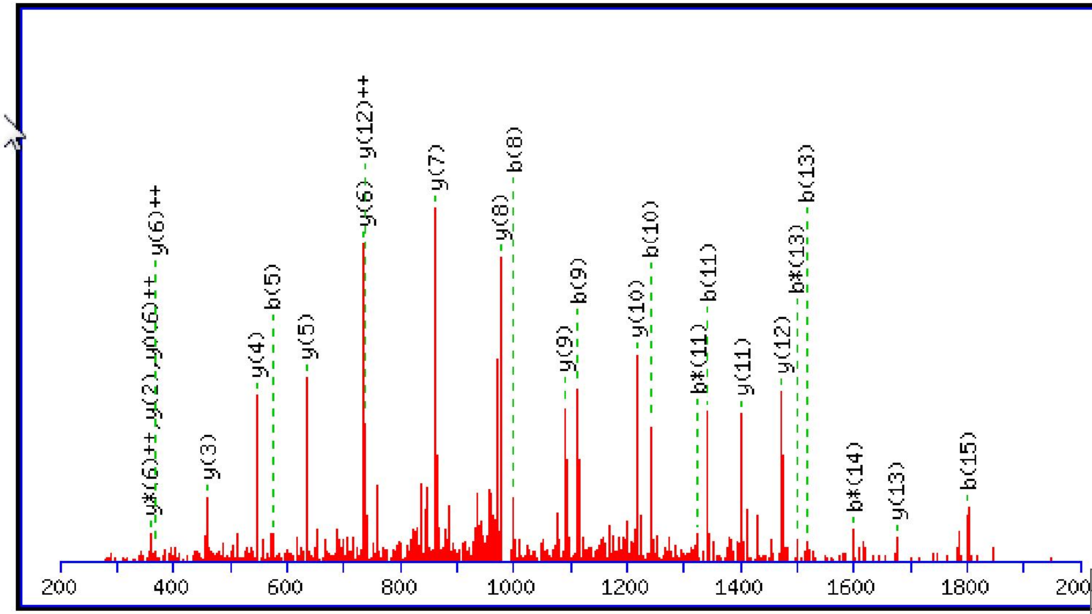
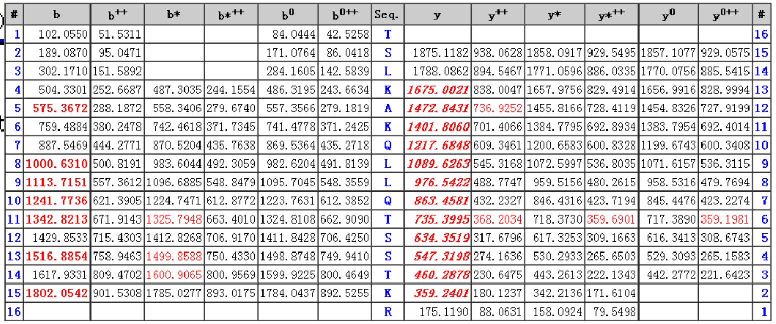
MS/MS Fragmentation of **TSLKAKQLLQTSSTKR**
Found in **H0Y9L2**, SLAIN motif-containing protein 2 (Fragment) OS=Homo sapiens GN=SLAIN2 PE=4 SV=1

Match to Query 14719: 1975.156108 from(988.585330,2+) intensity(194919.0938)
Title: File392 Spectrum14778 scans: 16369
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

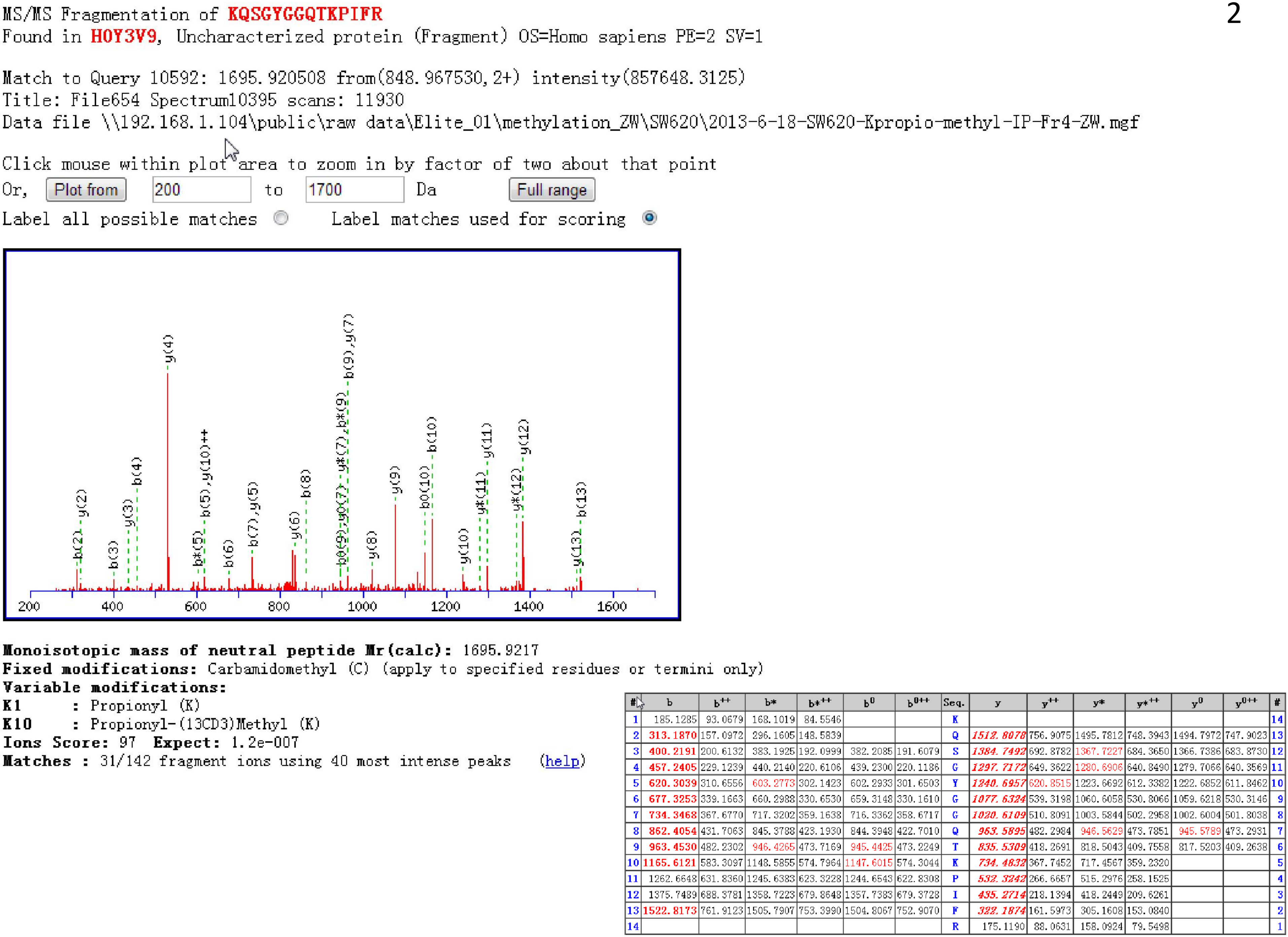
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1975.1586
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or t
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
K15 : Propionyl (K)
Ions Score: 99 **Expect:** 3.1e-008
Matches : 26/170 fragment ions using 33 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							16
2	189.0870	95.0471			171.0764	86.0418	S	1875.1182	938.0628	1858.0917	929.5495	1857.1077	929.0575	15
3	302.1710	151.5892			284.1605	142.5839	L	1788.0862	894.5467	1771.0596	886.0335	1770.0756	885.5415	14
4	504.3301	252.6687	487.3035	244.1554	486.3195	243.6634	K	1675.0021	838.0047	1657.9756	829.4914	1656.9916	828.9994	13
5	575.3672	288.1872	558.3406	279.6740	557.3566	279.1819	A	1472.8431	736.9252	1455.8166	728.4119	1454.8326	727.9199	12
6	759.4884	380.2478	742.4618	371.7345	741.4778	371.2425	K	1401.8060	701.4066	1384.7795	692.8934	1383.7954	692.4014	11
7	887.5469	444.2771	870.5204	435.7638	869.5364	435.2718	Q	1217.6848	609.3461	1200.6583	600.8328	1199.6743	600.3408	10
8	1000.6310	500.8191	983.6044	492.3059	982.6204	491.8139	L	1089.6263	545.3168	1072.5997	536.8035	1071.6157	536.3115	9
9	1113.7151	557.3612	1096.6885	548.8479	1095.7045	548.3559	L	976.5422	488.7747	959.5156	480.2615	958.5316	479.7694	8
10	1241.7736	621.3905	1224.7471	612.8772	1223.7631	612.3852	Q	863.4581	432.2327	846.4316	423.7194	845.4476	423.2274	7
11	1342.8213	671.9143	1325.7948	663.4010	1324.8108	662.9090	T	735.3995	368.2034	718.3730	359.6901	717.3890	359.1981	6
12	1429.8533	715.4303	1412.8268	706.9170	1411.8428	706.4250	S	634.3519	317.6796	617.3253	309.1663	616.3413	308.6743	5
13	1516.8854	758.9463	1499.8588	750.4330	1498.8748	749.9410	S	547.3198	274.1636	530.2933	265.6503	529.3093	265.1583	4
14	1617.9331	809.4702	1600.9065	800.9569	1599.9225	800.4649	T	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	3
15	1802.0542	901.5308	1785.0277	893.0175	1784.0437	892.5255	K	359.2401	180.1237	342.2136	171.6104			2
16							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KQSGYGGQTKPIFR**
Found in **H0Y3V9**, Uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1

Match to Query 10592: 1695.920508 from(848.967530,2+) intensity(857648.3125)
Title: File654 Spectrum10395 scans: 11930
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

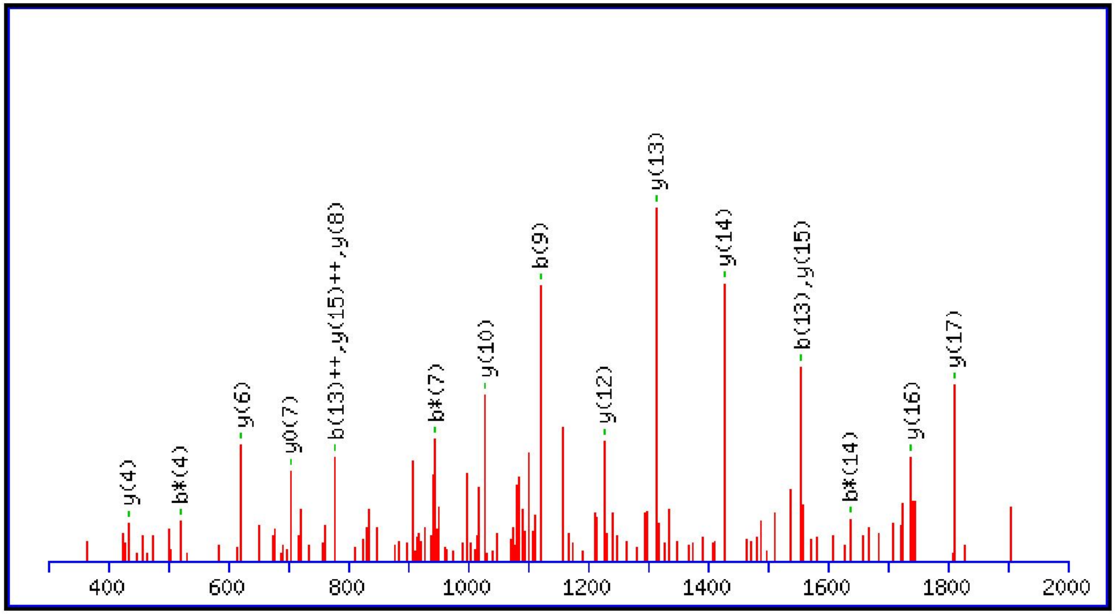
Monoisotopic mass of neutral peptide Mr(calc): 1695.9217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K10 : Propionyl-(13CD3)Methyl (K)
Ions Score: 97 **Expect:** 1.2e-007
Matches : 31/142 fragment ions using 40 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	**313.1870**	157.0972	296.1605	148.5839			Q	***1512.8078***	756.9075	1495.7812	748.3943	1494.7972	747.9023	13
3	**400.2191**	200.6132	383.1925	192.0999	382.2085	191.6079	S	***1384.7492***	692.8782	1367.7227	684.3650	1366.7386	683.8730	12
4	**457.2405**	229.1239	440.2140	220.6106	439.2300	220.1186	G	***1297.7172***	649.3622	1280.6906	640.8490	1279.7066	640.3569	11
5	**620.3039**	310.6556	603.2773	302.1423	602.2933	301.6503	Y	***1240.6957***	620.8515	1223.6692	612.3382	1222.6852	611.8462	10
6	**677.3253**	339.1663	660.2988	330.6530	659.3148	330.1610	G	***1077.6324***	539.3198	1060.6058	530.8066	1059.6218	530.3146	9
7	**734.3468**	367.6770	717.3202	359.1638	716.3362	358.6717	G	***1020.6109***	510.8091	1003.5844	502.2958	1002.6004	501.8038	8
8	**862.4054**	431.7063	845.3788	423.1930	844.3948	422.7010	Q	***963.5895***	482.2984	946.5629	473.7851	945.5789	473.2931	7
9	**963.4530**	482.2302	946.4265	473.7169	945.4425	473.2249	T	***835.5309***	418.2691	818.5043	409.7558	817.5203	409.2638	6
10	**1165.6121**	583.3097	1148.5855	574.7964	1147.6015	574.3044	K	***734.4832***	367.7452	717.4567	359.2320			5
11	1262.6648	631.8360	1245.6383	623.3228	1244.6543	622.8308	P	***532.3242***	266.6657	515.2976	258.1525			4
12	1375.7489	688.3781	1358.7223	679.8648	1357.7383	679.3728	I	***435.2714***	218.1394	418.2449	209.6261			3
13	**1522.8173**	761.9123	1505.7907	753.3990	1504.8067	752.9070	F	***322.1874***	161.5973	305.1608	153.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **QMKAKQLSAQSYGVTSSTAR**
Found in **F6QR24**, Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=2 SV=1

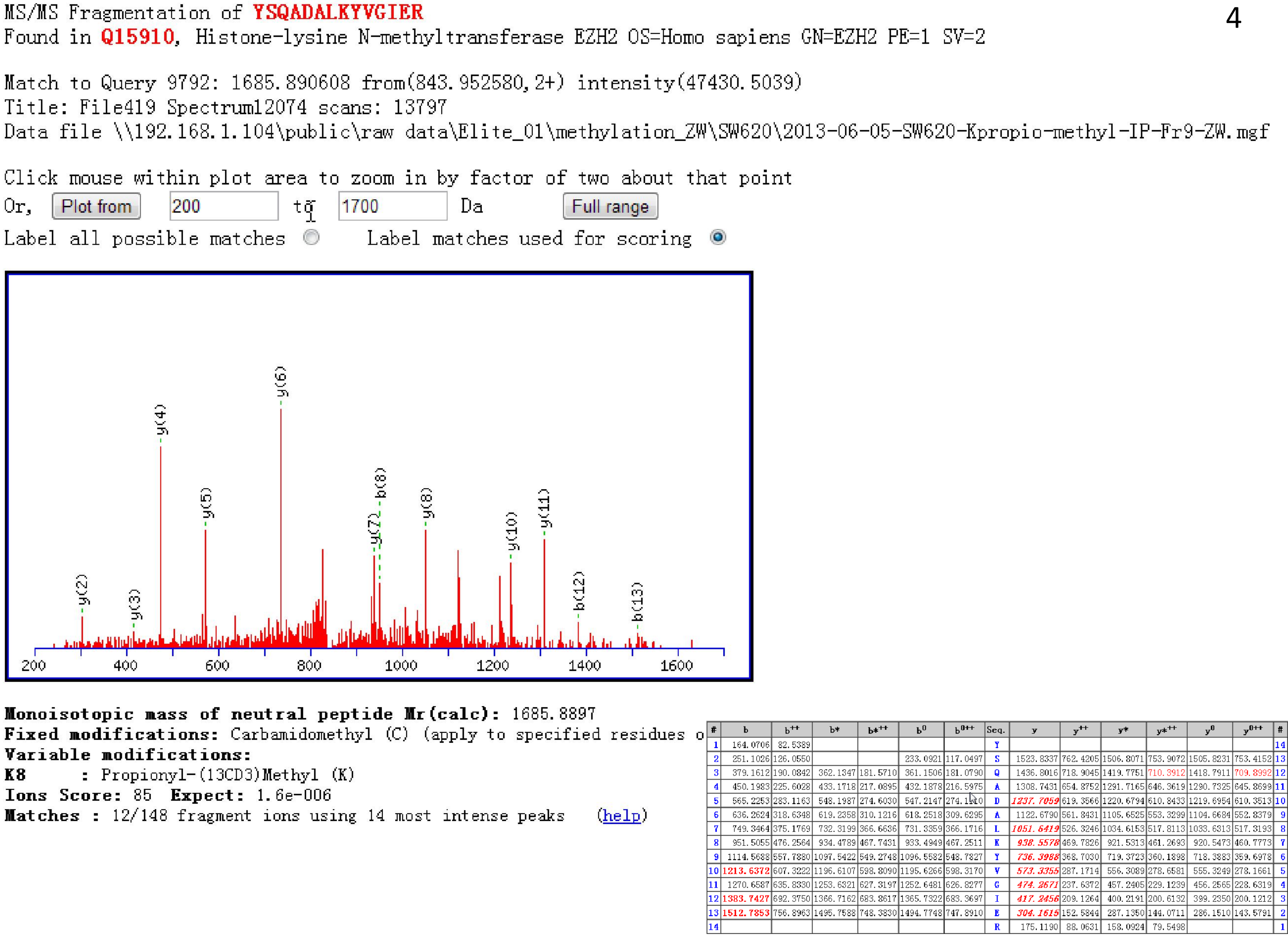
Match to Query 14797: 2275.205668 from(1138.610110,2+) intensity(0.0000)
Title: File422 Spectrum9337 scans: 10829
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2275.2023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
M2 : Label:13C(1)2H(3) (M)
K3 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
Ions Score: 92 **Expect:** 5.4e-007
Matches : 18/210 fragment ions using 16 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							20
2	264.1285	132.5679	247.1020	124.0546			M	2148.1511	1074.5792	2131.1245	1066.0659	2130.1405	1065.5739	19
3	466.2875	233.6474	449.2610	225.1341			K	2013.0884	1007.0478	1996.0618	998.5346	1995.0778	998.0425	18
4	537.3247	269.1660	520.2981	260.6527			A	**1810.9294**	905.9683	1793.9028	897.4550	1792.9188	896.9630	17
5	721.4458	361.2266	704.4193	352.7133			K	**1739.8923**	870.4498	1722.8657	861.9365	1721.8817	861.4445	16
6	849.5044	425.2558	832.4779	416.7426			Q	**1555.7711**	778.3892	1538.7445	769.8759	1537.7605	769.3839	15
7	962.5885	481.7979	945.5619	473.2846			L	**1427.7125**	714.3599	1410.6860	705.8466	1409.7019	705.3546	14
8	1049.6205	525.3139	1032.5940	516.8006	1031.6099	516.3086	S	**1314.6284**	657.8179	1297.6019	649.3046	1296.6179	648.8126	13
9	**1120.6576**	560.8324	1103.6311	552.3192	1102.6470	551.8272	A	**1227.5964**	614.3018	1210.5699	605.7886	1209.5858	605.2966	12
10	1248.7162	624.8617	1231.6896	616.3485	1230.7056	615.8565	Q	1156.5593	578.7833	1139.5327	570.2700	1138.5487	569.7780	11
11	1335.7482	668.3777	1318.7217	659.8645	1317.7377	659.3725	S	**1028.5007**	514.7540	1011.4742	506.2407	1010.4902	505.7487	10
12	1498.8115	749.9094	1481.7850	741.3961	1480.8010	740.9041	Y	941.4687	471.2380	924.4421	462.7247	923.4581	462.2327	9
13	**1555.8330**	778.4201	1538.8065	769.9069	1537.8224	769.4149	G	**778.4054**	389.7063	761.3788	381.1930	760.3948	380.7010	8
14	1654.9014	827.9544	1637.8749	819.4411	1636.8909	818.9491	V	721.3839	361.1956	704.3573	352.6823	703.3733	352.1903	7
15	1755.9491	878.4782	1738.9226	869.9649	1737.9385	869.4729	T	**622.3155**	311.6614	605.2889	303.1481	604.3049	302.6561	6
16	1842.9811	921.9942	1825.9546	913.4809	1824.9706	912.9889	S	521.2678	261.1375	504.2413	252.6243	503.2572	252.1323	5
17	1930.0132	965.5102	1912.9866	956.9969	1912.0026	956.5049	S	**434.2358**	217.6215	417.2092	209.1083	416.2252	208.6162	4
18	2031.0608	1016.0341	2014.0343	1007.5208	2013.0503	1007.0288	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
19	2102.0980	1051.5526	2085.0714	1043.0393	2084.0874	1042.5473	A	246.1561	123.5817	229.1295	115.0684			2
20							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **YSQADALKYVGIER**
Found in **Q15910**, Histone-lysine N-methyltransferase EZH2 OS=Homo sapiens GN=EZH2 PE=1 SV=2

Match to Query 9792: 1685.890608 from(843.952580,2+) intensity(47430.5039)
Title: File419 Spectrum12074 scans: 13797
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-06-05-SW620-Kpropio-methyl-IP-Fr9-ZW.mgf

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

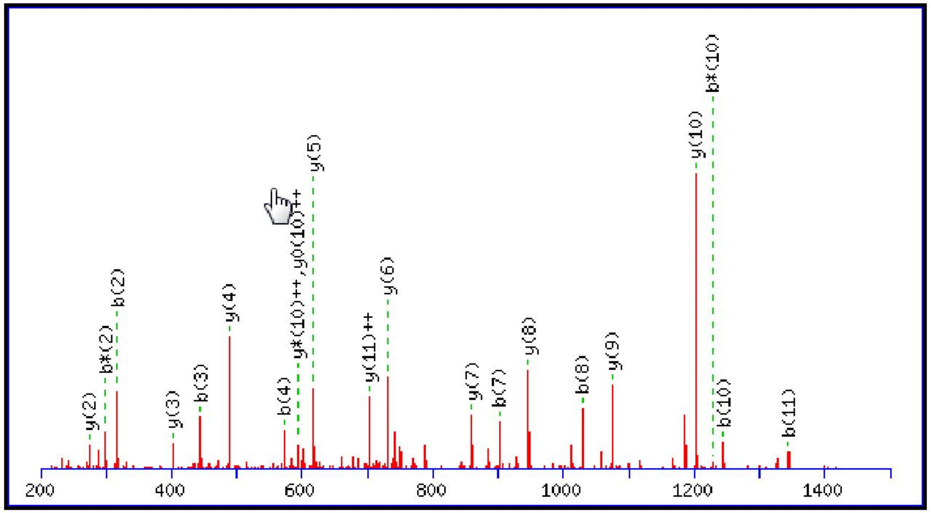
Monoisotopic mass of neutral peptide Mr(calc): 1685.8897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 85 **Expect:** 1.6e-006
Matches : 12/148 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389					Y							14
2	251.1026	126.0550			233.0921	117.0497	S	1523.8337	762.4205	1506.8071	753.9072	1505.8231	753.4152	13
3	379.1612	190.0842	362.1347	181.5710	361.1506	181.0790	Q	1436.8016	718.9045	1419.7751	710.3912	1418.7911	709.8992	12
4	450.1983	225.6028	433.1718	217.0895	432.1878	216.5975	A	1308.7431	654.8752	1291.7165	646.3619	1290.7325	645.8699	11
5	565.2253	283.1163	548.1987	274.6030	547.2147	274.1110	D	***1237.7059***	619.3566	1220.6794	610.8433	1219.6954	610.3513	10
6	636.2624	318.6348	619.2358	310.1216	618.2518	309.6295	A	1122.6790	561.8431	1105.6525	553.3299	1104.6684	552.8379	9
7	749.3464	375.1769	732.3199	366.6636	731.3359	366.1716	L	***1051.6419***	526.3246	1034.6153	517.8113	1033.6313	517.3193	8
8	951.5055	476.2564	934.4789	467.7431	933.4949	467.2511	K	***938.5578***	469.7826	921.5313	461.2693	920.5473	460.7773	7
9	1114.5688	557.7880	1097.5422	549.2748	1096.5582	548.7827	Y	***736.3988***	368.7030	719.3723	360.1898	718.3883	359.6978	6
10	**1213.6372**	607.3222	1196.6107	598.8090	1195.6266	598.3170	V	***573.3355***	287.1714	556.3089	278.6581	555.3249	278.1661	5
11	1270.6587	635.8330	1253.6321	627.3197	1252.6481	626.8277	G	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
12	**1383.7427**	692.3750	1366.7162	683.8617	1365.7322	683.3697	I	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
13	**1512.7853**	756.8963	1495.7588	748.3830	1494.7748	747.8910	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1

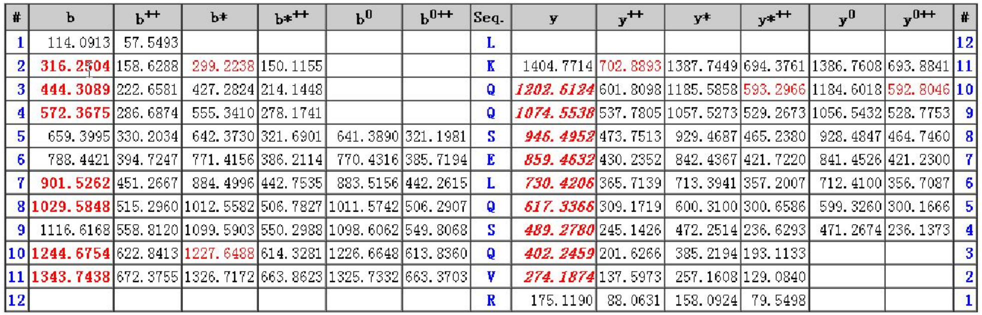
MS/MS Fragmentation of **LKQQSELQSQVR**
Found in **C9J9W2**, LIM and SH3 domain protein 1 (Fragment) OS=Homo sapiens GN=LASP1 PE=2 SV=1

Match to Query 7819: 1516.847868 from(759.431210,2+) intensity(891431.9375)
Title: File660 Spectrum4849 scans: 5963
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr3-ZW.mgf

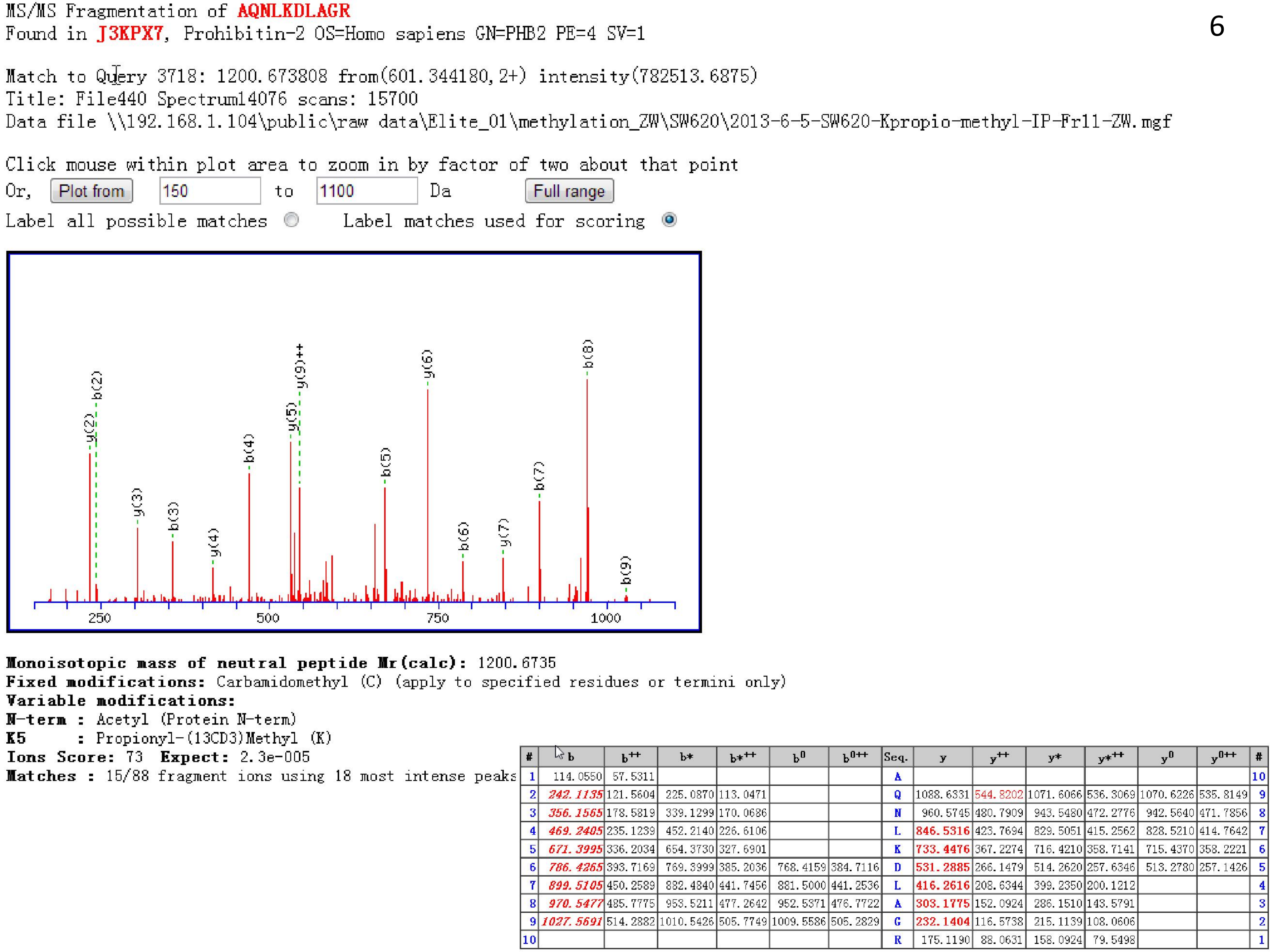
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1516.8482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 78 **Expect:** 8.6e-006
Matches : 21/116 fragment ions using 25 most intense peaks (help)



#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							12
2	**316.2504**	158.6288	299.2238	150.1155			K	1404.7714	702.8893	1387.7449	694.3761	1386.7608	693.8841	11
3	**444.3089**	222.6581	427.2824	214.1448			Q	***1202.6124***	601.8098	1185.5858	593.2966	1184.6018	592.8046	10
4	**572.3675**	286.6874	555.3410	278.1741			Q	***1074.5538***	537.7805	1057.5273	529.2673	1056.5432	528.7753	9
5	659.3995	330.2034	642.3730	321.6901	641.3890	321.1981	S	***946.4952***	473.7513	929.4687	465.2380	928.4847	464.7460	8
6	788.4421	394.7247	771.4156	386.2114	770.4316	385.7194	E	***859.4632***	430.2352	842.4367	421.7220	841.4526	421.2300	7
7	**901.5262**	451.2667	884.4996	442.7535	883.5156	442.2615	L	***730.4206***	365.7139	713.3941	357.2007	712.4100	356.7087	6
8	**1029.5848**	515.2960	1012.5582	506.7827	1011.5742	506.2907	Q	***617.3366***	309.1719	600.3100	300.6586	599.3260	300.1666	5
9	1116.6168	558.8120	1099.5903	550.2988	1098.6062	549.8068	S	***489.2780***	245.1426	472.2514	236.6293	471.2674	236.1373	4
10	**1244.6754**	622.8413	1227.6488	614.3281	1226.6648	613.8360	Q	***402.2459***	201.6266	385.2194	193.1133			3
11	**1343.7438**	672.3755	1326.7172	663.8623	1325.7332	663.3703	V	***274.1874***	137.5973	257.1608	129.0840			2
12							R	175.1190	88.0631	158.0924	79.5498			1



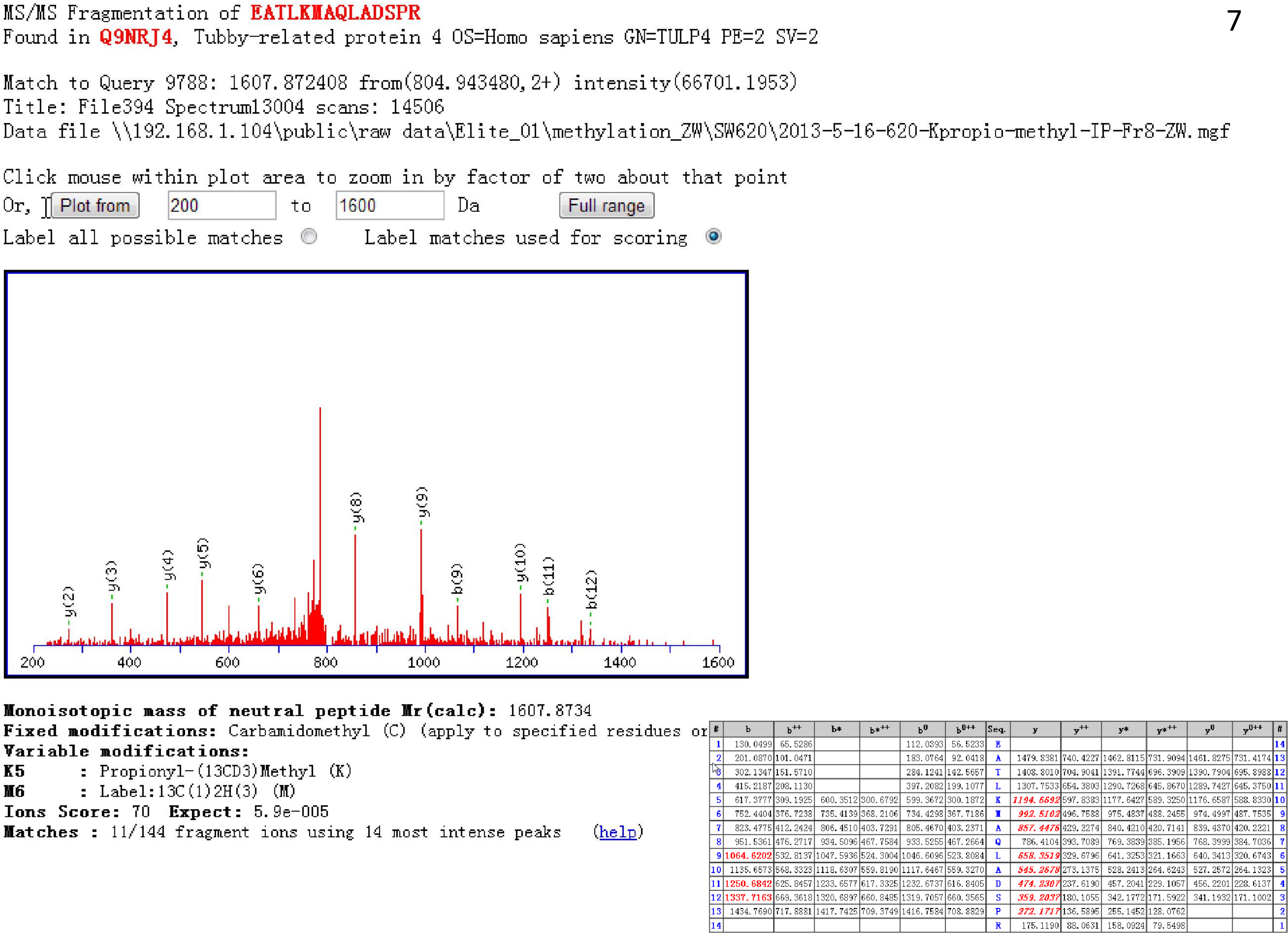
MS/MS Fragmentation of **AQNLKDLAGR**
Found in **J3KPX7**, Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=4 SV=1

Match to Query 3718: 1200.673808 from(601.344180,2+) intensity(782513.6875)
Title: File440 Spectrum14076 scans: 15700
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1200.6735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 73 **Expect:** 2.3e-005
Matches : 15/88 fragment ions using 18 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0550	57.5311					A							10
2	***242.1135***	121.5604	225.0870	113.0471			Q	1088.6331	544.8202	1071.6066	536.3069	1070.6226	535.8149	9
3	***356.1565***	178.5819	339.1299	170.0686			N	960.5745	480.7909	943.5480	472.2776	942.5640	471.7856	8
4	***469.2405***	235.1239	452.2140	226.6106			L	**846.5316**	423.7694	829.5051	415.2562	828.5210	414.7642	7
5	***671.3995***	336.2034	654.3730	327.6901			K	**733.4476**	367.2274	716.4210	358.7141	715.4370	358.2221	6
6	***786.4265***	393.7169	769.3999	385.2036	768.4159	384.7116	D	**531.2885**	266.1479	514.2620	257.6346	513.2780	257.1426	5
7	***899.5105***	450.2589	882.4840	441.7456	881.5000	441.2536	L	**416.2616**	208.6344	399.2350	200.1212			4
8	***970.5477***	485.7775	953.5211	477.2642	952.5371	476.7722	A	**303.1775**	152.0924	286.1510	143.5791			3
9	***1027.5691***	514.2882	1010.5426	505.7749	1009.5586	505.2829	G	**232.1404**	116.5738	215.1139	108.0606			2
10							R	175.1190	88.0631	158.0924	79.5498			1



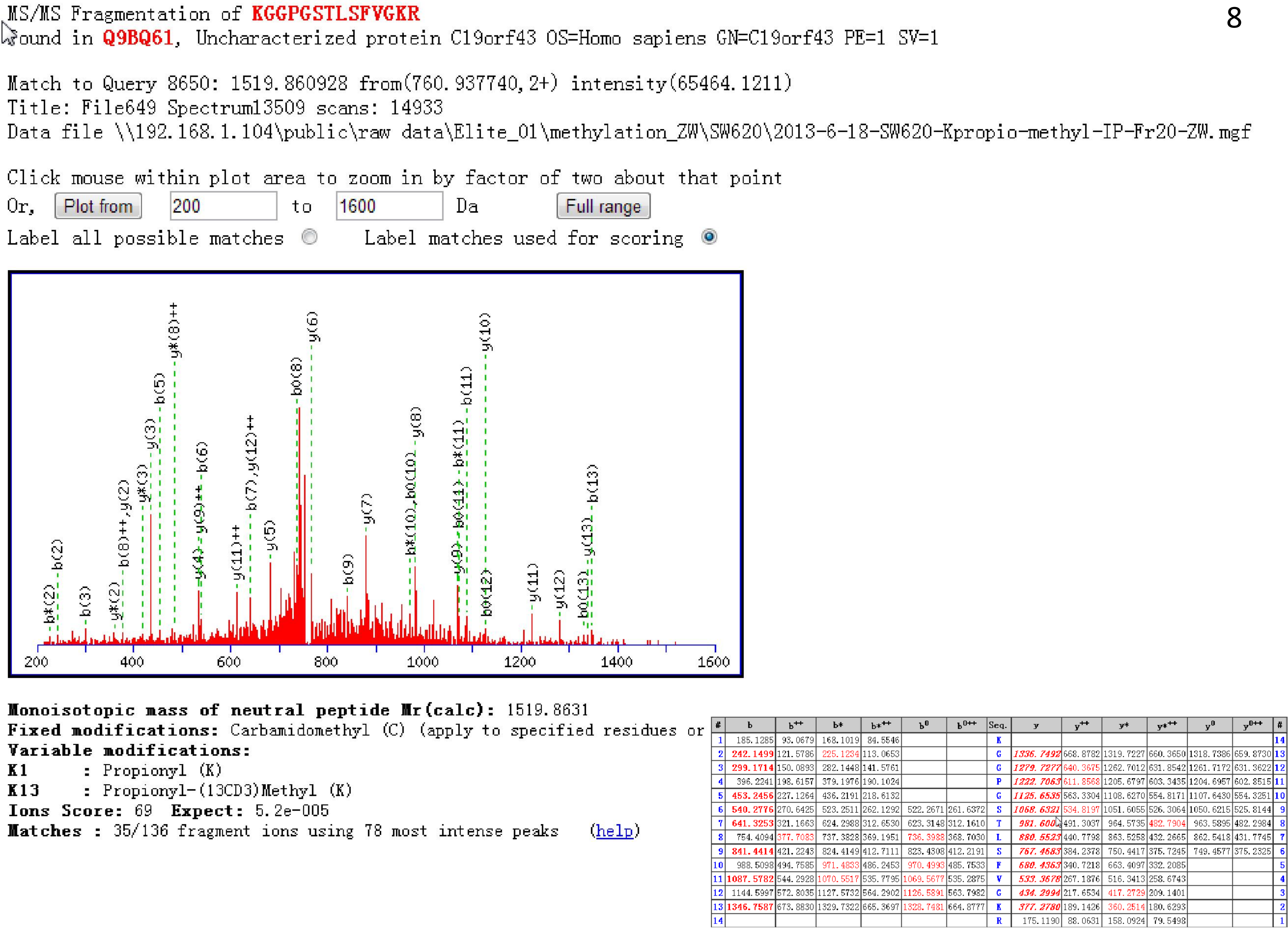
MS/MS Fragmentation of **EATLKMAQLADSPR**
Found in **Q9NRJ4**, Tubby-related protein 4 OS=Homo sapiens GN=TULP4 PE=2 SV=2

Match to Query 9788: 1607.872408 from(804.943480,2+) intensity(66701.1953)
Title: File394 Spectrum13004 scans: 14506
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1607.8734
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
M6 : Label:13C(1)2H(3) (M)
Ions Score: 70 **Expect:** 5.9e-005
Matches : 11/144 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	201.0870	101.0471			183.0764	92.0418	A	1479.8381	740.4227	1462.8115	731.9094	1461.8275	731.4174	13
3	302.1347	151.5710			284.1241	142.5657	T	1408.8010	704.9041	1391.7744	696.3909	1390.7904	695.8988	12
4	415.2187	208.1130			397.2082	199.1077	L	1307.7533	654.3803	1290.7268	645.8670	1289.7427	645.3750	11
5	617.3777	309.1925	600.3512	300.6792	599.3672	300.1872	K	***1194.6692***	597.8383	1177.6427	589.3250	1176.6587	588.8330	10
6	752.4404	376.7238	735.4139	368.2106	734.4298	367.7186	M	***992.5102***	496.7588	975.4837	488.2455	974.4997	487.7535	9
7	823.4775	412.2424	806.4510	403.7291	805.4670	403.2371	A	***857.4476***	429.2274	840.4210	420.7141	839.4370	420.2221	8
8	951.5361	476.2717	934.5096	467.7584	933.5255	467.2664	Q	786.4104	393.7089	769.3839	385.1956	768.3999	384.7036	7
9	**1064.6202**	532.8137	1047.5936	524.3004	1046.6096	523.8084	L	***658.3519***	329.6796	641.3253	321.1663	640.3413	320.6743	6
10	1135.6573	568.3323	1118.6307	559.8190	1117.6467	559.3270	A	***545.2678***	273.1375	528.2413	264.6243	527.2572	264.1323	5
11	**1250.6842**	625.8457	1233.6577	617.3325	1232.6737	616.8405	D	***474.2307***	237.6190	457.2041	229.1057	456.2201	228.6137	4
12	**1337.7163**	669.3618	1320.6897	660.8485	1319.7057	660.3565	S	***359.2037***	180.1055	342.1772	171.5922	341.1932	171.1002	3
13	1434.7690	717.8881	1417.7425	709.3749	1416.7584	708.8829	P	***272.1717***	136.5895	255.1452	128.0762			2
14							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KGGPGSTLSFVGKR**
Found in **Q9BQ61**, Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=1 SV=1

Match to Query 8650: 1519.860928 from(760.937740,2+) intensity(65464.1211)
Title: File649 Spectrum13509 scans: 14933
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr20-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

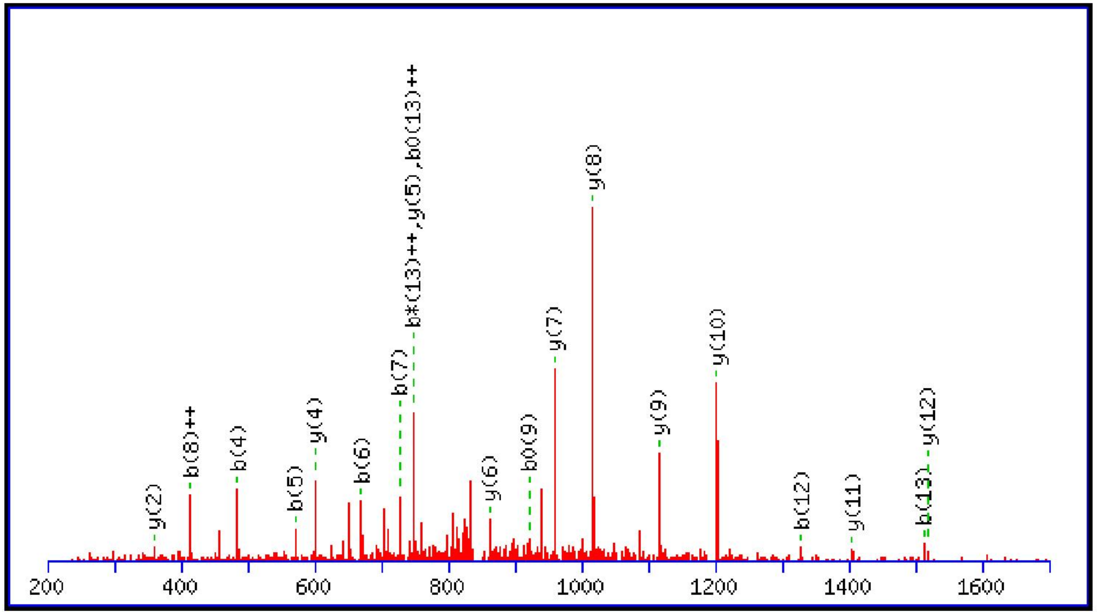
Monoisotopic mass of neutral peptide Mr(calc): 1519.8631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K1 : Propionyl (K)
K13 : Propionyl-(13CD3)Methyl (K)
Ions Score: 69 **Expect:** 5.2e-005
Matches : 35/136 fragment ions using 78 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	**242.1499**	121.5786	225.1234	113.0653			G	***1336.7492***	668.8782	1319.7227	660.3650	1318.7386	659.8730	13
3	**299.1714**	150.0893	282.1448	141.5761			G	***1279.7277***	640.3675	1262.7012	631.8542	1261.7172	631.3622	12
4	396.2241	198.6157	379.1976	190.1024			P	***1222.7063***	611.8568	1205.6797	603.3435	1204.6957	602.8515	11
5	**453.2456**	227.1264	436.2191	218.6132			G	***1125.6535***	563.3304	1108.6270	554.8171	1107.6430	554.3251	10
6	**540.2776**	270.6425	523.2511	262.1292	522.2671	261.6372	S	***1068.6321***	534.8197	1051.6055	526.3064	1050.6215	525.8144	9
7	**641.3253**	321.1663	624.2988	312.6530	623.3148	312.1610	T	***981.600***	491.3037	964.5735	482.7904	963.5895	482.2984	8
8	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	L	***880.5523***	440.7798	863.5258	432.2665	862.5418	431.7745	7
9	**841.4414**	421.2243	824.4149	412.7111	823.4308	412.2191	S	***767.4683***	384.2378	750.4417	375.7245	749.4577	375.2325	6
10	988.5098	494.7585	971.4833	486.2453	970.4993	485.7533	F	***680.4363***	340.7218	663.4097	332.2085			5
11	**1087.5782**	544.2928	1070.5517	535.7795	1069.5677	535.2875	V	***533.3678***	267.1876	516.3413	258.6743			4
12	1144.5997	572.8035	1127.5732	564.2902	1126.5891	563.7982	G	***434.2994***	217.6534	417.2729	209.1401			3
13	**1346.7587**	673.8830	1329.7322	665.3697	1328.7481	664.8777	K	***377.2780***	189.1426	360.2514	180.6293			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **APLKSVGPDFGKKR**
Found in **E7EUY0**, DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=2 SV=1

Match to Query 9012: 1684.978848 from(843.496700,2+) intensity(83880.1172)
Title: File667 Spectrum11996 scans: 13910
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr18-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



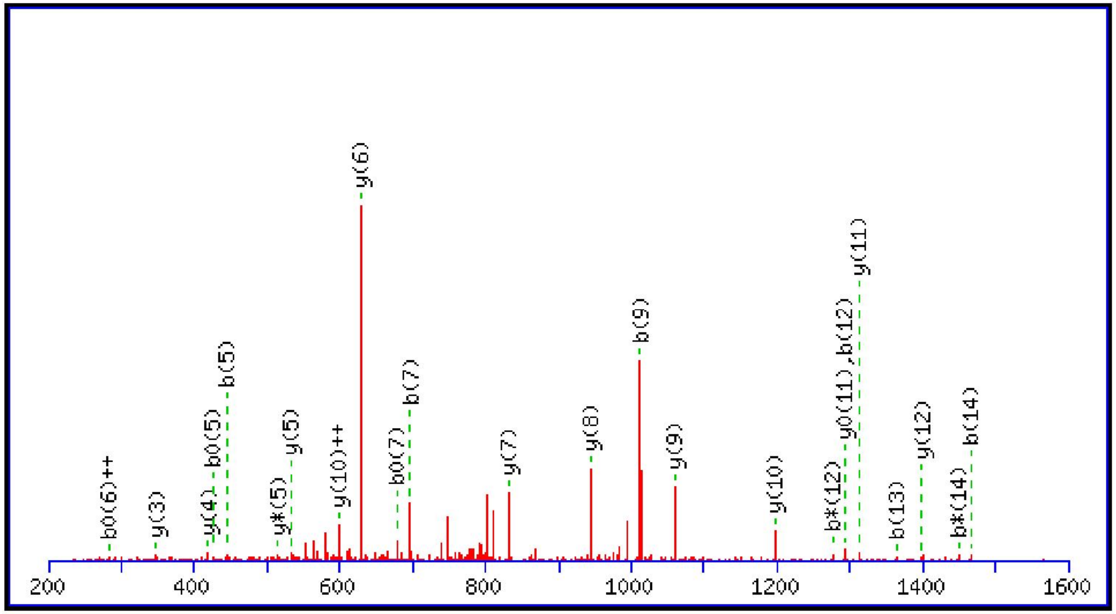
Monoisotopic mass of neutral peptide Mr(calc): 1684.9785
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K12 : Propionyl (K)
K13 : Propionyl (K)
Ions Score: 68 **Expect:** 5.1e-005
Matches : 20/132 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							14
2	169.0972	85.0522					P	1614.9486	807.9780	1597.9221	799.4647	1596.9381	798.9727	13
3	282.1812	141.5942					L	1517.8959	759.4516	1500.8693	750.9383	1499.8853	750.4463	12
4	484.3402	242.6738	467.3137	234.1605			K	1404.8118	702.9095	1387.7853	694.3963	1386.8012	693.9043	11
5	571.3723	286.1898	554.3457	277.6765	553.3617	277.1845	S	1202.6528	601.8300	1185.6263	593.3168	1184.6422	592.8248	10
6	670.4407	335.7240	653.4141	327.2107	652.4301	326.7187	V	1115.6208	558.3140	1098.5942	549.8007	1097.6102	549.3087	9
7	727.4621	364.2347	710.4356	355.7214	709.4516	355.2294	G	1016.5524	508.7798	999.5258	500.2665	998.5418	499.7745	8
8	824.5149	412.7611	807.4884	404.2478	806.5043	403.7558	P	959.5309	480.2691	942.5043	471.7558	941.5203	471.2638	7
9	939.5418	470.2746	922.5153	461.7613	921.5313	461.2693	D	862.4781	431.7427	845.4516	423.2294	844.4676	422.7374	6
10	1086.6103	543.8088	1069.5837	535.2955	1068.5997	534.8035	F	747.4512	374.2292	730.4246	365.7160			5
11	1143.6317	572.3195	1126.6052	563.8062	1125.6212	563.3142	G	600.3828	300.6950	583.3562	292.1817			4
12	1327.7529	664.3801	1310.7264	655.8668	1309.7423	655.3748	K	543.3613	272.1843	526.3348	263.6710			3
13	1511.8741	756.4407	1494.8475	747.9274	1493.8635	747.4354	K	359.2401	180.1237	342.2136	171.6104			2
14							R	175.1190	88.0631	158.0924	79.5498			1

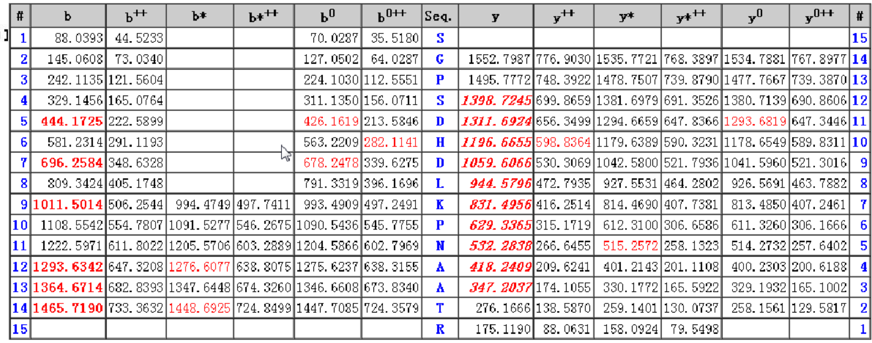
MS/MS Fragmentation of **SGPSDHDLKPNAATR**
Found in **A8MYT4**, Phosphatidylinositol 3-kinase catalytic subunit type 3 OS=Homo sapiens GN=PIK3C3 PE=2 SV=2

Match to Query 8779: 1638.823708 from(820.419130,2+) intensity(147951.2969)
Title: File386 Spectrum6160 scans: 7108
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1638.8234
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K9 : Propionyl-(13CD3)Methyl (K)
Ions Score: 67 **Expect:** 7.4e-005
Matches : 24/150 fragment ions using 40 most intense peaks (help)

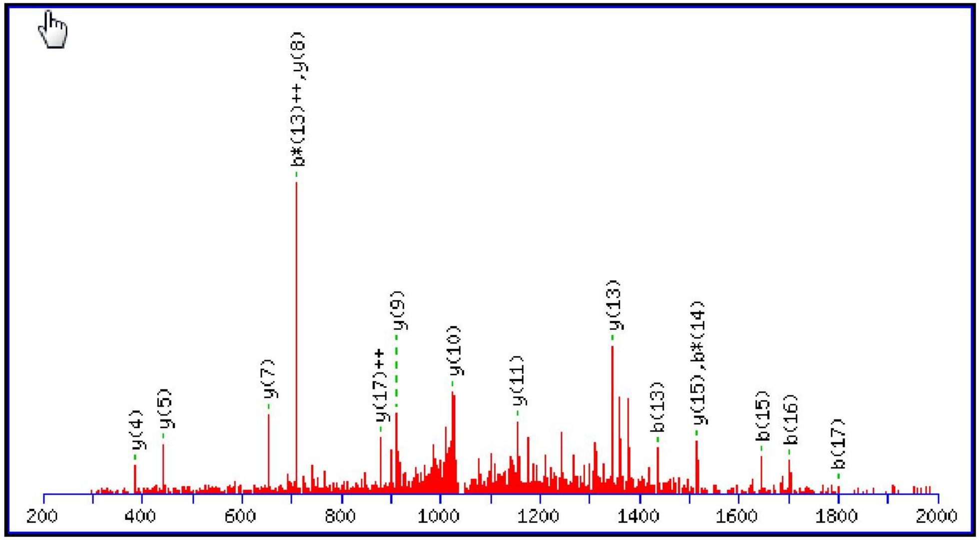


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	145.0608	73.0340			127.0502	64.0287	G	1552.7987	776.9030	1535.7721	768.3897	1534.7881	767.8977	14
3	242.1135	121.5604			224.1030	112.5551	P	1495.7772	748.3922	1478.7507	739.8790	1477.7667	739.3870	13
4	329.1456	165.0764			311.1350	156.0711	S	***1398.7245***	699.8659	1381.6979	691.3526	1380.7139	690.8606	12
5	**444.1725**	222.5899			426.1619	213.5846	D	***1311.6924***	656.3499	1294.6659	647.8366	1293.6819	647.3446	11
6	581.2314	291.1193			563.2209	282.1141	H	***1196.6655***	598.8364	1179.6389	590.3231	1178.6549	589.8311	10
7	**696.2584**	348.6328			678.2478	339.6275	D	***1059.6066***	530.3069	1042.5800	521.7936	1041.5960	521.3016	9
8	809.3424	405.1748			791.3319	396.1696	L	***944.5796***	472.7935	927.5531	464.2802	926.5691	463.7882	8
9	**1011.5014**	506.2544	994.4749	497.7411	993.4909	497.2491	K	***831.4956***	416.2514	814.4690	407.7381	813.4850	407.2461	7
10	1108.5542	554.7807	1091.5277	546.2675	1090.5436	545.7755	P	***629.3365***	315.1719	612.3100	306.6586	611.3260	306.1666	6
11	1222.5971	611.8022	1205.5706	603.2889	1204.5866	602.7969	N	***532.2838***	266.6455	515.2572	258.1323	514.2732	257.6402	5
12	**1293.6342**	647.3208	1276.6077	638.8075	1275.6237	638.3155	A	***418.2409***	209.6241	401.2143	201.1108	400.2303	200.6188	4
13	**1364.6714**	682.8393	1347.6448	674.3260	1346.6608	673.8340	A	***347.2037***	174.1055	330.1772	165.5922	329.1932	165.1002	3
14	**1465.7190**	733.3632	1448.6925	724.8499	1447.7085	724.3579	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
15							R	175.1190	88.0631	158.0924	79.5498			1

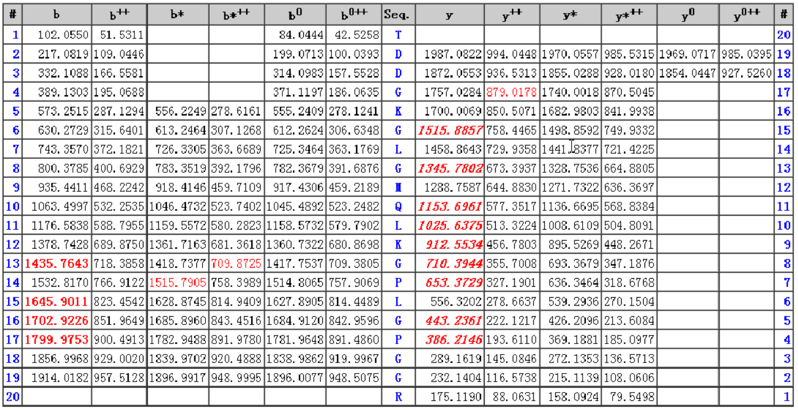
MS/MS Fragmentation of TDDGKGLGMQLKGPLGPGGR
Found in Q9NQS1, Cell death regulator Aven OS=Homo sapiens GN=AVEN PE=1 SV=1

Match to Query 15036: 2087.123148 from(1044.568850,2+) intensity(67384.5625)
Title: File658 Spectrum13479 scans: 15088
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr17-ZW.mgf

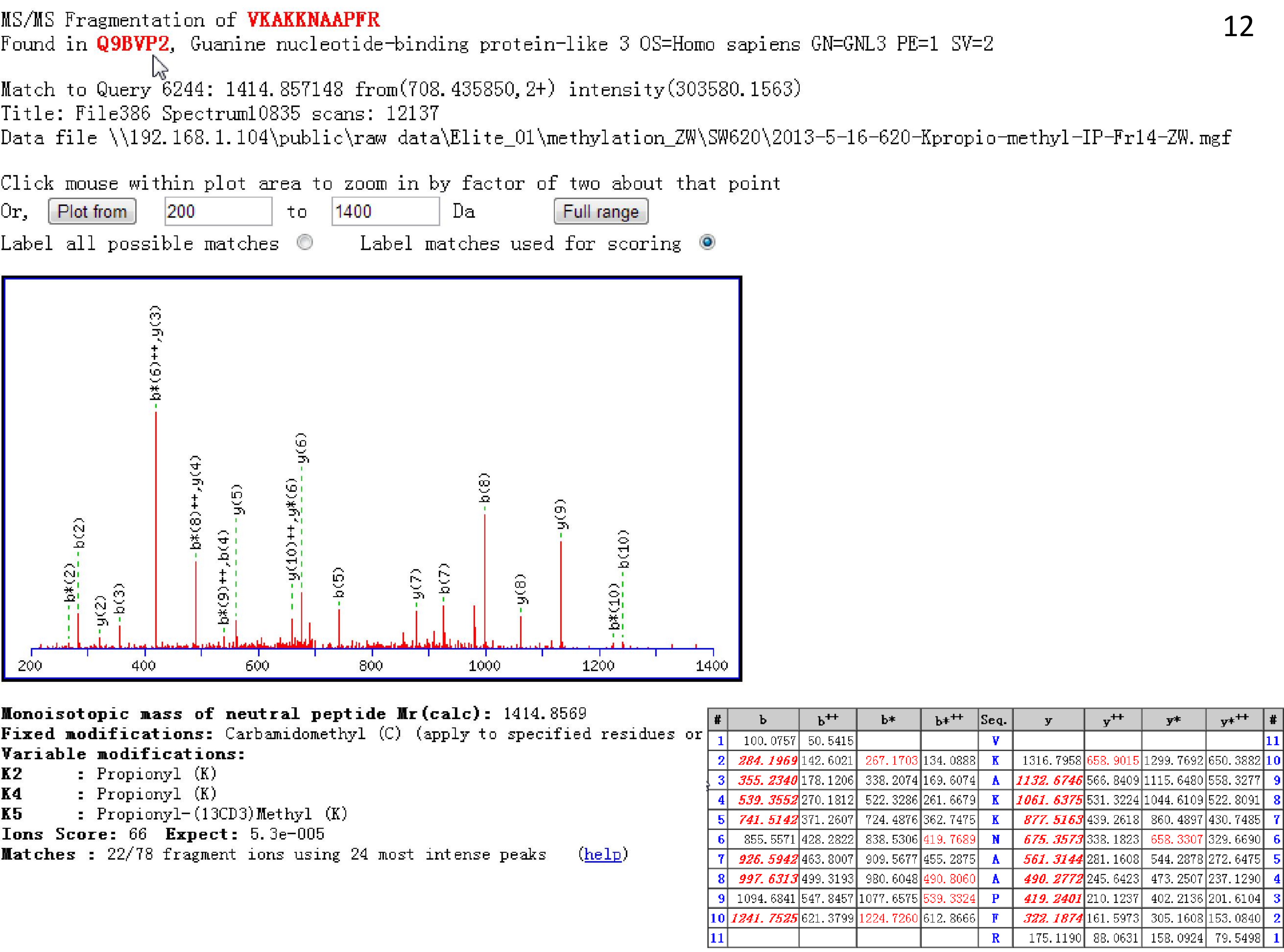
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2087.1227
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini onl
Variable modifications:
K5 : Propionyl (K)
M9 : Label:13C(1)2H(3) (M)
K12 : Propionyl-(13CD3)Methyl (K)
Ions Score: 67 **Expect:** 0.00014
Matches : 16/186 fragment ions using 17 most intense peaks (help)



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							20
2	217.0819	109.0446			199.0713	100.0393	D	1987.0822	994.0448	1970.0557	985.5315	1969.0717	985.0395	19
3	332.1088	166.5581			314.0983	157.5528	D	1872.0553	936.5313	1855.0288	928.0180	1854.0447	927.5260	18
4	389.1303	195.0688			371.1197	186.0635	G	1757.0284	879.0178	1740.0018	870.5045			17
5	573.2515	287.1294	556.2249	278.6161	555.2409	278.1241	K	1700.0069	850.5071	1682.9803	841.9938			16
6	630.2729	315.6401	613.2464	307.1268	612.2624	306.6348	G	***1515.8857***	758.4465	1498.8592	749.9332			15
7	743.3570	372.1821	726.3305	363.6689	725.3464	363.1769	L	1458.8643	729.9358	1441.8377	721.4225			14
8	800.3785	400.6929	783.3519	392.1796	782.3679	391.6876	G	***1345.7802***	673.3937	1328.7536	664.8805			13
9	935.4411	468.2242	918.4146	459.7109	917.4306	459.2189	M	1288.7587	644.8830	1271.7322	636.3697			12
10	1063.4997	532.2535	1046.4732	523.7402	1045.4892	523.2482	Q	***1153.6961***	577.3517	1136.6695	568.8384			11
11	1176.5838	588.7955	1159.5572	580.2823	1158.5732	579.7902	L	***1025.6375***	513.3224	1008.6109	504.8091			10
12	1378.7428	689.8750	1361.7163	681.3618	1360.7322	680.8698	K	***912.5534***	456.7803	895.5269	448.2671			9
13	**1435.7643**	718.3858	1418.7377	709.8725	1417.7537	709.3805	G	***710.3944***	355.7008	693.3679	347.1876			8
14	1532.8170	766.9122	1515.7905	758.3989	1514.8065	757.9069	P	***653.3729***	327.1901	636.3464	318.6768			7
15	**1645.9011**	823.4542	1628.8745	814.9409	1627.8905	814.4489	L	556.3202	278.6637	539.2936	270.1504			6
16	**1702.9226**	851.9649	1685.8960	843.4516	1684.9120	842.9596	G	***443.2361***	222.1217	426.2096	213.6084			5
17	**1799.9753**	900.4913	1782.9488	891.9780	1781.9648	891.4860	P	***386.2146***	193.6110	369.1881	185.0977			4
18	1856.9968	929.0020	1839.9702	920.4888	1838.9862	919.9967	G	289.1619	145.0846	272.1353	136.5713			3
19	1914.0182	957.5128	1896.9917	948.9995	1896.0077	948.5075	G	232.1404	116.5738	215.1139	108.0606			2
20							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **VKAKKNAAPFR**
Found in **Q9BVP2**, Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2

Match to Query 6244: 1414.857148 from(708.435850,2+) intensity(303580.1563)
Title: File386 Spectrum10835 scans: 12137
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.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 ●

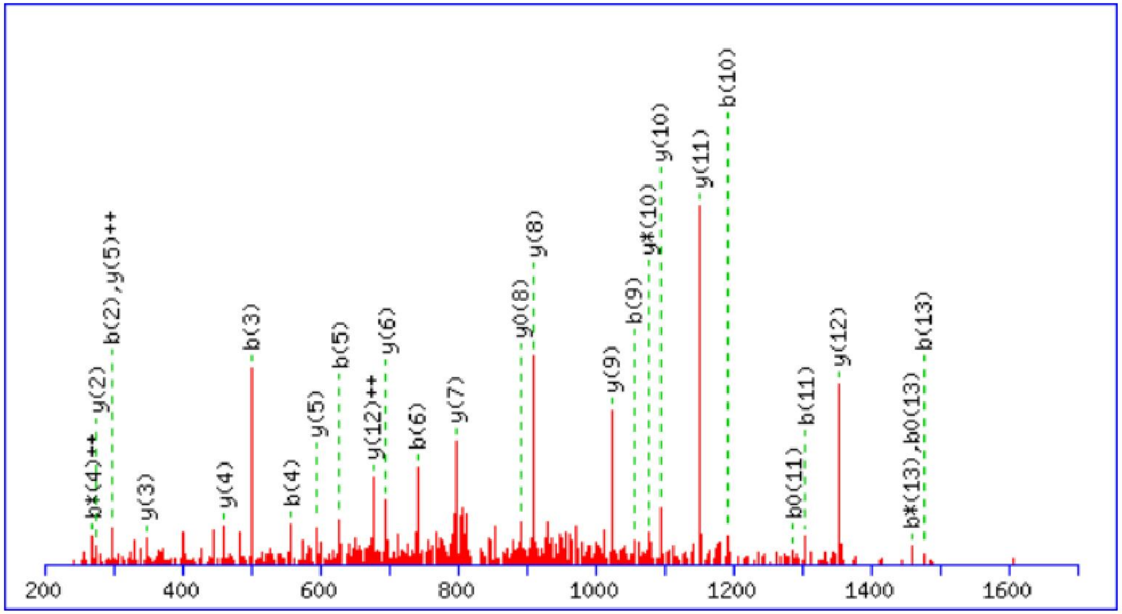
Monoisotopic mass of neutral peptide Mr(calc): 1414.8569
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K2 : Propionyl (K)
K4 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 66 **Expect:** 5.3e-005
Matches : 22/78 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	100.0757	50.5415			V					11
2	***284.1969***	142.6021	267.1703	134.0888	K	1316.7958	658.9015	1299.7692	650.3882	10
3	***355.2340***	178.1206	338.2074	169.6074	A	***1132.6746***	566.8409	1115.6480	558.3277	9
4	***539.3552***	270.1812	522.3286	261.6679	K	***1061.6375***	531.3224	1044.6109	522.8091	8
5	***741.5142***	371.2607	724.4876	362.7475	K	***877.5163***	439.2618	860.4897	430.7485	7
6	855.5571	428.2822	838.5306	419.7689	N	***675.3573***	338.1823	658.3307	329.6690	6
7	***926.5942***	463.8007	909.5677	455.2875	A	***561.3144***	281.1608	544.2878	272.6475	5
8	***997.6313***	499.3193	980.6048	490.8060	A	***490.2772***	245.6423	473.2507	237.1290	4
9	1094.6841	547.8457	1077.6575	539.3324	P	***419.2401***	210.1237	402.2136	201.6104	3
10	***1241.7525***	621.3799	1224.7260	612.8666	F	***322.1874***	161.5973	305.1608	153.0840	2
11					R	175.1190	88.0631	158.0924	79.5498	1

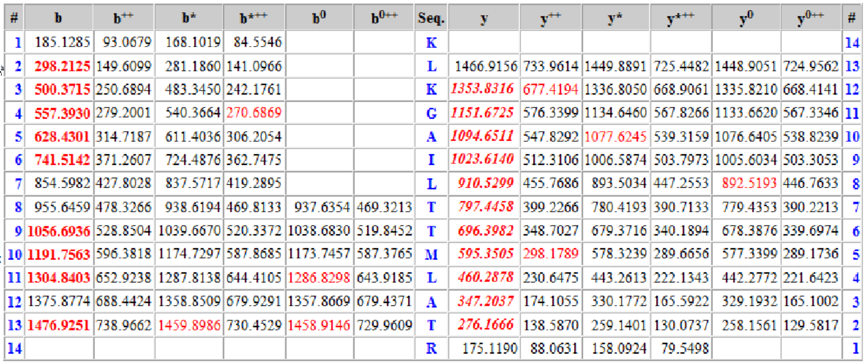
MS/MS Fragmentation of **KLKGAILTTMLATR**
Found in **E9PBG7**, Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=2 SV=1

Match to Query 10827: 1650.033788 from(826.024170,2+) intensity(613010.8125)
Title: File392 Spectrum18879 scans: 20903
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1650.0295
Fixed modifications: Carbamidomethyl (C) (apply to specified resi
Variable modifications:
K1      : Propionyl (K)
K3      : Propionyl-(13CD3)Methyl (K)
M10     : Label:13C(1)2H(3) (M)
Ions Score: 66  Expect: 2.1e-005
Matches : 28/140 fragment ions using 53 most intense peaks    (hel
```

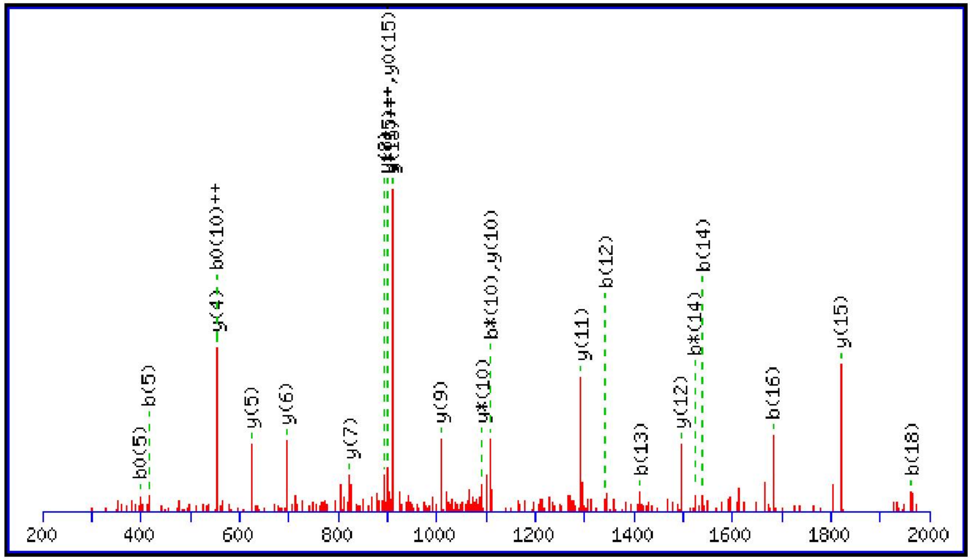


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	**298.2125**	149.6099	281.1860	141.0966			L	1466.9156	733.9614	1449.8891	725.4482	1448.9051	724.9562	13
3	**500.3715**	250.6894	483.3450	242.1761			K	***1353.8316***	677.4194	1336.8050	668.9061	1335.8210	668.4141	12
4	**557.3930**	279.2001	540.3664	270.6869			G	***1151.6725***	576.3399	1134.6460	567.8266	1133.6620	567.3346	11
5	**628.4301**	314.7187	611.4036	306.2054			A	***1094.6511***	547.8292	1077.6245	539.3159	1076.6405	538.8239	10
6	**741.5142**	371.2607	724.4876	362.7475			I	***1023.6140***	512.3106	1006.5874	503.7973	1005.6034	503.3053	9
7	854.5982	427.8028	837.5717	419.2895			L	***910.5299***	455.7686	893.5034	447.2553	892.5193	446.7633	8
8	955.6459	478.3266	938.6194	469.8133	937.6354	469.3213	T	***797.4458***	399.2266	780.4193	390.7133	779.4353	390.2213	7
9	**1056.6936**	528.8504	1039.6670	520.3372	1038.6830	519.8452	T	***696.3982***	348.7027	679.3716	340.1894	678.3876	339.6974	6
10	**1191.7563**	596.3818	1174.7297	587.8685	1173.7457	587.3765	M	***595.3505***	298.1789	578.3239	289.6656	577.3399	289.1736	5
11	**1304.8403**	652.9238	1287.8138	644.4105	1286.8298	643.9185	L	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	4
12	1375.8774	688.4424	1358.8509	679.9291	1357.8669	679.4371	A	***347.2037***	174.1055	330.1772	165.5922	329.1932	165.1002	3
13	**1476.9251**	738.9662	1459.8986	730.4529	1458.9146	729.9609	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AASSVPNLKKTNAQAAPKPR**
Found in **B4DH53**, MAP1S light chain OS=Homo sapiens GN=MAP1S PE=2 SV=1

Match to Query 16359: 2234.266448 from(1118.140500,2+) intensity(111044.6719)
Title: File386 Spectrum10990 scans: 12302
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.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 ●



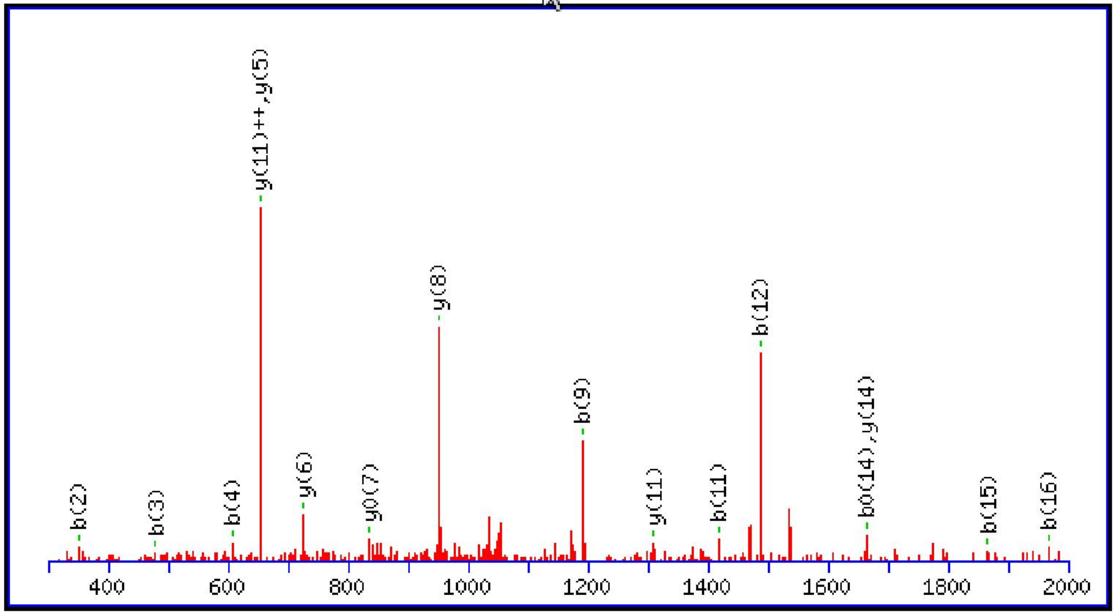
Monoisotopic mass of neutral peptide Mr(calc): 2234.2655
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
K18 : Propionyl (K)
Ions Score: 63 **Expect:** 0.00019
Matches : 24/194 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							20
2	143.0815	72.0444					A	2164.2357	1082.6215	2147.2092	1074.1082	2146.2251	1073.6162	19
3	230.1135	115.5604			212.1030	106.5551	S	2093.1986	1047.1029	2076.1721	1038.5897	2075.1880	1038.0977	18
4	317.1456	159.0764			299.1350	150.0711	S	2006.1666	1003.5869	1989.1400	995.0736	1988.1560	994.5816	17
5	**416.2140**	208.6106			398.2034	199.6053	V	1919.1345	960.0709	1902.1080	951.5576	1901.1240	951.0656	16
6	513.2667	257.1370			495.2562	248.1317	P	***1820.0661***	910.5367	1803.0396	902.0234	1802.0556	901.5314	15
7	627.3097	314.1585	610.2831	305.6452	609.2991	305.1532	N	1723.0134	862.0103	1705.9868	853.4970	1705.0028	853.0050	14
8	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	L	1608.9704	804.9889	1591.9439	796.4756	1590.9599	795.9836	13
9	942.5527	471.7800	925.5262	463.2667	924.5422	462.7747	K	***1495.8864***	748.4468	1478.8598	739.9336	1477.8758	739.4415	12
10	1126.6739	563.8406	1109.6474	555.3273	1108.6634	554.8353	K	***1293.7274***	647.3673	1276.7008	638.8540	1275.7168	638.3620	11
11	1227.7216	614.3644	1210.6951	605.8512	1209.7110	605.3592	T	***1109.6062***	555.3067	1092.5796	546.7935	1091.5956	546.3014	10
12	**1341.7645**	671.3859	1324.7380	662.8726	1323.7540	662.3806	N	***1008.5585***	504.7829	991.5320	496.2696			9
13	**1412.8016**	706.9045	1395.7751	698.3912	1394.7911	697.8992	A	***894.5156***	447.7614	877.4890	439.2482			8
14	**1540.8602**	770.9337	1523.8337	762.4205	1522.8497	761.9285	Q	***823.4785***	412.2429	806.4519	403.7296			7
15	1611.8973	806.4523	1594.8708	797.9390	1593.8868	797.4470	A	***695.4199***	348.2136	678.3933	339.7003			6
16	**1682.9344**	841.9709	1665.9079	833.4576	1664.9239	832.9656	A	***624.3828***	312.6950	607.3562	304.1817			5
17	1779.9872	890.4972	1762.9607	881.9840	1761.9766	881.4920	P	***553.3457***	277.1765	536.3191	268.6632			4
18	**1964.1084**	982.5578	1947.0818	974.0446	1946.0978	973.5525	K	456.2929	228.6501	439.2663	220.1368			3
19	2061.1612	1031.0842	2044.1346	1022.5709	2043.1506	1022.0789	P	272.1717	136.5895	255.1452	128.0762			2
20							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FKQEPEDELPEAPPKTR**
Found in **Q8NHM5**, Lysine-specific demethylase 2B OS=Homo sapiens GN=KDM2B PE=1 SV=1

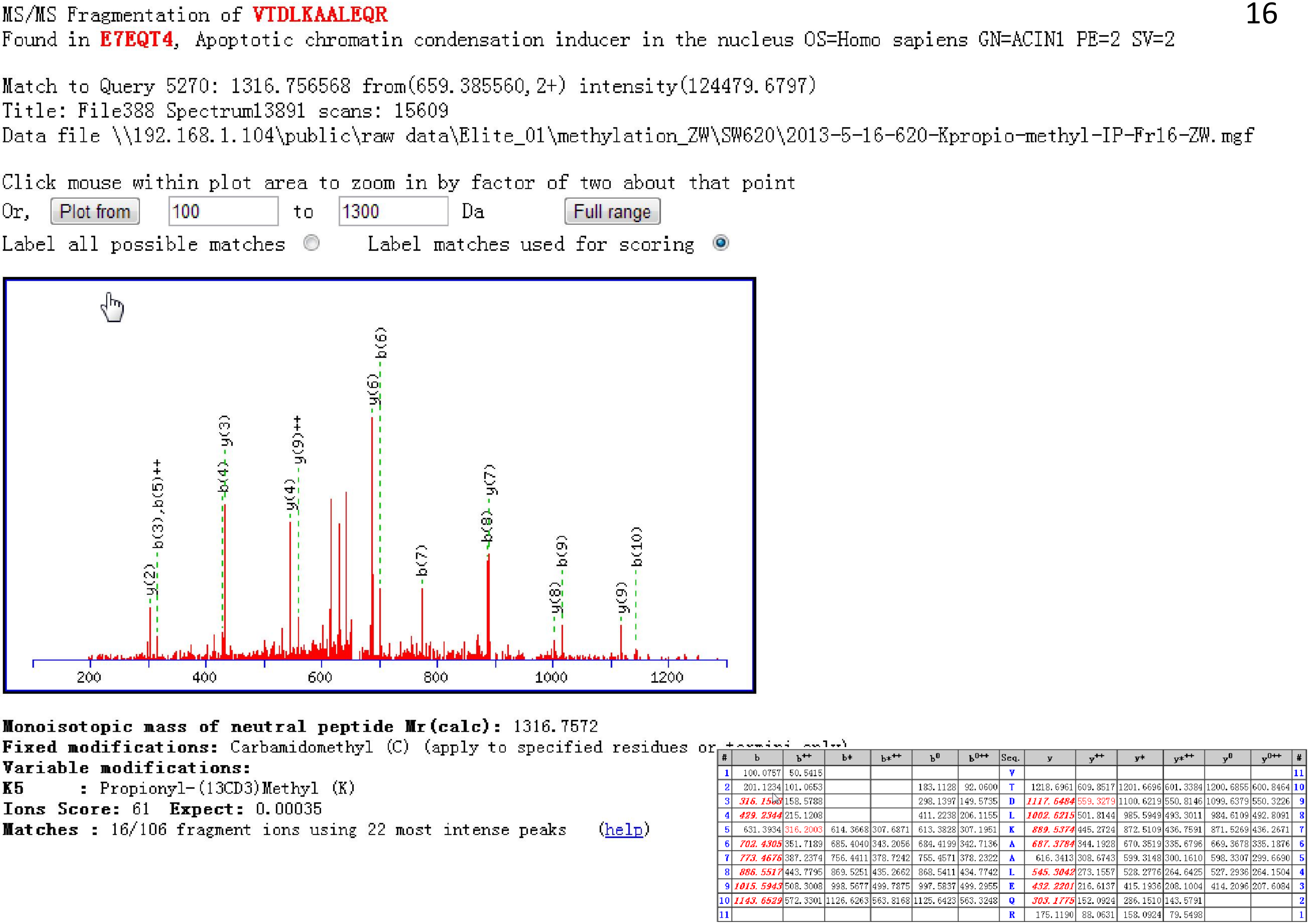
Match to Query 15626: 2140.088968 from(1071.051760,2+) intensity(60884.8594)
Title: File386 Spectrum11418 scans: 12758
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2140.0961
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K15 : Propionyl (K)
Ions Score: 61 **Expect:** 0.00051
Matches : 16/182 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							17
2	350.2347	175.6210	333.2082	167.1077			K	1994.0349	997.5211	1977.0084	989.0078	1976.0244	988.5158	16
3	478.2933	239.6503	461.2667	231.1370			Q	1791.8759	896.4416	1774.8494	887.9283	1773.8654	887.4363	15
4	607.3359	304.1716	590.3093	295.6583	589.3253	295.1663	E	1663.8174	832.4123	1646.7908	823.8990	1645.8068	823.4070	14
5	704.3886	352.6980	687.3621	344.1847	686.3781	343.6927	P	1534.7748	767.8910	1517.7482	759.3777	1516.7642	758.8857	13
6	833.4312	417.2193	816.4047	408.7060	815.4207	408.2140	E	1437.7220	719.3646	1420.6955	710.8514	1419.7114	710.3594	12
7	948.4582	474.7327	931.4316	466.2195	930.4476	465.7274	D	1308.6794	654.8433	1291.6529	646.3301	1290.6688	645.8381	11
8	1077.5008	539.2540	1060.4742	530.7407	1059.4902	530.2487	E	1193.6525	597.3299	1176.6259	588.8166	1175.6419	588.3246	10
9	1190.5848	595.7961	1173.5583	587.2828	1172.5743	586.7908	L	1064.6099	532.8086	1047.5833	524.2953	1046.5993	523.8033	9
10	1287.6376	644.3224	1270.6110	635.8092	1269.6270	635.3172	P	951.5258	476.2665	934.4993	467.7533	933.5152	467.2613	8
11	1416.6802	708.8437	1399.6536	700.3305	1398.6696	699.8384	E	854.4730	427.7402	837.4465	419.2269	836.4625	418.7349	7
12	1487.7173	744.3623	1470.6908	735.8490	1469.7067	735.3570	A	725.4305	363.2189	708.4039	354.7056	707.4199	354.2136	6
13	1584.7701	792.8887	1567.7435	784.3754	1566.7595	783.8834	P	654.3933	327.7003	637.3668	319.1870	636.3828	318.6950	5
14	1681.8228	841.4151	1664.7963	832.9018	1663.8123	832.4098	P	557.3406	279.1739	540.3140	270.6607	539.3300	270.1686	4
15	1865.9440	933.4756	1848.9175	924.9624	1847.9334	924.4704	K	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	3
16	1966.9917	983.9995	1949.9651	975.4862	1948.9811	974.9942	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
17							R	175.1190	88.0631	158.0924	79.5498			1



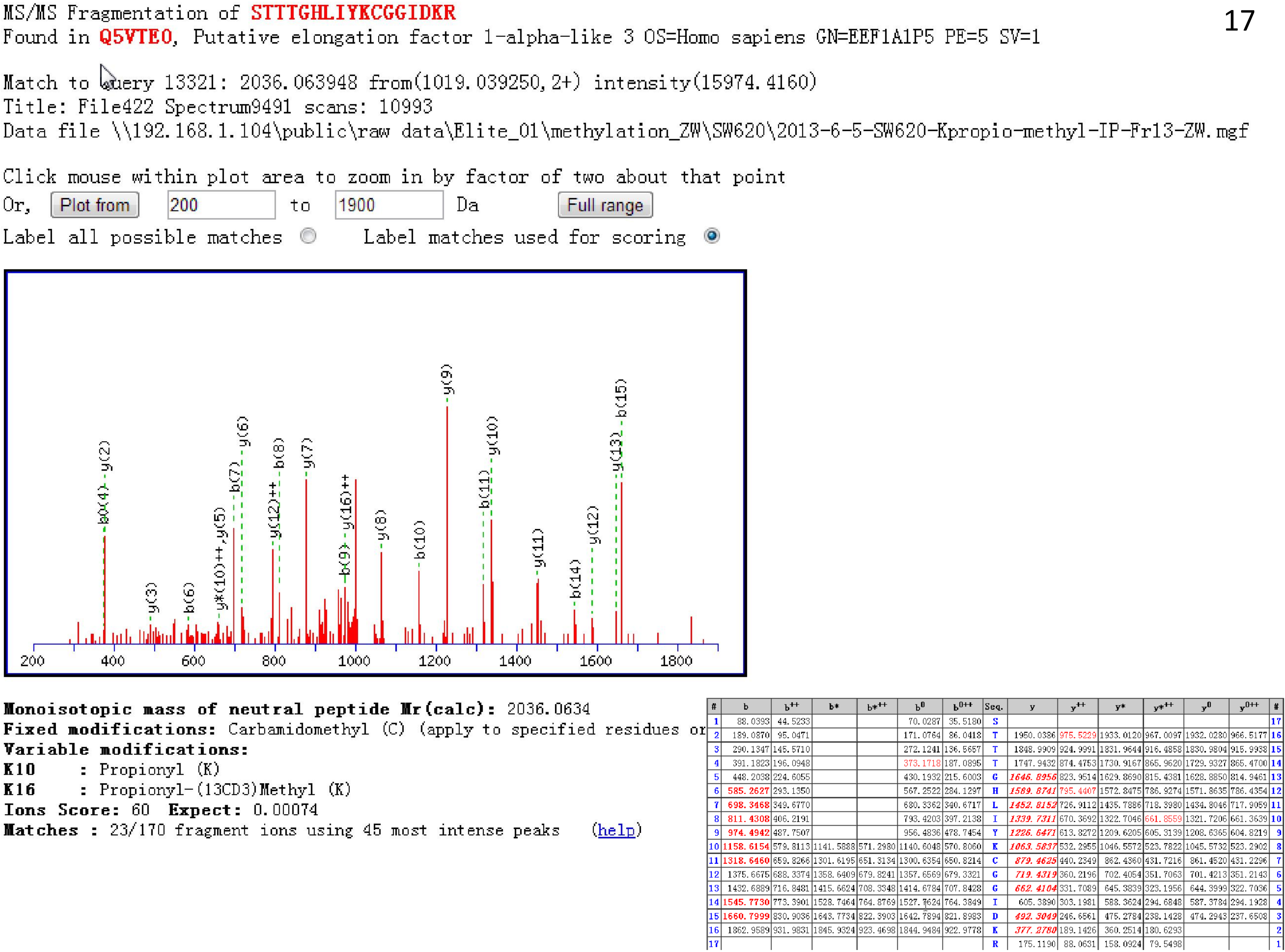
MS/MS Fragmentation of **VTDLKAALEQR**
Found in **E7EQT4**, Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=2 SV=2

Match to Query 5270: 1316.756568 from(659.385560,2+) intensity(124479.6797)
Title: File388 Spectrum13891 scans: 15609
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1316.7572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 61 **Expect:** 0.00035
Matches : 16/106 fragment ions using 22 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							11
2	201.1234	101.0653			183.1128	92.0600	T	1218.6961	609.8517	1201.6696	601.3384	1200.6855	600.8464	10
3	***316.15[illegible]***	158.5788			298.1397	149.5735	D	***1117.6484***	559.3279	1100.6219	550.8146	1099.6379	550.3226	9
4	***429.2344***	215.1208			411.2238	206.1155	L	***1002.6215***	501.8144	985.5949	493.3011	984.6109	492.8091	8
5	631.3934	316.2003	614.3668	307.6871	613.3828	307.1951	K	***889.5374***	445.2724	872.5109	436.7591	871.5269	436.2671	7
6	***702.4305***	351.7189	685.4040	343.2056	684.4199	342.7136	A	***687.3784***	344.1928	670.3519	335.6796	669.3678	335.1876	6
7	***773.4676***	387.2374	756.4411	378.7242	755.4571	378.2322	A	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
8	***886.5517***	443.7795	869.5251	435.2662	868.5411	434.7742	L	***545.3042***	273.1557	528.2776	264.6425	527.2936	264.1504	4
9	***1015.5943***	508.3008	998.5677	499.7875	997.5837	499.2955	E	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
10	***1143.6529***	572.3301	1126.6263	563.8168	1125.6423	563.3248	Q	***303.1775***	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



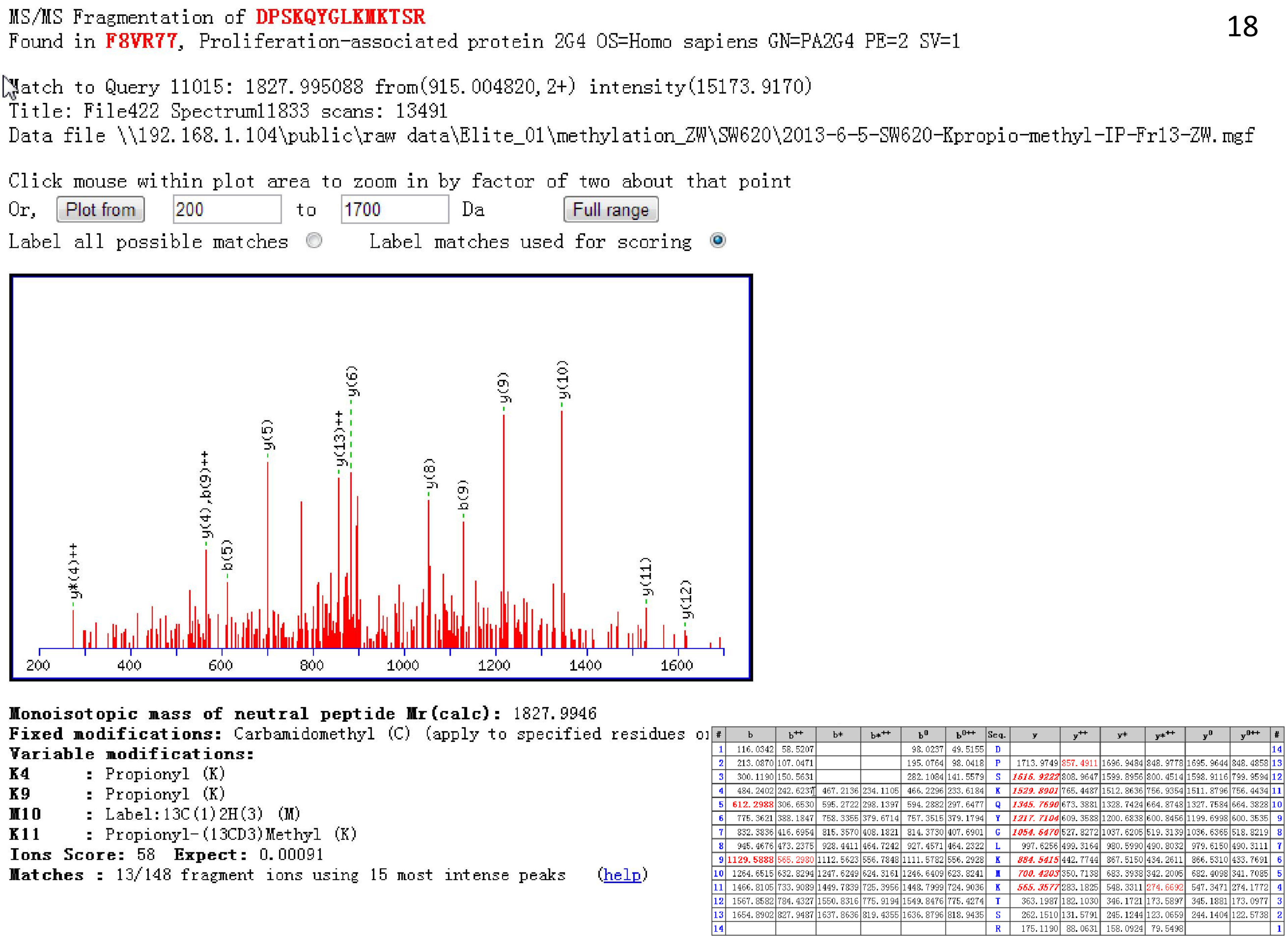
MS/MS Fragmentation of **STTTGHLIYKCGGIDKR**
Found in **Q5VTE0**, Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1

Match to Query 13321: 2036.063948 from(1019.039250,2+) intensity(15974.4160)
Title: File422 Spectrum9491 scans: 10993
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr13-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 2036.0634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K10 : Propionyl (K)
K16 : Propionyl-(13CD3)Methyl (K)
Ions Score: 60 **Expect:** 0.00074
Matches : 23/170 fragment ions using 45 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	189.0870	95.0471			171.0764	86.0418	T	1950.0386	975.5229	1933.0120	967.0097	1932.0280	966.5177	16
3	290.1347	145.5710			272.1241	136.5657	T	1848.9909	924.9991	1831.9644	916.4858	1830.9804	915.9938	15
4	391.1823	196.0948			373.1718	187.0895	T	1747.9432	874.4753	1730.9167	865.9620	1729.9327	865.4700	14
5	448.2038	224.6055			430.1932	215.6003	G	***1646.8956***	823.9514	1629.8690	815.4381	1628.8850	814.9461	13
6	**585.2627**	293.1350			567.2522	284.1297	H	***1589.8741***	795.4407	1572.8475	786.9274	1571.8635	786.4354	12
7	**698.3468**	349.6770			680.3362	340.6717	L	***1452.8152***	726.9112	1435.7886	718.3980	1434.8046	717.9059	11
8	**811.4308**	406.2191			793.4203	397.2138	I	***1339.7311***	670.3692	1322.7046	661.8559	1321.7206	661.3639	10
9	**974.4942**	487.7507			956.4836	478.7454	Y	***1226.6471***	613.8272	1209.6205	605.3139	1208.6365	604.8219	9
10	**1158.6154**	579.8113	1141.5888	571.2980	1140.6048	570.8060	K	***1063.5837***	532.2955	1046.5572	523.7822	1045.5732	523.2902	8
11	**1318.6460**	659.8266	1301.6195	651.3134	1300.6354	650.8214	C	***879.4625***	440.2349	862.4360	431.7216	861.4520	431.2296	7
12	1375.6675	688.3374	1358.6409	679.8241	1357.6569	679.3321	G	***719.4319***	360.2196	702.4054	351.7063	701.4213	351.2143	6
13	1432.6889	716.8481	1415.6624	708.3348	1414.6784	707.8428	G	***662.4104***	331.7089	645.3839	323.1956	644.3999	322.7036	5
14	**1545.7730**	773.3901	1528.7464	764.8769	1527.7624	764.3849	I	605.3890	303.1981	588.3624	294.6848	587.3784	294.1928	4
15	**1660.7999**	830.9036	1643.7734	822.3903	1642.7894	821.8983	D	***492.3049***	246.6561	475.2784	238.1428	474.2943	237.6508	3
16	1862.9589	931.9831	1845.9324	923.4698	1844.9484	922.9778	K	***377.2780***	189.1426	360.2514	180.6293			2
17							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **DPSKQYGLKMKTSR**
Found in **F8VR77**, Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=2 SV=1

Match to Query 11015: 1827.995088 from(915.004820,2+) intensity(15173.9170)
Title: File422 Spectrum11833 scans: 13491
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

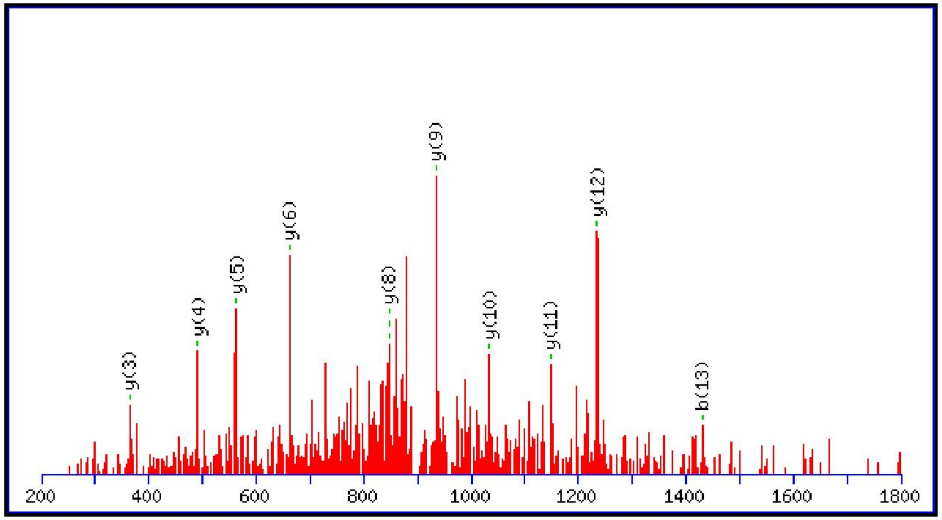
Monoisotopic mass of neutral peptide Mr(calc): 1827.9946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K4 : Propionyl (K)
K9 : Propionyl (K)
M10 : Label:13C(1)2H(3) (M)
K11 : Propionyl-(13CD3)Methyl (K)
Ions Score: 58 **Expect:** 0.00091
Matches : 13/148 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	213.0870	107.0471			195.0764	98.0418	P	1713.9749	857.4911	1696.9484	848.9778	1695.9644	848.4858	13
3	300.1190	150.5631			282.1084	141.5579	S	**1616.9222**	808.9647	1599.8956	800.4514	1598.9116	799.9594	12
4	484.2402	242.6237	467.2136	234.1105	466.2296	233.6184	K	**1529.8901**	765.4487	1512.8636	756.9354	1511.8796	756.4434	11
5	**612.2988**	306.6530	595.2722	298.1397	594.2882	297.6477	Q	**1345.7690**	673.3881	1328.7424	664.8748	1327.7584	664.3828	10
6	775.3621	388.1847	758.3355	379.6714	757.3515	379.1794	Y	**1217.7104**	609.3588	1200.6838	600.8456	1199.6998	600.3535	9
7	832.3836	416.6954	815.3570	408.1821	814.3730	407.6901	G	**1054.6470**	527.8272	1037.6205	519.3139	1036.6365	518.8219	8
8	945.4676	473.2375	928.4411	464.7242	927.4571	464.2322	L	997.6256	499.3164	980.5990	490.8032	979.6150	490.3111	7
9	**1129.5888**	565.2980	1112.5623	556.7848	1111.5782	556.2928	K	**884.5415**	442.7744	867.5150	434.2611	866.5310	433.7691	6
10	1264.6515	632.8294	1247.6249	624.3161	1246.6409	623.8241	M	**700.4203**	350.7138	683.3938	342.2005	682.4098	341.7085	5
11	1466.8105	733.9089	1449.7839	725.3956	1448.7999	724.9036	K	**565.3577**	283.1825	548.3311	274.6692	547.3471	274.1772	4
12	1567.8582	784.4327	1550.8316	775.9194	1549.8476	775.4274	T	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
13	1654.8902	827.9487	1637.8636	819.4355	1636.8796	818.9435	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GWLKSNVSDAVAQSTR**
Found in **P60174-1**, Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1

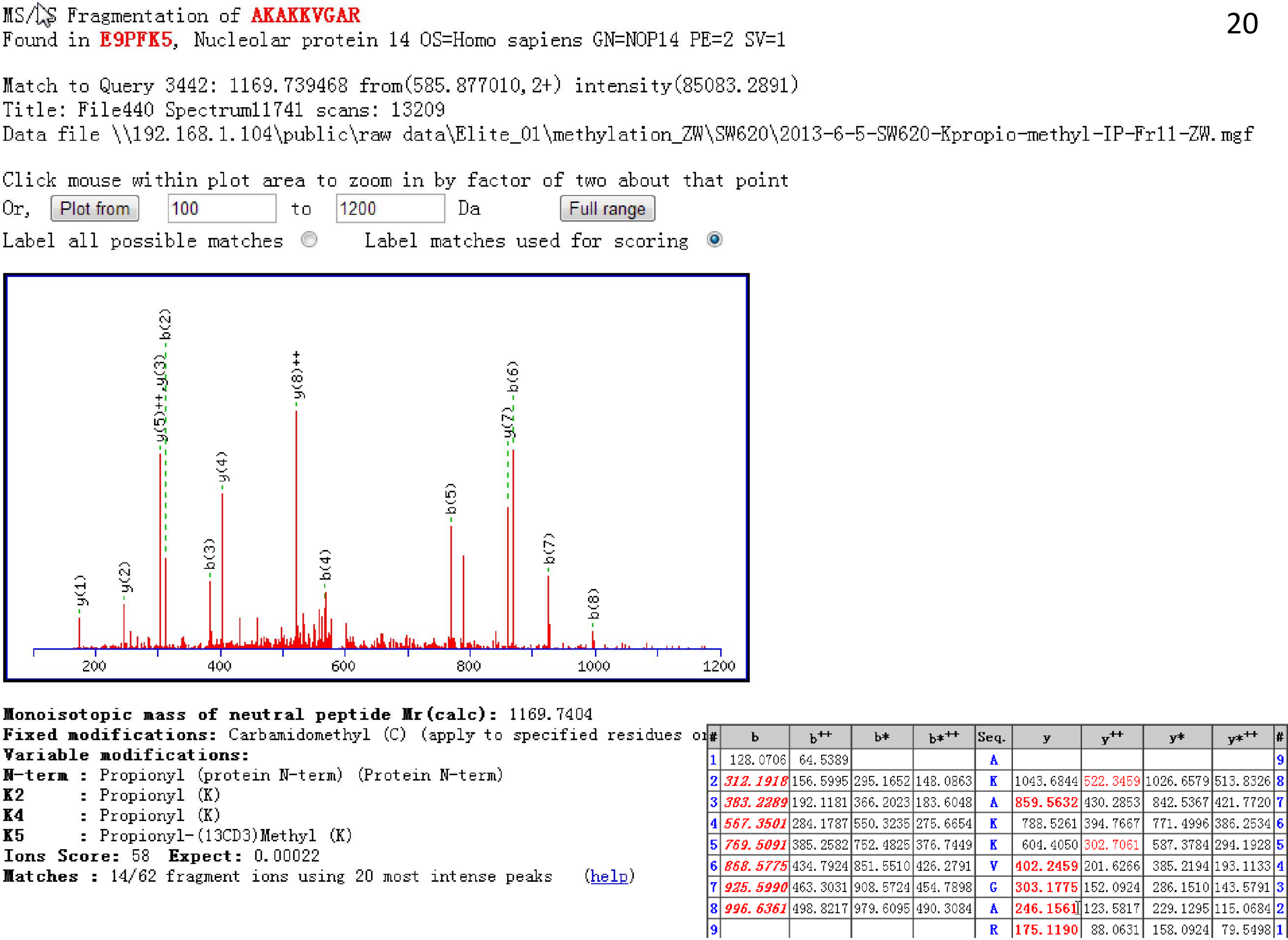
Match to Query 11677: 1791.937108 from(896.975830,2+) intensity(24611.7207)
Title: File388 Spectrum11845 scans: 13426
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1791.9388
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 58 **Expect:** 0.00092
Matches : 10/164 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							16
2	244.1081	122.5577					W	1735.9246	868.4659	1718.8981	859.9527	1717.9140	859.4607	15
3	357.1921	179.0997					L	1549.8453	775.4263	1532.8187	766.9130	1531.8347	766.4210	14
4	559.3511	280.1792	542.3246	271.6659			K	1436.7612	718.8843	1419.7347	710.3710	1418.7507	709.8790	13
5	646.3832	323.6952	629.3566	315.1819	628.3726	314.6899	S	***1234.6022***	617.8047	1217.5757	609.2915	1216.5917	608.7995	12
6	760.4261	380.7167	743.3995	372.2034	742.4155	371.7114	N	***1147.5702***	574.2887	1130.5436	565.7755	1129.5596	565.2835	11
7	859.4945	430.2509	842.4679	421.7376	841.4839	421.2456	V	***1033.5273***	517.2673	1016.5007	508.7540	1015.5167	508.2620	10
8	946.5265	473.7669	929.5000	465.2536	928.5160	464.7616	S	***934.4589***	467.7331	917.4323	459.2198	916.4483	458.7278	9
9	1061.5535	531.2804	1044.5269	522.7671	1043.5429	522.2751	D	***847.4268***	424.2170	830.4003	415.7038	829.4163	415.2118	8
10	1132.5906	566.7989	1115.5640	558.2857	1114.5800	557.7936	A	732.3999	366.7036	715.3733	358.1903	714.3893	357.6983	7
11	1231.6590	616.3331	1214.6324	607.8199	1213.6484	607.3279	V	***661.3628***	331.1850	644.3362	322.6717	643.3522	322.1797	6
12	1302.6961	651.8517	1285.6696	643.3384	1284.6855	642.8464	A	***562.2944***	281.6508	545.2678	273.1375	544.2838	272.6455	5
13	1430.7547	715.8810	1413.7281	707.3677	1412.7441	706.8757	Q	***491.2572***	246.1323	474.2307	237.6190	473.2467	237.1270	4
14	1517.7867	759.3970	1500.7602	750.8837	1499.7762	750.3917	S	***363.1987***	182.1030	346.1721	173.5897	345.1881	173.0977	3
15	1618.8344	809.9208	1601.8078	801.4076	1600.8238	800.9156	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1



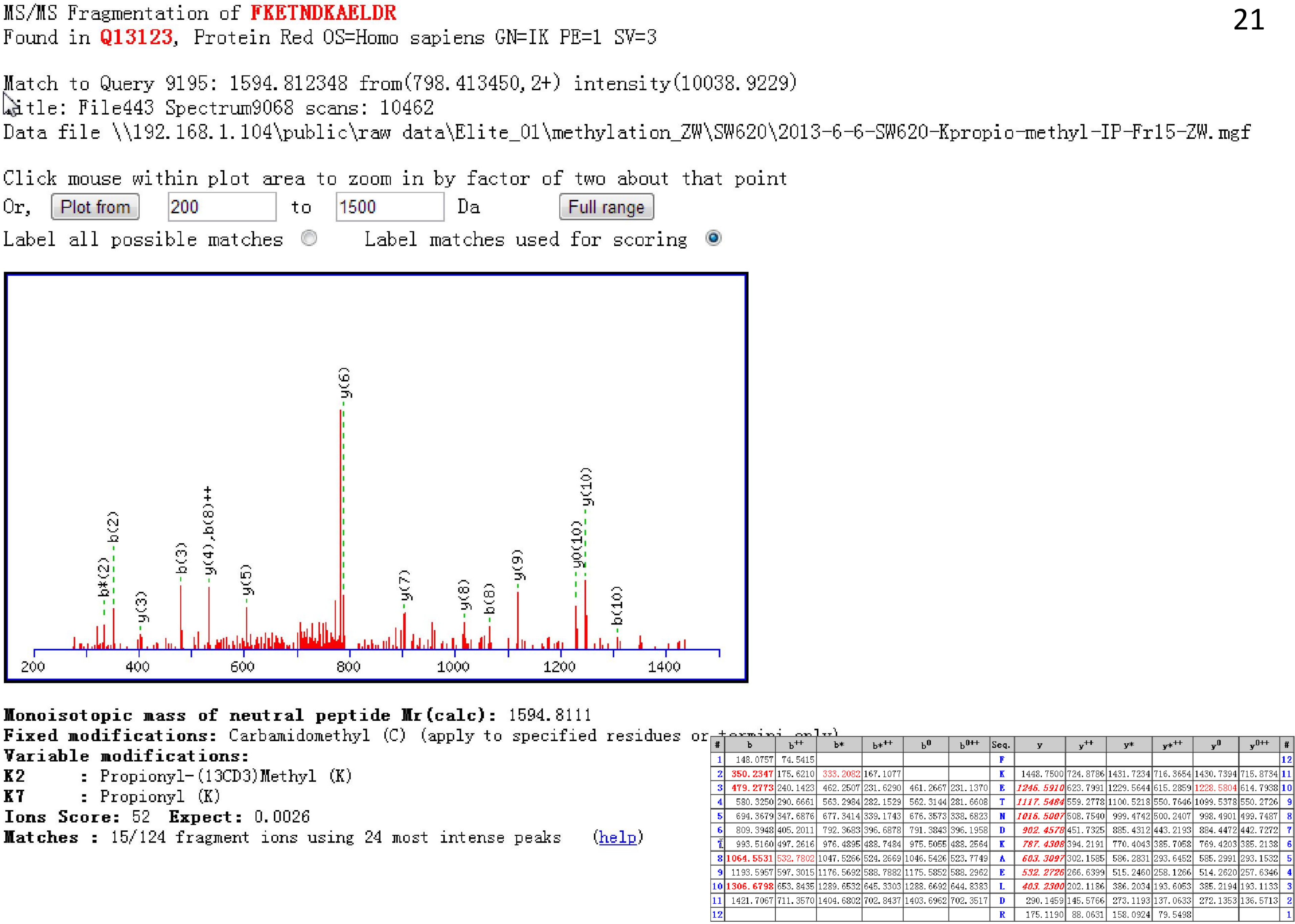
MS/MS Fragmentation of **AKAKKVGAR**
Found in **E9PFK5**, Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=2 SV=1

Match to Query 3442: 1169.739468 from(585.877010,2+) intensity(85083.2891)
Title: File440 Spectrum11741 scans: 13209
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1169.7404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K2 : Propionyl (K)
K4 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 58 **Expect:** 0.00022
Matches : 14/62 fragment ions using 20 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	128.0706	64.5389			A					9
2	312.1918	156.5995	295.1652	148.0863	K	1043.6844	522.3459	1026.6579	513.8326	8
3	383.2289	192.1181	366.2023	183.6048	A	859.5632	430.2853	842.5367	421.7720	7
4	567.3501	284.1787	550.3235	275.6654	K	788.5261	394.7667	771.4996	386.2534	6
5	769.5091	385.2582	752.4825	376.7449	K	604.4050	302.7061	587.3784	294.1928	5
6	868.5775	434.7924	851.5510	426.2791	V	402.2459	201.6266	385.2194	193.1133	4
7	925.5990	463.3031	908.5724	454.7898	G	303.1775	152.0924	286.1510	143.5791	3
8	996.6361	498.8217	979.6095	490.3084	A	246.1561	123.5817	229.1295	115.0684	2
9					R	175.1190	88.0631	158.0924	79.5498	1



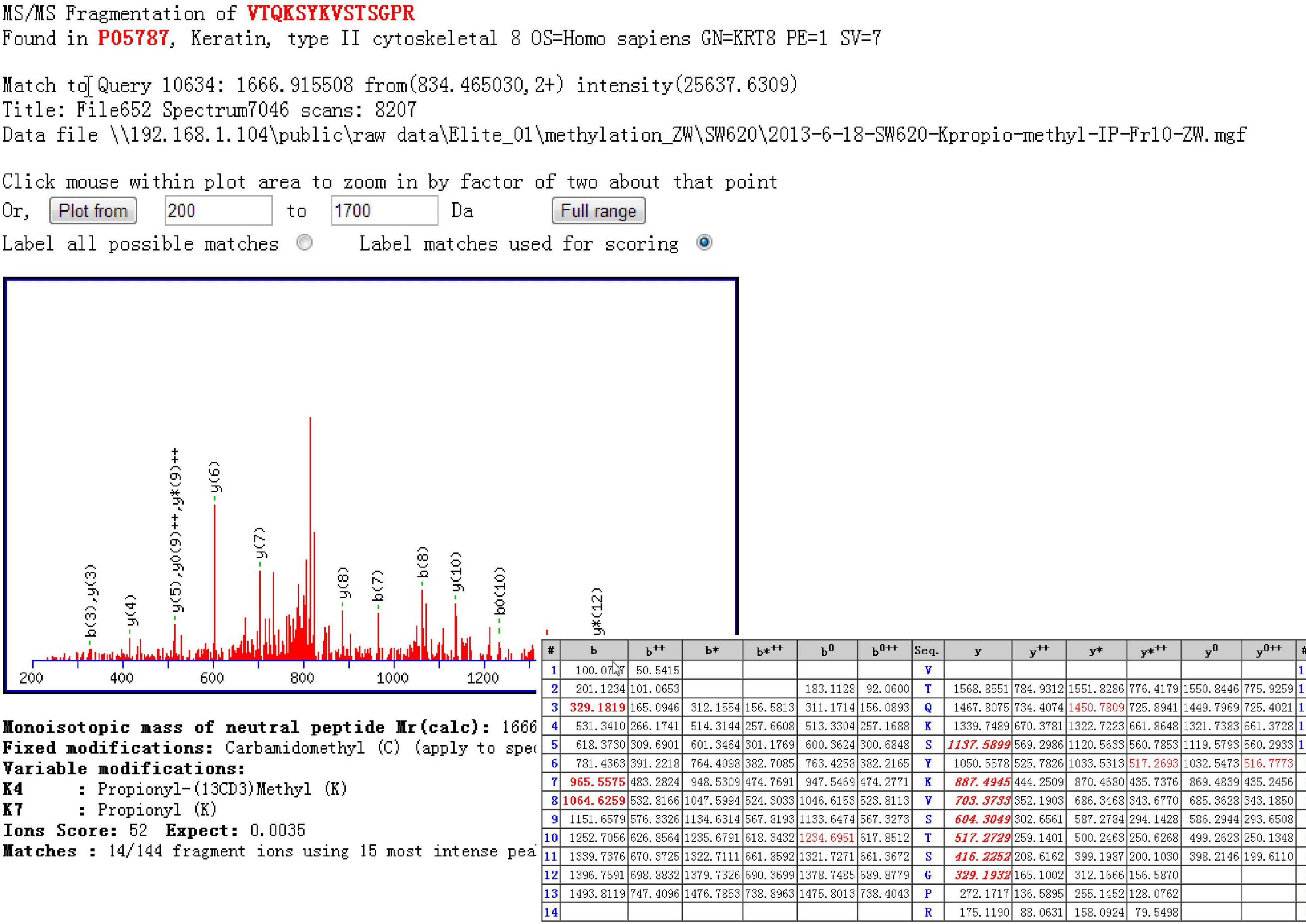
MS/MS Fragmentation of FKETNDKAELDR
Found in Q13123, Protein Red OS=Homo sapiens GN=IK PE=1 SV=3

Match to Query 9195: 1594.812348 from(798.413450,2+) intensity(10038.9229)
Title: File443 Spectrum9068 scans: 10462
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-6-SW620-Kpropio-methyl-IP-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1594.8111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 52 **Expect:** 0.0026
Matches : 15/124 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							12
2	**350.2347**	175.6210	333.2082	167.1077			K	1448.7500	724.8786	1431.7234	716.3654	1430.7394	715.8734	11
3	**479.2773**	240.1423	462.2507	231.6290	461.2667	231.1370	E	***1246.5910***	623.7991	1229.5644	615.2859	1228.5804	614.7938	10
4	580.3250	290.6661	563.2984	282.1529	562.3144	281.6608	T	***1117.5484***	559.2778	1100.5218	550.7646	1099.5378	550.2726	9
5	694.3679	347.6876	677.3414	339.1743	676.3573	338.6823	N	***1016.5007***	508.7540	999.4742	500.2407	998.4901	499.7487	8
6	809.3948	405.2011	792.3683	396.6878	791.3843	396.1958	D	***902.4578***	451.7325	885.4312	443.2193	884.4472	442.7272	7
7	993.5160	497.2616	976.4895	488.7484	975.5055	488.2564	K	***787.4308***	394.2191	770.4043	385.7058	769.4203	385.2138	6
8	**1064.5531**	532.7802	1047.5266	524.2669	1046.5426	523.7749	A	***603.3097***	302.1585	586.2831	293.6452	585.2991	293.1532	5
9	1193.5957	597.3015	1176.5692	588.7882	1175.5852	588.2962	E	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
10	**1306.6798**	653.8435	1289.6532	645.3303	1288.6692	644.8383	L	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
11	1421.7067	711.3570	1404.6802	702.8437	1403.6962	702.3517	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **VTQKSYKVSTSGPR**
Found in **P05787**, Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7

Match to Query 10634: 1666.915508 from(834.465030,2+) intensity(25637.6309)
Title: File652 Spectrum7046 scans: 8207
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

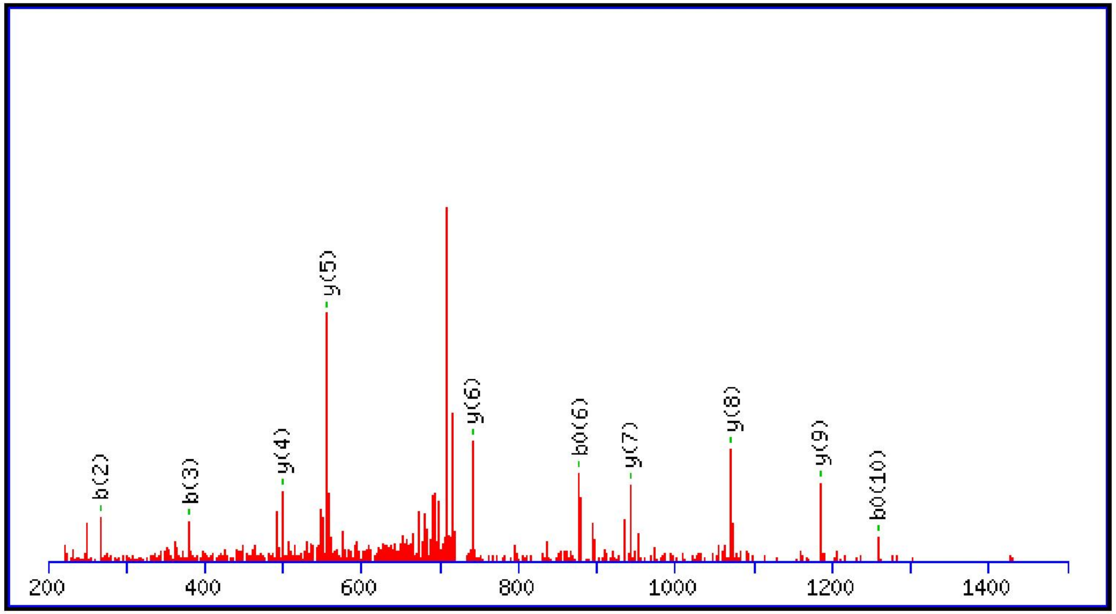
Monoisotopic mass of neutral peptide Mr(calc): 1666
Fixed modifications: Carbamidomethyl (C) (apply to spe
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 52 **Expect:** 0.0035
Matches : 14/144 fragment ions using 15 most intense pea

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.07[illegible]7	50.5415					V							14
2	201.1234	101.0653			183.1128	92.0600	T	1568.8551	784.9312	1551.8286	776.4179	1550.8446	775.9259	13
3	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	Q	1467.8075	734.4074	1450.7809	725.8941	1449.7969	725.4021	12
4	531.3410	266.1741	514.3144	257.6608	513.3304	257.1688	K	1339.7489	670.3781	1322.7223	661.8648	1321.7383	661.3728	11
5	618.3730	309.6901	601.3464	301.1769	600.3624	300.6848	S	***1137.5899***	569.2986	1120.5633	560.7853	1119.5793	560.2933	10
6	781.4363	391.2218	764.4098	382.7085	763.4258	382.2165	Y	1050.5578	525.7826	1033.5313	517.2693	1032.5473	516.7773	9
7	**965.5575**	483.2824	948.5309	474.7691	947.5469	474.2771	K	***887.4945***	444.2509	870.4680	435.7376	869.4839	435.2456	8
8	**1064.6259**	532.8166	1047.5994	524.3033	1046.6153	523.8113	V	***703.3733***	352.1903	686.3468	343.6770	685.3628	343.1850	7
9	1151.6579	576.3326	1134.6314	567.8193	1133.6474	567.3273	S	***604.3049***	302.6561	587.2784	294.1428	586.2944	293.6508	6
10	1252.7056	626.8564	1235.6791	618.3432	1234.6951	617.8512	T	***517.2729***	259.1401	500.2463	250.6268	499.2623	250.1348	5
11	1339.7376	670.3725	1322.7111	661.8592	1321.7271	661.3672	S	***416.2252***	208.6162	399.1987	200.1030	398.2146	199.6110	4
12	1396.7591	698.8832	1379.7326	690.3699	1378.7485	689.8779	G	***329.1932***	165.1002	312.1666	156.5870			3
13	1493.8119	747.4096	1476.7853	738.8963	1475.8013	738.4043	P	272.1717	136.5895	255.1452	128.0762			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **EHLEKKGPQVR**
Found in **F8VZY9**, Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=2 SV=1

Match to Query 6782: 1449.824928 from(725.919740,2+) intensity(66155.8906)
Title: File388 Spectrum6492 scans: 7687
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



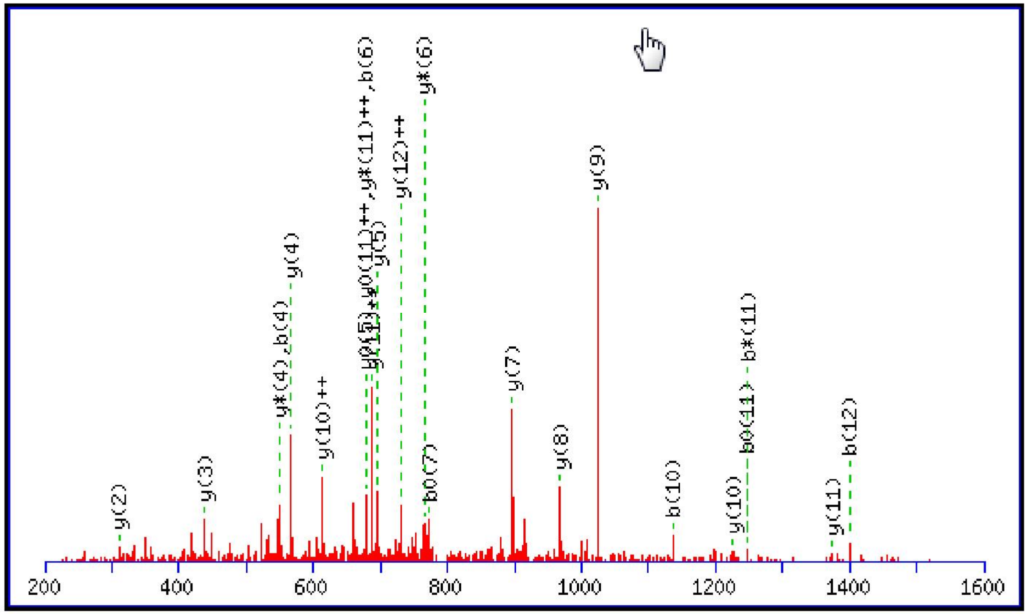
Monoisotopic mass of neutral peptide Mr(calc): 1449.8212
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 52 **Expect:** 0.0028
Matches : 10/98 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	**267.1088**	134.0580			249.0982	125.0527	H	1321.7859	661.3966	1304.7594	652.8833	1303.7754	652.3913	10
3	**380.1928**	190.6001			362.1823	181.5948	L	***1184.7270***	592.8671	1167.7005	584.3539	1166.7165	583.8619	9
4	509.2354	255.1214			491.2249	246.1161	E	***1071.6430***	536.3251	1054.6164	527.8118	1053.6324	527.3198	8
5	711.3945	356.2009	694.3679	347.6876	693.3839	347.1956	K	***942.6004***	471.8038	925.5738	463.2905			7
6	895.5156	448.2615	878.4891	439.7482	877.5051	439.2562	K	***740.4413***	370.7243	723.4148	362.2110			6
7	952.5371	476.7722	935.5105	468.2589	934.5265	467.7669	G	***556.3202***	278.6637	539.2936	270.1504			5
8	1049.5899	525.2986	1032.5633	516.7853	1031.5793	516.2933	P	***499.2987***	250.1530	482.2722	241.6397			4
9	1177.6484	589.3279	1160.6219	580.8146	1159.6379	580.3226	Q	402.2459	201.6266	385.2194	193.1133			3
10	1276.7168	638.8621	1259.6903	630.3488	1258.7063	629.8568	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1

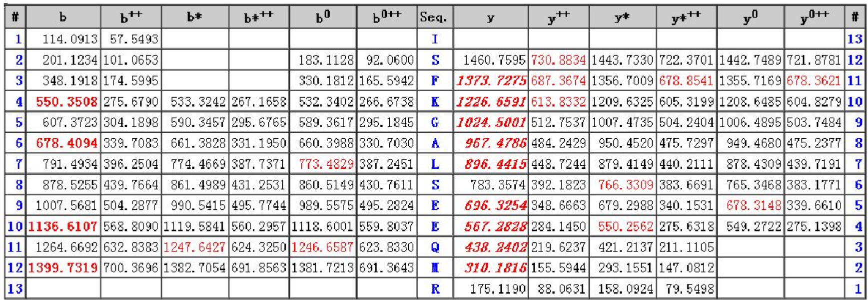
MS/MS Fragmentation of **ISFKGALSEEQMR**
Found in **F8VQX1**, RasGAP-activating-like protein 1 OS=Homo sapiens GN=RASAL1 PE=2 SV=1

Match to Query 8201: 1572.835788 from(787.425170,2+) intensity(259861.9531)
Title: File388 Spectrum14427 scans: 16181
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1572.8363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
M12 : Label:13C(1)2H(3) (M)
Ions Score: 51 **Expect:** 0.0046
Matches : 24/130 fragment ions using 39 most intense peaks (help)

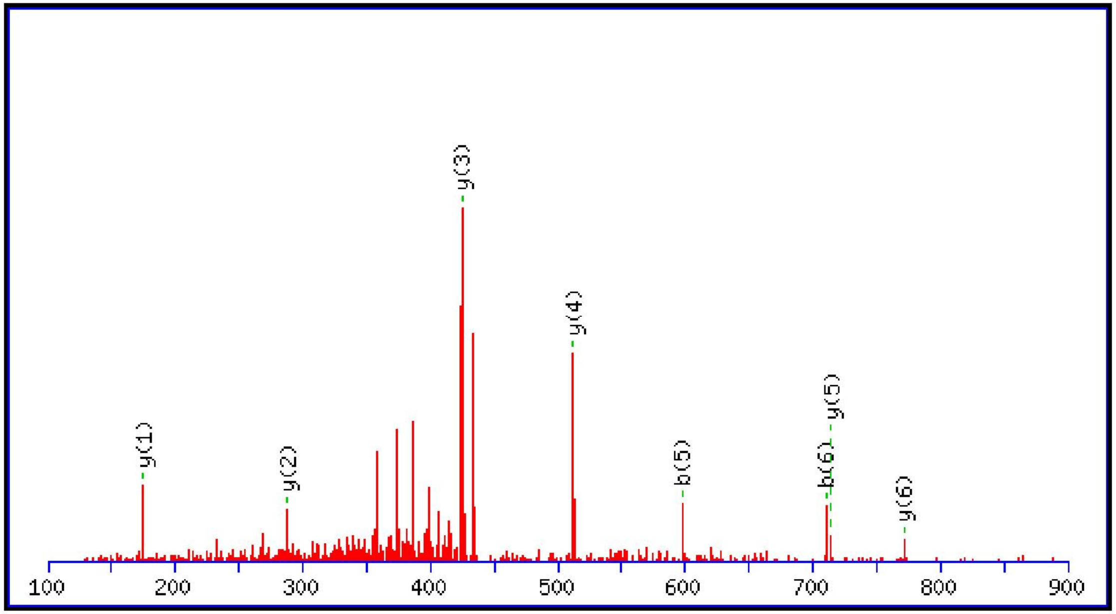


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							13
2	201.1234	101.0653			183.1128	92.0600	S	1460.7595	730.8834	1443.7330	722.3701	1442.7489	721.8781	12
3	348.1918	174.5995			330.1812	165.5942	F	***1373.7275***	687.3674	1356.7009	678.8541	1355.7169	678.3621	11
4	**550.3508**	275.6790	533.3242	267.1658	532.3402	266.6738	K	***1226.6591***	613.8332	1209.6325	605.3199	1208.6485	604.8279	10
5	607.3723	304.1898	590.3457	295.6765	589.3617	295.1845	G	***1024.5001***	512.7537	1007.4735	504.2404	1006.4895	503.7484	9
6	**678.4094**	339.7083	661.3828	331.1950	660.3988	330.7030	A	***967.4786***	484.2429	950.4520	475.7297	949.4680	475.2377	8
7	791.4934	396.2504	774.4669	387.7371	773.4829	387.2451	L	***896.4415***	448.7244	879.4149	440.2111	878.4309	439.7191	7
8	878.5255	439.7664	861.4989	431.2531	860.5149	430.7611	S	783.3574	392.1823	766.3309	383.6691	765.3468	383.1771	6
9	1007.5681	504.2877	990.5415	495.7744	989.5575	495.2824	E	***696.3254***	348.6663	679.2988	340.1531	678.3148	339.6610	5
10	**1136.6107**	568.8090	1119.5841	560.2957	1118.6001	559.8037	E	***567.2828***	284.1450	550.2562	275.6318	549.2722	275.1398	4
11	1264.6692	632.8383	1247.6427	624.3250	1246.6587	623.8330	Q	***438.2402***	219.6237	421.2137	211.1105			3
12	**1399.7319**	700.3696	1382.7054	691.8563	1381.7213	691.3643	M	***310.1816***	155.5944	293.1551	147.0812			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LGKSHIR**
Found in **Q92499**, ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2

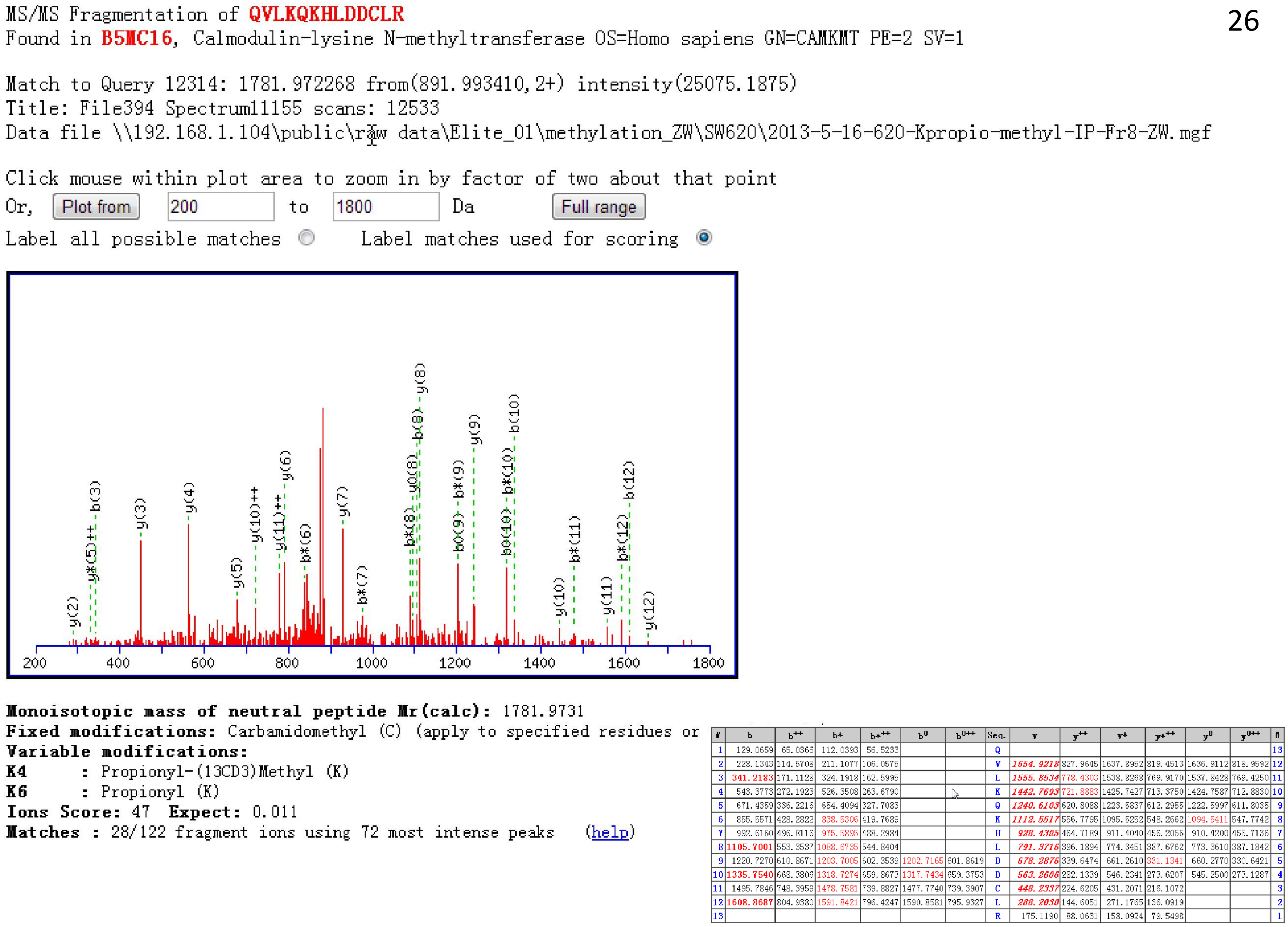
Match to Query 1229: 883.551368 from(442.782960,2+) intensity(23381.2656)
Title: File394 Spectrum4245 scans: 5060
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 883.5512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 47 **Expect:** 0.0034
Matches : 8/56 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							7
2	171.1128	86.0600					G	***771.4744***	386.2409	754.4479	377.7276	753.4639	377.2356	6
3	373.2718	187.1395	356.2453	178.6263			K	***714.4530***	357.7301	697.4264	349.2168	696.4424	348.7248	5
4	460.3038	230.6556	443.2773	222.1423	442.2933	221.6503	S	***512.2940***	256.6506	495.2674	248.1373	494.2834	247.6453	4
5	**597.3628**	299.1850	580.3362	290.6717	579.3522	290.1797	H	***425.2619***	213.1346	408.2354	204.6213			3
6	**710.4468**	355.7270	693.4203	347.2138	692.4363	346.7218	I	***288.2030***	144.6051	271.1765	136.0919			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **QVLKQKHLDDCLR**
Found in **B5MC16**, Calmodulin-lysine N-methyltransferase OS=Homo sapiens GN=CAMKMT PE=2 SV=1

Match to Query 12314: 1781.972268 from(891.993410,2+) intensity(25075.1875)
Title: File394 Spectrum11155 scans: 12533
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, 200 to 1800 Da
Label all possible matches ○ Label matches used for scoring ●

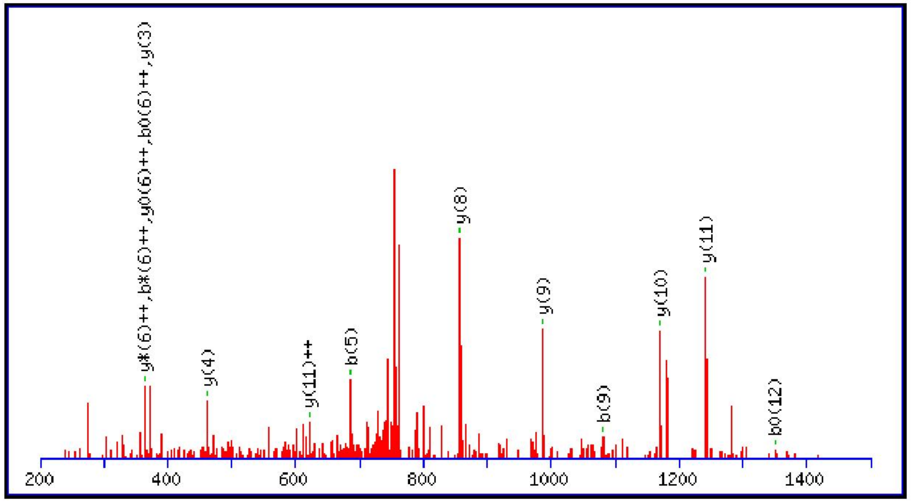
Monoisotopic mass of neutral peptide Mr(calc): 1781.9731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 47 **Expect:** 0.011
Matches : 28/122 fragment ions using 72 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							13
2	228.1343	114.5708	211.1077	106.0575			V	***1654.9218***	827.9645	1637.8952	819.4513	1636.9112	818.9592	12
3	**341.2183**	171.1128	324.1918	162.5995			L	***1555.8534***	778.4303	1538.8268	769.9170	1537.8428	769.4250	11
4	543.3773	272.1923	526.3508	263.6790			K	***1442.7693***	721.8883	1425.7427	713.3750	1424.7587	712.8830	10
5	671.4359	336.2216	654.4094	327.7083			Q	***1240.6103***	620.8088	1223.5837	612.2955	1222.5997	611.8035	9
6	855.5571	428.2822	838.5306	419.7689			K	***1112.5517***	556.7795	1095.5252	548.2662	1094.5411	547.7742	8
7	992.6160	496.8116	975.5895	488.2984			H	***928.4305***	464.7189	911.4040	456.2056	910.4200	455.7136	7
8	**1105.7001**	553.3537	1088.6735	544.8404			L	***791.3716***	396.1894	774.3451	387.6762	773.3610	387.1842	6
9	1220.7270	610.8671	1203.7005	602.3539	1202.7165	601.8619	D	***678.2876***	339.6474	661.2610	331.1341	660.2770	330.6421	5
10	**1335.7540**	668.3806	1318.7274	659.8673	1317.7434	659.3753	D	***563.2606***	282.1339	546.2341	273.6207	545.2500	273.1287	4
11	1495.7846	748.3959	1478.7581	739.8827	1477.7740	739.3907	C	***448.2337***	224.6205	431.2071	216.1072			3
12	**1608.8687**	804.9380	1591.8421	796.4247	1590.8581	795.9327	L	***288.2030***	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KVAKEGGPKVTSR**
Found in **Q15397**, Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3

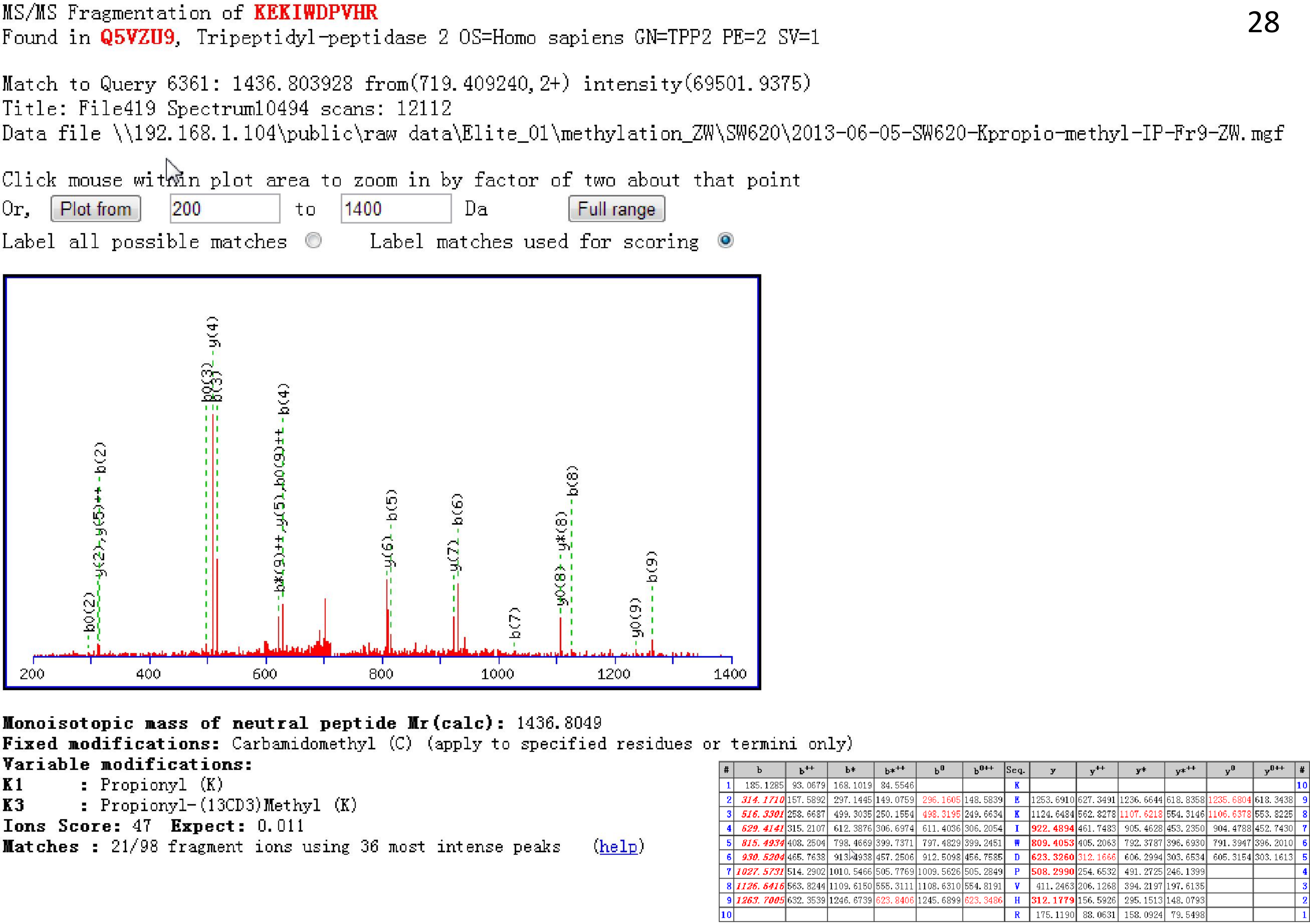
Match to Query 8103: 1541.904628 from(771.959590,2+) intensity(8409.0791)
Title: File660 Spectrum5207 scans: 6344
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1541.9050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K4 : Propionyl (K)
K9 : Propionyl (K)
Ions Score: 47 **Expect:** 0.0068
Matches : 14/134 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							13
2	302.2[illegible]47	151.6210	285.2082	143.1077			V	1340.7532	670.8803	1323.7267	662.3670	1322.7427	661.8750	12
3	373.2718	187.1395	356.2453	178.6263			A	***1241.6848***	621.3461	1224.6583	612.8328	1223.6743	612.3408	11
4	557.3930	279.2001	540.3664	270.6869			K	***1170.6477***	585.8275	1153.6212	577.3142	1152.6371	576.8222	10
5	**686.4356**	343.7214	669.4090	335.2082	668.4250	334.7161	E	***986.5265***	493.7669	969.5000	485.2536	968.5160	484.7616	9
6	743.4571	372.2322	726.4305	363.7189	725.4465	363.2269	G	***857.4839***	429.2456	840.4574	420.7323	839.4734	420.2403	8
7	800.4785	400.7429	783.4520	392.2296	782.4680	391.7376	G	800.4625	400.7349	783.4359	392.2216	782.4519	391.7296	7
8	897.5313	449.2693	880.5047	440.7560	879.5207	440.2640	P	743.4410	372.2241	726.4145	363.7109	725.4305	363.2189	6
9	**1081.6525**	541.3299	1064.6259	532.8166	1063.6419	532.3246	K	646.3883	323.6978	629.3617	315.1845	628.3777	314.6925	5
10	1180.7209	590.8641	1163.6943	582.3508	1162.7103	581.8588	V	***462.2671***	231.6372	445.2405	223.1239	444.2565	222.6319	4
11	1281.7686	641.3879	1264.7420	632.8746	1263.7580	632.3826	T	***363.1987***	182.1030	346.1721	173.5897	345.1881	173.0977	3
12	1368.8006	684.9039	1351.7740	676.3907	1350.7900	675.8986	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KEKIWDPVHR**
Found in **Q5VZU9**, Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=2 SV=1

Match to Query 6361: 1436.803928 from(719.409240,2+) intensity(69501.9375)
Title: File419 Spectrum10494 scans: 12112
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-06-05-SW620-Kpropio-methyl-IP-Fr9-ZW.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 ●

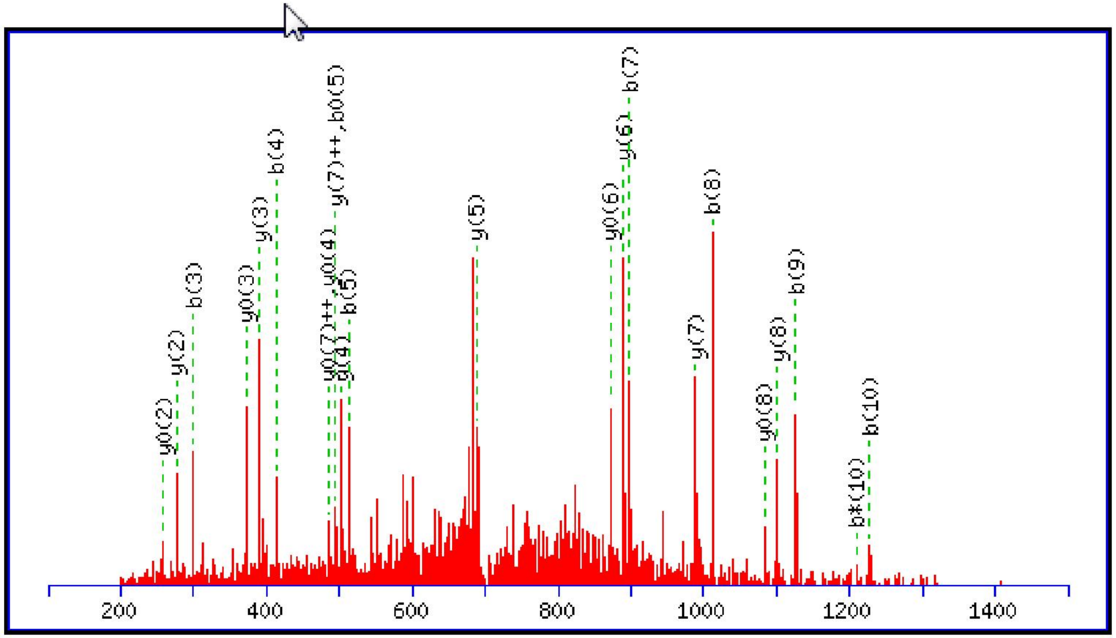
Monoisotopic mass of neutral peptide Mr(calc): 1436.8049
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 47 **Expect:** 0.011
Matches : 21/98 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							10
2	***314.1710***	157.5892	297.1445	149.0759	296.1605	148.5839	E	1253.6910	627.3491	1236.6644	618.8358	1235.6804	618.3438	9
3	***516.3301***	258.6687	499.3035	250.1554	498.3195	249.6634	K	1124.6484	562.8278	1107.6218	554.3146	1106.6378	553.8225	8
4	***629.4141***	315.2107	612.3876	306.6974	611.4036	306.2054	I	**922.4894**	461.7483	905.4628	453.2350	904.4788	452.7430	7
5	***815.4934***	408.2504	798.4669	399.7371	797.4829	399.2451	W	**809.4053**	405.2063	792.3787	396.6930	791.3947	396.2010	6
6	***930.5204***	465.7638	913.4938	457.2506	912.5098	456.7585	D	**623.3260**	312.1666	606.2994	303.6534	605.3154	303.1613	5
7	***1027.5731***	514.2902	1010.5466	505.7769	1009.5626	505.2849	P	**508.2990**	254.6532	491.2725	246.1399			4
8	***1126.6416***	563.8244	1109.6150	555.3111	1108.6310	554.8191	V	411.2463	206.1268	394.2197	197.6135			3
9	***1263.7005***	632.3539	1246.6739	623.8406	1245.6899	623.3486	H	**312.1779**	156.5926	295.1513	148.0793			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SLVIVKKLNTR**
Found in **Q8N655**, Uncharacterized protein C10orf12 OS=Homo sapiens GN=C10orf12 PE=1 SV=1

Match to Query 6095: 1399.904768 from(700.959660,2+) intensity(79978.1953)
Title: File388 Spectrum15903 scans: 17797
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.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 ●



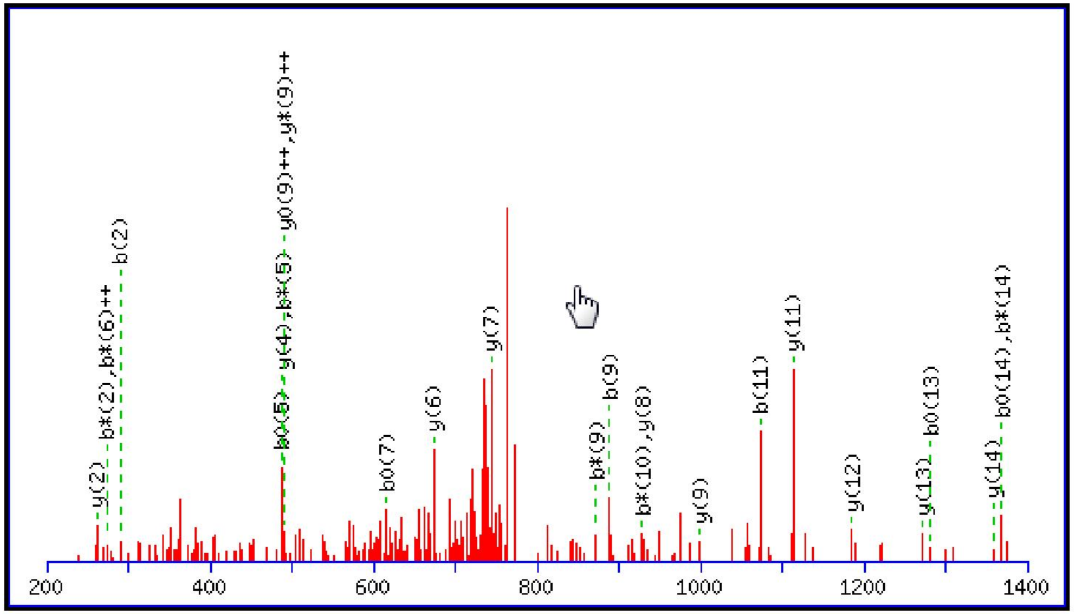
Monoisotopic mass of neutral peptide Mr(calc): 1399.9035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K6 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 46 **Expect:** 0.0015
Matches : 23/108 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	201.1234	101.0653			183.1128	92.0600	L	1313.8788	657.4430	1296.8522	648.9297	1295.8682	648.4377	10
3	**300.1918**	150.5995			282.1812	141.5942	V	1200.7947	600.9010	1183.7682	592.3877	1182.7841	591.8957	9
4	**413.2758**	207.1416			395.2653	198.1363	I	**1101.7263**	551.3668	1084.6997	542.8535	1083.7157	542.3615	8
5	**512.3443**	256.6758			494.3337	247.6705	V	**988.6422**	494.8248	971.6157	486.3115	970.6317	485.8195	7
6	714.5033	357.7553	697.4767	349.2420	696.4927	348.7500	K	**889.5738**	445.2905	872.5473	436.7773	871.5632	436.2853	6
7	**898.6245**	449.8159	881.5979	441.3026	880.6139	440.8106	K	**687.4148**	344.2110	670.3883	335.6978	669.4042	335.2058	5
8	**1011.7085**	506.3579	994.6820	497.8446	993.6979	497.3526	L	**503.2936**	252.1504	486.2671	243.6372	485.2831	243.1452	4
9	**1125.7514**	563.3794	1108.7249	554.8661	1107.7409	554.3741	N	**390.2096**	195.6084	373.1830	187.0951	372.1990	186.6031	3
10	**1226.7991**	613.9032	1209.7726	605.3899	1208.7886	604.8979	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KSSAGGAKAGQPESR**
Found in **P17098**, Zinc finger protein 8 OS=Homo sapiens GN=ZNF8 PE=1 SV=2

Match to Query 8060: 1559.821988 from(780.918270,2+) intensity(6126.0859)
Title: File440 Spectrum3286 scans: 4144
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.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 ●



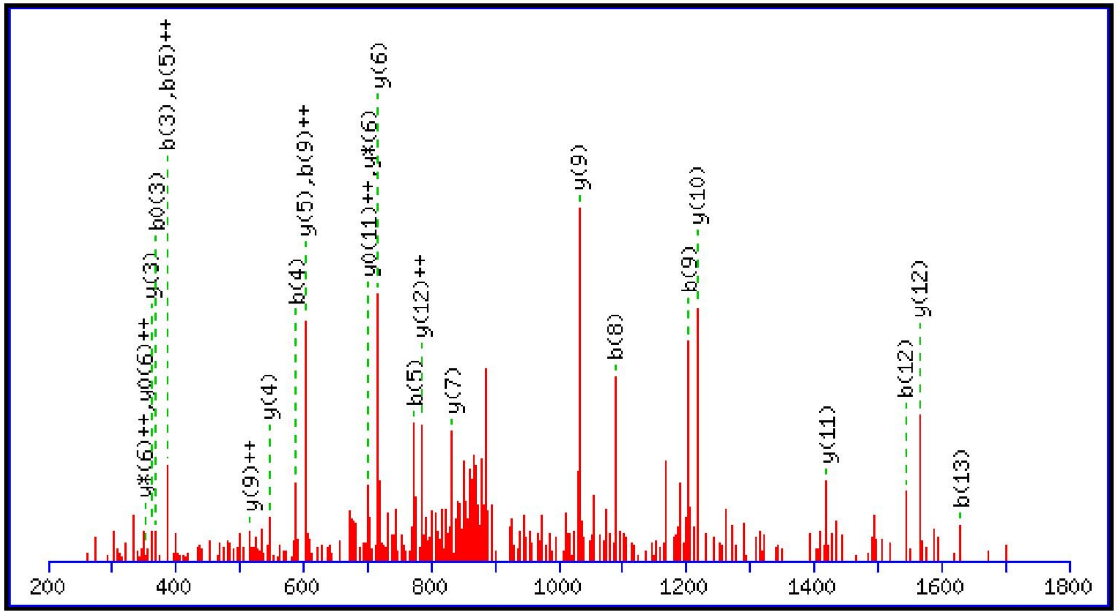
Monoisotopic mass of neutral peptide Mr(calc): 1559.8176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or te
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 45 **Expect:** 0.014
Matches : 25/164 fragment ions using 60 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	203.1663	102.0868	186.1397	93.5735			K							15
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	S	***1358.6659***	679.8366	1341.6393	671.3233	1340.6553	670.8313	14
3	377.2303	189.1188	360.2038	180.6055	359.2198	180.1135	S	***1271.6339***	636.3206	1254.6073	627.8073	1253.6233	627.3153	13
4	448.2675	224.6374	431.2409	216.1241	430.2569	215.6321	A	***1184.6018***	592.8046	1167.5753	584.2913	1166.5913	583.7993	12
5	505.2889	253.1481	488.2624	244.6348	487.2784	244.1428	G	***1113.5647***	557.2860	1096.5382	548.7727	1095.5541	548.2807	11
6	562.3104	281.6588	545.2838	273.1456	544.2998	272.6535	G	1056.5432	528.7753	1039.5167	520.2620	1038.5327	519.7700	10
7	633.3475	317.1774	616.3210	308.6641	615.3369	308.1721	A	***999.5218***	500.2645	982.4952	491.7513	981.5112	491.2592	9
8	817.4687	409.2380	800.4421	400.7247	799.4581	400.2327	K	***928.4847***	464.7460	911.4581	456.2327	910.4741	455.7407	8
9	**888.5058**	444.7565	871.4792	436.2433	870.4952	435.7513	A	***744.3635***	372.6854	727.3369	364.1721	726.3529	363.6801	7
10	945.5273	473.2673	928.5007	464.7540	927.5167	464.2620	G	***673.3264***	337.1668	656.2998	328.6536	655.3158	328.1615	6
11	**1073.5858**	537.2966	1056.5593	528.7833	1055.5753	528.2913	Q	616.3049	308.6561	599.2784	300.1428	598.2944	299.6508	5
12	1170.6386	585.8229	1153.6121	577.3097	1152.6280	576.8177	P	***488.2463***	244.6268	471.2198	236.1135	470.2358	235.6215	4
13	1299.6812	650.3442	1282.6546	641.8310	1281.6706	641.3390	E	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
14	1386.7132	693.8602	1369.6867	685.3470	1368.7027	684.8550	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
15							R	175.1190	88.0631	158.0924	79.5498			1

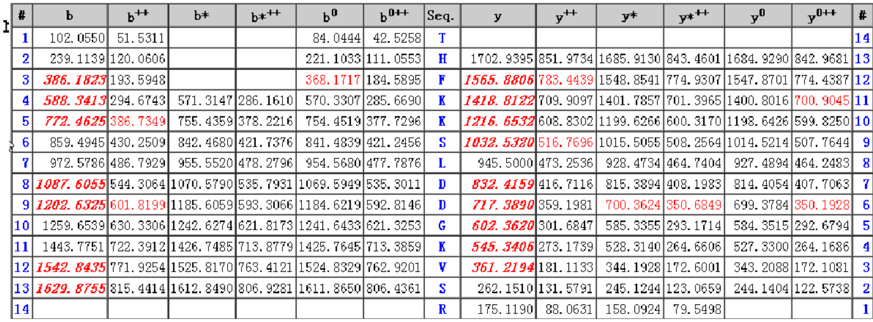
MS/MS Fragmentation of **THFKKSLDDGKVSR**
Found in **F5H0L8**, SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=2 SV=1

Match to Query 12640: 1802.979348 from(902.496950,2+) intensity(32097.1836)
Title: File394 Spectrum10127 scans: 11437
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1802.9799
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
K11 : Propionyl (K)
Ions Score: 45 **Expect:** 0.017
Matches : 25/148 fragment ions using 44 most intense peaks (help)

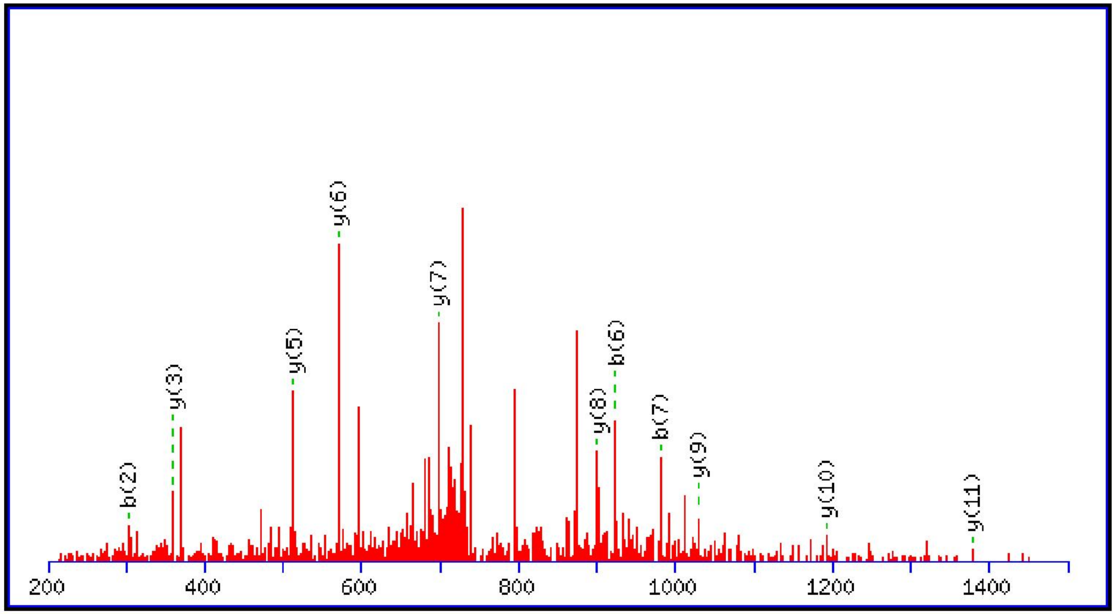


#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	239.1139	120.0606			221.1033	111.0553	H	1702.9395	851.9734	1685.9130	843.4601	1684.9290	842.9681	13
3	***386.1823***	193.5948			368.1717	184.5895	F	***1565.8806***	783.4439	1548.8541	774.9307	1547.8701	774.4387	12
4	***588.3413***	294.6743	571.3147	286.1610	570.3307	285.6690	K	***1418.8122***	709.9097	1401.7857	701.3965	1400.8016	700.9045	11
5	***772.4625***	386.7349	755.4359	378.2216	754.4519	377.7296	K	***1216.6532***	608.8302	1199.6266	600.3170	1198.6426	599.8250	10
6	859.4945	430.2509	842.4680	421.7376	841.4839	421.2456	S	***1032.5320***	516.7696	1015.5055	508.2564	1014.5214	507.7644	9
7	972.5786	486.7929	955.5520	478.2796	954.5680	477.7876	L	945.5000	473.2536	928.4734	464.7404	927.4894	464.2483	8
8	***1087.6055***	544.3064	1070.5790	535.7931	1069.5949	535.3011	D	***832.4159***	416.7116	815.3894	408.1983	814.4054	407.7063	7
9	***1202.6325***	601.8199	1185.6059	593.3066	1184.6219	592.8146	D	***717.3890***	359.1981	700.3624	350.6849	699.3784	350.1928	6
10	1259.6539	630.3306	1242.6274	621.8173	1241.6433	621.3253	G	***602.3620***	301.6847	585.3355	293.1714	584.3515	292.6794	5
11	1443.7751	722.3912	1426.7485	713.8779	1425.7645	713.3859	K	***545.3406***	273.1739	528.3140	264.6606	527.3300	264.1686	4
12	***1542.8435***	771.9254	1525.8170	763.4121	1524.8329	762.9201	V	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	3
13	***1629.8755***	815.4414	1612.8490	806.9281	1611.8650	806.4361	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1

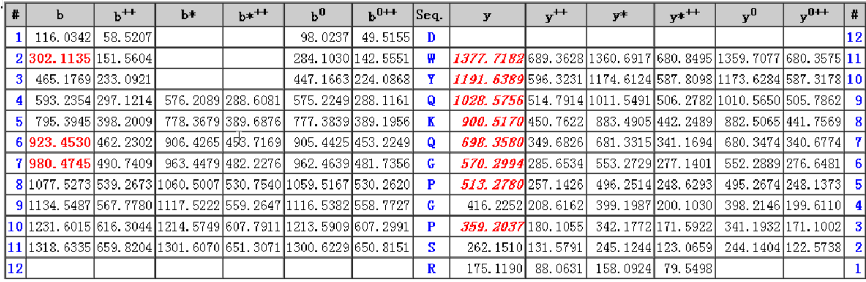
MS/MS Fragmentation of **DWYQKQGPGPSR**
Found in **P08727**, Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4

Match to Query 8577: 1491.736548 from(746.875550,2+) intensity(30655.0273)
Title: File392 Spectrum10177 scans: 11453
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

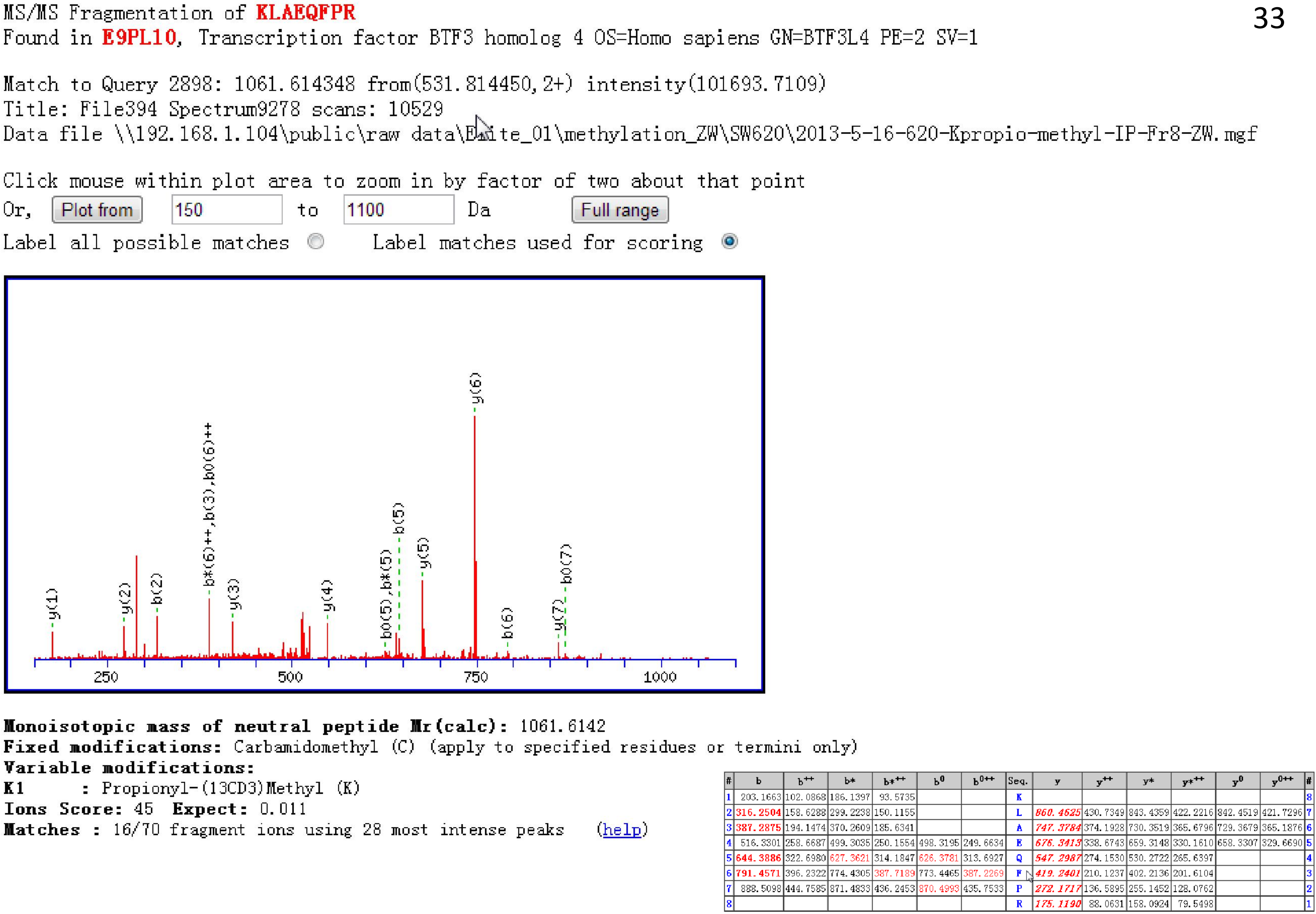
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1491.7379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.0096
Matches : 11/124 fragment ions using 26 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	302.1135	151.5604			284.1030	142.5551	W	1377.7182	689.3628	1360.6917	680.8495	1359.7077	680.3575	11
3	465.1769	233.0921			447.1663	224.0868	Y	1191.6389	596.3231	1174.6124	587.8098	1173.6284	587.3178	10
4	593.2354	297.1214	576.2089	288.6081	575.2249	288.1161	Q	1028.5756	514.7914	1011.5491	506.2782	1010.5650	505.7862	9
5	795.3945	398.2009	778.3679	389.6876	777.3839	389.1956	K	900.5170	450.7622	883.4905	442.2489	882.5065	441.7569	8
6	923.4530	462.2302	906.4265	453.7169	905.4425	453.2249	Q	698.3580	349.6826	681.3315	341.1694	680.3474	340.6774	7
7	980.4745	490.7409	963.4479	482.2276	962.4639	481.7356	G	570.2994	285.6534	553.2729	277.1401	552.2889	276.6481	6
8	1077.5273	539.2673	1060.5007	530.7540	1059.5167	530.2620	P	513.2780	257.1426	496.2514	248.6293	495.2674	248.1373	5
9	1134.5487	567.7780	1117.5222	559.2647	1116.5382	558.7727	G	416.2252	208.6162	399.1987	200.1030	398.2146	199.6110	4
10	1231.6015	616.3044	1214.5749	607.7911	1213.5909	607.2991	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
11	1318.6335	659.8204	1301.6070	651.3071	1300.6229	650.8151	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



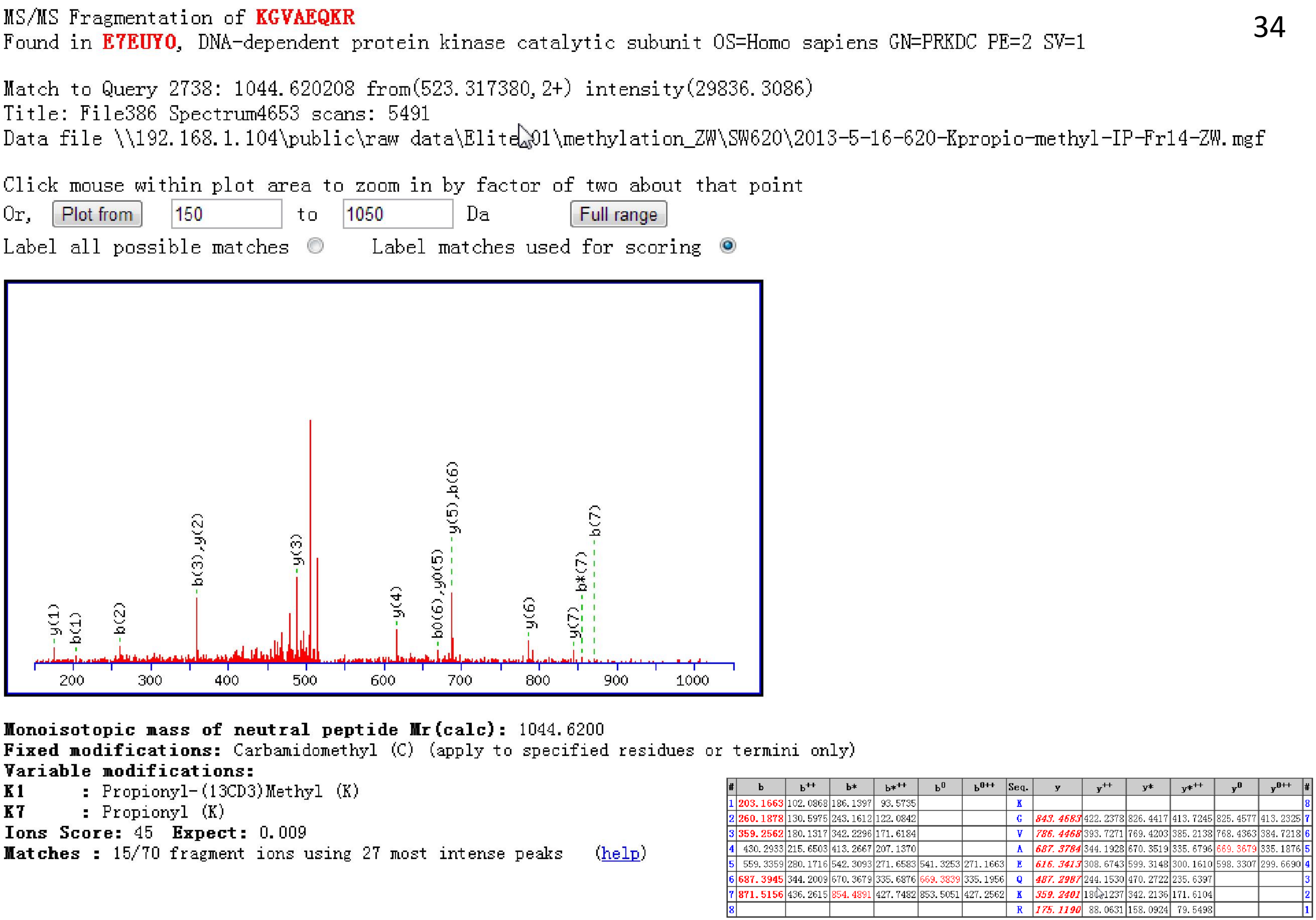
MS/MS Fragmentation of **KLAEQFPR**
Found in **E9PL10**, Transcription factor BTF3 homolog 4 OS=Homo sapiens GN=BTF3L4 PE=2 SV=1

Match to Query 2898: 1061.614348 from(531.814450,2+) intensity(101693.7109)
Title: File394 Spectrum9278 scans: 10529
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1061.6142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.011
Matches : 16/70 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	**316.2504**	158.6288	299.2238	150.1155			L	***860.4625***	430.7349	843.4359	422.2216	842.4519	421.7296	7
3	**387.2875**	194.1474	370.2609	185.6341			A	***747.3784***	374.1928	730.3519	365.6796	729.3679	365.1876	6
4	516.3301	258.6687	499.3035	250.1554	498.3195	249.6634	E	***676.3413***	338.6743	659.3148	330.1610	658.3307	329.6690	5
5	**644.3886**	322.6980	627.3621	314.1847	626.3781	313.6927	Q	***547.2987***	274.1530	530.2722	265.6397			4
6	**791.4571**	396.2322	774.4305	387.7189	773.4465	387.2269	F	***419.2401***	210.1237	402.2136	201.6104			3
7	888.5098	444.7585	871.4833	436.2453	870.4993	435.7533	P	***272.1717***	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KGVAEQKR**
Found in **E7EUY0**, DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=2 SV=1

Match to Query 2738: 1044.620208 from(523.317380,2+) intensity(29836.3086)
Title: File386 Spectrum4653 scans: 5491
Data file \\192.168.1.104\public\raw data\Elite[illegible]01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

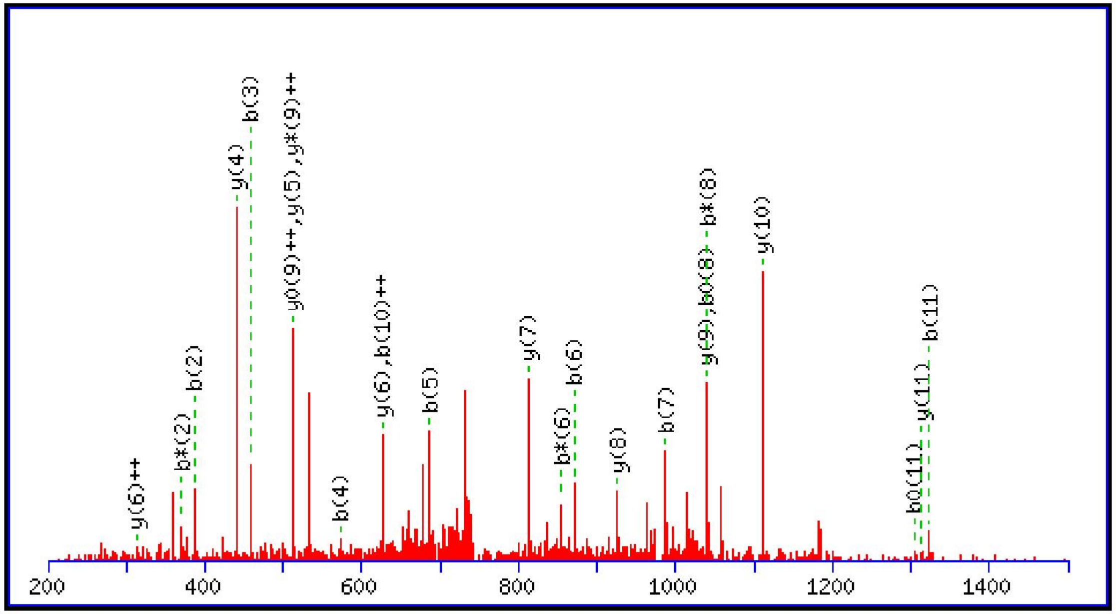
Monoisotopic mass of neutral peptide Mr(calc): 1044.6200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 45 **Expect:** 0.009
Matches : 15/70 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**203.1663**	102.0868	186.1397	93.5735			K							8
2	**260.1878**	130.5975	243.1612	122.0842			G	***843.4683***	422.2378	826.4417	413.7245	825.4577	413.2325	7
3	**359.2562**	180.1317	342.2296	171.6184			V	***786.4468***	393.7271	769.4203	385.2138	768.4363	384.7218	6
4	430.2933	215.6503	413.2667	207.1370			A	***687.3784***	344.1928	670.3519	335.6796	669.3679	335.1876	5
5	559.3359	280.1716	542.3093	271.6583	541.3253	271.1663	E	***616.3413***	308.6743	599.3148	300.1610	598.3307	299.6690	4
6	**687.3945**	344.2009	670.3679	335.6876	669.3839	335.1956	Q	***487.2987***	244.1530	470.2722	235.6397			3
7	**871.5156**	436.2615	854.4891	427.7482	853.5051	427.2562	K	***359.2401***	180.1237	342.2136	171.6104			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

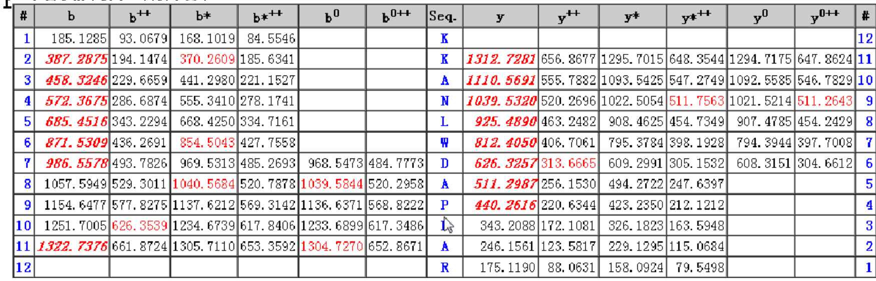
MS/MS Fragmentation of **KKANLWDAPPAR**
Found in **Q13470**, Non-receptor tyrosine-protein kinase TNK1 OS=Homo sapiens GN=TNK1 PE=1 SV=3

Match to Query 7464: 1495.840428 from(748.927490,2+) intensity(77194.1563)
Title: File388 Spectrum12472 scans: 14095
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

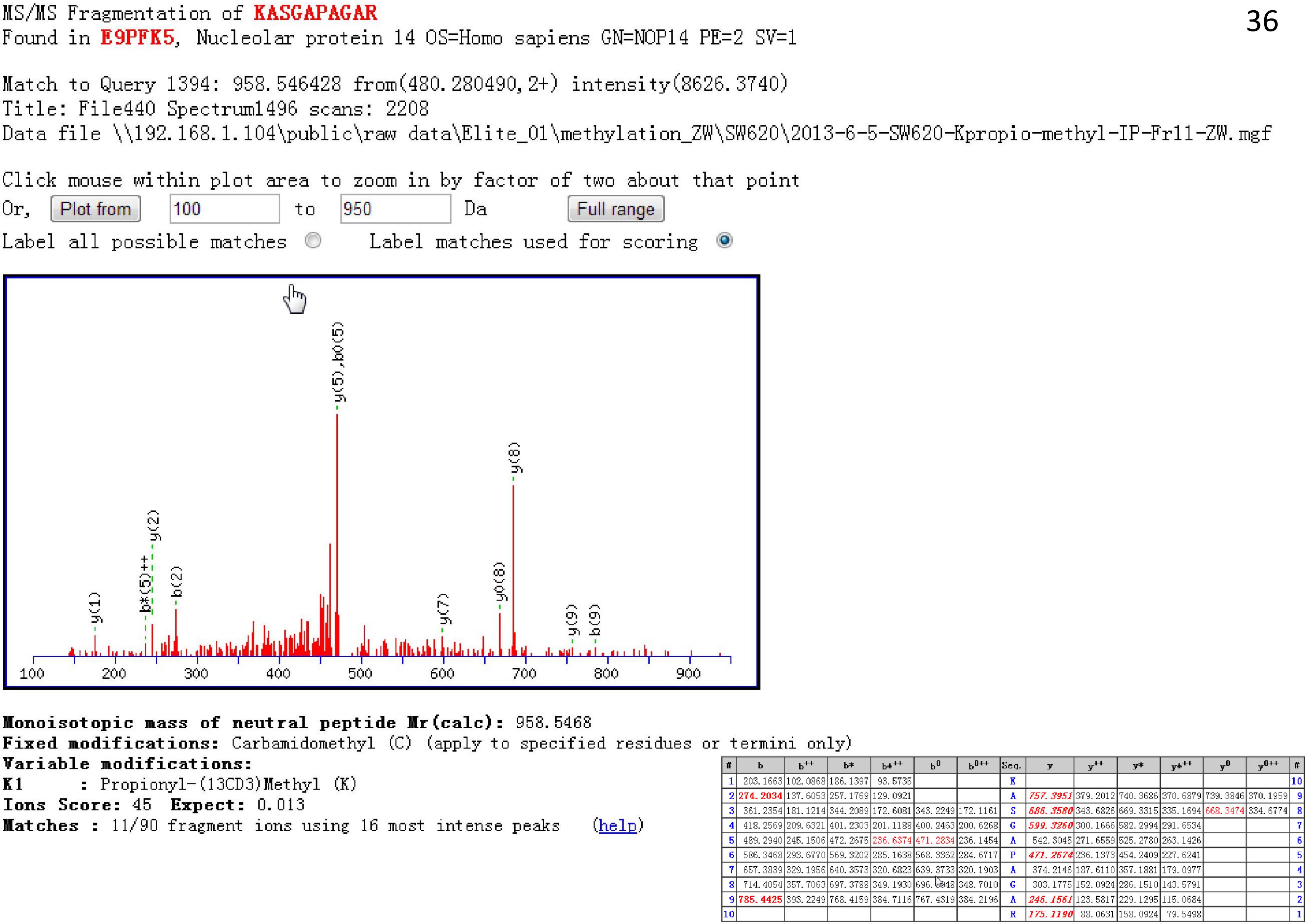
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1495.8419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.015
Matches : 24/110 fragment ions using 39 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							12
2	**387.2875**	194.1474	370.2609	185.6341			K	**1312.7281**	656.8677	1295.7015	648.3544	1294.7175	647.8624	11
3	**458.3246**	229.6659	441.2980	221.1527			A	**1110.5691**	555.7882	1093.5425	547.2749	1092.5585	546.7829	10
4	**572.3675**	286.6874	555.3410	278.1741			N	**1039.5320**	520.2696	1022.5054	511.7563	1021.5214	511.2643	9
5	**685.4516**	343.2294	668.4250	334.7161			L	**925.4890**	463.2482	908.4625	454.7349	907.4785	454.2429	8
6	**871.5309**	436.2691	854.5043	427.7558			W	**812.4050**	406.7061	795.3784	398.1928	794.3944	397.7008	7
7	**986.5578**	493.7826	969.5313	485.2693	968.5473	484.7773	D	**626.3257**	313.6665	609.2991	305.1532	608.3151	304.6612	6
8	1057.5949	529.3011	1040.5684	520.7878	1039.5844	520.2958	A	**511.2987**	256.1530	494.2722	247.6397			5
9	1154.6477	577.8275	1137.6212	569.3142	1136.6371	568.8222	P	**440.2616**	220.6344	423.2350	212.1212			4
10	1251.7005	626.3539	1234.6739	617.8406	1233.6899	617.3486	P	343.2088	172.1081	326.1823	163.5948			3
11	**1322.7376**	661.8724	1305.7110	653.3592	1304.7270	652.8671	A	246.1561	123.5817	229.1295	115.0684			2
12							R	175.1190	88.0631	158.0924	79.5498			1



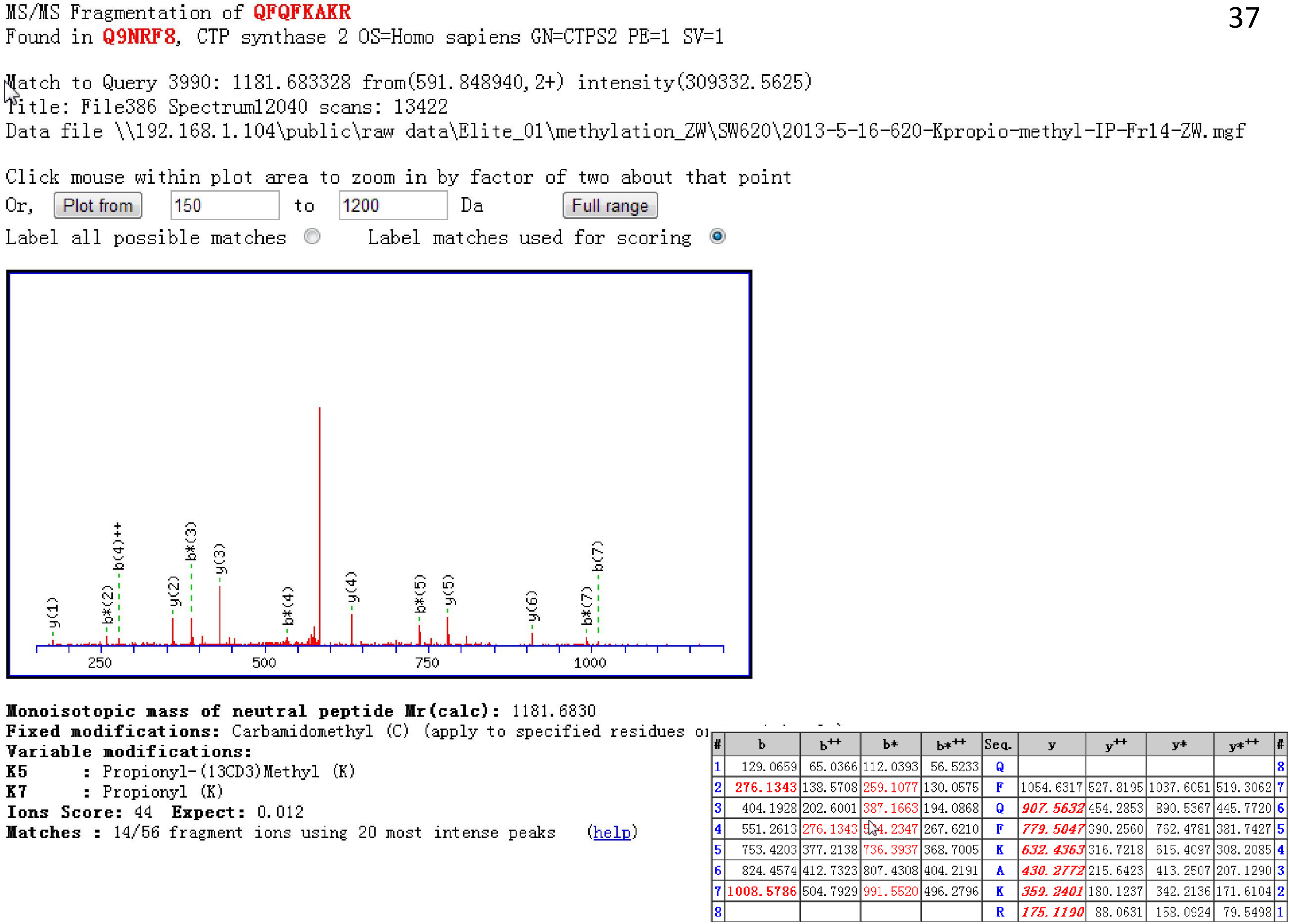
MS/MS Fragmentation of **KASGAPAGAR**
Found in **E9PFK5**, Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=2 SV=1

Match to Query 1394: 958.546428 from(480.280490,2+) intensity(8626.3740)
Title: File440 Spectrum1496 scans: 2208
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 958.5468
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.013
Matches : 11/90 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							10
2	**274.2034**	137.6053	257.1769	129.0921			A	***757.3951***	379.2012	740.3686	370.6879	739.3846	370.1959	9
3	361.2354	181.1214	344.2089	172.6081	343.2249	172.1161	S	***686.3580***	343.6826	669.3315	335.1694	668.3474	334.6774	8
4	418.2569	209.6321	401.2303	201.1188	400.2463	200.6268	G	***599.3260***	300.1666	582.2994	291.6534			7
5	489.2940	245.1506	472.2675	236.6374	471.2834	236.1454	A	542.3045	271.6559	525.2780	263.1426			6
6	586.3468	293.6770	569.3202	285.1638	568.3362	284.6717	P	***471.2674***	236.1373	454.2409	227.6241			5
7	657.3839	329.1956	640.3573	320.6823	639.3733	320.1903	A	374.2146	187.6110	357.1881	179.0977			4
8	714.4054	357.7063	697.3788	349.1930	696.[illegible]948	348.7010	G	303.1775	152.0924	286.1510	143.5791			3
9	**785.4425**	393.2249	768.4159	384.7116	767.4319	384.2196	A	***246.1561***	123.5817	229.1295	115.0684			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1



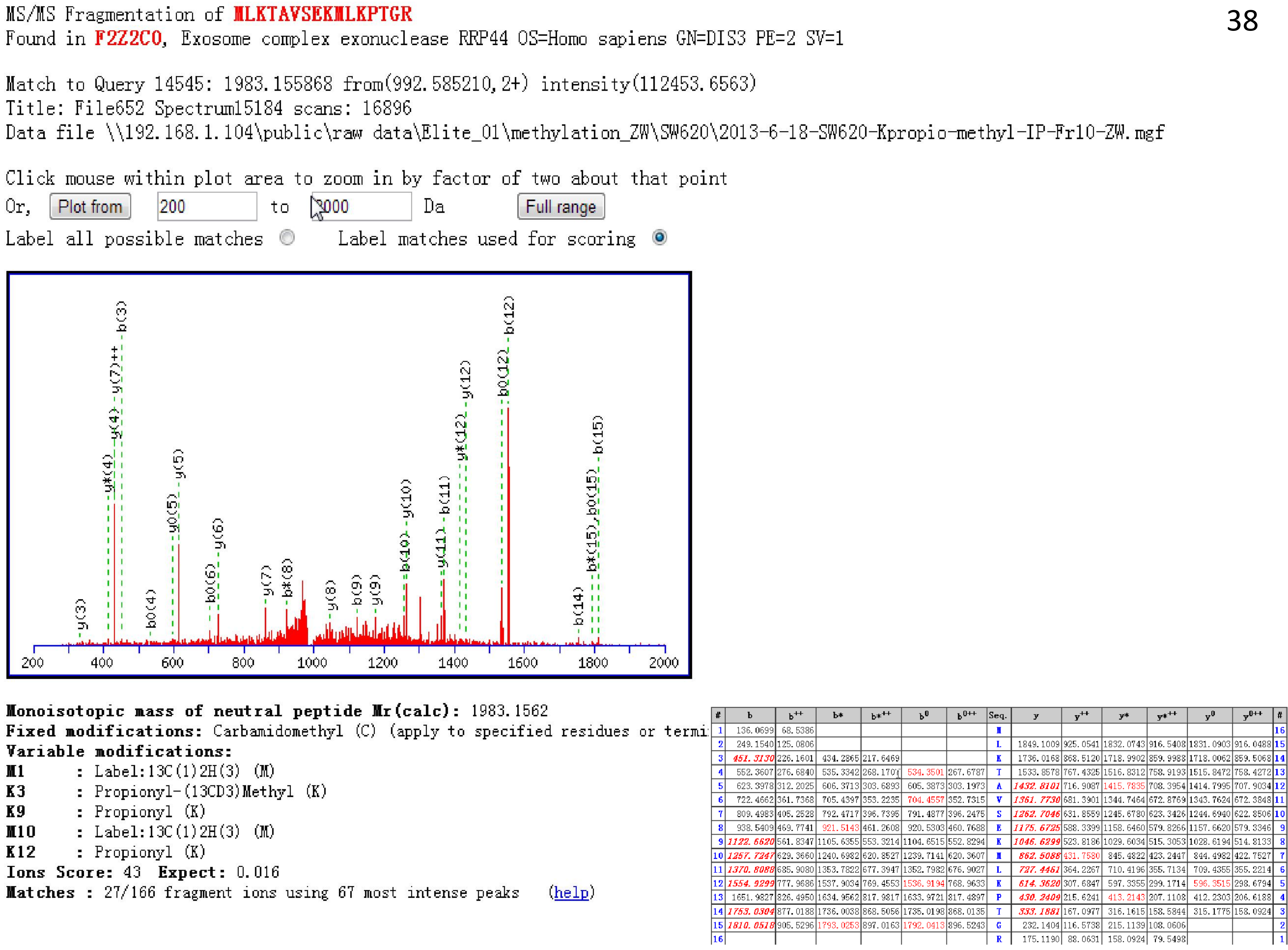
MS/MS Fragmentation of **QFQFKAKR**
Found in **Q9NRF8**, CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1

Match to Query 3990: 1181.683328 from(591.848940,2+) intensity(309332.5625)
Title: File386 Spectrum12040 scans: 13422
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1181.6830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 44 **Expect:** 0.012
Matches : 14/56 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	129.0659	65.0366	112.0393	56.5233	Q					8
2	**276.1343**	138.5708	259.1077	130.0575	F	1054.6317	527.8195	1037.6051	519.3062	7
3	404.1928	202.6001	387.1663	194.0868	Q	***907.5632***	454.2853	890.5367	445.7720	6
4	551.2613	276.1343	5[illegible]4.2347	267.6210	F	***779.5047***	390.2560	762.4781	381.7427	5
5	753.4203	377.2138	736.3937	368.7005	K	***632.4363***	316.7218	615.4097	308.2085	4
6	824.4574	412.7323	807.4308	404.2191	A	***430.2772***	215.6423	413.2507	207.1290	3
7	**1008.5786**	504.7929	991.5520	496.2796	K	***359.2401***	180.1237	342.2136	171.6104	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1



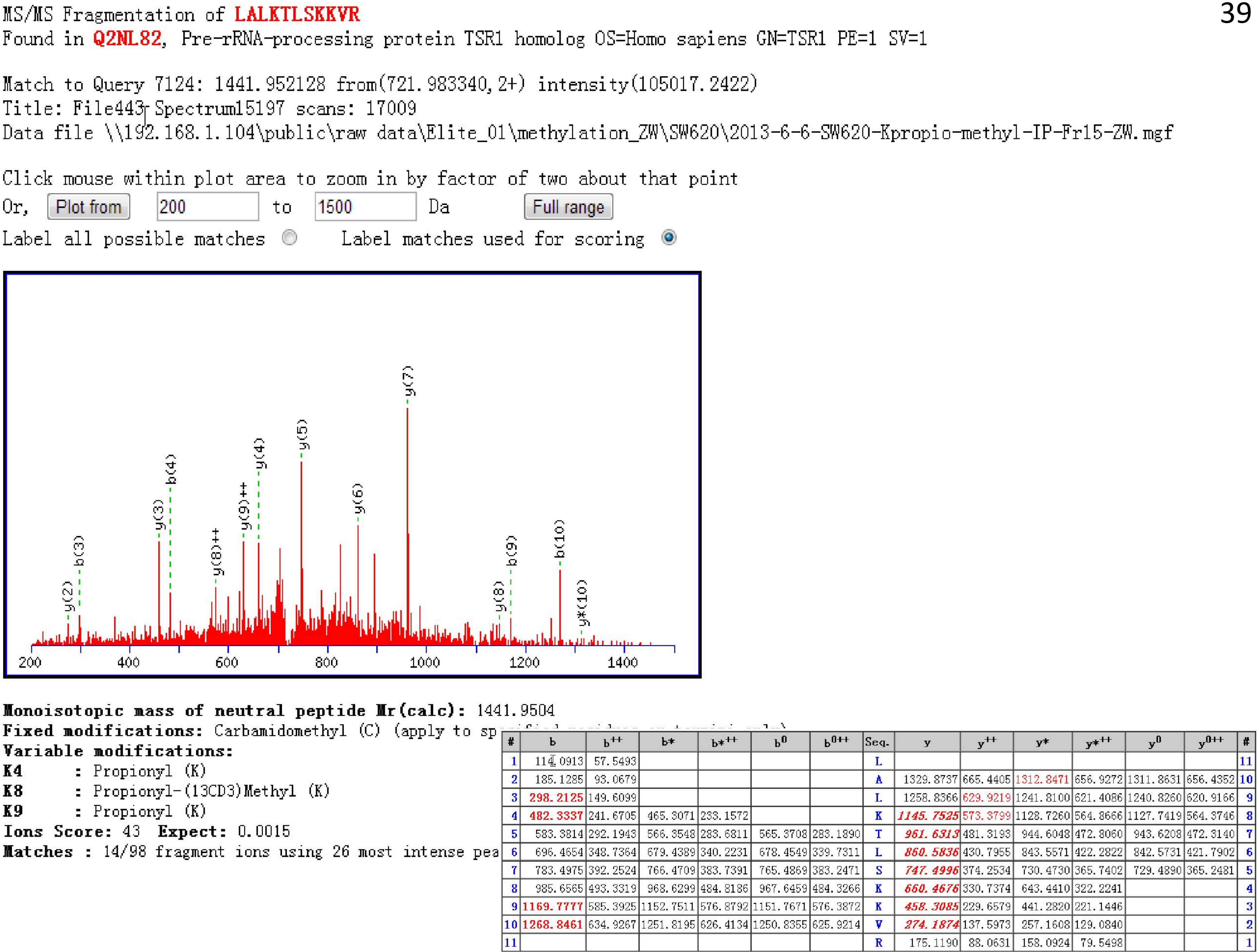
MS/MS Fragmentation of **MLKTAVSEKMLKPTGR**
Found in **F2Z2C0**, Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=2 SV=1

Match to Query 14545: 1983.155868 from(992.585210,2+) intensity(112453.6563)
Title: File652 Spectrum15184 scans: 16896
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr10-ZW.mgf

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

Monoisotopic mass of neutral peptide Mr(calc): 1983.1562
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termi
Variable modifications:
M1 : Label:13C(1)2H(3) (M)
K3 : Propionyl-(13CD3)Methyl (K)
K9 : Propionyl (K)
M10 : Label:13C(1)2H(3) (M)
K12 : Propionyl (K)
Ions Score: 43 **Expect:** 0.016
Matches : 27/166 fragment ions using 67 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	136.0699	68.5386					M							16
2	249.1540	125.0806					L	1849.1009	925.0541	1832.0743	916.5408	1831.0903	916.0488	15
3	***451.3130***	226.1601	434.2865	217.6469			K	1736.0168	868.5120	1718.9902	859.9988	1718.0062	859.5068	14
4	552.3607	276.6840	535.3342	268.1707	534.3501	267.6787	T	1533.8578	767.4325	1516.8312	758.9193	1515.8472	758.4272	13
5	623.3978	312.2025	606.3713	303.6893	605.3873	303.1973	A	***1432.8101***	716.9087	1415.7835	708.3954	1414.7995	707.9034	12
6	722.4662	361.7368	705.4397	353.2235	704.4557	352.7315	V	***1361.7730***	681.3901	1344.7464	672.8769	1343.7624	672.3848	11
7	809.4983	405.2528	792.4717	396.7395	791.4877	396.2475	S	***1262.7046***	631.8559	1245.6780	623.3426	1244.6940	622.8506	10
8	938.5409	469.7741	921.5143	461.2608	920.5303	460.7688	E	***1175.6725***	588.3399	1158.6460	579.8266	1157.6620	579.3346	9
9	***1122.6620***	561.8347	1105.6355	553.3214	1104.6515	552.8294	K	***1046.6299***	523.8186	1029.6034	515.3053	1028.6194	514.8133	8
10	***1257.7247***	629.3660	1240.6982	620.8527	1239.7141	620.3607	M	***862.5088***	431.7580	845.4822	423.2447	844.4982	422.7527	7
11	***1370.8088***	685.9080	1353.7822	677.3947	1352.7982	676.9027	L	***727.4461***	364.2267	710.4196	355.7134	709.4355	355.2214	6
12	***1554.9299***	777.9686	1537.9034	769.4553	1536.9194	768.9633	K	***614.3620***	307.6847	597.3355	299.1714	596.3515	298.6794	5
13	1651.9827	826.4950	1634.9562	817.9817	1633.9721	817.4897	P	***430.2409***	215.6241	413.2143	207.1108	412.2303	206.6188	4
14	***1753.0304***	877.0188	1736.0038	868.5056	1735.0198	868.0135	T	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
15	***1810.0518***	905.5296	1793.0253	897.0163	1792.0413	896.5243	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1



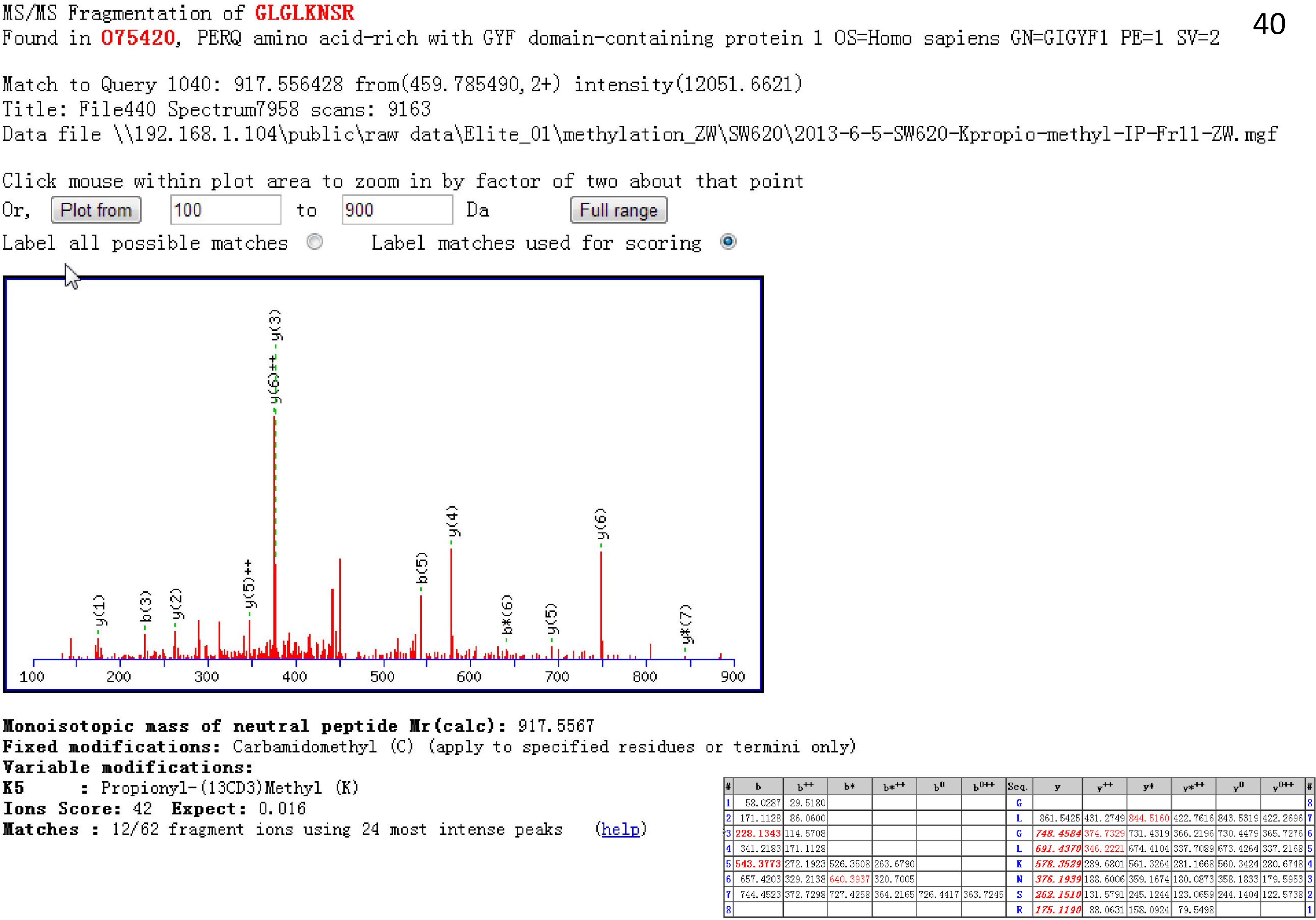
MS/MS Fragmentation of **LALKTLSKKVR**
Found in **Q2NL82**, Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1

Match to Query 7124: 1441.952128 from(721.983340,2+) intensity(105017.2422)
Title: File443 Spectrum15197 scans: 17009
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-6-SW620-Kpropio-methyl-IP-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1441.9504
Fixed modifications: Carbamidomethyl (C) (apply to sp
Variable modifications:
K4 : Propionyl (K)
K8 : Propionyl-(13CD3)Methyl (K)
K9 : Propionyl (K)
Ions Score: 43 **Expect:** 0.0015
Matches : 14/98 fragment ions using 26 most intense pea

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	185.1285	93.0679					A	1329.8737	665.4405	1312.8471	656.9272	1311.8631	656.4352	10
3	**298.2125**	149.6099					L	1258.8366	629.9219	1241.8100	621.4086	1240.8260	620.9166	9
4	**482.3337**	241.6705	465.3071	233.1572			K	***1145.7525***	573.3799	1128.7260	564.8666	1127.7419	564.3746	8
5	583.3814	292.1943	566.3548	283.6811	565.3708	283.1890	T	***961.6313***	481.3193	944.6048	472.8060	943.6208	472.3140	7
6	696.4654	348.7364	679.4389	340.2231	678.4549	339.7311	L	***860.5836***	430.7955	843.5571	422.2822	842.5731	421.7902	6
7	783.4975	392.2524	766.4709	383.7391	765.4869	383.2471	S	***747.4996***	374.2534	730.4730	365.7402	729.4890	365.2481	5
8	985.6565	493.3319	968.6299	484.8186	967.6459	484.3266	K	***660.4676***	330.7374	643.4410	322.2241			4
9	**1169.7777**	585.3925	1152.7511	576.8792	1151.7671	576.3872	K	***458.3085***	229.6579	441.2820	221.1446			3
10	**1268.8461**	634.9267	1251.8195	626.4134	1250.8355	625.9214	V	***274.1874***	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GLGLKNSR**
Found in **O75420**, PERQ amino acid-rich with GYF domain-containing protein 1 OS=Homo sapiens GN=GIGYF1 PE=1 SV=2

Match to Query 1040: 917.556428 from(459.785490,2+) intensity(12051.6621)
Title: File440 Spectrum7958 scans: 9163
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

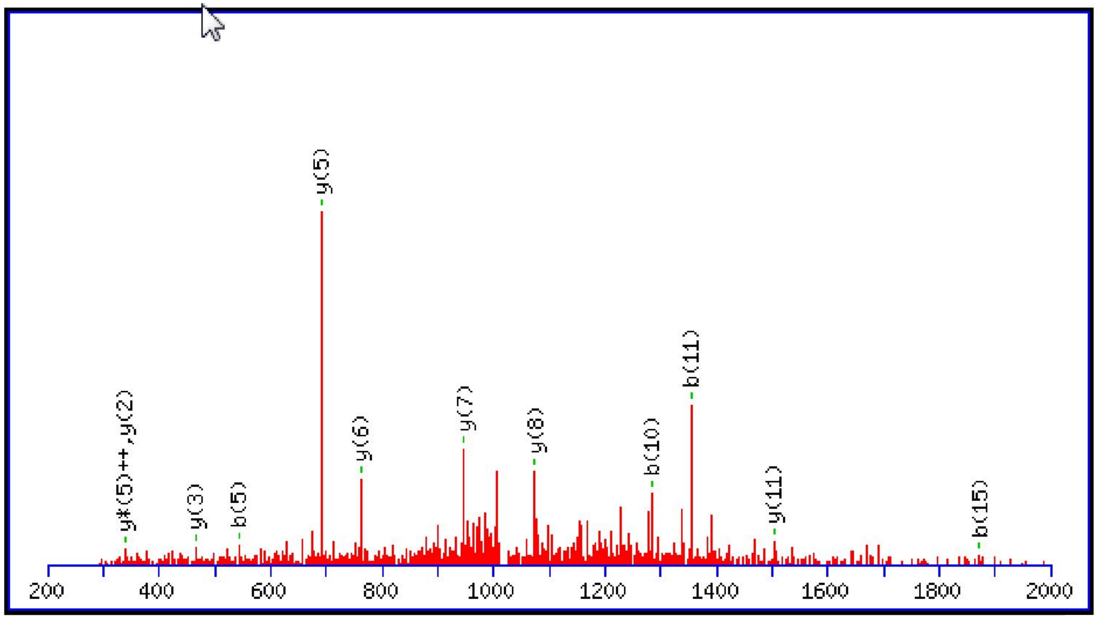
Monoisotopic mass of neutral peptide Mr(calc): 917.5567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 42 **Expect:** 0.016
Matches : 12/62 fragment ions using 24 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							8
2	171.1128	86.0600					L	861.5425	431.2749	844.5160	422.7616	843.5319	422.2696	7
3	**228.1343**	114.5708					G	***748.4584***	374.7329	731.4319	366.2196	730.4479	365.7276	6
4	341.2183	171.1128					L	***691.4370***	346.2221	674.4104	337.7089	673.4264	337.2168	5
5	**543.3773**	272.1923	526.3508	263.6790			K	***578.3529***	289.6801	561.3264	281.1668	560.3424	280.6748	4
6	657.4203	329.2138	640.3937	320.7005			N	***376.1939***	188.6006	359.1674	180.0873	358.1833	179.5953	3
7	744.4523	372.7298	727.4258	364.2165	726.4417	363.7245	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TPLCAILKQKAPQQYR**
Found in **A8MTK3**, POT1 protection of telomeres 1 homolog (S. pombe), isoform CRA_a OS=Homo sapiens GN=POT1 PE=2 SV=1

Match to Query 14754: 2044.142308 from(1023.078430,2+) intensity(112413.2500)
Title: File386 Spectrum16342 scans: 18040
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.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 ●



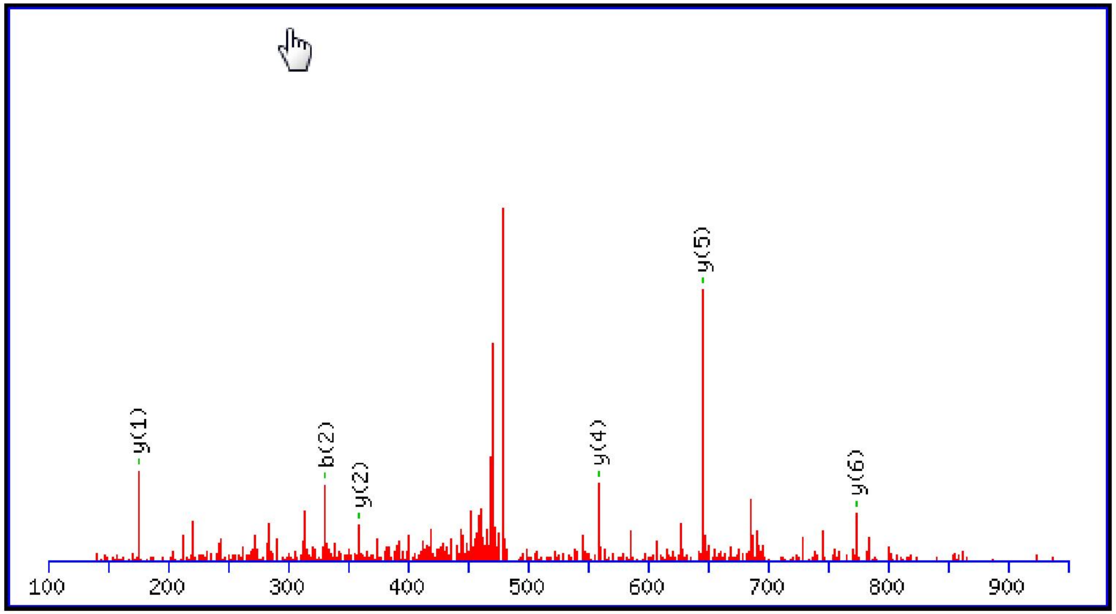
Monoisotopic mass of neutral peptide Mr(calc): 2044.1412
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or t
Variable modifications:
K8 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 41 **Expect:** 0.045
Matches : 12/136 fragment ions using 17 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	102.0550	51.5311			84.0444	42.5258	T					16
2	199.1077	100.0575			181.0972	91.0522	P	1944.1008	972.5540	1927.0743	964.0408	15
3	312.1918	156.5995			294.1812	147.5942	L	1847.0480	924.0277	1830.0215	915.5144	14
4	472.2224	236.6149			454.2119	227.6096	C	1733.9640	867.4856	1716.9374	858.9724	13
5	**543.2595**	272.1334			525.2490	263.1281	A	1573.9333	787.4703	1556.9068	778.9570	12
6	656.3436	328.6754			638.3330	319.6702	I	***1502.8962***	751.9517	1485.8697	743.4385	11
7	769.4277	385.2175			751.4171	376.2122	L	1389.8121	695.4097	1372.7856	686.8964	10
8	971.5867	486.2970	954.5601	477.7837	953.5761	477.2917	K	1276.7281	638.8677	1259.7015	630.3544	9
9	1099.6453	550.3263	1082.6187	541.8130	1081.6347	541.3210	Q	***1074.5691***	537.7882	1057.5425	529.2749	8
10	**1283.7664**	642.3869	1266.7399	633.8736	1265.7559	633.3816	K	***946.5105***	473.7589	929.4839	465.2456	7
11	**1354.8036**	677.9054	1337.7770	669.3921	1336.7930	668.9001	A	***762.3893***	381.6983	745.3628	373.1850	6
12	1451.8563	726.4318	1434.8298	717.9185	1433.8458	717.4265	P	***691.3522***	346.1797	674.3257	337.6665	5
13	1579.9149	790.4611	1562.8884	781.9478	1561.9043	781.4558	Q	594.2994	297.6534	577.2729	289.1401	4
14	1707.9735	854.4904	1690.9469	845.9771	1689.9629	845.4851	Q	***466.2409***	233.6241	449.2143	225.1108	3
15	**1871.0368**	936.0220	1854.0103	927.5088	1853.0262	927.0168	Y	***338.1823***	169.5948	321.1557	161.0815	2
16							R	175.1190	88.0631	158.0924	79.5498	1

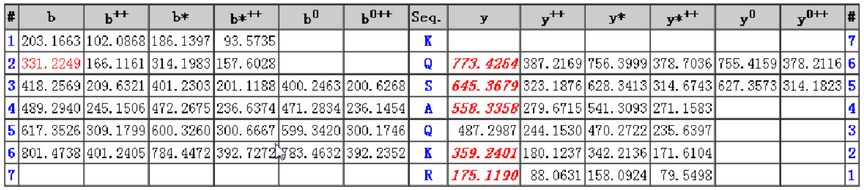
MS/MS Fragmentation of **KQSAQKR**
Found in **G3V1T4**, Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=2 SV=1

Match to Query 1550: 974.579748 from(488.297150,2+) intensity(23531.1719)
Title: File440 Spectrum1870 scans: 2624
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 974.5781
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 40 **Expect:** 0.026
Matches : 6/60 fragment ions using 8 most intense peaks (help)

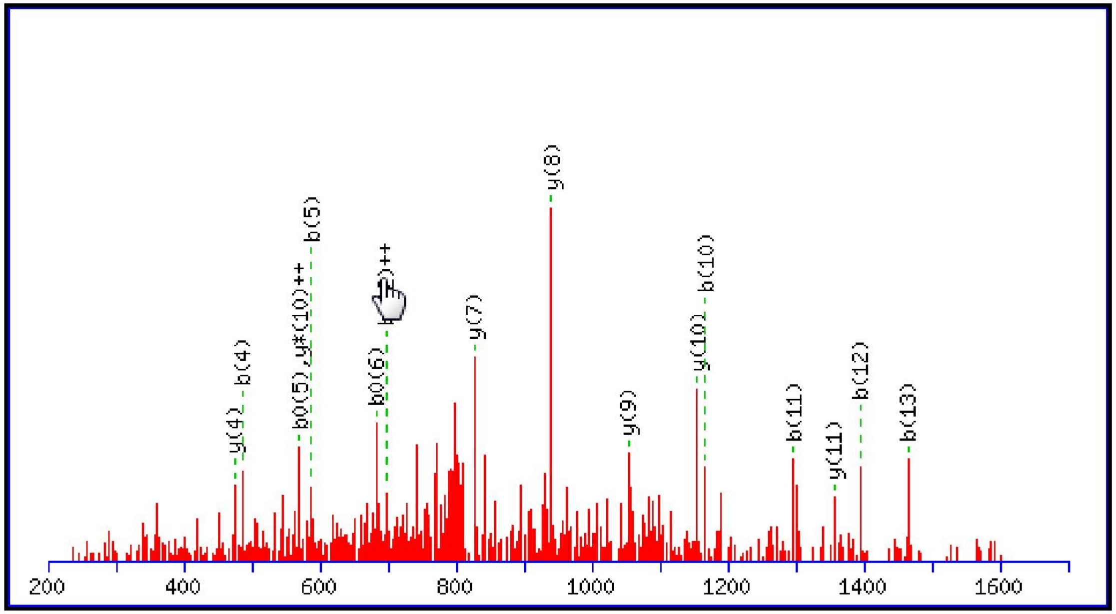


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							7
2	331.2249	166.1161	314.1983	157.6028			Q	**773.4264**	387.2169	756.3999	378.7036	755.4159	378.2116	6
3	418.2569	209.6321	401.2303	201.1188	400.2463	200.6268	S	**645.3679**	323.1876	628.3413	314.6743	627.3573	314.1823	5
4	489.2940	245.1506	472.2675	236.6374	471.2834	236.1454	A	**558.3358**	279.6715	541.3093	271.1583			4
5	617.3526	309.1799	600.3260	300.6667	599.3420	300.1746	Q	487.2987	244.1530	470.2722	235.6397			3
6	801.4738	401.2405	784.4472	392.7272	783.4632	392.2352	K	**359.2401**	180.1237	342.2136	171.6104			2
7							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AAVKTLNPKAEVAR**
Found in **P40227**, T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3

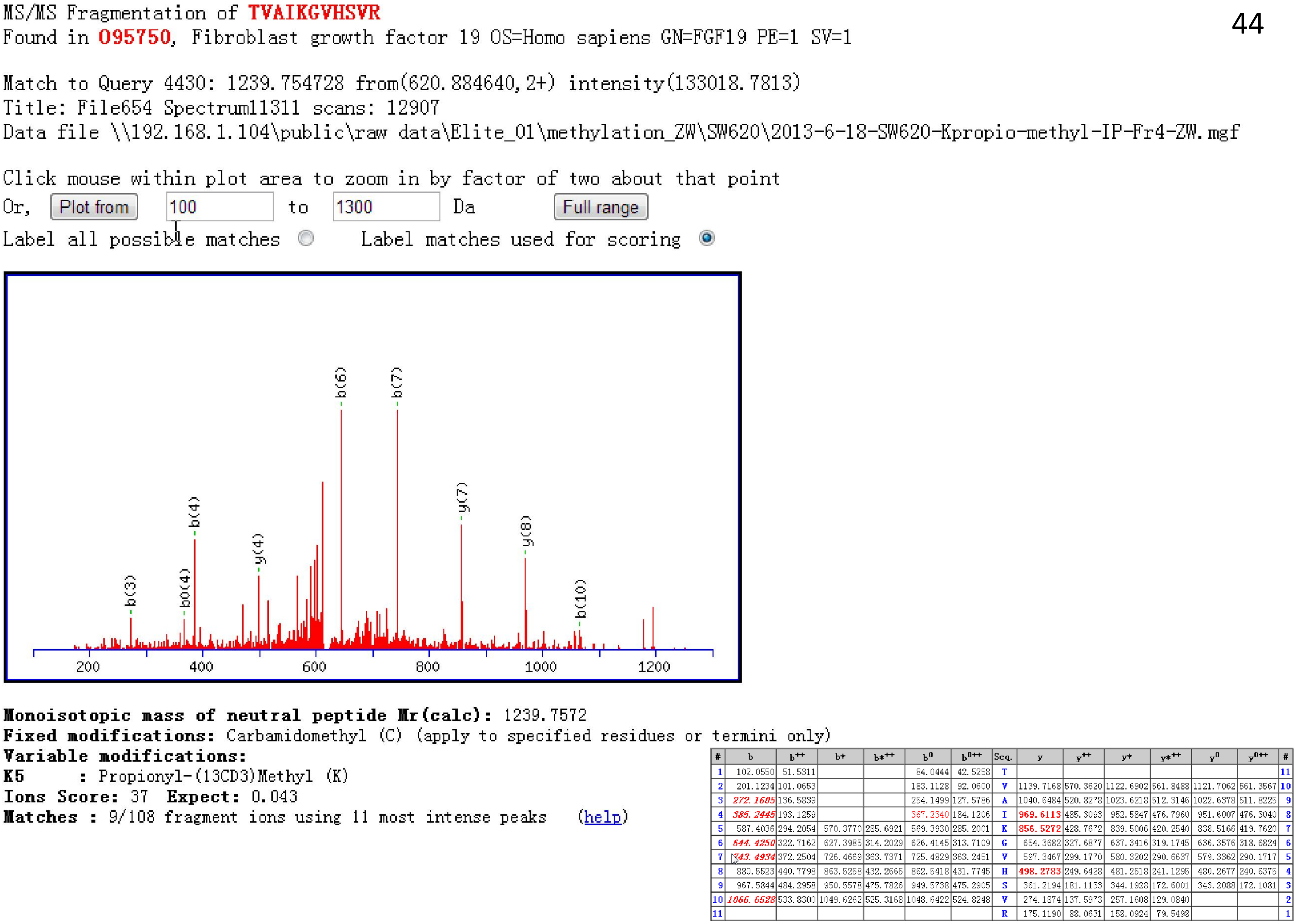
Match to Query 8805: 1638.958968 from(820.486760,2+) intensity(42681.8750)
Title: File386 Spectrum15176 scans: 16768
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1638.9577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
N-term : Acetyl (Protein N-term)
K4 : Propionyl-(13CD3)Methyl (K)
K9 : Propionyl (K)
Ions Score: 38 **Expect:** 0.06
Matches : 16/136 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0550	57.5311					A							14
2	185.0921	93.0497					A	1526.9173	763.9623	1509.8908	755.4490	1508.9068	754.9570	13
3	284.1605	142.5839					V	1455.8802	728.4438	1438.8537	719.9305	1437.8697	719.4385	12
4	***486.3195***	243.6634	469.2929	235.1501			K	***1356.8118***	678.9095	1339.7853	670.3963	1338.8012	669.9043	11
5	***587.3672***	294.1872	570.3406	285.6740	569.3566	285.1819	T	***1154.6528***	577.8300	1137.6263	569.3168	1136.6422	568.8248	10
6	700.4512	350.7293	683.4247	342.2160	682.4407	341.7240	L	***1053.6051***	527.3062	1036.5786	518.7929	1035.5946	518.3009	9
7	814.4942	407.7507	797.4676	399.2374	796.4836	398.7454	N	***940.5211***	470.7642	923.4945	462.2509	922.5105	461.7589	8
8	911.5469	456.2771	894.5204	447.7638	893.5364	447.2718	P	***826.4781***	413.7427	809.4516	405.2294	808.4676	404.7374	7
9	1095.6681	548.3377	1078.6416	539.8244	1077.6575	539.3324	K	729.4254	365.2163	712.3988	356.7030	711.4148	356.2110	6
10	***1166.7052***	583.8562	1149.6787	575.3430	1148.6947	574.8510	A	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
11	***1295.7478***	648.3775	1278.7213	639.8643	1277.7372	639.3723	E	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
12	***1394.8162***	697.9118	1377.7897	689.3985	1376.8057	688.9065	V	345.2245	173.1159	328.1979	164.6026			3
13	***1465.8533***	733.4303	1448.8268	724.9170	1447.8428	724.4250	A	246.1561	123.5817	229.1295	115.0684			2
14							R	175.1190	88.0631	158.0924	79.5498			1



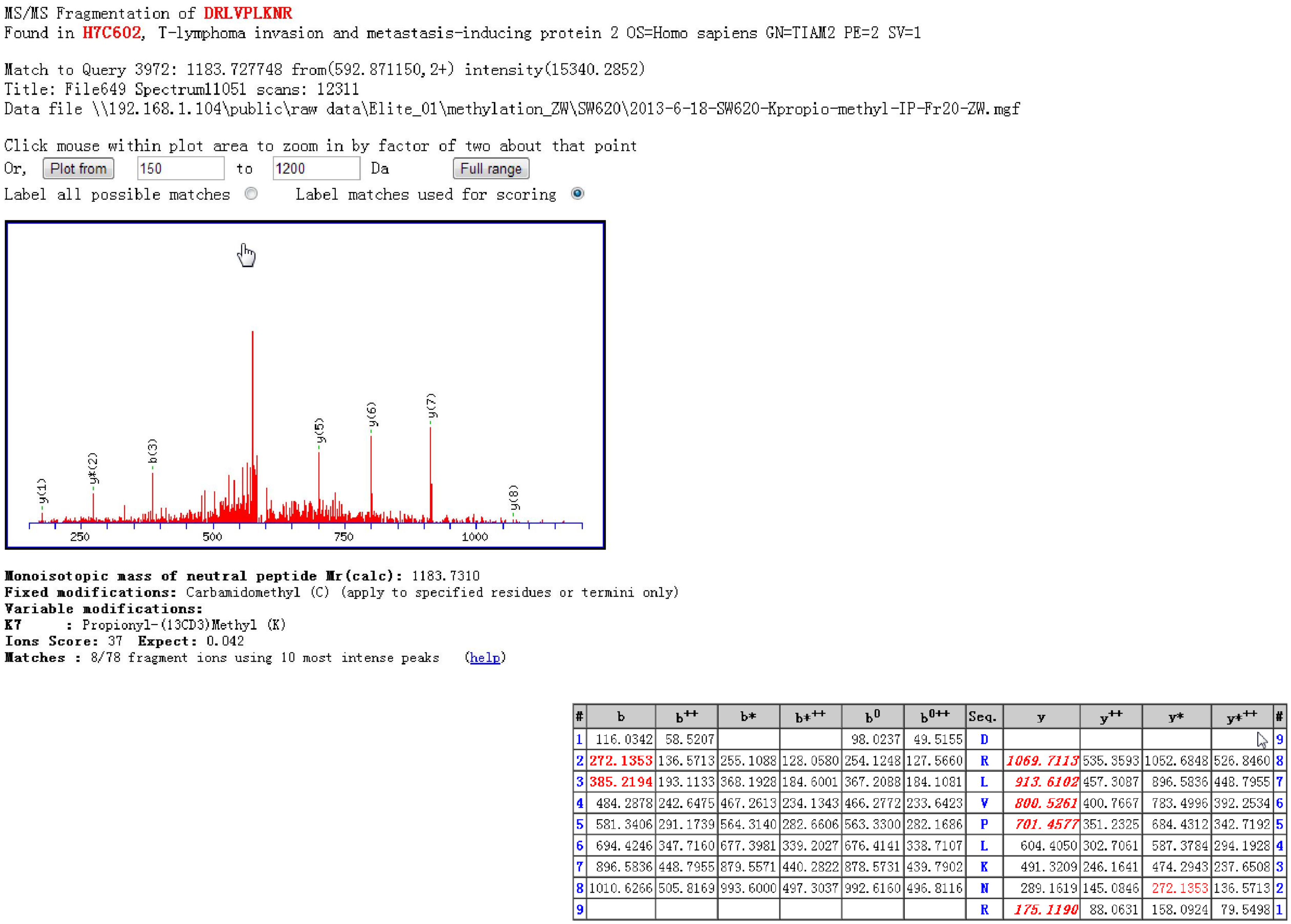
MS/MS Fragmentation of **TVAIKGVHSVR**
Found in **O95750**, Fibroblast growth factor 19 OS=Homo sapiens GN=FGF19 PE=1 SV=1

Match to Query 4430: 1239.754728 from(620.884640,2+) intensity(133018.7813)
Title: File654 Spectrum11311 scans: 12907
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr4-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1239.7572
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 37 **Expect:** 0.043
Matches : 9/108 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							11
2	201.1234	101.0653			183.1128	92.0600	V	1139.7168	570.3620	1122.6902	561.8488	1121.7062	561.3567	10
3	***272.1605***	136.5839			254.1499	127.5786	A	1040.6484	520.8278	1023.6218	512.3146	1022.6378	511.8225	9
4	***385.2445***	193.1259			367.2340	184.1206	I	**969.6113**	485.3093	952.5847	476.7960	951.6007	476.3040	8
5	587.4036	294.2054	570.3770	285.6921	569.3930	285.2001	K	**856.5272**	428.7672	839.5006	420.2540	838.5166	419.7620	7
6	***644.4250***	322.7162	627.3985	314.2029	626.4145	313.7109	G	654.3682	327.6877	637.3416	319.1745	636.3576	318.6824	6
7	***743.4934***	372.2504	726.4669	363.7371	725.4829	363.2451	V	597.3467	299.1770	580.3202	290.6637	579.3362	290.1717	5
8	880.5523	440.7798	863.5258	432.2665	862.5418	431.7745	H	**498.2783**	249.6428	481.2518	241.1295	480.2677	240.6375	4
9	967.5844	484.2958	950.5578	475.7826	949.5738	475.2905	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	***1066.6528***	533.8300	1049.6262	525.3168	1048.6422	524.8248	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **DRLVPLKNR**
Found in **H7C602**, T-lymphoma invasion and metastasis-inducing protein 2 OS=Homo sapiens GN=TIAM2 PE=2 SV=1

Match to Query 3972: 1183.727748 from(592.871150,2+) intensity(15340.2852)
Title: File649 Spectrum11051 scans: 12311
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr20-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

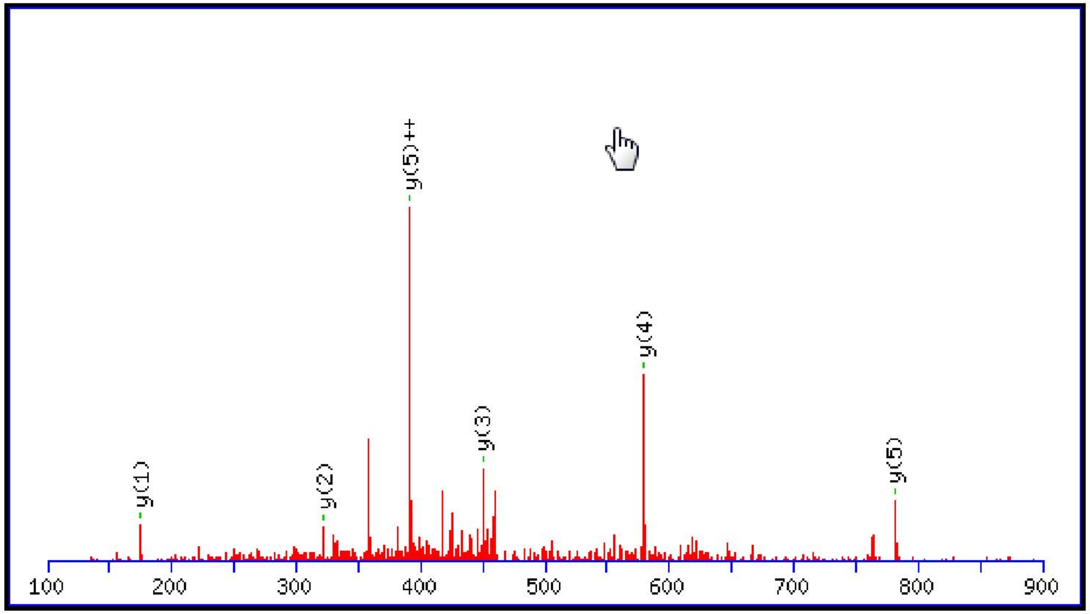
Monoisotopic mass of neutral peptide Mr(calc): 1183.7310
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 **:** Propionyl-(13CD3)Methyl (K)
Ions Score: 37 **Expect:** 0.042
Matches : 8/78 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**					9
2	**272.1353**	136.5713	255.1088	128.0580	254.1248	127.5660	**R**	***1069.7113***	535.3593	1052.6848	526.8460	8
3	**385.2194**	193.1133	368.1928	184.6001	367.2088	184.1081	**L**	***913.6102***	457.3087	896.5836	448.7955	7
4	484.2878	242.6475	467.2613	234.1343	466.2772	233.6423	**V**	***800.5261***	400.7667	783.4996	392.2534	6
5	581.3406	291.1739	564.3140	282.6606	563.3300	282.1686	**P**	***701.4577***	351.2325	684.4312	342.7192	5
6	694.4246	347.7160	677.3981	339.2027	676.4141	338.7107	**L**	604.4050	302.7061	587.3784	294.1928	4
7	896.5836	448.7955	879.5571	440.2822	878.5731	439.7902	**K**	491.3209	246.1641	474.2943	237.6508	3
8	1010.6266	505.8169	993.6000	497.3037	992.6160	496.8116	**N**	289.1619	145.0846	272.1353	136.5713	2
9							**R**	***175.1190***	88.0631	158.0924	79.5498	1

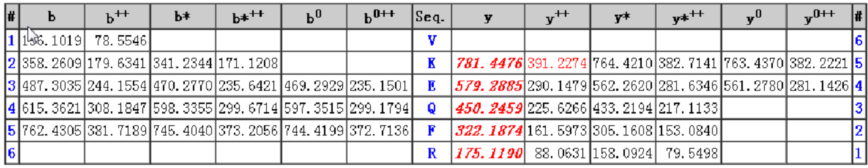
MS/MS Fragmentation of **VKEQFR**
Found in **O14802**, DNA-directed RNA polymerase III subunit RPC1 OS=Homo sapiens GN=POLR3A PE=1 SV=2

Match to Query 1533: 935.534088 from(468.774320,2+) intensity(22065.8086)
Title: File448 Spectrum12546 scans: 14308
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-6-SW620-Kpropio-methyl-IP-Fr7-ZW.mgf

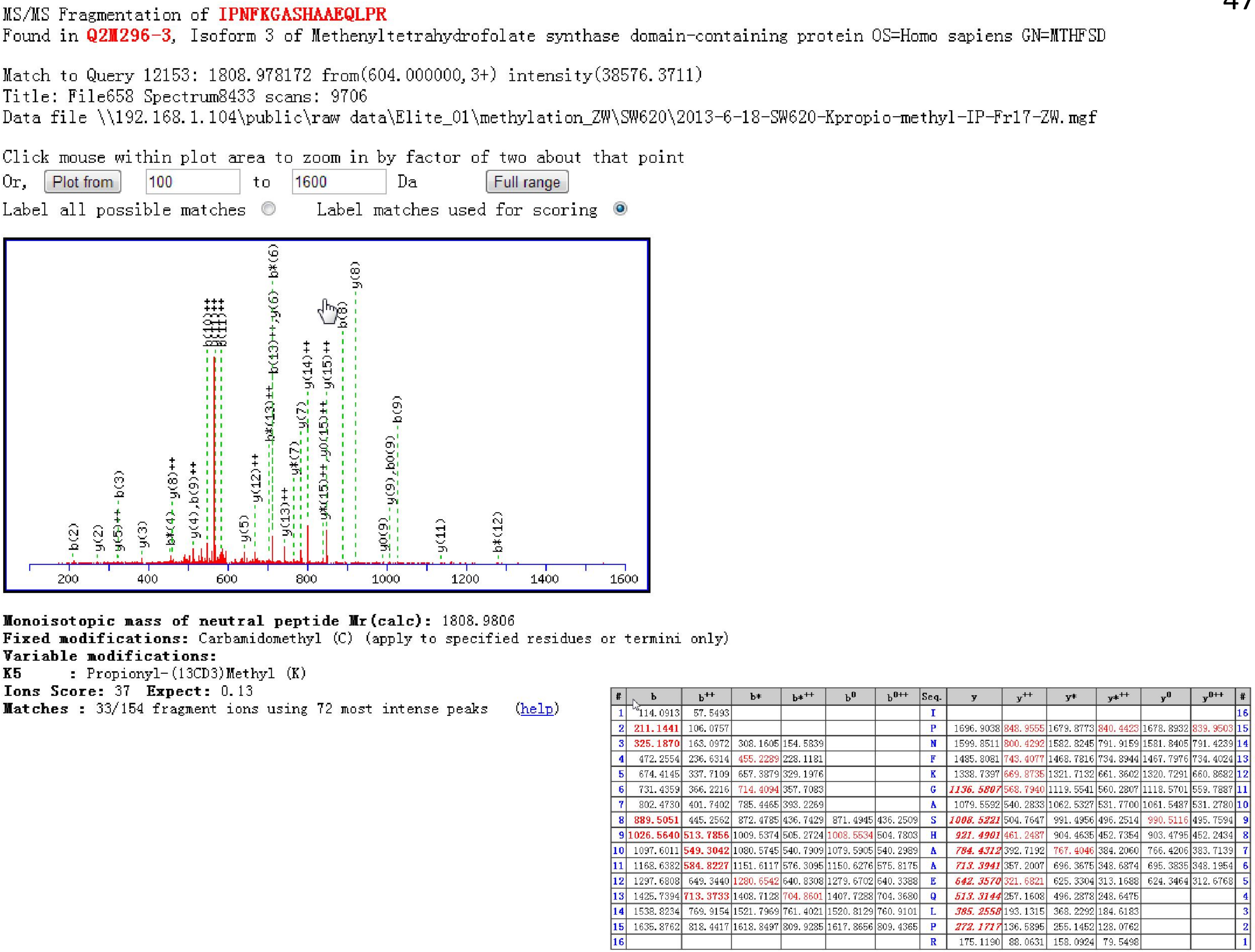
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 935.5349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 37 **Expect:** 0.066
Matches : 6/48 fragment ions using 8 most intense peaks (help)



#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	156.1019	78.5546					V							6
2	358.2609	179.6341	341.2344	171.1208			K	***781.4476***	391.2274	764.4210	382.7141	763.4370	382.2221	5
3	487.3035	244.1554	470.2770	235.6421	469.2929	235.1501	E	***579.2885***	290.1479	562.2620	281.6346	561.2780	281.1426	4
4	615.3621	308.1847	598.3355	299.6714	597.3515	299.1794	Q	***450.2459***	225.6266	433.2194	217.1133			3
5	762.4305	381.7189	745.4040	373.2056	744.4199	372.7136	F	***322.1874***	161.5973	305.1608	153.0840			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



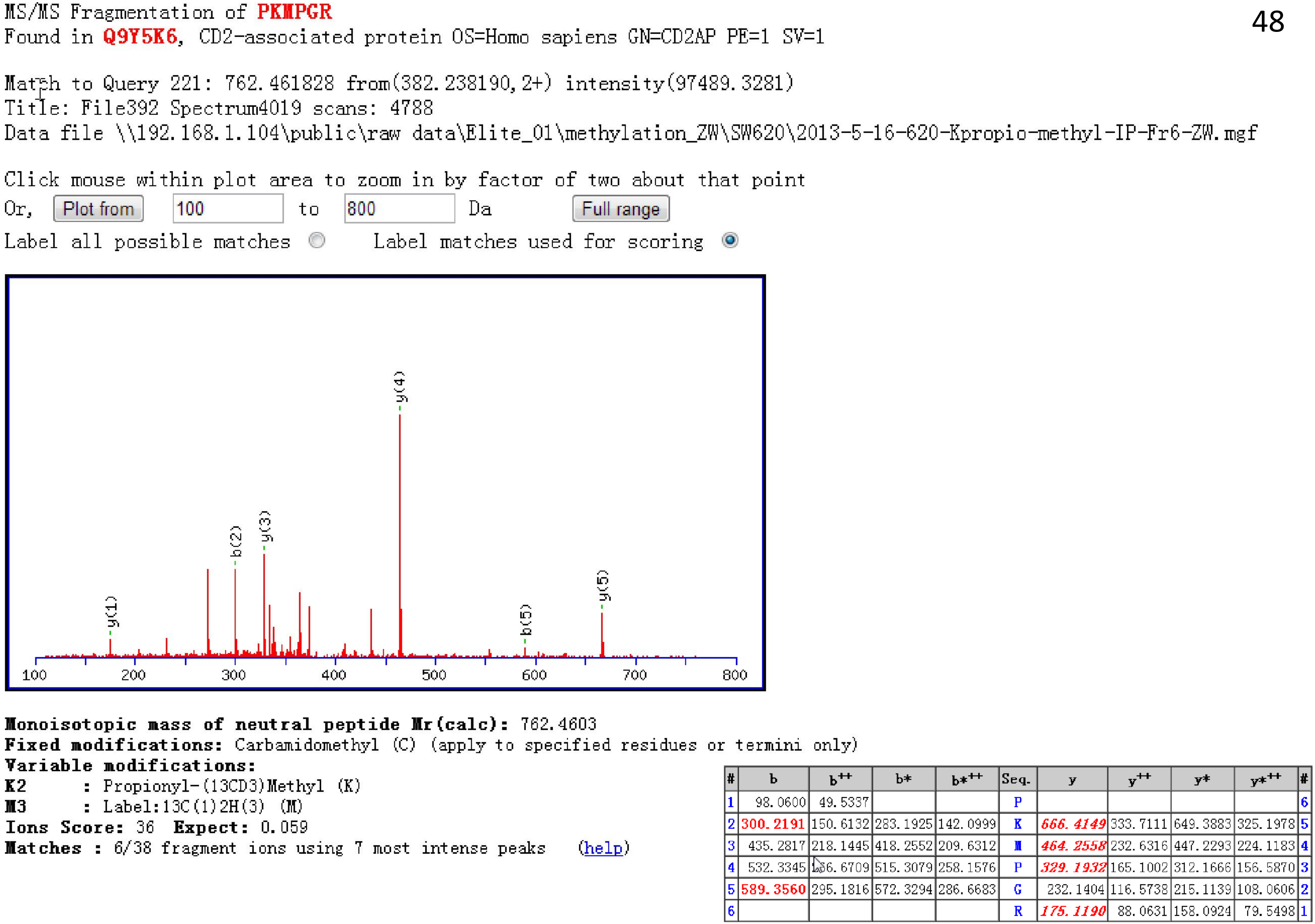
MS/MS Fragmentation of **IPNFKGASHAAEQLPR**
Found in **Q2M296-3**, Isoform 3 of Methenyltetrahydrofolate synthase domain-containing protein OS=Homo sapiens GN=MTHFSD

Match to Query 12153: 1808.978172 from(604.000000,3+) intensity(38576.3711)
Title: File658 Spectrum8433 scans: 9706
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr17-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1808.9806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 37 **Expect:** 0.13
Matches : 33/154 fragment ions using 72 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							16
2	**211.1441**	106.0757					P	1696.9038	848.9555	1679.8773	840.4423	1678.8932	839.9503	15
3	**325.1870**	163.0972	308.1605	154.5839			N	1599.8511	800.4292	1582.8245	791.9159	1581.8405	791.4239	14
4	472.2554	236.6314	455.2289	228.1181			F	1485.8081	743.4077	1468.7816	734.8944	1467.7976	734.4024	13
5	674.4145	337.7109	657.3879	329.1976			K	1338.7397	669.8735	1321.7132	661.3602	1320.7291	660.8682	12
6	731.4359	366.2216	714.4094	357.7083			G	***1136.5807***	568.7940	1119.5541	560.2807	1118.5701	559.7887	11
7	802.4730	401.7402	785.4465	393.2269			A	1079.5592	540.2833	1062.5327	531.7700	1061.5487	531.2780	10
8	**889.5051**	445.2562	872.4785	436.7429	871.4945	436.2509	S	***1008.5221***	504.7647	991.4956	496.2514	990.5116	495.7594	9
9	**1026.5640**	**513.7856**	1009.5374	505.2724	1008.5534	504.7803	H	***921.4901***	461.2487	904.4635	452.7354	903.4795	452.2434	8
10	1097.6011	**549.3042**	1080.5745	540.7909	1079.5905	540.2989	A	***784.4312***	392.7192	767.4046	384.2060	766.4206	383.7139	7
11	1168.6382	**584.8227**	1151.6117	576.3095	1150.6276	575.8175	A	***713.3941***	357.2007	696.3675	348.6874	695.3835	348.1954	6
12	1297.6808	649.3440	1280.6542	640.8308	1279.6702	640.3388	E	***642.3570***	321.6821	625.3304	313.1688	624.3464	312.6768	5
13	1425.7394	**713.3733**	1408.7128	704.8601	1407.7288	704.3680	Q	***513.3144***	257.1608	496.2878	248.6475			4
14	1538.8234	769.9154	1521.7969	761.4021	1520.8129	760.9101	L	***385.2558***	193.1315	368.2292	184.6183			3
15	1635.8762	818.4417	1618.8497	809.9285	1617.8656	809.4365	P	***272.1717***	136.5895	255.1452	128.0762			2
16							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **PKMPGR**

Found in **Q9Y5K6**, CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1

Match to Query 221: 762.461828 from(382.238190,2+) intensity(97489.3281)

Title: File392 Spectrum4019 scans: 4788

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

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

Or, Plot from 100 to 800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 762.4603

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

Variable modifications:

K2 : Propionyl-(13CD3)Methyl (K)

M3 : Label:13C(1)2H(3) (M)

Ions Score: 36 **Expect:** 0.059

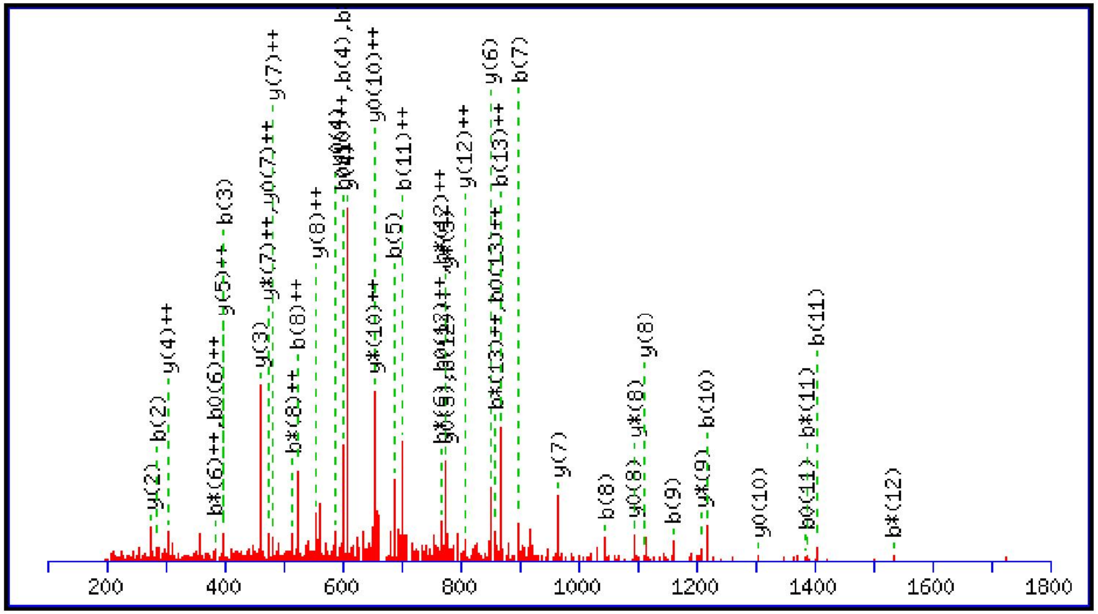
Matches : 6/38 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	98.0600	49.5337			P					6
2	**300.2191**	150.6132	283.1925	142.0999	K	***666.4149***	333.7111	649.3883	325.1978	5
3	435.2817	218.1445	418.2552	209.6312	M	***464.2558***	232.6316	447.2293	224.1183	4
4	532.3345	266.6709	515.3079	258.1576	P	***329.1932***	165.1002	312.1666	156.5870	3
5	**589.3560**	295.1816	572.3294	286.6683	G	232.1404	116.5738	215.1139	108.0606	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1

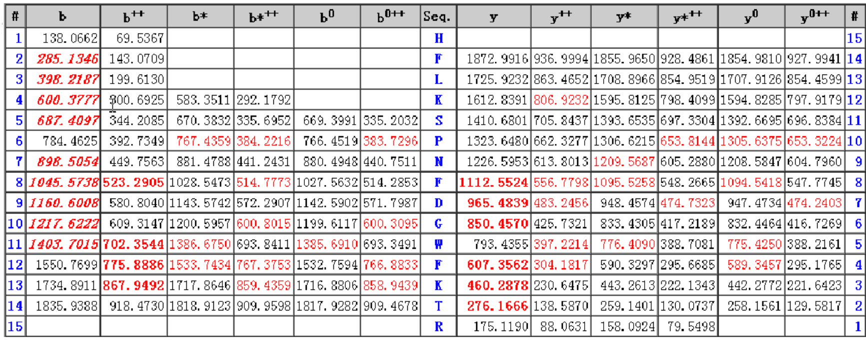
MS/MS Fragmentation of **HFLKSPNFDGWFKTR**
Found in **H7C5D0**, Protein DENND6A (Fragment) OS=Homo sapiens GN=DENND6A PE=4 SV=1

Match to Query 14565: 2009.043972 from(670.688600,3+) intensity(31107.2813)
Title: File388 Spectrum17027 scans: 19170
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

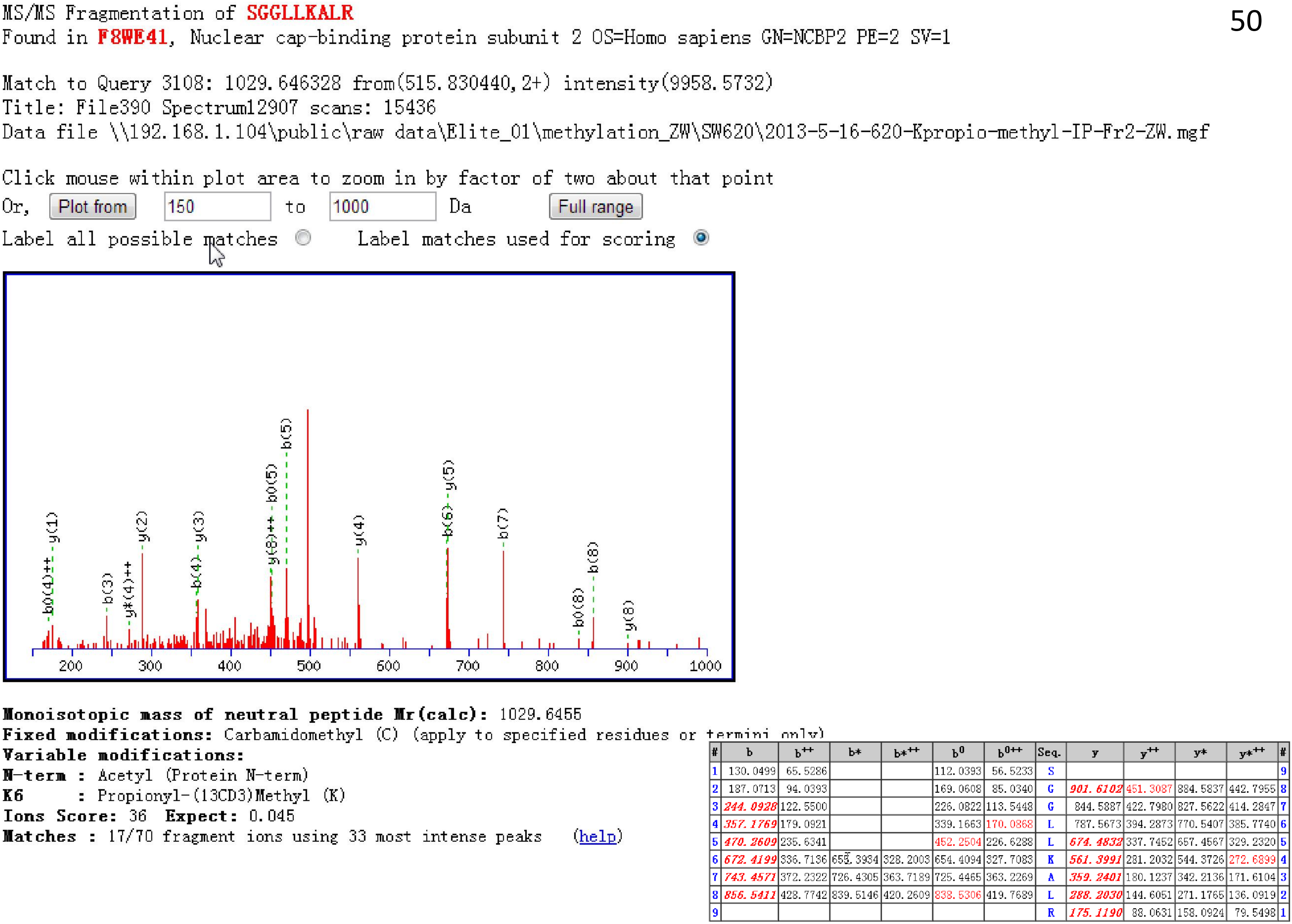
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2009.0432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K13 : Propionyl (K)
Ions Score: 36 **Expect:** 0.17
Matches : 48/152 fragment ions using 80 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							15
2	***285.1346***	143.0709					F	1872.9916	936.9994	1855.9650	928.4861	1854.9810	927.9941	14
3	***398.2187***	199.6130					L	1725.9232	863.4652	1708.8966	854.9519	1707.9126	854.4599	13
4	***600.3777***	300.6925	583.3511	292.1792			K	1612.8391	806.9232	1595.8125	798.4099	1594.8285	797.9179	12
5	***687.4097***	344.2085	670.3832	335.6952	669.3991	335.2032	S	1410.6801	705.8437	1393.6535	697.3304	1392.6695	696.8384	11
6	784.4625	392.7349	767.4359	384.2216	766.4519	383.7296	P	1323.6480	662.3277	1306.6215	653.8144	1305.6375	653.3224	10
7	***898.5054***	449.7563	881.4788	441.2431	880.4948	440.7511	N	1226.5953	613.8013	1209.5687	605.2880	1208.5847	604.7960	9
8	***1045.5738***	**523.2905**	1028.5473	514.7773	1027.5632	514.2853	F	**1112.5524**	556.7798	1095.5258	548.2665	1094.5418	547.7745	8
9	***1160.6008***	580.8040	1143.5742	572.2907	1142.5902	571.7987	D	**965.4839**	483.2456	948.4574	474.7323	947.4734	474.2403	7
10	***1217.6222***	609.3147	1200.5957	600.8015	1199.6117	600.3095	G	**850.4570**	425.7321	833.4305	417.2189	832.4464	416.7269	6
11	***1403.7015***	**702.3544**	1386.6750	693.8411	1385.6910	693.3491	W	793.4355	397.2214	776.4090	388.7081	775.4250	388.2161	5
12	1550.7699	**775.8886**	1533.7434	767.3753	1532.7594	766.8833	F	**607.3562**	304.1817	590.3297	295.6685	589.3457	295.1765	4
13	1734.8911	**867.9492**	1717.8646	859.4359	1716.8806	858.9439	K	**460.2878**	230.6475	443.2613	222.1343	442.2772	221.6423	3
14	1835.9388	918.4730	1818.9123	909.9598	1817.9282	909.4678	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
15							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **SGGLLKALR**
Found in **F8WE41**, Nuclear cap-binding protein subunit 2 OS=Homo sapiens GN=NCBP2 PE=2 SV=1

Match to Query 3108: 1029.646328 from(515.830440,2+) intensity(9958.5732)
Title: File390 Spectrum12907 scans: 15436
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

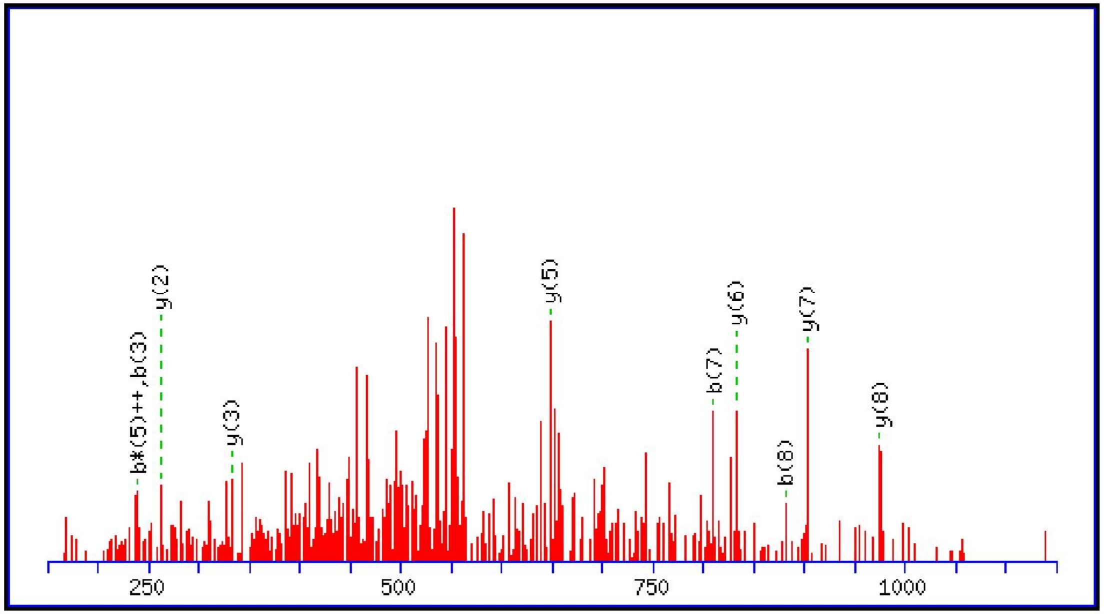
Monoisotopic mass of neutral peptide Mr(calc): 1029.6455
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 36 **Expect:** 0.045
Matches : 17/70 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	130.0499	65.5286			112.0393	56.5233	S					9
2	187.0713	94.0393			169.0608	85.0340	G	***901.6102***	451.3087	884.5837	442.7955	8
3	***244.0928***	122.5500			226.0822	113.5448	G	844.5887	422.7980	827.5622	414.2847	7
4	***357.1769***	179.0921			339.1663	170.0868	L	787.5673	394.2873	770.5407	385.7740	6
5	***470.2609***	235.6341			452.2504	226.6288	L	***674.4832***	337.7452	657.4567	329.2320	5
6	***672.4199***	336.7136	655.3934	328.2003	654.4094	327.7083	K	***561.3991***	281.2032	544.3726	272.6899	4
7	***743.4571***	372.2322	726.4305	363.7189	725.4465	363.2269	A	***359.2401***	180.1237	342.2136	171.6104	3
8	***856.5411***	428.7742	839.5146	420.2609	838.5306	419.7689	L	***288.2030***	144.6051	271.1765	136.0919	2
9							R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **PAAAKLKASR**
Found in **A7E2D7**, E1A-binding protein p400 (Fragment) OS=Homo sapiens GN=EP400 PE=2 SV=1

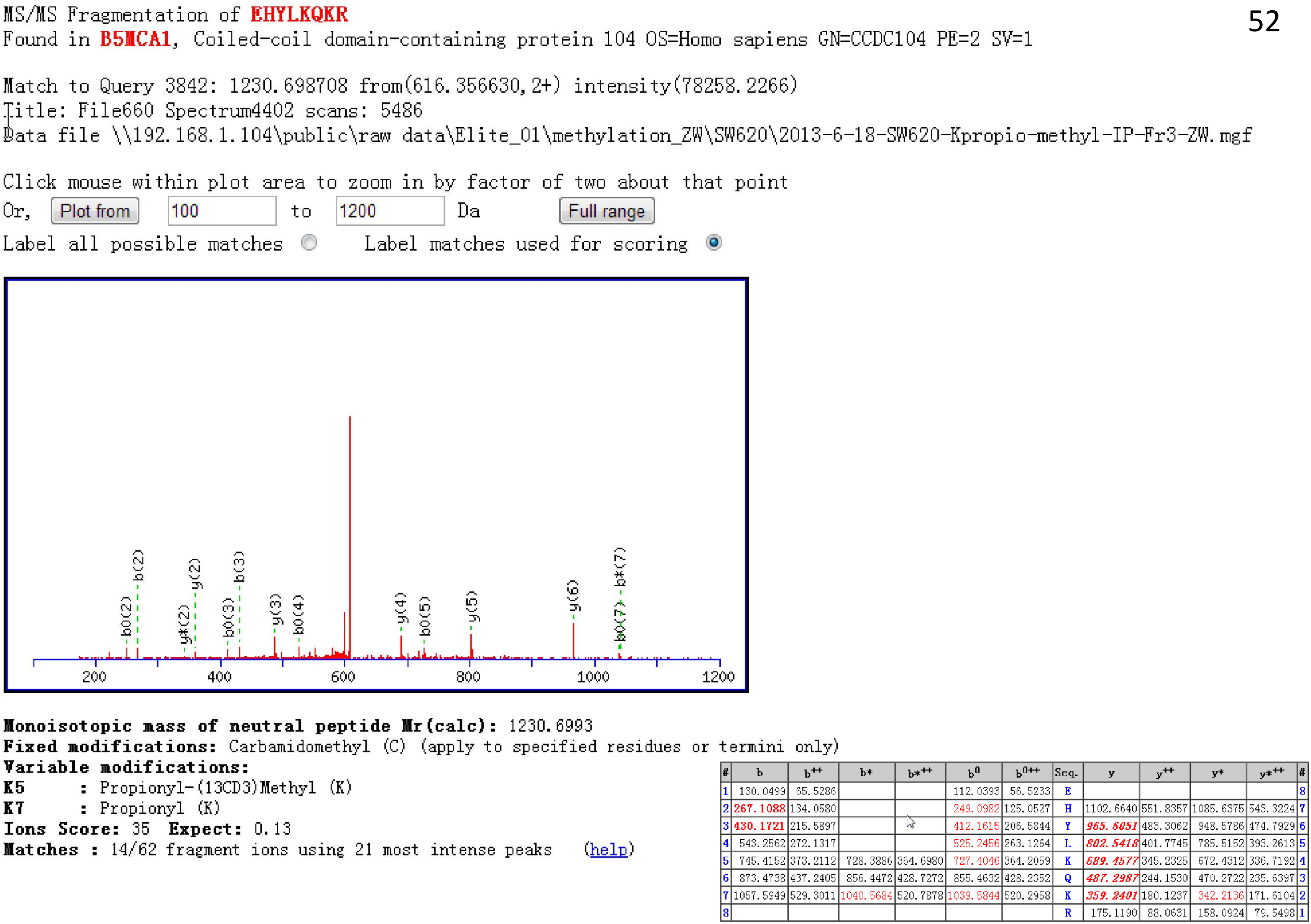
Match to Query 3401: 1141.707988 from(571.861270,2+) intensity(5912.1660)
Title: File443 Spectrum7209 scans: 8456
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-6-SW620-Kpropio-methyl-IP-Fr15-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide
Fixed modifications: Carbamidomethyl (C
Variable modifications:
K5 : Propionyl (K)
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 35 **Expect:** 0.059
Matches : 10/82 fragment ions using 19 mo

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	98.0600	49.5337					P							10
2	169.0972	85.0522					A	1045.6637	523.3355	1028.6371	514.8222	1027.6531	514.3302	9
3	**240.1343**	120.5708					A	***974.6266***	487.8169	957.6000	479.3037	956.6160	478.8116	8
4	311.1714	156.0893					A	***903.5895***	452.2984	886.5629	443.7851	885.5789	443.2931	7
5	495.2926	248.1499	478.2660	239.6366			K	***832.5523***	416.7798	815.5258	408.2665	814.5418	407.7745	6
6	608.3766	304.6920	591.3501	296.1787			L	***648.4312***	324.7192	631.4046	316.2059	630.4206	315.7139	5
7	**810.5356**	405.7715	793.5091	397.2582			K	535.3471	268.1772	518.3206	259.6639	517.3365	259.1719	4
8	**881.5728**	441.2900	864.5462	432.7767			A	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
9	968.6048	484.8060	951.5782	476.2928	950.5942	475.8007	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **EHYLKQKR**
Found in **B5MCA1**, Coiled-coil domain-containing protein 104 OS=Homo sapiens GN=CCDC104 PE=2 SV=1

Match to Query 3842: 1230.698708 from(616.356630,2+) intensity(78258.2266)
Title: File660 Spectrum4402 scans: 5486
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr3-ZW.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 ●

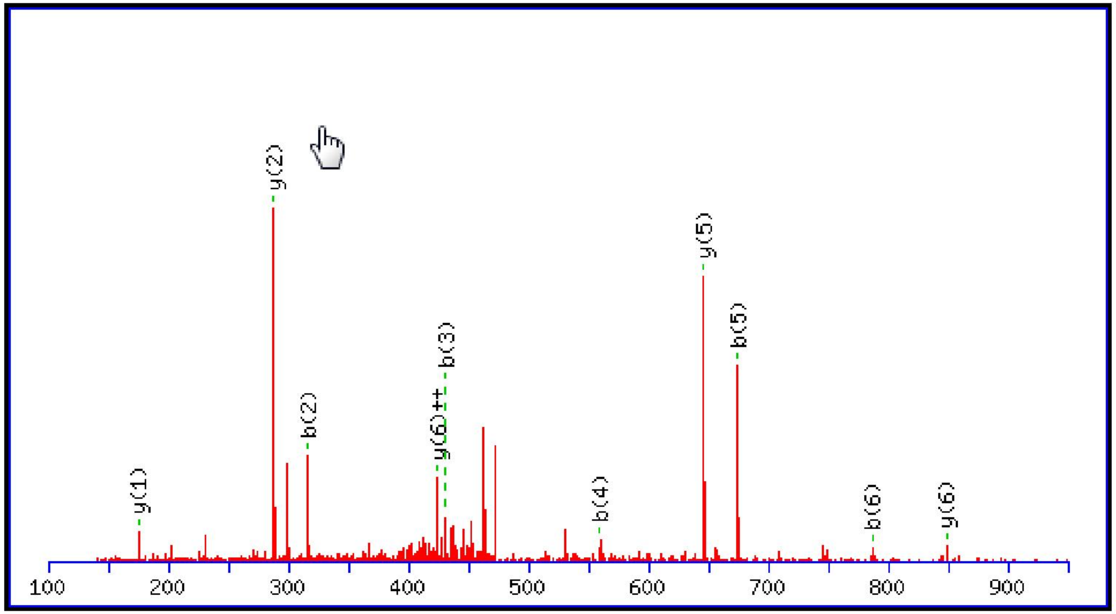
Monoisotopic mass of neutral peptide Mr(calc): 1230.6993
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 35 **Expect:** 0.13
Matches : 14/62 fragment ions using 21 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	130.0499	65.5286			112.0393	56.5233	E					8
2	**267.1088**	134.0580			249.0982	125.0527	H	1102.6640	551.8357	1085.6375	543.3224	7
3	**430.1721**	215.5897			412.1615	206.5844	Y	***965.6051***	483.3062	948.5786	474.7929	6
4	543.2562	272.1317			525.2456	263.1264	L	***802.5418***	401.7745	785.5152	393.2613	5
5	745.4152	373.2112	728.3886	364.6980	727.4046	364.2059	K	***689.4577***	345.2325	672.4312	336.7192	4
6	873.4738	437.2405	856.4472	428.7272	855.4632	428.2352	Q	***487.2987***	244.1530	470.2722	235.6397	3
7	1057.5949	529.3011	1040.5684	520.7878	1039.5844	520.2958	K	***359.2401***	180.1237	342.2136	171.6104	2
8							R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **LKDQDLR**
Found in **Q9UMY1**, Nucleolar protein 7 OS=Homo sapiens GN=NOL7 PE=1 SV=2

Match to Query 1545: 960.551188 from(481.282870,2+) intensity(66393.2109)
Title: File388 Spectrum5403 scans: 6512
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



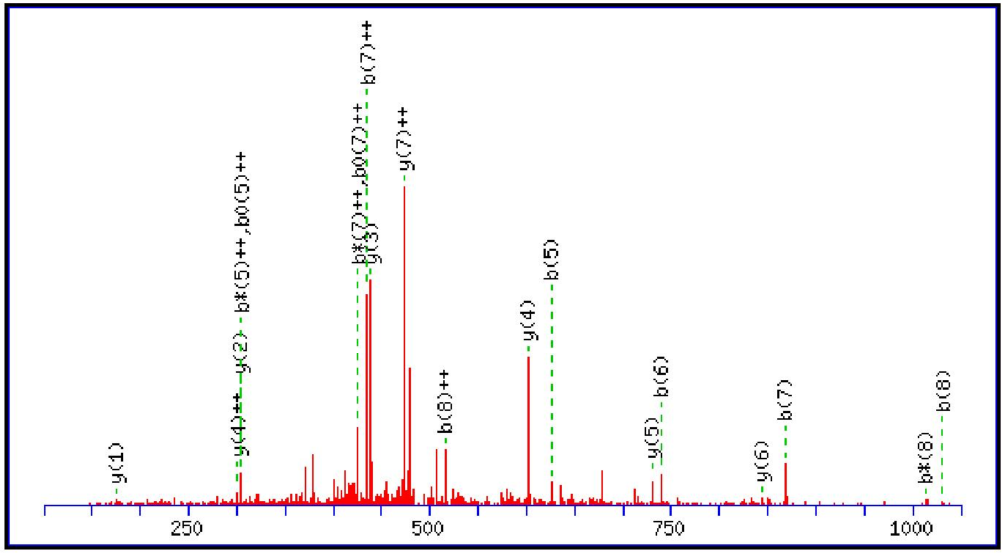
Monoisotopic mass of neutral peptide Mr(calc): 960.5513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 35 **Expect:** 0.1
Matches : 10/62 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							7
2	***316.2504***	158.6288	299.2238	150.1155			K	***848.4745***	424.7409	831.4479	416.2276	830.4639	415.7356	6
3	***431.2773***	216.1423	414.2507	207.6290	413.2667	207.1370	D	***646.3155***	323.6614	629.2889	315.1481	628.3049	314.6561	5
4	***559.3359***	280.1716	542.3093	271.6583	541.3253	271.1663	Q	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
5	***674.3628***	337.6850	657.3363	329.1718	656.3523	328.6798	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
6	***787.4469***	394.2271	770.4203	385.7138	769.4363	385.2218	L	***288.2030***	144.6051	271.1765	136.0919			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAHLTNQYMQR**
Found in **B1ANR0**, Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e OS=Homo sapiens GN=PABPC4 PE=2 SV=1

Match to Query 6842: 1466.783892 from(489.935240,3+) intensity(78308.3359)
Title: File440 Spectrum6594 scans: 7697
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



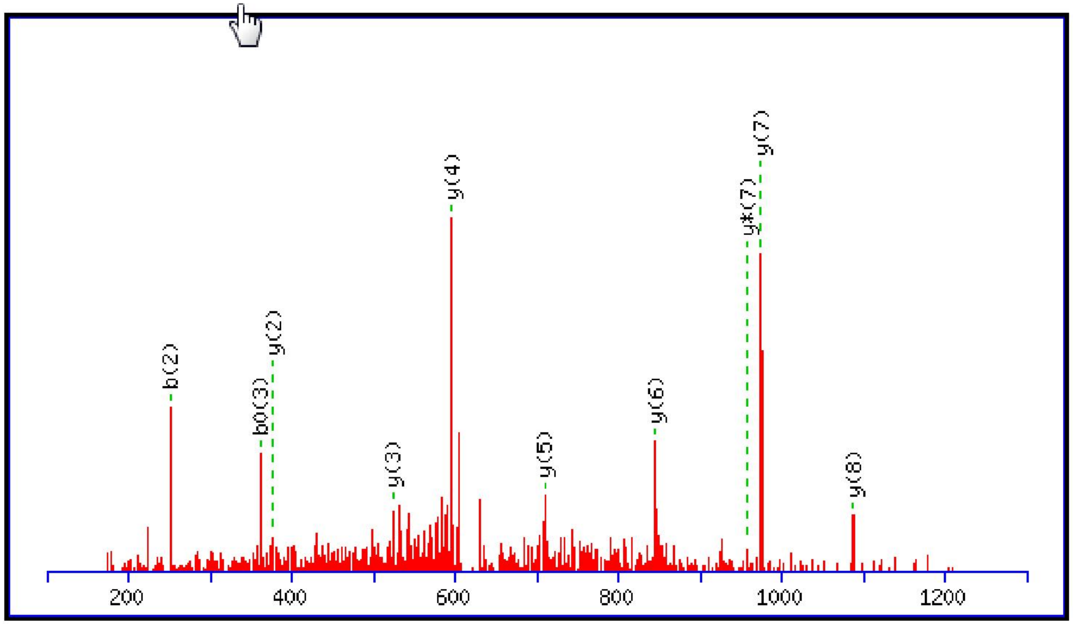
Monoisotopic mass of neutral peptide Mr(calc): 1466.7845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
M9 : Label:13C(1)2H(3) (M)
Ions Score: 35 **Expect:** 0.17
Matches : 19/100 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							11
2	274.2034	137.6053	257.1769	129.0921			A	1265.6328	633.3200	1248.6063	624.8068	1247.6222	624.3148	10
3	411.2623	206.1348	394.2358	197.6215			H	1194.5957	597.8015	1177.5691	589.2882	1176.5851	588.7962	9
4	524.3464	262.6768	507.3198	254.1636			L	1057.5368	529.2720	1040.5102	520.7588	1039.5262	520.2667	8
5	**625.3941**	313.2007	608.3675	304.6874	607.3835	304.1954	T	944.4527	472.7300	927.4262	464.2167	926.4421	463.7247	7
6	**739.4370**	370.2221	722.4104	361.7089	721.4264	361.2168	N	***843.4050***	422.2062	826.3785	413.6929			6
7	**867.4956**	**434.2514**	850.4690	425.7381	849.4850	425.2461	Q	***729.3621***	365.1847	712.3356	356.6714			5
8	**1030.5589**	**515.7831**	1013.5323	507.2698	1012.5483	506.7778	Y	***601.3035***	301.1554	584.2770	292.6421			4
9	1165.6216	583.3144	1148.5950	574.8011	1147.6110	574.3091	M	***438.2402***	219.6237	421.2137	211.1105			3
10	1293.6801	647.3437	1276.6536	638.8304	1275.6696	638.3384	Q	***303.1775***	152.0924	286.1510	143.5791			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1

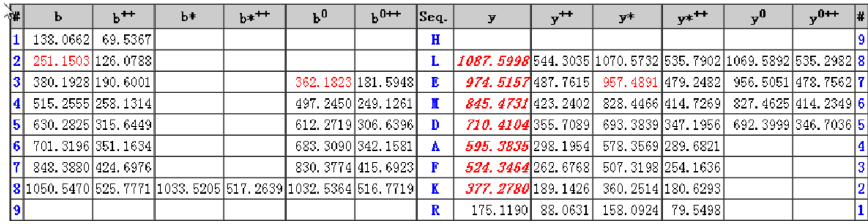
MS/MS Fragmentation of **HLEMDAFKR**
Found in **J3KPS2**, Protein FAM83H (Fragment) OS=Homo sapiens GN=FAM83H PE=4 SV=1

Match to Query 3757: 1223.649028 from(612.831790,2+) intensity(28718.8613)
Title: File419 Spectrum9103 scans: 10628
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-06-05-SW620-Kpropio-methyl-IP-Fr9-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1223.6514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Label:13C(1)2H(3) (M)
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 34 **Expect:** 0.15
Matches : 10/70 fragment ions using 22 most intense peaks (help)

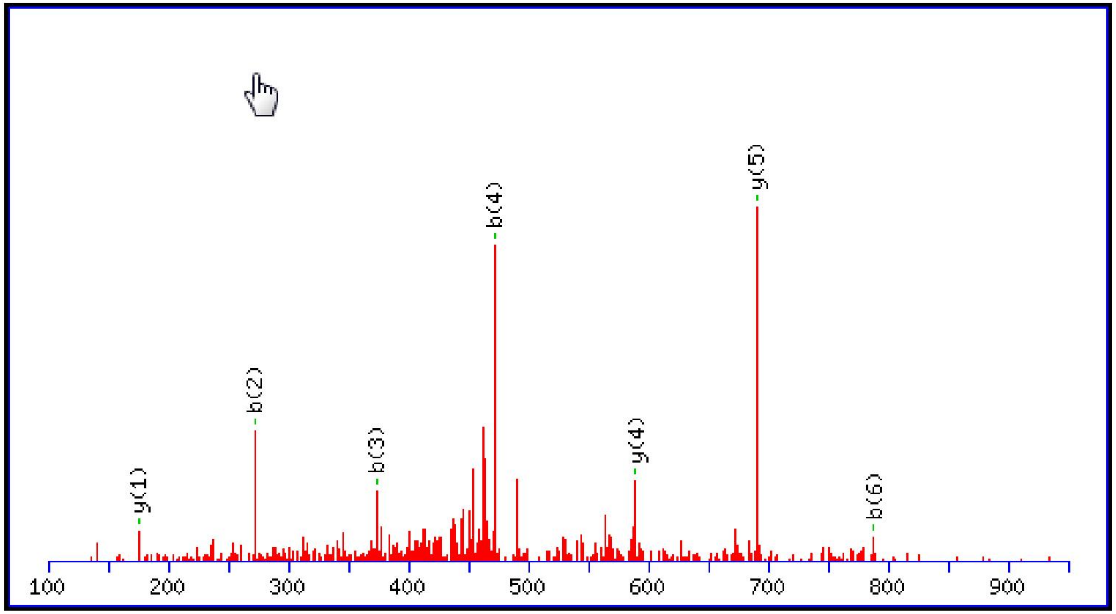


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.0662	69.5367					H							9
2	251.1503	126.0788					L	*1087.5998*	544.3035	1070.5732	535.7902	1069.5892	535.2982	8
3	380.1928	190.6001			362.1823	181.5948	E	*974.5157*	487.7615	957.4891	479.2482	956.5051	478.7562	7
4	515.2555	258.1314			497.2450	249.1261	M	*845.4731*	423.2402	828.4466	414.7269	827.4625	414.2349	6
5	630.2825	315.6449			612.2719	306.6396	D	*710.4104*	355.7089	693.3839	347.1956	692.3999	346.7036	5
6	701.3196	351.1634			683.3090	342.1581	A	*595.3835*	298.1954	578.3569	289.6821			4
7	848.3880	424.6976			830.3774	415.6923	F	*524.3464*	262.6768	507.3198	254.1636			3
8	1050.5470	525.7771	1033.5205	517.2639	1032.5364	516.7719	K	*377.2780*	189.1426	360.2514	180.6293			2
9							R	175.1190	88.0631	158.0924	79.5498			1

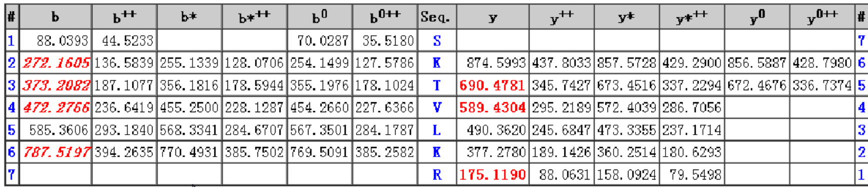
MS/MS Fragmentation of **SKTVLKR**
Found in **Q9UK61**, Protein FAM208A OS=Homo sapiens GN=FAM208A PE=1 SV=3

Match to Query 1822: 960.623748 from(481.319150,2+) intensity(19628.7578)
Title: File448 Spectrum7200 scans: 8578
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-6-SW620-Kpropio-methyl-IP-Fr7-ZW.mgf

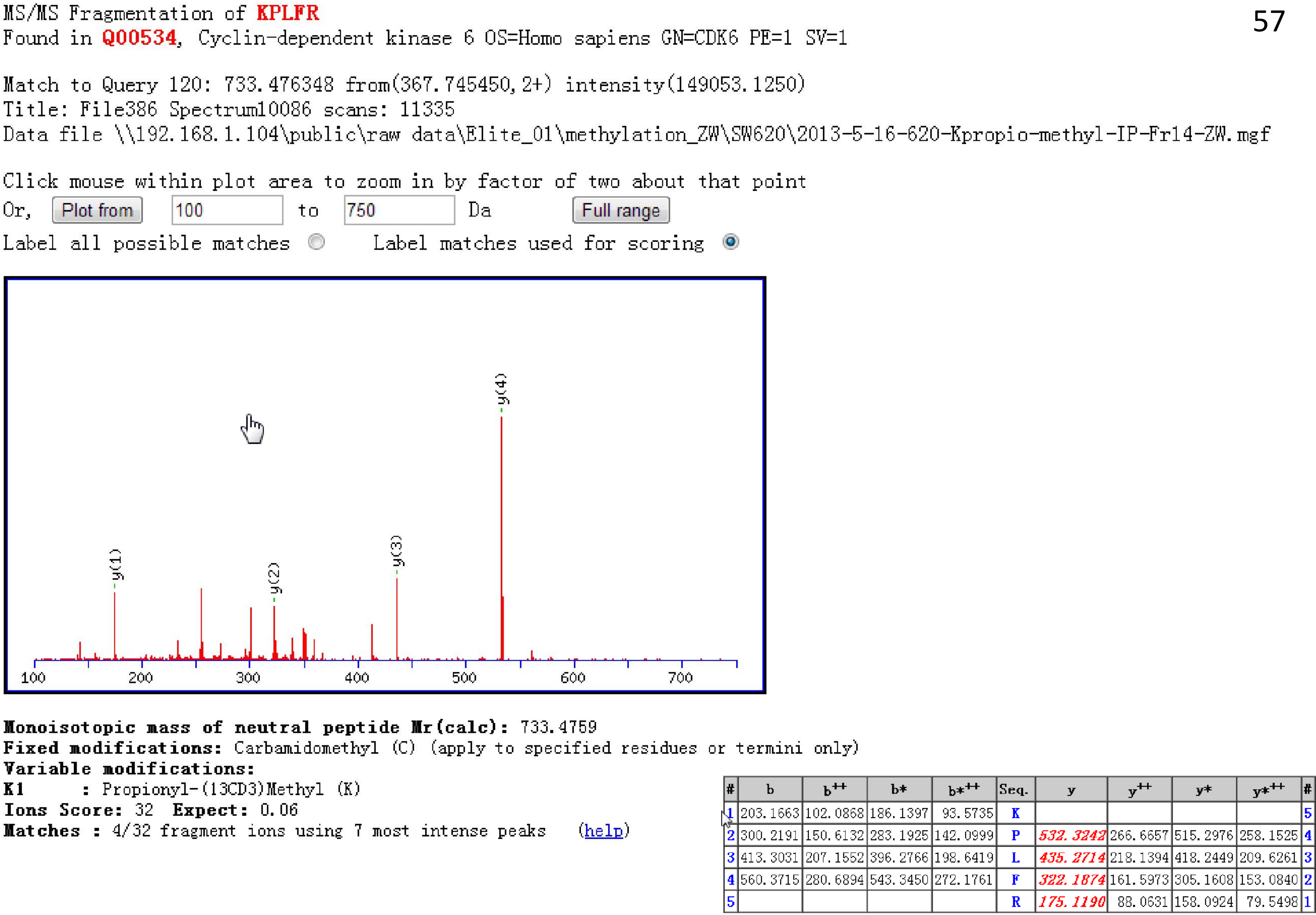
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 960.6240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 33 **Expect:** 0.054
Matches : 7/62 fragment ions using 8 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							7
2	*272.1605*	136.5839	255.1339	128.0706	254.1499	127.5786	K	874.5993	437.8033	857.5728	429.2900	856.5887	428.7980	6
3	*373.2082*	187.1077	356.1816	178.5944	355.1976	178.1024	T	**690.4781**	345.7427	673.4516	337.2294	672.4676	336.7374	5
4	*472.2766*	236.6419	455.2500	228.1287	454.2660	227.6366	V	**589.4304**	295.2189	572.4039	286.7056			4
5	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	L	490.3620	245.6847	473.3355	237.1714			3
6	*787.5197*	394.2635	770.4931	385.7502	769.5091	385.2582	K	377.2780	189.1426	360.2514	180.6293			2
7							R	**175.1190**	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KPLFR**
Found in **Q00534**, Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1

Match to Query 120: 733.476348 from(367.745450,2+) intensity(149053.1250)
Title: File386 Spectrum10086 scans: 11335
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

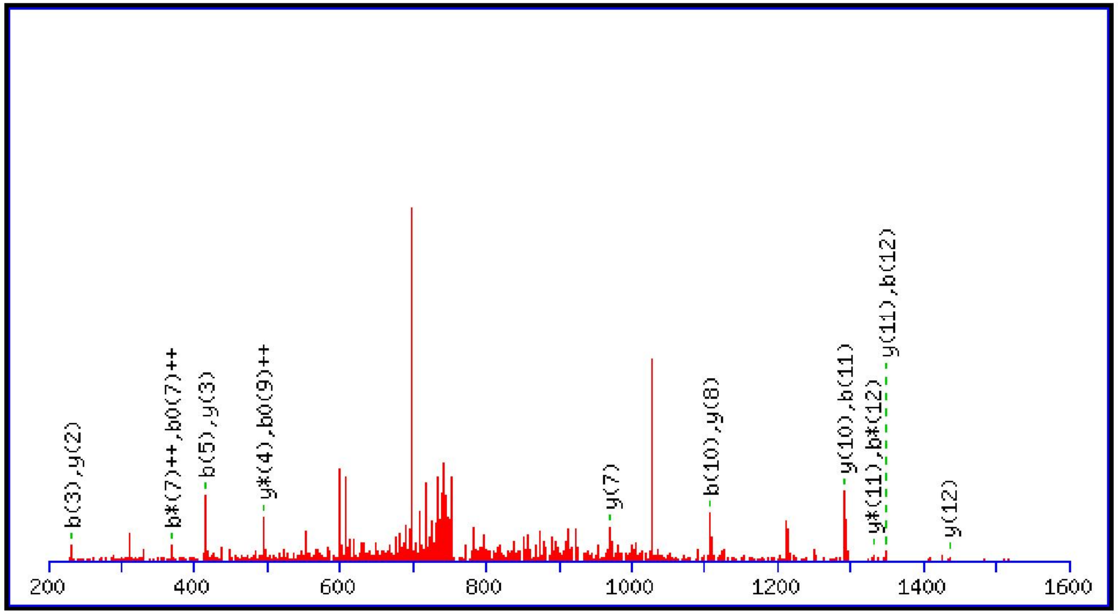
Monoisotopic mass of neutral peptide Mr(calc): 733.4759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 32 **Expect:** 0.06
Matches : 4/32 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	203.1663	102.0868	186.1397	93.5735	K					5
2	300.2191	150.6132	283.1925	142.0999	P	*532.3242*	266.6657	515.2976	258.1525	4
3	413.3031	207.1552	396.2766	198.6419	L	*435.2714*	218.1394	418.2449	209.6261	3
4	560.3715	280.6894	543.3450	272.1761	F	*322.1874*	161.5973	305.1608	153.0840	2
5					R	*175.1190*	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **SSGALHKRVPKGR**
Found in **Q9P2G4**, Microtubule-associated protein 10 OS=Homo sapiens GN=MAP10 PE=1 SV=2

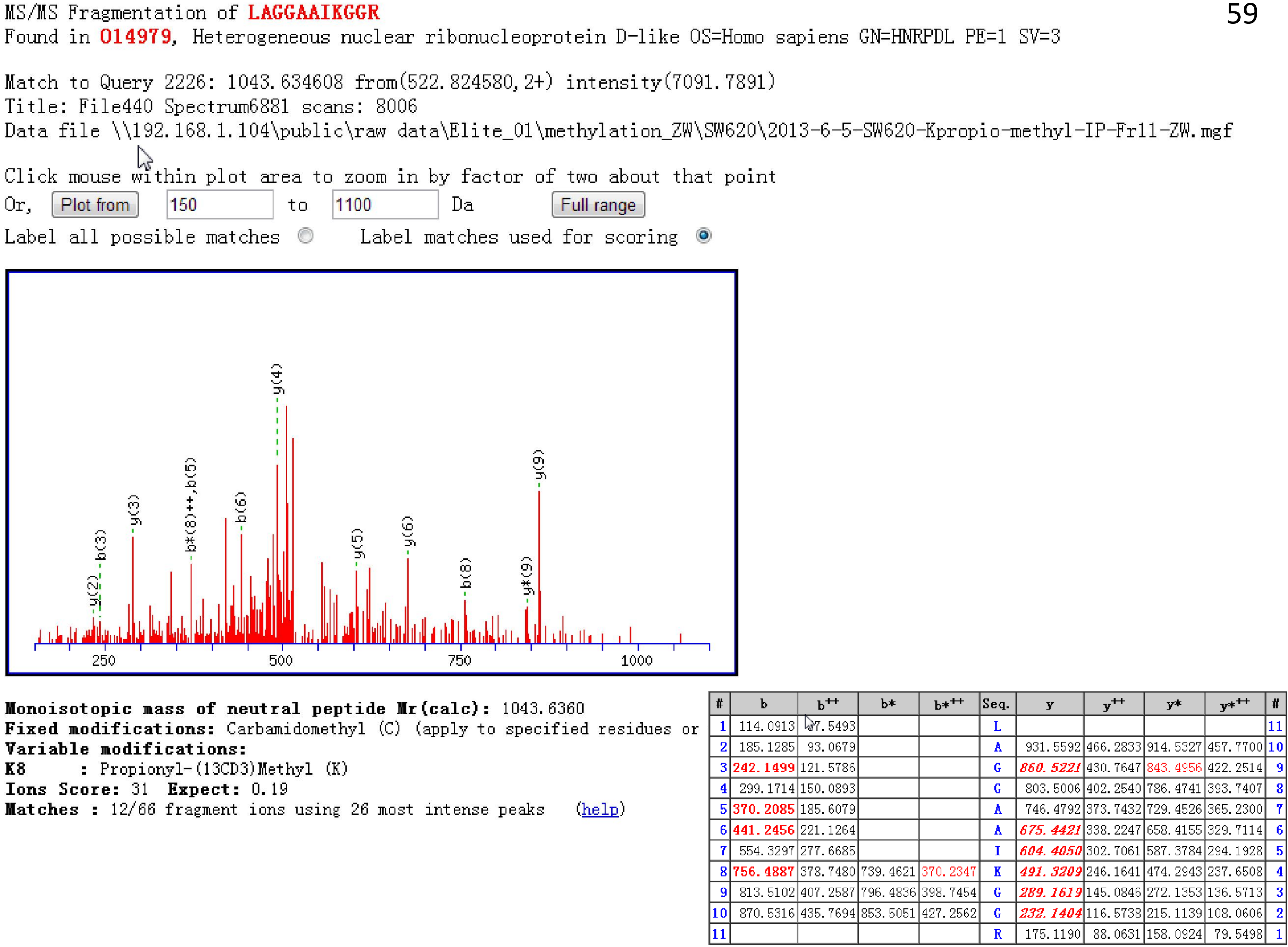
Match to Query 7903: 1521.887908 from(761.951230,2+) intensity(32169.0371)
Title: File660 Spectrum7847 scans: 9170
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1521.9012
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
K11 : Propionyl (K)
Ions Score: 31 **Expect:** 0.26
Matches : 18/110 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	175.0713	88.0393			157.0608	79.0340	S	***1435.8765***	718.4419	1418.8499	709.9286	1417.8659	709.4366	12
3	**232.0928**	116.5500			214.0822	107.5448	G	***1348.8445***	674.9259	1331.8179	666.4126			11
4	303.1299	152.0686			285.1193	143.0633	A	***1291.8230***	646.4151	1274.7964	637.9019			10
5	**416.2140**	208.6106			398.2034	199.6053	L	1220.7859	610.8966	1203.7593	602.3833			9
6	553.2729	277.1401			535.2623	268.1348	H	***1107.7018***	554.3545	1090.6753	545.8413			8
7	755.4319	378.2196	738.4054	369.7063	737.4213	369.2143	K	***970.6429***	485.8251	953.6163	477.3118			7
8	911.5330	456.2701	894.5065	447.7569	893.5224	447.2649	R	768.4839	384.7456	751.4573	376.2323			6
9	1010.6014	505.8044	993.5749	497.2911	992.5909	496.7991	V	612.3828	306.6950	595.3562	298.1817			5
10	**1107.6542**	554.3307	1090.6276	545.8175	1089.6436	545.3254	P	513.3144	257.1608	496.2878	248.6475			4
11	**1291.7754**	646.3913	1274.7488	637.8780	1273.7648	637.3860	K	***416.2616***	208.6344	399.2350	200.1212			3
12	**1348.7968**	674.9021	1331.7703	666.3888	1330.7863	665.8968	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1



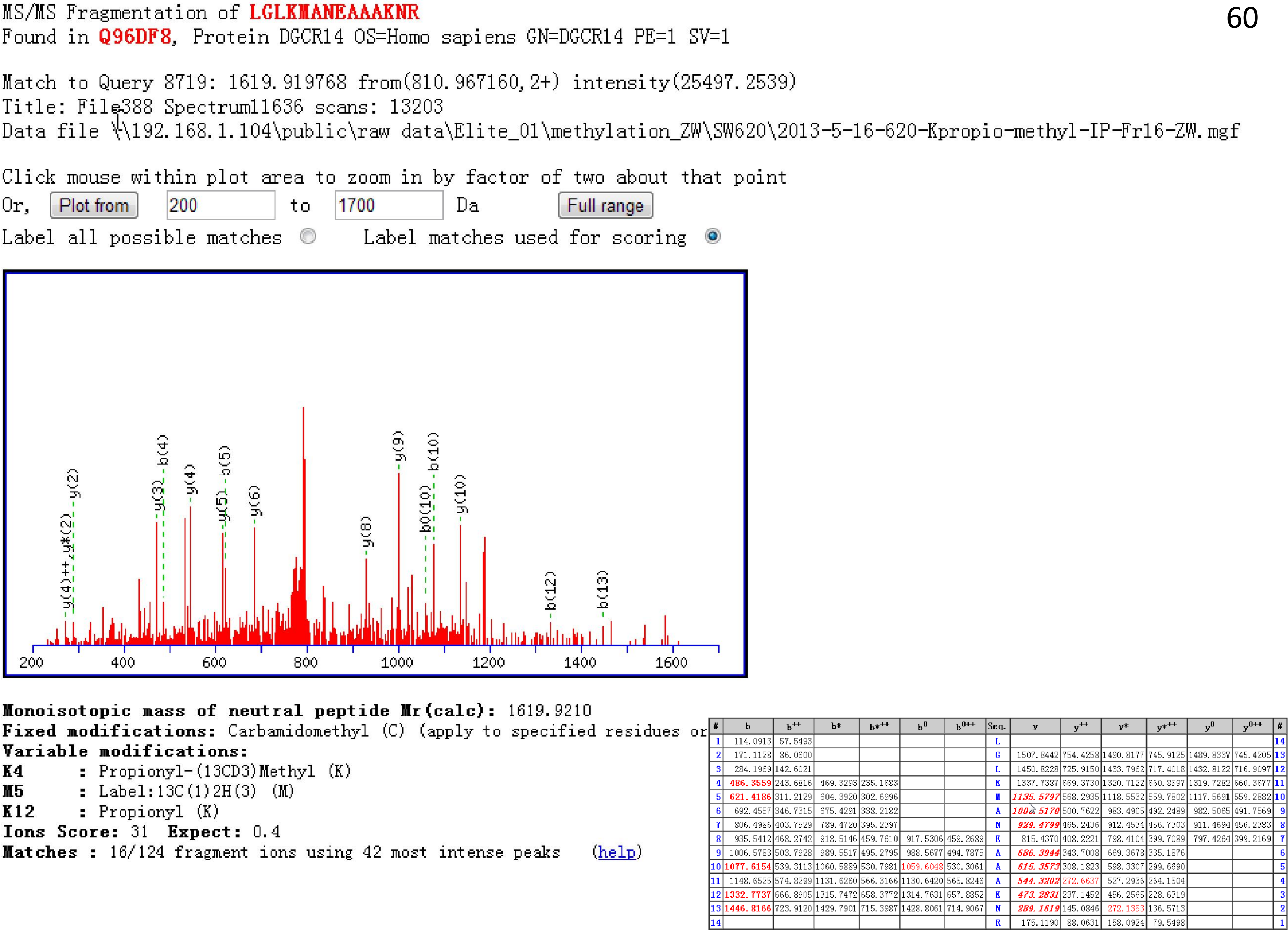
MS/MS Fragmentation of **LAGGAAIKGGR**
Found in **O14979**, Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3

Match to Query 2226: 1043.634608 from(522.824580,2+) intensity(7091.7891)
Title: File440 Spectrum6881 scans: 8006
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1043.6360
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 31 **Expect:** 0.19
Matches : 12/66 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			L					11
2	185.1285	93.0679			A	931.5592	466.2833	914.5327	457.7700	10
3	**242.1499**	121.5786			G	***860.5221***	430.7647	843.4956	422.2514	9
4	299.1714	150.0893			G	803.5006	402.2540	786.4741	393.7407	8
5	**370.2085**	185.6079			A	746.4792	373.7432	729.4526	365.2300	7
6	**441.2456**	221.1264			A	***675.4421***	338.2247	658.4155	329.7114	6
7	554.3297	277.6685			I	***604.4050***	302.7061	587.3784	294.1928	5
8	**756.4887**	378.7480	739.4621	370.2347	K	***491.3209***	246.1641	474.2943	237.6508	4
9	813.5102	407.2587	796.4836	398.7454	G	***289.1619***	145.0846	272.1353	136.5713	3
10	870.5316	435.7694	853.5051	427.2562	G	***232.1404***	116.5738	215.1139	108.0606	2
11					R	175.1190	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **LGLKMANEAAAKNR**
Found in **Q96DF8**, Protein DGCR14 OS=Homo sapiens GN=DGCR14 PE=1 SV=1

Match to Query 8719: 1619.919768 from(810.967160,2+) intensity(25497.2539)
Title: File388 Spectrum11636 scans: 13203
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1619.9210
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or

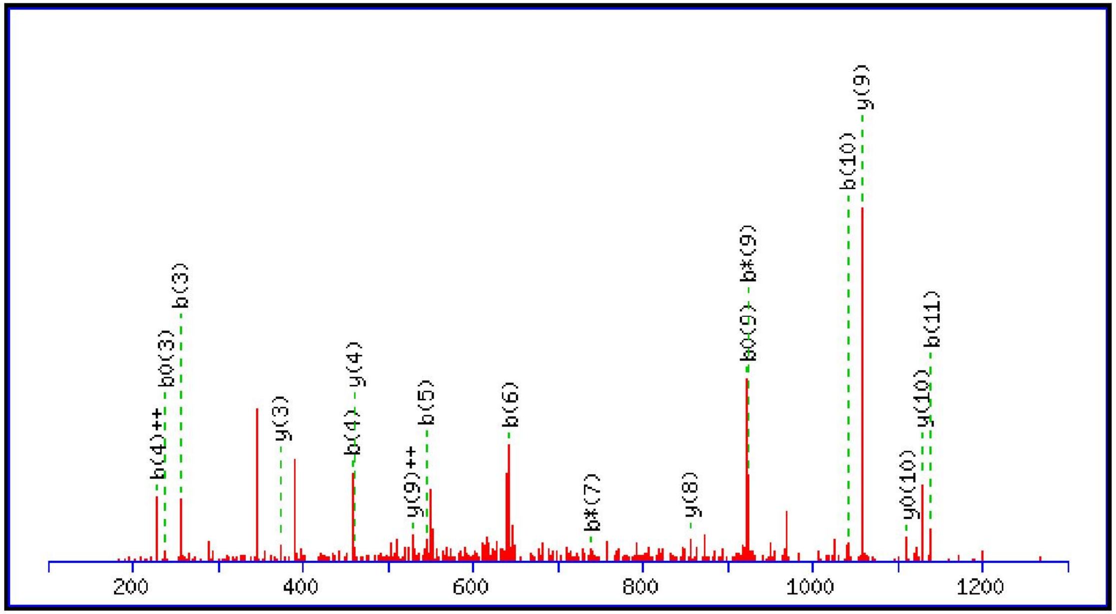
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
M5 : Label:13C(1)2H(3) (M)
K12 : Propionyl (K)
Ions Score: 31 **Expect:** 0.4
Matches : 16/124 fragment ions using 42 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							14
2	171.1128	86.0600					G	1507.8442	754.4258	1490.8177	745.9125	1489.8337	745.4205	13
3	284.1969	142.6021					L	1450.8228	725.9150	1433.7962	717.4018	1432.8122	716.9097	12
4	**486.3559**	243.6816	469.3293	235.1683			K	1337.7387	669.3730	1320.7122	660.8597	1319.7282	660.3677	11
5	**621.4186**	311.2129	604.3920	302.6996			M	***1135.5797***	568.2935	1118.5532	559.7802	1117.5691	559.2882	10
6	692.4557	346.7315	675.4291	338.2182			A	***1000.5170***	500.7622	983.4905	492.2489	982.5065	491.7569	9
7	806.4986	403.7529	789.4720	395.2397			N	***929.4799***	465.2436	912.4534	456.7303	911.4694	456.2383	8
8	935.5412	468.2742	918.5146	459.7610	917.5306	459.2689	E	815.4370	408.2221	798.4104	399.7089	797.4264	399.2169	7
9	1006.5783	503.7928	989.5517	495.2795	988.5677	494.7875	A	***686.3944***	343.7008	669.3678	335.1876			6
10	**1077.6154**	539.3113	1060.5889	530.7981	1059.6048	530.3061	A	***615.3573***	308.1823	598.3307	299.6690			5
11	1148.6525	574.8299	1131.6260	566.3166	1130.6420	565.8246	A	***544.3202***	272.6637	527.2936	264.1504			4
12	**1332.7737**	666.8905	1315.7472	658.3772	1314.7631	657.8852	K	***473.2831***	237.1452	456.2565	228.6319			3
13	**1446.8166**	723.9120	1429.7901	715.3987	1428.8061	714.9067	N	***289.1619***	145.0846	272.1353	136.5713			2
14							R	175.1190	88.0631	158.0924	79.5498			1

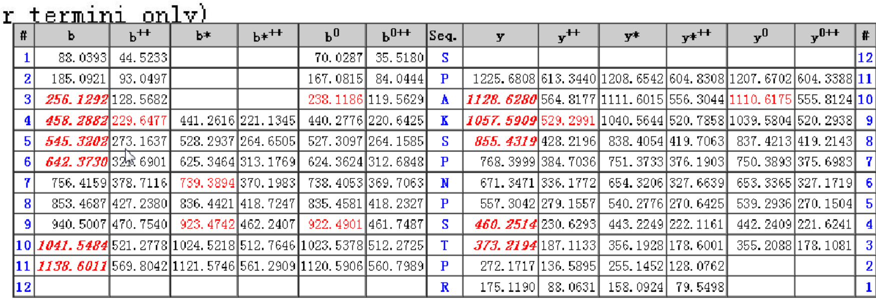
MS/MS Fragmentation of SPAKSPNPSTPR
Found in B4DJ58, Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=2 SV=1

Match to Query 4807: 1311.698208 from(656.856380,2+) intensity(215553.1875)
Title: File440 Spectrum11498 scans: 12950
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

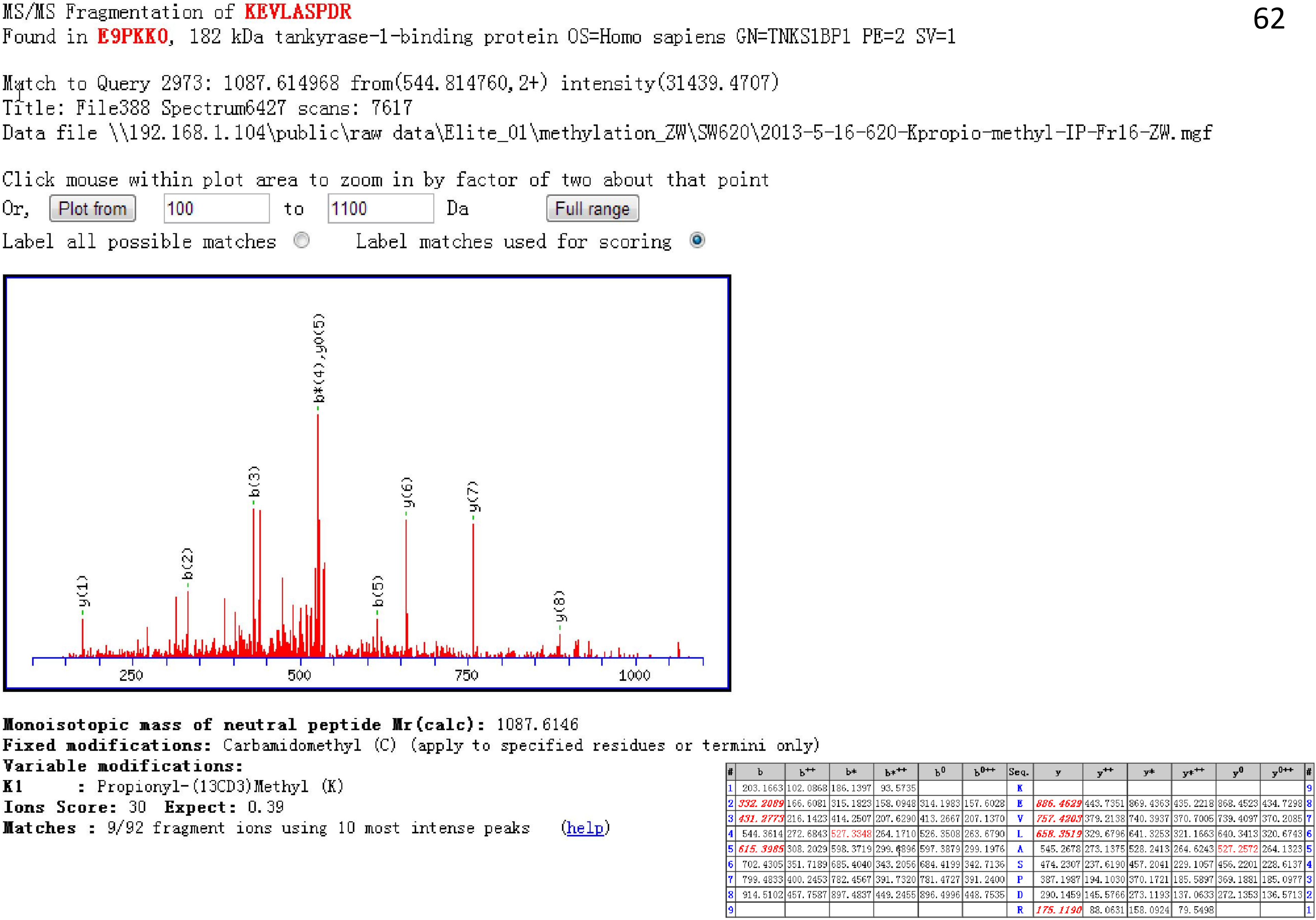
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1311.7055
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 31 **Expect:** 0.36
Matches : 18/122 fragment ions using 44 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	185.0921	93.0497			167.0815	84.0444	P	1225.6808	613.3440	1208.6542	604.8308	1207.6702	604.3388	11
3	***256.1292***	128.5682			238.1186	119.5629	A	***1128.6280***	564.8177	1111.6015	556.3044	1110.6175	555.8124	10
4	***458.2882***	229.6477	441.2616	221.1345	440.2776	220.6425	K	***1057.5909***	529.2991	1040.5644	520.7858	1039.5804	520.2938	9
5	***545.3202***	273.1637	528.2937	264.6505	527.3097	264.1585	S	***855.4319***	428.2196	838.4054	419.7063	837.4213	419.2143	8
6	***642.3730***	321.6901	625.3464	313.1769	624.3624	312.6848	P	768.3999	384.7036	751.3733	376.1903	750.3893	375.6983	7
7	756.4159	378.7116	739.3894	370.1983	738.4053	369.7063	N	671.3471	336.1772	654.3206	327.6639	653.3365	327.1719	6
8	853.4687	427.2380	836.4421	418.7247	835.4581	418.2327	P	557.3042	279.1557	540.2776	270.6425	539.2936	270.1504	5
9	940.5007	470.7540	923.4742	462.2407	922.4901	461.7487	S	***460.2514***	230.6293	443.2249	222.1161	442.2409	221.6241	4
10	***1041.5484***	521.2778	1024.5218	512.7646	1023.5378	512.2725	T	***373.2194***	187.1133	356.1928	178.6001	355.2088	178.1081	3
11	***1138.6011***	569.8042	1121.5746	561.2909	1120.5906	560.7989	P	272.1717	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of KEVLASPDR
Found in E9PKK0, 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=2 SV=1

Match to Query 2973: 1087.614968 from(544.814760,2+) intensity(31439.4707)
Title: File388 Spectrum6427 scans: 7617
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

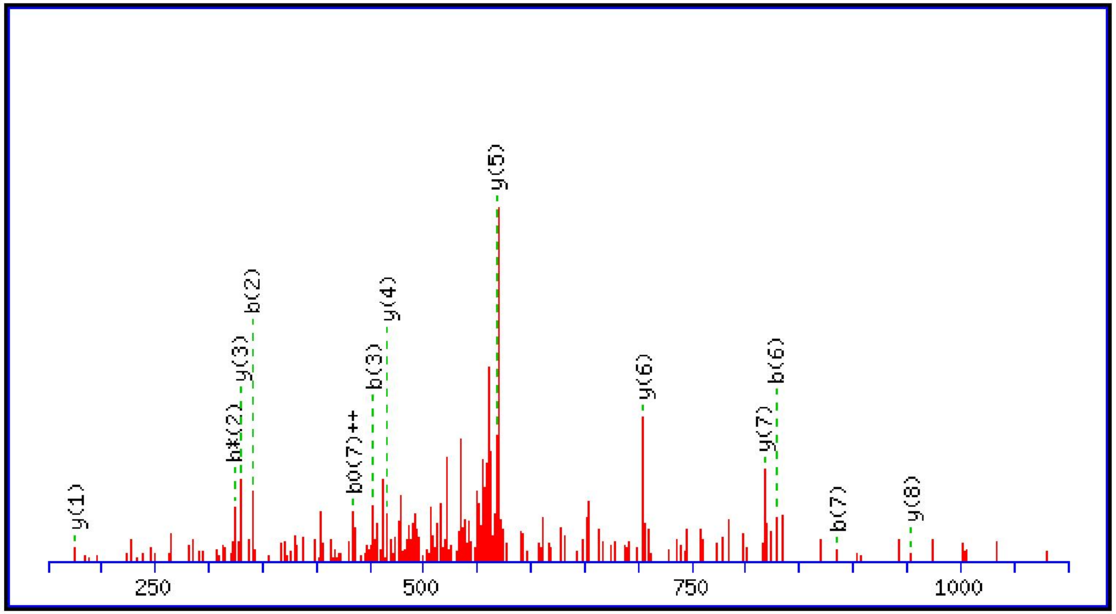
Monoisotopic mass of neutral peptide Mr(calc): 1087.6146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 30 **Expect:** 0.39
Matches : 9/92 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	*332.2089*	166.6081	315.1823	158.0948	314.1983	157.6028	E	*886.4629*	443.7351	869.4363	435.2218	868.4523	434.7298	8
3	*431.2773*	216.1423	414.2507	207.6290	413.2667	207.1370	V	*757.4203*	379.2138	740.3937	370.7005	739.4097	370.2085	7
4	544.3614	272.6843	527.3348	264.1710	526.3508	263.6790	L	*658.3519*	329.6796	641.3253	321.1663	640.3413	320.6743	6
5	*615.3985*	308.2029	598.3719	299.6896	597.3879	299.1976	A	545.2678	273.1375	528.2413	264.6243	527.2572	264.1323	5
6	702.4305	351.7189	685.4040	343.2056	684.4199	342.7136	S	474.2307	237.6190	457.2041	229.1057	456.2201	228.6137	4
7	799.4833	400.2453	782.4567	391.7320	781.4727	391.2400	P	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	3
8	914.5102	457.7587	897.4837	449.2455	896.4996	448.7535	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
9							R	*175.1190*	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KHLHTHGPR**
Found in **P25490**, Transcriptional repressor protein YY1 OS=Homo sapiens GN=YY1 PE=1 SV=2

Match to Query 3002: 1155.653548 from(578.834050,2+) intensity(4199.0898)
Title: File660 Spectrum373 scans: 902
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



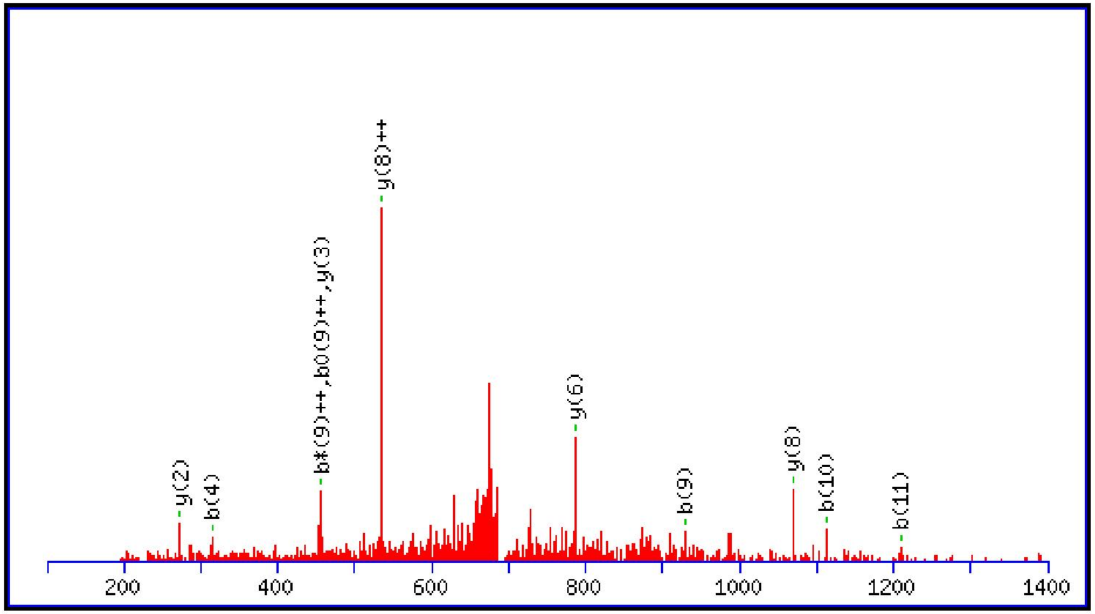
Monoisotopic mass of neutral peptide Mr(calc): 1155.6534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 30 **Expect:** 0.43
Matches : 13/80 fragment ions using 45 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**340.2252**	170.6162	323.1987	162.1030			H	***954.5017***	477.7545	937.4751	469.2412	936.4911	468.7492	8
3	**453.3093**	227.1583	436.2827	218.6450			L	***817.4427***	409.2250	800.4162	400.7117	799.4322	400.2197	7
4	590.3682	295.6877	573.3416	287.1745			H	***704.3587***	352.6830	687.3321	344.1697	686.3481	343.6777	6
5	691.4159	346.2116	674.3893	337.6983	673.4053	337.2063	T	***567.2998***	284.1535	550.2732	275.6402	549.2892	275.1482	5
6	**828.4748**	414.7410	811.4482	406.2277	810.4642	405.7357	H	***466.2521***	233.6297	449.2255	225.1164			4
7	**885.4962**	443.2518	868.4697	434.7385	867.4857	434.2465	G	***329.1932***	165.1002	312.1666	156.5870			3
8	982.5490	491.7781	965.5224	483.2649	964.5384	482.7729	P	272.1717	136.5895	255.1452	128.0762			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

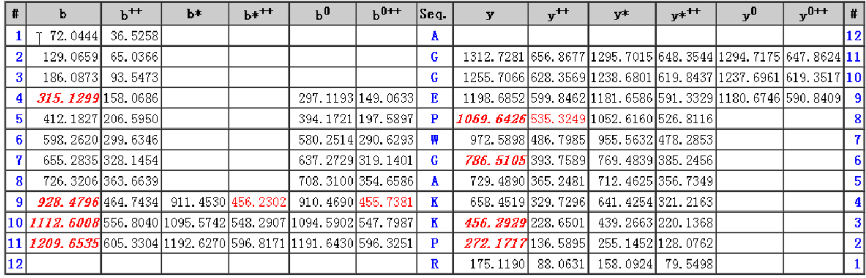
MS/MS Fragmentation of **AGGEPWGAKKPR**
Found in **E5RHJ4**, DBIRD complex subunit KIAA1967 (Fragment) OS=Homo sapiens GN=KIAA1967 PE=2 SV=1

Match to Query 6455: 1382.759128 from(692.386840,2+) intensity(46311.7227)
Title: File394 Spectrum11304 scans: 12692
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

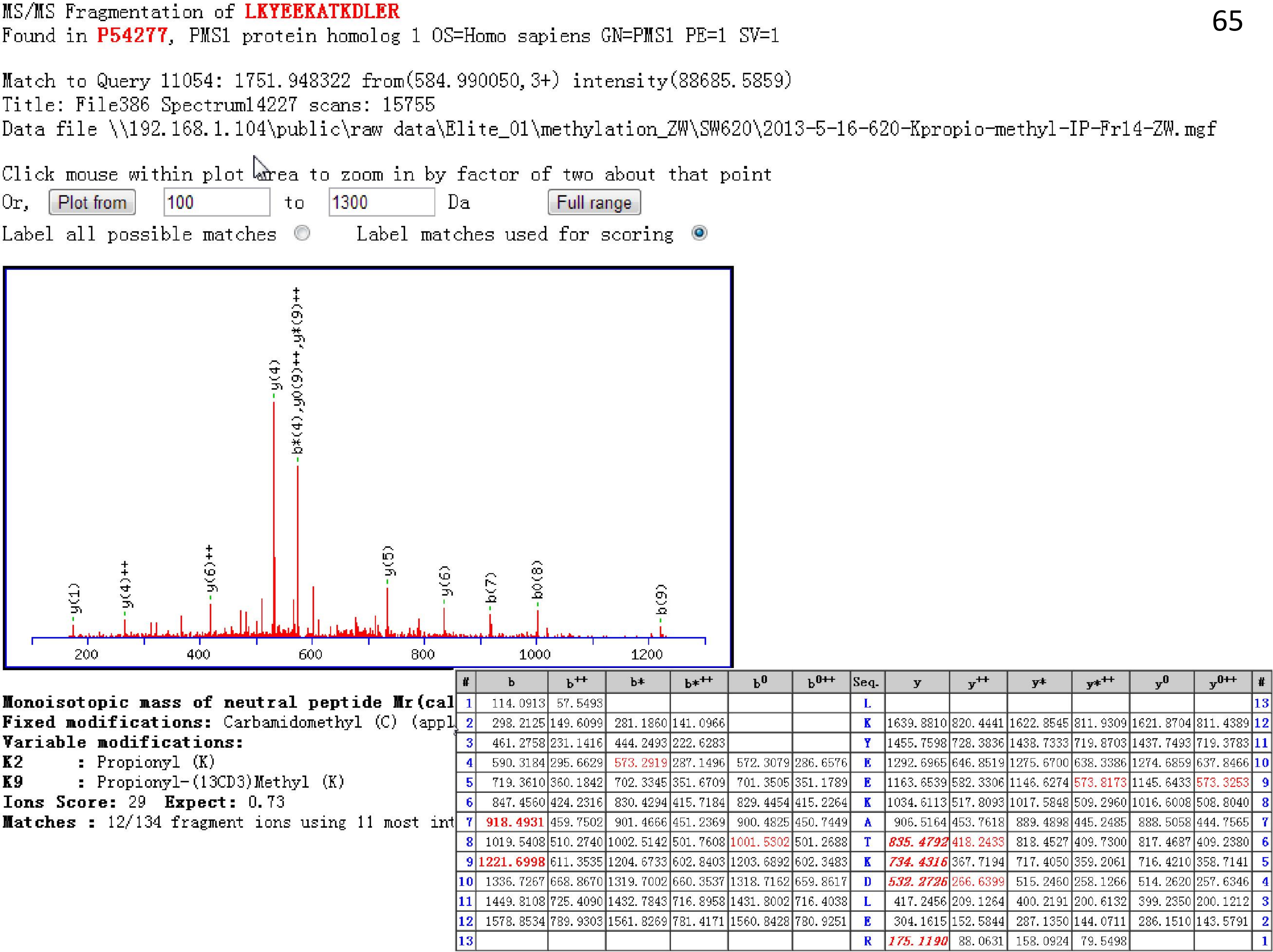
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1382.7579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 29 **Expect:** 0.55
Matches : 11/94 fragment ions using 12 most intense peaks (help)



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	129.0659	65.0366					G	1312.7281	656.8677	1295.7015	648.3544	1294.7175	647.8624	11
3	186.0873	93.5473					G	1255.7066	628.3569	1238.6801	619.8437	1237.6961	619.3517	10
4	***315.1299***	158.0686			297.1193	149.0633	E	1198.6852	599.8462	1181.6586	591.3329	1180.6746	590.8409	9
5	412.1827	206.5950			394.1721	197.5897	P	***1069.6426***	535.3249	1052.6160	526.8116			8
6	598.2620	299.6346			580.2514	290.6293	W	972.5898	486.7985	955.5632	478.2853			7
7	655.2835	328.1454			637.2729	319.1401	G	***786.5105***	393.7589	769.4839	385.2456			6
8	726.3206	363.6639			708.3100	354.6586	A	729.4890	365.2481	712.4625	356.7349			5
9	***928.4796***	464.7434	911.4530	456.2302	910.4690	455.7381	K	658.4519	329.7296	641.4254	321.2163			4
10	***1112.6008***	556.8040	1095.5742	548.2907	1094.5902	547.7987	K	***456.2929***	228.6501	439.2663	220.1368			3
11	***1209.6535***	605.3304	1192.6270	596.8171	1191.6430	596.3251	P	***272.1717***	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LKYEEKATKDLER**
Found in **P54277**, PMS1 protein homolog 1 OS=Homo sapiens GN=PMS1 PE=1 SV=1

Match to Query 11054: 1751.948322 from(584.990050,3+) intensity(88685.5859)
Title: File386 Spectrum14227 scans: 15755
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.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 ●

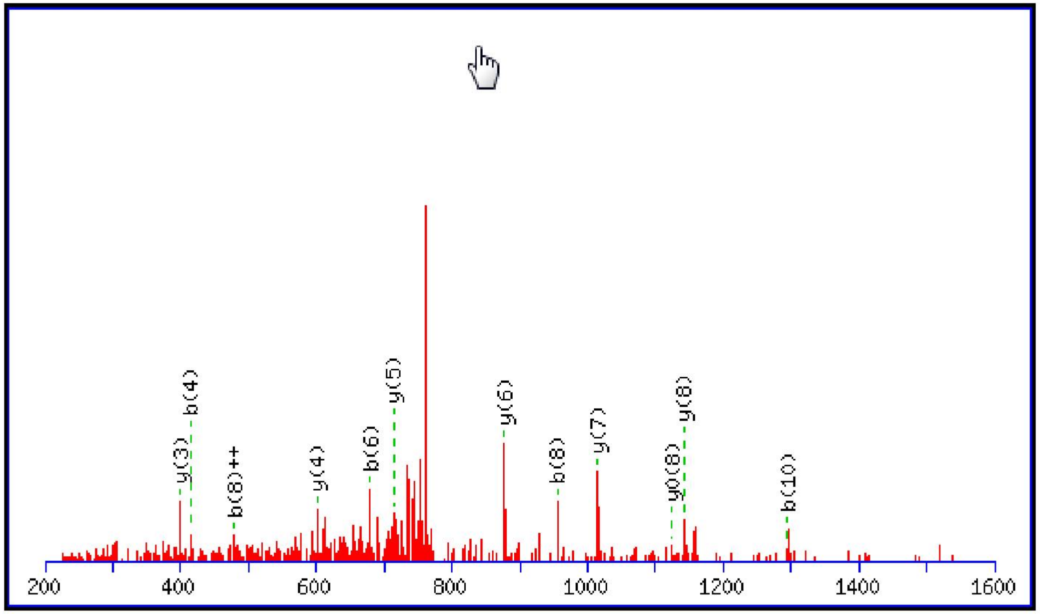
Monoisotopic mass of neutral peptide Mr(cal
Fixed modifications: Carbamidomethyl (C) (appl
Variable modifications:
K2 : Propionyl (K)
K9 : Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.73
Matches : 12/134 fragment ions using 11 most int

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							13
2	298.2125	149.6099	281.1860	141.0966			K	1639.8810	820.4441	1622.8545	811.9309	1621.8704	811.4389	12
3	461.2758	231.1416	444.2493	222.6283			Y	1455.7598	728.3836	1438.7333	719.8703	1437.7493	719.3783	11
4	590.3184	295.6629	573.2919	287.1496	572.3079	286.6576	E	1292.6965	646.8519	1275.6700	638.3386	1274.6859	637.8466	10
5	719.3610	360.1842	702.3345	351.6709	701.3505	351.1789	E	1163.6539	582.3306	1146.6274	573.8173	1145.6433	573.3253	9
6	847.4560	424.2316	830.4294	415.7184	829.4454	415.2264	K	1034.6113	517.8093	1017.5848	509.2960	1016.6008	508.8040	8
7	**918.4931**	459.7502	901.4666	451.2369	900.4825	450.7449	A	906.5164	453.7618	889.4898	445.2485	888.5058	444.7565	7
8	1019.5408	510.2740	1002.5142	501.7608	1001.5302	501.2688	T	***835.4792***	418.2433	818.4527	409.7300	817.4687	409.2380	6
9	**1221.6998**	611.3535	1204.6733	602.8403	1203.6892	602.3483	K	***734.4316***	367.7194	717.4050	359.2061	716.4210	358.7141	5
10	1336.7267	668.8670	1319.7002	660.3537	1318.7162	659.8617	D	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
11	1449.8108	725.4090	1432.7843	716.8958	1431.8002	716.4038	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
12	1578.8534	789.9303	1561.8269	781.4171	1560.8428	780.9251	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SAAKQHYLKHSR**
Found in **Q9UPZ9**, Serine/threonine-protein kinase ICK OS=Homo sapiens GN=ICK PE=1 SV=1

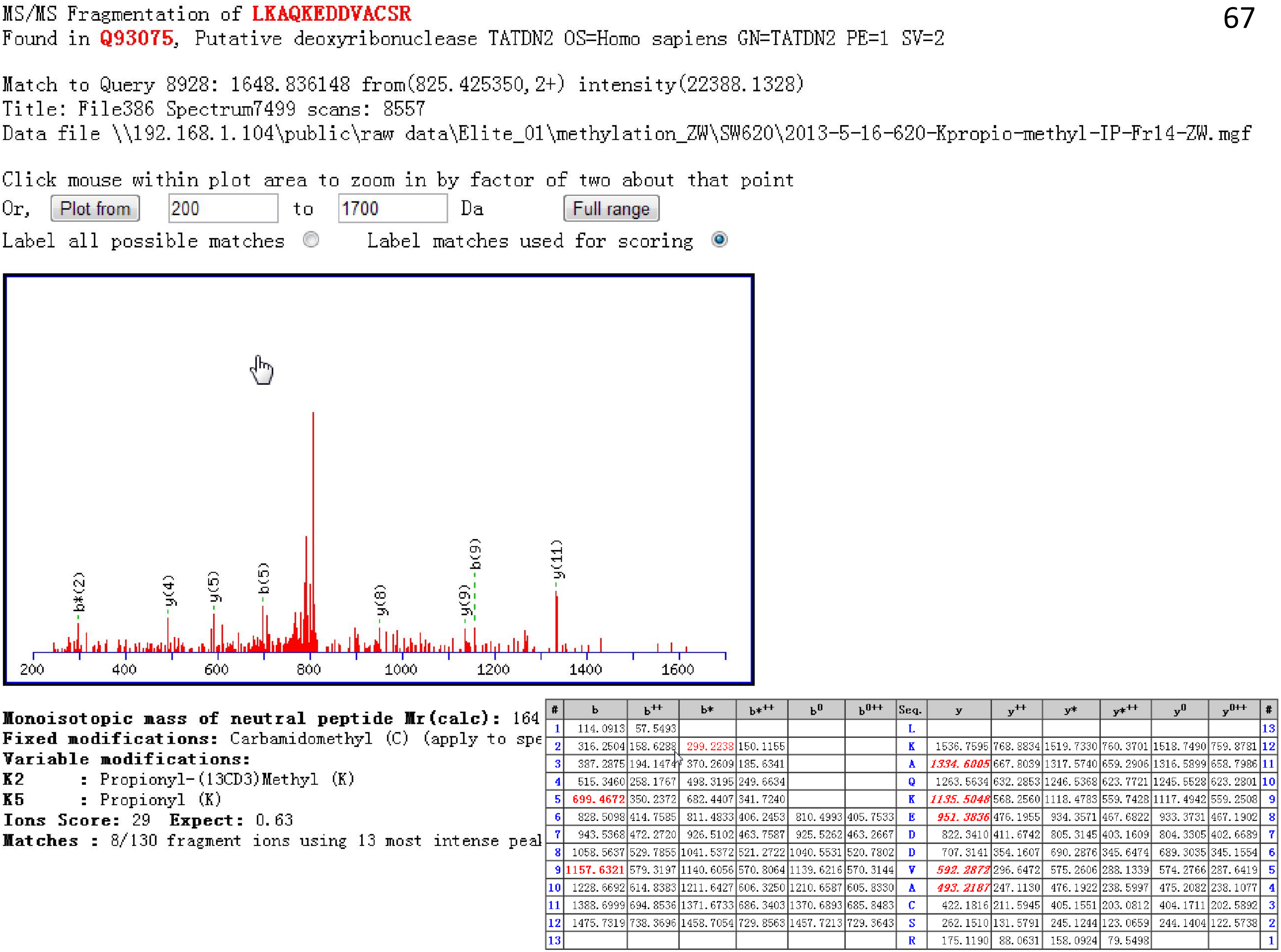
Match to Query 9041: 1555.858008 from(778.936280,2+) intensity(28214.5996)
Title: File394 Spectrum5163 scans: 6065
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1554.8539
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl (K)
K9 : Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.69
Matches : 12/124 fragment ions using 27 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	159.0764	80.0418			141.0659	71.0366	A	1468.8292	734.9182	1451.8026	726.4050	1450.8186	725.9130	11
3	230.1135	115.5604			212.1030	106.5551	A	1397.7921	699.3997	1380.7655	690.8864	1379.7815	690.3944	10
4	**414.2347**	207.6210	397.2082	199.1077	396.2241	198.6157	K	1326.7550	663.8811	1309.7284	655.3678	1308.7444	654.8758	9
5	542.2933	271.6503	525.2667	263.1370	524.2827	262.6450	Q	***1142.6338***	571.8205	1125.6072	563.3073	1124.6232	562.8152	8
6	**679.3522**	340.1797	662.3257	331.6665	661.3416	331.1745	H	***1014.5752***	507.7912	997.5487	499.2780	996.5646	498.7860	7
7	842.4155	421.7114	825.3890	413.1981	824.4050	412.7061	Y	***877.5163***	439.2618	860.4897	430.7485	859.5057	430.2565	6
8	**955.4996**	478.2534	938.4730	469.7402	937.4890	469.2482	L	***714.4530***	357.7301	697.4264	349.2168	696.4424	348.7248	5
9	1157.6586	579.3329	1140.6321	570.8197	1139.6480	570.3277	K	***601.3689***	301.1881	584.3424	292.6748	583.3583	292.1828	4
10	**1294.7175**	647.8624	1277.6910	639.3491	1276.7070	638.8571	H	***399.2099***	200.1086	382.1833	191.5953	381.1993	191.1033	3
11	1381.7495	691.3784	1364.7230	682.8651	1363.7390	682.3731	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



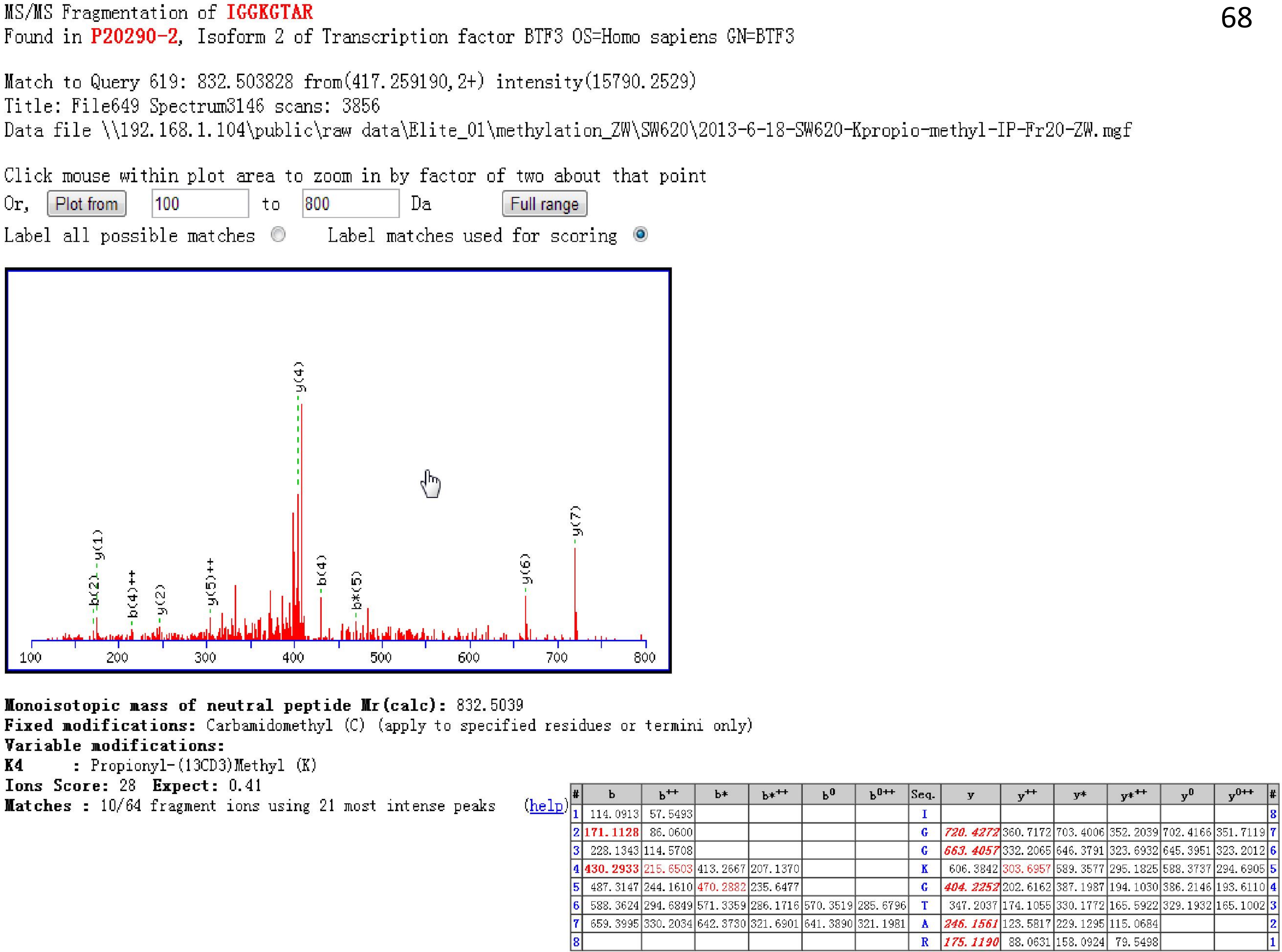
MS/MS Fragmentation of **LKAQKEDDVACSR**
Found in **Q93075**, Putative deoxyribonuclease TATDN2 OS=Homo sapiens GN=TATDN2 PE=1 SV=2

Match to Query 8928: 1648.836148 from(825.425350,2+) intensity(22388.1328)
Title: File386 Spectrum7499 scans: 8557
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 164
Fixed modifications: Carbamidomethyl (C) (apply to spe
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
Ions Score: 29 **Expect:** 0.63
Matches : 8/130 fragment ions using 13 most intense peal

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							13
2	316.2504	158.6288	299.2238	150.1155			K	1536.7595	768.8834	1519.7330	760.3701	1518.7490	759.8781	12
3	387.2875	194.1474	370.2609	185.6341			A	***1334.6005***	667.8039	1317.5740	659.2906	1316.5899	658.7986	11
4	515.3460	258.1767	498.3195	249.6634			Q	1263.5634	632.2853	1246.5368	623.7721	1245.5528	623.2801	10
5	**699.4672**	350.2372	682.4407	341.7240			K	***1135.5048***	568.2560	1118.4783	559.7428	1117.4942	559.2508	9
6	828.5098	414.7585	811.4833	406.2453	810.4993	405.7533	E	***951.3836***	476.1955	934.3571	467.6822	933.3731	467.1902	8
7	943.5368	472.2720	926.5102	463.7587	925.5262	463.2667	D	822.3410	411.6742	805.3145	403.1609	804.3305	402.6689	7
8	1058.5637	529.7855	1041.5372	521.2722	1040.5531	520.7802	D	707.3141	354.1607	690.2876	345.6474	689.3035	345.1554	6
9	**1157.6321**	579.3197	1140.6056	570.8064	1139.6216	570.3144	V	***592.2872***	296.6472	575.2606	288.1339	574.2766	287.6419	5
10	1228.6692	614.8383	1211.6427	606.3250	1210.6587	605.8330	A	***493.2187***	247.1130	476.1922	238.5997	475.2082	238.1077	4
11	1388.6999	694.8536	1371.6733	686.3403	1370.6893	685.8483	C	422.1816	211.5945	405.1551	203.0812	404.1711	202.5892	3
12	1475.7319	738.3696	1458.7054	729.8563	1457.7213	729.3643	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



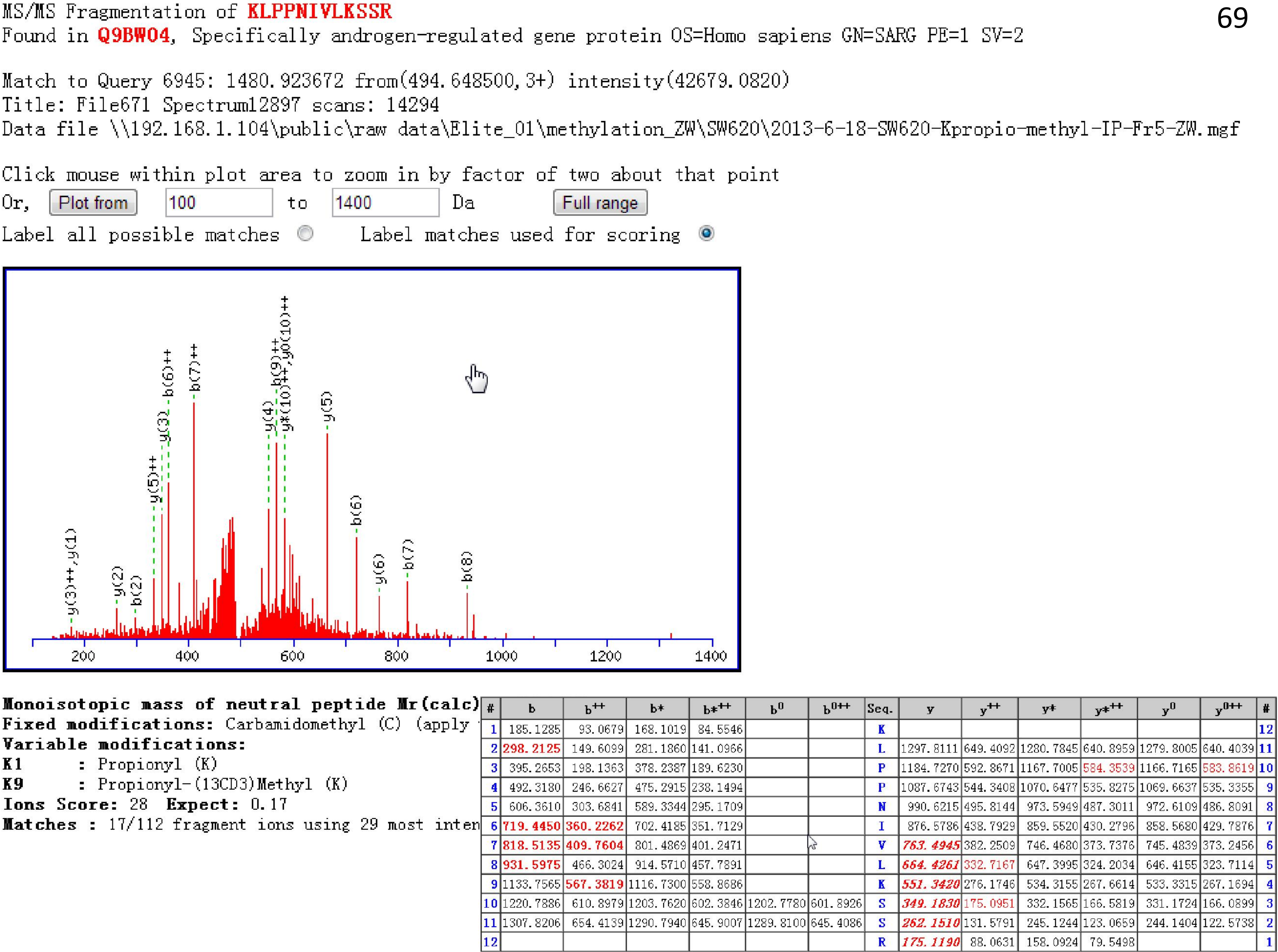
MS/MS Fragmentation of IGGKGTAR
Found in P20290-2, Isoform 2 of Transcription factor BTF3 OS=Homo sapiens GN=BTF3

Match to Query 619: 832.503828 from(417.259190,2+) intensity(15790.2529)
Title: File649 Spectrum3146 scans: 3856
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr20-ZW.mgf

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

Monoisotopic mass of neutral peptide Mr(calc): 832.5039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 28 **Expect:** 0.41
Matches : 10/64 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							8
2	**171.1128**	86.0600					G	***720.4272***	360.7172	703.4006	352.2039	702.4166	351.7119	7
3	228.1343	114.5708					G	***663.4057***	332.2065	646.3791	323.6932	645.3951	323.2012	6
4	**430.2933**	215.6503	413.2667	207.1370			K	606.3842	303.6957	589.3577	295.1825	588.3737	294.6905	5
5	487.3147	244.1610	470.2882	235.6477			G	***404.2252***	202.6162	387.1987	194.1030	386.2146	193.6110	4
6	588.3624	294.6849	571.3359	286.1716	570.3519	285.6796	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
7	659.3995	330.2034	642.3730	321.6901	641.3890	321.1981	A	***246.1561***	123.5817	229.1295	115.0684			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



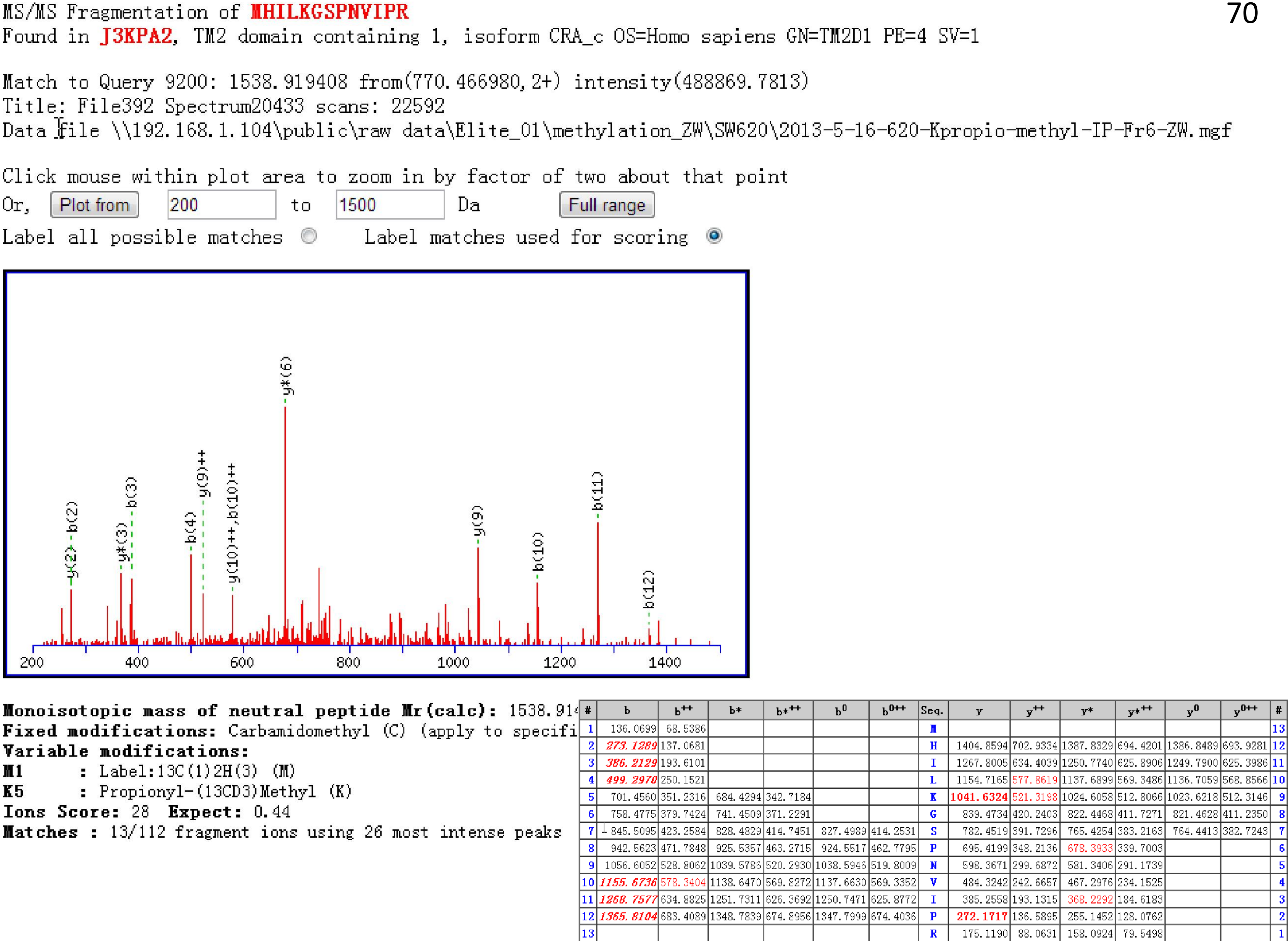
MS/MS Fragmentation of **KLPPNIVLKSSR**
Found in **Q9BW04**, Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2

Match to Query 6945: 1480.923672 from(494.648500,3+) intensity(42679.0820)
Title: File671 Spectrum12897 scans: 14294
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr5-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc)
Fixed modifications: Carbamidomethyl (C) (apply
Variable modifications:
K1 : Propionyl (K)
K9 : Propionyl-(13CD3)Methyl (K)
Ions Score: 28 **Expect:** 0.17
Matches : 17/112 fragment ions using 29 most inten

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							12
2	**298.2125**	149.6099	281.1860	141.0966			L	1297.8111	649.4092	1280.7845	640.8959	1279.8005	640.4039	11
3	395.2653	198.1363	378.2387	189.6230			P	1184.7270	592.8671	1167.7005	584.3539	1166.7165	583.8619	10
4	492.3180	246.6627	475.2915	238.1494			P	1087.6743	544.3408	1070.6477	535.8275	1069.6637	535.3355	9
5	606.3610	303.6841	589.3344	295.1709			N	990.6215	495.8144	973.5949	487.3011	972.6109	486.8091	8
6	**719.4450**	**360.2262**	702.4185	351.7129			I	876.5786	438.7929	859.5520	430.2796	858.5680	429.7876	7
7	**818.5135**	**409.7604**	801.4869	401.2471			V	***763.4945***	382.2509	746.4680	373.7376	745.4839	373.2456	6
8	**931.5975**	466.3024	914.5710	457.7891			L	***664.4261***	332.7167	647.3995	324.2034	646.4155	323.7114	5
9	1133.7565	**567.3819**	1116.7300	558.8686			K	***551.3420***	276.1746	534.3155	267.6614	533.3315	267.1694	4
10	1220.7886	610.8979	1203.7620	602.3846	1202.7780	601.8926	S	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	3
11	1307.8206	654.4139	1290.7940	645.9007	1289.8100	645.4086	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	***175.1190***	88.0631	158.0924	79.5498			1



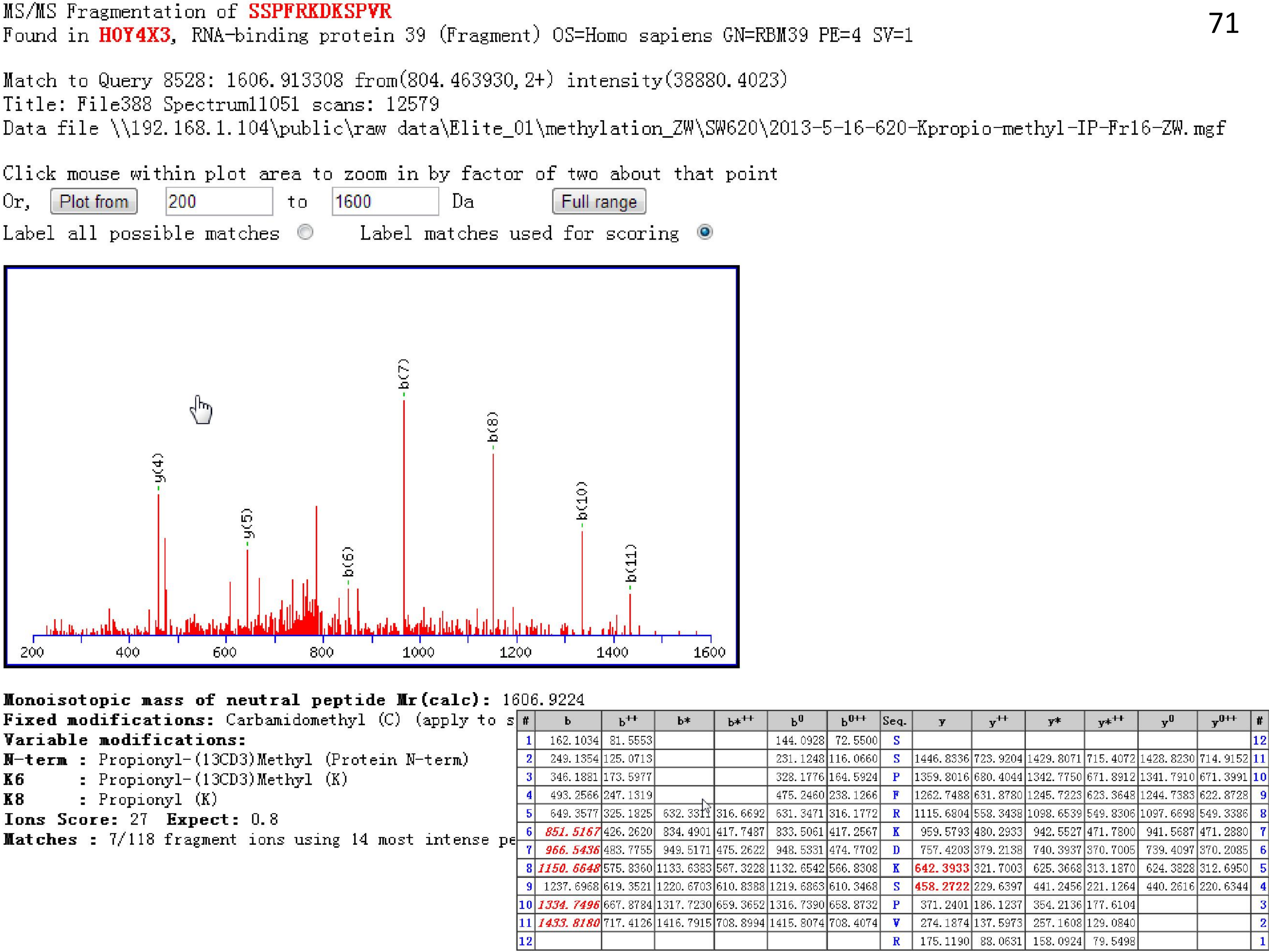
MS/MS Fragmentation of MHILKGSPNVIPR
Found in J3KPA2, TM2 domain containing 1, isoform CRA_c OS=Homo sapiens GN=TM2D1 PE=4 SV=1

Match to Query 9200: 1538.919408 from(770.466980,2+) intensity(488869.7813)
Title: File392 Spectrum20433 scans: 22592
Data File \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1538.91
Fixed modifications: Carbamidomethyl (C) (apply to specifi
Variable modifications:
M1 : Label:13C(1)2H(3) (M)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 28 **Expect:** 0.44
Matches : 13/112 fragment ions using 26 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	136.0699	68.5386					M							13
2	***273.1289***	137.0681					H	1404.8594	702.9334	1387.8329	694.4201	1386.8489	693.9281	12
3	***386.2129***	193.6101					I	1267.8005	634.4039	1250.7740	625.8906	1249.7900	625.3986	11
4	***499.2970***	250.1521					L	1154.7165	577.8619	1137.6899	569.3486	1136.7059	568.8566	10
5	701.4560	351.2316	684.4294	342.7184			K	**1041.6324**	521.3198	1024.6058	512.8066	1023.6218	512.3146	9
6	758.4775	379.7424	741.4509	371.2291			G	839.4734	420.2403	822.4468	411.7271	821.4628	411.2350	8
7	845.5095	423.2584	828.4829	414.7451	827.4989	414.2531	S	782.4519	391.7296	765.4254	383.2163	764.4413	382.7243	7
8	942.5623	471.7848	925.5357	463.2715	924.5517	462.7795	P	695.4199	348.2136	678.3933	339.7003			6
9	1056.6052	528.8062	1039.5786	520.2930	1038.5946	519.8009	N	598.3671	299.6872	581.3406	291.1739			5
10	***1155.6736***	578.3404	1138.6470	569.8272	1137.6630	569.3352	V	484.3242	242.6657	467.2976	234.1525			4
11	***1268.7577***	634.8825	1251.7311	626.3692	1250.7471	625.8772	I	385.2558	193.1315	368.2292	184.6183			3
12	***1365.8104***	683.4089	1348.7839	674.8956	1347.7999	674.4036	P	**272.1717**	136.5895	255.1452	128.0762			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **SSPFRKDKSPVR**
Found in **H0Y4X3**, RNA-binding protein 39 (Fragment) OS=Homo sapiens GN=RBM39 PE=4 SV=1

Match to Query 8528: 1606.913308 from(804.463930,2+) intensity(38880.4023)
Title: File388 Spectrum11051 scans: 12579
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

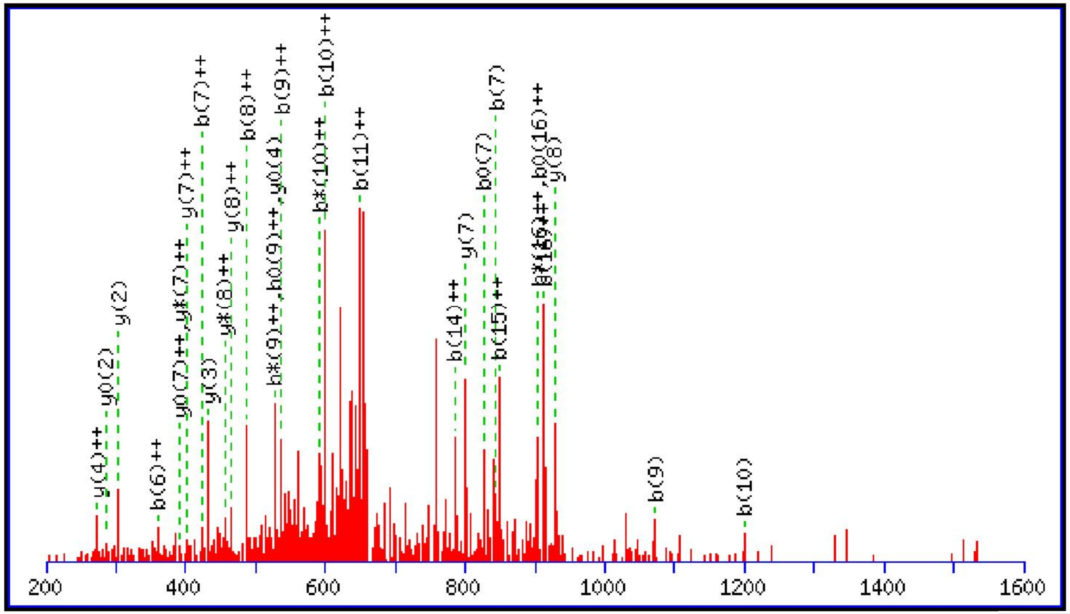
Monoisotopic mass of neutral peptide Mr(calc): 1606.9224
Fixed modifications: Carbamidomethyl (C) (apply to s
Variable modifications:
N-term : Propionyl-(13CD3)Methyl (Protein N-term)
K6 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 27 **Expect:** 0.8
Matches : 7/118 fragment ions using 14 most intense pe

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	162.1034	81.5553			144.0928	72.5500	S							12
2	249.1354	125.0713			231.1248	116.0660	S	1446.8336	723.9204	1429.8071	715.4072	1428.8230	714.9152	11
3	346.1881	173.5977			328.1776	164.5924	P	1359.8016	680.4044	1342.7750	671.8912	1341.7910	671.3991	10
4	493.2566	247.1319			475.2460	238.1266	F	1262.7488	631.8780	1245.7223	623.3648	1244.7383	622.8728	9
5	649.3577	325.1825	632.3311	316.6692	631.3471	316.1772	R	1115.6804	558.3438	1098.6539	549.8306	1097.6698	549.3386	8
6	***851.5167***	426.2620	834.4901	417.7487	833.5061	417.2567	K	959.5793	480.2933	942.5527	471.7800	941.5687	471.2880	7
7	***966.5436***	483.7755	949.5171	475.2622	948.5331	474.7702	D	757.4203	379.2138	740.3937	370.7005	739.4097	370.2085	6
8	***1150.6648***	575.8360	1133.6383	567.3228	1132.6542	566.8308	K	**642.3933**	321.7003	625.3668	313.1870	624.3828	312.6950	5
9	1237.6968	619.3521	1220.6703	610.8388	1219.6863	610.3468	S	**458.2722**	229.6397	441.2456	221.1264	440.2616	220.6344	4
10	***1334.7496***	667.8784	1317.7230	659.3652	1316.7390	658.8732	P	371.2401	186.1237	354.2136	177.6104			3
11	***1433.8180***	717.4126	1416.7915	708.8994	1415.8074	708.4074	V	274.1874	137.5973	257.1608	129.0840			2
12							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VLEDGKQQVQVVGLQER**
Found in **E9PB70**, Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=2 SV=1

Match to Query 13898: 1998.088572 from(667.036800,3+) intensity(7883.1938)
Title: File669 Spectrum7002 scans: 8134
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



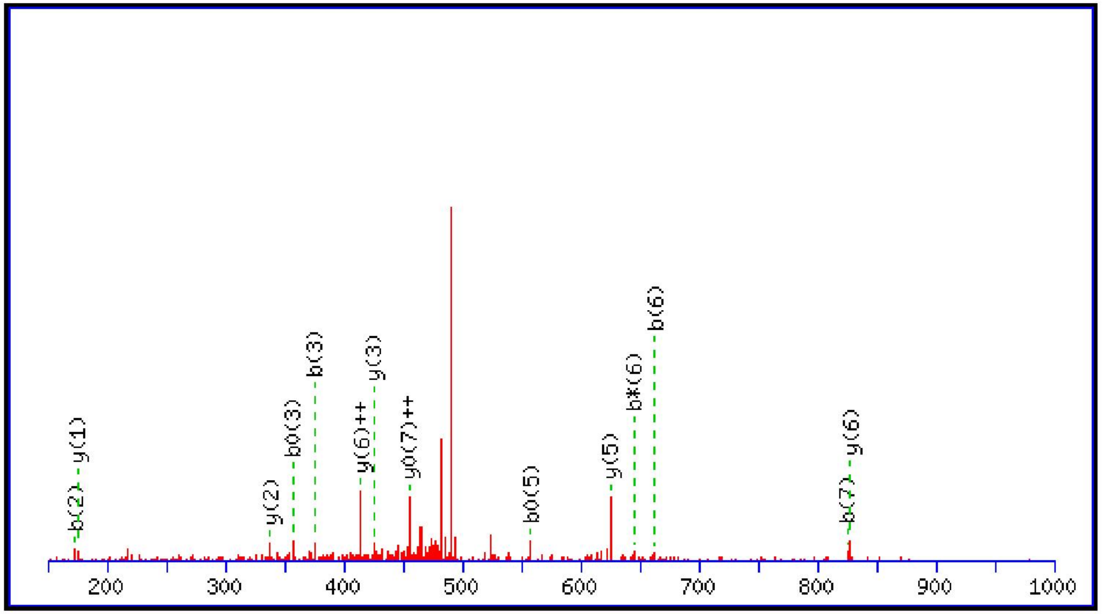
Monoisotopic mass of neutral peptide Mr(calc): 1998.1019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 27 **Expect:** 1.3
Matches : 30/176 fragment ions using 74 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							17
2	213.1598	107.0835					L	1900.0407	950.5240	1883.0142	942.0107	1882.0301	941.5187	16
3	342.2023	171.6048			324.1918	162.5995	E	1786.9566	893.9820	1769.9301	885.4687	1768.9461	884.9767	15
4	457.2293	229.1183			439.2187	220.1130	D	1657.9140	829.4607	1640.8875	820.9474	1639.9035	820.4554	14
5	514.2508	257.6290			496.2402	248.6237	G	1542.8871	771.9472	1525.8606	763.4339	1524.8765	762.9419	13
6	716.4098	***358.7085***	699.3832	350.1952	698.3992	349.7032	K	1485.8656	743.4365	1468.8391	734.9232	1467.8551	734.4312	12
7	**844.4683**	***422.7378***	827.4418	414.2245	826.4578	413.7325	Q	1283.7066	642.3570	1266.6801	633.8437	1265.6961	633.3517	11
8	972.5269	***486.7671***	955.5004	478.2538	954.5164	477.7618	Q	1155.6480	578.3277	1138.6215	569.8144	1137.6375	569.3224	10
9	**1071.5953**	***536.3013***	1054.5688	527.7880	1053.5848	527.2960	V	1027.5895	514.2984	1010.5629	505.7851	1009.5789	505.2931	9
10	**1199.6539**	***600.3306***	1182.6274	591.8173	1181.6434	591.3253	Q	**928.5211**	464.7642	911.4945	456.2509	910.5105	455.7589	8
11	1298.7223	***649.8648***	1281.6958	641.3515	1280.7118	640.8595	V	**800.4625**	400.7349	783.4359	392.2216	782.4519	391.7296	7
12	1397.7907	699.3990	1380.7642	690.8857	1379.7802	690.3937	V	701.3941	351.2007	684.3675	342.6874	683.3835	342.1954	6
13	1454.8122	727.9097	1437.7857	719.3965	1436.8016	718.9045	G	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	5
14	1567.8963	***784.4518***	1550.8697	775.9385	1549.8857	775.4465	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
15	1695.9548	***848.4811***	1678.9283	839.9678	1677.9443	839.4758	Q	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	3
16	1824.9974	***913.0024***	1807.9709	904.4891	1806.9869	903.9971	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
17							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ATKTVSYR**
Found in **Q8N8U2**, Chromodomain Y-like protein 2 OS=Homo sapiens GN=CDYL2 PE=1 SV=2

Match to Query 1110: 998.567168 from(500.290860,2+) intensity(14889.3145)
Title: File667 Spectrum2963 scans: 4199
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr18-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



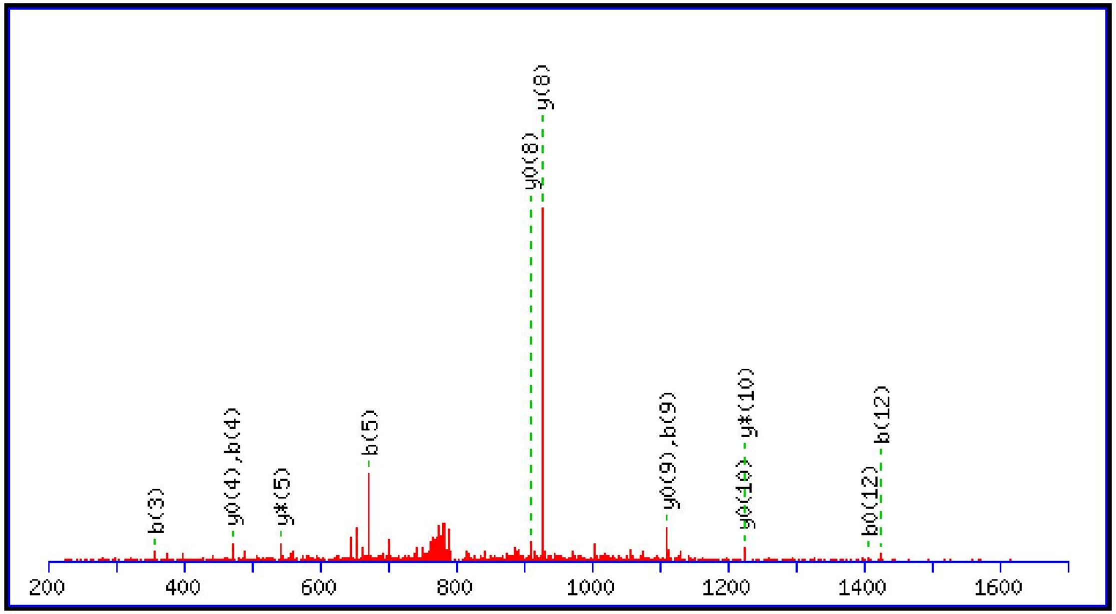
Monoisotopic mass of neutral peptide Mr(calc): 998.5669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 26 **Expect:** 0.88
Matches : 14/74 fragment ions using 32 most

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							8
2	**173.0921**	87.0497			155.0815	78.0444	T	928.5371	464.7722	911.5105	456.2589	910.5265	455.7669	7
3	**375.2511**	188.1292	358.2245	179.6159	357.2405	179.1239	K	***827.4894***	414.2483	810.4629	405.7351	809.4788	405.2431	6
4	476.2988	238.6530	459.2722	230.1397	458.2882	229.6477	T	***625.3304***	313.1688	608.3039	304.6556	607.3198	304.1636	5
5	575.3672	288.18[illegible]	558.3406	279.6740	557.3566	279.1819	V	524.2827	262.6450	507.2562	254.1317	506.2722	253.6397	4
6	**662.3992**	331.7032	645.3727	323.1900	644.3886	322.6980	S	***425.2143***	213.1108	408.1878	204.5975	407.2037	204.1055	3
7	**825.4625**	413.2349	808.4360	404.7216	807.4520	404.2296	Y	***338.1823***	169.5948	321.1557	161.0815			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

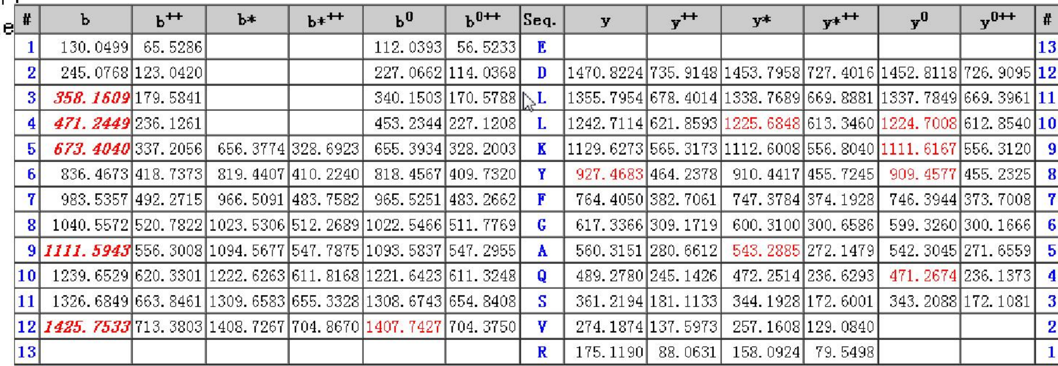
MS/MS Fragmentation of **EDLLKYFGAQSVR**
Found in **A8K1C9**, RNA-binding protein 40 OS=Homo sapiens GN=RNPC3 PE=2 SV=1

Match to Query 8475: 1598.867888 from(800.441220,2+) intensity(49615.4648)
Title: File671 Spectrum11798 scans: 13122
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1598.8577
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 24 **Expect:** 2.1
Matches : 13/132 fragment ions using 14 most intense peaks

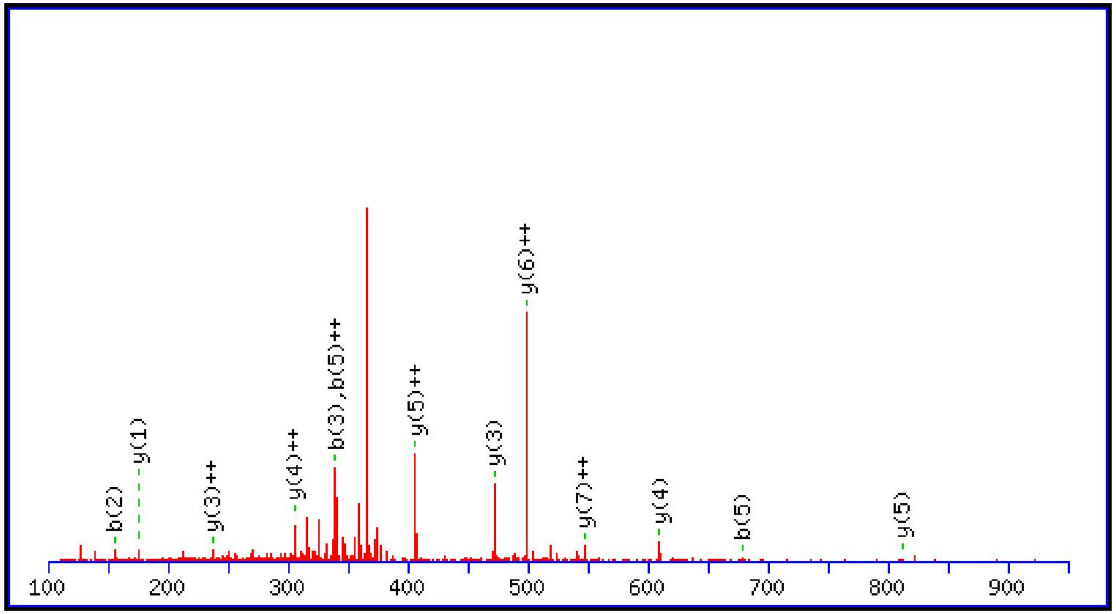


#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	245.0768	123.0420			227.0662	114.0368	D	1470.8224	735.9148	1453.7958	727.4016	1452.8118	726.9095	12
3	***358.1609***	179.5841			340.1503	170.5788	L	1355.7954	678.4014	1338.7689	669.8881	1337.7849	669.3961	11
4	***471.2449***	236.1261			453.2344	227.1208	L	1242.7114	621.8593	1225.6848	613.3460	1224.7008	612.8540	10
5	***673.4040***	337.2056	656.3774	328.6923	655.3934	328.2003	K	1129.6273	565.3173	1112.6008	556.8040	1111.6167	556.3120	9
6	836.4673	418.7373	819.4407	410.2240	818.4567	409.7320	Y	927.4683	464.2378	910.4417	455.7245	909.4577	455.2325	8
7	983.5357	492.2715	966.5091	483.7582	965.5251	483.2662	F	764.4050	382.7061	747.3784	374.1928	746.3944	373.7008	7
8	1040.5572	520.7822	1023.5306	512.2689	1022.5466	511.7769	G	617.3366	309.1719	600.3100	300.6586	599.3260	300.1666	6
9	***1111.5943***	556.3008	1094.5677	547.7875	1093.5837	547.2955	A	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
10	1239.6529	620.3301	1222.6263	611.8168	1221.6423	611.3248	Q	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
11	1326.6849	663.8461	1309.6583	655.3328	1308.6743	654.8408	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
12	***1425.7533***	713.3803	1408.7267	704.8670	1407.7427	704.3750	V	274.1874	137.5973	257.1608	129.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GPKKHLKR**
Found in **P62701**, 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2

Match to Query 3780: 1148.730162 from(383.917330,3+) intensity(57175.6484)
Title: File394 Spectrum6552 scans: 7614
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 950 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



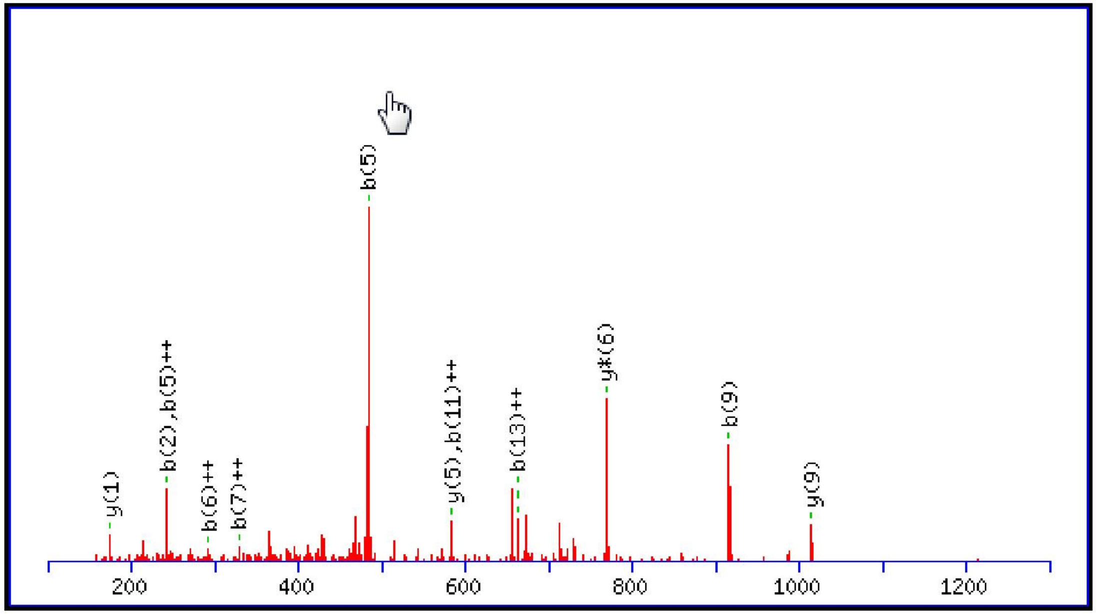
Monoisotopic mass of neutral peptide Mr(calc): 1148.7302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl (K)
K4 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 24 **Expect:** 0.63
Matches : 13/52 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.5180			G					8
2	**155.0815**	78.0444			P	1092.7161	546.8617	1075.6895	538.3484	7
3	**339.2027**	170.1050	322.1761	161.5917	K	995.6633	498.3353	978.6367	489.8220	6
4	541.3617	271.1845	524.3351	262.6712	K	***811.5421***	406.2747	794.5156	397.7614	5
5	**678.4206**	339.7139	661.3941	331.2007	H	***609.3831***	305.1952	592.3566	296.6819	4
6	791.5047	396.2560	774.4781	387.7427	L	***472.3242***	236.6657	455.2976	228.1525	3
7	975.6258	488.3166	958.5993	479.8033	K	359.2401	180.1237	342.2136	171.6104	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1

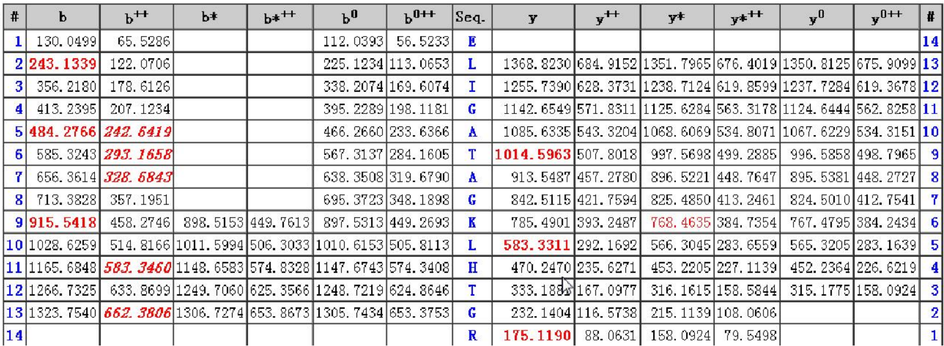
MS/MS Fragmentation of **ELIGATAGKLHTGR**
Found in **F8W943**, Argininosuccinate lyase (Fragment) OS=Homo sapiens GN=ASL PE=2 SV=1

Match to Query 8650: 1496.860992 from(499.960940,3+) intensity(332980.7813)
Title: File392 Spectrum16961 scans: 18761
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

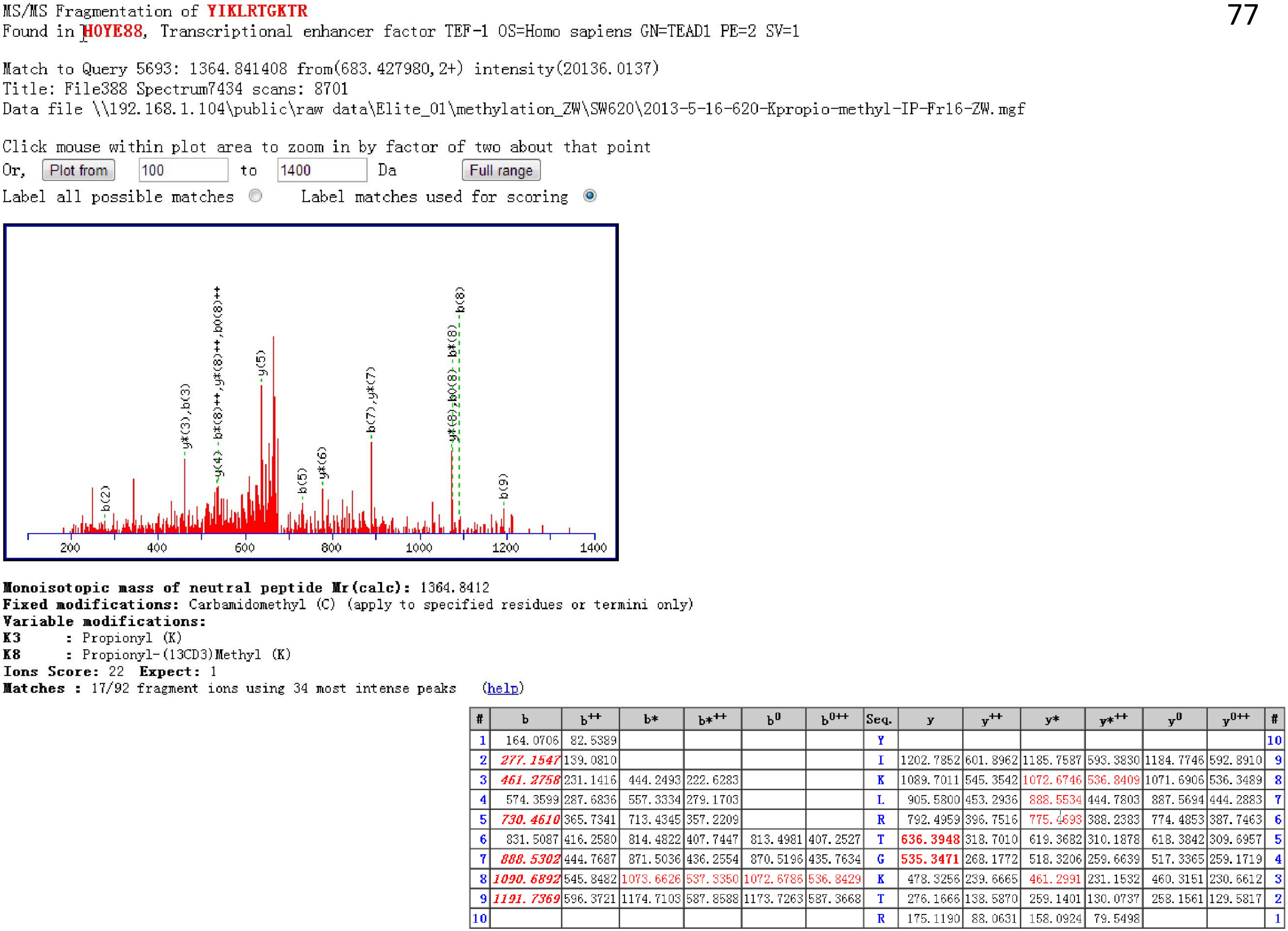
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1496.8584
Fixed modifications: Carbamidomethyl (C) (apply to specified residu
Variable modifications:
K9 : Propionyl-(13CD3)Methyl (K)
Ions Score: 24 **Expect:** 1.8
Matches : 12/136 fragment ions using 19 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	**243.1339**	122.0706			225.1234	113.0653	L	1368.8230	684.9152	1351.7965	676.4019	1350.8125	675.9099	13
3	356.2180	178.6126			338.2074	169.6074	I	1255.7390	628.3731	1238.7124	619.8599	1237.7284	619.3678	12
4	413.2395	207.1234			395.2289	198.1181	G	1142.6549	571.8311	1125.6284	563.3178	1124.6444	562.8258	11
5	**484.2766**	***242.6419***			466.2660	233.6366	A	1085.6335	543.3204	1068.6069	534.8071	1067.6229	534.3151	10
6	585.3243	***293.1658***			567.3137	284.1605	T	**1014.5963**	507.8018	997.5698	499.2885	996.5858	498.7965	9
7	656.3614	***328.6843***			638.3508	319.6790	A	913.5487	457.2780	896.5221	448.7647	895.5381	448.2727	8
8	713.3828	357.1951			695.3723	348.1898	G	842.5115	421.7594	825.4850	413.2461	824.5010	412.7541	7
9	**915.5418**	458.2746	898.5153	449.7613	897.5313	449.2693	K	785.4901	393.2487	768.4635	384.7354	767.4795	384.2434	6
10	1028.6259	514.8166	1011.5994	506.3033	1010.6153	505.8113	L	**583.3311**	292.1692	566.3045	283.6559	565.3205	283.1639	5
11	1165.6848	***583.3460***	1148.6583	574.8328	1147.6743	574.3408	H	470.2470	235.6271	453.2205	227.1139	452.2364	226.6219	4
12	1266.7325	633.8699	1249.7060	625.3566	1248.7219	624.8646	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
13	1323.7540	***662.3806***	1306.7274	653.8673	1305.7434	653.3753	G	232.1404	116.5738	215.1139	108.0606			2
14							R	**175.1190**	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **YIKLRTGKTR**

Found in **H0YE88**, Transcriptional enhancer factor TEF-1 OS=Homo sapiens GN=TEAD1 PE=2 SV=1

Match to Query 5693: 1364.841408 from(683.427980,2+) intensity(20136.0137)

Title: File388 Spectrum7434 scans: 8701

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1364.8412

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

Variable modifications:

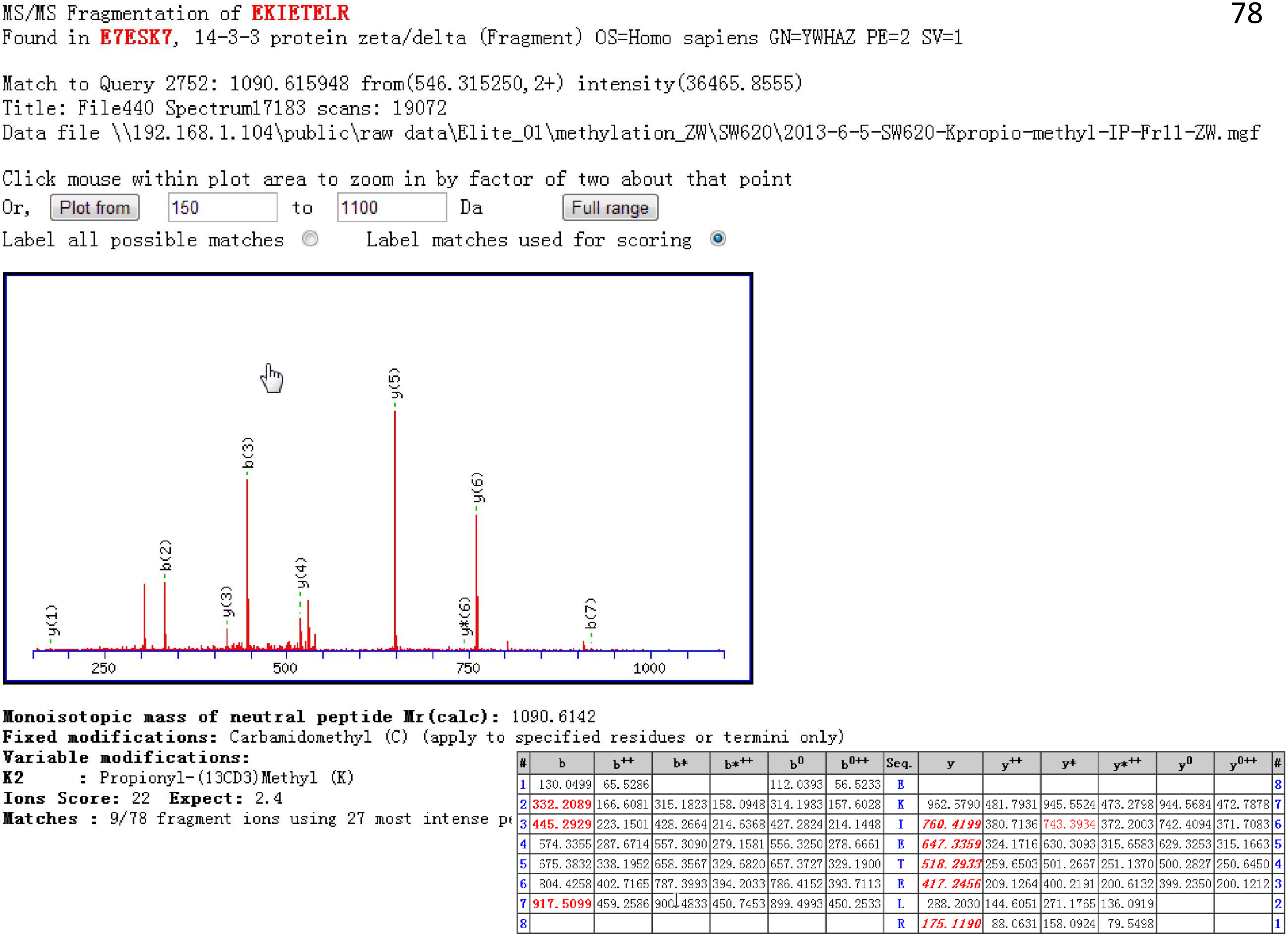
K3 : Propionyl (K)

K8 : Propionyl-(13CD3)Methyl (K)

Ions Score: 22 **Expect:** 1

Matches : 17/92 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							10
2	***277.1547***	139.0810					I	1202.7852	601.8962	1185.7587	593.3830	1184.7746	592.8910	9
3	***461.2758***	231.1416	444.2493	222.6283			K	1089.7011	545.3542	1072.6746	536.8409	1071.6906	536.3489	8
4	574.3599	287.6836	557.3334	279.1703			L	905.5800	453.2936	888.5534	444.7803	887.5694	444.2883	7
5	***730.4610***	365.7341	713.4345	357.2209			R	792.4959	396.7516	775.4693	388.2383	774.4853	387.7463	6
6	831.5087	416.2580	814.4822	407.7447	813.4981	407.2527	T	**636.3948**	318.7010	619.3682	310.1878	618.3842	309.6957	5
7	***888.5302***	444.7687	871.5036	436.2554	870.5196	435.7634	G	**535.3471**	268.1772	518.3206	259.6639	517.3365	259.1719	4
8	***1090.6892***	545.8482	1073.6626	537.3350	1072.6786	536.8429	K	478.3256	239.6665	461.2991	231.1532	460.3151	230.6612	3
9	***1191.7369***	596.3721	1174.7103	587.8588	1173.7263	587.3668	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **EKIETELR**
Found in **E7ESK7**, 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1

Match to Query 2752: 1090.615948 from(546.315250,2+) intensity(36465.8555)
Title: File440 Spectrum17183 scans: 19072
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Label all possible matches ○ Label matches used for scoring ●

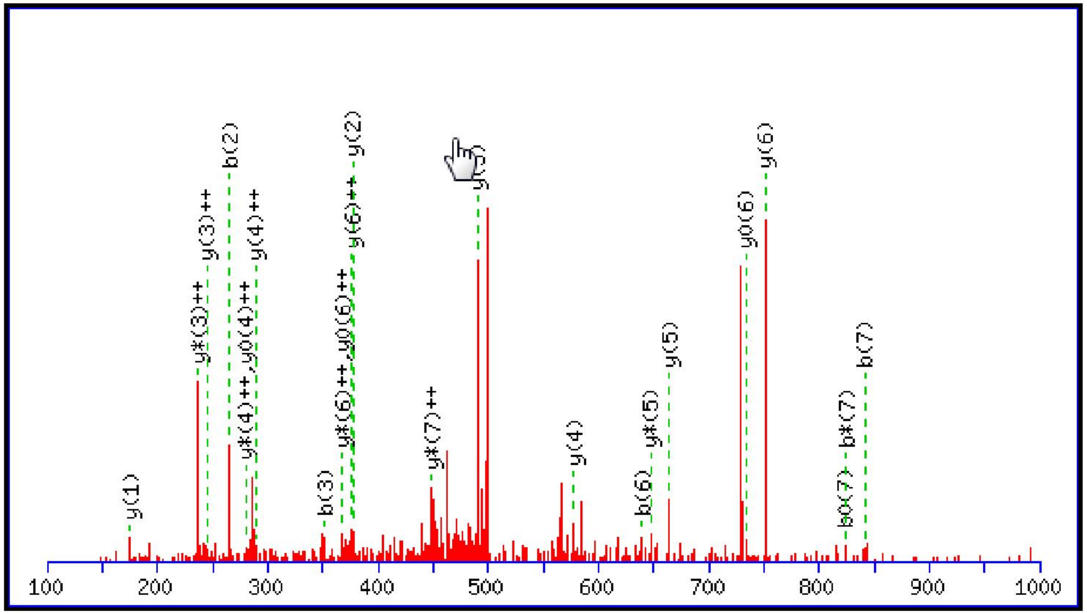
Monoisotopic mass of neutral peptide Mr(calc): 1090.6142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 22 **Expect:** 2.4
Matches : 9/78 fragment ions using 27 most intense pe

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							8
2	**332.2089**	166.6081	315.1823	158.0948	314.1983	157.6028	K	962.5790	481.7931	945.5524	473.2798	944.5684	472.7878	7
3	**445.2929**	223.1501	428.2664	214.6368	427.2824	214.1448	I	***760.4199***	380.7136	743.3934	372.2003	742.4094	371.7083	6
4	574.3355	287.6714	557.3090	279.1581	556.3250	278.6661	E	***647.3359***	324.1716	630.3093	315.6583	629.3253	315.1663	5
5	675.3832	338.1952	658.3567	329.6820	657.3727	329.1900	T	***518.2933***	259.6503	501.2667	251.1370	500.2827	250.6450	4
6	804.4258	402.7165	787.3993	394.2033	786.4152	393.7113	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
7	**917.5099**	459.2586	900.4833	450.7453	899.4993	450.2533	L	288.2030	144.6051	271.1765	136.0919			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

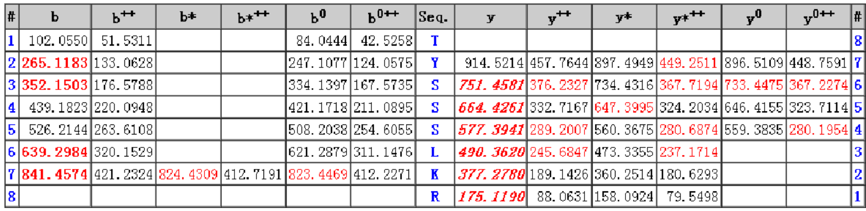
MS/MS Fragmentation of **TYSSSLKR**
Found in **H0Y901**, Ladinin-1 (Fragment) OS=Homo sapiens GN=LAD1 PE=2 SV=1

Match to Query 1345: 1014.561488 from(508.288020,2+) intensity(15789.7627)
Title: File669 Spectrum5264 scans: 6280
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr1-ZW.mgf

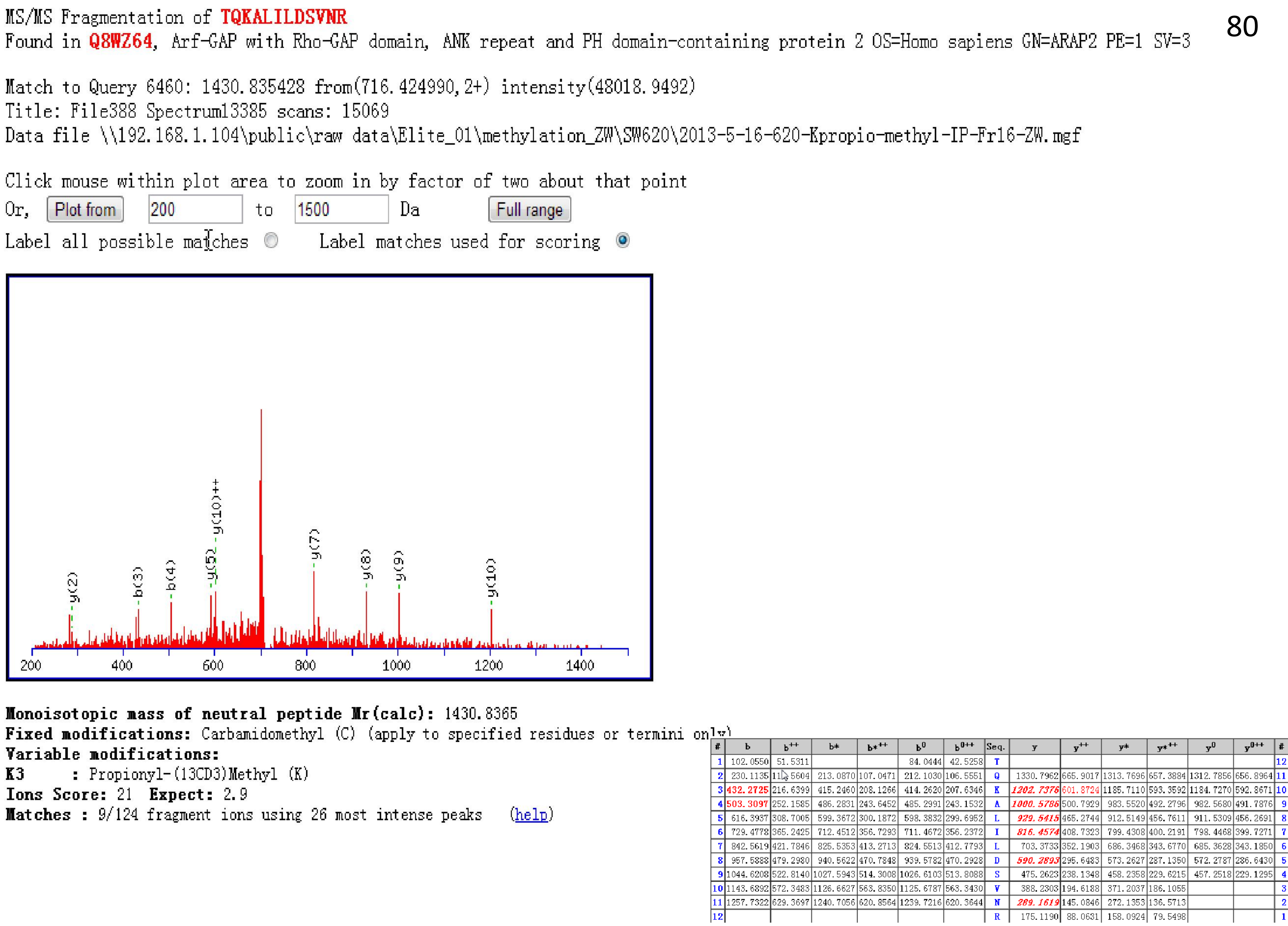
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1014.5618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 21 **Expect:** 3.1
Matches : 23/66 fragment ions using 67 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							8
2	**265.1183**	133.0628			247.1077	124.0575	Y	914.5214	457.7644	897.4949	449.2511	896.5109	448.7591	7
3	**352.1503**	176.5788			334.1397	167.5735	S	***751.4581***	376.2327	734.4316	367.7194	733.4475	367.2274	6
4	439.1823	220.0948			421.1718	211.0895	S	***664.4261***	332.7167	647.3995	324.2034	646.4155	323.7114	5
5	526.2144	263.6108			508.2038	254.6055	S	***577.3941***	289.2007	560.3675	280.6874	559.3835	280.1954	4
6	**639.2984**	320.1529			621.2879	311.1476	L	***490.3620***	245.6847	473.3355	237.1714			3
7	**841.4574**	421.2324	824.4309	412.7191	823.4469	412.2271	K	***377.2780***	189.1426	360.2514	180.6293			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **TQKALILDSVNR**

Found in **Q8WZ64**, Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ARAP2 PE=1 SV=3

Match to Query 6460: 1430.835428 from(716.424990,2+) intensity(48018.9492)

Title: File388 Spectrum13385 scans: 15069

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr16-ZW.mgf

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

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1430.8365

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

Variable modifications:

K3 : Propionyl-(13CD3)Methyl (K)

Ions Score: 21 **Expect:** 2.9

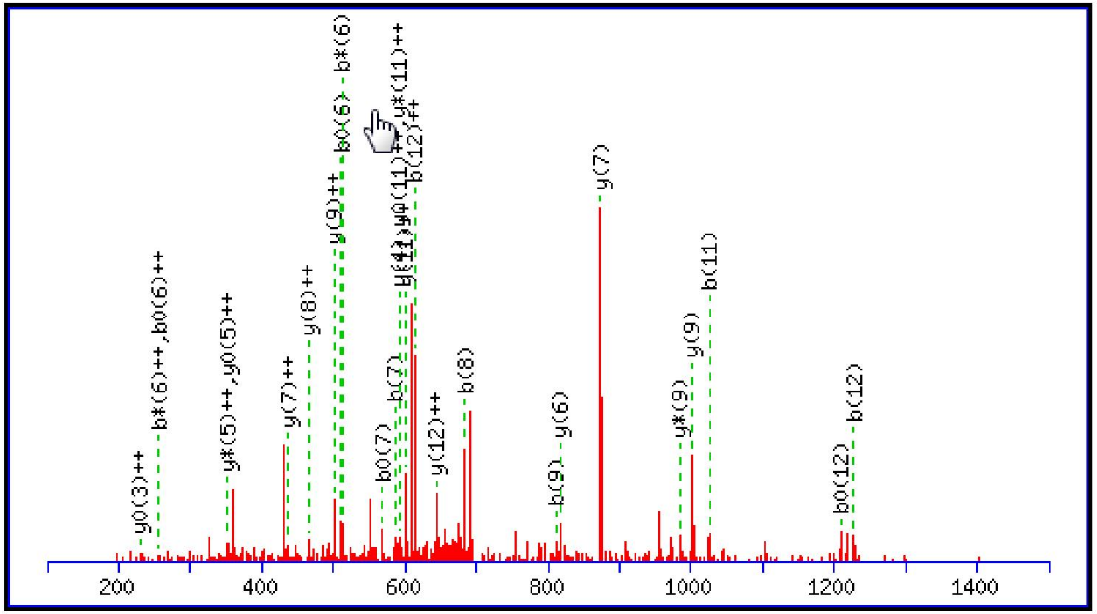
Matches : 9/124 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1330.7962	665.9017	1313.7696	657.3884	1312.7856	656.8964	11
3	**432.2725**	216.6399	415.2460	208.1266	414.2620	207.6346	K	***1202.7376***	601.8724	1185.7110	593.3592	1184.7270	592.8671	10
4	**503.3097**	252.1585	486.2831	243.6452	485.2991	243.1532	A	***1000.5786***	500.7929	983.5520	492.2796	982.5680	491.7876	9
5	616.3937	308.7005	599.3672	300.1872	598.3832	299.6952	L	***929.5415***	465.2744	912.5149	456.7611	911.5309	456.2691	8
6	729.4778	365.2425	712.4512	356.7293	711.4672	356.2372	I	***816.4574***	408.7323	799.4308	400.2191	798.4468	399.7271	7
7	842.5619	421.7846	825.5353	413.2713	824.5513	412.7793	L	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	6
8	957.5888	479.2980	940.5622	470.7848	939.5782	470.2928	D	***590.2893***	295.6483	573.2627	287.1350	572.2787	286.6430	5
9	1044.6208	522.8140	1027.5943	514.3008	1026.6103	513.8088	S	475.2623	238.1348	458.2358	229.6215	457.2518	229.1295	4
10	1143.6892	572.3483	1126.6627	563.8350	1125.6787	563.3430	V	388.2303	194.6188	371.2037	186.1055			3
11	1257.7322	629.3697	1240.7056	620.8564	1239.7216	620.3644	N	***289.1619***	145.0846	272.1353	136.5713			2
12							R	175.1190	88.0631	158.0924	79.5498			1

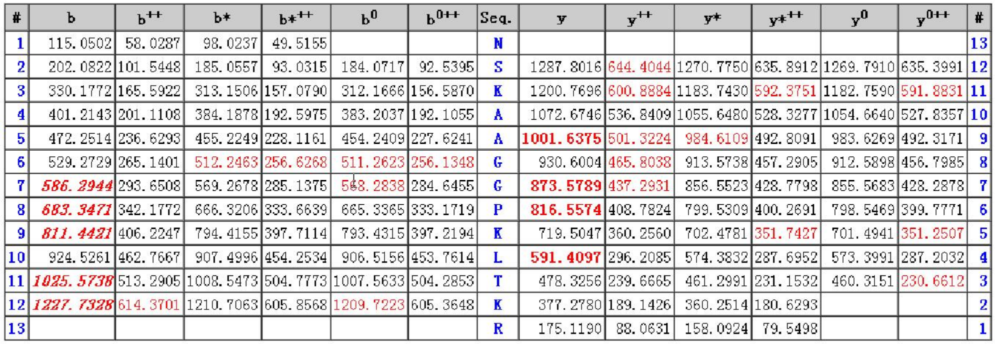
MS/MS Fragmentation of **NSKAAGGPKLTKR**
Found in **H9KVB4**, Trinucleotide repeat-containing gene 18 protein OS=Homo sapiens GN=TNRC18 PE=2 SV=1

Match to Query 6564: 1400.827728 from(701.421140,2+) intensity(38974.1602)
Title: File443 Spectrum6130 scans: 7298
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-6-SW620-Kpropio-methyl-IP-Fr15-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1400.8372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K12 : Propionyl-(13CD3)Methyl (K)
Ions Score: 20 **Expect:** 3.2
Matches : 27/138 fragment ions using 90 most intense peaks (hel

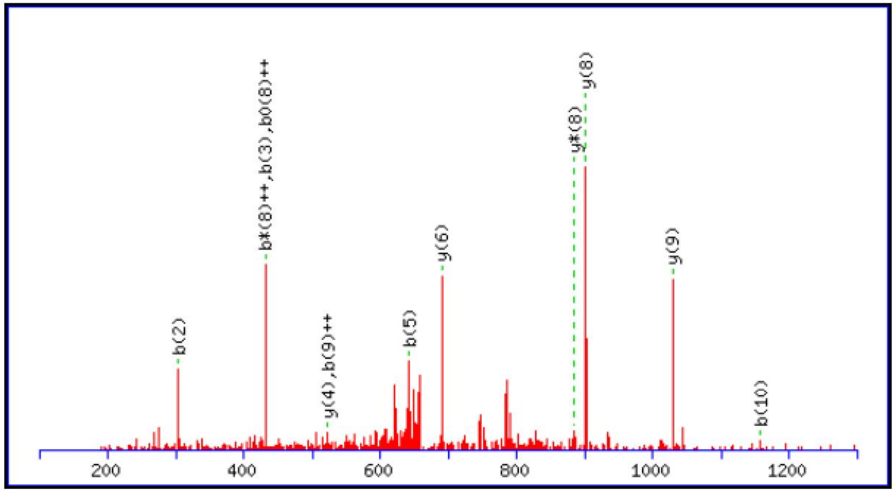


#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	1287.8016	644.4044	1270.7750	635.8912	1269.7910	635.3991	12
3	330.1772	165.5922	313.1506	157.0790	312.1666	156.5870	K	1200.7696	600.8884	1183.7430	592.3751	1182.7590	591.8831	11
4	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	A	1072.6746	536.8409	1055.6480	528.3277	1054.6640	527.8357	10
5	472.2514	236.6293	455.2249	228.1161	454.2409	227.6241	A	**1001.6375**	501.3224	984.6109	492.8091	983.6269	492.3171	9
6	529.2729	265.1401	512.2463	256.6268	511.2623	256.1348	G	930.6004	465.8038	913.5738	457.2905	912.5898	456.7985	8
7	***586.2944***	293.6508	569.2678	285.1375	568.2838	284.6455	G	**873.5789**	437.2931	856.5523	428.7798	855.5683	428.2878	7
8	***683.3471***	342.1772	666.3206	333.6639	665.3365	333.1719	P	**816.5574**	408.7824	799.5309	400.2691	798.5469	399.7771	6
9	***811.4421***	406.2247	794.4155	397.7114	793.4315	397.2194	K	719.5047	360.2560	702.4781	351.7427	701.4941	351.2507	5
10	924.5261	462.7667	907.4996	454.2534	906.5156	453.7614	L	**591.4097**	296.2085	574.3832	287.6952	573.3991	287.2032	4
11	***1025.5738***	513.2905	1008.5473	504.7773	1007.5633	504.2853	T	478.3256	239.6665	461.2991	231.1532	460.3151	230.6612	3
12	***1227.7328***	614.3701	1210.7063	605.8568	1209.7223	605.3648	K	377.2780	189.1426	360.2514	180.6293			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TKQPIPAAYNR**
Found in **Q6P1J9**, Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1

Match to Query 4790: 1331.746688 from(666.880620,2+) intensity(34781.2969)
Title: File671 Spectrum7222 scans: 8241
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr5-ZW.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 ●



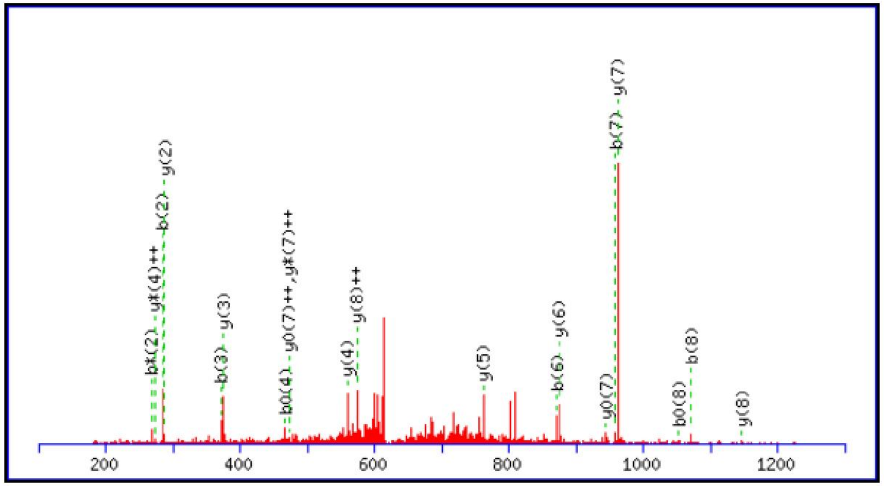
Monoisotopic mass of neutral peptide Mr(calc): 1331.7470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 31 **Expect:** 0.36
Matches : 12/98 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					11
2	***304.2140***	152.6106	287.1874	144.0973	286.2034	143.6053	K	1231.7066	616.3569	1214.6801	607.8437	10
3	***432.2725***	216.6399	415.2460	208.1266	414.2620	207.6346	Q	***1029.5476***	515.2774	1012.5211	506.7642	9
4	529.3253	265.1663	512.2988	256.6530	511.3147	256.1610	P	***901.4890***	451.2482	884.4625	442.7349	8
5	***642.4094***	321.7083	625.3828	313.1951	624.3988	312.7030	I	804.4363	402.7218	787.4097	394.2085	7
6	739.4621	370.2347	722.4356	361.7214	721.4516	361.2294	P	***691.3522***	346.1797	674.3257	337.6665	6
7	810.4993	405.7533	793.4727	397.2400	792.4887	396.7480	A	594.2994	297.6534	577.2729	289.1401	5
8	881.5364	441.2718	864.5098	432.7585	863.5258	432.2665	A	***523.2623***	262.1348	506.2358	253.6215	4
9	1044.5997	522.8035	1027.5731	514.2902	1026.5891	513.7982	Y	452.2252	226.6162	435.1987	218.1030	3
10	***1158.6426***	579.8249	1141.6161	571.3117	1140.6321	570.8197	N	289.1619	145.0846	272.1353	136.5713	2
11							R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **VKSLKKSLR**
Found in **J3QRV5**, Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=4 SV=1

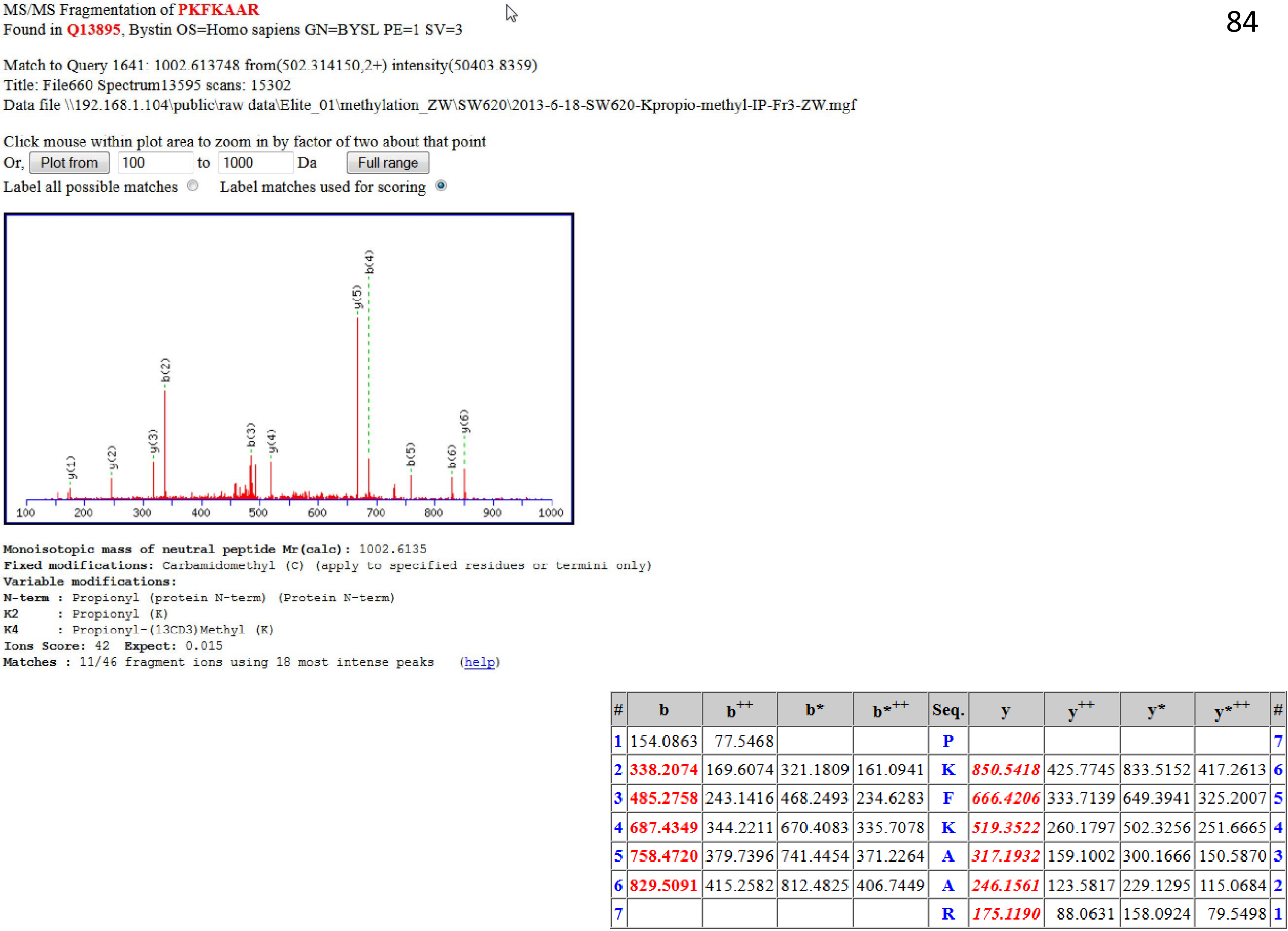
Match to Query 3778: 1243.812968 from(622.913760,2+) intensity(46833.3438)
Title: File671 Spectrum11978 scans: 13314
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr5-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1243.8136
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 34 **Expect:** 0.028
Matches : 20/86 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							9
2	**284.1969**	142.6021	267.1703	134.0888			K	***1145.7525***	573.3799	1128.7260	564.8666	1127.7419	564.3746	8
3	**371.2289**	186.1181	354.2023	177.6048	353.2183	177.1128	S	***961.6313***	481.3193	944.6048	472.8060	943.6208	472.3140	7
4	484.3130	242.6601	467.2864	234.1468	466.3024	233.6548	L	***874.5993***	437.8033	857.5727	429.2900	856.5887	428.7980	6
5	686.4720	343.7396	669.4454	335.2264	668.4614	334.7343	K	***761.5152***	381.2613	744.4887	372.7480	743.5047	372.2560	5
6	**870.5932**	435.8002	853.5666	427.2869	852.5826	426.7949	K	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	4
7	**957.6252**	479.3162	940.5986	470.8030	939.6146	470.3109	S	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
8	**1070.7092**	535.8583	1053.6827	527.3450	1052.6987	526.8530	L	***288.2030***	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1



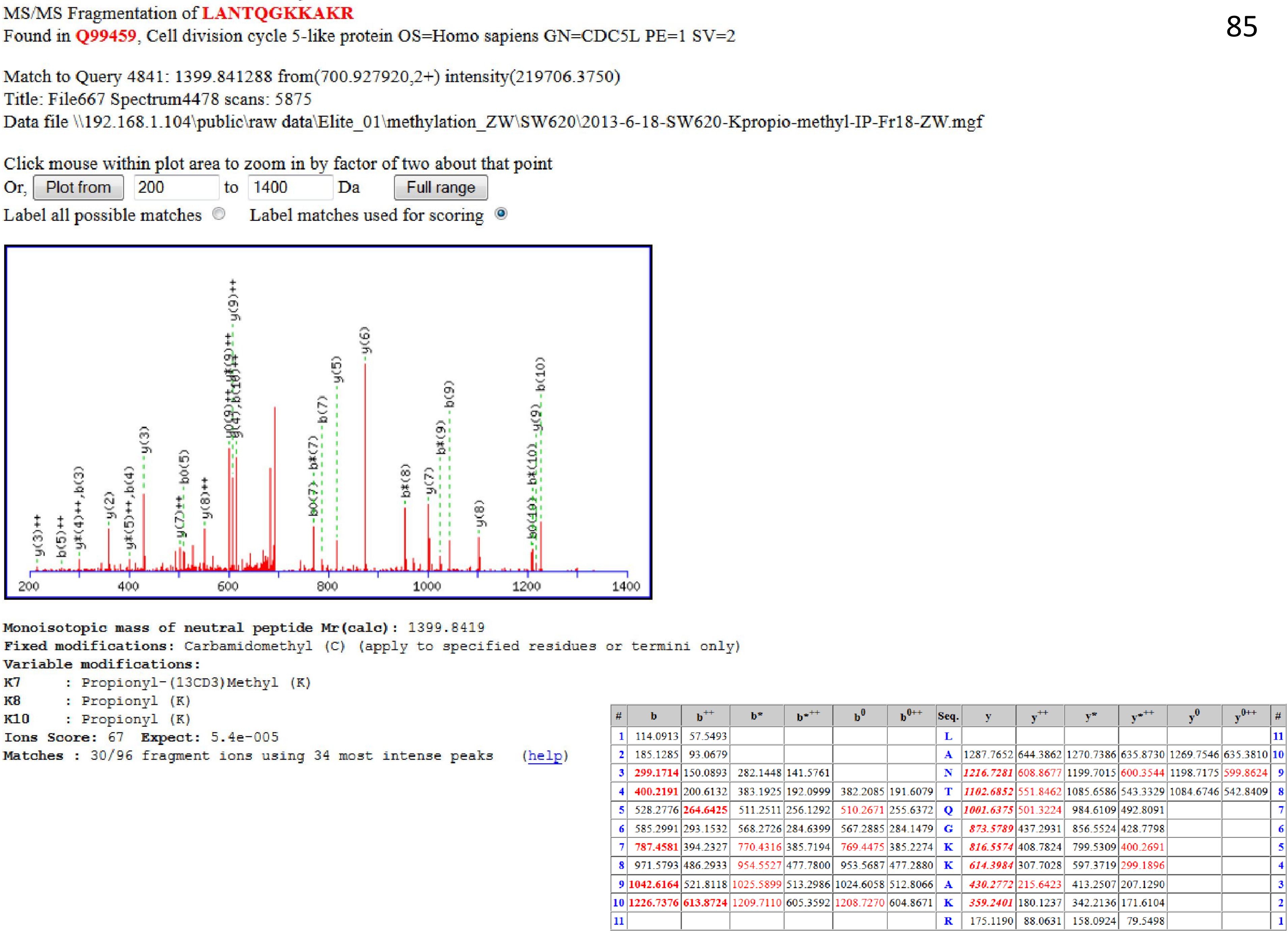
MS/MS Fragmentation of **PKFKAAR**
Found in **Q13895**, Bystin OS=Homo sapiens GN=BYSL PE=1 SV=3

Match to Query 1641: 1002.613748 from(502.314150,2+) intensity(50403.8359)
Title: File660 Spectrum13595 scans: 15302
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1002.6135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K2     : Propionyl (K)
K4     : Propionyl-(13CD3)Methyl (K)
Ions Score: 42  Expect: 0.015
Matches : 11/46 fragment ions using 18 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	154.0863	77.5468			P					7
2	**338.2074**	169.6074	321.1809	161.0941	K	*850.5418*	425.7745	833.5152	417.2613	6
3	**485.2758**	243.1416	468.2493	234.6283	F	*666.4206*	333.7139	649.3941	325.2007	5
4	**687.4349**	344.2211	670.4083	335.7078	K	*519.3522*	260.1797	502.3256	251.6665	4
5	**758.4720**	379.7396	741.4454	371.2264	A	*317.1932*	159.1002	300.1666	150.5870	3
6	**829.5091**	415.2582	812.4825	406.7449	A	*246.1561*	123.5817	229.1295	115.0684	2
7					R	*175.1190*	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **LANTQGKKAKR**
Found in **Q99459**, Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2

Match to Query 4841: 1399.841288 from(700.927920,2+) intensity(219706.3750)
Title: File667 Spectrum4478 scans: 5875
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr18-ZW.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 ●

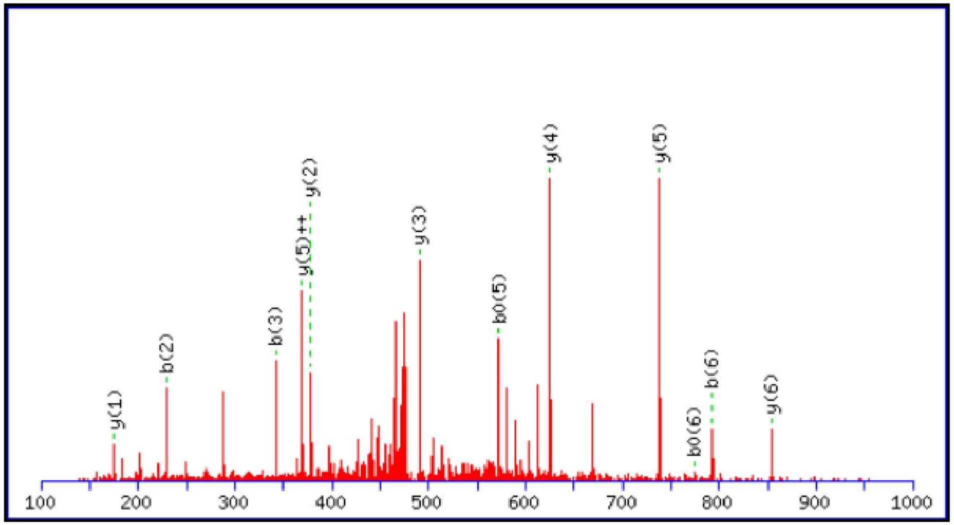
Monoisotopic mass of neutral peptide Mr(calc): 1399.8419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 67 **Expect:** 5.4e-005
Matches : 30/96 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	185.1285	93.0679					A	1287.7652	644.3862	1270.7386	635.8730	1269.7546	635.3810	10
3	**299.1714**	150.0893	282.1448	141.5761			N	***1216.7281***	608.8677	1199.7015	600.3544	1198.7175	599.8624	9
4	**400.2191**	200.6132	383.1925	192.0999	382.2085	191.6079	T	***1102.6852***	551.8462	1085.6586	543.3329	1084.6746	542.8409	8
5	528.2776	**264.6425**	511.2511	256.1292	510.2671	255.6372	Q	***1001.6375***	501.3224	984.6109	492.8091			7
6	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	G	***873.5789***	437.2931	856.5524	428.7798			6
7	**787.4581**	394.2327	770.4316	385.7194	769.4475	385.2274	K	***816.5574***	408.7824	799.5309	400.2691			5
8	971.5793	486.2933	954.5527	477.7800	953.5687	477.2880	K	***614.3984***	307.7028	597.3719	299.1896			4
9	**1042.6164**	521.8118	1025.5899	513.2986	1024.6058	512.8066	A	***430.2772***	215.6423	413.2507	207.1290			3
10	**1226.7376**	**613.8724**	1209.7110	605.3592	1208.7270	604.8671	K	***359.2401***	180.1237	342.2136	171.6104			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LDIMLKR**
Found in **I3L2C9**, Phospholipase D2 OS=Homo sapiens GN=PLD2 PE=2 SV=1

Match to Query 1688: 965.613128 from(483.813840,2+) intensity(56794.9336)
Title: File649 Spectrum14158 scans: 15625
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr20-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



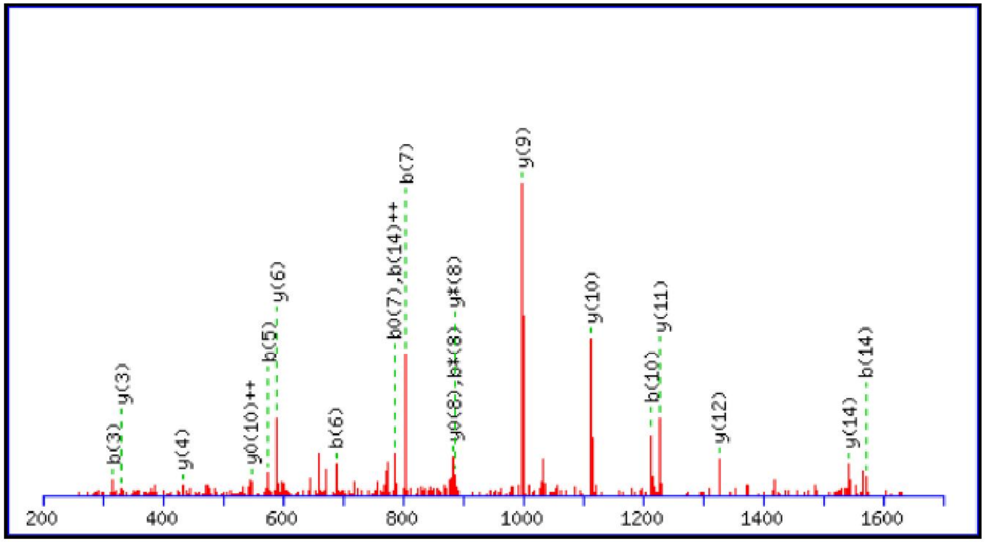
Monoisotopic mass of neutral peptide Mr(calc): 965.6125
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Label:13C(1)2H(3) (M)
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 35 **Expect:** 0.042
Matches : 12/50 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							7
2	**229.1183**	115.0628			211.1077	106.0575	D	***853.5357***	427.2715	836.5092	418.7582	835.5251	418.2662	6
3	**342.2023**	171.6048			324.1918	162.5995	I	***738.5088***	369.7580	721.4822	361.2447			5
4	477.2650	239.1361			459.2545	230.1309	M	***625.4247***	313.2160	608.3981	304.7027			4
5	590.3491	295.6782			572.3385	286.6729	L	***490.3620***	245.6847	473.3355	237.1714			3
6	**792.5081**	396.7577	775.4815	388.2444	774.4975	387.7524	K	***377.2780***	189.1426	360.2514	180.6293			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of GKGCVLDPQKGTTVGR
Found in Q2PPJ7, Ral GTPase-activating protein subunit alpha-2 OS=Homo sapiens GN=RALGAPA2 PE=1 SV=2

Match to Query 12620: 1801.964948 from(901.989750,2+) intensity(227886.9688)
Title: File394 Spectrum10738 scans: 12089
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



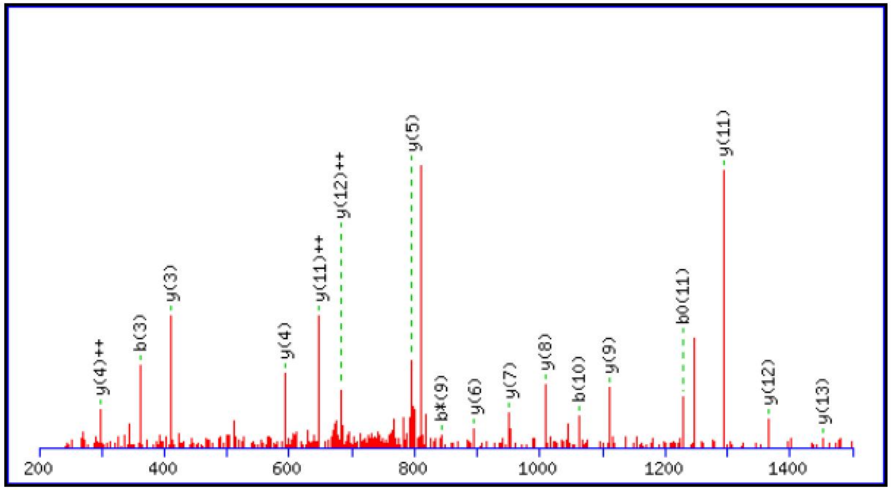
Monoisotopic mass of neutral peptide Mr(calc): 1801.9629
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 53 **Expect:** 0.003
Matches : 20/160 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							16
2	260.1878	130.5975	243.1612	122.0842			K	1745.9487	873.4780	1728.9222	864.9647	1727.9382	864.4727	15
3	***317.2092***	159.1082	300.1827	150.5950			G	***1543.7897***	772.3985	1526.7632	763.8852	1525.7791	763.3932	14
4	477.2399	239.1236	460.2133	230.6103			C	1486.7682	743.8878	1469.7417	735.3745	1468.7577	734.8825	13
5	***576.3083***	288.6578	559.2817	280.1445			V	***1326.7376***	663.8724	1309.7110	655.3592	1308.7270	654.8672	12
6	***689.3923***	345.1998	672.3658	336.6865			L	***1227.6692***	614.3382	1210.6426	605.8250	1209.6586	605.3329	11
7	***804.4193***	402.7133	787.3927	394.2000	786.4087	393.7080	D	***1114.5851***	557.7962	1097.5586	549.2829	1096.5746	548.7909	10
8	901.4721	451.2397	884.4455	442.7264	883.4615	442.2344	P	***999.5582***	500.2827	982.5316	491.7694	981.5476	491.2774	9
9	1029.5306	515.2690	1012.5041	506.7557	1011.5201	506.2637	Q	902.5054	451.7563	885.4789	443.2431	884.4948	442.7511	8
10	***1213.6518***	607.3295	1196.6253	598.8163	1195.6412	598.3243	K	774.4468	387.7271	757.4203	379.2138	756.4363	378.7218	7
11	1270.6733	635.8403	1253.6467	627.3270	1252.6627	626.8350	G	***590.3257***	295.6665	573.2991	287.1532	572.3151	286.6612	6
12	1371.7210	686.3641	1354.6944	677.8508	1353.7104	677.3588	T	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
13	1472.7686	736.8880	1455.7421	728.3747	1454.7581	727.8827	T	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	4
14	***1571.8370***	786.4222	1554.8105	777.9089	1553.8265	777.4169	V	***331.2088***	166.1081	314.1823	157.5948			3
15	1628.8585	814.9329	1611.8320	806.4196	1610.8479	805.9276	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KSAPSTGGVKKPHR**
Found in **B4DEB1**, Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1

Match to Query 10911: 1652.976908 from(827.495730,2+) intensity(70017.6875)
Title: File392 Spectrum6683 scans: 7707
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



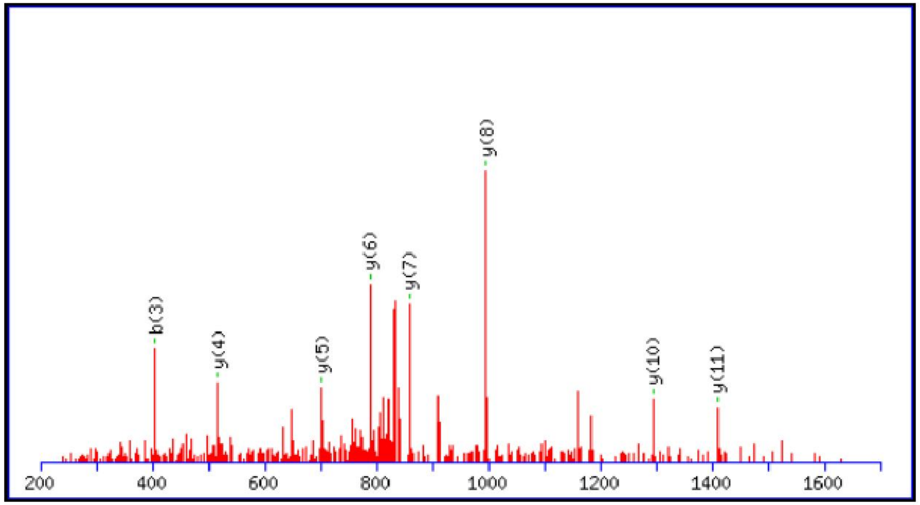
Monoisotopic mass of neutral peptide Mr(calc): 1652.9755
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl-(13CD3)Methyl (K)
K11 : Propionyl (K)
Ions Score: 79 **Expect:** 3.6e-006
Matches : 17/138 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							14
2	290.1983	145.6028	273.1718	137.0895	272.1878	136.5975	S	***1451.8238***	726.4155	1434.7972	717.9023	1433.8132	717.4102	13
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	A	***1364.7917***	682.8995	1347.7652	674.3862	1346.7812	673.8942	12
4	458.2882	229.6477	441.2616	221.1345	440.2776	220.6425	P	***1293.7546***	647.3810	1276.7281	638.8677	1275.7441	638.3757	11
5	545.3202	273.1637	528.2937	264.6505	527.3097	264.1585	S	1196.7019	598.8546	1179.6753	590.3413	1178.6913	589.8493	10
6	646.3679	323.6876	629.3414	315.1743	628.3573	314.6823	T	***1109.6698***	555.3386	1092.6433	546.8253	1091.6593	546.3333	9
7	703.3894	352.1983	686.3628	343.6850	685.3788	343.1930	G	***1008.6222***	504.8147	991.5956	496.3014			8
8	760.4108	380.7091	743.3843	372.1958	742.4003	371.7038	G	***951.6007***	476.3040	934.5741	467.7907			7
9	859.4792	430.2433	842.4527	421.7300	841.4687	421.2380	V	***894.5792***	447.7933	877.5527	439.2800			6
10	**1061.6383**	531.3228	1044.6117	522.8095	1043.6277	522.3175	K	***795.5108***	398.2590	778.4843	389.7458			5
11	1245.7594	623.3834	1228.7329	614.8701	1227.7489	614.3781	K	***593.3518***	297.1795	576.3253	288.6663			4
12	1342.8122	671.9097	1325.7857	663.3965	1324.8016	662.9045	P	***409.2306***	205.1190	392.2041	196.6057			3
13	1479.8711	740.4392	1462.8446	731.9259	1461.8605	731.4339	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SKDMYHASKSAKR**
Found in **Q8N5A5**, Zinc finger CCCH-type with G patch domain-containing protein OS=Homo sapiens GN=ZGPAT PE=1 SV=3

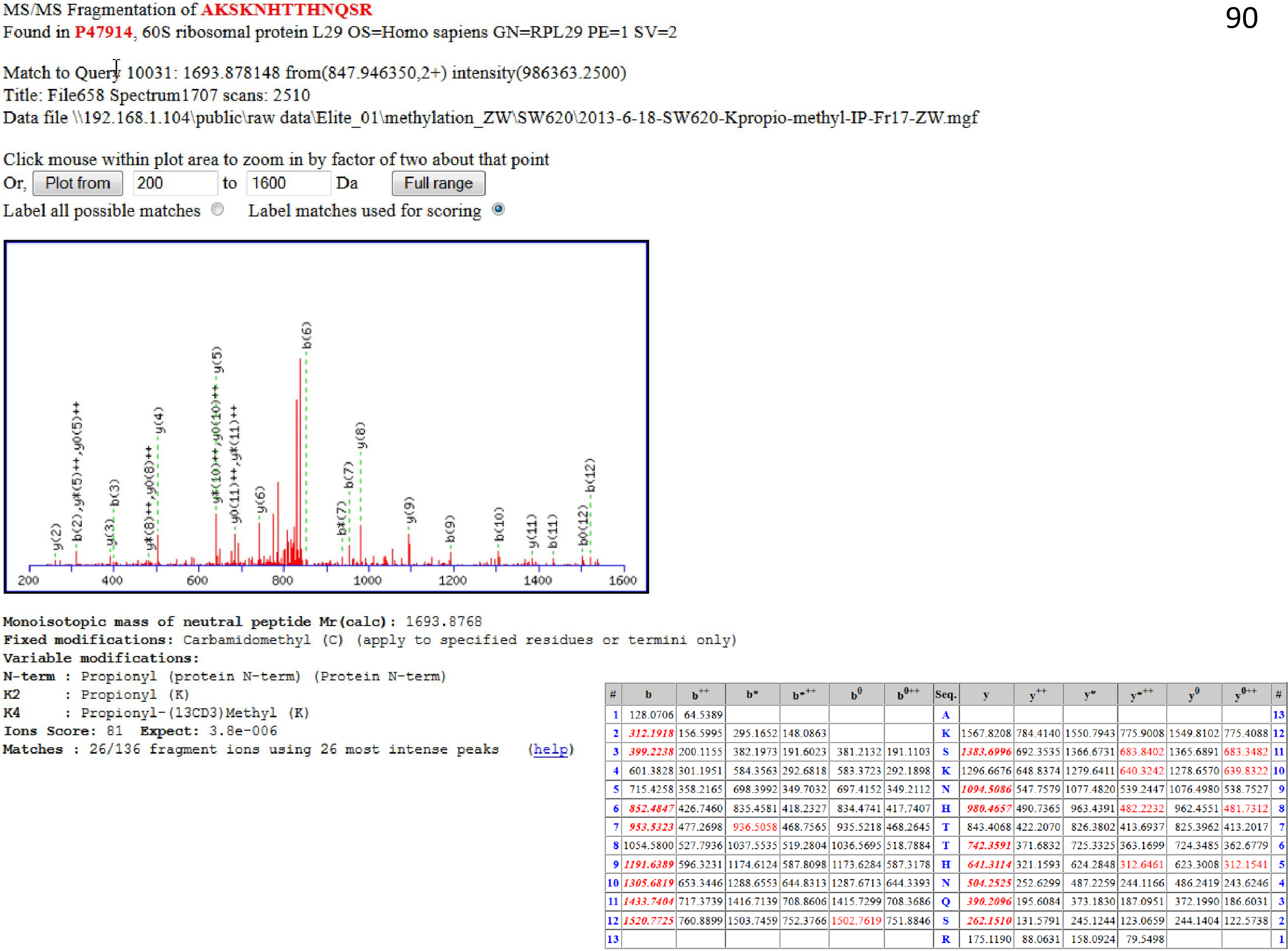
Match to Query 11597: 1697.896828 from(849.955690,2+) intensity(25783.1309)
Title: File392 Spectrum7778 scans: 8884
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1697.8952
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
M4      : Label:13C(1)2H(3) (M)
K9      : Propionyl (K)
K12     : Propionyl (K)
Ions Score: 39  Expect: 0.07
Matches : 8/136 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	290.1983	145.6028	273.1718	137.0895	272.1878	136.5975	K	1611.8705	806.4389	1594.8439	797.9256	1593.8599	797.4336	12
3	405.2253	203.1163	388.1987	194.6030	387.2147	194.1110	D	***1409.7114***	705.3594	1392.6849	696.8461	1391.7009	696.3541	11
4	540.2879	270.6476	523.2614	262.1343	522.2774	261.6423	M	***1294.6845***	647.8459	1277.6580	639.3326	1276.6739	638.8406	10
5	703.3513	352.1793	686.3247	343.6660	685.3407	343.1740	Y	1159.6218	580.3146	1142.5953	571.8013	1141.6113	571.3093	9
6	840.4102	420.7087	823.3836	412.1954	822.3996	411.7034	H	***996.5585***	498.7829	979.5320	490.2696	978.5479	489.7776	8
7	911.4473	456.2273	894.4207	447.7140	893.4367	447.2220	A	***859.4996***	430.2534	842.4730	421.7402	841.4890	421.2482	7
8	998.4793	499.7433	981.4528	491.2300	980.4687	490.7380	S	***788.4625***	394.7349	771.4359	386.2216	770.4519	385.7296	6
9	1182.6005	591.8039	1165.5739	583.2906	1164.5899	582.7986	K	***701.4305***	351.2189	684.4039	342.7056	683.4199	342.2136	5
10	1269.6325	635.3199	1252.6060	626.8066	1251.6220	626.3146	S	***517.3093***	259.1583	500.2827	250.6450	499.2987	250.1530	4
11	1340.6696	670.8385	1323.6431	662.3252	1322.6591	661.8332	A	430.2772	215.6423	413.2507	207.1290			3
12	1524.7908	762.8990	1507.7643	754.3858	1506.7802	753.8938	K	359.2401	180.1237	342.2136	171.6104			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKSKNHTTHNQSR**
Found in **P47914**, 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2

Match to Query 10031: 1693.878148 from(847.946350,2+) intensity(986363.2500)
Title: File658 Spectrum1707 scans: 2510
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr17-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

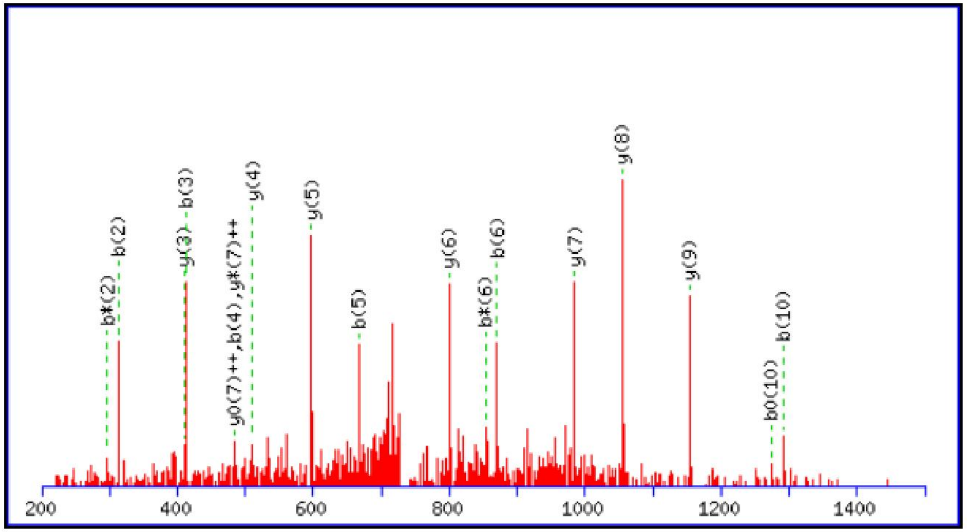
```
Monoisotopic mass of neutral peptide Mr(calc): 1693.8768
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K2     : Propionyl (K)
K4     : Propionyl-(13CD3)Methyl (K)
Ions Score: 81  Expect: 3.8e-006
Matches : 26/136 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	128.0706	64.5389					A							13
2	***312.1918***	156.5995	295.1652	148.0863			K	1567.8208	784.4140	1550.7943	775.9008	1549.8102	775.4088	12
3	***399.2238***	200.1155	382.1973	191.6023	381.2132	191.1103	S	***1383.6996***	692.3535	1366.6731	683.8402	1365.6891	683.3482	11
4	601.3828	301.1951	584.3563	292.6818	583.3723	292.1898	K	1296.6676	648.8374	1279.6411	640.3242	1278.6570	639.8322	10
5	715.4258	358.2165	698.3992	349.7032	697.4152	349.2112	N	***1094.5086***	547.7579	1077.4820	539.2447	1076.4980	538.7527	9
6	***852.4847***	426.7460	835.4581	418.2327	834.4741	417.7407	H	***980.4657***	490.7365	963.4391	482.2232	962.4551	481.7312	8
7	***953.5323***	477.2698	936.5058	468.7565	935.5218	468.2645	T	843.4068	422.2070	826.3802	413.6937	825.3962	413.2017	7
8	1054.5800	527.7936	1037.5535	519.2804	1036.5695	518.7884	T	***742.3591***	371.6832	725.3325	363.1699	724.3485	362.6779	6
9	***1191.6389***	596.3231	1174.6124	587.8098	1173.6284	587.3178	H	***641.3114***	321.1593	624.2848	312.6461	623.3008	312.1541	5
10	***1305.6819***	653.3446	1288.6553	644.8313	1287.6713	644.3393	N	***504.2525***	252.6299	487.2259	244.1166	486.2419	243.6246	4
11	***1433.7404***	717.3739	1416.7139	708.8606	1415.7299	708.3686	Q	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	3
12	***1520.7725***	760.8899	1503.7459	752.3766	1502.7619	751.8846	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KQVAKKSTSFR**
Found in **E9PRF4**, Histone-lysine N-methyltransferase SETDB1 (Fragment) OS=Homo sapiens GN=SETDB1 PE=2 SV=1

Match to Query 6806: 1464.857768 from(733.436160,2+) intensity(27188.8887)
Title: File440 Spectrum10055 scans: 11410
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



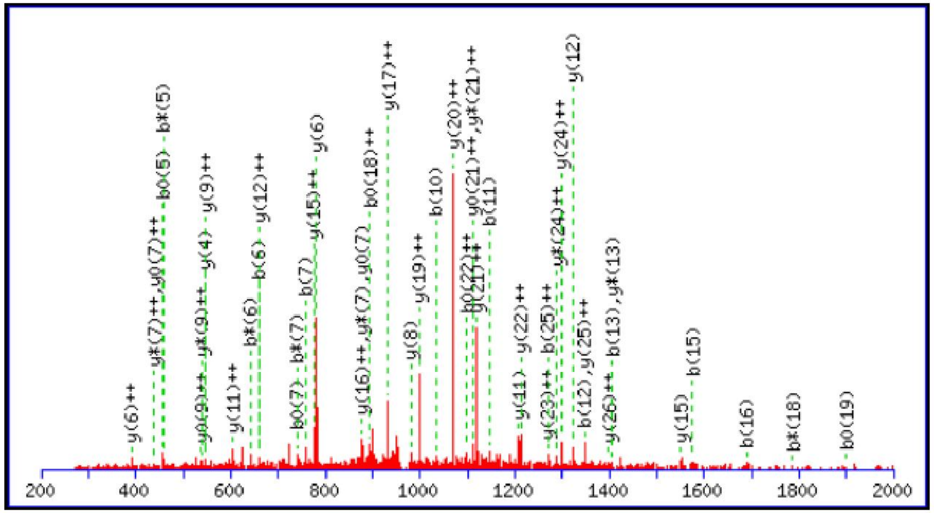
Monoisotopic mass of neutral peptide Mr(calc): 1464.8573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K5 : Propionyl (K)
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 48 **Expect:** 0.0052
Matches : 18/104 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							11
2	***313.1870***	157.0972	296.1605	148.5839			Q	1281.7434	641.3753	1264.7168	632.8621	1263.7328	632.3701	10
3	***412.2554***	206.6314	395.2289	198.1181			V	***1153.6848***	577.3460	1136.6583	568.8328	1135.6743	568.3408	9
4	***483.2926***	242.1499	466.2660	233.6366			A	***1054.6164***	527.8118	1037.5899	519.2986	1036.6058	518.8066	8
5	***667.4137***	334.2105	650.3872	325.6972			K	***983.5793***	492.2933	966.5527	483.7800	965.5687	483.2880	7
6	***869.5728***	435.2900	852.5462	426.7767			K	***799.4581***	400.2327	782.4316	391.7194	781.4475	391.2274	6
7	956.6048	478.8060	939.5782	470.2928	938.5942	469.8007	S	***597.2991***	299.1532	580.2726	290.6399	579.2885	290.1479	5
8	1057.6525	529.3299	1040.6259	520.8166	1039.6419	520.3246	T	***510.2671***	255.6372	493.2405	247.1239	492.2565	246.6319	4
9	1144.6845	572.8459	1127.6579	564.3326	1126.6739	563.8406	S	***409.2194***	205.1133	392.1928	196.6001	391.2088	196.1081	3
10	***1291.7529***	646.3801	1274.7264	637.8668	1273.7423	637.3748	F	322.1874	161.5973	305.1608	153.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TTTGNKVFGALKGAVDGGLSIPHSTKR**
Found in **P46777**, 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3

Match to Query 19843: 2897.590362 from(966.870730,3+) intensity(230322.1563)
Title: File440 Spectrum18095 scans: 20210
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-5-SW620-Kpropio-methyl-IP-Fr11-ZW.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 ●



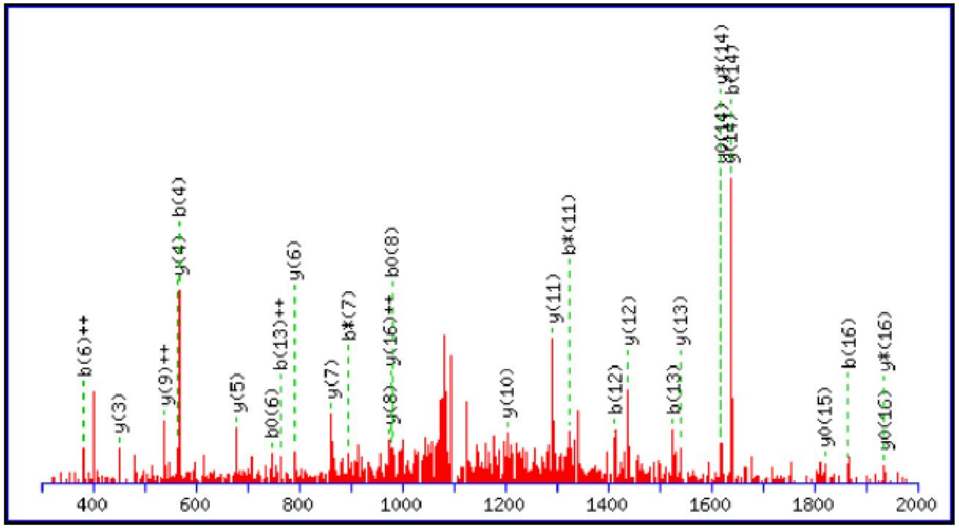
```
Monoisotopic mass of neutral peptide Mr(calc): 2897.5884
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or ter
Variable modifications:
K6     : Propionyl (K)
K12    : Propionyl-(13CD3)Methyl (K)
K26    : Propionyl (K)
Ions Score: 58  Expect: 0.0009
Matches : 49/300 fragment ions using 105 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							27
2	203.1026	102.0550			185.0921	93.0497	T	2797.5479	1399.2776	2780.5214	1390.7643	2779.5374	1390.2723	26
3	304.1503	152.5788			286.1397	143.5735	T	2696.5003	1348.7538	2679.4737	1340.2405	2678.4897	1339.7485	25
4	361.1718	181.0895			343.1612	172.0842	G	2595.4526	1298.2299	2578.4260	1289.7167	2577.4420	1289.2246	24
5	475.2147	238.1110	458.1882	229.5977	457.2041	229.1057	N	2538.4311	1269.7192	2521.4046	1261.2059	2520.4206	1260.7139	23
6	**659.3359**	330.1716	642.3093	321.6583	641.3253	321.1663	K	2424.3882	1212.6977	2407.3616	1204.1845	2406.3776	1203.6925	22
7	**758.4043**	379.7058	741.3777	371.1925	740.3937	370.7005	V	2240.2670	1120.6371	2223.2405	1112.1239	2222.2564	1111.6319	21
8	905.4727	453.2400	888.4462	444.7267	887.4621	444.2347	F	2141.1986	1071.1029	2124.1721	1062.5897	2123.1880	1062.0977	20
9	962.4942	481.7507	945.4676	473.2375	944.4836	472.7454	G	1994.1302	997.5687	1977.1036	989.0555	1976.1196	988.5634	19
10	**1033.5313**	517.2693	1016.5047	508.7560	1015.5207	508.2640	A	1937.1087	969.0580	1920.0822	960.5447	1919.0982	960.0527	18
11	**1146.6154**	573.8113	1129.5888	565.2980	1128.6048	564.8060	L	1866.0716	933.5394	1849.0451	925.0262	1848.0610	924.5342	17
12	**1348.7744**	674.8908	1331.7478	666.3775	1330.7638	665.8855	K	1752.9875	876.9974	1735.9610	868.4841	1734.9770	867.9921	16
13	**1405.7958**	703.4016	1388.7693	694.8883	1387.7853	694.3963	G	**1550.8285**	775.9179	1533.8020	767.4046	1532.8180	766.9126	15
14	1476.8329	738.9201	1459.8064	730.4068	1458.8224	729.9148	A	1493.8071	747.4072	1476.7805	738.8939	1475.7965	738.4019	14
15	**1575.9014**	788.4543	1558.8748	779.9410	1557.8908	779.4490	V	1422.7700	711.8886	1405.7434	703.3753	1404.7594	702.8833	13
16	**1690.9283**	845.9678	1673.9018	837.4545	1672.9177	836.9625	D	**1323.7015**	662.3544	1306.6750	653.8411	1305.6910	653.3491	12
17	1747.9498	874.4785	1730.9232	865.9652	1729.9392	865.4732	G	**1208.6746**	604.8409	1191.6480	596.3277	1190.6640	595.8357	11
18	1804.9712	902.9893	1787.9447	894.4760	1786.9607	893.9840	G	1151.6531	576.3302	1134.6266	567.8169	1133.6426	567.3249	10
19	1918.0553	959.5313	1901.0287	951.0180	1900.0447	950.5260	L	1094.6317	547.8195	1077.6051	539.3062	1076.6211	538.8142	9
20	2005.0873	1003.0473	1988.0608	994.5340	1987.0768	994.0420	S	**981.5476**	491.2774	964.5211	482.7642	963.5370	482.2722	8
21	2118.1714	1059.5893	2101.1448	1051.0761	2100.1608	1050.5840	I	894.5156	447.7614	877.4890	439.2482	876.5050	438.7561	7
22	2215.2241	1108.1157	2198.1976	1099.6024	2197.2136	1099.1104	P	**781.4315**	391.2194	764.4050	382.7061	763.4209	382.2141	6
23	2352.2831	1176.6452	2335.2565	1168.1319	2334.2725	1167.6399	H	684.3787	342.6930	667.3522	334.1797	666.3682	333.6877	5
24	2439.3151	1220.1612	2422.2885	1211.6479	2421.3045	1211.1559	S	**547.3198**	274.1636	530.2933	265.6503	529.3093	265.1583	4
25	2540.3628	1270.6850	2523.3362	1262.1717	2522.3522	1261.6797	T	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	3
26	2724.4839	1362.7456	2707.4574	1354.2323	2706.4734	1353.7403	K	359.2401	180.1237	342.2136	171.6104			2
27							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LHNKPTFSQTIALLNIYR**
Found in **Q01081**, Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3

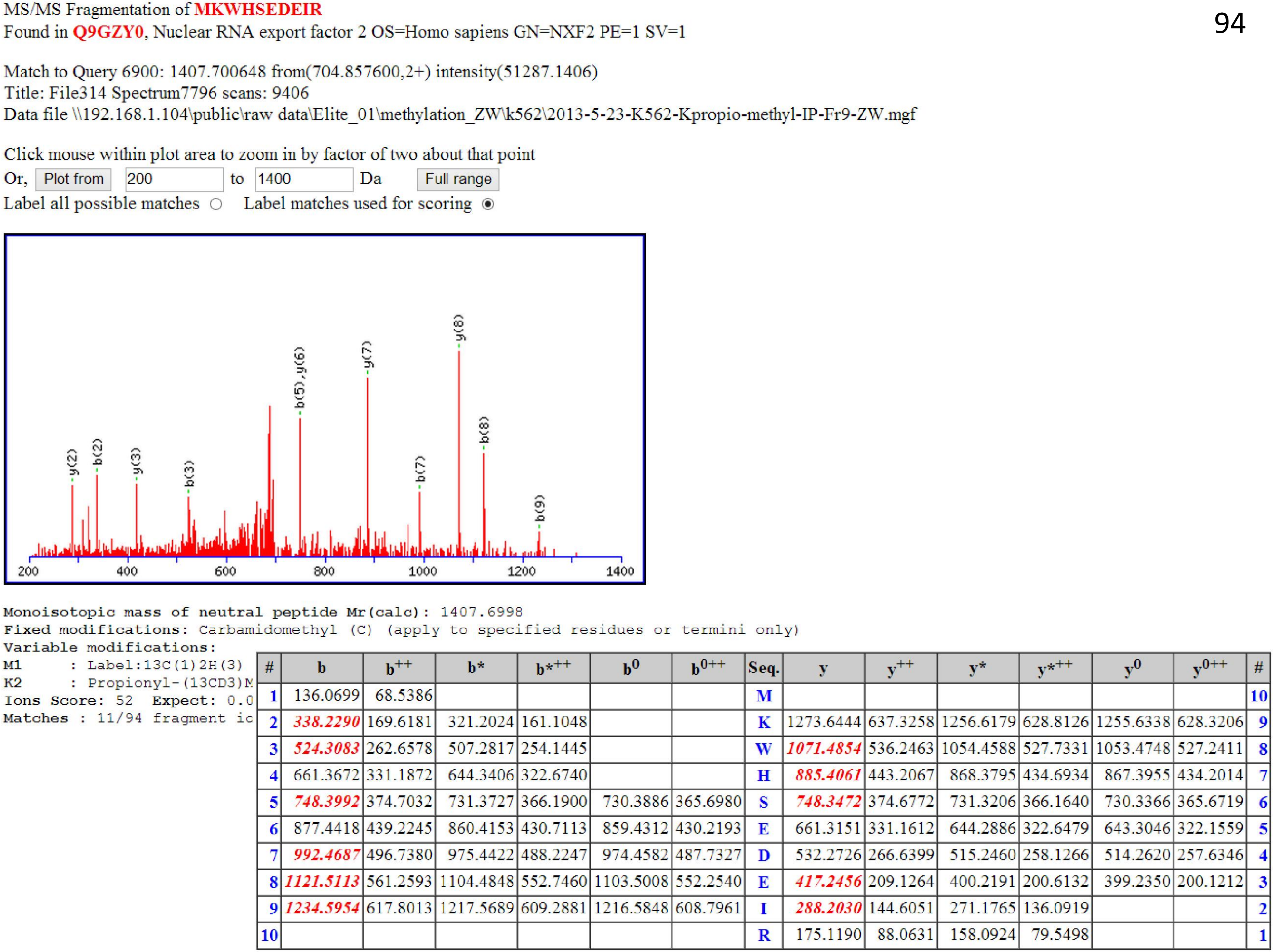
Match to Query 15638: 2202.249368 from(1102.131960,2+) intensity(60800.7969)
Title: File669 Spectrum17598 scans: 19485
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-6-18-SW620-Kpropio-methyl-IP-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2202.2433
Fixed modifications: Carbamidomethyl (C) (apply to specified residue
Variable modifications:
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 41  Expect: 0.032
Matches : 29/174 fragment ions using 68 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							18
2	251.1503	126.0788					H	2090.1666	1045.5869	2073.1400	1037.0736	2072.1560	1036.5816	17
3	365.1932	183.1002	348.1666	174.5870			N	1953.1077	977.0575	1936.0811	968.5442	1935.0971	968.0522	16
4	**567.3522**	284.1797	550.3256	275.6665			K	1839.0647	920.0360	1822.0382	911.5227	1821.0542	911.0307	15
5	664.4050	332.7061	647.3784	324.1928			P	***1636.9057***	818.9565	1619.8792	810.4432	1618.8952	809.9512	14
6	765.4526	383.2300	748.4261	374.7167	747.4421	374.2247	T	***1539.8530***	770.4301	1522.8264	761.9168	1521.8424	761.4248	13
7	912.5210	456.7642	895.4945	448.2509	894.5105	447.7589	F	***1438.8053***	719.9063	1421.7787	711.3930	1420.7947	710.9010	12
8	999.5531	500.2802	982.5265	491.7669	981.5425	491.2749	S	***1291.7369***	646.3721	1274.7103	637.8588	1273.7263	637.3668	11
9	1127.6117	564.3095	1110.5851	555.7962	1109.6011	555.3042	Q	***1204.7048***	602.8561	1187.6783	594.3428	1186.6943	593.8508	10
10	1228.6593	614.8333	1211.6328	606.3200	1210.6488	605.8280	T	1076.6463	538.8268	1059.6197	530.3135	1058.6357	529.8215	9
11	1341.7434	671.3753	1324.7168	662.8621	1323.7328	662.3701	I	***975.5986***	488.3029	958.5720	479.7897			8
12	**1412.7805**	706.8939	1395.7540	698.3806	1394.7699	697.8886	A	***862.5145***	431.7609	845.4880	423.2476			7
13	**1525.8646**	763.4359	1508.8380	754.9227	1507.8540	754.4306	L	***791.4774***	396.2423	774.4509	387.7291			6
14	**1638.9486**	819.9780	1621.9221	811.4647	1620.9381	810.9727	L	***678.3933***	339.7003	661.3668	331.1870			5
15	1752.9916	876.9994	1735.9650	868.4861	1734.9810	867.9941	N	***565.3093***	283.1583	548.2827	274.6450			4
16	**1866.0756**	933.5415	1849.0491	925.0282	1848.0651	924.5362	I	***451.2663***	226.1368	434.2398	217.6235			3
17	2029.1390	1015.0731	2012.1124	1006.5598	2011.1284	1006.0678	Y	338.1823	169.5948	321.1557	161.0815			2
18							R	175.1190	88.0631	158.0924	79.5498			1



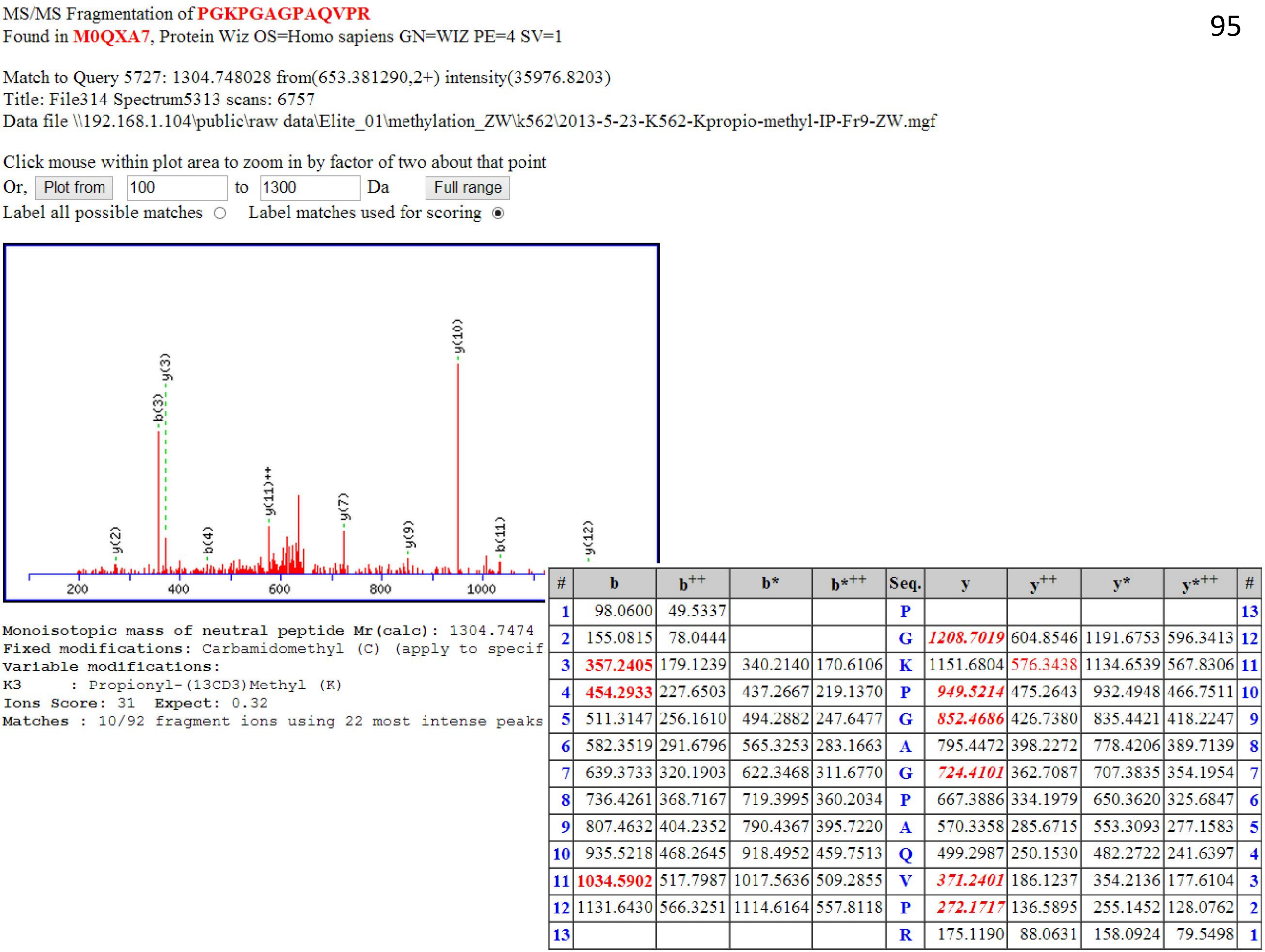
MS/MS Fragmentation of **MKWHSEDEIR**
Found in **Q9GZY0**, Nuclear RNA export factor 2 OS=Homo sapiens GN=NXF2 PE=1 SV=1

Match to Query 6900: 1407.700648 from(704.857600,2+) intensity(51287.1406)
Title: File314 Spectrum7796 scans: 9406
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr9-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1407.6998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Label:13C(1)2H(3)
K2      : Propionyl-(13CD3)M
Ions Score: 52  Expect: 0.0
Matches : 11/94 fragment ic
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	136.0699	68.5386					M							10
2	***338.2290***	169.6181	321.2024	161.1048			K	1273.6444	637.3258	1256.6179	628.8126	1255.6338	628.3206	9
3	***524.3083***	262.6578	507.2817	254.1445			W	***1071.4854***	536.2463	1054.4588	527.7331	1053.4748	527.2411	8
4	661.3672	331.1872	644.3406	322.6740			H	***885.4061***	443.2067	868.3795	434.6934	867.3955	434.2014	7
5	***748.3992***	374.7032	731.3727	366.1900	730.3886	365.6980	S	***748.3472***	374.6772	731.3206	366.1640	730.3366	365.6719	6
6	877.4418	439.2245	860.4153	430.7113	859.4312	430.2193	E	661.3151	331.1612	644.2886	322.6479	643.3046	322.1559	5
7	***992.4687***	496.7380	975.4422	488.2247	974.4582	487.7327	D	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
8	***1121.5113***	561.2593	1104.4848	552.7460	1103.5008	552.2540	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
9	***1234.5954***	617.8013	1217.5689	609.2881	1216.5848	608.7961	I	***288.2030***	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



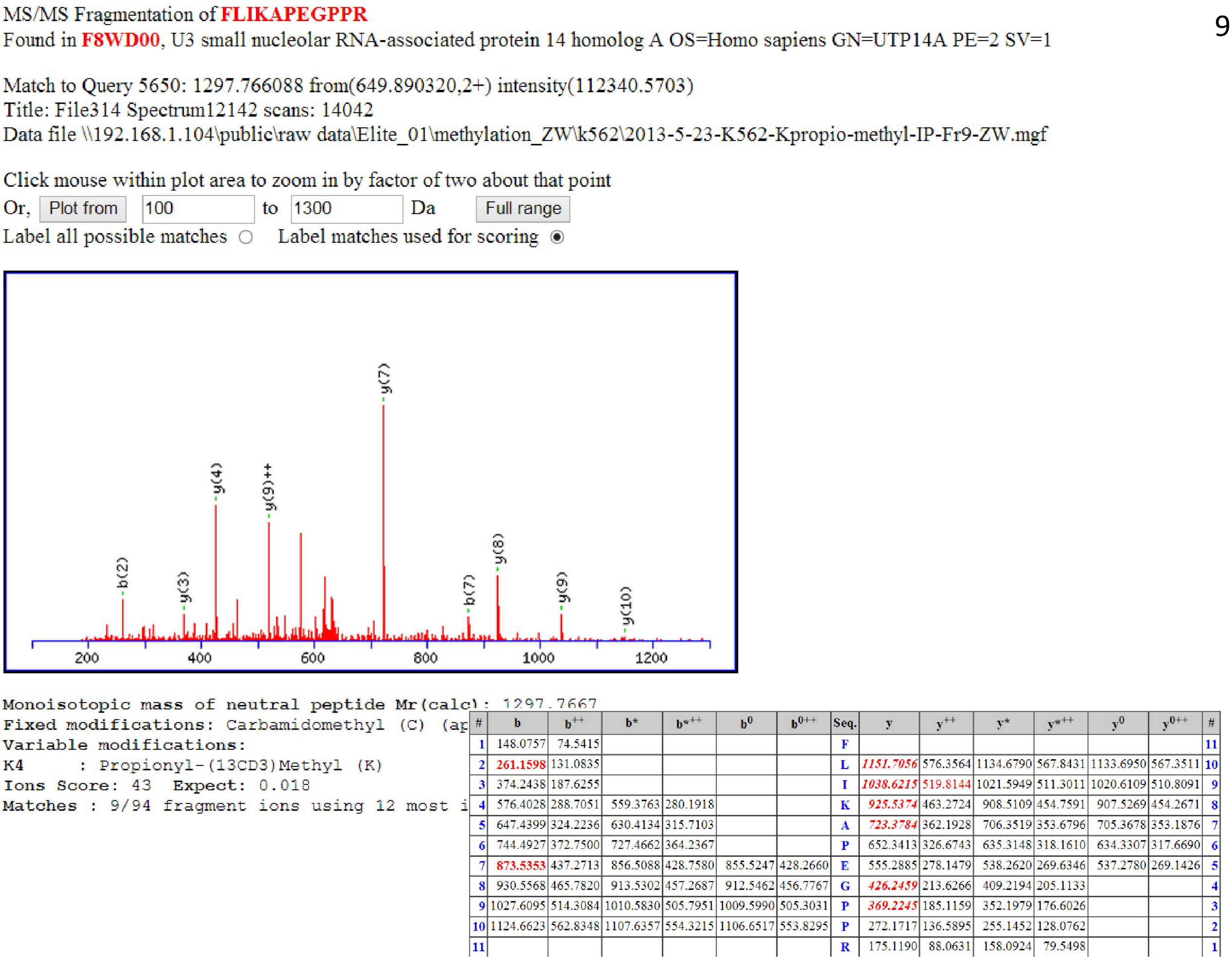
MS/MS Fragmentation of **PGKPGAGPAQVPR**
Found in **M0QXA7**, Protein Wiz OS=Homo sapiens GN=WIZ PE=4 SV=1

Match to Query 5727: 1304.748028 from(653.381290,2+) intensity(35976.8203)
Title: File314 Spectrum5313 scans: 6757
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr9-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1304.7474
Fixed modifications: Carbamidomethyl (C) (apply to specif
Variable modifications:
K3      : Propionyl-(13CD3)Methyl (K)
Ions Score: 31  Expect: 0.32
Matches : 10/92 fragment ions using 22 most intense peaks
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	98.0600	49.5337			P					13
2	155.0815	78.0444			G	***1208.7019***	604.8546	1191.6753	596.3413	12
3	**357.2405**	179.1239	340.2140	170.6106	K	1151.6804	576.3438	1134.6539	567.8306	11
4	**454.2933**	227.6503	437.2667	219.1370	P	***949.5214***	475.2643	932.4948	466.7511	10
5	511.3147	256.1610	494.2882	247.6477	G	***852.4686***	426.7380	835.4421	418.2247	9
6	582.3519	291.6796	565.3253	283.1663	A	795.4472	398.2272	778.4206	389.7139	8
7	639.3733	320.1903	622.3468	311.6770	G	***724.4101***	362.7087	707.3835	354.1954	7
8	736.4261	368.7167	719.3995	360.2034	P	667.3886	334.1979	650.3620	325.6847	6
9	807.4632	404.2352	790.4367	395.7220	A	570.3358	285.6715	553.3093	277.1583	5
10	935.5218	468.2645	918.4952	459.7513	Q	499.2987	250.1530	482.2722	241.6397	4
11	**1034.5902**	517.7987	1017.5636	509.2855	V	***371.2401***	186.1237	354.2136	177.6104	3
12	1131.6430	566.3251	1114.6164	557.8118	P	***272.1717***	136.5895	255.1452	128.0762	2
13					R	175.1190	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **FLIKAPEGPPR**
Found in **F8WD00**, U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=2 SV=1

Match to Query 5650: 1297.766088 from(649.890320,2+) intensity(112340.5703)
Title: File314 Spectrum12142 scans: 14042
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr9-ZW.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 ●

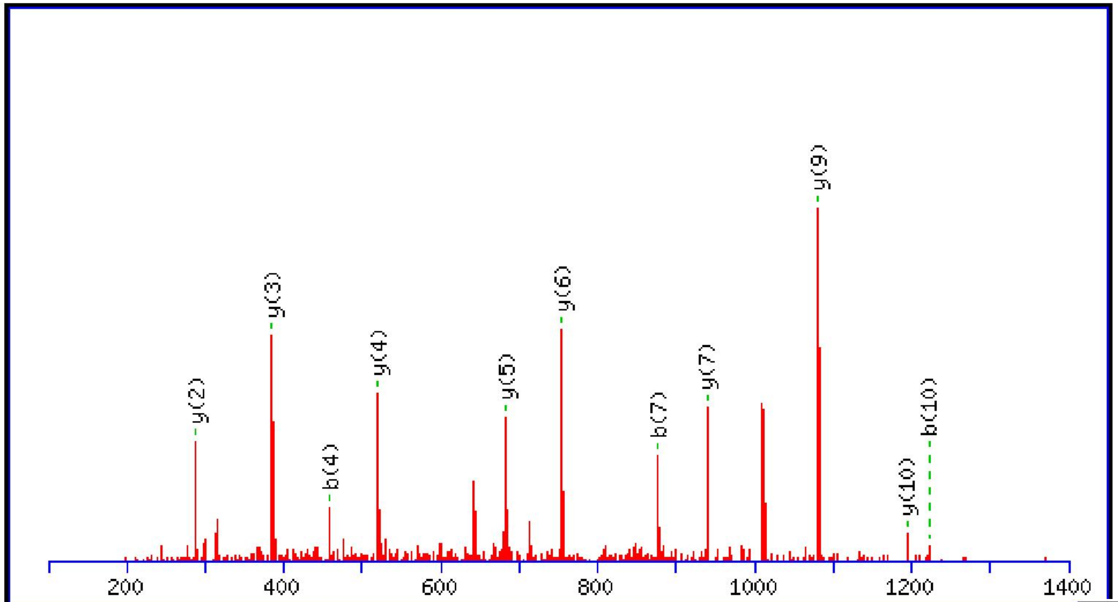
```
Monoisotopic mass of neutral peptide Mr(calc): 1297.7667
Fixed modifications: Carbamidomethyl (C) (ap
Variable modifications:
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 43  Expect: 0.018
Matches : 9/94 fragment ions using 12 most i
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							11
2	**261.1598**	131.0835					L	***1151.7056***	576.3564	1134.6790	567.8431	1133.6950	567.3511	10
3	374.2438	187.6255					I	***1038.6215***	519.8144	1021.5949	511.3011	1020.6109	510.8091	9
4	576.4028	288.7051	559.3763	280.1918			K	***925.5374***	463.2724	908.5109	454.7591	907.5269	454.2671	8
5	647.4399	324.2236	630.4134	315.7103			A	***723.3784***	362.1928	706.3519	353.6796	705.3678	353.1876	7
6	744.4927	372.7500	727.4662	364.2367			P	652.3413	326.6743	635.3148	318.1610	634.3307	317.6690	6
7	**873.5353**	437.2713	856.5088	428.7580	855.5247	428.2660	E	555.2885	278.1479	538.2620	269.6346	537.2780	269.1426	5
8	930.5568	465.7820	913.5302	457.2687	912.5462	456.7767	G	***426.2459***	213.6266	409.2194	205.1133			4
9	1027.6095	514.3084	1010.5830	505.7951	1009.5990	505.3031	P	***369.2245***	185.1159	352.1979	176.6026			3
10	1124.6623	562.8348	1107.6357	554.3215	1106.6517	553.8295	P	272.1717	136.5895	255.1452	128.0762			2
11							R	175.1190	88.0631	158.0924	79.5498			1

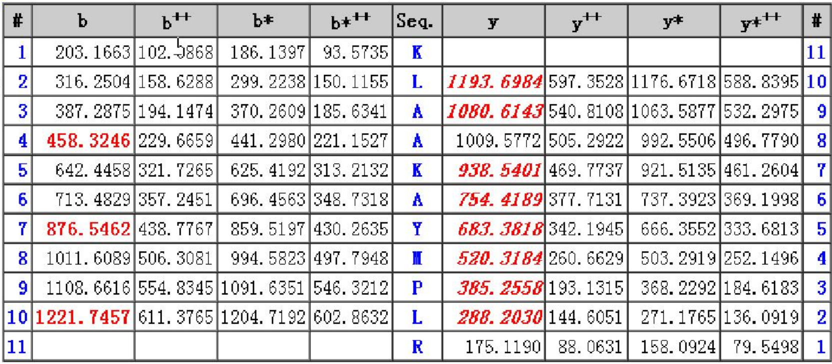
MS/MS Fragmentation of **KLAAKAYMPLR**
Found in **F5H8K3**, PHD finger protein 19 OS=Homo sapiens GN=PHF19 PE=2 SV=1

Match to Query 6707: 1394.850188 from(698.432370,2+) intensity(214282.7969)
Title: File314 Spectrum14179 scans: 16215
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr9-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1394.8501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or t
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
M8 : Label:13C(1)2H(3) (M)
Ions Score: 78 **Expect:** 2.9e-006
Matches : 11/80 fragment ions using 12 most intense peaks (help)

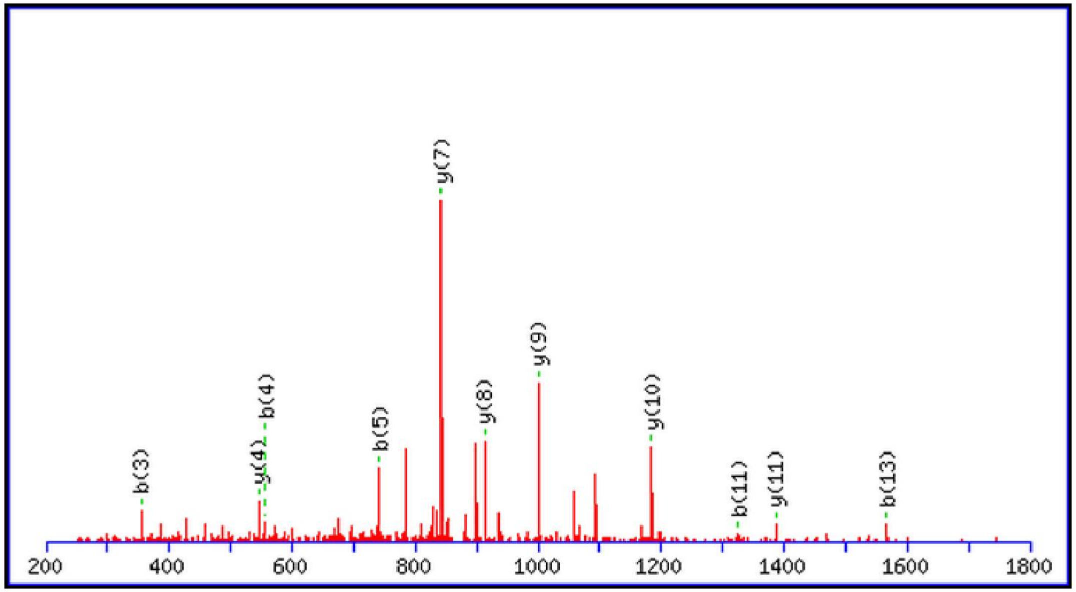


#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	203.1663	102.0868	186.1397	93.5735	K					11
2	316.2504	158.6288	299.2238	150.1155	L	***1193.6984***	597.3528	1176.6718	588.8395	10
3	387.2875	194.1474	370.2609	185.6341	A	***1080.6143***	540.8108	1063.5877	532.2975	9
4	**458.3246**	229.6659	441.2980	221.1527	A	1009.5772	505.2922	992.5506	496.7790	8
5	642.4458	321.7265	625.4192	313.2132	K	***938.5401***	469.7737	921.5135	461.2604	7
6	713.4829	357.2451	696.4563	348.7318	A	***754.4189***	377.7131	737.3923	369.1998	6
7	**876.5462**	438.7767	859.5197	430.2635	Y	***683.3818***	342.1945	666.3552	333.6813	5
8	1011.6089	506.3081	994.5823	497.7948	M	***520.3184***	260.6629	503.2919	252.1496	4
9	1108.6616	554.8345	1091.6351	546.3212	P	***385.2558***	193.1315	368.2292	184.6183	3
10	**1221.7457**	611.3765	1204.7192	602.8632	L	***288.2030***	144.6051	271.1765	136.0919	2
11					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **VAKKKSAPAEEQLR**
Found in **Q96BK5**, PIN2/TERF1-interacting telomerase inhibitor 1 OS=Homo sapiens GN=PINX1 PE=1 SV=2

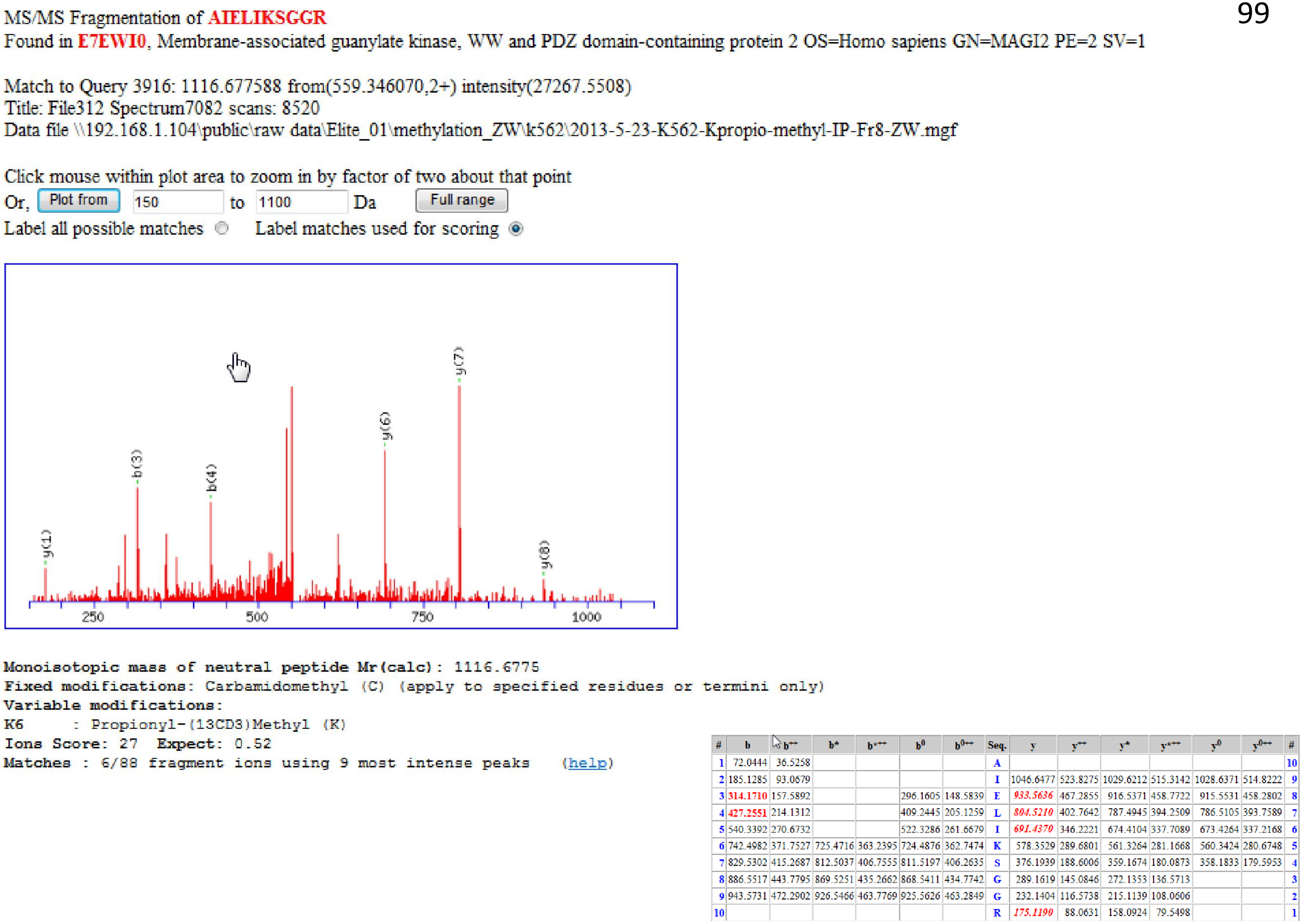
Match to Query 12905: 1740.004988 from(871.009770,2+) intensity(133428.2969)
Title: File312 Spectrum8804 scans: 10358
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1740.
Fixed modifications: Carbamidomethyl (C) (apply to s
Variable modifications:
K3      : Propionyl (K)
K4      : Propionyl-(13CD3)Methyl (K)
K5      : Propionyl (K)
Ions Score: 47  Expect: 0.0074
Matches : 11/136 fragment ions using 15 most intense
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							14
2	171.1128	86.0600					A	1641.9443	821.4758	1624.9177	812.9625	1623.9337	812.4705	13
3	***355.2340***	178.1206	338.2074	169.6074			K	1570.9072	785.9572	1553.8806	777.4439	1552.8966	776.9519	12
4	***557.3930***	279.2001	540.3664	270.6869			K	***1386.7860***	693.8966	1369.7594	685.3834	1368.7754	684.8914	11
5	***741.5142***	371.2607	724.4876	362.7475			K	***1184.6270***	592.8171	1167.6004	584.3039	1166.6164	583.8118	10
6	828.5462	414.7767	811.5197	406.2635	810.5356	405.7715	S	***1000.5058***	500.7565	983.4793	492.2433	982.4952	491.7513	9
7	899.5833	450.2953	882.5568	441.7820	881.5727	441.2900	A	***913.4738***	457.2405	896.4472	448.7272	895.4632	448.2352	8
8	996.6361	498.8217	979.6095	490.3084	978.6255	489.8164	P	***842.4367***	421.7220	825.4101	413.2087	824.4261	412.7167	7
9	1067.6732	534.3402	1050.6466	525.8270	1049.6626	525.3350	A	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	6
10	1196.7158	598.8615	1179.6892	590.3483	1178.7052	589.8562	E	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	5
11	***1325.7584***	663.3828	1308.7318	654.8696	1307.7478	654.3775	E	***545.3042***	273.1557	528.2776	264.6425	527.2936	264.1504	4
12	1453.8170	727.4121	1436.7904	718.8988	1435.8064	718.4068	Q	416.2616	208.6344	399.2350	200.1212			3
13	***1566.9010***	783.9541	1549.8745	775.4409	1548.8905	774.9489	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1



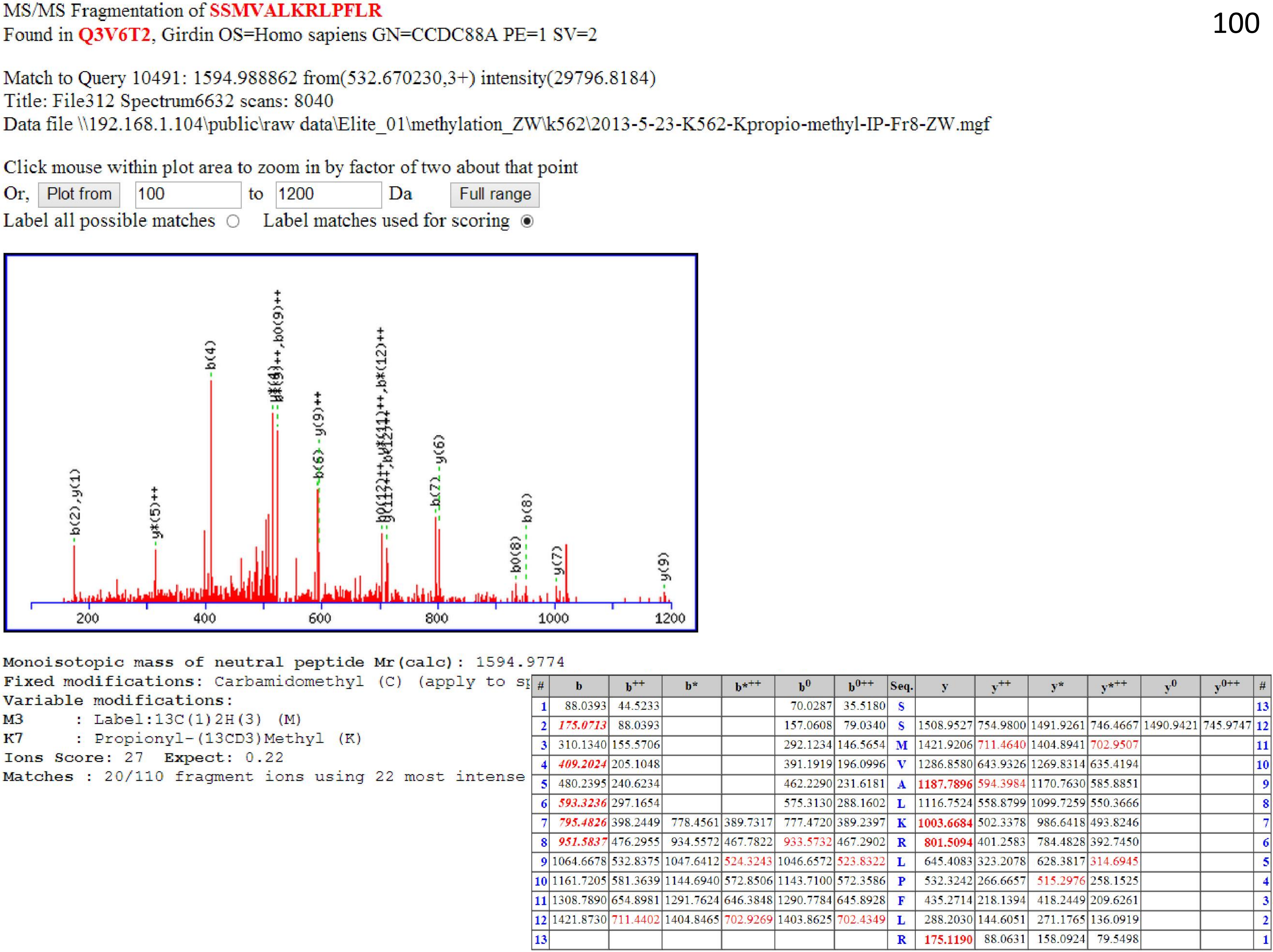
MS/MS Fragmentation of **AIELIKSGGR**
Found in **E7EWI0**, Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2 OS=Homo sapiens GN=MAGI2 PE=2 SV=1

Match to Query 3916: 1116.677588 from(559.346070,2+) intensity(27267.5508)
Title: File312 Spectrum7082 scans: 8520
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1116.6775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6      : Propionyl-(13CD3)Methyl (K)
Ions Score: 27  Expect: 0.52
Matches : 6/88 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							10
2	185.1285	93.0679					I	1046.6477	523.8275	1029.6212	515.3142	1028.6371	514.8222	9
3	**314.1710**	157.5892			296.1605	148.5839	E	***933.5636***	467.2855	916.5371	458.7722	915.5531	458.2802	8
4	**427.2551**	214.1312			409.2445	205.1259	L	***804.5210***	402.7642	787.4945	394.2509	786.5105	393.7589	7
5	540.3392	270.6732			522.3286	261.6679	I	***691.4370***	346.2221	674.4104	337.7089	673.4264	337.2168	6
6	742.4982	371.7527	725.4716	363.2395	724.4876	362.7474	K	578.3529	289.6801	561.3264	281.1668	560.3424	280.6748	5
7	829.5302	415.2687	812.5037	406.7555	811.5197	406.2635	S	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	4
8	886.5517	443.7795	869.5251	435.2662	868.5411	434.7742	G	289.1619	145.0846	272.1353	136.5713			3
9	943.5731	472.2902	926.5466	463.7769	925.5626	463.2849	G	232.1404	116.5738	215.1139	108.0606			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1



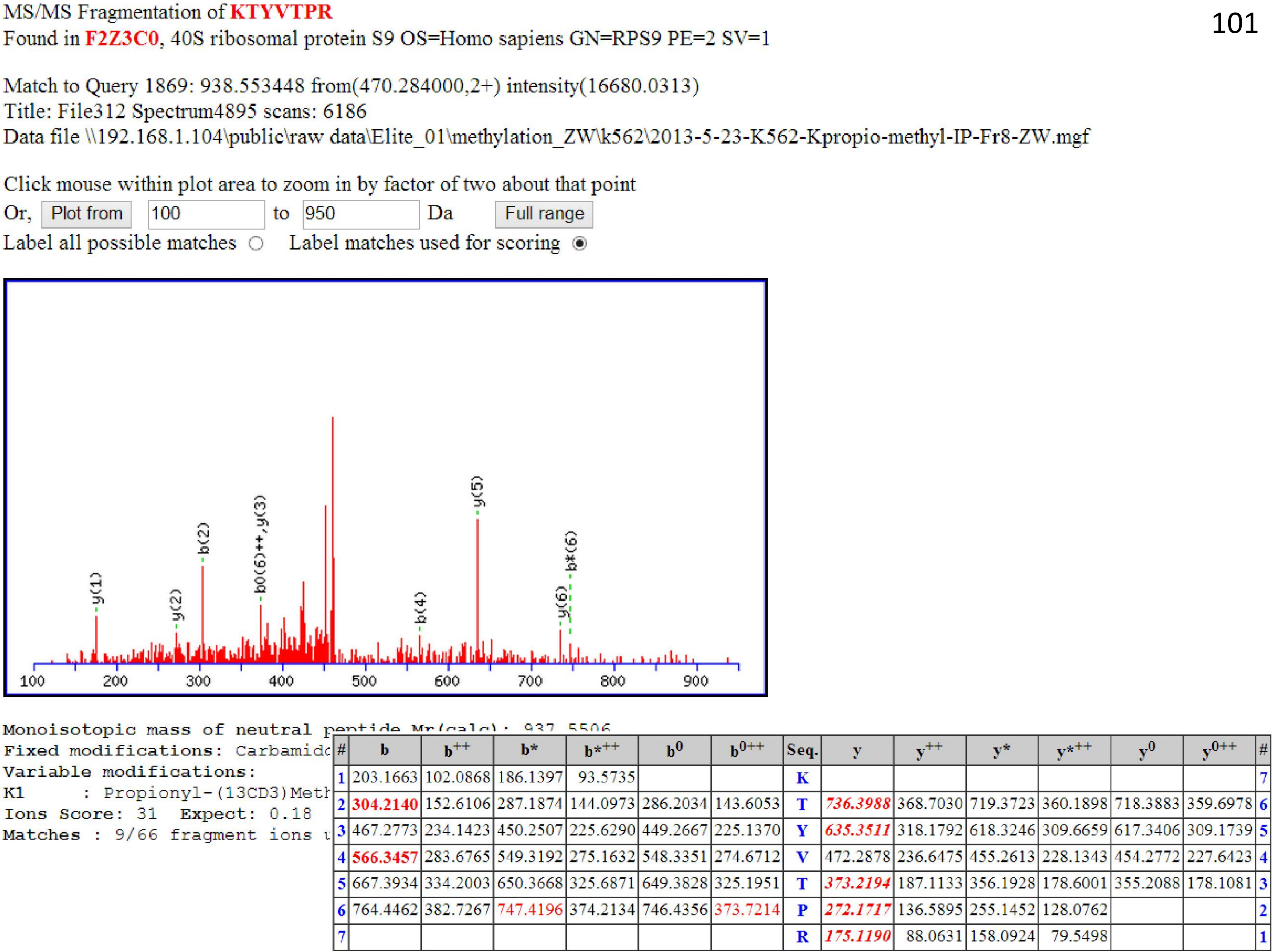
MS/MS Fragmentation of **SSMVALKRLPFLR**
Found in **Q3V6T2**, Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2

Match to Query 10491: 1594.988862 from(532.670230,3+) intensity(29796.8184)
Title: File312 Spectrum6632 scans: 8040
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1594.9774
Fixed modifications: Carbamidomethyl (C) (apply to sp
Variable modifications:
M3      : Label:13C(1)2H(3) (M)
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 27   Expect: 0.22
Matches : 20/110 fragment ions using 22 most intense
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	***175.0713***	88.0393			157.0608	79.0340	S	1508.9527	754.9800	1491.9261	746.4667	1490.9421	745.9747	12
3	310.1340	155.5706			292.1234	146.5654	M	1421.9206	711.4640	1404.8941	702.9507			11
4	***409.2024***	205.1048			391.1919	196.0996	V	1286.8580	643.9326	1269.8314	635.4194			10
5	480.2395	240.6234			462.2290	231.6181	A	**1187.7896**	594.3984	1170.7630	585.8851			9
6	***593.3236***	297.1654			575.3130	288.1602	L	1116.7524	558.8799	1099.7259	550.3666			8
7	***795.4826***	398.2449	778.4561	389.7317	777.4720	389.2397	K	**1003.6684**	502.3378	986.6418	493.8246			7
8	***951.5837***	476.2955	934.5572	467.7822	933.5732	467.2902	R	**801.5094**	401.2583	784.4828	392.7450			6
9	1064.6678	532.8375	1047.6412	524.3243	1046.6572	523.8322	L	645.4083	323.2078	628.3817	314.6945			5
10	1161.7205	581.3639	1144.6940	572.8506	1143.7100	572.3586	P	532.3242	266.6657	515.2976	258.1525			4
11	1308.7890	654.8981	1291.7624	646.3848	1290.7784	645.8928	F	435.2714	218.1394	418.2449	209.6261			3
12	1421.8730	711.4402	1404.8465	702.9269	1403.8625	702.4349	L	288.2030	144.6051	271.1765	136.0919			2
13							R	**175.1190**	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KTYVTPR**
Found in **F2Z3C0**, 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=2 SV=1

Match to Query 1869: 938.553448 from(470.284000,2+) intensity(16680.0313)
Title: File312 Spectrum4895 scans: 6186
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

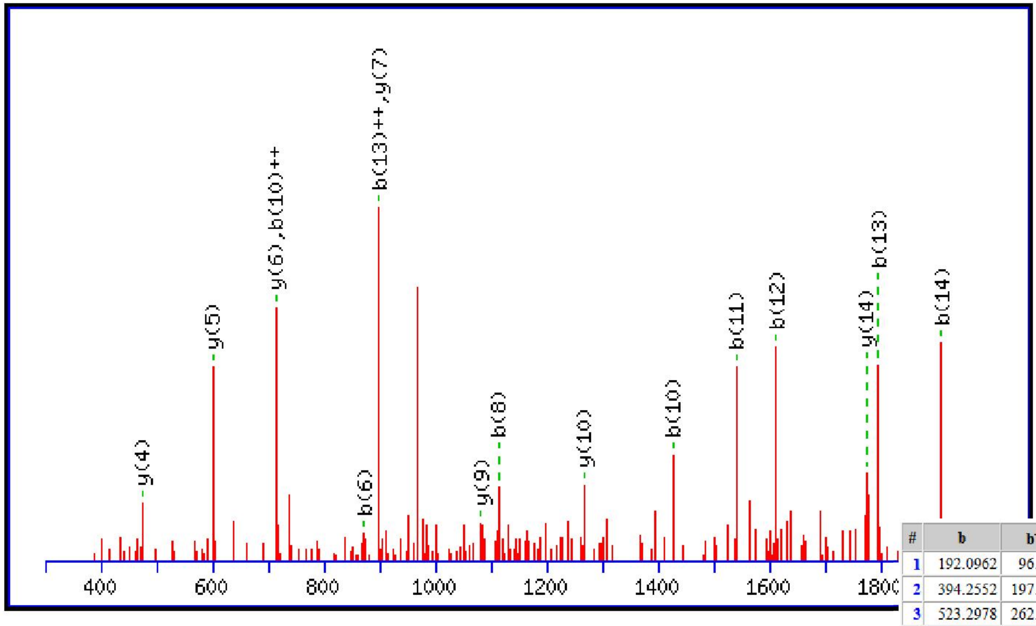
Monoisotopic mass of neutral peptide Mr(calc): 937.5506
Fixed modifications: Carbamido
Variable modifications:
K1 : Propionyl-(13CD3)Meth
Ions Score: 31 Expect: 0.18
Matches : 9/66 fragment ions u

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							7
2	**304.2140**	152.6106	287.1874	144.0973	286.2034	143.6053	T	***736.3988***	368.7030	719.3723	360.1898	718.3883	359.6978	6
3	467.2773	234.1423	450.2507	225.6290	449.2667	225.1370	Y	***635.3511***	318.1792	618.3246	309.6659	617.3406	309.1739	5
4	**566.3457**	283.6765	549.3192	275.1632	548.3351	274.6712	V	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
5	667.3934	334.2003	650.3668	325.6871	649.3828	325.1951	T	***373.2194***	187.1133	356.1928	178.6001	355.2088	178.1081	3
6	764.4462	382.7267	747.4196	374.2134	746.4356	373.7214	P	***272.1717***	136.5895	255.1452	128.0762			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **MKETIMNQEKLAKLQAQVR**
Found in **D6RDG3**, Transcription factor BTF3 (Fragment) OS=Homo sapiens GN=BTF3 PE=2 SV=1

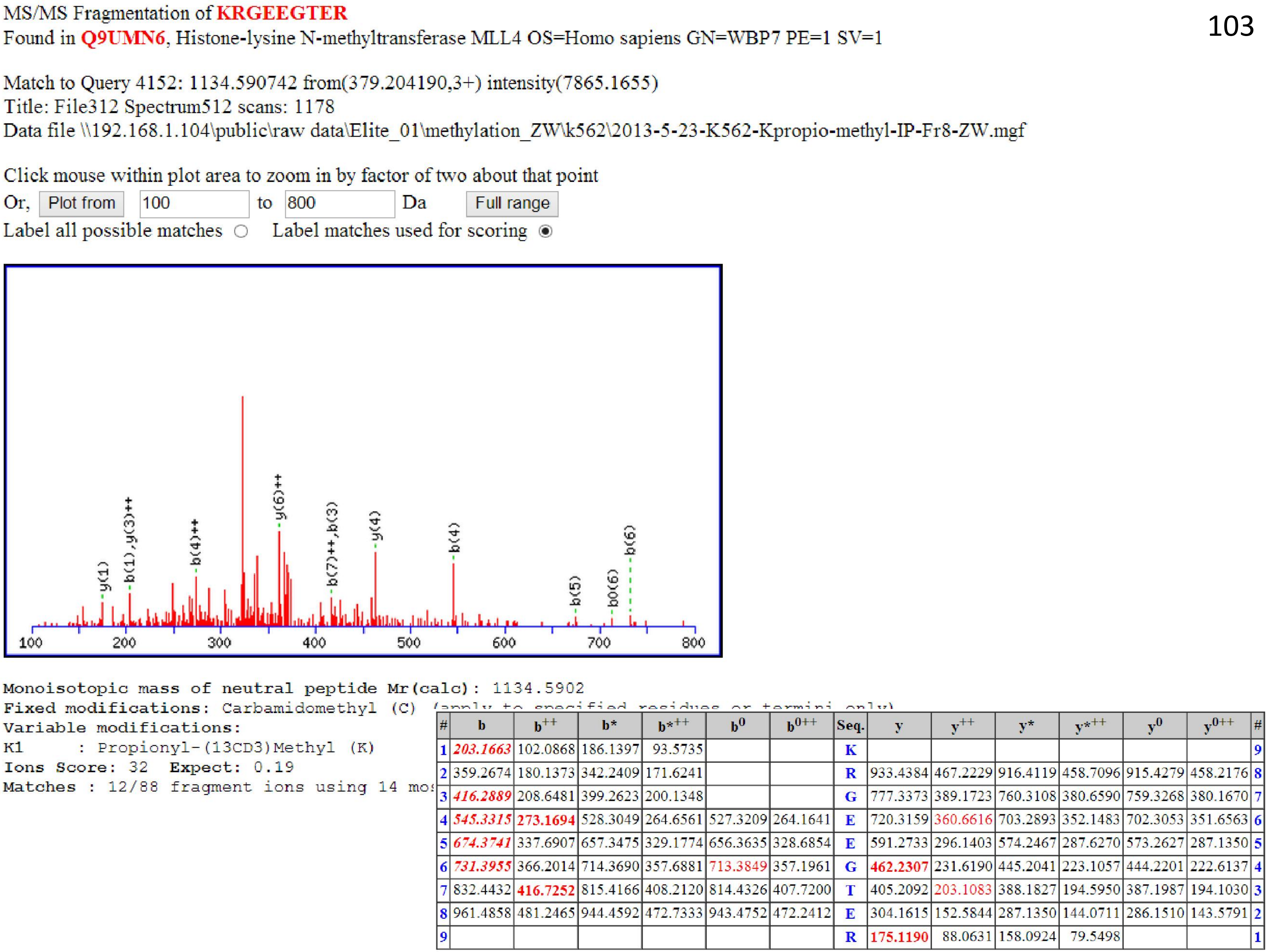
Match to Query 18897: 2508.413668 from(1255.214110,2+) intensity(430861.0313)
Title: File312 Spectrum19338 scans: 21701
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2508.4109
Fixed modifications: Carbamidomethyl (C) (apply to specified resid
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
M1 : Label:13C(1)2H(3) (M)
K2 : Propionyl-(13CD3)Methyl (K)
M6 : Label:13C(1)2H(3) (M)
K10 : Propionyl (K)
K13 : Propionyl (K)
Ions Score: 68 **Expect:** 5.8e-005
Matches : 16/190 fragment ions using 16 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	192.0962	96.5517					M							19
2	394.2552	197.6312	377.2286	189.1180			K	2318.3294	1159.6683	2301.3028	1151.1550	2300.3188	1150.6630	18
3	523.2978	262.1525	506.2712	253.6392	505.2872	253.1472	E	2116.1703	1058.5888	2099.1438	1050.0755	2098.1598	1049.5835	17
4	624.3454	312.6764	607.3189	304.1631	606.3349	303.6711	T	1987.1277	994.0675	1970.1012	985.5542	1969.1172	985.0622	16
5	737.4295	369.2184	720.4030	360.7051	719.4189	360.2131	I	1886.0801	943.5437	1869.0535	935.0304	1868.0695	934.5384	15
6	*872.4922*	436.7497	855.4656	428.2365	854.4816	427.7444	M	*1772.9960*	887.0016	1755.9695	878.4884	1754.9854	877.9964	14
7	986.5351	493.7712	969.5086	485.2579	968.5245	484.7659	N	1637.9333	819.4703	1620.9068	810.9570	1619.9228	810.4650	13
8	*1114.5937*	557.8005	1097.5671	549.2872	1096.5831	548.7952	Q	1523.8904	762.4488	1506.8639	753.9356	1505.8798	753.4436	12
9	1243.6363	62[illegible].3218	1226.6097	613.8085	1225.6257	613.3165	E	1395.8318	698.4196	1378.8053	689.9063	1377.8213	689.4143	11
10	*1427.7575*	**714.3824**	1410.7309	705.8691	1409.7469	705.3771	K	*1266.7892*	633.8983	1249.7627	625.3850			10
11	*1540.8415*	770.9244	1523.8150	762.4111	1522.8310	761.9191	L	*1082.6681*	541.8377	1065.6415	533.3244			9
12	*1611.8786*	806.4430	1594.8521	797.9297	1593.8681	797.4377	A	969.5840	485.2956	952.5574	476.7824			8
13	*1795.9998*	**898.5035**	1778.9733	889.9903	1777.9892	889.4983	K	*898.5469*	449.7771	881.5203	441.2638			7
14	*1909.0839*	955.0456	1892.0573	946.5323	1891.0733	946.0403	L	*714.4257*	357.7165	697.3992	349.2032			6
15	2037.1425	1019.0749	2020.1159	1010.5616	2019.1319	1010.0696	Q	*601.3416*	301.1745	584.3151	292.6612			5
16	2108.1796	1054.5934	2091.1530	1046.0801	2090.1690	1045.5881	A	*473.2831*	237.1452	456.2565	228.6319			4
17	2236.2381	1118.6227	2219.2116	1110.1094	2218.2276	1109.6174	Q	402.2459	201.6266	385.2194	193.1133			3
18	2335.3066	1168.1569	2318.2800	1159.6436	2317.2960	1159.1516	V	274.1874	137.5973	257.1608	129.0840			2
19							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KRGEEGTER**
Found in **Q9UMN6**, Histone-lysine N-methyltransferase MLL4 OS=Homo sapiens GN=WBP7 PE=1 SV=1

Match to Query 4152: 1134.590742 from(379.204190,3+) intensity(7865.1655)
Title: File312 Spectrum512 scans: 1178
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

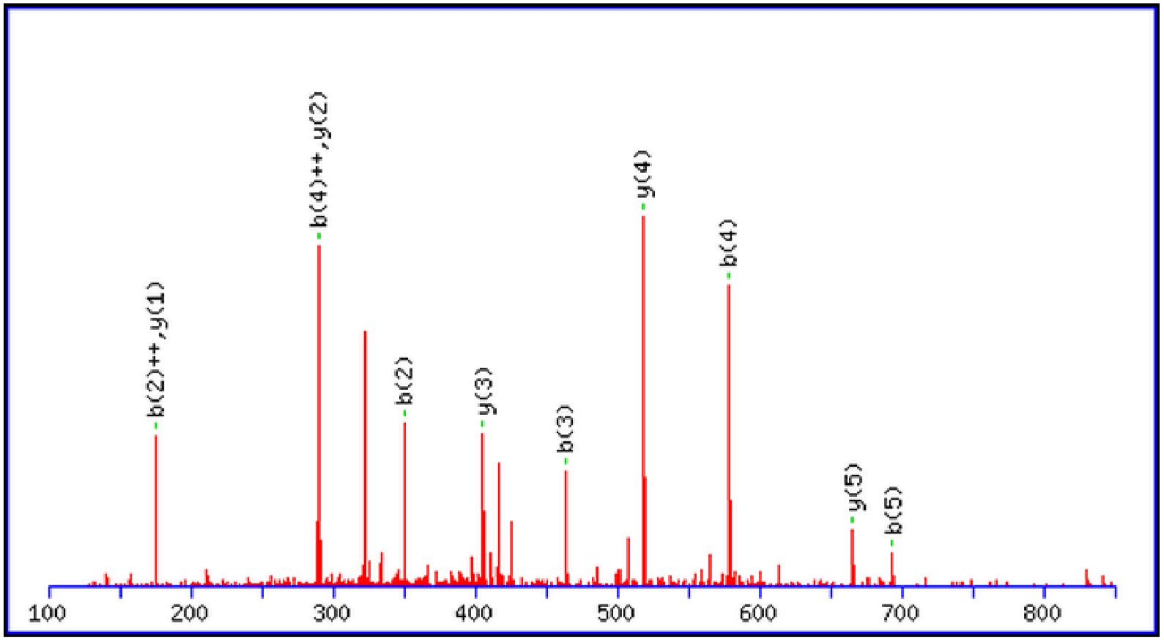
```
Monoisotopic mass of neutral peptide Mr(calc): 1134.5902
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
Ions Score: 32  Expect: 0.19
Matches : 12/88 fragment ions using 14 mos
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***203.1663***	102.0868	186.1397	93.5735			K							9
2	359.2674	180.1373	342.2409	171.6241			R	933.4384	467.2229	916.4119	458.7096	915.4279	458.2176	8
3	***416.2889***	208.6481	399.2623	200.1348			G	777.3373	389.1723	760.3108	380.6590	759.3268	380.1670	7
4	***545.3315***	**273.1694**	528.3049	264.6561	527.3209	264.1641	E	720.3159	360.6616	703.2893	352.1483	702.3053	351.6563	6
5	***674.3741***	337.6907	657.3475	329.1774	656.3635	328.6854	E	591.2733	296.1403	574.2467	287.6270	573.2627	287.1350	5
6	***731.3955***	366.2014	714.3690	357.6881	713.3849	357.1961	G	**462.2307**	231.6190	445.2041	223.1057	444.2201	222.6137	4
7	832.4432	**416.7252**	815.4166	408.2120	814.4326	407.7200	T	405.2092	203.1083	388.1827	194.5950	387.1987	194.1030	3
8	961.4858	481.2465	944.4592	472.7333	943.4752	472.2412	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KFIDDR**
Found in **C9JQG7**, Chromodomain Y-like protein (Fragment) OS=Homo sapiens GN=CDYL PE=2 SV=1

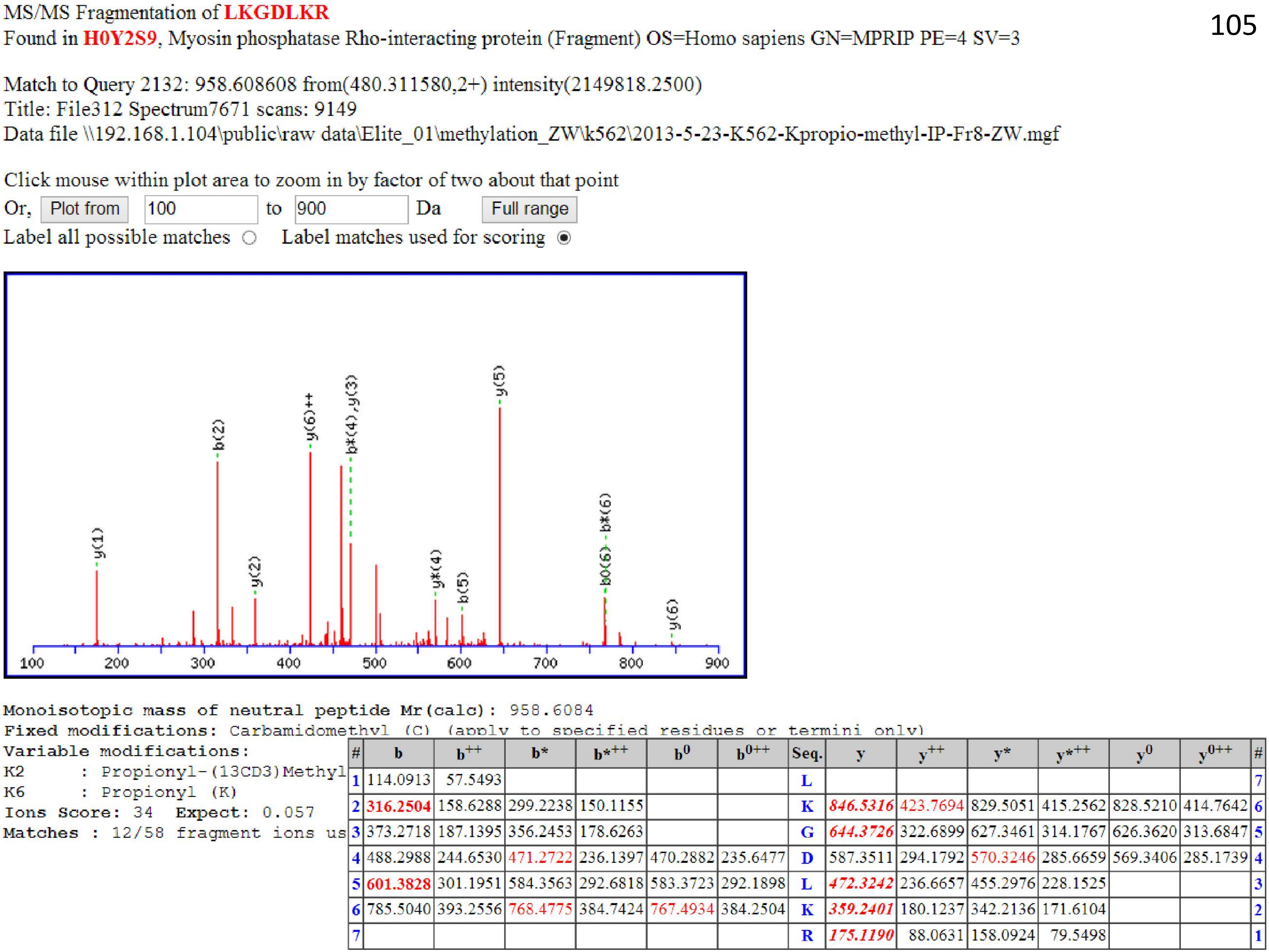
Match to Query 1155: 866.476968 from(434.245760,2+) intensity(121829.0703)
Title: File312 Spectrum7538 scans: 9007
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 866.4771
Fixed modifications:
Variable modificatio
K1         : Propionyl-(
Ions Score: 33   Expe
Matches : 11/52 frag
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			**K**							6
2	**350.2347**	**175.6210**	333.2082	167.1077			**F**	***665.3253***	333.1663	648.2988	324.6530	647.3148	324.1610	5
3	**463.3188**	232.1630	446.2922	223.6497			**I**	***518.2569***	259.6321	501.2304	251.1188	500.2463	250.6268	4
4	**578.3457**	**289.6765**	561.3192	281.1632	560.3351	280.6712	**D**	***405.1728***	203.0901	388.1463	194.5768	387.1623	194.0848	3
5	**693.3727**	347.1900	676.3461	338.6767	675.3621	338.1847	**D**	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
6							**R**	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LKGDLKR**

Found in **H0Y2S9**, Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIP PE=4 SV=3

Match to Query 2132: 958.608608 from(480.311580,2+) intensity(2149818.2500)

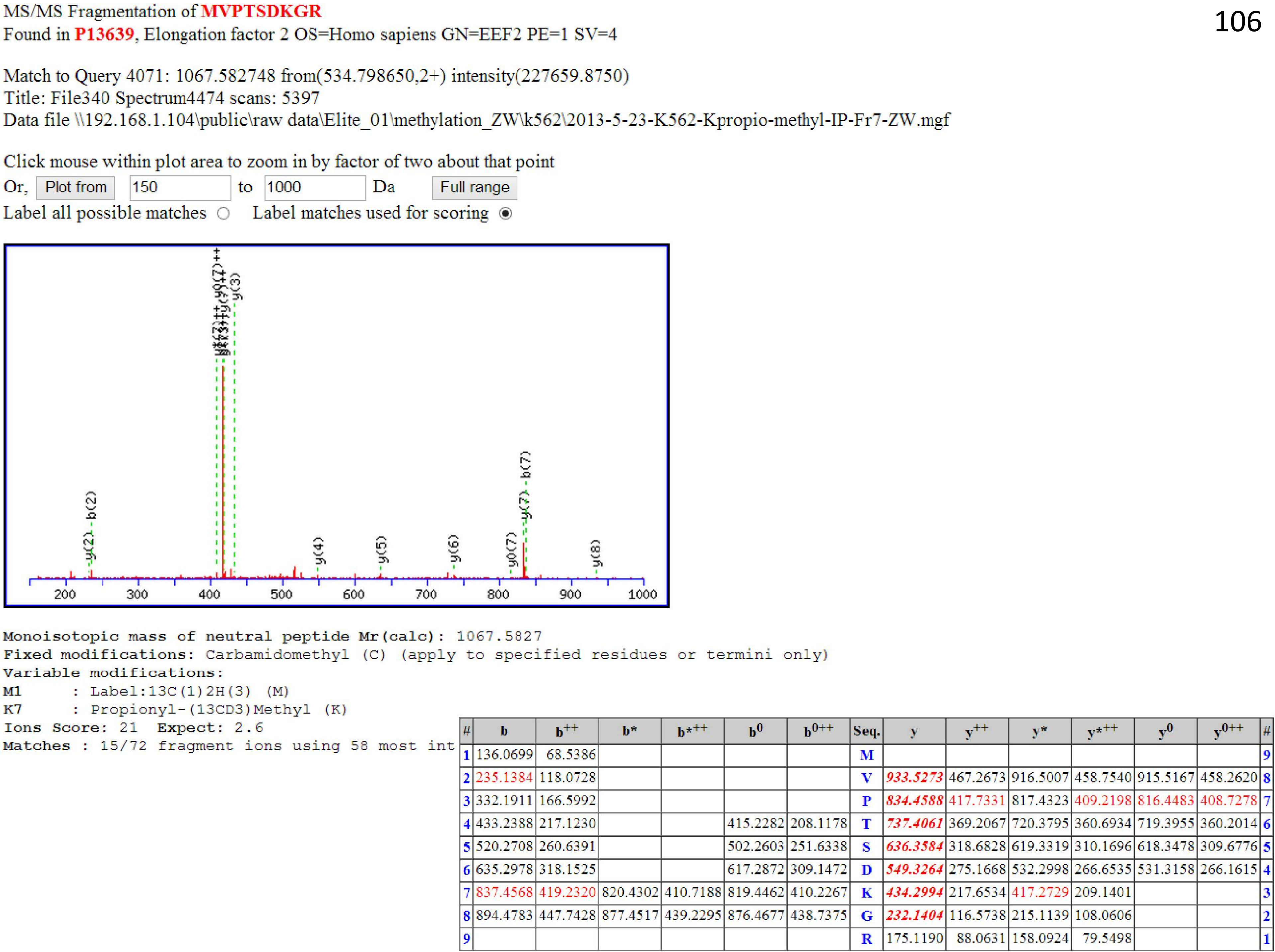
Title: File312 Spectrum7671 scans: 9149

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.mgf

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

```
Monoisotopic mass of neutral peptide Mr(calc): 958.6084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2       : Propionyl-(13CD3)Methyl
K6       : Propionyl (K)
Ions Score: 34  Expect: 0.057
Matches : 12/58 fragment ions us
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							7
2	**316.2504**	158.6288	299.2238	150.1155			K	***846.5316***	423.7694	829.5051	415.2562	828.5210	414.7642	6
3	373.2718	187.1395	356.2453	178.6263			G	***644.3726***	322.6899	627.3461	314.1767	626.3620	313.6847	5
4	488.2988	244.6530	471.2722	236.1397	470.2882	235.6477	D	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	4
5	**601.3828**	301.1951	584.3563	292.6818	583.3723	292.1898	L	***472.3242***	236.6657	455.2976	228.1525			3
6	785.5040	393.2556	768.4775	384.7424	767.4934	384.2504	K	***359.2401***	180.1237	342.2136	171.6104			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **MVPTSDKGR**
Found in **P13639**, Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Match to Query 4071: 1067.582748 from(534.798650,2+) intensity(227659.8750)
Title: File340 Spectrum4474 scans: 5397
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

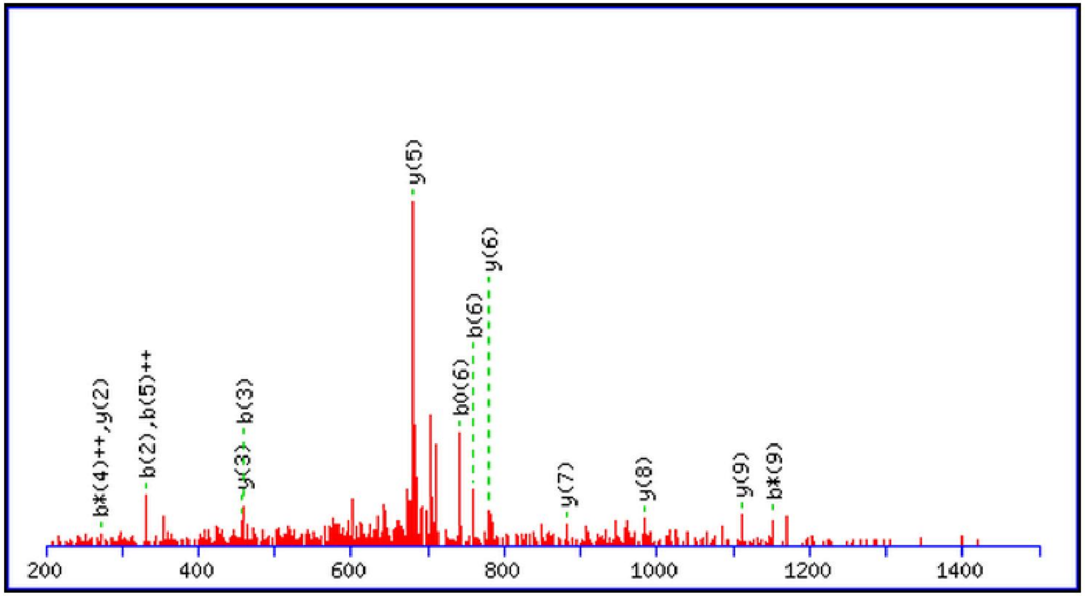
```
Monoisotopic mass of neutral peptide Mr(calc): 1067.5827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Label:13C(1)2H(3) (M)
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 21  Expect: 2.6
Matches : 15/72 fragment ions using 58 most int
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	136.0699	68.5386					M							9
2	235.1384	118.0728					V	***933.5273***	467.2673	916.5007	458.7540	915.5167	458.2620	8
3	332.1911	166.5992					P	***834.4588***	417.7331	817.4323	409.2198	816.4483	408.7278	7
4	433.2388	217.1230			415.2282	208.1178	T	***737.4061***	369.2067	720.3795	360.6934	719.3955	360.2014	6
5	520.2708	260.6391			502.2603	251.6338	S	***636.3584***	318.6828	619.3319	310.1696	618.3478	309.6776	5
6	635.2978	318.1525			617.2872	309.1472	D	***549.3264***	275.1668	532.2998	266.6535	531.3158	266.1615	4
7	837.4568	419.2320	820.4302	410.7188	819.4462	410.2267	K	***434.2994***	217.6534	417.2729	209.1401			3
8	894.4783	447.7428	877.4517	439.2295	876.4677	438.7375	G	***232.1404***	116.5738	215.1139	108.0606			2
9							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KQQTTVPQKPR**
Found in **Q6R954**, Polymerase delta interacting protein 46 OS=Homo sapiens GN=PDIP46 PE=2 SV=1

Match to Query 8879: 1439.836288 from(720.925420,2+) intensity(24912.3145)
Title: File340 Spectrum6426 scans: 7483
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



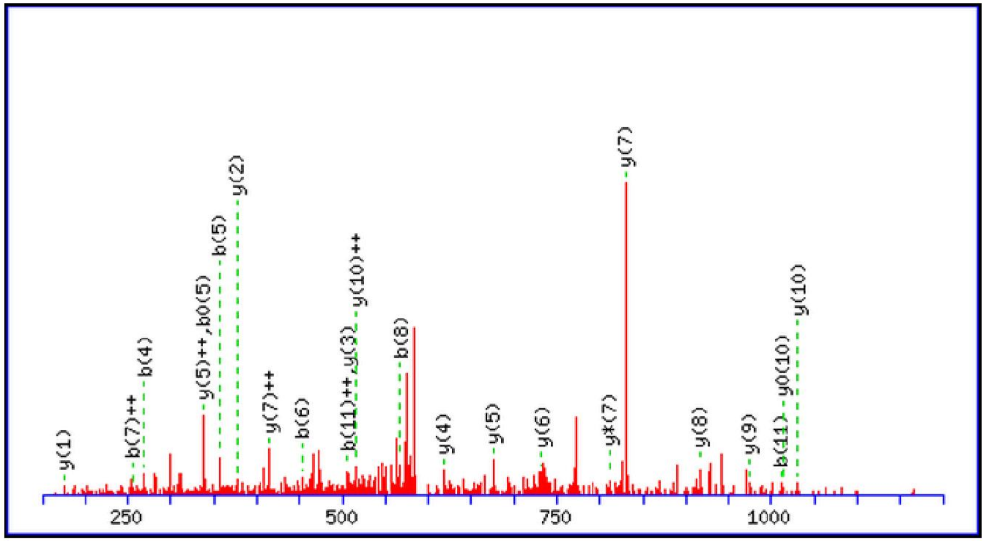
```
Monoisotopic mass of neutral peptide Mr(calc): 1439.8369
Fixed modifications: Carbamidomethyl (C) (a
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
K9      : Propionyl (K)
Ions Score: 23  Expect: 1.9
Matches : 14/102 fragment ions using 47 mos
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							11
2	**331.2249**	166.1161	314.1983	157.6028			Q	1238.6852	619.8462	1221.6586	611.3329	1220.6746	610.8409	10
3	**459.2834**	230.1454	442.2569	221.6321			Q	***1110.6266***	555.8169	1093.6000	547.3037	1092.6160	546.8116	9
4	560.3311	280.6692	543.3046	272.1559	542.3206	271.6639	T	***982.5680***	491.7876	965.5415	483.2744	964.5574	482.7824	8
5	661.3788	331.1930	644.3523	322.6798	643.3682	322.1878	T	***881.5203***	441.2638	864.4938	432.7505	863.5098	432.2585	7
6	**760.4472**	380.7272	743.4207	372.2140	742.4367	371.7220	V	***780.4727***	390.7400	763.4461	382.2267			6
7	857.5000	429.2536	840.4734	420.7404	839.4894	420.2483	P	***681.4042***	341.2058	664.3777	332.6925			5
8	985.5586	493.2829	968.5320	484.7696	967.5480	484.2776	Q	584.3515	292.6794	567.3249	284.1661			4
9	1169.6797	585.3435	1152.6532	576.8302	1151.6692	576.3382	K	***456.2929***	228.6501	439.2663	220.1368			3
10	1266.7325	633.8699	1249.7060	625.3566	1248.7219	624.8646	P	***272.1717***	136.5895	255.1452	128.0762			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GPGGSPGGLQKR**
Found in **K7EJB8**, Protein phosphatase 1 regulatory subunit 14A OS=Homo sapiens GN=PPP1R14A PE=4 SV=1

Match to Query 5445: 1183.657328 from(592.835940,2+) intensity(31017.3262)
Title: File340 Spectrum5712 scans: 6722
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



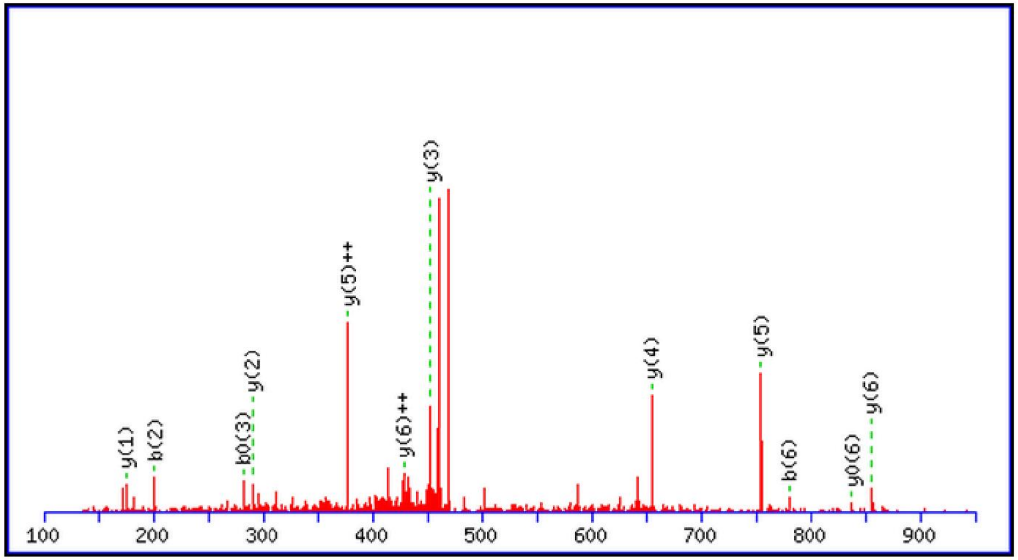
```
Monoisotopic mass of neutral peptide Mr(calc): 1183.6582
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K11     : Propionyl-(13CD3)Methyl (K)
Ions Score: 33  Expect: 0.2
Matches : 23/92 fragment ions using 87 most in
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							12
2	155.0815	78.0444					P	1127.6440	564.3256	1110.6175	555.8124	1109.6335	555.3204	11
3	212.1030	106.5551					G	***1030.5913***	515.7993	1013.5647	507.2860	1012.5807	506.7940	10
4	**269.1244**	135.0659					G	***973.5698***	487.2885	956.5432	478.7753	955.5592	478.2833	9
5	**356.1565**	178.5819			338.1459	169.5766	S	***916.5483***	458.7778	899.5218	450.2645	898.5378	449.7725	8
6	**453.2092**	227.1083			435.1987	218.1030	P	***829.5163***	415.2618	812.4897	406.7485			7
7	510.2307	255.6190			492.2201	246.6137	G	***732.4635***	366.7354	715.4370	358.2221			6
8	**567.2522**	284.1297			549.2416	275.1244	G	***675.4421***	338.2247	658.4155	329.7114			5
9	680.3362	340.6717			662.3257	331.6665	L	***618.4206***	309.7139	601.3941	301.2007			4
10	808.3948	404.7010	791.3682	396.1878	790.3842	395.6958	Q	***505.3365***	253.1719	488.3100	244.6586			3
11	**1010.5538**	505.7805	993.5273	497.2673	992.5432	496.7753	K	***377.2780***	189.1426	360.2514	180.6293			2
12							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VTVKYDR**
Found in **K7EJB8**, Protein phosphatase 1 regulatory subunit 14A OS=Homo sapiens GN=PPP1R14A PE=4 SV=1

Match to Query 2516: 953.545568 from(477.780060,2+) intensity(46758.8008)
Title: File340 Spectrum5861 scans: 6881
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



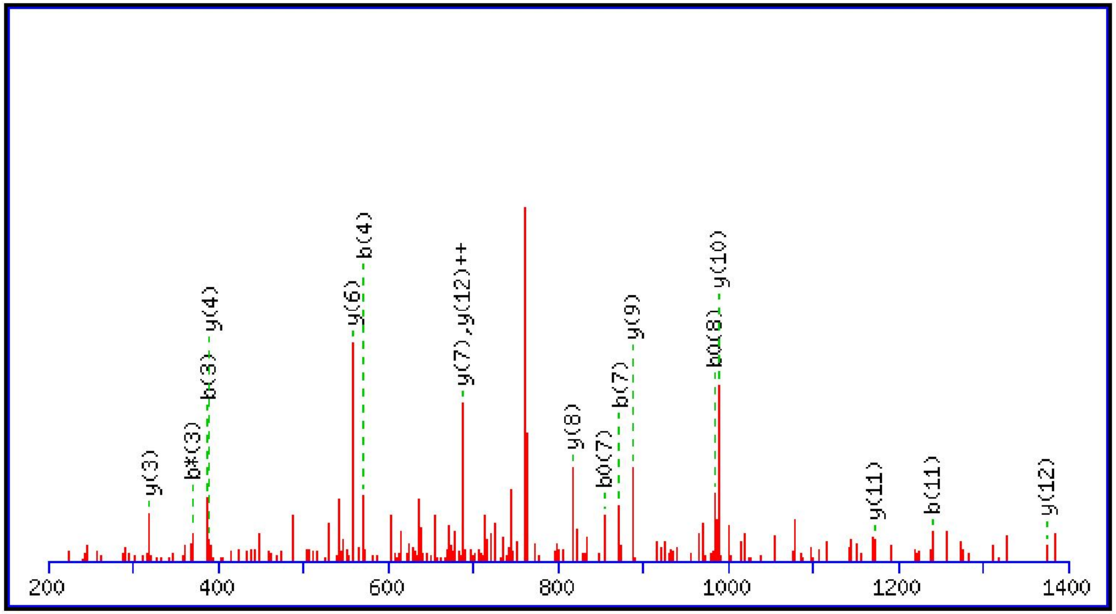
```
Monoisotopic mass of neutral peptide Mr(calc): 953.5455
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 39   Expec
Matches : 12/62 fragm
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							7
2	**201.1234**	101.0653			183.1128	92.0600	T	***855.4843***	428.2458	838.4578	419.7325	837.4738	419.2405	6
3	300.1918	150.5995			282.1812	141.5942	V	***754.4367***	377.7220	737.4101	369.2087	736.4261	368.7167	5
4	502.3508	251.6790	485.3242	243.1658	484.3402	242.6738	K	***655.3682***	328.1878	638.3417	319.6745	637.3577	319.1825	4
5	665.4141	333.2107	648.3876	324.6974	647.4036	324.2054	Y	***453.2092***	227.1082	436.1827	218.5950	435.1987	218.1030	3
6	**780.4411**	390.7242	763.4145	382.2109	762.4305	381.7189	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LAKKTAEEPAASGR**
Found in **Q9NQS7**, Inner centromere protein OS=Homo sapiens GN=INCENP PE=1 SV=3

Match to Query 9030: 1557.863248 from(779.938900,2+) intensity(19372.4043)
Title: File309 Spectrum5796 scans: 7064
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr6-ZW.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 ●



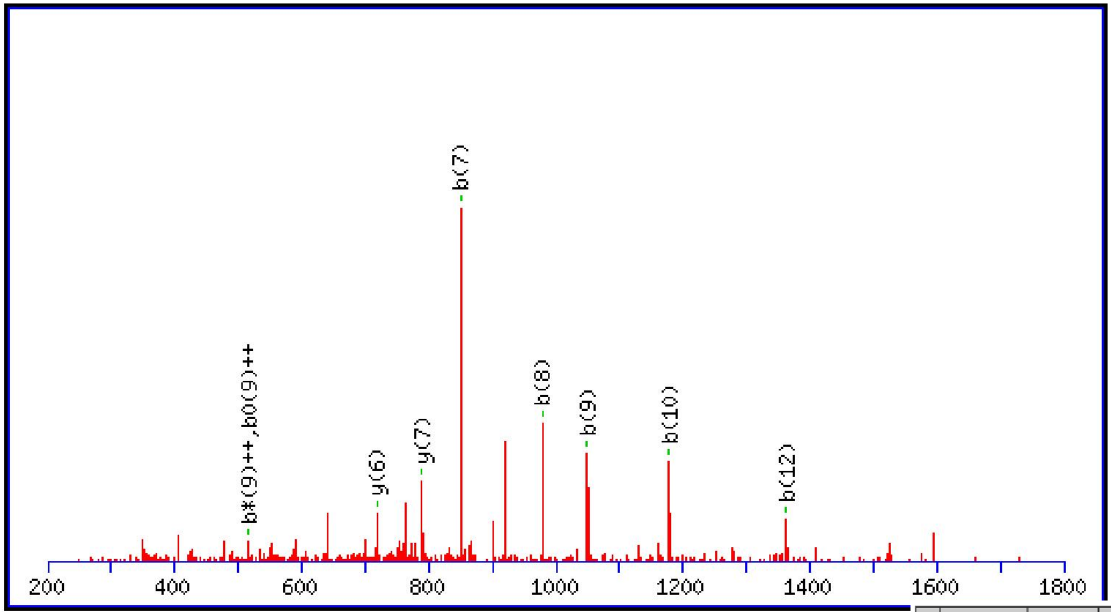
Monoisotopic mass of neutral peptide Mr(calc): 1557.8635
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
K4 : Propionyl (K)
Ions Score: 51 **Expect:** 0.0039
Matches : 17/140 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							14
2	185.1285	93.0679					A	1445.7867	723.3970	1428.7602	714.8837	1427.7762	714.3917	13
3	**387.2875**	194.1474	370.2609	185.6341			K	***1374.7496***	687.8784	1357.7231	679.3652	1356.7390	678.8732	12
4	**571.4086**	286.2080	554.3821	277.6947			K	***1172.5906***	586.7989	1155.5640	578.2857	1154.5800	577.7937	11
5	672.4563	336.7318	655.4298	328.2185	654.4458	327.7265	T	***988.4694***	494.7383	971.4429	486.2251	970.4588	485.7331	10
6	743.4934	372.2504	726.4669	363.7371	725.4829	363.2451	A	***887.4217***	444.2145	870.3952	435.7012	869.4112	435.2092	9
7	**872.5360**	436.7717	855.5095	428.2584	854.5255	427.7664	E	***816.3846***	408.6959	799.3581	400.1827	798.3741	399.6907	8
8	1001.5786	501.2930	984.5521	492.7797	983.5681	492.2877	E	***687.3420***	344.1747	670.3155	335.6614	669.3315	335.1694	7
9	1098.6314	549.8193	1081.6048	541.3061	1080.6208	540.8140	P	***558.2994***	279.6534	541.2729	271.1401	540.2889	270.6481	6
10	1169.6685	585.3379	1152.6420	576.8246	1151.6579	576.3326	A	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	5
11	**1240.7056**	620.8564	1223.6791	612.3432	1222.6951	611.8512	A	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	4
12	1327.7376	664.3725	1310.7111	655.8592	1309.7271	655.3672	S	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	3
13	1384.7591	692.8832	1367.7326	684.3699	1366.7485	683.8779	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **MKTPNAQEAEGQQTR**
Found in **Q5JZB7**, Spindlin-2B OS=Homo sapiens GN=SPIN2B PE=2 SV=1

Match to Query 11948: 1765.876448 from(883.945500,2+) intensity(111218.6563)
Title: File309 Spectrum8373 scans: 9815
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr6-ZW.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 ●



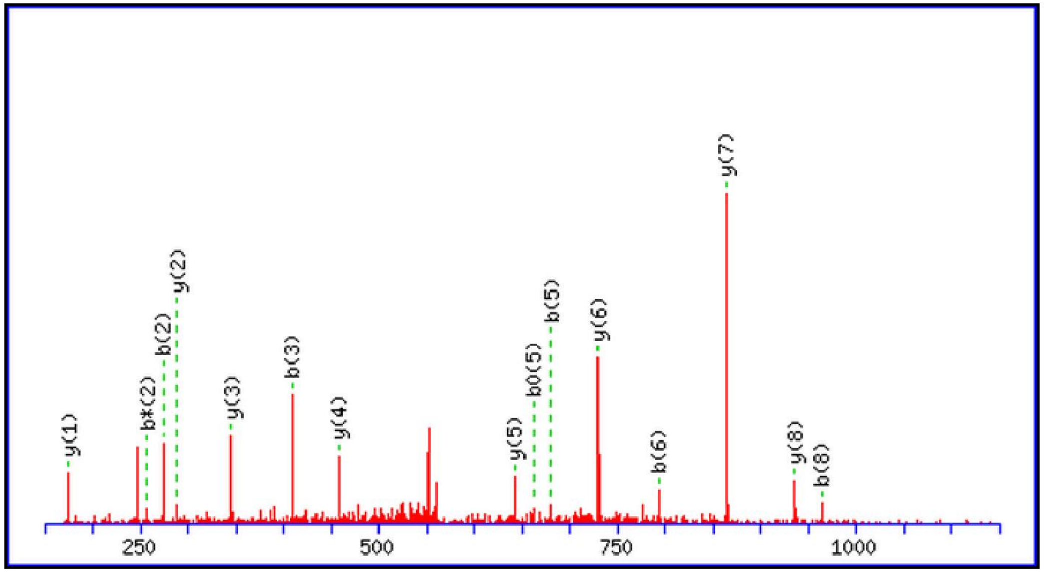
Monoisotopic mass of neutral peptide Mr(calc): 1765.8810
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
M1 : Label:13C(1)2H(3) (M)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 23 **Expect:** 1.9
Matches : 9/160 fragment ions using 15 most intense peaks (hel

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	136.0699	68.5386					M							15
2	338.2290	169.6181	321.2024	161.1048			K	1631.8256	816.4165	1614.7991	807.9032	1613.8151	807.4112	14
3	439.2766	220.1420	422.2501	211.6287	421.2661	211.1367	T	1429.6666	715.3369	1412.6401	706.8237	1411.6560	706.3317	13
4	536.3294	268.6683	519.3029	260.1551	518.3188	259.6631	P	1328.6189	664.8131	1311.5924	656.2998	1310.6084	655.8078	12
5	650.3723	325.6898	633.3458	317.1765	632.3618	316.6845	N	1231.5662	616.2867	1214.5396	607.7734	1213.5556	607.2814	11
6	721.4094	361.2084	704.3829	352.6951	703.3989	352.2031	A	1117.5232	559.2653	1100.4967	550.7520	1099.5127	550.2600	10
7	***849.4680***	425.2376	832.4415	416.7244	831.4575	416.2324	Q	1046.4861	523.7467	1029.4596	515.2334	1028.4756	514.7414	9
8	***978.5106***	489.7589	961.4841	481.2457	960.5000	480.7537	E	918.4276	459.7174	901.4010	451.2041	900.4170	450.7121	8
9	***1049.5477***	525.2775	1032.5212	516.7642	1031.5372	516.2722	A	**789.3850**	395.1961	772.3584	386.6828	771.3744	386.1908	7
10	***1178.5903***	589.7988	1161.5638	581.2855	1160.5798	580.7935	E	**718.3478**	359.6776	701.3213	351.1643	700.3373	350.6723	6
11	1235.6118	618.3095	1218.5852	609.7963	1217.6012	609.3042	G	589.3053	295.1563	572.2787	286.6430	571.2947	286.1510	5
12	***1363.6704***	682.3388	1346.6438	673.8255	1345.6598	673.3335	Q	532.2838	266.6455	515.2572	258.1323	514.2732	257.6402	4
13	1491.7289	746.3681	1474.7024	737.8548	1473.7184	737.3628	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
14	1592.7766	796.8919	1575.7501	788.3787	1574.7661	787.8867	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
15							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAMSKLGLR**
Found in **H0YHX9**, Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2 SV=1

Match to Query 5366: 1136.712748 from(569.363650,2+) intensity(117938.2891)
Title: File320 Spectrum12847 scans: 14333
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●



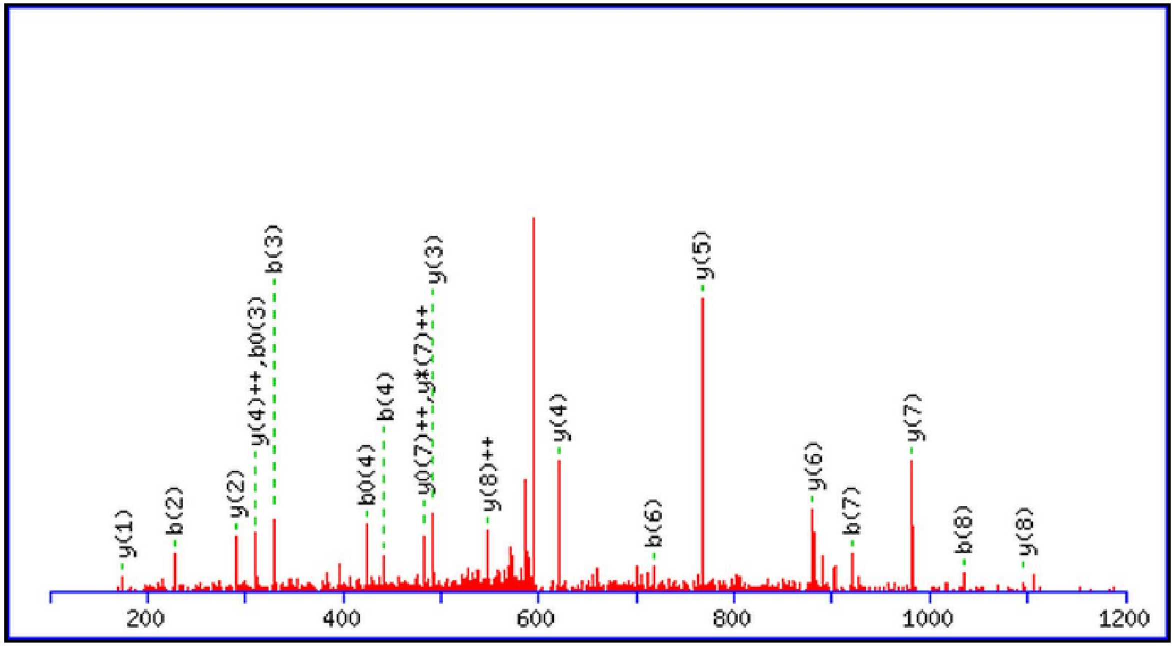
```
Monoisotopic mass of neutral peptide Mr(calc): 1136.7132
Fixed modifications: Ca
Variable modifications:
K1       : Propionyl-(13C
M3       : Label:13C(1)2H
K5       : Propionyl (K)
Ions Score: 57  Expect:
Matches : 15/80 fragmen
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**274.2034**	137.6053	257.1769	129.0921			A	***935.5615***	468.2844	918.5350	459.7711	917.5510	459.2791	8
3	**409.2661**	205.1367	392.2395	196.6234			M	***864.5244***	432.7658	847.4979	424.2526	846.5139	423.7606	7
4	496.2981	248.6527	479.2716	240.1394	478.2875	239.6474	S	***729.4618***	365.2345	712.4352	356.7212	711.4512	356.2292	6
5	**680.4193**	340.7133	663.3927	332.2000	662.4087	331.7080	K	***642.4297***	321.7185	625.4032	313.2052			5
6	**793.5033**	397.2553	776.4768	388.7420	775.4928	388.2500	L	***458.3085***	229.6579	441.2820	221.1446			4
7	850.5248	425.7660	833.4983	417.2528	832.5142	416.7608	G	***345.2245***	173.1159	328.1979	164.6026			3
8	**963.6089**	482.3081	946.5823	473.7948	945.5983	473.3028	L	***288.2030***	144.6051	271.1765	136.0919			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **INTLFQKDR**
Found in **I3L3Z8**, Pre-mRNA-processing-splicing factor 8 (Fragment) OS=Homo sapiens GN=PRPF8 PE=4 SV=1

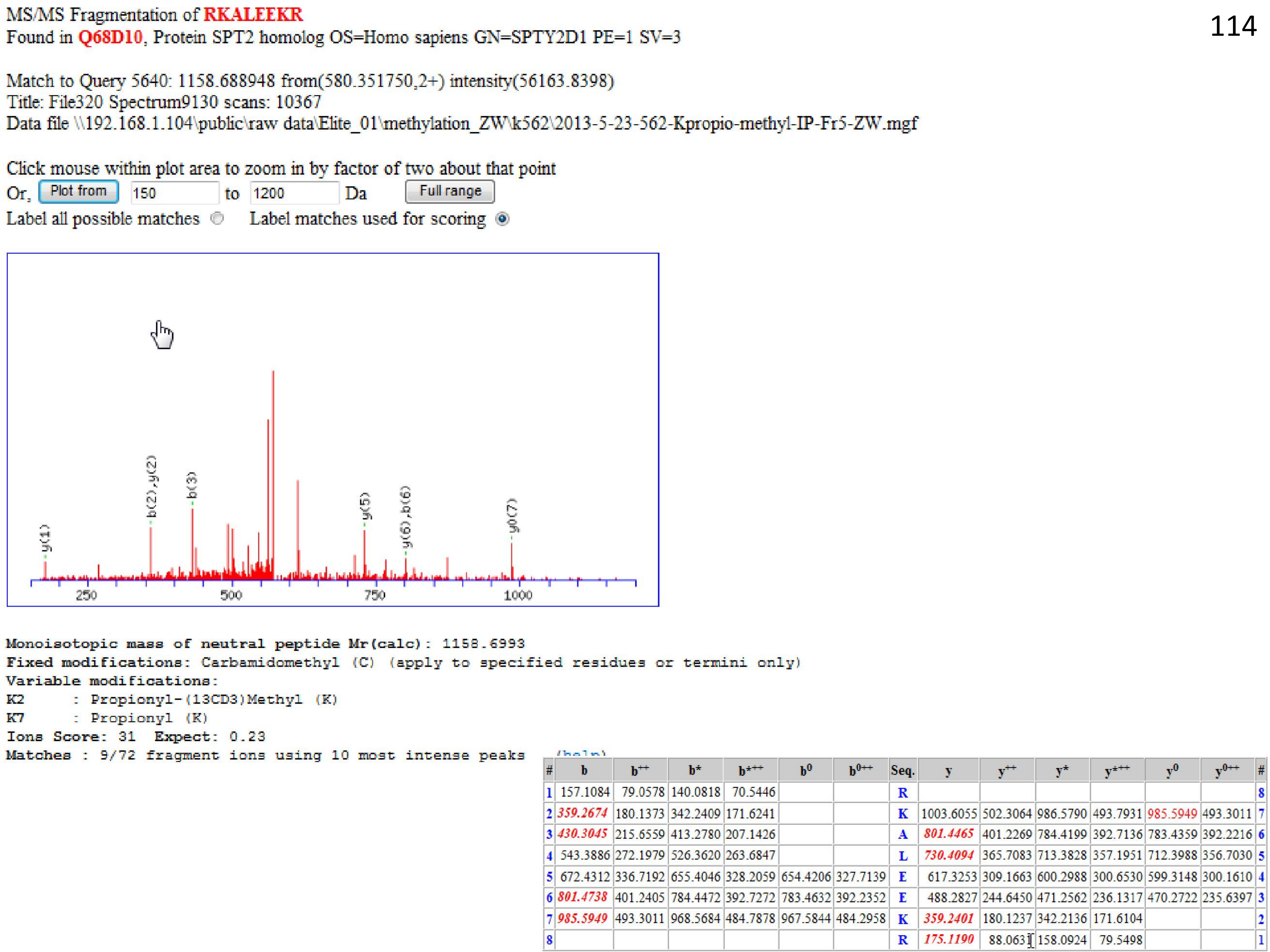
Match to Query 6346: 1207.681608 from(604.848080,2+) intensity(116592.1484)
Title: File320 Spectrum12819 scans: 14303
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(c
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 58   Expect: 0.00062
Matches : 20/88 fragment ions using 32 mo
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							9
2	**228.1343**	114.5708	211.1077	106.0575			N	***1095.6066***	548.3069	1078.5800	539.7936	1077.5960	539.3016	8
3	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	T	***981.5636***	491.2855	964.5371	482.7722	963.5531	482.2802	7
4	**442.2660**	221.6366	425.2395	213.1234	424.2554	212.6314	L	***880.5160***	440.7616	863.4894	432.2483	862.5054	431.7563	6
5	589.3344	295.1709	572.3079	286.6576	571.3239	286.1656	F	***767.4319***	384.2196	750.4054	375.7063	749.4213	375.2143	5
6	**717.3930**	359.2001	700.3665	350.6869	699.3824	350.1949	Q	***620.3635***	310.6854	603.3369	302.1721	602.3529	301.6801	4
7	**919.5520**	460.2796	902.5255	451.7664	901.5414	451.2744	K	***492.3049***	246.6561	475.2784	238.1428	474.2943	237.6508	3
8	**1034.5790**	517.7931	1017.5524	509.2798	1016.5684	508.7878	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **RKALEEKR**
Found in **Q68D10**, Protein SPT2 homolog OS=Homo sapiens GN=SPTY2D1 PE=1 SV=3

Match to Query 5640: 1158.688948 from(580.351750,2+) intensity(56163.8398)
Title: File320 Spectrum9130 scans: 10367
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1158.6993
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K7      : Propionyl (K)
Ions Score: 31  Expect: 0.23
Matches : 9/72 fragment ions using 10 most intense peaks
```

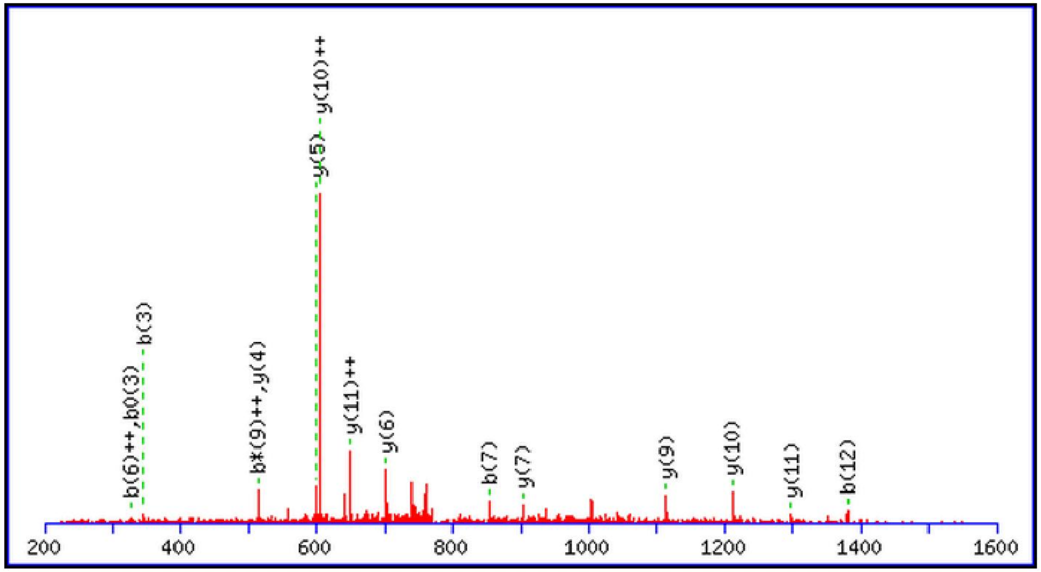
(help)

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							8
2	***359.2674***	180.1373	342.2409	171.6241			K	1003.6055	502.3064	986.5790	493.7931	985.5949	493.3011	7
3	***430.3045***	215.6559	413.2780	207.1426			A	***801.4465***	401.2269	784.4199	392.7136	783.4359	392.2216	6
4	543.3886	272.1979	526.3620	263.6847			L	***730.4094***	365.7083	713.3828	357.1951	712.3988	356.7030	5
5	672.4312	336.7192	655.4046	328.2059	654.4206	327.7139	E	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	4
6	***801.4738***	401.2405	784.4472	392.7272	783.4632	392.2352	E	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	3
7	***985.5949***	493.3011	968.5684	484.7878	967.5844	484.2958	K	***359.2401***	180.1237	342.2136	171.6104			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **WASPPLKTSPQLR**
Found in **Q9UMN6**, Histone-lysine N-methyltransferase MLL4 OS=Homo sapiens GN=WBP7 PE=1 SV=1

Match to Query 11378: 1553.887548 from(777.951050,2+) intensity(126050.6250)
Title: File320 Spectrum13553 scans: 15086
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



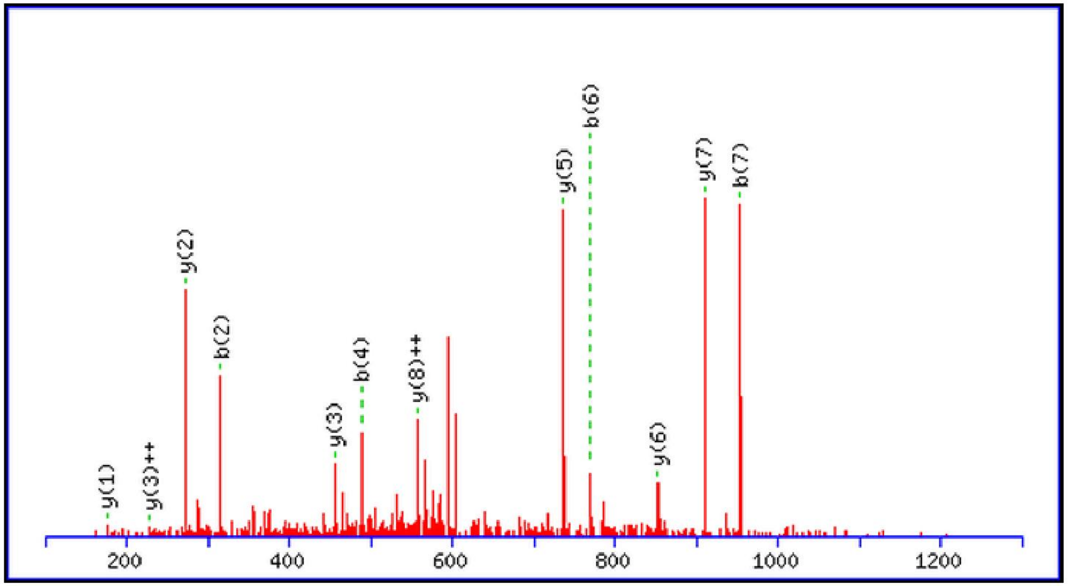
```
Monoisotopic mass of neutral peptide Mr(calc): 1553.8838
Fixed modifications: Carbamidomethyl (C) (apply t
Variable modifications:
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 37   Expect: 0.088
Matches : 15/120 fragment ions using 28 most inte
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							13
2	258.1237	129.5655					A	1368.8118	684.9095	1351.7853	676.3963	1350.8012	675.9043	12
3	**345.1557**	173.0815			327.1452	164.0762	S	***1297.7747***	649.3910	1280.7481	640.8777	1279.7641	640.3857	11
4	442.2085	221.6079			424.1979	212.6026	P	***1210.7427***	605.8750	1193.7161	597.3617	1192.7321	596.8697	10
5	539.2613	270.1343			521.2507	261.1290	P	***1113.6899***	557.3486	1096.6634	548.8353	1095.6793	548.3433	9
6	652.3453	326.6763			634.3348	317.6710	L	1016.6371	508.8222	999.6106	500.3089	998.6266	499.8169	8
7	**854.5043**	427.7558	837.4778	419.2425	836.4938	418.7505	K	***903.5531***	452.2802	886.5265	443.7669	885.5425	443.2749	7
8	955.5520	478.2796	938.5255	469.7664	937.5415	469.2744	T	***701.3941***	351.2007	684.3675	342.6874	683.3835	342.1954	6
9	1042.5840	521.7957	1025.5575	513.2824	1024.5735	512.7904	S	***600.3464***	300.6768	583.3198	292.1636	582.3358	291.6715	5
10	1139.6368	570.3220	1122.6103	561.8088	1121.6262	561.3168	P	***513.3144***	257.1608	496.2878	248.6475			4
11	1267.6954	634.3513	1250.6688	625.8381	1249.6848	625.3460	Q	416.2616	208.6344	399.2350	200.1212			3
12	**1380.7794**	690.8934	1363.7529	682.3801	1362.7689	681.8881	L	288.2030	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GKGDPKKPR**
Found in **B2RPK0**, Putative high mobility group protein B1-like 1 OS=Homo sapiens GN=HMGB1P1 PE=5 SV=1

Match to Query 6613: 1223.714208 from(612.864380,2+) intensity(135332.8750)
Title: File320 Spectrum9934 scans: 11226
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●



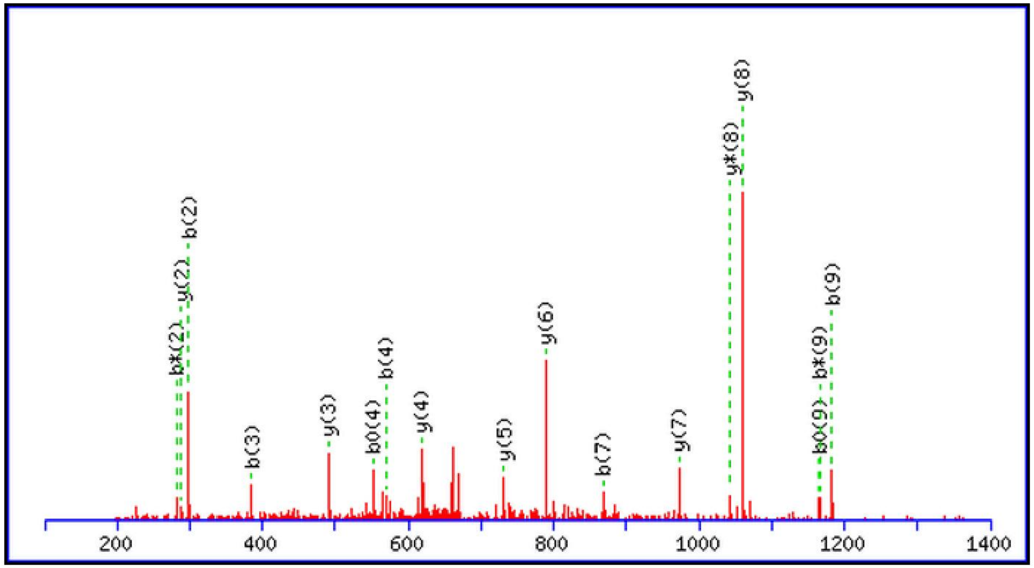
```
Monoisotopic mass of neutral peptide Mr(calc): 1223.7146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term)
K2     : Propionyl-(13CD3)Methyl (K
K6     : Propionyl (K)
K7     : Propionyl (K)
Ions Score: 37  Expect: 0.068
Matches : 12/78 fragment ions using
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0550	57.5311					G							9
2	**316.2140**	158.6106	299.1874	150.0973			K	1111.6743	556.3408	1094.6477	547.8275	1093.6637	547.3355	8
3	373.2354	187.1214	356.2089	178.6081			G	***909.5152***	455.2613	892.4887	446.7480	891.5047	446.2560	7
4	**488.2624**	244.6348	471.2358	236.1216	470.2518	235.6295	D	***852.4938***	426.7505	835.4672	418.2373	834.4832	417.7452	6
5	585.3151	293.1612	568.2886	284.6479	567.3046	284.1559	P	***737.4668***	369.2371	720.4403	360.7238			5
6	**769.4363**	385.2218	752.4098	376.7085	751.4258	376.2165	K	640.4141	320.7107	623.3875	312.1974			4
7	**953.5575**	477.2824	936.5309	468.7691	935.5469	468.2771	K	***456.2929***	228.6501	439.2663	220.1368			3
8	1050.6103	525.8088	1033.5837	517.2955	1032.5997	516.8035	P	***272.1717***	136.5895	255.1452	128.0762			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IKSKGLQKLR**
Found in **B4DX32**, DNA/RNA-binding protein KIN17 OS=Homo sapiens GN=KIN PE=2 SV=1

Match to Query 8520: 1355.876928 from(678.945740,2+) intensity(285733.1250)
Title: File320 Spectrum13216 scans: 14727
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●



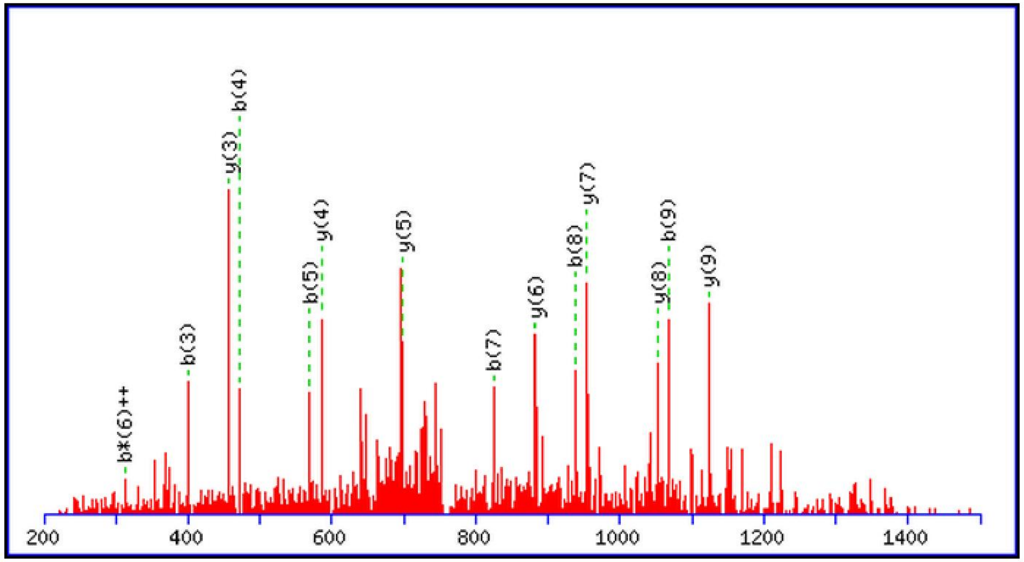
```
Monoisotopic mass of neutral peptide Mr(calc): 1355.8773
Fixed modifications: Carbamido
Variable modifications:
K2      : Propionyl (K)
K4      : Propionyl (K)
K8      : Propionyl-(13CD3)Meth
Ions Score: 39  Expect: 0.0083
Matches : 17/88 fragment ions
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							10
2	**298.2125**	149.6099	281.1860	141.0966			K	1243.8005	622.4039	1226.7740	613.8906	1225.7900	613.3986	9
3	**385.2445**	193.1259	368.2180	184.6126	367.2340	184.1206	S	***1059.6793***	530.3433	1042.6528	521.8300	1041.6688	521.3380	8
4	**569.3657**	285.1865	552.3392	276.6732	551.3552	276.1812	K	***972.6473***	486.8273	955.6208	478.3140			7
5	626.3872	313.6972	609.3606	305.1840	608.3766	304.6919	G	***788.5261***	394.7667	771.4996	386.2534			6
6	739.4713	370.2393	722.4447	361.7260	721.4607	361.2340	L	***731.5047***	366.2560	714.4781	357.7427			5
7	**867.5298**	434.2686	850.5033	425.7553	849.5193	425.2633	Q	***618.4206***	309.7139	601.3941	301.2007			4
8	1069.6888	535.3481	1052.6623	526.8348	1051.6783	526.3428	K	***490.3620***	245.6847	473.3355	237.1714			3
9	**1182.7729**	591.8901	1165.7464	583.3768	1164.7623	582.8848	L	***288.2030***	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **PVKAVAKLEPKR**
Found in **Q9C0D4**, Zinc finger protein 518B OS=Homo sapiens GN=ZNF518B PE=2 SV=2

Match to Query 10987: 1520.958708 from(761.486630,2+) intensity(53742.7578)
Title: File320 Spectrum13604 scans: 15140
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.mgf

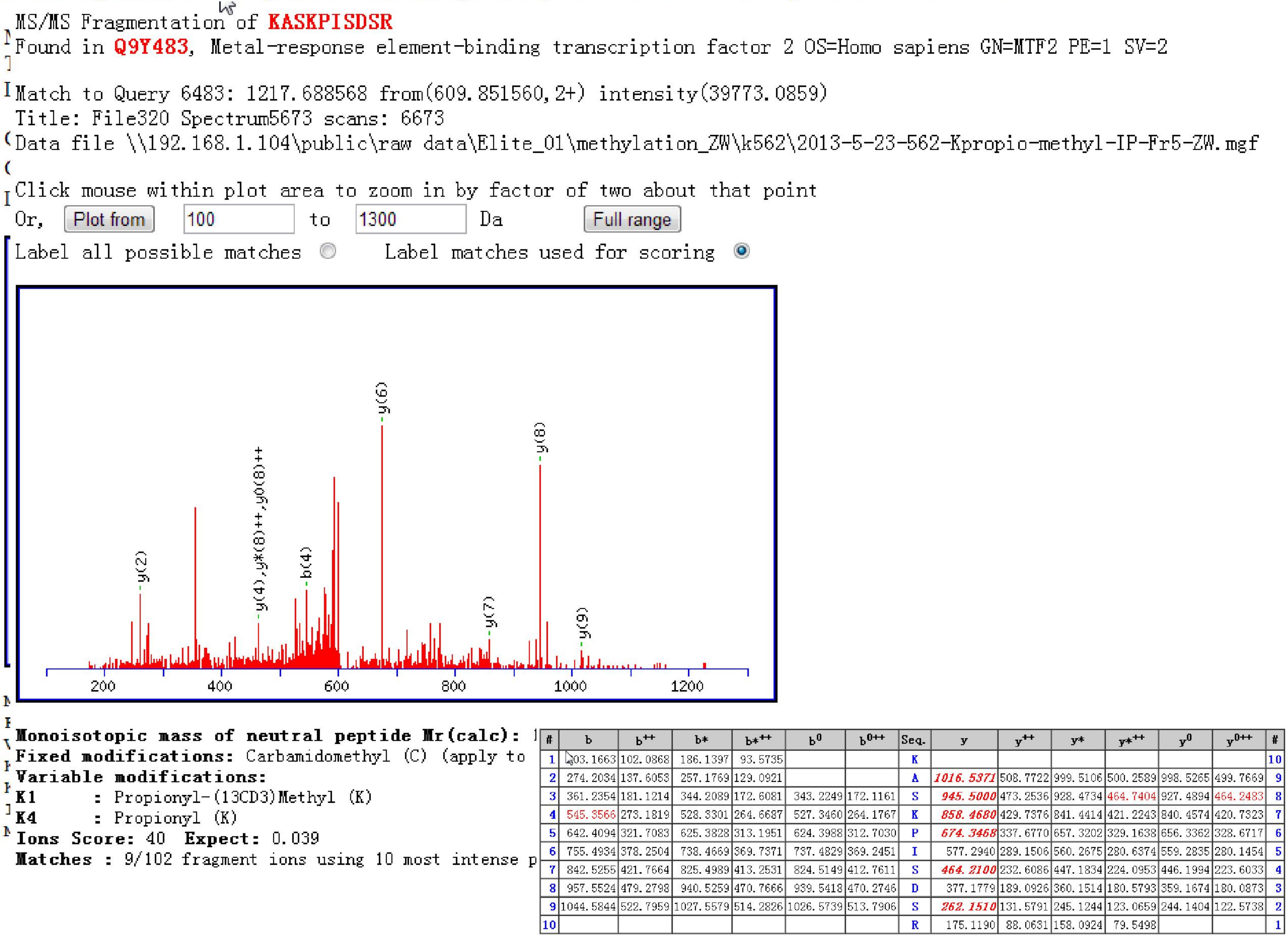
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1520.9563
Fixed modifications: Carbamidomethyl (C) (a
Variable modifications:
K3      : Propionyl-(13CD3)Methyl (K)
K7      : Propionyl (K)
K11     : Propionyl (K)
Ions Score: 40  Expect: 0.0085
Matches : 14/106 fragment ions using 26 mos
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	98.0600	49.5337					P							12
2	197.1285	99.0679					V	1424.9108	712.9590	1407.8842	704.4458	1406.9002	703.9538	11
3	**399.2875**	200.1474	382.2609	191.6341			K	1325.8424	663.4248	1308.8158	654.9116	1307.8318	654.4195	10
4	**470.3246**	235.6659	453.2980	227.1527			A	***1123.6834***	562.3453	1106.6568	553.8320	1105.6728	553.3400	9
5	**569.3930**	285.2001	552.3664	276.6869			V	***1052.6463***	526.8268	1035.6197	518.3135	1034.6357	517.8215	8
6	640.4301	320.7187	623.4036	312.2054			A	***953.5778***	477.2926	936.5513	468.7793	935.5673	468.2873	7
7	**824.5513**	412.7793	807.5247	404.2660			K	***882.5407***	441.7740	865.5142	433.2607	864.5302	432.7687	6
8	**937.6354**	469.3213	920.6088	460.8080			L	***698.4196***	349.7134	681.3930	341.2001	680.4090	340.7081	5
9	**1066.6779**	533.8426	1049.6514	525.3293	1048.6674	524.8373	E	***585.3355***	293.1714	568.3089	284.6581	567.3249	284.1661	4
10	1163.7307	582.3690	1146.7042	573.8557	1145.7201	573.3637	P	***456.2929***	228.6501	439.2663	220.1368			3
11	1347.8519	674.4296	1330.8253	665.9163	1329.8413	665.4243	K	359.2401	180.1237	342.2136	171.6104			2
12							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KASKPISDSR**
Found in **Q9Y483**, Metal-response element-binding transcription factor 2 OS=Homo sapiens GN=MTF2 PE=1 SV=2



MS/MS Fragmentation of **KASKPISDSR**
Found in **Q9Y483**, Metal-response element-binding transcription factor 2 OS=Homo sapiens GN=MTF2 PE=1 SV=2

Match to Query 6483: 1217.688568 from(609.851560,2+) intensity(39773.0859)
Title: File320 Spectrum5673 scans: 6673
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●

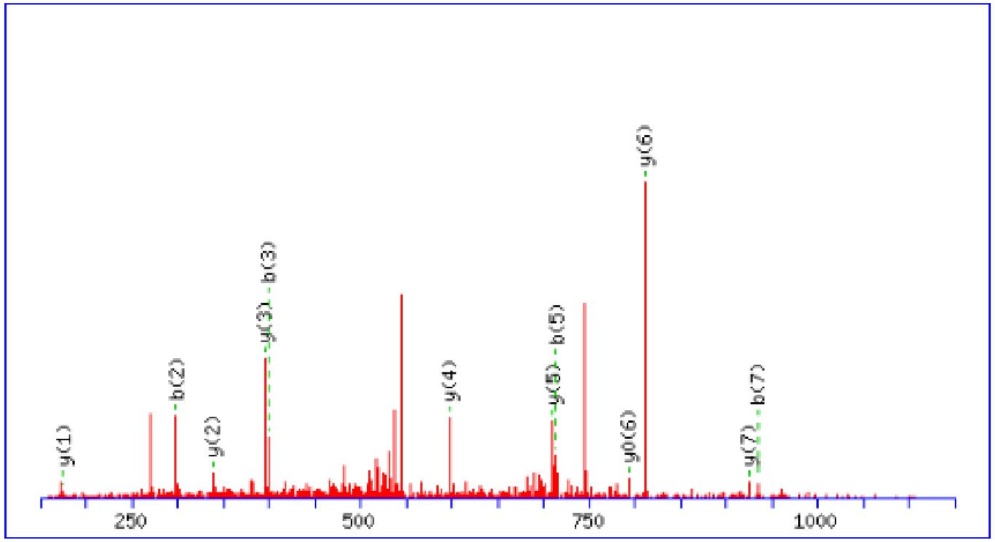
Monoisotopic mass of neutral peptide Mr(calc):
Fixed modifications: Carbamidomethyl (C) (apply to
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K4 : Propionyl (K)
Ions Score: 40 **Expect:** 0.039
Matches : 9/102 fragment ions using 10 most intense p

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	03.1663	102.0868	186.1397	93.5735			K							10
2	274.2034	137.6053	257.1769	129.0921			A	1016.5371	508.7722	999.5106	500.2589	998.5265	499.7669	9
3	361.2354	181.1214	344.2089	172.6081	343.2249	172.1161	S	945.5000	473.2536	928.4734	464.7404	927.4894	464.2483	8
4	545.3566	273.1819	528.3301	264.6687	527.3460	264.1767	K	858.4680	429.7376	841.4414	421.2243	840.4574	420.7323	7
5	642.4094	321.7083	625.3828	313.1951	624.3988	312.7030	P	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	6
6	755.4934	378.2504	738.4669	369.7371	737.4829	369.2451	I	577.2940	289.1506	560.2675	280.6374	559.2835	280.1454	5
7	842.5255	421.7664	825.4989	413.2531	824.5149	412.7611	S	464.2100	232.6086	447.1834	224.0953	446.1994	223.6033	4
8	957.5524	479.2798	940.5259	470.7666	939.5418	470.2746	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
9	1044.5844	522.7959	1027.5579	514.2826	1026.5739	513.7906	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KLTLKGYR**
Found in **Q86UX7**, Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1

Match to Query 4952: 1107.692348 from(554.853450,2+) intensity(127852.6641)
Title: File320 Spectrum13283 scans: 14798
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●



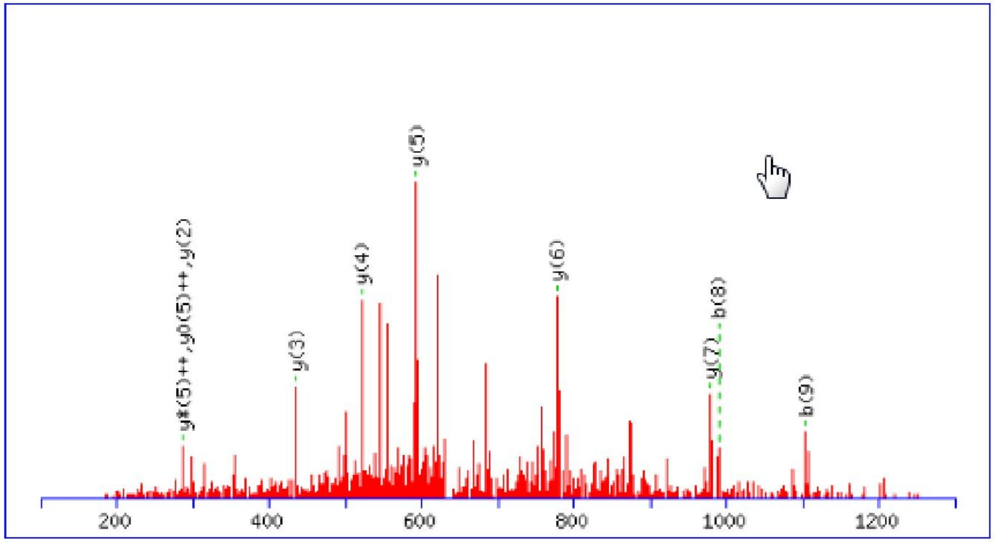
Monoisotopic mass of neutral peptide Mr(calc): 1107.6924
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 43 **Expect:** 0.0082
Matches : 12/70 fragment ions using 30 most intense peaks (hel

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	**298.2125**	149.6099	281.1860	141.0966			L	***924.5786***	462.7929	907.5520	454.2796	906.5680	453.7876	7
3	**399.2602**	200.1337	382.2336	191.6205	381.2496	191.1285	T	***811.4945***	406.2509	794.4680	397.7376	793.4839	397.2456	6
4	512.3443	256.6758	495.3177	248.1625	494.3337	247.6705	L	***710.4468***	355.7270	693.4203	347.2138			5
5	**714.5033**	357.7553	697.4767	349.2420	696.4927	348.7500	K	***597.3628***	299.1850	580.3362	290.6717			4
6	771.5247	386.2660	754.4982	377.7527	753.5142	377.2607	G	***395.2037***	198.1055	378.1772	189.5922			3
7	**934.5881**	467.7977	917.5615	459.2844	916.5775	458.7924	Y	***338.1823***	169.5948	3[illegible]1.1557	161.0815			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VAQKKASFLR**
Found in **P46777**, 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3

Match to Query 7346: 1276.776828 from(639.395690,2+) intensity(72028.1797)
Title: File320 Spectrum13018 scans: 14515
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●



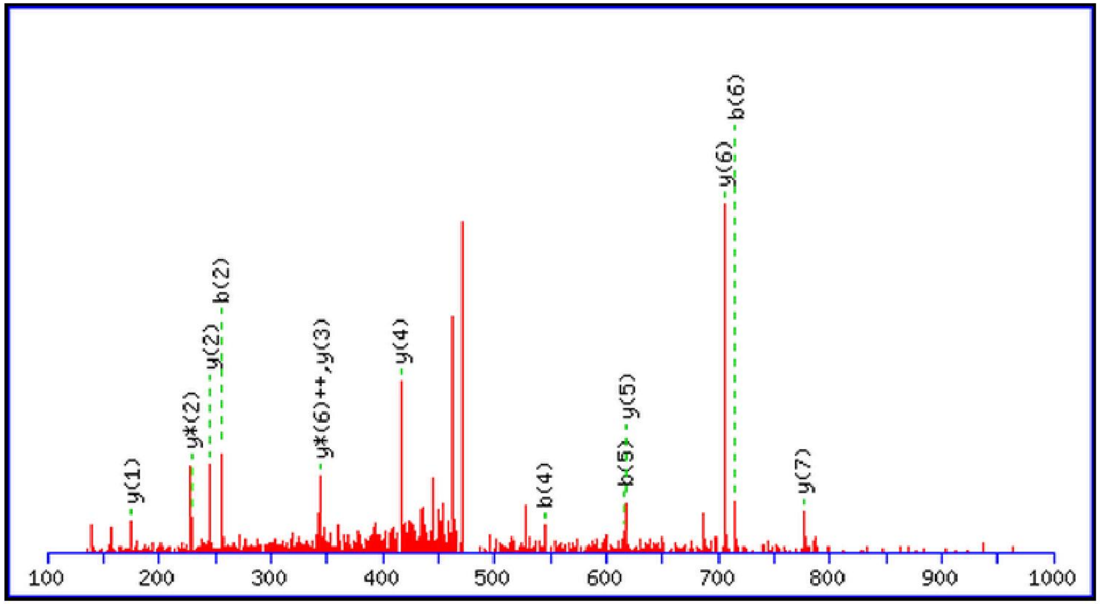
```
Monoisotopic mass of neutral peptide Mr(calc): 1276.7776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4      : Propionyl-(13CD3)Methyl (K)
K5      : Propionyl (K)
Ions Score: 44  Expect: 0.011
Matches : 10/86 fragment ions using 11 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							10
2	171.1128	86.0600					A	1178.7165	589.8619	1161.6899	581.3486	1160.7059	580.8566	9
3	299.1714	150.0893	282.1448	141.5761			Q	1107.6793	554.3433	1090.6528	545.8300	1089.6688	545.3380	8
4	501.3304	251.1688	484.3038	242.6556			K	***979.6208***	490.3140	962.5942	481.8007	961.6102	481.3087	7
5	685.4516	343.2294	668.4250	334.7162			K	***777.4617***	389.2345	760.4352	380.7212	759.4512	380.2292	6
6	756.4887	378.7480	739.4621	370.2347			A	***593.3406***	297.1739	576.3140	288.6606	575.3300	288.1686	5
7	843.5207	422.2640	826.4942	413.7507	825.5101	413.2587	S	***522.3035***	261.6554	505.2769	253.1421	504.2929	252.6501	4
8	**990.5891**	495.7982	973.5626	487.2849	972.5786	486.7929	F	***435.2714***	218.1394	418.2449	209.6261			3
9	**1103.6732**	552.3402	1086.6466	543.8270	1085.6626	543.3350	L	***288.2030***	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KASKAVAR**
Found in **K7EL20**, Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=3 SV=1

Match to Query 2730: 959.604108 from(480.809330,2+) intensity(37284.5273)
Title: File320 Spectrum4575 scans: 5500
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



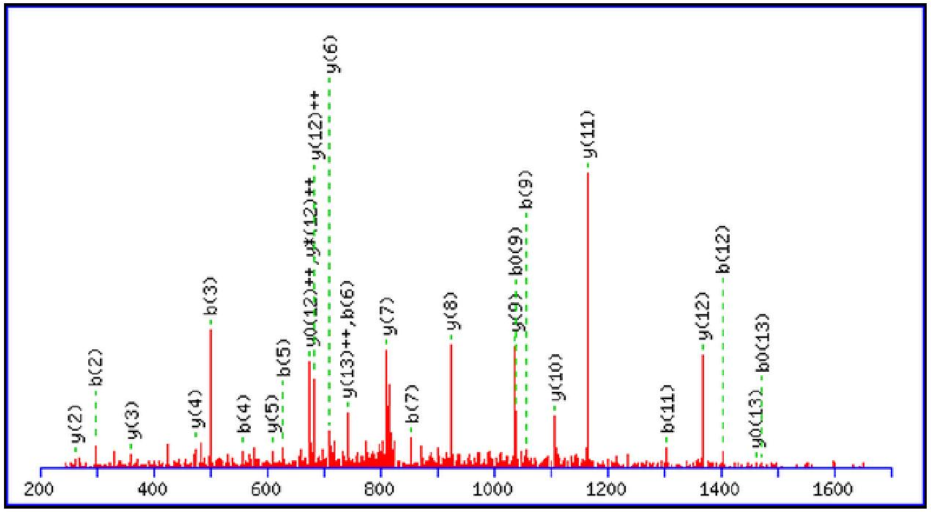
```
Monoisotopic mass of neutral peptide Mr(calc): 959.6036
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K4      : Propionyl-(13CD3)Methyl (K
Ions Score: 50  Expect: 0.0019
Matches : 13/70 fragment ions using
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	**256.1656**	128.5864	239.1390	120.0731			A	***776.4897***	388.7485	759.4632	380.2352	758.4792	379.7432	7
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	S	***705.4526***	353.2300	688.4261	344.7167	687.4421	344.2247	6
4	**545.3566**	273.1819	528.3301	264.6687	527.3460	264.1767	K	***618.4206***	309.7139	601.3941	301.2007			5
5	**616.3937**	308.7005	599.3672	300.1872	598.3832	299.6952	A	***416.2616***	208.6344	399.2350	200.1212			4
6	**715.4621**	358.2347	698.4356	349.7214	697.4516	349.2294	V	***345.2245***	173.1159	328.1979	164.6026			3
7	786.4993	393.7533	769.4727	385.2400	768.4887	384.7480	A	***246.1561***	123.5817	229.1295	115.0684			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KLKGAILTTMLVSR**
Found in **H0Y6G2**, Calcium/calmodulin-dependent protein kinase type II subunit gamma (Fragment) OS=Homo sapiens GN=CAMK2G PE=4 SV=1

Match to Query 11054: 1664.045628 from(833.030090,2+) intensity(97248.1016)
Title: File375 Spectrum15750 scans: 18267
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



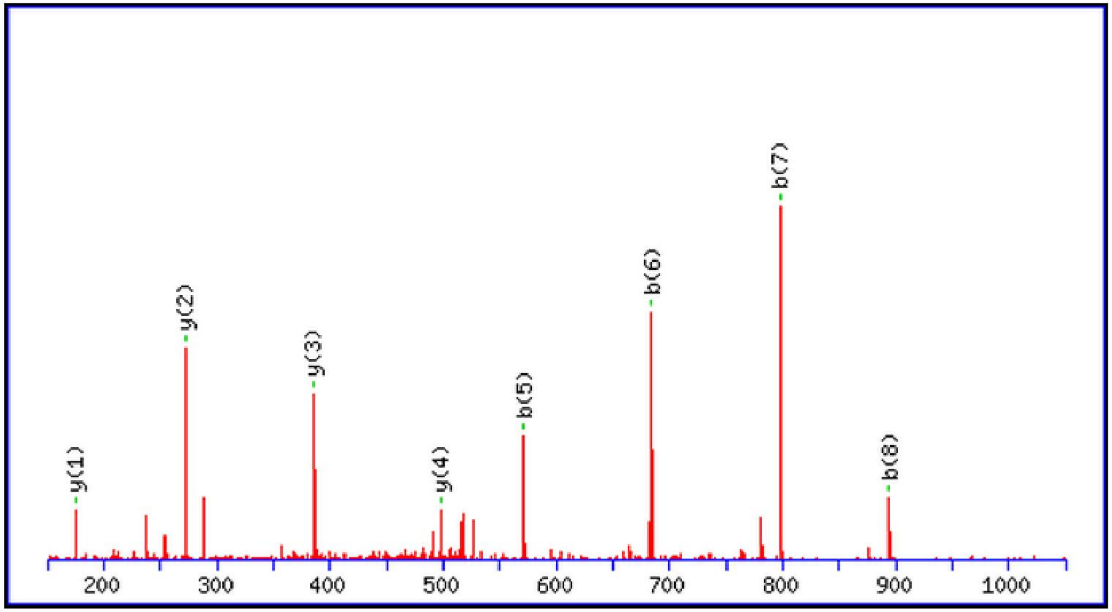
Monoisotopic mass of neutral peptide Mr(calc): 1664.0452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
M10 : Label:13C(1)2H(3) (M)
Ions Score: 60 **Expect:** 6.7e-005
Matches : 27/140 fragment ions using 58 most intense

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	**298.2125**	149.6099	281.1860	141.0966			L	1480.9313	740.9693	1463.9047	732.4560	1462.9207	731.9640	13
3	**500.3715**	250.6894	483.3450	242.1761			K	***1367.8472***	684.4272	1350.8207	675.9140	1349.8366	675.4220	12
4	**557.3930**	279.2001	540.3664	270.6869			G	***1165.6882***	583.3477	1148.6616	574.8345	1147.6776	574.3425	11
5	**628.4301**	314.7187	611.4036	306.2054			A	***1108.6667***	554.8370	1091.6402	546.3237	1090.6562	545.8317	10
6	**741.5142**	371.2607	724.4876	362.7475			I	***1037.6296***	519.3184	1020.6031	510.8052	1019.6190	510.3132	9
7	**854.5982**	427.8028	837.5717	419.2895			L	***924.5456***	462.7764	907.5190	454.2631	906.5350	453.7711	8
8	955.6459	478.3266	938.6194	469.8133	937.6354	469.3213	T	***811.4615***	406.2344	794.4349	397.7211	793.4509	397.2291	7
9	**1056.6936**	528.8504	1039.6670	520.3372	1038.6830	519.8452	T	***710.4138***	355.7105	693.3873	347.1973	692.4032	346.7053	6
10	1191.7563	596.3818	1174.7297	587.8685	1173.7457	587.3765	M	***609.3661***	305.1867	592.3396	296.6734	591.3556	296.1814	5
11	**1304.8403**	652.9238	1287.8138	644.4105	1286.8298	643.9185	L	***474.3035***	237.6554	457.2769	229.1421	456.2929	228.6501	4
12	**1403.9087**	702.4580	1386.8822	693.9447	1385.8982	693.4527	V	***361.2194***	181.1133	344.1928	172.6001	343.2088	172.1081	3
13	1490.9408	745.9740	1473.9142	737.4607	1472.9302	736.9687	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **PGTKLLLPR**
Found in **Q9NYZ3**, G2 and S phase-expressed protein 1 OS=Homo sapiens GN=GTSE1 PE=1 SV=3

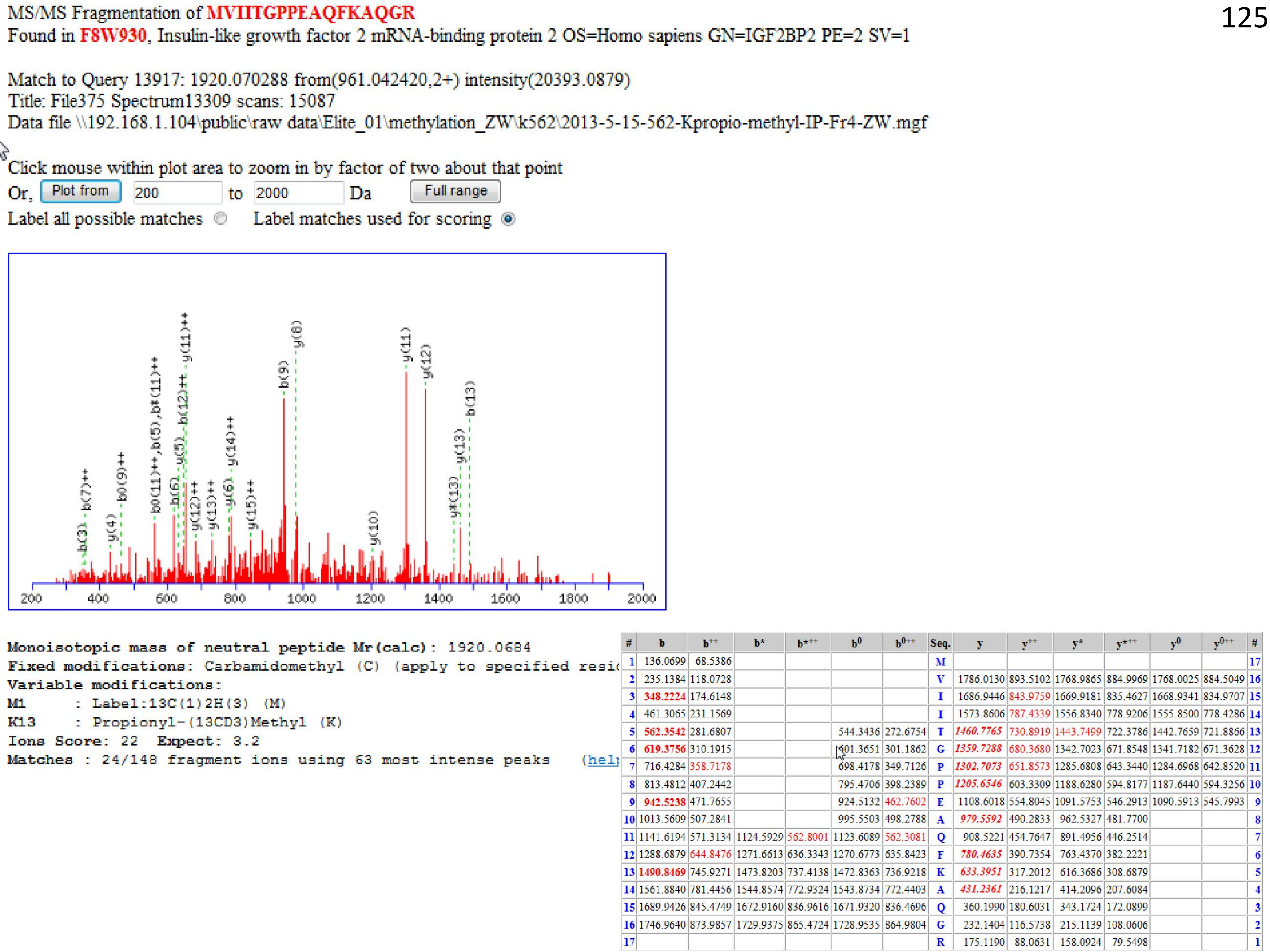
Match to Query 3191: 1067.707128 from(534.860840,2+) intensity(79356.2031)
Title: File375 Spectrum12028 scans: 13721
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral pept
Fixed modifications: Carbamidomet
Variable modifications:
K4      : Propionyl-(13CD3)Methyl
Ions Score: 36  Expect: 0.016
Matches : 8/74 fragment ions usin
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.0600	49.5337					**P**							9
2	155.0815	78.0444					**G**	971.6521	486.3297	954.6255	477.8164	953.6415	477.3244	8
3	256.1292	128.5682			238.1186	119.5629	**T**	914.6306	457.8189	897.6041	449.3057	896.6200	448.8137	7
4	458.2882	229.6477	441.2616	221.1345	440.2776	220.6425	**K**	813.5829	407.2951	796.5564	398.7818			6
5	***571.3723***	286.1898	554.3457	277.6765	553.3617	277.1845	**L**	611.4239	306.2156	594.3974	297.7023			5
6	***684.4563***	342.7318	667.4298	334.2185	666.4458	333.7265	**L**	***498.3398***	249.6736	481.3133	241.1603			4
7	***797.5404***	399.2738	780.5138	390.7606	779.5298	390.2685	**L**	***385.2558***	193.1315	368.2292	184.6183			3
8	***894.5932***	447.8002	877.5666	439.2869	876.5826	438.7949	**P**	***272.1717***	136.5895	255.1452	128.0762			2
9							**R**	***175.1190***	88.0631	158.0924	79.5498			1



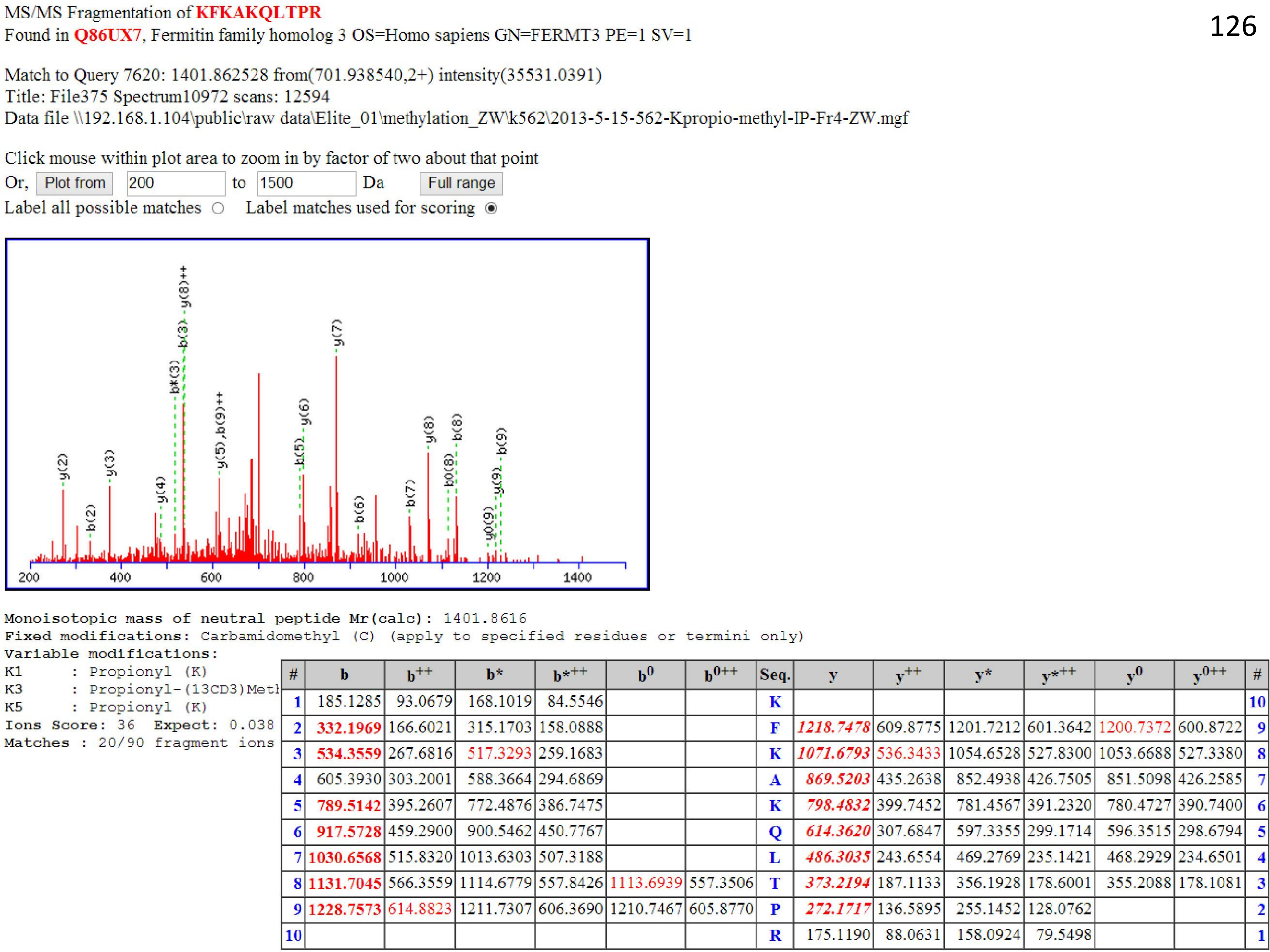
MS/MS Fragmentation of **MVIITGPPEAQFKAQGR**
Found in **F8W930**, Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=2 SV=1

Match to Query 13917: 1920.070288 from(961.042420,2+) intensity(20393.0879)
Title: File375 Spectrum13309 scans: 15087
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr4-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1920.0684
Fixed modifications: Carbamidomethyl (C) (apply to specified resi
Variable modifications:
M1      : Label:13C(1)2H(3) (M)
K13     : Propionyl-(13CD3)Methyl (K)
Ions Score: 22  Expect: 3.2
Matches : 24/148 fragment ions using 63 most intense peaks   (hel
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	136.0699	68.5386					M							17
2	235.1384	118.0728					V	1786.0130	893.5102	1768.9865	884.9969	1768.0025	884.5049	16
3	**348.2224**	174.6148					I	1686.9446	843.9759	1669.9181	835.4627	1668.9341	834.9707	15
4	461.3065	231.1569					I	1573.8606	787.4339	1556.8340	778.9206	1555.8500	778.4286	14
5	**562.3542**	281.6807			544.3436	272.6754	T	***1460.7765***	730.8919	1443.7499	722.3786	1442.7659	721.8866	13
6	**619.3756**	310.1915			601.3651	301.1862	G	***1359.7288***	680.3680	1342.7023	671.8548	1341.7182	671.3628	12
7	716.4284	358.7178			698.4178	349.7126	P	***1302.7073***	651.8573	1285.6808	643.3440	1284.6968	642.8520	11
8	813.4812	407.2442			795.4706	398.2389	P	***1205.6546***	603.3309	1188.6280	594.8177	1187.6440	594.3256	10
9	**942.5238**	471.7655			924.5132	462.7602	E	1108.6018	554.8045	1091.5753	546.2913	1090.5913	545.7993	9
10	1013.5609	507.2841			995.5503	498.2788	A	***979.5592***	490.2833	962.5327	481.7700			8
11	1141.6194	571.3134	1124.5929	562.8001	1123.6089	562.3081	Q	908.5221	454.7647	891.4956	446.2514			7
12	1288.6879	644.8476	1271.6613	636.3343	1270.6773	635.8423	F	***780.4635***	390.7354	763.4370	382.2221			6
13	**1490.8469**	745.9271	1473.8203	737.4138	1472.8363	736.9218	K	***633.3951***	317.2012	616.3686	308.6879			5
14	1561.8840	781.4456	1544.8574	772.9324	1543.8734	772.4403	A	***431.2361***	216.1217	414.2096	207.6084			4
15	1689.9426	845.4749	1672.9160	836.9616	1671.9320	836.4696	Q	360.1990	180.6031	343.1724	172.0899			3
16	1746.9640	873.9857	1729.9375	865.4724	1728.9535	864.9804	G	232.1404	116.5738	215.1139	108.0606			2
17							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KFKAKQLTPR**
Found in **Q86UX7**, Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1

Match to Query 7620: 1401.862528 from(701.938540,2+) intensity(35531.0391)
Title: File375 Spectrum10972 scans: 12594
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

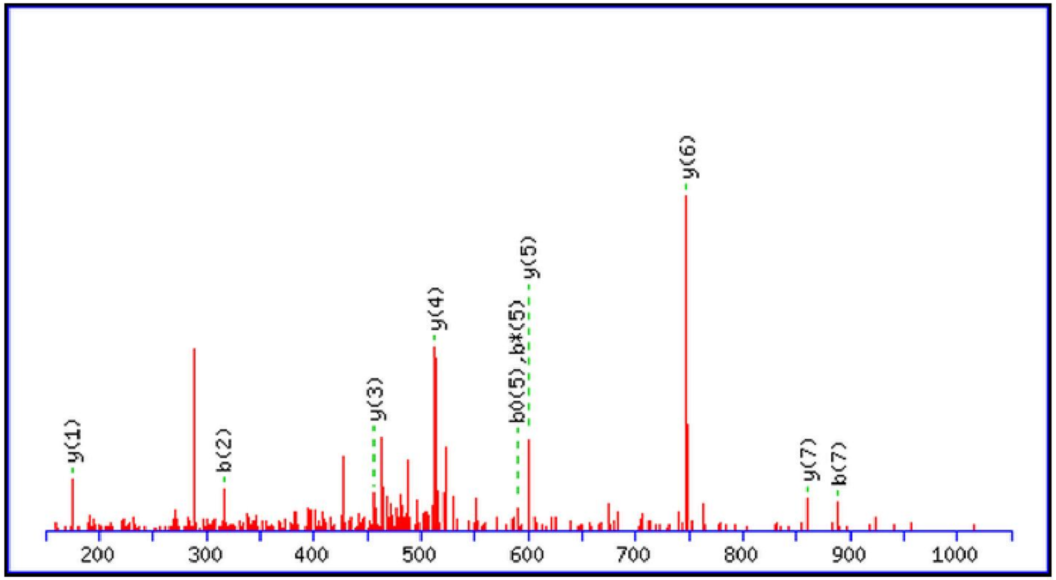
```
Monoisotopic mass of neutral peptide Mr(calc): 1401.8616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K3      : Propionyl-(13CD3)Meth
K5      : Propionyl (K)
Ions Score: 36  Expect: 0.038
Matches : 20/90 fragment ions
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	185.1285	93.0679	168.1019	84.5546			K							10
2	**332.1969**	166.6021	315.1703	158.0888			F	***1218.7478***	609.8775	1201.7212	601.3642	1200.7372	600.8722	9
3	**534.3559**	267.6816	517.3293	259.1683			K	***1071.6793***	536.3433	1054.6528	527.8300	1053.6688	527.3380	8
4	605.3930	303.2001	588.3664	294.6869			A	***869.5203***	435.2638	852.4938	426.7505	851.5098	426.2585	7
5	**789.5142**	395.2607	772.4876	386.7475			K	***798.4832***	399.7452	781.4567	391.2320	780.4727	390.7400	6
6	**917.5728**	459.2900	900.5462	450.7767			Q	***614.3620***	307.6847	597.3355	299.1714	596.3515	298.6794	5
7	**1030.6568**	515.8320	1013.6303	507.3188			L	***486.3035***	243.6554	469.2769	235.1421	468.2929	234.6501	4
8	**1131.7045**	566.3559	1114.6779	557.8426	1113.6939	557.3506	T	***373.2194***	187.1133	356.1928	178.6001	355.2088	178.1081	3
9	**1228.7573**	614.8823	1211.7307	606.3690	1210.7467	605.8770	P	***272.1717***	136.5895	255.1452	128.0762			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KIFSGPKR**
Found in **Q7Z5K2**, Wings apart-like protein homolog OS=Homo sapiens GN=WAPAL PE=1 SV=1

Match to Query 3109: 1061.650248 from(531.832400,2+) intensity(14045.9766)
Title: File375 Spectrum8977 scans: 10464
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



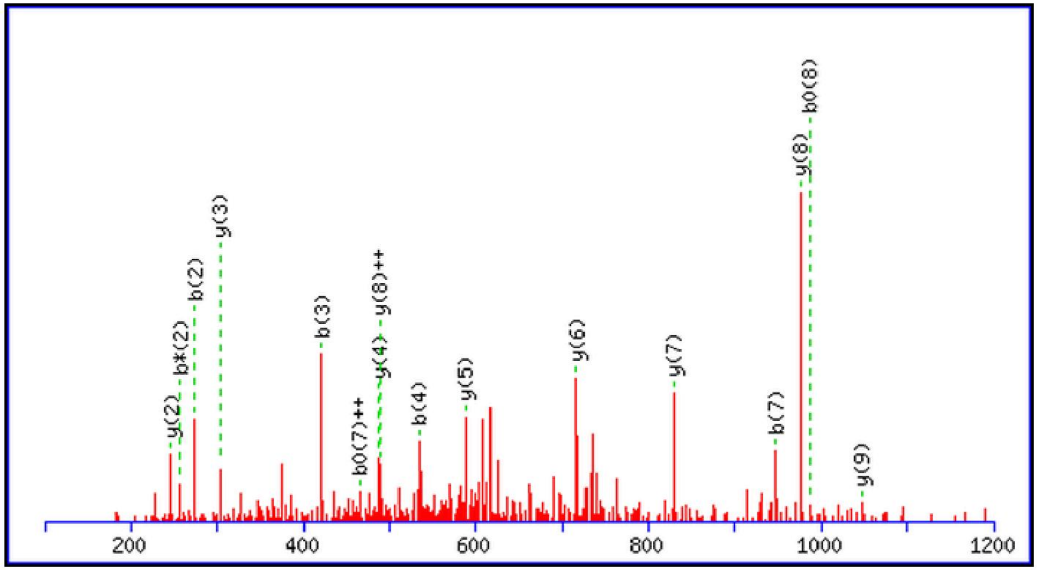
```
Monoisotopic mass of neutral peptide Mr(calc): 1061.6506
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Me
K7      : Propionyl (K)
Ions Score: 40  Expect: 0.02
Matches : 10/70 fragment ion
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	**316.2504**	158.6288	299.2238	150.1155			I	***860.4989***	430.7531	843.4723	422.2398	842.4883	421.7478	7
3	463.3188	232.1630	446.2922	223.6497			F	***747.4148***	374.2110	730.3883	365.6978	729.4042	365.2058	6
4	550.3508	275.6790	533.3242	267.1658	532.3402	266.6738	S	***600.3464***	300.6768	583.3198	292.1636	582.3358	291.6715	5
5	607.3723	304.1898	590.3457	295.6765	589.3617	295.1845	G	***513.3144***	257.1608	496.2878	248.6475			4
6	704.4250	352.7161	687.3985	344.2029	686.4145	343.7109	P	***456.2929***	228.6501	439.2663	220.1368			3
7	**888.5462**	444.7767	871.5197	436.2635	870.5356	435.7715	K	359.2401	180.1237	342.2136	171.6104			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAFLQTKGAR**
Found in **O15156**, Zinc finger and BTB domain-containing protein 7B OS=Homo sapiens GN=ZBTB7B PE=1 SV=2

Match to Query 5584: 1248.746428 from(625.380490,2+) intensity(36088.4766)
Title: File375 Spectrum10089 scans: 11652
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr4-ZW.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 ●



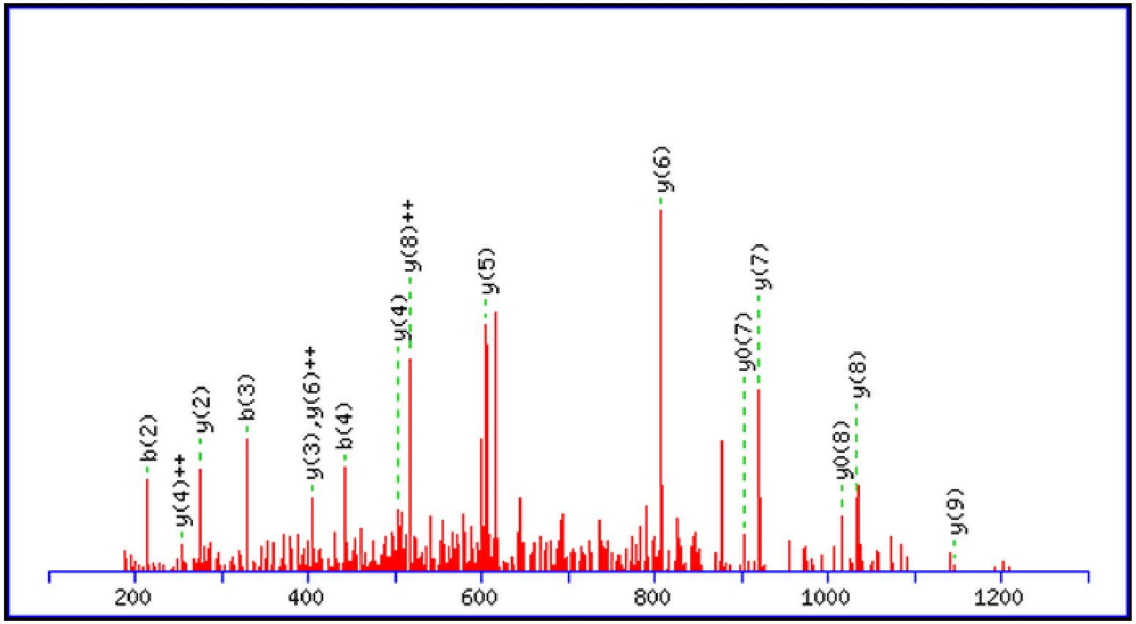
```
Monoisotopic mass of neutral peptide Mr(calc): 1248.7463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
K7      : Propionyl (K)
Ions Score: 51  Expect: 0.0023
Matches : 16/90 fragment ions using
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	203.1663	102.0868	186.1397	93.5735			K							10
2	**274.2034**	137.6053	257.1769	129.0921			A	***1047.5946***	524.3009	1030.5680	515.7876	1029.5840	515.2956	9
3	**421.2718**	211.1395	404.2453	202.6263			F	***976.5574***	488.7824	959.5309	480.2691	958.5469	479.7771	8
4	**534.3559**	267.6816	517.3293	259.1683			L	***829.4890***	415.2482	812.4625	406.7349	811.4785	406.2429	7
5	662.4145	331.7109	645.3879	323.1976			Q	***716.4050***	358.7061	699.3784	350.1928	698.3944	349.7008	6
6	763.4621	382.2347	746.4356	373.7214	745.4516	373.2294	T	***588.3464***	294.6768	571.3198	286.1636	570.3358	285.6715	5
7	**947.5833**	474.2953	930.5568	465.7820	929.5728	465.2900	K	***487.2987***	244.1530	470.2722	235.6397			4
8	1004.6048	502.8060	987.5782	494.2928	986.5942	493.8007	G	***303.1775***	152.0924	286.1510	143.5791			3
9	1075.6419	538.3246	1058.6153	529.8113	1057.6313	529.3193	A	***246.1561***	123.5817	229.1295	115.0684			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TLLIKTVETR**
Found in **P08670**, Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Match to Query 5689: 1246.775728 from(624.395140,2+) intensity(33411.3242)
Title: File373 Spectrum13349 scans: 14945
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr3-ZW.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 ●



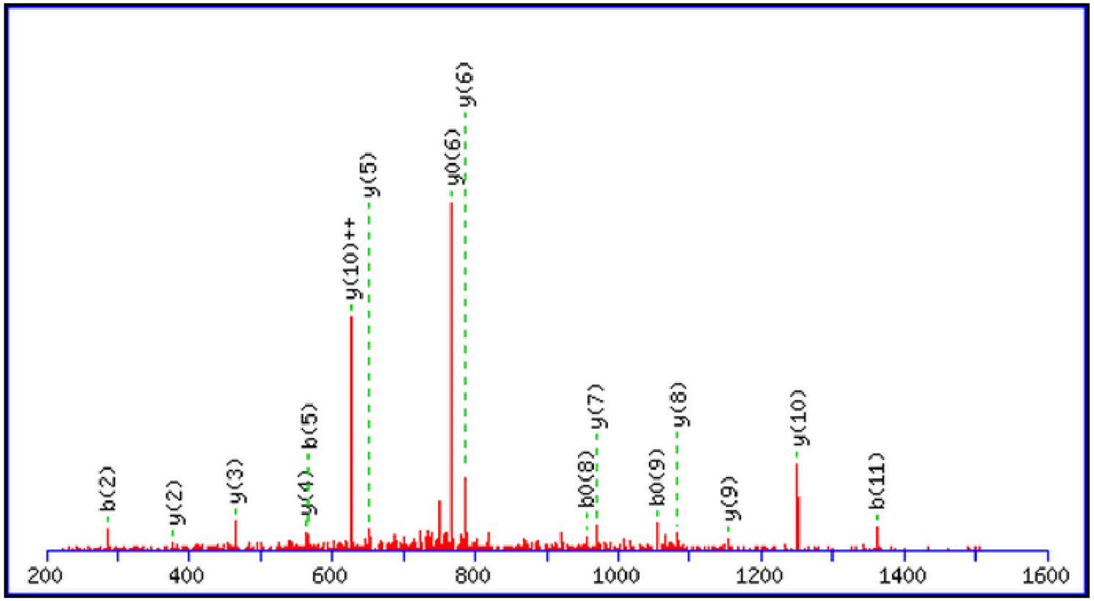
```
Monoisotopic mass of neutral peptid
Fixed modifications: Carbamidomethy
Variable modifications:
K5      : Propionyl-(13CD3)Methyl (K
Ions Score: 50  Expect: 0.0016
Matches : 16/98 fragment ions using
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	**215.1390**	108.0731			197.1285	99.0679	L	***1146.7365***	573.8719	1129.7100	565.3586	1128.7260	564.8666	9
3	**328.2231**	164.6152			310.2125	155.6099	L	***1033.6525***	517.3299	1016.6259	508.8166	1015.6419	508.3246	8
4	**441.3071**	221.1572			423.2966	212.1519	I	***920.5684***	460.7878	903.5418	452.2746	902.5578	451.7826	7
5	643.4662	322.2367	626.4396	313.7234	625.4556	313.2314	K	***807.4843***	404.2458	790.4578	395.7325	789.4738	395.2405	6
6	744.5138	372.7606	727.4873	364.2473	726.5033	363.7553	T	***605.3253***	303.1663	588.2988	294.6530	587.3148	294.1610	5
7	843.5823	422.2948	826.5557	413.7815	825.5717	413.2895	V	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
8	972.6248	486.8161	955.5983	478.3028	954.6143	477.8108	E	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	3
9	1073.6725	537.3399	1056.6460	528.8266	1055.6620	528.3346	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KTPALKMSVSKR**
Found in **I3L080**, Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=2 SV=1

Match to Query 10032: 1534.930888 from(768.472720,2+) intensity(45496.5938)
Title: File373 Spectrum12189 scans: 13708
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



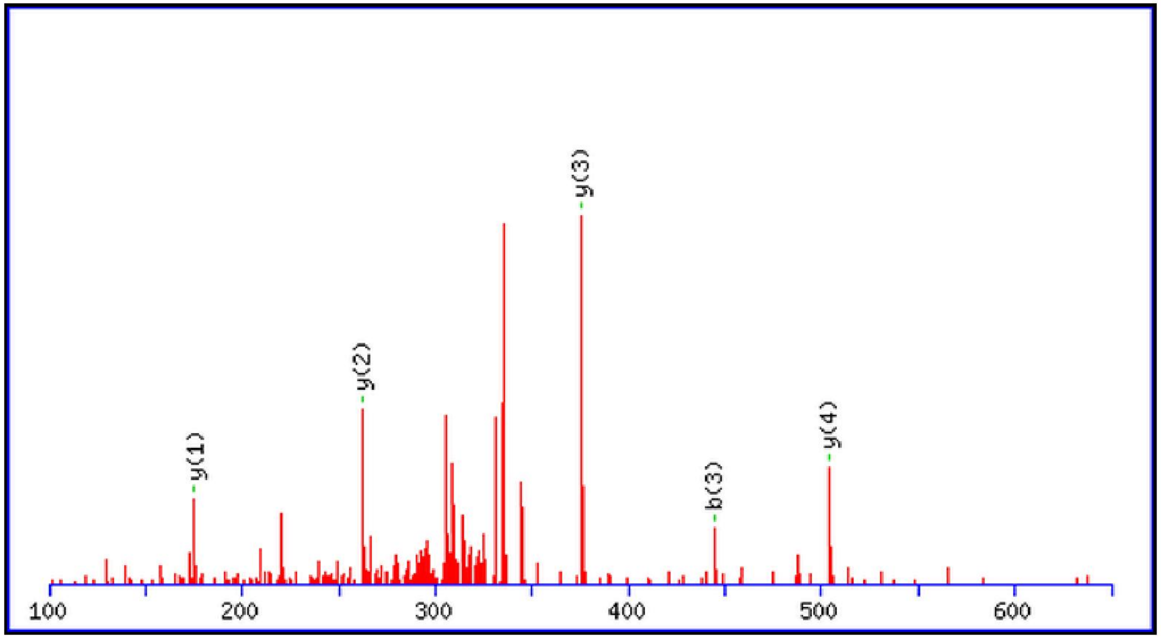
```
Monoisotopic mass of neutral peptide Mr(ca
Fixed modifications: Carbamidomethyl (C) (
Variable modifications:
K1      : Propionyl (K)
K6      : Propionyl (K)
M7      : Label:13C(1)2H(3) (M)
K11     : Propionyl-(13CD3)Methyl (K)
Ions Score: 65  Expect: 6e-005
Matches : 16/126 fragment ions using 26 mo
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							12
2	**286.1761**	143.5917	269.1496	135.0784	268.1656	134.5864	T	1351.8159	676.4116	1334.7894	667.8983	1333.8053	667.4063	11
3	383.2289	192.1181	366.2023	183.6048	365.2183	183.1128	P	***1250.7682***	625.8878	1233.7417	617.3745	1232.7577	616.8825	10
4	454.2660	227.6366	437.2395	219.1234	436.2554	218.6314	A	***1153.7155***	577.3614	1136.6889	568.8481	1135.7049	568.3561	9
5	**567.3501**	284.1787	550.3235	275.6654	549.3395	275.1734	L	***1082.6783***	541.8428	1065.6518	533.3295	1064.6678	532.8375	8
6	751.4713	376.2393	734.4447	367.7260	733.4607	367.2340	K	***969.5943***	485.3008	952.5677	476.7875	951.5837	476.2955	7
7	886.5339	443.7706	869.5074	435.2573	868.5234	434.7653	M	***785.4731***	393.2402	768.4466	384.7269	767.4625	384.2349	6
8	973.5660	487.2866	956.5394	478.7733	955.5554	478.2813	S	***650.4104***	325.7089	633.3839	317.1956	632.3999	316.7036	5
9	1072.6344	536.8208	1055.6078	528.3075	1054.6238	527.8155	V	***563.3784***	282.1928	546.3519	273.6796	545.3678	273.1876	4
10	1159.6664	580.3368	1142.6398	571.8236	1141.6558	571.3316	S	***464.3100***	232.6586	447.2834	224.1454	446.2994	223.6534	3
11	**1361.8254**	681.4163	1344.7989	672.9031	1343.8148	672.4111	K	***377.2780***	189.1426	360.2514	180.6293			2
12							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KQISR**
Found in **A0JNW5**, UHRF1-binding protein 1-like OS=Homo sapiens GN=UHRF1BP1L PE=1 SV=2

Match to Query 18: 704.445048 from(353.229800,2+) intensity(8895.4434)
Title: File373 Spectrum2309 scans: 3078
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●



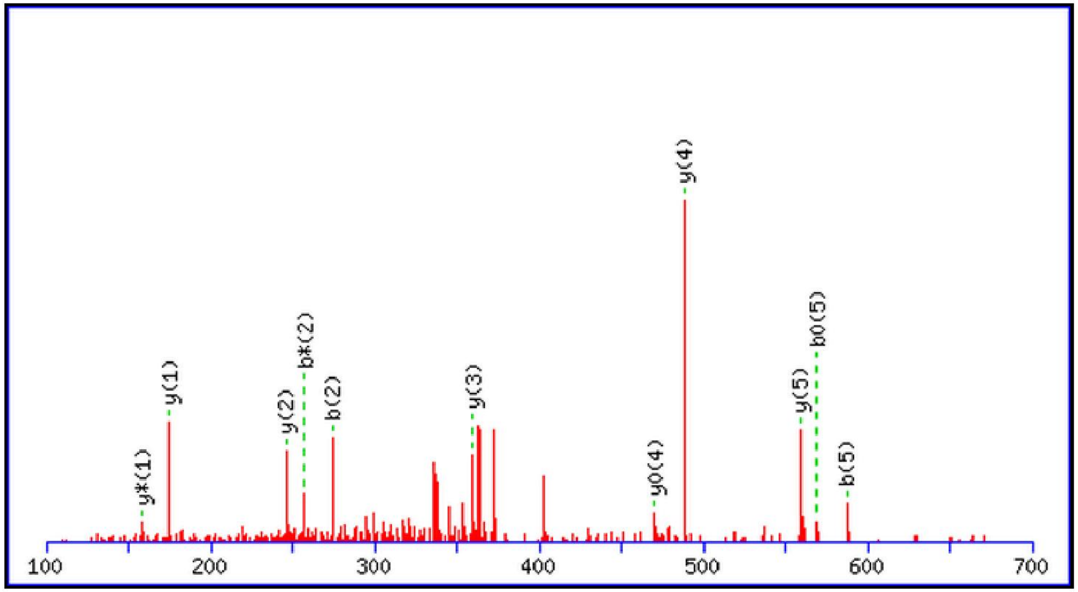
```
Monoisotopic mass of neutral peptide Mr(calc): 704.4453
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Met
Ions Score: 30  Expect: 0.26
Matches : 5/40 fragment ions
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							5
2	331.2249	166.1161	314.1983	157.6028			Q	***503.2936***	252.1504	486.2671	243.6372	485.2831	243.1452	4
3	444.3089	222.6581	427.2824	214.1448			I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
4	531.3410	266.1741	514.3144	257.6608	513.3304	257.1688	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
5							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAEIAR**
Found in **Q8IWV8**, E3 ubiquitin-protein ligase UBR2 OS=Homo sapiens GN=UBR2 PE=1 SV=1

Match to Query 211: 760.471968 from(381.243260,2+) intensity(12606.0537)
Title: File373 Spectrum3382 scans: 4234
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr3-ZW.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 ●



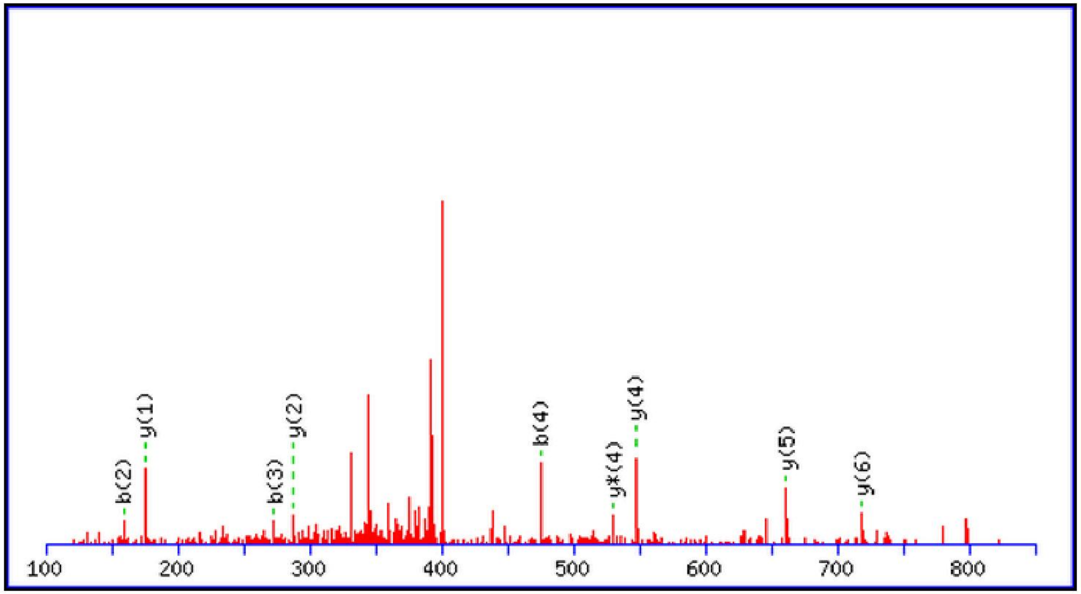
```
Monoisotopic mass of neutral peptide Mr(calc): 760.4715
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modificat
K1      : Propionyl
Ions Score: 34   Ex
Matches : 11/50 fr
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							6
2	**274.2034**	137.6053	257.1769	129.0921			A	***559.3198***	280.1636	542.2933	271.6503	541.3093	271.1583	5
3	403.2460	202.1266	386.2194	193.6134	385.2354	193.1214	E	***488.2827***	244.6450	471.2562	236.1317	470.2722	235.6397	4
4	516.3301	258.6687	499.3035	250.1554	498.3195	249.6634	I	***359.2401***	180.1237	342.2136	171.6104			3
5	**587.3672**	294.1872	570.3406	285.6740	569.3566	285.1819	A	***246.1561***	123.5817	229.1295	115.0684			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TGNKGLR**
Found in **H3BRB3**, Kinesin-like protein KIF22 OS=Homo sapiens GN=KIF22 PE=2 SV=1

Match to Query 586: 818.487528 from(410.251040,2+) intensity(42031.4531)
Title: File373 Spectrum3261 scans: 4105
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



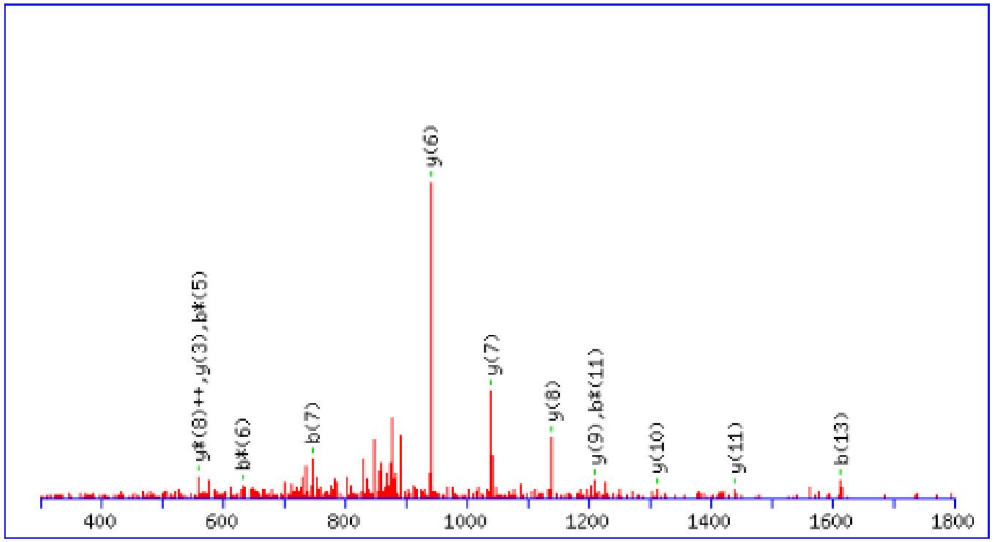
```
Monoisotopic mass of neutral peptide Mr(calc): 818.4883
Fixed modifications: Carbamido
Variable modifications:
K4     : Propionyl-(13CD3)Meth
Ions Score: 38   Expect: 0.039
Matches : 9/56 fragment ions u
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					7
2	**159.0764**	80.0418			141.0659	71.0366	G	***718.4479***	359.7276	701.4213	351.2143	6
3	**273.1193**	137.0633	256.0928	128.5500	255.1088	128.0580	N	***661.4264***	331.2168	644.3999	322.7036	5
4	**475.2784**	238.1428	458.2518	229.6295	457.2678	229.1375	K	***547.3835***	274.1954	530.3569	265.6821	4
5	532.2998	266.6535	515.2733	258.1403	514.2893	257.6483	G	345.2245	173.1159	328.1979	164.6026	3
6	645.3839	323.1956	628.3573	314.6823	627.3733	314.1903	L	***288.2030***	144.6051	271.1765	136.0919	2
7							R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **NMVQTAVVPVKKKR**
Found in **Q12972**, Nuclear inhibitor of protein phosphatase 1 OS=Homo sapiens GN=PPP1R8 PE=1 SV=2

Match to Query 13778: 1787.090068 from(894.552310,2+) intensity(25304.2461)
Title: File276 Spectrum12603 scans: 14135
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



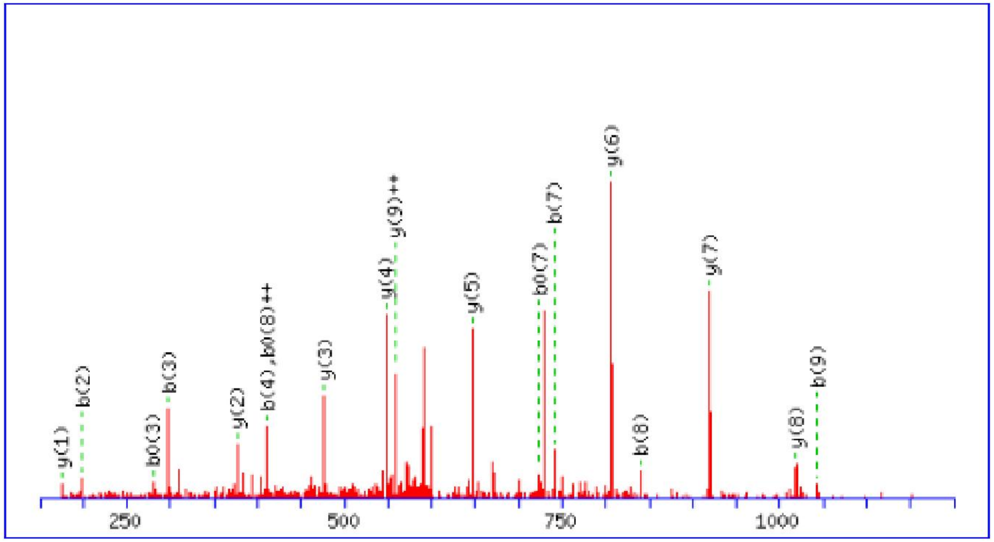
```
Monoisotopic mass of neutral peptide Mr(calc): 1787.0884
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2      : Label:13C(1)2H(3) (M)
K11     : Propionyl (K)
K12     : Propionyl (K)
K13     : Propionyl-(13CD3)Methyl (K)
Ions Score: 49  Expect: 0.0017
Matches : 13/130 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							14
2	250.1129	125.5601	233.0863	117.0468			M	1674.0528	837.5300	1657.0262	829.0168	1656.0422	828.5247	13
3	349.1813	175.0943	332.1547	166.5810			V	1538.9901	769.9987	1521.9636	761.4854	1520.9795	760.9934	12
4	477.2399	239.1236	460.2133	230.6103			Q	***1439.9217***	720.4645	1422.8951	711.9512	1421.9111	711.4592	11
5	578.2875	289.6474	561.2610	281.1341	560.2770	280.6421	T	***1311.8631***	656.4352	1294.8366	647.9219	1293.8526	647.4299	10
6	649.3247	325.1660	632.2981	316.6527	631.3141	316.1607	A	***1210.8154***	605.9114	1193.7889	597.3981			9
7	**748.3931**	374.7002	731.3665	366.1869	730.3825	365.6949	V	***1139.7783***	570.3928	1122.7518	561.8795			8
8	847.4615	424.2344	830.4349	415.7211	829.4509	415.2291	V	***1040.7099***	520.8586	1023.6834	512.3453			7
9	944.5142	472.7608	927.4877	464.2475	926.5037	463.7555	P	***941.6415***	471.3244	924.6150	462.8111			6
10	1043.5827	522.2950	1026.5561	513.7817	1025.5721	513.2897	V	844.5887	422.7980	827.5622	414.2847			5
11	1227.7038	614.3556	1210.6773	605.8423	1209.6933	605.3503	K	745.5203	373.2638	728.4938	364.7505			4
12	1411.8250	706.4161	1394.7985	697.9029	1393.8145	697.4109	K	***561.3991***	281.2032	544.3726	272.6899			3
13	**1613.9840**	807.4957	1596.9575	798.9824	1595.9735	798.4904	K	377.2780	189.1426	360.2514	180.6293			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TPVLCVAVKR**
Found in **Q6DT37**, Serine/threonine-protein kinase MRCK gamma OS=Homo sapiens GN=CDC42BPG PE=1 SV=2

Match to Query 6108: 1215.728248 from(608.871400,2+) intensity(102705.3516)
Title: File276 Spectrum11504 scans: 12963
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



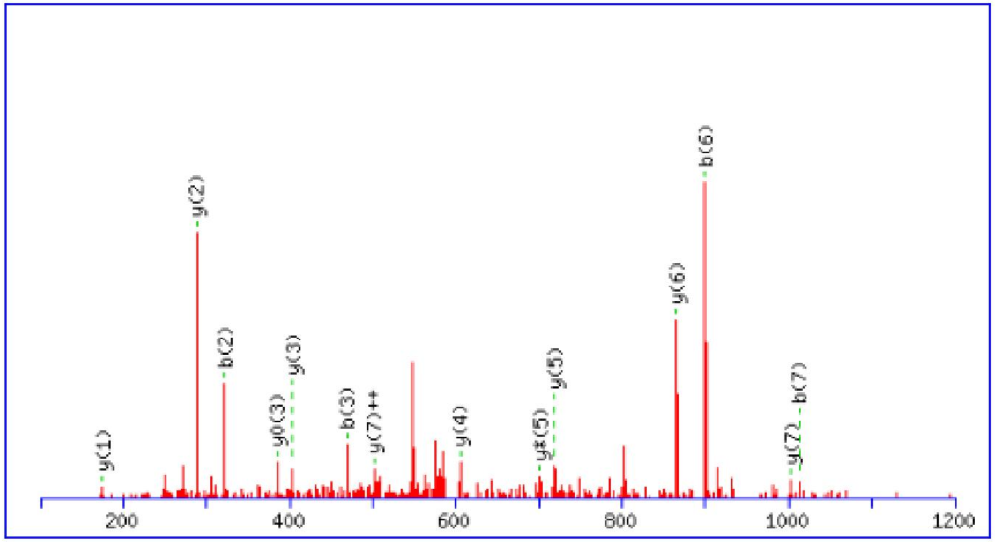
```
Monoisotopic mass of neutral peptide Mr(calc): 1215.7282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K9      : Propionyl-(13CD3)Methyl (K)
Ions Score: 57  Expect: 0.00055
Matches : 18/74 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					10
2	**199.1077**	100.0575			181.0972	91.0522	P	1115.6878	558.3475	1098.6612	549.8343	9
3	**298.1761**	149.5917			280.1656	140.5864	V	***1018.6350***	509.8212	1001.6085	501.3079	8
4	**411.2602**	206.1337			393.2496	197.1285	L	***919.5666***	460.2869	902.5401	451.7737	7
5	571.2908	286.1491			553.2803	277.1438	C	***806.4826***	403.7449	789.4560	395.2316	6
6	670.3593	335.6833			652.3487	326.6780	V	***646.4519***	323.7296	629.4254	315.2163	5
7	**741.3964**	371.2018			723.3858	362.1965	A	***547.3835***	274.1954	530.3569	265.6821	4
8	**840.4648**	420.7360			822.4542	411.7307	V	***476.3464***	238.6768	459.3198	230.1636	3
9	**1042.6238**	521.8155	1025.5973	513.3023	1024.6132	512.8103	K	***377.2780***	189.1426	360.2514	180.6293	2
10							R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KHFIKDIR**
Found in **Q03701**, CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3

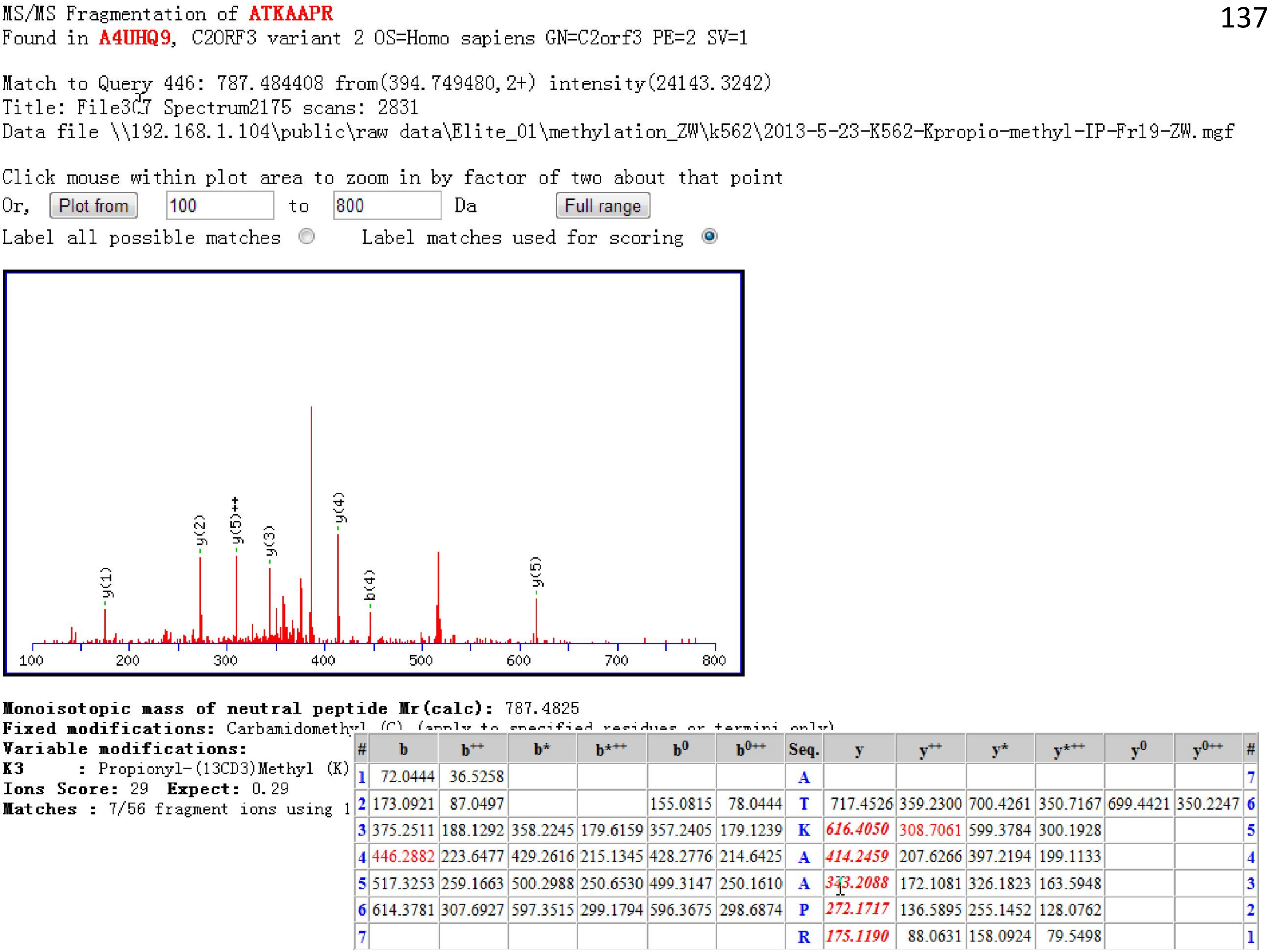
Match to Query 3442: 1185.714328 from(593.864440,2+) intensity(25360.4883)
Title: File365 Spectrum9386 scans: 10900
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr20-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1185.7142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K5      : Propionyl-(13CD3)Methyl (K)
Ions Score: 43  Expect: 0.013
Matches : 14/70 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	**322.1874**	161.5973	305.1608	153.0840			H	***1002.6004***	501.8038	985.5738	493.2905	984.5898	492.7985	7
3	**469.2558**	235.1315	452.2292	226.6183			F	***865.5414***	433.2744	848.5149	424.7611	847.5309	424.2691	6
4	582.3398	291.6736	565.3133	283.1603			I	***718.4730***	359.7402	701.4465	351.2269	700.4625	350.7349	5
5	784.4989	392.7531	767.4723	384.2398			K	***605.3890***	303.1981	588.3624	294.6848	587.3784	294.1928	4
6	**899.5258**	450.2665	882.4993	441.7533	881.5152	441.2613	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
7	**1012.6099**	506.8086	995.5833	498.2953	994.5993	497.8033	I	***288.2030***	144.6051	271.1765	136.0919			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **ATKAAPR**
Found in **A4UHQ9**, C2ORF3 variant 2 OS=Homo sapiens GN=C2orf3 PE=2 SV=1

Match to Query 446: 787.484408 from(394.749480,2+) intensity(24143.3242)
Title: File307 Spectrum2175 scans: 2831
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr19-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

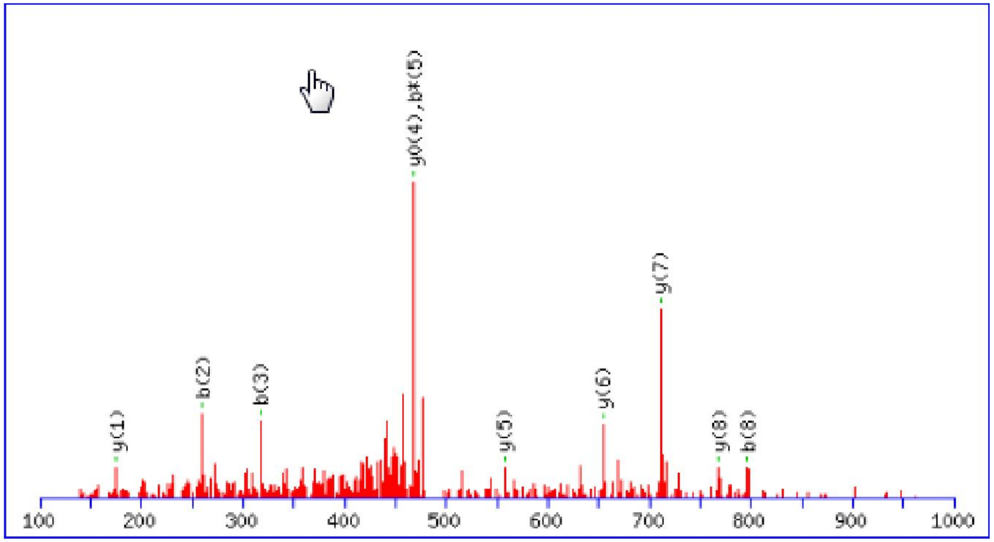
Monoisotopic mass of neutral peptide Mr(calc): 787.4825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.29
Matches : 7/56 fragment ions using 1

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							7
2	173.0921	87.0497			155.0815	78.0444	T	717.4526	359.2300	700.4261	350.7167	699.4421	350.2247	6
3	375.2511	188.1292	358.2245	179.6159	357.2405	179.1239	K	***616.4050***	308.7061	599.3784	300.1928			5
4	446.2882	223.6477	429.2616	215.1345	428.2776	214.6425	A	***414.2459***	207.6266	397.2194	199.1133			4
5	517.3253	259.1663	500.2988	250.6530	499.3147	250.1610	A	***343.2088***	172.1081	326.1823	163.5948			3
6	614.3781	307.6927	597.3515	299.1794	596.3675	298.6874	P	***272.1717***	136.5895	255.1452	128.0762			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

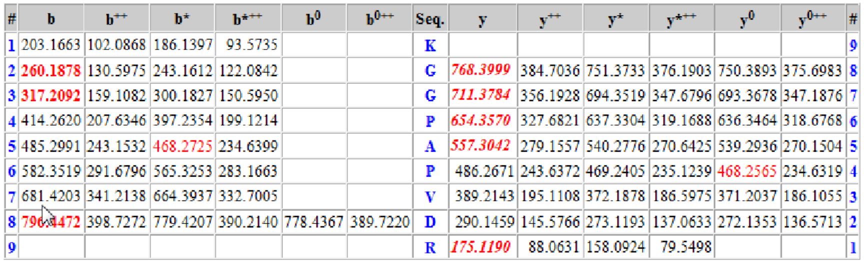
MS/MS Fragmentation of **KGGPAPVDR**
Found in **E7EU24**, Protein CBFA2T3 OS=Homo sapiens GN=CBFA2T3 PE=2 SV=2

Match to Query 2120: 969.551848 from(485.783200,2+) intensity(16014.0156)
Title: File307 Spectrum3376 scans: 4114
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr19-ZW.mgf

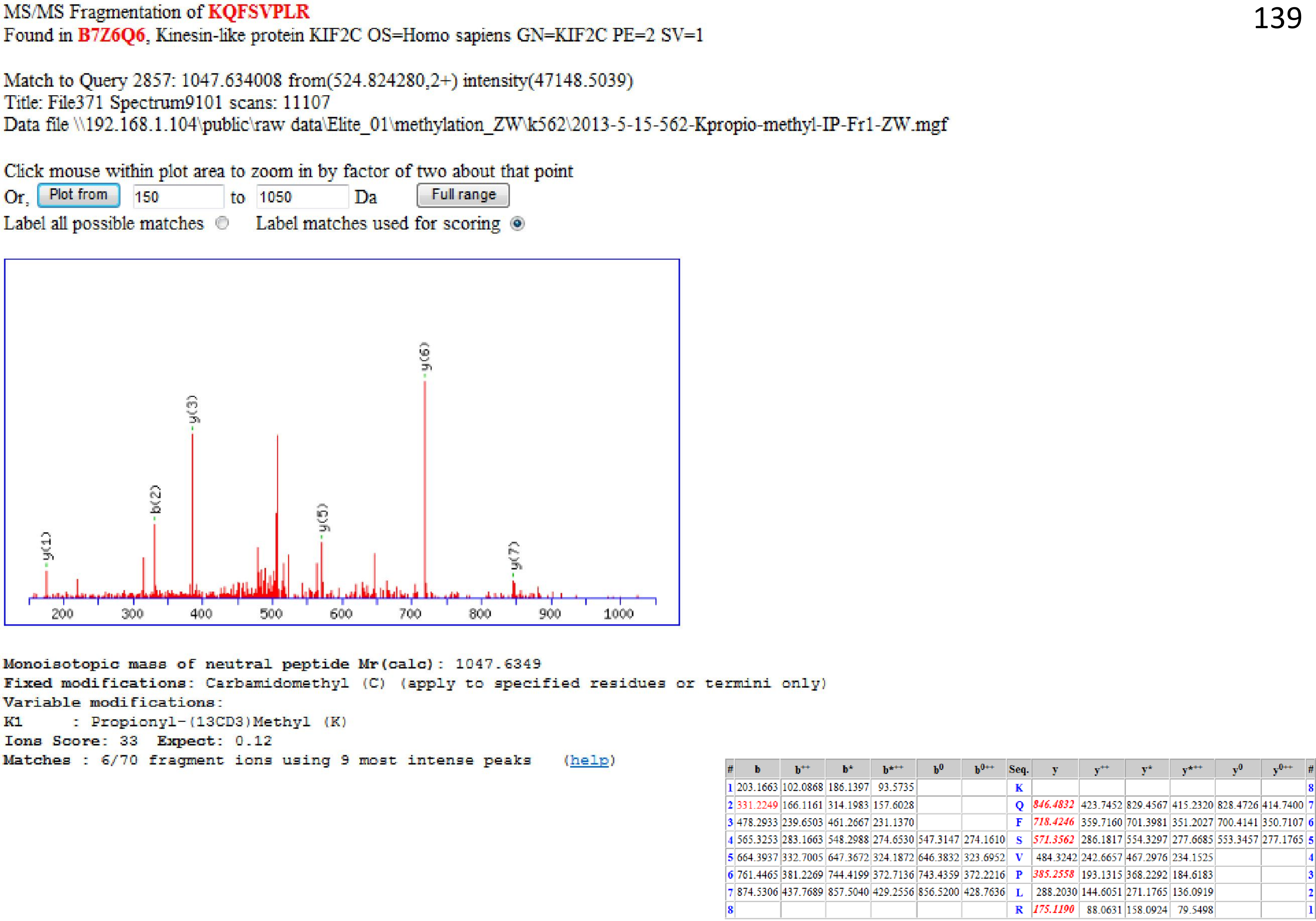
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 969.5516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 30 **Expect:** 0.37
Matches : 10/80 fragment ions using 18 most intense peaks (help)



#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**260.1878**	130.5975	243.1612	122.0842			G	***768.3999***	384.7036	751.3733	376.1903	750.3893	375.6983	8
3	**317.2092**	159.1082	300.1827	150.5950			G	***711.3784***	356.1928	694.3519	347.6796	693.3678	347.1876	7
4	414.2620	207.6346	397.2354	199.1214			P	***654.3570***	327.6821	637.3304	319.1688	636.3464	318.6768	6
5	485.2991	243.1532	468.2725	234.6399			A	***557.3042***	279.1557	540.2776	270.6425	539.2936	270.1504	5
6	582.3519	291.6796	565.3253	283.1663			P	486.2671	243.6372	469.2405	235.1239	468.2565	234.6319	4
7	681.4203	341.2138	664.3937	332.7005			V	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
8	**796.4472**	398.7272	779.4207	390.2140	778.4367	389.7220	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



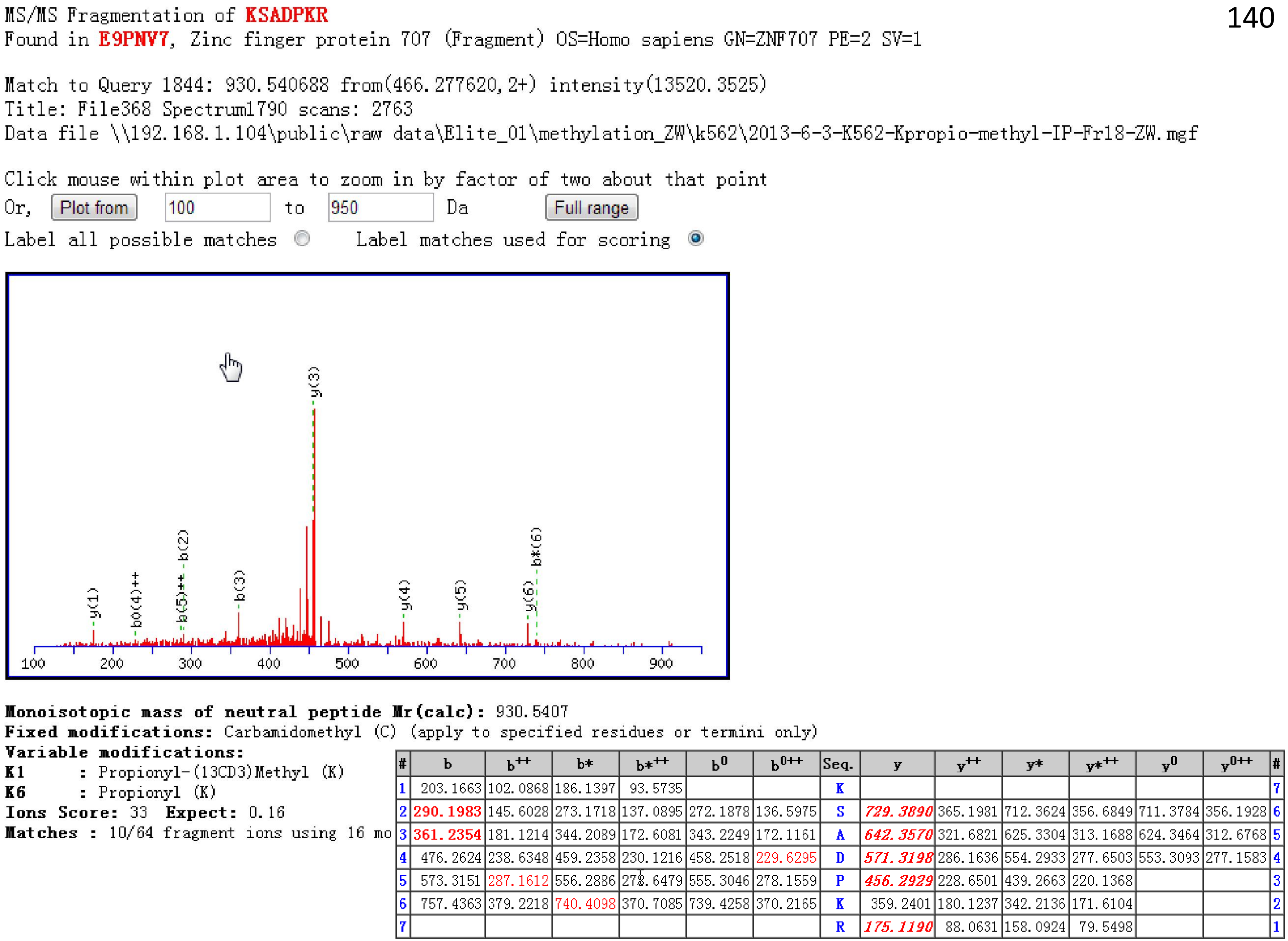
MS/MS Fragmentation of **KQFSVPLR**
Found in **B7Z6Q6**, Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C PE=2 SV=1

Match to Query 2857: 1047.634008 from(524.824280,2+) intensity(47148.5039)
Title: File371 Spectrum9101 scans: 11107
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1047.6349
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
Ions Score: 33  Expect: 0.12
Matches : 6/70 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	331.2249	166.1161	314.1983	157.6028			Q	*846.4832*	423.7452	829.4567	415.2320	828.4726	414.7400	7
3	478.2933	239.6503	461.2667	231.1370			F	*718.4246*	359.7160	701.3981	351.2027	700.4141	350.7107	6
4	565.3253	283.1663	548.2988	274.6530	547.3147	274.1610	S	*571.3562*	286.1817	554.3297	277.6685	553.3457	277.1765	5
5	664.3937	332.7005	647.3672	324.1872	646.3832	323.6952	V	484.3242	242.6657	467.2976	234.1525			4
6	761.4465	381.2269	744.4199	372.7136	743.4359	372.2216	P	*385.2558*	193.1315	368.2292	184.6183			3
7	874.5306	437.7689	857.5040	429.2556	856.5200	428.7636	L	288.2030	144.6051	271.1765	136.0919			2
8							R	*175.1190*	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KSADPKR**
Found in **E9PNV7**, Zinc finger protein 707 (Fragment) OS=Homo sapiens GN=ZNF707 PE=2 SV=1

Match to Query 1844: 930.540688 from(466.277620,2+) intensity(13520.3525)
Title: File368 Spectrum1790 scans: 2763
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr18-ZW.mgf

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

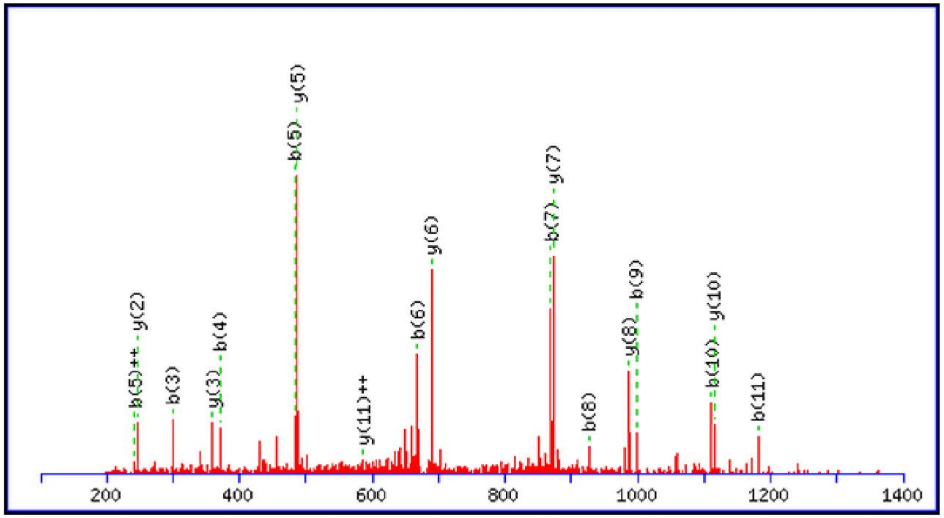
Monoisotopic mass of neutral peptide Mr(calc): 930.5407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 33 **Expect:** 0.16
Matches : 10/64 fragment ions using 16 mo

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							7
2	290.1983	145.6028	273.1718	137.0895	272.1878	136.5975	S	*729.3890*	365.1981	712.3624	356.6849	711.3784	356.1928	6
3	361.2354	181.1214	344.2089	172.6081	343.2249	172.1161	A	*642.3570*	321.6821	625.3304	313.1688	624.3464	312.6768	5
4	476.2624	238.6348	459.2358	230.1216	458.2518	229.6295	D	*571.3198*	286.1636	554.2933	277.6503	553.3093	277.1583	4
5	573.3151	287.1612	556.2886	278.6479	555.3046	278.1559	P	*456.2929*	228.6501	439.2663	220.1368			3
6	757.4363	379.2218	740.4098	370.7085	739.4258	370.2165	K	359.2401	180.1237	342.2136	171.6104			2
7							R	*175.1190*	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KGGALKKGAIAR**
Found in **Q5T6S3**, PHD finger protein 19 OS=Homo sapiens GN=PHF19 PE=1 SV=1

Match to Query 7205: 1354.857388 from(678.435970,2+) intensity(117963.9531)
Title: File338 Spectrum11325 scans: 12646
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr17-ZW.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 ●



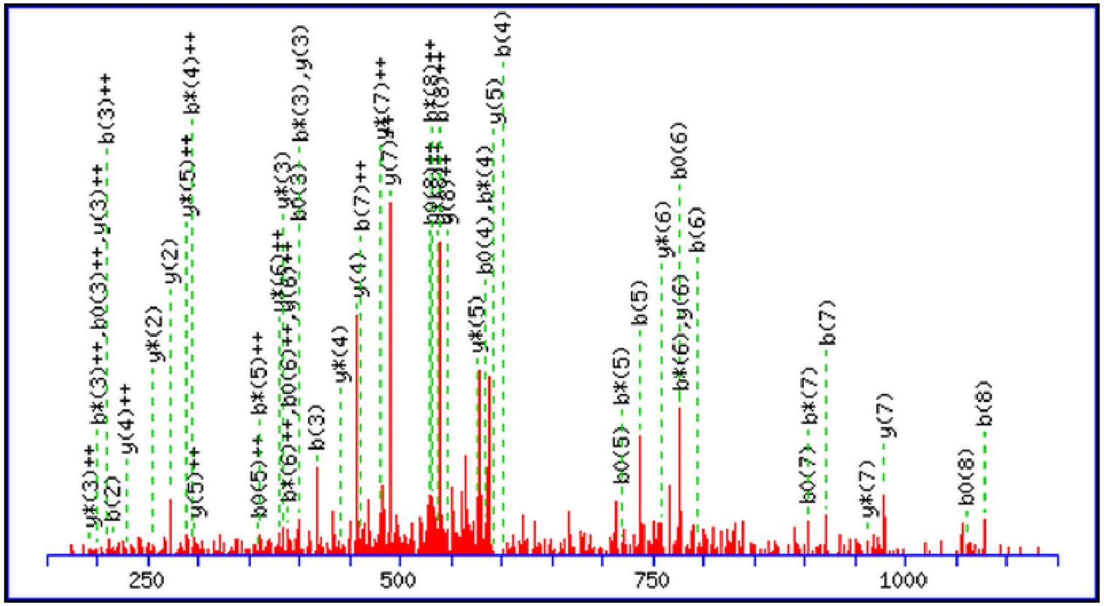
```
Monoisotopic mass of neutral peptide Mr(calc): 1354.8569
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K1      : Propionyl (K)
K6      : Propionyl (K)
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 66  Expect: 3.1e-005
Matches : 19/88 fragment ions using 35 most intense peaks    (h
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	185.1285	93.0679	168.1019	84.5546	K					12
2	***242.1499***	121.5786	225.1234	113.0653	G	1171.7430	586.3751	1154.7165	577.8619	11
3	***299.1714***	150.0893	282.1448	141.5761	G	**1114.7215**	557.8644	1097.6950	549.3511	10
4	***370.2085***	185.6079	353.1819	177.0946	A	1057.7001	529.3537	1040.6735	520.8404	9
5	***483.2926***	242.1499	466.2660	233.6366	L	**986.6630**	493.8351	969.6364	485.3218	8
6	***667.4137***	334.2105	650.3872	325.6972	K	**873.5789**	437.2931	856.5523	428.7798	7
7	***869.5728***	435.2900	852.5462	426.7767	K	**689.4577**	345.2325	672.4312	336.7192	6
8	***926.5942***	463.8007	909.5677	455.2875	G	**487.2987**	244.1530	470.2722	235.6397	5
9	***997.6313***	499.3193	980.6048	490.8060	A	430.2772	215.6423	413.2507	207.1290	4
10	***1110.7154***	555.8613	1093.6888	547.3481	I	**359.2401**	180.1237	342.2136	171.6104	3
11	***1181.7525***	591.3799	1164.7260	582.8666	A	**246.1561**	123.5817	229.1295	115.0684	2
12					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **TLKKMGQRP**
Found in **B0QY89**, Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1

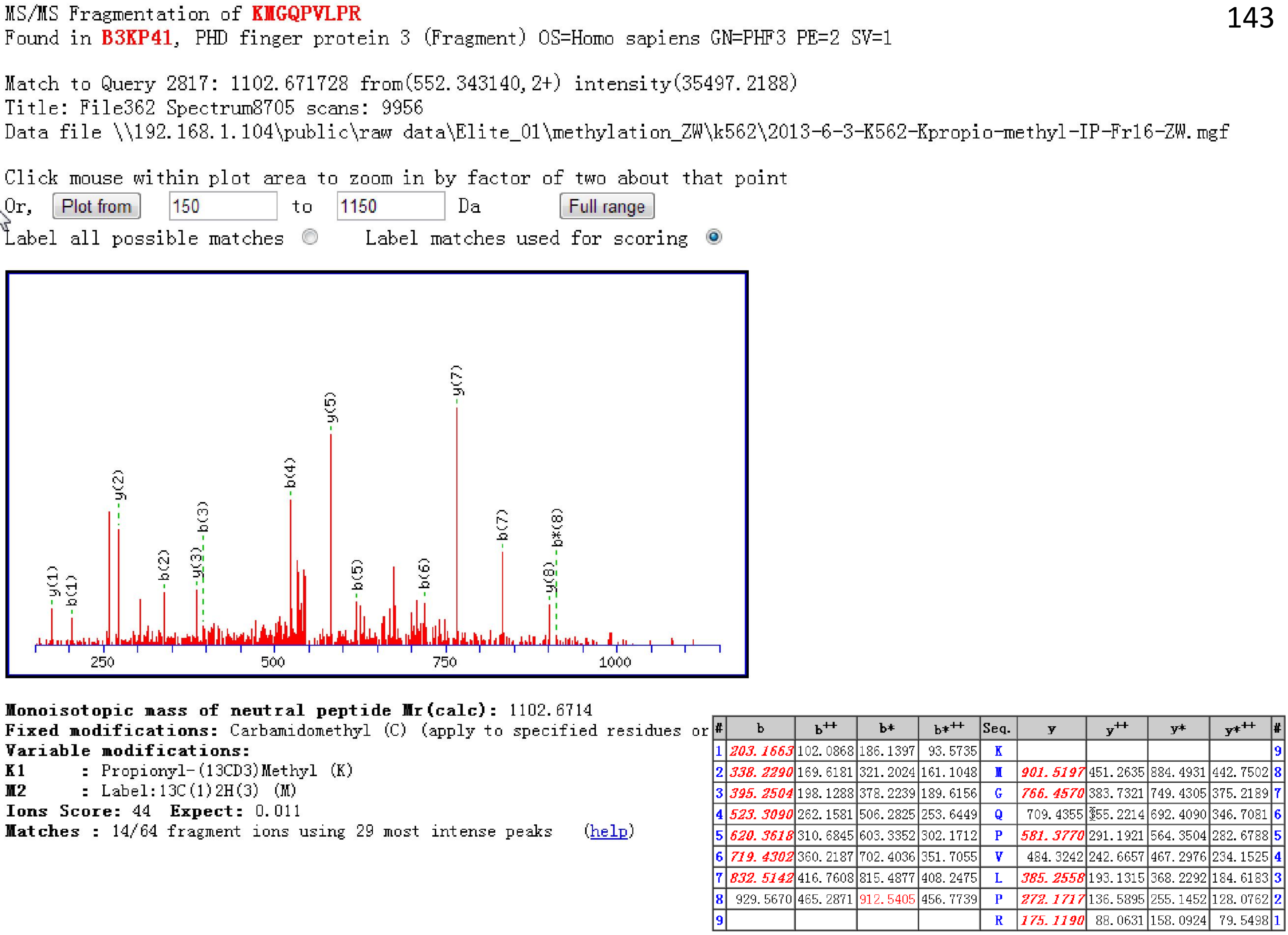
Match to Query 5063: 1191.717988 from(596.866270,2+) intensity(30733.3301)
Title: File338 Spectrum9670 scans: 10880
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr17-ZW.mgf

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 ○



```
Monoisotopic mass of neutral peptide Mr(ca
Fixed modifications: Carbamidomethyl (C) (
Variable modifications:
K3       : Propionyl-(13CD3)Methyl (K)
K4       : Propionyl (K)
M5       : Label:13C(1)2H(3) (M)
Ions Score: 26   Expect: 0.65    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					9
2	**215.1390**	108.0731			197.1285	99.0679	L	1091.6787	**546.3430**	1074.6521	**537.8297**	8
3	**417.2980**	**209.1527**	**400.2715**	**200.6394**	**399.2875**	**200.1474**	K	**978.5946**	**489.8009**	**961.5681**	**481.2877**	7
4	**601.4192**	301.2132	**584.3927**	**292.7000**	**583.4086**	292.2080	K	**776.4356**	**388.7214**	**759.4091**	**380.2082**	6
5	**736.4819**	368.7446	**719.4553**	**360.2313**	**718.4713**	**359.7393**	M	**592.3144**	**296.6609**	**575.2879**	**288.1476**	5
6	**793.5033**	397.2553	**776.4768**	**388.7420**	**775.4928**	**388.2500**	G	**457.2518**	**229.1295**	**440.2252**	220.6162	4
7	**921.5619**	**461.2846**	**904.5354**	452.7713	**903.5514**	452.2793	Q	**400.2303**	**200.6188**	**383.2037**	**192.1055**	3
8	**1077.6630**	**539.3352**	1060.6365	**530.8219**	**1059.6525**	**530.3299**	R	**272.1717**	136.5895	**255.1452**	128.0762	2
9							P	116.0706	58.5389			1



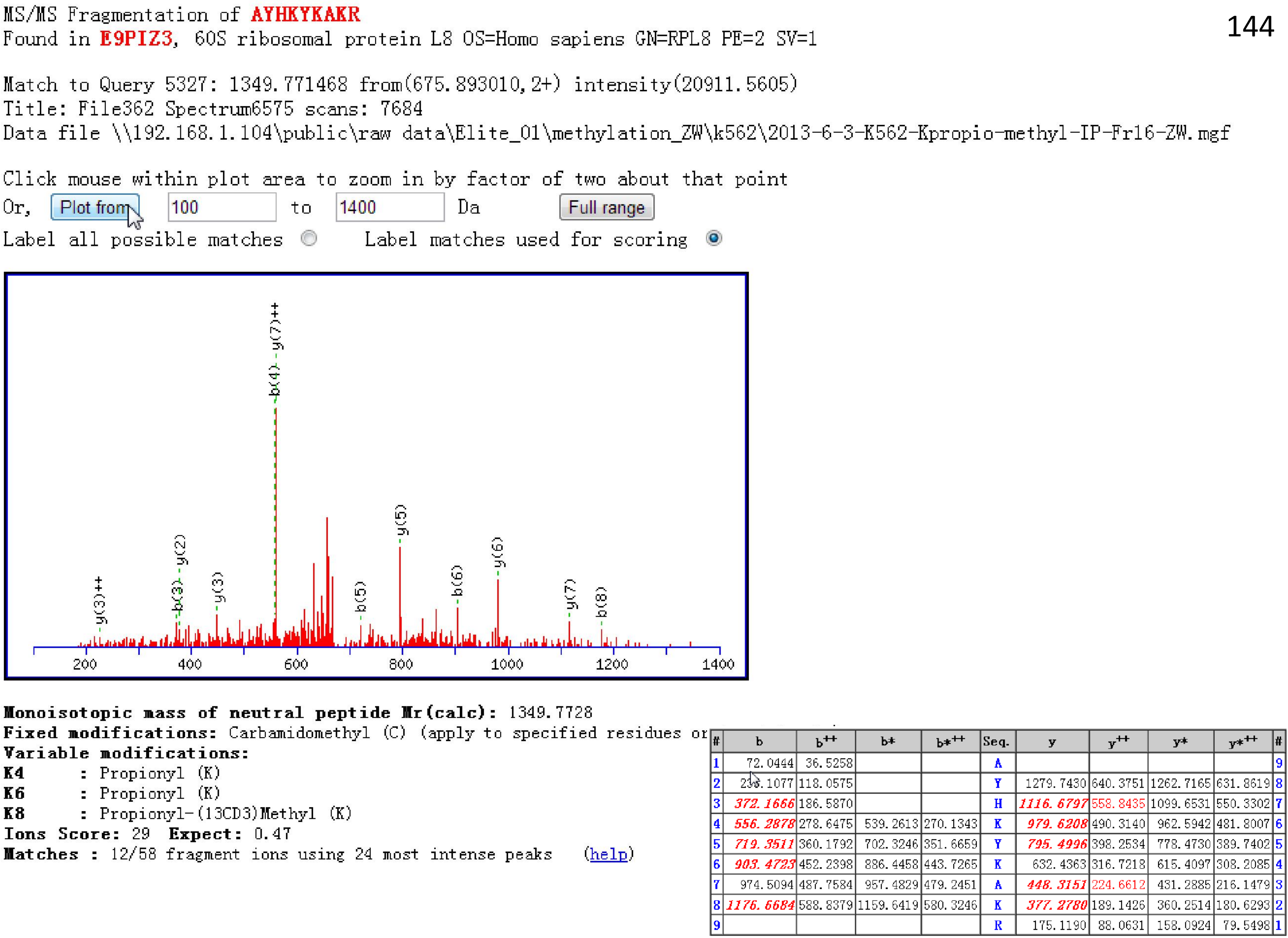
MS/MS Fragmentation of **KMGQPVLPR**
Found in **B3KP41**, PHD finger protein 3 (Fragment) OS=Homo sapiens GN=PHF3 PE=2 SV=1

Match to Query 2817: 1102.671728 from(552.343140,2+) intensity(35497.2188)
Title: File362 Spectrum8705 scans: 9956
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr16-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1102.6714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
M2 : Label:13C(1)2H(3) (M)
Ions Score: 44 **Expect:** 0.011
Matches : 14/64 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	***203.1663***	102.0868	186.1397	93.5735	K					9
2	***338.2290***	169.6181	321.2024	161.1048	M	***901.5197***	451.2635	884.4931	442.7502	8
3	***395.2504***	198.1288	378.2239	189.6156	G	***766.4570***	383.7321	749.4305	375.2189	7
4	***523.3090***	262.1581	506.2825	253.6449	Q	709.4355	355.2214	692.4090	346.7081	6
5	***620.3618***	310.6845	603.3352	302.1712	P	***581.3770***	291.1921	564.3504	282.6788	5
6	***719.4302***	360.2187	702.4036	351.7055	V	484.3242	242.6657	467.2976	234.1525	4
7	***832.5142***	416.7608	815.4877	408.2475	L	***385.2558***	193.1315	368.2292	184.6183	3
8	929.5670	465.2871	912.5405	456.7739	P	***272.1717***	136.5895	255.1452	128.0762	2
9					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **AYHKYKAKR**
Found in **E9PIZ3**, 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=2 SV=1

Match to Query 5327: 1349.771468 from(675.893010,2+) intensity(20911.5605)
Title: File362 Spectrum6575 scans: 7684
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr16-ZW.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 ●

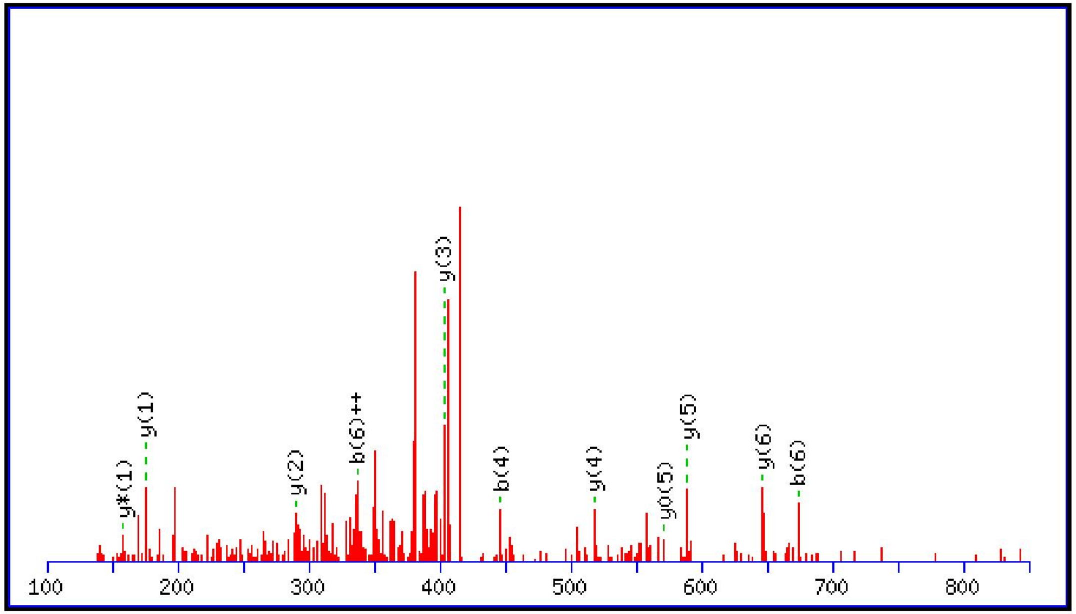
Monoisotopic mass of neutral peptide Mr(calc): 1349.7728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl (K)
K6 : Propionyl (K)
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.47
Matches : 12/58 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	72.0444	36.5258			A					9
2	235.1077	118.0575			Y	1279.7430	640.3751	1262.7165	631.8619	8
3	***372.1666***	186.5870			H	***1116.6797***	558.8435	1099.6531	550.3302	7
4	***556.2878***	278.6475	539.2613	270.1343	K	***979.6208***	490.3140	962.5942	481.8007	6
5	***719.3511***	360.1792	702.3246	351.6659	Y	***795.4996***	398.2534	778.4730	389.7402	5
6	***903.4723***	452.2398	886.4458	443.7265	K	632.4363	316.7218	615.4097	308.2085	4
7	974.5094	487.7584	957.4829	479.2451	A	***448.3151***	224.6612	431.2885	216.1479	3
8	***1176.6684***	588.8379	1159.6419	580.3246	K	***377.2780***	189.1426	360.2514	180.6293	2
9					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KGADLDR**
Found in **B3KNZ8**, Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 OS=Homo sapiens GN=CENTG3 PE=2 SV=1

Match to Query 531: 847.467808 from(424.741180,2+) intensity(8125.7539)
Title: File362 Spectrum3602 scans: 4510
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



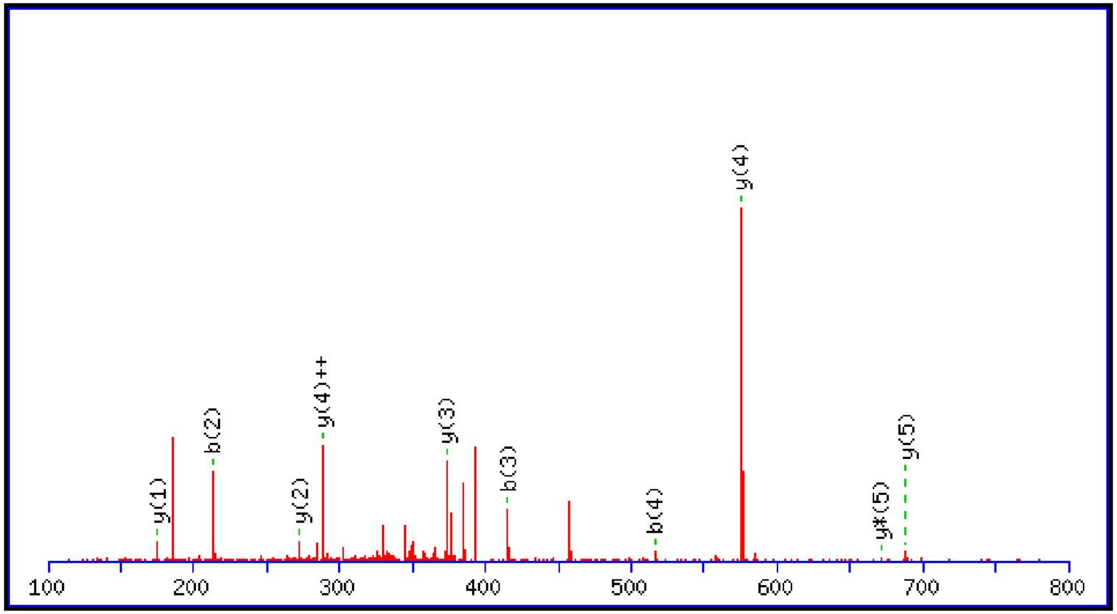
Monoisotopic mass of neutral peptide Mr(calc): 847.4672
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 30 **Expect:** 0.21
Matches : 11/64 fragment ions using 3

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							7
2	260.1878	130.5975	243.1612	122.0842			G	***646.3155***	323.6614	629.2889	315.1481	628.3049	314.6561	6
3	331.2249	166.1161	314.1983	157.6028			A	***589.2940***	295.1506	572.2675	286.6374	571.2835	286.1454	5
4	**446.2518**	223.6295	429.2253	215.1163	428.2412	214.6243	D	***518.2569***	259.6321	501.2304	251.1188	500.2463	250.6268	4
5	559.3359	280.1716	542.3093	271.6583	541.3253	271.1663	L	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
6	**674.3628**	337.6850	657.3363	329.1718	656.3523	328.6798	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VIKTPR**
Found in **Q9UMN6**, Histone-lysine N-methyltransferase MLL4 OS=Homo sapiens GN=WBP7 PE=1 SV=1

Match to Query 638: 786.523168 from(394.268860,2+) intensity(120378.4922)
Title: File322 Spectrum4776 scans: 5610
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



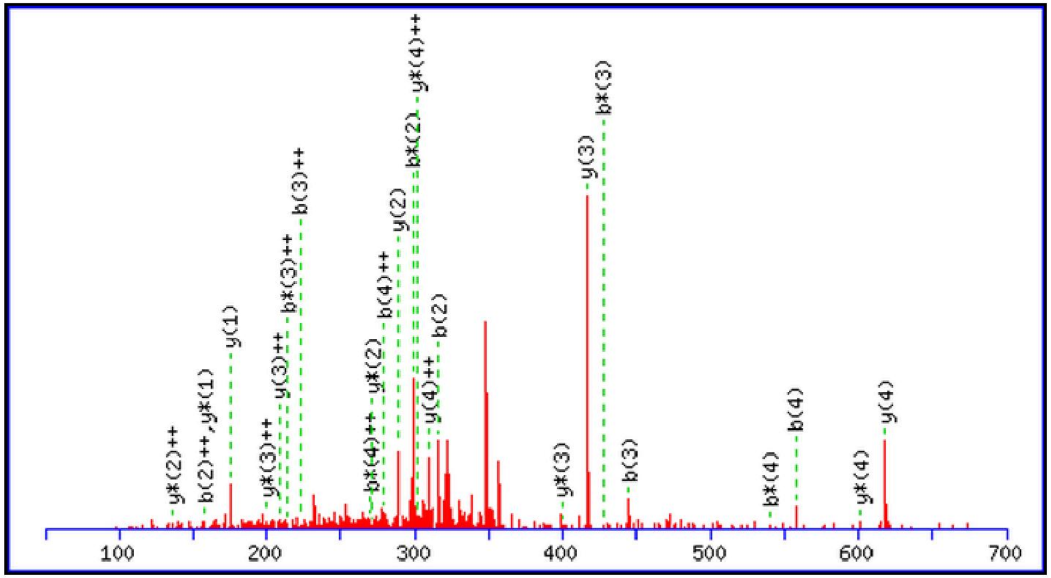
Monoisotopic mass of neutral peptide Mr(calc): 786.5236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 **:** Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.13
Matches : 10/46 fragment ions using 21 most intens

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							6
2	**213.1598**	107.0835					I	***688.4625***	344.7349	671.4359	336.2216	670.4519	335.7296	5
3	**415.3188**	208.1630	398.2922	199.6497			K	***575.3784***	288.1928	558.3519	279.6796	557.3678	279.1876	4
4	**516.3664**	258.6869	499.3399	250.1736	498.3559	249.6816	T	***373.2194***	187.1133	356.1928	178.6001	355.2088	178.1081	3
5	613.4192	307.2132	596.3927	298.7000	595.4086	298.2080	P	***272.1717***	136.5895	255.1452	128.0762			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IKQIR**
Found in **Q5T6W5**, Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1

Match to Query 203: 730.496248 from(366.255400,2+) intensity(11531.8877)
Title: File322 Spectrum6074 scans: 7020
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 50 to 700 Da Full range
Label all possible matches ● Label matches used for scoring ○



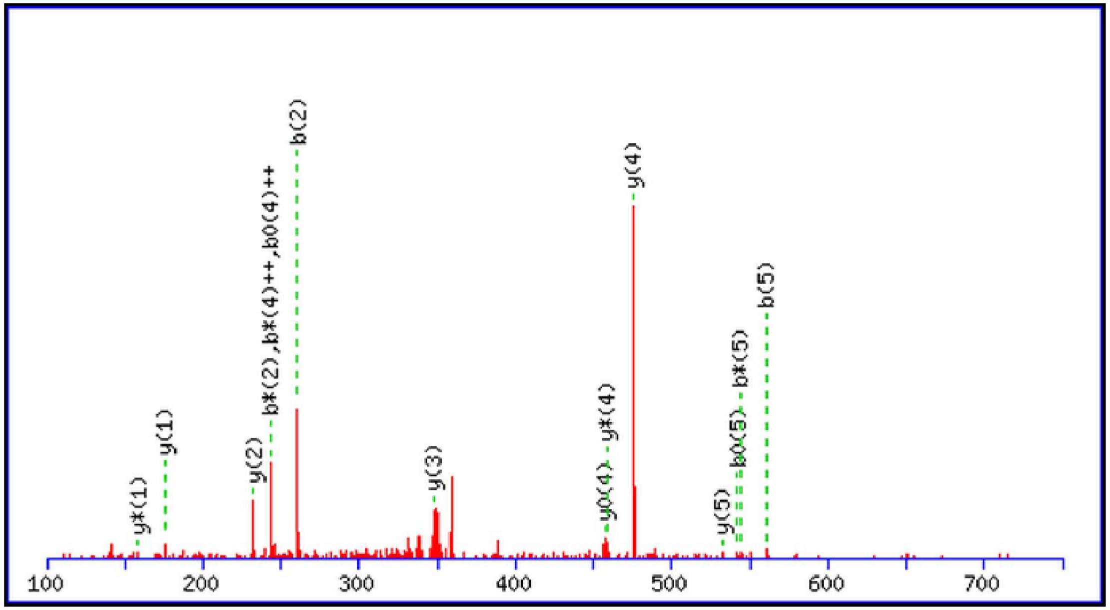
```
Monoisotopic mass of neutral peptide Mr(calc): 730.4974
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Met
Ions Score: 30   Expect: 0.12
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.0913	57.5493			I					5
2	316.2504	158.6288	299.2238	150.1155	K	618.4206	309.7139	601.3941	301.2007	4
3	444.3089	222.6581	427.2824	214.1448	Q	416.2616	208.6344	399.2350	200.1212	3
4	557.3930	279.2001	540.3664	270.6869	I	288.2030	144.6051	271.1765	136.0919	2
5					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KGKDGR**
Found in **J3KR15**, N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D OS=Homo sapiens GN=NAPEPLD PE=4 SV=1

Match to Query 217: 733.435708 from(367.725130,2+) intensity(31839.1367)
Title: File322 Spectrum1004 scans: 1475
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



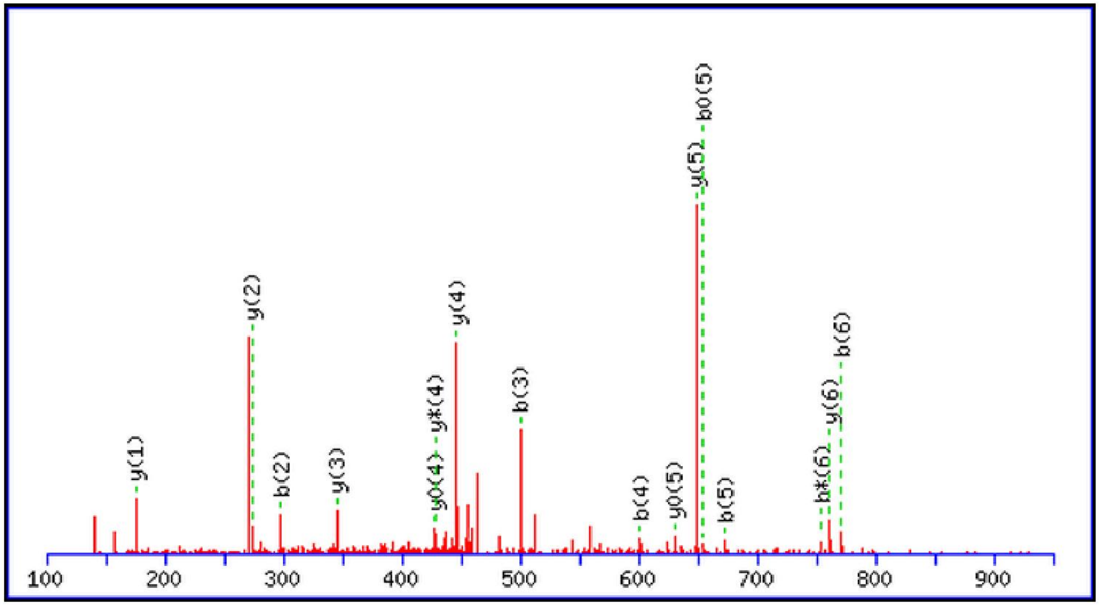
```
Monoisotopic mass of neutral peptide Mr(calc): 733.4355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CI
Ions Score: 36  Expect:
Matches : 15/50 fragment
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							6
2	**260.1878**	130.5975	243.1612	122.0842			G	***532.2838***	266.6455	515.2572	258.1323	514.2732	257.6402	5
3	388.2827	194.6450	371.2562	186.1317			K	***475.2623***	238.1348	458.2358	229.6215	457.2518	229.1295	4
4	503.3097	252.1585	486.2831	243.6452	485.2991	243.1532	D	***347.1674***	174.0873	330.1408	165.5740	329.1568	165.0820	3
5	**560.3311**	280.6692	543.3046	272.1559	542.3206	271.6639	G	***232.1404***	116.5738	215.1139	108.0606			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KIKTAVR**
Found in **F6QR24**, Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=2 SV=1

Match to Query 2027: 944.628208 from(473.321380,2+) intensity(59718.7695)
Title: File359 Spectrum6194 scans: 7336
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



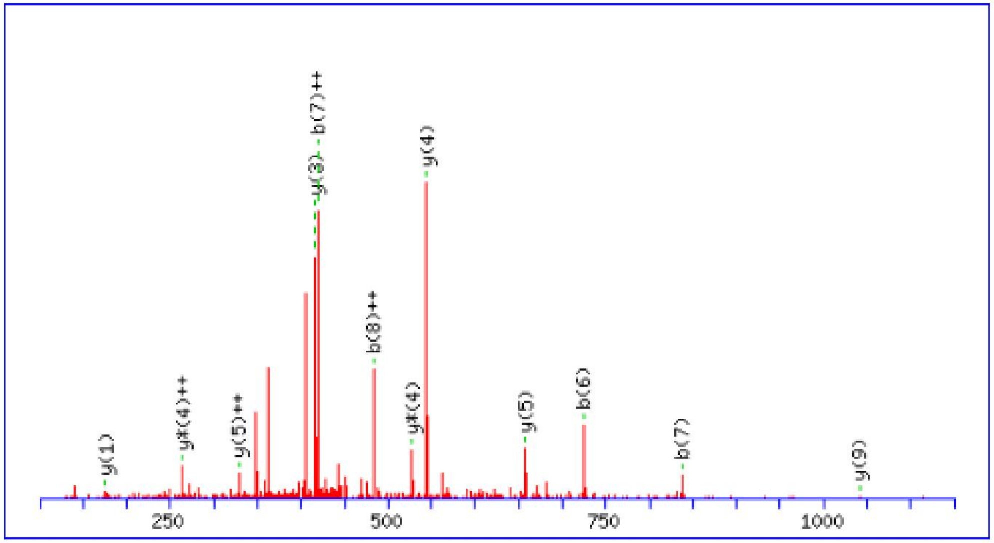
```
Monoisotopic mass of neutral peptide Mr(calc): 944.6291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K3      : Propionyl-(13CD3)Me
Ions Score: 37   Expect: 0.02
Matches : 16/60 fragment ion
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							7
2	**298.2125**	149.6099	281.1860	141.0966			I	***761.5152***	381.2613	744.4887	372.7480	743.5047	372.2560	6
3	**500.3715**	250.6894	483.3450	242.1761			K	***648.4312***	324.7192	631.4046	316.2059	630.4206	315.7139	5
4	**601.4192**	301.2132	584.3927	292.7000	583.4086	292.2080	T	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
5	**672.4563**	336.7318	655.4298	328.2185	654.4458	327.7265	A	***345.2245***	173.1159	328.1979	164.6026			3
6	**771.5247**	386.2660	754.4982	377.7527	753.5142	377.2607	V	***274.1874***	137.5973	257.1608	129.0840			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **HKIALSIQKLR**
Found in **M0QZ22**, Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=4 SV=1

Match to Query 7830: 1379.879382 from(460.967070,3+) intensity(103940.1094)
Title: File359 Spectrum6643 scans: 7815
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



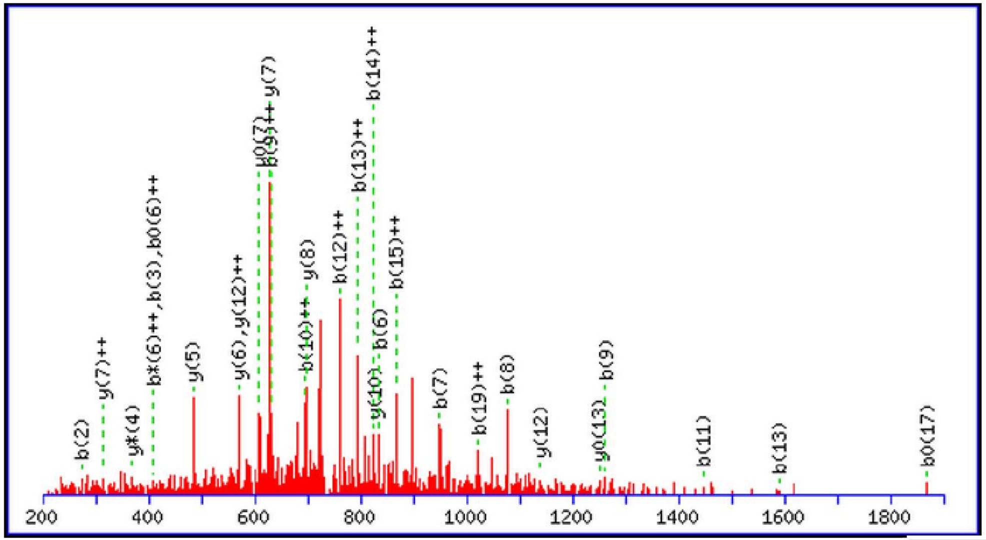
```
Monoisotopic mass of neutral peptide Mr(calc): 1379.8885
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
Ions Score: 26  Expect: 0.24
Matches : 12/98 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							11
2	340.2252	170.6162	323.1987	162.1030			K	1243.8369	622.4221	1226.8104	613.9088	1225.8263	613.4168	10
3	453.3093	227.1583	436.2827	218.6450			I	***1041.6779***	521.3426	1024.6513	512.8293	1023.6673	512.3373	9
4	524.3464	262.6768	507.3198	254.1636			A	928.5938	464.8006	911.5673	456.2873	910.5833	455.7953	8
5	637.4304	319.2189	620.4039	310.7056			L	857.5567	429.2820	840.5302	420.7687	839.5461	420.2767	7
6	**724.4625**	362.7349	707.4359	354.2216	706.4519	353.7296	S	744.4726	372.7400	727.4461	364.2267	726.4621	363.7347	6
7	**837.5465**	**419.2769**	820.5200	410.7636	819.5360	410.2716	I	***657.4406***	329.2239	640.4141	320.7107			5
8	965.6051	**483.3062**	948.5786	474.7929	947.5945	474.3009	Q	***544.3566***	272.6819	527.3300	264.1686			4
9	1093.7001	547.3537	1076.6735	538.8404	1075.6895	538.3484	K	***416.2980***	208.6526	399.2714	200.1394			3
10	1206.7841	603.8957	1189.7576	595.3824	1188.7736	594.8904	L	288.2030	144.6051	271.1765	136.0919			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAMIEKLEKEGAAGSPGGPR**
Found in **B5MCI0**, Smoothelin OS=Homo sapiens GN=SMTN PE=2 SV=1

Match to Query 16027: 2215.205892 from(739.409240,3+) intensity(84502.7578)
Title: File359 Spectrum14992 scans: 16720
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-6-3-K562-Kpropio-methyl-IP-Fr14-ZW.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 ●



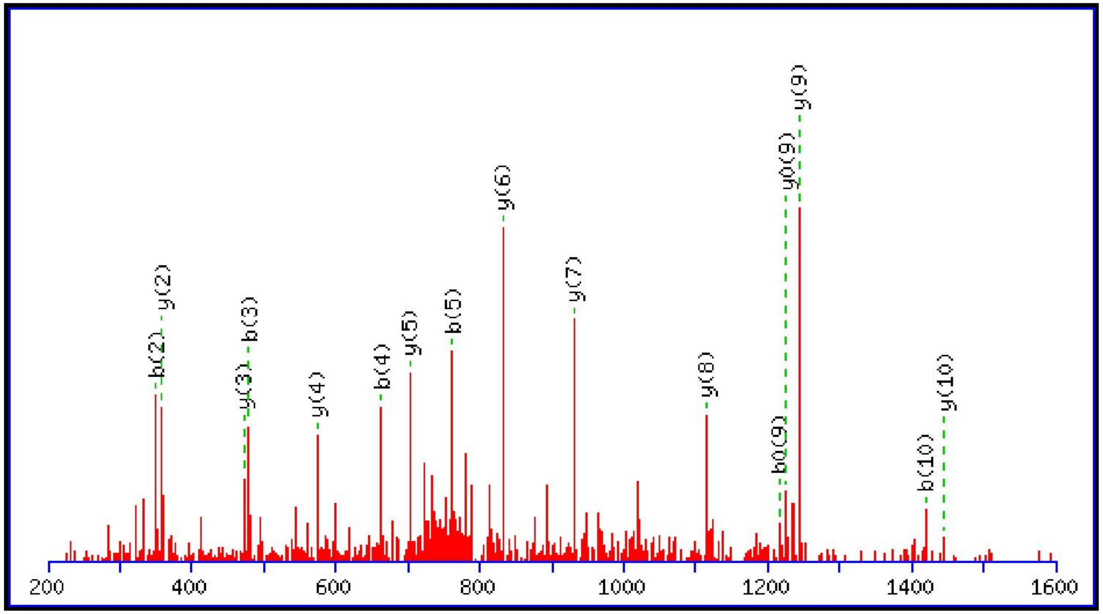
```
Monoisotopic mass of neutral peptide Mr(calc): 2215.2063
Fixed modifications: Carbamidomethyl (C) (apply to specified res
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
M3      : Label:13C(1)2H(3) (M)
K6      : Propionyl (K)
K9      : Propionyl (K)
Ions Score: 31  Expect: 0.53
Matches : 29/210 fragment ions using 72 most intense peaks   (he
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	203.1663	102.0868	186.1397	93.5735			K							20
2	***274.2034***	137.6053	257.1769	129.0921			A	2014.0546	1007.5310	1997.0281	999.0177	1996.0441	998.5257	19
3	***409.2661***	205.1367	392.2395	196.6234			M	1943.0175	972.0124	1925.9910	963.4991	1925.0070	963.0071	18
4	522.3501	261.6787	505.3236	253.1654			I	1807.9549	904.4811	1790.9283	895.9678	1789.9443	895.4758	17
5	651.3927	326.2000	634.3662	317.6867	633.3822	317.1947	E	1694.8708	847.9390	1677.8442	839.4258	1676.8602	838.9338	16
6	***835.5139***	418.2606	818.4874	409.7473	817.5033	409.2553	K	1565.8282	783.4177	1548.8016	774.9045	1547.8176	774.4125	15
7	***948.5980***	474.8026	931.5714	466.2893	930.5874	465.7973	L	1381.7070	691.3571	1364.6805	682.8439	1363.6965	682.3519	14
8	***1077.6406***	539.3239	1060.6140	530.8106	1059.6300	530.3186	E	1268.6230	634.8151	1251.5964	626.3018	1250.6124	625.8098	13
9	***1261.7617***	***631.3845***	1244.7352	622.8712	1243.7512	622.3792	K	**1139.5804**	570.2938	1122.5538	561.7805	1121.5698	561.2885	12
10	1390.8043	***695.9058***	1373.7778	687.3925	1372.7938	686.9005	E	955.4592	478.2332	938.4326	469.7200	937.4486	469.2279	11
11	***1447.8258***	724.4165	1430.7993	715.9033	1429.8152	715.4113	G	**826.4166**	413.7119	809.3900	405.1987	808.4060	404.7067	10
12	1518.8629	***759.9351***	1501.8364	751.4218	1500.8523	750.9298	A	769.3951	385.2012	752.3686	376.6879	751.3846	376.1959	9
13	***1589.9000***	***795.4537***	1572.8735	786.9404	1571.8895	786.4484	A	**698.3580**	349.6826	681.3315	341.1694	680.3474	340.6774	8
14	1646.9215	***823.9644***	1629.8949	815.4511	1628.9109	814.9591	G	**627.3209**	314.1641	610.2944	305.6508	609.3103	305.1588	7
15	1733.9535	***867.4804***	1716.9270	858.9671	1715.9430	858.4751	S	**570.2994**	285.6534	553.2729	277.1401	552.2889	276.6481	6
16	1831.0063	916.0068	1813.9797	907.4935	1812.9957	907.0015	P	**483.2674**	242.1373	466.2409	233.6241			5
17	1888.0277	944.5175	1871.0012	936.0042	1870.0172	935.5122	G	386.2146	193.6110	369.1881	185.0977			4
18	1945.0492	973.0282	1928.0227	964.5150	1927.0386	964.0230	G	329.1932	165.1002	312.1666	156.5870			3
19	2042.1020	***1021.5546***	2025.0754	1013.0414	2024.0914	1012.5493	P	272.1717	136.5895	255.1452	128.0762			2
20							R	175.1190	88.0631	158.0924	79.5498			1

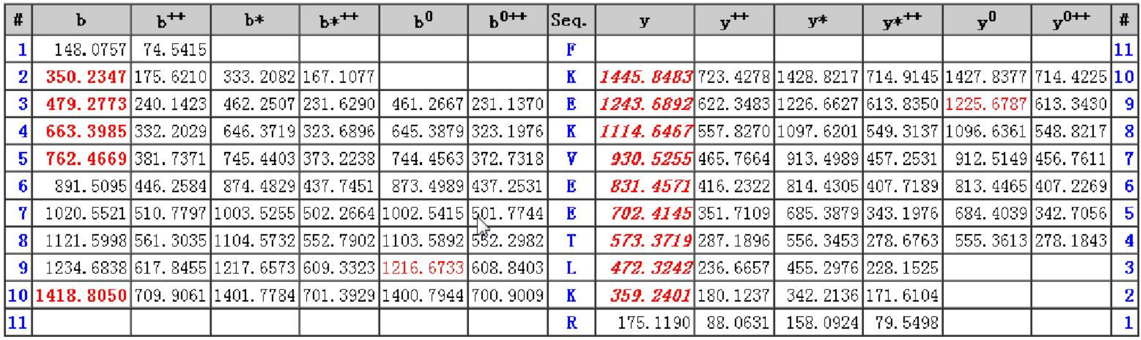
MS/MS Fragmentation of **FKEKVEETLKR**
Found in **Q9Y6V7**, Probable ATP-dependent RNA helicase DDX49 OS=Homo sapiens GN=DDX49 PE=1 SV=1

Match to Query 9979: 1591.910248 from(796.962400,2+) intensity(52408.3398)
Title: File336 Spectrum12200 scans: 13758
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1591.9094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K4 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 62 **Expect:** 0.00027
Matches : 16/108 fragment ions using 27 most intense p

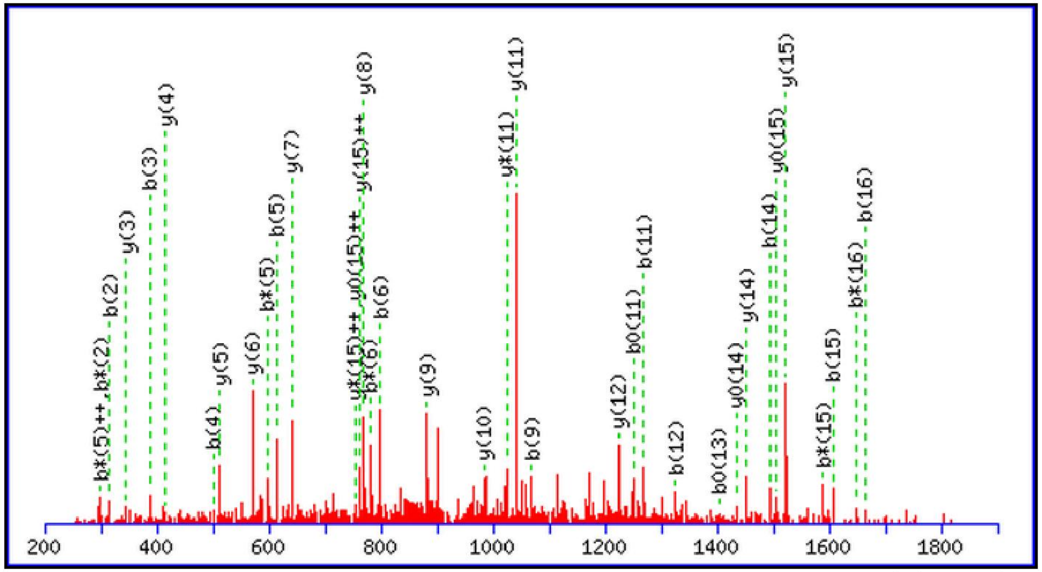


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							11
2	**350.2347**	175.6210	333.2082	167.1077			K	***1445.8483***	723.4278	1428.8217	714.9145	1427.8377	714.4225	10
3	**479.2773**	240.1423	462.2507	231.6290	461.2667	231.1370	E	***1243.6892***	622.3483	1226.6627	613.8350	1225.6787	613.3430	9
4	**663.3985**	332.2029	646.3719	323.6896	645.3879	323.1976	K	***1114.6467***	557.8270	1097.6201	549.3137	1096.6361	548.8217	8
5	**762.4669**	381.7371	745.4403	373.2238	744.4563	372.7318	V	***930.5255***	465.7664	913.4989	457.2531	912.5149	456.7611	7
6	891.5095	446.2584	874.4829	437.7451	873.4989	437.2531	E	***831.4571***	416.2322	814.4305	407.7189	813.4465	407.2269	6
7	1020.5521	510.7797	1003.5255	502.2664	1002.5415	501.7744	E	***702.4145***	351.7109	685.3879	343.1976	684.4039	342.7056	5
8	1121.5998	561.3035	1104.5732	552.7902	1103.5892	552.2982	T	***573.3719***	287.1896	556.3453	278.6763	555.3613	278.1843	4
9	1234.6838	617.8455	1217.6573	609.3323	1216.6733	608.8403	L	***472.3242***	236.6657	455.2976	228.1525			3
10	**1418.8050**	709.9061	1401.7784	701.3929	1400.7944	700.9009	K	***359.2401***	180.1237	342.2136	171.6104			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LKANLKGTLQAGPALGR**
Found in **O94761**, ATP-dependent DNA helicase Q4 OS=Homo sapiens GN=RECQL4 PE=1 SV=1

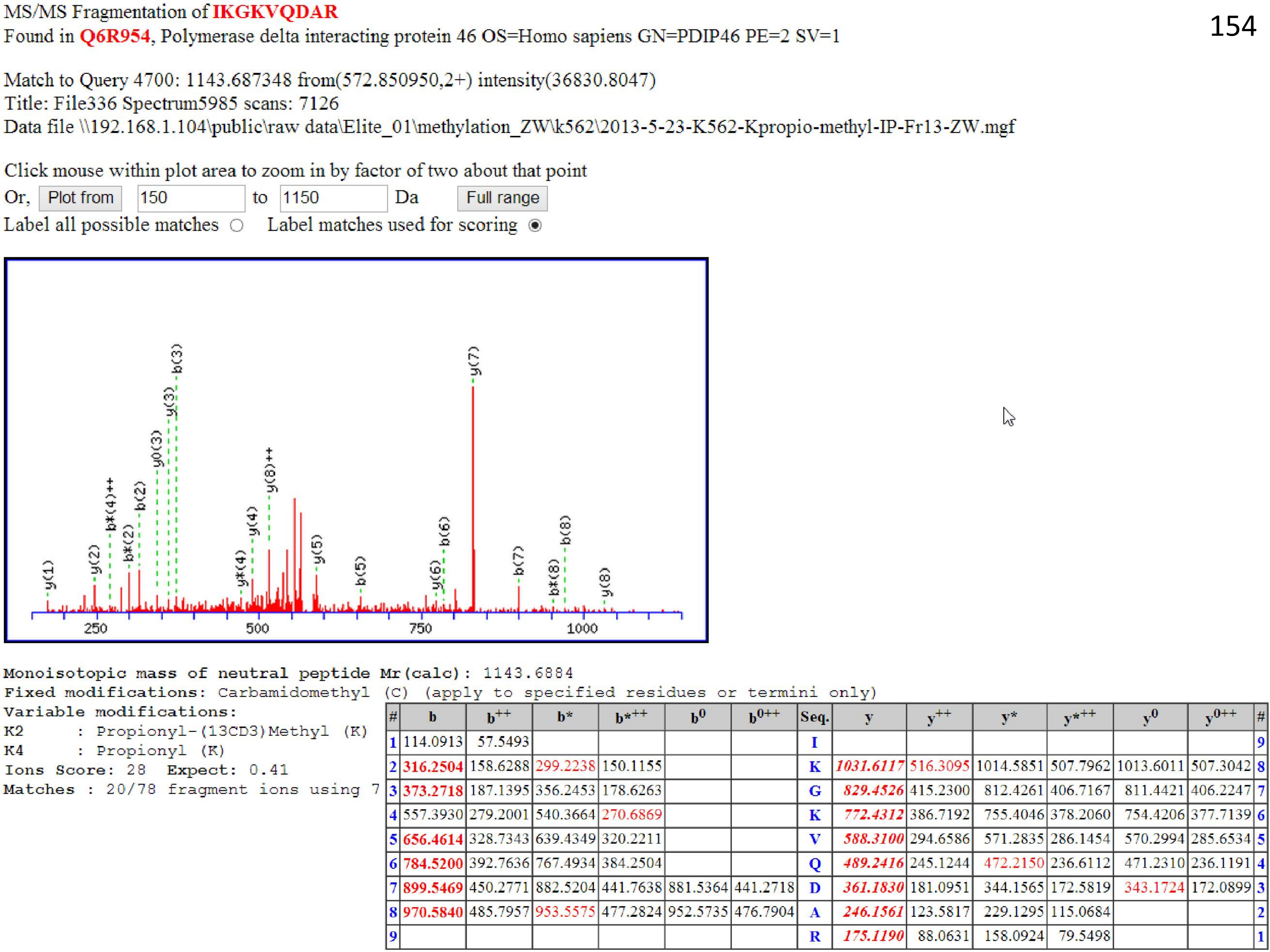
Match to Query 12792: 1837.107388 from(919.560970,2+) intensity(66936.5391)
Title: File336 Spectrum14773 scans: 16502
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr13-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1837.1058
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K6      : Propionyl (K)
Ions Score: 67  Expect: 3e-005
Matches : 37/158 fragment ions using 78 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							17
2	***316.2504***	158.6288	299.2238	150.1155			K	1725.0290	863.0181	1708.0025	854.5049	1707.0185	854.0129	16
3	***387.2875***	194.1474	370.2609	185.6341			A	***1522.8700***	761.9386	1505.8435	753.4254	1504.8594	752.9334	15
4	***501.3304***	251.1688	484.3038	242.6556			N	***1451.8329***	726.4201	1434.8063	717.9068	1433.8223	717.4148	14
5	***614.4145***	307.7109	597.3879	299.1976			L	1337.7900	669.3986	1320.7634	660.8853	1319.7794	660.3933	13
6	***798.5356***	399.7715	781.5091	391.2582			K	***1224.7059***	612.8566	1207.6793	604.3433	1206.6953	603.8513	12
7	855.5571	428.2822	838.5306	419.7689			G	***1040.5847***	520.7960	1023.5582	512.2827	1022.5742	511.7907	11
8	956.6048	478.8060	939.5782	470.2928	938.5942	469.8007	T	***983.5633***	492.2853	966.5367	483.7720	965.5527	483.2800	10
9	***1069.6888***	535.3481	1052.6623	526.8348	1051.6783	526.3428	L	***882.5156***	441.7614	865.4890	433.2482			9
10	1197.7474	599.3773	1180.7209	590.8641	1179.7369	590.3721	Q	***769.4315***	385.2194	752.4050	376.7061			8
11	***1268.7845***	634.8959	1251.7580	626.3826	1250.7740	625.8906	A	***641.3729***	321.1901	624.3464	312.6768			7
12	***1325.8060***	663.4066	1308.7795	654.8934	1307.7954	654.4014	G	***570.3358***	285.6715	553.3093	277.1583			6
13	1422.8588	711.9330	1405.8322	703.4197	1404.8482	702.9277	P	***513.3144***	257.1608	496.2878	248.6475			5
14	***1493.8959***	747.4516	1476.8693	738.9383	1475.8853	738.4463	A	***416.2616***	208.6344	399.2350	200.1212			4
15	***1606.9799***	803.9936	1589.9534	795.4803	1588.9694	794.9883	L	***345.2245***	173.1159	328.1979	164.6026			3
16	***1664.0014***	832.5043	1646.9749	823.9911	1645.9908	823.4991	G	232.1404	116.5738	215.1139	108.0606			2
17							R	175.1190	88.0631	158.0924	79.5498			1



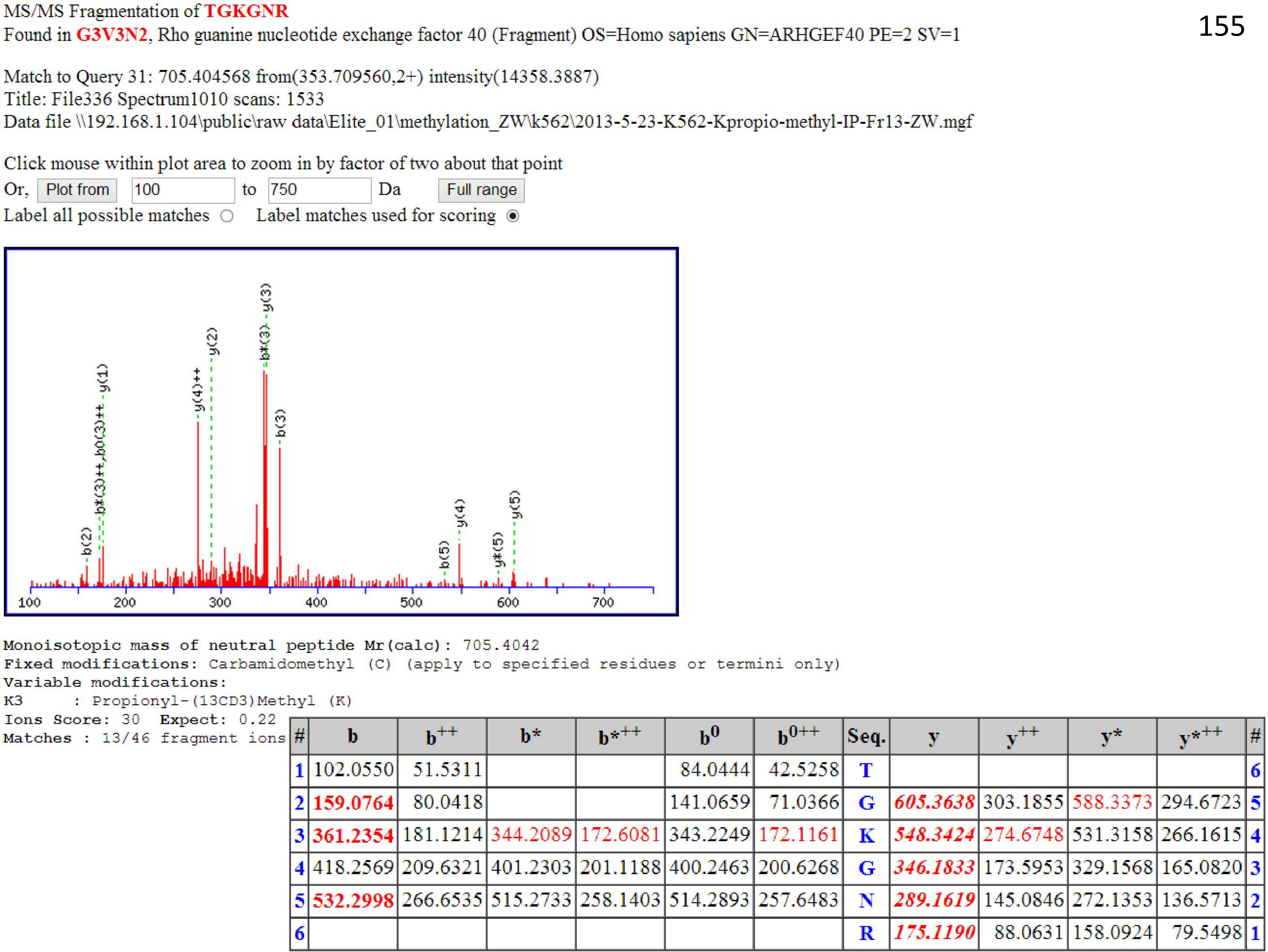
MS/MS Fragmentation of **IKGKVQDAR**
Found in **Q6R954**, Polymerase delta interacting protein 46 OS=Homo sapiens GN=PDIP46 PE=2 SV=1

Match to Query 4700: 1143.687348 from(572.850950,2+) intensity(36830.8047)
Title: File336 Spectrum5985 scans: 7126
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr13-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1143.6884
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K4      : Propionyl (K)
Ions Score: 28  Expect: 0.41
Matches : 20/78 fragment ions using 7
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					I							9
2	**316.2504**	158.6288	299.2238	150.1155			K	***1031.6117***	516.3095	1014.5851	507.7962	1013.6011	507.3042	8
3	**373.2718**	187.1395	356.2453	178.6263			G	***829.4526***	415.2300	812.4261	406.7167	811.4421	406.2247	7
4	557.3930	279.2001	540.3664	270.6869			K	***772.4312***	386.7192	755.4046	378.2060	754.4206	377.7139	6
5	**656.4614**	328.7343	639.4349	320.2211			V	***588.3100***	294.6586	571.2835	286.1454	570.2994	285.6534	5
6	**784.5200**	392.7636	767.4934	384.2504			Q	***489.2416***	245.1244	472.2150	236.6112	471.2310	236.1191	4
7	**899.5469**	450.2771	882.5204	441.7638	881.5364	441.2718	D	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
8	**970.5840**	485.7957	953.5575	477.2824	952.5735	476.7904	A	***246.1561***	123.5817	229.1295	115.0684			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



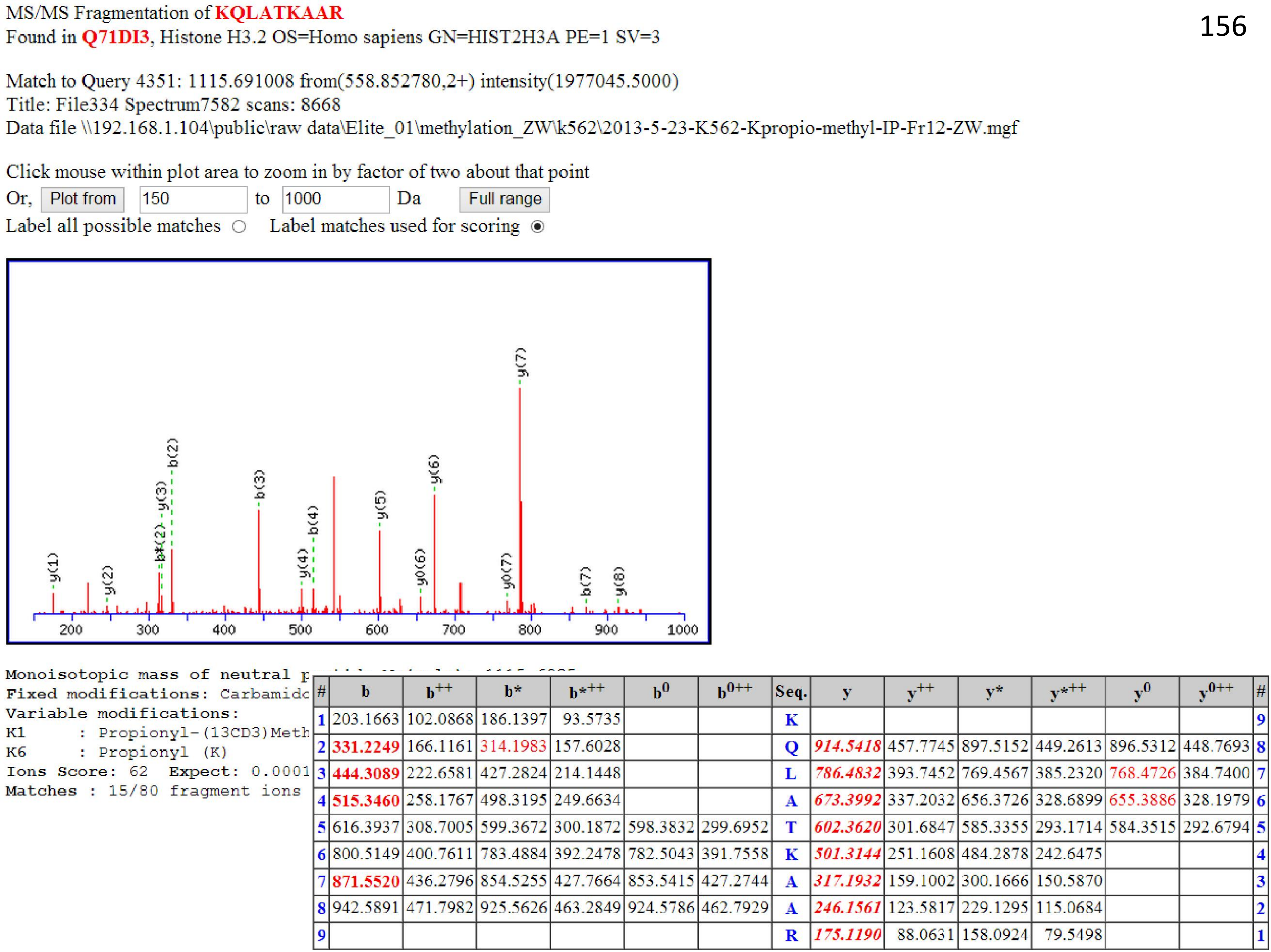
MS/MS Fragmentation of **TGKGNR**
Found in **G3V3N2**, Rho guanine nucleotide exchange factor 40 (Fragment) OS=Homo sapiens GN=ARHGEF40 PE=2 SV=1

Match to Query 31: 705.404568 from(353.709560,2+) intensity(14358.3887)
Title: File336 Spectrum1010 scans: 1533
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 705.4042
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3      : Propionyl-(13CD3)Methyl (K)
Ions Score: 30  Expect: 0.22
Matches : 13/46 fragment ions
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					6
2	**159.0764**	80.0418			141.0659	71.0366	G	***605.3638***	303.1855	588.3373	294.6723	5
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	K	***548.3424***	274.6748	531.3158	266.1615	4
4	418.2569	209.6321	401.2303	201.1188	400.2463	200.6268	G	***346.1833***	173.5953	329.1568	165.0820	3
5	**532.2998**	266.6535	515.2733	258.1403	514.2893	257.6483	N	***289.1619***	145.0846	272.1353	136.5713	2
6							R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **KQLATKAAR**
Found in **Q71DI3**, Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3

Match to Query 4351: 1115.691008 from(558.852780,2+) intensity(1977045.5000)
Title: File334 Spectrum7582 scans: 8668
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

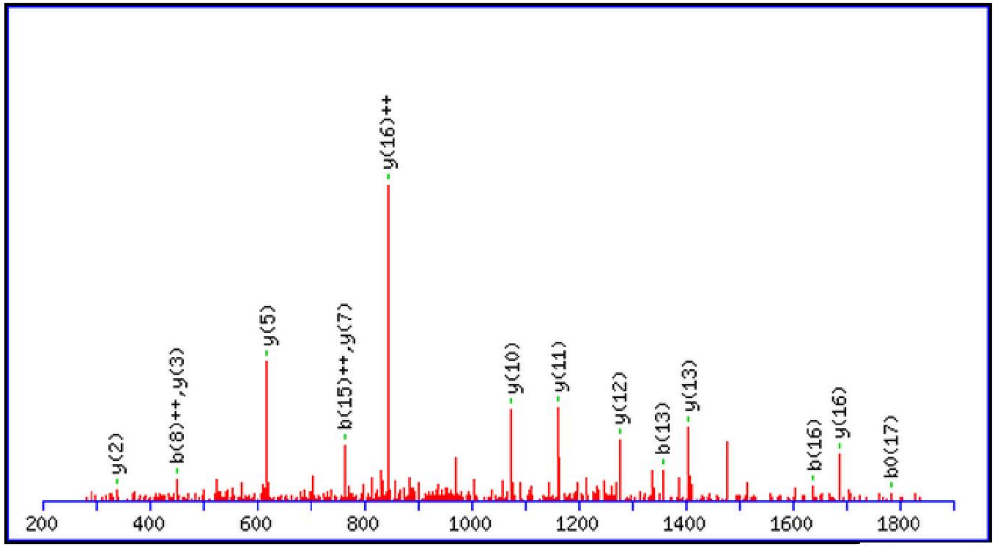
```
Monoisotopic mass of neutral p
Fixed modifications: Carbamidc
Variable modifications:
K1      : Propionyl-(13CD3)Meth
K6      : Propionyl (K)
Ions Score: 62  Expect: 0.0001
Matches : 15/80 fragment ions
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**331.2249**	166.1161	314.1983	157.6028			Q	***914.5418***	457.7745	897.5152	449.2613	896.5312	448.7693	8
3	**444.3089**	222.6581	427.2824	214.1448			L	***786.4832***	393.7452	769.4567	385.2320	768.4726	384.7400	7
4	**515.3460**	258.1767	498.3195	249.6634			A	***673.3992***	337.2032	656.3726	328.6899	655.3886	328.1979	6
5	616.3937	308.7005	599.3672	300.1872	598.3832	299.6952	T	***602.3620***	301.6847	585.3355	293.1714	584.3515	292.6794	5
6	800.5149	400.7611	783.4884	392.2478	782.5043	391.7558	K	***501.3144***	251.1608	484.2878	242.6475			4
7	**871.5520**	436.2796	854.5255	427.7664	853.5415	427.2744	A	***317.1932***	159.1002	300.1666	150.5870			3
8	942.5891	471.7982	925.5626	463.2849	924.5786	462.7929	A	***246.1561***	123.5817	229.1295	115.0684			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KSPLAQDSPSQGSPALYR**
Found in **E9PEI0**, Cell division cycle-associated protein 2 OS=Homo sapiens GN=CDCA2 PE=2 SV=1

Match to Query 14607: 1975.026708 from(988.520630,2+) intensity(55254.6367)
Title: File334 Spectrum10677 scans: 11969
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.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 ●



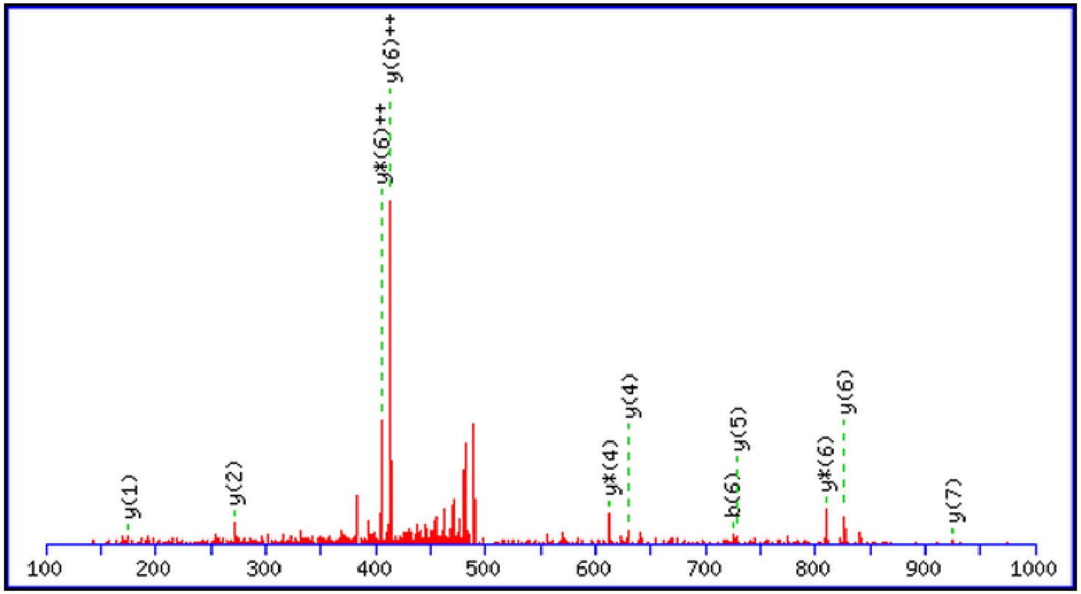
```
Monoisotopic mass of neutral peptide Mr(calc): 1975.0283
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K1       : Propionyl-(13CD3)Methyl (K)
Ions Score: 74  Expect: 2.5e-005
Matches : 15/192 fragment ions using 16 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							18
2	290.1983	145.6028	273.1718	137.0895	272.1878	136.5975	S	1773.8766	887.4419	1756.8501	878.9287	1755.8660	878.4367	17
3	387.2511	194.1292	370.2245	185.6159	369.2405	185.1239	P	***1686.8446***	843.9259	1669.8180	835.4127	1668.8340	834.9206	16
4	500.3351	250.6712	483.3086	242.1579	482.3246	241.6659	L	1589.7918	795.3995	1572.7653	786.8863	1571.7812	786.3943	15
5	571.3723	286.1898	554.3457	277.6765	553.3617	277.1845	A	1476.7077	738.8575	1459.6812	730.3442	1458.6972	729.8522	14
6	699.4308	350.2191	682.4043	341.7058	681.4203	341.2138	Q	***1405.6706***	703.3390	1388.6441	694.8257	1387.6601	694.3337	13
7	814.4578	407.7325	797.4312	399.2193	796.4472	398.7272	D	***1277.6121***	639.3097	1260.5855	630.7964	1259.6015	630.3044	12
8	901.4898	**451.2485**	884.4633	442.7353	883.4792	442.2433	S	***1162.5851***	581.7962	1145.5586	573.2829	1144.5745	572.7909	11
9	998.5426	499.7749	981.5160	491.2616	980.5320	490.7696	P	***1075.5531***	538.2802	1058.5265	529.7669	1057.5425	529.2749	10
10	1085.5746	543.2909	1068.5481	534.7777	1067.5640	534.2857	S	978.5003	489.7538	961.4738	481.2405	960.4898	480.7485	9
11	1213.6332	607.3202	1196.6066	598.8070	1195.6226	598.3149	Q	891.4683	446.2378	874.4417	437.7245	873.4577	437.2325	8
12	1270.6546	635.8310	1253.6281	627.3177	1252.6441	626.8257	G	***763.4097***	382.2085	746.3832	373.6952	745.3991	373.2032	7
13	**1357.6867**	679.3470	1340.6601	670.8337	1339.6761	670.3417	S	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
14	1454.7394	727.8734	1437.7129	719.3601	1436.7289	718.8681	P	***619.3562***	310.1817	602.3297	301.6685			5
15	1525.7765	**763.3919**	1508.7500	754.8786	1507.7660	754.3866	A	522.3035	261.6554	505.2769	253.1421			4
16	**1638.8606**	819.9339	1621.8341	811.4207	1620.8500	810.9287	L	***451.2663***	226.1368	434.2398	217.6235			3
17	1801.9239	901.4656	1784.8974	892.9523	1783.9134	892.4603	Y	***338.1823***	169.5948	321.1557	161.0815			2
18							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AVPVKRPR**
Found in **Q5QPL9**, RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1

Match to Query 2907: 995.653608 from(498.834080,2+) intensity(53707.6211)
Title: File334 Spectrum4162 scans: 4987
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



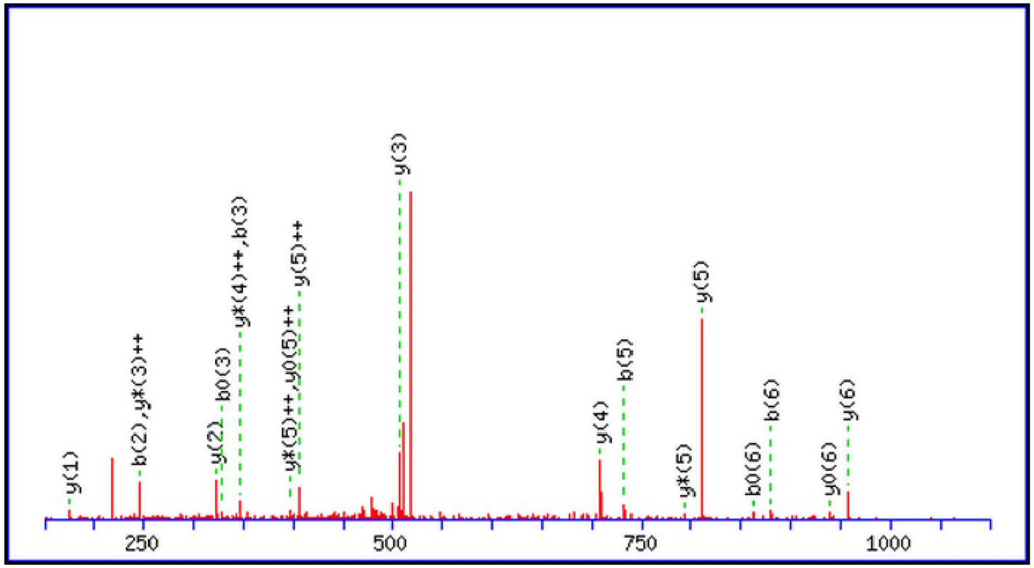
```
Monoisotopic mass of neutral peptide Mr(calc):
Fixed modifications: Carbamidomethyl (C) (appl
Variable modifications:
K5       : Propionyl-(13CD3)Methyl (K)
Ions Score: 40   Expect: 0.0079
Matches : 11/48 fragment ions using 17 most in
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.0444	36.5258			A					8
2	171.1128	86.0600			V	***925.6214***	463.3144	908.5949	454.8011	7
3	268.1656	134.5864			P	***826.5530***	413.7801	809.5265	405.2669	6
4	367.2340	184.1206			V	***729.5003***	365.2538	712.4737	356.7405	5
5	569.3930	285.2001	552.3664	276.6869	K	***630.4318***	315.7196	613.4053	307.2063	4
6	725.4941	363.2507	708.4676	354.7374	R	428.2728	214.6401	411.2463	206.1268	3
7	822.5469	411.7771	805.5203	403.2638	P	***272.1717***	136.5895	255.1452	128.0762	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **PFTKKFR**
Found in **M0QXA7**, Protein Wiz OS=Homo sapiens GN=WIZ PE=4 SV=1

Match to Query 3620: 1052.628028 from(527.321290,2+) intensity(202455.3750)
Title: File334 Spectrum13253 scans: 14717
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



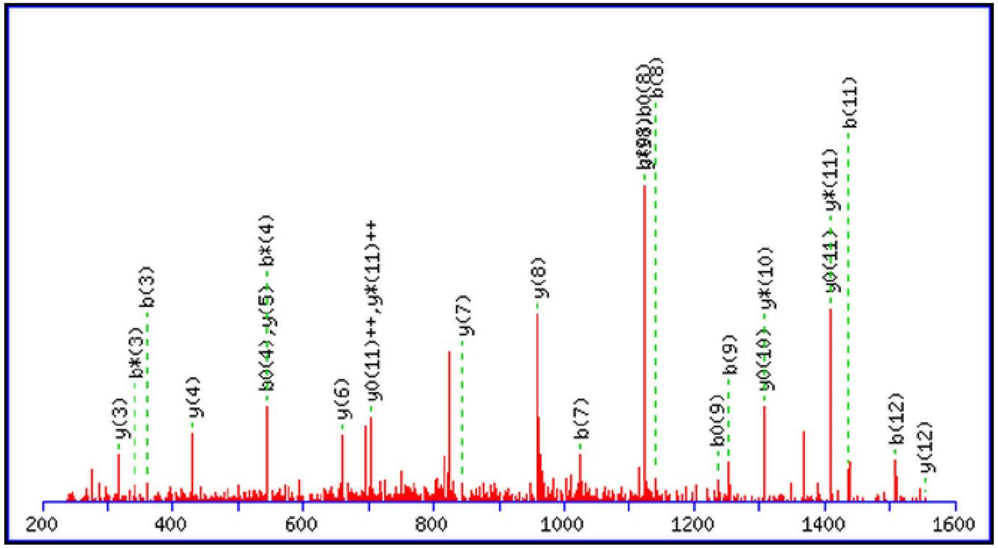
```
Monoisotopic mass of neutral peptide Mr(calc): 1052.6291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4      : Propionyl-(13CD3)Methyl (K)
K5      : Propionyl (K)
Ions Score: 42  Expect: 0.
Matches : 19/54 fragment i
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	98.0600	49.5337					P							7
2	**245.1285**	123.0679					F	***956.5837***	478.7955	939.5571	470.2822	938.5731	469.7902	6
3	**346.1761**	173.5917			328.1656	164.5864	T	***809.5152***	405.2613	792.4887	396.7480	791.5047	396.2560	5
4	548.3351	274.6712	531.3086	266.1579	530.3246	265.6659	K	***708.4676***	354.7374	691.4410	346.2241			4
5	**732.4563**	366.7318	715.4298	358.2185	714.4458	357.7265	K	***506.3085***	253.6579	489.2820	245.1446			3
6	**879.5247**	440.2660	862.4982	431.7527	861.5142	431.2607	F	***322.1874***	161.5973	305.1608	153.0840			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **EQTKYDWDLLAAR**
Found in **K7EJ74**, 116 kDa U5 small nuclear ribonucleoprotein component (Fragment) OS=Homo sapiens GN=EFTUD2 PE=4 SV=1

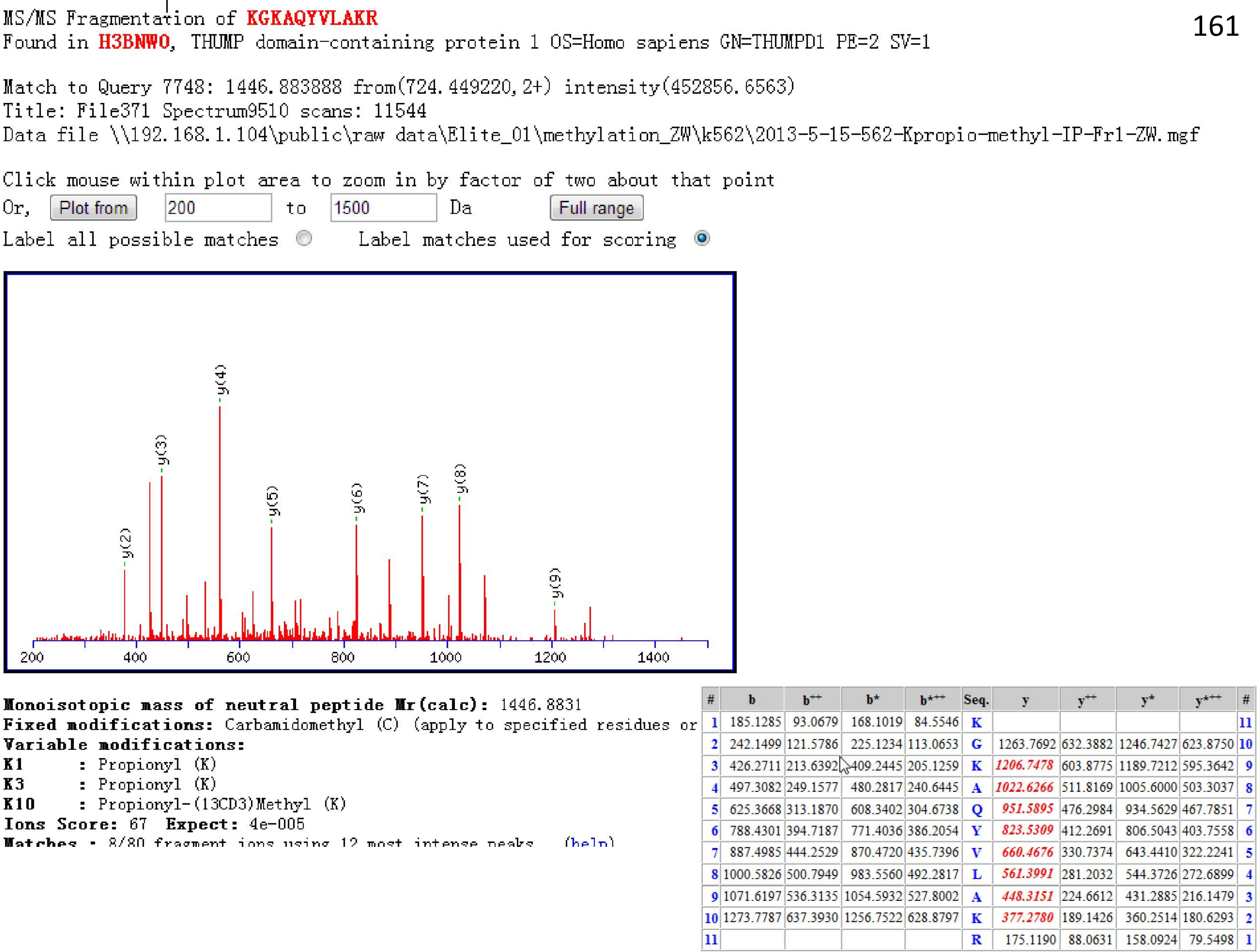
Match to Query 11999: 1681.849088 from(841.931820,2+) intensity(221610.8125)
Title: File334 Spectrum18414 scans: 20231
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1681.8584
Fixed modifications: Carbamidomethyl (C) (apply
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 51 **Expect:** 0.0036
Matches : 26/132 fragment ions using 42 most i

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	***1553.8231***	777.4152	1536.7966	768.9019	1535.8125	768.4099	12
3	***359.1561***	180.0817	342.1296	171.5684	341.1456	171.0764	T	1425.7645	713.3859	1408.7380	704.8726	1407.7540	704.3806	11
4	561.3151	281.1612	544.2886	272.6479	543.3046	272.1559	K	1324.7168	662.8621	1307.6903	654.3488	1306.7063	653.8568	10
5	724.3785	362.6929	707.3519	354.1796	706.3679	353.6876	Y	***1122.5578***	561.7826	1105.5313	553.2693	1104.5473	552.7773	9
6	839.4054	420.2063	822.3789	411.6931	821.3948	411.2011	D	***959.4945***	480.2509	942.4680	471.7376	941.4839	471.2456	8
7	***1025.4847***	513.2460	1008.4582	504.7327	1007.4742	504.2407	W	***844.4676***	422.7374	827.4410	414.2241	826.4570	413.7321	7
8	***1140.5117***	570.7595	1123.4851	562.2462	1122.5011	561.7542	D	***658.3883***	329.6978	641.3617	321.1845	640.3777	320.6925	6
9	***1253.5957***	627.3015	1236.5692	618.7882	1235.5852	618.2962	L	***543.3613***	272.1843	526.3348	263.6710			5
10	1366.6798	683.8435	1349.6532	675.3303	1348.6692	674.8383	L	***430.2772***	215.6423	413.2507	207.1290			4
11	***1437.7169***	719.3621	1420.6904	710.8488	1419.7063	710.3568	A	***317.1932***	159.1002	300.1666	150.5870			3
12	***1508.7540***	754.8806	1491.7275	746.3674	1490.7435	745.8754	A	246.1561	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KGKAQYVLAKR**

Found in **H3BNW0**, THUMP domain-containing protein 1 OS=Homo sapiens GN=THUMPD1 PE=2 SV=1

Match to Query 7748: 1446.883888 from(724.449220,2+) intensity(452856.6563)

Title: File371 Spectrum9510 scans: 11544

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr1-ZW.mgf

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

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1446.8831

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

Variable modifications:

K1 : Propionyl (K)

K3 : Propionyl (K)

K10 : Propionyl-(13CD3)Methyl (K)

Ions Score: 67 **Expect:** 4e-005

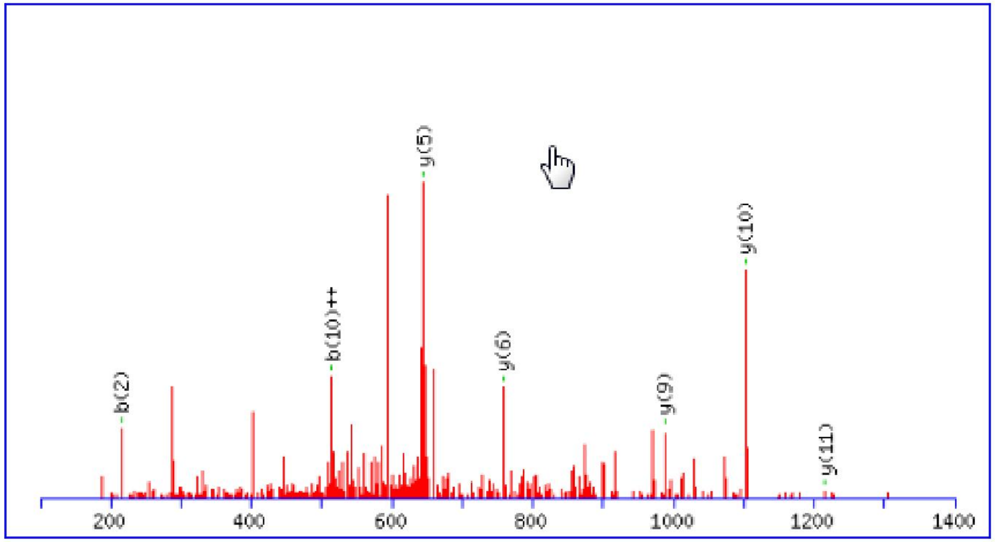
Matches : 8/80 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	185.1285	93.0679	168.1019	84.5546	K					11
2	242.1499	121.5786	225.1234	113.0653	G	1263.7692	632.3882	1246.7427	623.8750	10
3	426.2711	213.6392	409.2445	205.1259	K	***1206.7478***	603.8775	1189.7212	595.3642	9
4	497.3082	249.1577	480.2817	240.6445	A	***1022.6266***	511.8169	1005.6000	503.3037	8
5	625.3668	313.1870	608.3402	304.6738	Q	***951.5895***	476.2984	934.5629	467.7851	7
6	788.4301	394.7187	771.4036	386.2054	Y	***823.5309***	412.2691	806.5043	403.7558	6
7	887.4985	444.2529	870.4720	435.7396	V	***660.4676***	330.7374	643.4410	322.2241	5
8	1000.5826	500.7949	983.5560	492.2817	L	***561.3991***	281.2032	544.3726	272.6899	4
9	1071.6197	536.3135	1054.5932	527.8002	A	***448.3151***	224.6612	431.2885	216.1479	3
10	1273.7787	637.3930	1256.7522	628.8797	K	***377.2780***	189.1426	360.2514	180.6293	2
11					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **TLDTGAIPGKNR**
Found in **Q96QE3**, ATPase family AAA domain-containing protein 5 OS=Homo sapiens GN=ATAD5 PE=1 SV=4

Match to Query 6217: 1316.743868 from(659.379210,2+) intensity(37110.5195)
Title: File371 Spectrum13424 scans: 16061
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr1-ZW.mgf

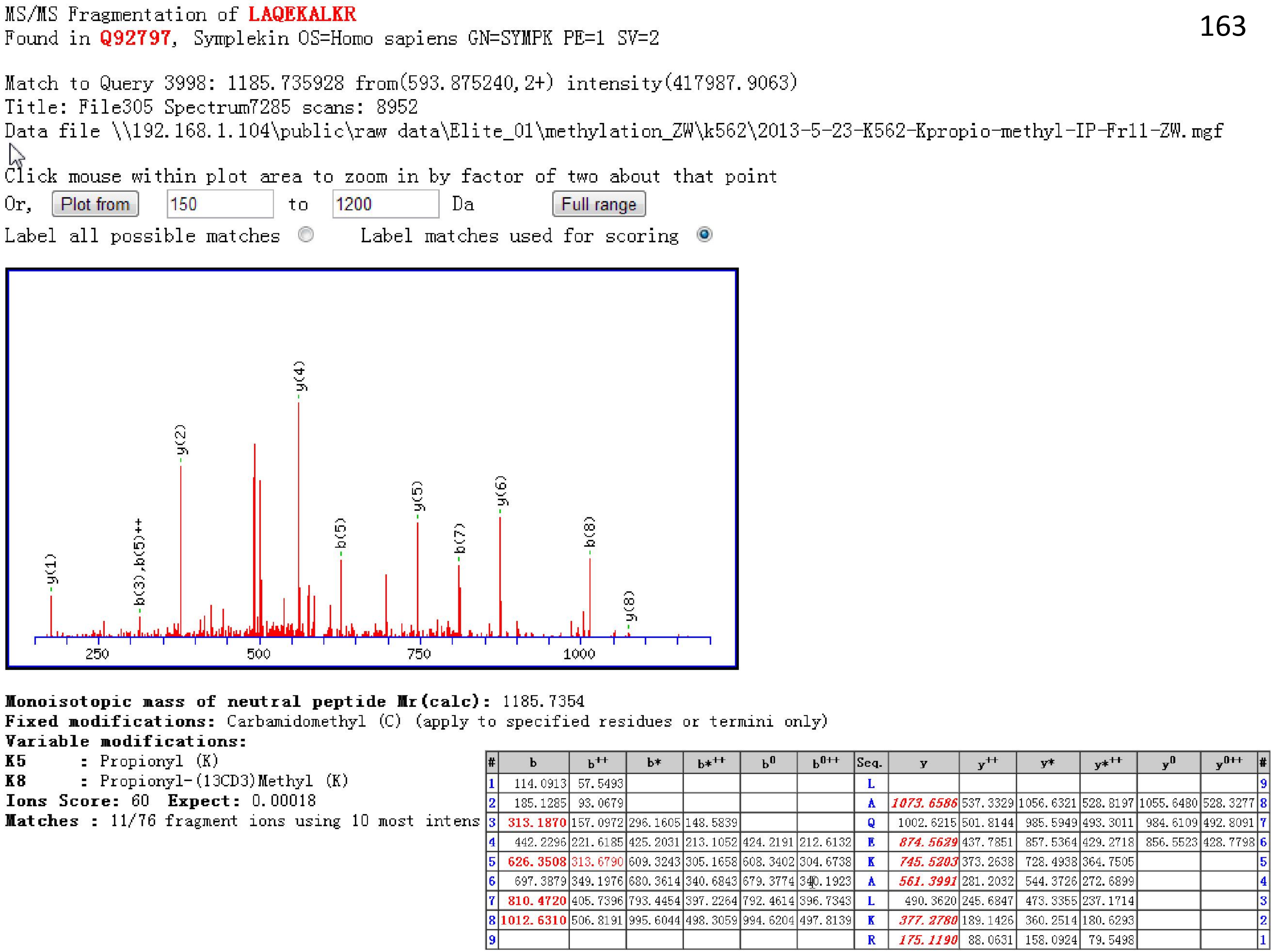
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1315.7368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K10     : Propionyl-(13CD3)Methyl (K)
Ions Score: 22  Expect: 2.7
Matches : 7/98 fragment ions using 12 most intense peaks
```

(he

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	215.1390	108.0731			197.1285	99.0679	L	***1215.6964***	608.3519	1198.6699	599.8386	1197.6859	599.3466	11
3	330.1660	165.5866			312.1554	156.5813	D	***1102.6124***	551.8098	1085.5858	543.2966	1084.6018	542.8045	10
4	431.2136	216.1105			413.2031	207.1052	T	***987.5854***	494.2964	970.5589	485.7831	969.5749	485.2911	9
5	488.2351	244.6212			470.2245	235.6159	G	886.5378	443.7725	869.5112	435.2592			8
6	559.2722	280.1397			541.2617	271.1345	A	829.5163	415.2618	812.4897	406.7485			7
7	672.3563	336.6818			654.3457	327.6765	I	***758.4792***	379.7432	741.4526	371.2300			6
8	769.4090	385.2082			751.3985	376.2029	P	***645.3951***	323.2012	628.3686	314.6879			5
9	826.4305	413.7189			808.4199	404.7136	G	548.3424	274.6748	531.3158	266.1615			4
10	1028.5895	514.7984	1011.5630	506.2851	1010.5790	505.7931	K	491.3209	246.1641	474.2943	237.6508			3
11	1142.6325	571.8199	1125.6059	563.3066	1124.6219	562.8146	N	289.1619	145.0846	272.1353	136.5713			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LAQEKALKR**
Found in **Q92797**, Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2

Match to Query 3998: 1185.735928 from(593.875240,2+) intensity(417987.9063)
Title: File305 Spectrum7285 scans: 8952
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

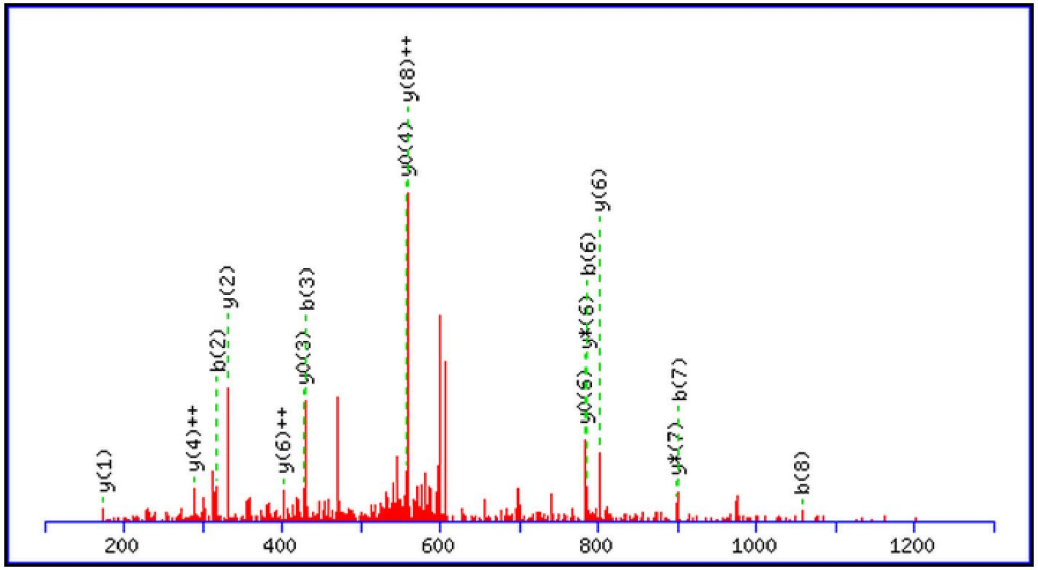
Monoisotopic mass of neutral peptide Mr(calc): 1185.7354
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl (K)
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 60 **Expect:** 0.00018
Matches : 11/76 fragment ions using 10 most intens

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							9
2	185.1285	93.0679					A	***1073.6586***	537.3329	1056.6321	528.8197	1055.6480	528.3277	8
3	**313.1870**	157.0972	296.1605	148.5839			Q	1002.6215	501.8144	985.5949	493.3011	984.6109	492.8091	7
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	E	***874.5629***	437.7851	857.5364	429.2718	856.5523	428.7798	6
5	**626.3508**	313.6790	609.3243	305.1658	608.3402	304.6738	K	***745.5203***	373.2638	728.4938	364.7505			5
6	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	A	***561.3991***	281.2032	544.3726	272.6899			4
7	**810.4720**	405.7396	793.4454	397.2264	792.4614	396.7343	L	490.3620	245.6847	473.3355	237.1714			3
8	**1012.6310**	506.8191	995.6044	498.3059	994.6204	497.8139	K	***377.2780***	189.1426	360.2514	180.6293			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **DKIPEEDRR**
Found in **P17066**, Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2

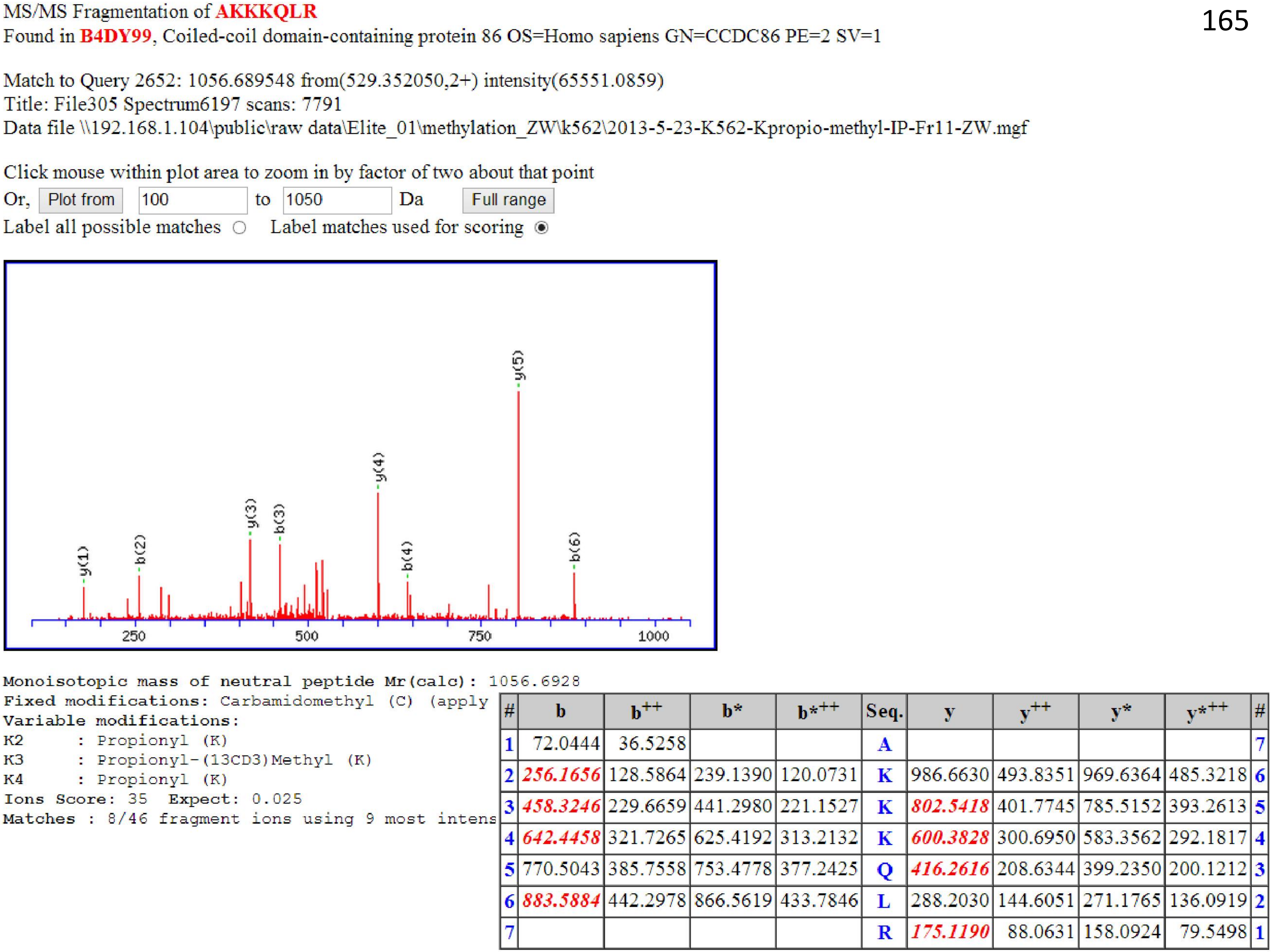
Match to Query 4381: 1230.647188 from(616.330870,2+) intensity(56340.2852)
Title: File305 Spectrum3589 scans: 4953
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr11-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1230.6477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (F
Ions Score: 21  Expect: 3.2
Matches : 16/90 fragment ions using
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							9
2	***318.1932***	159.6003	301.1667	151.0870	300.1827	150.5950	K	1116.6280	558.8177	1099.6015	550.3044	1098.6175	549.8124	8
3	***431.2773***	216.1423	414.2507	207.6290	413.2667	207.1370	I	914.4690	457.7381	897.4425	449.2249	896.4585	448.7329	7
4	528.3301	264.6687	511.3035	256.1554	510.3195	255.6634	P	**801.3850**	401.1961	784.3584	392.6828	783.3744	392.1908	6
5	657.3727	329.1900	640.3461	320.6767	639.3621	320.1847	E	704.3322	352.6697	687.3056	344.1565	686.3216	343.6645	5
6	***786.4152***	393.7113	769.3887	385.1980	768.4047	384.7060	E	575.2896	288.1484	558.2630	279.6352	557.2790	279.1432	4
7	***901.4422***	451.2247	884.4156	442.7115	883.4316	442.2195	D	446.2470	223.6271	429.2205	215.1139	428.2364	214.6219	3
8	***1057.5433***	529.2753	1040.5168	520.7620	1039.5327	520.2700	R	**331.2201**	166.1137	314.1935	157.6004			2
9							R	**175.1190**	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKKKQLR**
Found in **B4DY99**, Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=2 SV=1

Match to Query 2652: 1056.689548 from(529.352050,2+) intensity(65551.0859)
Title: File305 Spectrum6197 scans: 7791
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

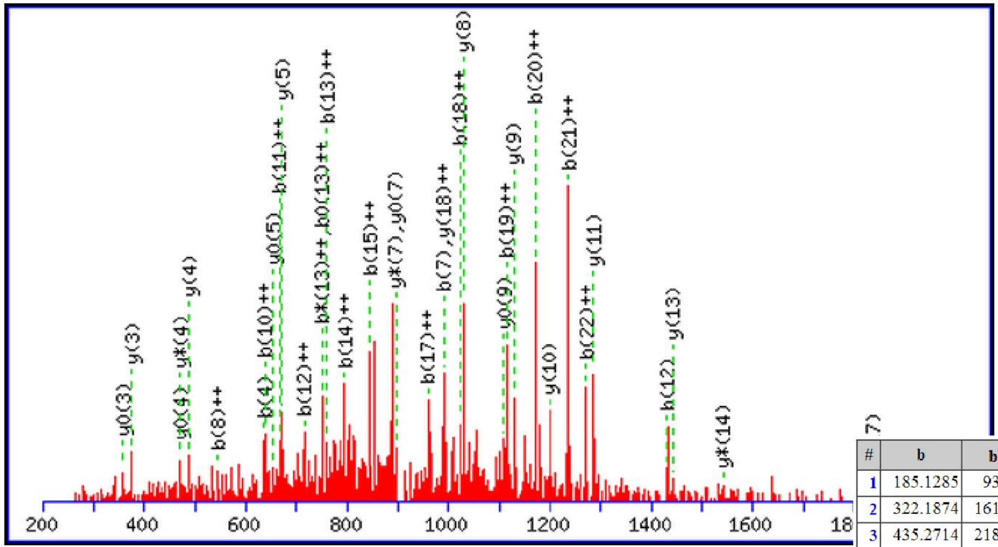
```
Monoisotopic mass of neutral peptide Mr(calc): 1056.6928
Fixed modifications: Carbamidomethyl (C) (apply
Variable modifications:
K2      : Propionyl (K)
K3      : Propionyl-(13CD3)Methyl (K)
K4      : Propionyl (K)
Ions Score: 35  Expect: 0.025
Matches : 8/46 fragment ions using 9 most intens
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	72.0444	36.5258			A					7
2	*256.1656*	128.5864	239.1390	120.0731	K	986.6630	493.8351	969.6364	485.3218	6
3	*458.3246*	229.6659	441.2980	221.1527	K	*802.5418*	401.7745	785.5152	393.2613	5
4	*642.4458*	321.7265	625.4192	313.2132	K	*600.3828*	300.6950	583.3562	292.1817	4
5	770.5043	385.7558	753.4778	377.2425	Q	*416.2616*	208.6344	399.2350	200.1212	3
6	*883.5884*	442.2978	866.5619	433.7846	L	288.2030	144.6051	271.1765	136.0919	2
7					R	*175.1190*	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KHLKPEQPADGVSAVDLEKLEAR**
Found in **Q96T58**, Msx2-interacting protein OS=Homo sapiens GN=SPEN PE=1 SV=1

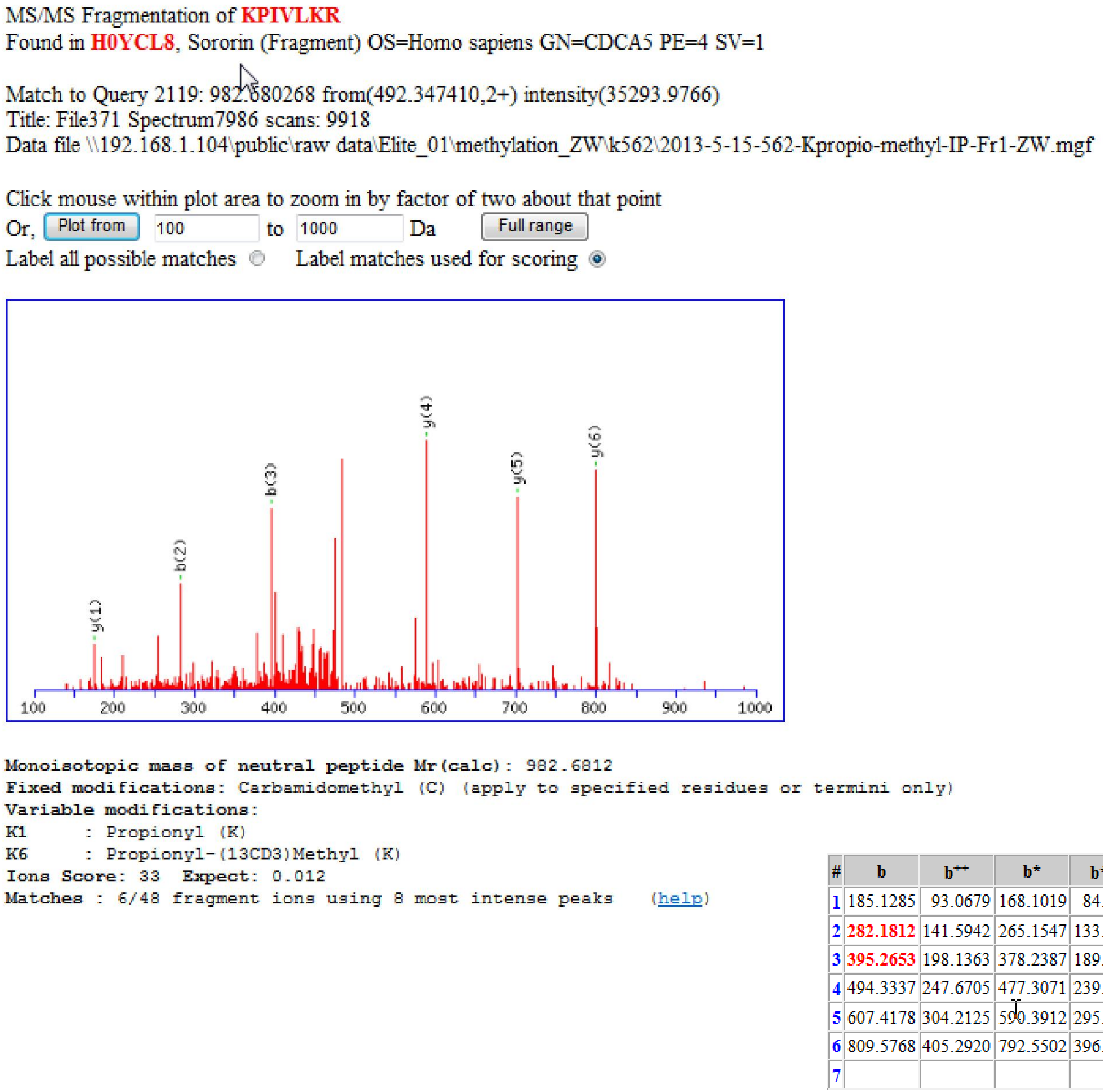
Match to Query 19077: 2715.470922 from(906.164250,3+) intensity(55584.5977)
Title: File305 Spectrum14427 scans: 16570
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr11-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2715.4715
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K1      : Propionyl (K)
K4      : Propionyl-(13CD3)Methyl (K)
K19     : Propionyl (K)
Ions Score: 45  Expect: 0.021
Matches : 36/250 fragment ions using 85 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							23
2	322.1874	161.5973	305.1608	153.0840			H	2532.3577	1266.6825	2515.3311	1258.1692	2514.3471	1257.6772	22
3	435.2714	218.1394	418.2449	209.6261			L	2395.2988	1198.1530	2378.2722	1189.6397	2377.2882	1189.1477	21
4	637.4304	319.2189	620.4039	310.7056			K	2282.2147	1141.6110	2265.1882	1133.0977	2264.2041	1132.6057	20
5	734.4832	367.7452	717.4567	359.2320			P	2080.0557	1040.5315	2063.0291	1032.0182	2062.0451	1031.5262	19
6	863.5258	432.2665	846.4993	423.7533	845.5152	423.2613	E	1983.0029	992.0051	1965.9764	983.4918	1964.9924	982.9998	18
7	991.5844	496.2958	974.5578	487.7826	973.5738	487.2905	Q	1853.9603	927.4838	1836.9338	918.9705	1835.9498	918.4785	17
8	1088.6371	***544.8222***	1071.6106	536.3089	1070.6266	535.8169	P	1725.9018	863.4545	1708.8752	854.9412	1707.8912	854.4492	16
9	1159.6743	580.3408	1142.6477	571.8275	1141.6637	571.3355	A	1628.8490	814.9281	1611.8224	806.4149	1610.8384	805.9229	15
10	1274.7012	***637.8542***	1257.6747	629.3410	1256.6906	628.8490	D	1557.8119	779.4096	1540.7853	770.8963	1539.8013	770.4043	14
11	1331.7227	***666.3650***	1314.6961	657.8517	1313.7121	657.3597	G	**1442.7849**	721.8961	1425.7584	713.3828	1424.7744	712.8908	13
12	1430.7911	***715.8992***	1413.7645	707.3859	1412.7805	706.8939	V	1385.7635	693.3854	1368.7369	684.8721	1367.7529	684.3801	12
13	1517.8231	***759.4152***	1500.7966	750.9019	1499.8125	750.4099	S	**1286.6951**	643.8512	1269.6685	635.3379	1268.6845	634.8459	11
14	1588.8602	***794.9337***	1571.8337	786.4205	1570.8497	785.9285	A	**1199.6630**	600.3352	1182.6365	591.8219	1181.6525	591.3299	10
15	1687.9286	***844.4680***	1670.9021	835.9547	1669.9181	835.4627	V	**1128.6259**	564.8166	1111.5994	556.3033	1110.6154	555.8113	9
16	1802.9556	901.9814	1785.9290	893.4682	1784.9450	892.9761	D	**1029.5575**	515.2824	1012.5310	506.7691	1011.5469	506.2771	8
17	1916.0396	***958.5235***	1899.0131	950.0102	1898.0291	949.5182	L	914.5306	457.7689	897.5040	449.2556	896.5200	448.7636	7
18	2045.0822	***1023.0448***	2028.0557	1014.5315	2027.0717	1014.0395	E	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	6
19	2229.2034	***1115.1053***	2212.1769	1106.5921	2211.1928	1106.1001	K	**672.4039**	336.7056	655.3774	328.1923	654.3933	327.7003	5
20	2342.2875	***1171.6474***	2325.2609	1163.1341	2324.2769	1162.6421	L	**488.2827**	244.6450	471.2562	236.1317	470.2722	235.6397	4
21	2471.3301	***1236.1687***	2454.3035	1227.6554	2453.3195	1227.1634	E	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	3
22	2542.3672	***1271.6872***	2525.3406	1263.1740	2524.3566	1262.6819	A	246.1561	123.5817	229.1295	115.0684			2
23							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KPIVLKR**

Found in **H0YCL8**, Sororin (Fragment) OS=Homo sapiens GN=CDCA5 PE=4 SV=1

Match to Query 2119: 982.680268 from(492.347410,2+) intensity(35293.9766)

Title: File371 Spectrum7986 scans: 9918

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-15-562-Kpropio-methyl-IP-Fr1-ZW.mgf

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

Or, Plot from 100 to 1000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 982.6812

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

Variable modifications:

K1 : Propionyl (K)

K6 : Propionyl-(13CD3)Methyl (K)

Ions Score: 33 **Expect:** 0.012

Matches : 6/48 fragment ions using 8 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	185.1285	93.0679	168.1019	84.5546	K					7
2	**282.1812**	141.5942	265.1547	133.0810	P	***799.5673***	400.2873	782.5407	391.7740	6
3	**395.2653**	198.1363	378.2387	189.6230	I	***702.5145***	351.7609	685.4880	343.2476	5
4	494.3337	247.6705	477.3071	239.1572	V	***589.4304***	295.2189	572.4039	286.7056	4
5	607.4178	304.2125	590.3912	295.6992	L	490.3620	245.6847	473.3355	237.1714	3
6	809.5768	405.2920	792.5502	396.7788	K	377.2780	189.1426	360.2514	180.6293	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **EKTHGEVER**

Found in **P55072**, Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Match to Query 5009: 1157.594948 from(579.804750,2+) intensity(399530.6250)

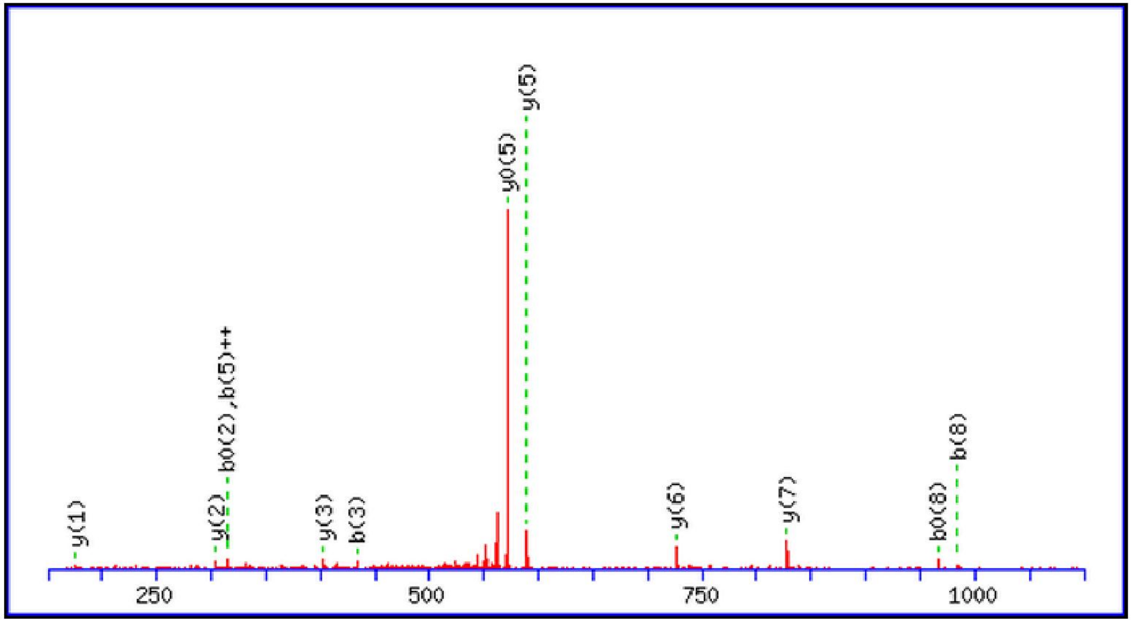
Title: File332 Spectrum2158 scans: 2842

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr10-ZW.mgf

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

Or, Plot from 150 to 1100 Da Full range

Label all possible matches ○ Label matches used for scoring ●



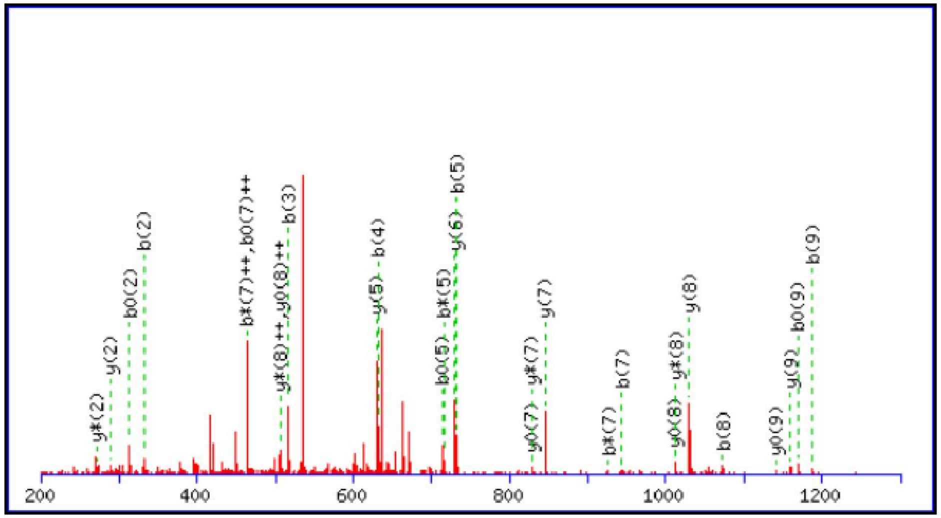
```
Monoisotopic mass of neutral peptide
Fixed modifications: Carbamidomethyl
Variable modifications:
K2        : Propionyl-(13CD3)Methyl (K)
Ions Score: 42  Expect: 0.019
Matches : 12/92 fragment ions using
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	332.2089	166.6081	315.1823	158.0948	314.1983	157.6028	K	1029.5596	515.2834	1012.5331	506.7702	1011.5491	506.2782	8
3	**433.2566**	217.1319	416.2300	208.6186	415.2460	208.1266	T	***827.4006***	414.2039	810.3741	405.6907	809.3900	405.1987	7
4	570.3155	285.6614	553.2889	277.1481	552.3049	276.6561	H	***726.3529***	363.6801	709.3264	355.1668	708.3424	354.6748	6
5	627.3369	314.1721	610.3104	305.6588	609.3264	305.1668	G	***589.2940***	295.1506	572.2675	286.6374	571.2835	286.1454	5
6	756.3795	378.6934	739.3530	370.1801	738.3690	369.6881	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
7	855.4479	428.2276	838.4214	419.7143	837.4374	419.2223	V	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
8	**984.4905**	492.7489	967.4640	484.2356	966.4800	483.7436	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KEKDTPNENR**
Found in **Q15022**, Polycomb protein SUZ12 OS=Homo sapiens GN=SUZ12 PE=1 SV=3

Match to Query 7274: 1359.691268 from(680.852910,2+) intensity(121536.6484)
Title: File334 Spectrum4187 scans: 5014
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



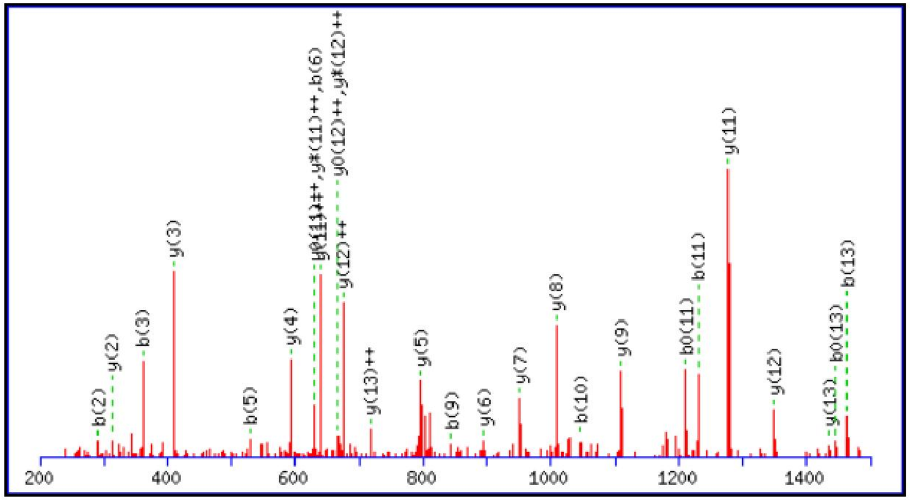
Monoisotopic mass of neutral peptide Mr(calc): 1359.6903
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 35 **Expect:** 0.12
Matches : 28/102 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							10
2	*332.2089*	166.6081	315.1823	158.0948	314.1983	157.6028	E	**1158.5386**	579.7729	1141.5120	571.2596	1140.5280	570.7676	9
3	*516.3301*	258.6687	499.3035	250.1554	498.3195	249.6634	K	**1029.4960**	515.2516	1012.4694	506.7383	1011.4854	506.2463	8
4	*631.3570*	316.1821	614.3305	307.6689	613.3464	307.1769	D	**845.3748**	423.1910	828.3482	414.6778	827.3642	414.1857	7
5	*732.4047*	366.7060	715.3781	358.1927	714.3941	357.7007	T	**730.3478**	365.6776	713.3213	357.1643	712.3373	356.6723	6
6	829.4574	415.2324	812.4309	406.7191	811.4469	406.2271	P	**629.3002**	315.1537	612.2736	306.6404	611.2896	306.1484	5
7	*943.5004*	472.2538	926.4738	463.7406	925.4898	463.2485	N	532.2474	266.6273	515.2209	258.1141	514.2368	257.6221	4
8	*1072.5430*	536.7751	1055.5164	528.2618	1054.5324	527.7698	E	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
9	*1186.5859*	593.7966	1169.5593	585.2833	1168.5753	584.7913	N	**289.1619**	145.0846	272.1353	136.5713			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KSAPATGGVKKPHR**
Found in **Q71DI3**, Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3

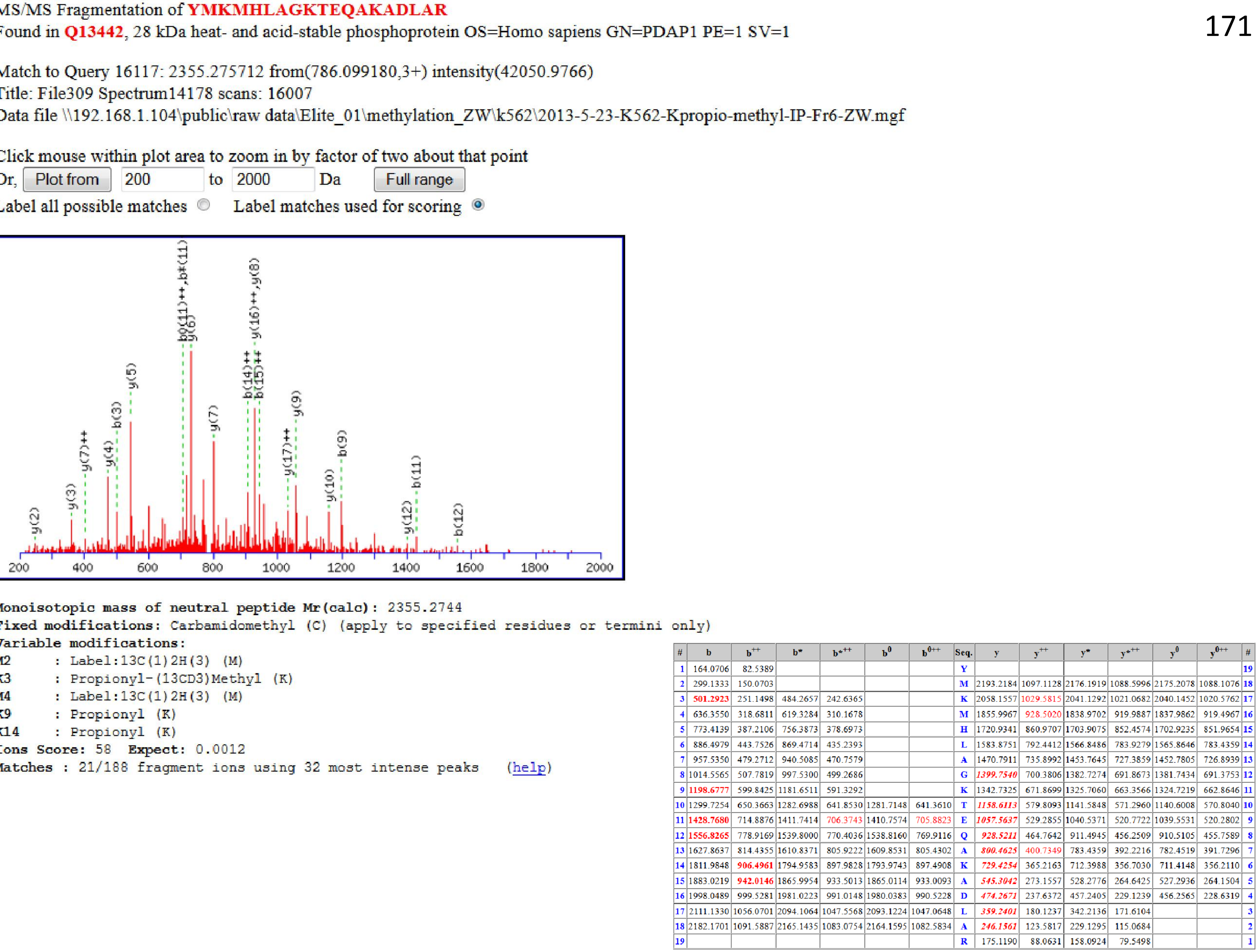
Match to Query 11298: 1636.979948 from(819.497250,2+) intensity(857586.5000)
Title: File334 Spectrum8017 scans: 9132
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1636.9806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
K10     : Propionyl-(13CD3)Methyl (K)
K11     : Propionyl (K)
Ions Score: 86  Expect: 5.2e-007
Matches : 28/138 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							14
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	S	***1435.8289***	718.4181	1418.8023	709.9048	1417.8183	709.4128	13
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	A	***1348.7968***	674.9021	1331.7703	666.3888	1330.7863	665.8968	12
4	458.2882	229.6477	441.2616	221.1345	440.2776	220.6425	P	***1277.7597***	639.3835	1260.7332	630.8702	1259.7492	630.3782	11
5	**529.3253**	265.1663	512.2988	256.6530	511.3147	256.1610	A	1180.7070	590.8571	1163.6804	582.3438	1162.6964	581.8518	10
6	**630.3730**	315.6901	613.3464	307.1769	612.3624	306.6848	T	***1109.6698***	555.3386	1092.6433	546.8253	1091.6593	546.3333	9
7	687.3945	344.2009	670.3679	335.6876	669.3839	335.1956	G	***1008.6222***	504.8147	991.5956	496.3014			8
8	744.4159	372.7116	727.3894	364.1983	726.4054	363.7063	G	***951.6007***	476.3040	934.5741	467.7907			7
9	**843.4843**	422.2458	826.4578	413.7325	825.4738	413.2405	V	***894.5792***	447.7933	877.5527	439.2800			6
10	**1045.6433**	523.3253	1028.6168	514.8120	1027.6328	514.3200	K	***795.5108***	398.2590	778.4843	389.7458			5
11	**1229.7645**	615.3859	1212.7380	606.8726	1211.7540	606.3806	K	***593.3518***	297.1795	576.3253	288.6663			4
12	1326.8173	663.9123	1309.7907	655.3990	1308.8067	654.9070	P	***409.2306***	205.1190	392.2041	196.6057			3
13	**1463.8762**	732.4417	1446.8496	723.9285	1445.8656	723.4365	H	***312.1779***	156.5926	295.1513	148.0793			2
14							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **YMKMHLAGKTEQAKADLAR**
Found in **Q13442**, 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1

Match to Query 16117: 2355.275712 from(786.099180,3+) intensity(42050.9766)
Title: File309 Spectrum14178 scans: 16007
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr6-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2355.2744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2      : Label:13C(1)2H(3) (M)
K3      : Propionyl-(13CD3)Methyl (K)
M4      : Label:13C(1)2H(3) (M)
K9      : Propionyl (K)
K14     : Propionyl (K)
Ions Score: 58  Expect: 0.0012
Matches : 21/188 fragment ions using 32 most intense peaks  (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							19
2	299.1333	150.0703					M	2193.2184	1097.1128	2176.1919	1088.5996	2175.2078	1088.1076	18
3	**501.2923**	251.1498	484.2657	242.6365			K	2058.1557	1029.5815	2041.1292	1021.0682	2040.1452	1020.5762	17
4	636.3550	318.6811	619.3284	310.1678			M	1855.9967	928.5020	1838.9702	919.9887	1837.9862	919.4967	16
5	773.4139	387.2106	756.3873	378.6973			H	1720.9341	860.9707	1703.9075	852.4574	1702.9235	851.9654	15
6	886.4979	443.7526	869.4714	435.2393			L	1583.8751	792.4412	1566.8486	783.9279	1565.8646	783.4359	14
7	957.5350	479.2712	940.5085	470.7579			A	1470.7911	735.8992	1453.7645	727.3859	1452.7805	726.8939	13
8	1014.5565	507.7819	997.5300	499.2686			G	***1399.7540***	700.3806	1382.7274	691.8673	1381.7434	691.3753	12
9	**1198.6777**	599.8425	1181.6511	591.3292			K	1342.7325	671.8699	1325.7060	663.3566	1324.7219	662.8646	11
10	1299.7254	650.3663	1282.6988	641.8530	1281.7148	641.3610	T	***1158.6113***	579.8093	1141.5848	571.2960	1140.6008	570.8040	10
11	**1428.7680**	714.8876	1411.7414	706.3743	1410.7574	705.8823	E	***1057.5637***	529.2855	1040.5371	520.7722	1039.5531	520.2802	9
12	**1556.8265**	778.9169	1539.8000	770.4036	1538.8160	769.9116	Q	***928.5211***	464.7642	911.4945	456.2509	910.5105	455.7589	8
13	1627.8637	814.4355	1610.8371	805.9222	1609.8531	805.4302	A	***800.4625***	400.7349	783.4359	392.2216	782.4519	391.7296	7
14	1811.9848	**906.4961**	1794.9583	897.9828	1793.9743	897.4908	K	***729.4254***	365.2163	712.3988	356.7030	711.4148	356.2110	6
15	1883.0219	**942.0146**	1865.9954	933.5013	1865.0114	933.0093	A	***545.3042***	273.1557	528.2776	264.6425	527.2936	264.1504	5
16	1998.0489	999.5281	1981.0223	991.0148	1980.0383	990.5228	D	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
17	2111.1330	1056.0701	2094.1064	1047.5568	2093.1224	1047.0648	L	***359.2401***	180.1237	342.2136	171.6104			3
18	2182.1701	1091.5887	2165.1435	1083.0754	2164.1595	1082.5834	A	***246.1561***	123.5817	229.1295	115.0684			2
19							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **YIGIVKQAGLER**

Found in **P52597**, Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3

Match to Query 7163: 1419.836888 from(710.925720,2+) intensity(76685.4297)

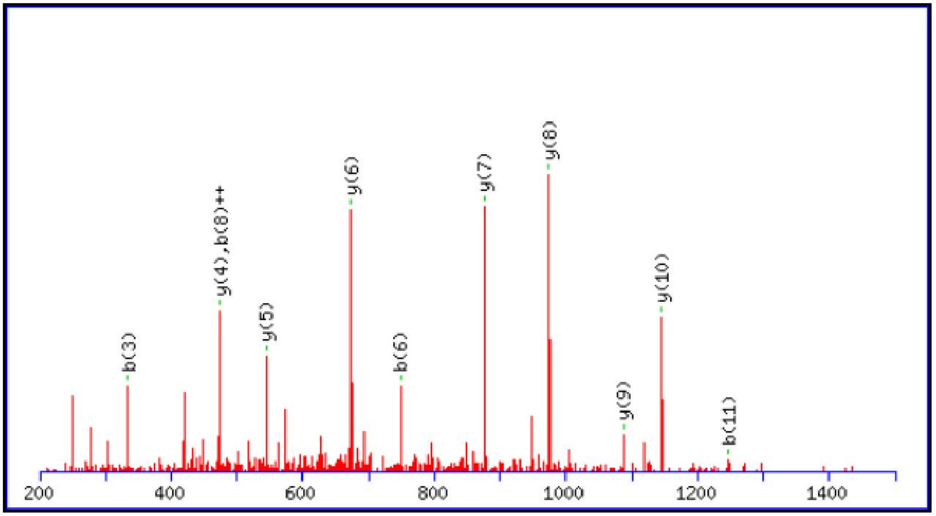
Title: File309 Spectrum12005 scans: 13689

Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr6-ZW.mgf

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

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1419.8358

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

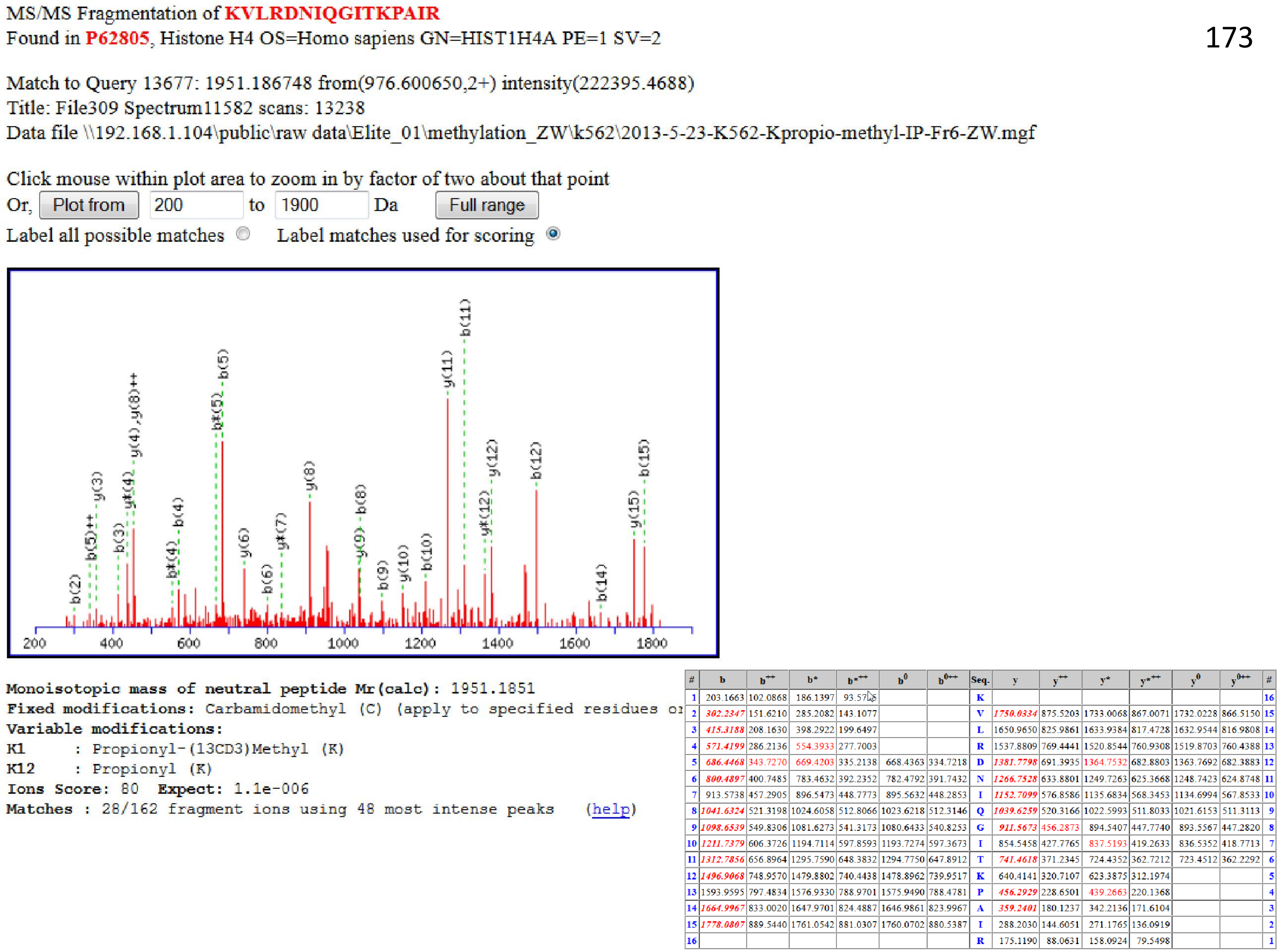
Variable modifications:

K6 : Propionyl-(13CD3)Methyl (K)

Ions Score: 61 **Expect:** 0.00024

Matches : 11/100 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							12
2	277.1547	139.0810					I	1257.7798	629.3935	1240.7532	620.8803	1239.7692	620.3882	11
3	**334.1761**	167.5917					G	***1144.6957***	572.8515	1127.6692	564.3382	1126.6852	563.8462	10
4	447.2602	224.1337					I	***1087.6743***	544.3408	1070.6477	535.8275	1069.6637	535.3355	9
5	546.3286	273.6679					V	***974.5902***	487.7987	957.5636	479.2855	956.5796	478.7935	8
6	**748.4876**	374.7475	731.4611	366.2342			K	***875.5218***	438.2645	858.4952	429.7513	857.5112	429.2592	7
7	876.5462	438.7767	859.5197	430.2635			Q	***673.3628***	337.1850	656.3362	328.6717	655.3522	328.1797	6
8	947.5833	474.2953	930.5568	465.7820			A	***545.3042***	273.1557	528.2776	264.6425	527.2936	264.1504	5
9	1004.6048	502.8060	987.5782	494.2928			G	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
10	1117.6888	559.3481	1100.6623	550.8348			L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
11	**1246.7314**	623.8694	1229.7049	615.3561	1228.7209	614.8641	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KVLRDNIQGITKPAIR**
Found in **P62805**, Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

Match to Query 13677: 1951.186748 from(976.600650,2+) intensity(222395.4688)
Title: File309 Spectrum11582 scans: 13238
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr6-ZW.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 ●

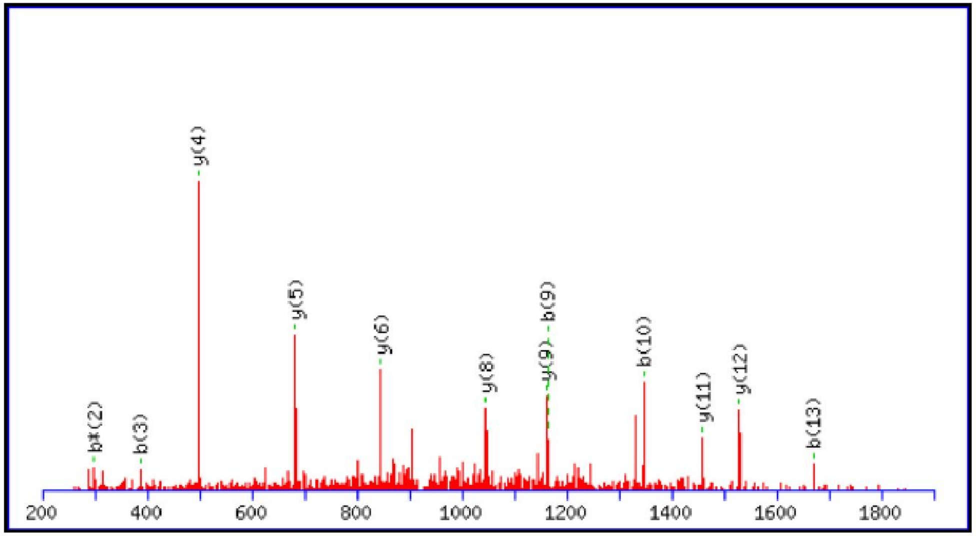
Monoisotopic mass of neutral peptide Mr(calc): 1951.1851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K12 : Propionyl (K)
Ions Score: 80 **Expect:** 1.1e-006
Matches : 28/162 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.57[illegible]5			K							16
2	***302.2347***	151.6210	285.2082	143.1077			V	***1750.0334***	875.5203	1733.0068	867.0071	1732.0228	866.5150	15
3	***415.3188***	208.1630	398.2922	199.6497			L	1650.9650	825.9861	1633.9384	817.4728	1632.9544	816.9808	14
4	***571.4199***	286.2136	554.3933	277.7003			R	1537.8809	769.4441	1520.8544	760.9308	1519.8703	760.4388	13
5	***686.4468***	343.7270	669.4203	335.2138	668.4363	334.7218	D	***1381.7798***	691.3935	1364.7532	682.8803	1363.7692	682.3883	12
6	***800.4897***	400.7485	783.4632	392.2352	782.4792	391.7432	N	***1266.7528***	633.8801	1249.7263	625.3668	1248.7423	624.8748	11
7	913.5738	457.2905	896.5473	448.7773	895.5632	448.2853	I	***1152.7099***	576.8586	1135.6834	568.3453	1134.6994	567.8533	10
8	***1041.6324***	521.3198	1024.6058	512.8066	1023.6218	512.3146	Q	***1039.6259***	520.3166	1022.5993	511.8033	1021.6153	511.3113	9
9	***1098.6539***	549.8306	1081.6273	541.3173	1080.6433	540.8253	G	***911.5673***	456.2873	894.5407	447.7740	893.5567	447.2820	8
10	***1211.7379***	606.3726	1194.7114	597.8593	1193.7274	597.3673	I	854.5458	427.7765	837.5193	419.2633	836.5352	418.7713	7
11	***1312.7856***	656.8964	1295.7590	648.3832	1294.7750	647.8912	T	***741.4618***	371.2345	724.4352	362.7212	723.4512	362.2292	6
12	***1496.9068***	748.9570	1479.8802	740.4438	1478.8962	739.9517	K	640.4141	320.7107	623.3875	312.1974			5
13	1593.9595	797.4834	1576.9330	788.9701	1575.9490	788.4781	P	***456.2929***	228.6501	439.2663	220.1368			4
14	***1664.9967***	833.0020	1647.9701	824.4887	1646.9861	823.9967	A	***359.2401***	180.1237	342.2136	171.6104			3
15	***1778.0807***	889.5440	1761.0542	881.0307	1760.0702	880.5387	I	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LKANKDSLYKPILR**
Found in **Q14692**, Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1

Match to Query 14025: 1844.104348 from(923.059450,2+) intensity(154355.6250)
Title: File312 Spectrum16529 scans: 18598
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr8-ZW.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 ●



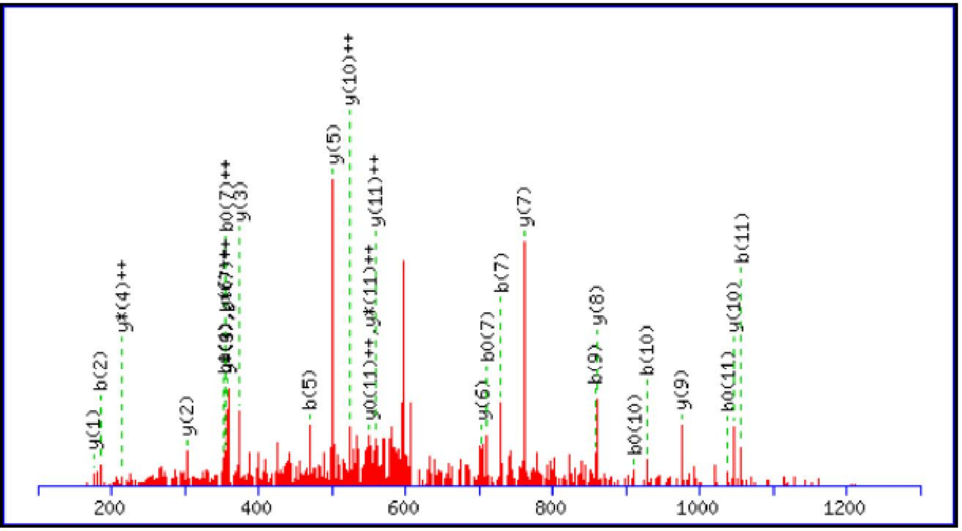
Monoisotopic mass of neutral peptide Mr(calc): 1844.1044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 53 **Expect:** 0.00099
Matches : 12/130 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							14
2	316.2504	158.6288	299.2238	150.1155			K	1732.0276	866.5174	1715.0011	858.0042	1714.0171	857.5122	13
3	**387.2875**	194.1474	370.2609	185.6341			A	***1529.8686***	765.4379	1512.8421	756.9247	1511.8580	756.4327	12
4	501.3304	251.1688	484.3038	242.6556			N	***1458.8315***	729.9194	1441.8049	721.4061	1440.8209	720.9141	11
5	685.4516	343.2294	668.4250	334.7161			K	1344.7886	672.8979	1327.7620	664.3846	1326.7780	663.8926	10
6	800.4785	400.7429	783.4520	392.2296	782.4679	391.7376	D	***1160.6674***	580.8373	1143.6408	572.3241	1142.6568	571.8320	9
7	887.5105	444.2589	870.4840	435.7456	869.5000	435.2536	S	***1045.6404***	523.3239	1028.6139	514.8106	1027.6299	514.3186	8
8	1000.5946	500.8009	983.5681	492.2877	982.5840	491.7957	L	958.6084	479.8078	941.5819	471.2946			7
9	**1163.6579**	582.3326	1146.6314	573.8193	1145.6474	573.3273	Y	***845.5244***	423.2658	828.4978	414.7525			6
10	**1347.7791**	674.3932	1330.7526	665.8799	1329.7685	665.3879	K	***682.4610***	341.7341	665.4345	333.2209			5
11	1444.8319	722.9196	1427.8053	714.4063	1426.8213	713.9143	P	***498.3398***	249.6736	481.3133	241.1603			4
12	1557.9159	779.4616	1540.8894	770.9483	1539.9054	770.4563	I	401.2871	201.1472	384.2605	192.6339			3
13	**1671.0000**	836.0036	1653.9735	827.4904	1652.9894	826.9984	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1

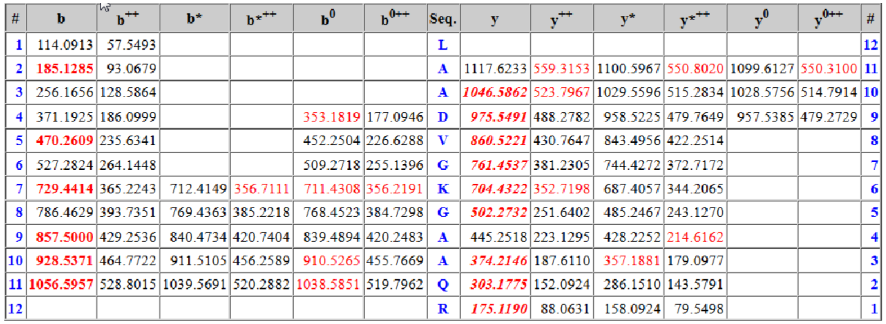
MS/MS Fragmentation of **LAADVGKGAAQR**
Found in **P12235**, ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4

Match to Query 4722: 1229.697848 from(615.856200,2+) intensity(20065.5801)
Title: File314 Spectrum4887 scans: 6302
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-K562-Kpropio-methyl-IP-Fr9-ZW.mgf

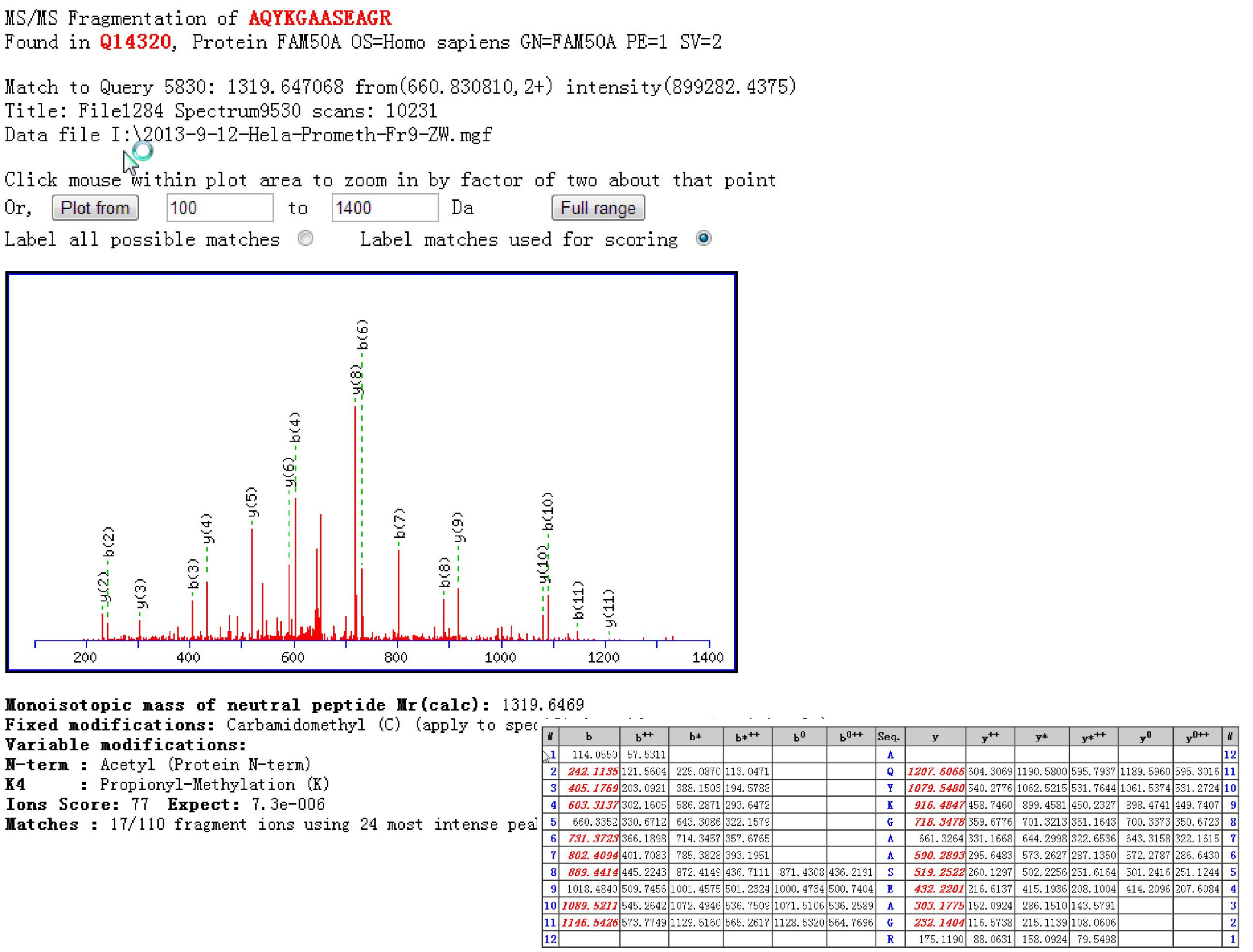
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1229.7001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 41 **Expect:** 0.034
Matches : 28/98 fragment ions using 72 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							12
2	**185.1285**	93.0679					A	1117.6233	559.3153	1100.5967	550.8020	1099.6127	550.3100	11
3	256.1656	128.5864					A	***1046.5862***	523.7967	1029.5596	515.2834	1028.5756	514.7914	10
4	371.1925	186.0999			353.1819	177.0946	D	***975.5491***	488.2782	958.5225	479.7649	957.5385	479.2729	9
5	**470.2609**	235.6341			452.2504	226.6288	V	***860.5221***	430.7647	843.4956	422.2514			8
6	527.2824	264.1448			509.2718	255.1396	G	***761.4537***	381.2305	744.4272	372.7172			7
7	**729.4414**	365.2243	712.4149	356.7111	711.4308	356.2191	K	***704.4322***	352.7198	687.4057	344.2065			6
8	786.4629	393.7351	769.4363	385.2218	768.4523	384.7298	G	***502.2732***	251.6402	485.2467	243.1270			5
9	**857.5000**	429.2536	840.4734	420.7404	839.4894	420.2483	A	445.2518	223.1295	428.2252	214.6162			4
10	**928.5371**	464.7722	911.5105	456.2589	910.5265	455.7669	A	***374.2146***	187.6110	357.1881	179.0977			3
11	**1056.5957**	528.8015	1039.5691	520.2882	1038.5851	519.7962	Q	***303.1775***	152.0924	286.1510	143.5791			2
12							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AQYKGAASEAGR**
Found in **Q14320**, Protein FAM50A OS=Homo sapiens GN=FAM50A PE=1 SV=2

Match to Query 5830: 1319.647068 from(660.830810,2+) intensity(899282.4375)
Title: File1284 Spectrum9530 scans: 10231
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.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 ●

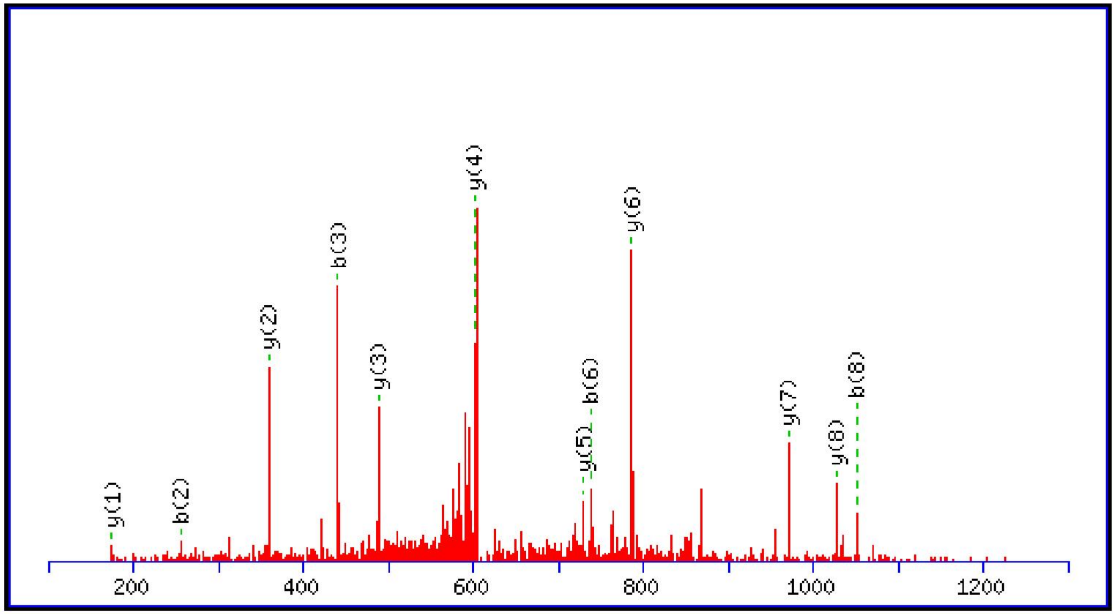
Monoisotopic mass of neutral peptide Mr(calc): 1319.6469
Fixed modifications: Carbamidomethyl (C) (apply to spec
Variable modifications:
N-term : Acetyl (Protein N-term)
K4 : Propionyl-Methylation (K)
Ions Score: 77 **Expect:** 7.3e-006
Matches : 17/110 fragment ions using 24 most intense peal

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0550	57.5311					A							12
2	***242.1135***	121.5604	225.0870	113.0471			Q	***1207.6066***	604.3069	1190.5800	595.7937	1189.5960	595.3016	11
3	***405.1769***	203.0921	388.1503	194.5788			Y	***1079.5480***	540.2776	1062.5215	531.7644	1061.5374	531.2724	10
4	***603.3137***	302.1605	586.2871	293.6472			K	***916.4847***	458.7460	899.4581	450.2327	898.4741	449.7407	9
5	660.3352	330.6712	643.3086	322.1579			G	***718.3478***	359.6776	701.3213	351.1643	700.3373	350.6723	8
6	***731.3723***	366.1898	714.3457	357.6765			A	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	7
7	***802.4094***	401.7083	785.3828	393.1951			A	***590.2893***	295.6483	573.2627	287.1350	572.2787	286.6430	6
8	***889.4414***	445.2243	872.4149	436.7111	871.4308	436.2191	S	***519.2522***	260.1297	502.2256	251.6164	501.2416	251.1244	5
9	1018.4840	509.7456	1001.4575	501.2324	1000.4734	500.7404	E	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	4
10	***1089.5211***	545.2642	1072.4946	536.7509	1071.5106	536.2589	A	***303.1775***	152.0924	286.1510	143.5791			3
11	***1146.5426***	573.7749	1129.5160	565.2617	1128.5320	564.7696	G	***232.1404***	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KGKGQIEKR**
Found in **Q96IZ0**, PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1

Match to Query 4910: 1224.717008 from(613.365780,2+) intensity(136380.3906)
Title: File1284 Spectrum8249 scans: 8896
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.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 ●



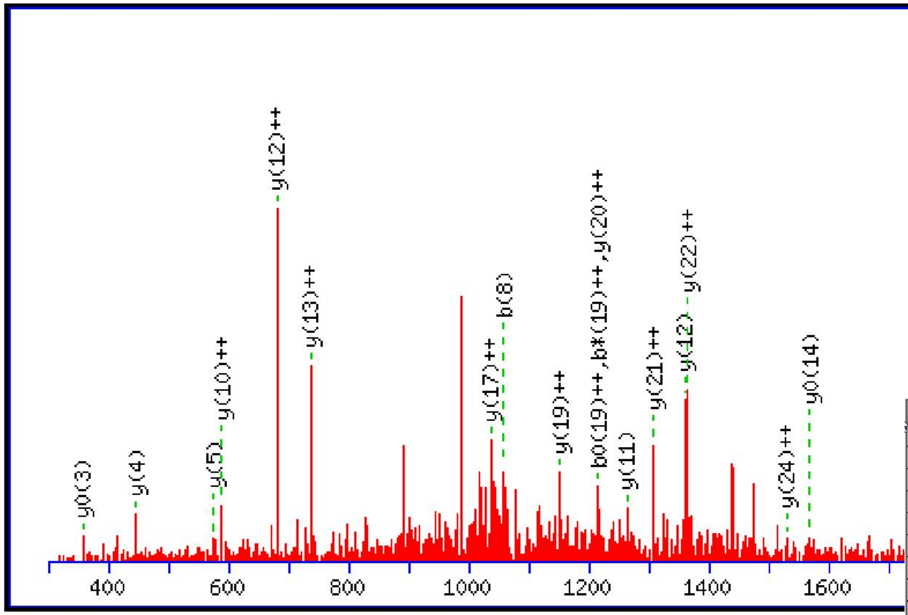
Monoisotopic mass of neutral peptide Mr(calc): 1224.7190
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
K3 : Propionyl (K)
K8 : Propionyl (K)
Ions Score: 57 **Expect:** 0.001
Matches : 12/80 fragment ions using 22 most intense pea

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							9
2	**256.1656**	128.5864	239.1390	120.0731			G	*1027.5895*	514.2984	1010.5629	505.7851	1009.5789	505.2931	8
3	**440.2867**	220.647	423.2602	212.1337			K	*970.5680*	485.7876	953.5415	477.2744	952.5574	476.7824	7
4	497.3082	249.1577	480.2817	240.6445			G	*786.4468*	393.7271	769.4203	385.2138	768.4363	384.7218	6
5	625.3668	313.1870	608.3402	304.6738			Q	*729.4254*	365.2163	712.3988	356.7030	711.4148	356.2110	5
6	**738.4509**	369.7291	721.4243	361.2158			I	*601.3668*	301.1870	584.3402	292.6738	583.3562	292.1817	4
7	867.4934	434.2504	850.4669	425.7371	849.4829	425.2451	E	*488.2827*	244.6450	471.2562	236.1317	470.2722	235.6397	3
8	**1051.6146**	526.3109	1034.5881	517.7977	1033.6041	517.3057	K	*359.2401*	180.1237	342.2136	171.6104			2
9							R	*175.1190*	88.0631	158.0924	79.5498			1

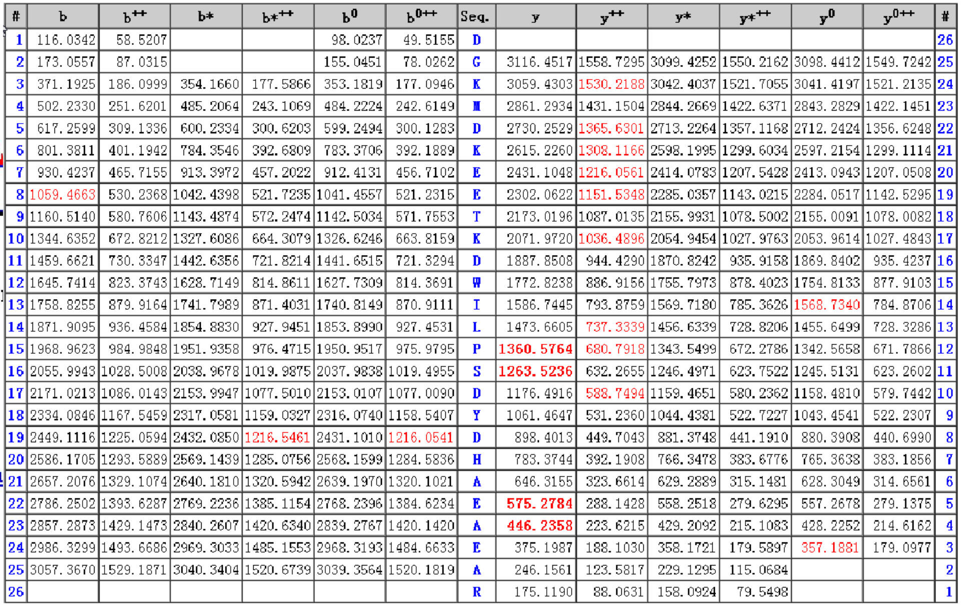
MS/MS Fragmentation of DGKMDKEETKDWILPSDYDHAEAEAR
Found in HOY875, Calumenin (Fragment) OS=Homo sapiens GN=CALU PE=4 SV=1

Match to Query 22039: 3231.443622 from(1078.155150,3+) intensity(15968.8232)
Title: File1284 Spectrum16424 scans: 17412
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.mgf

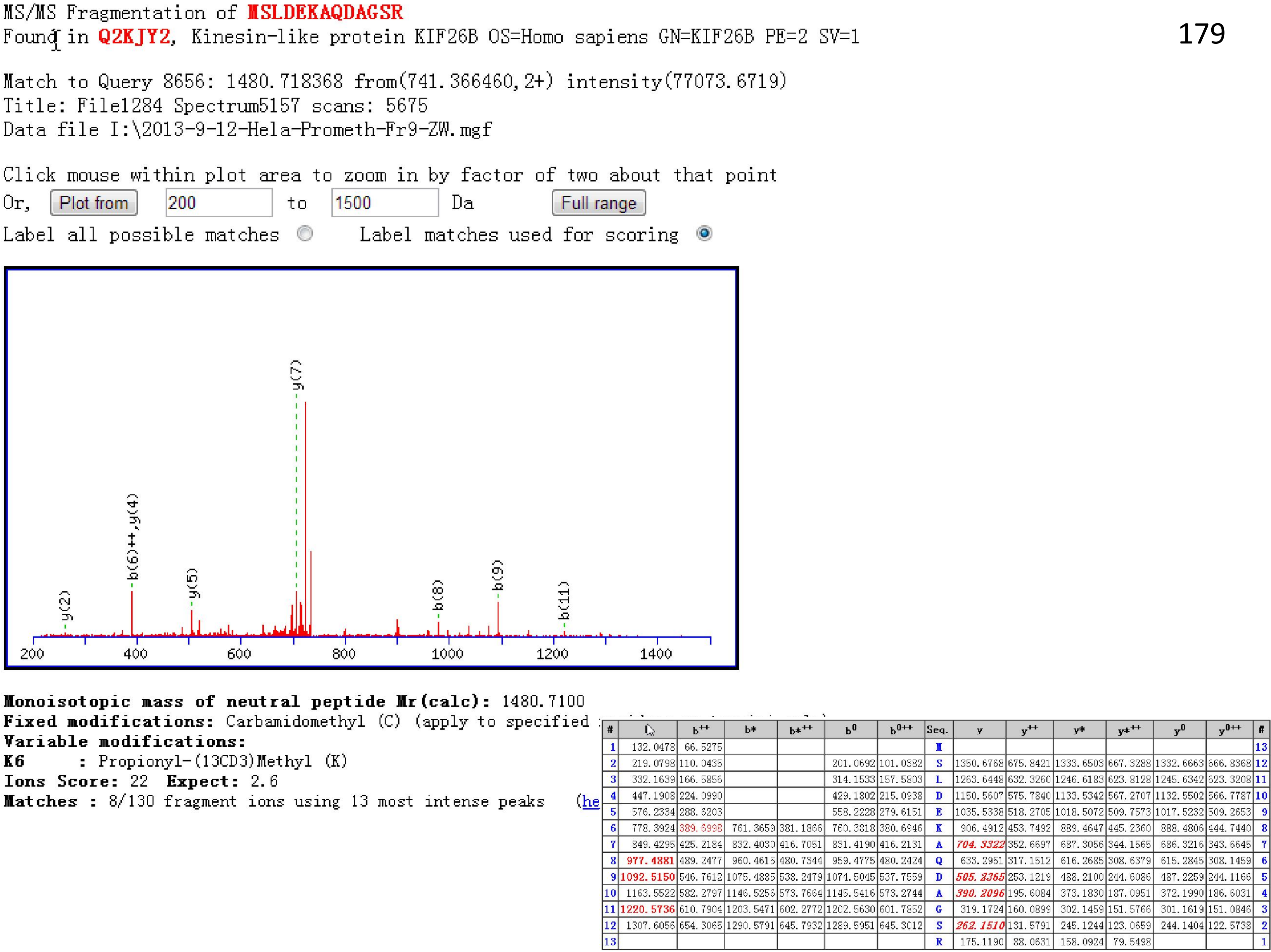
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3230.4713
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K3 : Propionyl-Methylation (K)
K6 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 32 **Expect:** 0.17
Matches : 18/292 fragment ions using 34 most intense peaks (h



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							26
2	173.0557	87.0315			155.0451	78.0262	G	3116.4517	1558.7295	3099.4252	1550.2162	3098.4412	1549.7242	25
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	K	3059.4303	1530.2188	3042.4037	1521.7055	3041.4197	1521.2135	24
4	502.2330	251.6201	485.2064	243.1069	484.2224	242.6149	M	2861.2934	1431.1504	2844.2669	1422.6371	2843.2829	1422.1451	23
5	617.2599	309.1336	600.2334	300.6203	599.2494	300.1283	D	2730.2529	1365.6301	2713.2264	1357.1168	2712.2424	1356.6248	22
6	801.3811	401.1942	784.3546	392.6809	783.3706	392.1889	K	2615.2260	1308.1166	2598.1995	1299.6034	2597.2154	1299.1114	21
7	930.4237	465.7155	913.3972	457.2022	912.4131	456.7102	E	2431.1048	1216.0561	2414.0783	1207.5428	2413.0943	1207.0508	20
8	1059.4663	530.2368	1042.4398	521.7235	1041.4557	521.2315	E	2302.0622	1151.5348	2285.0357	1143.0215	2284.0517	1142.5295	19
9	1160.5140	580.7606	1143.4874	572.2474	1142.5034	571.7553	T	2173.0196	1087.0135	2155.9931	1078.5002	2155.0091	1078.0082	18
10	1344.6352	672.8212	1327.6086	664.3079	1326.6246	663.8159	K	2071.9720	1036.4896	2054.9454	1027.9763	2053.9614	1027.4843	17
11	1459.6621	730.3347	1442.6356	721.8214	1441.6515	721.3294	D	1887.8508	944.4290	1870.8242	935.9158	1869.8402	935.4237	16
12	1645.7414	823.3743	1628.7149	814.8611	1627.7309	814.3691	W	1772.8238	886.9156	1755.7973	878.4023	1754.8133	877.9103	15
13	1758.8255	879.9164	1741.7989	871.4031	1740.8149	870.9111	I	1586.7445	793.8759	1569.7180	785.3626	1568.7340	784.8706	14
14	1871.9095	936.4584	1854.8830	927.9451	1853.8990	927.4531	L	1473.6605	737.3339	1456.6339	728.8206	1455.6499	728.3286	13
15	1968.9623	984.9848	1951.9358	976.4715	1950.9517	975.9795	P	**1360.5764**	680.7918	1343.5499	672.2786	1342.5658	671.7866	12
16	2055.9943	1028.5008	2038.9678	1019.9875	2037.9838	1019.4955	S	**1263.5236**	632.2655	1246.4971	623.7522	1245.5131	623.2602	11
17	2171.0213	1086.0143	2153.9947	1077.5010	2153.0107	1077.0090	D	1176.4916	588.7494	1159.4651	580.2362	1158.4810	579.7442	10
18	2334.0846	1167.5459	2317.0581	1159.0327	2316.0740	1158.5407	Y	1061.4647	531.2360	1044.4381	522.7227	1043.4541	522.2307	9
19	2449.1116	1225.0594	2432.0850	1216.5461	2431.1010	1216.0541	D	898.4013	449.7043	881.3748	441.1910	880.3908	440.6990	8
20	2586.1705	1293.5889	2569.1439	1285.0756	2568.1599	1284.5836	H	783.3744	392.1908	766.3478	383.6776	765.3638	383.1856	7
21	2657.2076	1329.1074	2640.1810	1320.5942	2639.1970	1320.1021	A	646.3155	323.6614	629.2889	315.1481	628.3049	314.6561	6
22	2786.2502	1393.6287	2769.2236	1385.1154	2768.2396	1384.6234	E	**575.2784**	288.1428	558.2518	279.6295	557.2678	279.1375	5
23	2857.2873	1429.1473	2840.2607	1420.6340	2839.2767	1420.1420	A	**446.2358**	223.6215	429.2092	215.1083	428.2252	214.6162	4
24	2986.3299	1493.6686	2969.3033	1485.1553	2968.3193	1484.6633	E	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
25	3057.3670	1529.1871	3040.3404	1520.6739	3039.3564	1520.1819	A	246.1561	123.5817	229.1295	115.0684			2
26							R	175.1190	88.0631	158.0924	79.5498			1



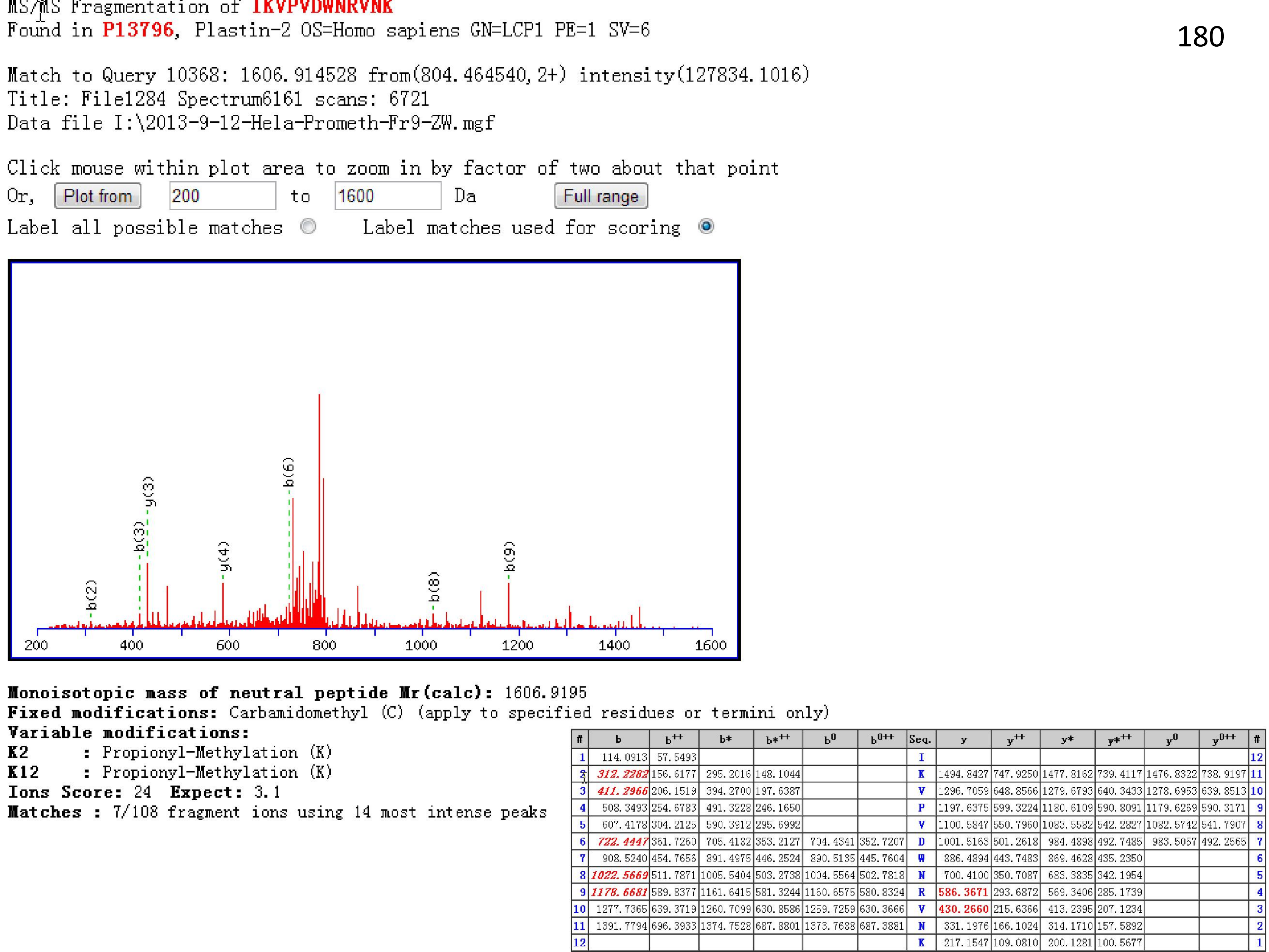
MS/MS Fragmentation of **MSLDEKAQDAGSR**
Found in **Q2KJY2**, Kinesin-like protein KIF26B OS=Homo sapiens GN=KIF26B PE=2 SV=1

Match to Query 8656: 1480.718368 from(741.366460,2+) intensity(77073.6719)
Title: File1284 Spectrum5157 scans: 5675
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1480.7100
Fixed modifications: Carbamidomethyl (C) (apply to specified :
Variable modifications:
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 22 **Expect:** 2.6
Matches : 8/130 fragment ions using 13 most intense peaks (he

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275					M							13
2	219.0798	110.0435			201.0692	101.0382	S	1350.6768	675.8421	1333.6503	667.3288	1332.6663	666.8368	12
3	332.1639	166.5856			314.1533	157.5803	L	1263.6448	632.3260	1246.6183	623.8128	1245.6342	623.3208	11
4	447.1908	224.0990			429.1802	215.0938	D	1150.5607	575.7840	1133.5342	567.2707	1132.5502	566.7787	10
5	576.2334	288.6203			558.2228	279.6151	E	1035.5338	518.2705	1018.5072	509.7573	1017.5232	509.2653	9
6	778.3924	389.6998	761.3659	381.1866	760.3818	380.6946	K	906.4912	453.7492	889.4647	445.2360	888.4806	444.7440	8
7	849.4295	425.2184	832.4030	416.7051	831.4190	416.2131	A	***704.3322***	352.6697	687.3056	344.1565	686.3216	343.6645	7
8	**977.4881**	489.2477	960.4615	480.7344	959.4775	480.2424	Q	633.2951	317.1512	616.2685	308.6379	615.2845	308.1459	6
9	**1092.5150**	546.7612	1075.4885	538.2479	1074.5045	537.7559	D	***505.2365***	253.1219	488.2100	244.6086	487.2259	244.1166	5
10	1163.5522	582.2797	1146.5256	573.7664	1145.5416	573.2744	A	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	4
11	**1220.5736**	610.7904	1203.5471	602.2772	1202.5630	601.7852	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
12	1307.6056	654.3065	1290.5791	645.7932	1289.5951	645.3012	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



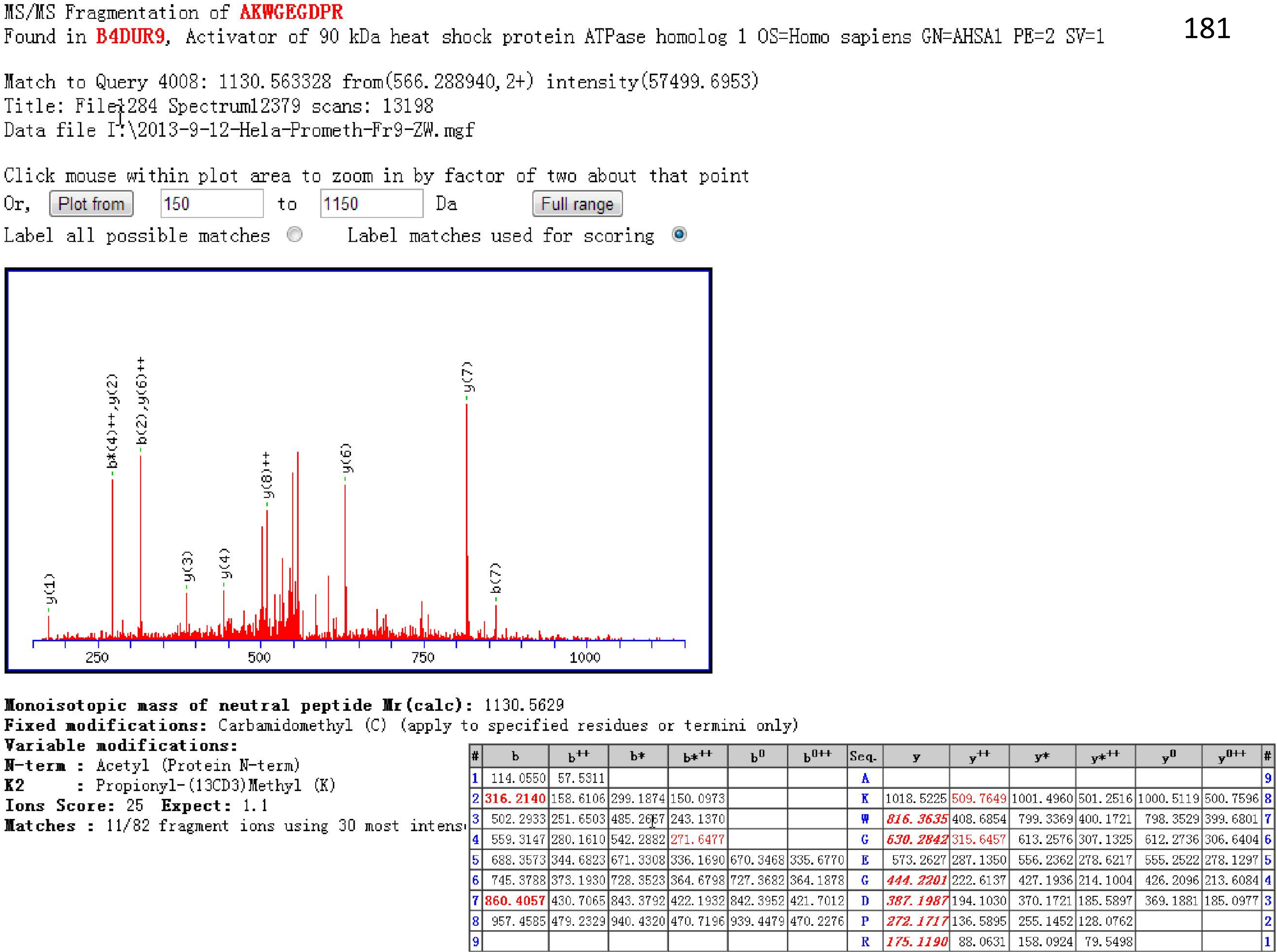
MS/MS Fragmentation of **IKVPVDWNRVNK**
Found in **P13796**, Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6

Match to Query 10368: 1606.914528 from(804.464540,2+) intensity(127834.1016)
Title: File1284 Spectrum6161 scans: 6721
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1606.9195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
K12 : Propionyl-Methylation (K)
Ions Score: 24 **Expect:** 3.1
Matches : 7/108 fragment ions using 14 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							12
2	***312.2282***	156.6177	295.2016	148.1044			K	1494.8427	747.9250	1477.8162	739.4117	1476.8322	738.9197	11
3	***411.2966***	206.1519	394.2700	197.6387			V	1296.7059	648.8566	1279.6793	640.3433	1278.6953	639.8513	10
4	508.3493	254.6783	491.3228	246.1650			P	1197.6375	599.3224	1180.6109	590.8091	1179.6269	590.3171	9
5	607.4178	304.2125	590.3912	295.6992			V	1100.5847	550.7960	1083.5582	542.2827	1082.5742	541.7907	8
6	***722.4447***	361.7260	705.4182	353.2127	704.4341	352.7207	D	1001.5163	501.2618	984.4898	492.7485	983.5057	492.2565	7
7	908.5240	454.7656	891.4975	446.2524	890.5135	445.7604	W	886.4894	443.7483	869.4628	435.2350			6
8	***1022.5669***	511.7871	1005.5404	503.2738	1004.5564	502.7818	N	700.4100	350.7087	683.3835	342.1954			5
9	***1178.6681***	589.8377	1161.6415	581.3244	1160.6575	580.8324	R	**586.3671**	293.6872	569.3406	285.1739			4
10	1277.7365	639.3719	1260.7099	630.8586	1259.7259	630.3666	V	**430.2660**	215.6366	413.2395	207.1234			3
11	1391.7794	696.3933	1374.7528	687.8801	1373.7688	687.3881	N	331.1976	166.1024	314.1710	157.5892			2
12							K	217.1547	109.0810	200.1281	100.5677			1



MS/MS Fragmentation of AKWGEGDPR

Found in B4DUR9, Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=2 SV=1

Match to Query 4008: 1130.563328 from(566.288940,2+) intensity(57499.6953)

Title: File1284 Spectrum12379 scans: 13198

Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1130.5629

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

Variable modifications:

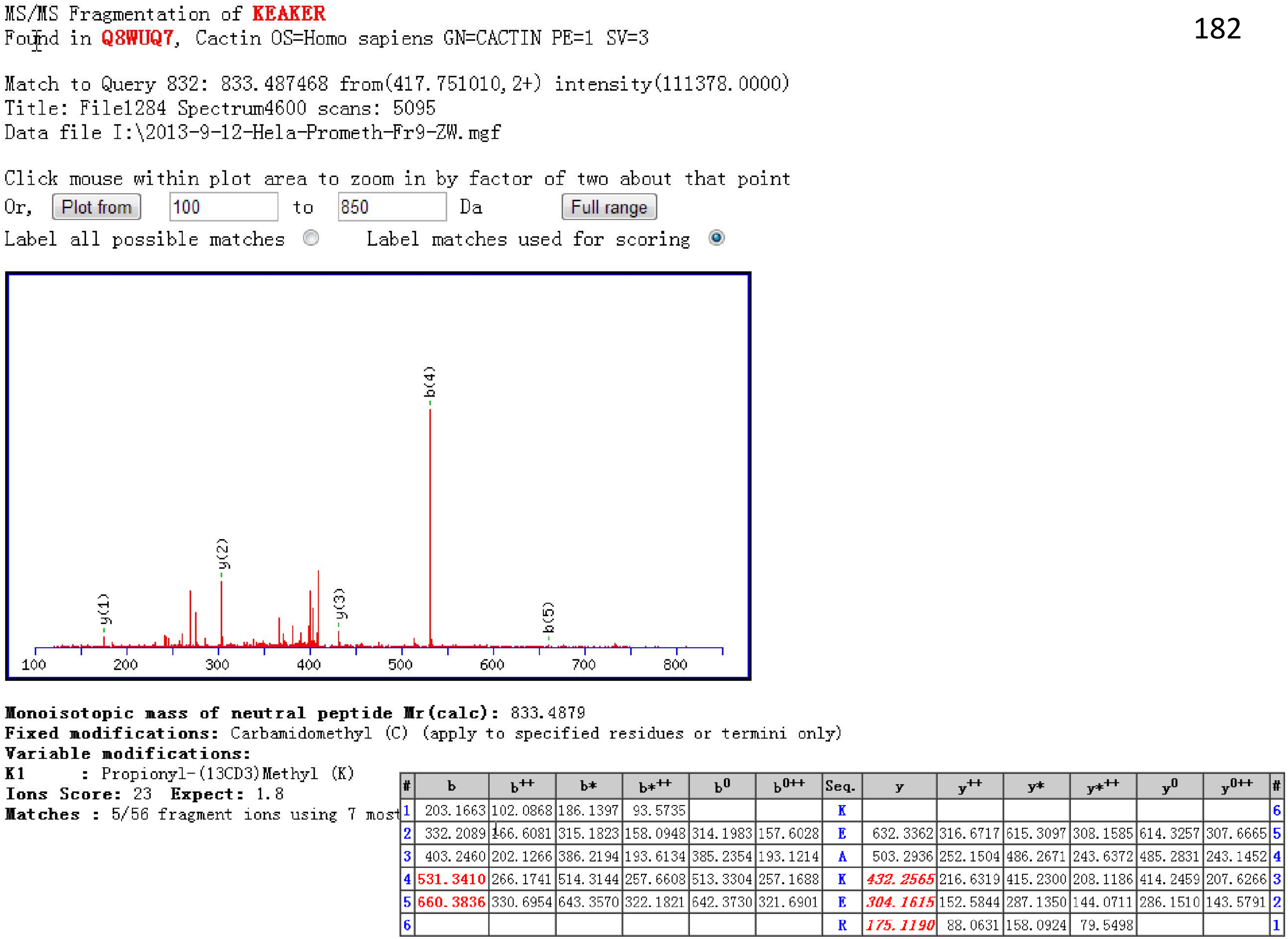
N-term : Acetyl (Protein N-term)

K2 : Propionyl-(13CD3)Methyl (K)

Ions Score: 25 **Expect:** 1.1

Matches : 11/82 fragment ions using 30 most intens

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	114.0550	57.5311					A							9
2	**316.2140**	158.6106	299.1874	150.0973			K	1018.5225	509.7649	1001.4960	501.2516	1000.5119	500.7596	8
3	502.2933	251.6503	485.2667	243.1370			W	***816.3635***	408.6854	799.3369	400.1721	798.3529	399.6801	7
4	559.3147	280.1610	542.2882	271.6477			G	***630.2842***	315.6457	613.2576	307.1325	612.2736	306.6404	6
5	688.3573	344.6823	671.3308	336.1690	670.3468	335.6770	E	573.2627	287.1350	556.2362	278.6217	555.2522	278.1297	5
6	745.3788	373.1930	728.3523	364.6798	727.3682	364.1878	G	***444.2201***	222.6137	427.1936	214.1004	426.2096	213.6084	4
7	**860.4057**	430.7065	843.3792	422.1932	842.3952	421.7012	D	***387.1987***	194.1030	370.1721	185.5897	369.1881	185.0977	3
8	957.4585	479.2329	940.4320	470.7196	939.4479	470.2276	P	***272.1717***	136.5895	255.1452	128.0762			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



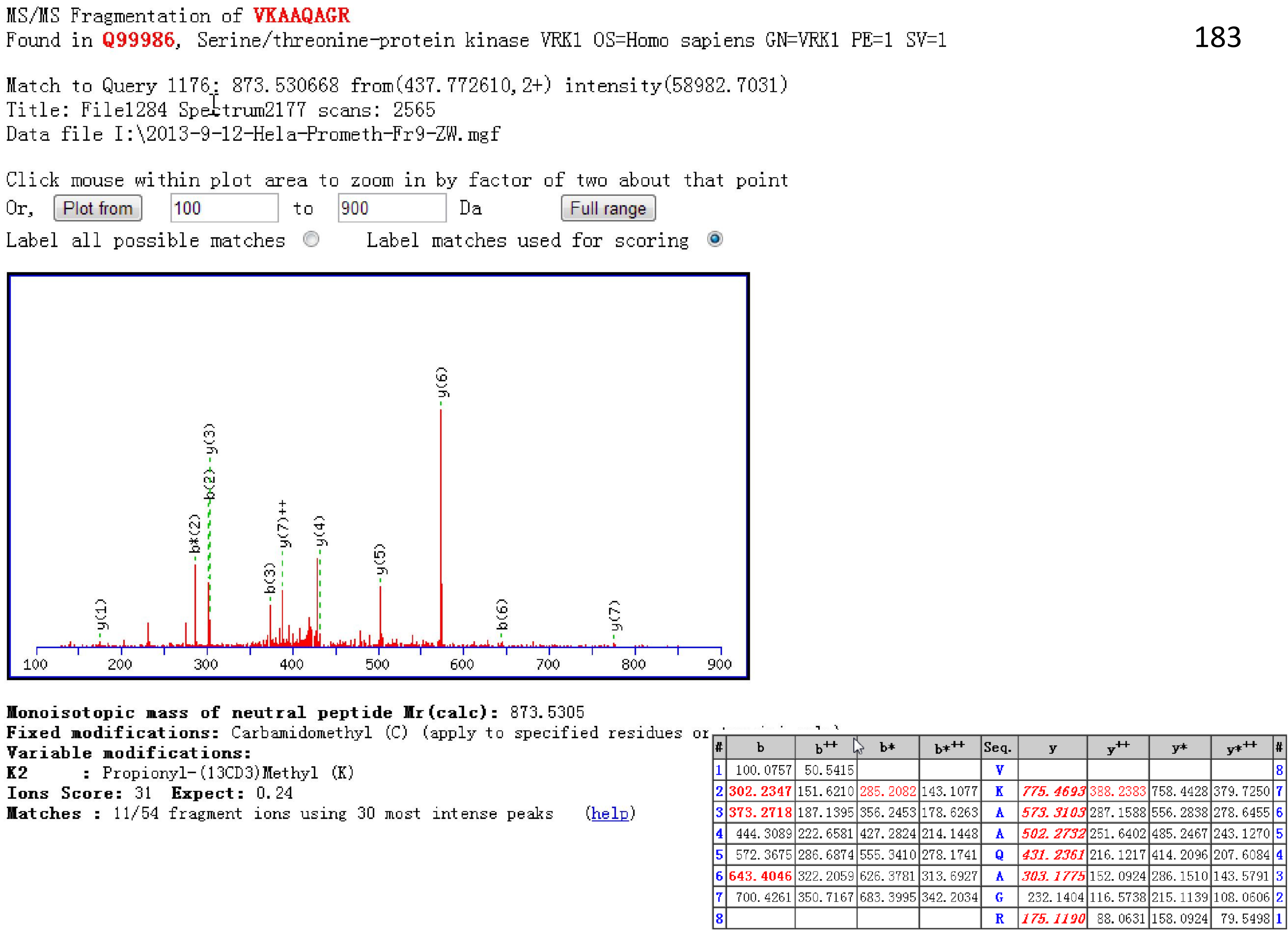
MS/MS Fragmentation of **KEAKER**
Found in **Q8WUQ7**, Cactin OS=Homo sapiens GN=CACTIN PE=1 SV=3

Match to Query 832: 833.487468 from(417.751010,2+) intensity(111378.0000)
Title: File1284 Spectrum4600 scans: 5095
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 833.4879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 23 **Expect:** 1.8
Matches : 5/56 fragment ions using 7 most

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			**K**							6
2	332.2089	166.6081	315.1823	158.0948	314.1983	157.6028	**E**	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	5
3	403.2460	202.1266	386.2194	193.6134	385.2354	193.1214	**A**	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
4	531.3410	266.1741	514.3144	257.6608	513.3304	257.1688	**K**	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	3
5	660.3836	330.6954	643.3570	322.1821	642.3730	321.6901	**E**	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
6							**R**	***175.1190***	88.0631	158.0924	79.5498			1



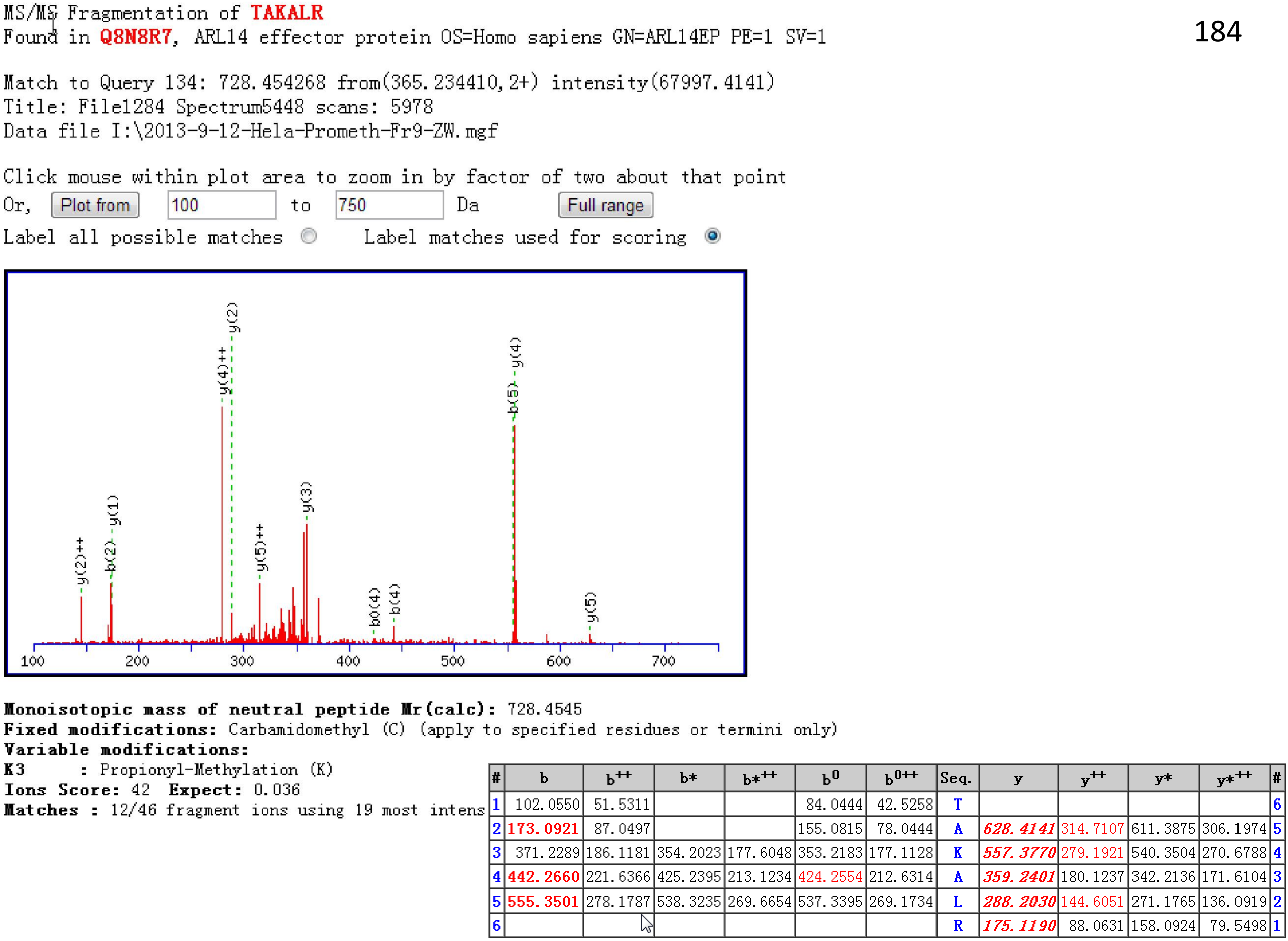
MS/MS Fragmentation of **VKAAQAGR**
Found in **Q99986**, Serine/threonine-protein kinase VRK1 OS=Homo sapiens GN=VRK1 PE=1 SV=1

Match to Query 1176: 873.530668 from(437.772610,2+) intensity(58982.7031)
Title: File1284 Spectrum2177 scans: 2565
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 873.5305
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 31 **Expect:** 0.24
Matches : 11/54 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.0757	50.5415			V					8
2	**302.2347**	151.6210	285.2082	143.1077	K	***775.4693***	388.2383	758.4428	379.7250	7
3	**373.2718**	187.1395	356.2453	178.6263	A	***573.3103***	287.1588	556.2838	278.6455	6
4	444.3089	222.6581	427.2824	214.1448	A	***502.2732***	251.6402	485.2467	243.1270	5
5	572.3675	286.6874	555.3410	278.1741	Q	***431.2361***	216.1217	414.2096	207.6084	4
6	**643.4046**	322.2059	626.3781	313.6927	A	***303.1775***	152.0924	286.1510	143.5791	3
7	700.4261	350.7167	683.3995	342.2034	G	232.1404	116.5738	215.1139	108.0606	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1



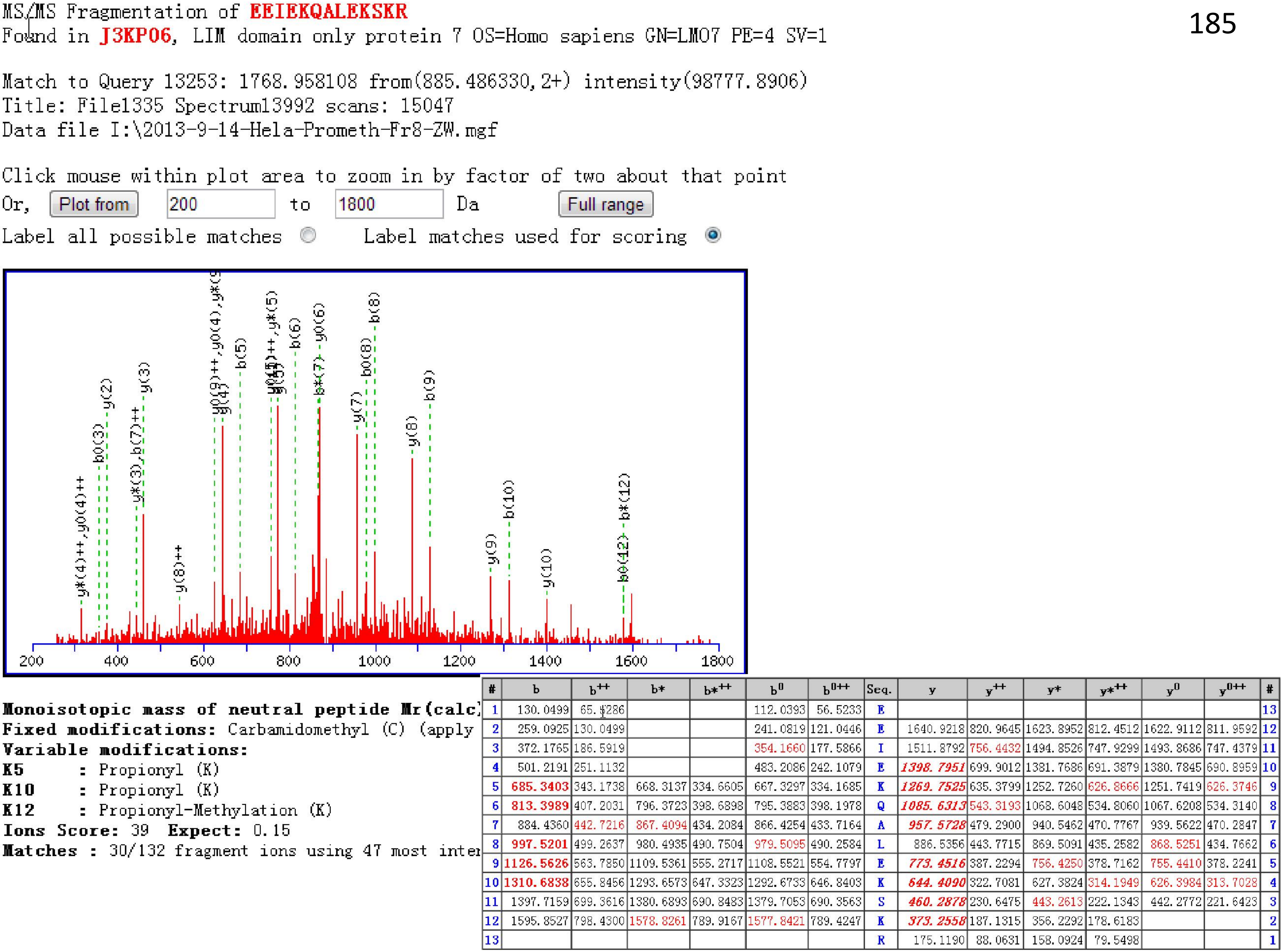
MS/MS Fragmentation of **TAKALR**
Found in **Q8N8R7**, ARL14 effector protein OS=Homo sapiens GN=ARL14EP PE=1 SV=1

Match to Query 134: 728.454268 from(365.234410,2+) intensity(67997.4141)
Title: File1284 Spectrum5448 scans: 5978
Data file I:\2013-9-12-Hela-Prometh-Fr9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 728.4545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-Methylation (K)
Ions Score: 42 **Expect:** 0.036
Matches : 12/46 fragment ions using 19 most intens

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					6
2	**173.0921**	87.0497			155.0815	78.0444	A	***628.4141***	314.7107	611.3875	306.1974	5
3	371.2289	186.1181	354.2023	177.6048	353.2183	177.1128	K	***557.3770***	279.1921	540.3504	270.6788	4
4	**442.2660**	221.6366	425.2395	213.1234	424.2554	212.6314	A	***359.2401***	180.1237	342.2136	171.6104	3
5	**555.3501**	278.1787	538.3235	269.6654	537.3395	269.1734	L	***288.2030***	144.6051	271.1765	136.0919	2
6							R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **EEIEKQALEKSKR**
Found in **J3KP06**, LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=4 SV=1

Match to Query 13253: 1768.958108 from(885.486330,2+) intensity(98777.8906)
Title: File1335 Spectrum13992 scans: 15047
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.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 ●

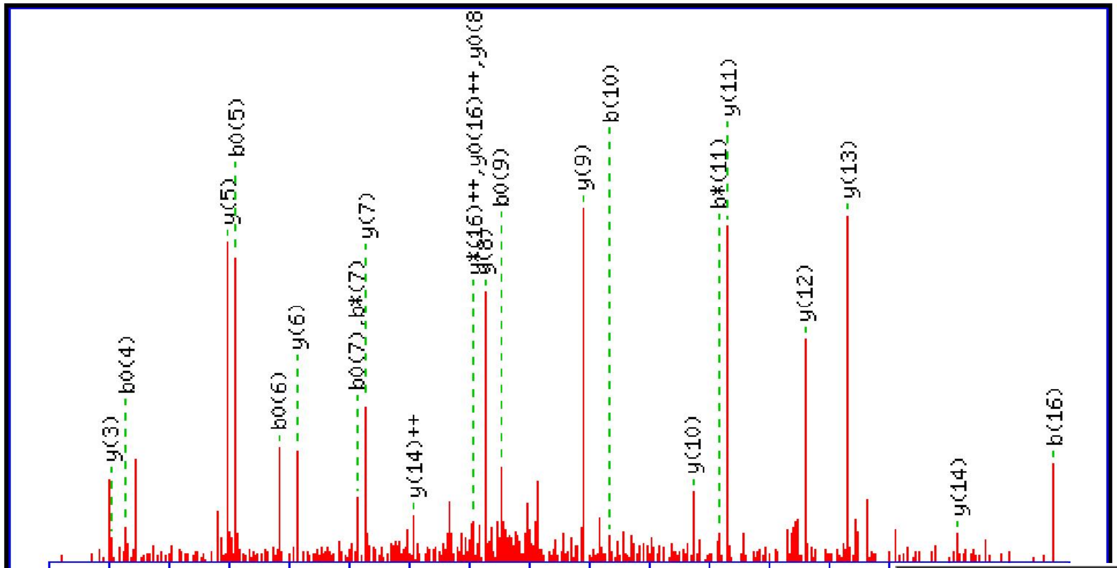
Monoisotopic mass of neutral peptide Mr(calc
Fixed modifications: Carbamidomethyl (C) (apply
Variable modifications:
K5 : Propionyl (K)
K10 : Propionyl (K)
K12 : Propionyl-Methylation (K)
Ions Score: 39 **Expect:** 0.15
Matches : 30/132 fragment ions using 47 most inter

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	259.0925	130.0499			241.0819	121.0446	E	1640.9218	820.9645	1623.8952	812.4512	1622.9112	811.9592	12
3	372.1765	186.5919			354.1660	177.5866	I	1511.8792	756.4432	1494.8526	747.9299	1493.8686	747.4379	11
4	501.2191	251.1132			483.2086	242.1079	E	***1398.7951***	699.9012	1381.7686	691.3879	1380.7845	690.8959	10
5	**685.3403**	343.1738	668.3137	334.6605	667.3297	334.1685	K	***1269.7525***	635.3799	1252.7260	626.8666	1251.7419	626.3746	9
6	**813.3989**	407.2031	796.3723	398.6898	795.3883	398.1978	Q	***1085.6313***	543.3193	1068.6048	534.8060	1067.6208	534.3140	8
7	884.4360	442.7216	867.4094	434.2084	866.4254	433.7164	A	***957.5728***	479.2900	940.5462	470.7767	939.5622	470.2847	7
8	**997.5201**	499.2637	980.4935	490.7504	979.5095	490.2584	L	886.5356	443.7715	869.5091	435.2582	868.5251	434.7662	6
9	**1126.5626**	563.7850	1109.5361	555.2717	1108.5521	554.7797	E	***773.4516***	387.2294	756.4250	378.7162	755.4410	378.2241	5
10	**1310.6838**	655.8456	1293.6573	647.3323	1292.6733	646.8403	K	***644.4090***	322.7081	627.3824	314.1949	626.3984	313.7028	4
11	1397.7159	699.3616	1380.6893	690.8483	1379.7053	690.3563	S	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	3
12	1595.8527	798.4300	1578.8261	789.9167	1577.8421	789.4247	K	***373.2558***	187.1315	356.2292	178.6183			2
13							R	175.1190	88.0631	158.0924	79.5498			1

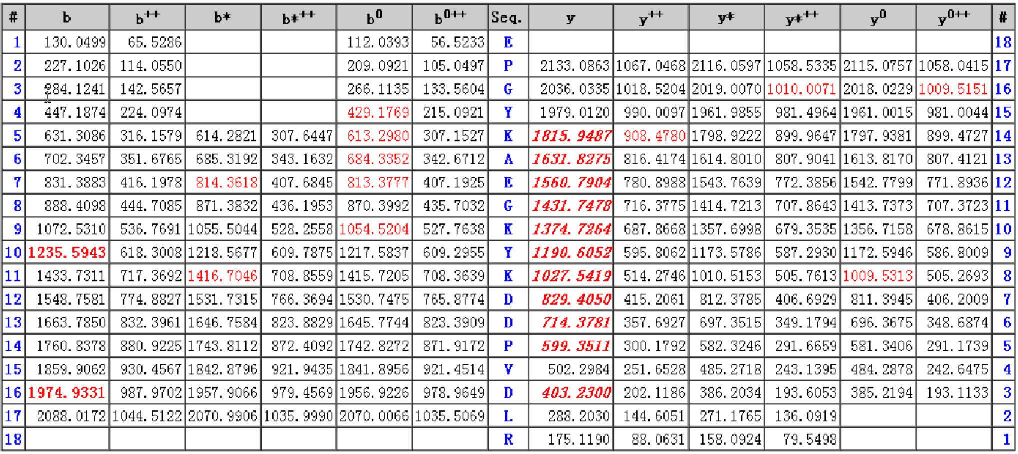
MS/MS Fragmentation of **EPGYKAEGKYKDDPVDLR**
Found in **Q9Y2W1**, Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2

Match to Query 17355: 2261.124128 from(1131.569340,2+) intensity(220357.1875)
Title: File1335 Spectrum15418 scans: 16533
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

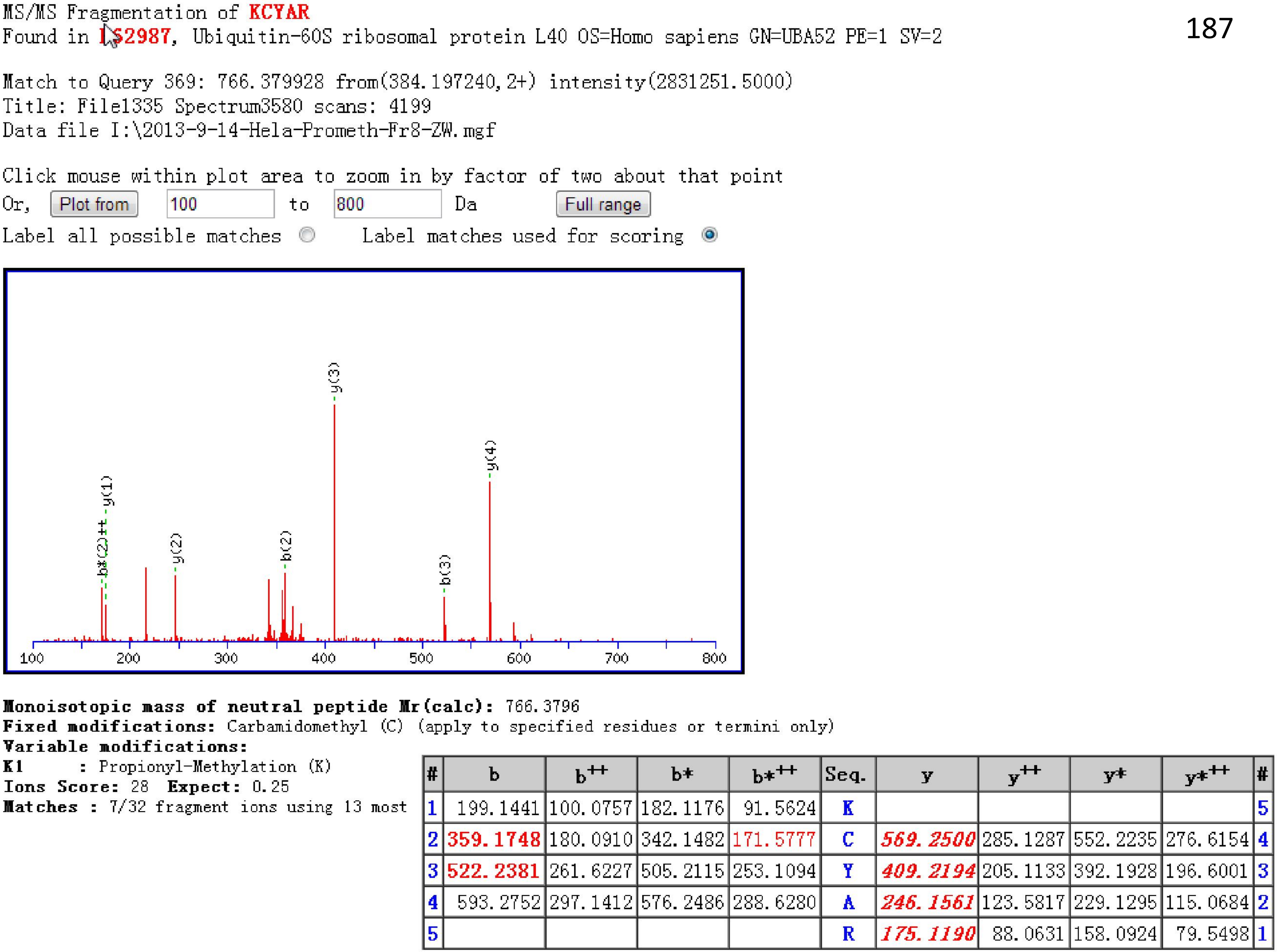
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2261.1216
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K5 : Propionyl (K)
K9 : Propionyl (K)
K11 : Propionyl-Methylation (K)
Ions Score: 69 **Expect:** 0.00015
Matches : 24/192 fragment ions using 34 most intense peaks (



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							18
2	227.1026	114.0550			209.0921	105.0497	P	2133.0863	1067.0468	2116.0597	1058.5335	2115.0757	1058.0415	17
3	284.1241	142.5657			266.1135	133.5604	G	2036.0335	1018.5204	2019.0070	1010.0071	2018.0229	1009.5151	16
4	447.1874	224.0974			429.1769	215.0921	Y	1979.0120	990.0097	1961.9855	981.4964	1961.0015	981.0044	15
5	631.3086	316.1579	614.2821	307.6447	613.2980	307.1527	K	***1815.9487***	908.4780	1798.9222	899.9647	1797.9381	899.4727	14
6	702.3457	351.6765	685.3192	343.1632	684.3352	342.6712	A	***1631.8275***	816.4174	1614.8010	807.9041	1613.8170	807.4121	13
7	831.3883	416.1978	814.3618	407.6845	813.3777	407.1925	E	***1560.7904***	780.8988	1543.7639	772.3856	1542.7799	771.8936	12
8	888.4098	444.7085	871.3832	436.1953	870.3992	435.7032	G	***1431.7478***	716.3775	1414.7213	707.8643	1413.7373	707.3723	11
9	1072.5310	536.7691	1055.5044	528.2558	1054.5204	527.7638	K	***1374.7264***	687.8668	1357.6998	679.3535	1356.7158	678.8615	10
10	**1235.5943**	618.3008	1218.5677	609.7875	1217.5837	609.2955	Y	***1190.6052***	595.8062	1173.5786	587.2930	1172.5946	586.8009	9
11	1433.7311	717.3692	1416.7046	708.8559	1415.7205	708.3639	K	***1027.5419***	514.2746	1010.5153	505.7613	1009.5313	505.2693	8
12	1548.7581	774.8827	1531.7315	766.3694	1530.7475	765.8774	D	***829.4050***	415.2061	812.3785	406.6929	811.3945	406.2009	7
13	1663.7850	832.3961	1646.7584	823.8829	1645.7744	823.3909	D	***714.3781***	357.6927	697.3515	349.1794	696.3675	348.6874	6
14	1760.8378	880.9225	1743.8112	872.4092	1742.8272	871.9172	P	***599.3511***	300.1792	582.3246	291.6659	581.3406	291.1739	5
15	1859.9062	930.4567	1842.8796	921.9435	1841.8956	921.4514	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
16	**1974.9331**	987.9702	1957.9066	979.4569	1956.9226	978.9649	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
17	2088.0172	1044.5122	2070.9906	1035.9990	2070.0066	1035.5069	L	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1



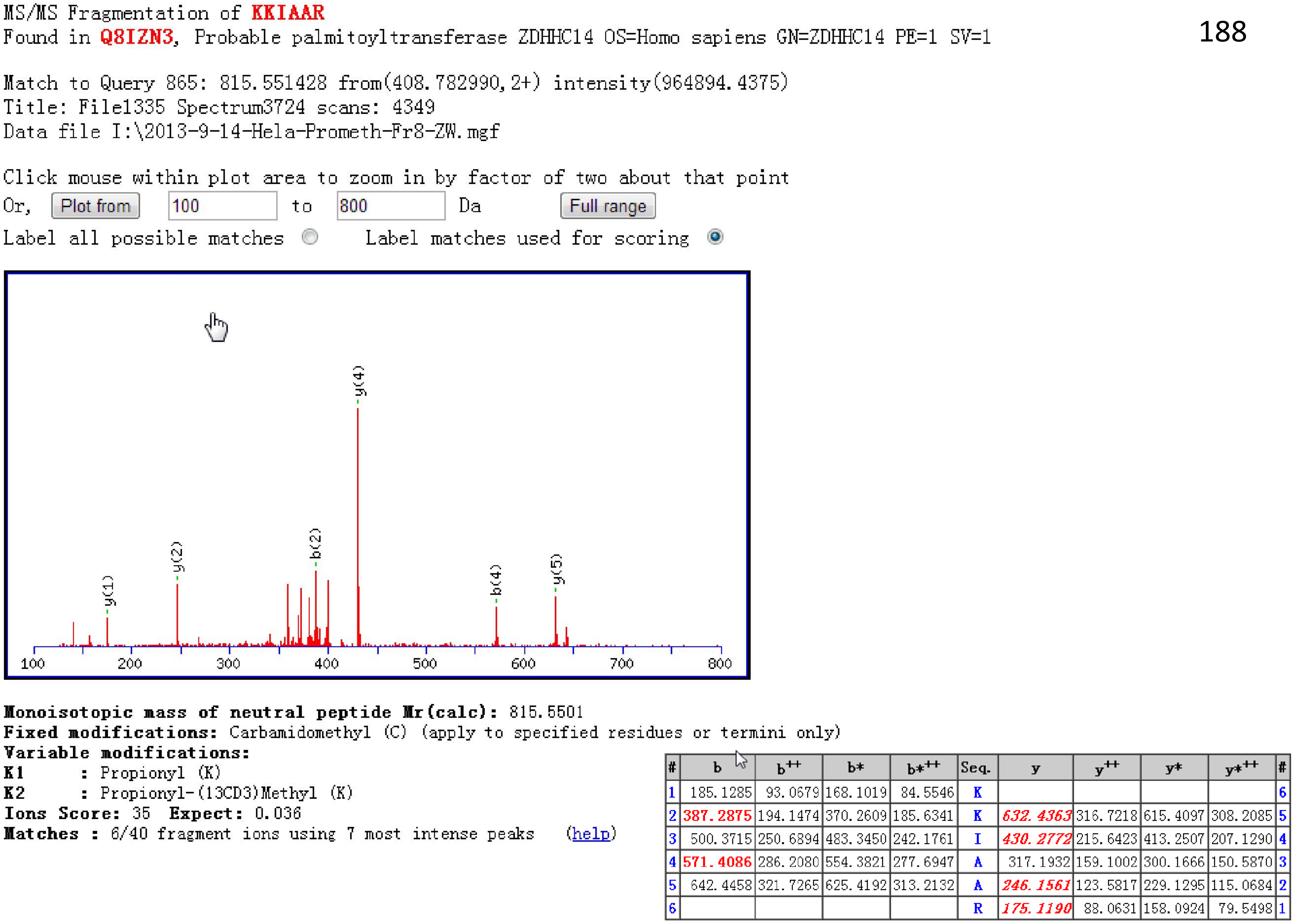
MS/MS Fragmentation of **KCYAR**
Found in **IS2987**, Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2

Match to Query 369: 766.379928 from(384.197240,2+) intensity(2831251.5000)
Title: File1335 Spectrum3580 scans: 4199
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 766.3796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 28 **Expect:** 0.25
Matches : 7/32 fragment ions using 13 most

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	199.1441	100.0757	182.1176	91.5624	K					5
2	**359.1748**	180.0910	342.1482	171.5777	C	***569.2500***	285.1287	552.2235	276.6154	4
3	**522.2381**	261.6227	505.2115	253.1094	Y	***409.2194***	205.1133	392.1928	196.6001	3
4	593.2752	297.1412	576.2486	288.6280	A	***246.1561***	123.5817	229.1295	115.0684	2
5					R	***175.1190***	88.0631	158.0924	79.5498	1



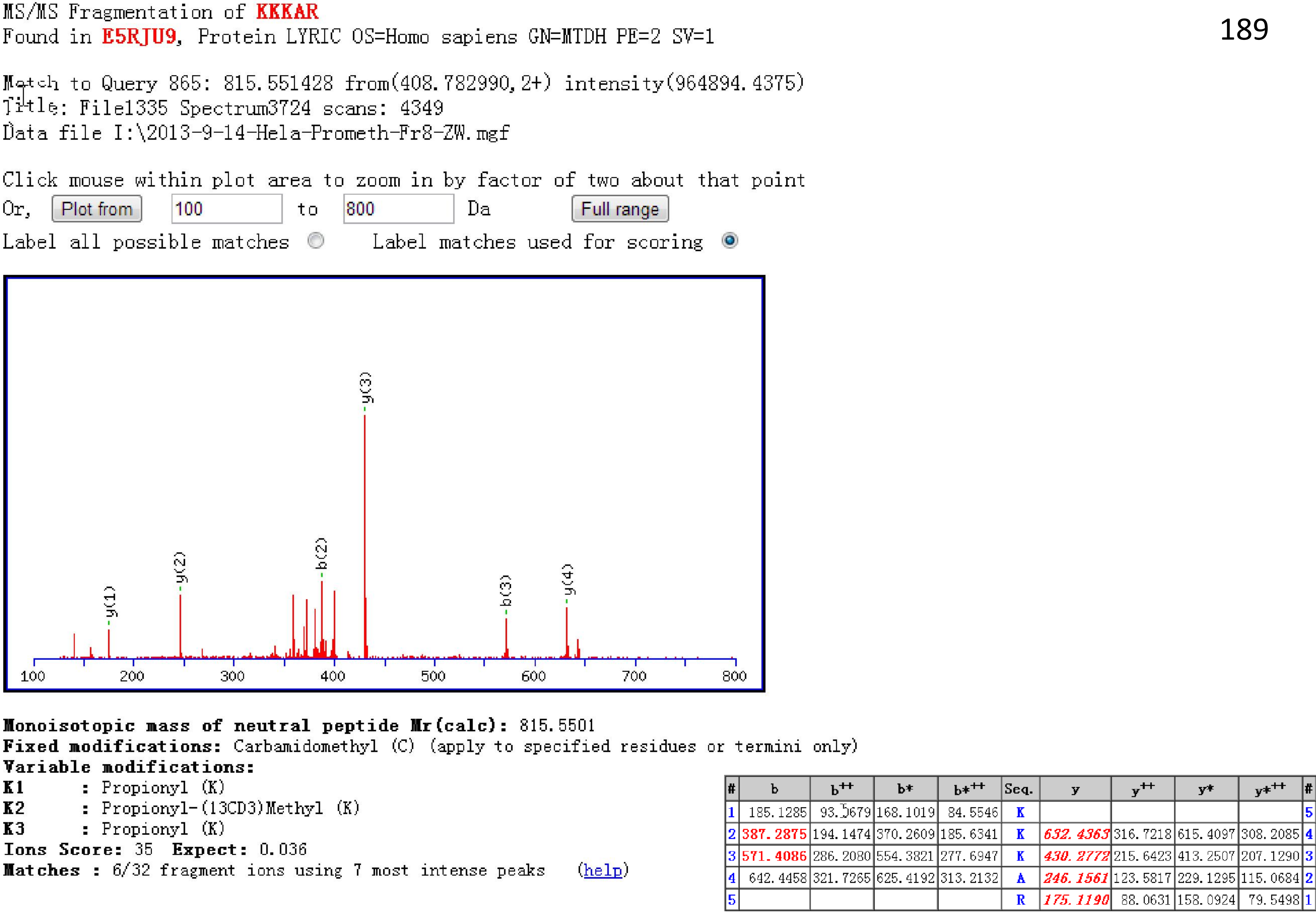
MS/MS Fragmentation of **KKIAAR**
Found in **Q8IZN3**, Probable palmitoyltransferase ZDHHC14 OS=Homo sapiens GN=ZDHHC14 PE=1 SV=1

Match to Query 865: 815.551428 from(408.782990,2+) intensity(964894.4375)
Title: File1335 Spectrum3724 scans: 4349
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 815.5501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 35 **Expect:** 0.036
Matches : 6/40 fragment ions using 7 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	185.1285	93.0679	168.1019	84.5546	K					6
2	**387.2875**	194.1474	370.2609	185.6341	K	***632.4363***	316.7218	615.4097	308.2085	5
3	500.3715	250.6894	483.3450	242.1761	I	***430.2772***	215.6423	413.2507	207.1290	4
4	**571.4086**	286.2080	554.3821	277.6947	A	317.1932	159.1002	300.1666	150.5870	3
5	642.4458	321.7265	625.4192	313.2132	A	***246.1561***	123.5817	229.1295	115.0684	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **KKKAR**
Found in **E5RJU9**, Protein LYRIC OS=Homo sapiens GN=MTDH PE=2 SV=1

Match to Query 865: 815.551428 from(408.782990,2+) intensity(964894.4375)
Title: File1335 Spectrum3724 scans: 4349
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

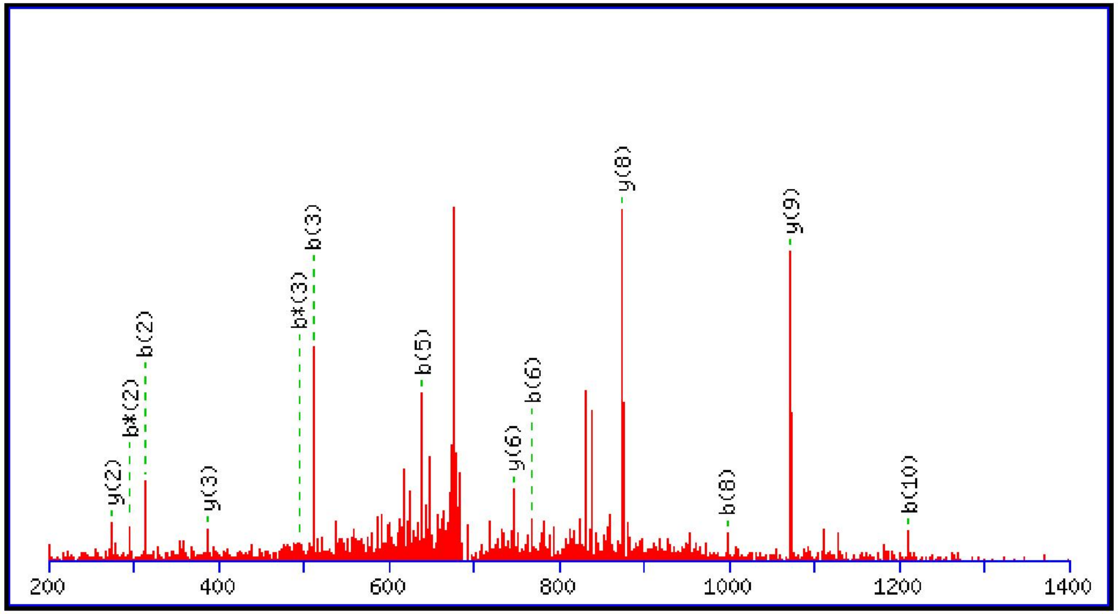
Monoisotopic mass of neutral peptide Mr(calc): 815.5501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K2 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 35 **Expect:** 0.036
Matches : 6/32 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	185.1285	93.5679	168.1019	84.5546	K					5
2	**387.2875**	194.1474	370.2609	185.6341	K	***632.4363***	316.7218	615.4097	308.2085	4
3	**571.4086**	286.2080	554.3821	277.6947	K	***430.2772***	215.6423	413.2507	207.1290	3
4	642.4458	321.7265	625.4192	313.2132	A	***246.1561***	123.5817	229.1295	115.0684	2
5					R	***175.1190***	88.0631	158.0924	79.5498	1
)

MS/MS Fragmentation of **KQKGAETELVR**
Found in **F5GWB7**, Putative ribosomal RNA methyltransferase NOP2 (Fragment) OS=Homo sapiens GN=NOP2 PE=2 SV=1

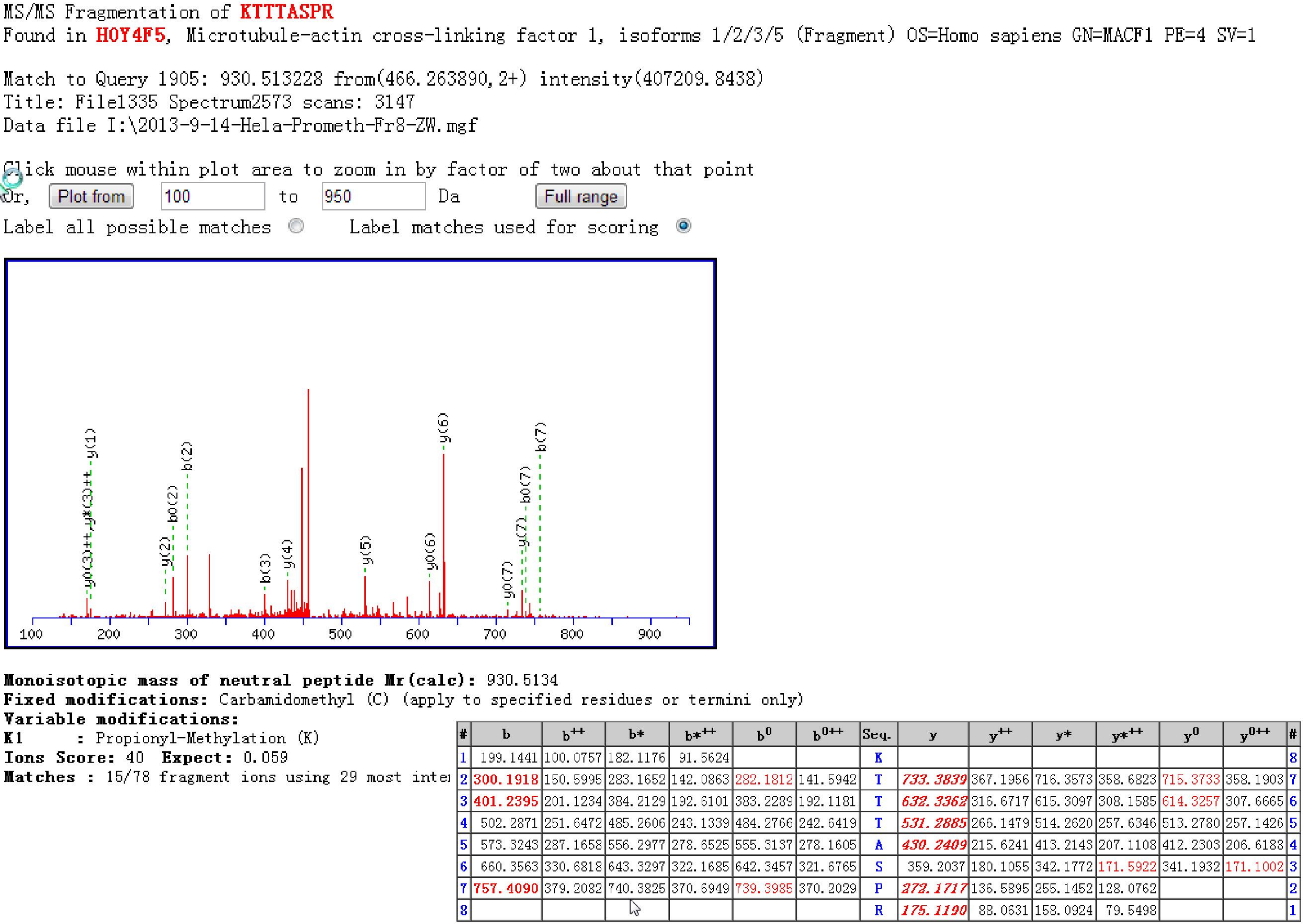
Match to Query 8071: 1383.771708 from(692.893130,2+) intensity(148107.1250)
Title: File1335 Spectrum10460 scans: 11368
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1383.7722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-Methylation (K)
Ions Score: 35 **Expect:** 0.28
Matches : 13/104 fragment ions using 24 most intense pea

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							11
2	***313.1870***	157.0972	296.1605	148.5839			Q	1200.6583	600.8328	1183.6317	592.3195	1182.6477	591.8275	10
3	***511.3239***	256.1656	494.2973	247.6523			K	***1072.5997***	536.8035	1055.5732	528.2902	1054.5891	527.7982	9
4	568.3453	284.6763	551.3188	276.1630			G	***874.4629***	437.7351	857.4363	429.2218	856.4523	428.7298	8
5	***639.3824***	320.1948	622.3559	311.6816			A	817.4414	409.2243	800.4149	400.7111	799.4308	400.2191	7
6	***768.4250***	384.7162	751.3985	376.2029	750.4145	375.7109	E	***746.4043***	373.7058	729.3777	365.1925	728.3937	364.7005	6
7	869.4727	435.2400	852.4462	426.7267	851.4621	426.2347	T	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
8	***998.5153***	499.7613	981.4888	491.2480	980.5047	490.7560	E	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
9	1111.5994	556.3033	1094.5728	547.7900	1093.5888	547.2980	L	***387.2714***	194.1394	370.2449	185.6261			3
10	***1210.6678***	605.8375	1193.6412	597.3243	1192.6572	596.8322	V	***274.1874***	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KTTTASPR**

Found in **H0Y4F5**, Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Fragment) OS=Homo sapiens GN=MACF1 PE=4 SV=1

Match to Query 1905: 930.513228 from(466.263890,2+) intensity(407209.8438)

Title: File1335 Spectrum2573 scans: 3147

Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

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

Monoisotopic mass of neutral peptide Mr(calc): 930.5134

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

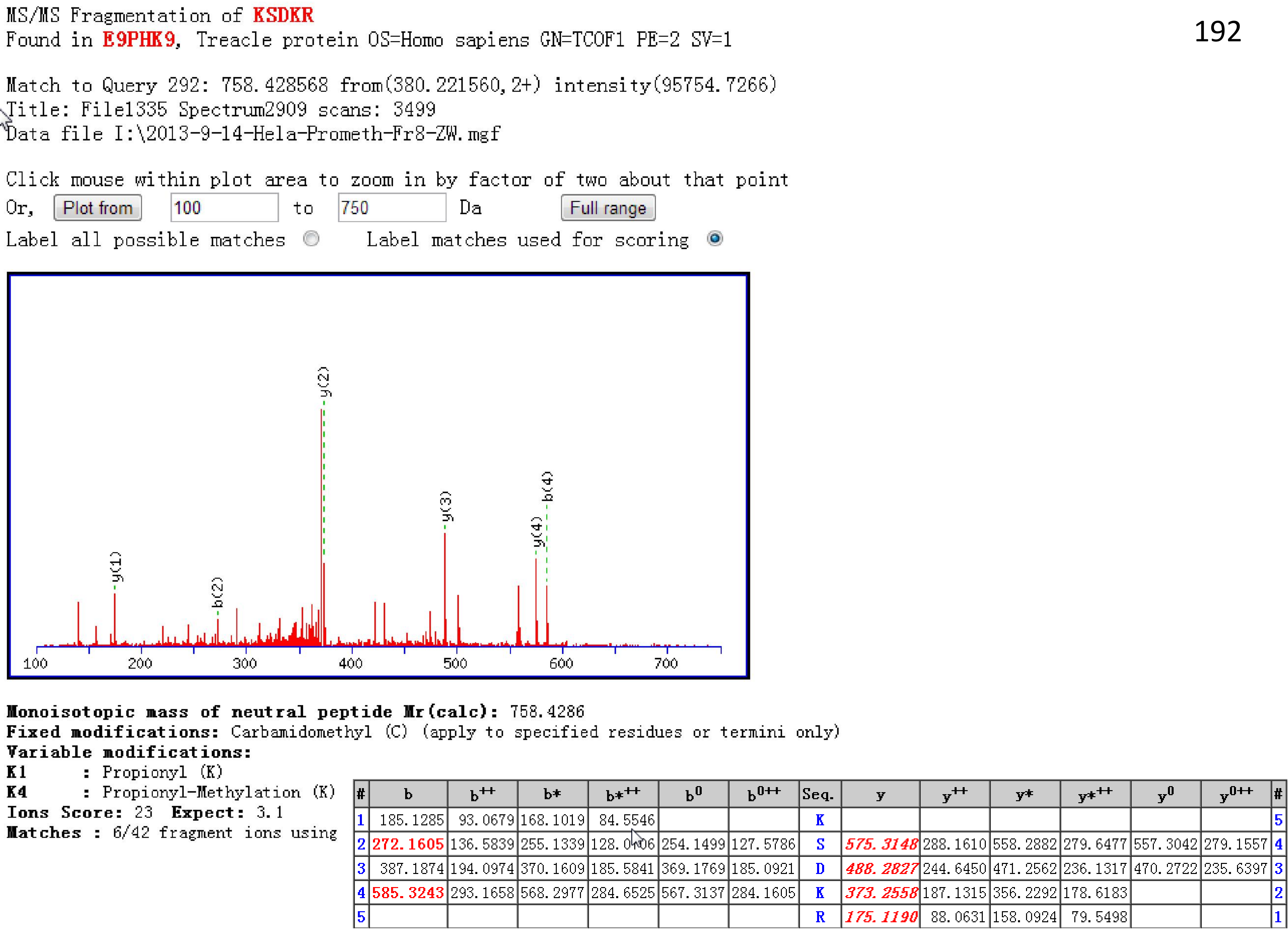
Variable modifications:

K1 : Propionyl-Methylation (K)

Ions Score: 40 **Expect:** 0.059

Matches : 15/78 fragment ions using 29 most inte

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							8
2	**300.1918**	150.5995	283.1652	142.0863	282.1812	141.5942	T	***733.3839***	367.1956	716.3573	358.6823	715.3733	358.1903	7
3	**401.2395**	201.1234	384.2129	192.6101	383.2289	192.1181	T	***632.3362***	316.6717	615.3097	308.1585	614.3257	307.6665	6
4	502.2871	251.6472	485.2606	243.1339	484.2766	242.6419	T	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	5
5	573.3243	287.1658	556.2977	278.6525	555.3137	278.1605	A	***430.2409***	215.6241	413.2143	207.1108	412.2303	206.6188	4
6	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
7	**757.4090**	379.2082	740.3825	370.6949	739.3985	370.2029	P	***272.1717***	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KSDKR**
Found in **E9PHK9**, Treacle protein OS=Homo sapiens GN=TCOF1 PE=2 SV=1

Match to Query 292: 758.428568 from(380.221560,2+) intensity(95754.7266)
Title: File1335 Spectrum2909 scans: 3499
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

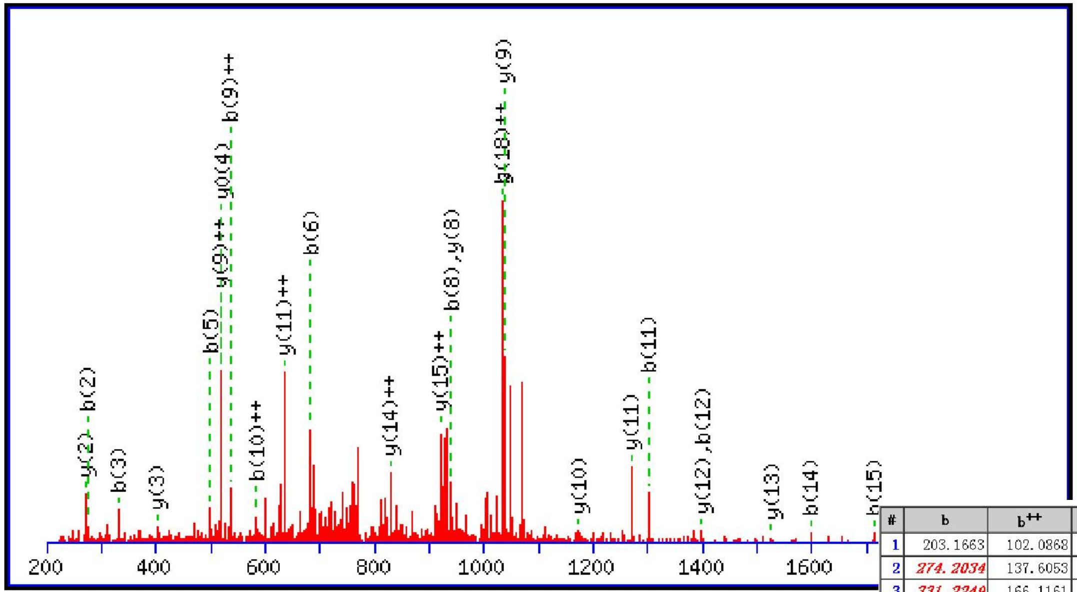
Monoisotopic mass of neutral peptide Mr(calc): 758.4286
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K4 : Propionyl-Methylation (K)
Ions Score: 23 **Expect:** 3.1
Matches : 6/42 fragment ions using

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							5
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	S	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	4
3	387.1874	194.0974	370.1609	185.5841	369.1769	185.0921	D	***488.2827***	244.6450	471.2562	236.1317	470.2722	235.6397	3
4	**585.3243**	293.1658	568.2977	284.6525	567.3137	284.1605	K	***373.2558***	187.1315	356.2292	178.6183			2
5							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAGPAKEQEPMPTVDSHEPR**
Found in **H3BU16**, Hematological and neurological-expressed 1-like protein (Fragment) OS=Homo sapiens GN=HN1L PE=2 SV=1

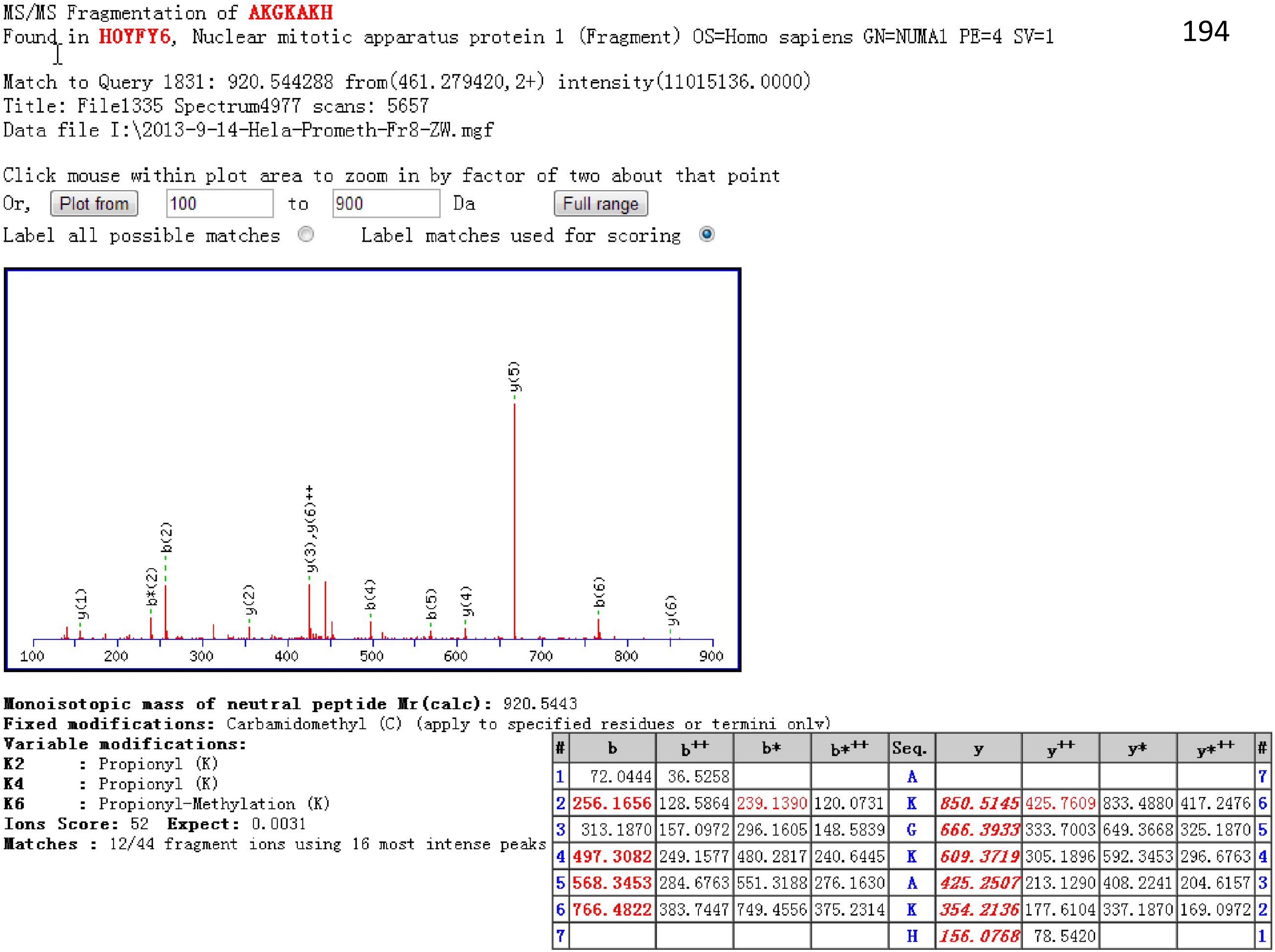
Match to Query 17788: 2337.181782 from(780.067870,3+) intensity(170386.1250)
Title: File1335 Spectrum9443 scans: 10309
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2337.1816
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
M11 : Label:13C(1)2H(3) (M)
Ions Score: 52 **Expect:** 0.0088
Matches : 26/212 fragment ions using 49 most intense peaks (he

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							20
2	***274.2034***	137.6053	257.1769	129.0921			A	2136.0299	1068.5186	2119.0033	1060.0053	2118.0193	1059.5133	19
3	***331.2249***	166.1161	314.1983	157.6028			G	2064.9928	1033.0000	2047.9662	1024.4867	2046.9822	1023.9947	18
4	428.2776	214.6425	411.2511	206.1292			P	2007.9713	1004.4893	1990.9448	995.9760	1989.9607	995.4840	17
5	***499.3147***	250.1610	482.2882	241.6477			A	1910.9185	955.9629	1893.8920	947.4496	1892.9080	946.9576	16
6	***683.4359***	342.2216	666.4094	333.7083			K	1839.8814	920.4444	1822.8549	911.9311	1821.8709	911.4391	15
7	812.4785	406.7429	795.4520	398.2296	794.4680	397.7376	E	1655.7602	828.3838	1638.7337	819.8705	1637.7497	819.3785	14
8	***940.5371***	470.7722	923.5105	462.2589	922.5265	461.7669	Q	***1526.7177***	763.8625	1509.6911	755.3492	1508.7071	754.8572	13
9	1069.5797	**535.2935**	1052.5531	526.7802	1051.5691	526.2882	E	***1398.6591***	699.8332	1381.6325	691.3199	1380.6485	690.8279	12
10	1166.6325	**583.8199**	1149.6059	575.3066	1148.6219	574.8146	P	***1269.6165***	635.3119	1252.5899	626.7986	1251.6059	626.3066	11
11	***1301.6951***	651.3512	1284.6686	642.8379	1283.6846	642.3459	M	***1172.5637***	586.7855	1155.5372	578.2722	1154.5532	577.7802	10
12	***1398.7479***	699.8776	1381.7213	691.3643	1380.7373	690.8723	P	***1037.5010***	519.2542	1020.4745	510.7409	1019.4905	510.2489	9
13	1499.7956	750.4014	1482.7690	741.8881	1481.7850	741.3961	T	***940.4483***	470.7278	923.4217	462.2145	922.4377	461.7225	8
14	***1598.8640***	799.9356	1581.8374	791.4224	1580.8534	790.9303	V	839.4006	420.2039	822.3741	411.6907	821.3900	411.1987	7
15	***1713.8909***	857.4491	1696.8644	848.9358	1695.8804	848.4438	D	740.3322	370.6697	723.3056	362.1565	722.3216	361.6645	6
16	1800.9229	900.9651	1783.8964	892.4518	1782.9124	891.9598	S	625.3052	313.1563	608.2787	304.6430	607.2947	304.1510	5
17	1937.9819	969.4946	1920.9553	960.9813	1919.9713	960.4893	H	538.2732	269.6402	521.2467	261.1270	520.2627	260.6350	4
18	2067.0245	**1034.0159**	2049.9979	1025.5026	2049.0139	1025.0106	E	***401.2143***	201.1108	384.1878	192.5975	383.2037	192.1055	3
19	2164.0772	1082.5422	2147.0507	1074.0290	2146.0667	1073.5370	P	***272.1717***	136.5895	255.1452	128.0762			2
20							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKGKAKH**
Found in **H0YFY6**, Nuclear mitotic apparatus protein 1 (Fragment) OS=Homo sapiens GN=NUMA1 PE=4 SV=1

Match to Query 1831: 920.544288 from(461.279420,2+) intensity(11015136.0000)
Title: File1335 Spectrum4977 scans: 5657
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

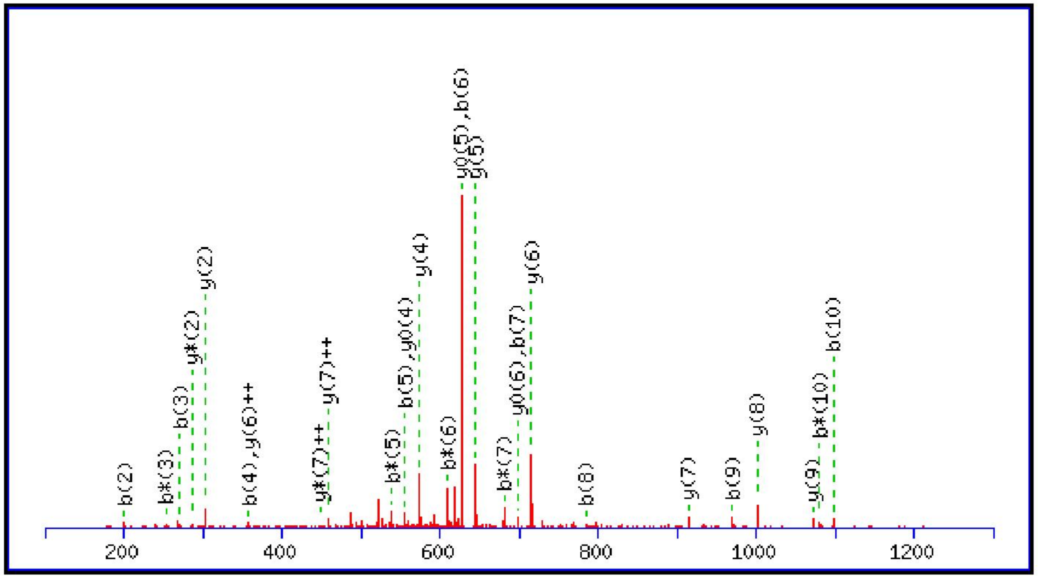
Monoisotopic mass of neutral peptide Mr(calc): 920.5443
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K4 : Propionyl (K)
K6 : Propionyl-Methylation (K)
Ions Score: 52 **Expect:** 0.0031
Matches : 12/44 fragment ions using 16 most intense peaks

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.0444	36.5258			A					7
2	**256.1656**	128.5864	239.1390	120.0731	K	***850.5145***	425.7609	833.4880	417.2476	6
3	313.1870	157.0972	296.1605	148.5839	G	***666.3933***	333.7003	649.3668	325.1870	5
4	**497.3082**	249.1577	480.2817	240.6445	K	***609.3719***	305.1896	592.3453	296.6763	4
5	**568.3453**	284.6763	551.3188	276.1630	A	***425.2507***	213.1290	408.2241	204.6157	3
6	**766.4822**	383.7447	749.4556	375.2314	K	***354.2136***	177.6104	337.1870	169.0972	2
7					H	***156.0768***	78.5420			1

MS/MS Fragmentation of QAASKAASKQR
Found in Q9H1E3, Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1

Match to Query 6574: 1270.698588 from(636.356570,2+) intensity(3423992.7500)
Title: File1335 Spectrum4404 scans: 5060
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.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 ●



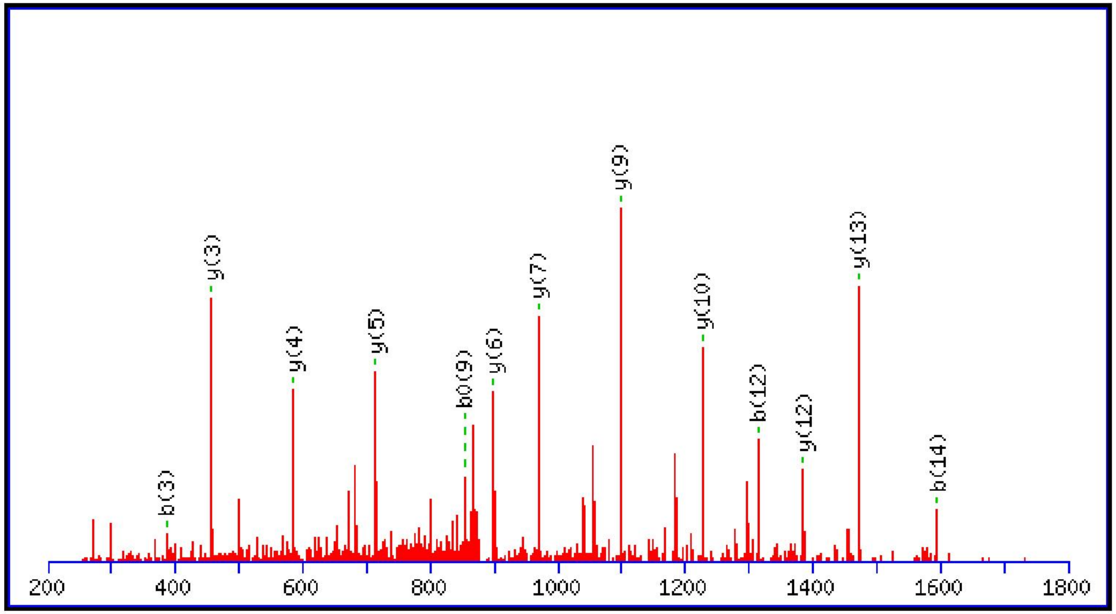
Monoisotopic mass of neutral peptide Mr(calc): 1270.6993
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-Methylation (K)
K9 : Propionyl (K)
Ions Score: 60 **Expect:** 0.00069
Matches : 28/108 fragment ions using 43 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	200.1030	100.5551	183.0764	92.0418			A	1143.6480	572.3277	1126.6215	563.8144	1125.6375	563.3224	10
3	271.1401	136.0737	254.1135	127.5604			A	1072.6109	536.8091	1055.5844	528.2958	1054.6004	527.8038	9
4	358.1721	179.5897	341.1456	171.0764	340.1615	170.5844	S	1001.5738	501.2905	984.5473	492.7773	983.5633	492.2853	8
5	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	K	914.5418	457.7745	897.5152	449.2613	896.5312	448.7693	7
6	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	A	716.4050	358.7061	699.3784	350.1928	698.3944	349.7008	6
7	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	A	645.3678	323.1876	628.3413	314.6743	627.3573	314.1823	5
8	785.4152	393.2112	768.3886	384.6980	767.4046	384.2060	S	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	4
9	969.5364	485.2718	952.5098	476.7585	951.5258	476.2665	K	487.2987	244.1530	470.2722	235.6397			3
10	1097.5949	549.3011	1080.5684	540.7878	1079.5844	540.2958	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KVSSAEGAAKEEPKR**
Found in **P05114**, Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3

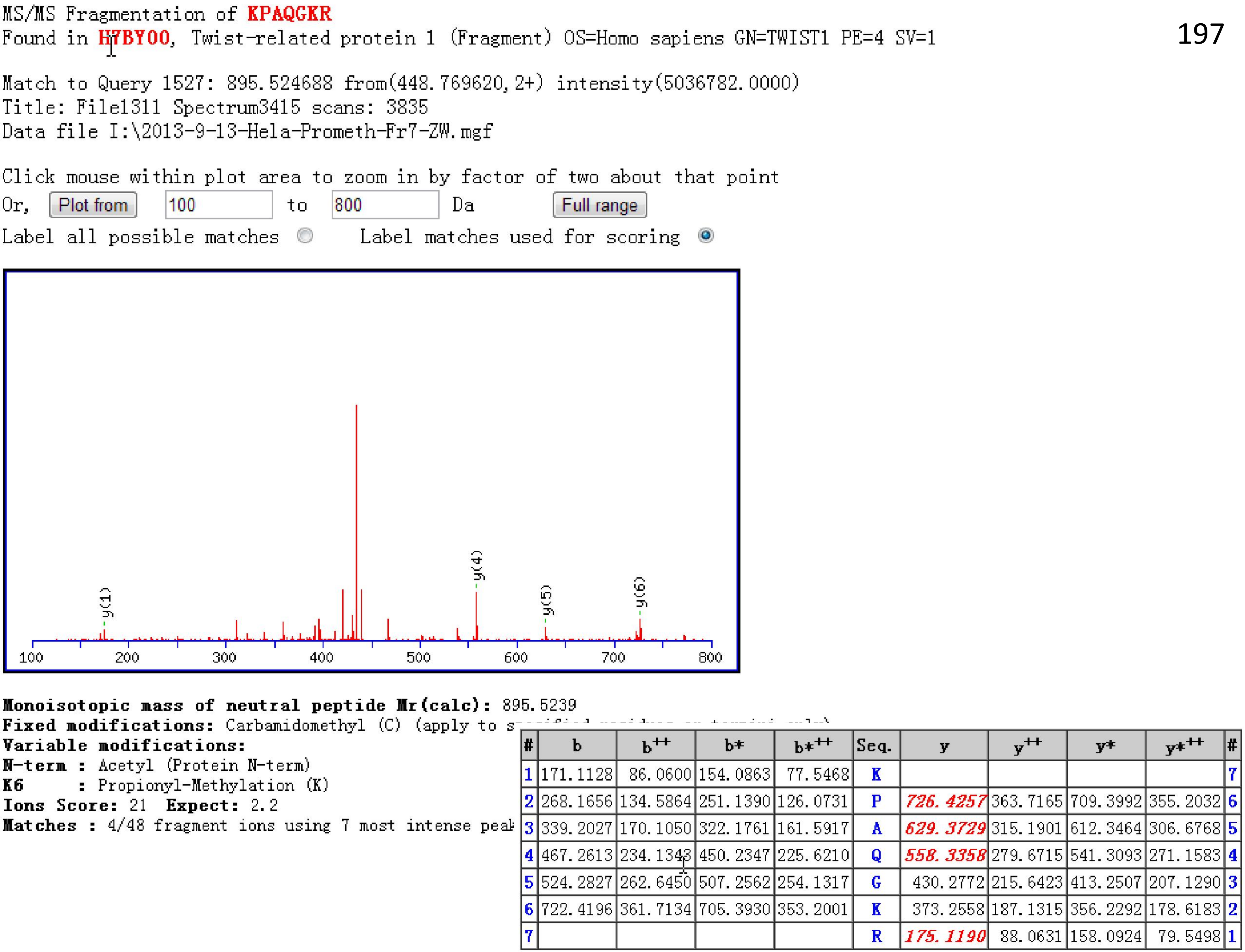
Match to Query 10403: 1767.936628 from(884.975590,2+) intensity(180978.7031)
Title: File1311 Spectrum7689 scans: 8288
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1767.93
Fixed modifications: Carbamidomethyl (C) (apply to specifi
Variable modifications:
K1 : Propionyl-Methylation (K)
K10 : Propionyl (K)
K14 : Propionyl (K)
Ions Score: 81 **Expect:** 8.2e-006
Matches : 13/158 fragment ions using 15 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							15
2	298.2125	149.6099	281.1860	141.0966			V	1570.8071	785.9072	1553.7806	777.3939	1552.7966	776.9019	14
3	**385.2445**	193.1259	368.2180	184.6126	367.2340	184.1206	S	***1471.7387***	736.3730	1454.7122	727.8597	1453.7281	727.3677	13
4	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	S	***1384.7067***	692.8570	1367.6801	684.3437	1366.6961	683.8517	12
5	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	A	1297.6747	649.3410	1280.6481	640.8277	1279.6641	640.3357	11
6	672.3563	336.6818	655.3297	328.1685	654.3457	327.6765	E	***1226.6375***	613.8224	1209.6110	605.3091	1208.6270	604.8171	10
7	729.3777	365.1925	712.3512	356.6792	711.3672	356.1872	G	***1097.5950***	549.3011	1080.5684	540.7878	1079.5844	540.2958	9
8	800.4149	400.7111	783.3883	392.1978	782.4043	391.7058	A	1040.5735	520.7904	1023.5469	512.2771	1022.5629	511.7851	8
9	871.4520	436.2296	854.4254	427.7163	853.4414	427.2243	A	***969.5364***	485.2718	952.5098	476.7585	951.5258	476.2665	7
10	1055.5732	528.2902	1038.5466	519.7769	1037.5626	519.2849	K	***898.4993***	449.7533	881.4727	441.2400	880.4887	440.7480	6
11	1184.6157	592.8115	1167.5892	584.2982	1166.6052	583.8062	E	***714.3781***	357.6927	697.3515	349.1794	696.3675	348.6874	5
12	**1313.6583**	657.3328	1296.6318	648.8195	1295.6478	648.3275	E	***585.3355***	293.1714	568.3089	284.6581	567.3249	284.1661	4
13	1410.7111	705.8592	1393.6846	697.3459	1392.7005	696.8539	P	***456.2929***	228.6501	439.2663	220.1368			3
14	**1594.8323**	797.9198	1577.8057	789.4065	1576.8217	788.9145	K	359.2401	180.1237	342.2136	171.6104			2
15							R	175.1190	88.0631	158.0924	79.5498			1



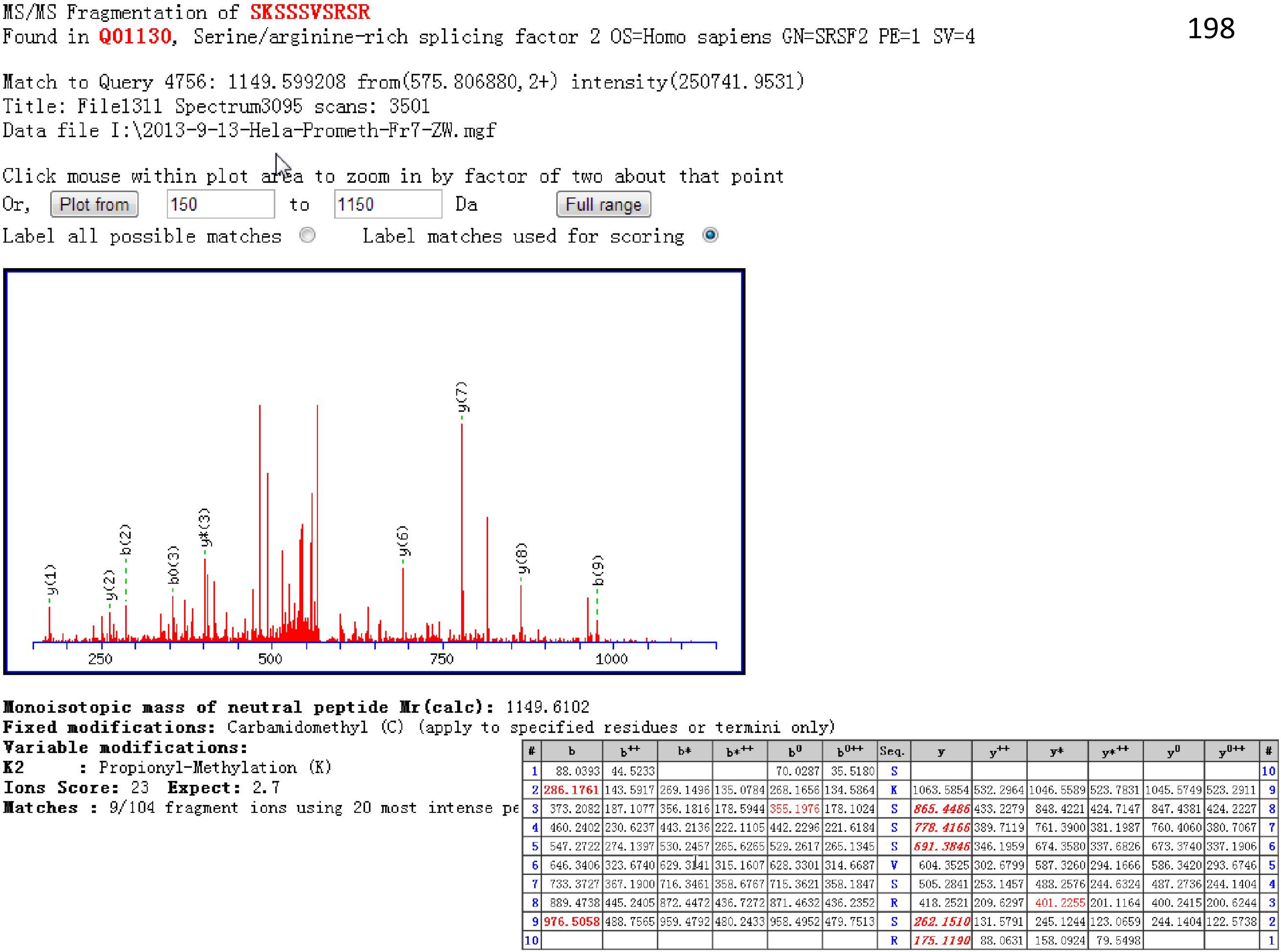
MS/MS Fragmentation of **KPAQGKR**
Found in **H7BY00**, Twist-related protein 1 (Fragment) OS=Homo sapiens GN=TWIST1 PE=4 SV=1

Match to Query 1527: 895.524688 from(448.769620,2+) intensity(5036782.0000)
Title: File1311 Spectrum3415 scans: 3835
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 895.5239
Fixed modifications: Carbamidomethyl (C) (apply to s
Variable modifications:
N-term : Acetyl (Protein N-term)
K6 : Propionyl-Methylation (K)
Ions Score: 21 **Expect:** 2.2
Matches : 4/48 fragment ions using 7 most intense peak

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	171.1128	86.0600	154.0863	77.5468	K					7
2	268.1656	134.5864	251.1390	126.0731	P	***726.4257***	363.7165	709.3992	355.2032	6
3	339.2027	170.1050	322.1761	161.5917	A	***629.3729***	315.1901	612.3464	306.6768	5
4	467.2613	234.1343	450.2347	225.6210	Q	***558.3358***	279.6715	541.3093	271.1583	4
5	524.2827	262.6450	507.2562	254.1317	G	430.2772	215.6423	413.2507	207.1290	3
6	722.4196	361.7134	705.3930	353.2001	K	373.2558	187.1315	356.2292	178.6183	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1



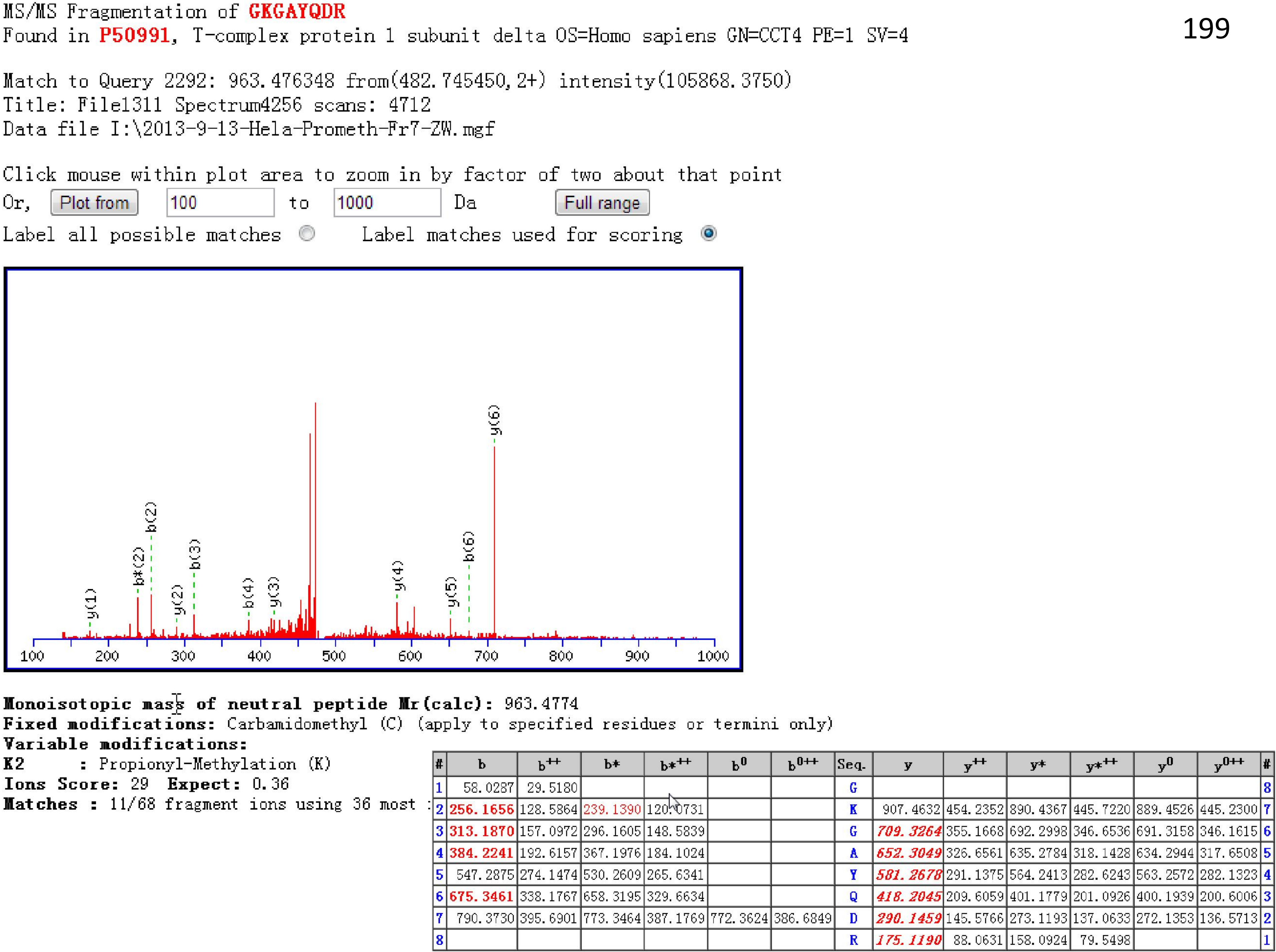
MS/MS Fragmentation of **SKSSSVSRSR**
Found in **Q01130**, Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4

Match to Query 4756: 1149.599208 from(575.806880,2+) intensity(250741.9531)
Title: File1311 Spectrum3095 scans: 3501
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1149.6102
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
Ions Score: 23 **Expect:** 2.7
Matches : 9/104 fragment ions using 20 most intense pe

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							10
2	**286.1761**	143.5917	269.1496	135.0784	268.1656	134.5864	K	1063.5854	532.2964	1046.5589	523.7831	1045.5749	523.2911	9
3	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	S	***865.4486***	433.2279	848.4221	424.7147	847.4381	424.2227	8
4	460.2402	230.6237	443.2136	222.1105	442.2296	221.6184	S	***778.4166***	389.7119	761.3900	381.1987	760.4060	380.7067	7
5	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	S	***691.3846***	346.1959	674.3580	337.6826	673.3740	337.1906	6
6	646.3406	323.6740	629.3141	315.1607	628.3301	314.6687	V	604.3525	302.6799	587.3260	294.1666	586.3420	293.6746	5
7	733.3727	367.1900	716.3461	358.6767	715.3621	358.1847	S	505.2841	253.1457	488.2576	244.6324	487.2736	244.1404	4
8	889.4738	445.2405	872.4472	436.7272	871.4632	436.2352	R	418.2521	209.6297	401.2255	201.1164	400.2415	200.6244	3
9	**976.5058**	488.7565	959.4792	480.2433	958.4952	479.7513	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	***175.1190***	88.0631	158.0924	79.5498			1



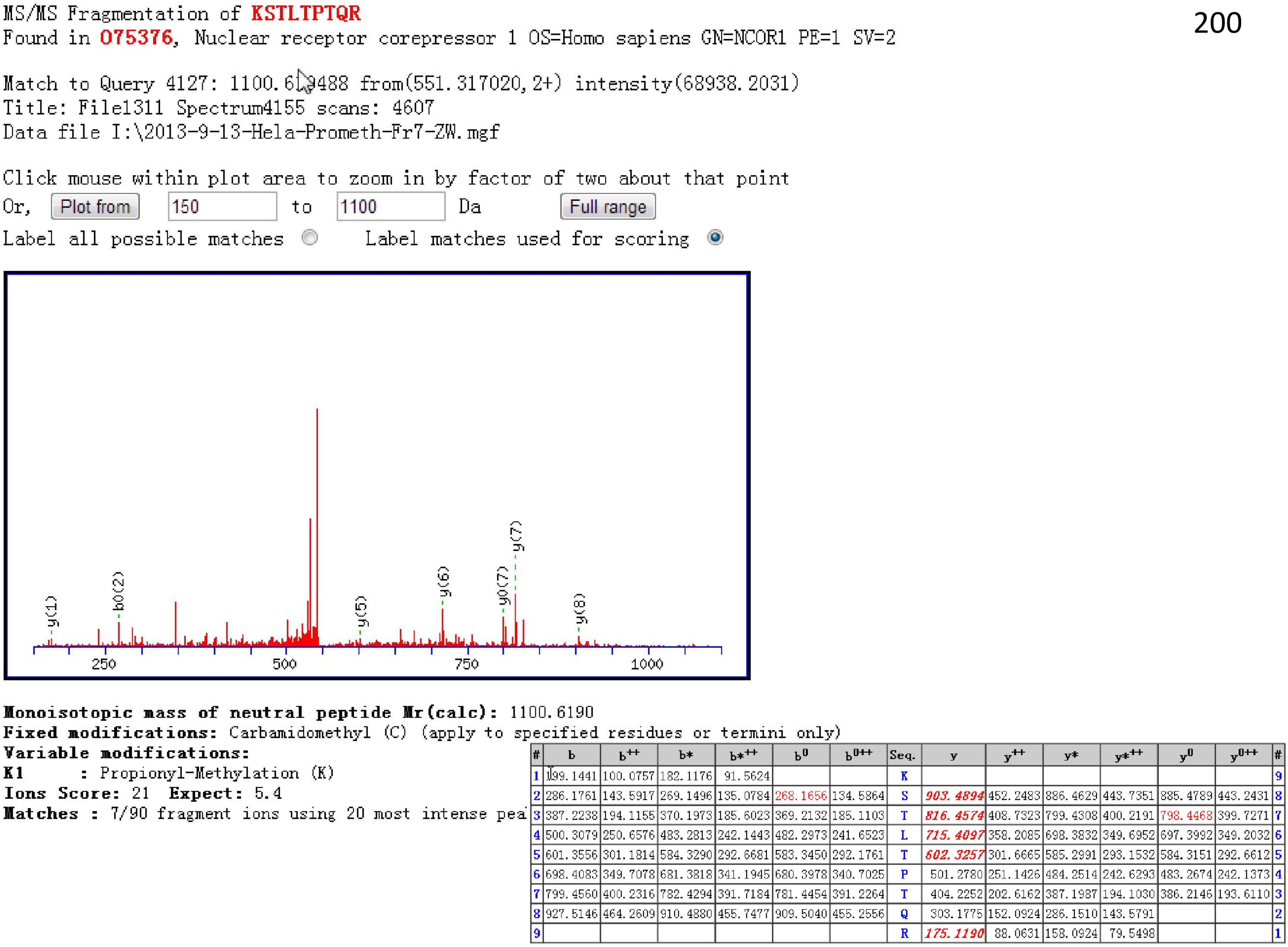
MS/MS Fragmentation of **GKGAYQDR**
Found in **P50991**, T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4

Match to Query 2292: 963.476348 from(482.745450,2+) intensity(105868.3750)
Title: File1311 Spectrum4256 scans: 4712
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 963.4774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
Ions Score: 29 **Expect:** 0.36
Matches : 11/68 fragment ions using 36 most :

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							8
2	**256.1656**	128.5864	239.1390	120.0731			K	907.4632	454.2352	890.4367	445.7220	889.4526	445.2300	7
3	**313.1870**	157.0972	296.1605	148.5839			G	***709.3264***	355.1668	692.2998	346.6536	691.3158	346.1615	6
4	**384.2241**	192.6157	367.1976	184.1024			A	***652.3049***	326.6561	635.2784	318.1428	634.2944	317.6508	5
5	547.2875	274.1474	530.2609	265.6341			Y	***581.2678***	291.1375	564.2413	282.6243	563.2572	282.1323	4
6	**675.3461**	338.1767	658.3195	329.6634			Q	***418.2045***	209.6059	401.1779	201.0926	400.1939	200.6006	3
7	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



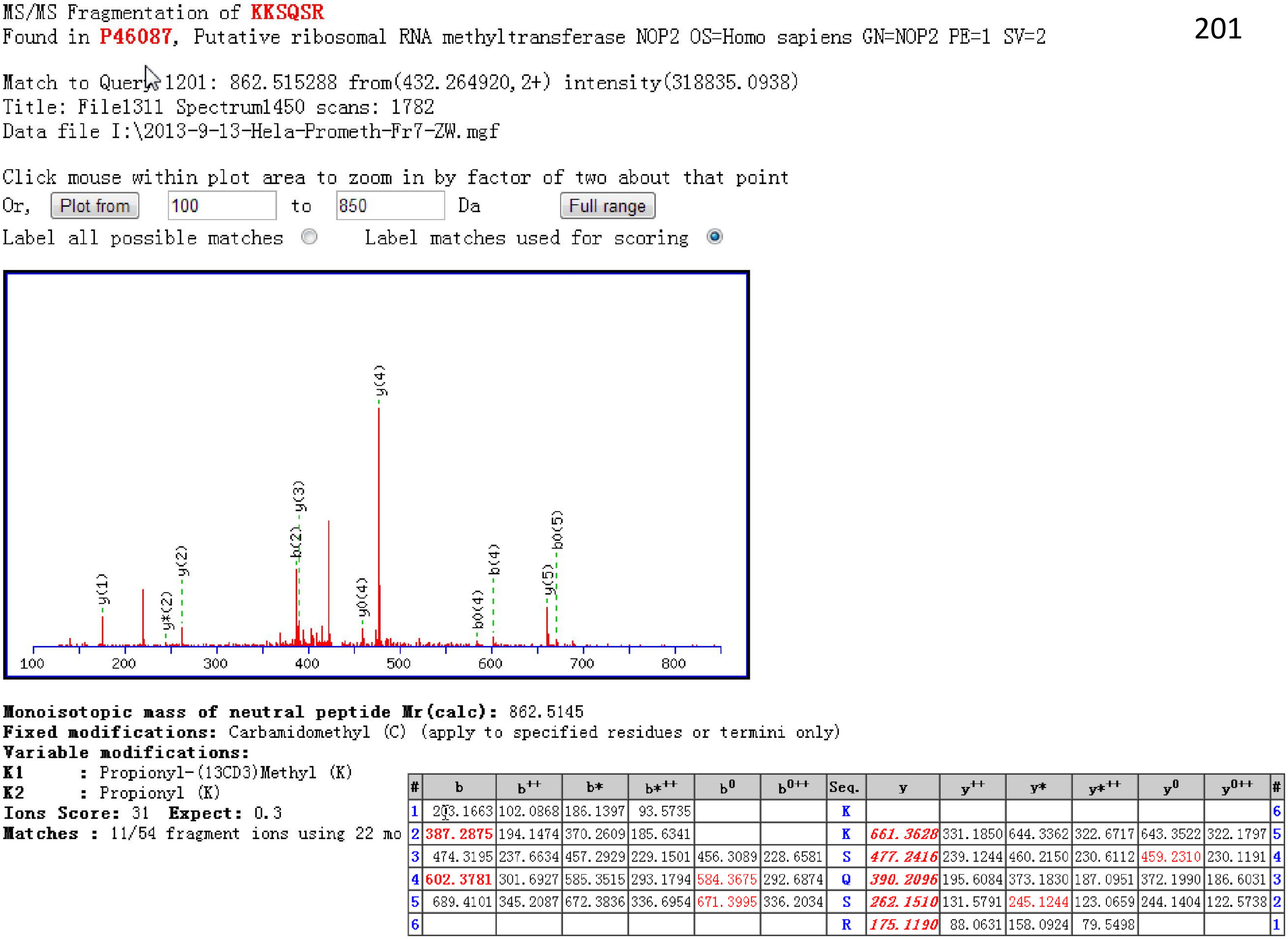
MS/MS Fragmentation of **KSTLTPTQR**
Found in **O75376**, Nuclear receptor corepressor 1 OS=Homo sapiens GN=NCOR1 PE=1 SV=2

Match to Query 4127: 1100.619488 from(551.317020,2+) intensity(68938.2031)
Title: File1311 Spectrum4155 scans: 4607
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1100.6190
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 21 **Expect:** 5.4
Matches : 7/90 fragment ions using 20 most intense pea

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							9
2	286.1761	143.5917	269.1496	135.0784	268.1656	134.5864	S	***903.4894***	452.2483	886.4629	443.7351	885.4789	443.2431	8
3	387.2238	194.1155	370.1973	185.6023	369.2132	185.1103	T	***816.4574***	408.7323	799.4308	400.2191	798.4468	399.7271	7
4	500.3079	250.6576	483.2813	242.1443	482.2973	241.6523	L	***715.4097***	358.2085	698.3832	349.6952	697.3992	349.2032	6
5	601.3556	301.1814	584.3290	292.6681	583.3450	292.1761	T	***602.3257***	301.6665	585.2991	293.1532	584.3151	292.6612	5
6	698.4083	349.7078	681.3818	341.1945	680.3978	340.7025	P	501.2780	251.1426	484.2514	242.6293	483.2674	242.1373	4
7	799.4560	400.2316	782.4294	391.7184	781.4454	391.2264	T	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
8	927.5146	464.2609	910.4880	455.7477	909.5040	455.2556	Q	303.1775	152.0924	286.1510	143.5791			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KKSQSR**

Found in **P46087**, Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2

Match to Query 1201: 862.515288 from(432.264920,2+) intensity(318835.0938)

Title: File1311 Spectrum1450 scans: 1782

Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

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

Or, 100 to 850 Da

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 862.5145

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

Variable modifications:

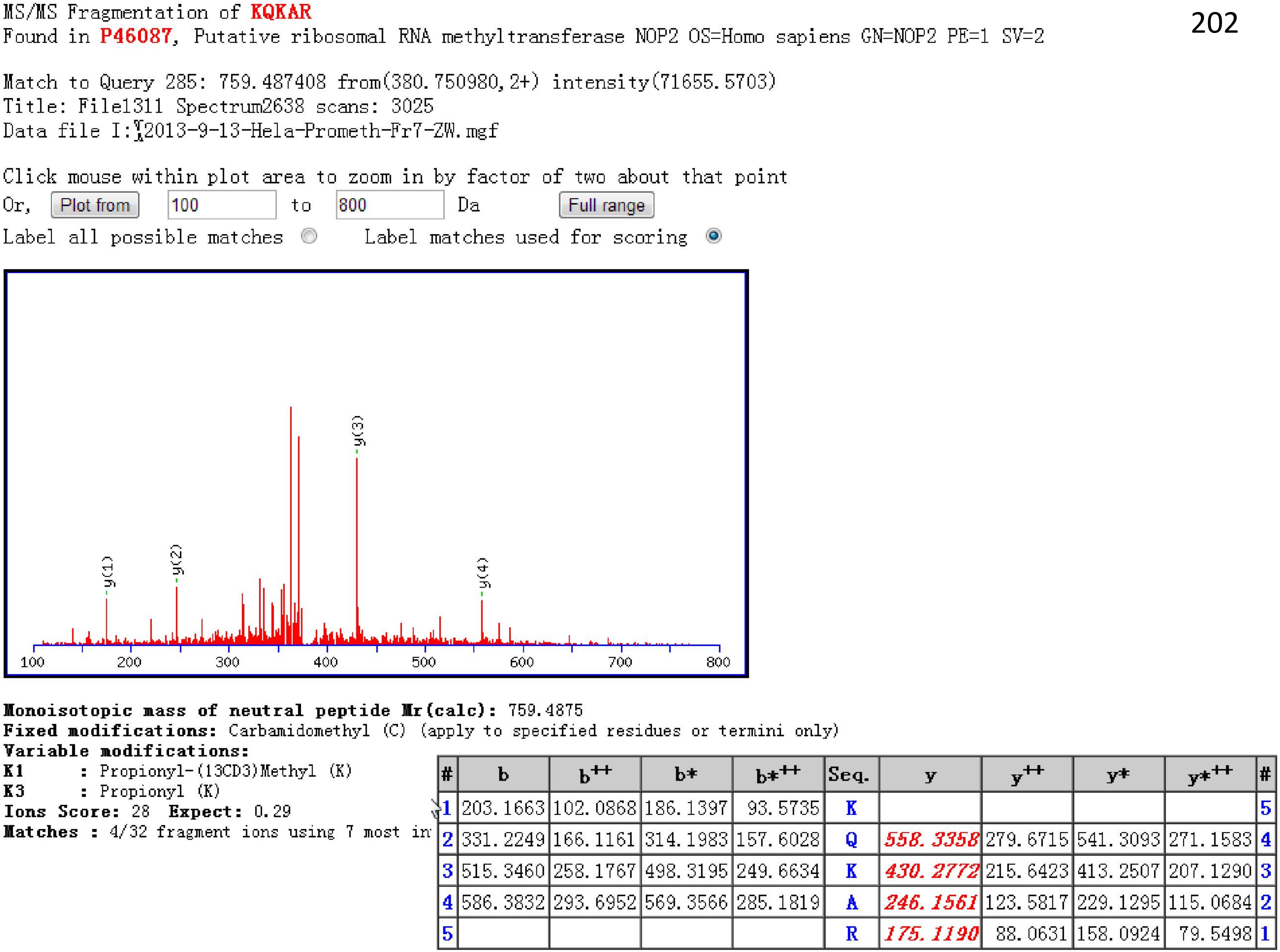
K1 : Propionyl-(13CD3)Methyl (K)

K2 : Propionyl (K)

Ions Score: 31 **Expect:** 0.3

Matches : 11/54 fragment ions using 22 mo

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							6
2	**387.2875**	194.1474	370.2609	185.6341			K	***661.3628***	331.1850	644.3362	322.6717	643.3522	322.1797	5
3	474.3195	237.6634	457.2929	229.1501	456.3089	228.6581	S	***477.2416***	239.1244	460.2150	230.6112	459.2310	230.1191	4
4	**602.3781**	301.6927	585.3515	293.1794	584.3675	292.6874	Q	***390.2096***	195.6084	373.1830	187.0951	372.1990	186.6031	3
5	689.4101	345.2087	672.3836	336.6954	671.3995	336.2034	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



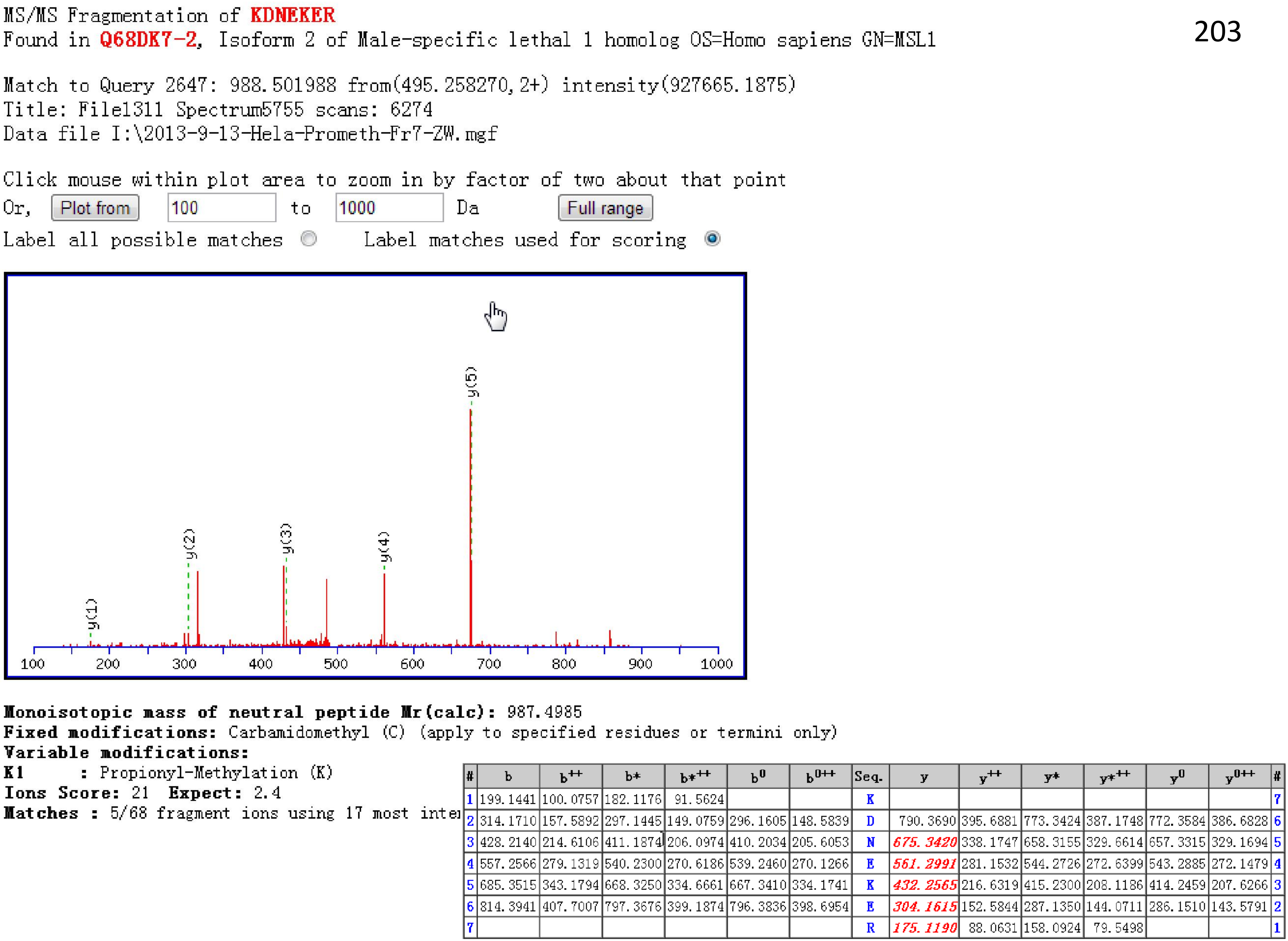
MS/MS Fragmentation of **KQKAR**
Found in **P46087**, Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2

Match to Query 285: 759.487408 from(380.750980,2+) intensity(71655.5703)
Title: File1311 Spectrum2638 scans: 3025
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 759.4875
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 28 **Expect:** 0.29
Matches : 4/32 fragment ions using 7 most in

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	203.1663	102.0868	186.1397	93.5735	K					5
2	331.2249	166.1161	314.1983	157.6028	Q	***558.3358***	279.6715	541.3093	271.1583	4
3	515.3460	258.1767	498.3195	249.6634	K	***430.2772***	215.6423	413.2507	207.1290	3
4	586.3832	293.6952	569.3566	285.1819	A	***246.1561***	123.5817	229.1295	115.0684	2
5					R	***175.1190***	88.0631	158.0924	79.5498	1



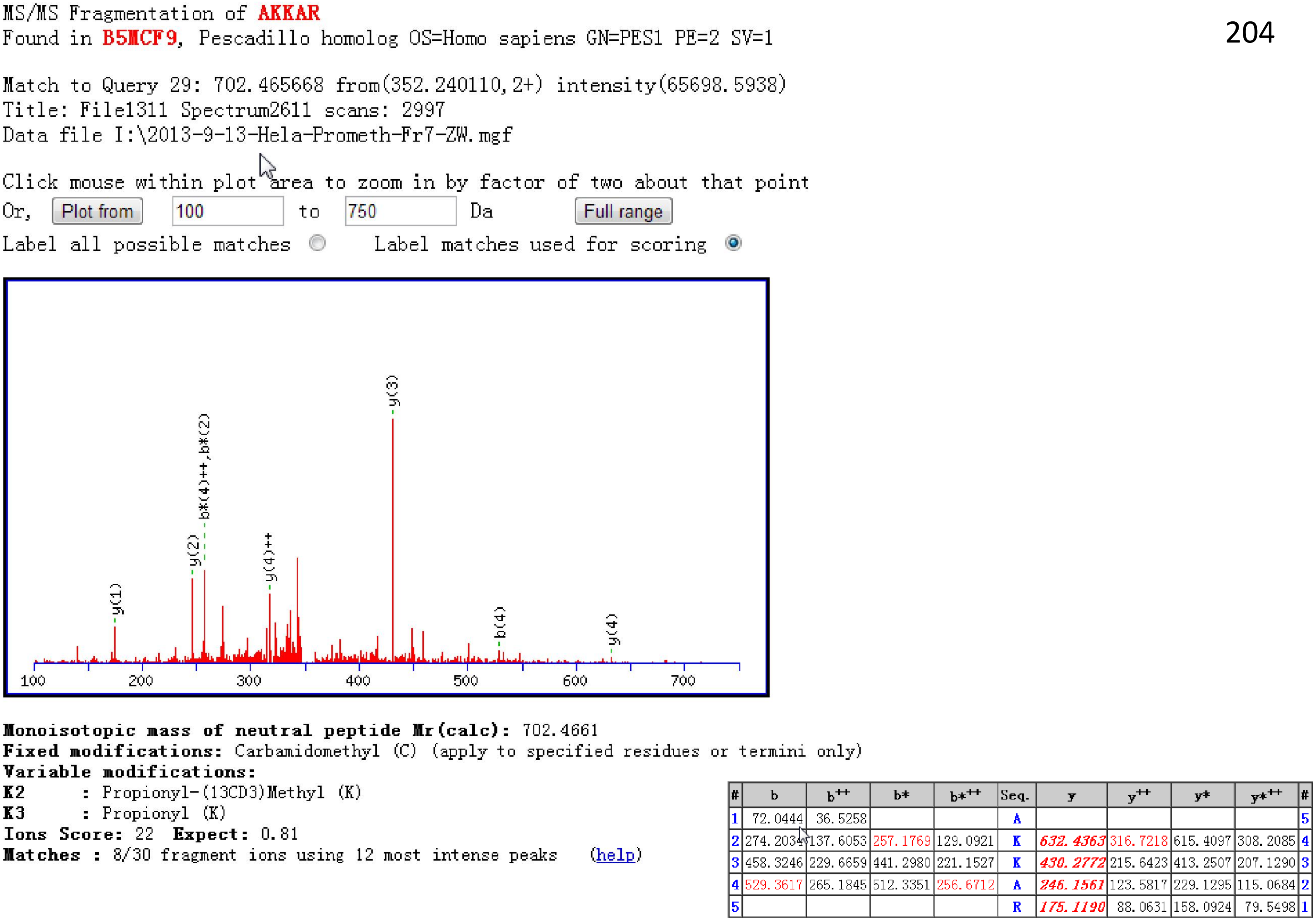
MS/MS Fragmentation of **KDNEKER**
Found in **Q68DK7-2**, Isoform 2 of Male-specific lethal 1 homolog OS=Homo sapiens GN=MSL1

Match to Query 2647: 988.501988 from(495.258270,2+) intensity(927665.1875)
Title: File1311 Spectrum5755 scans: 6274
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 987.4985
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 21 **Expect:** 2.4
Matches : 5/68 fragment ions using 17 most inte

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							7
2	314.1710	157.5892	297.1445	149.0759	296.1605	148.5839	D	790.3690	395.6881	773.3424	387.1748	772.3584	386.6828	6
3	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	N	***675.3420***	338.1747	658.3155	329.6614	657.3315	329.1694	5
4	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	E	***561.2991***	281.1532	544.2726	272.6399	543.2885	272.1479	4
5	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	K	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	3
6	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
7							R	***175.1190***	88.0631	158.0924	79.5498			1



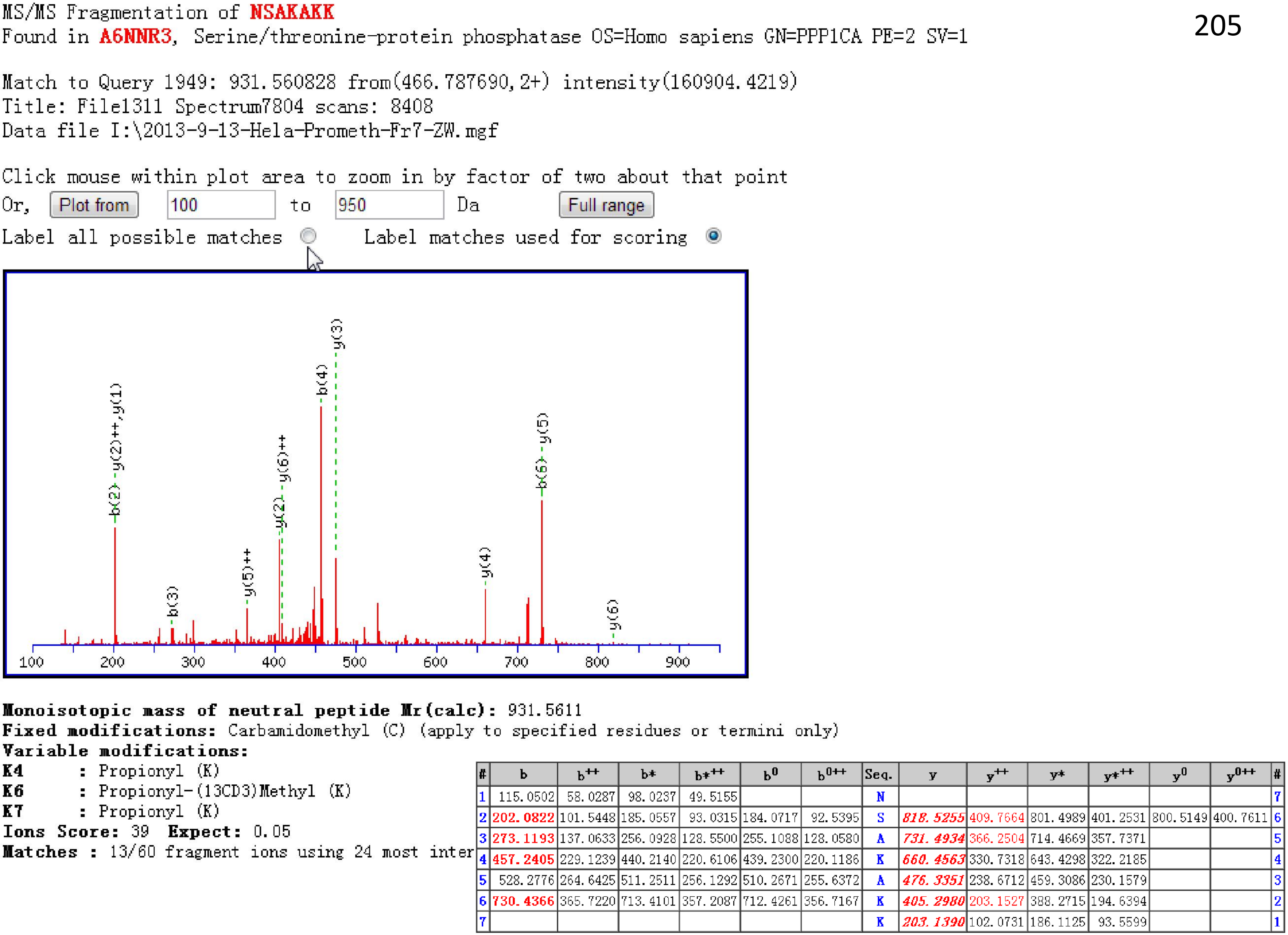
MS/MS Fragmentation of **AKKAR**
Found in **B5MCF9**, Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1

Match to Query 29: 702.465668 from(352.240110,2+) intensity(65698.5938)
Title: File1311 Spectrum2611 scans: 2997
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 702.4661
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 22 **Expect:** 0.81
Matches : 8/30 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.0444	36.5258			A					5
2	274.2034	137.6053	257.1769	129.0921	K	***632.4363***	316.7218	615.4097	308.2085	4
3	458.3246	229.6659	441.2980	221.1527	K	***430.2772***	215.6423	413.2507	207.1290	3
4	529.3617	265.1845	512.3351	256.6712	A	***246.1561***	123.5817	229.1295	115.0684	2
5					R	***175.1190***	88.0631	158.0924	79.5498	1



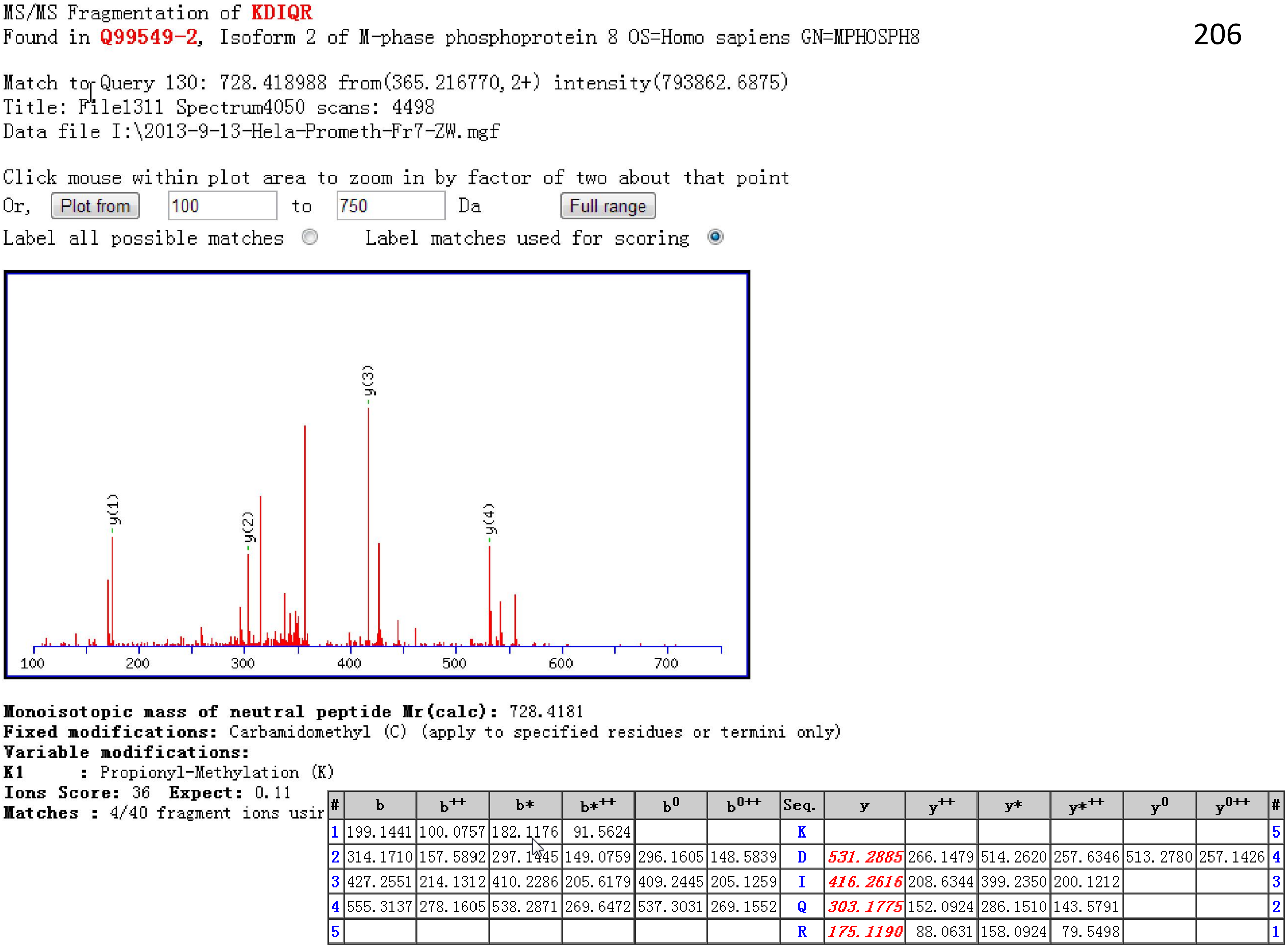
MS/MS Fragmentation of **NSAKAKK**
Found in **A6NNR3**, Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CA PE=2 SV=1

Match to Query 1949: 931.560828 from(466.787690,2+) intensity(160904.4219)
Title: File1311 Spectrum7804 scans: 8408
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 931.5611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl (K)
K6 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 39 **Expect:** 0.05
Matches : 13/60 fragment ions using 24 most inter

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							7
2	**202.0822**	101.5448	185.0557	93.0315	184.0717	92.5395	S	***818.5255***	409.7664	801.4989	401.2531	800.5149	400.7611	6
3	**273.1193**	137.0633	256.0928	128.5500	255.1088	128.0580	A	***731.4934***	366.2504	714.4669	357.7371			5
4	**457.2405**	229.1239	440.2140	220.6106	439.2300	220.1186	K	***660.4563***	330.7318	643.4298	322.2185			4
5	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	A	***476.3351***	238.6712	459.3086	230.1579			3
6	**730.4366**	365.7220	713.4101	357.2087	712.4261	356.7167	K	***405.2980***	203.1527	388.2715	194.6394			2
7							K	***203.1390***	102.0731	186.1125	93.5599			1



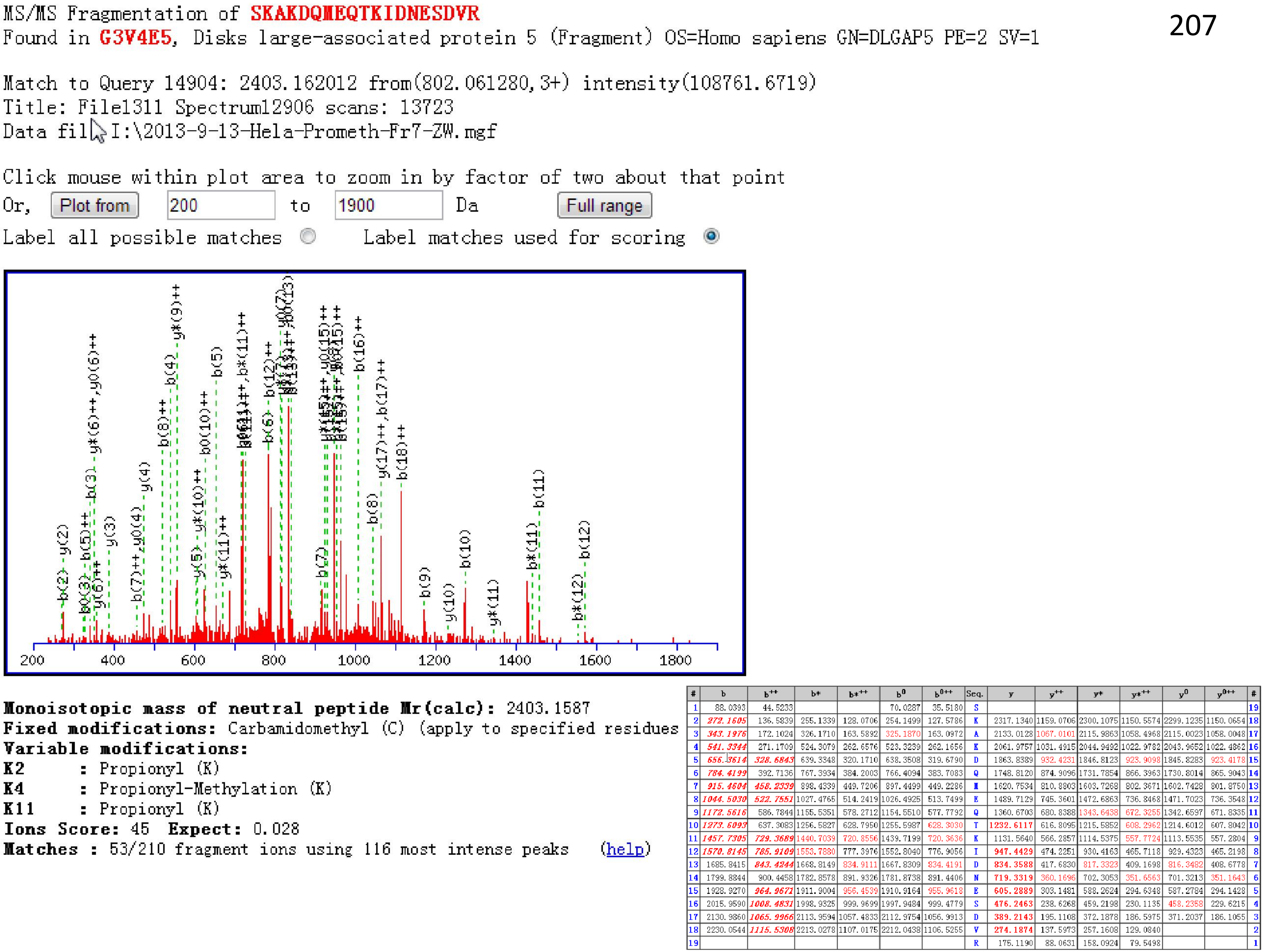
MS/MS Fragmentation of **KDIQR**
Found in **Q99549-2**, Isoform 2 of M-phase phosphoprotein 8 OS=Homo sapiens GN=MPHOSPH8

Match to Query 130: 728.418988 from(365.216770,2+) intensity(793862.6875)
Title: File1311 Spectrum4050 scans: 4498
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 728.4181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 36 **Expect:** 0.11
Matches : 4/40 fragment ions usir

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							5
2	314.1710	157.5892	297.1445	149.0759	296.1605	148.5839	D	*531.2885*	266.1479	514.2620	257.6346	513.2780	257.1426	4
3	427.2551	214.1312	410.2286	205.6179	409.2445	205.1259	I	*416.2616*	208.6344	399.2350	200.1212			3
4	555.3137	278.1605	538.2871	269.6472	537.3031	269.1552	Q	*303.1775*	152.0924	286.1510	143.5791			2
5							R	*175.1190*	88.0631	158.0924	79.5498			1



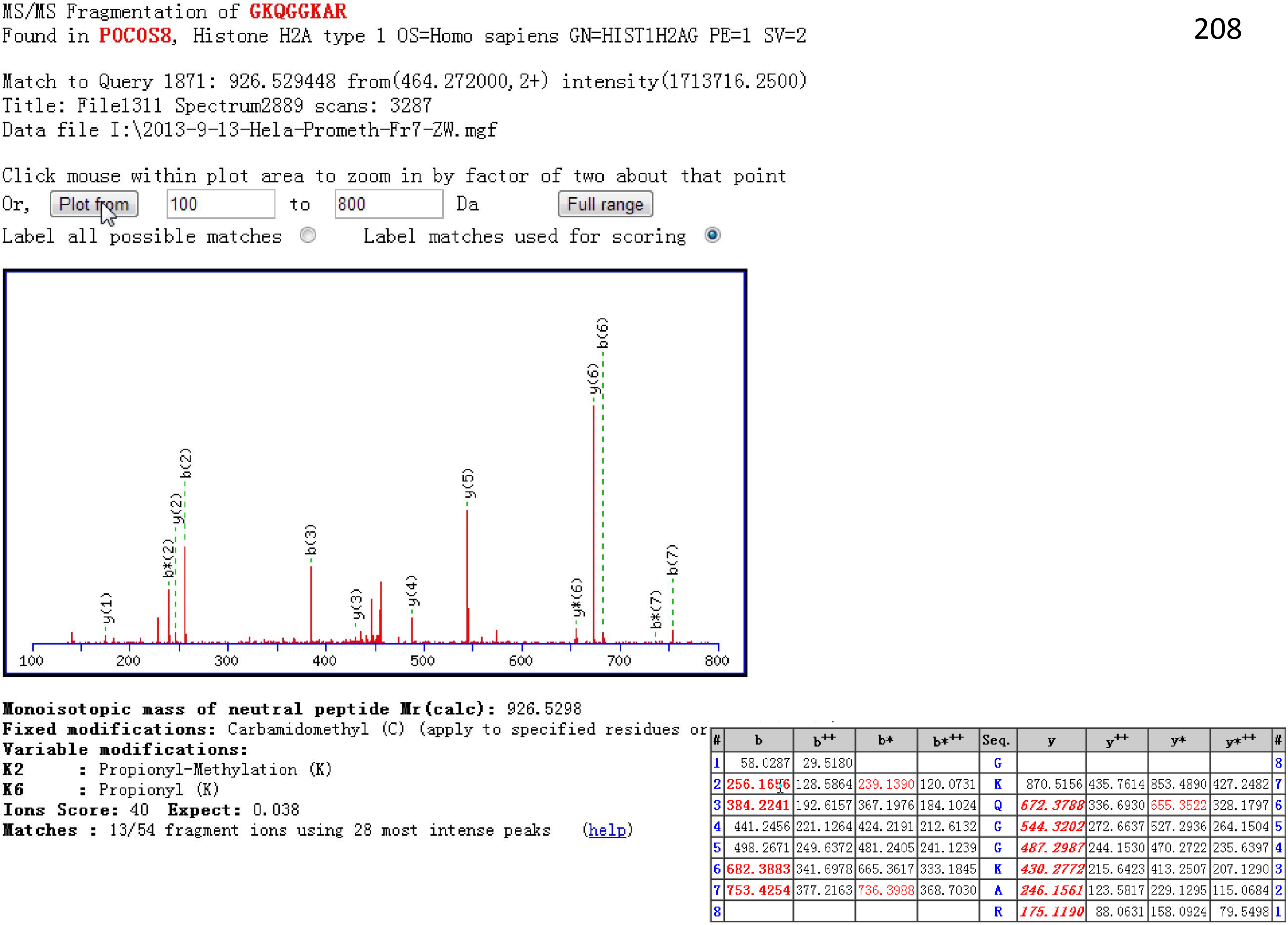
MS/MS Fragmentation of **SKAKDQMEQTKIDNESDVR**
Found in **G3V4E5**, Disks large-associated protein 5 (Fragment) OS=Homo sapiens GN=DLGAP5 PE=2 SV=1

Match to Query 14904: 2403.162012 from(802.061280,3+) intensity(108761.6719)
Title: File1311 Spectrum12906 scans: 13723
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 2403.1587
Fixed modifications: Carbamidomethyl (C) (apply to specified residues
Variable modifications:
K2 : Propionyl (K)
K4 : Propionyl-Methylation (K)
K11 : Propionyl (K)
Ions Score: 45 **Expect:** 0.028
Matches : 53/210 fragment ions using 116 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	K	2317.1340	1159.0706	2300.1075	1150.5574	2299.1235	1150.0654	18
3	**343.1976**	172.1024	326.1710	163.5892	325.1870	163.0972	A	2133.0128	1067.0101	2115.9863	1058.4968	2115.0023	1058.0048	17
4	**541.3344**	271.1709	524.3079	262.6576	523.3239	262.1656	K	2061.9757	1031.4915	2044.9492	1022.9782	2043.9652	1022.4862	16
5	**656.3614**	**328.6843**	639.3348	320.1710	638.3508	319.6790	D	1863.8389	932.4231	1846.8123	923.9098	1845.8283	923.4178	15
6	**784.4199**	392.7136	767.3934	384.2003	766.4094	383.7083	Q	1748.8120	874.9096	1731.7854	866.3963	1730.8014	865.9043	14
7	**915.4604**	**458.2339**	898.4339	449.7206	897.4499	449.2286	M	1620.7534	810.8803	1603.7268	802.3671	1602.7428	801.8750	13
8	**1044.5030**	**522.7551**	1027.4765	514.2419	1026.4925	513.7499	E	1489.7129	745.3601	1472.6863	736.8468	1471.7023	736.3548	12
9	**1172.5616**	586.7844	1155.5351	578.2712	1154.5510	577.7792	Q	1360.6703	680.8388	1343.6438	672.3255	1342.6597	671.8335	11
10	**1273.6093**	637.3083	1256.5827	628.7950	1255.5987	628.3030	T	**1232.6117**	616.8095	1215.5852	608.2962	1214.6012	607.8042	10
11	**1457.7305**	**729.3689**	1440.7039	720.8556	1439.7199	720.3636	K	1131.5640	566.2857	1114.5375	557.7724	1113.5535	557.2804	9
12	**1570.8145**	**785.9109**	1553.7880	777.3976	1552.8040	776.9056	I	**947.4429**	474.2251	930.4163	465.7118	929.4323	465.2198	8
13	1685.8415	**843.4244**	1668.8149	834.9111	1667.8309	834.4191	D	**834.3588**	417.6830	817.3323	409.1698	816.3482	408.6778	7
14	1799.8844	900.4458	1782.8578	891.9326	1781.8738	891.4406	N	**719.3319**	360.1696	702.3053	351.6563	701.3213	351.1643	6
15	1928.9270	**964.9671**	1911.9004	956.4539	1910.9164	955.9618	E	**605.2889**	303.1481	588.2624	294.6348	587.2784	294.1428	5
16	2015.9590	**1008.4831**	1998.9325	999.9699	1997.9484	999.4779	S	**476.2463**	238.6268	459.2198	230.1135	458.2358	229.6215	4
17	2130.9860	**1065.9966**	2113.9594	1057.4833	2112.9754	1056.9913	D	**389.2143**	195.1108	372.1878	186.5975	371.2037	186.1055	3
18	2230.0544	**1115.5308**	2213.0278	1107.0175	2212.0438	1106.5255	V	**274.1874**	137.5973	257.1608	129.0840			2
19							R	175.1190	88.0631	158.0924	79.5498			1



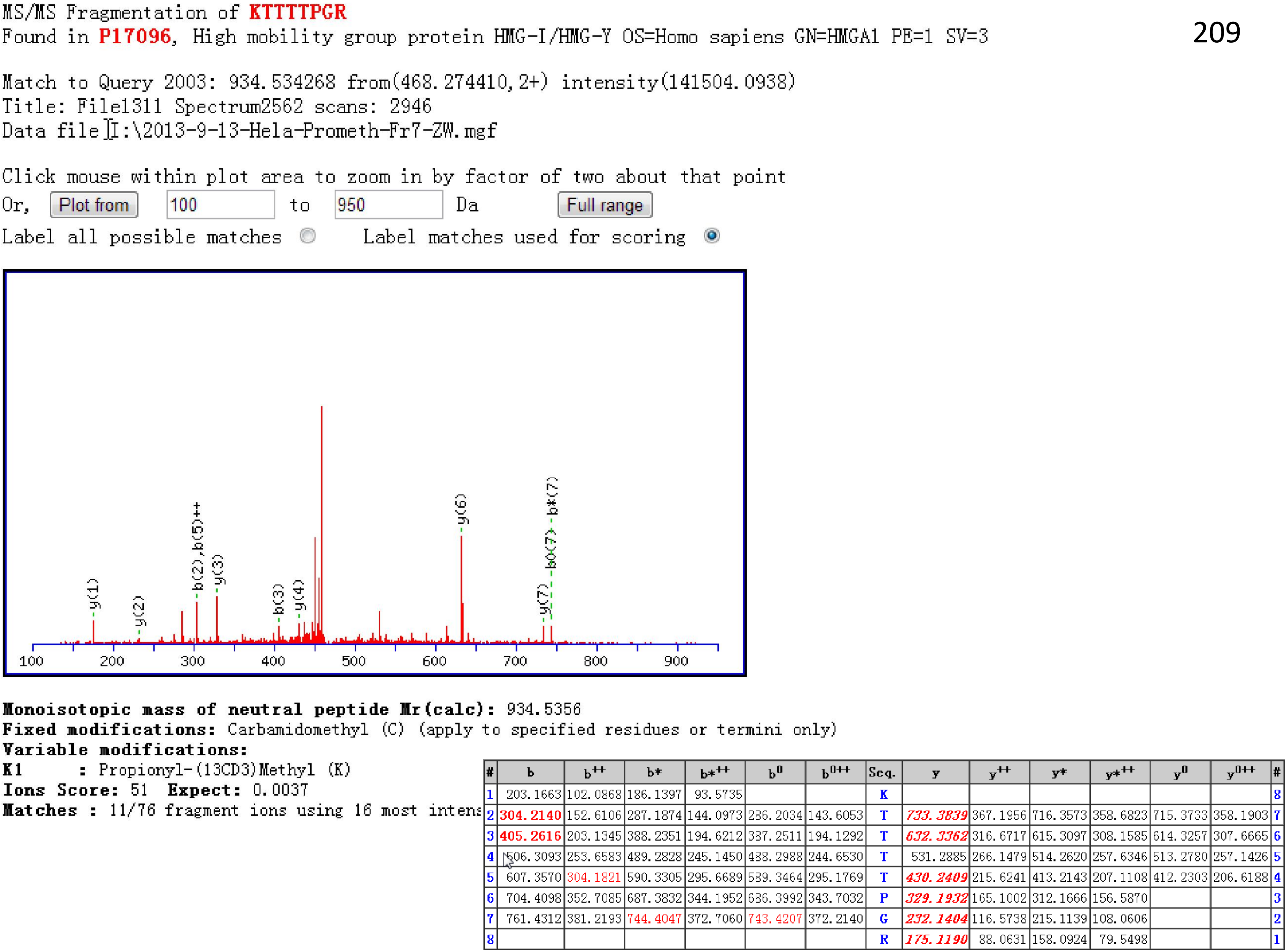
MS/MS Fragmentation of GKQGGKAR
Found in P0C0S8, Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2

Match to Query 1871: 926.529448 from(464.272000,2+) intensity(1713716.2500)
Title: File1311 Spectrum2889 scans: 3287
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 926.5298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K2 : Propionyl-Methylation (K)
K6 : Propionyl (K)
Ions Score: 40 **Expect:** 0.038
Matches : 13/54 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	58.0287	29.5180			G					8
2	**256.1656**	128.5864	239.1390	120.0731	K	870.5156	435.7614	853.4890	427.2482	7
3	**384.2241**	192.6157	367.1976	184.1024	Q	***672.3788***	336.6930	655.3522	328.1797	6
4	441.2456	221.1264	424.2191	212.6132	G	***544.3202***	272.6637	527.2936	264.1504	5
5	498.2671	249.6372	481.2405	241.1239	G	***487.2987***	244.1530	470.2722	235.6397	4
6	**682.3883**	341.6978	665.3617	333.1845	K	***430.2772***	215.6423	413.2507	207.1290	3
7	**753.4254**	377.2163	736.3988	368.7030	A	***246.1561***	123.5817	229.1295	115.0684	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1



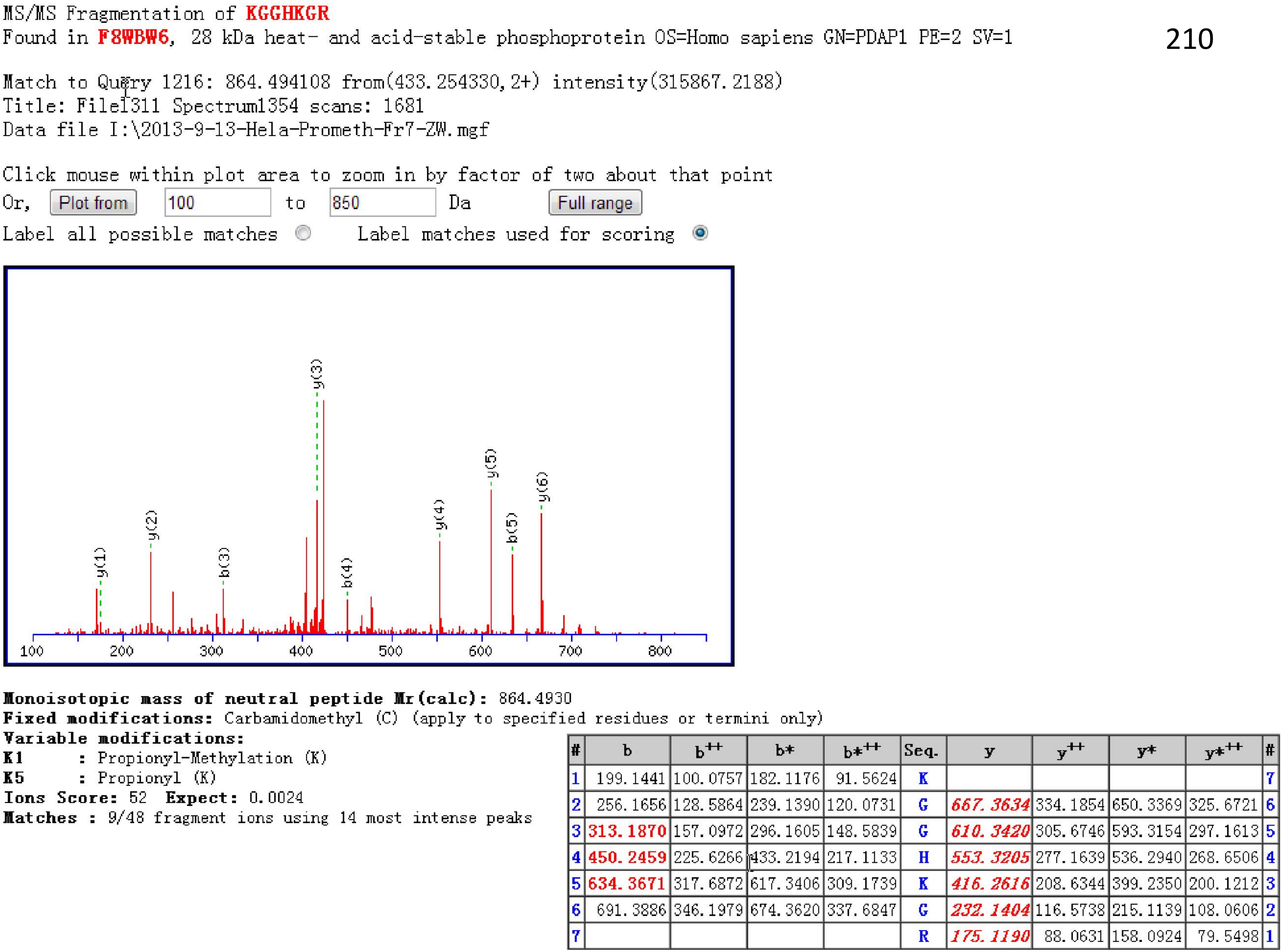
MS/MS Fragmentation of **KTTTTPGR**
Found in **P17096**, High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3

Match to Query 2003: 934.534268 from(468.274410,2+) intensity(141504.0938)
Title: File1311 Spectrum2562 scans: 2946
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 934.5356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 51 **Expect:** 0.0037
Matches : 11/76 fragment ions using 16 most intens

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	**304.2140**	152.6106	287.1874	144.0973	286.2034	143.6053	T	***733.3839***	367.1956	716.3573	358.6823	715.3733	358.1903	7
3	**405.2616**	203.1345	388.2351	194.6212	387.2511	194.1292	T	***632.3362***	316.6717	615.3097	308.1585	614.3257	307.6665	6
4	506.3093	253.6583	489.2828	245.1450	488.2988	244.6530	T	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
5	607.3570	304.1821	590.3305	295.6689	589.3464	295.1769	T	***430.2409***	215.6241	413.2143	207.1108	412.2303	206.6188	4
6	704.4098	352.7085	687.3832	344.1952	686.3992	343.7032	P	***329.1932***	165.1002	312.1666	156.5870			3
7	761.4312	381.2193	744.4047	372.7060	743.4207	372.2140	G	***232.1404***	116.5738	215.1139	108.0606			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



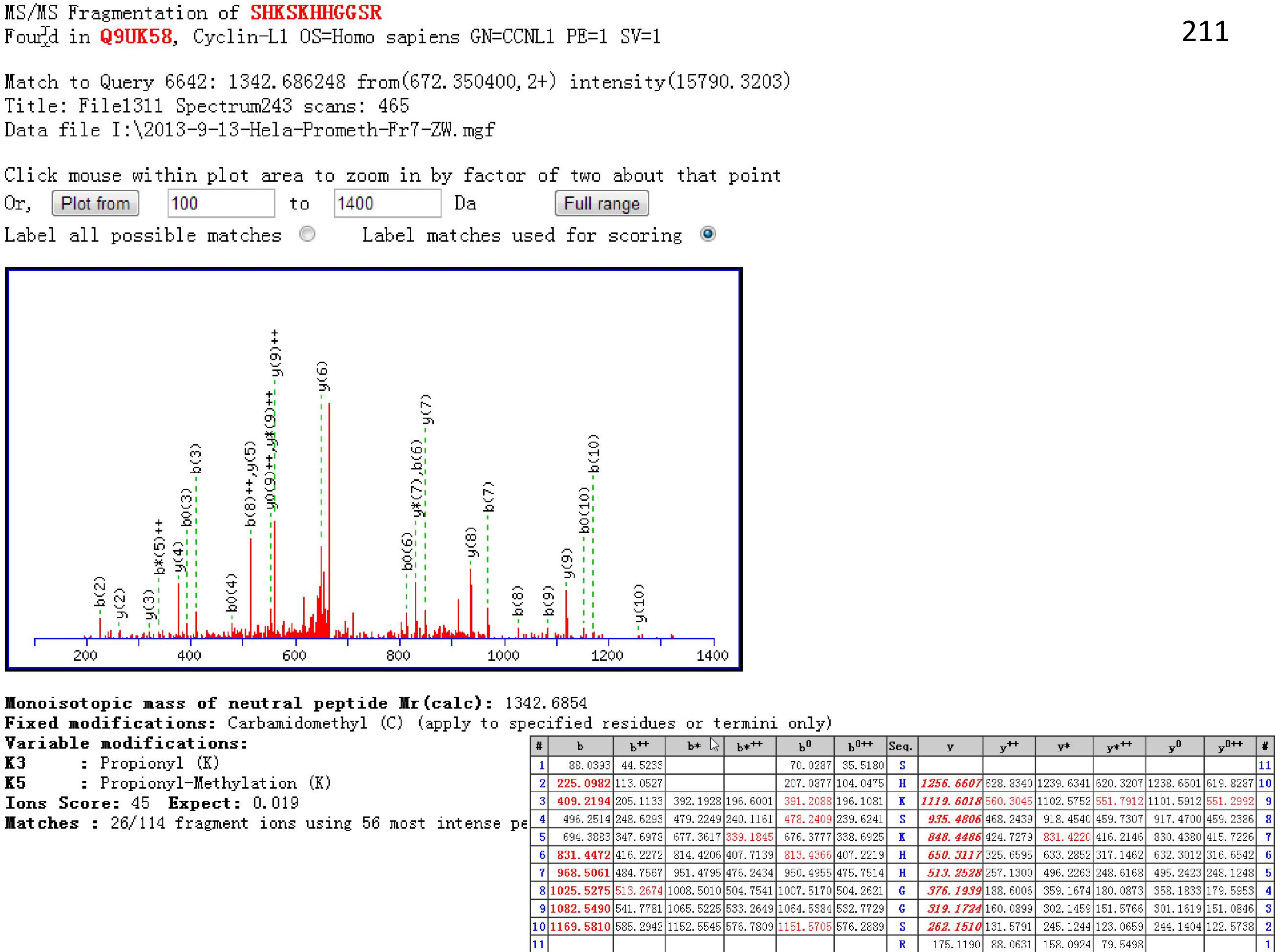
MS/MS Fragmentation of **KGGHKGR**
Found in **F8WBW6**, 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=2 SV=1

Match to Query 1216: 864.494108 from(433.254330,2+) intensity(315867.2188)
Title: File1311 Spectrum1354 scans: 1681
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 864.4930
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
K5 : Propionyl (K)
Ions Score: 52 **Expect:** 0.0024
Matches : 9/48 fragment ions using 14 most intense peaks

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	199.1441	100.0757	182.1176	91.5624	K					7
2	256.1656	128.5864	239.1390	120.0731	G	***667.3634***	334.1854	650.3369	325.6721	6
3	**313.1870**	157.0972	296.1605	148.5839	G	***610.3420***	305.6746	593.3154	297.1613	5
4	**450.2459**	225.6266	433.2194	217.1133	H	***553.3205***	277.1639	536.2940	268.6506	4
5	**634.3671**	317.6872	617.3406	309.1739	K	***416.2616***	208.6344	399.2350	200.1212	3
6	691.3886	346.1979	674.3620	337.6847	G	***232.1404***	116.5738	215.1139	108.0606	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1



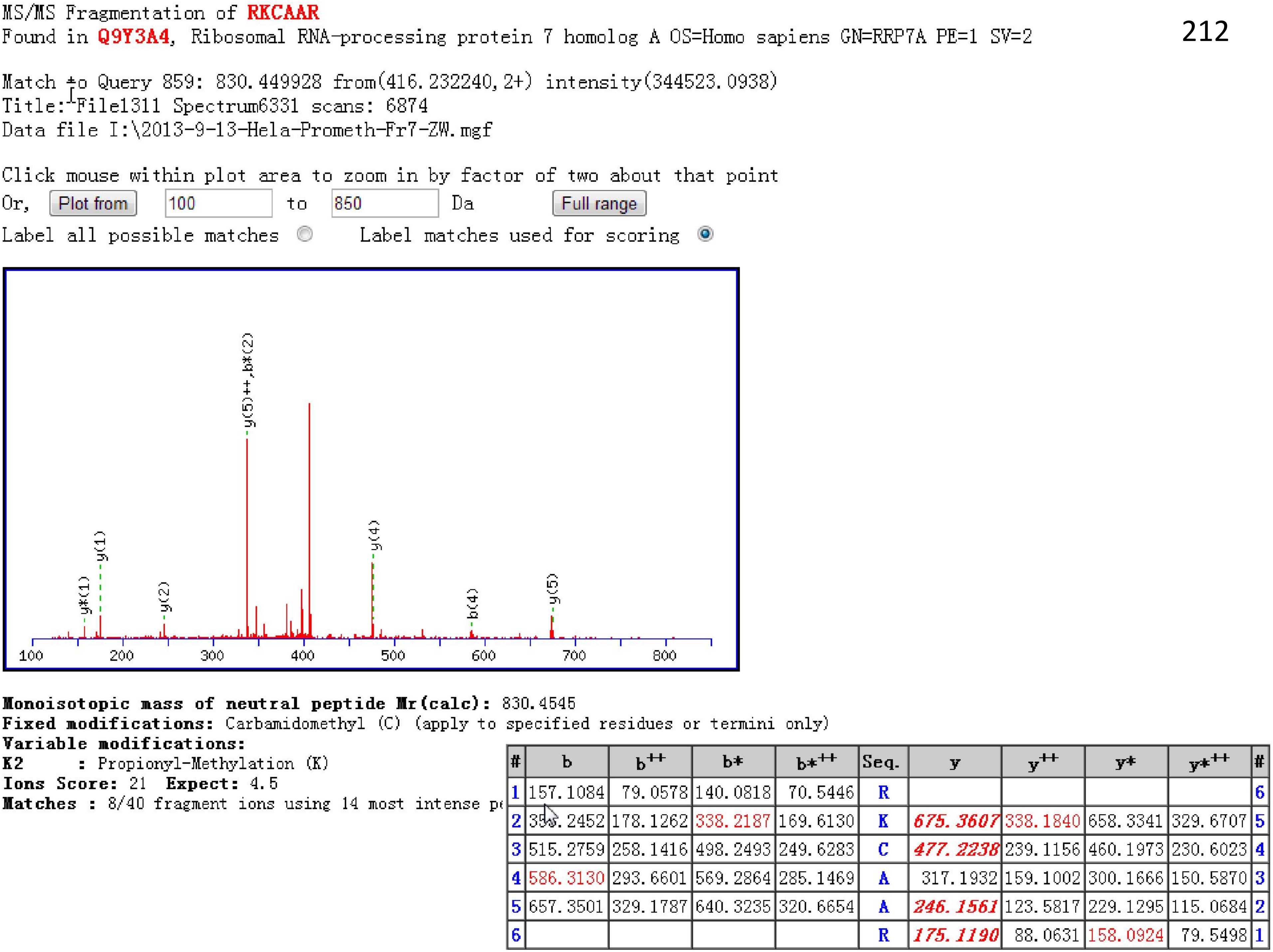
MS/MS Fragmentation of **SHKSKHHGGSR**
Found in **Q9UK58**, Cyclin-L1 OS=Homo sapiens GN=CCNL1 PE=1 SV=1

Match to Query 6642: 1342.686248 from(672.350400,2+) intensity(15790.3203)
Title: File1311 Spectrum243 scans: 465
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1342.6854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl (K)
K5 : Propionyl-Methylation (K)
Ions Score: 45 **Expect:** 0.019
Matches : 26/114 fragment ions using 56 most intense pe

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	**225.0982**	113.0527			207.0877	104.0475	H	***1256.6607***	628.8340	1239.6341	620.3207	1238.6501	619.8287	10
3	**409.2194**	205.1133	392.1928	196.6001	391.2088	196.1081	K	***1119.6018***	560.3045	1102.5752	551.7912	1101.5912	551.2992	9
4	496.2514	248.6293	479.2249	240.1161	478.2409	239.6241	S	***935.4806***	468.2439	918.4540	459.7307	917.4700	459.2386	8
5	694.3883	347.6978	677.3617	339.1845	676.3777	338.6925	K	***848.4486***	424.7279	831.4220	416.2146	830.4380	415.7226	7
6	**831.4472**	416.2272	814.4206	407.7139	813.4366	407.2219	H	***650.3117***	325.6595	633.2852	317.1462	632.3012	316.6542	6
7	**968.5061**	484.7567	951.4795	476.2434	950.4955	475.7514	H	***513.2528***	257.1300	496.2263	248.6168	495.2423	248.1248	5
8	**1025.5275**	513.2674	1008.5010	504.7541	1007.5170	504.2621	G	***376.1939***	188.6006	359.1674	180.0873	358.1833	179.5953	4
9	**1082.5490**	541.7781	1065.5225	533.2649	1064.5384	532.7729	G	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	3
10	**1169.5810**	585.2942	1152.5545	576.7809	1151.5705	576.2889	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498			1



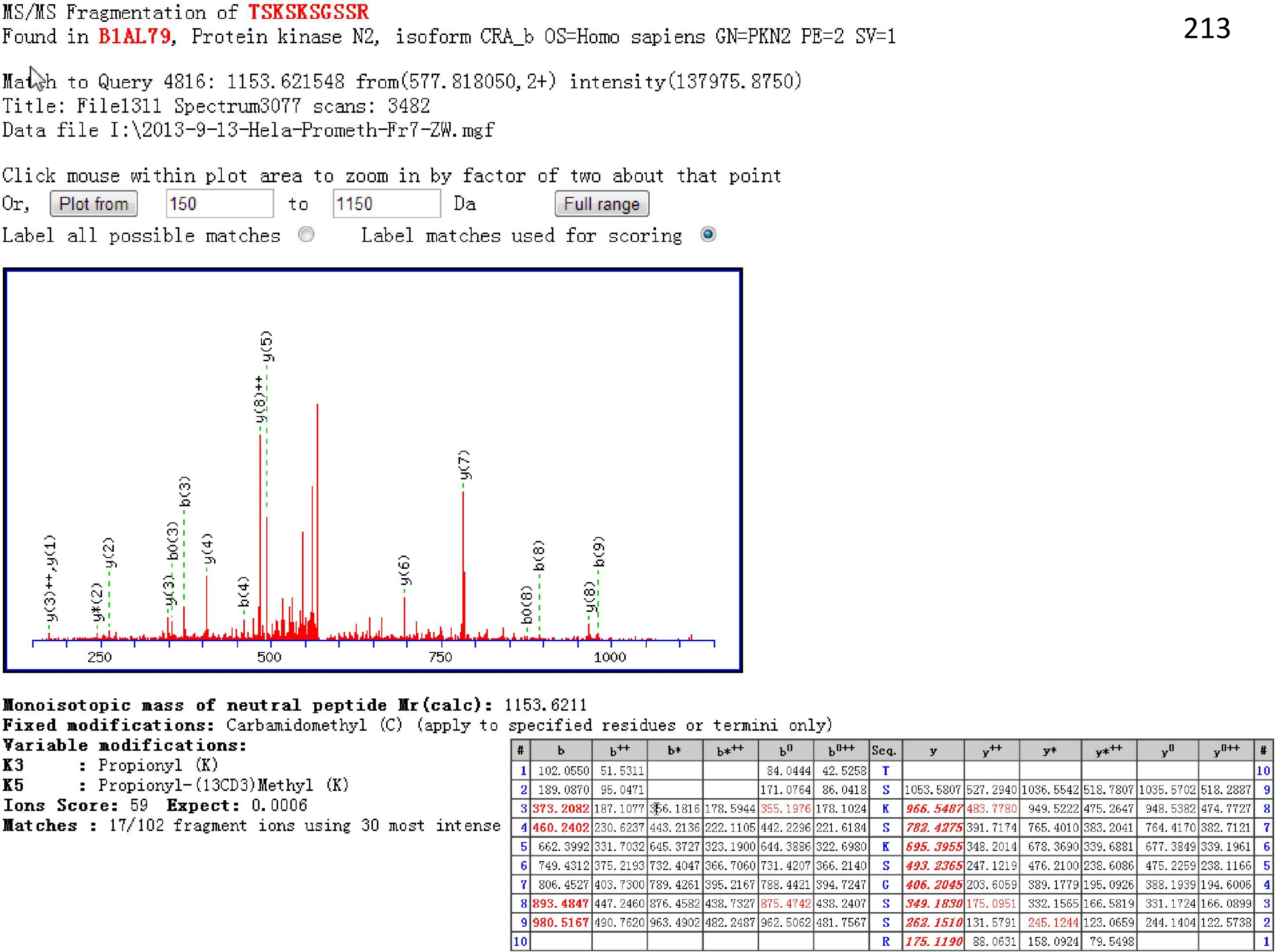
MS/MS Fragmentation of **RKCAAR**
Found in **Q9Y3A4**, Ribosomal RNA-processing protein 7 homolog A OS=Homo sapiens GN=RRP7A PE=1 SV=2

Match to Query 859: 830.449928 from(416.232240,2+) intensity(344523.0938)
Title: File1311 Spectrum6331 scans: 6874
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 830.4545
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
Ions Score: 21 **Expect:** 4.5
Matches : 8/40 fragment ions using 14 most intense pe

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	157.1084	79.0578	140.0818	70.5446	R					6
2	355.2452	178.1262	338.2187	169.6130	K	***675.3607***	338.1840	658.3341	329.6707	5
3	515.2759	258.1416	498.2493	249.6283	C	***477.2238***	239.1156	460.1973	230.6023	4
4	586.3130	293.6601	569.2864	285.1469	A	317.1932	159.1002	300.1666	150.5870	3
5	657.3501	329.1787	640.3235	320.6654	A	***246.1561***	123.5817	229.1295	115.0684	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1



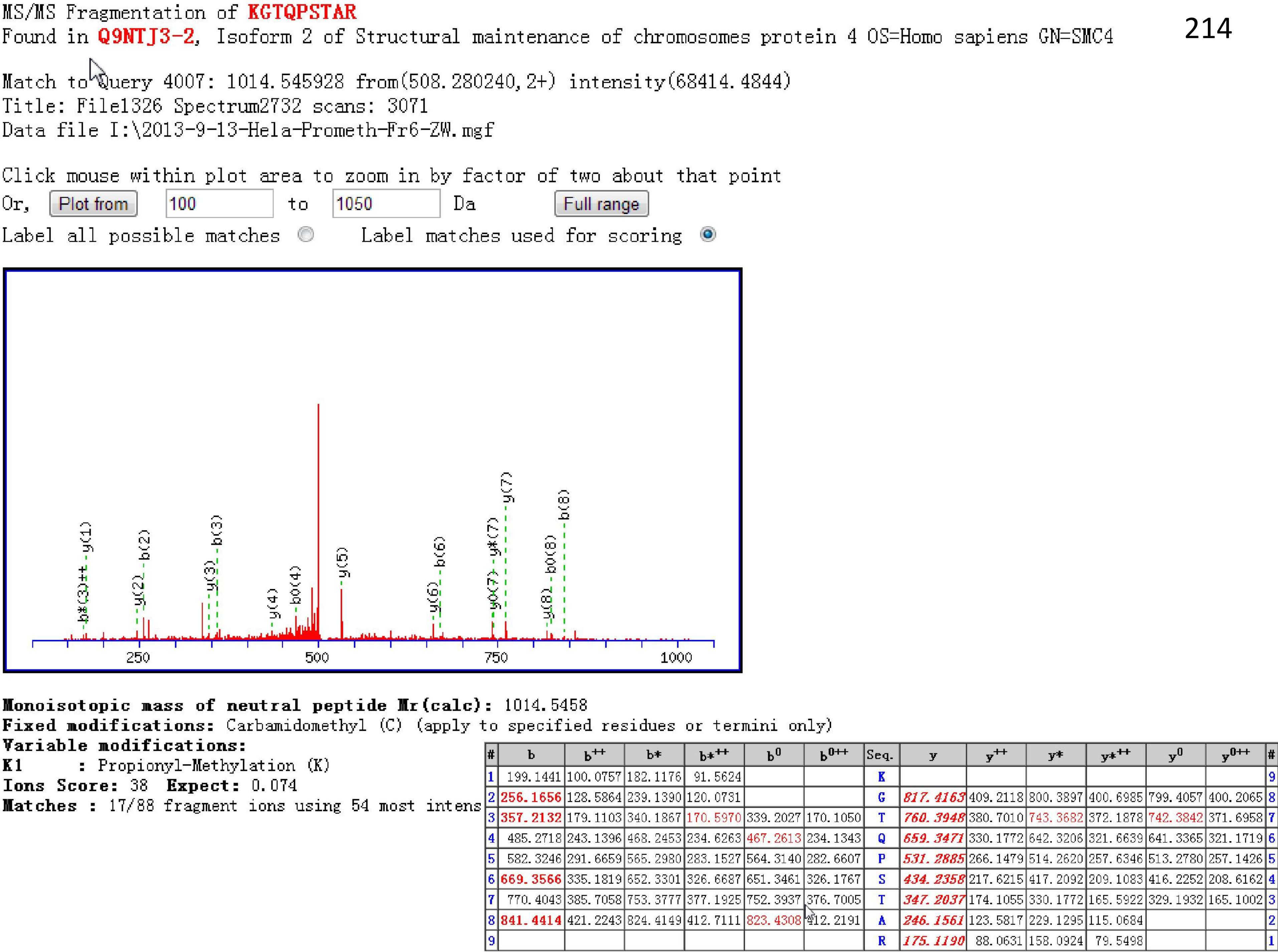
MS/MS Fragmentation of TSKSKSGSSR
Found in B1AL79, Protein kinase N2, isoform CRA_b OS=Homo sapiens GN=PKN2 PE=2 SV=1

Match to Query 4816: 1153.621548 from(577.818050,2+) intensity(137975.8750)
Title: File1311 Spectrum3077 scans: 3482
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1153.6211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 59 **Expect:** 0.0006
Matches : 17/102 fragment ions using 30 most intense

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	189.0870	95.0471			171.0764	86.0418	S	1053.5807	527.2940	1036.5542	518.7807	1035.5702	518.2887	9
3	**373.2082**	187.1077	356.1816	178.5944	355.1976	178.1024	K	***966.5487***	483.7780	949.5222	475.2647	948.5382	474.7727	8
4	**460.2402**	230.6237	443.2136	222.1105	442.2296	221.6184	S	***782.4275***	391.7174	765.4010	383.2041	764.4170	382.7121	7
5	662.3992	331.7032	645.3727	323.1900	644.3886	322.6980	K	***695.3955***	348.2014	678.3690	339.6881	677.3849	339.1961	6
6	749.4312	375.2193	732.4047	366.7060	731.4207	366.2140	S	***493.2365***	247.1219	476.2100	238.6086	475.2259	238.1166	5
7	806.4527	403.7300	789.4261	395.2167	788.4421	394.7247	G	***406.2045***	203.6059	389.1779	195.0926	388.1939	194.6006	4
8	**893.4847**	447.2460	876.4582	438.7327	875.4742	438.2407	S	***349.1830***	175.0951	332.1565	166.5819	331.1724	166.0899	3
9	**980.5167**	490.7620	963.4902	482.2487	962.5062	481.7567	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	***175.1190***	88.0631	158.0924	79.5498			1



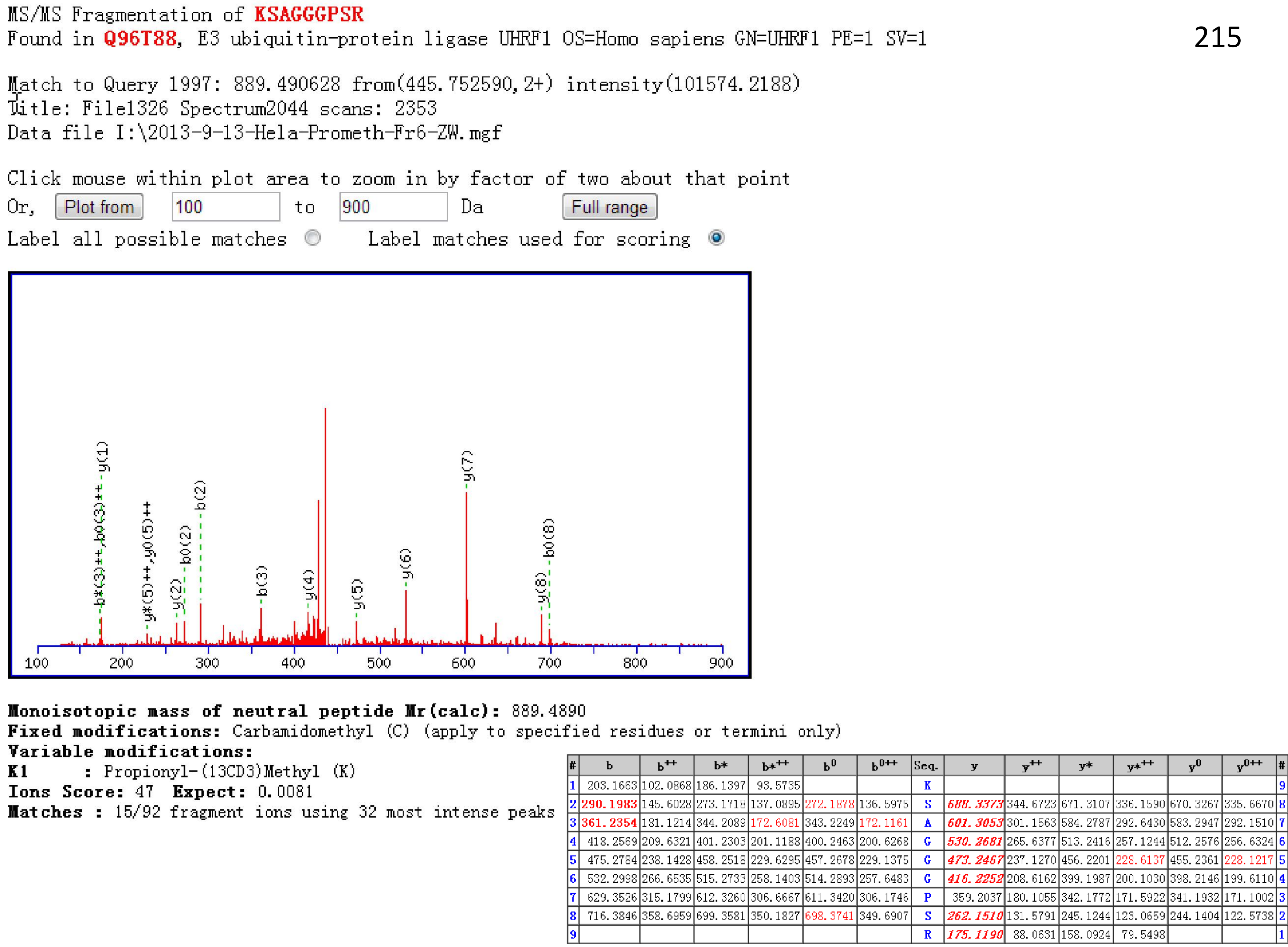
MS/MS Fragmentation of **KGTQPSTAR**
Found in **Q9NTJ3-2**, Isoform 2 of Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4

Match to Query 4007: 1014.545928 from(508.280240,2+) intensity(68414.4844)
Title: File1326 Spectrum2732 scans: 3071
Data file I:\2013-9-13-Hela-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1014.5458
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 38 **Expect:** 0.074
Matches : 17/88 fragment ions using 54 most intens

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							9
2	**256.1656**	128.5864	239.1390	120.0731			G	***817.4163***	409.2118	800.3897	400.6985	799.4057	400.2065	8
3	**357.2132**	179.1103	340.1867	170.5970	339.2027	170.1050	T	***760.3948***	380.7010	743.3682	372.1878	742.3842	371.6958	7
4	485.2718	243.1396	468.2453	234.6263	467.2613	234.1343	Q	***659.3471***	330.1772	642.3206	321.6639	641.3365	321.1719	6
5	582.3246	291.6659	565.2980	283.1527	564.3140	282.6607	P	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	5
6	**669.3566**	335.1819	652.3301	326.6687	651.3461	326.1767	S	***434.2358***	217.6215	417.2092	209.1083	416.2252	208.6162	4
7	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	T	***347.2037***	174.1055	330.1772	165.5922	329.1932	165.1002	3
8	**841.4414**	421.2243	824.4149	412.7111	823.4308	412.2191	A	***246.1561***	123.5817	229.1295	115.0684			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KSAGGGPSR**

Found in **Q96T88**, E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1

Match to Query 1997: 889.490628 from(445.752590,2+) intensity(101574.2188)

Title: File1326 Spectrum2044 scans: 2353

Data file I:\2013-9-13-Hela-Prometh-Fr6-ZW.mgf

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

Or, Plot from 100 to 900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 889.4890

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

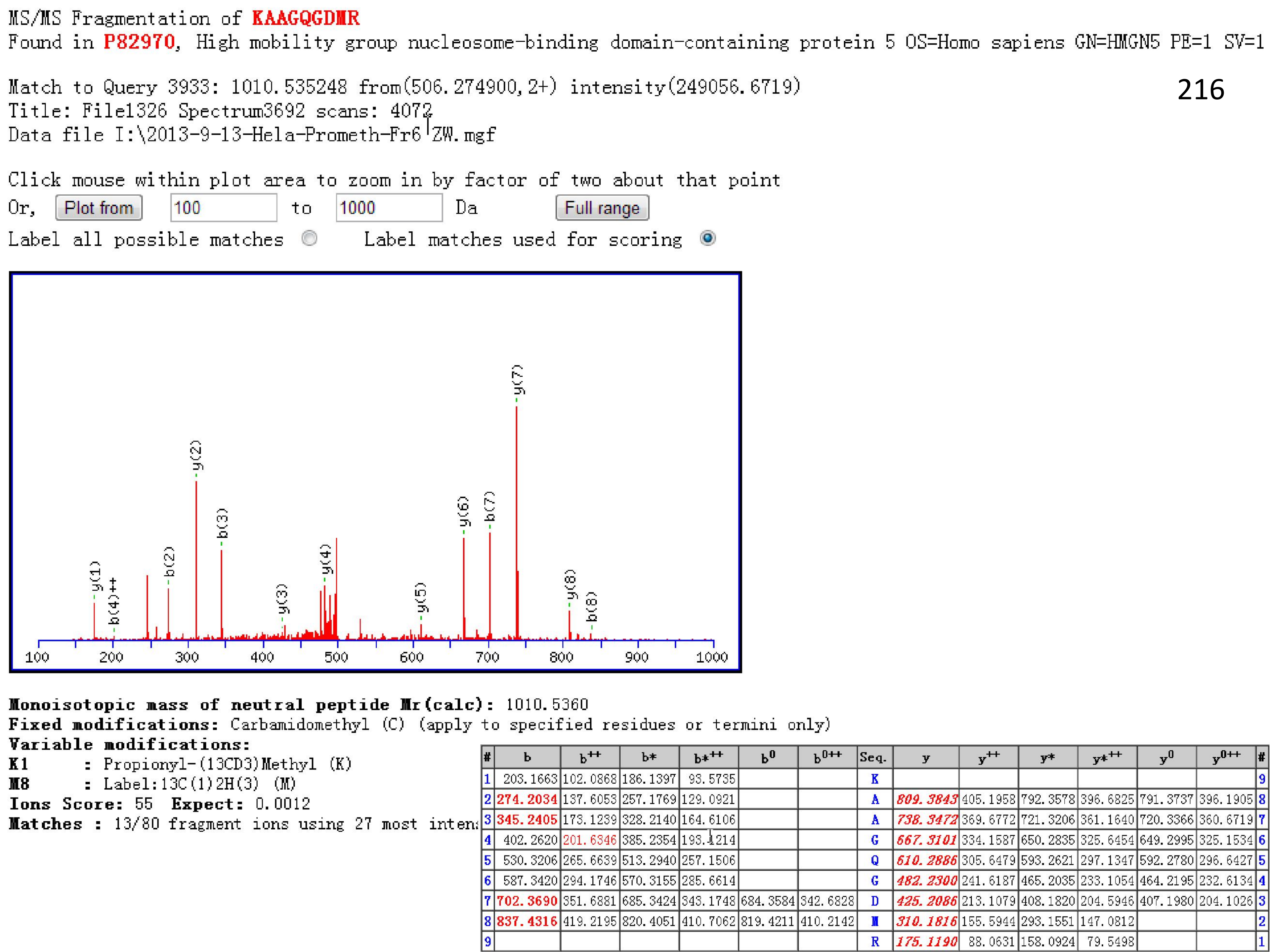
Variable modifications:

K1 : Propionyl-(13CD3)Methyl (K)

Ions Score: 47 **Expect:** 0.0081

Matches : 15/92 fragment ions using 32 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	S	***688.3373***	344.6723	671.3107	336.1590	670.3267	335.6670	8
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	A	***601.3053***	301.1563	584.2787	292.6430	583.2947	292.1510	7
4	418.2569	209.6321	401.2303	201.1188	400.2463	200.6268	G	***530.2681***	265.6377	513.2416	257.1244	512.2576	256.6324	6
5	475.2784	238.1428	458.2518	229.6295	457.2678	229.1375	G	***473.2467***	237.1270	456.2201	228.6137	455.2361	228.1217	5
6	532.2998	266.6535	515.2733	258.1403	514.2893	257.6483	G	***416.2252***	208.6162	399.1987	200.1030	398.2146	199.6110	4
7	629.3526	315.1799	612.3260	306.6667	611.3420	306.1746	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
8	716.3846	358.6959	699.3581	350.1827	698.3741	349.6907	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KAAGQGDMR**
Found in **P82970**, High mobility group nucleosome-binding domain-containing protein 5 OS=Homo sapiens GN=HMGN5 PE=1 SV=1

Match to Query 3933: 1010.535248 from(506.274900,2+) intensity(249056.6719)
Title: File1326 Spectrum3692 scans: 4072
Data file I:\2013-9-13-Hela-Prometh-Fr6 ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

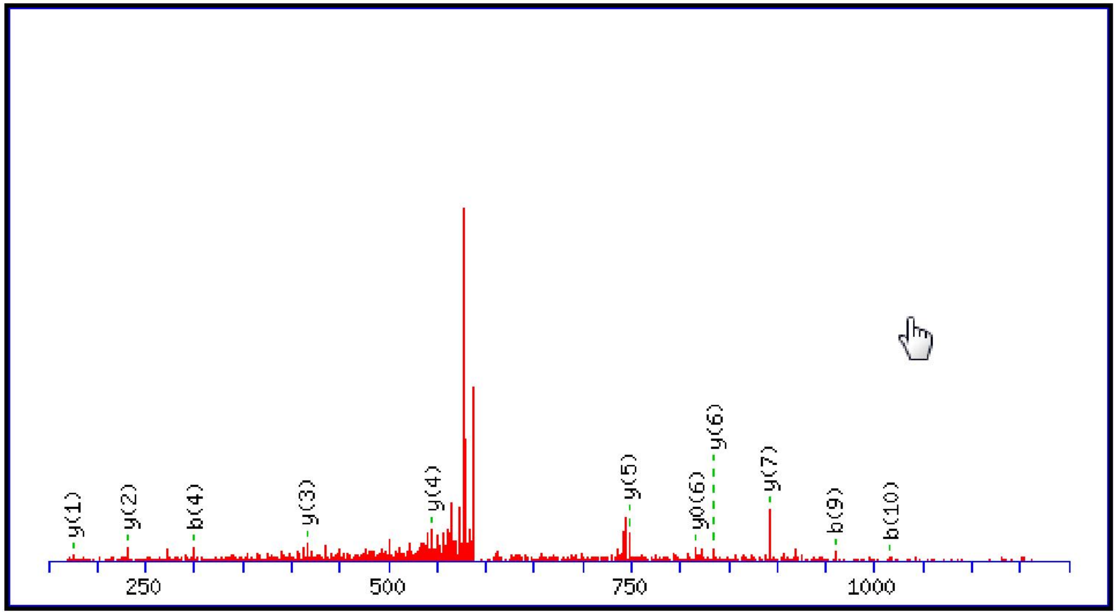
Monoisotopic mass of neutral peptide Mr(calc): 1010.5360
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
M8 : Label:13C(1)2H(3) (M)
Ions Score: 55 **Expect:** 0.0012
Matches : 13/80 fragment ions using 27 most intens

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**274.2034**	137.6053	257.1769	129.0921			A	***809.3843***	405.1958	792.3578	396.6825	791.3737	396.1905	8
3	**345.2405**	173.1239	328.2140	164.6106			A	***738.3472***	369.6772	721.3206	361.1640	720.3366	360.6719	7
4	402.2620	201.6346	385.2354	193.1214			G	***667.3101***	334.1587	650.2835	325.6454	649.2995	325.1534	6
5	530.3206	265.6639	513.2940	257.1506			Q	***610.2886***	305.6479	593.2621	297.1347	592.2780	296.6427	5
6	587.3420	294.1746	570.3155	285.6614			G	***482.2300***	241.6187	465.2035	233.1054	464.2195	232.6134	4
7	**702.3690**	351.6881	685.3424	343.1748	684.3584	342.6828	D	***425.2086***	213.1079	408.1820	204.5946	407.1980	204.1026	3
8	**837.4316**	419.2195	820.4051	410.7062	819.4211	410.2142	M	***310.1816***	155.5944	293.1551	147.0812			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

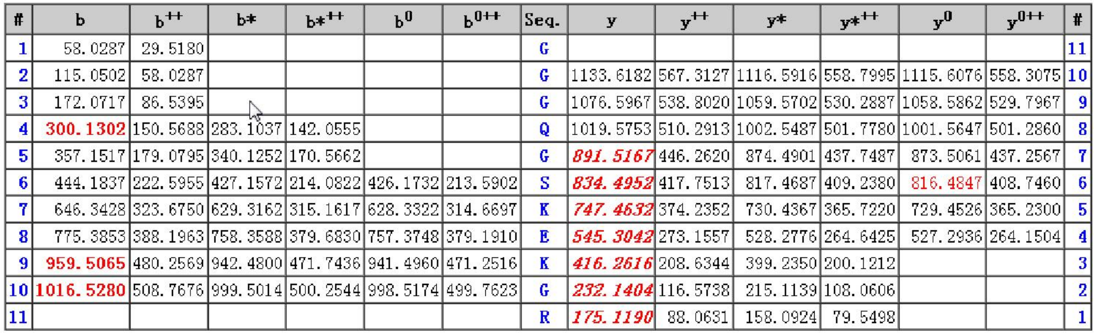
MS/MS Fragmentation of **GGGQGSKEKGR**
Found in **Q7L2J0**, 7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1

Match to Query 6867: 1189.629368 from(595.821960,2+) intensity(22659.0156)
Title: File1326 Spectrum4117 scans: 4514
Data file I:\2013-9-13-Hela-Prometh-Fr6-ZW.mgf

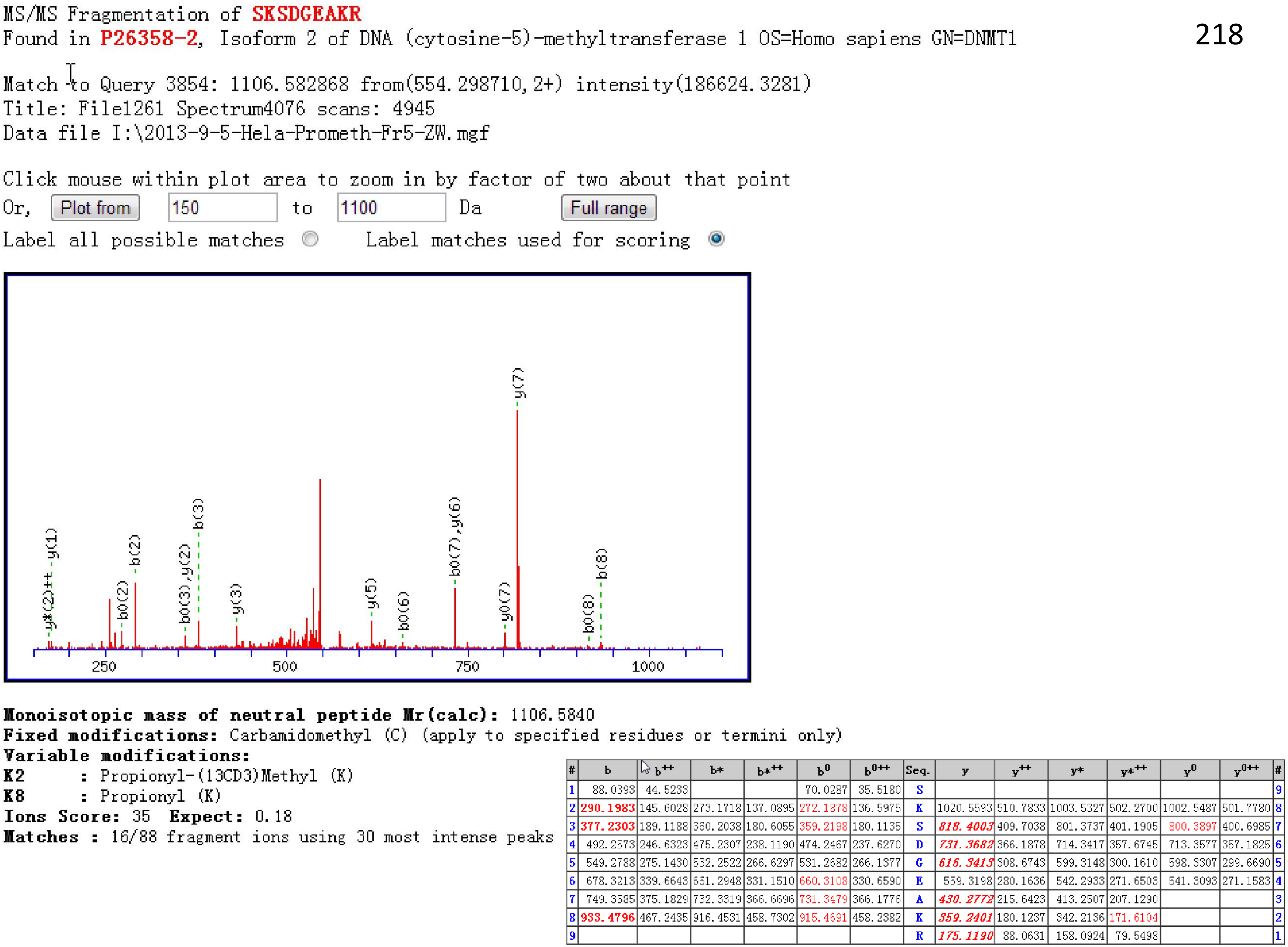
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1189.6324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
K9 : Propionyl (K)
Ions Score: 30 **Expect:** 0.58
Matches : 11/98 fragment ions using 40 most intense peaks



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							11
2	115.0502	58.0287					G	1133.6182	567.3127	1116.5916	558.7995	1115.6076	558.3075	10
3	172.0717	86.5395					G	1076.5967	538.8020	1059.5702	530.2887	1058.5862	529.7967	9
4	**300.1302**	150.5688	283.1037	142.0555			Q	1019.5753	510.2913	1002.5487	501.7780	1001.5647	501.2860	8
5	357.1517	179.0795	340.1252	170.5662			G	***891.5167***	446.2620	874.4901	437.7487	873.5061	437.2567	7
6	444.1837	222.5955	427.1572	214.0822	426.1732	213.5902	S	***834.4952***	417.7513	817.4687	409.2380	816.4847	408.7460	6
7	646.3428	323.6750	629.3162	315.1617	628.3322	314.6697	K	***747.4632***	374.2352	730.4367	365.7220	729.4526	365.2300	5
8	775.3853	388.1963	758.3588	379.6830	757.3748	379.1910	E	***545.3042***	273.1557	528.2776	264.6425	527.2936	264.1504	4
9	**959.5065**	480.2569	942.4800	471.7436	941.4960	471.2516	K	***416.2616***	208.6344	399.2350	200.1212			3
10	**1016.5280**	508.7676	999.5014	500.2544	998.5174	499.7623	G	***232.1404***	116.5738	215.1139	108.0606			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1



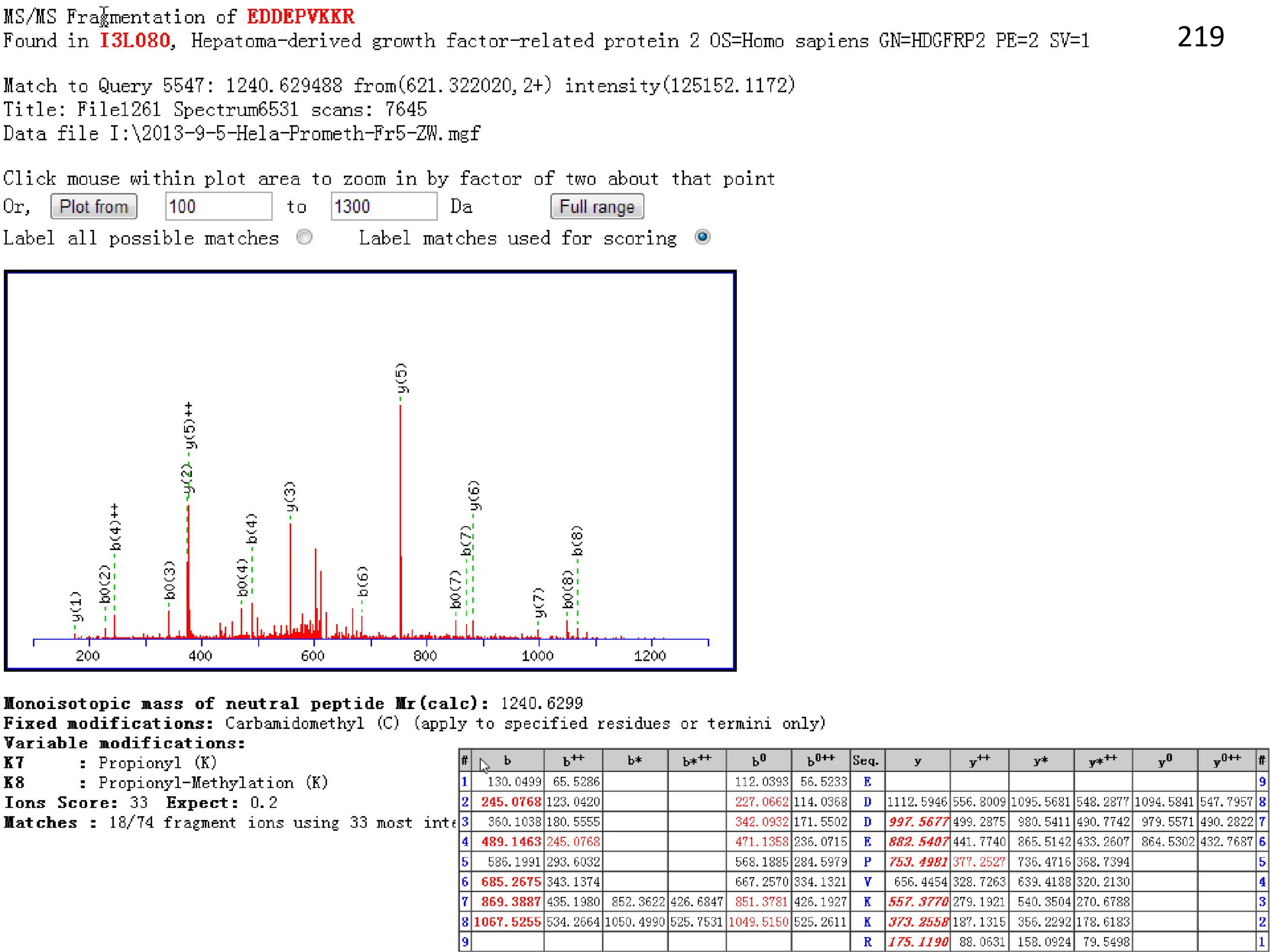
MS/MS Fragmentation of **SKSDGEAKR**
Found in **P26358-2**, Isoform 2 of DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1

Match to Query 3854: 1106.582868 from(554.298710,2+) intensity(186624.3281)
Title: File1261 Spectrum4076 scans: 4945
Data file I:\2013-9-5-Hela-Prometh-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1106.5840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 35 **Expect:** 0.18
Matches : 16/88 fragment ions using 30 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	K	1020.5593	510.7833	1003.5327	502.2700	1002.5487	501.7780	8
3	**377.2303**	189.1188	360.2038	180.6055	359.2198	180.1135	S	***818.4003***	409.7038	801.3737	401.1905	800.3897	400.6985	7
4	492.2573	246.6323	475.2307	238.1190	474.2467	237.6270	D	***731.3682***	366.1878	714.3417	357.6745	713.3577	357.1825	6
5	549.2788	275.1430	532.2522	266.6297	531.2682	266.1377	G	***616.3413***	308.6743	599.3148	300.1610	598.3307	299.6690	5
6	678.3213	339.6643	661.2948	331.1510	660.3108	330.6590	E	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	4
7	749.3585	375.1829	732.3319	366.6696	731.3479	366.1776	A	***430.2772***	215.6423	413.2507	207.1290			3
8	**933.4796**	467.2435	916.4531	458.7302	915.4691	458.2382	K	***359.2401***	180.1237	342.2136	171.6104			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



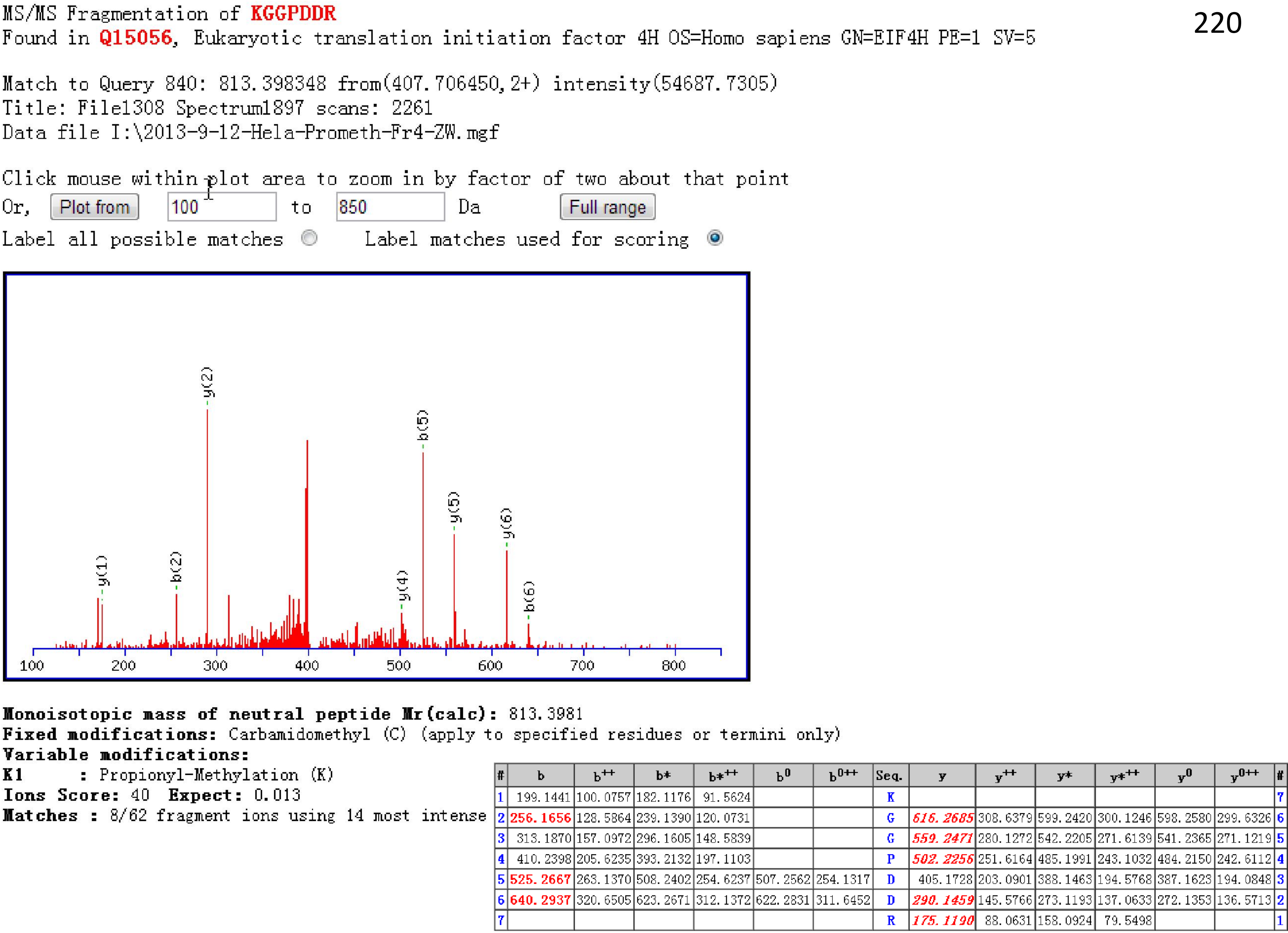
MS/MS Fragmentation of **EDDEPVKKR**
Found in **I3L080**, Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=2 SV=1

Match to Query 5547: 1240.629488 from(621.322020,2+) intensity(125152.1172)
Title: File1261 Spectrum6531 scans: 7645
Data file I:\2013-9-5-Hela-Prometh-Fr5-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1240.6299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl (K)
K8 : Propionyl-Methylation (K)
Ions Score: 33 **Expect:** 0.2
Matches : 18/74 fragment ions using 33 most inte

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							9
2	**245.0768**	123.0420			227.0662	114.0368	D	1112.5946	556.8009	1095.5681	548.2877	1094.5841	547.7957	8
3	360.1038	180.5555			342.0932	171.5502	D	***997.5677***	499.2875	980.5411	490.7742	979.5571	490.2822	7
4	**489.1463**	245.0768			471.1358	236.0715	E	***882.5407***	441.7740	865.5142	433.2607	864.5302	432.7687	6
5	586.1991	293.6032			568.1885	284.5979	P	***753.4981***	377.2527	736.4716	368.7394			5
6	**685.2675**	343.1374			667.2570	334.1321	V	656.4454	328.7263	639.4188	320.2130			4
7	**869.3887**	435.1980	852.3622	426.6847	851.3781	426.1927	K	***557.3770***	279.1921	540.3504	270.6788			3
8	**1067.5255**	534.2664	1050.4990	525.7531	1049.5150	525.2611	K	***373.2558***	187.1315	356.2292	178.6183			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



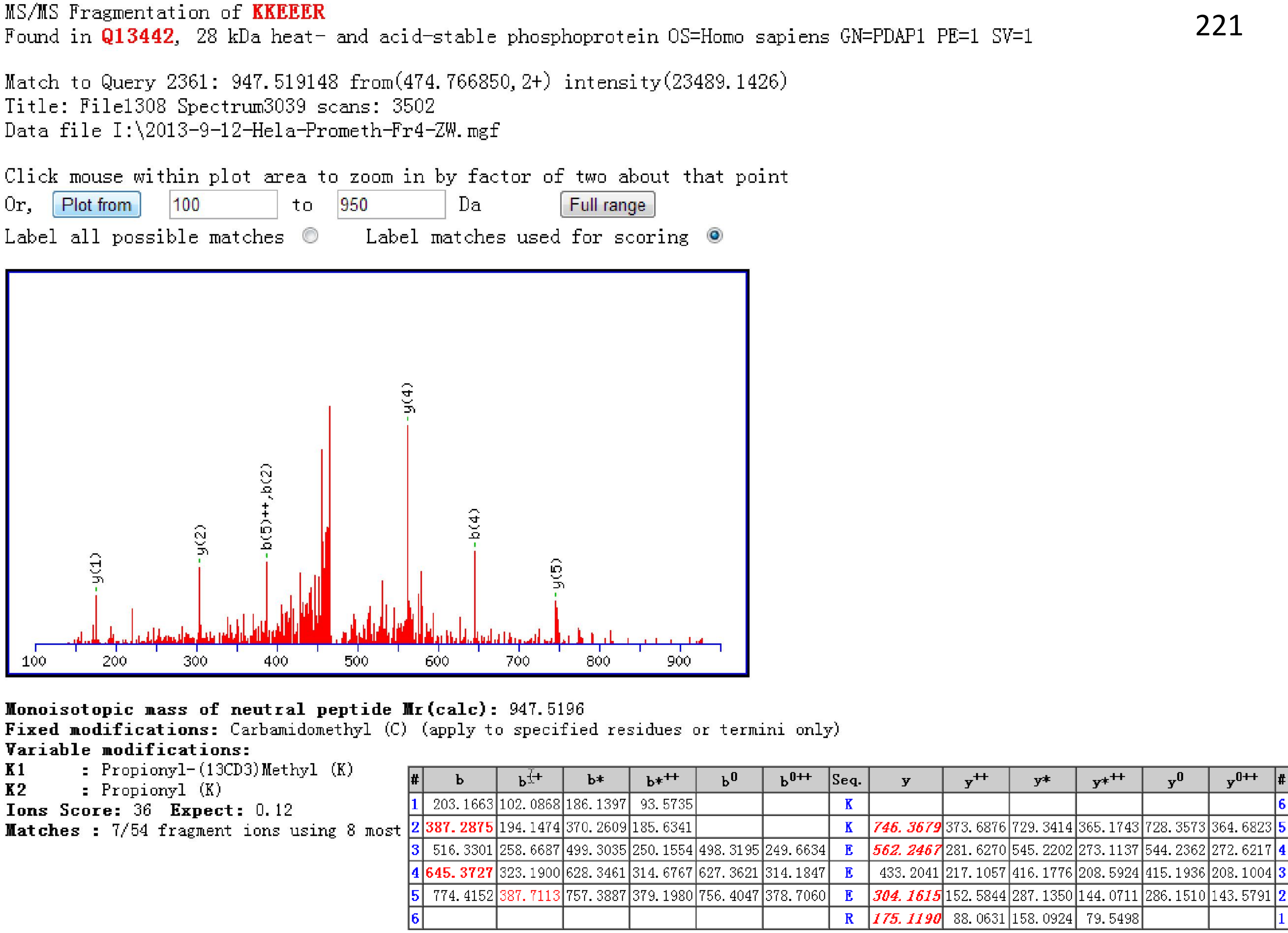
MS/MS Fragmentation of **KGGPDDR**
Found in **Q15056**, Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5

Match to Query 840: 813.398348 from(407.706450,2+) intensity(54687.7305)
Title: File1308 Spectrum1897 scans: 2261
Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 813.3981
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 40 **Expect:** 0.013
Matches : 8/62 fragment ions using 14 most intense

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							7
2	**256.1656**	128.5864	239.1390	120.0731			G	***616.2685***	308.6379	599.2420	300.1246	598.2580	299.6326	6
3	313.1870	157.0972	296.1605	148.5839			G	***559.2471***	280.1272	542.2205	271.6139	541.2365	271.1219	5
4	410.2398	205.6235	393.2132	197.1103			P	***502.2256***	251.6164	485.1991	243.1032	484.2150	242.6112	4
5	**525.2667**	263.1370	508.2402	254.6237	507.2562	254.1317	D	405.1728	203.0901	388.1463	194.5768	387.1623	194.0848	3
6	**640.2937**	320.6505	623.2671	312.1372	622.2831	311.6452	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
7							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KKEEER**

Found in **Q13442**, 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1

Match to Query 2361: 947.519148 from(474.766850,2+) intensity(23489.1426)

Title: File1308 Spectrum3039 scans: 3502

Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.mgf

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

Or, Plot from 100 to 950 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 947.5196

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

Variable modifications:

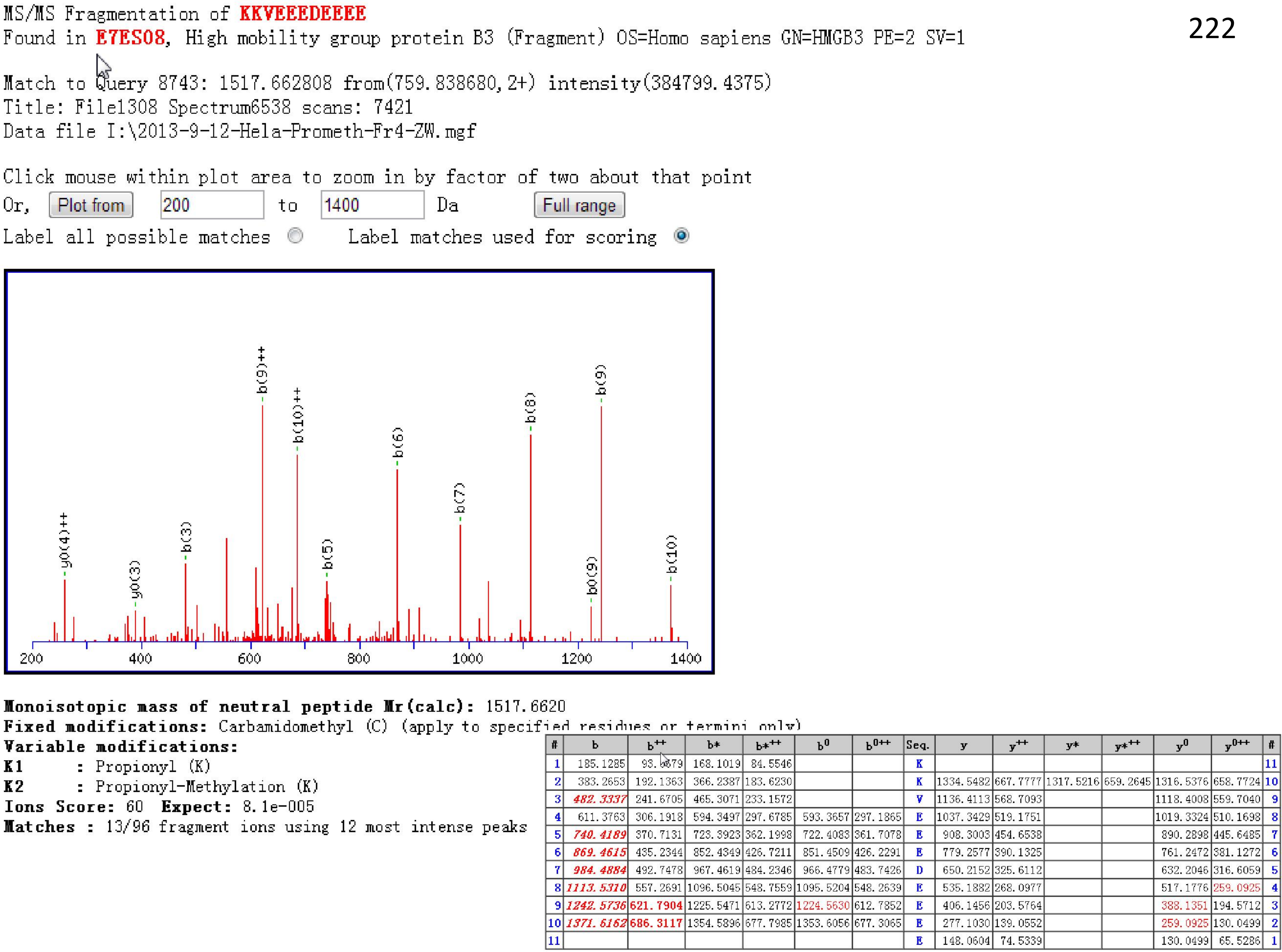
K1 : Propionyl-(13CD3)Methyl (K)

K2 : Propionyl (K)

Ions Score: 36 **Expect:** 0.12

Matches : 7/54 fragment ions using 8 most

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							6
2	**387.2875**	194.1474	370.2609	185.6341			K	***746.3679***	373.6876	729.3414	365.1743	728.3573	364.6823	5
3	516.3301	258.6687	499.3035	250.1554	498.3195	249.6634	E	***562.2467***	281.6270	545.2202	273.1137	544.2362	272.6217	4
4	**645.3727**	323.1900	628.3461	314.6767	627.3621	314.1847	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
5	774.4152	387.7113	757.3887	379.1980	756.4047	378.7060	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



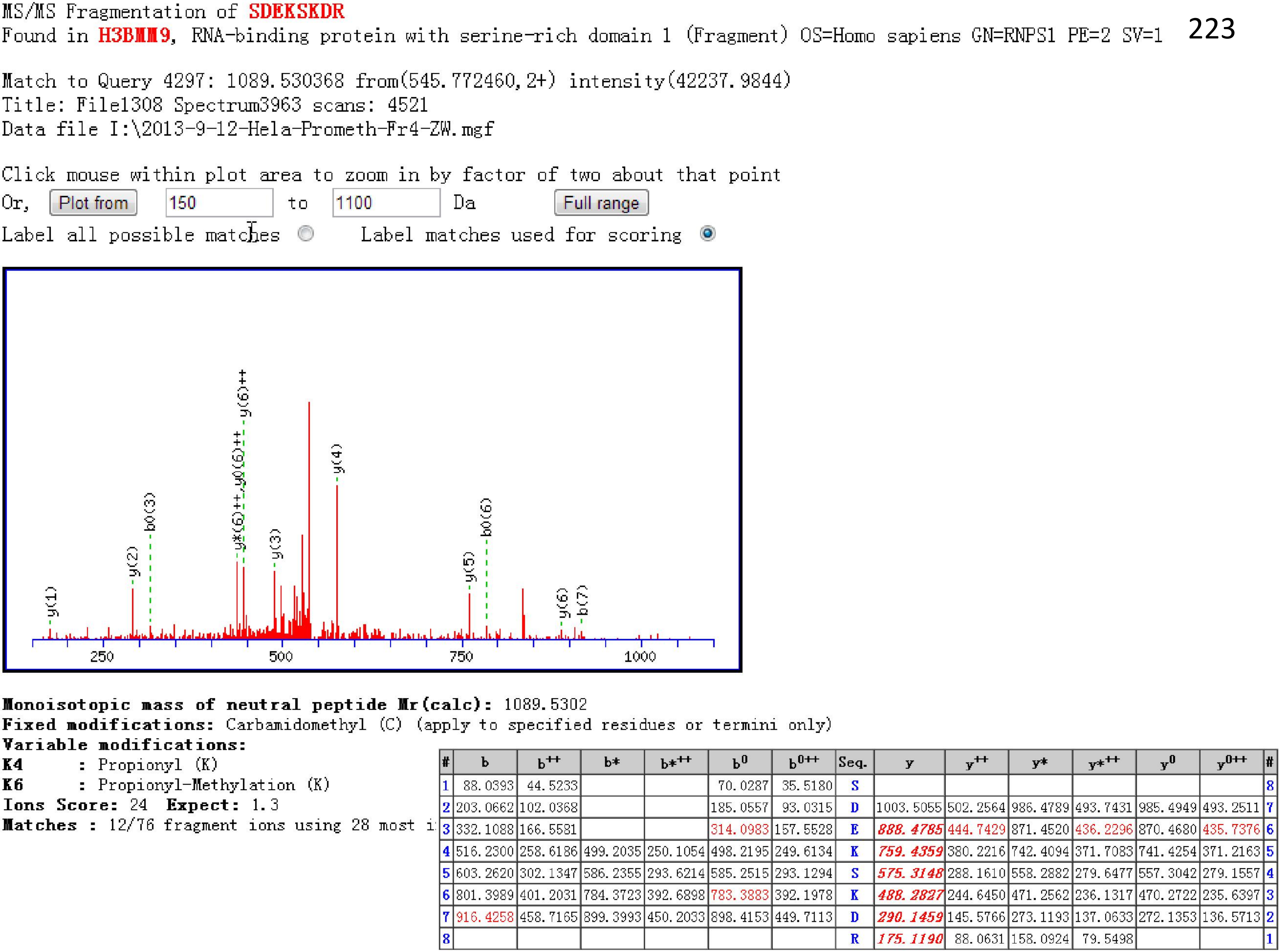
MS/MS Fragmentation of **KKVEEEDEEEE**
Found in **E7ES08**, High mobility group protein B3 (Fragment) OS=Homo sapiens GN=HMGB3 PE=2 SV=1

Match to Query 8743: 1517.662808 from(759.838680,2+) intensity(384799.4375)
Title: File1308 Spectrum6538 scans: 7421
Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1517.6620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K2 : Propionyl-Methylation (K)
Ions Score: 60 **Expect:** 8.1e-005
Matches : 13/96 fragment ions using 12 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							11
2	383.2653	192.1363	366.2387	183.6230			K	1334.5482	667.7777	1317.5216	659.2645	1316.5376	658.7724	10
3	***482.3337***	241.6705	465.3071	233.1572			V	1136.4113	568.7093			1118.4008	559.7040	9
4	611.3763	306.1918	594.3497	297.6785	593.3657	297.1865	E	1037.3429	519.1751			1019.3324	510.1698	8
5	***740.4189***	370.7131	723.3923	362.1998	722.4083	361.7078	E	908.3003	454.6538			890.2898	445.6485	7
6	***869.4615***	435.2344	852.4349	426.7211	851.4509	426.2291	E	779.2577	390.1325			761.2472	381.1272	6
7	***984.4884***	492.7478	967.4619	484.2346	966.4779	483.7426	D	650.2152	325.6112			632.2046	316.6059	5
8	***1113.5310***	557.2691	1096.5045	548.7559	1095.5204	548.2639	E	535.1882	268.0977			517.1776	259.0925	4
9	***1242.5736***	**621.7904**	1225.5471	613.2772	1224.5630	612.7852	E	406.1456	203.5764			388.1351	194.5712	3
10	***1371.6162***	**686.3117**	1354.5896	677.7985	1353.6056	677.3065	E	277.1030	139.0552			259.0925	130.0499	2
11							E	148.0604	74.5339			130.0499	65.5286	1



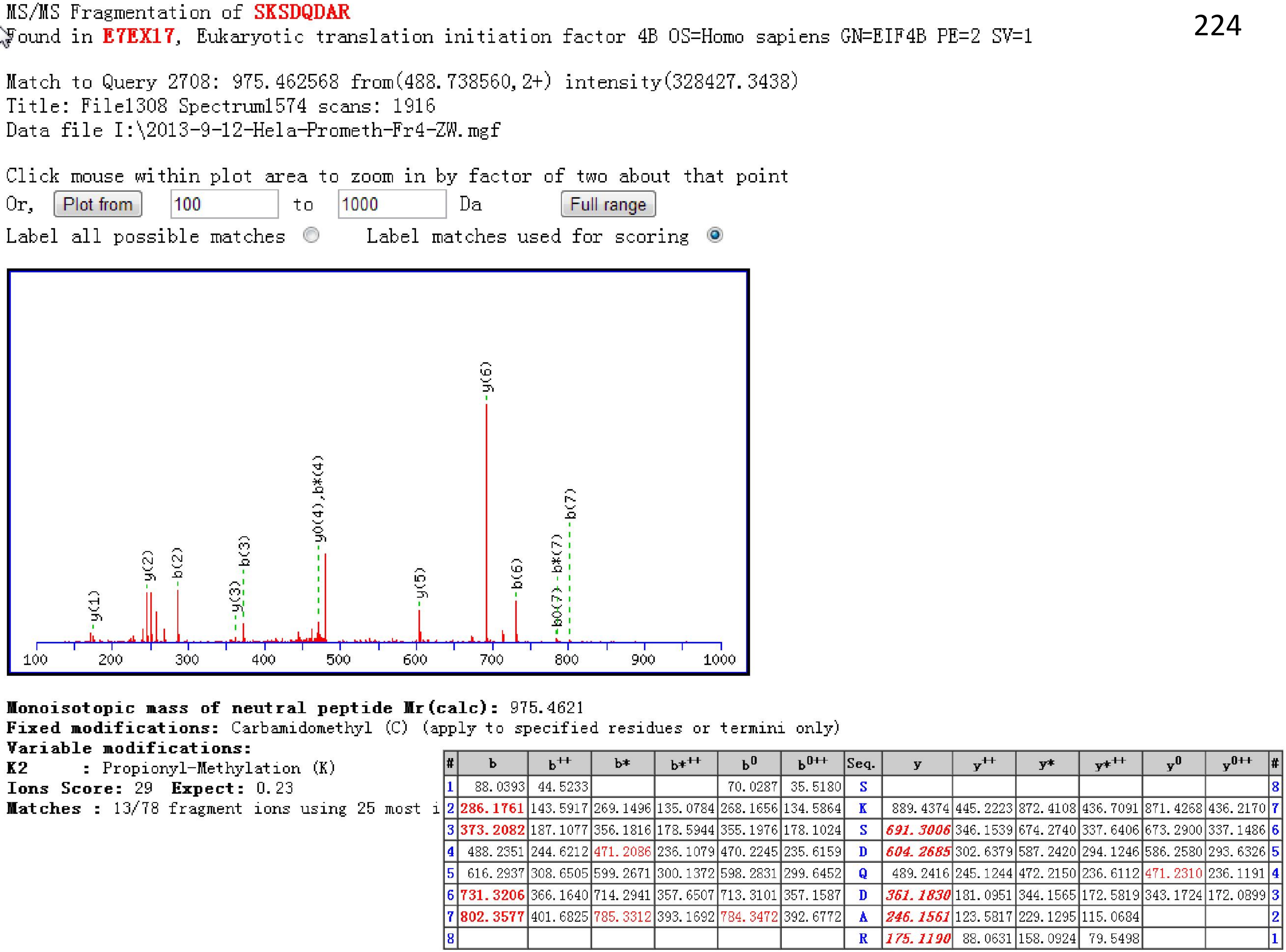
MS/MS Fragmentation of SDEKSKDR
Found in H3BMM9, RNA-binding protein with serine-rich domain 1 (Fragment) OS=Homo sapiens GN=RNPS1 PE=2 SV=1

Match to Query 4297: 1089.530368 from(545.772460,2+) intensity(42237.9844)
Title: File1308 Spectrum3963 scans: 4521
Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1089.5302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl (K)
K6 : Propionyl-Methylation (K)
Ions Score: 24 **Expect:** 1.3
Matches : 12/76 fragment ions using 28 most i

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							8
2	203.0662	102.0368			185.0557	93.0315	D	1003.5055	502.2564	986.4789	493.7431	985.4949	493.2511	7
3	332.1088	166.5581			314.0983	157.5528	E	***888.4785***	444.7429	871.4520	436.2296	870.4680	435.7376	6
4	516.2300	258.6186	499.2035	250.1054	498.2195	249.6134	K	***759.4359***	380.2216	742.4094	371.7083	741.4254	371.2163	5
5	603.2620	302.1347	586.2355	293.6214	585.2515	293.1294	S	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	4
6	801.3989	401.2031	784.3723	392.6898	783.3883	392.1978	K	***488.2827***	244.6450	471.2562	236.1317	470.2722	235.6397	3
7	916.4258	458.7165	899.3993	450.2033	898.4153	449.7113	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



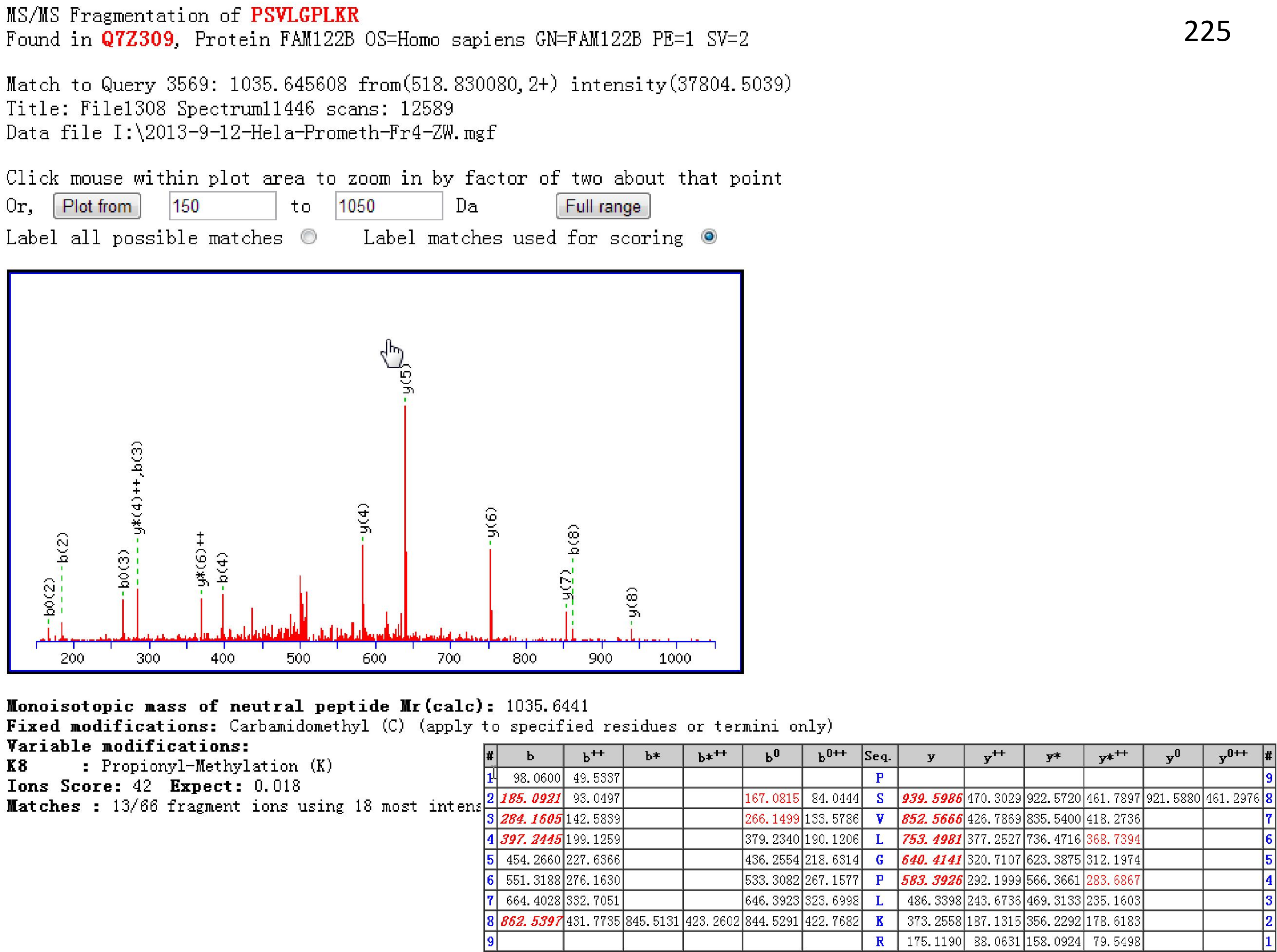
MS/MS Fragmentation of SKSDQDAR
Found in E7EX17, Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1

Match to Query 2708: 975.462568 from(488.738560,2+) intensity(328427.3438)
Title: File1308 Spectrum1574 scans: 1916
Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 975.4621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
Ions Score: 29 **Expect:** 0.23
Matches : 13/78 fragment ions using 25 most i

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							8
2	**286.1761**	143.5917	269.1496	135.0784	268.1656	134.5864	K	889.4374	445.2223	872.4108	436.7091	871.4268	436.2170	7
3	**373.2082**	187.1077	356.1816	178.5944	355.1976	178.1024	S	***691.3006***	346.1539	674.2740	337.6406	673.2900	337.1486	6
4	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	D	***604.2685***	302.6379	587.2420	294.1246	586.2580	293.6326	5
5	616.2937	308.6505	599.2671	300.1372	598.2831	299.6452	Q	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	4
6	**731.3206**	366.1640	714.2941	357.6507	713.3101	357.1587	D	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
7	**802.3577**	401.6825	785.3312	393.1692	784.3472	392.6772	A	***246.1561***	123.5817	229.1295	115.0684			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



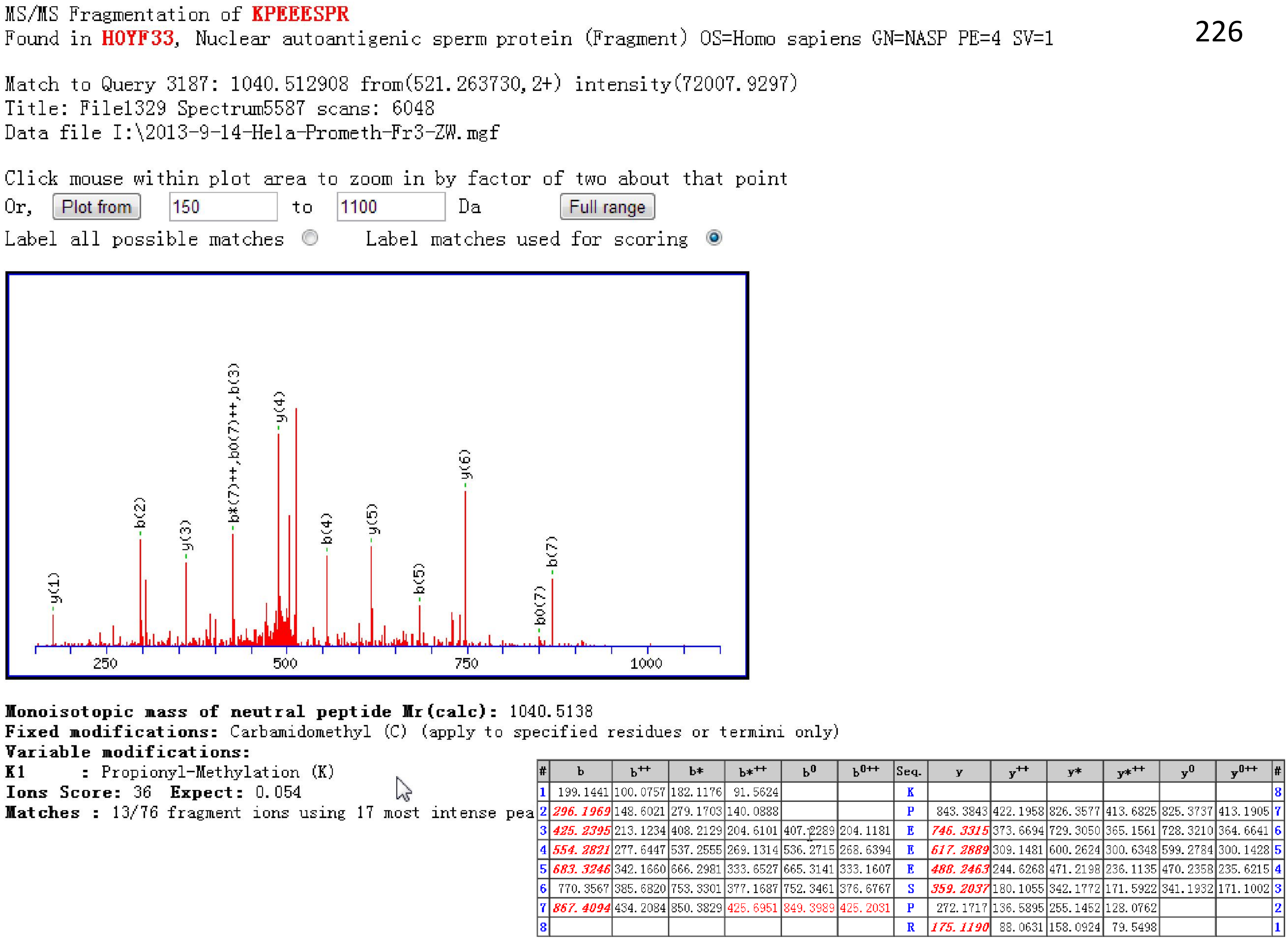
MS/MS Fragmentation of **PSVLGPLKR**
Found in **Q7Z309**, Protein FAM122B OS=Homo sapiens GN=FAM122B PE=1 SV=2

Match to Query 3569: 1035.645608 from(518.830080,2+) intensity(37804.5039)
Title: File1308 Spectrum11446 scans: 12589
Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1035.6441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K8 : Propionyl-Methylation (K)
Ions Score: 42 **Expect:** 0.018
Matches : 13/66 fragment ions using 18 most intens

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	98.0600	49.5337					P							9
2	***185.0921***	93.0497			167.0815	84.0444	S	***939.5986***	470.3029	922.5720	461.7897	921.5880	461.2976	8
3	***284.1605***	142.5839			266.1499	133.5786	V	***852.5666***	426.7869	835.5400	418.2736			7
4	***397.2445***	199.1259			379.2340	190.1206	L	***753.4981***	377.2527	736.4716	368.7394			6
5	454.2660	227.6366			436.2554	218.6314	G	***640.4141***	320.7107	623.3875	312.1974			5
6	551.3188	276.1630			533.3082	267.1577	P	***583.3926***	292.1999	566.3661	283.6867			4
7	664.4028	332.7051			646.3923	323.6998	L	486.3398	243.6736	469.3133	235.1603			3
8	***862.5397***	431.7735	845.5131	423.2602	844.5291	422.7682	K	373.2558	187.1315	356.2292	178.6183			2
9							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KPEEESPR**
Found in **H0YF33**, Nuclear autoantigenic sperm protein (Fragment) OS=Homo sapiens GN=NASP PE=4 SV=1

Match to Query 3187: 1040.512908 from(521.263730,2+) intensity(72007.9297)
Title: File1329 Spectrum5587 scans: 6048
Data file I:\2013-9-14-Hela-Prometh-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

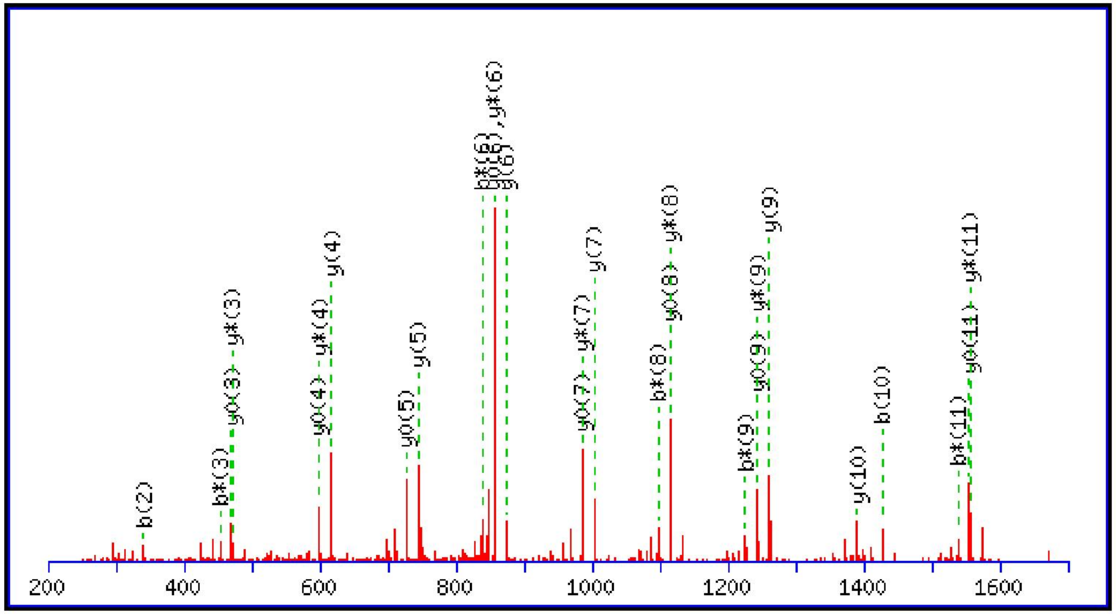
Monoisotopic mass of neutral peptide Mr(calc): 1040.5138
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 36 **Expect:** 0.054
Matches : 13/76 fragment ions using 17 most intense pea

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							8
2	***296.1969***	148.6021	279.1703	140.0888			P	843.3843	422.1958	826.3577	413.6825	825.3737	413.1905	7
3	***425.2395***	213.1234	408.2129	204.6101	407.2289	204.1181	E	***746.3315***	373.6694	729.3050	365.1561	728.3210	364.6641	6
4	***554.2821***	277.6447	537.2555	269.1314	536.2715	268.6394	E	***617.2889***	309.1481	600.2624	300.6348	599.2784	300.1428	5
5	***683.3246***	342.1660	666.2981	333.6527	665.3141	333.1607	E	***488.2463***	244.6268	471.2198	236.1135	470.2358	235.6215	4
6	770.3567	385.6820	753.3301	377.1687	752.3461	376.6767	S	***359.2037***	180.1055	342.1772	171.5922	341.1932	171.1002	3
7	***867.4094***	434.2084	850.3829	425.6951	849.3989	425.2031	P	272.1717	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **RKEQEEEEQKER**
Found in **E7EQT4**, Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=2 SV=2

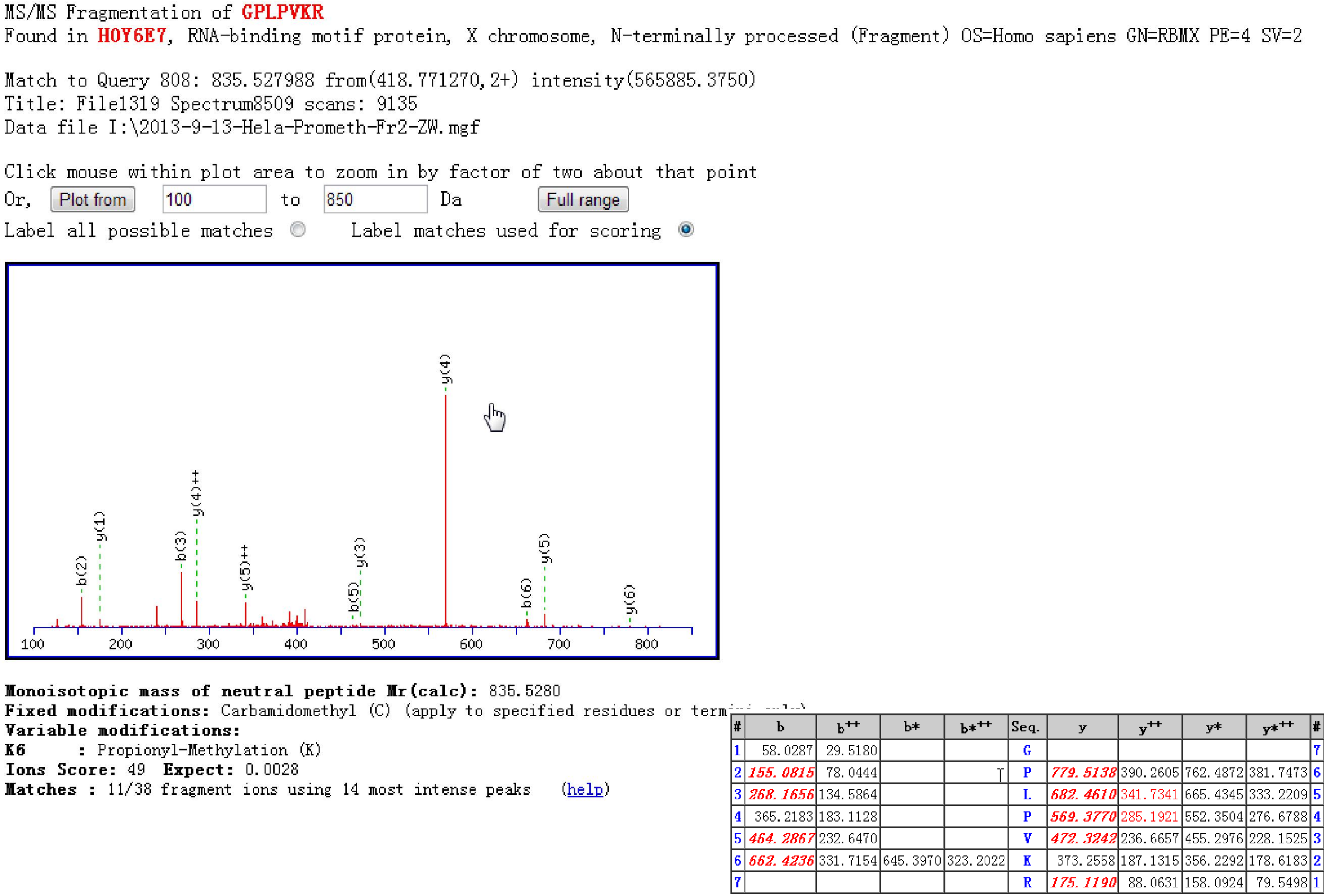
Match to Query 11533: 1728.830428 from(865.422490,2+) intensity(310533.7500)
Title: File1329 Spectrum3428 scans: 3799
Data file I:\2013-9-14-Hela-Prometh-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, 200 to 1700 Da
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1728.8278
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K2 : Propionyl (K)
K10 : Propionyl (K)
Ions Score: 67 **Expect:** 8.9e-005
Matches : 36/126 fragment ions using 45 most intense peak

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	***341.2296***	171.1184	324.2030	162.6051			K	1573.7340	787.3706	1556.7075	778.8574	1555.7235	778.3654	11
3	***470.2722***	235.6397	453.2456	227.1264	452.2616	226.6344	E	**1389.6128**	695.3101	1372.5863	686.7968	1371.6023	686.3048	10
4	***598.3307***	299.6690	581.3042	291.1557	580.3202	290.6637	Q	**1260.5703**	630.7888	1243.5437	622.2755	1242.5597	621.7835	9
5	***727.3733***	364.1903	710.3468	355.6770	709.3628	355.1850	E	1132.5117	566.7595	1115.4851	558.2462	1114.5011	557.7542	8
6	***856.4159***	428.7116	839.3894	420.1983	838.4054	419.7063	E	**1003.4691**	502.2382	986.4425	493.7249	985.4585	493.2329	7
7	***985.4585***	493.2329	968.4320	484.7196	967.4480	484.2276	E	**874.4265**	437.7169	857.3999	429.2036	856.4159	428.7116	6
8	***1114.5011***	557.7542	1097.4746	549.2409	1096.4905	548.7489	E	**745.3839**	373.1956	728.3573	364.6823	727.3733	364.1903	5
9	***1242.5597***	621.7835	1225.5331	613.2702	1224.5491	612.7782	Q	**616.3413**	308.6743	599.3148	300.1610	598.3307	299.6690	4
10	***1426.6809***	713.8441	1409.6543	705.3308	1408.6703	704.8388	K	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	3
11	***1555.7235***	778.3654	1538.6969	769.8521	1537.7129	769.3601	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GPLPVKR**

Found in **H0Y6E7**, RNA-binding motif protein, X chromosome, N-terminally processed (Fragment) OS=Homo sapiens GN=RBMX PE=4 SV=2

Match to Query 808: 835.527988 from(418.771270,2+) intensity(565885.3750)

Title: File1319 Spectrum8509 scans: 9135

Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

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

Or, Plot from 100 to 850 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 835.5280

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

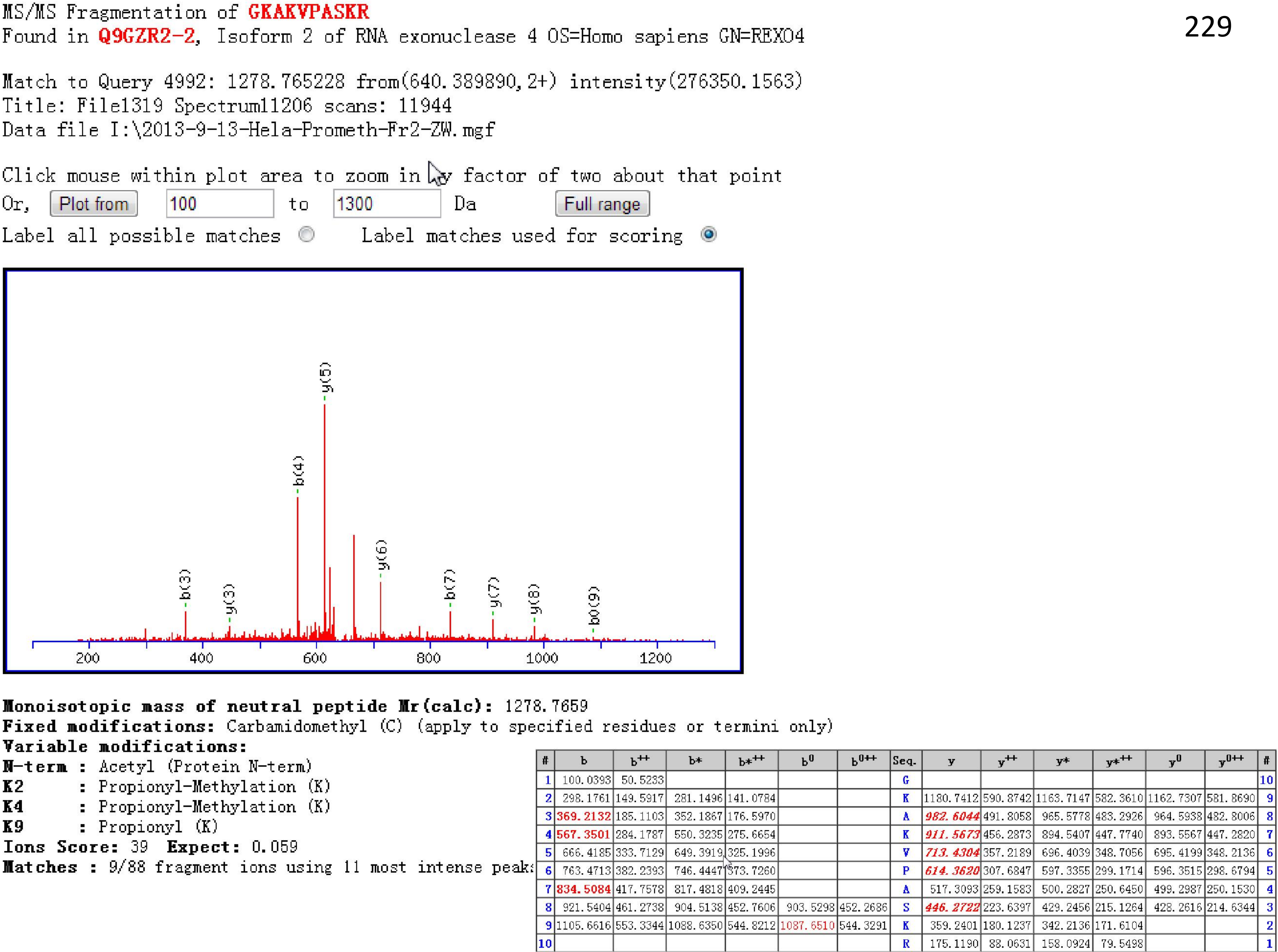
Variable modifications:

K6 : Propionyl-Methylation (K)

Ions Score: 49 **Expect:** 0.0028

Matches : 11/38 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.5180			G					7
2	***155.0815***	78.0444			P	***779.5138***	390.2605	762.4872	381.7473	6
3	***268.1656***	134.5864			L	***682.4610***	341.7341	665.4345	333.2209	5
4	365.2183	183.1128			P	***569.3770***	285.1921	552.3504	276.6788	4
5	***464.2867***	232.6470			V	***472.3242***	236.6657	455.2976	228.1525	3
6	***662.4236***	331.7154	645.3970	323.2022	K	373.2558	187.1315	356.2292	178.6183	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **GKAKVPASKR**
Found in **Q9GZR2-2**, Isoform 2 of RNA exonuclease 4 OS=Homo sapiens GN=REXO4

Match to Query 4992: 1278.765228 from(640.389890,2+) intensity(276350.1563)
Title: File1319 Spectrum11206 scans: 11944
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.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 ●

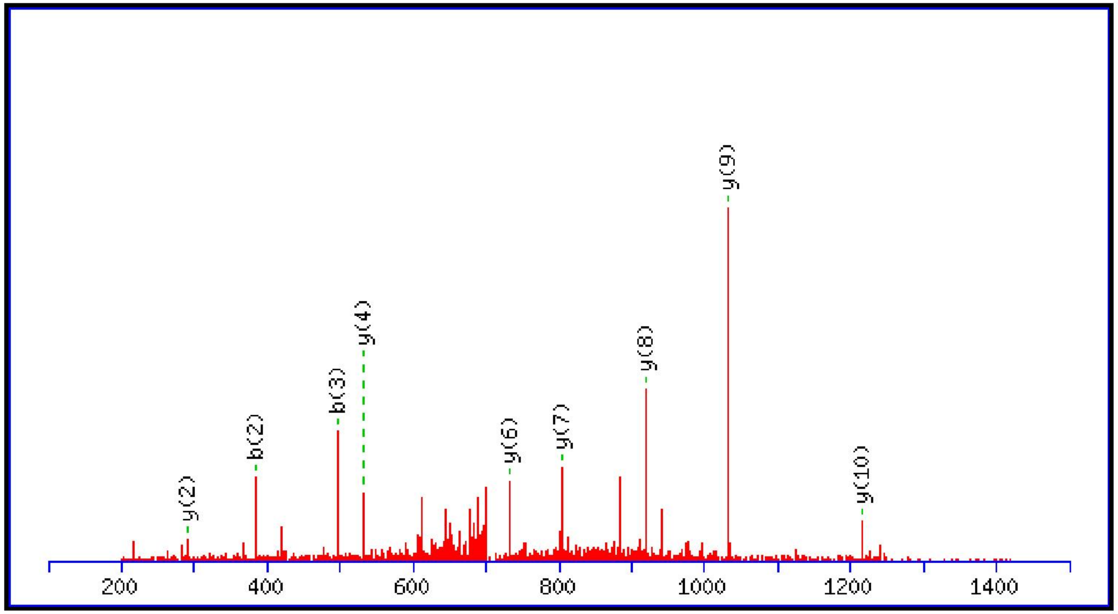
Monoisotopic mass of neutral peptide Mr(calc): 1278.7659
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
K2 : Propionyl-Methylation (K)
K4 : Propionyl-Methylation (K)
K9 : Propionyl (K)
Ions Score: 39 **Expect:** 0.059
Matches : 9/88 fragment ions using 11 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0393	50.5233					G							10
2	298.1761	149.5917	281.1496	141.0784			K	1180.7412	590.8742	1163.7147	582.3610	1162.7307	581.8690	9
3	**369.2132**	185.1103	352.1867	176.5970			A	***982.6044***	491.8058	965.5778	483.2926	964.5938	482.8006	8
4	**567.3501**	284.1787	550.3235	275.6654			K	***911.5673***	456.2873	894.5407	447.7740	893.5567	447.2820	7
5	666.4185	333.7129	649.3919	325.1996			V	***713.4304***	357.2189	696.4039	348.7056	695.4199	348.2136	6
6	763.4713	382.2393	746.4447	373.7260			P	***614.3620***	307.6847	597.3355	299.1714	596.3515	298.6794	5
7	**834.5084**	417.7578	817.4818	409.2445			A	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	4
8	921.5404	461.2738	904.5138	452.7606	903.5298	452.2686	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	3
9	1105.6616	553.3344	1088.6350	544.8212	1087.6510	544.3291	K	359.2401	180.1237	342.2136	171.6104			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KKLDASILEDR**
Found in **J3KMZ8**, Zinc finger protein ubi-d4 OS=Homo sapiens GN=DPF2 PE=4 SV=1

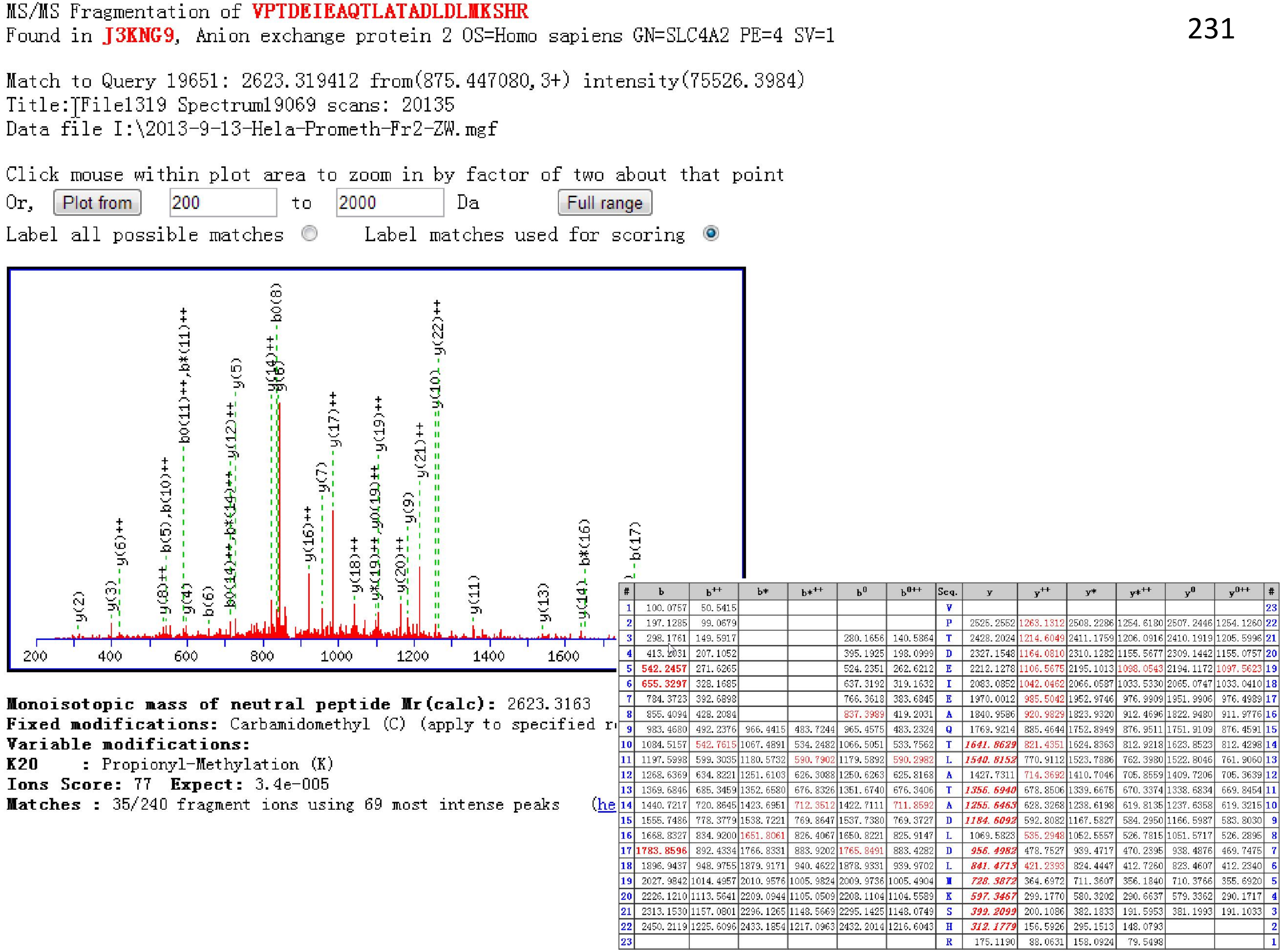
Match to Query 6324: 1412.788188 from(707.401370,2+) intensity(402113.6250)
Title: File1319 Spectrum14746 scans: 15632
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1412.7875
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
K2 : Propionyl (K)
Ions Score: 57 **Expect:** 0.0016
Matches : 9/112 fragment ions using 13 most intense peak

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							11
2	**383.2653**	192.1363	366.2387	183.6230			K	***1215.6579***	608.3326	1198.6314	599.8193	1197.6474	599.3273	10
3	**496.3493**	248.6783	479.3228	240.1650			L	***1031.5368***	516.2720	1014.5102	507.7587	1013.5262	507.2667	9
4	611.3763	306.1918	594.3497	297.6785	593.3657	297.1865	D	***918.4527***	459.7300	901.4262	451.2167	900.4421	450.7247	8
5	682.4134	341.7103	665.3869	333.1971	664.4028	332.7051	A	***803.4258***	402.2165	786.3992	393.7032	785.4152	393.2112	7
6	769.4454	385.2264	752.4189	376.7131	751.4349	376.2211	S	***732.3886***	366.6980	715.3621	358.1847	714.3781	357.6927	6
7	882.5295	441.7684	865.5029	433.2551	864.5189	432.7631	I	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
8	995.6136	498.3104	978.5870	489.7971	977.6030	489.3051	L	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	4
9	1124.6562	562.8317	1107.6296	554.3184	1106.6456	553.8264	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
10	1239.6831	620.3452	1222.6565	611.8319	1221.6725	611.3399	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **VPTDEIEAQTLATADLDLMKSHR**
Found in **J3KNG9**, Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=4 SV=1

Match to Query 19651: 2623.319412 from(875.447080,3+) intensity(75526.3984)
Title: File1319 Spectrum19069 scans: 20135
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

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

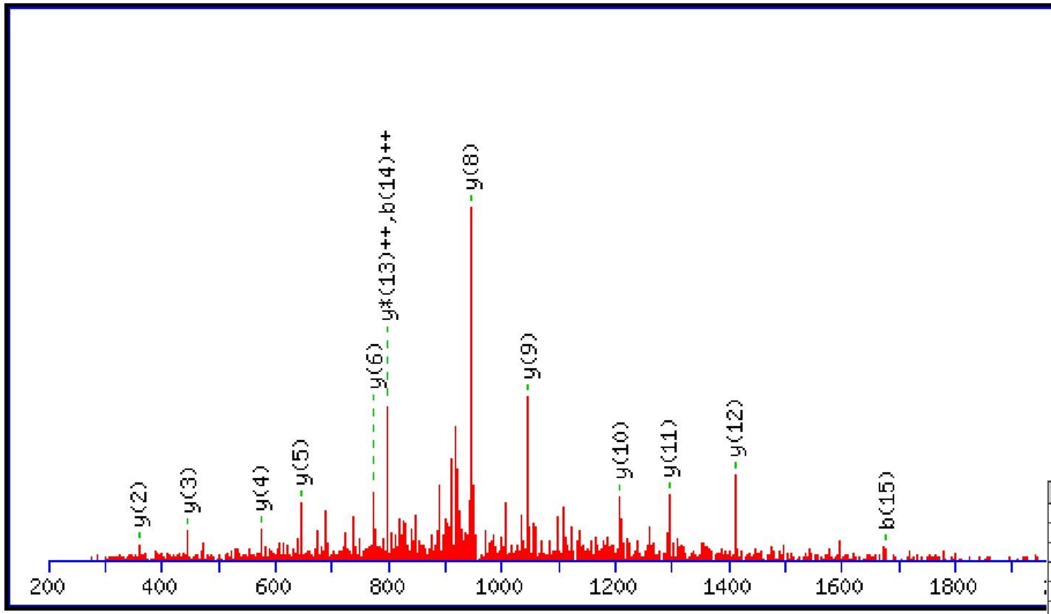
Monoisotopic mass of neutral peptide Mr(calc): 2623.3163
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K20 : Propionyl-Methylation (K)
Ions Score: 77 **Expect:** 3.4e-005
Matches : 35/240 fragment ions using 69 most intense peaks (he

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							23
2	197.1285	99.0679					P	2525.2552	1263.1312	2508.2286	1254.6180	2507.2446	1254.1260	22
3	298.1761	149.5917			280.1656	140.5864	T	2428.2024	1214.6049	2411.1759	1206.0916	2410.1919	1205.5996	21
4	413.2031	207.1052			395.1925	198.0999	D	2327.1548	1164.0810	2310.1282	1155.5677	2309.1442	1155.0757	20
5	**542.2457**	271.6265			524.2351	262.6212	E	2212.1278	1106.5675	2195.1013	1098.0543	2194.1172	1097.5623	19
6	**655.3297**	328.1685			637.3192	319.1632	I	2083.0852	1042.0462	2066.0587	1033.5330	2065.0747	1033.0410	18
7	784.3723	392.6898			766.3618	383.6845	E	1970.0012	985.5042	1952.9746	976.9909	1951.9906	976.4989	17
8	855.4094	428.2084			837.3989	419.2031	A	1840.9586	920.9829	1823.9320	912.4696	1822.9480	911.9776	16
9	983.4680	492.2376	966.4415	483.7244	965.4575	483.2324	Q	1769.9214	885.4644	1752.8949	876.9511	1751.9109	876.4591	15
10	1084.5157	542.7615	1067.4891	534.2482	1066.5051	533.7562	T	***1641.8629***	821.4351	1624.8363	812.9218	1623.8523	812.4298	14
11	1197.5998	599.3035	1180.5732	590.7902	1179.5892	590.2982	L	***1540.8152***	770.9112	1523.7886	762.3980	1522.8046	761.9060	13
12	1268.6369	634.8221	1251.6103	626.3088	1250.6263	625.8168	A	1427.7311	714.3692	1410.7046	705.8559	1409.7206	705.3639	12
13	1369.6846	685.3459	1352.6580	676.8326	1351.6740	676.3406	T	***1356.6940***	678.8506	1339.6675	670.3374	1338.6834	669.8454	11
14	1440.7217	720.8645	1423.6951	712.3512	1422.7111	711.8592	A	***1255.6463***	628.3268	1238.6198	619.8135	1237.6358	619.3215	10
15	1555.7486	778.3779	1538.7221	769.8647	1537.7380	769.3727	D	***1184.6092***	592.8082	1167.5827	584.2950	1166.5987	583.8030	9
16	1668.8327	834.9200	1651.8061	826.4067	1650.8221	825.9147	L	1069.5823	535.2948	1052.5557	526.7815	1051.5717	526.2895	8
17	**1783.8596**	892.4334	1766.8331	883.9202	1765.8491	883.4282	D	***956.4982***	478.7527	939.4717	470.2395	938.4876	469.7475	7
18	1896.9437	948.9755	1879.9171	940.4622	1878.9331	939.9702	L	***841.4713***	421.2393	824.4447	412.7260	823.4607	412.2340	6
19	2027.9842	1014.4957	2010.9576	1005.9824	2009.9736	1005.4904	M	***728.3872***	364.6972	711.3607	356.1840	710.3766	355.6920	5
20	2226.1210	1113.5641	2209.0944	1105.0509	2208.1104	1104.5589	K	***597.3467***	299.1770	580.3202	290.6637	579.3362	290.1717	4
21	2313.1530	1157.0801	2296.1265	1148.5669	2295.1425	1148.0749	S	***399.2099***	200.1086	382.1833	191.5953	381.1993	191.1033	3
22	2450.2119	1225.6096	2433.1854	1217.0963	2432.2014	1216.6043	H	***312.1779***	156.5926	295.1513	148.0793			2
23							R	175.1190	88.0631	158.0924	79.5498			1

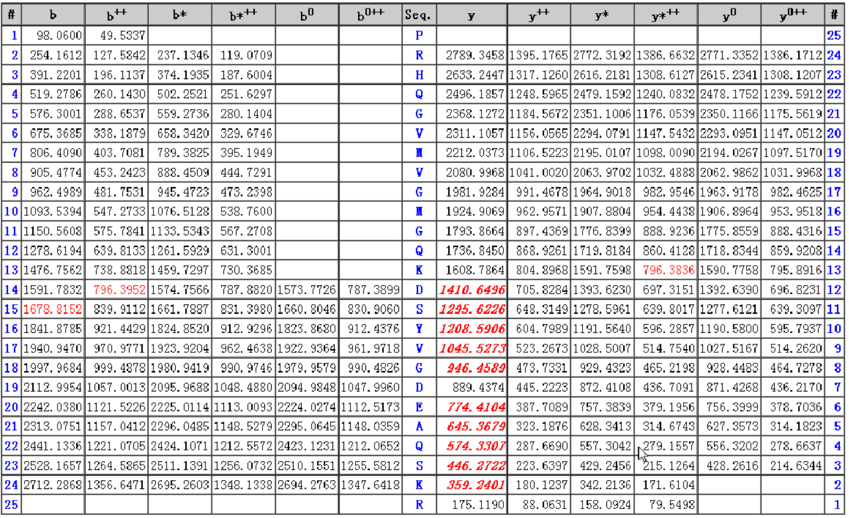
MS/MS Fragmentation of PRHQGVMVGMGQKDSYVGDEAQSKR
Found in I3L3I4, Actin, cytoplasmic 2, N-terminally processed OS=Homo sapiens GN=ACTG1 PE=2 SV=1

Match to Query 21386: 2885.380692 from(962.800840,3+) intensity(91224.3594)
Title: File1319 Spectrum11628 scans: 12384
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2885.3913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K13 : Propionyl-Methylation (K)
K24 : Propionyl (K)
Ions Score: 64 **Expect:** 0.00041
Matches : 13/256 fragment ions using 17 most intense peaks (help)

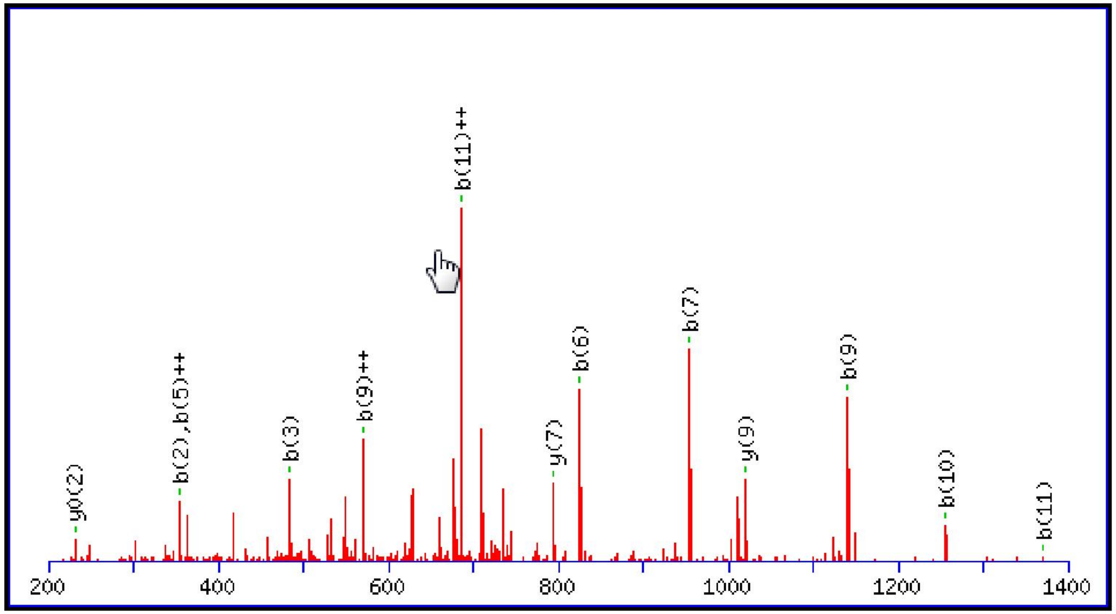


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	98.0600	49.5337					P							25
2	254.1612	127.5842	237.1346	119.0709			R	2789.3458	1395.1765	2772.3192	1386.6632	2771.3352	1386.1712	24
3	391.2201	196.1137	374.1935	187.6004			H	2633.2447	1317.1260	2616.2181	1308.6127	2615.2341	1308.1207	23
4	519.2786	260.1430	502.2521	251.6297			Q	2496.1857	1248.5965	2479.1592	1240.0832	2478.1752	1239.5912	22
5	576.3001	288.6537	559.2736	280.1404			G	2368.1272	1184.5672	2351.1006	1176.0539	2350.1166	1175.5619	21
6	675.3685	338.1879	658.3420	329.6746			V	2311.1057	1156.0565	2294.0791	1147.5432	2293.0951	1147.0512	20
7	806.4090	403.7081	789.3825	395.1949			M	2212.0373	1106.5223	2195.0107	1098.0090	2194.0267	1097.5170	19
8	905.4774	453.2423	888.4509	444.7291			V	2080.9968	1041.0020	2063.9702	1032.4888	2062.9862	1031.9968	18
9	962.4989	481.7531	945.4723	473.2398			G	1981.9284	991.4678	1964.9018	982.9546	1963.9178	982.4625	17
10	1093.5394	547.2733	1076.5128	538.7600			M	1924.9069	962.9571	1907.8804	954.4438	1906.8964	953.9518	16
11	1150.5608	575.7841	1133.5343	567.2708			G	1793.8664	897.4369	1776.8399	888.9236	1775.8559	888.4316	15
12	1278.6194	639.8133	1261.5929	631.3001			Q	1736.8450	868.9261	1719.8184	860.4128	1718.8344	859.9208	14
13	1476.7562	738.8818	1459.7297	730.3685			K	1608.7864	804.8968	1591.7598	796.3836	1590.7758	795.8916	13
14	1591.7832	796.3952	1574.7566	787.8820	1573.7726	787.3899	D	***1410.6496***	705.8284	1393.6230	697.3151	1392.6390	696.8231	12
15	1678.8152	839.9112	1661.7887	831.3980	1660.8046	830.9060	S	***1295.6226***	648.3149	1278.5961	639.8017	1277.6121	639.3097	11
16	1841.8785	921.4429	1824.8520	912.9296	1823.8680	912.4376	Y	***1208.5906***	604.7989	1191.5640	596.2857	1190.5800	595.7937	10
17	1940.9470	970.9771	1923.9204	962.4638	1922.9364	961.9718	V	***1045.5273***	523.2673	1028.5007	514.7540	1027.5167	514.2620	9
18	1997.9684	999.4878	1980.9419	990.9746	1979.9579	990.4826	G	***946.4589***	473.7331	929.4323	465.2198	928.4483	464.7278	8
19	2112.9954	1057.0013	2095.9688	1048.4880	2094.9848	1047.9960	D	889.4374	445.2223	872.4108	436.7091	871.4268	436.2170	7
20	2242.0380	1121.5226	2225.0114	1113.0093	2224.0274	1112.5173	E	***774.4104***	387.7089	757.3839	379.1956	756.3999	378.7036	6
21	2313.0751	1157.0412	2296.0485	1148.5279	2295.0645	1148.0359	A	***645.3679***	323.1876	628.3413	314.6743	627.3573	314.1823	5
22	2441.1336	1221.0705	2424.1071	1212.5572	2423.1231	1212.0652	Q	***574.3307***	287.6690	557.3042	279.1557	556.3202	278.6637	4
23	2528.1657	1264.5865	2511.1391	1256.0732	2510.1551	1255.5812	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	3
24	2712.2868	1356.6471	2695.2603	1348.1338	2694.2763	1347.6418	K	***359.2401***	180.1237	342.2136	171.6104			2
25							R	175.1190	88.0631	158.0924	79.5498			1

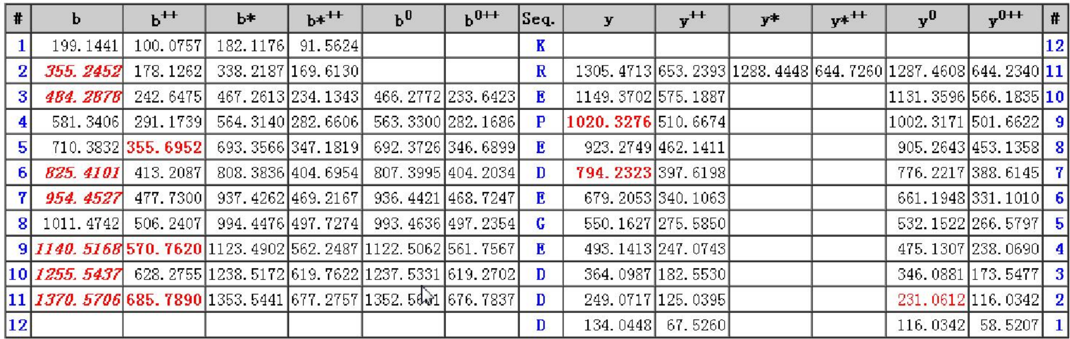
MS/MS Fragmentation of **KREPEDEGEDDD**
Found in **P39687**, Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1

Match to Query 7668: 1502.602388 from(752.308470,2+) intensity(470317.4688)
Title: File1319 Spectrum4011 scans: 4441
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

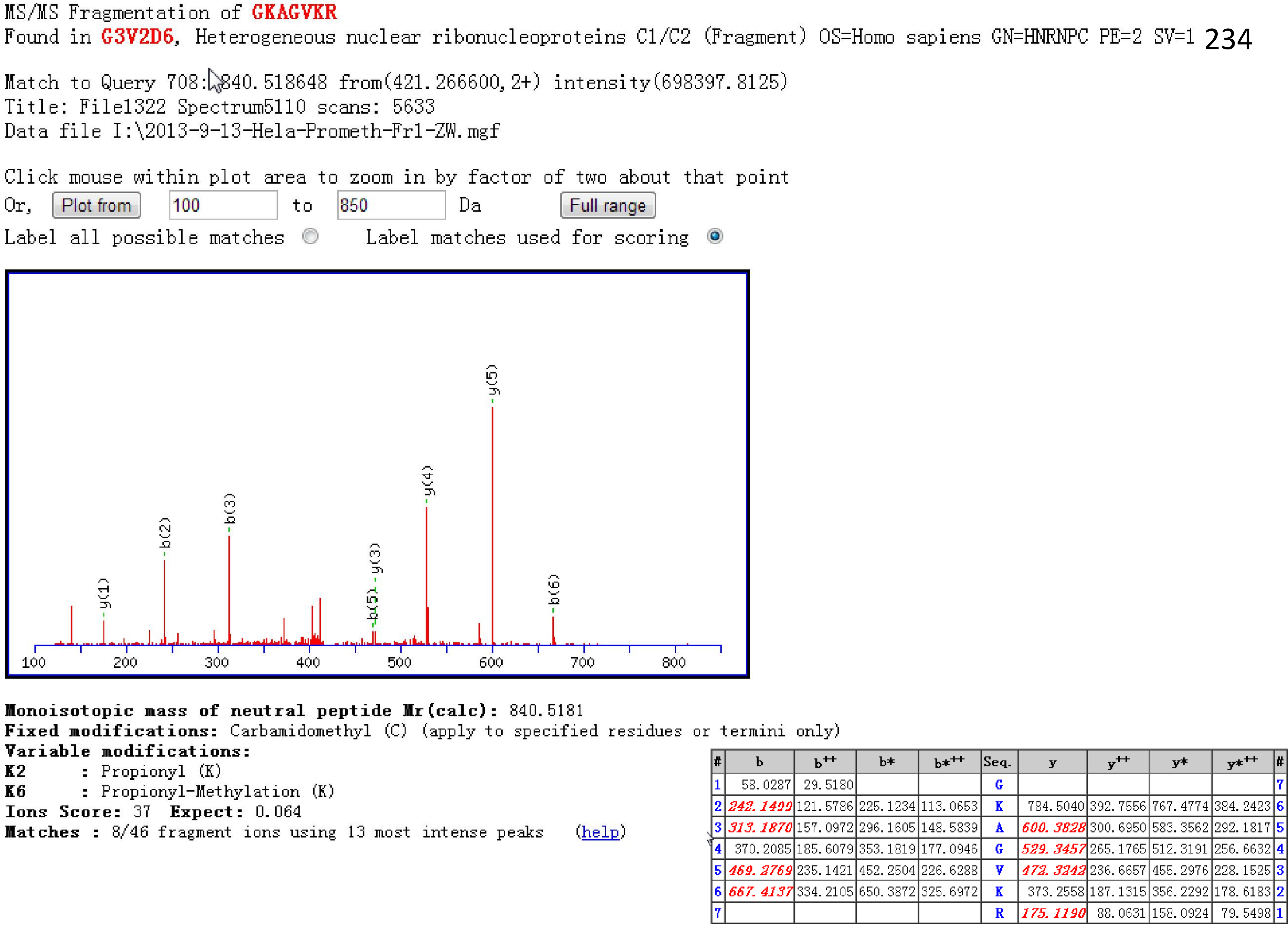
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1502.6009
Fixed modifications: Carbamidomethyl (C) (apply to specif
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 70 **Expect:** 1.7e-006
Matches : 13/108 fragment ions using 12 most intense peaks



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							12
2	***355.2452***	178.1262	338.2187	169.6130			R	1305.4713	653.2393	1288.4448	644.7260	1287.4608	644.2340	11
3	***484.2878***	242.6475	467.2613	234.1343	466.2772	233.6423	E	1149.3702	575.1887			1131.3596	566.1835	10
4	581.3406	291.1739	564.3140	282.6606	563.3300	282.1686	P	**1020.3276**	510.6674			1002.3171	501.6622	9
5	710.3832	**355.6952**	693.3566	347.1819	692.3726	346.6899	E	923.2749	462.1411			905.2643	453.1358	8
6	***825.4101***	413.2087	808.3836	404.6954	807.3995	404.2034	D	**794.2323**	397.6198			776.2217	388.6145	7
7	***954.4527***	477.7300	937.4262	469.2167	936.4421	468.7247	E	679.2053	340.1063			661.1948	331.1010	6
8	1011.4742	506.2407	994.4476	497.7274	993.4636	497.2354	G	550.1627	275.5850			532.1522	266.5797	5
9	***1140.5168***	**570.7620**	1123.4902	562.2487	1122.5062	561.7567	E	493.1413	247.0743			475.1307	238.0690	4
10	***1255.5437***	628.2755	1238.5172	619.7622	1237.5331	619.2702	D	364.0987	182.5530			346.0881	173.5477	3
11	***1370.5706***	**685.7890**	1353.5441	677.2757	1352.5601	676.7837	D	249.0717	125.0395			231.0612	116.0342	2
12							D	134.0448	67.5260			116.0342	58.5207	1



MS/MS Fragmentation of **GKAGVKR**
Found in **G3V2D6**, Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=2 SV=1

Match to Query 708: 840.518648 from(421.266600,2+) intensity(698397.8125)
Title: File1322 Spectrum5110 scans: 5633
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

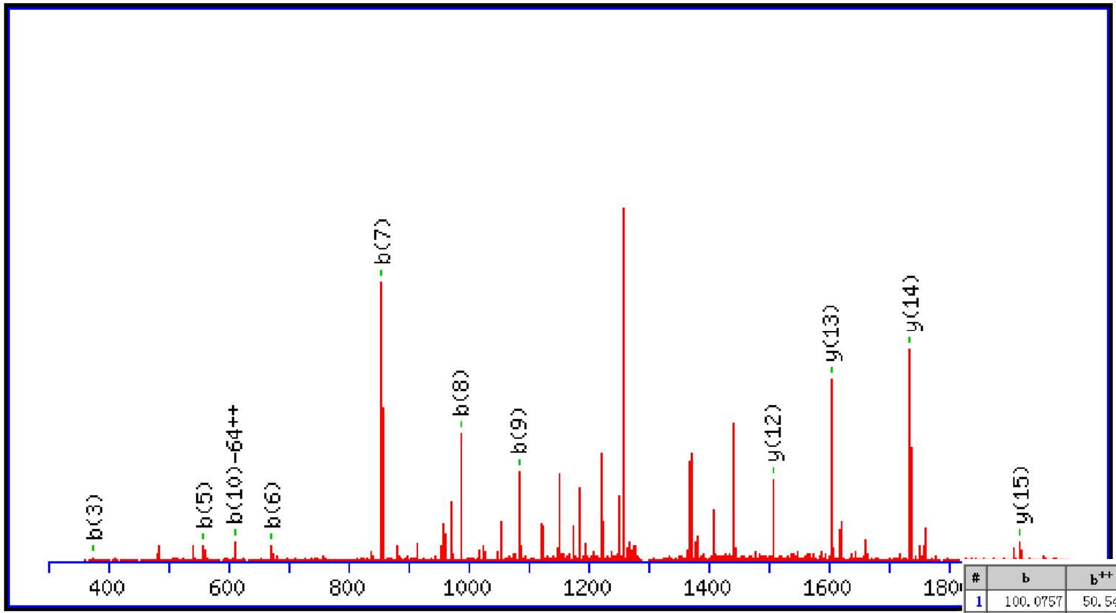
Monoisotopic mass of neutral peptide Mr(calc): 840.5181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K6 : Propionyl-Methylation (K)
Ions Score: 37 **Expect:** 0.064
Matches : 8/46 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.5180			G					7
2	***242.1499***	121.5786	225.1234	113.0653	K	784.5040	392.7556	767.4774	384.2423	6
3	***313.1870***	157.0972	296.1605	148.5839	A	***600.3828***	300.6950	583.3562	292.1817	5
4	370.2085	185.6079	353.1819	177.0946	G	***529.3457***	265.1765	512.3191	256.6632	4
5	***469.2769***	235.1421	452.2504	226.6288	V	***472.3242***	236.6657	455.2976	228.1525	3
6	***667.4137***	334.2105	650.3872	325.6972	K	373.2558	187.1315	356.2292	178.6183	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **VQMPSLKMPKVDLKGPQVEVR**
Found in **Q8IVF2**, Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2

Match to Query 15938: 2591.407328 from(1296.710940,2+) intensity(102551.4297)
Title: File281 Spectrum21228 scans: 22802
Data file I:\2013-9-12-Hela-Prometh-Fr19-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



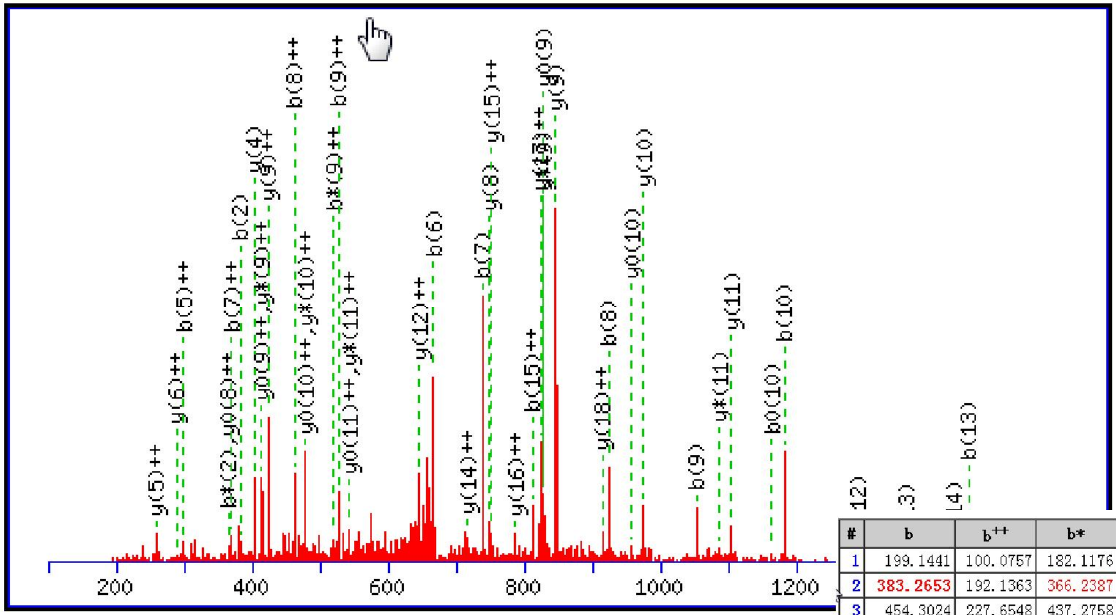
Monoisotopic mass of neutral peptide Mr(calc): 2590.4227
Fixed modifications: Carbamidomethyl (C) (apply to specified resi
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table),
K7 : Propionyl (K)
K10 : Propionyl-Methylation (K)
K14 : Propionyl-Methylation (K)
Ions Score: 28 **Expect:** 1.9
Matches : 11/342 fragment ions using 17 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							21
2	228.1343	114.5708	211.1077	106.0575			Q	2492.3615	1246.6844	2475.3350	1238.1711	2474.3510	1237.6791	20
3	375.1697	188.0885	358.1431	179.5752			M	2364.3029	1182.6551	2347.2764	1174.1418	2346.2924	1173.6498	19
4	472.2224	236.6149	455.1959	228.1016			P	2217.2675	1109.1374	2200.2410	1100.6241	2199.2570	1100.1321	18
5	559.2545	280.1309	542.2279	271.6176	541.2439	271.1256	S	2120.2148	1060.6110	2103.1882	1052.0978	2102.2042	1051.6057	17
6	672.3385	336.6729	655.3120	328.1596	654.3280	327.6676	L	2033.1827	1017.0950	2016.1562	1008.5817	2015.1722	1008.0897	16
7	856.4597	428.7335	839.4332	420.2202	838.4491	419.7282	K	1920.0987	960.5530	1903.0721	952.0397	1902.0881	951.5477	15
8	987.5002	494.2537	970.4736	485.7405	969.4896	485.2484	M	1735.9775	868.4924	1718.9510	859.9791	1717.9669	859.4871	14
9	1084.5530	542.7801	1067.5264	534.2668	1066.5424	533.7748	P	1604.9370	802.9721	1587.9105	794.4589	1586.9265	793.9669	13
10	1282.6898	641.8485	1265.6632	633.3353	1264.6792	632.8432	K	1507.8843	754.4458	1490.8577	745.9325	1489.8737	745.4405	12
11	1381.7582	691.3827	1364.7316	682.8695	1363.7476	682.3775	V	1309.7474	655.3774	1292.7209	646.8641	1291.7369	646.3721	11
12	1496.7851	748.8962	1479.7586	740.3829	1478.7746	739.8909	D	1210.6790	605.8431	1193.6525	597.3299	1192.6684	596.8379	10
13	1609.8692	805.4382	1592.8427	796.9250	1591.8586	796.4330	L	1095.6521	548.3297	1078.6255	539.8164	1077.6415	539.3244	9
14	1808.0060	904.5067	1790.9795	895.9934	1789.9955	895.5014	K	982.5680	491.7876	965.5415	483.2744	964.5574	482.7824	8
15	1865.0275	933.0174	1848.0009	924.5041	1847.0169	924.0121	G	784.4312	392.7192	767.4046	384.2060	766.4206	383.7139	7
16	1962.0803	981.5438	1945.0537	973.0305	1944.0697	972.5385	P	727.4097	364.2085	710.3832	355.6952	709.3991	355.2032	6
17	2090.1388	1045.5731	2073.1123	1037.0598	2072.1283	1036.5678	Q	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	5
18	2189.2072	1095.1073	2172.1807	1086.5940	2171.1967	1086.1020	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
19	2318.2498	1159.6286	2301.2233	1151.1153	2300.2393	1150.6233	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
20	2417.3183	1209.1628	2400.2917	1200.6495	2399.3077	1200.1575	V	274.1874	137.5973	257.1608	129.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KKAAAAAWEEPSSGNGTAR**
Found in **Q9P258**, Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2

Match to Query 15937: 2027.009922 from(676.677250,3+) intensity(207188.5625)
Title: File1322 Spectrum9575 scans: 10284
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.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 ●



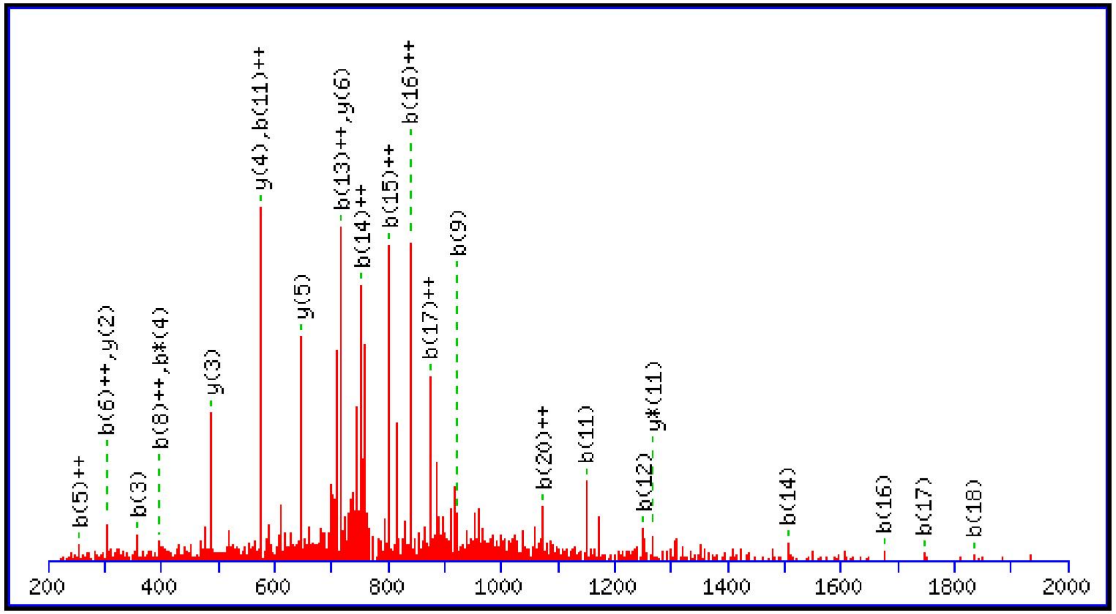
Monoisotopic mass of neutral peptide Mr(calc): 2027.0
Fixed modifications: Carbamidomethyl (C) (apply to specit
Variable modifications:
K1 : Propionyl-Methylation (K)
K2 : Propionyl (K)
Ions Score: 40 **Expect:** 0.1
Matches : 43/196 fragment ions using 104 most intense peak

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	199.1441	100.0757	182.1176	91.5624			K							19
2	**383.2653**	192.1363	366.2387	183.6230			K	1829.8777	915.4425	1812.8511	906.9292	1811.8671	906.4372	18
3	454.3024	227.6548	437.2758	219.1416			A	1645.7565	823.3819	1628.7299	814.8686	1627.7459	814.3766	17
4	525.3395	263.1734	508.3130	254.6601			A	1574.7194	787.8633	1557.6928	779.3501	1556.7088	778.8580	16
5	596.3766	**298.6920**	579.3501	290.1787			A	1503.6823	752.3448	1486.6557	743.8315	1485.6717	743.3395	15
6	**667.4137**	334.2105	650.3872	325.6972			A	***1432.6451***	716.8262	1415.6186	708.3129	1414.6346	707.8209	14
7	**738.4509**	**369.7291**	721.4243	361.2158			A	***1361.6080***	681.3077	1344.5815	672.7944	1343.5975	672.3024	13
8	**924.5302**	**462.7687**	907.5036	454.2554			W	***1290.5709***	645.7891	1273.5444	637.2758	1272.5604	636.7838	12
9	**1053.5728**	**527.2900**	1036.5462	518.7767	1035.5622	518.2847	E	***1104.4916***	552.7494	1087.4651	544.2362	1086.4810	543.7442	11
10	**1182.6154**	591.8113	1165.5888	583.2980	1164.6048	582.8060	E	***975.4490***	488.2281	958.4225	479.7149	957.4384	479.2229	10
11	1279.6681	640.3377	1262.6416	631.8244	1261.6576	631.3324	P	***846.4064***	423.7068	829.3799	415.1936	828.3959	414.7016	9
12	1366.7001	683.8537	1349.6736	675.3404	1348.6896	674.8484	S	***749.3537***	375.1805	732.3271	366.6672	731.3431	366.1752	8
13	**1453.7322**	727.3697	1436.7056	718.8564	1435.7216	718.3644	S	662.3216	331.6645	645.2951	323.1512	644.3111	322.6592	7
14	1510.7536	755.8805	1493.7271	747.3672	1492.7431	746.8752	G	575.2896	288.1484	558.2631	279.6352	557.2790	279.1432	6
15	1624.7966	**812.9019**	1607.7700	804.3886	1606.7860	803.8966	N	518.2681	259.6377	501.2416	251.1244	500.2576	250.6324	5
16	1681.8180	841.4127	1664.7915	832.8994	1663.8075	832.4074	G	***404.2252***	202.6162	387.1987	194.1030	386.2146	193.6110	4
17	1782.8657	891.9365	1765.8392	883.4232	1764.8551	882.9312	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
18	1853.9028	927.4550	1836.8763	918.9418	1835.8923	918.4498	A	246.1561	123.5817	229.1295	115.0684			2
19							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KASGPPVSELITKAVAASKER**
Found in **P10412**, Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2

Match to Query 15046: 2320.301472 from(774.441100,3+) intensity(36450.2734)
Title: File1314 Spectrum18970 scans: 20490
Data file I:\2013-9-13-Hela-Prometh-Fr16-ZW.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 ●



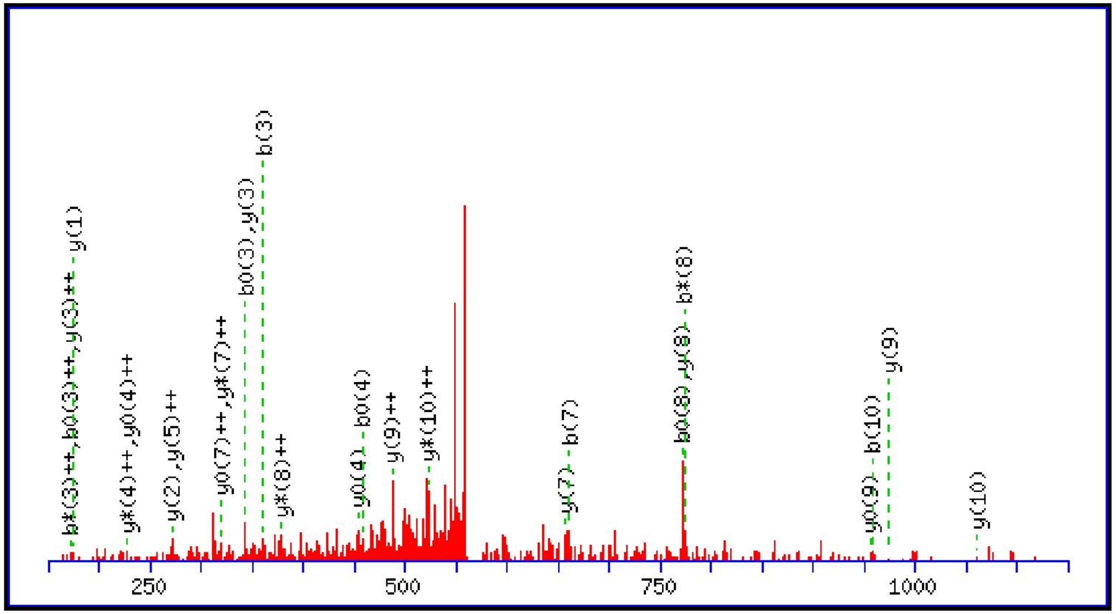
Monoisotopic mass of neutral peptide Mr(calc): 2320.3002
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or t
Variable modifications:
K1 : Propionyl-Methylation (K)
K13 : Propionyl (K)
K19 : Propionyl (K)
Ions Score: 62 **Expect:** 0.00056
Matches : 25/234 fragment ions using 35 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							21
2	270.1812	135.5942	253.1547	127.0810			A	2123.1707	1062.0890	2106.1441	1053.5757	2105.1601	1053.0837	20
3	**357.2132**	179.1103	340.1867	170.5970	339.2027	170.1050	S	2052.1335	1026.5704	2035.1070	1018.0571	2034.1230	1017.5651	19
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	G	1965.1015	983.0544	1948.0750	974.5411	1947.0910	974.0491	18
5	511.2875	**256.1474**	494.2609	247.6341	493.2769	247.1421	P	1908.0801	954.5437	1891.0535	946.0304	1890.0695	945.5384	17
6	608.3402	**304.6738**	591.3137	296.1605	590.3297	295.6685	P	1811.0273	906.0173	1794.0007	897.5040	1793.0167	897.0120	16
7	707.4087	354.2080	690.3821	345.6947	689.3981	345.2027	V	1713.9745	857.4909	1696.9480	848.9776	1695.9640	848.4856	15
8	794.4407	**397.7240**	777.4141	389.2107	776.4301	388.7187	S	1614.9061	807.9567	1597.8796	799.4434	1596.8955	798.9514	14
9	**923.4833**	462.2453	906.4567	453.7320	905.4727	453.2400	E	1527.8741	764.4407	1510.8475	755.9274	1509.8635	755.4354	13
10	1036.5673	518.7873	1019.5408	510.2740	1018.5568	509.7820	L	1398.8315	699.9194	1381.8049	691.4061	1380.8209	690.9141	12
11	**1149.6514**	**575.3293**	1132.6249	566.8161	1131.6408	566.3241	I	1285.7474	643.3774	1268.7209	634.8641	1267.7369	634.3721	11
12	**1250.6991**	625.8532	1233.6725	617.3399	1232.6885	616.8479	T	1172.6634	586.8353	1155.6368	578.3220	1154.6528	577.8300	10
13	1434.8203	**717.9138**	1417.7937	709.4005	1416.8097	708.9085	K	1071.6157	536.3115	1054.5891	527.7982	1053.6051	527.3062	9
14	**1505.8574**	**753.4323**	1488.8308	744.9190	1487.8468	744.4270	A	887.4945	444.2509	870.4680	435.7376	869.4839	435.2456	8
15	1604.9258	**802.9665**	1587.8992	794.4533	1586.9152	793.9612	V	816.4574	408.7323	799.4308	400.2191	798.4468	399.7271	7
16	**1675.9629**	**838.4851**	1658.9364	829.9718	1657.9523	829.4798	A	**717.3890**	359.1981	700.3624	350.6849	699.3784	350.1928	6
17	**1747.0000**	**874.0036**	1729.9735	865.4904	1728.9894	864.9984	A	**646.3519**	323.6796	629.3253	315.1663	628.3413	314.6743	5
18	**1834.0320**	917.5197	1817.0055	909.0064	1816.0215	908.5144	S	**575.3148**	288.1610	558.2882	279.6477	557.3042	279.1557	4
19	2018.1532	1009.5802	2001.1267	1001.0670	2000.1427	1000.5750	K	**488.2827**	244.6450	471.2562	236.1317	470.2722	235.6397	3
20	2147.1958	**1074.1015**	2130.1693	1065.5883	2129.1852	1065.0963	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
21							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ASKDGGAEAPR**
Found in **Q8N3D4**, EH domain-binding protein 1-like protein 1 OS=Homo sapiens GN=EHBP1L1 PE=1 SV=2

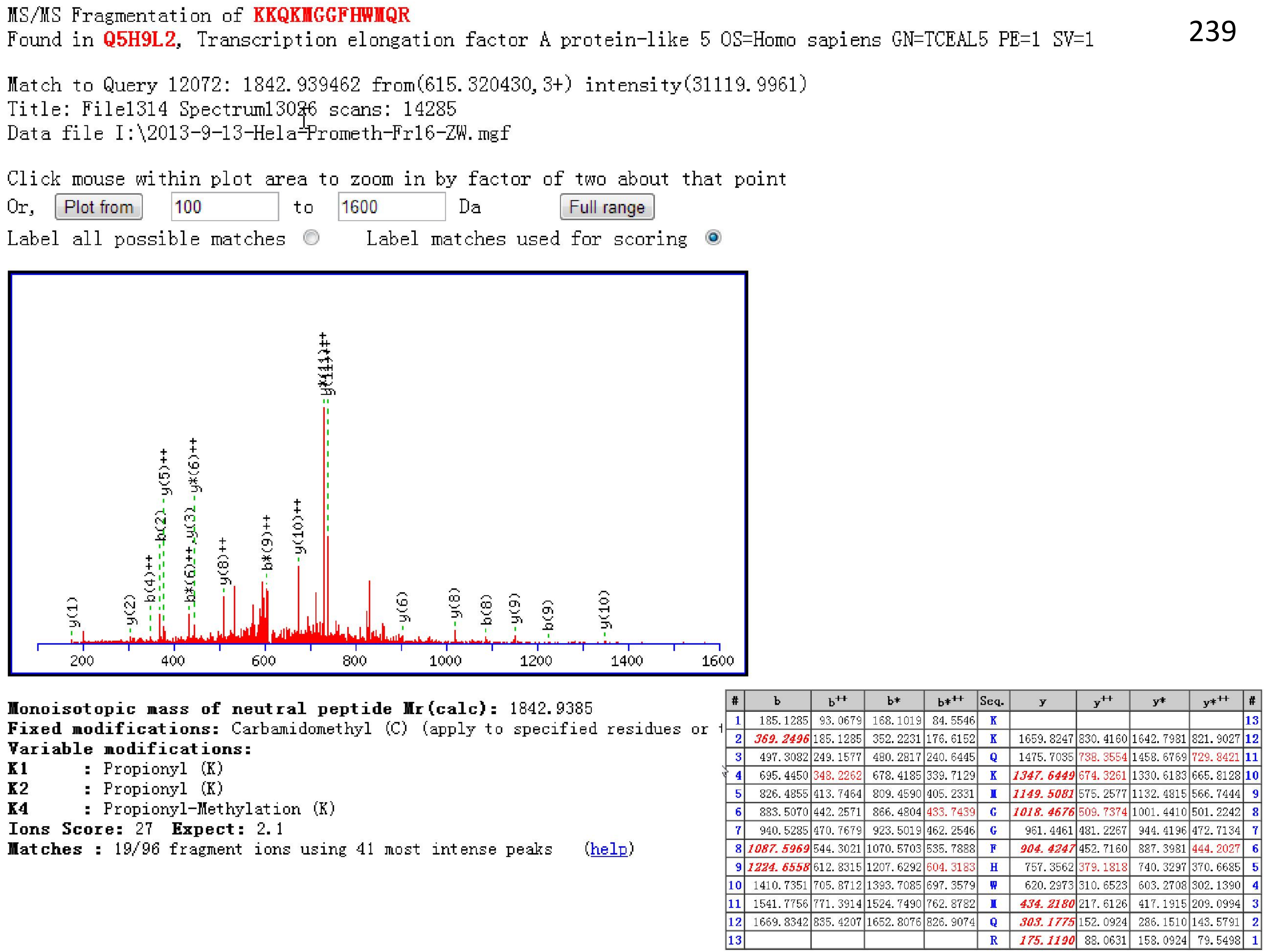
Match to Query 5212: 1131.578468 from(566.796510,2+) intensity(5204.7188)
Title: File1314 Spectrum3445 scans: 3985
Data file I:\2013-9-13-Hela-Prometh-Fr16-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1131.5793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 23 **Expect:** 2.5
Matches : 27/108 fragment ions using 77 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							11
2	159.0764	80.0418			141.0659	71.0366	S	***1061.5494***	531.2784	1044.5229	522.7651	1043.5389	522.2731	10
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	K	***974.5174***	487.7623	957.4909	479.2491	956.5069	478.7571	9
4	476.2624	238.6348	459.2358	230.1216	458.2518	229.6295	D	***772.3584***	386.6828	755.3319	378.1696	754.3478	377.6776	8
5	533.2838	267.1456	516.2573	258.6323	515.2733	258.1403	G	***657.3315***	329.1694	640.3049	320.6561	639.3209	320.1641	7
6	590.3053	295.6563	573.2788	287.1430	572.2947	286.6510	G	600.3100	300.6586	583.2835	292.1454	582.2994	291.6534	6
7	**661.3424**	331.1748	644.3159	322.6616	643.3319	322.1696	A	543.2885	272.1479	526.2620	263.6346	525.2780	263.1426	5
8	790.3850	395.6961	773.3585	387.1829	772.3744	386.6909	E	472.2514	236.6293	455.2249	228.1161	454.2409	227.6241	4
9	861.4221	431.2147	844.3956	422.7014	843.4116	422.2094	A	***343.2088***	172.1081	326.1823	163.5948			3
10	**958.4749**	479.7411	941.4483	471.2278	940.4643	470.7358	P	***272.1717***	136.5895	255.1452	128.0762			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1



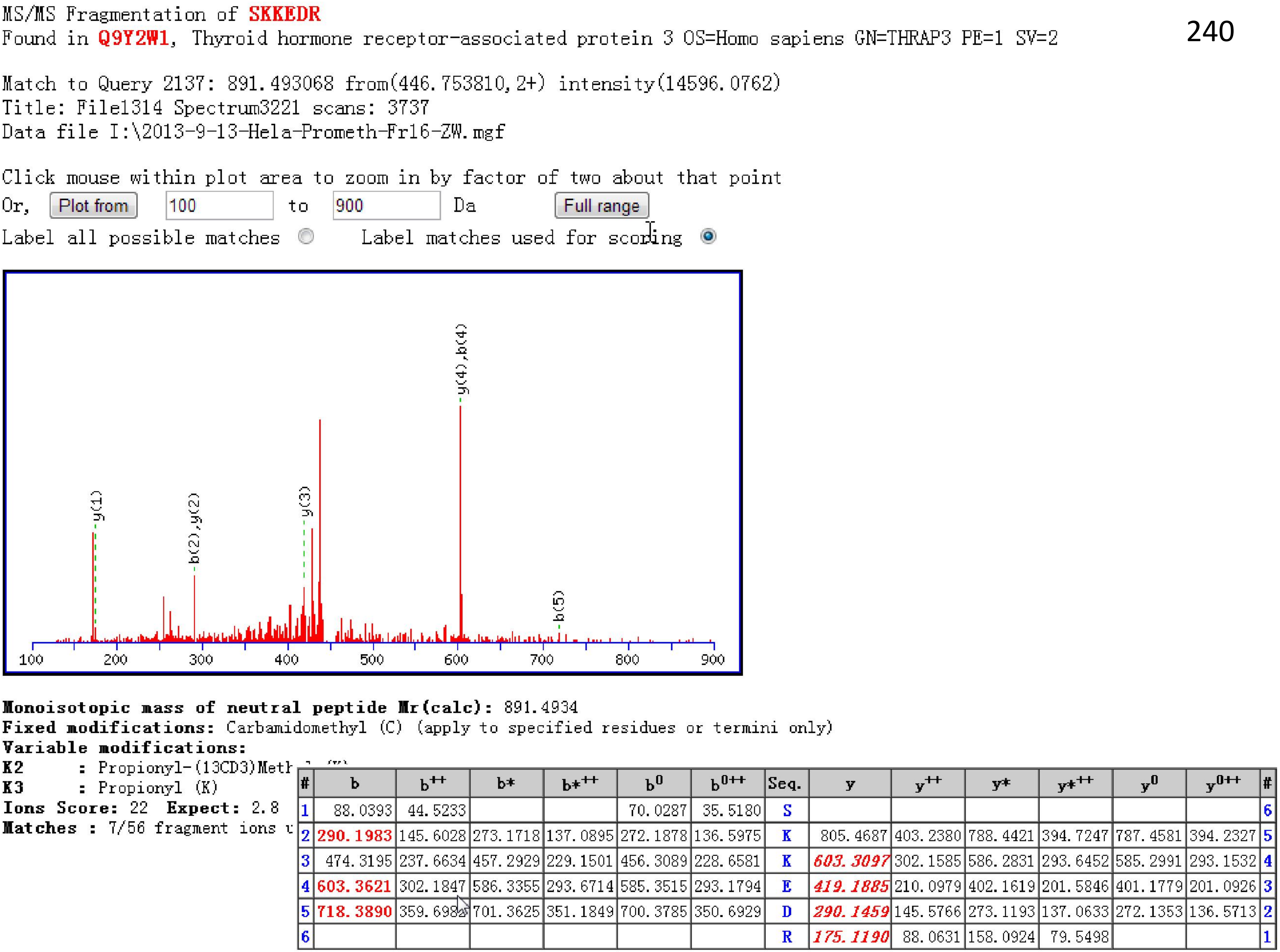
MS/MS Fragmentation of **KKQKMGGFHWMQR**
Found in **Q5H9L2**, Transcription elongation factor A protein-like 5 OS=Homo sapiens GN=TCEAL5 PE=1 SV=1

Match to Query 12072: 1842.939462 from(615.320430,3+) intensity(31119.9961)
Title: File1314 Spectrum13026 scans: 14285
Data file I:\2013-9-13-Hela-Prometh-Fr16-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1842.9385
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K1 : Propionyl (K)
K2 : Propionyl (K)
K4 : Propionyl-Methylation (K)
Ions Score: 27 **Expect:** 2.1
Matches : 19/96 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	185.1285	93.0679	168.1019	84.5546	K					13
2	***369.2496***	185.1285	352.2231	176.6152	K	1659.8247	830.4160	1642.7981	821.9027	12
3	497.3082	249.1577	480.2817	240.6445	Q	1475.7035	738.3554	1458.6769	729.8421	11
4	695.4450	348.2262	678.4185	339.7129	K	***1347.6449***	674.3261	1330.6183	665.8128	10
5	826.4855	413.7464	809.4590	405.2331	M	***1149.5081***	575.2577	1132.4815	566.7444	9
6	883.5070	442.2571	866.4804	433.7439	G	***1018.4676***	509.7374	1001.4410	501.2242	8
7	940.5285	470.7679	923.5019	462.2546	G	961.4461	481.2267	944.4196	472.7134	7
8	***1087.5969***	544.3021	1070.5703	535.7888	F	***904.4247***	452.7160	887.3981	444.2027	6
9	***1224.6558***	612.8315	1207.6292	604.3183	H	757.3562	379.1818	740.3297	370.6685	5
10	1410.7351	705.8712	1393.7085	697.3579	W	620.2973	310.6523	603.2708	302.1390	4
11	1541.7756	771.3914	1524.7490	762.8782	M	***434.2180***	217.6126	417.1915	209.0994	3
12	1669.8342	835.4207	1652.8076	826.9074	Q	***303.1775***	152.0924	286.1510	143.5791	2
13					R	***175.1190***	88.0631	158.0924	79.5498	1



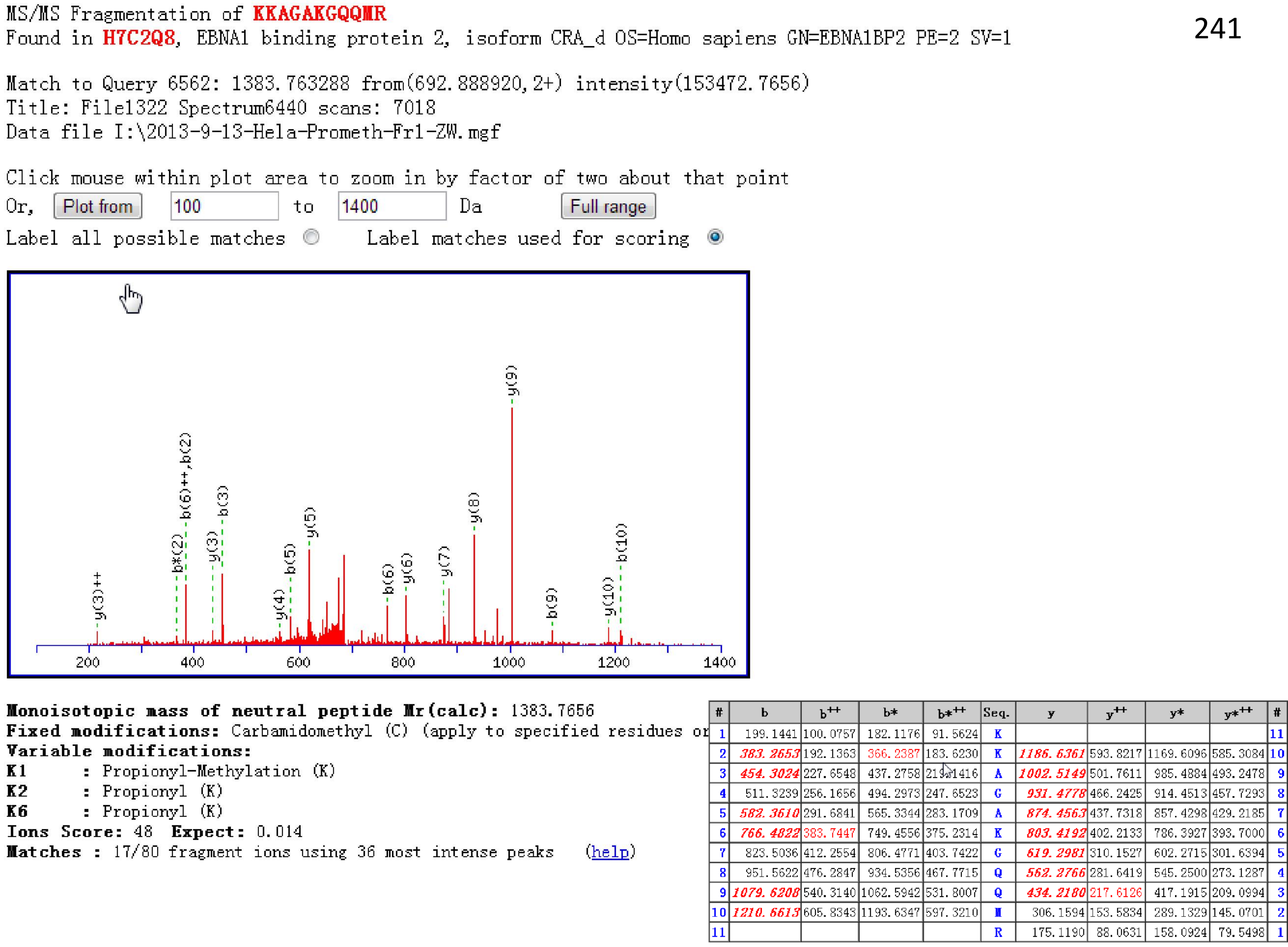
MS/MS Fragmentation of **SKKEDR**
Found in **Q9Y2W1**, Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2

Match to Query 2137: 891.493068 from(446.753810,2+) intensity(14596.0762)
Title: File1314 Spectrum3221 scans: 3737
Data file I:\2013-9-13-Hela-Prometh-Fr16-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 891.4934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Meth
K3 : Propionyl (K)
Ions Score: 22 **Expect:** 2.8
Matches : 7/56 fragment ions u

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							6
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	K	805.4687	403.2380	788.4421	394.7247	787.4581	394.2327	5
3	474.3195	237.6634	457.2929	229.1501	456.3089	228.6581	K	***603.3097***	302.1585	586.2831	293.6452	585.2991	293.1532	4
4	**603.3621**	302.1847	586.3355	293.6714	585.3515	293.1794	E	***419.1885***	210.0979	402.1619	201.5846	401.1779	201.0926	3
5	**718.3890**	359.6982	701.3625	351.1849	700.3785	350.6929	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KKAGAKGQQMR**
Found in **H7C2Q8**, EBNA1 binding protein 2, isoform CRA_d OS=Homo sapiens GN=EBNA1BP2 PE=2 SV=1

Match to Query 6562: 1383.763288 from(692.888920,2+) intensity(153472.7656)
Title: File1322 Spectrum6440 scans: 7018
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.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 ●

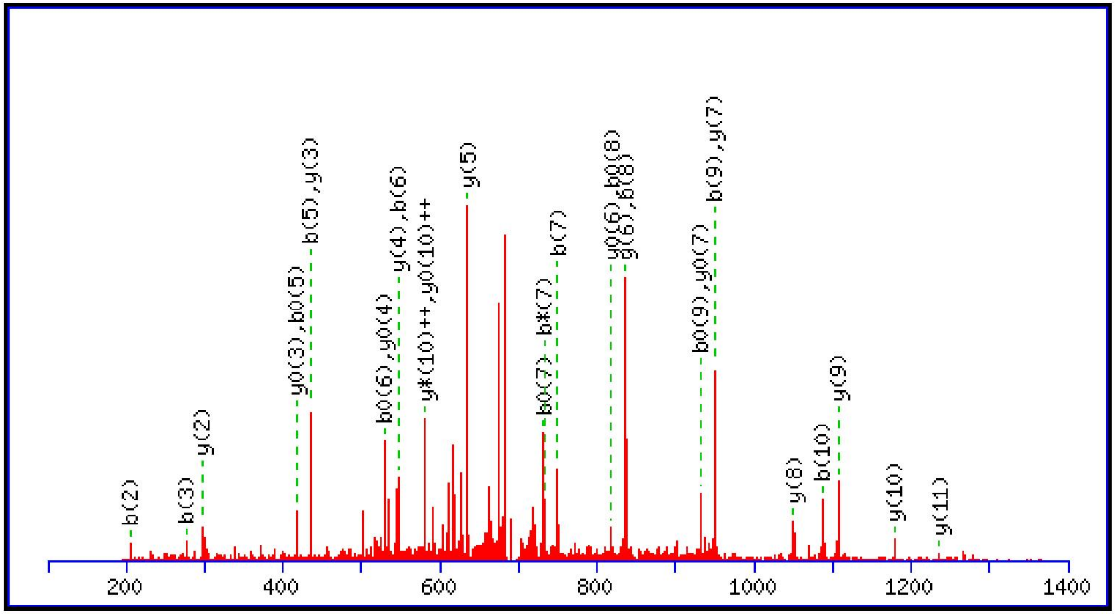
Monoisotopic mass of neutral peptide Mr(calc): 1383.7656
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K1 : Propionyl-Methylation (K)
K2 : Propionyl (K)
K6 : Propionyl (K)
Ions Score: 48 **Expect:** 0.014
Matches : 17/80 fragment ions using 36 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	199.1441	100.0757	182.1176	91.5624	K					11
2	**383.2653**	192.1363	366.2387	183.6230	K	**1186.6361**	593.8217	1169.6096	585.3084	10
3	**454.3024**	227.6548	437.2758	219.1416	A	**1002.5149**	501.7611	985.4884	493.2478	9
4	511.3239	256.1656	494.2973	247.6523	G	**931.4778**	466.2425	914.4513	457.7293	8
5	**582.3610**	291.6841	565.3344	283.1709	A	**874.4563**	437.7318	857.4298	429.2185	7
6	**766.4822**	383.7447	749.4556	375.2314	K	**803.4192**	402.2133	786.3927	393.7000	6
7	823.5036	412.2554	806.4771	403.7422	G	**619.2981**	310.1527	602.2715	301.6394	5
8	951.5622	476.2847	934.5356	467.7715	Q	**562.2766**	281.6419	545.2500	273.1287	4
9	**1079.6208**	540.3140	1062.5942	531.8007	Q	**434.2180**	217.6126	417.1915	209.0994	3
10	**1210.6613**	605.8343	1193.6347	597.3210	M	306.1594	153.5834	289.1329	145.0701	2
11					R	175.1190	88.0631	158.0924	79.5498	1

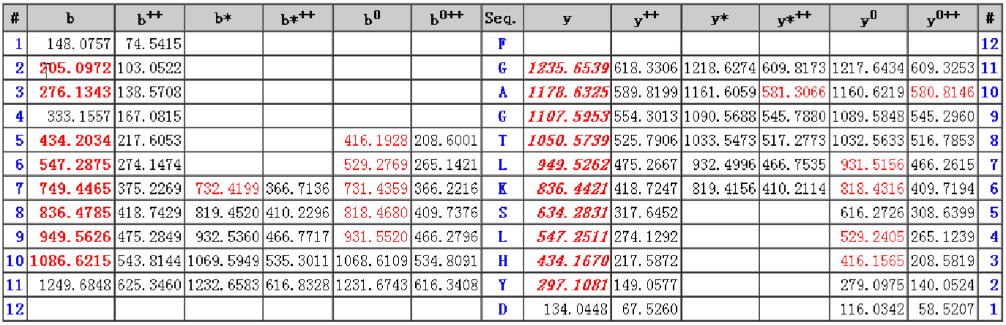
MS/MS Fragmentation of **FGAGTLKSLHYD**
Found in **Q5HYI8**, Rab-like protein 3 OS=Homo sapiens GN=RABL3 PE=1 SV=1

Match to Query 4724: 1381.714088 from(691.864320,2+) intensity(154506.0469)
Title: File1296 Spectrum10302 scans: 11892
Data file I:\2013-9-12-Hela-Prometh-Fr14-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1381.7151
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 80 **Expect:** 5.8e-006
Matches : 30/102 fragment ions using 36 most intense peaks (he

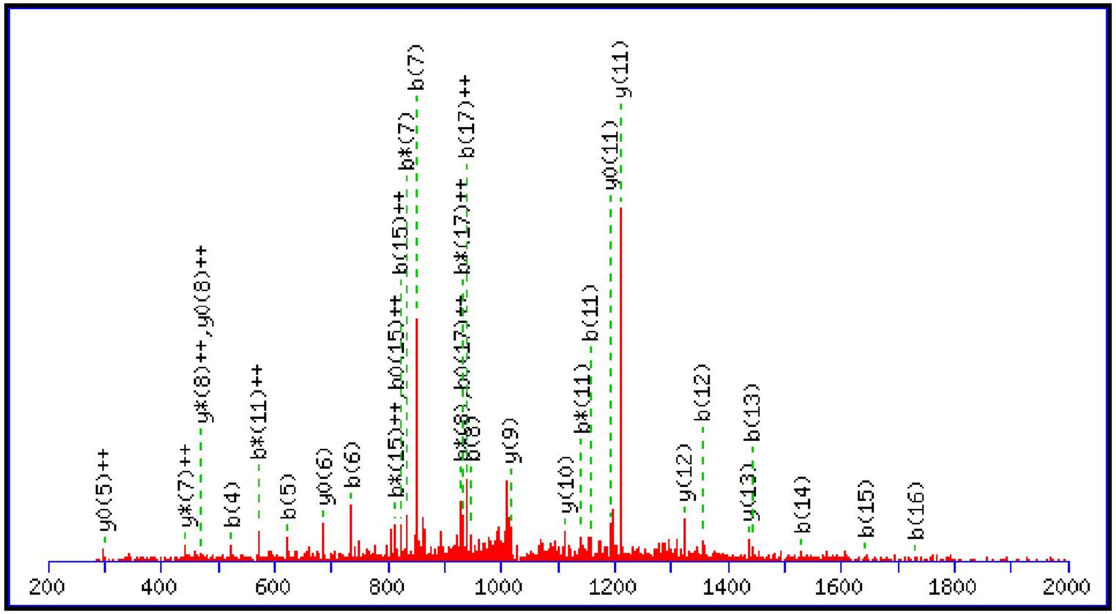


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							12
2	205.0972	103.0522					G	1235.6539	618.3306	1218.6274	609.8173	1217.6434	609.3253	11
3	276.1343	138.5708					A	1178.6325	589.8199	1161.6059	581.3066	1160.6219	580.8146	10
4	333.1557	167.0815					G	1107.5953	554.3013	1090.5688	545.7880	1089.5848	545.2960	9
5	434.2034	217.6053			416.1928	208.6001	T	1050.5739	525.7906	1033.5473	517.2773	1032.5633	516.7853	8
6	547.2875	274.1474			529.2769	265.1421	L	949.5262	475.2667	932.4996	466.7535	931.5156	466.2615	7
7	749.4465	375.2269	732.4199	366.7136	731.4359	366.2216	K	836.4421	418.7247	819.4156	410.2114	818.4316	409.7194	6
8	836.4785	418.7429	819.4520	410.2296	818.4680	409.7376	S	634.2831	317.6452			616.2726	308.6399	5
9	949.5626	475.2849	932.5360	466.7717	931.5520	466.2796	L	547.2511	274.1292			529.2405	265.1239	4
10	1086.6215	543.8144	1069.5949	535.3011	1068.6109	534.8091	H	434.1670	217.5872			416.1565	208.5819	3
11	1249.6848	625.3460	1232.6583	616.8328	1231.6743	616.3408	Y	297.1081	149.0577			279.0975	140.0524	2
12							D	134.0448	67.5260			116.0342	58.5207	1

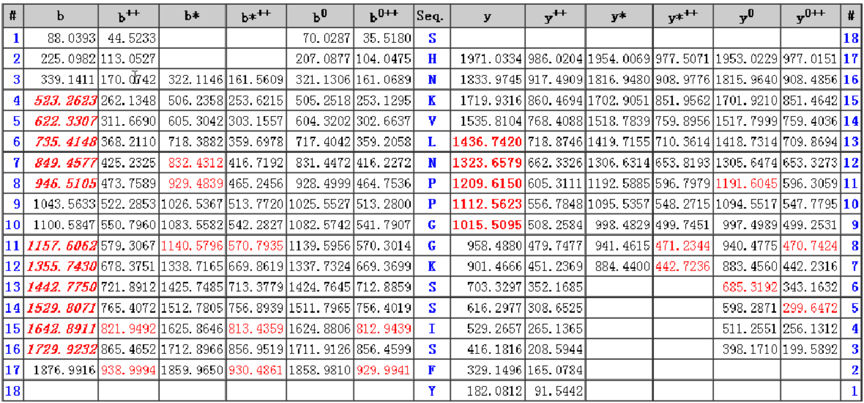
MS/MS Fragmentation of **SHNKVLNPPGGKSSISFY**
Found in **B4DLH4**, Hematological and neurological-expressed 1-like protein OS=Homo sapiens GN=HN1L PE=2 SV=1

Match to Query 11319: 2057.057708 from(1029.536130,2+) intensity(86979.5938)
Title: File1296 Spectrum11710 scans: 13359
Data file I:\2013-9-12-Hela-Prometh-Fr14-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2057.0582
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl (K)
K12 : Propionyl-Methylation (K)
Ions Score: 29 **Expect:** 1.4
Matches : 32/184 fragment ions using 103 most intense peaks (help)

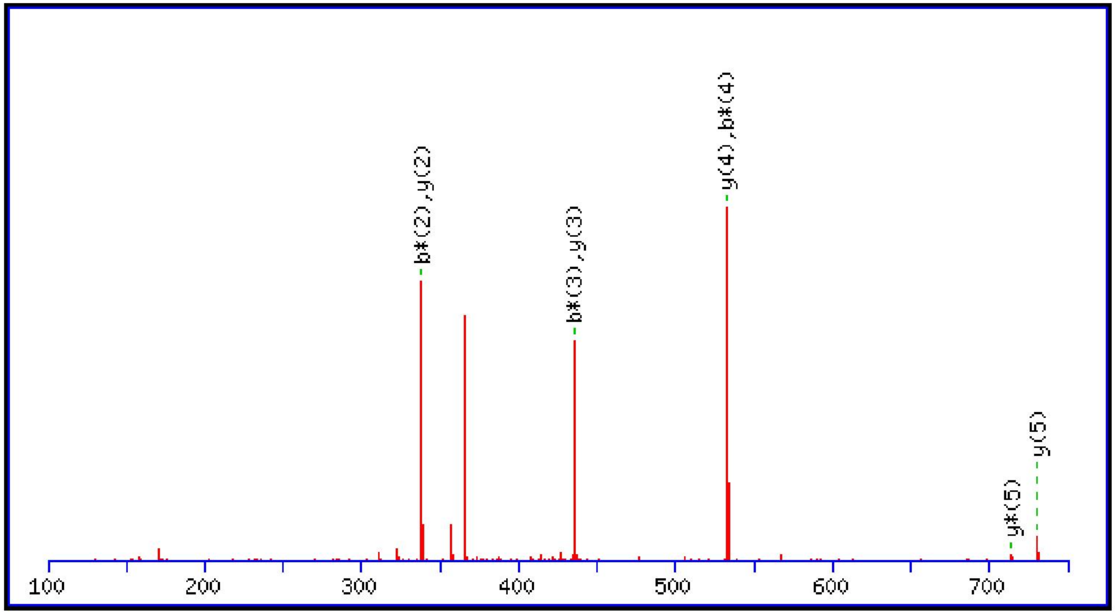


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							18
2	225.0982	113.0527			207.0877	104.0475	H	1971.0334	986.0204	1954.0069	977.5071	1953.0229	977.0151	17
3	339.1411	170.0742	322.1146	161.5609	321.1306	161.0689	N	1833.9745	917.4909	1816.9480	908.9776	1815.9640	908.4856	16
4	523.2623	262.1348	506.2358	253.6215	505.2518	253.1295	K	1719.9316	860.4694	1702.9051	851.9562	1701.9210	851.4642	15
5	622.3307	311.6690	605.3042	303.1557	604.3202	302.6637	V	1535.8104	768.4088	1518.7839	759.8956	1517.7999	759.4036	14
6	735.4148	368.2110	718.3882	359.6978	717.4042	359.2058	L	1436.7420	718.8746	1419.7155	710.3614	1418.7314	709.8694	13
7	849.4577	425.2325	832.4312	416.7192	831.4472	416.2272	N	1323.6579	662.3326	1306.6314	653.8193	1305.6474	653.3273	12
8	946.5105	473.7589	929.4839	465.2456	928.4999	464.7536	P	1209.6150	605.3111	1192.5885	596.7979	1191.6045	596.3059	11
9	1043.5633	522.2853	1026.5367	513.7720	1025.5527	513.2800	P	1112.5623	556.7848	1095.5357	548.2715	1094.5517	547.7795	10
10	1100.5847	550.7960	1083.5582	542.2827	1082.5742	541.7907	G	1015.5095	508.2584	998.4829	499.7451	997.4989	499.2531	9
11	1157.6062	579.3067	1140.5796	570.7935	1139.5956	570.3014	G	958.4880	479.7477	941.4615	471.2344	940.4775	470.7424	8
12	1355.7430	678.3751	1338.7165	669.8619	1337.7324	669.3699	K	901.4666	451.2369	884.4400	442.7236	883.4560	442.2316	7
13	1442.7750	721.8912	1425.7485	713.3779	1424.7645	712.8859	S	703.3297	352.1685			685.3192	343.1632	6
14	1529.8071	765.4072	1512.7805	756.8939	1511.7965	756.4019	S	616.2977	308.6525			598.2871	299.6472	5
15	1642.8911	821.9492	1625.8646	813.4359	1624.8806	812.9439	I	529.2657	265.1365			511.2551	256.1312	4
16	1729.9232	865.4652	1712.8966	856.9519	1711.9126	856.4599	S	416.1816	208.5944			398.1710	199.5892	3
17	1876.9916	938.9994	1859.9650	930.4861	1858.9810	929.9941	F	329.1496	165.0784					2
18							Y	182.0812	91.5442					1

MS/MS Fragmentation of **RKPPYR**
Found in **J3KRC3**, Centrosomal protein of 95 kDa (Fragment) OS=Homo sapiens GN=CEP95 PE=4 SV=1

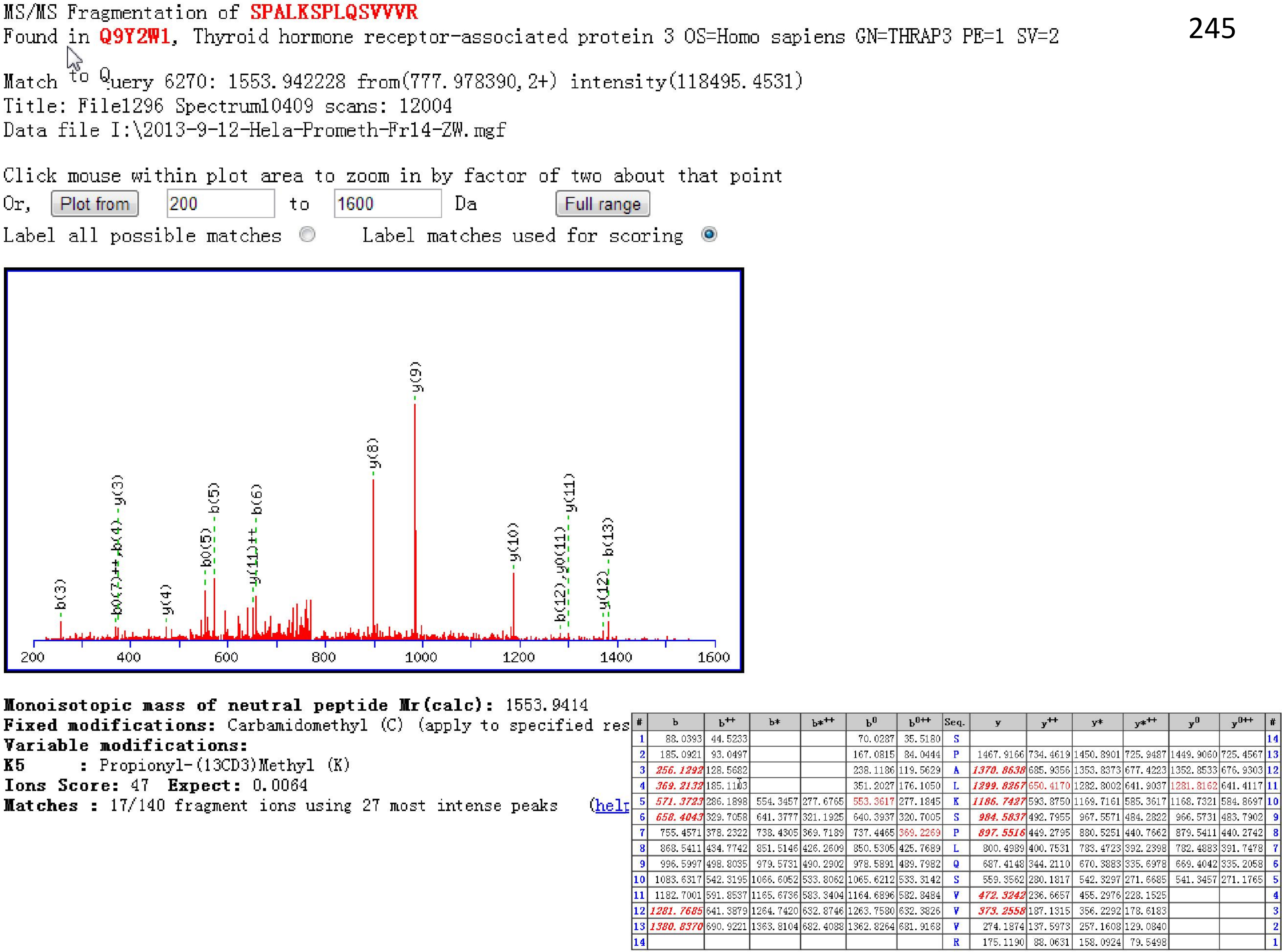
Match to Query 965: 886.527628 from(444.271090,2+) intensity(2175662.0000)
Title: File1296 Spectrum11768 scans: 13420
Data file I:\2013-9-12-Hela-Prometh-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 885.5184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
Ions Score: 33 **Expect:** 0.3
Matches : 8/40 fragment ions using 7 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	157.1084	79.0578	140.0818	70.5446	R					6
2	355.2452	178.1262	338.2187	169.6130	K	***730.4246***	365.7160	713.3981	357.2027	5
3	452.2980	226.6526	435.2714	218.1394	P	***532.2878***	266.6475	515.2613	258.1343	4
4	549.3507	275.1790	532.3242	266.6657	P	***435.2350***	218.1212	418.2085	209.6079	3
5	712.4141	356.7107	695.3875	348.1974	Y	***338.1823***	169.5948	321.1557	161.0815	2
6					R	175.1190	88.0631	158.0924	79.5498	1



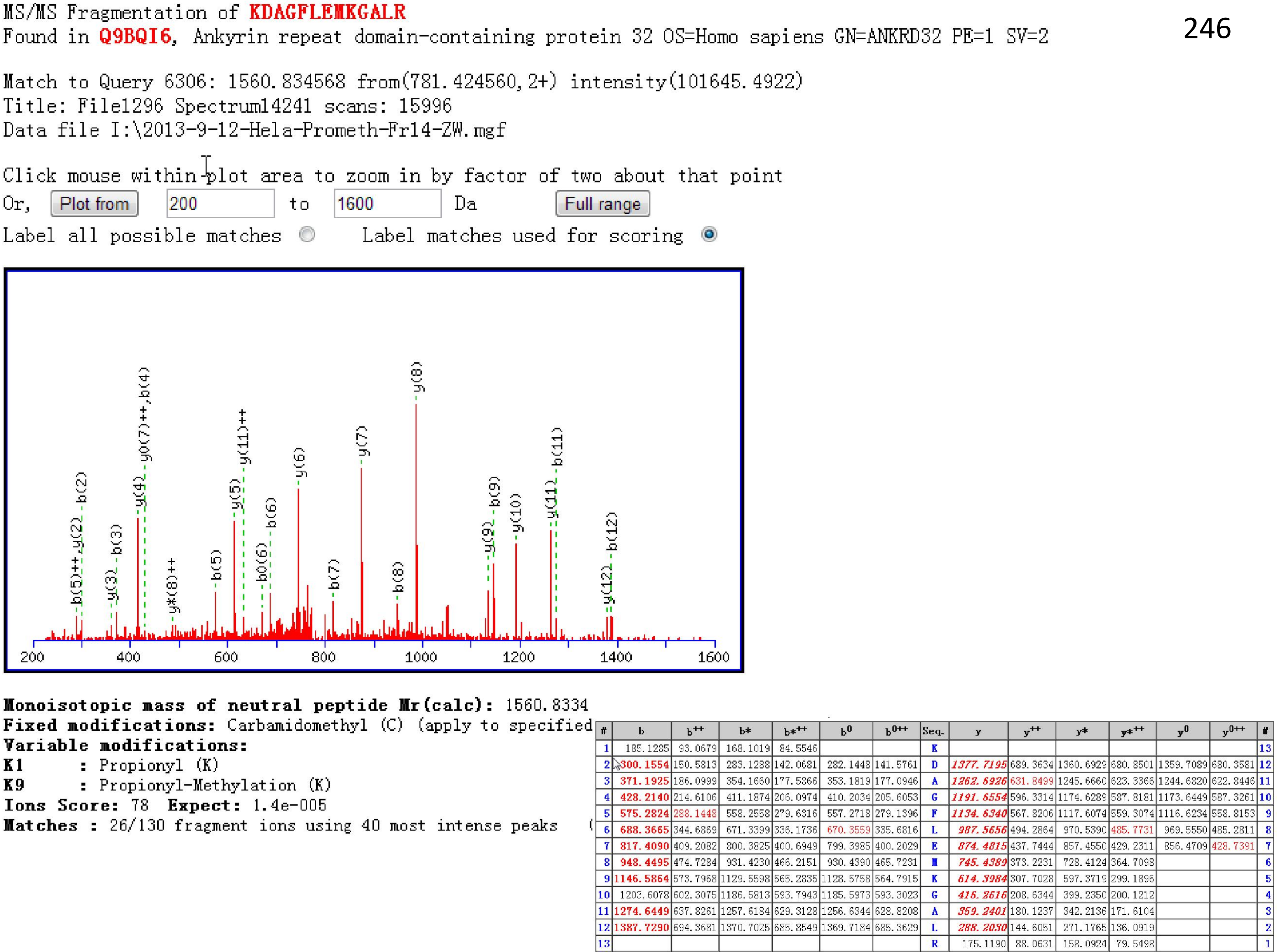
MS/MS Fragmentation of **SPALKSPLQSVVVR**
Found in **Q9Y2W1**, Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2

Match to Query 6270: 1553.942228 from(777.978390,2+) intensity(118495.4531)
Title: File1296 Spectrum10409 scans: 12004
Data file I:\2013-9-12-Hela-Prometh-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1553.9414
Fixed modifications: Carbamidomethyl (C) (apply to specified res
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 47 **Expect:** 0.0064
Matches : 17/140 fragment ions using 27 most intense peaks (hel

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	185.0921	93.0497			167.0815	84.0444	P	1467.9166	734.4619	1450.8901	725.9487	1449.9060	725.4567	13
3	***256.1292***	128.5682			238.1186	119.5629	A	***1370.8638***	685.9356	1353.8373	677.4223	1352.8533	676.9303	12
4	***369.2132***	185.1103			351.2027	176.1050	L	***1299.8267***	650.4170	1282.8002	641.9037	1281.8162	641.4117	11
5	***571.3723***	286.1898	554.3457	277.6765	553.3617	277.1845	K	***1186.7427***	593.8750	1169.7161	585.3617	1168.7321	584.8697	10
6	***658.4043***	329.7058	641.3777	321.1925	640.3937	320.7005	S	***984.5837***	492.7955	967.5571	484.2822	966.5731	483.7902	9
7	755.4571	378.2322	738.4305	369.7189	737.4465	369.2269	P	***897.5516***	449.2795	880.5251	440.7662	879.5411	440.2742	8
8	868.5411	434.7742	851.5146	426.2609	850.5305	425.7689	L	800.4989	400.7531	783.4723	392.2398	782.4883	391.7478	7
9	996.5997	498.8035	979.5731	490.2902	978.5891	489.7982	Q	687.4148	344.2110	670.3883	335.6978	669.4042	335.2058	6
10	1083.6317	542.3195	1066.6052	533.8062	1065.6212	533.3142	S	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
11	1182.7001	591.8537	1165.6736	583.3404	1164.6896	582.8484	V	***472.3242***	236.6657	455.2976	228.1525			4
12	***1281.7685***	641.3879	1264.7420	632.8746	1263.7580	632.3826	V	***373.2558***	187.1315	356.2292	178.6183			3
13	***1380.8370***	690.9221	1363.8104	682.4088	1362.8264	681.9168	V	274.1874	137.5973	257.1608	129.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KDAGFLEMKGALR**
Found in **Q9BQI6**, Ankyrin repeat domain-containing protein 32 OS=Homo sapiens GN=ANKRD32 PE=1 SV=2

Match to Query 6306: 1560.834568 from(781.424560,2+) intensity(101645.4922)
Title: File1296 Spectrum14241 scans: 15996
Data file I:\2013-9-12-Hela-Prometh-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

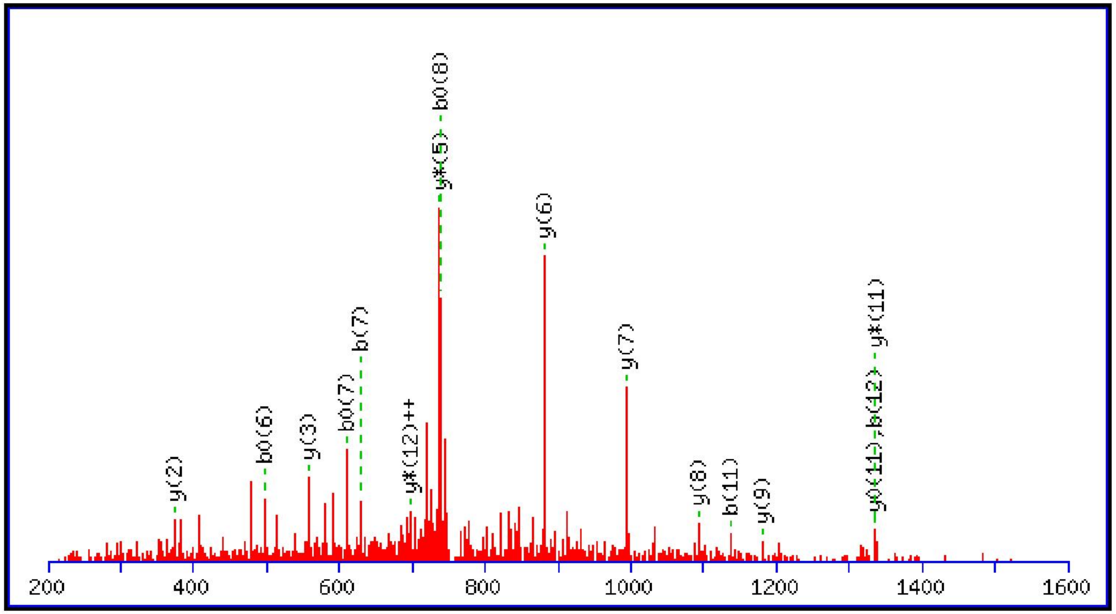
Monoisotopic mass of neutral peptide Mr(calc): 1560.8334
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K1 : Propionyl (K)
K9 : Propionyl-Methylation (K)
Ions Score: 78 **Expect:** 1.4e-005
Matches : 26/130 fragment ions using 40 most intense peaks (

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							13
2	**300.1554**	150.5813	283.1288	142.0681	282.1448	141.5761	D	***1377.7195***	689.3634	1360.6929	680.8501	1359.7089	680.3581	12
3	**371.1925**	186.0999	354.1660	177.5866	353.1819	177.0946	A	***1262.6926***	631.8499	1245.6660	623.3366	1244.6820	622.8446	11
4	**428.2140**	214.6106	411.1874	206.0974	410.2034	205.6053	G	***1191.6554***	596.3314	1174.6289	587.8181	1173.6449	587.3261	10
5	**575.2824**	288.1448	558.2558	279.6316	557.2718	279.1396	F	***1134.6340***	567.8206	1117.6074	559.3074	1116.6234	558.8153	9
6	**688.3665**	344.6869	671.3399	336.1736	670.3559	335.6816	L	***987.5656***	494.2864	970.5390	485.7731	969.5550	485.2811	8
7	**817.4090**	409.2082	800.3825	400.6949	799.3985	400.2029	E	***874.4815***	437.7444	857.4550	429.2311	856.4709	428.7391	7
8	**948.4495**	474.7284	931.4230	466.2151	930.4390	465.7231	M	***745.4389***	373.2231	728.4124	364.7098			6
9	**1146.5864**	573.7968	1129.5598	565.2835	1128.5758	564.7915	K	***614.3984***	307.7028	597.3719	299.1896			5
10	1203.6078	602.3075	1186.5813	593.7943	1185.5973	593.3023	G	***416.2616***	208.6344	399.2350	200.1212			4
11	**1274.6449**	637.8261	1257.6184	629.3128	1256.6344	628.8208	A	***359.2401***	180.1237	342.2136	171.6104			3
12	**1387.7290**	694.3681	1370.7025	685.8549	1369.7184	685.3629	L	***288.2030***	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VGTASVLQPVKKR**
Found in **Q2TAL8**, Glutamine-rich protein 1 OS=Homo sapiens GN=QRICH1 PE=1 SV=1

Match to Query 8301: 1507.909268 from(754.961910,2+) intensity(45624.3164)
Title File1264 Spectrum9247 scans: 10947
Data file I:\2013-9-5-Hela-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



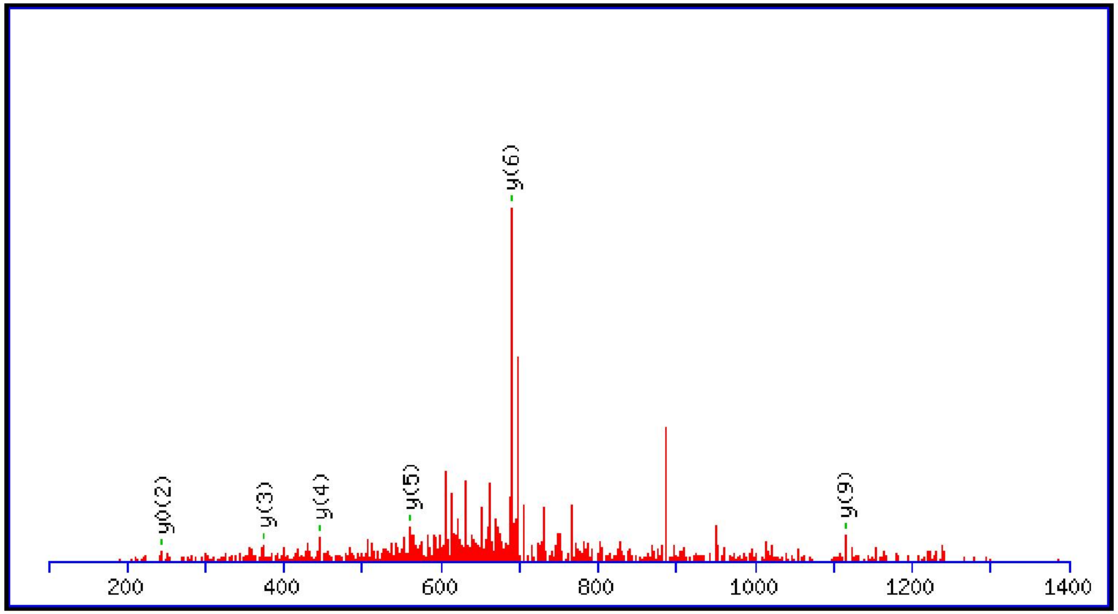
Monoisotopic mass of neutral peptide Mr(calc): 1507.9086
Fixed modifications: Carbamidomethyl (C) (apply to specified res
Variable modifications:
K11 : Propionyl (K)
K12 : Propionyl-Methylation (K)
Ions Score: 31 **Expect:** 0.3
Matches : 16/110 fragment ions using 26 most intense peaks (hel

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							13
2	157.0972	79.0522					G	1409.8475	705.4274	1392.8209	696.9141	1391.8369	696.4221	12
3	258.1448	129.5761			240.1343	120.5708	T	1352.8260	676.9166	1335.7995	668.4034	1334.8154	667.9114	11
4	329.1819	165.0946			311.1714	156.0893	A	1251.7783	626.3928	1234.7518	617.8795	1233.7678	617.3875	10
5	416.2140	208.6106			398.2034	199.6053	S	***1180.7412***	590.8742	1163.7147	582.3610	1162.7307	581.8690	9
6	515.2824	258.1448			497.2718	249.1395	V	***1093.7092***	547.3582	1076.6826	538.8450			8
7	**628.3665**	314.6869			610.3559	305.6816	L	***994.6408***	497.8240	977.6142	489.3108			7
8	756.4250	378.7162	739.3985	370.2029	738.4145	369.7109	Q	***881.5567***	441.2820	864.5302	432.7687			6
9	853.4778	427.2425	836.4512	418.7293	835.4672	418.2373	P	753.4981	377.2527	736.4716	368.7394			5
10	952.5462	476.7767	935.5197	468.2635	934.5356	467.7715	V	656.4454	328.7263	639.4188	320.2130			4
11	**1136.6674**	568.8373	1119.6408	560.3241	1118.6568	559.8320	K	***557.3770***	279.1921	540.3504	270.6788			3
12	**1334.8042**	667.9057	1317.7777	659.3925	1316.7936	658.9005	K	***373.2558***	187.1315	356.2292	178.6183			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KLKLNENAISR**
Found in **B3KP96**, Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=2 SV=1

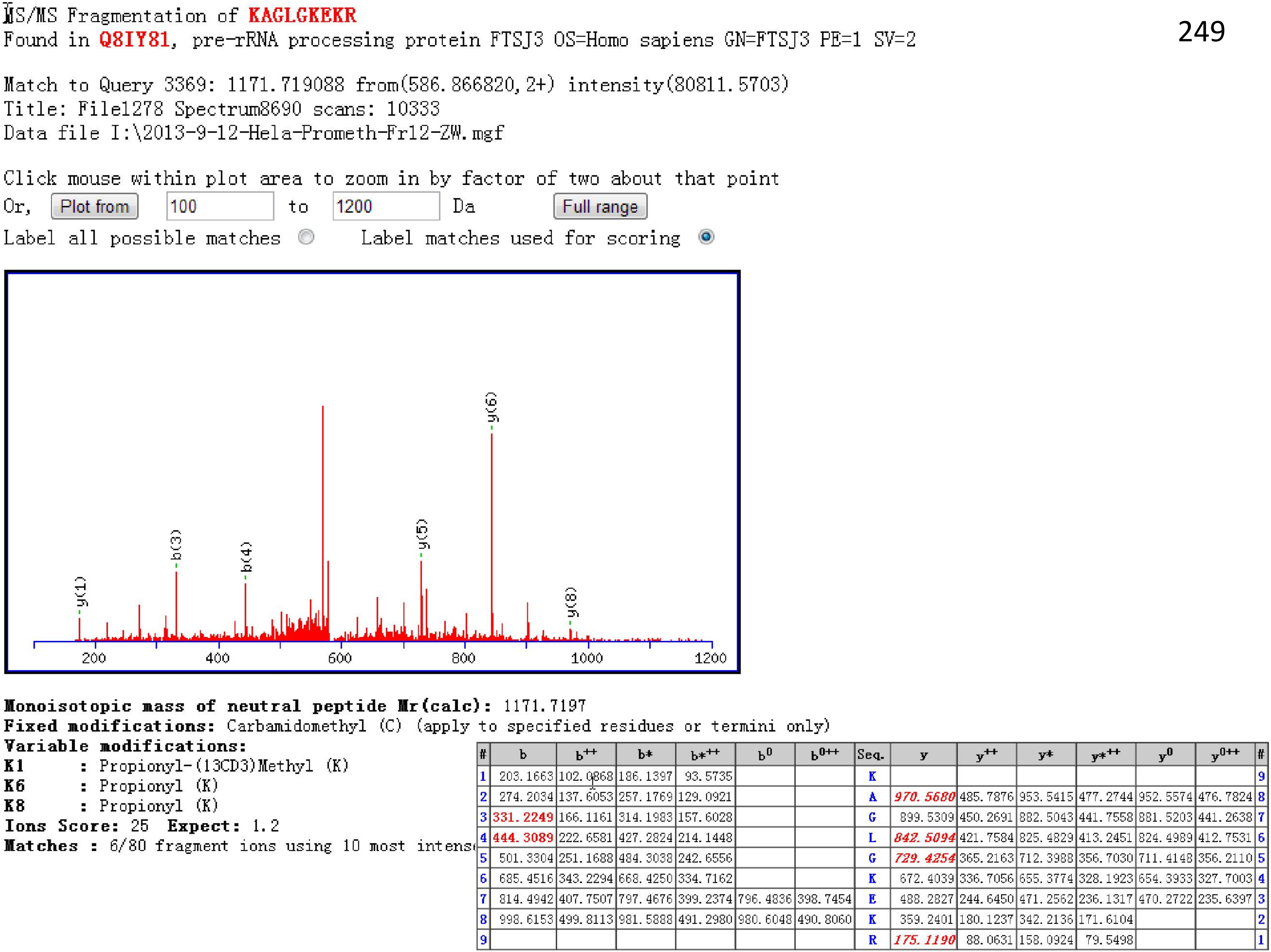
Match to Query 5785: 1411.814188 from(706.914370,2+) intensity(23202.8145)
Title: File1278 Spectrum3656 scans: 5066
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1410.8194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-Methylation (K)
Ions Score: 27 **Expect:** 1.3
Matches : 6/108 fragment ions using 12 most intense peak:

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							11
2	298.2125	149.6099	281.1860	141.0966			L	1227.7056	614.3564	1210.6790	605.8431	1209.6950	605.3511	10
3	496.3493	248.6783	479.3228	240.1650			K	***1114.6215***	557.8144	1097.5949	549.3011	1096.6109	548.8091	9
4	609.4334	305.2203	592.4069	296.7071			L	916.4847	458.7460	899.4581	450.2327	898.4741	449.7407	8
5	723.4763	362.2418	706.4498	353.7285			N	803.4006	402.2039	786.3741	393.6907	785.3900	393.1987	7
6	852.5189	426.7631	835.4924	418.2498	834.5084	417.7578	E	***689.3577***	345.1825	672.3311	336.6692	671.3471	336.1772	6
7	966.5619	483.7846	949.5353	475.2713	948.5513	474.7793	N	***560.3151***	280.6612	543.2885	272.1479	542.3045	271.6559	5
8	1037.5990	519.3031	1020.5724	510.7898	1019.5884	510.2978	A	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
9	1150.6830	575.8452	1133.6565	567.3319	1132.6725	566.8399	I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1237.7151	619.3612	1220.6885	610.8479	1219.7045	610.3559	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498			1



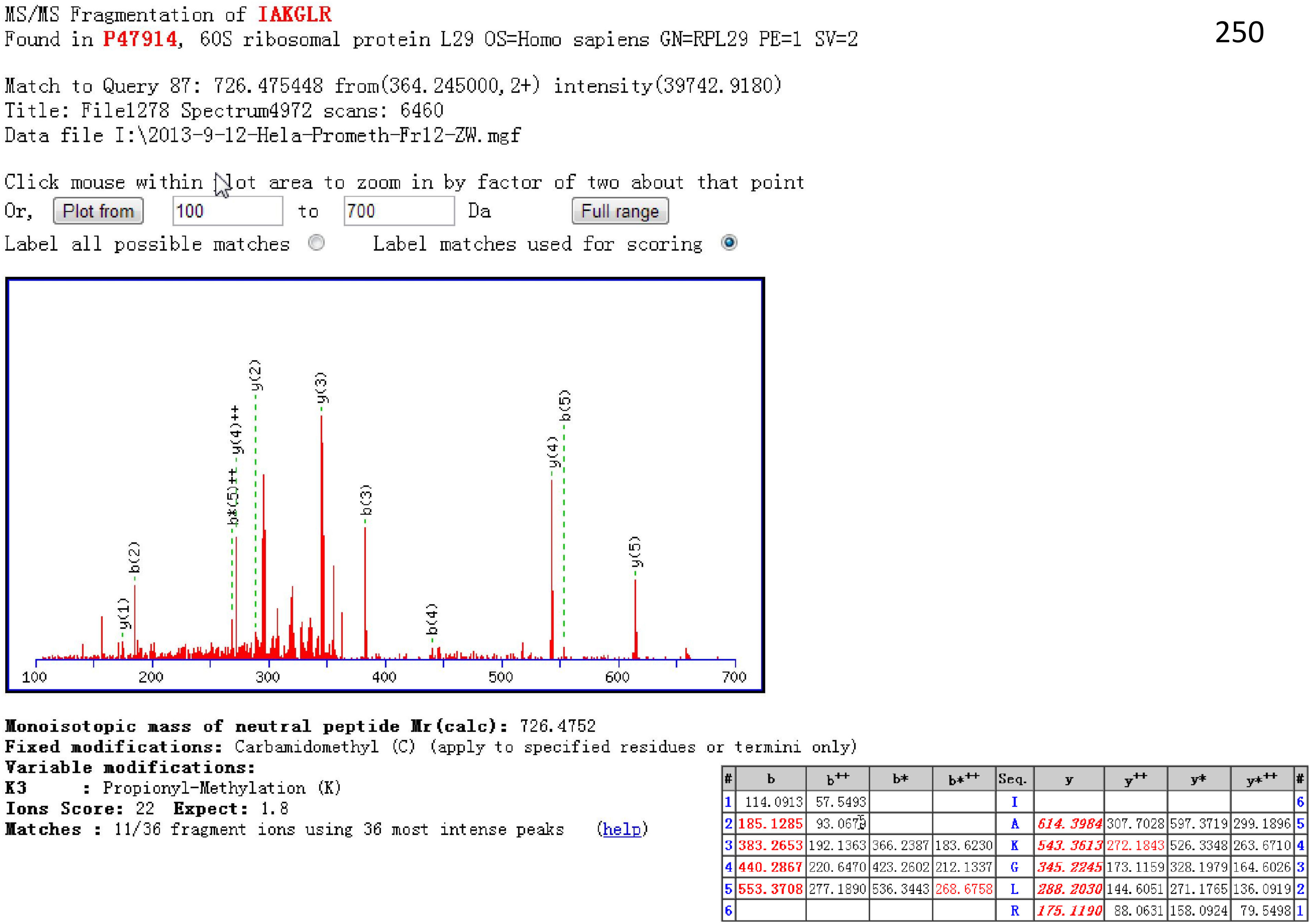
MS/MS Fragmentation of **KAGLGKEKR**
Found in **Q8IY81**, pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2

Match to Query 3369: 1171.719088 from(586.866820,2+) intensity(80811.5703)
Title: File1278 Spectrum8690 scans: 10333
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1171.7197
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
K8 : Propionyl (K)
Ions Score: 25 **Expect:** 1.2
Matches : 6/80 fragment ions using 10 most intens

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	274.2034	137.6053	257.1769	129.0921			A	***970.5680***	485.7876	953.5415	477.2744	952.5574	476.7824	8
3	**331.2249**	166.1161	314.1983	157.6028			G	899.5309	450.2691	882.5043	441.7558	881.5203	441.2638	7
4	**444.3089**	222.6581	427.2824	214.1448			L	***842.5094***	421.7584	825.4829	413.2451	824.4989	412.7531	6
5	501.3304	251.1688	484.3038	242.6556			G	***729.4254***	365.2163	712.3988	356.7030	711.4148	356.2110	5
6	685.4516	343.2294	668.4250	334.7162			K	672.4039	336.7056	655.3774	328.1923	654.3933	327.7003	4
7	814.4942	407.7507	797.4676	399.2374	796.4836	398.7454	E	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	3
8	998.6153	499.8113	981.5888	491.2980	980.6048	490.8060	K	359.2401	180.1237	342.2136	171.6104			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



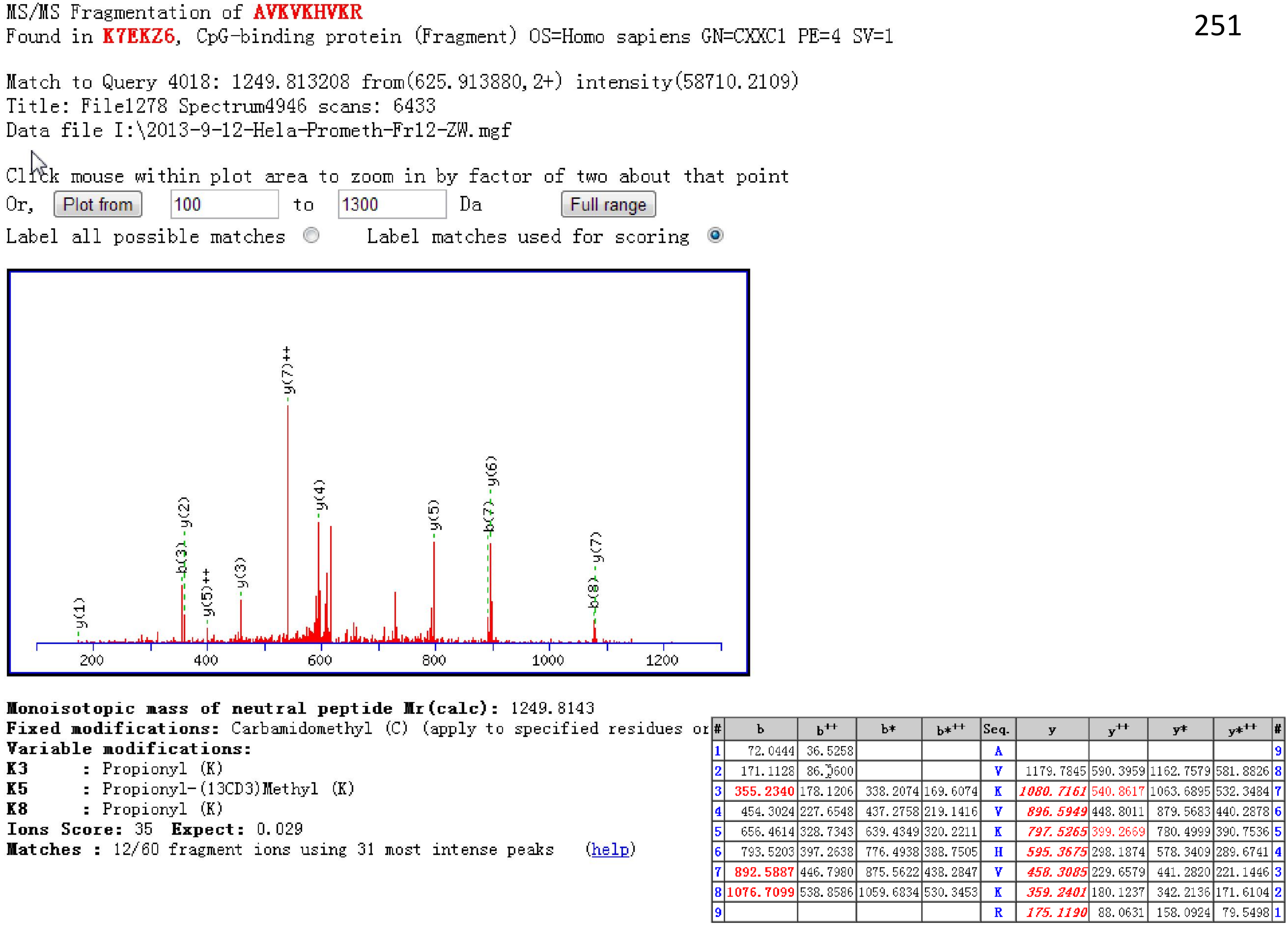
MS/MS Fragmentation of **IAKGLR**
Found in **P47914**, 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2

Match to Query 87: 726.475448 from(364.245000,2+) intensity(39742.9180)
Title: File1278 Spectrum4972 scans: 6460
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 726.4752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-Methylation (K)
Ions Score: 22 **Expect:** 1.8
Matches : 11/36 fragment ions using 36 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			I					6
2	**185.1285**	93.0679			A	***614.3984***	307.7028	597.3719	299.1896	5
3	**383.2653**	192.1363	366.2387	183.6230	K	***543.3613***	272.1843	526.3348	263.6710	4
4	**440.2867**	220.6470	423.2602	212.1337	G	***345.2245***	173.1159	328.1979	164.6026	3
5	**553.3708**	277.1890	536.3443	268.6758	L	***288.2030***	144.6051	271.1765	136.0919	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **AVKVKHVKR**
Found in **K7EKZ6**, CpG-binding protein (Fragment) OS=Homo sapiens GN=CXXC1 PE=4 SV=1

Match to Query 4018: 1249.813208 from(625.913880,2+) intensity(58710.2109)
Title: File1278 Spectrum4946 scans: 6433
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.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 ●

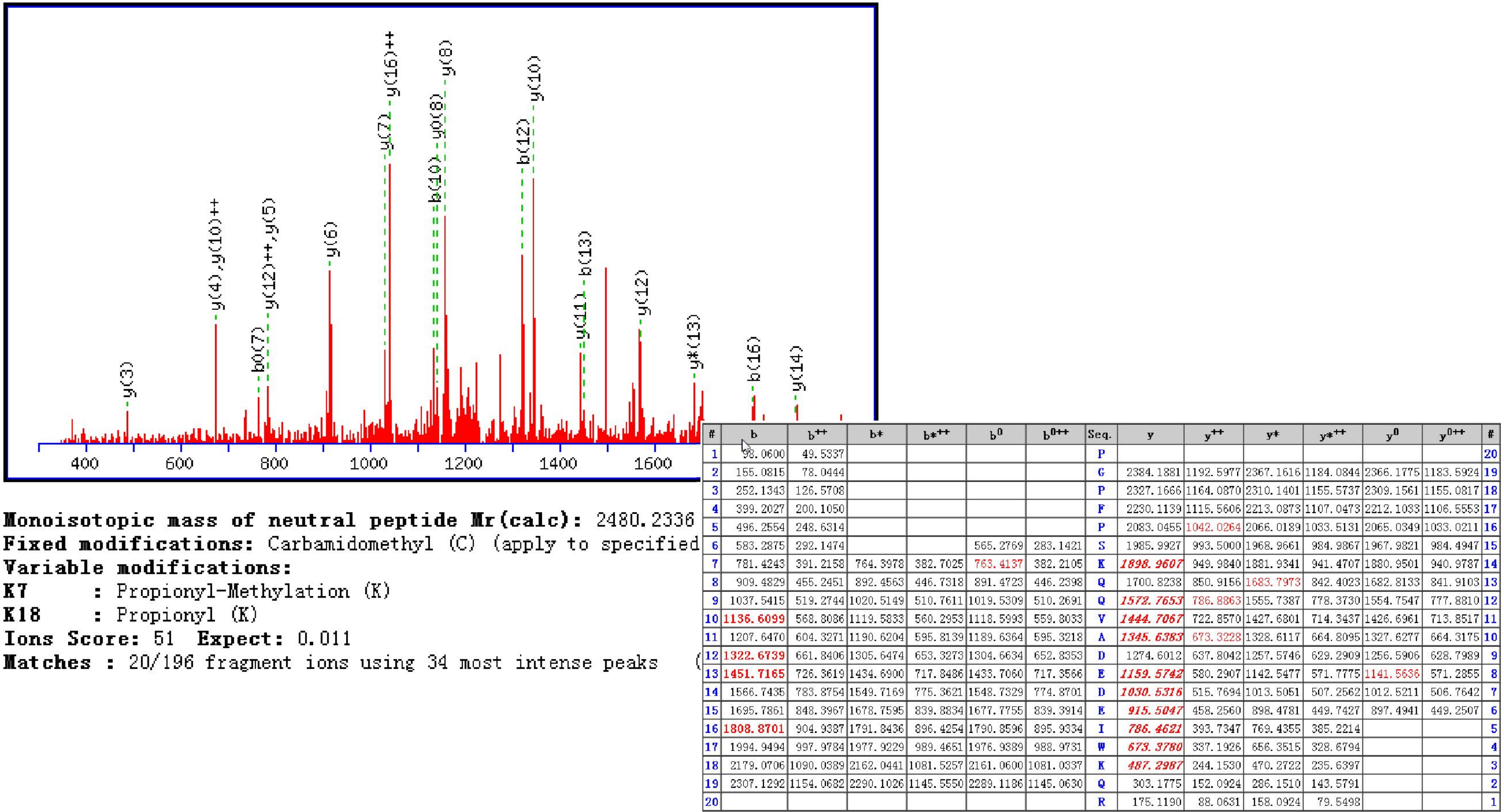
Monoisotopic mass of neutral peptide Mr(calc): 1249.8143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K3 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 35 **Expect:** 0.029
Matches : 12/60 fragment ions using 31 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.0444	36.5258			A					9
2	171.1128	86.0600			V	1179.7845	590.3959	1162.7579	581.8826	8
3	**355.2340**	178.1206	338.2074	169.6074	K	***1080.7161***	540.8617	1063.6895	532.3484	7
4	454.3024	227.6548	437.2758	219.1416	V	***896.5949***	448.8011	879.5683	440.2878	6
5	656.4614	328.7343	639.4349	320.2211	K	***797.5265***	399.2669	780.4999	390.7536	5
6	793.5203	397.2638	776.4938	388.7505	H	***595.3675***	298.1874	578.3409	289.6741	4
7	**892.5887**	446.7980	875.5622	438.2847	V	***458.3085***	229.6579	441.2820	221.1446	3
8	**1076.7099**	538.8586	1059.6834	530.3453	K	***359.2401***	180.1237	342.2136	171.6104	2
9					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **PGPFPSKQQVADEDEIWKQR**
Found in **Q9Y520-6**, Isoform 6 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C

Match to Query 15645: 2480.235448 from(1241.125000,2+) intensity(43261.8477)
Title: File1278 Spectrum16732 scans: 18710
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



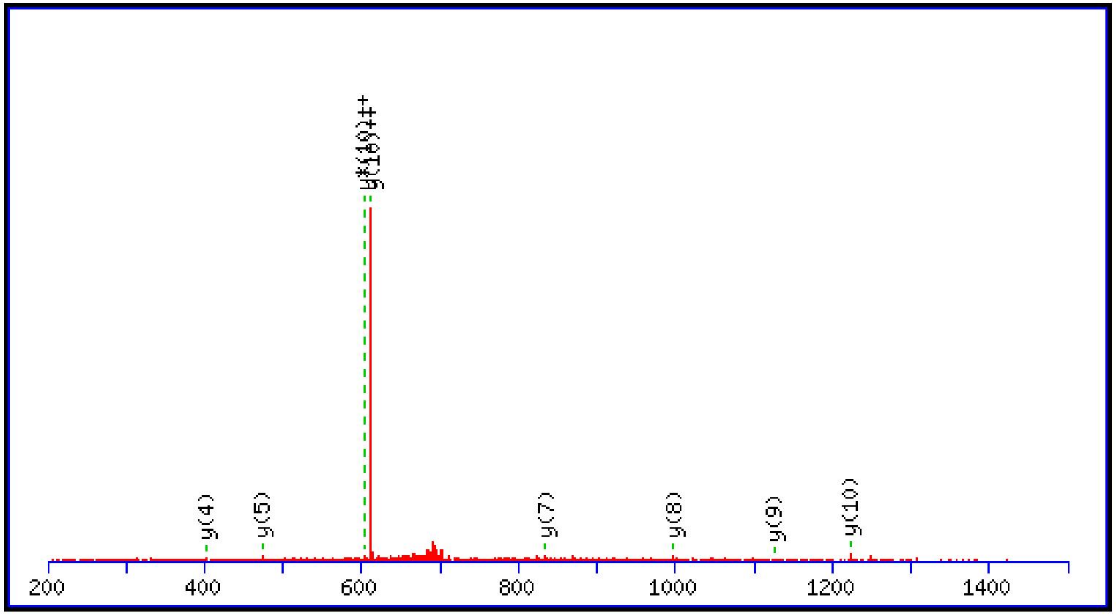
Monoisotopic mass of neutral peptide Mr(calc): 2480.2336
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K7 : Propionyl-Methylation (K)
K18 : Propionyl (K)
Ions Score: 51 **Expect:** 0.011
Matches : 20/196 fragment ions using 34 most intense peaks (

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	98.0600	49.5337					P							20
2	155.0815	78.0444					G	2384.1881	1192.5977	2367.1616	1184.0844	2366.1775	1183.5924	19
3	252.1343	126.5708					P	2327.1666	1164.0870	2310.1401	1155.5737	2309.1561	1155.0817	18
4	399.2027	200.1050					F	2230.1139	1115.5606	2213.0873	1107.0473	2212.1033	1106.5553	17
5	496.2554	248.6314					P	2083.0455	1042.0264	2066.0189	1033.5131	2065.0349	1033.0211	16
6	583.2875	292.1474			565.2769	283.1421	S	1985.9927	993.5000	1968.9661	984.9867	1967.9821	984.4947	15
7	781.4243	391.2158	764.3978	382.7025	763.4137	382.2105	K	***1898.9607***	949.9840	1881.9341	941.4707	1880.9501	940.9787	14
8	909.4829	455.2451	892.4563	446.7318	891.4723	446.2398	Q	1700.8238	850.9156	1683.7973	842.4023	1682.8133	841.9103	13
9	1037.5415	519.2744	1020.5149	510.7611	1019.5309	510.2691	Q	***1572.7653***	786.8863	1555.7387	778.3730	1554.7547	777.8810	12
10	**1136.6099**	568.8086	1119.5833	560.2953	1118.5993	559.8033	V	***1444.7067***	722.8570	1427.6801	714.3437	1426.6961	713.8517	11
11	1207.6470	604.3271	1190.6204	595.8139	1189.6364	595.3218	A	***1345.6383***	673.3228	1328.6117	664.8095	1327.6277	664.3175	10
12	**1322.6739**	661.8406	1305.6474	653.3273	1304.6634	652.8353	D	1274.6012	637.8042	1257.5746	629.2909	1256.5906	628.7989	9
13	**1451.7165**	726.3619	1434.6900	717.8486	1433.7060	717.3566	E	***1159.5742***	580.2907	1142.5477	571.7775	1141.5636	571.2855	8
14	1566.7435	783.8754	1549.7169	775.3621	1548.7329	774.8701	D	***1030.5316***	515.7694	1013.5051	507.2562	1012.5211	506.7642	7
15	1695.7861	848.3967	1678.7595	839.8834	1677.7755	839.3914	E	***915.5047***	458.2560	898.4781	449.7427	897.4941	449.2507	6
16	**1808.8701**	904.9387	1791.8436	896.4254	1790.8596	895.9334	I	***786.4621***	393.7347	769.4355	385.2214			5
17	1994.9494	997.9784	1977.9229	989.4651	1976.9389	988.9731	W	***673.3780***	337.1926	656.3515	328.6794			4
18	2179.0706	1090.0389	2162.0441	1081.5257	2161.0600	1081.0337	K	***487.2987***	244.1530	470.2722	235.6397			3
19	2307.1292	1154.0682	2290.1026	1145.5550	2289.1186	1145.0630	Q	303.1775	152.0924	286.1510	143.5791			2
20							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TVPQYKYAAGVR**
Found in **E7EQV3**, Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=2 SV=1

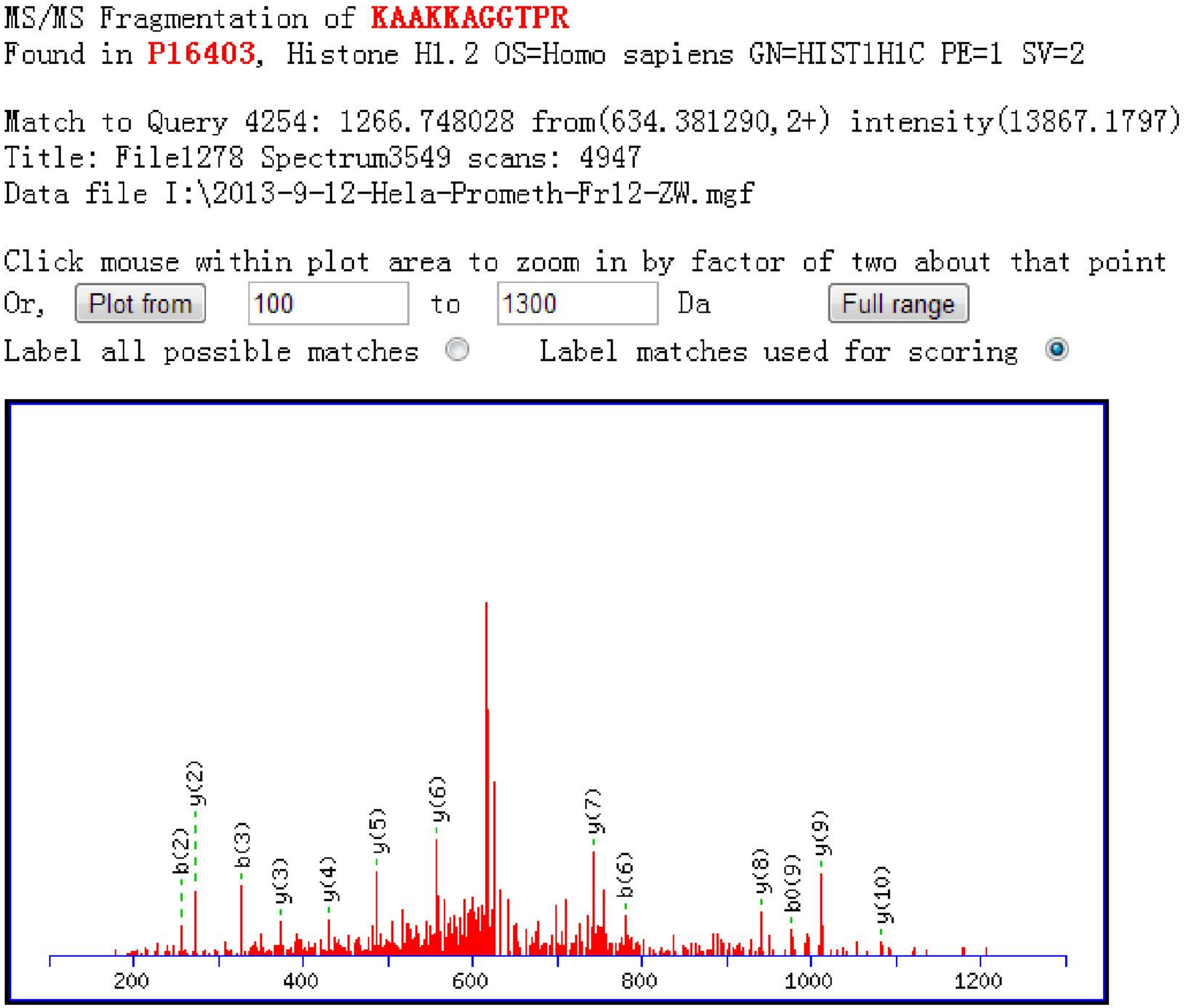
Match to Query 5896: 1421.765968 from(711.890260,2+) intensity(48765.4180)
Title: File1278 Spectrum8466 scans: 10100
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1421.7667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K6 : Propionyl-Methylation (K)
Ions Score: 38 **Expect:** 0.13
Matches : 8/104 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	102.0550	51.5311			84.0444	42.5258	T					12
2	201.1234	101.0653			183.1128	92.0600	V	1321.7263	661.3668	1304.6998	652.8535	11
3	298.1761	149.5917			280.1656	140.5864	P	***1222.6579***	611.8326	1205.6313	603.3193	10
4	426.2347	213.6210	409.2082	205.1077	408.2241	204.6157	Q	***1125.6051***	563.3062	1108.5786	554.7929	9
5	589.2980	295.1527	572.2715	286.6394	571.2875	286.1474	Y	***997.5465***	499.2769	980.5200	490.7636	8
6	787.4349	394.2211	770.4083	385.7078	769.4243	385.2158	K	***834.4832***	417.7452	817.4567	409.2320	7
7	950.4982	475.7527	933.4716	467.2395	932.4876	466.7475	Y	636.3464	318.6768	619.3198	310.1636	6
8	1021.5353	511.2713	1004.5088	502.7580	1003.5247	502.2660	A	***473.2831***	237.1452	456.2565	228.6319	5
9	1092.5724	546.7899	1075.5459	538.2766	1074.5619	537.7846	A	***402.2459***	201.6266	385.2194	193.1133	4
10	1149.5939	575.3006	1132.5673	566.7873	1131.5833	566.2953	G	331.2088	166.1081	314.1823	157.5948	3
11	1248.6623	624.8348	1231.6358	616.3215	1230.6517	615.8295	V	274.1874	137.5973	257.1608	129.0840	2
12							R	175.1190	88.0631	158.0924	79.5498	1

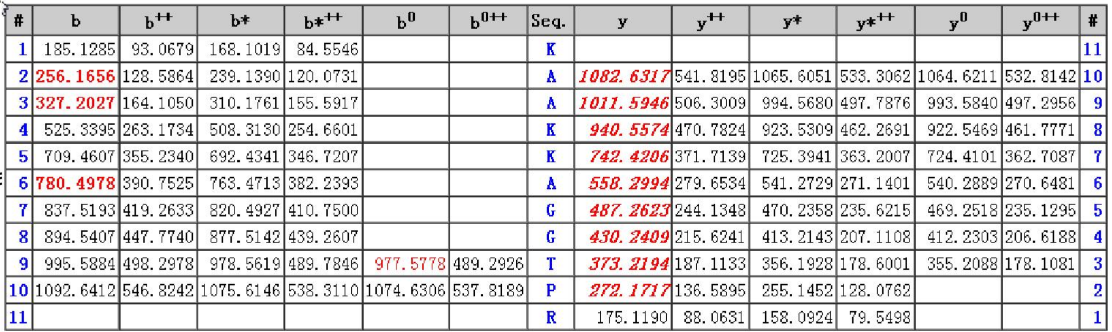


MS/MS Fragmentation of **KAAKKAGGTPR**
Found in **P16403**, Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2

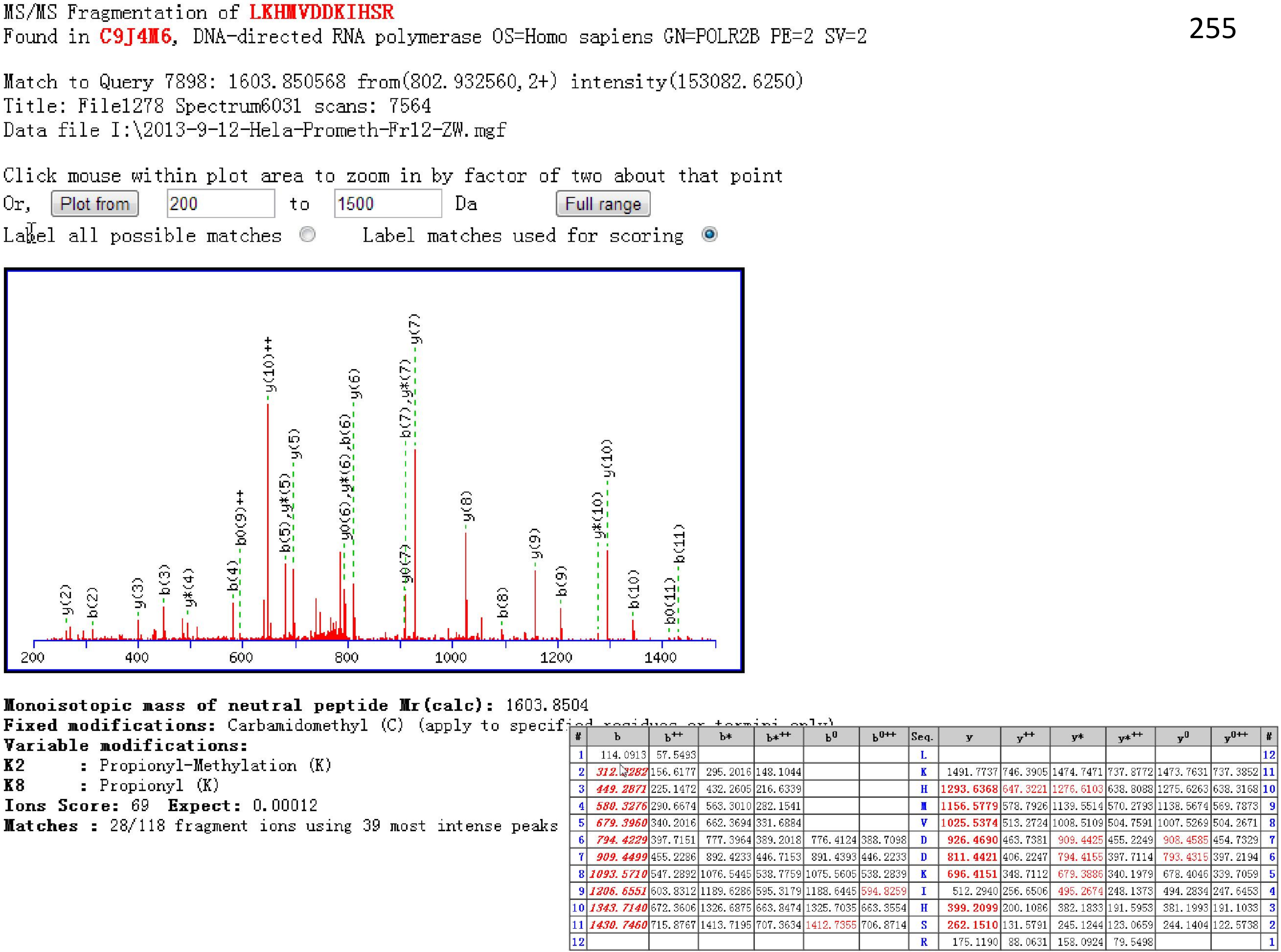
Match to Query 4254: 1266.748028 from(634.381290,2+) intensity(13867.1797)
Title: File1278 Spectrum3549 scans: 4947
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.mgf

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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1265.7455
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K4 : Propionyl-Methylation (K)
K5 : Propionyl (K)
Ions Score: 65 **Expect:** 0.00014
Matches : 13/100 fragment ions using 22 most intense pea



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							11
2	256.1656	128.5864	239.1390	120.0731			A	*1082.6317*	541.8195	1065.6051	533.3062	1064.6211	532.8142	10
3	327.2027	164.1050	310.1761	155.5917			A	*1011.5946*	506.3009	994.5680	497.7876	993.5840	497.2956	9
4	525.3395	263.1734	508.3130	254.6601			K	*940.5574*	470.7824	923.5309	462.2691	922.5469	461.7771	8
5	709.4607	355.2340	692.4341	346.7207			K	*742.4206*	371.7139	725.3941	363.2007	724.4101	362.7087	7
6	780.4978	390.7525	763.4713	382.2393			A	*558.2994*	279.6534	541.2729	271.1401	540.2889	270.6481	6
7	837.5193	419.2633	820.4927	410.7500			G	*487.2623*	244.1348	470.2358	235.6215	469.2518	235.1295	5
8	894.5407	447.7740	877.5142	439.2607			G	*430.2409*	215.6241	413.2143	207.1108	412.2303	206.6188	4
9	995.5884	498.2978	978.5619	489.7846	977.5778	489.2926	T	*373.2194*	187.1133	356.1928	178.6001	355.2088	178.1081	3
10	1092.6412	546.8242	1075.6146	538.3110	1074.6306	537.8189	P	*272.1717*	136.5895	255.1452	128.0762			2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LKHMVDDKIHSR**
Found in **C9J4M6**, DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2

Match to Query 7898: 1603.850568 from(802.932560,2+) intensity(153082.6250)
Title: File1278 Spectrum6031 scans: 7564
Data file I:\2013-9-12-Hela-Prometh-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

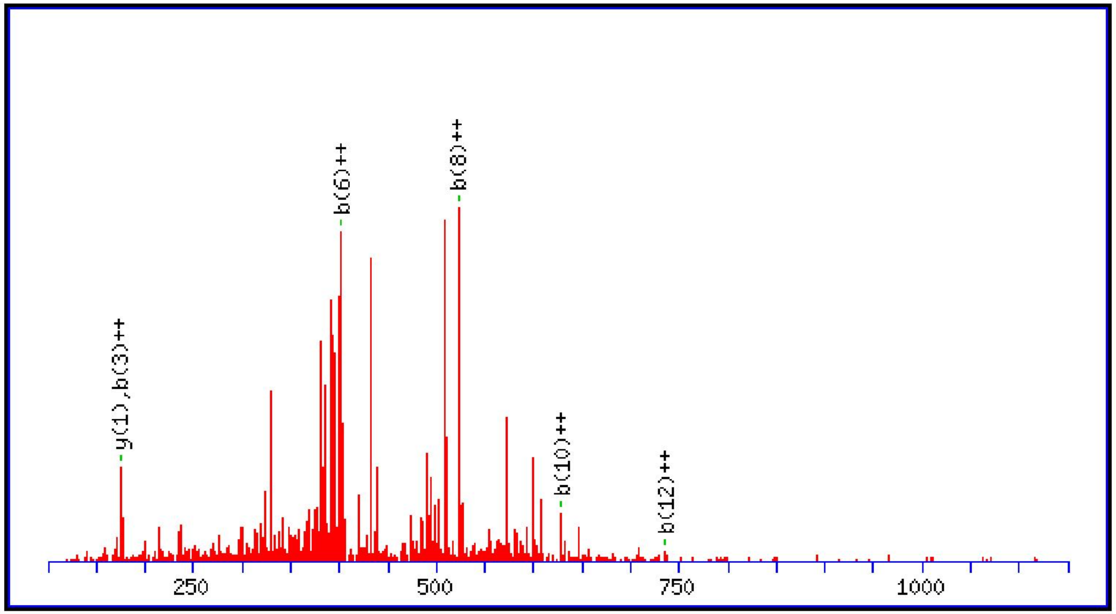
Monoisotopic mass of neutral peptide Mr(calc): 1603.8504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
K8 : Propionyl (K)
Ions Score: 69 **Expect:** 0.00012
Matches : 28/118 fragment ions using 39 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							12
2	***312.2282***	156.6177	295.2016	148.1044			K	1491.7737	746.3905	1474.7471	737.8772	1473.7631	737.3852	11
3	***449.2871***	225.1472	432.2605	216.6339			H	**1293.6368**	647.3221	1276.6103	638.8088	1275.6263	638.3168	10
4	***580.3276***	290.6674	563.3010	282.1541			M	**1156.5779**	578.7926	1139.5514	570.2793	1138.5674	569.7873	9
5	***679.3960***	340.2016	662.3694	331.6884			V	**1025.5374**	513.2724	1008.5109	504.7591	1007.5269	504.2671	8
6	***794.4229***	397.7151	777.3964	389.2018	776.4124	388.7098	D	**926.4690**	463.7381	909.4425	455.2249	908.4585	454.7329	7
7	***909.4499***	455.2286	892.4233	446.7153	891.4393	446.2233	D	**811.4421**	406.2247	794.4155	397.7114	793.4315	397.2194	6
8	***1093.5710***	547.2892	1076.5445	538.7759	1075.5605	538.2839	K	**696.4151**	348.7112	679.3886	340.1979	678.4046	339.7059	5
9	***1206.6551***	603.8312	1189.6286	595.3179	1188.6445	594.8259	I	512.2940	256.6506	495.2674	248.1373	494.2834	247.6453	4
10	***1343.7140***	672.3606	1326.6875	663.8474	1325.7035	663.3554	H	**399.2099**	200.1086	382.1833	191.5953	381.1993	191.1033	3
11	***1430.7460***	715.8767	1413.7195	707.3634	1412.7355	706.8714	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1

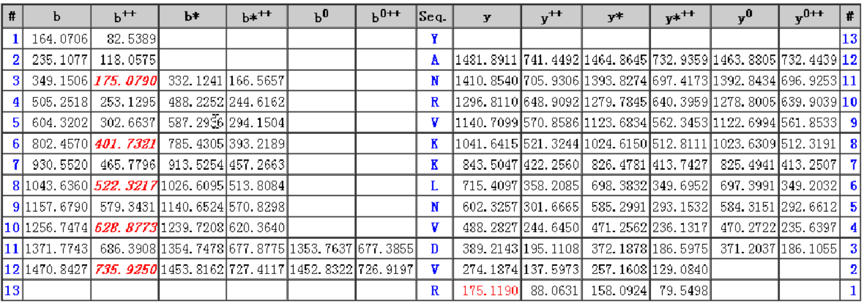
MS/MS Fragmentation of **YANRVKKLNVDVR**
Found in **Q8N4N8**, Kinesin-like protein KIF2B OS=Homo sapiens GN=KIF2B PE=1 SV=3

Match to Query 10508: 1643.945616 from(411.993680,4+) intensity(184554.3906)
Title: File1322 Spectrum4320 scans: 4810
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

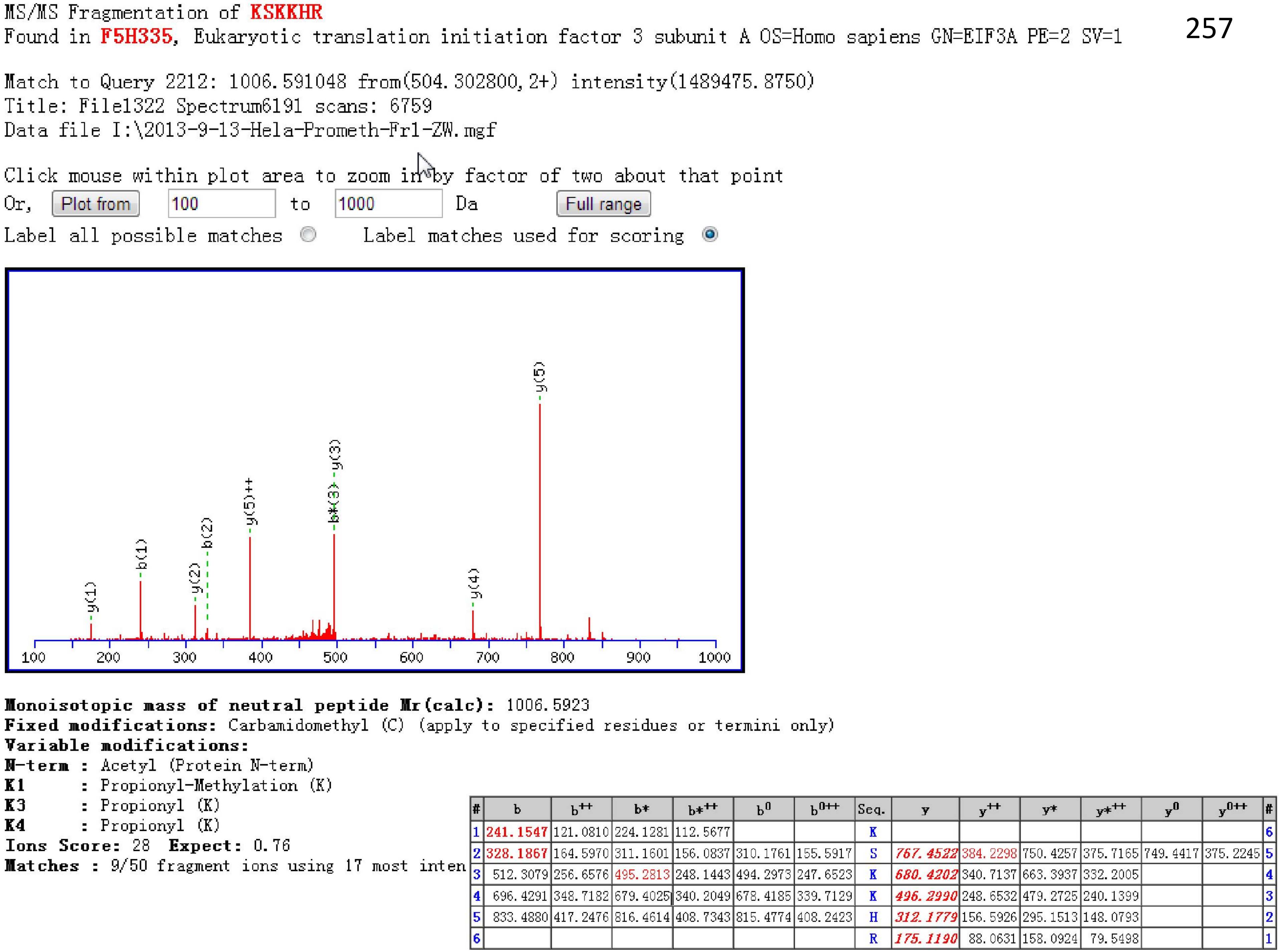
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1643.9471
Fixed modifications: Carbamidometryl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : Propionyl-Methylation (K)
Ions Score: 23 **Expect:** 3.8
Matches : 6/116 fragment ions using 10 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							13
2	235.1077	118.0575					A	1481.8911	741.4492	1464.8645	732.9359	1463.8805	732.4439	12
3	349.1506	***175.0790***	332.1241	166.5657			N	1410.8540	705.9306	1393.8274	697.4173	1392.8434	696.9253	11
4	505.2518	253.1295	488.2252	244.6162			R	1296.8110	648.9092	1279.7845	640.3959	1278.8005	639.9039	10
5	604.3202	302.6637	587.2936	294.1504			V	1140.7099	570.8586	1123.6834	562.3453	1122.6994	561.8533	9
6	802.4570	***401.7321***	785.4305	393.2189			K	1041.6415	521.3244	1024.6150	512.8111	1023.6309	512.3191	8
7	930.5520	465.7796	913.5254	457.2663			K	843.5047	422.2560	826.4781	413.7427	825.4941	413.2507	7
8	1043.6360	***522.3217***	1026.6095	513.8084			L	715.4097	358.2085	698.3832	349.6952	697.3991	349.2032	6
9	1157.6790	579.3431	1140.6524	570.8298			N	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	5
10	1256.7474	***628.8773***	1239.7208	620.3640			V	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
11	1371.7743	686.3908	1354.7478	677.8775	1353.7637	677.3855	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
12	1470.8427	***735.9250***	1453.8162	727.4117	1452.8322	726.9197	V	274.1874	137.5973	257.1608	129.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1



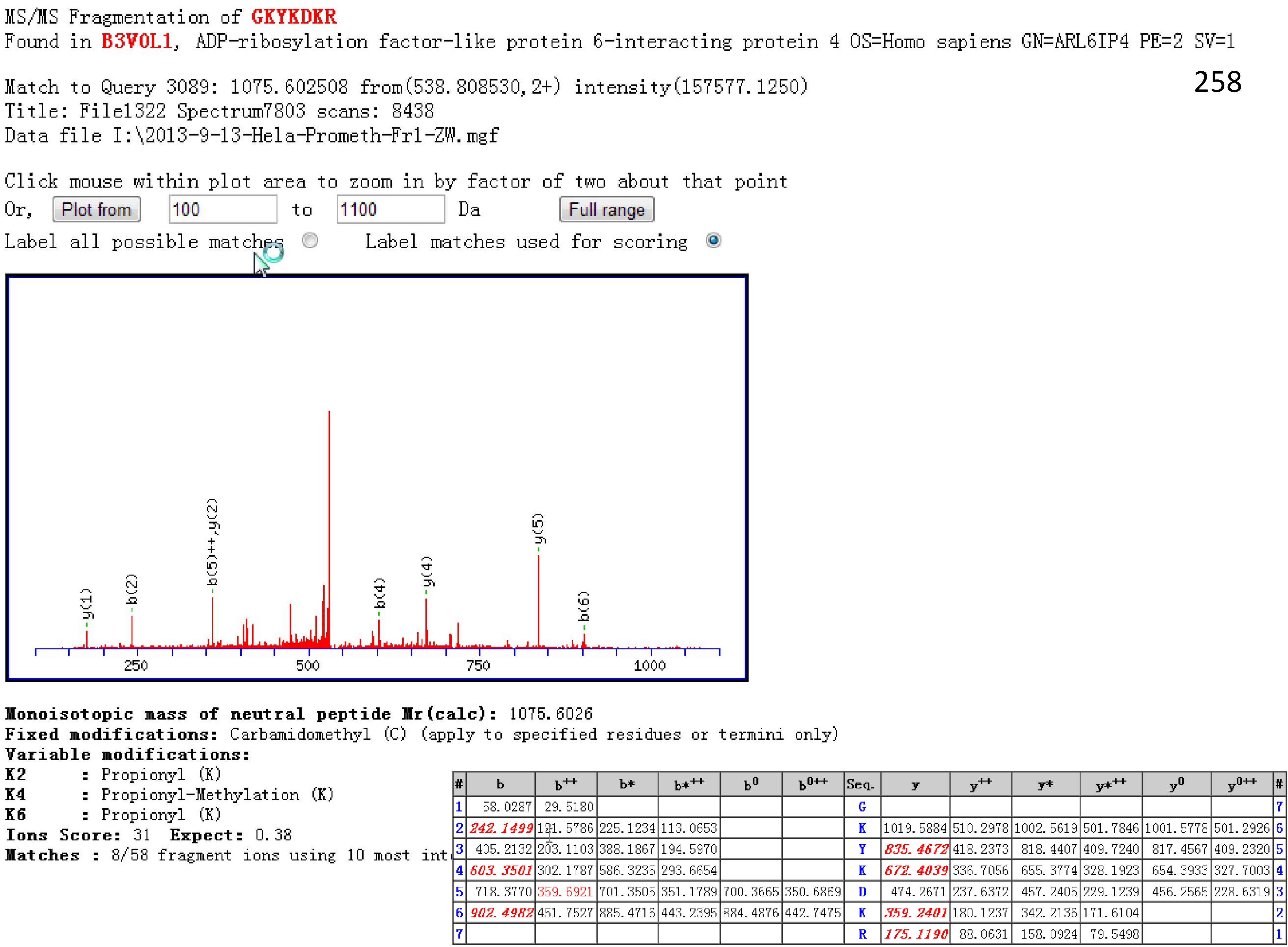
MS/MS Fragmentation of **KSKKHR**
Found in **F5H335**, Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1

Match to Query 2212: 1006.591048 from(504.302800,2+) intensity(1489475.8750)
Title: File1322 Spectrum6191 scans: 6759
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1006.5923
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
K1 : Propionyl-Methylation (K)
K3 : Propionyl (K)
K4 : Propionyl (K)
Ions Score: 28 **Expect:** 0.76
Matches : 9/50 fragment ions using 17 most inten

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**241.1547**	121.0810	224.1281	112.5677			K							6
2	**328.1867**	164.5970	311.1601	156.0837	310.1761	155.5917	S	***767.4522***	384.2298	750.4257	375.7165	749.4417	375.2245	5
3	512.3079	256.6576	495.2813	248.1443	494.2973	247.6523	K	***680.4202***	340.7137	663.3937	332.2005			4
4	696.4291	348.7182	679.4025	340.2049	678.4185	339.7129	K	***496.2990***	248.6532	479.2725	240.1399			3
5	833.4880	417.2476	816.4614	408.7343	815.4774	408.2423	H	***312.1779***	156.5926	295.1513	148.0793			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GKYKDKR**
Found in **B3V0L1**, ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Homo sapiens GN=ARL6IP4 PE=2 SV=1

Match to Query 3089: 1075.602508 from(538.808530,2+) intensity(157577.1250)
Title: File1322 Spectrum7803 scans: 8438
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

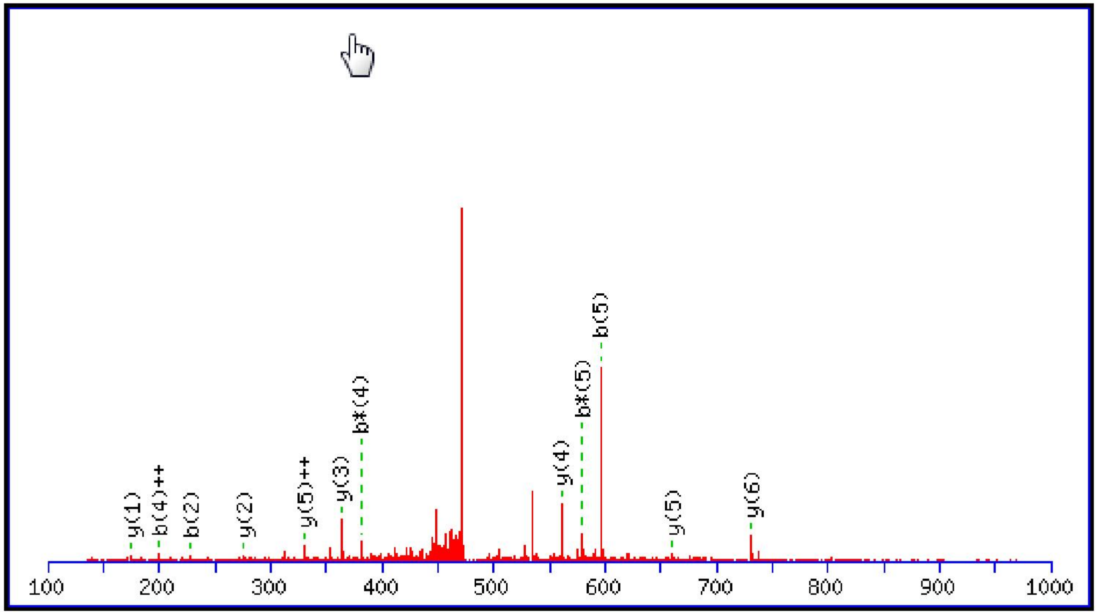
Monoisotopic mass of neutral peptide Mr(calc): 1075.6026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K4 : Propionyl-Methylation (K)
K6 : Propionyl (K)
Ions Score: 31 **Expect:** 0.38
Matches : 8/58 fragment ions using 10 most int

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							7
2	***242.1499***	121.5786	225.1234	113.0653			K	1019.5884	510.2978	1002.5619	501.7846	1001.5778	501.2926	6
3	405.2132	203.1103	388.1867	194.5970			Y	***835.4672***	418.2373	818.4407	409.7240	817.4567	409.2320	5
4	***603.3501***	302.1787	586.3235	293.6654			K	***672.4039***	336.7056	655.3774	328.1923	654.3933	327.7003	4
5	718.3770	359.6921	701.3505	351.1789	700.3665	350.6869	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	3
6	***902.4982***	451.7527	885.4716	443.2395	884.4876	442.7475	K	***359.2401***	180.1237	342.2136	171.6104			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **QVAVKSTR**
Found in **E9PRF4**, Histone-lysine N-methyltransferase SETDB1 (Fragment) OS=Homo sapiens GN=SETDB1 PE=2 SV=1

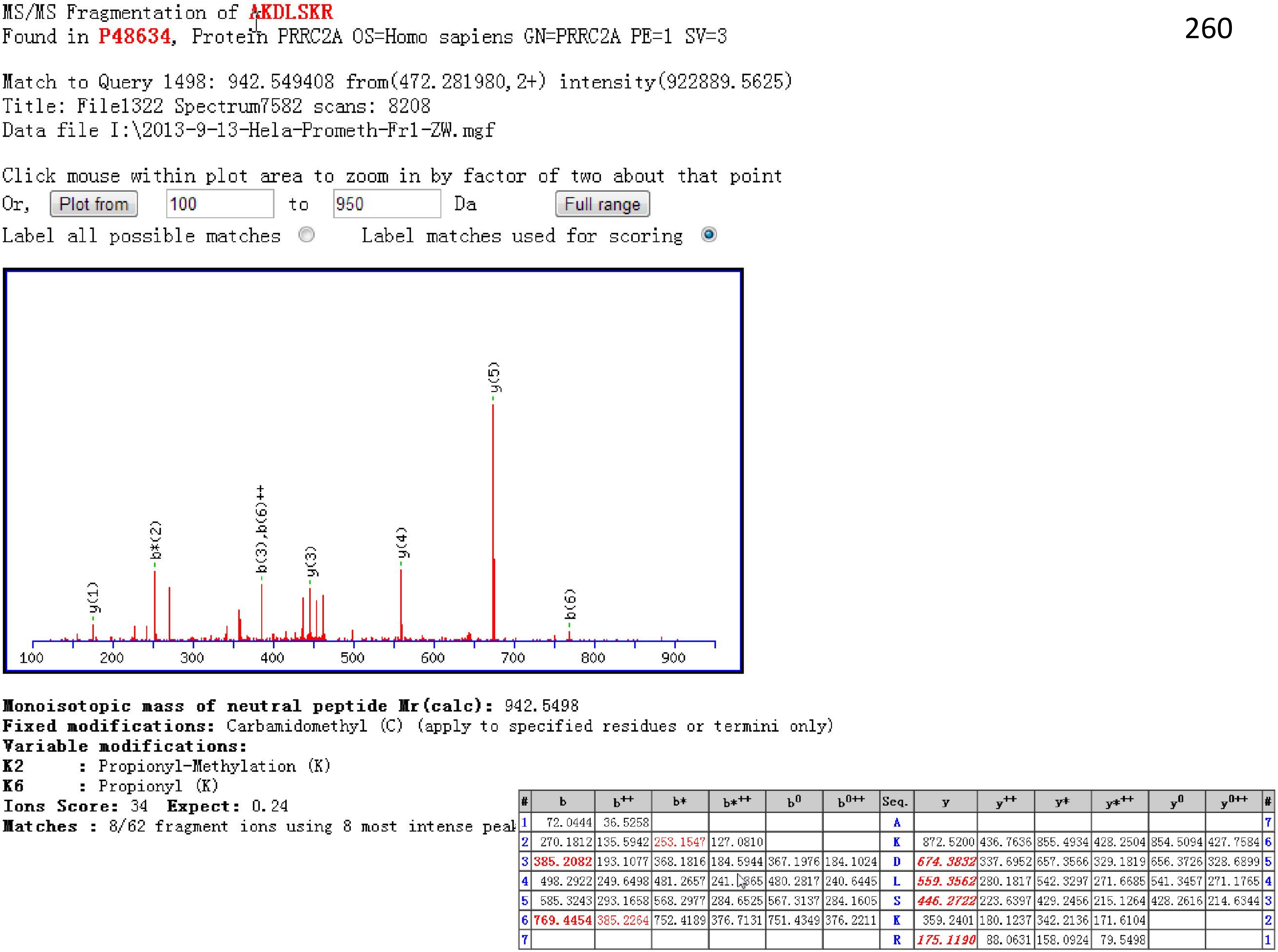
Match to Query 1634: 957.560948 from(479.787750,2+) intensity(182960.3281)
Title: File1322 Spectrum5025 scans: 5544
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 957.5607
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5 : Propionyl-Methylation (K)
Ions Score: 32 **Expect:** 0.38
Matches : 12/72 fragment ions using 27 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							8
2	**228.1343**	114.5708	211.1077	106.0575			V	830.5094	415.7584	813.4829	407.2451	812.4989	406.7531	7
3	299.1714	150.0893	282.1448	141.5761			A	***731.4410***	366.2241	714.4145	357.7109	713.4305	357.2189	6
4	398.2398	199.6235	381.2132	191.1103			V	***660.4039***	330.7056	643.3774	322.1923	642.3933	321.7003	5
5	**596.3766**	298.6920	579.3501	290.1787			K	***561.3355***	281.1714	544.3089	272.6581	543.3249	272.1661	4
6	683.4087	342.2080	666.3[illegible]21	333.6947	665.3981	333.2027	S	***363.1987***	182.1030	346.1721	173.5897	345.1881	173.0977	3
7	784.4563	392.7318	767.4298	384.2185	766.4458	383.7265	T	***276.1666***	138.5870	259.1401	130.0737	258.1561	129.5817	2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKDLSKR**
Found in **P48634**, Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3

Match to Query 1498: 942.549408 from(472.281980,2+) intensity(922889.5625)
Title: File1322 Spectrum7582 scans: 8208
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

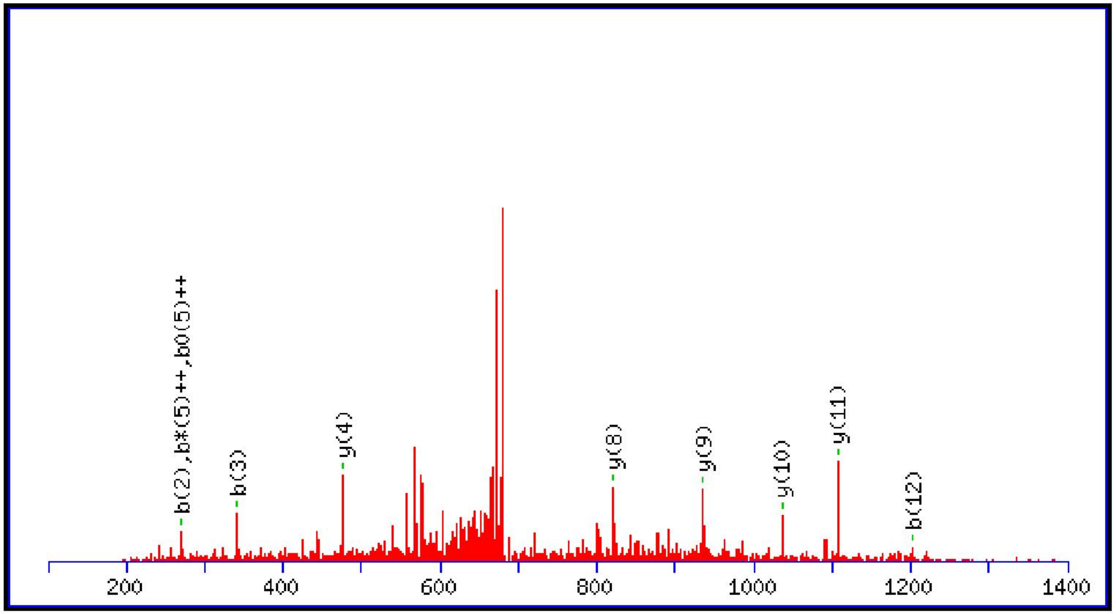
Monoisotopic mass of neutral peptide Mr(calc): 942.5498
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
K6 : Propionyl (K)
Ions Score: 34 **Expect:** 0.24
Matches : 8/62 fragment ions using 8 most intense peal

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							7
2	270.1812	135.5942	253.1547	127.0810			K	872.5200	436.7636	855.4934	428.2504	854.5094	427.7584	6
3	**385.2082**	193.1077	368.1816	184.5944	367.1976	184.1024	D	***674.3832***	337.6952	657.3566	329.1819	656.3726	328.6899	5
4	498.2922	249.6498	481.2657	241.[illegible]365	480.2817	240.6445	L	***559.3562***	280.1817	542.3297	271.6685	541.3457	271.1765	4
5	585.3243	293.1658	568.2977	284.6525	567.3137	284.1605	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	3
6	**769.4454**	385.2264	752.4189	376.7131	751.4349	376.2211	K	359.2401	180.1237	342.2136	171.6104			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAATDGADTPFGR**
Found in **K7EN03**, RelA-associated inhibitor (Fragment) OS=Homo sapiens GN=PPP1R13L PE=4 SV=1

Match to Query 6436: 1375.672208 from(688.843380,2+) intensity(93149.6563)
Title: File1322 Spectrum9232 scans: 9926
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.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 ●



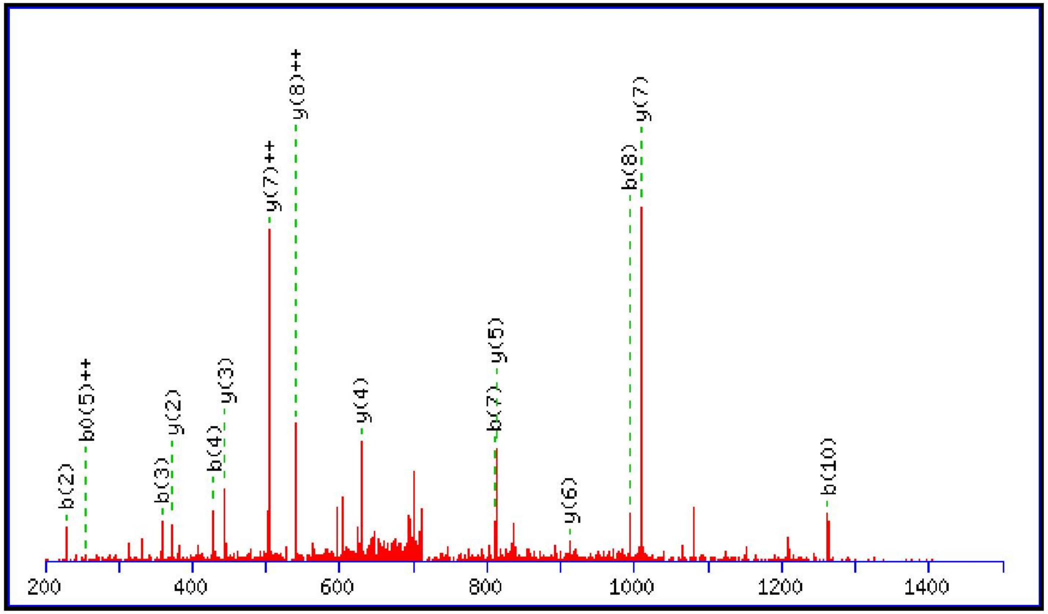
Monoisotopic mass of neutral peptide Mr(calc): 1375.6732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-Methylation (K)
Ions Score: 33 **Expect:** 0.22
Matches : 10/130 fragment ions using 12 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	199.1441	100.0757	182.1176	91.5624			K							13
2	**270.1812**	135.5942	253.1547	127.0810			A	1178.5436	589.7755	1161.5171	581.2622	1160.5331	580.7702	12
3	**341.2183**	171.1128	324.1918	162.5995			A	***1107.5065***	554.2569	1090.4800	545.7436	1089.4960	545.2516	11
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	T	***1036.4694***	518.7383	1019.4429	510.2251	1018.4589	509.7331	10
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	D	***935.4217***	468.2145	918.3952	459.7012	917.4112	459.2092	9
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	G	***820.3948***	410.7010	803.3682	402.1878	802.3842	401.6958	8
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	A	763.3733	382.1903	746.3468	373.6770	745.3628	373.1850	7
8	800.3785	400.6929	783.3519	392.1796	782.3679	391.6876	D	692.3362	346.6717	675.3097	338.1585	674.3257	337.6665	6
9	901.4262	451.2167	884.3996	442.7034	883.4156	442.2114	T	577.3093	289.1583	560.2827	280.6450	559.2987	280.1530	5
10	998.4789	499.7431	981.4524	491.2298	980.4684	490.7378	P	***476.2616***	238.6344	459.2350	230.1212			4
11	1145.5473	573.2773	1128.5208	564.7640	1127.5368	564.2720	F	379.2088	190.1081	362.1823	181.5948			3
12	**1202.5688**	601.7880	1185.5422	593.2748	1184.5582	592.7828	G	232.1404	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VEEAPVKKAKR**
Found in **H0Y9Y2**, Biorientation of chromosomes in cell division protein 1-like 1 (Fragment) OS=Homo sapiens GN=BOD1L1 PE=4 SV=1

Match to Query 7444: 1435.838588 from(718.926570,2+) intensity(478861.4688)
Title: File1322 Spectrum10007 scans: 10734
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



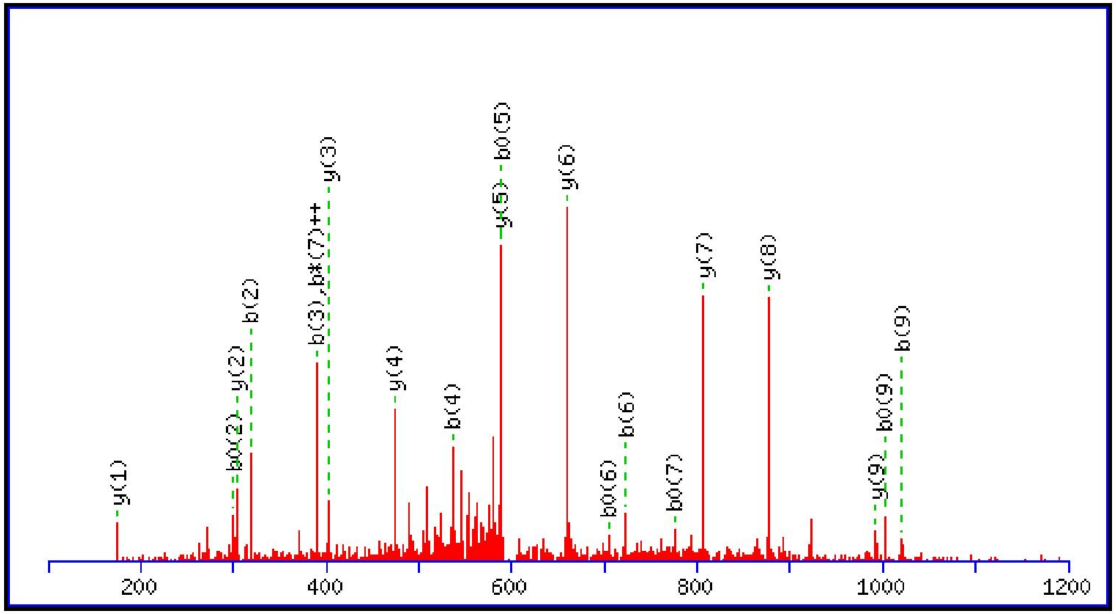
Monoisotopic mass of neutral peptide Mr(calc): 1435.8398
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl (K)
K8 : Propionyl (K)
K10 : Propionyl-Methylation (K)
Ions Score: 51 **Expect:** 0.004
Matches : 15/90 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							11
2	***229.1183***	115.0628			211.1077	106.0575	E	1337.7787	669.3930	1320.7522	660.8797	1319.7682	660.3877	10
3	***358.1609***	179.5841			340.1503	170.5788	E	1208.7361	604.8717	1191.7096	596.3584	1190.7256	595.8664	9
4	***429.1980***	215.1026			411.1874	206.0974	A	1079.6935	540.3504	1062.6670	531.8371			8
5	526.2508	263.6290			508.2402	254.6237	P	***1008.6564***	504.8319	991.6299	496.3186			7
6	625.3192	313.1632			607.3086	304.1579	V	***911.6037***	456.3055	894.5771	447.7922			6
7	***809.4403***	405.2238	792.4138	396.7105	791.4298	396.2185	K	***812.5353***	406.7713	795.5087	398.2580			5
8	***993.5615***	497.2844	976.5350	488.7711	975.5510	488.2791	K	***628.4141***	314.7107	611.3875	306.1974			4
9	1064.5986	532.8030	1047.5721	524.2897	1046.5881	523.7977	A	***444.2929***	222.6501	427.2663	214.1368			3
10	***1262.7355***	631.8714	1245.7089	623.3581	1244.7249	622.8661	K	***373.2558***	187.1315	356.2292	178.6183			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KDAFADAVQR**
Found in **M0R0I5**, Far upstream element-binding protein 2 (Fragment) OS=Homo sapiens GN=KHSRP PE=4 SV=1

Match to Query 4389: 1193.631068 from(597.822810,2+) intensity(275242.0313)
Title: File1322 Spectrum10083 scans: 10813
Data file I:\2013-9-13-Hela-Prometh-Fr1-ZW.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 ●



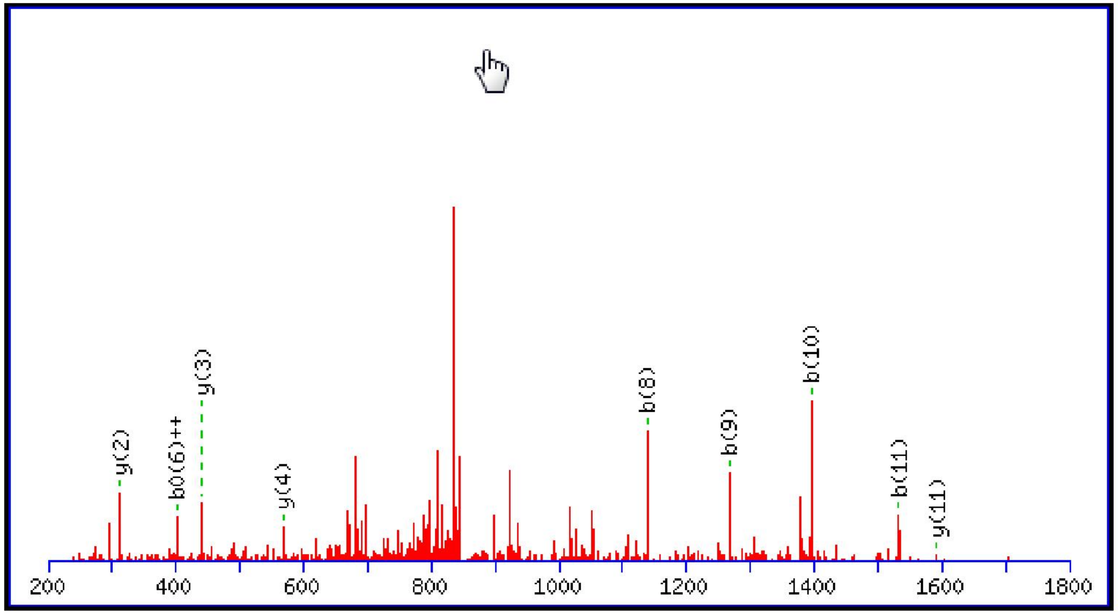
Monoisotopic mass of neutral peptide Mr(calc): 1193.6313
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 70 **Expect:** 6.7e-005
Matches : 20/98 fragment ions using 31 most intense peaks (

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			**K**							10
2	**318.1932**	159.6003	301.1667	151.0870	300.1827	150.5950	**D**	***992.4796***	496.7434	975.4530	488.2302	974.4690	487.7381	9
3	**389.2303**	195.1188	372.2038	186.6055	371.2198	186.1135	**A**	***877.4526***	439.2300	860.4261	430.7167	859.4421	430.2247	8
4	**536.2988**	268.6530	519.2722	260.1397	518.2882	259.6477	**F**	***806.4155***	403.7114	789.3890	395.1981	788.4050	394.7061	7
5	607.3359	304.1716	590.3093	295.6583	589.3253	295.1663	**A**	***659.3471***	330.1772	642.3206	321.6639	641.3365	321.1719	6
6	**722.3628**	361.6850	705.3363	353.1718	704.3523	352.6798	**D**	***588.3100***	294.6586	571.2835	286.1454	570.2994	285.6534	5
7	793.3999	397.2036	776.3734	388.6903	775.3894	388.1983	**A**	***473.2831***	237.1452	456.2565	228.6319			4
8	892.4683	446.7378	875.4418	438.2245	874.4578	437.7325	**V**	***402.2459***	201.6266	385.2194	193.1133			3
9	**1020.5269**	510.7671	1003.5004	502.2538	1002.5164	501.7618	**Q**	***303.1775***	152.0924	286.1510	143.5791			2
10							**R**	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **DKNRHDKDQQHR**
Found in **J3KQL8**, Apolipoprotein L2 OS=Homo sapiens GN=APOL2 PE=4 SV=1

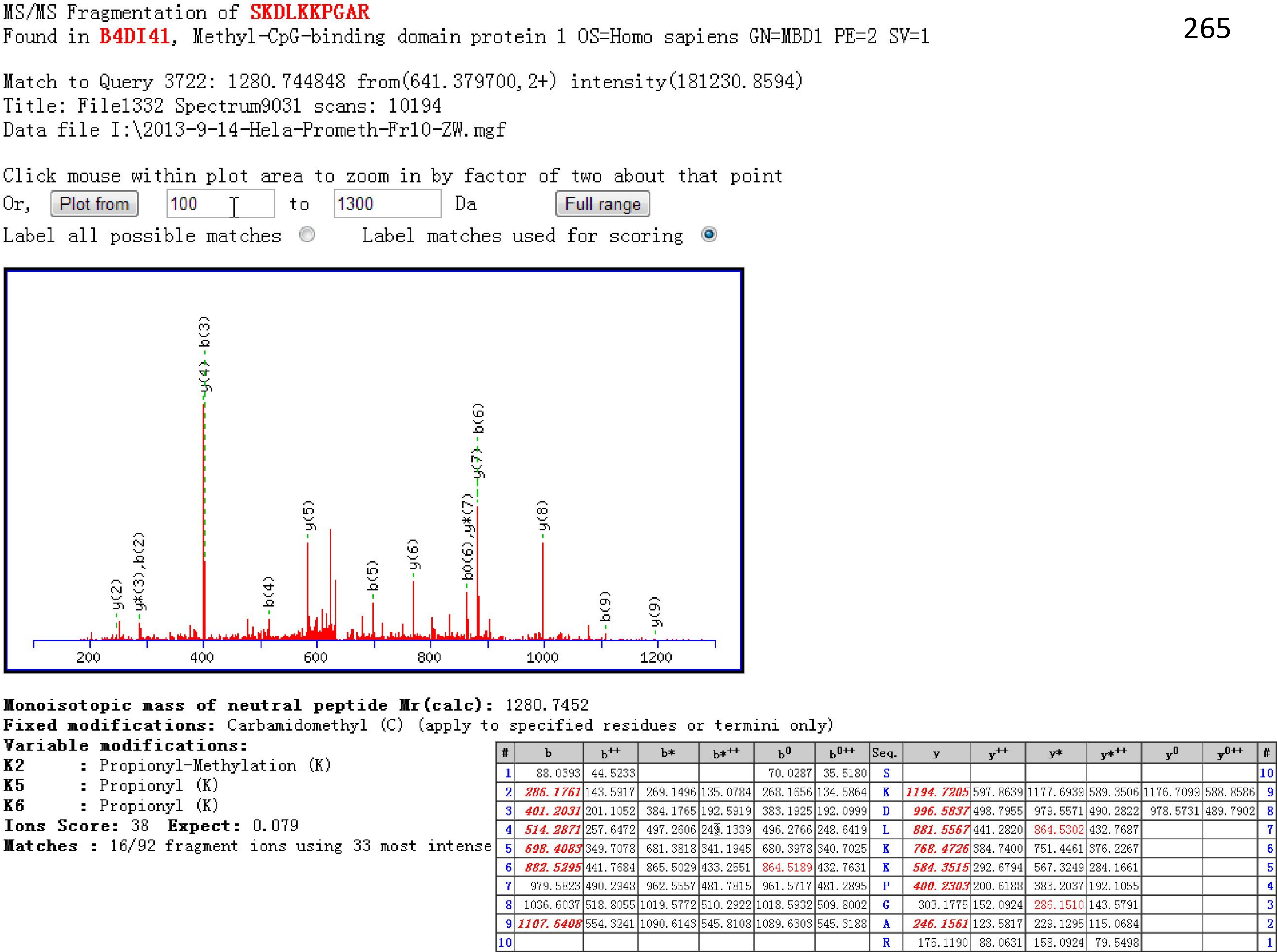
Match to Query 10319: 1705.851288 from(853.932920,2+) intensity(74072.5781)
Title: File1332 Spectrum6206 scans: 7251
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1705.8517
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 26 **Expect:** 1.9
Matches : 9/122 fragment ions using 15 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							12
2	300.1554	150.5813	283.1288	142.0681	282.1448	141.5761	K	***1591.8320***	796.4197	1574.8055	787.9064	1573.8215	787.4144	11
3	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	N	1407.7109	704.3591	1390.6843	695.8458	1389.7003	695.3538	10
4	570.2994	285.6534	553.2729	277.1401	552.2889	276.6481	R	1293.6679	647.3376	1276.6414	638.8243	1275.6574	638.3323	9
5	707.3583	354.1828	690.3318	345.6695	689.3478	345.1775	H	1137.5668	569.2871	1120.5403	560.7738	1119.5563	560.2818	8
6	822.3853	411.6963	805.3587	403.1830	804.3747	402.6910	D	1000.5079	500.7576	983.4814	492.2443	982.4974	491.7523	7
7	1024.5443	512.7758	1007.5178	504.2625	1006.5337	503.7705	K	885.4810	443.2441	868.4544	434.7309	867.4704	434.2388	6
8	***1139.5712***	570.2893	1122.5447	561.7760	1121.5607	561.2840	D	683.3220	342.1646	666.2954	333.6513	665.3114	333.1593	5
9	***1267.6298***	634.3185	1250.6033	625.8053	1249.6193	625.3133	Q	***568.2950***	284.6511	551.2685	276.1379			4
10	***1395.6884***	698.3478	1378.6619	689.8346	1377.6778	689.3426	Q	***440.2364***	220.6219	423.2099	212.1086			3
11	***1532.7473***	766.8773	1515.7208	758.3640	1514.7367	757.8720	H	***312.1779***	156.5926	295.1513	148.0793			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **SKDLKKPGAR**
Found in **B4DI41**, Methyl-CpG-binding domain protein 1 OS=Homo sapiens GN=MBD1 PE=2 SV=1

Match to Query 3722: 1280.744848 from(641.379700,2+) intensity(181230.8594)
Title: File1332 Spectrum9031 scans: 10194
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.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 ●

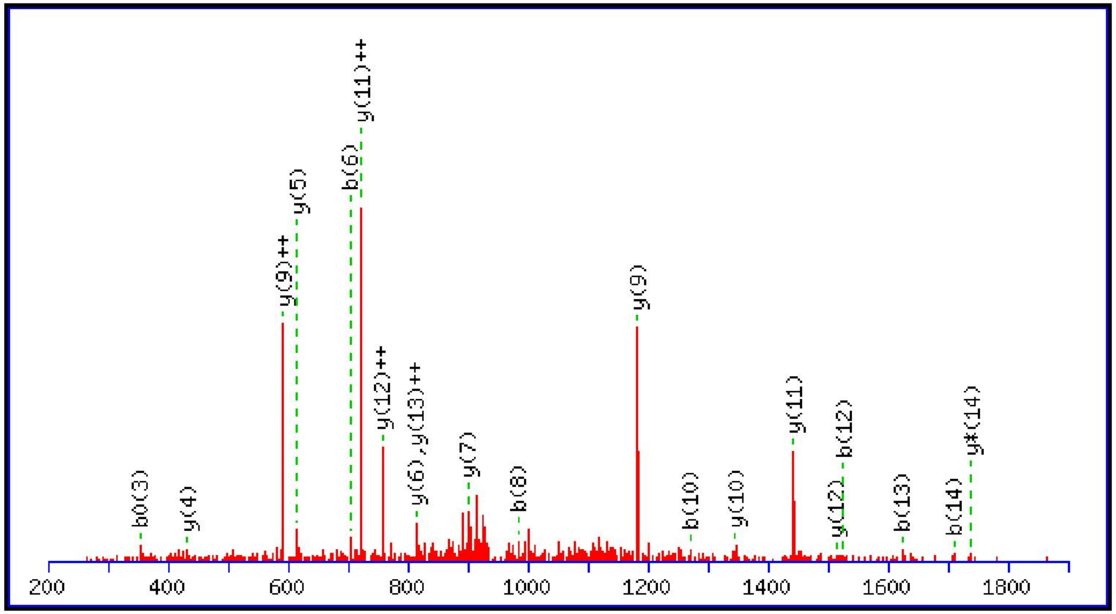
Monoisotopic mass of neutral peptide Mr(calc): 1280.7452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-Methylation (K)
K5 : Propionyl (K)
K6 : Propionyl (K)
Ions Score: 38 **Expect:** 0.079
Matches : 16/92 fragment ions using 33 most intense

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							10
2	***286.1761***	143.5917	269.1496	135.0784	268.1656	134.5864	K	***1194.7205***	597.8639	1177.6939	589.3506	1176.7099	588.8586	9
3	***401.2031***	201.1052	384.1765	192.5919	383.1925	192.0999	D	***996.5837***	498.7955	979.5571	490.2822	978.5731	489.7902	8
4	***514.2871***	257.6472	497.2606	249.1339	496.2766	248.6419	L	***881.5567***	441.2820	864.5302	432.7687			7
5	***698.4083***	349.7078	681.3818	341.1945	680.3978	340.7025	K	***768.4726***	384.7400	751.4461	376.2267			6
6	***882.5295***	441.7684	865.5029	433.2551	864.5189	432.7631	K	***584.3515***	292.6794	567.3249	284.1661			5
7	979.5823	490.2948	962.5557	481.7815	961.5717	481.2895	P	***400.2303***	200.6188	383.2037	192.1055			4
8	1036.6037	518.8055	1019.5772	510.2922	1018.5932	509.8002	G	303.1775	152.0924	286.1510	143.5791			3
9	***1107.6408***	554.3241	1090.6143	545.8108	1089.6303	545.3188	A	***246.1561***	123.5817	229.1295	115.0684			2
10							R	175.1190	88.0631	158.0924	79.5498			1

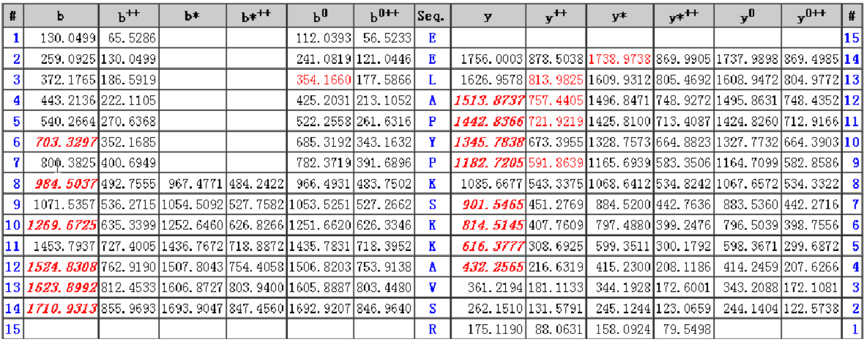
MS/MS Fragmentation of **EELAPYPKSKKAVSR**
Found in **C9JQA1**, Polyglutamine-binding protein 1 (Fragment) OS=Homo sapiens GN=PQBP1 PE=2 SV=1

Match to Query 13687: 1884.034768 from(943.024660,2+) intensity(38959.1758)
Title: File1332 Spectrum11611 scans: 12881
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

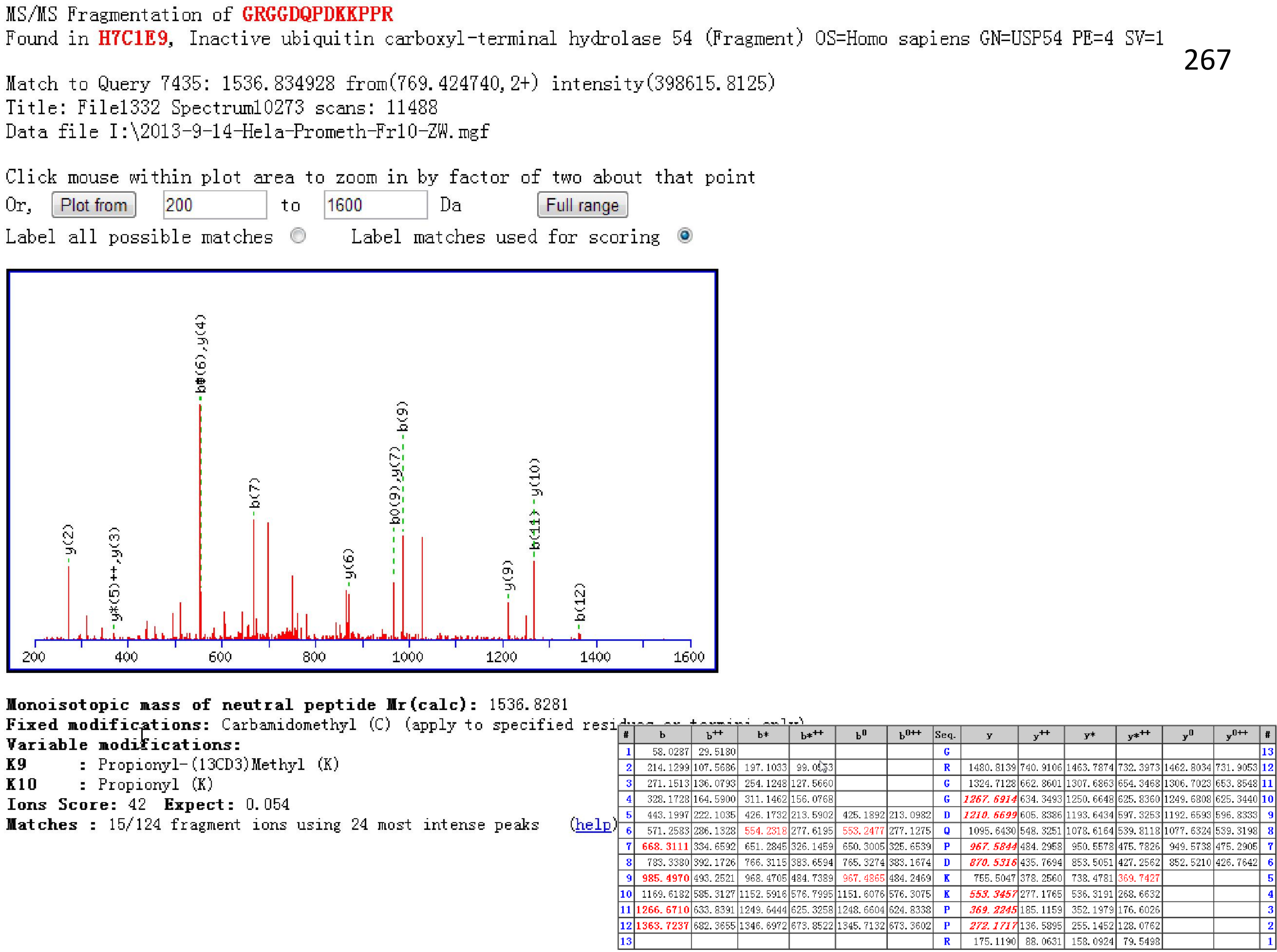
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1884.0356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K8 : Propionyl (K)
K10 : Propionyl-Methylation (K)
K11 : Propionyl (K)
Ions Score: 33 **Expect:** 0.59
Matches : 20/152 fragment ions using 47 most intense peaks (help)



#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	259.0925	130.0499			241.0819	121.0446	E	1756.0003	878.5038	1738.9738	869.9905	1737.9898	869.4985	14
3	372.1765	186.5919			354.1660	177.5866	L	1626.9578	813.9825	1609.9312	805.4692	1608.9472	804.9772	13
4	443.2136	222.1105			425.2031	213.1052	A	***1513.8737***	757.4405	1496.8471	748.9272	1495.8631	748.4352	12
5	540.2664	270.6368			522.2558	261.6316	P	***1442.8366***	721.9219	1425.8100	713.4087	1424.8260	712.9166	11
6	***703.3297***	352.1685			685.3192	343.1632	Y	***1345.7838***	673.3955	1328.7573	664.8823	1327.7732	664.3903	10
7	800.3825	400.6949			782.3719	391.6896	P	***1182.7205***	591.8639	1165.6939	583.3506	1164.7099	582.8586	9
8	***984.5037***	492.7555	967.4771	484.2422	966.4931	483.7502	K	1085.6677	543.3375	1068.6412	534.8242	1067.6572	534.3322	8
9	1071.5357	536.2715	1054.5092	527.7582	1053.5251	527.2662	S	***901.5465***	451.2769	884.5200	442.7636	883.5360	442.2716	7
10	***1269.6725***	635.3399	1252.6460	626.8266	1251.6620	626.3346	K	***814.5145***	407.7609	797.4880	399.2476	796.5039	398.7556	6
11	1453.7937	727.4005	1436.7672	718.8872	1435.7831	718.3952	K	***616.3777***	308.6925	599.3511	300.1792	598.3671	299.6872	5
12	***1524.8308***	762.9190	1507.8043	754.4058	1506.8203	753.9138	A	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	4
13	***1623.8992***	812.4533	1606.8727	803.9400	1605.8887	803.4480	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
14	***1710.9313***	855.9693	1693.9047	847.4560	1692.9207	846.9640	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
15							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GRGGDQPDKKPPR**

Found in **H7C1E9**, Inactive ubiquitin carboxyl-terminal hydrolase 54 (Fragment) OS=Homo sapiens GN=USP54 PE=4 SV=1

Match to Query 7435: 1536.834928 from(769.424740,2+) intensity(398615.8125)

Title: File1332 Spectrum10273 scans: 11488

Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

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

Or, Plot from 200 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1536.8281

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

Variable modifications:

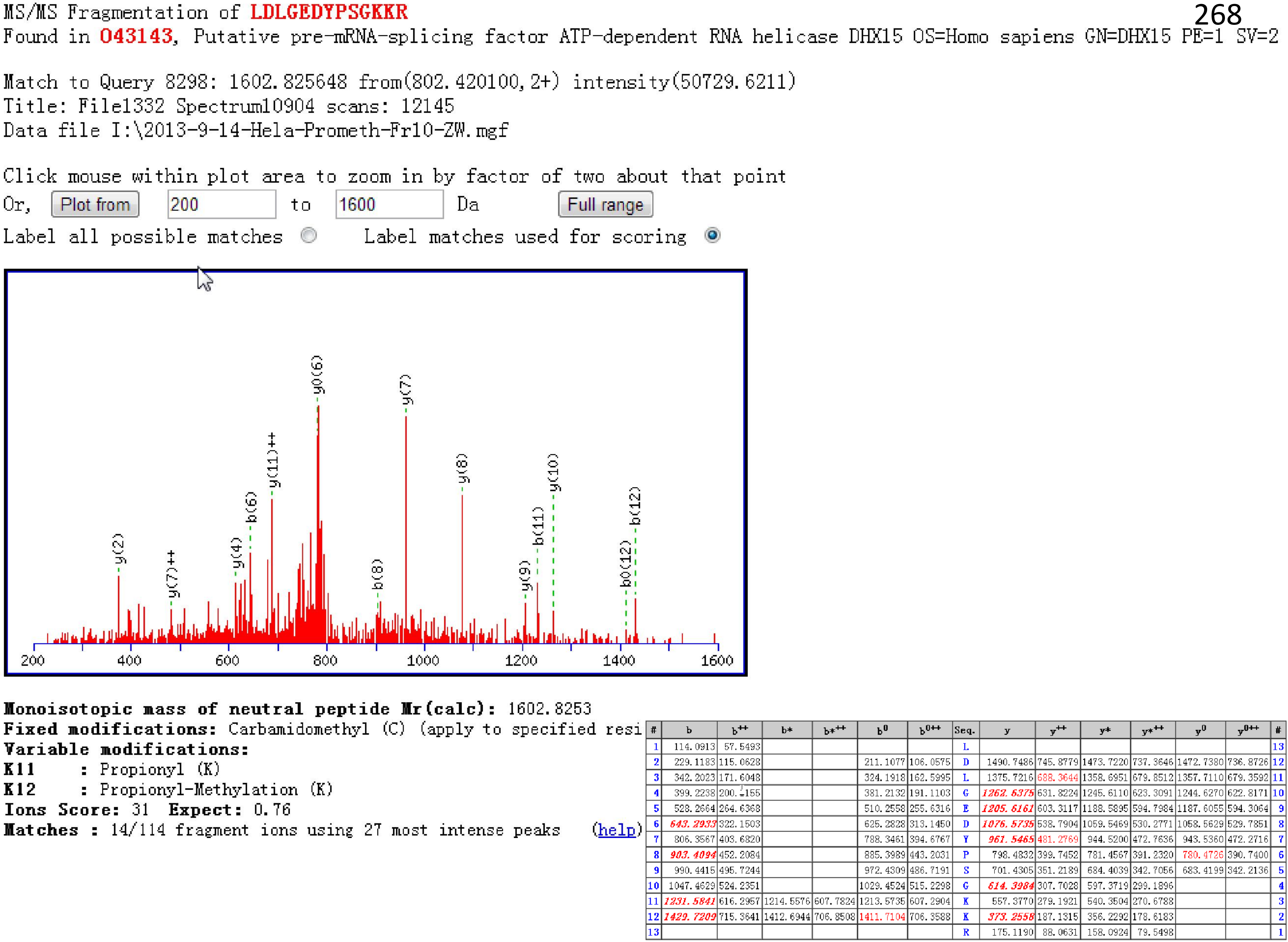
K9 : Propionyl-(13CD3)Methyl (K)

K10 : Propionyl (K)

Ions Score: 42 **Expect:** 0.054

Matches : 15/124 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							13
2	214.1299	107.5686	197.1033	99.0553			R	1480.8139	740.9106	1463.7874	732.3973	1462.8034	731.9053	12
3	271.1513	136.0793	254.1248	127.5660			G	1324.7128	662.8601	1307.6863	654.3468	1306.7023	653.8548	11
4	328.1728	164.5900	311.1462	156.0768			G	***1267.6914***	634.3493	1250.6648	625.8360	1249.6808	625.3440	10
5	443.1997	222.1035	426.1732	213.5902	425.1892	213.0982	D	***1210.6699***	605.8386	1193.6434	597.3253	1192.6593	596.8333	9
6	571.2583	286.1328	554.2318	277.6195	553.2477	277.1275	Q	1095.6430	548.3251	1078.6164	539.8118	1077.6324	539.3198	8
7	**668.3111**	334.6592	651.2845	326.1459	650.3005	325.6539	P	***967.5844***	484.2958	950.5578	475.7826	949.5738	475.2905	7
8	783.3380	392.1726	766.3115	383.6594	765.3274	383.1674	D	***870.5316***	435.7694	853.5051	427.2562	852.5210	426.7642	6
9	**985.4970**	493.2521	968.4705	484.7389	967.4865	484.2469	K	755.5047	378.2560	738.4781	369.7427			5
10	1169.6182	585.3127	1152.5916	576.7995	1151.6076	576.3075	K	***553.3457***	277.1765	536.3191	268.6632			4
11	**1266.6710**	633.8391	1249.6444	625.3258	1248.6604	624.8338	P	***369.2245***	185.1159	352.1979	176.6026			3
12	**1363.7237**	682.3655	1346.6972	673.8522	1345.7132	673.3602	P	***272.1717***	136.5895	255.1452	128.0762			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LDLGEDYPSGKKR**
Found in **O43143**, Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2

Match to Query 8298: 1602.825648 from(802.420100,2+) intensity(50729.6211)
Title: File1332 Spectrum10904 scans: 12145
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

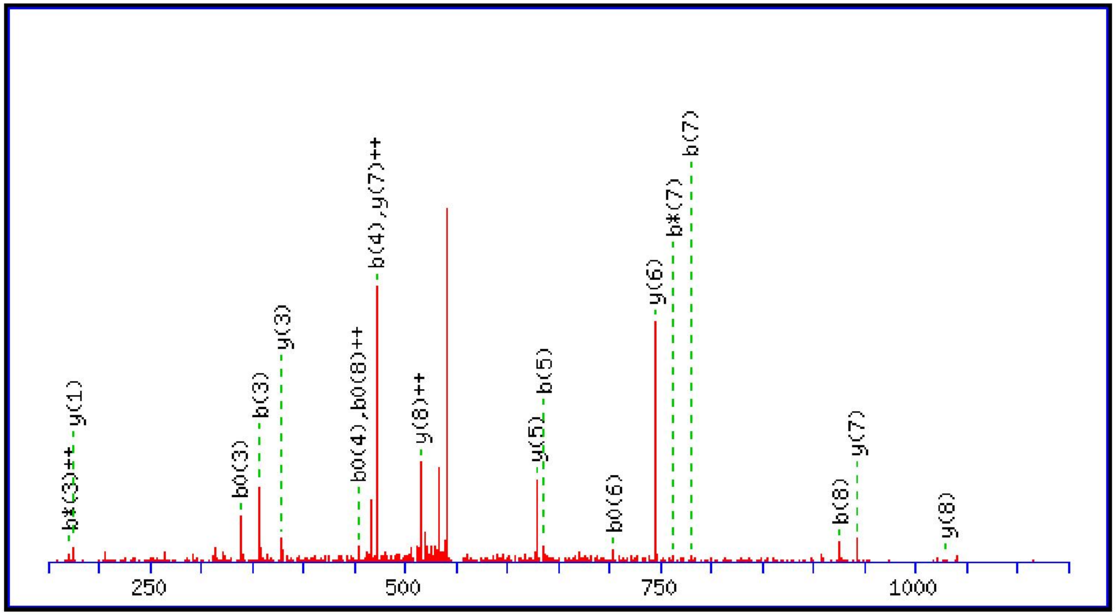
Monoisotopic mass of neutral peptide Mr(calc): 1602.8253
Fixed modifications: Carbamidomethyl (C) (apply to specified resi
Variable modifications:
K11 : Propionyl (K)
K12 : Propionyl-Methylation (K)
Ions Score: 31 **Expect:** 0.76
Matches : 14/114 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							13
2	229.1183	115.0628			211.1077	106.0575	D	1490.7486	745.8779	1473.7220	737.3646	1472.7380	736.8726	12
3	342.2023	171.6048			324.1918	162.5995	L	1375.7216	688.3644	1358.6951	679.8512	1357.7110	679.3592	11
4	399.2238	200.1155			381.2132	191.1103	G	***1262.6375***	631.8224	1245.6110	623.3091	1244.6270	622.8171	10
5	528.2664	264.6368			510.2558	255.6316	E	***1205.6161***	603.3117	1188.5895	594.7984	1187.6055	594.3064	9
6	***643.2933***	322.1503			625.2828	313.1450	D	***1076.5735***	538.7904	1059.5469	530.2771	1058.5629	529.7851	8
7	806.3567	403.6820			788.3461	394.6767	Y	***961.5465***	481.2769	944.5200	472.7636	943.5360	472.2716	7
8	***903.4094***	452.2084			885.3989	443.2031	P	798.4832	399.7452	781.4567	391.2320	780.4726	390.7400	6
9	990.4415	495.7244			972.4309	486.7191	S	701.4305	351.2189	684.4039	342.7056	683.4199	342.2136	5
10	1047.4629	524.2351			1029.4524	515.2298	G	***614.3984***	307.7028	597.3719	299.1896			4
11	***1231.5841***	616.2957	1214.5576	607.7824	1213.5735	607.2904	K	557.3770	279.1921	540.3504	270.6788			3
12	***1429.7209***	715.3641	1412.6944	706.8508	1411.7104	706.3588	K	***373.2558***	187.1315	356.2292	178.6183			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ASKDYSGFR**
Found in **G3XAA8**, La ribonucleoprotein domain family, member 4, isoform CRA_j OS=Homo sapiens GN=LARP4 PE=2 SV=1

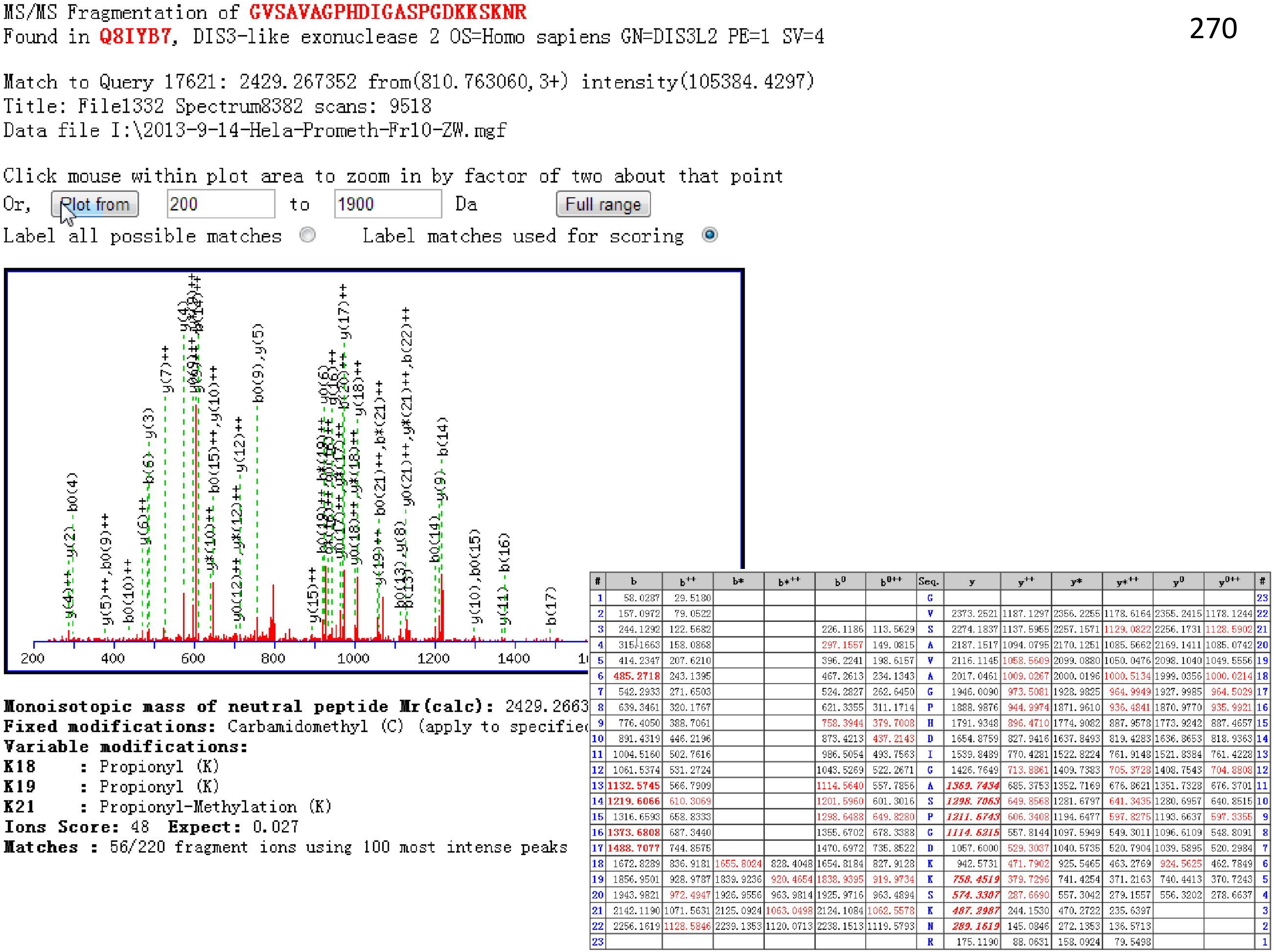
Match to Query 2199: 1099.528908 from(550.771730,2+) intensity(348793.2813)
Title: File1332 Spectrum8043 scans: 9165
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1099.5298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-Methylation (K)
Ions Score: 48 **Expect:** 0.0032
Matches : 19/84 fragment ions using 27 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							9
2	159.0764	80.0418			141.0659	71.0366	S	***1029.5000***	515.2536	1012.4734	506.7404	1011.4894	506.2483	8
3	***357.2132***	179.1103	340.1867	170.5970	339.2027	170.1050	K	***942.4680***	471.7376	925.4414	463.2243	924.4574	462.7323	7
4	***472.2402***	236.6237	455.2136	228.1105	454.2296	227.6185	D	***744.3311***	372.6692	727.3046	364.1559	726.3206	363.6639	6
5	***635.3035***	318.1554	618.2770	309.6421	617.2930	309.1501	Y	***629.3042***	315.1557	612.2776	306.6425	611.2936	306.1504	5
6	722.3355	361.6714	705.3090	353.1581	704.3250	352.6661	S	466.2409	233.6241	449.2143	225.1108	448.2303	224.6188	4
7	***779.3570***	390.1821	762.3305	381.6689	761.3464	381.1769	G	***379.2088***	190.1081	362.1823	181.5948			3
8	***926.4254***	463.7164	909.3989	455.2031	908.4149	454.7111	F	322.1874	161.5973	305.1608	153.0840			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GVSAVAGPHDIGASPGDKKSKNR**
Found in **Q8IYB7**, DIS3-like exonuclease 2 OS=Homo sapiens GN=DIS3L2 PE=1 SV=4

Match to Query 17621: 2429.267352 from(810.763060,3+) intensity(105384.4297)
Title: File1332 Spectrum8382 scans: 9518
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.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 ●

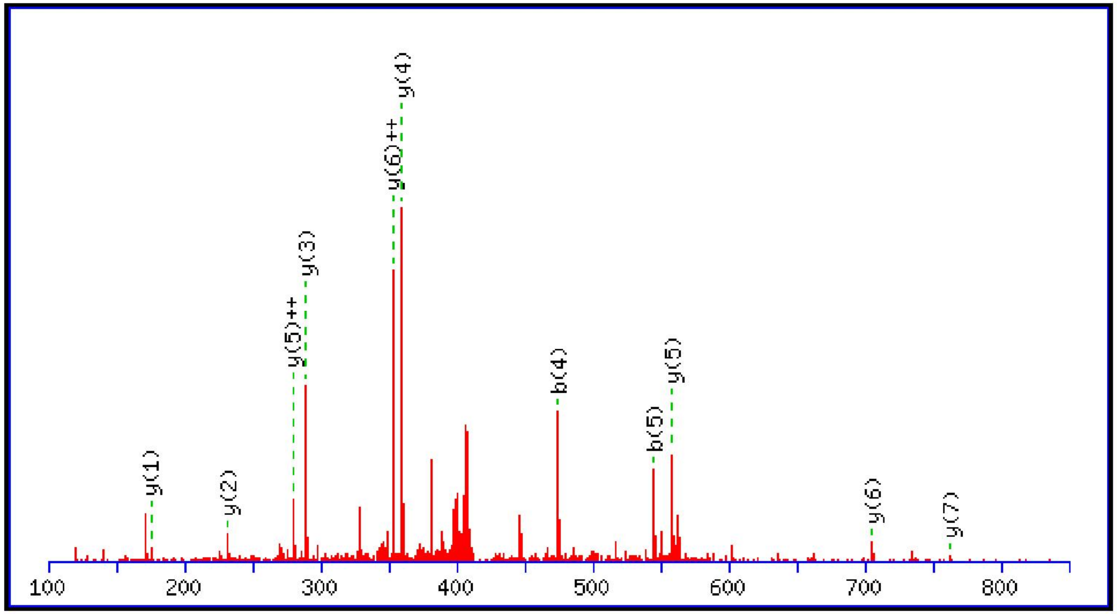
Monoisotopic mass of neutral peptide Mr(calc): 2429.2663
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K18 : Propionyl (K)
K19 : Propionyl (K)
K21 : Propionyl-Methylation (K)
Ions Score: 48 **Expect:** 0.027
Matches : 56/220 fragment ions using 100 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	58.0287	29.5180					G							23
2	157.0972	79.0522					V	2373.2521	1187.1297	2356.2255	1178.6164	2355.2415	1178.1244	22
3	244.1292	122.5682			226.1186	113.5629	S	2274.1837	1137.5955	2257.1571	1129.0822	2256.1731	1128.5902	21
4	315.1663	158.0868			297.1557	149.0815	A	2187.1517	1094.0795	2170.1251	1085.5662	2169.1411	1085.0742	20
5	414.2347	207.6210			396.2241	198.6157	V	2116.1145	1058.5609	2099.0880	1050.0476	2098.1040	1049.5556	19
6	**485.2718**	243.1395			467.2613	234.1343	A	2017.0461	1009.0267	2000.0196	1000.5134	1999.0356	1000.0214	18
7	542.2933	271.6503			524.2827	262.6450	G	1946.0090	973.5081	1928.9825	964.9949	1927.9985	964.5029	17
8	639.3461	320.1767			621.3355	311.1714	P	1888.9876	944.9974	1871.9610	936.4841	1870.9770	935.9921	16
9	776.4050	388.7061			758.3944	379.7008	H	1791.9348	896.4710	1774.9082	887.9578	1773.9242	887.4657	15
10	891.4319	446.2196			873.4213	437.2143	D	1654.8759	827.9416	1637.8493	819.4283	1636.8653	818.9363	14
11	1004.5160	502.7616			986.5054	493.7563	I	1539.8489	770.4281	1522.8224	761.9148	1521.8384	761.4228	13
12	1061.5374	531.2724			1043.5269	522.2671	G	1426.7649	713.8861	1409.7383	705.3728	1408.7543	704.8808	12
13	**1132.5745**	566.7909			1114.5640	557.7856	A	***1369.7434***	685.3753	1352.7169	676.8621	1351.7328	676.3701	11
14	**1219.6066**	610.3069			1201.5960	601.3016	S	***1298.7063***	649.8568	1281.6797	641.3435	1280.6957	640.8515	10
15	1316.6593	658.8333			1298.6488	649.8280	P	***1211.6743***	606.3408	1194.6477	597.8275	1193.6637	597.3355	9
16	**1373.6808**	687.3440			1355.6702	678.3388	G	***1114.6215***	557.8144	1097.5949	549.3011	1096.6109	548.8091	8
17	**1488.7077**	744.8575			1470.6972	735.8522	D	1057.6000	529.3037	1040.5735	520.7904	1039.5895	520.2984	7
18	1672.8289	836.9181	1655.8024	828.4048	1654.8184	827.9128	K	942.5731	471.7902	925.5465	463.2769	924.5625	462.7849	6
19	1856.9501	928.9787	1839.9236	920.4654	1838.9395	919.9734	K	***758.4519***	379.7296	741.4254	371.2163	740.4413	370.7243	5
20	1943.9821	972.4947	1926.9556	963.9814	1925.9716	963.4894	S	***574.3307***	287.6690	557.3042	279.1557	556.3202	278.6637	4
21	2142.1190	1071.5631	2125.0924	1063.0498	2124.1084	1062.5578	K	***487.2987***	244.1530	470.2722	235.6397			3
22	2256.1619	1128.5846	2239.1353	1120.0713	2238.1513	1119.5793	N	***289.1619***	145.0846	272.1353	136.5713			2
23							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AGFKAGGR**
Found in **Q9H9A6**, Leucine-rich repeat-containing protein 40 OS=Homo sapiens GN=LRRC40 PE=1 SV=1

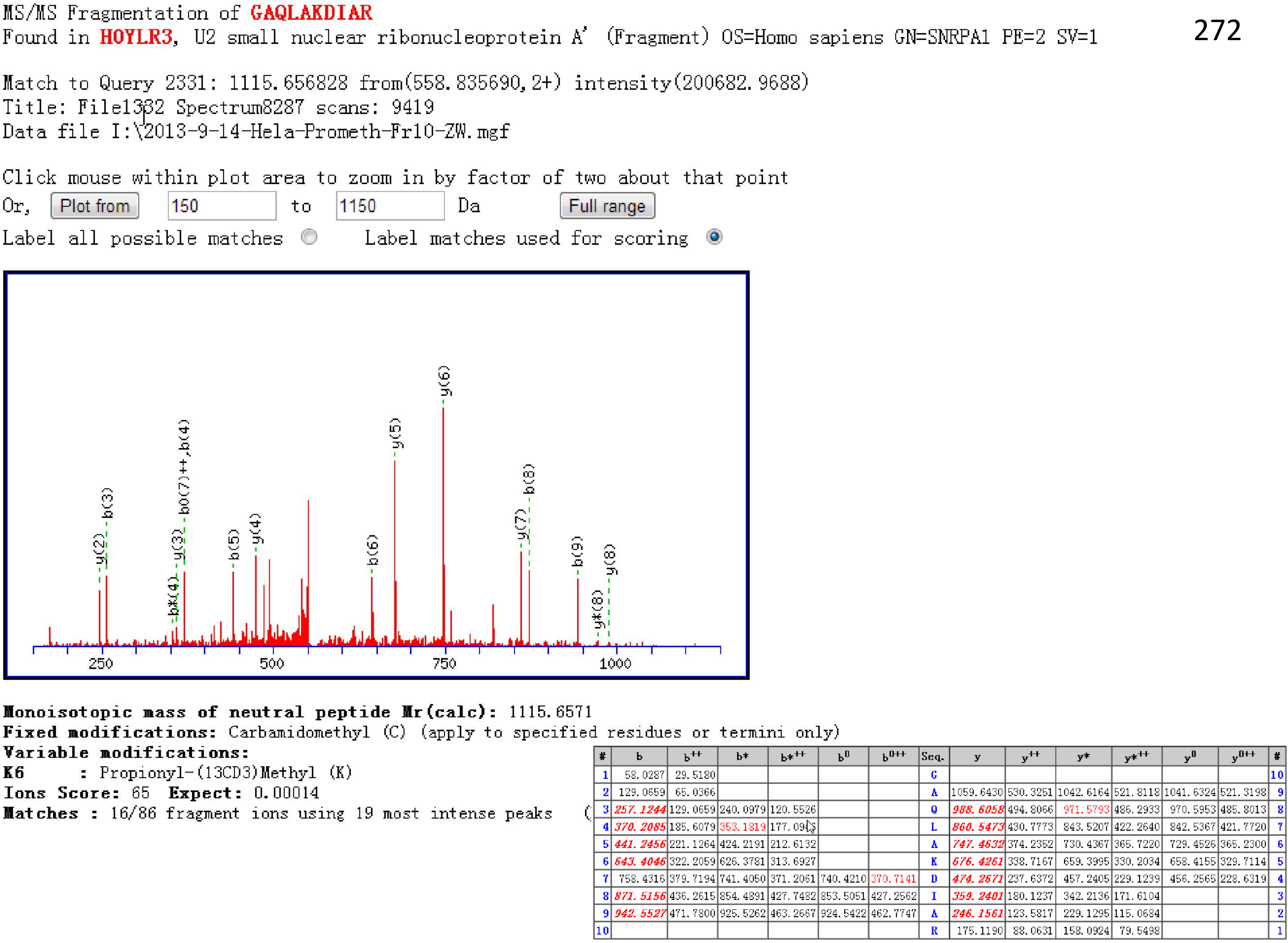
Match to Query 466: 832.454808 from(417.234680,2+) intensity(115552.1172)
Title: File1332 Spectrum4990 scans: 5984
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 832.4555
Fixed modifications: Carbamidomethyl (C) (apply to specified residues o
Variable modifications:
K4 : Propionyl-Methylation (K)
Ions Score: 53 **Expect:** 0.0019
Matches : 11/50 fragment ions using 21 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.0444	36.5258			A					8
2	129.0659	65.0366			G	***762.4257***	381.7165	745.3992	373.2032	7
3	276.1343	138.5708			F	***705.4042***	353.2058	688.3777	344.6925	6
4	**474.2711**	237.6392	457.2445	229.1259	K	***558.3358***	279.6715	541.3093	271.1583	5
5	**545.3082**	273.1577	528.2817	264.6445	A	***360.1990***	180.6031	343.1724	172.0899	4
6	602.3297	301.6685	585.3031	293.1552	G	***289.1619***	145.0846	272.1353	136.5713	3
7	659.3511	330.1792	642.3246	321.6659	G	***232.1404***	116.5738	215.1139	108.0606	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **GAQLAKDIAR**
Found in **H0YLR3**, U2 small nuclear ribonucleoprotein A' (Fragment) OS=Homo sapiens GN=SNRPA1 PE=2 SV=1

Match to Query 2331: 1115.656828 from(558.835690,2+) intensity(200682.9688)
Title: File1332 Spectrum8287 scans: 9419
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.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 ●

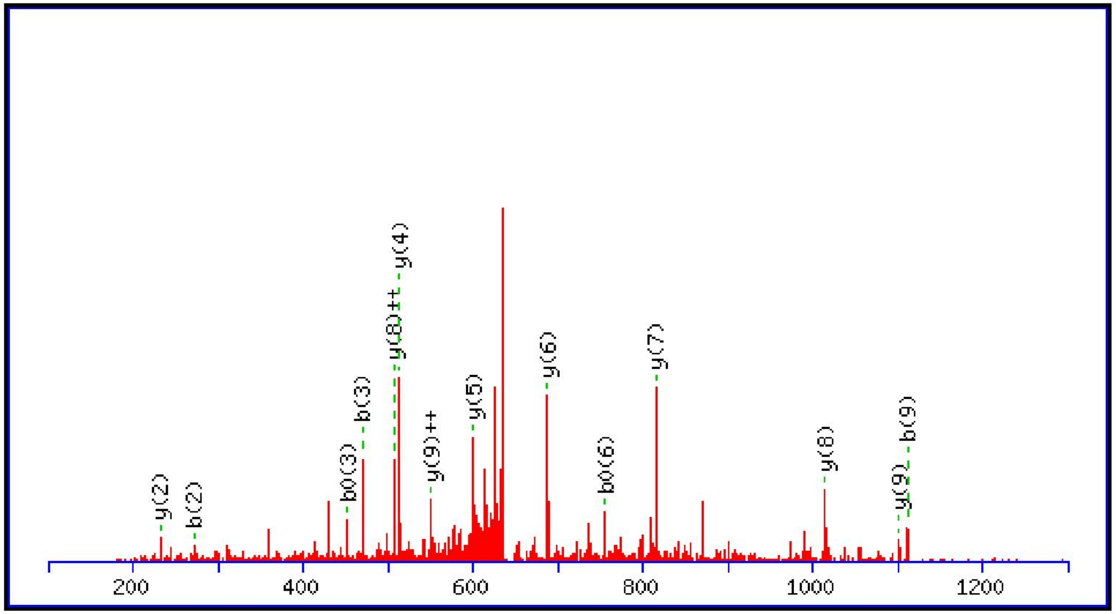
Monoisotopic mass of neutral peptide Mr(calc): 1115.6571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 65 **Expect:** 0.00014
Matches : 16/86 fragment ions using 19 most intense peaks (

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	129.0659	65.0366					A	1059.6430	530.3251	1042.6164	521.8118	1041.6324	521.3198	9
3	***257.1244***	129.0659	240.0979	120.5526			Q	***988.6058***	494.8066	971.5793	486.2933	970.5953	485.8013	8
4	***370.2085***	185.6079	353.1819	177.09[illegible]			L	***860.5473***	430.7773	843.5207	422.2640	842.5367	421.7720	7
5	***441.2456***	221.1264	424.2191	212.6132			A	***747.4632***	374.2352	730.4367	365.7220	729.4526	365.2300	6
6	***643.4046***	322.2059	626.3781	313.6927			K	***676.4261***	338.7167	659.3995	330.2034	658.4155	329.7114	5
7	758.4316	379.7194	741.4050	371.2061	740.4210	370.7141	D	***474.2671***	237.6372	457.2405	229.1239	456.2565	228.6319	4
8	***871.5156***	436.2615	854.4891	427.7482	853.5051	427.2562	I	***359.2401***	180.1237	342.2136	171.6104			3
9	***942.5527***	471.7800	925.5262	463.2667	924.5422	462.7747	A	***246.1561***	123.5817	229.1295	115.0684			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KSKESSPKGR**
Found in **P51608**, Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1

Match to Query 6792: 1284.703948 from(643.359250,2+) intensity(320897.4375)
Title: File1335 Spectrum6402 scans: 7141
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.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 ●



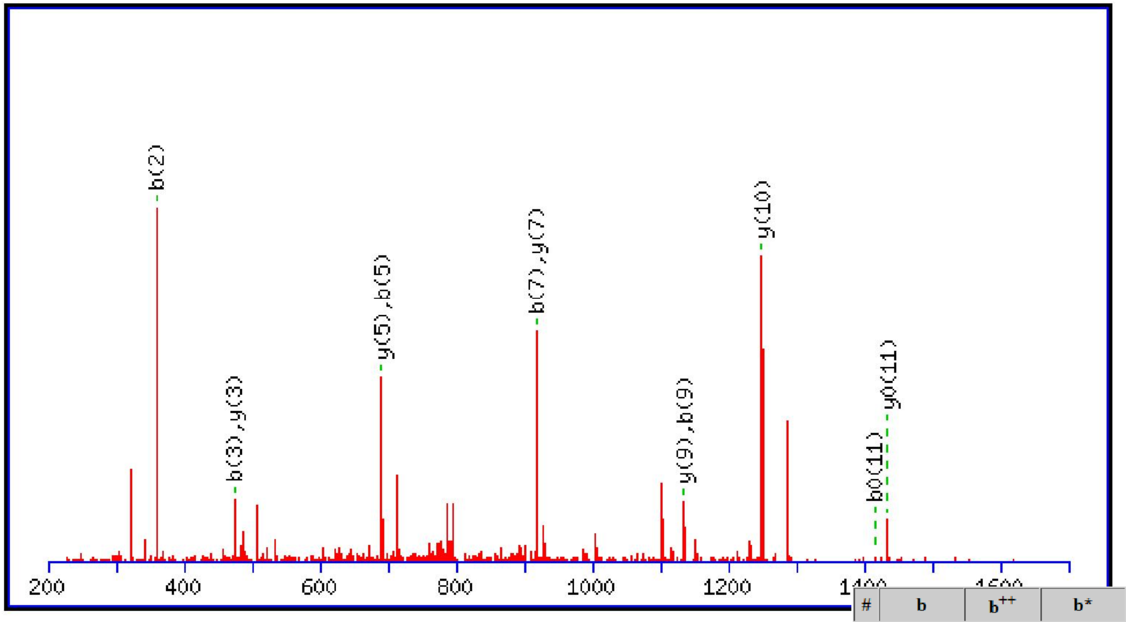
```
Monoisotopic mass of neutral peptide Mr(calc): 1284.7037
Fixed modifications: Carbamidomethyl (C) (apply to specified residu
Variable modifications:
K1      : Propionyl (K)
K3      : Propionyl-Methylation (K)
K8      : Propionyl (K)
Ions Score: 37  Expect: 0.15
Matches : 14/98 fragment ions using 33 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							10
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	S	***1101.5899***	551.2986	1084.5633	542.7853	1083.5793	542.2933	9
3	**470.2973**	235.6523	453.2708	227.1390	452.2867	226.6470	K	***1014.5578***	507.7826	997.5313	499.2693	996.5473	498.7773	8
4	599.3399	300.1736	582.3134	291.6603	581.3293	291.1683	E	***816.4210***	408.7141	799.3945	400.2009	798.4104	399.7089	7
5	686.3719	343.6896	669.3454	335.1763	668.3614	334.6843	S	***687.3784***	344.1928	670.3519	335.6796	669.3678	335.1876	6
6	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	S	***600.3464***	300.6768	583.3198	292.1636	582.3358	291.6715	5
7	870.4567	435.7320	853.4302	427.2187	852.4462	426.7267	P	***513.3144***	257.1608	496.2878	248.6475			4
8	1054.5779	527.7926	1037.5514	519.2793	1036.5673	518.7873	K	416.2616	208.6344	399.2350	200.1212			3
9	**1111.5994**	556.3033	1094.5728	547.7900	1093.5888	547.2980	G	***232.1404***	116.5738	215.1139	108.0606			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **RKDTDDIESPKR**
Found in **G5EA03**, LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=2 SV=1

Match to Query 9205: 1606.867288 from(804.440920,2+) intensity(470954.3125)
Title: File1311 Spectrum7603 scans: 8199
Data file I:\2013-9-13-Hela-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



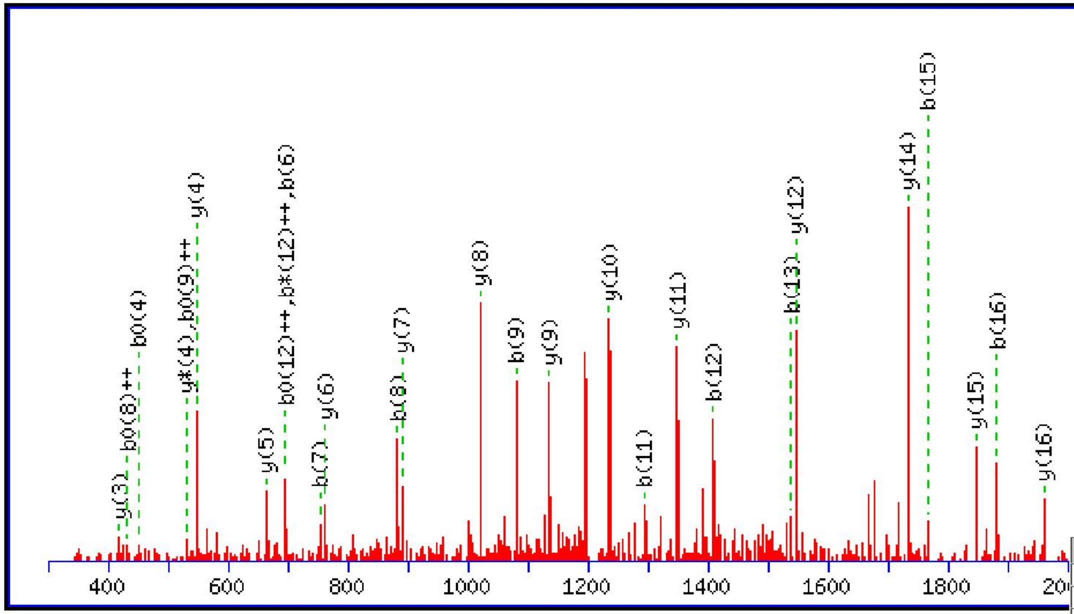
```
Monoisotopic mass of neutral peptide Mr(calc): 1606.8
Fixed modifications: Carbamidomethyl (C) (apply to sp
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K11     : Propionyl-(13CD3)Methyl (K)
Ions Score: 38   Expect: 0.16
Matches : 13/122 fragment ions using 14 most intense
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	***359.2674***	180.1373	342.2409	171.6241			K	1451.7769	726.3921	1434.7504	717.8788	1433.7664	717.3868	11
3	***474.2943***	237.6508	457.2678	229.1375	456.2838	228.6455	D	**1249.6179**	625.3126	1232.5914	616.7993	1231.6074	616.3073	10
4	575.3420	288.1746	558.3155	279.6614	557.3315	279.1694	T	**1134.5910**	567.7991	1117.5644	559.2859	1116.5804	558.7938	9
5	***690.3690***	345.6881	673.3424	337.1748	672.3584	336.6828	D	1033.5433	517.2753	1016.5168	508.7620	1015.5327	508.2700	8
6	805.3959	403.2016	788.3694	394.6883	787.3853	394.1963	D	**918.5164**	459.7618	901.4898	451.2485	900.5058	450.7565	7
7	***918.4800***	459.7436	901.4534	451.2303	900.4694	450.7383	I	803.4894	402.2483	786.4629	393.7351	785.4788	393.2431	6
8	1047.5226	524.2649	1030.4960	515.7516	1029.5120	515.2596	E	**690.4054**	345.7063	673.3788	337.1930	672.3948	336.7010	5
9	***1134.5546***	567.7809	1117.5280	559.2677	1116.5440	558.7757	S	561.3628	281.1850	544.3362	272.6717	543.3522	272.1797	4
10	1231.6074	616.3073	1214.5808	607.7940	1213.5968	607.3020	P	**474.3307**	237.6690	457.3042	229.1557			3
11	***1433.7664***	717.3868	1416.7398	708.8735	1415.7558	708.3815	K	377.2780	189.1426	360.2514	180.6293			2
12							R	175.1190	88.0631	158.0924	79.5498			1

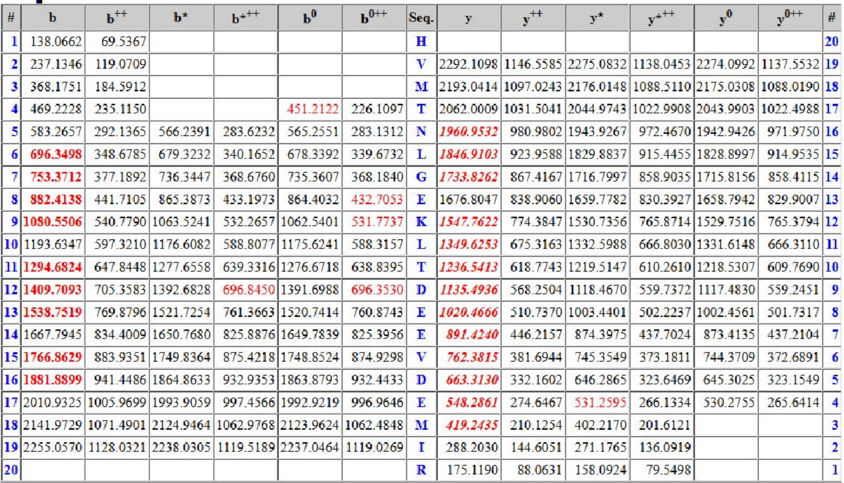
MS/MS Fragmentation of **HVMTNLGEKLTDEEVDEMIR**
Found in **P62158**, Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2

Match to Query 18308: 2428.162208 from(1215.088380,2+) intensity(122499.4766)
Title: File1319 Spectrum17600 scans: 18605
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2428.1614
Fixed modifications: Carbamidomethyl (C) (apply to specified residu
Variable modifications:
K9      : Propionyl-Methylation (K)
Ions Score: 100  Expect: 7.8e-008
Matches : 28/208 fragment ions using 34 most intense peaks    (help)
```

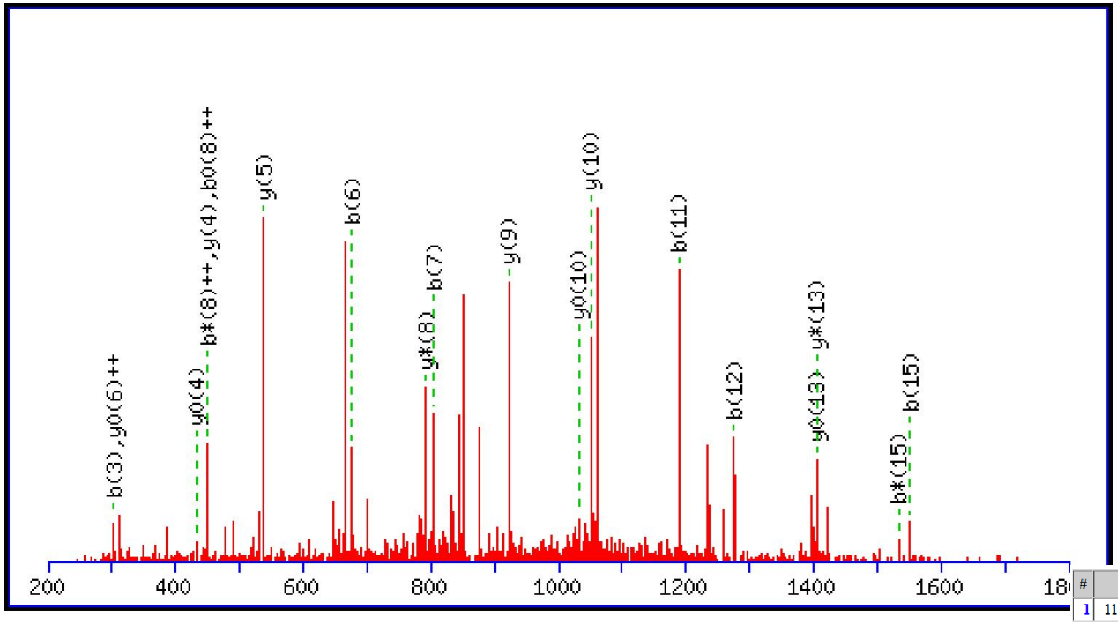


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							20
2	237.1346	119.0709					V	2292.1098	1146.5585	2275.0832	1138.0453	2274.0992	1137.5532	19
3	368.1751	184.5912					M	2193.0414	1097.0243	2176.0148	1088.5110	2175.0308	1088.0190	18
4	469.2228	235.1150			451.2122	226.1097	T	2062.0009	1031.5041	2044.9743	1022.9908	2043.9903	1022.4988	17
5	583.2657	292.1365	566.2391	283.6232	565.2551	283.1312	N	***1960.9532***	980.9802	1943.9267	972.4670	1942.9426	971.9750	16
6	**696.3498**	348.6785	679.3232	340.1652	678.3392	339.6732	L	***1846.9103***	923.9588	1829.8837	915.4455	1828.8997	914.9535	15
7	**753.3712**	377.1892	736.3447	368.6760	735.3607	368.1840	G	***1733.8262***	867.4167	1716.7997	858.9035	1715.8156	858.4115	14
8	**882.4138**	441.7105	865.3873	433.1973	864.4032	432.7053	E	1676.8047	838.9060	1659.7782	830.3927	1658.7942	829.9007	13
9	**1080.5506**	540.7790	1063.5241	532.2657	1062.5401	531.7737	K	***1547.7622***	774.3847	1530.7356	765.8714	1529.7516	765.3794	12
10	1193.6347	597.3210	1176.6082	588.8077	1175.6241	588.3157	L	***1349.6253***	675.3163	1332.5988	666.8030	1331.6148	666.3110	11
11	**1294.6824**	647.8448	1277.6558	639.3316	1276.6718	638.8395	T	***1236.5413***	618.7743	1219.5147	610.2610	1218.5307	609.7690	10
12	**1409.7093**	705.3583	1392.6828	696.8450	1391.6988	696.3530	D	***1135.4936***	568.2504	1118.4670	559.7372	1117.4830	559.2451	9
13	**1538.7519**	769.8796	1521.7254	761.3663	1520.7414	760.8743	E	***1020.4666***	510.7370	1003.4401	502.2237	1002.4561	501.7317	8
14	1667.7945	834.4009	1650.7680	825.8876	1649.7839	825.3956	E	***891.4240***	446.2157	874.3975	437.7024	873.4135	437.2104	7
15	**1766.8629**	883.9351	1749.8364	875.4218	1748.8524	874.9298	V	***762.3815***	381.6944	745.3549	373.1811	744.3709	372.6891	6
16	**1881.8899**	941.4486	1864.8633	932.9353	1863.8793	932.4433	D	***663.3130***	332.1602	646.2865	323.6469	645.3025	323.1549	5
17	2010.9325	1005.9699	1993.9059	997.4566	1992.9219	996.9646	E	***548.2861***	274.6467	531.2595	266.1334	530.2755	265.6414	4
18	2141.9729	1071.4901	2124.9464	1062.9768	2123.9624	1062.4848	M	***419.2435***	210.1254	402.2170	201.6121			3
19	2255.0570	1128.0321	2238.0305	1119.5189	2237.0464	1119.0269	I	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **NTSAKVELPSSSTSSR**
Found in **C9J2C7**, Protein NT5C1B-RDH14 (Fragment) OS=Homo sapiens GN=NT5C1B-RDH14 PE=4 SV=2

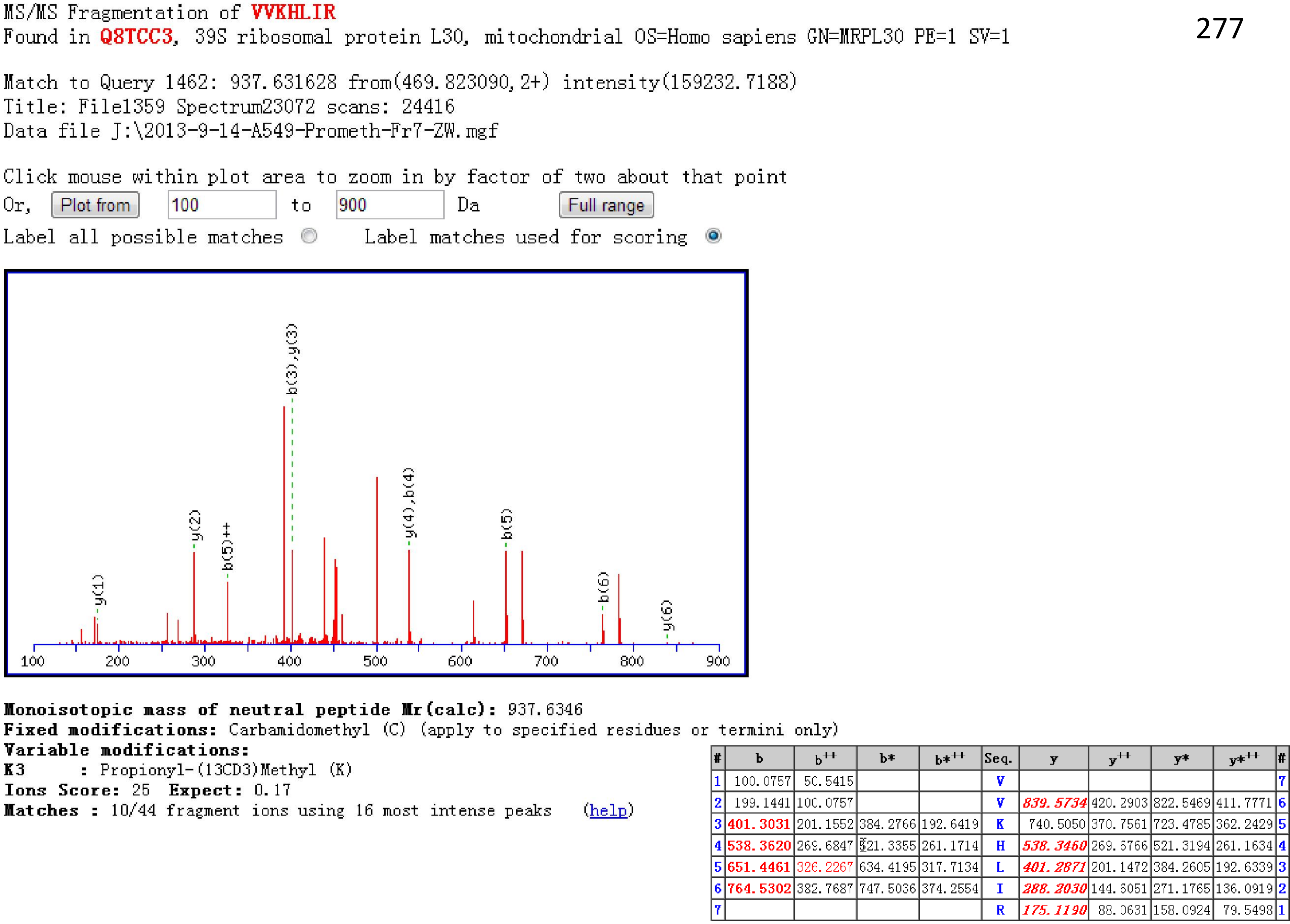
Match to Query 10736: 1723.880108 from(862.947330,2+) intensity(604150.8125)
Title: File1319 Spectrum16970 scans: 17949
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1723.8861
Fixed modifications: Carbamidomethyl (C) (apply to specified residu
Variable modifications:
K5      : Propionyl-(13CD3)Methyl (K)
Ions Score: 27   Expect: 1.6
Matches : 19/176 fragment ions using 30 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							16
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	T	1610.8504	805.9289	1593.8239	797.4156	1592.8399	796.9236	15
3	***303.1299***	152.0686	286.1034	143.5553	285.1193	143.0633	S	1509.8028	755.4050	1492.7762	746.8917	1491.7922	746.3997	14
4	374.1670	187.5872	357.1405	179.0739	356.1565	178.5819	A	1422.7707	711.8890	1405.7442	703.3757	1404.7602	702.8837	13
5	576.3260	288.6667	559.2995	280.1534	558.3155	279.6614	K	1351.7336	676.3704	1334.7071	667.8572	1333.7231	667.3652	12
6	***675.3945***	338.2009	658.3679	329.6876	657.3839	329.1956	V	1149.5746	575.2909	1132.5481	566.7777	1131.5640	566.2857	11
7	***804.4370***	402.7222	787.4105	394.2089	786.4265	393.7169	E	**1050.5062**	525.7567	1033.4796	517.2435	1032.4956	516.7515	10
8	917.5211	459.2642	900.4946	450.7509	899.5105	450.2589	L	**921.4636**	461.2354	904.4371	452.7222	903.4530	452.2302	9
9	1014.5739	507.7906	997.5473	499.2773	996.5633	498.7853	P	808.3795	404.6934	791.3530	396.1801	790.3690	395.6881	8
10	1101.6059	551.3066	1084.5794	542.7933	1083.5953	542.3013	S	711.3268	356.1670	694.3002	347.6537	693.3162	347.1617	7
11	***1188.6379***	594.8226	1171.6114	586.3093	1170.6274	585.8173	S	624.2947	312.6510	607.2682	304.1377	606.2842	303.6457	6
12	***1275.6700***	638.3386	1258.6434	629.8253	1257.6594	629.3333	S	**537.2627**	269.1350	520.2362	260.6217	519.2522	260.1297	5
13	1376.7176	688.8625	1359.6911	680.3492	1358.7071	679.8572	T	**450.2307**	225.6190	433.2041	217.1057	432.2201	216.6137	4
14	1463.7497	732.3785	1446.7231	723.8652	1445.7391	723.3732	S	349.1830	175.0951	332.1565	166.5819	331.1724	166.0899	3
15	***1550.7817***	775.8945	1533.7551	767.3812	1532.7711	766.8892	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **VVKHLIR**
Found in **Q8TCC3**, 39S ribosomal protein L30, mitochondrial OS=Homo sapiens GN=MRPL30 PE=1 SV=1

Match to Query 1462: 937.631628 from(469.823090,2+) intensity(159232.7188)
Title: File1359 Spectrum23072 scans: 24416
Data file J:\2013-9-14-A549-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

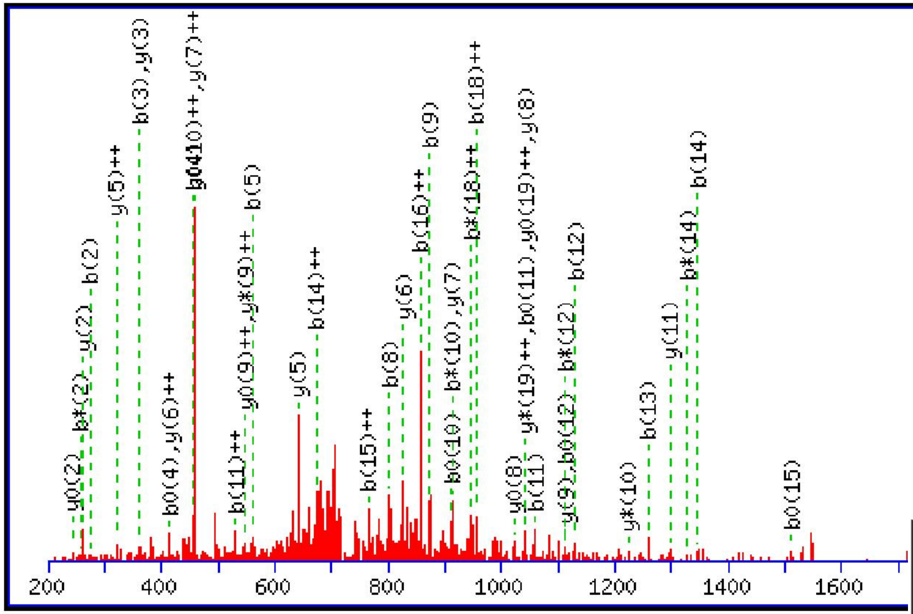
Monoisotopic mass of neutral peptide Mr(calc): 937.6346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 25 **Expect:** 0.17
Matches : 10/44 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	100.0757	50.5415			V					7
2	199.1441	100.0757			V	***839.5734***	420.2903	822.5469	411.7771	6
3	**401.3031**	201.1552	384.2766	192.6419	K	740.5050	370.7561	723.4785	362.2429	5
4	**538.3620**	269.6847	521.3355	261.1714	H	***538.3460***	269.6766	521.3194	261.1634	4
5	**651.4461**	326.2267	634.4195	317.7134	L	***401.2871***	201.1472	384.2605	192.6339	3
6	**764.5302**	382.7687	747.5036	374.2554	I	***288.2030***	144.6051	271.1765	136.0919	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1

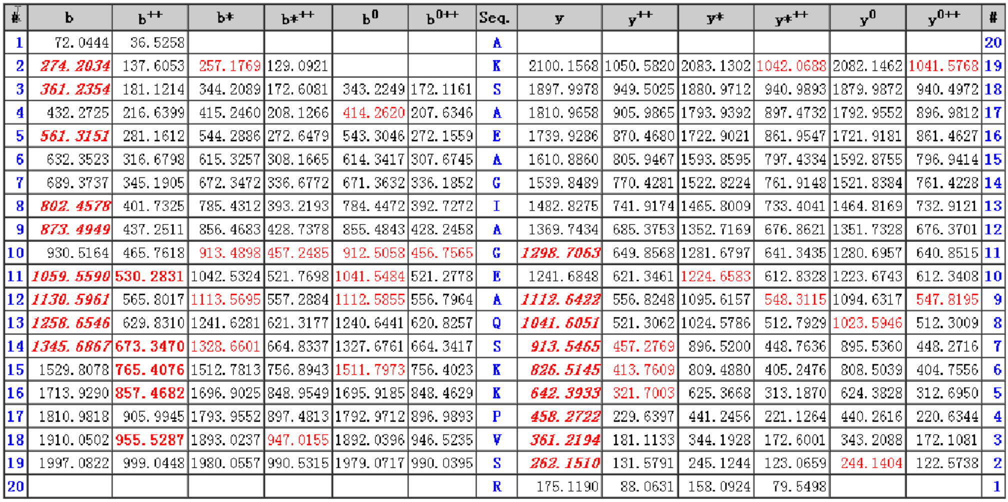
MS/MS Fragmentation of AKSAEAGIAGEAQSKKPVSR
Found in Q7Z478, ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2

Match to Query 14229: 2170.185762 from(724.402530,3+) intensity(27088.4707)
Title: File1359 Spectrum10130 scans: 10868
Data file J:\2013-9-14-A549-Prometh-Fr7-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2170.1866
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K15 : Propionyl (K)
K16 : Propionyl (K)
Ions Score: 42 **Expect:** 0.044
Matches : 45/220 fragment ions using 73 most intense peaks (h

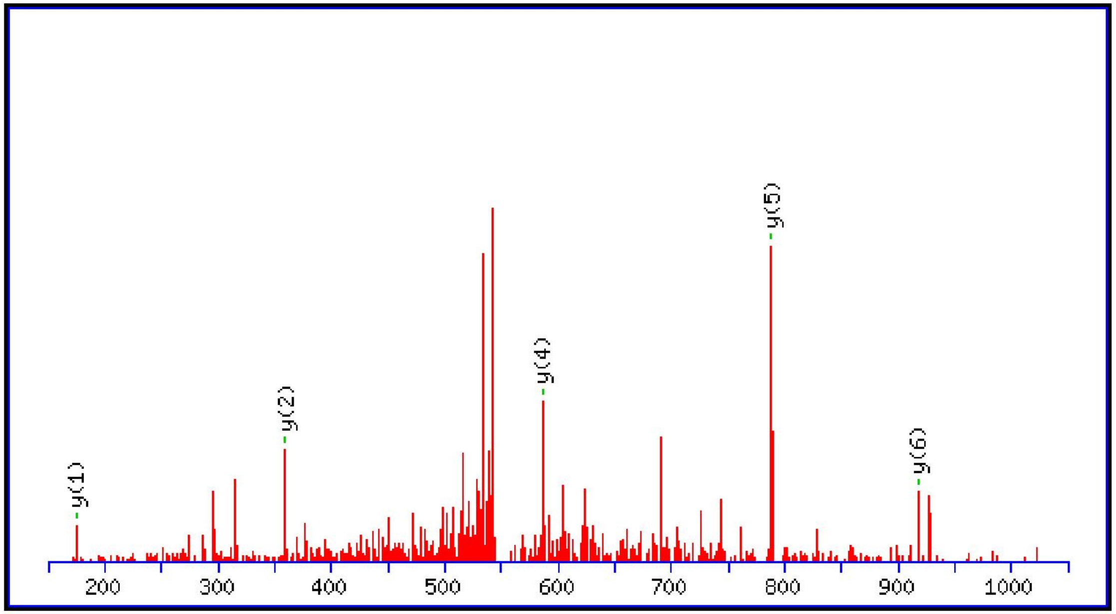


#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							20
2	**274.2034**	137.6053	257.1769	129.0921			K	2100.1568	1050.5820	2083.1302	1042.0688	2082.1462	1041.5768	19
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	S	1897.9978	949.5025	1880.9712	940.9893	1879.9872	940.4972	18
4	432.2725	216.6399	415.2460	208.1266	414.2620	207.6346	A	1810.9658	905.9865	1793.9392	897.4732	1792.9552	896.9812	17
5	**561.3151**	281.1612	544.2886	272.6479	543.3046	272.1559	E	1739.9286	870.4680	1722.9021	861.9547	1721.9181	861.4627	16
6	632.3523	316.6798	615.3257	308.1665	614.3417	307.6745	A	1610.8860	805.9467	1593.8595	797.4334	1592.8755	796.9414	15
7	689.3737	345.1905	672.3472	336.6772	671.3632	336.1852	G	1539.8489	770.4281	1522.8224	761.9148	1521.8384	761.4228	14
8	**802.4578**	401.7325	785.4312	393.2193	784.4472	392.7272	I	1482.8275	741.9174	1465.8009	733.4041	1464.8169	732.9121	13
9	**873.4949**	437.2511	856.4683	428.7378	855.4843	428.2458	A	1369.7434	685.3753	1352.7169	676.8621	1351.7328	676.3701	12
10	930.5164	465.7618	913.4898	457.2485	912.5058	456.7565	G	**1298.7063**	649.8568	1281.6797	641.3435	1280.6957	640.8515	11
11	**1059.5590**	**530.2831**	1042.5324	521.7698	1041.5484	521.2778	E	1241.6848	621.3461	1224.6583	612.8328	1223.6743	612.3408	10
12	**1130.5961**	565.8017	1113.5695	557.2884	1112.5855	556.7964	A	**1112.6422**	556.8248	1095.6157	548.3115	1094.6317	547.8195	9
13	**1258.6546**	629.8310	1241.6281	621.3177	1240.6441	620.8257	Q	**1041.6051**	521.3062	1024.5786	512.7929	1023.5946	512.3009	8
14	**1345.6867**	**673.3470**	1328.6601	664.8337	1327.6761	664.3417	S	**913.5465**	457.2769	896.5200	448.7636	895.5360	448.2716	7
15	1529.8078	**765.4076**	1512.7813	756.8943	1511.7973	756.4023	K	**826.5145**	413.7609	809.4880	405.2476	808.5039	404.7556	6
16	1713.9290	**857.4682**	1696.9025	848.9549	1695.9185	848.4629	K	**642.3933**	321.7003	625.3668	313.1870	624.3828	312.6950	5
17	1810.9818	905.9945	1793.9552	897.4813	1792.9712	896.9893	P	**458.2722**	229.6397	441.2456	221.1264	440.2616	220.6344	4
18	1910.0502	**955.5287**	1893.0237	947.0155	1892.0396	946.5235	V	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
19	1997.0822	999.0448	1980.0557	990.5315	1979.0717	990.0395	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
20							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KEKNIKR**
Found in **M0QYQ7**, Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1

Match to Query 2841: 1100.681248 from(551.347900,2+) intensity(40095.6563)
Title: File1359 Spectrum7767 scans: 8407
Data file J:\2013-9-14-A549-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 150 to 1050 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



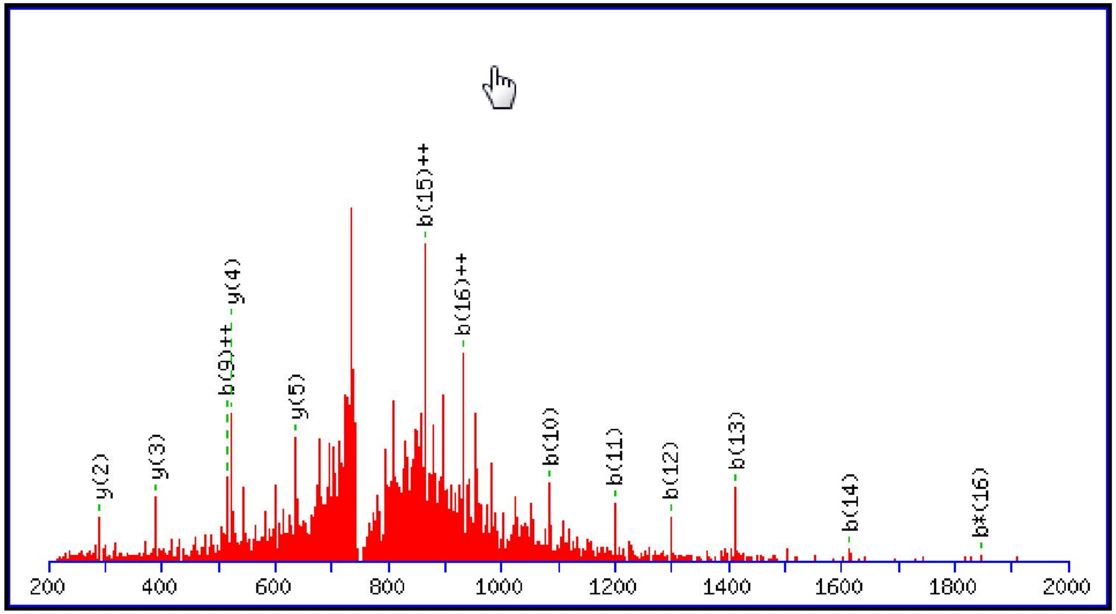
Monoisotopic mass of neutral peptide Mr(calc): 1100.6826
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 35 **Expect:** 0.072
Matches : 5/60 fragment ions using 9 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							7
2	314.1710	157.5892	297.1445	149.0759	296.1605	148.5839	E	*917.5687*	459.2880	900.5422	450.7747	899.5582	450.2827	6
3	516.3301	258.6687	499.3035	250.1554	498.3195	249.6634	K	*788.5261*	394.7667	771.4996	386.2534			5
4	630.3730	315.6901	613.3464	307.1769	612.3624	306.6848	N	*586.3671*	293.6872	569.3406	285.1739			4
5	743.4571	372.2322	726.4305	363.7189	725.4465	363.2269	I	472.3242	236.6657	455.2976	228.1525			3
6	927.5782	464.2928	910.5517	455.7795	909.5677	455.2875	K	*359.2401*	180.1237	342.2136	171.6104			2
7							R	*175.1190*	88.0631	158.0924	79.5498			1

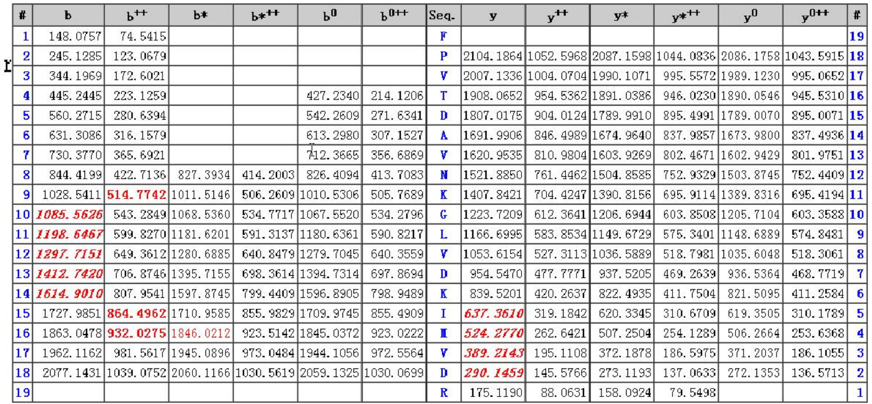
MS/MS Fragmentation of **FPVTDAVNKGLVDKIMVDR**
Found in **Q15149**, Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3

Match to Query 14835: 2250.248082 from(751.089970,3+) intensity(81341.5703)
Title: File1359 Spectrum19464 scans: 20597
Data file J:\2013-9-14-A549-Prometh-Fr7-ZW.mgf

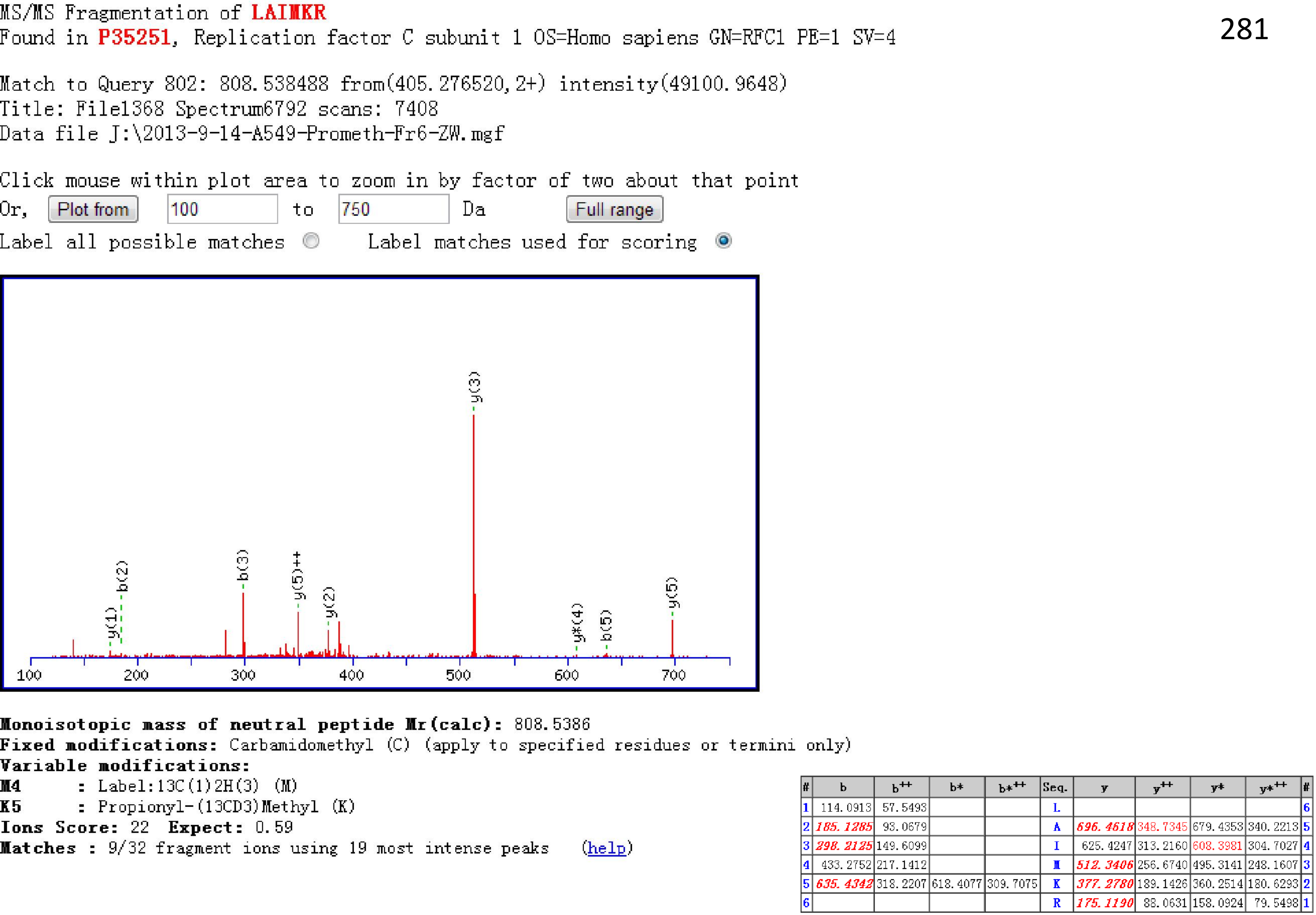
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2250.2475
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K9 : Propionyl (K)
K14 : Propionyl-(13CD3)Methyl (K)
M16 : Label:13C(1)2H(3) (M)
Ions Score: 33 **Expect:** 0.27
Matches : 13/194 fragment ions using 17 most intense peaks (help)



#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							19
2	245.1285	123.0679					P	2104.1864	1052.5968	2087.1598	1044.0836	2086.1758	1043.5915	18
3	344.1969	172.6021					V	2007.1336	1004.0704	1990.1071	995.5572	1989.1230	995.0652	17
4	445.2445	223.1259			427.2340	214.1206	T	1908.0652	954.5362	1891.0386	946.0230	1890.0546	945.5310	16
5	560.2715	280.6394			542.2609	271.6341	D	1807.0175	904.0124	1789.9910	895.4991	1789.0070	895.0071	15
6	631.3086	316.1579			613.2980	307.1527	A	1691.9906	846.4989	1674.9640	837.9857	1673.9800	837.4936	14
7	730.3770	365.6921			712.3665	356.6869	V	1620.9535	810.9804	1603.9269	802.4671	1602.9429	801.9751	13
8	844.4199	422.7136	827.3934	414.2003	826.4094	413.7083	N	1521.8850	761.4462	1504.8585	752.9329	1503.8745	752.4409	12
9	1028.5411	**514.7742**	1011.5146	506.2609	1010.5306	505.7689	K	1407.8421	704.4247	1390.8156	695.9114	1389.8316	695.4194	11
10	***1085.5626***	543.2849	1068.5360	534.7717	1067.5520	534.2796	G	1223.7209	612.3641	1206.6944	603.8508	1205.7104	603.3588	10
11	***1198.6467***	599.8270	1181.6201	591.3137	1180.6361	590.8217	L	1166.6995	583.8534	1149.6729	575.3401	1148.6889	574.8481	9
12	***1297.7151***	649.3612	1280.6885	640.8479	1279.7045	640.3559	V	1053.6154	527.3113	1036.5889	518.7981	1035.6048	518.3061	8
13	***1412.7420***	706.8746	1395.7155	698.3614	1394.7314	697.8694	D	954.5470	477.7771	937.5205	469.2639	936.5364	468.7719	7
14	***1614.9010***	807.9541	1597.8745	799.4409	1596.8905	798.9489	K	839.5201	420.2637	822.4935	411.7504	821.5095	411.2584	6
15	1727.9851	**864.4962**	1710.9585	855.9829	1709.9745	855.4909	I	***637.3610***	319.1842	620.3345	310.6709	619.3505	310.1789	5
16	1863.0478	**932.0275**	1846.0212	923.5142	1845.0372	923.0222	M	***524.2770***	262.6421	507.2504	254.1289	506.2664	253.6368	4
17	1962.1162	981.5617	1945.0896	973.0484	1944.1056	972.5564	V	***389.2143***	195.1108	372.1878	186.5975	371.2037	186.1055	3
18	2077.1431	1039.0752	2060.1166	1030.5619	2059.1325	1030.0699	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
19							R	175.1190	88.0631	158.0924	79.5498			1



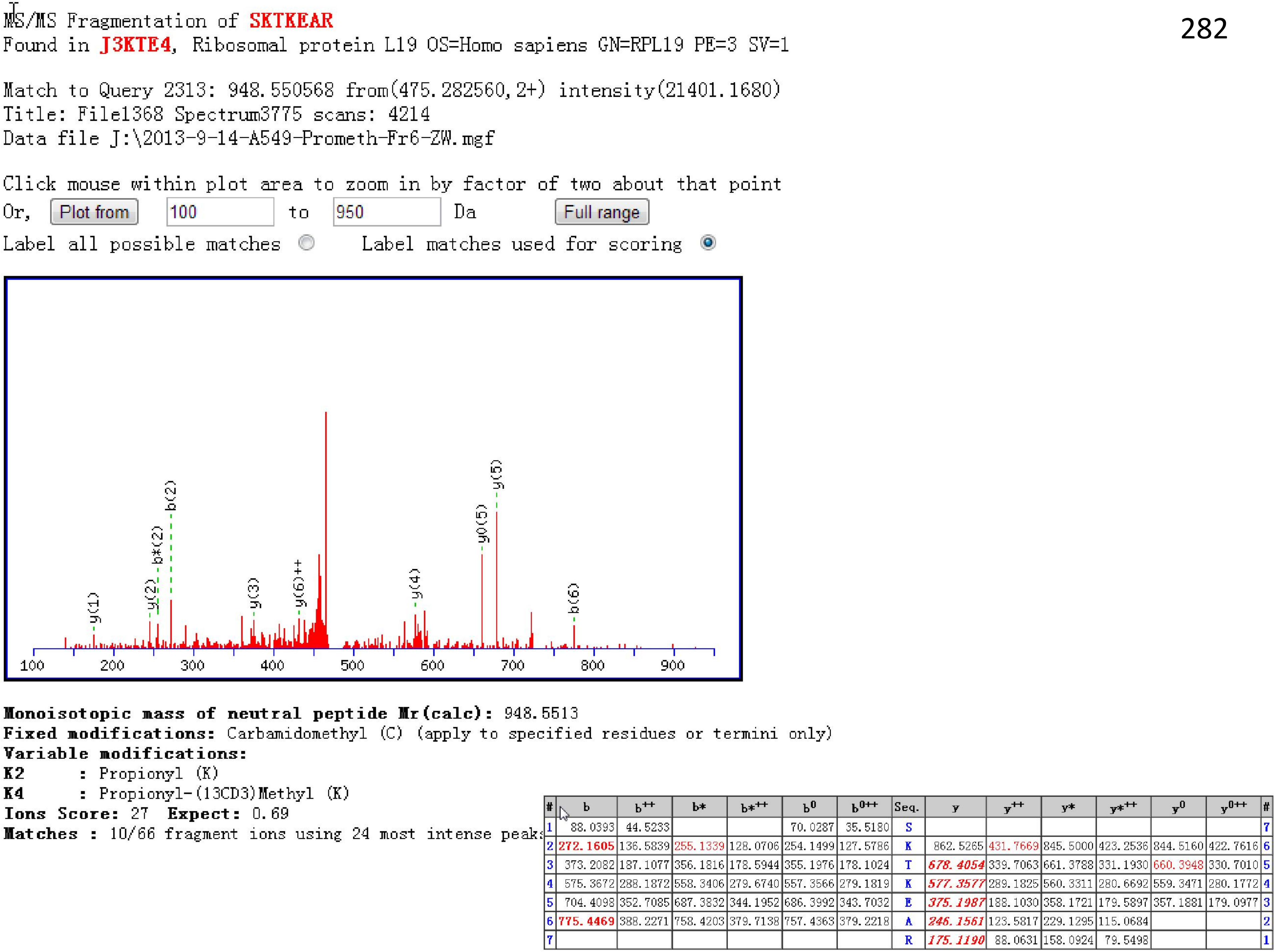
MS/MS Fragmentation of **LAIMKR**
Found in **P35251**, Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4

Match to Query 802: 808.538488 from(405.276520,2+) intensity(49100.9648)
Title: File1368 Spectrum6792 scans: 7408
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 808.5386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Label:13C(1)2H(3) (M)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 22 **Expect:** 0.59
Matches : 9/32 fragment ions using 19 most intense peaks (help)

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.0913	57.5493			L					6
2	***185.1285***	93.0679			A	***696.4618***	348.7345	679.4353	340.2213	5
3	***298.2125***	149.6099			I	625.4247	313.2160	608.3981	304.7027	4
4	433.2752	217.1412			M	***512.3406***	256.6740	495.3141	248.1607	3
5	***635.4342***	318.2207	618.4077	309.7075	K	***377.2780***	189.1426	360.2514	180.6293	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **SKTKEAR**
Found in **J3KTE4**, Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3 SV=1

Match to Query 2313: 948.550568 from(475.282560,2+) intensity(21401.1680)
Title: File1368 Spectrum3775 scans: 4214
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

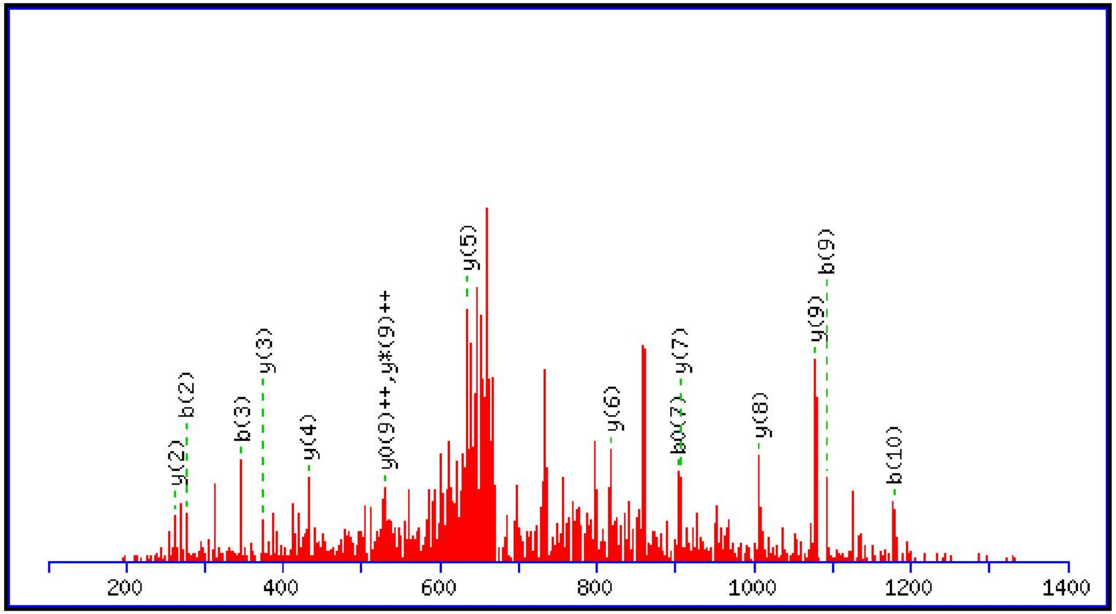
Monoisotopic mass of neutral peptide Mr(calc): 948.5513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 27 **Expect:** 0.69
Matches : 10/66 fragment ions using 24 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							7
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	K	862.5265	431.7669	845.5000	423.2536	844.5160	422.7616	6
3	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	T	***678.4054***	339.7063	661.3788	331.1930	660.3948	330.7010	5
4	575.3672	288.1872	558.3406	279.6740	557.3566	279.1819	K	***577.3577***	289.1825	560.3311	280.6692	559.3471	280.1772	4
5	704.4098	352.7085	687.3832	344.1952	686.3992	343.7032	E	***375.1987***	188.1030	358.1721	179.5897	357.1881	179.0977	3
6	**775.4469**	388.2271	758.4203	379.7138	757.4363	379.2218	A	***246.1561***	123.5817	229.1295	115.0684			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FQATSKKGISR**
Found in **Q96ST2**, Protein IWS1 homolog OS=Homo sapiens GN=IWS1 PE=1 SV=2

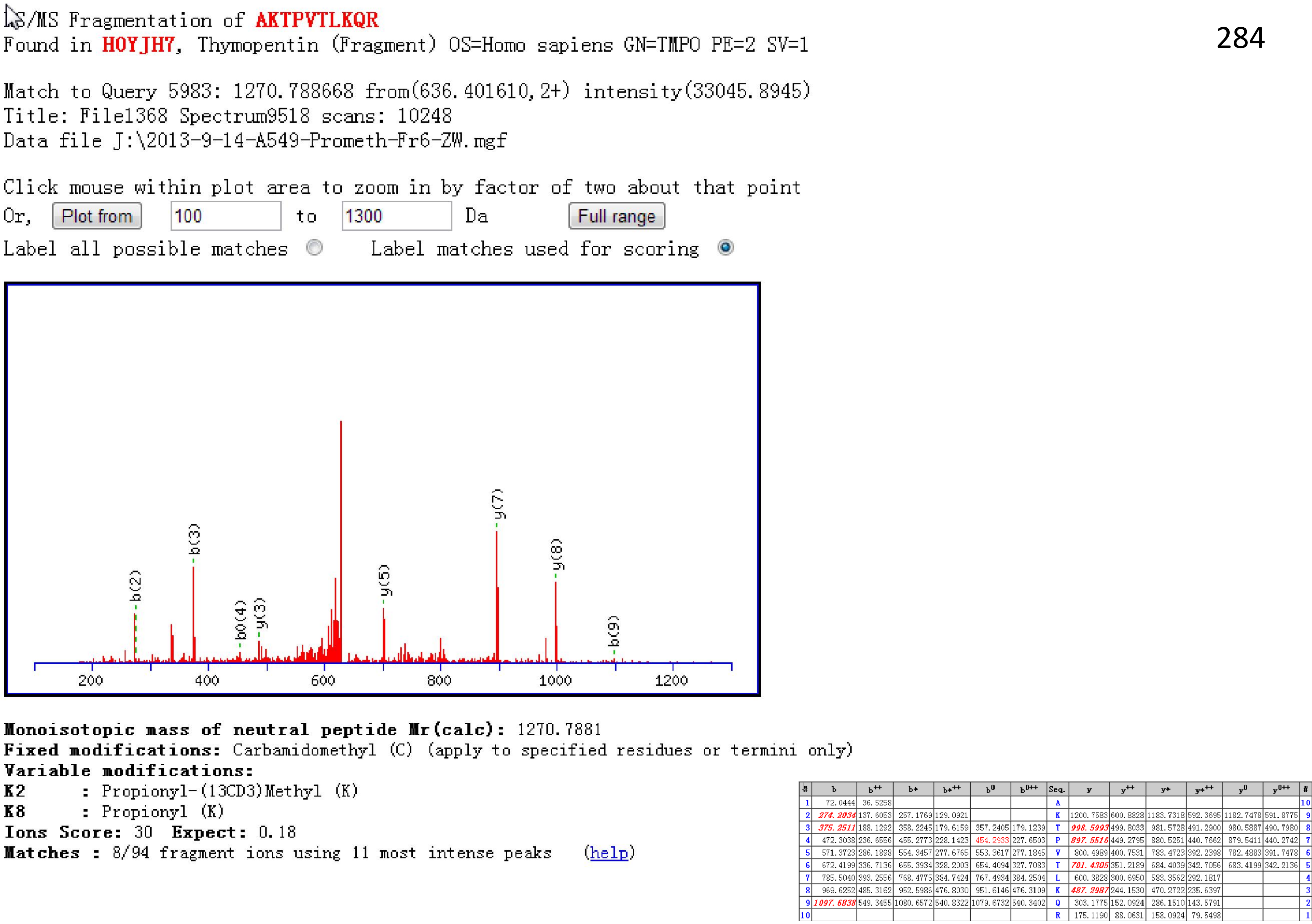
Match to Query 6627: 1351.773168 from(676.893860,2+) intensity(22756.0352)
Title: File1368 Spectrum8828 scans: 9530
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1351.7732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : Propionyl (K)
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.48
Matches : 15/110 fragment ions using 48 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415					F							11
2	**276.1343**	138.5708	259.1077	130.0575			Q	1205.7121	603.3597	1188.6855	594.8464	1187.7015	594.3544	10
3	**347.1714**	174.0893	330.1448	165.5761			A	***1077.6535***	539.3304	1060.6270	530.8171	1059.6430	530.3251	9
4	448.2191	224.6132	431.1925	216.0999	430.2085	215.6079	T	***1006.6164***	503.8118	989.5899	495.2986	988.6058	494.8066	8
5	535.2511	268.1292	518.2245	259.6159	517.2405	259.1239	S	***905.5687***	453.2880	888.5422	444.7747	887.5582	444.2827	7
6	719.3723	360.1898	702.3457	351.6765	701.3617	351.1845	K	***818.5367***	409.7720	801.5102	401.2587	800.5261	400.7667	6
7	921.5313	461.2693	904.5047	452.7560	903.5207	452.2640	K	***634.4155***	317.7114	617.3890	309.1981	616.4050	308.7061	5
8	978.5527	489.7800	961.5262	481.2667	960.5422	480.7747	G	***432.2565***	216.6319	415.2300	208.1186	414.2459	207.6266	4
9	**1091.6368**	546.3220	1074.6103	537.8088	1073.6262	537.3168	I	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	**1178.6688**	589.8381	1161.6423	581.3248	1160.6583	580.8328	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKTPVTLKQR**
Found in **H0YJH7**, Thymopentin (Fragment) OS=Homo sapiens GN=TMPO PE=2 SV=1

Match to Query 5983: 1270.788668 from(636.401610,2+) intensity(33045.8945)
Title: File1368 Spectrum9518 scans: 10248
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.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 ●

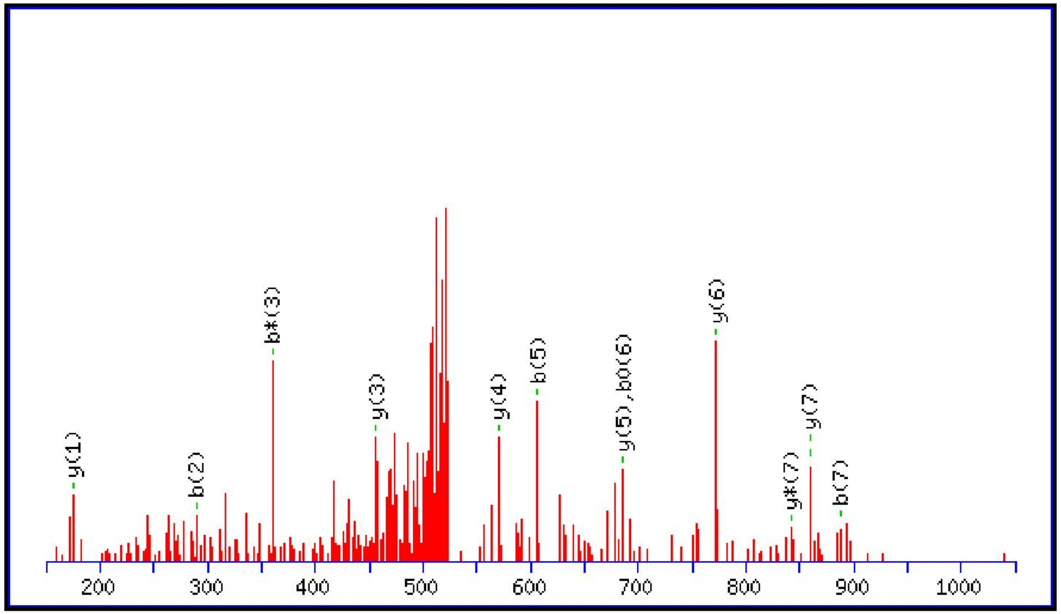
Monoisotopic mass of neutral peptide Mr(calc): 1270.7881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 30 **Expect:** 0.18
Matches : 8/94 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							10
2	***274.2034***	137.6053	257.1769	129.0921			K	1200.7583	600.8828	1183.7318	592.3695	1182.7478	591.8775	9
3	***375.2511***	188.1292	358.2245	179.6159	357.2405	179.1239	T	***998.5993***	499.8033	981.5728	491.2900	980.5887	490.7980	8
4	472.3038	236.6556	455.2773	228.1423	454.2933	227.6503	P	***897.5516***	449.2795	880.5251	440.7662	879.5411	440.2742	7
5	571.3723	286.1898	554.3457	277.6765	553.3617	277.1845	V	800.4989	400.7531	783.4723	392.2398	782.4883	391.7478	6
6	672.4199	336.7136	655.3934	328.2003	654.4094	327.7083	T	***701.4305***	351.2189	684.4039	342.7056	683.4199	342.2136	5
7	785.5040	393.2556	768.4775	384.7424	767.4934	384.2504	L	600.3828	300.6950	583.3562	292.1817			4
8	969.6252	485.3162	952.5986	476.8030	951.6146	476.3109	K	***487.2987***	244.1530	470.2722	235.6397			3
9	***1097.6838***	549.3455	1080.6572	540.8322	1079.6732	540.3402	Q	303.1775	152.0924	286.1510	143.5791			2
10							R	175.1190	88.0631	158.0924	79.5498			1

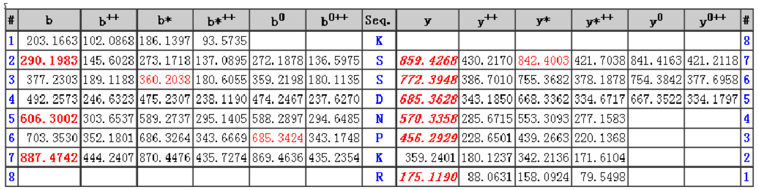
MS/MS Fragmentation of **KSSDNPKR**
Found in **Q96L73**, Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific OS=Homo sapiens GN=NSD1 PE=1 SV=1

Match to Query 3622: 1060.578108 from(531.296330,2+) intensity(6147.5298)
Title: File1368 Spectrum3200 scans: 3592
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1060.5785
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 31 **Expect:** 0.26
Matches : 12/74 fragment ions using 25 most intense peaks (help)

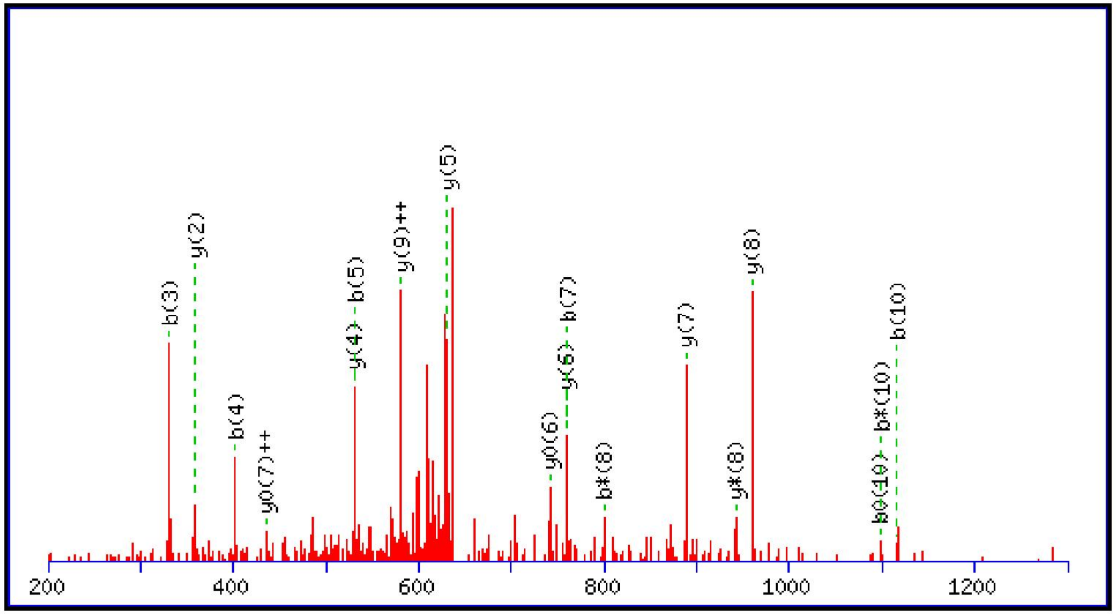


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	S	***859.4268***	430.2170	842.4003	421.7038	841.4163	421.2118	7
3	377.2303	189.1188	360.2038	180.6055	359.2198	180.1135	S	***772.3948***	386.7010	755.3682	378.1878	754.3842	377.6958	6
4	492.2573	246.6323	475.2307	238.1190	474.2467	237.6270	D	***685.3628***	343.1850	668.3362	334.6717	667.3522	334.1797	5
5	**606.3002**	303.6537	589.2737	295.1405	588.2897	294.6485	N	***570.3358***	285.6715	553.3093	277.1583			4
6	703.3530	352.1801	686.3264	343.6669	685.3424	343.1748	P	***456.2929***	228.6501	439.2663	220.1368			3
7	**887.4742**	444.2407	870.4476	435.7274	869.4636	435.2354	K	359.2401	180.1237	342.2136	171.6104			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of AGKAEQTGNKR
Found in Q5UIP0, Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2

Match to Query 6142: 1288.700648 from(645.357600,2+) intensity(19868.2969)
Title: File1368 Spectrum3927 scans: 4376
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



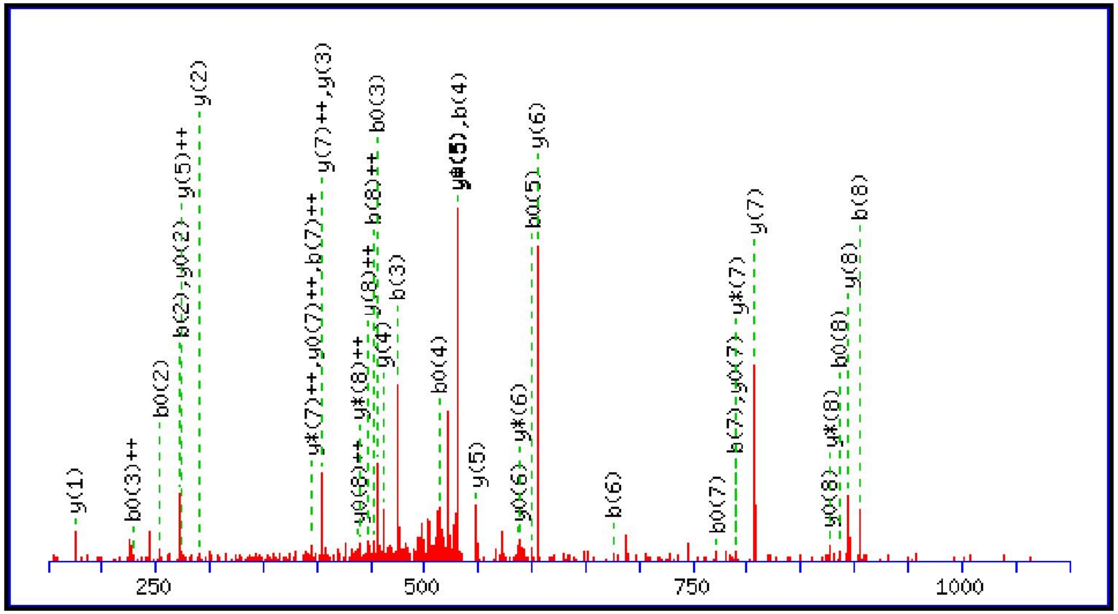
Monoisotopic mass of neutral peptide Mr(calc): 1288.7008
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 34 **Expect:** 0.19
Matches : 18/100 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							11
2	129.0659	65.0366					G	1218.6710	609.8391	1201.6444	601.3258	1200.6604	600.8338	10
3	***331.2249***	166.1161	314.1983	157.6028			K	1161.6495	581.3284	1144.6229	572.8151	1143.6389	572.3231	9
4	***402.2620***	201.6346	385.2354	193.1214			A	***959.4905***	480.2489	942.4639	471.7356	941.4799	471.2436	8
5	***531.3046***	266.1559	514.2780	257.6427	513.2940	257.1506	E	***888.4534***	444.7303	871.4268	436.2170	870.4428	435.7250	7
6	659.3632	330.1852	642.3366	321.6719	641.3526	321.1799	Q	***759.4108***	380.2090	742.3842	371.6958	741.4002	371.2037	6
7	***760.4108***	380.7091	743.3843	372.1958	742.4003	371.7038	T	***631.3522***	316.1797	614.3257	307.6665	613.3416	307.1745	5
8	817.4323	409.2198	800.4057	400.7065	799.4217	400.2145	G	***530.3045***	265.6559	513.2780	257.1426			4
9	931.4752	466.2412	914.4487	457.7280	913.4647	457.2360	N	473.2831	237.1452	456.2565	228.6319			3
10	***1115.5964***	558.3018	1098.5699	549.7886	1097.5858	549.2966	K	***359.2401***	180.1237	342.2136	171.6104			2
11							R	175.1190	88.0631	158.0924	79.5498			1

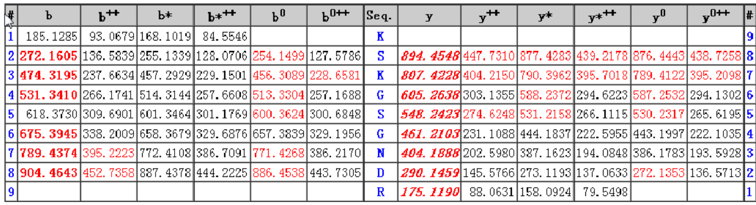
MS/MS Fragmentation of **KSKGSGNDR**
Found in **Q9UHG0**, Doublecortin domain-containing protein 2 OS=Homo sapiens GN=DCDC2 PE=1 SV=2

Match to Query 3865: 1077.567968 from(539.791260,2+) intensity(67747.7891)
Title: File1368 Spectrum2886 scans: 3262
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1077.5687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 41 **Expect:** 0.028
Matches : 39/92 fragment ions using 78 most intense peaks (help)

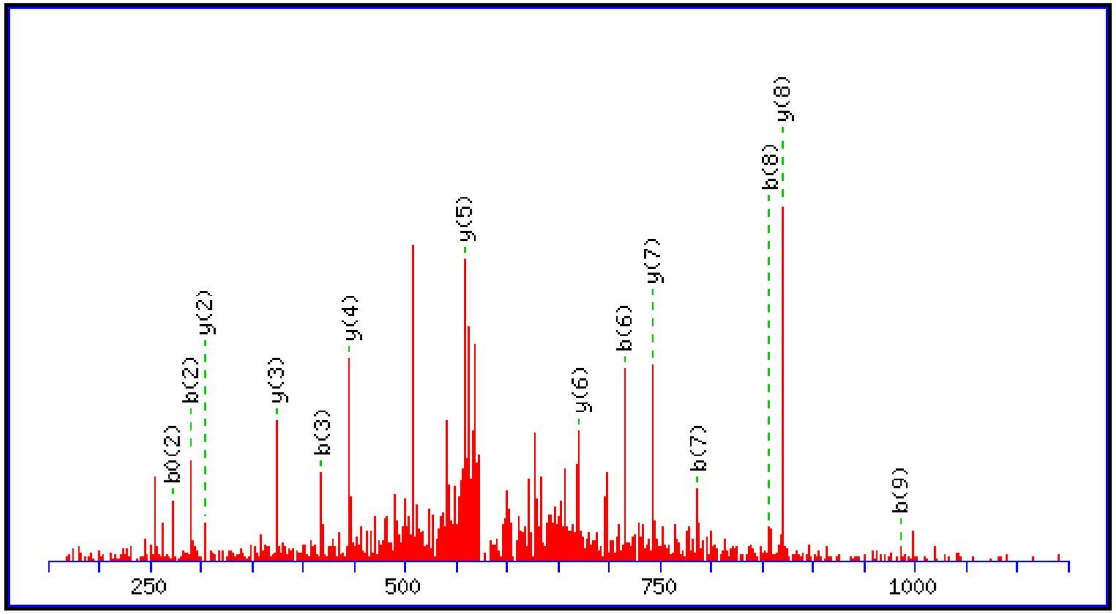


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							9
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	S	***894.4548***	447.7310	877.4283	439.2178	876.4443	438.7258	8
3	**474.3195**	237.6634	457.2929	229.1501	456.3089	228.6581	K	***807.4228***	404.2150	790.3962	395.7018	789.4122	395.2098	7
4	**531.3410**	266.1741	514.3144	257.6608	513.3304	257.1688	G	***605.2638***	303.1355	588.2372	294.6223	587.2532	294.1302	6
5	618.3730	309.6901	601.3464	301.1769	600.3624	300.6848	S	***548.2423***	274.6248	531.2158	266.1115	530.2317	265.6195	5
6	**675.3945**	338.2009	658.3679	329.6876	657.3839	329.1956	G	***461.2103***	231.1088	444.1837	222.5955	443.1997	222.1035	4
7	**789.4374**	395.2223	772.4108	386.7091	771.4268	386.2170	N	***404.1888***	202.5980	387.1623	194.0848	386.1783	193.5928	3
8	**904.4643**	452.7358	887.4378	444.2225	886.4538	443.7305	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

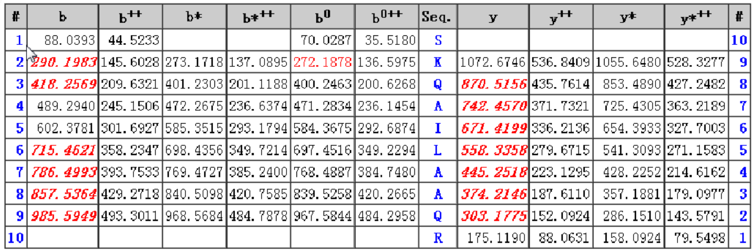
MS/MS Fragmentation of **SKQAILAAQR**
Found in **O60869-2**, Isoform 2 of Endothelial differentiation-related factor 1 OS=Homo sapiens GN=EDF1

Match to Query 4896: 1158.697728 from(580.356140,2+) intensity(51590.8477)
Title: File1368 Spectrum9029 scans: 9739
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1158.6993
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.0079
Matches : 14/88 fragment ions using 30 most intense peaks (help)

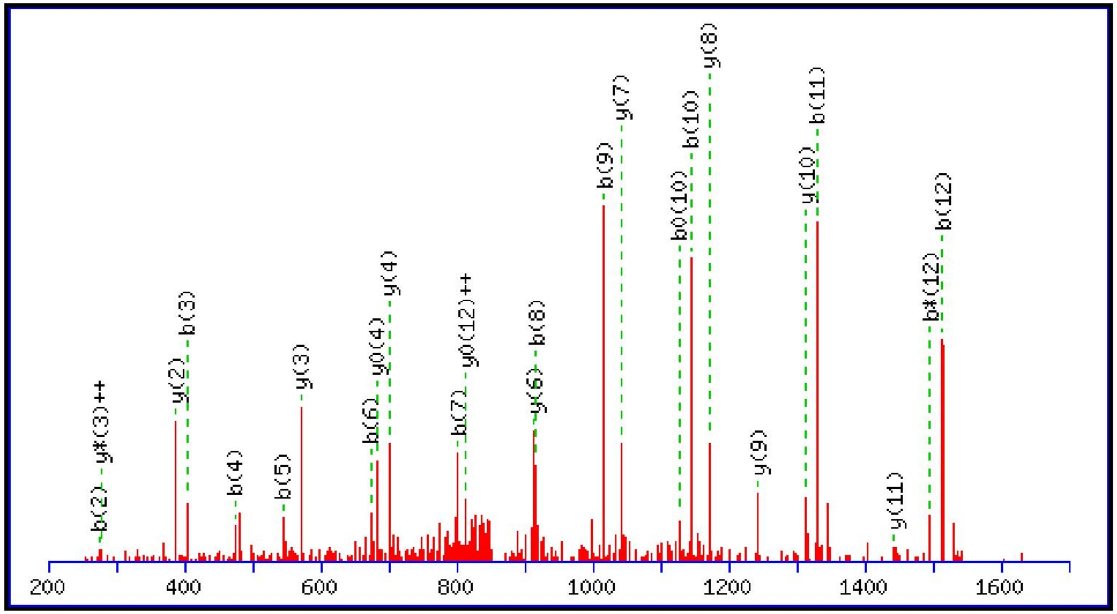


#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	88.0393	44.5233			70.0287	35.5180	S					10
2	***290.1983***	145.6028	273.1718	137.0895	272.1878	136.5975	K	1072.6746	536.8409	1055.6480	528.3277	9
3	***418.2569***	209.6321	401.2303	201.1188	400.2463	200.6268	Q	***870.5156***	435.7614	853.4890	427.2482	8
4	489.2940	245.1506	472.2675	236.6374	471.2834	236.1454	A	***742.4570***	371.7321	725.4305	363.2189	7
5	602.3781	301.6927	585.3515	293.1794	584.3675	292.6874	I	***671.4199***	336.2136	654.3933	327.7003	6
6	***715.4621***	358.2347	698.4356	349.7214	697.4516	349.2294	L	***558.3358***	279.6715	541.3093	271.1583	5
7	***786.4993***	393.7533	769.4727	385.2400	768.4887	384.7480	A	***445.2518***	223.1295	428.2252	214.6162	4
8	***857.5364***	429.2718	840.5098	420.7585	839.5258	420.2665	A	***374.2146***	187.6110	357.1881	179.0977	3
9	***985.5949***	493.3011	968.5684	484.7878	967.5844	484.2958	Q	***303.1775***	152.0924	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498	1

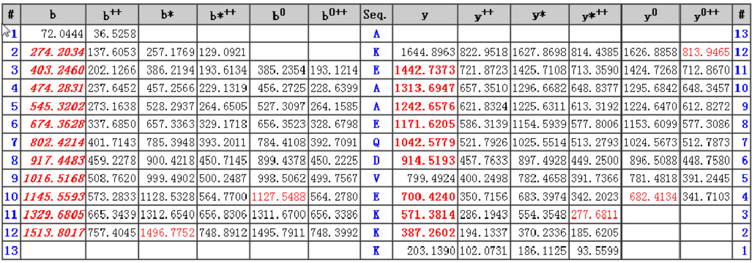
MS/MS Fragmentation of **AKEAAEQDVEKKK**
Found in **J3KS98**, 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 PE=4 SV=1

Match to Query 10247: 1714.928688 from(858.471620,2+) intensity(75932.7734)
Title: File1368 Spectrum10291 scans: 11054
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1714.9261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K11 : Propionyl (K)
K12 : Propionyl (K)
K13 : Propionyl (K)
Ions Score: 76 **Expect:** 1.3e-005
Matches : 25/132 fragment ions using 41 most intense peaks (help)

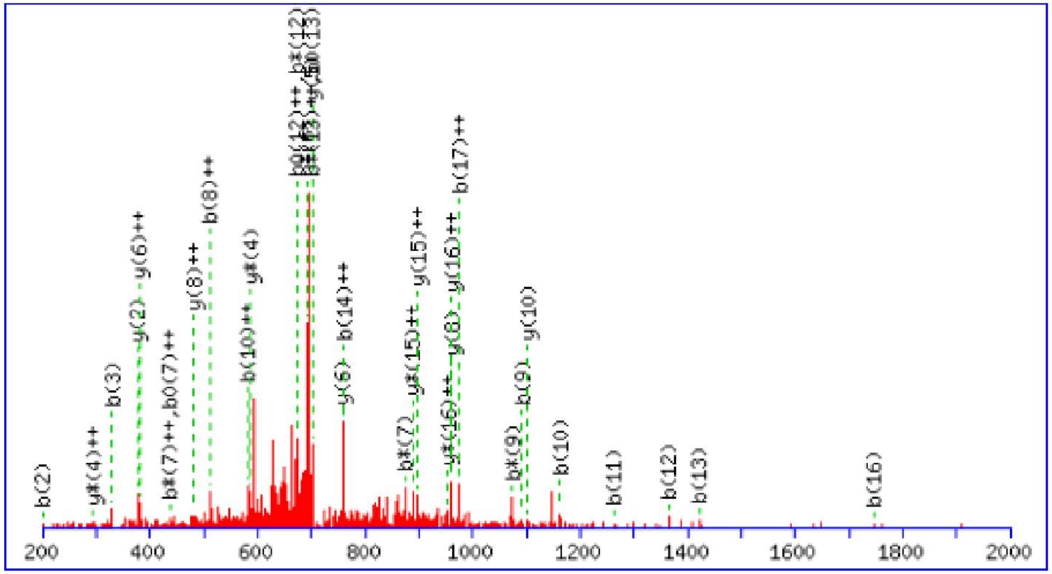


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							13
2	***274.2034***	137.6053	257.1769	129.0921			K	1644.8963	822.9518	1627.8698	814.4385	1626.8858	813.9465	12
3	***403.2460***	202.1266	386.2194	193.6134	385.2354	193.1214	E	**1442.7373**	721.8723	1425.7108	713.3590	1424.7268	712.8670	11
4	***474.2831***	237.6452	457.2566	229.1319	456.2725	228.6399	A	**1313.6947**	657.3510	1296.6682	648.8377	1295.6842	648.3457	10
5	***545.3202***	273.1638	528.2937	264.6505	527.3097	264.1585	A	**1242.6576**	621.8324	1225.6311	613.3192	1224.6470	612.8272	9
6	***674.3628***	337.6850	657.3363	329.1718	656.3523	328.6798	E	**1171.6205**	586.3139	1154.5939	577.8006	1153.6099	577.3086	8
7	***802.4214***	401.7143	785.3948	393.2011	784.4108	392.7091	Q	**1042.5779**	521.7926	1025.5514	513.2793	1024.5673	512.7873	7
8	***917.4483***	459.2278	900.4218	450.7145	899.4378	450.2225	D	**914.5193**	457.7633	897.4928	449.2500	896.5088	448.7580	6
9	***1016.5168***	508.7620	999.4902	500.2487	998.5062	499.7567	V	799.4924	400.2498	782.4658	391.7366	781.4818	391.2445	5
10	***1145.5593***	573.2833	1128.5328	564.7700	1127.5488	564.2780	E	**700.4240**	350.7156	683.3974	342.2023	682.4134	341.7103	4
11	***1329.6805***	665.3439	1312.6540	656.8306	1311.6700	656.3386	K	**571.3814**	286.1943	554.3548	277.6811			3
12	***1513.8017***	757.4045	1496.7752	748.8912	1495.7911	748.3992	K	**387.2602**	194.1337	370.2336	185.6205			2
13							K	203.1390	102.0731	186.1125	93.5599			1

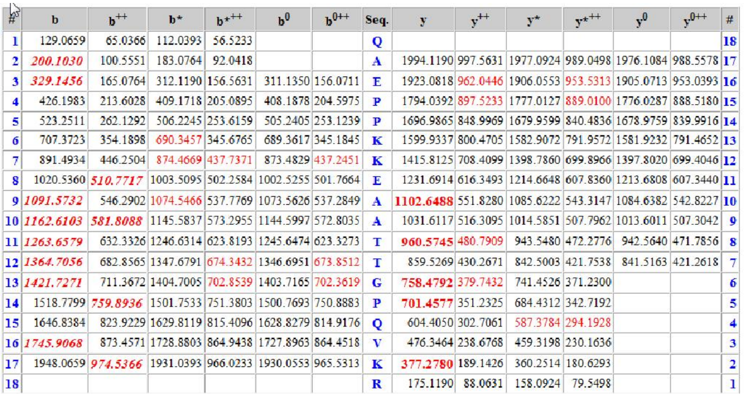
MS/MS Fragmentation of **QAEPPKKEAATTGPQVKR**
Found in **H3BP01**, Zinc finger CCCH domain-containing protein 18 (Fragment) OS=Homo sapiens GN=ZC3H18 PE=4 SV=1

Match to Query 13960: 2121.168972 from(708.063600,3+) intensity(21604.1992)
Title: File1353 Spectrum9085 scans: 9769
Data file J:\2013-9-14-A549-Prometh-Fr5-ZW.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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2121.1702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini on
Variable modifications:
K6      : Propionyl (K)
K7      : Propionyl (K)
K17     : Propionyl-(13CD3)Methyl (K)
Ions Score: 22  Expect: 3.8
Matches : 34/188 fragment ions using 83 most intense peaks   (help)
```

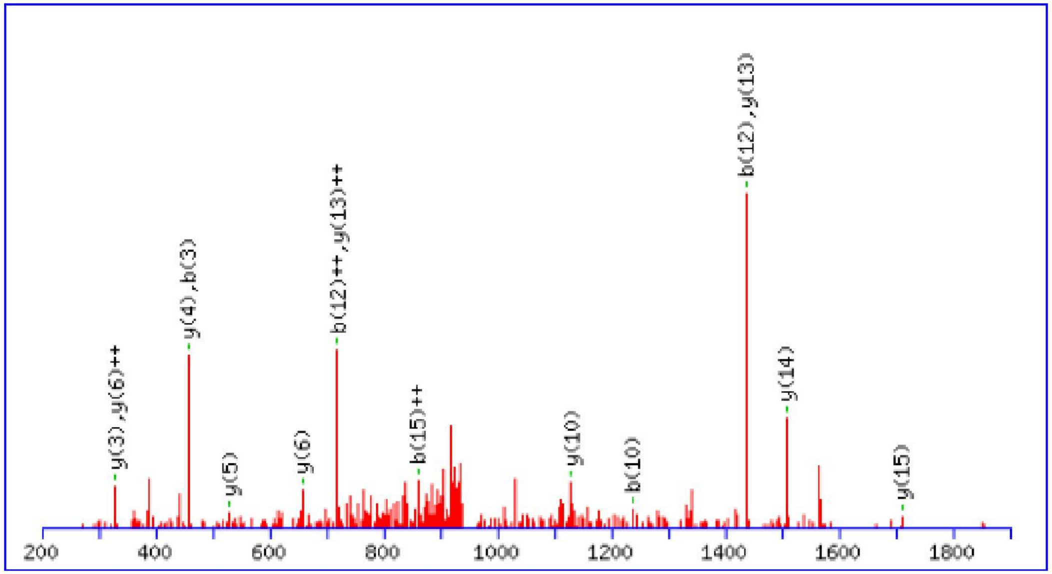


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							18
2	***200.1030***	100.5551	183.0764	92.0418			A	1994.1190	997.5631	1977.0924	989.0498	1976.1084	988.5578	17
3	***329.1456***	165.0764	312.1190	156.5631	311.1350	156.0711	E	1923.0818	962.0446	1906.0553	953.5313	1905.0713	953.0393	16
4	426.1983	213.6028	409.1718	205.0895	408.1878	204.5975	P	1794.0392	897.5233	1777.0127	889.0100	1776.0287	888.5180	15
5	523.2511	262.1292	506.2245	253.6159	505.2405	253.1239	P	1696.9865	848.9969	1679.9599	840.4836	1678.9759	839.9916	14
6	707.3723	354.1898	690.3457	345.6765	689.3617	345.1845	K	1599.9337	800.4705	1582.9072	791.9572	1581.9232	791.4652	13
7	891.4934	446.2504	874.4669	437.7371	873.4829	437.2451	K	1415.8125	708.4099	1398.7860	699.8966	1397.8020	699.4046	12
8	1020.5360	***510.7717***	1003.5095	502.2584	1002.5255	501.7664	E	1231.6914	616.3493	1214.6648	607.8360	1213.6808	607.3440	11
9	***1091.5732***	546.2902	1074.5466	537.7769	1073.5626	537.2849	A	**1102.6488**	551.8280	1085.6222	543.3147	1084.6382	542.8227	10
10	***1162.6103***	***581.8088***	1145.5837	573.2955	1144.5997	572.8035	A	1031.6117	516.3095	1014.5851	507.7962	1013.6011	507.3042	9
11	***1263.6579***	632.3326	1246.6314	623.8193	1245.6474	623.3273	T	**960.5745**	480.7909	943.5480	472.2776	942.5640	471.7856	8
12	***1364.7056***	682.8565	1347.6791	674.3432	1346.6951	673.8512	T	859.5269	430.2671	842.5003	421.7538	841.5163	421.2618	7
13	***1421.7271***	711.3672	1404.7005	702.8539	1403.7165	702.3619	G	**758.4792**	379.7432	741.4526	371.2300			6
14	1518.7799	***759.8936***	1501.7533	751.3803	1500.7693	750.8883	P	**701.4577**	351.2325	684.4312	342.7192			5
15	1646.8384	823.9229	1629.8119	815.4096	1628.8279	814.9176	Q	604.4050	302.7061	587.3784	294.1928			4
16	***1745.9068***	873.4571	1728.8803	864.9438	1727.8963	864.4518	V	476.3464	238.6768	459.3198	230.1636			3
17	1948.0659	***974.5366***	1931.0393	966.0233	1930.0553	965.5313	K	**377.2780**	189.1426	360.2514	180.6293			2
18							R	175.1190	88.0631	158.0924	79.5498			1

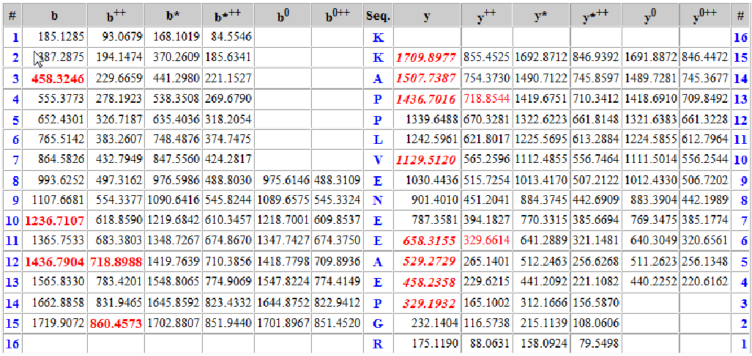
MS/MS Fragmentation of **KKAPPLVENEEAEPGR**
Found in **K7ELJ2**, PDZ domain-containing protein GIPC1 (Fragment) OS=Homo sapiens GN=GIPC1 PE=4 SV=1

Match to Query 11448: 1893.012428 from(947.513490,2+) intensity(12001.0371)
Title: File1353 Spectrum10527 scans: 11271
Data file J:\2013-9-14-A549-Prometh-Fr5-ZW.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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1893.0116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini o
Variable modifications:
K1      : Propionyl (K)
K2      : Propionyl-(13CD3)Methyl (K)
Ions Score: 55  Expect: 0.0024
Matches : 15/160 fragment ions using 16 most intense peaks   (help)
```

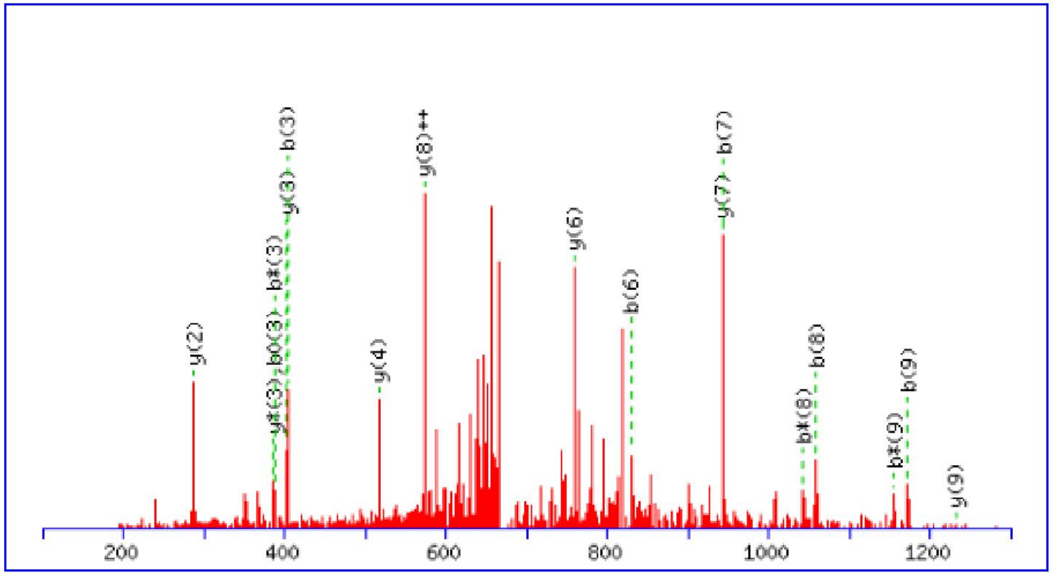


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							16
2	387.2875	194.1474	370.2609	185.6341			K	***1709.8977***	855.4525	1692.8712	846.9392	1691.8872	846.4472	15
3	**458.3246**	229.6659	441.2980	221.1527			A	***1507.7387***	754.3730	1490.7122	745.8597	1489.7281	745.3677	14
4	555.3773	278.1923	538.3508	269.6790			P	***1436.7016***	718.8544	1419.6751	710.3412	1418.6910	709.8492	13
5	652.4301	326.7187	635.4036	318.2054			P	1339.6488	670.3281	1322.6223	661.8148	1321.6383	661.3228	12
6	765.5142	383.2607	748.4876	374.7475			L	1242.5961	621.8017	1225.5695	613.2884	1224.5855	612.7964	11
7	864.5826	432.7949	847.5560	424.2817			V	***1129.5120***	565.2596	1112.4855	556.7464	1111.5014	556.2544	10
8	993.6252	497.3162	976.5986	488.8030	975.6146	488.3109	E	1030.4436	515.7254	1013.4170	507.2122	1012.4330	506.7202	9
9	1107.6681	554.3377	1090.6416	545.8244	1089.6575	545.3324	N	901.4010	451.2041	884.3745	442.6909	883.3904	442.1989	8
10	**1236.7107**	618.8590	1219.6842	610.3457	1218.7001	609.8537	E	787.3581	394.1827	770.3315	385.6694	769.3475	385.1774	7
11	1365.7533	683.3803	1348.7267	674.8670	1347.7427	674.3750	E	***658.3155***	329.6614	641.2889	321.1481	640.3049	320.6561	6
12	**1436.7904**	**718.8988**	1419.7639	710.3856	1418.7798	709.8936	A	***529.2729***	265.1401	512.2463	256.6268	511.2623	256.1348	5
13	1565.8330	783.4201	1548.8065	774.9069	1547.8224	774.4149	E	***458.2358***	229.6215	441.2092	221.1082	440.2252	220.6162	4
14	1662.8858	831.9465	1645.8592	823.4332	1644.8752	822.9412	P	***329.1932***	165.1002	312.1666	156.5870			3
15	1719.9072	**860.4573**	1702.8807	851.9440	1701.8967	851.4520	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **NSKKELNDIR**
Found in **C9JIG9**, Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=2 SV=1

Match to Query 4699: 1345.747048 from(673.880800,2+) intensity(89151.6641)
Title: File1353 Spectrum10080 scans: 10806
Data file J:\2013-9-14-A549-Prometh-Fr5-ZW.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 ●



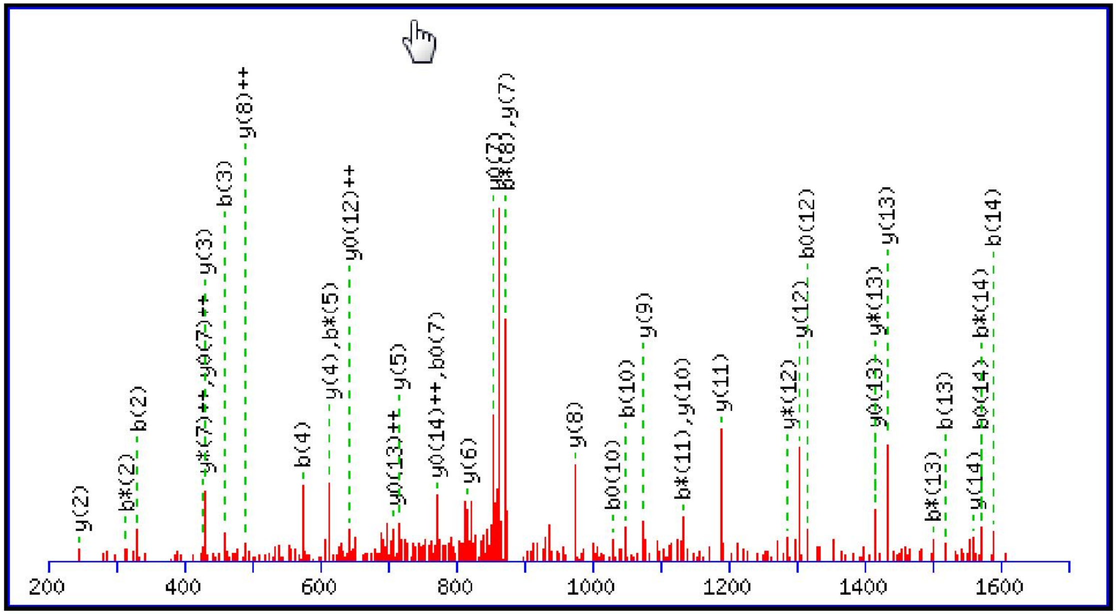
```
Monoisotopic mass of neutral peptide Mr(calc): 1345.7474
Fixed modifications: Carbamidomethyl (C) (apply to specified residu
Variable modifications:
K3     : Propionyl-(13CD3)Methyl (K)
K4     : Propionyl (K)
Ions Score: 45  Expect: 0.015
Matches : 17/102 fragment ions using 22 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							10
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	***1232.7118***	616.8595	1215.6852	608.3462	1214.7012	607.8542	9
3	***404.2412***	202.6243	387.2147	194.1110	386.2307	193.6190	K	1145.6797	573.3435	1128.6532	564.8302	1127.6692	564.3382	8
4	588.3624	294.6848	571.3359	286.1716	570.3519	285.6796	K	***943.5207***	472.2640	926.4942	463.7507	925.5102	463.2587	7
5	717.4050	359.2061	700.3785	350.6929	699.3945	350.2009	E	***759.3995***	380.2034	742.3730	371.6901	741.3890	371.1981	6
6	***830.4891***	415.7482	813.4625	407.2349	812.4785	406.7429	L	630.3569	315.6821	613.3304	307.1688	612.3464	306.6768	5
7	***944.5320***	472.7696	927.5055	464.2564	926.5214	463.7644	N	***517.2729***	259.1401	500.2463	250.6268	499.2623	250.1348	4
8	***1059.5589***	530.2831	1042.5324	521.7698	1041.5484	521.2778	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	***1172.6430***	586.8251	1155.6165	578.3119	1154.6324	577.8199	I	***288.2030***	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KQQDGGTTGTTKKAR**
Found in **F5H8F7**, Set1/Ash2 histone methyltransferase complex subunit ASH2 OS=Homo sapiens GN=ASH2L PE=2 SV=1

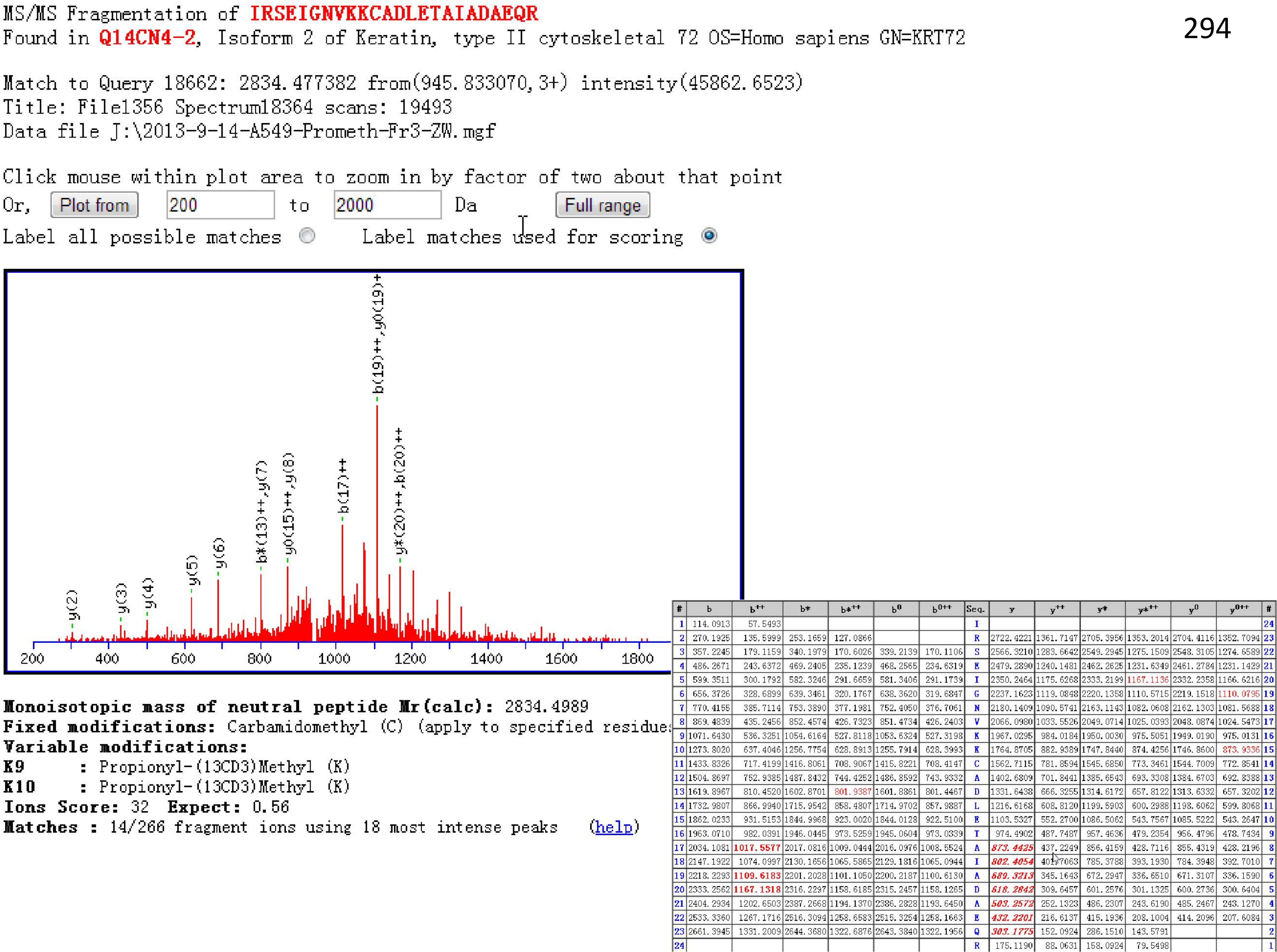
Match to Query 9358: 1761.949428 from(881.981990,2+) intensity(36421.2500)
Title: File1353 Spectrum4760 scans: 5262
Data file J:\2013-9-14-A549-Prometh-Fr5-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1761.9494
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K12 : Propionyl (K)
K13 : Propionyl (K)
Ions Score: 94 **Expect:** 2.2e-007
Matches : 39/154 fragment ions using 56 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							15
2	**331.2249**	166.1161	314.1983	157.6028			Q	***1560.7976***	780.9025	1543.7711	772.3892	1542.7871	771.8972	14
3	**459.2834**	230.1454	442.2569	221.6321			Q	***1432.7391***	716.8732	1415.7125	708.3599	1414.7285	707.8679	13
4	**574.3104**	287.6588	557.2838	279.1456	556.2998	278.6535	D	***1304.6805***	652.8439	1287.6539	644.3306	1286.6699	643.8386	12
5	631.3319	316.1696	614.3053	307.6563	613.3213	307.1643	G	***1189.6535***	595.3304	1172.6270	586.8171	1171.6430	586.3251	11
6	688.3533	344.6803	671.3268	336.1670	670.3428	335.6750	G	***1132.6321***	566.8197	1115.6055	558.3064	1114.6215	557.8144	10
7	789.4010	395.2041	772.3744	386.6909	771.3904	386.1989	T	***1075.6106***	538.3089	1058.5841	529.7957	1057.6000	529.3037	9
8	890.4487	445.7280	873.4221	437.2147	872.4381	436.7227	T	***974.5629***	487.7851	957.5364	479.2718	956.5524	478.7798	8
9	947.4701	474.2387	930.4436	465.7254	929.4596	465.2334	G	***873.5152***	437.2613	856.4887	428.7480	855.5047	428.2560	7
10	**1048.5178**	524.7625	1031.4913	516.2493	1030.5073	515.7573	T	***816.4938***	408.7505	799.4672	400.2373	798.4832	399.7452	6
11	1149.5655	575.2864	1132.5389	566.7731	1131.5549	566.2811	T	***715.4461***	358.2267	698.4196	349.7134	697.4355	349.2214	5
12	1333.6867	667.3470	1316.6601	658.8337	1315.6761	658.3417	K	***614.3984***	307.7028	597.3719	299.1896			4
13	**1517.8079**	759.4076	1500.7813	750.8943	1499.7973	750.4023	K	***430.2772***	215.6423	413.2507	207.1290			3
14	**1588.8450**	794.9261	1571.8184	786.4128	1570.8344	785.9208	A	***246.1561***	123.5817	229.1295	115.0684			2
15							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **IRSEIGNVKKCADLETAIADAEQR**
Found in **Q14CN4-2**, Isoform 2 of Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72

Match to Query 18662: 2834.477382 from(945.833070,3+) intensity(45862.6523)
Title: File1356 Spectrum18364 scans: 19493
Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.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 ●

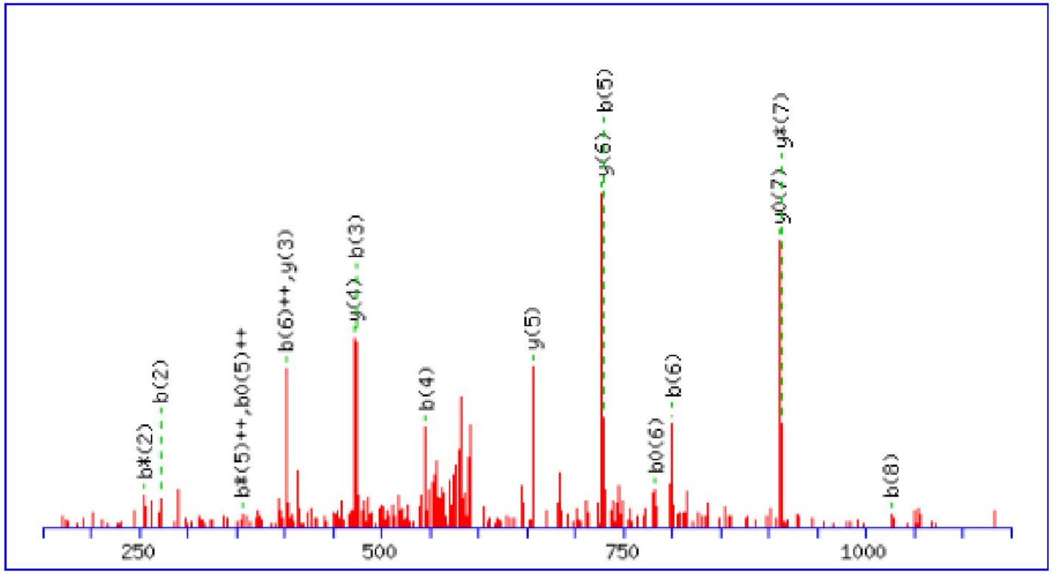
Monoisotopic mass of neutral peptide Mr(calc): 2834.4989
Fixed modifications: Carbamidomethyl (C) (apply to specified residues
Variable modifications:
K9 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl-(13CD3)Methyl (K)
Ions Score: 32 **Expect:** 0.56
Matches : 14/266 fragment ions using 18 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					I							24
2	270.1925	135.5999	253.1659	127.0866			R	2722.4221	1361.7147	2705.3956	1353.2014	2704.4116	1352.7094	23
3	357.2245	179.1159	340.1979	170.6026	339.2139	170.1106	S	2566.3210	1283.6642	2549.2945	1275.1509	2548.3105	1274.6589	22
4	486.2671	243.6372	469.2405	235.1239	468.2565	234.6319	E	2479.2890	1240.1481	2462.2625	1231.6349	2461.2784	1231.1429	21
5	599.3511	300.1792	582.3246	291.6659	581.3406	291.1739	I	2350.2464	1175.6268	2333.2199	1167.1136	2332.2358	1166.6216	20
6	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	G	2237.1623	1119.0848	2220.1358	1110.5715	2219.1518	1110.0795	19
7	770.4155	385.7114	753.3890	377.1981	752.4050	376.7061	N	2180.1409	1090.5741	2163.1143	1082.0608	2162.1303	1081.5688	18
8	869.4839	435.2456	852.4574	426.7323	851.4734	426.2403	V	2066.0980	1033.5526	2049.0714	1025.0393	2048.0874	1024.5473	17
9	1071.6430	536.3251	1054.6164	527.8118	1053.6324	527.3198	K	1967.0295	984.0184	1950.0030	975.5051	1949.0190	975.0131	16
10	1273.8020	637.4046	1256.7754	628.8913	1255.7914	628.3993	K	1764.8705	882.9389	1747.8440	874.4256	1746.8600	873.9336	15
11	1433.8326	717.4199	1416.8061	708.9067	1415.8221	708.4147	C	1562.7115	781.8594	1545.6850	773.3461	1544.7009	772.8541	14
12	1504.8697	752.9385	1487.8432	744.4252	1486.8592	743.9332	A	1402.6809	701.8441	1385.6543	693.3308	1384.6703	692.8388	13
13	1619.8967	810.4520	1602.8701	801.9387	1601.8861	801.4467	D	1331.6438	666.3255	1314.6172	657.8122	1313.6332	657.3202	12
14	1732.9807	866.9940	1715.9542	858.4807	1714.9702	857.9887	L	1216.6168	608.8120	1199.5903	600.2988	1198.6062	599.8068	11
15	1862.0233	931.5153	1844.9968	923.0020	1844.0128	922.5100	E	1103.5327	552.2700	1086.5062	543.7567	1085.5222	543.2647	10
16	1963.0710	982.0391	1946.0445	973.5259	1945.0604	973.0339	T	974.4902	487.7487	957.4636	479.2354	956.4796	478.7434	9
17	2034.1081	**1017.5577**	2017.0816	1009.0444	2016.0976	1008.5524	A	***873.4425***	437.2249	856.4159	428.7116	855.4319	428.2196	8
18	2147.1922	1074.0997	2130.1656	1065.5865	2129.1816	1065.0944	I	***802.4054***	401.7063	785.3788	393.1930	784.3948	392.7010	7
19	2218.2293	**1109.6183**	2201.2028	1101.1050	2200.2187	1100.6130	A	***689.3213***	345.1643	672.2947	336.6510	671.3107	336.1590	6
20	2333.2562	**1167.1318**	2316.2297	1158.6185	2315.2457	1158.1265	D	***618.2842***	309.6457	601.2576	301.1325	600.2736	300.6404	5
21	2404.2934	1202.6503	2387.2668	1194.1370	2386.2828	1193.6450	A	***503.2572***	252.1323	486.2307	243.6190	485.2467	243.1270	4
22	2533.3360	1267.1716	2516.3094	1258.6583	2515.3254	1258.1663	E	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	3
23	2661.3945	1331.2009	2644.3680	1322.6876	2643.3840	1322.1956	Q	***303.1775***	152.0924	286.1510	143.5791			2
24							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SKKAKAPER**
Found in **Q6ZRS2**, Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3

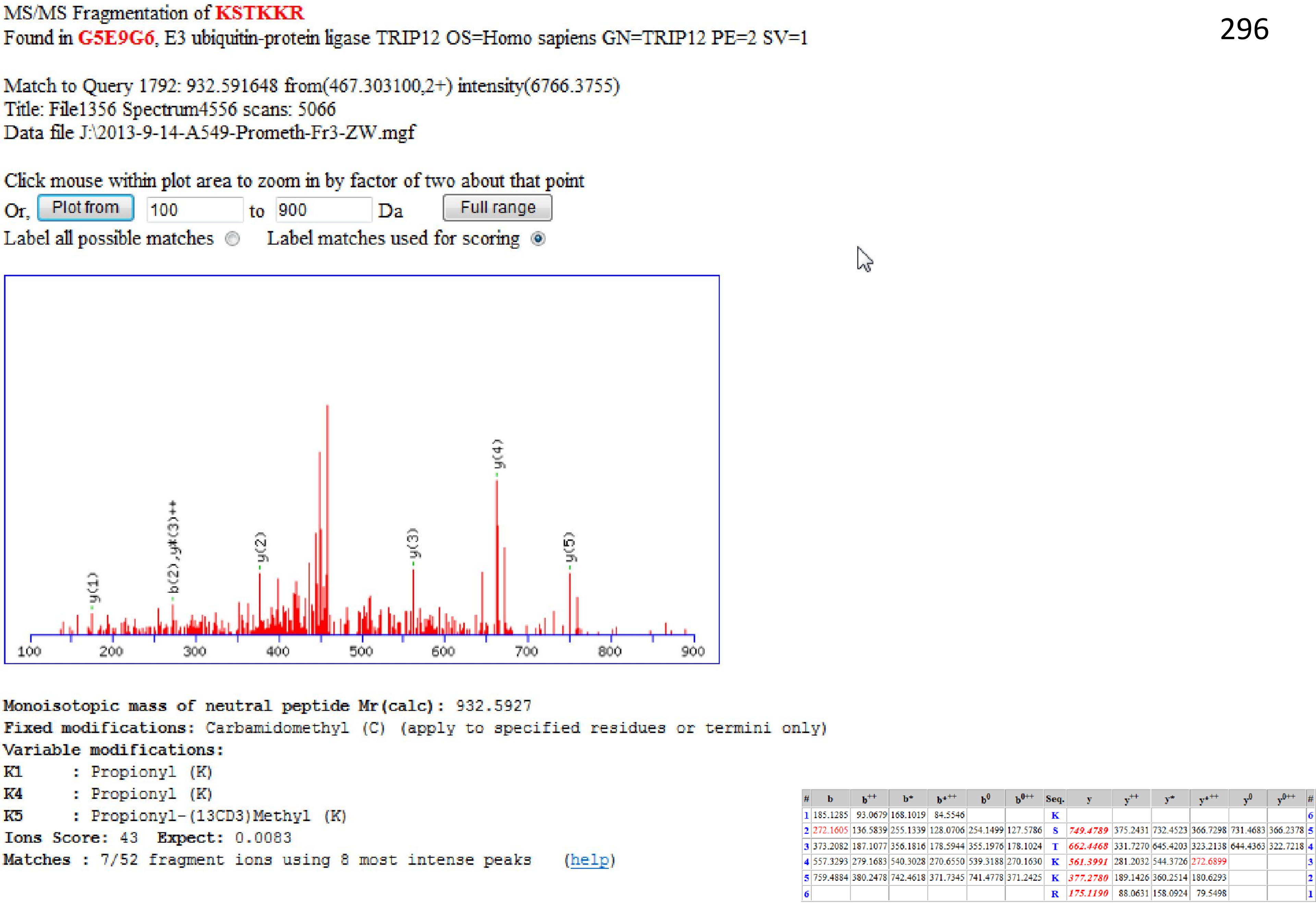
Match to Query 4492: 1199.714448 from(600.864500,2+) intensity(23520.7617)
Title: File1356 Spectrum6144 scans: 6722
Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1199.7146
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
Ions Score: 35 **Expect:** 0.09
Matches : 17/92 fragment ions using 29 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	***272.1605***	136.5839	255.1339	128.0706	254.1499	127.5786	K	1113.6899	557.3486	1096.6634	548.8353	1095.6793	548.3433	8
3	***474.3195***	237.6634	457.2929	229.1501	456.3089	228.6581	K	929.5687	465.2880	912.5422	456.7747	911.5582	456.2827	7
4	***545.3566***	273.1819	528.3301	264.6687	527.3460	264.1767	A	**727.4097**	364.2085	710.3832	355.6952	709.3991	355.2032	6
5	***729.4778***	365.2425	712.4512	356.7293	711.4672	356.2372	K	**656.3726**	328.6899	639.3461	320.1767	638.3620	319.6847	5
6	***800.5149***	400.7611	783.4884	392.2478	782.5043	391.7558	A	**472.2514**	236.6293	455.2249	228.1161	454.2409	227.6241	4
7	897.5677	449.2875	880.5411	440.7742	879.5571	440.2822	P	**401.2143**	201.1108	384.1878	192.5975	383.2037	192.1055	3
8	***1026.6103***	513.8088	1009.5837	505.2955	1008.5997	504.8035	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KSTKKR**
Found in **G5E9G6**, E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=2 SV=1

Match to Query 1792: 932.591648 from(467.303100,2+) intensity(6766.3755)
Title: File1356 Spectrum4556 scans: 5066
Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●

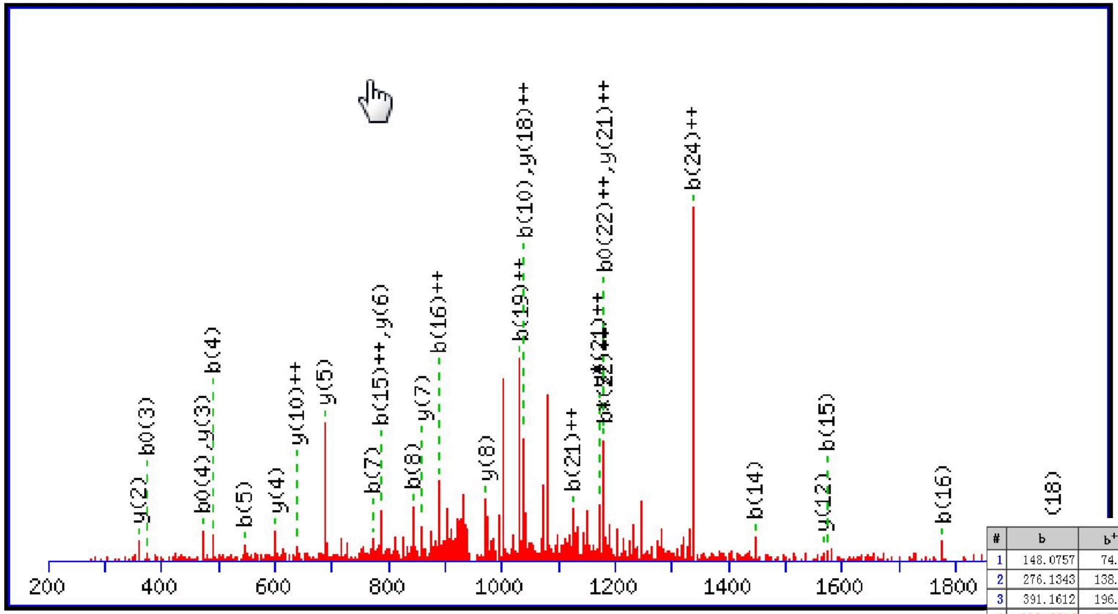
Monoisotopic mass of neutral peptide Mr(calc): 932.5927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K4 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 43 **Expect:** 0.0083
Matches : 7/52 fragment ions using 8 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							6
2	272.1605	136.5839	255.1339	128.0706	254.1499	127.5786	S	*749.4789*	375.2431	732.4523	366.7298	731.4683	366.2378	5
3	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	T	*662.4468*	331.7270	645.4203	323.2138	644.4363	322.7218	4
4	557.3293	279.1683	540.3028	270.6550	539.3188	270.1630	K	*561.3991*	281.2032	544.3726	272.6899			3
5	759.4884	380.2478	742.4618	371.7345	741.4778	371.2425	K	*377.2780*	189.1426	360.2514	180.6293			2
6							R	*175.1190*	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FQDVGPQAPVGSVYQKTNAVSEIKR**
Found in **H0Y5J4**, Drebrin-like protein (Fragment) OS=Homo sapiens GN=DBNL PE=4 SV=1

Match to Query 18714: 2847.508092 from(950.176640,3+) intensity(58247.6367)
Title: File1356 Spectrum16044 scans: 17045
Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.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 ●



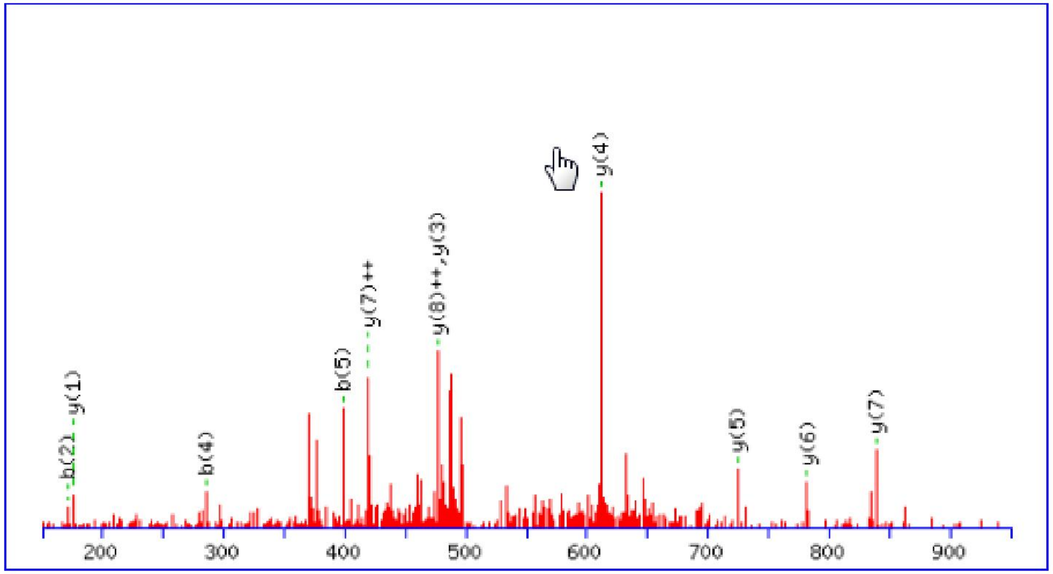
Monoisotopic mass of neutral peptide Mr(calc): 2847.5040
Fixed modifications: Carbamidomethyl (C) (apply to specified residu
Variable modifications:
K16 : Propionyl-(13CD3)Methyl (K)
K24 : Propionyl (K)
Ions Score: 45 **Expect:** 0.025
Matches : 30/276 fragment ions using 51 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							25
2	276.1343	138.5708	259.1077	130.0575			Q	2701.4428	1351.2250	2684.4163	1342.7118	2683.4322	1342.2198	24
3	391.1612	196.0842	374.1347	187.5710	373.1506	187.0790	D	2573.3842	1287.1958	2556.3577	1278.6825	2555.3737	1278.1905	23
4	**490.2296**	245.6185	473.2031	237.1052	472.2191	236.6132	V	2458.3573	1229.6823	2441.3307	1221.1690	2440.3467	1220.6770	22
5	**547.2511**	274.1292	530.2245	265.6159	529.2405	265.1239	G	2359.2889	1180.1481	2342.2623	1171.6348	2341.2783	1171.1428	21
6	644.3039	322.6556	627.2773	314.1423	626.2933	313.6503	P	2302.2674	1151.6373	2285.2409	1143.1241	2284.2568	1142.6321	20
7	**772.3624**	386.6849	755.3359	378.1716	754.3519	377.6796	Q	2205.2146	1103.1110	2188.1881	1094.5977	2187.2041	1094.1057	19
8	**843.3995**	422.2034	826.3730	413.6901	825.3890	413.1981	A	2077.1561	1039.0817	2060.1295	1030.5684	2059.1455	1030.0764	18
9	940.4523	470.7298	923.4258	462.2165	922.4417	461.7245	P	2006.1190	1003.5631	1989.0924	995.0498	1988.1084	994.5578	17
10	**1039.5207**	520.2640	1022.4942	511.7507	1021.5102	511.2587	V	1909.0662	955.0367	1892.0396	946.5235	1891.0556	946.0315	16
11	1096.5422	548.7747	1079.5156	540.2615	1078.5316	539.7694	G	1809.9973	905.5025	1792.9712	896.9893	1791.9872	896.4972	15
12	1183.5742	592.2907	1166.5477	583.7775	1165.5637	583.2855	S	1752.9763	876.9918	1735.9498	868.4785	1734.9657	867.9865	14
13	1282.6426	641.8250	1265.6161	633.3117	1264.6321	632.8197	V	1665.9443	833.4758	1648.9177	824.9625	1647.9337	824.4705	13
14	**1445.7060**	723.3566	1428.6794	714.8433	1427.6954	714.3513	Y	**1566.8759**	783.9416	1549.8493	775.4283	1548.8653	774.9363	12
15	**1573.7645**	**787.3859**	1556.7380	778.8726	1555.7540	778.3806	Q	1403.8125	702.4099	1386.7860	693.8966	1385.8020	693.4046	11
16	**1775.9235**	**888.4654**	1758.8970	879.9521	1757.9130	879.4601	K	1275.7540	638.3806	1258.7274	629.8673	1257.7434	629.3753	10
17	1876.9712	938.9893	1859.9447	930.4760	1858.9607	929.9840	T	1073.5949	537.3011	1056.5684	528.7878	1055.5844	528.2958	9
18	1991.0142	996.0107	1973.9876	987.4974	1973.0036	987.0054	N	**972.5473**	486.7773	955.5207	478.2640	954.5367	477.7720	8
19	2062.0513	**1031.5293**	2045.0247	1023.0160	2044.0407	1022.5240	A	**858.5043**	429.7558	841.4778	421.2425	840.4938	420.7505	7
20	2161.1197	1081.0635	2144.0931	1072.5502	2143.1091	1072.0582	V	**787.4672**	394.2373	770.4407	385.7240	769.4567	385.2320	6
21	2248.1517	**1124.5795**	2231.1252	1116.0662	2230.1411	1115.5742	S	**688.3988**	344.7030	671.3723	336.1898	670.3883	335.6978	5
22	2377.1943	1189.1008	2360.1678	1180.5875	2359.1837	1180.0955	E	**601.3668**	301.1870	584.3402	292.6738	583.3562	292.1817	4
23	2490.2784	1245.6428	2473.2518	1237.1295	2472.2678	1236.6375	I	**472.3242**	236.6657	455.2976	228.1525			3
24	2674.3995	**1337.7034**	2657.3730	1329.1901	2656.3890	1328.6981	K	**359.2401**	180.1237	342.2136	171.6104			2
25							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GLGGIMVKR**
Found in **O94776**, Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1

Match to Query 2535: 1007.633648 from(504.824100,2+) intensity(17939.4902)
Title: File1356 Spectrum12225 scans: 13066
Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



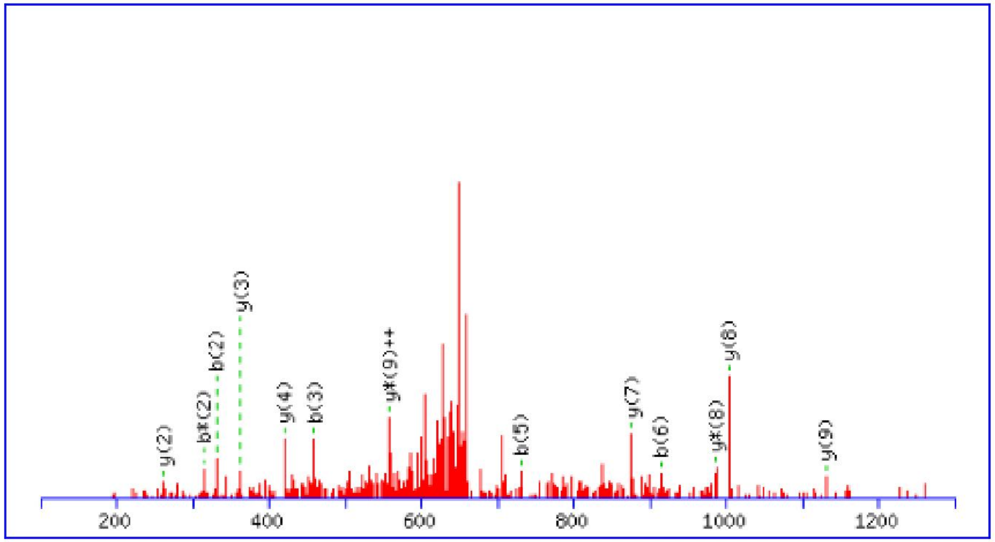
Monoisotopic mass of neutral peptide Mr(calc): 1007.6343
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M6 : Label:13C(1)2H(3) (M)
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.0056
Matches : 11/50 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	58.0287	29.5180			G					9
2	**171.1128**	86.0600			L	951.6201	476.3137	934.5936	467.8004	8
3	228.1343	114.5708			G	***838.5360***	419.7717	821.5095	411.2584	7
4	**285.1557**	143.0815			G	***781.5146***	391.2609	764.4880	382.7477	6
5	**398.2398**	199.6235			I	***724.4931***	362.7502	707.4666	354.2369	5
6	533.3025	267.1549			M	***611.4090***	306.2082	594.3825	297.6949	4
7	632.3709	316.6891			V	***476.3464***	238.6768	459.3198	230.1636	3
8	834.5299	417.7686	817.5033	409.2553	K	377.2780	189.1426	360.2514	180.6293	2
9					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KQQSKKGTSR**
Found in **Q6UX04**, Peptidyl-prolyl cis-trans isomerase CWC27 homolog OS=Homo sapiens GN=CWC27 PE=1 SV=1

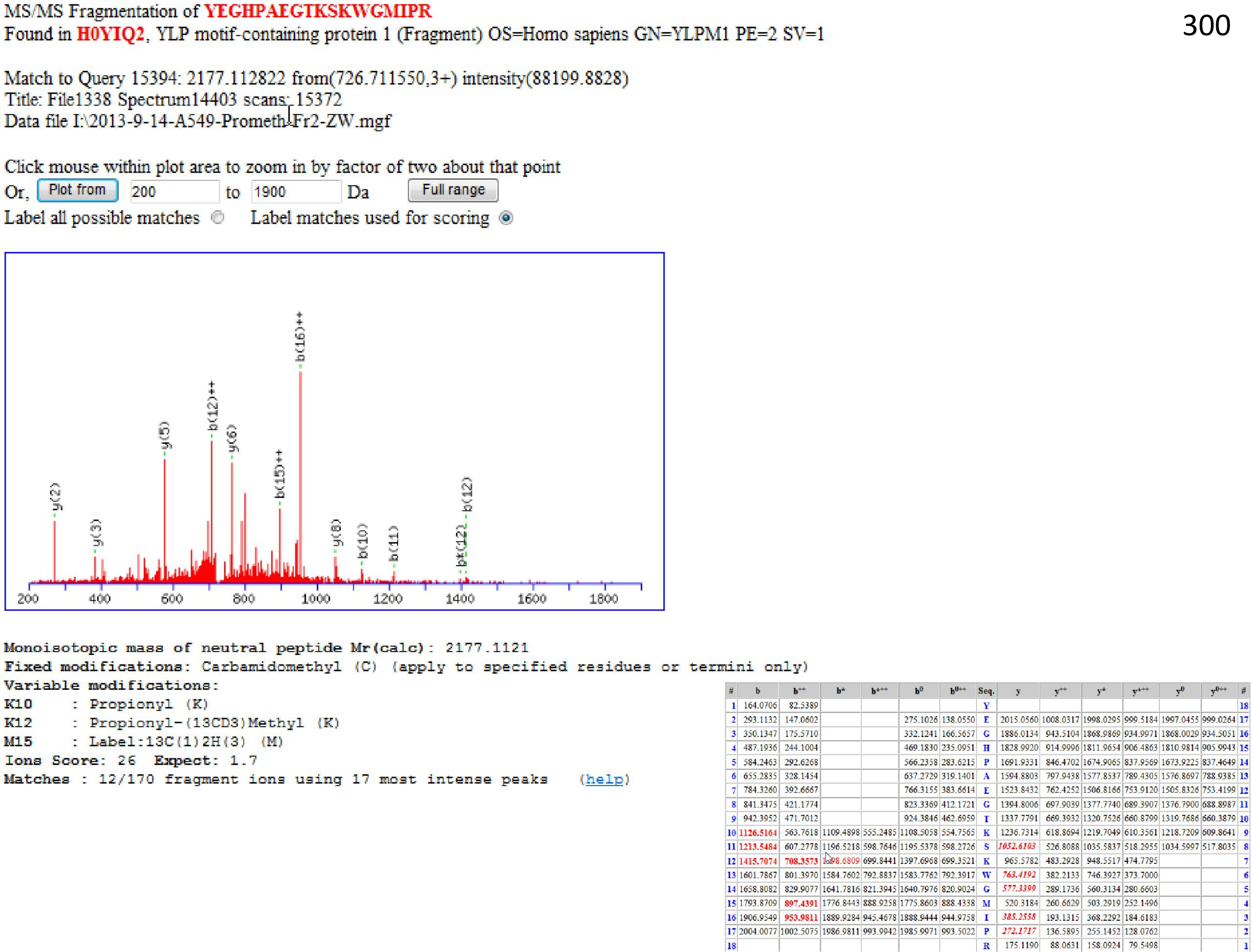
Match to Query 6287: 1332.763288 from(667.388920,2+) intensity(11596.7998)
Title: File1338 Spectrum4165 scans: 4664
Data file I:\2013-9-14-A549-Prometh-Fr2-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1332.7634
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
K5      : Propionyl (K)
K6      : Propionyl (K)
Ions Score: 26  Expect: 0.97
Matches : 13/100 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							10
2	**331.2249**	166.1161	314.1983	157.6028			Q	***1131.6117***	566.3095	1114.5851	557.7962	1113.6011	557.3042	9
3	**459.2834**	230.1454	442.2569	221.6321			Q	***1003.5531***	502.2802	986.5265	493.7669	985.5425	493.2749	8
4	546.3155	273.6614	529.2889	265.1481	528.3049	264.6561	S	***875.4945***	438.2509	858.4680	429.7376	857.4839	429.2456	7
5	**730.4367**	365.7220	713.4101	357.2087	712.4261	356.7167	K	788.4625	394.7349	771.4359	386.2216	770.4519	385.7296	6
6	**914.5578**	457.7826	897.5313	449.2693	896.5473	448.7773	K	604.3413	302.6743	587.3148	294.1610	586.3307	293.6690	5
7	971.5793	486.2933	954.5527	477.7800	953.5687	477.2880	G	***420.2201***	210.6137	403.1936	202.1004	402.2096	201.6084	4
8	1072.6270	536.8171	1055.6004	528.3038	1054.6164	527.8118	T	***363.1987***	182.1030	346.1721	173.5897	345.1881	173.0977	3
9	1159.6590	580.3331	1142.6325	571.8199	1141.6484	571.3279	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **YEGHPAEGTKSKWGMIPR**
Found in **H0YIQ2**, YLP motif-containing protein 1 (Fragment) OS=Homo sapiens GN=YLPM1 PE=2 SV=1

Match to Query 15394: 2177.112822 from(726.711550,3+) intensity(88199.8828)
Title: File1338 Spectrum14403 scans: 15372
Data file I:\2013-9-14-A549-Prometh-Fr2-ZW.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 ●

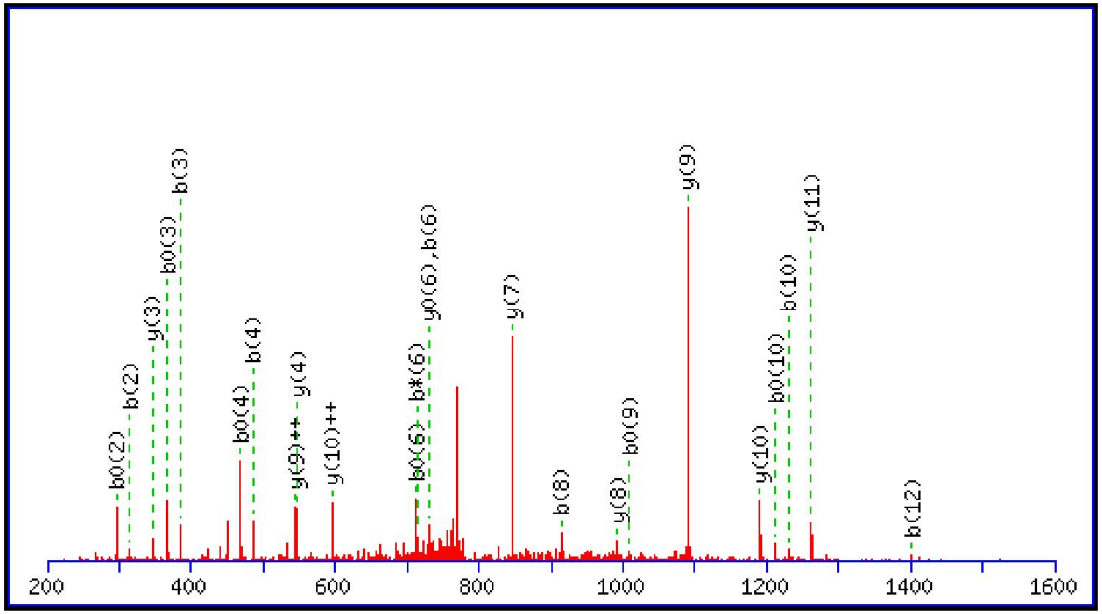
```
Monoisotopic mass of neutral peptide Mr(calc): 2177.1121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K10     : Propionyl (K)
K12     : Propionyl-(13CD3)Methyl (K)
M15     : Label:13C(1)2H(3) (M)
Ions Score: 26  Expect: 1.7
Matches : 12/170 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							18
2	293.1132	147.0602			275.1026	138.0550	E	2015.0560	1008.0317	1998.0295	999.5184	1997.0455	999.0264	17
3	350.1347	175.5710			332.1241	166.5657	G	1886.0134	943.5104	1868.9869	934.9971	1868.0029	934.5051	16
4	487.1936	244.1004			469.1830	235.0951	H	1828.9920	914.9996	1811.9654	906.4863	1810.9814	905.9943	15
5	584.2463	292.6268			566.2358	283.6215	P	1691.9331	846.4702	1674.9065	837.9569	1673.9225	837.4649	14
6	655.2835	328.1454			637.2729	319.1401	A	1594.8803	797.9438	1577.8537	789.4305	1576.8697	788.9385	13
7	784.3260	392.6667			766.3155	383.6614	E	1523.8432	762.4252	1506.8166	753.9120	1505.8326	753.4199	12
8	841.3475	421.1774			823.3369	412.1721	G	1394.8006	697.9039	1377.7740	689.3907	1376.7900	688.8987	11
9	942.3952	471.7012			924.3846	462.6959	T	1337.7791	669.3932	1320.7526	660.8799	1319.7686	660.3879	10
10	**1126.5164**	563.7618	1109.4898	555.2485	1108.5058	554.7565	K	1236.7314	618.8694	1219.7049	610.3561	1218.7209	609.8641	9
11	**1213.5484**	607.2778	1196.5218	598.7646	1195.5378	598.2726	S	***1052.6103***	526.8088	1035.5837	518.2955	1034.5997	517.8035	8
12	**1415.7074**	**708.3573**	1[illegible]98.6809	699.8441	1397.6968	699.3521	K	965.5782	483.2928	948.5517	474.7795			7
13	1601.7867	801.3970	1584.7602	792.8837	1583.7762	792.3917	W	***763.4192***	382.2133	746.3927	373.7000			6
14	1658.8082	829.9077	1641.7816	821.3945	1640.7976	820.9024	G	***577.3399***	289.1736	560.3134	280.6603			5
15	1793.8709	**897.4391**	1776.8443	888.9258	1775.8603	888.4338	M	520.3184	260.6629	503.2919	252.1496			4
16	1906.9549	**953.9811**	1889.9284	945.4678	1888.9444	944.9758	I	***385.2558***	193.1315	368.2292	184.6183			3
17	2004.0077	1002.5075	1986.9811	993.9942	1985.9971	993.5022	P	***272.1717***	136.5895	255.1452	128.0762			2
18							R	175.1190	88.0631	158.0924	79.5498			1

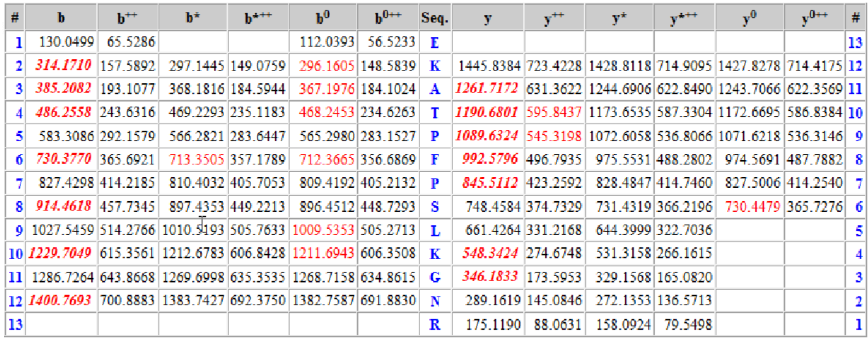
MS/MS Fragmentation of **EKATPFPSLKGNR**
Found in **Q8WXG6-3**, Isoform 3 of MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD

Match to Query 8467: 1573.879728 from(787.947140,2+) intensity(352652.6250)
Title: File1338 Spectrum13723 scans: 14664
Data file I:\2013-9-14-A549-Prometh-Fr2-ZW.mgf

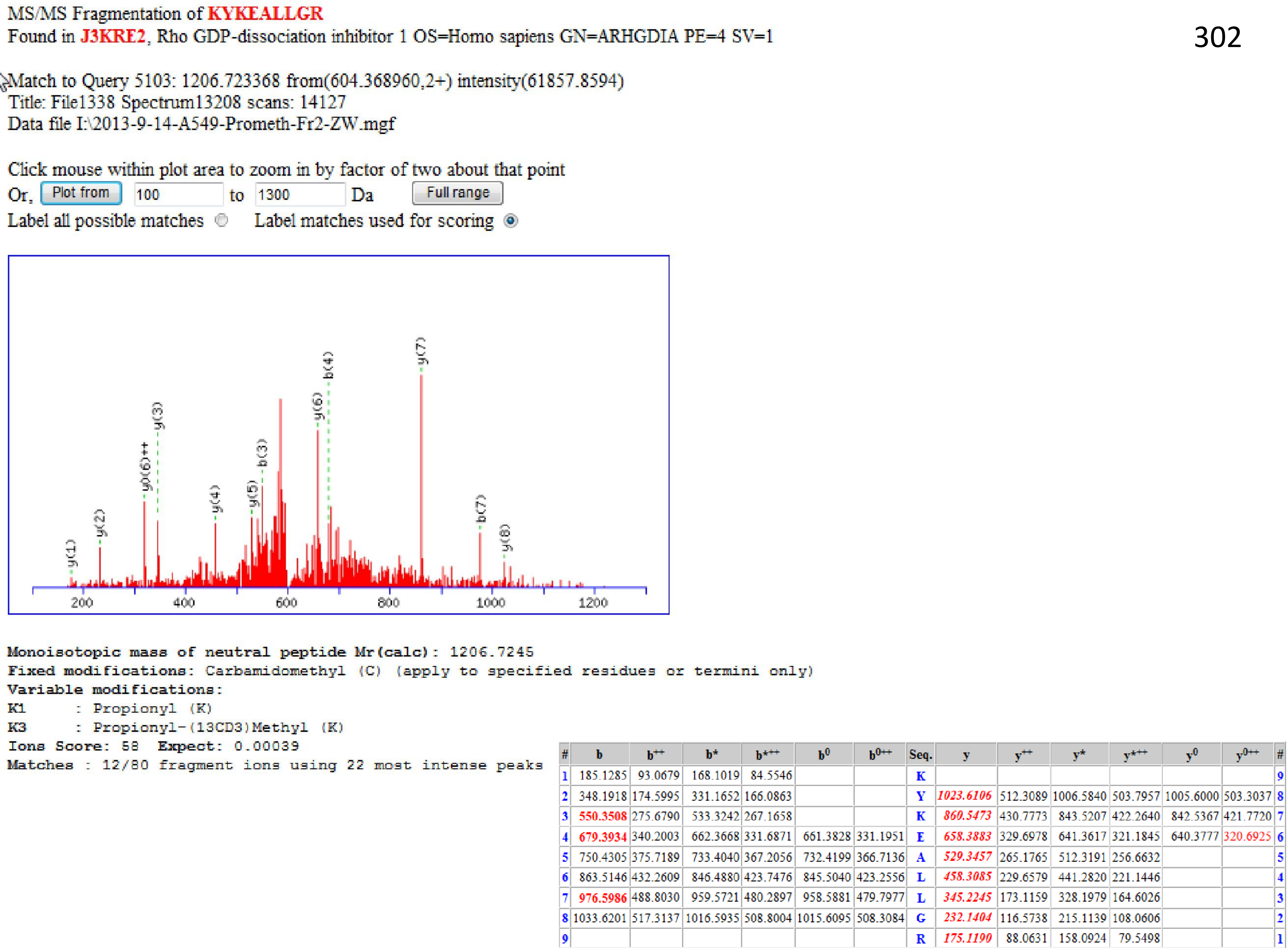
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1573.8737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K2 : Propionyl (K)
K10 : Propionyl-(13CD3)Methyl (K)
Ions Score: 45 **Expect:** 0.016
Matches : 24/132 fragment ions using 40 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	***314.1710***	157.5892	297.1445	149.0759	296.1605	148.5839	K	1445.8384	723.4228	1428.8118	714.9095	1427.8278	714.4175	12
3	***385.2082***	193.1077	368.1816	184.5944	367.1976	184.1024	A	***1261.7172***	631.3622	1244.6906	622.8490	1243.7066	622.3569	11
4	***486.2558***	243.6316	469.2293	235.1183	468.2453	234.6263	T	***1190.6801***	595.8437	1173.6535	587.3304	1172.6695	586.8384	10
5	583.3086	292.1579	566.2821	283.6447	565.2980	283.1527	P	***1089.6324***	545.3198	1072.6058	536.8066	1071.6218	536.3146	9
6	***730.3770***	365.6921	713.3505	357.1789	712.3665	356.6869	F	***992.5796***	496.7935	975.5531	488.2802	974.5691	487.7882	8
7	827.4298	414.2185	810.4032	405.7053	809.4192	405.2132	P	***845.5112***	423.2592	828.4847	414.7460	827.5006	414.2540	7
8	***914.4618***	457.7345	897.4353	449.2213	896.4512	448.7293	S	748.4584	374.7329	731.4319	366.2196	730.4479	365.7276	6
9	1027.5459	514.2766	1010.5193	505.7633	1009.5353	505.2713	L	661.4264	331.2168	644.3999	322.7036			5
10	***1229.7049***	615.3561	1212.6783	606.8428	1211.6943	606.3508	K	***548.3424***	274.6748	531.3158	266.1615			4
11	1286.7264	643.8668	1269.6998	635.3535	1268.7158	634.8615	G	***346.1833***	173.5953	329.1568	165.0820			3
12	***1400.7693***	700.8883	1383.7427	692.3750	1382.7587	691.8830	N	289.1619	145.0846	272.1353	136.5713			2
13							R	175.1190	88.0631	158.0924	79.5498			1



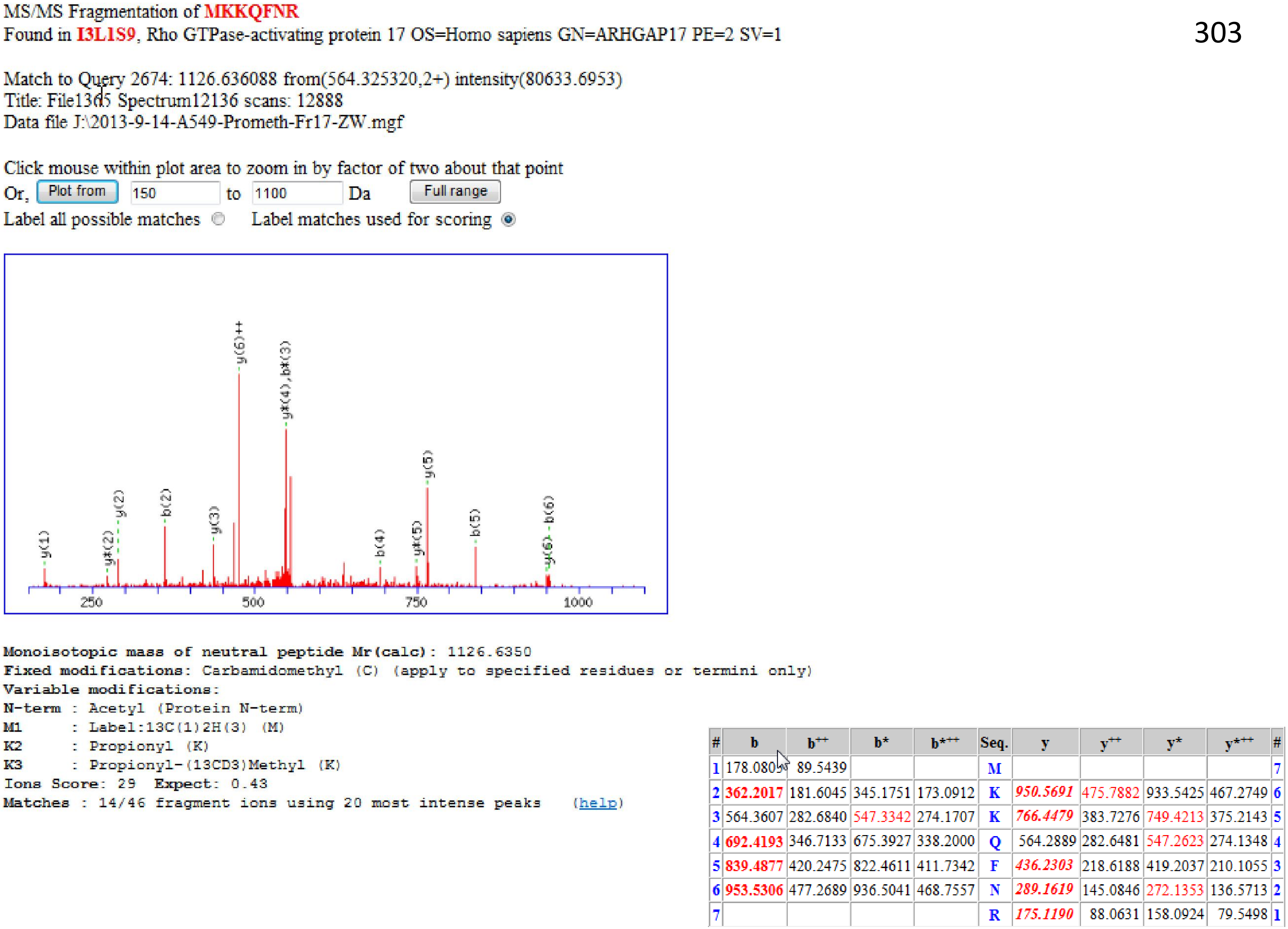
MS/MS Fragmentation of **KYKEALLGR**
Found in **J3KRE2**, Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=4 SV=1

Match to Query 5103: 1206.723368 from(604.368960,2+) intensity(61857.8594)
Title: File1338 Spectrum13208 scans: 14127
Data file I:\2013-9-14-A549-Prometh-Fr2-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1206.7245
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 58 **Expect:** 0.00039
Matches : 12/80 fragment ions using 22 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							9
2	348.1918	174.5995	331.1652	166.0863			Y	***1023.6106***	512.3089	1006.5840	503.7957	1005.6000	503.3037	8
3	**550.3508**	275.6790	533.3242	267.1658			K	***860.5473***	430.7773	843.5207	422.2640	842.5367	421.7720	7
4	**679.3934**	340.2003	662.3668	331.6871	661.3828	331.1951	E	***658.3883***	329.6978	641.3617	321.1845	640.3777	320.6925	6
5	750.4305	375.7189	733.4040	367.2056	732.4199	366.7136	A	***529.3457***	265.1765	512.3191	256.6632			5
6	863.5146	432.2609	846.4880	423.7476	845.5040	423.2556	L	***458.3085***	229.6579	441.2820	221.1446			4
7	**976.5986**	488.8030	959.5721	480.2897	958.5881	479.7977	L	***345.2245***	173.1159	328.1979	164.6026			3
8	1033.6201	517.3137	1016.5935	508.8004	1015.6095	508.3084	G	***232.1404***	116.5738	215.1139	108.0606			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of MKKQFNR
Found in I3L1S9, Rho GTPase-activating protein 17 OS=Homo sapiens GN=ARHGAP17 PE=2 SV=1

Match to Query 2674: 1126.636088 from(564.325320,2+) intensity(80633.6953)
Title: File1365 Spectrum12136 scans: 12888
Data file J:\2013-9-14-A549-Prometh-Fr17-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

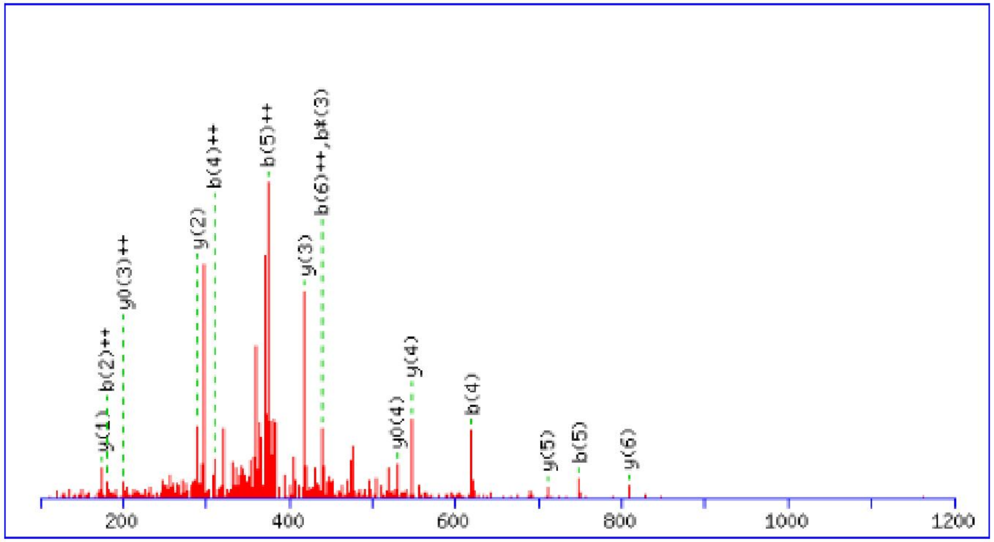
```
Monoisotopic mass of neutral peptide Mr(calc): 1126.6350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
M1     : Label:13C(1)2H(3) (M)
K2     : Propionyl (K)
K3     : Propionyl-(13CD3)Methyl (K)
Ions Score: 29  Expect: 0.43
Matches : 14/46 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	178.080	89.5439			M					7
2	**362.2017**	181.6045	345.1751	173.0912	K	***950.5691***	475.7882	933.5425	467.2749	6
3	564.3607	282.6840	547.3342	274.1707	K	***766.4479***	383.7276	749.4213	375.2143	5
4	**692.4193**	346.7133	675.3927	338.2000	Q	564.2889	282.6481	547.2623	274.1348	4
5	**839.4877**	420.2475	822.4611	411.7342	F	***436.2303***	218.6188	419.2037	210.1055	3
6	**953.5306**	477.2689	936.5041	468.7557	N	***289.1619***	145.0846	272.1353	136.5713	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KRPYEENR**
Found in **M0QYI8**, Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Fragment) OS=Homo sapiens GN=HNRNPUL1 PE=4 SV=1

Match to Query 2935: 1164.618042 from(389.213290,3+) intensity(27002.0938)
Title: File1365 Spectrum3202 scans: 3557
Data file J:\2013-9-14-A549-Prometh-Fr17-ZW.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 ●



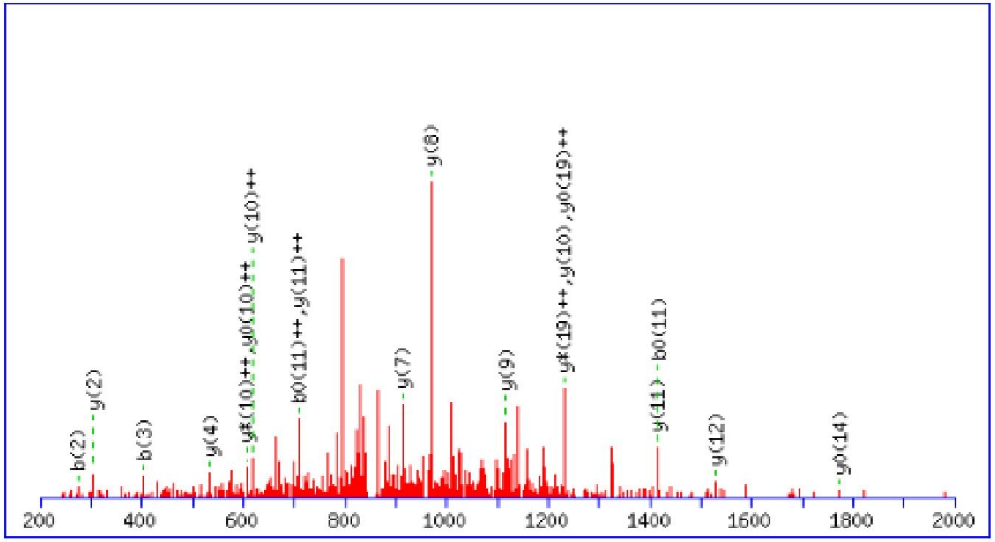
```
Monoisotopic mass of neutral peptide Mr(calc): 1164.6160
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
Ions Score: 35  Expect: 0.11
Matches : 15/72 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	359.2674	**180.1373**	342.2409	171.6241			R	963.4643	482.2358	946.4377	473.7225	945.4537	473.2305	7
3	456.3202	228.6637	439.2936	220.1504			P	***807.3632***	404.1852	790.3366	395.6719	789.3526	395.1799	6
4	**619.3835**	**310.1954**	602.3569	301.6821			Y	***710.3104***	355.6588	693.2838	347.1456	692.2998	346.6536	5
5	**748.4261**	**374.7167**	731.3995	366.2034	730.4155	365.7114	E	***547.2471***	274.1272	530.2205	265.6139	529.2365	265.1219	4
6	877.4687	**439.2380**	860.4421	430.7247	859.4581	430.2327	E	***418.2045***	209.6059	401.1779	201.0926	400.1939	200.6006	3
7	991.5116	496.2594	974.4851	487.7462	973.5010	487.2542	N	***289.1619***	145.0846	272.1353	136.5713			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

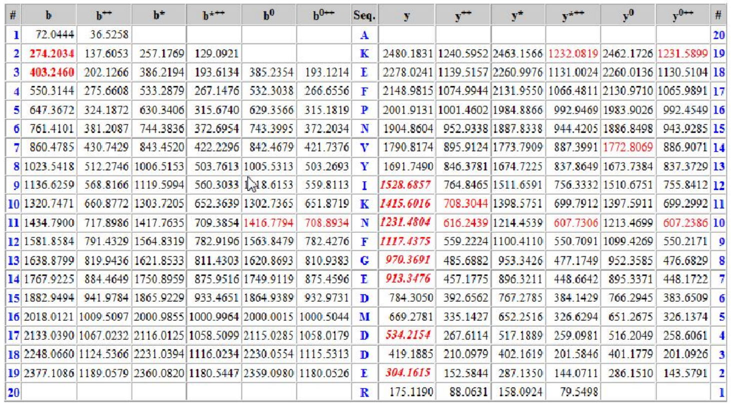
MS/MS Fragmentation of **AKEFPNVYIKNFGEDMDDER**
Found in **Q9H361**, Polyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1 SV=2

Match to Query 14519: 2550.190572 from(851.070800,3+) intensity(26727.1250)
Title: File1365 Spectrum17380 scans: 18356
Data file J:\2013-9-14-A549-Prometh-Fr17-ZW.mgf

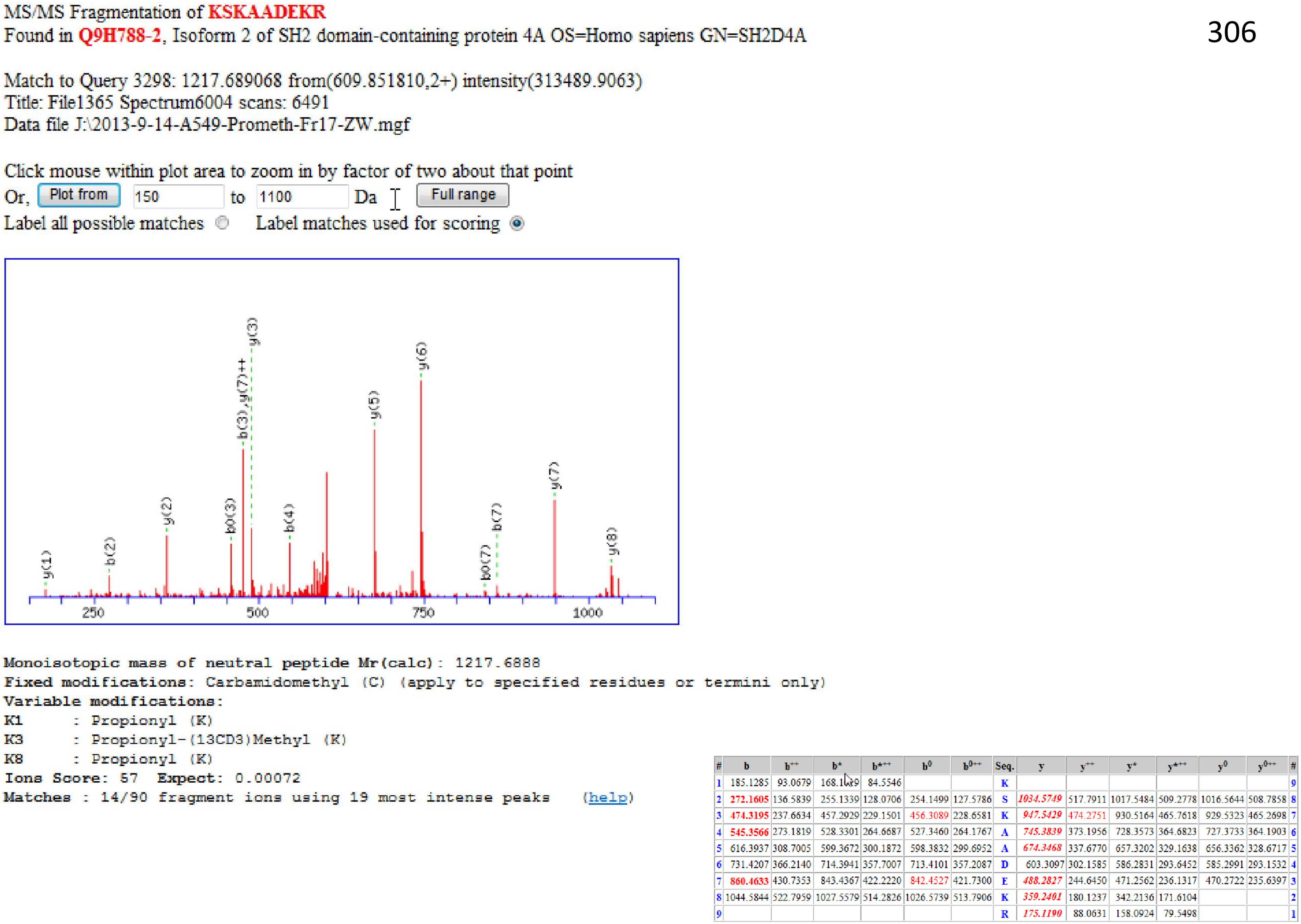
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2550.2130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K10     : Propionyl (K)
M16     : Label:13C(1)2H(3) (M)
Ions Score: 30   Expect: 0.28
Matches : 19/220 fragment ions using 33 most intense peaks   (help)
```



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							20
2	**274.2034**	137.6053	257.1769	129.0921			K	2480.1831	1240.5952	2463.1566	1232.0819	2462.1726	1231.5899	19
3	**403.2460**	202.1266	386.2194	193.6134	385.2354	193.1214	E	2278.0241	1139.5157	2260.9976	1131.0024	2260.0136	1130.5104	18
4	550.3144	275.6608	533.2879	267.1476	532.3038	266.6556	F	2148.9815	1074.9944	2131.9550	1066.4811	2130.9710	1065.9891	17
5	647.3672	324.1872	630.3406	315.6740	629.3566	315.1819	P	2001.9131	1001.4602	1984.8866	992.9469	1983.9026	992.4549	16
6	761.4101	381.2087	744.3836	372.6954	743.3995	372.2034	N	1904.8604	952.9338	1887.8338	944.4205	1886.8498	943.9285	15
7	860.4785	430.7429	843.4520	422.2296	842.4679	421.7376	V	1790.8174	895.9124	1773.7909	887.3991	1772.8069	886.9071	14
8	1023.5418	512.2746	1006.5153	503.7613	1005.5313	503.2693	Y	1691.7490	846.3781	1674.7225	837.8649	1673.7384	837.3729	13
9	1136.6259	568.8166	1119.5994	560.3033	1118.6153	559.8113	I	***1528.6857***	764.8465	1511.6591	756.3332	1510.6751	755.8412	12
10	1320.7471	660.8772	1303.7205	652.3639	1302.7365	651.8719	K	***1415.6016***	708.3044	1398.5751	699.7912	1397.5911	699.2992	11
11	1434.7900	717.8986	1417.7635	709.3854	1416.7794	708.8934	N	***1231.4804***	616.2439	1214.4539	607.7306	1213.4699	607.2386	10
12	1581.8584	791.4329	1564.8319	782.9196	1563.8479	782.4276	F	***1117.4375***	559.2224	1100.4110	550.7091	1099.4269	550.2171	9
13	1638.8799	819.9436	1621.8533	811.4303	1620.8693	810.9383	G	***970.3691***	485.6882	953.3426	477.1749	952.3585	476.6829	8
14	1767.9225	884.4649	1750.8959	875.9516	1749.9119	875.4596	E	***913.3476***	457.1775	896.3211	448.6642	895.3371	448.1722	7
15	1882.9494	941.9784	1865.9229	933.4651	1864.9389	932.9731	D	784.3050	392.6562	767.2785	384.1429	766.2945	383.6509	6
16	2018.0121	1009.5097	2000.9855	1000.9964	2000.0015	1000.5044	M	669.2781	335.1427	652.2516	326.6294	651.2675	326.1374	5
17	2133.0390	1067.0232	2116.0125	1058.5099	2115.0285	1058.0179	D	***534.2154***	267.6114	517.1889	259.0981	516.2049	258.6061	4
18	2248.0660	1124.5366	2231.0394	1116.0234	2230.0554	1115.5313	D	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
19	2377.1086	1189.0579	2360.0820	1180.5447	2359.0980	1180.0526	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498			1



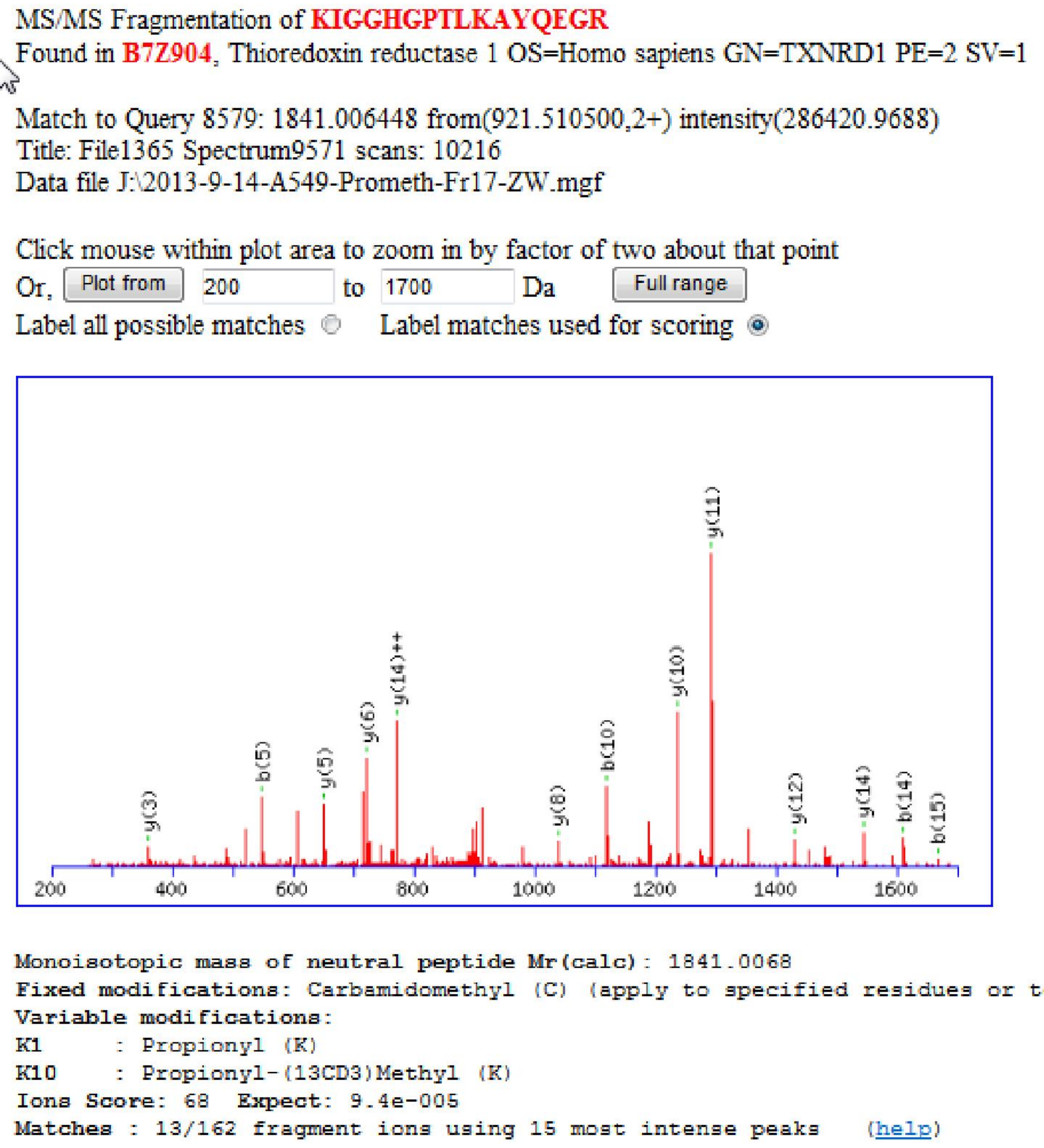
MS/MS Fragmentation of **KSKAADEKR**
Found in **Q9H788-2**, Isoform 2 of SH2 domain-containing protein 4A OS=Homo sapiens GN=SH2D4A

Match to Query 3298: 1217.689068 from(609.851810,2+) intensity(313489.9063)
Title: File1365 Spectrum6004 scans: 6491
Data file J:\2013-9-14-A549-Prometh-Fr17-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1217.6888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K3      : Propionyl-(13CD3)Methyl (K)
K8      : Propionyl (K)
Ions Score: 57  Expect: 0.00072
Matches : 14/90 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1[illegible]9	84.5546			K							9
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	S	***1034.5749***	517.7911	1017.5484	509.2778	1016.5644	508.7858	8
3	**474.3195**	237.6634	457.2929	229.1501	456.3089	228.6581	K	***947.5429***	474.2751	930.5164	465.7618	929.5323	465.2698	7
4	**545.3566**	273.1819	528.3301	264.6687	527.3460	264.1767	A	***745.3839***	373.1956	728.3573	364.6823	727.3733	364.1903	6
5	616.3937	308.7005	599.3672	300.1872	598.3832	299.6952	A	***674.3468***	337.6770	657.3202	329.1638	656.3362	328.6717	5
6	731.4207	366.2140	714.3941	357.7007	713.4101	357.2087	D	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	4
7	**860.4633**	430.7353	843.4367	422.2220	842.4527	421.7300	E	***488.2827***	244.6450	471.2562	236.1317	470.2722	235.6397	3
8	1044.5844	522.7959	1027.5579	514.2826	1026.5739	513.7906	K	***359.2401***	180.1237	342.2136	171.6104			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

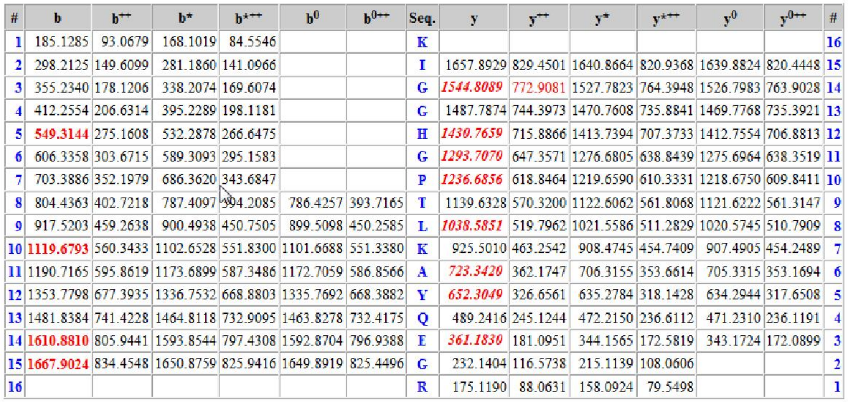


MS/MS Fragmentation of **KIGGHGPTLKAYQEGR**
Found in **B7Z904**, Thioredoxin reductase 1 OS=Homo sapiens GN=TXNRD1 PE=2 SV=1

Match to Query 8579: 1841.006448 from(921.510500,2+) intensity(286420.9688)
Title: File1365 Spectrum9571 scans: 10216
Data file J:\2013-9-14-A549-Prometh-Fr17-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1841.0068
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K10 : Propionyl-(13CD3)Methyl (K)
Ions Score: 68 Expect: 9.4e-005
Matches : 13/162 fragment ions using 15 most intense peaks (help)

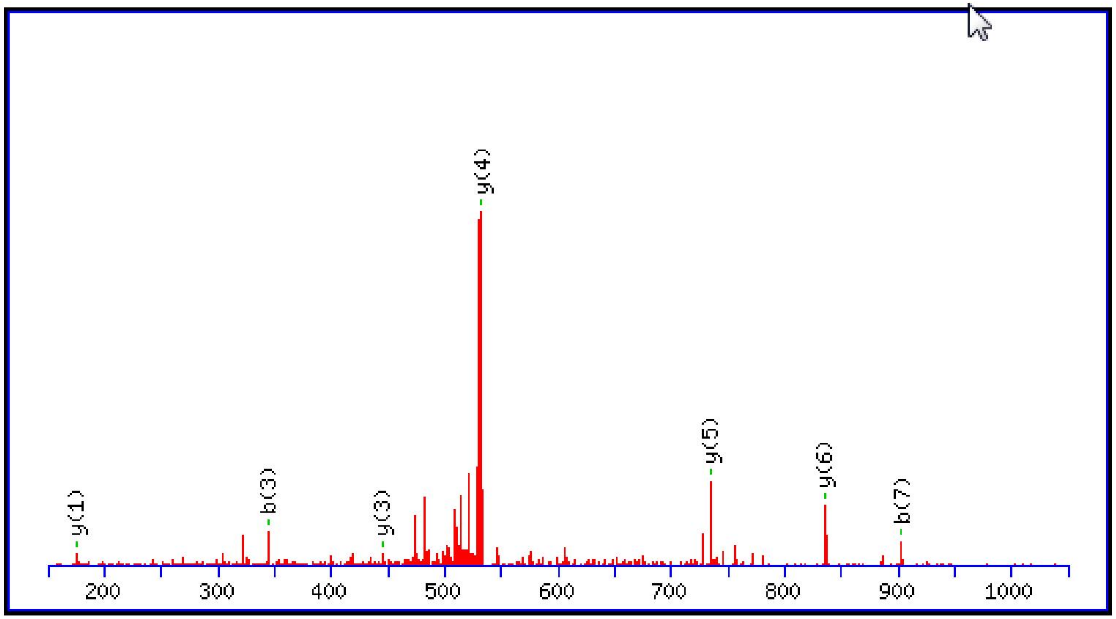


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							16
2	298.2125	149.6099	281.1860	141.0966			I	1657.8929	829.4501	1640.8664	820.9368	1639.8824	820.4448	15
3	355.2340	178.1206	338.2074	169.6074			G	***1544.8089***	772.9081	1527.7823	764.3948	1526.7983	763.9028	14
4	412.2554	206.6314	395.2289	198.1181			G	1487.7874	744.3973	1470.7608	735.8841	1469.7768	735.3921	13
5	**549.3144**	275.1608	532.2878	266.6475			H	***1430.7659***	715.8866	1413.7394	707.3733	1412.7554	706.8813	12
6	606.3358	303.6715	589.3093	295.1583			G	***1293.7070***	647.3571	1276.6805	638.8439	1275.6964	638.3519	11
7	703.3886	352.1979	686.3620	343.6847			P	***1236.6856***	618.8464	1219.6590	610.3331	1218.6750	609.8411	10
8	804.4363	402.7218	787.4097	394.2085	786.4257	393.7165	T	1139.6328	570.3200	1122.6062	561.8068	1121.6222	561.3147	9
9	917.5203	459.2638	900.4938	450.7505	899.5098	450.2585	L	***1038.5851***	519.7962	1021.5586	511.2829	1020.5745	510.7909	8
10	**1119.6793**	560.3433	1102.6528	551.8300	1101.6688	551.3380	K	925.5010	463.2542	908.4745	454.7409	907.4905	454.2489	7
11	1190.7165	595.8619	1173.6899	587.3486	1172.7059	586.8566	A	***723.3420***	362.1747	706.3155	353.6614	705.3315	353.1694	6
12	1353.7798	677.3935	1336.7532	668.8803	1335.7692	668.3882	Y	***652.3049***	326.6561	635.2784	318.1428	634.2944	317.6508	5
13	1481.8384	741.4228	1464.8118	732.9095	1463.8278	732.4175	Q	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	4
14	**1610.8810**	805.9441	1593.8544	797.4308	1592.8704	796.9388	E	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
15	**1667.9024**	834.4548	1650.8759	825.9416	1649.8919	825.4496	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KNTKSRNR**
Found in **J3KN98**, Leucine-rich repeat serine/threonine-protein kinase 1 OS=Homo sapiens GN=LRRK1 PE=4 SV=1

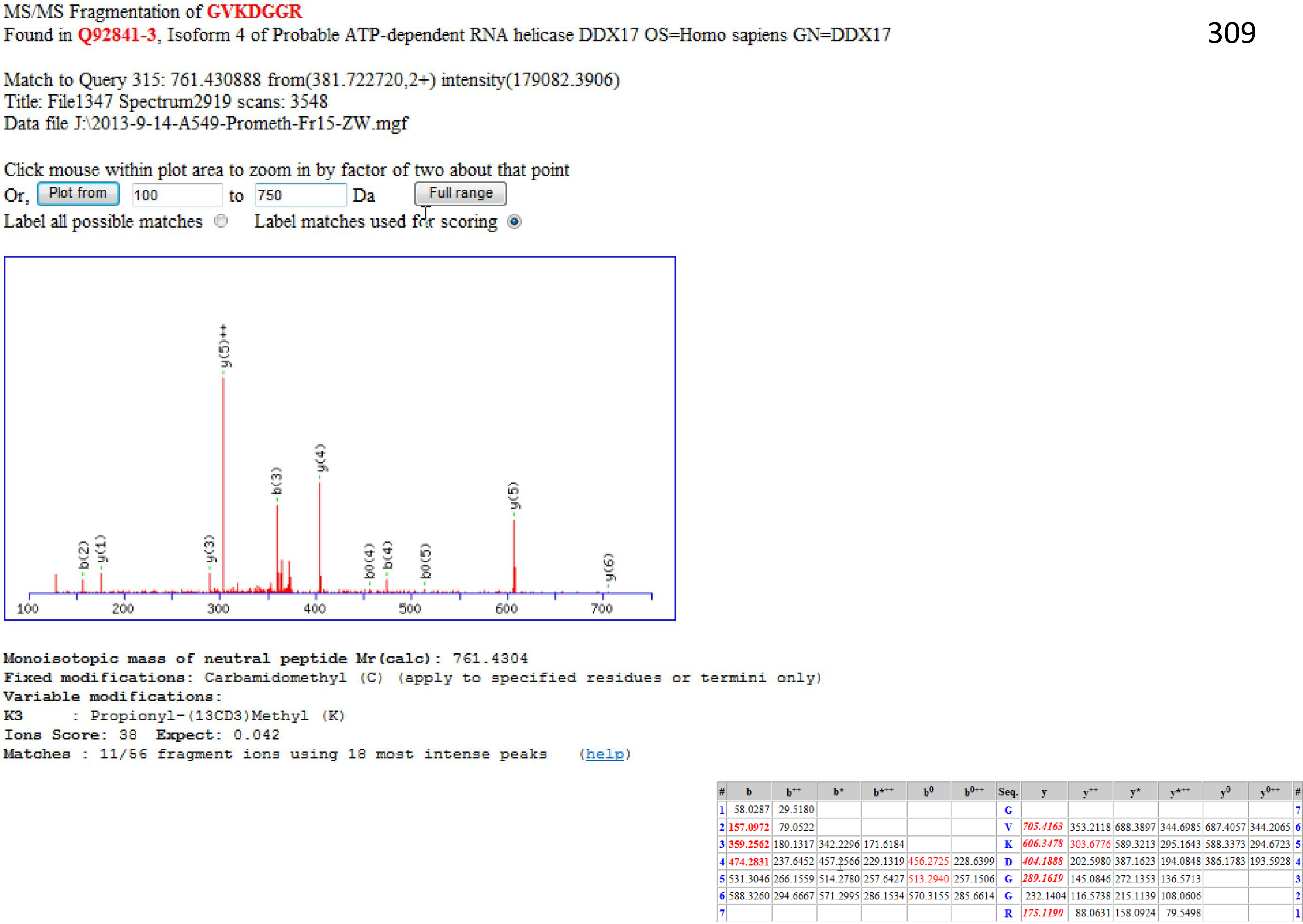
Match to Query 3472: 1076.625088 from(539.319820,2+) intensity(146545.1875)
Title: File1347 Spectrum9994 scans: 11017
Data file J:\2013-9-14-A549-Prometh-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1076.6323
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 39 **Expect:** 0.047
Matches : 7/74 fragment ions using 9 most intense peaks (he]

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.1022	65.0548	112.0757	56.5415			**K**							8
2	243.1452	122.0762	226.1186	113.5629			**N**	949.5446	475.2760	932.5181	466.7627	931.5341	466.2707	7
3	**344.1928**	172.6001	327.1663	164.0868	326.1823	163.5948	**T**	***835.5017***	418.2545	818.4752	409.7412	817.4911	409.2492	6
4	546.3519	273.6796	529.3253	26[illegible]1663	528.3413	264.6743	**K**	***734.4540***	367.7307	717.4275	359.2174	716.4435	358.7254	5
5	633.3839	317.1956	616.3573	308.6823	615.3733	308.1903	**S**	***532.2950***	266.6511	515.2685	258.1379	514.2845	257.6459	4
6	789.4850	395.2461	772.4584	386.7329	771.4744	386.2409	**R**	***445.2630***	223.1351	428.2364	214.6219			3
7	**903.5279**	452.2676	886.5014	443.7543	885.5174	443.2623	**N**	289.1619	145.0846	272.1353	136.5713			2
8							**R**	***175.1190***	88.0631	158.0924	79.5498			1



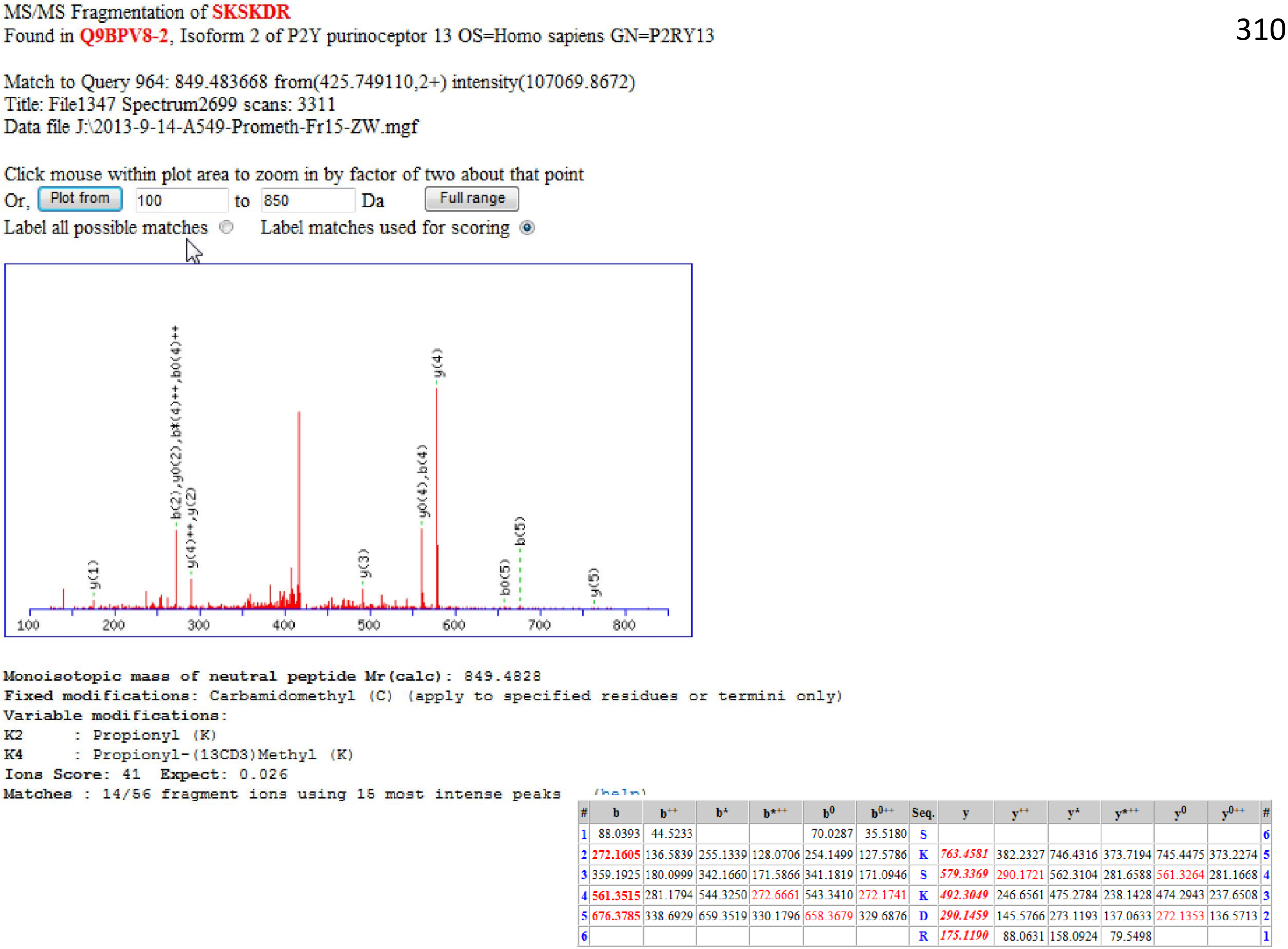
MS/MS Fragmentation of **GVKDGGR**
Found in **Q92841-3**, Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17

Match to Query 315: 761.430888 from(381.722720,2+) intensity(179082.3906)
Title: File1347 Spectrum2919 scans: 3548
Data file J:\2013-9-14-A549-Prometh-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 761.4304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 38 **Expect:** 0.042
Matches : 11/56 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							7
2	**157.0972**	79.0522					V	***705.4163***	353.2118	688.3897	344.6985	687.4057	344.2065	6
3	**359.2562**	180.1317	342.2296	171.6184			K	***606.3478***	303.6776	589.3213	295.1643	588.3373	294.6723	5
4	**474.2831**	237.6452	457.2566	229.1319	456.2725	228.6399	D	***404.1888***	202.5980	387.1623	194.0848	386.1783	193.5928	4
5	531.3046	266.1559	514.2780	257.6427	513.2940	257.1506	G	***289.1619***	145.0846	272.1353	136.5713			3
6	588.3260	294.6667	571.2995	286.1534	570.3155	285.6614	G	232.1404	116.5738	215.1139	108.0606			2
7							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **SKSKDR**
Found in **Q9BPV8-2**, Isoform 2 of P2Y purinoceptor 13 OS=Homo sapiens GN=P2RY13

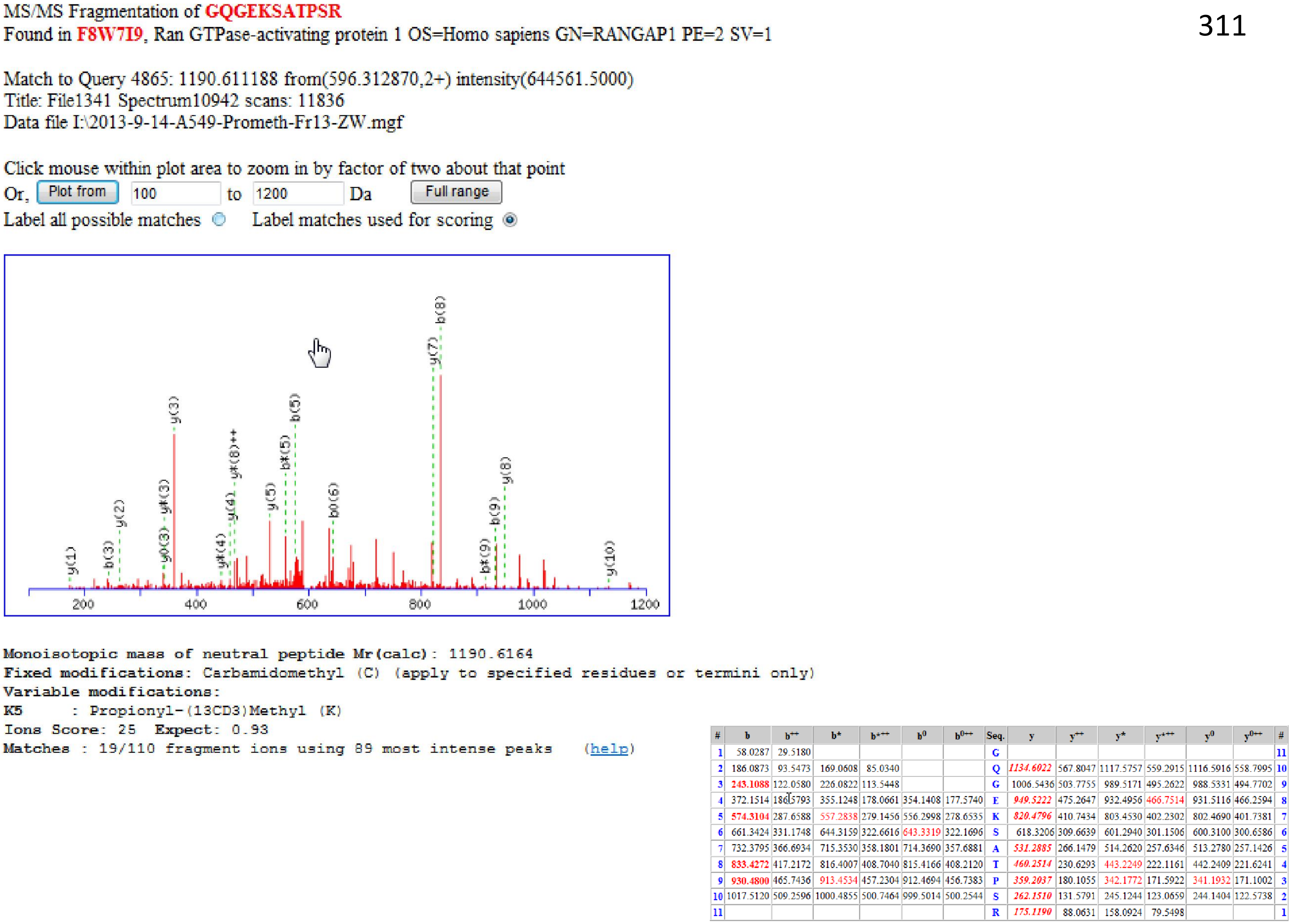
Match to Query 964: 849.483668 from(425.749110,2+) intensity(107069.8672)
Title: File1347 Spectrum2699 scans: 3311
Data file J:\2013-9-14-A549-Prometh-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 849.4828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl (K)
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 41  Expect: 0.026
Matches : 14/56 fragment ions using 15 most intense peaks
```

(help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							6
2	**272.1605**	136.5839	255.1339	128.0706	254.1499	127.5786	K	***763.4581***	382.2327	746.4316	373.7194	745.4475	373.2274	5
3	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	S	***579.3369***	290.1721	562.3104	281.6588	561.3264	281.1668	4
4	**561.3515**	281.1794	544.3250	272.6661	543.3410	272.1741	K	***492.3049***	246.6561	475.2784	238.1428	474.2943	237.6508	3
5	**676.3785**	338.6929	659.3519	330.1796	658.3679	329.6876	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GQGEKSATPSR**

Found in **F8W7I9**, Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=2 SV=1

Match to Query 4865: 1190.611188 from(596.312870,2+) intensity(644561.5000)

Title: File1341 Spectrum10942 scans: 11836

Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.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 ●

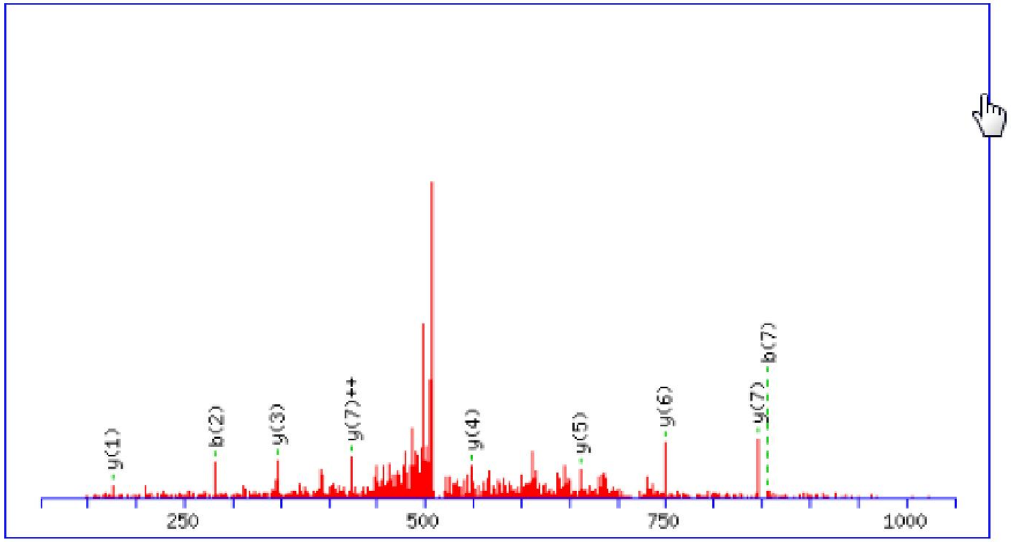
```
Monoisotopic mass of neutral peptide Mr(calc): 1190.6164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5      : Propionyl-(13CD3)Methyl (K)
Ions Score: 25  Expect: 0.93
Matches : 19/110 fragment ions using 89 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							11
2	186.0873	93.5473	169.0608	85.0340			Q	*1134.6022*	567.8047	1117.5757	559.2915	1116.5916	558.7995	10
3	**243.1088**	122.0580	226.0822	113.5448			G	1006.5436	503.7755	989.5171	495.2622	988.5331	494.7702	9
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	E	*949.5222*	475.2647	932.4956	466.7514	931.5116	466.2594	8
5	**574.3104**	287.6588	557.2838	279.1456	556.2998	278.6535	K	*820.4796*	410.7434	803.4530	402.2302	802.4690	401.7381	7
6	661.3424	331.1748	644.3159	322.6616	643.3319	322.1696	S	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
7	732.3795	366.6934	715.3530	358.1801	714.3690	357.6881	A	*531.2885*	266.1479	514.2620	257.6346	513.2780	257.1426	5
8	**833.4272**	417.2172	816.4007	408.7040	815.4166	408.2120	T	*460.2514*	230.6293	443.2249	222.1161	442.2409	221.6241	4
9	**930.4800**	465.7436	913.4534	457.2304	912.4694	456.7383	P	*359.2037*	180.1055	342.1772	171.5922	341.1932	171.1002	3
10	1017.5120	509.2596	1000.4855	500.7464	999.5014	500.2544	S	*262.1510*	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	*175.1190*	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KPSLKGNR**
Found in **Q494U1**, Pleckstrin homology domain-containing family N member 1 OS=Homo sapiens GN=PLEKHN1 PE=1 SV=2

Match to Query 2939: 1028.626068 from(515.320310,2+) intensity(19779.6758)
Title: File1341 Spectrum8010 scans: 8781
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



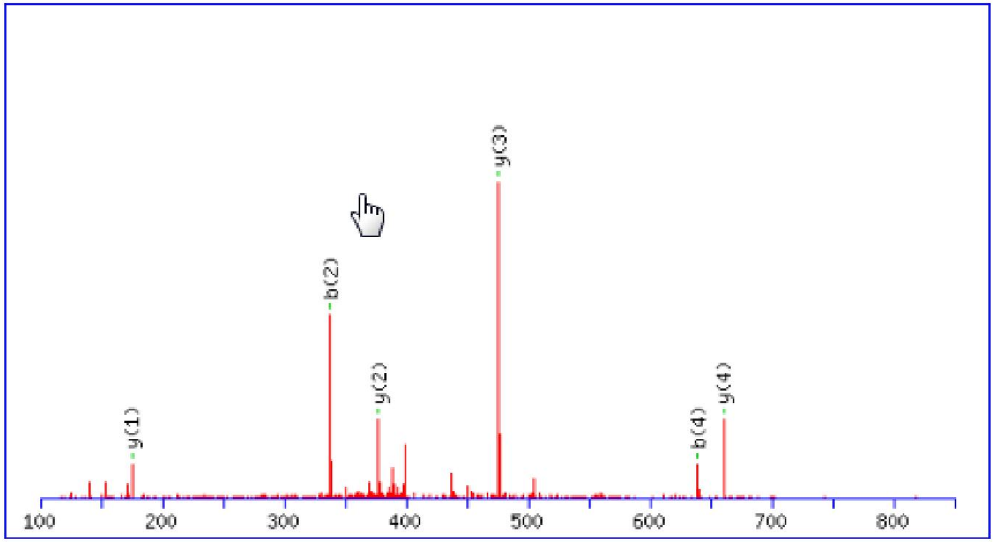
```
Monoisotopic mass of neutral peptide Mr(calc): 1028.6251
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K5      : Propionyl-(13CD3)Methyl (K)
Ions Score: 38  Expect: 0.039
Matches : 9/70 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	**282.1812**	141.5942	265.1547	133.0810			P	***845.5112***	423.2592	828.4847	414.7460	827.5006	414.2540	7
3	369.2132	185.1103	352.1867	176.5970	351.2027	176.1050	S	***748.4584***	374.7329	731.4319	366.2196	730.4479	365.7276	6
4	482.2973	241.6523	465.2708	233.1390	464.2867	232.6470	L	***661.4264***	331.2168	644.3999	322.7036			5
5	684.4563	342.7318	667.4298	334.2185	666.4458	333.7265	K	***548.3424***	274.6748	531.3158	266.1615			4
6	741.4778	371.2425	724.4512	362.7293	723.4672	362.2372	G	***346.1833***	173.5953	329.1568	165.0820			3
7	**855.5207**	428.2640	838.4942	419.7507	837.5101	419.2587	N	289.1619	145.0846	272.1353	136.5713			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

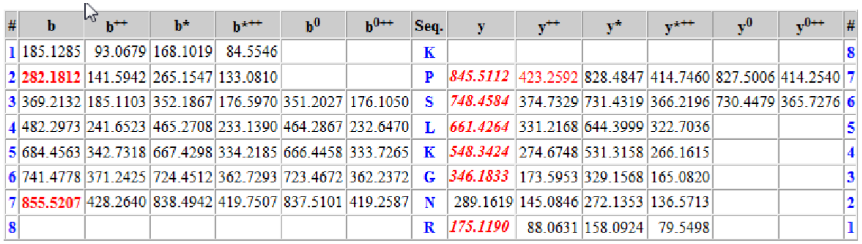
MS/MS Fragmentation of **PKVKR**
Found in **C9JCD9**, Protein BUD31 homolog OS=Homo sapiens GN=BUD31 PE=2 SV=1

Match to Query 781: 812.538788 from(407.276670,2+) intensity(319013.8750)
Title: File1341 Spectrum11041 scans: 11939
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 812.5392
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K2 : Propionyl (K)
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 23 **Expect:** 0.67
Matches : 6/30 fragment ions using 13 most intense peaks (help)

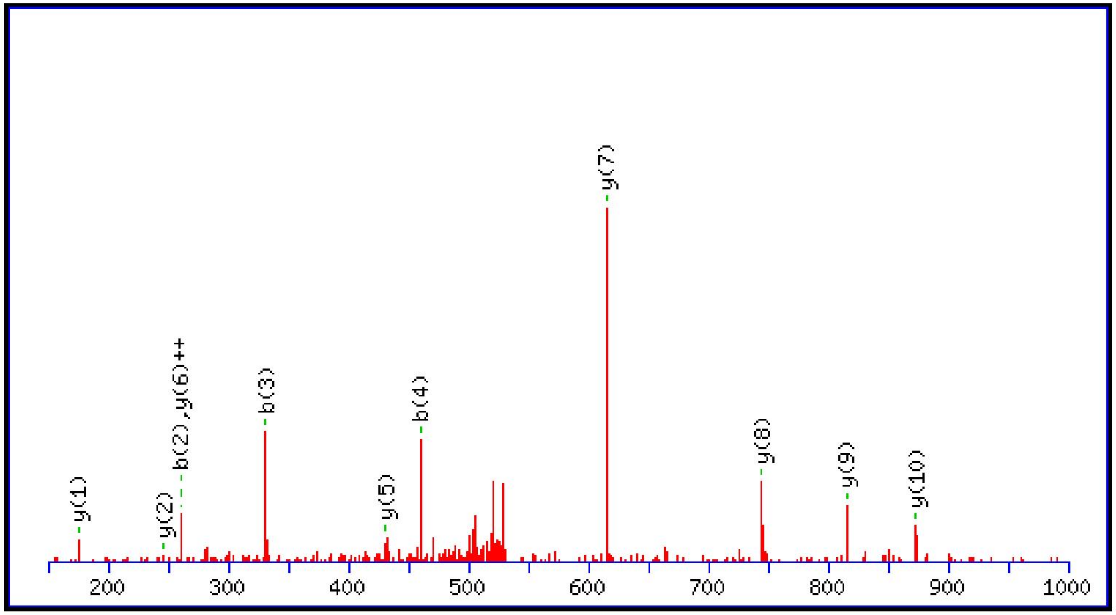


#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	**282.1812**	141.5942	265.1547	133.0810			P	***845.5112***	423.2592	828.4847	414.7460	827.5006	414.2540	7
3	369.2132	185.1103	352.1867	176.5970	351.2027	176.1050	S	***748.4584***	374.7329	731.4319	366.2196	730.4479	365.7276	6
4	482.2973	241.6523	465.2708	233.1390	464.2867	232.6470	L	***661.4264***	331.2168	644.3999	322.7036			5
5	684.4563	342.7318	667.4298	334.2185	666.4458	333.7265	K	***548.3424***	274.6748	531.3158	266.1615			4
6	741.4778	371.2425	724.4512	362.7293	723.4672	362.2372	G	***346.1833***	173.5953	329.1568	165.0820			3
7	**855.5207**	428.2640	838.4942	419.7507	837.5101	419.2587	N	289.1619	145.0846	272.1353	136.5713			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KGAEPSGGAAR**
Found in **K4DI81**, Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=4 SV=1

Match to Query 3436: 1073.573828 from(537.794190,2+) intensity(36450.6797)
Title: File1341 Spectrum2209 scans: 2678
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



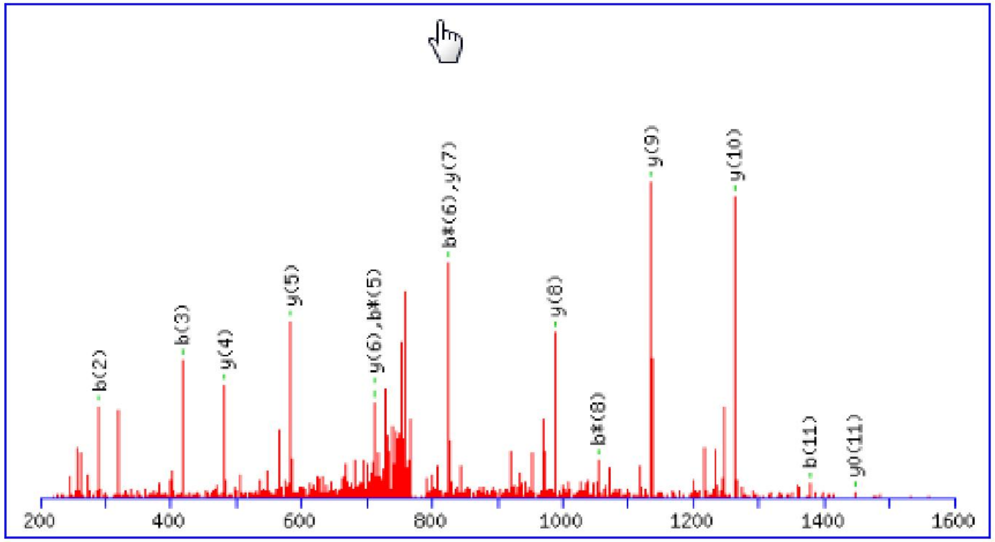
Monoisotopic mass of neutral peptide Mr(calc): 1073.5738
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 51 **Expect:** 0.0028
Matches : 11/104 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	1[illegible]6.1397	93.5735			K							11
2	**260.1878**	130.5975	243.1612	122.0842			G	***872.4221***	436.7147	855.3955	428.2014	854.4115	427.7094	10
3	**331.2249**	166.1161	314.1983	157.6028			A	***815.4006***	408.2039	798.3741	399.6907	797.3900	399.1987	9
4	**460.2675**	230.6374	443.2409	222.1241	442.2569	221.6321	E	***744.3635***	372.6854	727.3369	364.1721	726.3529	363.6801	8
5	557.3202	279.1638	540.2937	270.6505	539.3097	270.1585	P	***615.3209***	308.1641	598.2944	299.6508	597.3103	299.1588	7
6	644.3523	322.6798	627.3257	314.1665	626.3417	313.6745	S	518.2681	259.6377	501.2416	251.1244	500.2576	250.6324	6
7	701.3737	351.1905	684.3472	342.6772	683.3632	342.1852	G	***431.2361***	216.1217	414.2096	207.6084			5
8	758.3952	379.7012	741.3686	371.1880	740.3846	370.6959	G	374.2146	187.6110	357.1881	179.0977			4
9	829.4323	415.2198	812.4057	406.7065	811.4217	406.2145	A	317.1932	159.1002	300.1666	150.5870			3
10	900.4694	450.7383	883.4429	442.2251	882.4588	441.7331	A	***246.1561***	123.5817	229.1295	115.0684			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1

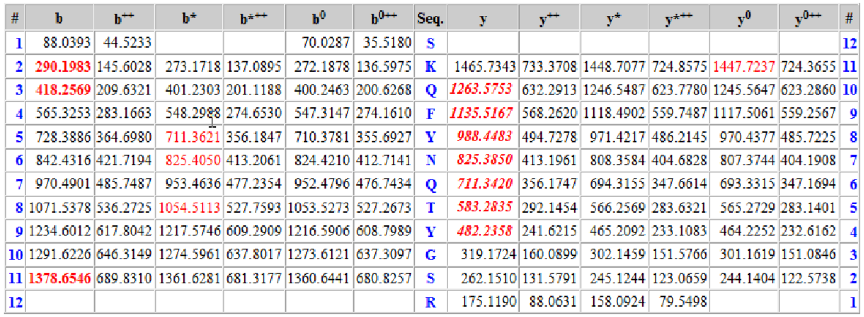
MS/MS Fragmentation of **SKQFYNQTYGSR**
Found in **G3V0I6**, OTU domain containing 4, isoform CRA_f OS=Homo sapiens GN=OTUD4 PE=2 SV=1

Match to Query 9179: 1551.758528 from(776.886540,2+) intensity(124892.4063)
Title: File1341 Spectrum9081 scans: 9897
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1551.7590
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 64 **Expect:** 0.00012
Matches : 14/128 fragment ions using 14 most intense peaks (help)

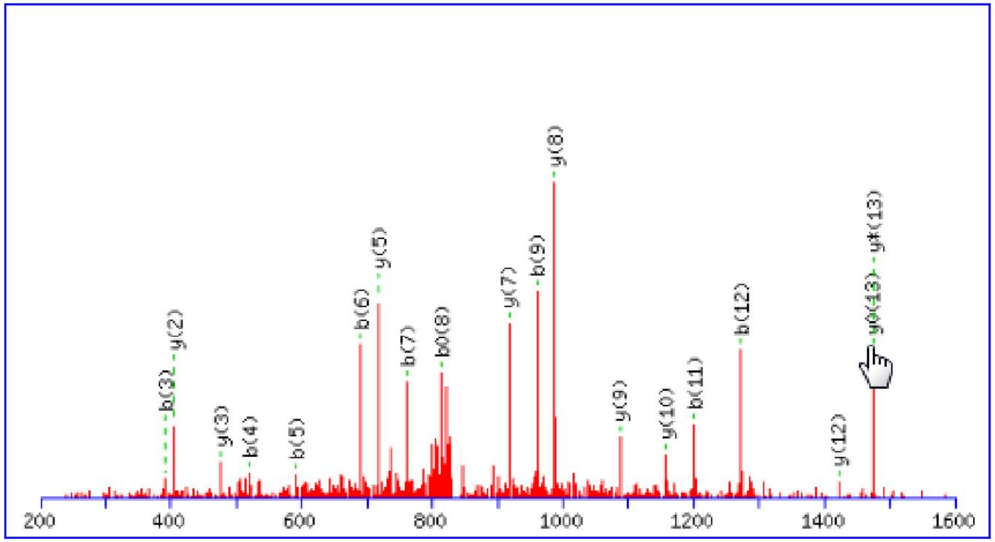


#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	K	1465.7343	733.3708	1448.7077	724.8575	1447.7237	724.3655	11
3	**418.2569**	209.6321	401.2303	201.1188	400.2463	200.6268	Q	***1263.5753***	632.2913	1246.5487	623.7780	1245.5647	623.2860	10
4	565.3253	283.1663	548.2988	274.6530	547.3147	274.1610	F	***1135.5167***	568.2620	1118.4902	559.7487	1117.5061	559.2567	9
5	728.3886	364.6980	711.3621	356.1847	710.3781	355.6927	Y	***988.4483***	494.7278	971.4217	486.2145	970.4377	485.7225	8
6	842.4316	421.7194	825.4050	413.2061	824.4210	412.7141	N	***825.3850***	413.1961	808.3584	404.6828	807.3744	404.1908	7
7	970.4901	485.7487	953.4636	477.2354	952.4796	476.7434	Q	***711.3420***	356.1747	694.3155	347.6614	693.3315	347.1694	6
8	1071.5378	536.2725	1054.5113	527.7593	1053.5273	527.2673	T	***583.2835***	292.1454	566.2569	283.6321	565.2729	283.1401	5
9	1234.6012	617.8042	1217.5746	609.2909	1216.5906	608.7989	Y	***482.2358***	241.6215	465.2092	233.1083	464.2252	232.6162	4
10	1291.6226	646.3149	1274.5961	637.8017	1273.6121	637.3097	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
11	**1378.6546**	689.8310	1361.6281	681.3177	1360.6441	680.8257	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAMEAVAAQGKAKK**
Found in **P18669**, Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2

Match to Query 10447: 1675.972628 from(838.993590,2+) intensity(335509.1875)
Title: File1341 Spectrum11978 scans: 12915
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



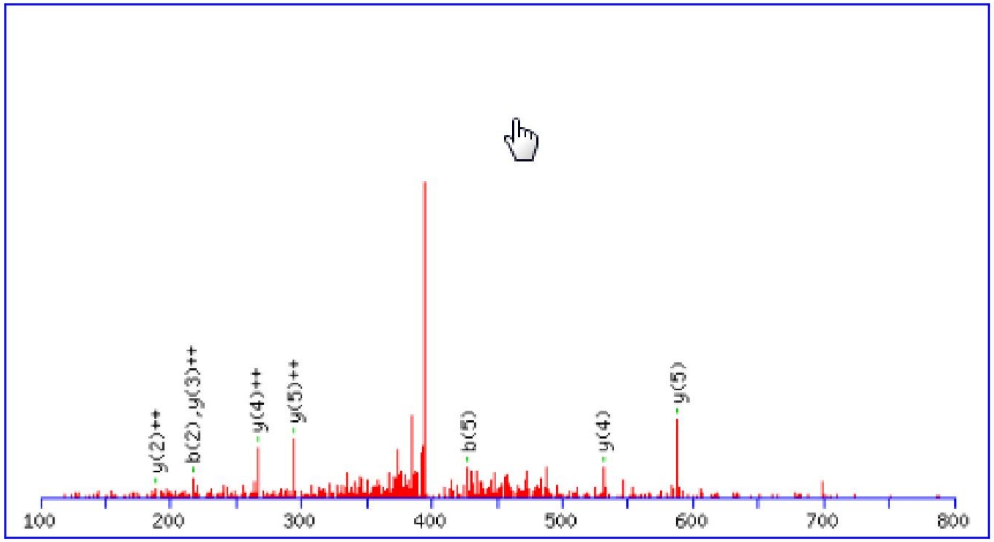
```
Monoisotopic mass of neutral peptide Mr(calc): 1675.9724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1     : Propionyl (K)
M3     : Label:13C(1)2H(3) (M)
K11    : Propionyl (K)
K13    : Propionyl-(13CD3)Methyl (K)
K14    : Propionyl (K)
Ions Score: 66  Expect: 7.8e-005
Matches : 20/130 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	256.1656	128.5864	239.1390	120.0731			A	1492.8585	746.9329	1475.8320	738.4196	1474.8479	737.9276	13
3	***391.2282***	196.1178	374.2017	187.6045			M	***1421.8214***	711.4143	1404.7948	702.9011	1403.8108	702.4090	12
4	***520.2708***	260.6391	503.2443	252.1258	502.2603	251.6338	E	1286.7587	643.8830	1269.7322	635.3697	1268.7482	634.8777	11
5	***591.3079***	296.1576	574.2814	287.6443	573.2974	287.1523	A	***1157.7161***	579.3617	1140.6896	570.8484			10
6	***690.3764***	345.6918	673.3498	337.1785	672.3658	336.6865	V	***1086.6790***	543.8431	1069.6525	535.3299			9
7	***761.4135***	381.2104	744.3869	372.6971	743.4029	372.2051	A	***987.6106***	494.3089	970.5840	485.7957			8
8	832.4506	416.7289	815.4240	408.2157	814.4400	407.7236	A	***916.5735***	458.7904	899.5469	450.2771			7
9	***960.5092***	480.7582	943.4826	472.2449	942.4986	471.7529	Q	845.5364	423.2718	828.5098	414.7585			6
10	1017.5306	509.2690	1000.5041	500.7557	999.5201	500.2637	G	***717.4778***	359.2425	700.4512	350.7293			5
11	***1201.6518***	601.3295	1184.6253	592.8163	1183.6412	592.3243	K	660.4563	330.7318	643.4298	322.2185			4
12	***1272.6889***	636.8481	1255.6624	628.3348	1254.6784	627.8428	A	***476.3351***	238.6712	459.3086	230.1579			3
13	***1474.8479***	737.9276	1457.8214	729.4143	1456.8374	728.9223	K	***405.2980***	203.1527	388.2715	194.6394			2
14							K	203.1390	102.0731	186.1125	93.5599			1

MS/MS Fragmentation of **DTGPGKR**
Found in **A6NHB5**, Zinc finger MYM-type protein 3 OS=Homo sapiens GN=ZMYM3 PE=2 SV=1

Match to Query 510: 803.441808 from(402.728180,2+) intensity(12087.5791)
Title: File1344 Spectrum1354 scans: 2002
Data file I:\2013-9-14-A549-Prometh-Fr12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



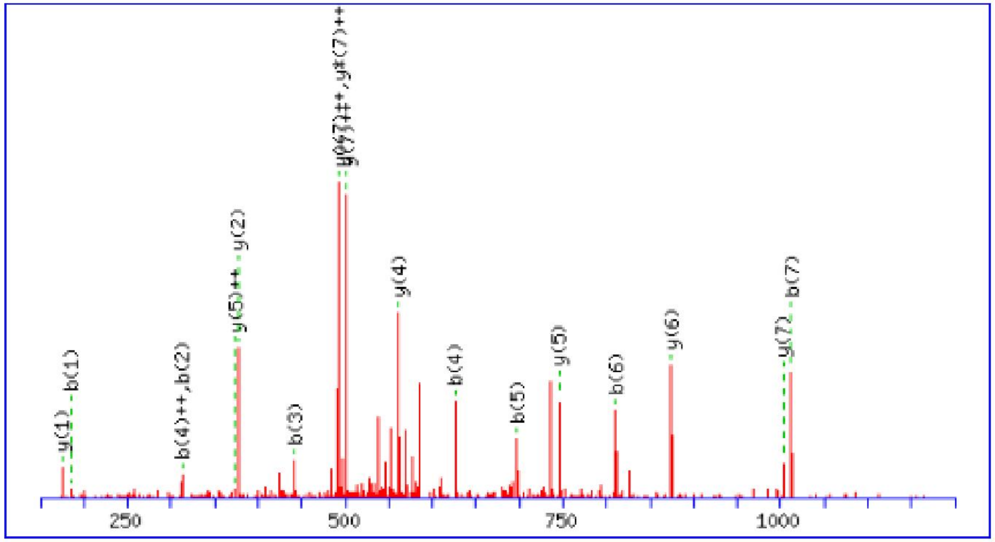
```
Monoisotopic mass of neutral peptide Mr(calc): 803.4410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6      : Propionyl-(13CD3)Methyl (K)
Ions Score: 21  Expect: 2
Matches : 8/52 fragment ions using 21 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207			98.0237	49.5155	D							7
2	**217.0819**	109.0446			199.0713	100.0393	T	689.4213	345.2143	672.3948	336.7010	671.4108	336.2090	6
3	274.1034	137.5553			256.0928	128.5500	G	**588.3737**	294.6905	571.3471	286.1772			5
4	371.1561	186.0817			353.1456	177.0764	P	**531.3522**	266.1797	514.3256	257.6665			4
5	**428.1776**	214.5924			410.1670	205.5872	G	434.2994	217.6534	417.2729	209.1401			3
6	630.3366	315.6719	613.3101	307.1587	612.3260	306.6667	K	377.2780	189.1426	360.2514	180.6293			2
7							R	175.1190	88.0631	158.0924	79.5498			1

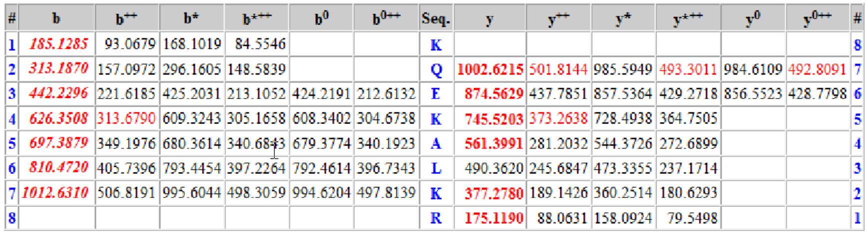
MS/MS Fragmentation of **KQEKALKR**
Found in **A4D1E1**, Zinc finger protein 804B OS=Homo sapiens GN=ZNF804B PE=2 SV=2

Match to Query 4023: 1185.735808 from(593.875180,2+) intensity(435725.2813)
Title: File1344 Spectrum6891 scans: 8054
Data file I:\2013-9-14-A549-Prometh-Fr12-ZW.mgf

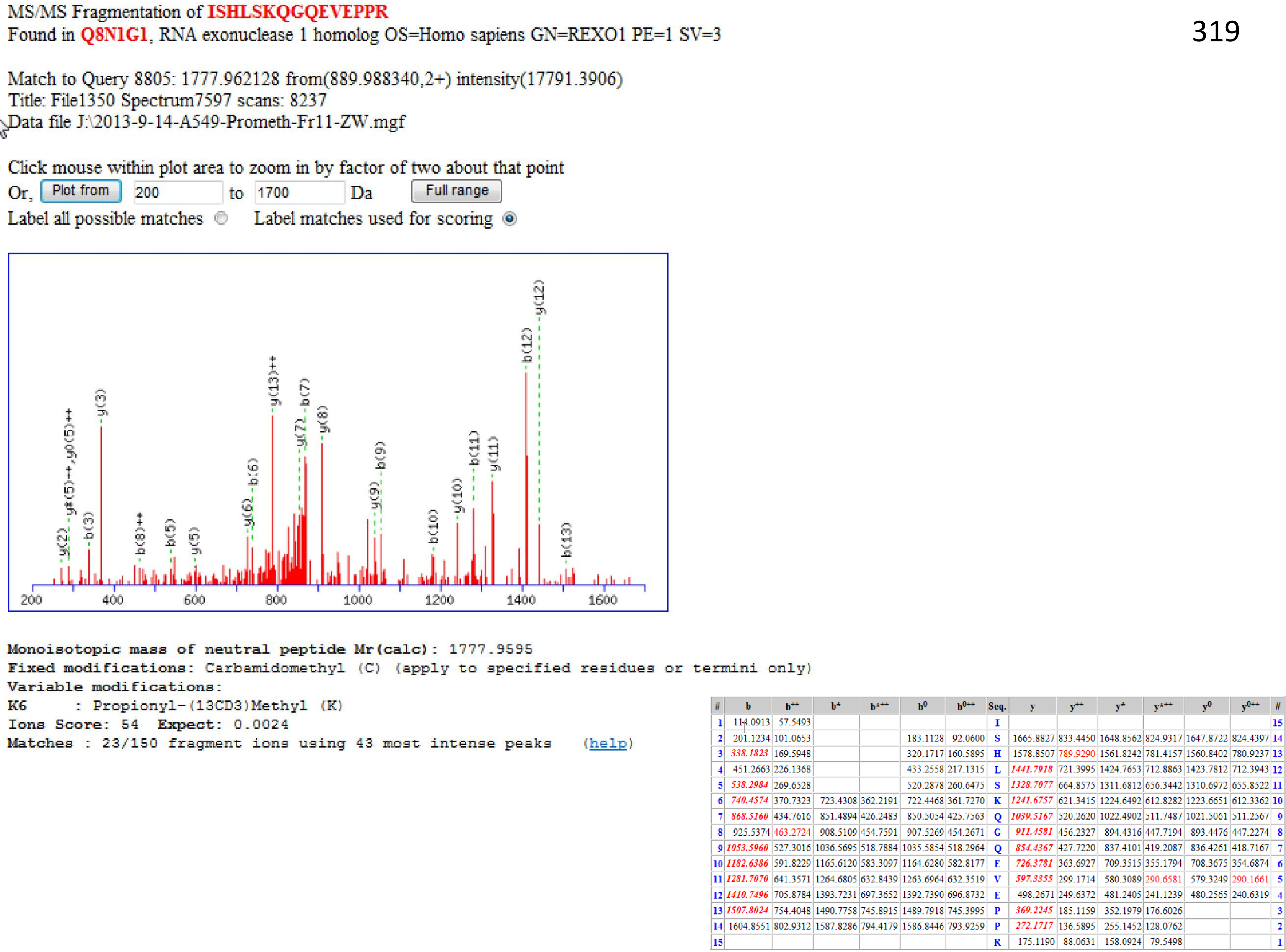
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1185.7354
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K4      : Propionyl (K)
K7      : Propionyl-(13CD3)Methyl (K)
Ions Score: 46  Expect: 0.0042
Matches : 18/70 fragment ions using 30 most intense peaks   (help)
```



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	*185.1285*	93.0679	168.1019	84.5546			K							8
2	*313.1870*	157.0972	296.1605	148.5839			Q	**1002.6215**	501.8144	985.5949	493.3011	984.6109	492.8091	7
3	*442.2296*	221.6185	425.2031	213.1052	424.2191	212.6132	E	**874.5629**	437.7851	857.5364	429.2718	856.5523	428.7798	6
4	*626.3508*	313.6790	609.3243	305.1658	608.3402	304.6738	K	**745.5203**	373.2638	728.4938	364.7505			5
5	*697.3879*	349.1976	680.3614	340.6843	679.3774	340.1923	A	**561.3991**	281.2032	544.3726	272.6899			4
6	*810.4720*	405.7396	793.4454	397.2264	792.4614	396.7343	L	490.3620	245.6847	473.3355	237.1714			3
7	*1012.6310*	506.8191	995.6044	498.3059	994.6204	497.8139	K	**377.2780**	189.1426	360.2514	180.6293			2
8							R	**175.1190**	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **ISHLSKQGQEVEPPR**
Found in **Q8N1G1**, RNA exonuclease 1 homolog OS=Homo sapiens GN=REXO1 PE=1 SV=3

Match to Query 8805: 1777.962128 from(889.988340,2+) intensity(17791.3906)
Title: File1350 Spectrum7597 scans: 8237
Data file J:\2013-9-14-A549-Prometh-Fr11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

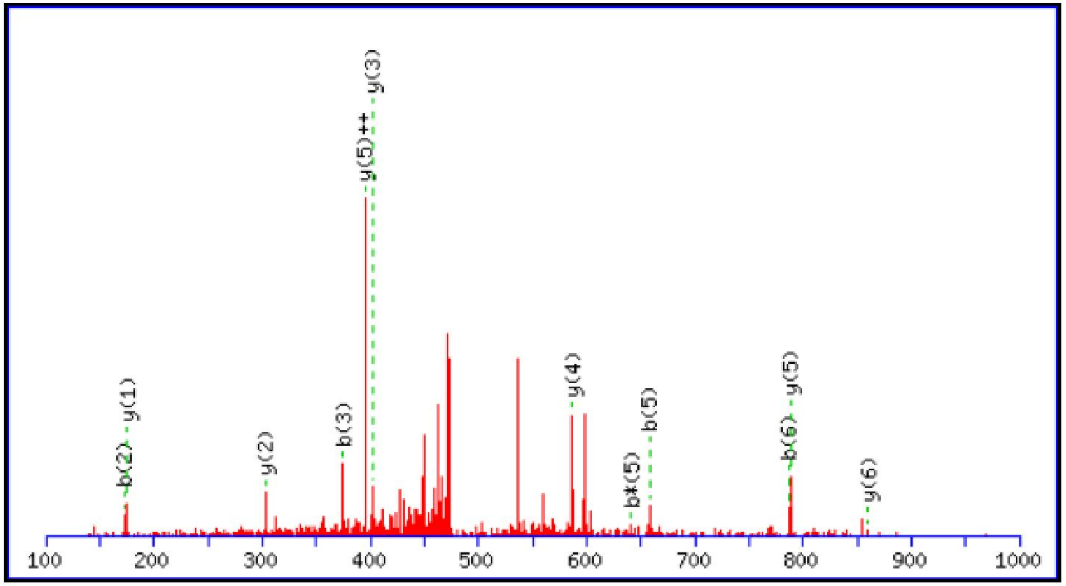
```
Monoisotopic mass of neutral peptide Mr(calc): 1777.9595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6      : Propionyl-(13CD3)Methyl (K)
Ions Score: 54  Expect: 0.0024
Matches : 23/150 fragment ions using 43 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.0913	57.5493					I							15
2	201.1234	101.0653			183.1128	92.0600	S	1665.8827	833.4450	1648.8562	824.9317	1647.8722	824.4397	14
3	***338.1823***	169.5948			320.1717	160.5895	H	1578.8507	789.9290	1561.8242	781.4157	1560.8402	780.9237	13
4	451.2663	226.1368			433.2558	217.1315	L	***1441.7918***	721.3995	1424.7653	712.8863	1423.7812	712.3943	12
5	***538.2984***	269.6528			520.2878	260.6475	S	***1328.7077***	664.8575	1311.6812	656.3442	1310.6972	655.8522	11
6	***740.4574***	370.7323	723.4308	362.2191	722.4468	361.7270	K	***1241.6757***	621.3415	1224.6492	612.8282	1223.6651	612.3362	10
7	***868.5160***	434.7616	851.4894	426.2483	850.5054	425.7563	Q	***1039.5167***	520.2620	1022.4902	511.7487	1021.5061	511.2567	9
8	925.5374	463.2724	908.5109	454.7591	907.5269	454.2671	G	***911.4581***	456.2327	894.4316	447.7194	893.4476	447.2274	8
9	***1053.5960***	527.3016	1036.5695	518.7884	1035.5854	518.2964	Q	***854.4367***	427.7220	837.4101	419.2087	836.4261	418.7167	7
10	***1182.6386***	591.8229	1165.6120	583.3097	1164.6280	582.8177	E	***726.3781***	363.6927	709.3515	355.1794	708.3675	354.6874	6
11	***1281.7070***	641.3571	1264.6805	632.8439	1263.6964	632.3519	V	***597.3355***	299.1714	580.3089	290.6581	579.3249	290.1661	5
12	***1410.7496***	705.8784	1393.7231	697.3652	1392.7390	696.8732	E	498.2671	249.6372	481.2405	241.1239	480.2565	240.6319	4
13	***1507.8024***	754.4048	1490.7758	745.8915	1489.7918	745.3995	P	***369.2245***	185.1159	352.1979	176.6026			3
14	1604.8551	802.9312	1587.8286	794.4179	1586.8446	793.9259	P	***272.1717***	136.5895	255.1452	128.0762			2
15							R	175.1190	88.0631	158.0924	79.5498			1

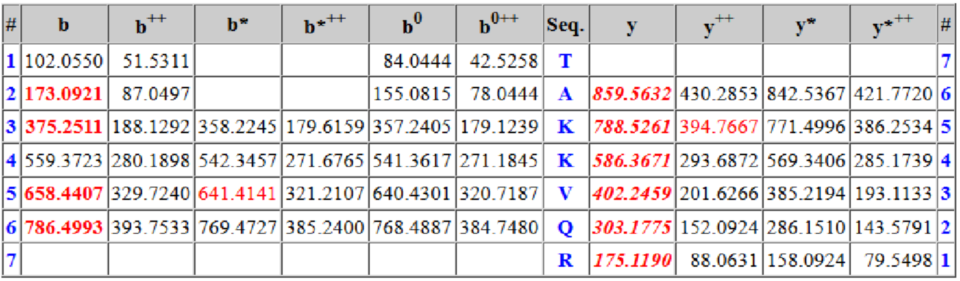
MS/MS Fragmentation of **TAKKVQR**
Found in **B4DY13**, Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=2 SV=1

Match to Query 2365: 959.603068 from(480.808810,2+) intensity(49457.5820)
Title: File1338 Spectrum4649 scans: 5169
Data file I:\2013-9-14-A549-Prometh-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc): 959.6036`
`Fixed modifications: Carbamidomethyl (C) (apply to specified resid`
`Variable modifications:`
`K3 : Propionyl-(13CD3)Methyl (K)`
`K4 : Propionyl (K)`
`Ions Score: 38 Expect: 0.033`
`Matches : 12/56 fragment ions using 24 most intense peaks (help)`

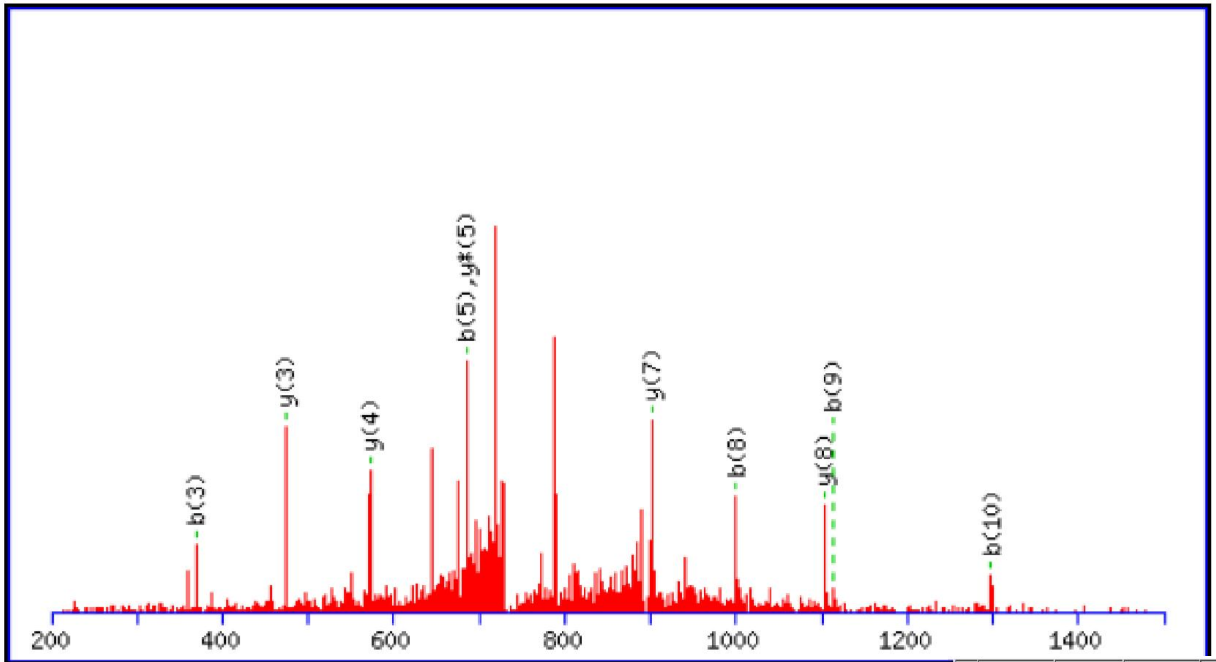


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**					7
2	**173.0921**	87.0497			155.0815	78.0444	**A**	***859.5632***	430.2853	842.5367	421.7720	6
3	**375.2511**	188.1292	358.2245	179.6159	357.2405	179.1239	**K**	***788.5261***	394.7667	771.4996	386.2534	5
4	559.3723	280.1898	542.3457	271.6765	541.3617	271.1845	**K**	***586.3671***	293.6872	569.3406	285.1739	4
5	**658.4407**	329.7240	641.4141	321.2107	640.4301	320.7187	**V**	***402.2459***	201.6266	385.2194	193.1133	3
6	**786.4993**	393.7533	769.4727	385.2400	768.4887	384.7480	**Q**	***303.1775***	152.0924	286.1510	143.5791	2
7							**R**	***175.1190***	88.0631	158.0924	79.5498	1

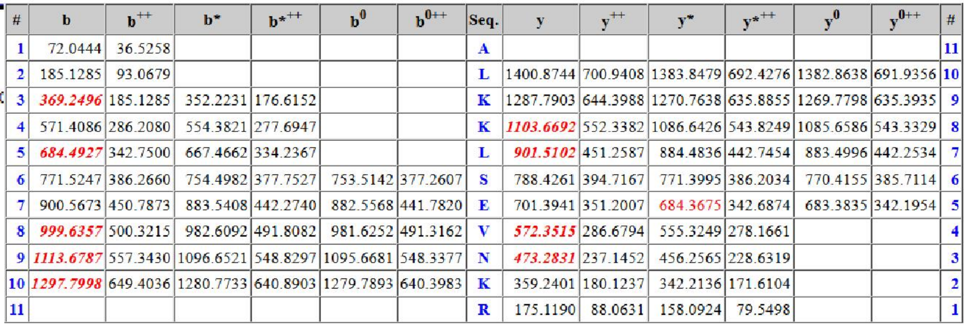
MS/MS Fragmentation of **ALKKLSEVNKR**
Found in **Q8NCF5**, NFATC2-interacting protein OS=Homo sapiens GN=NFATC2IP PE=1 SV=1

Match to Query 7460: 1470.902928 from(736.458740,2+) intensity(34848.6563)
Title: File1338 Spectrum12611 scans: 13505
Data file I:\2013-9-14-A549-Prometh-Fr2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1470.9042
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K3 : Propionyl (K)
K4 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 43 **Expect:** 0.0093
Matches : 10/98 fragment ions using 13 most intense peaks

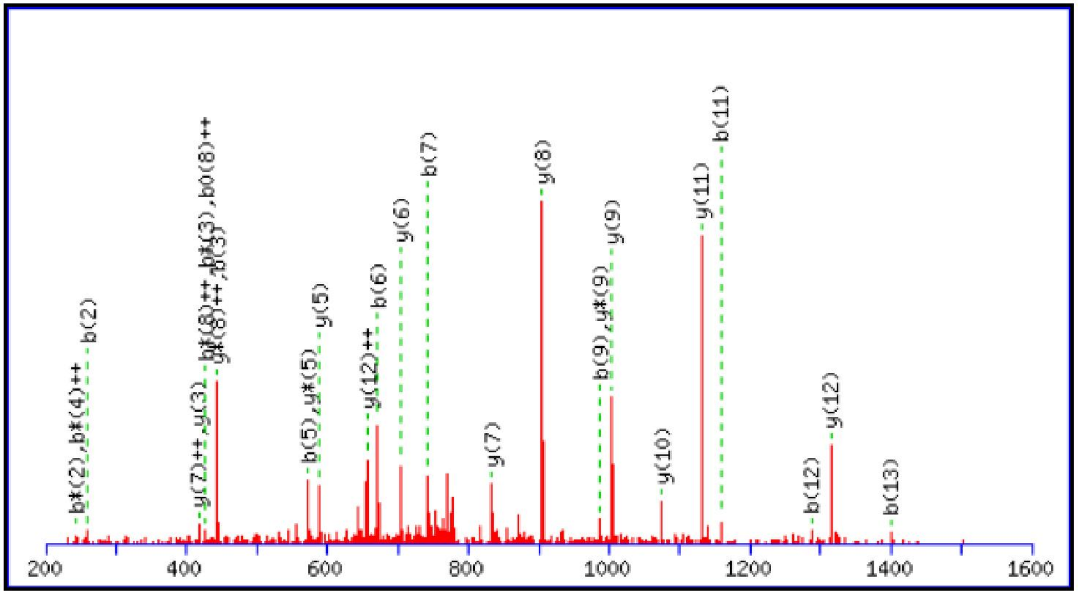


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							11
2	185.1285	93.0679					L	1400.8744	700.9408	1383.8479	692.4276	1382.8638	691.9356	10
3	***369.2496***	185.1285	352.2231	176.6152			K	1287.7903	644.3988	1270.7638	635.8855	1269.7798	635.3935	9
4	571.4086	286.2080	554.3821	277.6947			K	***1103.6692***	552.3382	1086.6426	543.8249	1085.6586	543.3329	8
5	***684.4927***	342.7500	667.4662	334.2367			L	***901.5102***	451.2587	884.4836	442.7454	883.4996	442.2534	7
6	771.5247	386.2660	754.4982	377.7527	753.5142	377.2607	S	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	6
7	900.5673	450.7873	883.5408	442.2740	882.5568	441.7820	E	701.3941	351.2007	684.3675	342.6874	683.3835	342.1954	5
8	***999.6357***	500.3215	982.6092	491.8082	981.6252	491.3162	V	***572.3515***	286.6794	555.3249	278.1661			4
9	***1113.6787***	557.3430	1096.6521	548.8297	1095.6681	548.3377	N	***473.2831***	237.1452	456.2565	228.6319			3
10	***1297.7998***	649.4036	1280.7733	640.8903	1279.7893	640.3983	K	359.2401	180.1237	342.2136	171.6104			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GKKGAVAEDGDELR**
Found in **G3V2D9**, DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=2 SV=1

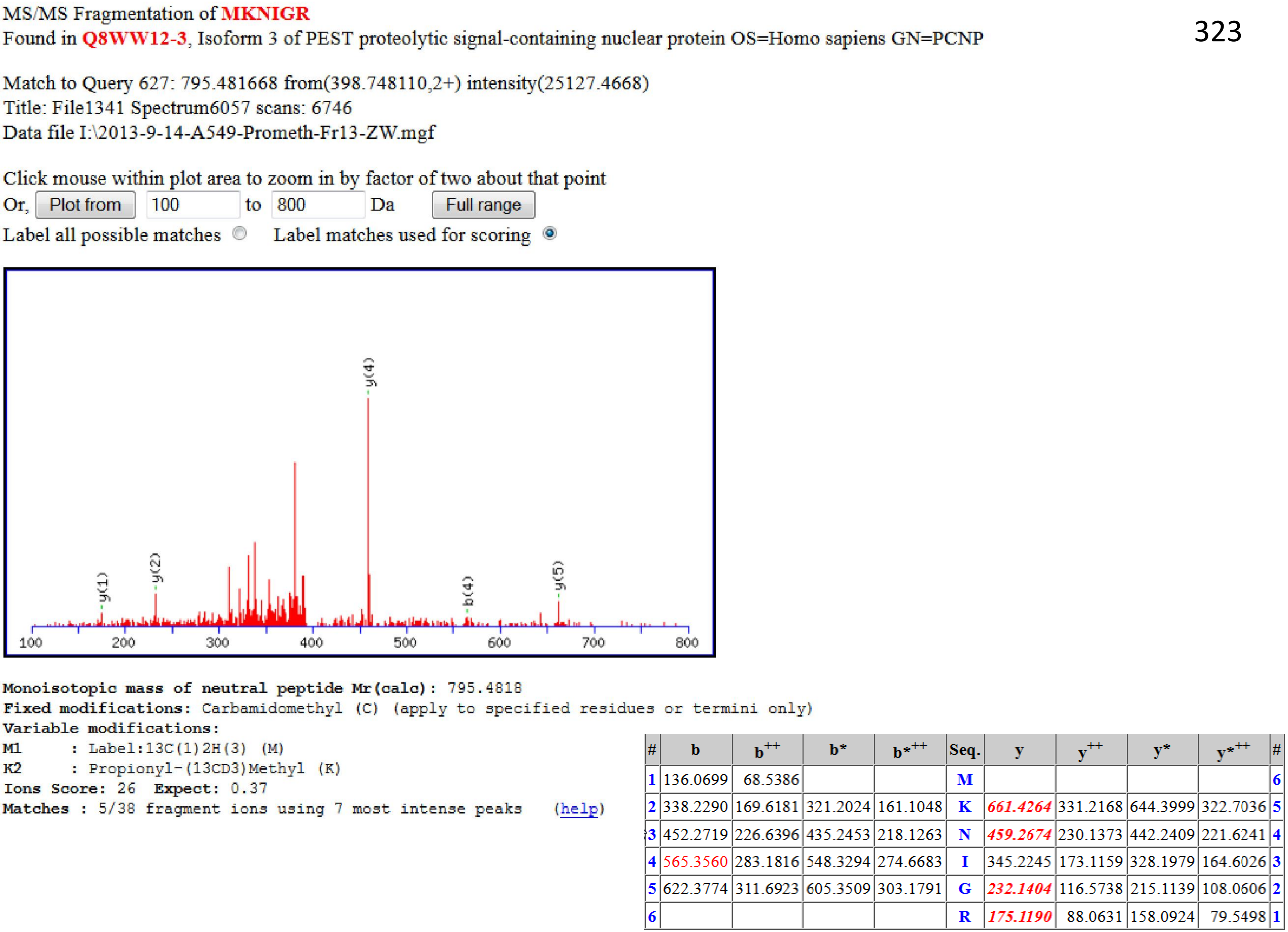
Match to Query 9028: 1573.821988 from(787.918270,2+) intensity(44815.3320)
Title: File1368 Spectrum9031 scans: 9741
Data file J:\2013-9-14-A549-Prometh-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1573.8220
Fixed modifications: Carbamidomethyl (C) (apply to specified residue
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 63 **Expect:** 0.00027
Matches : 28/136 fragment ions using 39 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							14
2	***260.1878***	130.5975	243.1612	122.0842			K	1517.8078	759.4076	1500.7813	750.8943	1499.7973	750.4023	13
3	***444.3089***	222.6581	427.2824	214.1448			K	***1315.6488***	658.3281	1298.6223	649.8148	1297.6383	649.3228	12
4	501.3304	251.1688	484.3038	242.6556			G	***1131.5277***	566.2675	1114.5011	557.7542	1113.5171	557.2622	11
5	***572.3675***	286.6874	555.3410	278.1741			A	***1074.5062***	537.7567	1057.4796	529.2435	1056.4956	528.7515	10
6	***671.4359***	336.2216	654.4094	327.7083			V	***1003.4691***	502.2382	986.4425	493.7249	985.4585	493.2329	9
7	***742.4730***	371.7402	725.4465	363.2269			A	***904.4007***	452.7040	887.3741	444.1907	886.3901	443.6987	8
8	871.5156	436.2615	854.4891	427.7482	853.5051	427.2562	E	***833.3636***	417.1854	816.3370	408.6721	815.3530	408.1801	7
9	***986.5426***	493.7749	969.5160	485.2616	968.5320	484.7696	D	***704.3210***	352.6641	687.2944	344.1508	686.3104	343.6588	6
10	1043.5640	522.2857	1026.5375	513.7724	1025.5535	513.2804	G	***589.2940***	295.1506	572.2675	286.6374	571.2835	286.1454	5
11	***1158.5910***	579.7991	1141.5644	571.2859	1140.5804	570.7938	D	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
12	***1287.6336***	644.3204	1270.6070	635.8071	1269.6230	635.3151	E	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
13	***1400.7176***	700.8625	1383.6911	692.3492	1382.7071	691.8572	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **MKNIGR**
Found in **Q8WW12-3**, Isoform 3 of PEST proteolytic signal-containing nuclear protein OS=Homo sapiens GN=PCNP

Match to Query 627: 795.481668 from(398.748110,2+) intensity(25127.4668)
Title: File1341 Spectrum6057 scans: 6746
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

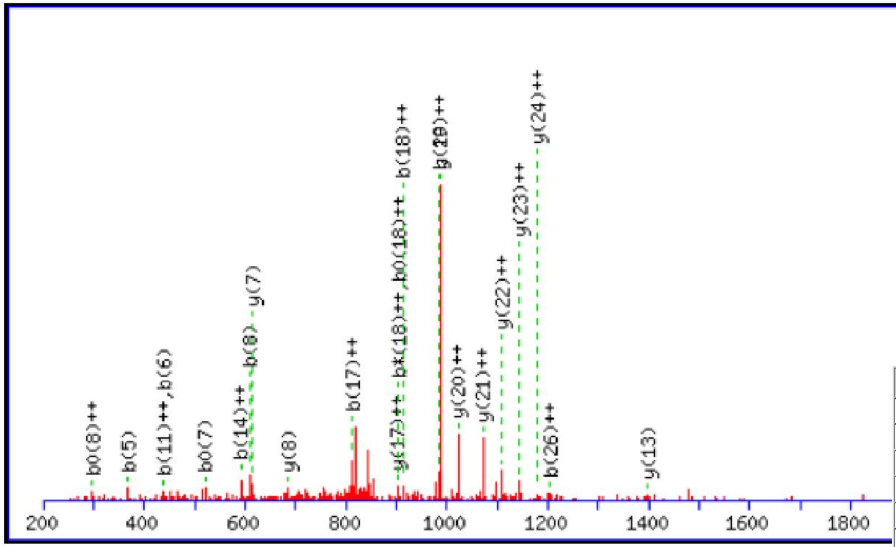
```
Monoisotopic mass of neutral peptide Mr(calc): 795.4818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1      : Label:13C(1)2H(3) (M)
K2      : Propionyl-(13CD3)Methyl (K)
Ions Score: 26  Expect: 0.37
Matches : 5/38 fragment ions using 7 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	136.0699	68.5386			M					6
2	338.2290	169.6181	321.2024	161.1048	K	*661.4264*	331.2168	644.3999	322.7036	5
3	452.2719	226.6396	435.2453	218.1263	N	*459.2674*	230.1373	442.2409	221.6241	4
4	565.3560	283.1816	548.3294	274.6683	I	345.2245	173.1159	328.1979	164.6026	3
5	622.3774	311.6923	605.3509	303.1791	G	*232.1404*	116.5738	215.1139	108.0606	2
6					R	*175.1190*	88.0631	158.0924	79.5498	1

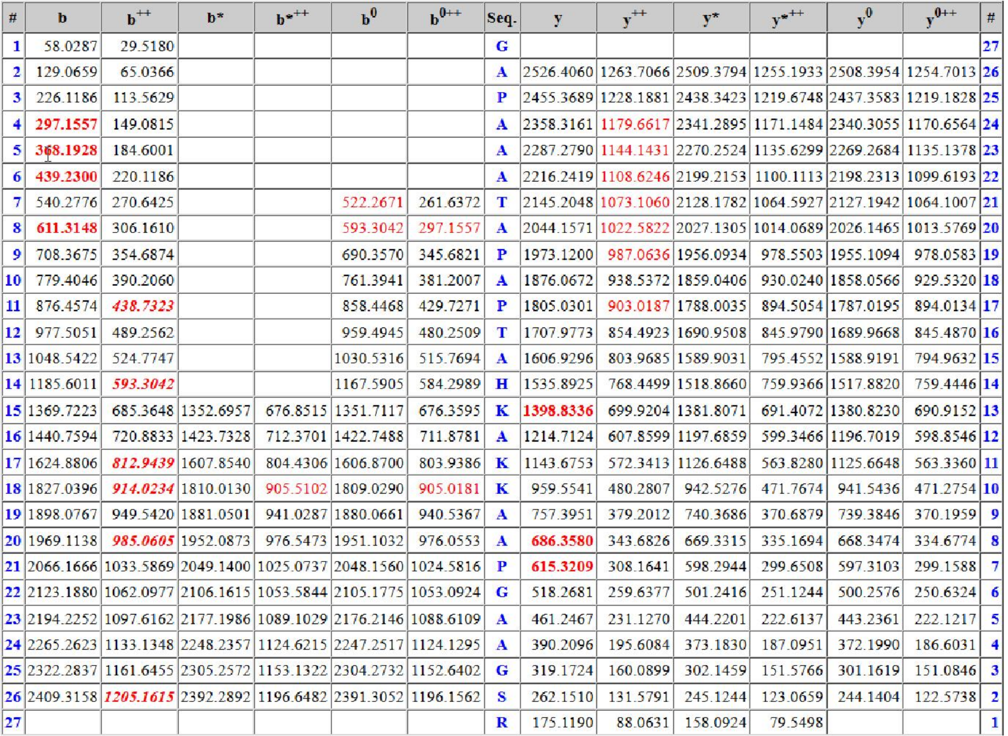
Found in Q92522, Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1

Match to Query 18515: 2582.422812 from(861.814880,3+) intensity(30429.6426)
Title: File1341 Spectrum7601 scans: 8355
Data file I:\2013-9-14-A549-Prometh-Fr13-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2582.4201
Fixed modifications: Carbamidomethyl (C) (apply to specified residue
Variable modifications:
K15 : Propionyl (K)
K17 : Propionyl (K)
K18 : Propionyl-(13CD3)Methyl (K)
Ions Score: 28 **Expect:** 0.88
Matches : 25/270 fragment ions using 58 most intense peaks (help)

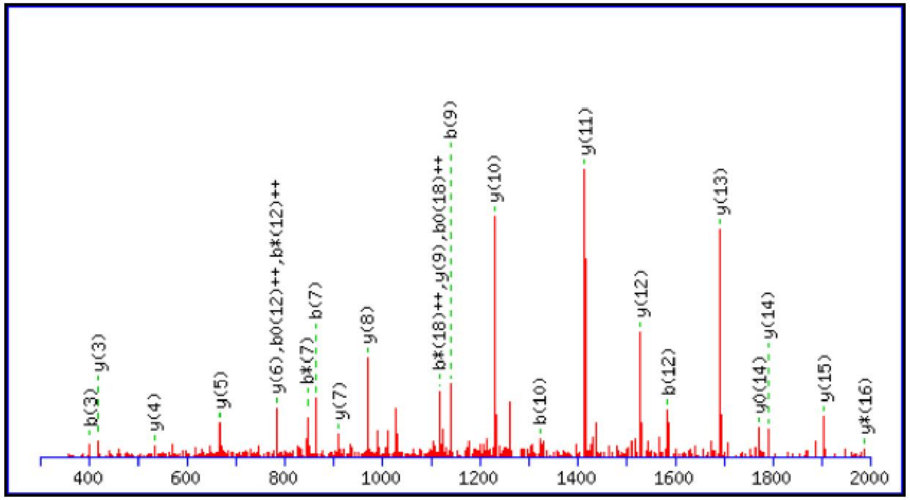


#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							27
2	129.0659	65.0366					A	2526.4060	1263.7066	2509.3794	1255.1933	2508.3954	1254.7013	26
3	226.1186	113.5629					P	2455.3689	1228.1881	2438.3423	1219.6748	2437.3583	1219.1828	25
4	**297.1557**	149.0815					A	2358.3161	1179.6617	2341.2895	1171.1484	2340.3055	1170.6564	24
5	**368.1928**	184.6001					A	2287.2790	1144.1431	2270.2524	1135.6299	2269.2684	1135.1378	23
6	**439.2300**	220.1186					A	2216.2419	1108.6246	2199.2153	1100.1113	2198.2313	1099.6193	22
7	540.2776	270.6425			522.2671	261.6372	T	2145.2048	1073.1060	2128.1782	1064.5927	2127.1942	1064.1007	21
8	**611.3148**	306.1610			593.3042	297.1557	A	2044.1571	1022.5822	2027.1305	1014.0689	2026.1465	1013.5769	20
9	708.3675	354.6874			690.3570	345.6821	P	1973.1200	987.0636	1956.0934	978.5503	1955.1094	978.0583	19
10	779.4046	390.2060			761.3941	381.2007	A	1876.0672	938.5372	1859.0406	930.0240	1858.0566	929.5320	18
11	876.4574	***438.7323***			858.4468	429.7271	P	1805.0301	903.0187	1788.0035	894.5054	1787.0195	894.0134	17
12	977.5051	489.2562			959.4945	480.2509	T	1707.9773	854.4923	1690.9508	845.9790	1689.9668	845.4870	16
13	1048.5422	524.7747			1030.5316	515.7694	A	1606.9296	803.9685	1589.9031	795.4552	1588.9191	794.9632	15
14	1185.6011	***593.3042***			1167.5905	584.2989	H	1535.8925	768.4499	1518.8660	759.9366	1517.8820	759.4446	14
15	1369.7223	685.3648	1352.6957	676.8515	1351.7117	676.3595	K	**1398.8336**	699.9204	1381.8071	691.4072	1380.8230	690.9152	13
16	1440.7594	720.8833	1423.7328	712.3701	1422.7488	711.8781	A	1214.7124	607.8599	1197.6859	599.3466	1196.7019	598.8546	12
17	1624.8806	***812.9439***	1607.8540	804.4306	1606.8700	803.9386	K	1143.6753	572.3413	1126.6488	563.8280	1125.6648	563.3360	11
18	1827.0396	***914.0234***	1810.0130	905.5102	1809.0290	905.0181	K	959.5541	480.2807	942.5276	471.7674	941.5436	471.2754	10
19	1898.0767	949.5420	1881.0501	941.0287	1880.0661	940.5367	A	757.3951	379.2012	740.3686	370.6879	739.3846	370.1959	9
20	1969.1138	***985.0605***	1952.0873	976.5473	1951.1032	976.0553	A	**686.3580**	343.6826	669.3315	335.1694	668.3474	334.6774	8
21	2066.1666	1033.5869	2049.1400	1025.0737	2048.1560	1024.5816	P	**615.3209**	308.1641	598.2944	299.6508	597.3103	299.1588	7
22	2123.1880	1062.0977	2106.1615	1053.5844	2105.1775	1053.0924	G	518.2681	259.6377	501.2416	251.1244	500.2576	250.6324	6
23	2194.2252	1097.6162	2177.1986	1089.1029	2176.2146	1088.6109	A	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	5
24	2265.2623	1133.1348	2248.2357	1124.6215	2247.2517	1124.1295	A	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	4
25	2322.2837	1161.6455	2305.2572	1153.1322	2304.2732	1152.6402	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
26	2409.3158	***1205.1615***	2392.2892	1196.6482	2391.3052	1196.1562	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
27							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AKEFTNVYIKNFGEDMDDER**
Found in **H0YAR2**, Polyadenylate-binding protein 1 (Fragment) OS=Homo sapiens GN=PABPC1 PE=4 SV=1

Match to Query 14545: 2554.211528 from(1278.113040,2+) intensity(57242.3477)
Title: File1365 Spectrum17316 scans: 18289
Data file J:\2013-9-14-A549-Prometh-Fr17-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



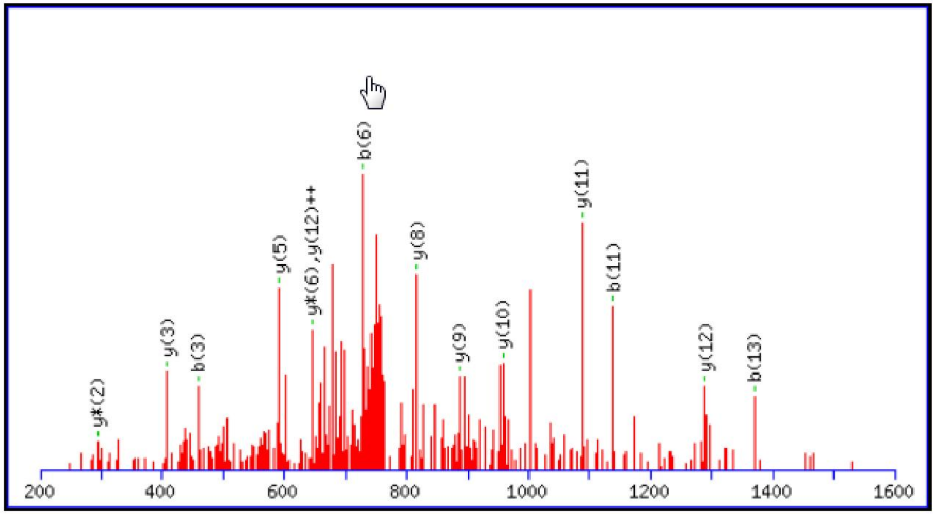
Monoisotopic mass of neutral peptide Mr(calc): 2554.2079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
M16 : Label:13C(1)2H(3) (M)
Ions Score: 87 **Expect:** 7.5e-007
Matches : 25/220 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							20
2	274.2034	137.6053	257.1769	129.0921			K	2484.1781	1242.5927	2467.1515	1234.0794	2466.1675	1233.5874	19
3	**403.2460**	202.1266	386.2194	193.6134	385.2354	193.1214	E	2282.0190	1141.5132	2264.9925	1132.9999	2264.0085	1132.5079	18
4	550.3144	275.6608	533.2879	267.1476	532.3038	266.6556	F	2152.9764	1076.9919	2135.9499	1068.4786	2134.9659	1067.9866	17
5	651.3621	326.1847	634.3355	317.6714	633.3515	317.1794	T	2005.9080	1003.4577	1988.8815	994.9444	1987.8975	994.4524	16
6	765.4050	383.2061	748.3785	374.6929	747.3945	374.2009	N	***1904.8604***	952.9338	1887.8338	944.4205	1886.8498	943.9285	15
7	**864.4734**	432.7404	847.4469	424.2271	846.4629	423.7351	V	***1790.8174***	895.9124	1773.7909	887.3991	1772.8069	886.9071	14
8	1027.5368	514.2720	1010.5102	505.7587	1009.5262	505.2667	Y	***1691.7490***	846.3781	1674.7225	837.8649	1673.7384	837.3729	13
9	**1140.6208**	570.8140	1123.5943	562.3008	1122.6103	561.8088	I	***1528.6857***	764.8465	1511.6591	756.3332	1510.6751	755.8412	12
10	**1324.7420**	662.8746	1307.7155	654.3614	1306.7314	653.8694	K	***1415.6016***	708.3044	1398.5751	699.7912	1397.5911	699.2992	11
11	1438.7849	719.8961	1421.7584	711.3828	1420.7744	710.8908	N	***1231.4804***	616.2439	1214.4539	607.7306	1213.4699	607.2386	10
12	**1585.8533**	793.4303	1568.8268	784.9170	1567.8428	784.4250	F	***1117.4375***	559.2224	1100.4110	550.7091	1099.4270	550.2171	9
13	1642.8748	821.9410	1625.8483	813.4278	1624.8642	812.9358	G	***970.3691***	485.6882	953.3426	477.1749	952.3585	476.6829	8
14	1771.9174	886.4623	1754.8909	877.9491	1753.9068	877.4571	E	***913.3476***	457.1775	896.3211	448.6642	895.3371	448.1722	7
15	1886.9443	943.9758	1869.9178	935.4625	1868.9338	934.9705	D	***784.3050***	392.6562	767.2785	384.1429	766.2945	383.6509	6
16	2022.0070	1011.5071	2004.9805	1002.9939	2003.9964	1002.5019	M	***669.2781***	335.1427	652.2516	326.6294	651.2675	326.1374	5
17	2137.0340	1069.0206	2120.0074	1060.5073	2119.0234	1060.0153	D	***534.2154***	267.6114	517.1889	259.0981	516.2049	258.6061	4
18	2252.0609	1126.5341	2235.0343	1118.0208	2234.0503	1117.5288	D	***419.1885***	210.0979	402.1619	201.5846	401.1779	201.0926	3
19	2381.1035	1191.0554	2364.0769	1182.5421	2363.0929	1182.0501	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of KAKEAAGPAPSPMR
Found in Q12834, Cell division cycle protein 20 homolog OS=Homo sapiens GN=CDC20 PE=1 SV=2

Match to Query 6623: 1543.858248 from(772.936400,2+) intensity(9178.1299)
Title: File1359 Spectrum7752 scans: 8391
Data file J:\2013-9-14-A549-Prometh-Fr7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1543.8573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
M13 : Label:13C(1)2H(3) (M)
Ions Score: 35 **Expect:** 0.17
Matches : 14/144 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	256.1656	128.5864	239.1390	120.0731			A	1360.7435	680.8754	1343.7169	672.3621	1342.7329	671.8701	13
3	**458.3246**	229.6659	441.2980	221.1527			K	***1289.7064***	645.3568	1272.6798	636.8435	1271.6958	636.3515	12
4	587.3672	294.1872	570.3406	285.6740	569.3566	285.1819	E	***1087.5473***	544.2773	1070.5208	535.7640	1069.5368	535.2720	11
5	658.4043	329.7058	641.3777	321.1925	640.3937	320.7005	A	***958.5047***	479.7560	941.4782	471.2427	940.4942	470.7507	10
6	**729.4414**	365.2243	712.4149	356.7111	711.4308	356.2191	A	***887.4676***	444.2375	870.4411	435.7242	869.4571	435.2322	9
7	786.4629	393.7351	769.4363	385.2218	768.4523	384.7298	G	***816.4305***	408.7189	799.4040	400.2056	798.4200	399.7136	8
8	883.5156	442.2615	866.4891	433.7482	865.5051	433.2562	P	759.4091	380.2082	742.3825	371.6949	741.3985	371.2029	7
9	954.5527	477.7800	937.5262	469.2667	936.5422	468.7747	A	662.3563	331.6818	645.3297	323.1685	644.3457	322.6765	6
10	1051.6055	526.3064	1034.5790	517.7931	1033.5949	517.3011	P	***591.3192***	296.1632	574.2926	287.6500	573.3086	287.1579	5
11	**1138.6375**	569.8224	1121.6110	561.3091	1120.6270	560.8171	S	494.2664	247.6368	477.2399	239.1236	476.2558	238.6316	4
12	1235.6903	618.3488	1218.6638	609.8355	1217.6797	609.3435	P	***407.2344***	204.1208	390.2078	195.6076			3
13	**1370.7530**	685.8801	1353.7264	677.3668	1352.7424	676.8748	M	310.1816	155.5944	293.1551	147.0812			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TDFKEEPEPGFKR**

Found in **B4DWJ2**, Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=2 SV=1

Match to Query 9203: 1708.859708 from(855.437130,2+) intensity(8724.8760)

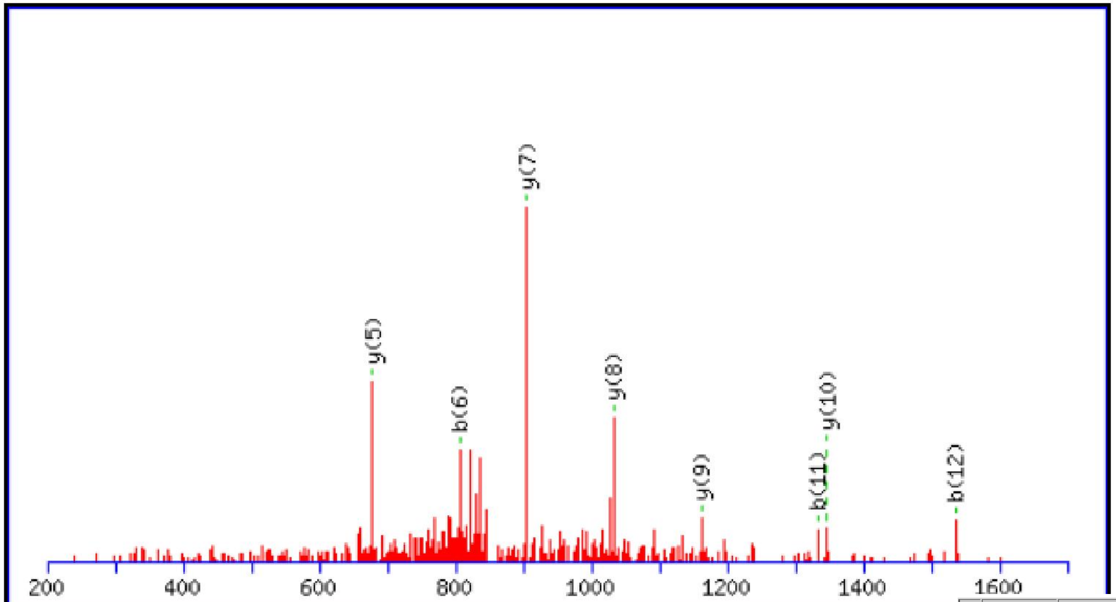
Title: File1356 Spectrum12268 scans: 13111

Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.mgf

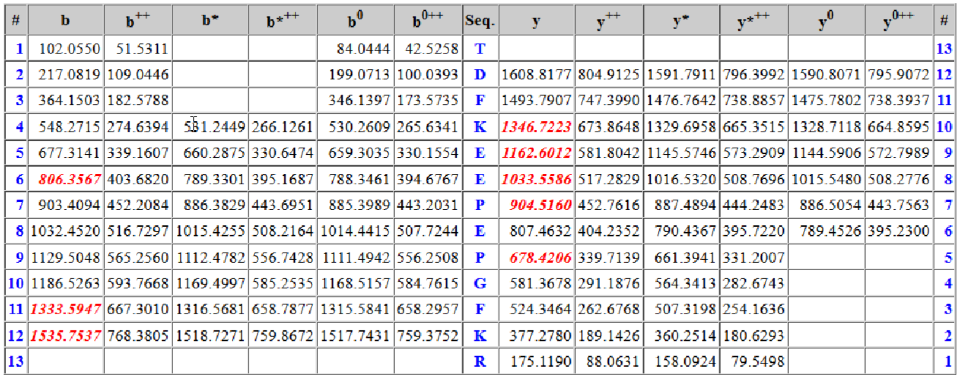
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1700 Da Full range

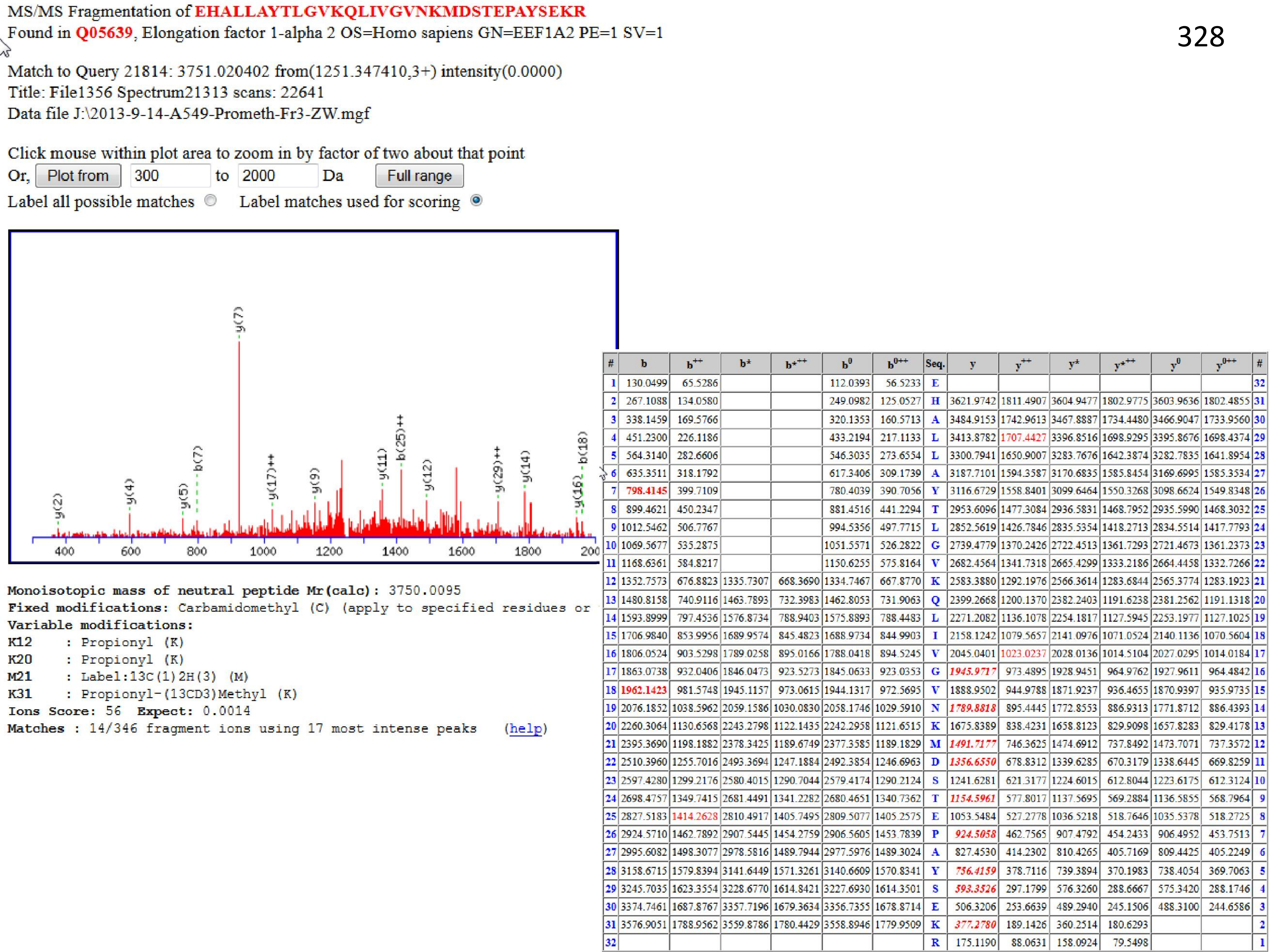
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1708.8581
Fixed modifications: Carbamidomethyl (C) (apply to specified resi
Variable modifications:
K4 : Propionyl (K)
K12 : Propionyl-(13CD3)Methyl (K)
Ions Score: 27 **Expect:** 0.93
Matches : 8/128 fragment ions using 14 most intense peaks (help



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							13
2	217.0819	109.0446			199.0713	100.0393	D	1608.8177	804.9125	1591.7911	796.3992	1590.8071	795.9072	12
3	364.1503	182.5788			346.1397	173.5735	F	1493.7907	747.3990	1476.7642	738.8857	1475.7802	738.3937	11
4	548.2715	274.6394	531.2449	266.1261	530.2609	265.6341	K	***1346.7223***	673.8648	1329.6958	665.3515	1328.7118	664.8595	10
5	677.3141	339.1607	660.2875	330.6474	659.3035	330.1554	E	***1162.6012***	581.8042	1145.5746	573.2909	1144.5906	572.7989	9
6	***806.3567***	403.6820	789.3301	395.1687	788.3461	394.6767	E	***1033.5586***	517.2829	1016.5320	508.7696	1015.5480	508.2776	8
7	903.4094	452.2084	886.3829	443.6951	885.3989	443.2031	P	***904.5160***	452.7616	887.4894	444.2483	886.5054	443.7563	7
8	1032.4520	516.7297	1015.4255	508.2164	1014.4415	507.7244	E	807.4632	404.2352	790.4367	395.7220	789.4526	395.2300	6
9	1129.5048	565.2560	1112.4782	556.7428	1111.4942	556.2508	P	***678.4206***	339.7139	661.3941	331.2007			5
10	1186.5263	593.7668	1169.4997	585.2535	1168.5157	584.7615	G	581.3678	291.1876	564.3413	282.6743			4
11	***1333.5947***	667.3010	1316.5681	658.7877	1315.5841	658.2957	F	524.3464	262.6768	507.3198	254.1636			3
12	***1535.7537***	768.3805	1518.7271	759.8672	1517.7431	759.3752	K	377.2780	189.1426	360.2514	180.6293			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **EHALLAYTLGVKQLIVGVNKMDSTEPAYSEKR**

Found in **Q05639**, Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1

Match to Query 21814: 3751.020402 from(1251.347410,3+) intensity(0.0000)

Title: File1356 Spectrum21313 scans: 22641

Data file J:\2013-9-14-A549-Prometh-Fr3-ZW.mgf

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

Or, Plot from 300 to 2000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

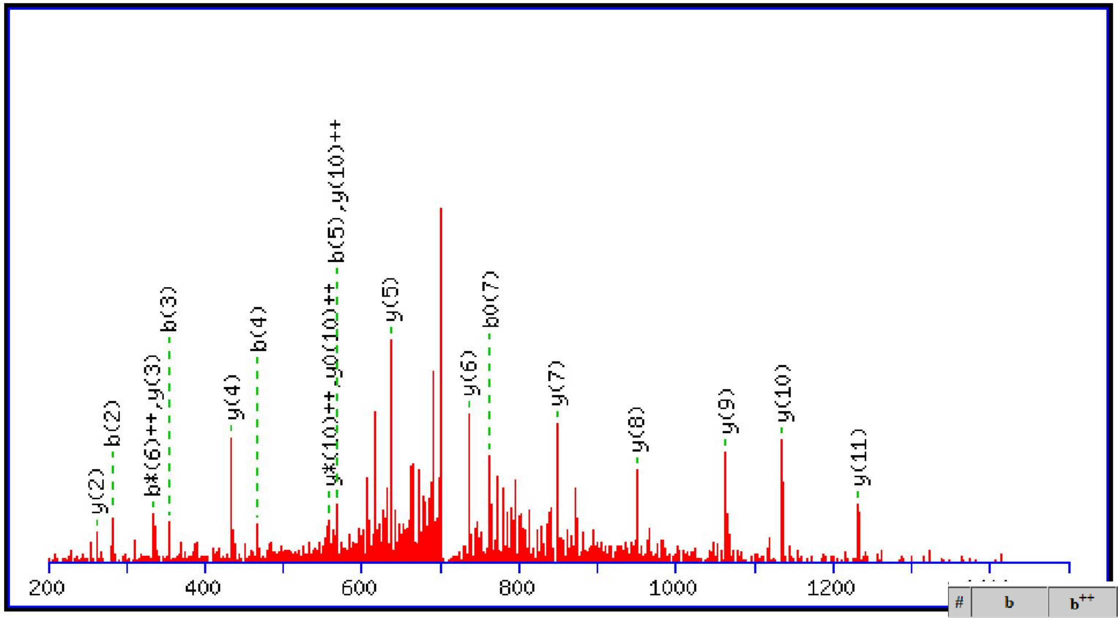
```
Monoisotopic mass of neutral peptide Mr(calc): 3750.0095
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K12    : Propionyl (K)
K20    : Propionyl (K)
M21    : Label:13C(1)2H(3) (M)
K31    : Propionyl-(13CD3)Methyl (K)
Ions Score: 56  Expect: 0.0014
Matches : 14/346 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							32
2	267.1088	134.0580			249.0982	125.0527	H	3621.9742	1811.4907	3604.9477	1802.9775	3603.9636	1802.4855	31
3	338.1459	169.5766			320.1353	160.5713	A	3484.9153	1742.9613	3467.8887	1734.4480	3466.9047	1733.9560	30
4	451.2300	226.1186			433.2194	217.1133	L	3413.8782	1707.4427	3396.8516	1698.9295	3395.8676	1698.4374	29
5	564.3140	282.6606			546.3035	273.6554	L	3300.7941	1650.9007	3283.7676	1642.3874	3282.7835	1641.8954	28
6	635.3511	318.1792			617.3406	309.1739	A	3187.7101	1594.3587	3170.6835	1585.8454	3169.6995	1585.3534	27
7	**798.4145**	399.7109			780.4039	390.7056	Y	3116.6729	1558.8401	3099.6464	1550.3268	3098.6624	1549.8348	26
8	899.4621	450.2347			881.4516	441.2294	T	2953.6096	1477.3084	2936.5831	1468.7952	2935.5990	1468.3032	25
9	1012.5462	506.7767			994.5356	497.7715	L	2852.5619	1426.7846	2835.5354	1418.2713	2834.5514	1417.7793	24
10	1069.5677	535.2875			1051.5571	526.2822	G	2739.4779	1370.2426	2722.4513	1361.7293	2721.4673	1361.2373	23
11	1168.6361	584.8217			1150.6255	575.8164	V	2682.4564	1341.7318	2665.4299	1333.2186	2664.4458	1332.7266	22
12	1352.7573	676.8823	1335.7307	668.3690	1334.7467	667.8770	K	2583.3880	1292.1976	2566.3614	1283.6844	2565.3774	1283.1923	21
13	1480.8158	740.9116	1463.7893	732.3983	1462.8053	731.9063	Q	2399.2668	1200.1370	2382.2403	1191.6238	2381.2562	1191.1318	20
14	1593.8999	797.4536	1576.8734	788.9403	1575.8893	788.4483	L	2271.2082	1136.1078	2254.1817	1127.5945	2253.1977	1127.1025	19
15	1706.9840	853.9956	1689.9574	845.4823	1688.9734	844.9903	I	2158.1242	1079.5657	2141.0976	1071.0524	2140.1136	1070.5604	18
16	1806.0524	903.5298	1789.0258	895.0166	1788.0418	894.5245	V	2045.0401	1023.0237	2028.0136	1014.5104	2027.0295	1014.0184	17
17	1863.0738	932.0406	1846.0473	923.5273	1845.0633	923.0353	G	***1945.9717***	973.4895	1928.9451	964.9762	1927.9611	964.4842	16
18	**1962.1423**	981.5748	1945.1157	973.0615	1944.1317	972.5695	V	1888.9502	944.9788	1871.9237	936.4655	1870.9397	935.9735	15
19	2076.1852	1038.5962	2059.1586	1030.0830	2058.1746	1029.5910	N	***1789.8818***	895.4445	1772.8553	886.9313	1771.8712	886.4393	14
20	2260.3064	1130.6568	2243.2798	1122.1435	2242.2958	1121.6515	K	1675.8389	838.4231	1658.8123	829.9098	1657.8283	829.4178	13
21	2395.3690	1198.1882	2378.3425	1189.6749	2377.3585	1189.1829	M	***1491.7177***	746.3625	1474.6912	737.8492	1473.7071	737.3572	12
22	2510.3960	1255.7016	2493.3694	1247.1884	2492.3854	1246.6963	D	***1356.6550***	678.8312	1339.6285	670.3179	1338.6445	669.8259	11
23	2597.4280	1299.2176	2580.4015	1290.7044	2579.4174	1290.2124	S	1241.6281	621.3177	1224.6015	612.8044	1223.6175	612.3124	10
24	2698.4757	1349.7415	2681.4491	1341.2282	2680.4651	1340.7362	T	***1154.5961***	577.8017	1137.5695	569.2884	1136.5855	568.7964	9
25	2827.5183	1414.2628	2810.4917	1405.7495	2809.5077	1405.2575	E	1053.5484	527.2778	1036.5218	518.7646	1035.5378	518.2725	8
26	2924.5710	1462.7892	2907.5445	1454.2759	2906.5605	1453.7839	P	***924.5058***	462.7565	907.4792	454.2433	906.4952	453.7513	7
27	2995.6082	1498.3077	2978.5816	1489.7944	2977.5976	1489.3024	A	827.4530	414.2302	810.4265	405.7169	809.4425	405.2249	6
28	3158.6715	1579.8394	3141.6449	1571.3261	3140.6609	1570.8341	Y	***756.4159***	378.7116	739.3894	370.1983	738.4054	369.7063	5
29	3245.7035	1623.3554	3228.6770	1614.8421	3227.6930	1614.3501	S	***593.3526***	297.1799	576.3260	288.6667	575.3420	288.1746	4
30	3374.7461	1687.8767	3357.7196	1679.3634	3356.7355	1678.8714	E	506.3206	253.6639	489.2940	245.1506	488.3100	244.6586	3
31	3576.9051	1788.9562	3559.8786	1780.4429	3558.8946	1779.9509	K	***377.2780***	189.1426	360.2514	180.6293			2
32							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KPANTLVKTASR**
Found in **Q9Y6X9**, MORC family CW-type zinc finger protein 2 OS=Homo sapiens GN=MORC2 PE=1 SV=2

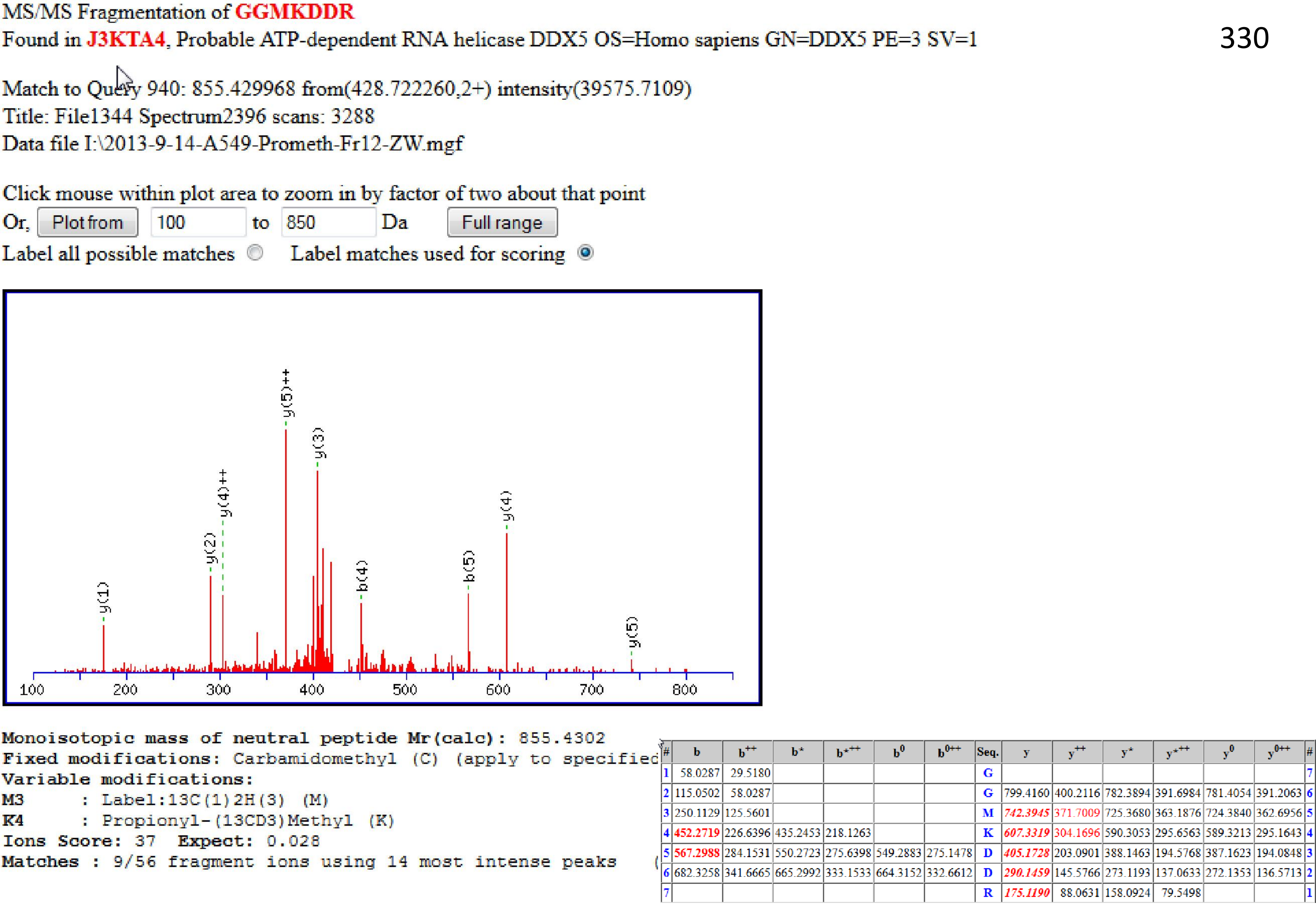
Match to Query 6421: 1414.842128 from(708.428340,2+) intensity(52117.8945)
Title: File1347 Spectrum8753 scans: 9724
Data file J:\2013-9-14-A549-Prometh-Fr15-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1414.8416
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K1      : Propionyl (K)
K8      : Propionyl-(13CD3)Methyl (K)
Ions Score: 80  Expect: 3.4e-006
Matches : 19/122 fragment ions using 26 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							12
2	**282.1812**	141.5942	265.1547	133.0810			P	***1231.7277***	616.3675	1214.7012	607.8542	1213.7172	607.3622	11
3	**353.2183**	177.1128	336.1918	168.5995			A	***1134.6750***	567.8411	1117.6484	559.3279	1116.6644	558.8358	10
4	**467.2613**	234.1343	450.2347	225.6210			N	***1063.6379***	532.3226	1046.6113	523.8093	1045.6273	523.3173	9
5	**568.3089**	284.6581	551.2824	276.1448	550.2984	275.6528	T	***949.5949***	475.3011	932.5684	466.7878	931.5844	466.2958	8
6	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	L	***848.5473***	424.7773	831.5207	416.2640	830.5367	415.7720	7
7	780.4614	390.7343	763.4349	382.2211	762.4509	381.7291	V	***735.4632***	368.2352	718.4367	359.7220	717.4526	359.2300	6
8	982.6204	491.8139	965.5939	483.3006	964.6099	482.8086	K	***636.3948***	318.7010	619.3682	310.1878	618.3842	309.6957	5
9	1083.6681	542.3377	1066.6416	533.8244	1065.6575	533.3324	T	***434.2358***	217.6215	417.2092	209.1082	416.2252	208.6162	4
10	1154.7052	577.8562	1137.6787	569.3430	1136.6947	568.8510	A	***333.1881***	167.0977	316.1615	158.5844	315.1775	158.0924	3
11	1241.7372	621.3723	1224.7107	612.8590	1223.7267	612.3670	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GGMKDDR**

Found in **J3KTA4**, Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=3 SV=1

Match to Query 940: 855.429968 from(428.722260,2+) intensity(39575.7109)

Title: File1344 Spectrum2396 scans: 3288

Data file I:\2013-9-14-A549-Prometh-Fr12-ZW.mgf

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

Or, Plot from 100 to 850 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 855.4302

Fixed modifications: Carbamidomethyl (C) (apply to specifie

Variable modifications:

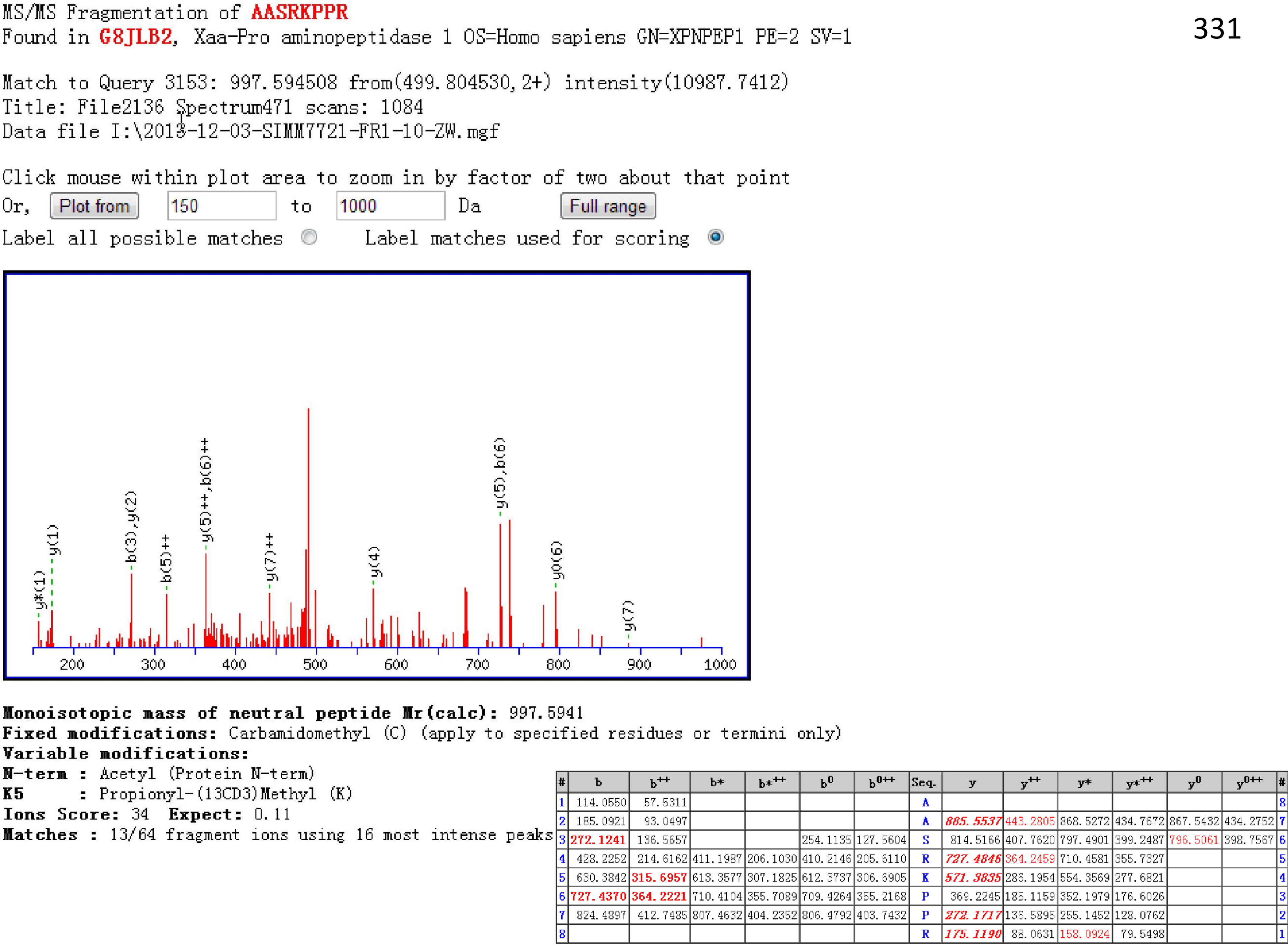
M3 : Label:13C(1)2H(3) (M)

K4 : Propionyl-(13CD3)Methyl (K)

Ions Score: 37 **Expect:** 0.028

Matches : 9/56 fragment ions using 14 most intense peaks (

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							7
2	115.0502	58.0287					G	799.4160	400.2116	782.3894	391.6984	781.4054	391.2063	6
3	250.1129	125.5601					M	***742.3945***	371.7009	725.3680	363.1876	724.3840	362.6956	5
4	**452.2719**	226.6396	435.2453	218.1263			K	***607.3319***	304.1696	590.3053	295.6563	589.3213	295.1643	4
5	**567.2988**	284.1531	550.2723	275.6398	549.2883	275.1478	D	***405.1728***	203.0901	388.1463	194.5768	387.1623	194.0848	3
6	682.3258	341.6665	665.2992	333.1533	664.3152	332.6612	D	***290.1459***	145.5766	273.1193	137.0633	272.1353	136.5713	2
7							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of AASRKPPR
Found in G8JLB2, Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=2 SV=1

Match to Query 3153: 997.594508 from(499.804530,2+) intensity(10987.7412)
Title: File2136 Spectrum471 scans: 1084
Data file I:\2013-12-03-SIMM7721-FR1-10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, 150 to 1000 Da
Label all possible matches ○ Label matches used for scoring ●

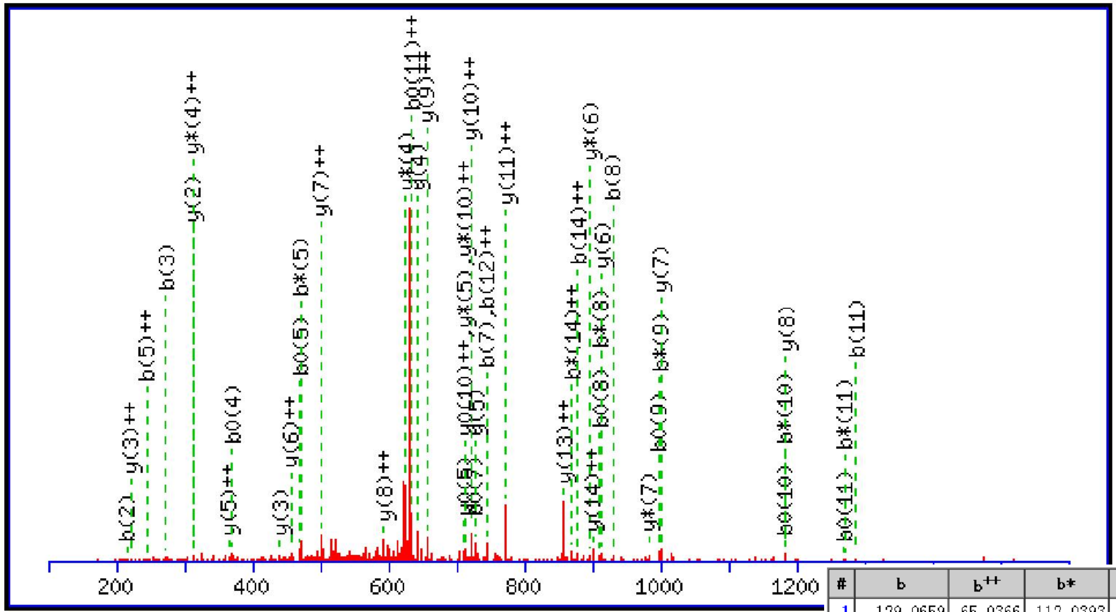
Monoisotopic mass of neutral peptide Mr(calc): 997.5941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 34 **Expect:** 0.11
Matches : 13/64 fragment ions using 16 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	114.0550	57.5311					A							8
2	185.0921	93.0497					A	***885.5537***	443.2805	868.5272	434.7672	867.5432	434.2752	7
3	**272.1241**	136.5657			254.1135	127.5604	S	814.5166	407.7620	797.4901	399.2487	796.5061	398.7567	6
4	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	R	***727.4846***	364.2459	710.4581	355.7327			5
5	630.3842	**315.6957**	613.3577	307.1825	612.3737	306.6905	K	***571.3835***	286.1954	554.3569	277.6821			4
6	**727.4370**	**364.2221**	710.4104	355.7089	709.4264	355.2168	P	369.2245	185.1159	352.1979	176.6026			3
7	824.4897	412.7485	807.4632	404.2352	806.4792	403.7432	P	***272.1717***	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **QSGNTEQKSKSKQHR**
Found in **A9IYQ1**, Sister chromatid cohesion protein PDS5 homolog B (Fragment) OS=Homo sapiens GN=PDS5B PE=2 SV=1

Match to Query 12808: 1927.997652 from(643.673160,3+) intensity(30005.7617)
Title: File2136 Spectrum3681 scans: 4551
Data file I:\2013-12-03-SIMM7721-FR1-10-ZW.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 ●



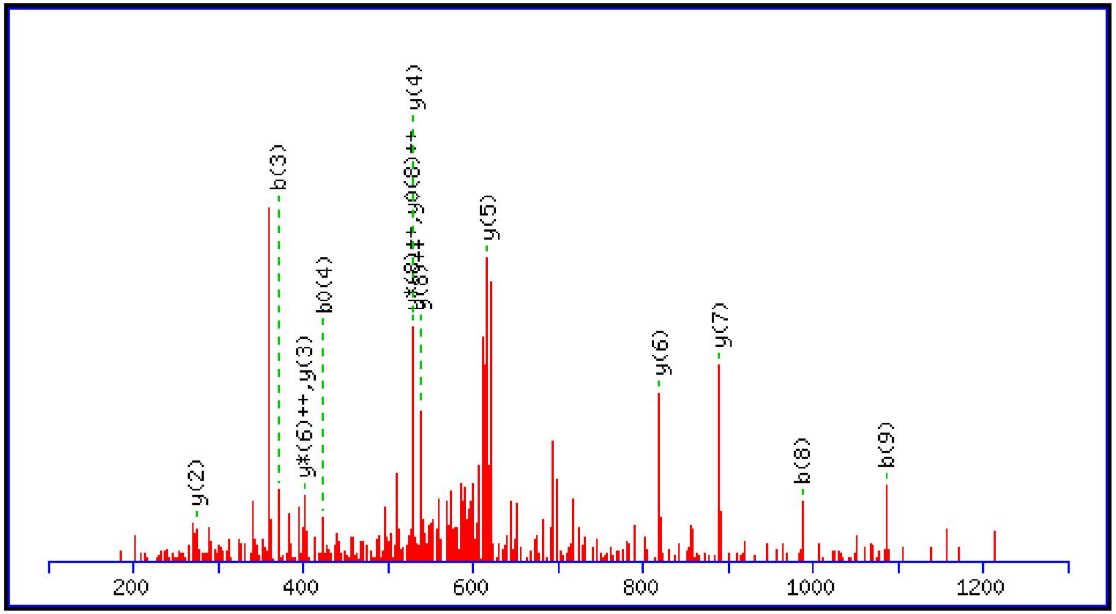
Monoisotopic mass of neutral peptide Mr(calc): 1927.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K8 : Propionyl (K)
K10 : Propionyl (K)
K12 : Propionyl-(13CD3)Methyl (K)
Ions Score: 34 **Expect:** 0.25
Matches : 47/158 fragment ions using 103 most intense peal

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							15
2	**216.0979**	108.5526	199.0713	100.0393	198.0873	99.5473	S	1800.9471	900.9772	1783.9206	892.4639	1782.9366	891.9719	14
3	**273.1193**	137.0633	256.0928	128.5500	255.1088	128.0580	G	1713.9151	857.4612	1696.8886	848.9479	1695.9045	848.4559	13
4	387.1623	194.0848	370.1357	185.5715	369.1517	185.0795	N	1656.8936	828.9505	1639.8671	820.4372	1638.8831	819.9452	12
5	488.2100	244.6086	471.1834	236.0953	470.1994	235.6033	T	1542.8507	771.9290	1525.8242	763.4157	1524.8402	762.9237	11
6	617.2525	309.1299	600.2260	300.6166	599.2420	300.1246	E	1441.8030	721.4052	1424.7765	712.8919	1423.7925	712.3999	10
7	**745.3111**	373.1592	728.2846	364.6459	727.3006	364.1539	Q	1312.7604	656.8839	1295.7339	648.3706	1294.7499	647.8786	9
8	**929.4323**	465.2198	912.4058	456.7065	911.4217	456.2145	K	**1184.7019**	592.8546	1167.6753	584.3413	1166.6913	583.8493	8
9	1016.4643	508.7358	999.4378	500.2225	998.4538	499.7305	S	**1000.5807**	500.7940	983.5541	492.2807	982.5701	491.7887	7
10	1200.5855	600.7964	1183.5590	592.2831	1182.5749	591.7911	K	**913.5487**	457.2780	896.5221	448.7647	895.5381	448.2727	6
11	**1287.6175**	644.3124	1270.5910	635.7991	1269.6070	635.3071	S	**729.4275**	365.2174	712.4009	356.7041	711.4169	356.2121	5
12	1489.7765	745.3919	1472.7500	736.8786	1471.7660	736.3866	K	**642.3955**	321.7014	625.3689	313.1881			4
13	1617.8351	809.4212	1600.8086	800.9079	1599.8246	800.4159	Q	**440.2364**	220.6219	423.2099	212.1086			3
14	1754.8940	877.9507	1737.8675	869.4374	1736.8835	868.9454	H	**312.1779**	156.5926	295.1513	148.0793			2
15							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ADKAKSQQVR**
Found in **H7C0Q2**, Glucocorticoid-induced transcript 1 protein (Fragment) OS=Homo sapiens GN=GLCCI1 PE=2 SV=1

Match to Query 6763: 1259.711648 from(630.863100,2+) intensity(9468.4912)
Title: File2136 Spectrum4390 scans: 5310
Data file I:\2013-12-03-SIMM7721-FR1-10-ZW.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 ●



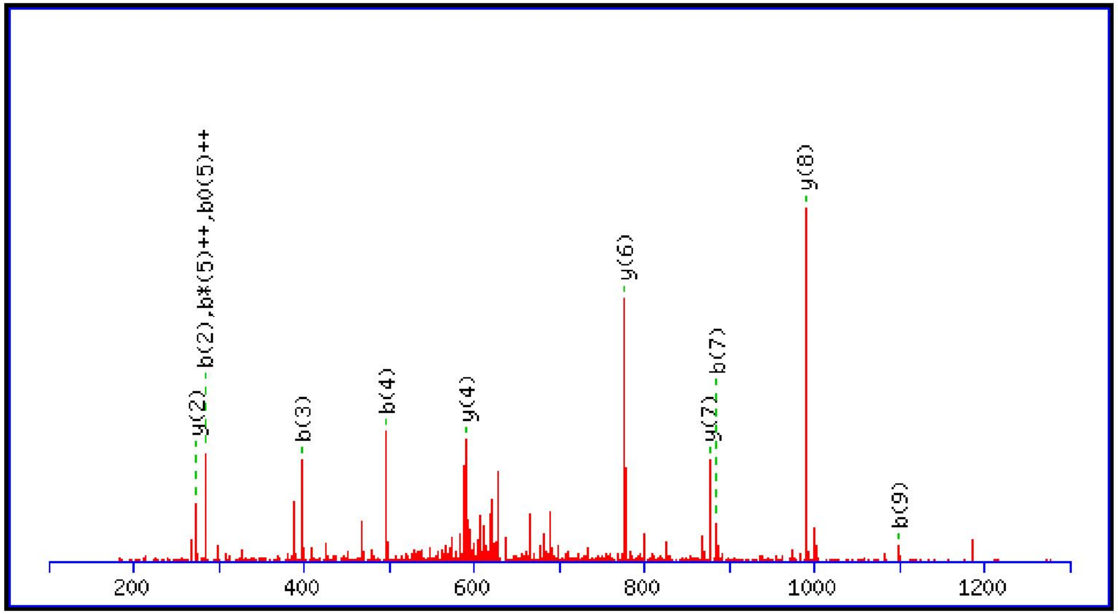
Monoisotopic mass of neutral peptide Mr(calc): 1259.7106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 24 **Expect:** 2
Matches : 14/94 fragment ions using 33 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							10
2	187.0713	94.0393			169.0608	85.0340	D	1189.6808	595.3440	1172.6542	586.8308	1171.6702	586.3388	9
3	**371.1925**	186.0999	354.1660	177.5866	353.1819	177.0946	K	1074.6539	537.8306	1057.6273	529.3173	1056.6433	528.8253	8
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	A	***890.5327***	445.7700	873.5061	437.2567	872.5221	436.7647	7
5	644.3886	322.6980	627.3621	314.1847	626.3781	313.6927	K	***819.4956***	410.2514	802.4690	401.7381	801.4850	401.2461	6
6	731.4207	366.2140	714.3941	357.7007	713.4101	357.2087	S	***617.3366***	309.1719	600.3100	300.6586	599.3260	300.1666	5
7	859.4792	430.2433	842.4527	421.7300	841.4687	421.2380	Q	***530.3045***	265.6559	513.2780	257.1426			4
8	**987.5378**	494.2725	970.5113	485.7593	969.5273	485.2673	Q	***402.2459***	201.6266	385.2194	193.1133			3
9	**1086.6062**	543.8068	1069.5797	535.2935	1068.5957	534.8015	V	***274.1874***	137.5973	257.1608	129.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VKNVSVKDVR**
Found in **Q5VTE0**, Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1

Match to Query 6289: 1272.766208 from(637.390380,2+) intensity(306396.1563)
Title: File2138 Spectrum9095 scans: 10259
Data file I:\2013-12-03-SIMM7721-FR1-11-ZW.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 ●



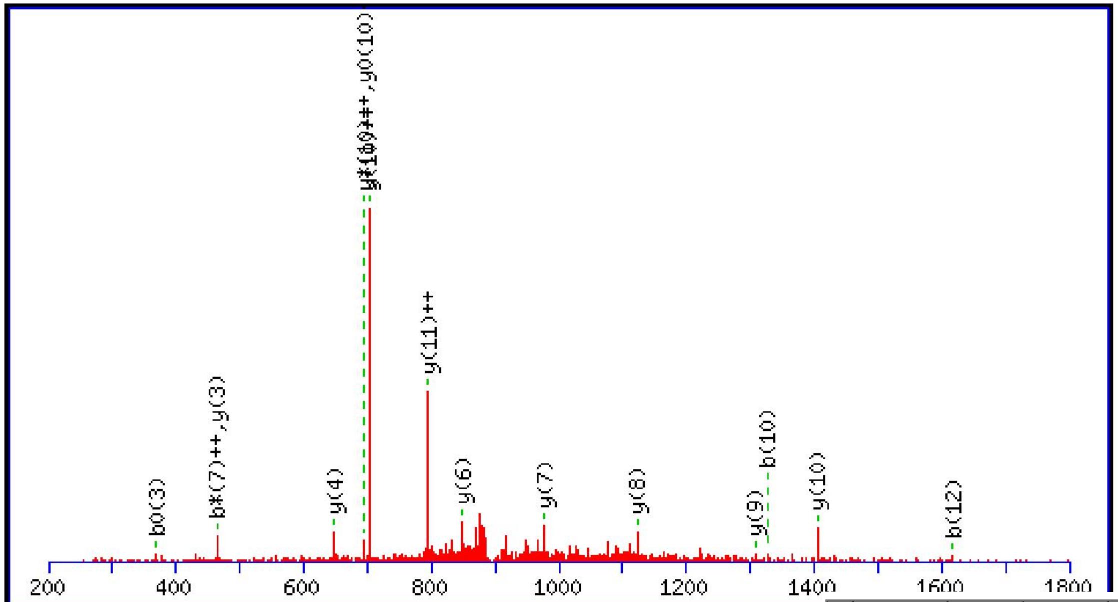
Monoisotopic mass of neutral peptide Mr(calc): 1272.7674
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl (K)
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 54 **Expect:** 0.0011
Matches : 12/94 fragment ions using 11 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415					V							10
2	***284.1969***	142.6021	267.1703	134.0888			K	1174.7063	587.8568	1157.6797	579.3435	1156.6957	578.8515	9
3	***398.2398***	199.6235	381.2132	191.1103			N	***990.5851***	495.7962	973.5586	487.2829	972.5745	486.7909	8
4	***497.3082***	249.1577	480.2817	240.6445			V	***876.5422***	438.7747	859.5156	430.2615	858.5316	429.7694	7
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	S	***777.4738***	389.2405	760.4472	380.7272	759.4632	380.2352	6
6	683.4087	342.2080	666.3821	333.6947	665.3981	333.2027	V	690.4417	345.7245	673.4152	337.2112	672.4312	336.7192	5
7	***885.5677***	443.2875	868.5411	434.7742	867.5571	434.2822	K	***591.3733***	296.1903	574.3468	287.6770	573.3628	287.1850	4
8	1000.5946	500.8009	983.5681	492.2877	982.5840	491.7957	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
9	***1099.6630***	550.3351	1082.6365	541.8219	1081.6525	541.3299	V	***274.1874***	137.5973	257.1608	129.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LSWPKFQSIKSKR**
Found in **Q8IVF2**, Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2

Match to Query 13911: 1790.038428 from(896.026490,2+) intensity(62980.0117)
Title: File2138 Spectrum17295 scans: 18827
Data file I:\2013-12-03-SIMM7721-FR1-11-ZW.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 ●



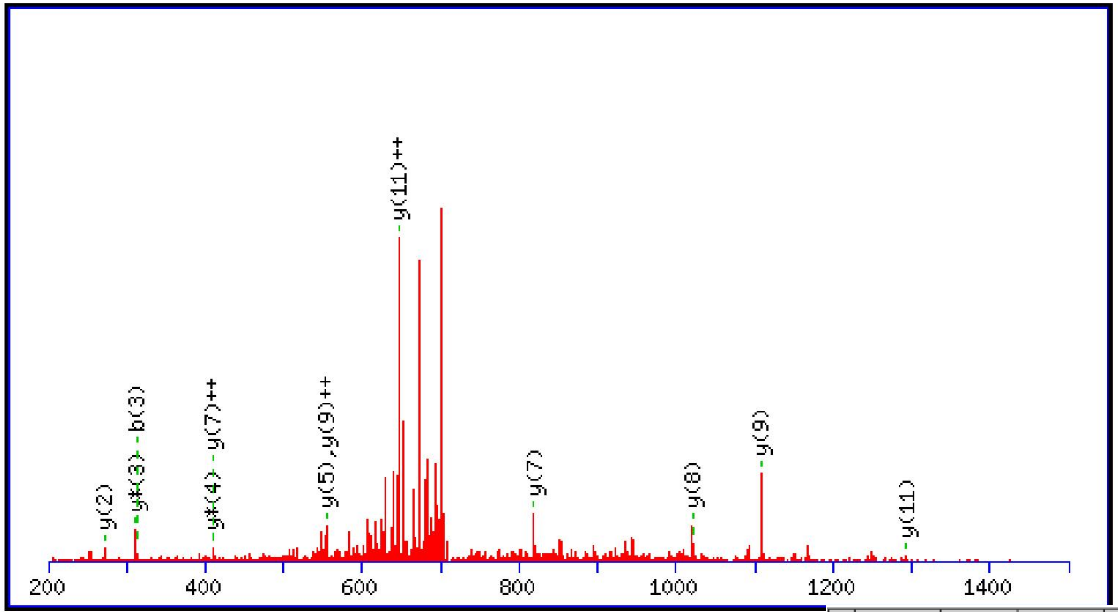
Monoisotopic mass of neutral peptide Mr(calc): 1790.
Fixed modifications: Carbamidomethyl (C) (apply to spec:
Variable modifications:
K5 : Propionyl (K)
K10 : Propionyl (K)
K12 : Propionyl-(13CD3)Methyl (K)
Ions Score: 32 **Expect:** 0.23
Matches : 15/130 fragment ions using 31 most intense peak

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							13
2	201.1234	101.0653			183.1128	92.0600	S	1677.9595	839.4834	1660.9330	830.9701	1659.9490	830.4781	12
3	387.2027	194.1050			369.1921	185.0997	W	1590.9275	795.9674	1573.9010	787.4541	1572.9169	786.9621	11
4	484.2554	242.6314			466.2449	233.6261	P	***1404.8482***	702.9277	1387.8216	694.4145	1386.8376	693.9225	10
5	668.3766	334.6919	651.3501	326.1787	650.3661	325.6867	K	***1307.7954***	654.4014	1290.7689	645.8881	1289.7849	645.3961	9
6	815.4450	408.2262	798.4185	399.7129	797.4345	399.2209	F	***1123.6743***	562.3408	1106.6477	553.8275	1105.6637	553.3355	8
7	943.5036	472.2554	926.4771	463.7422	925.4930	463.2502	Q	***976.6058***	488.8066	959.5793	480.2933	958.5953	479.8013	7
8	1030.5356	515.7715	1013.5091	507.2582	1012.5251	506.7662	S	***848.5473***	424.7773	831.5207	416.2640	830.5367	415.7720	6
9	1143.6197	572.3135	1126.5932	563.8002	1125.6091	563.3082	I	761.5152	381.2613	744.4887	372.7480	743.5047	372.2560	5
10	**1327.7409**	664.3741	1310.7143	655.8608	1309.7303	655.3688	K	***648.4312***	324.7192	631.4046	316.2059	630.4206	315.7139	4
11	1414.7729	707.8901	1397.7464	699.3768	1396.7623	698.8848	S	***464.3100***	232.6586	447.2834	224.1454	446.2994	223.6534	3
12	**1616.9319**	808.9696	1599.9054	800.4563	1598.9214	799.9643	K	377.2780	189.1426	360.2514	180.6293			2
13							R	175.1190	88.0631	158.0924	79.5498			1

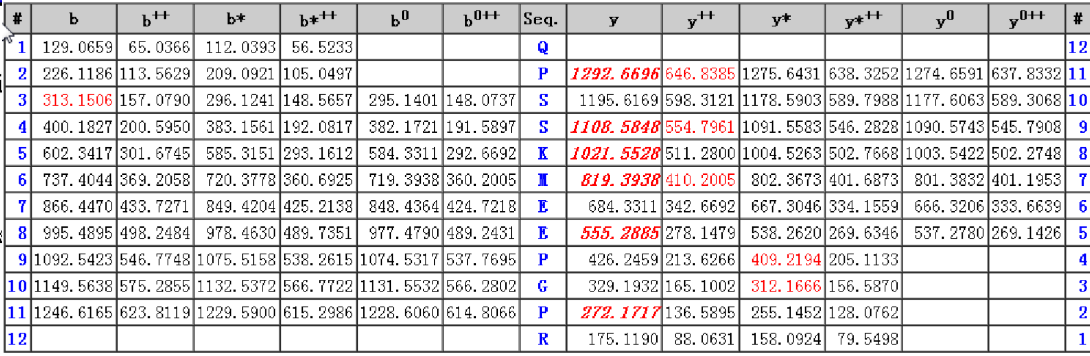
MS/MS Fragmentation of **QPSSKMEEPGPR**
Found in **E5RI52**, UPF0544 protein C5orf45 OS=Homo sapiens GN=C5orf45 PE=2 SV=1

Match to Query 7979: 1419.715188 from(710.864870,2+) intensity(35569.4453)
Title: File2138 Spectrum8989 scans: 10148
Data file I:\2013-12-03-SIMM7721-FR1-11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1419.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K5 : Propionyl-(13CD3)Methyl (K)
M6 : Label:13C(1)2H(3) (M)
Ions Score: 27 **Expect:** 0.62
Matches : 12/120 fragment ions using 24 most intense peak

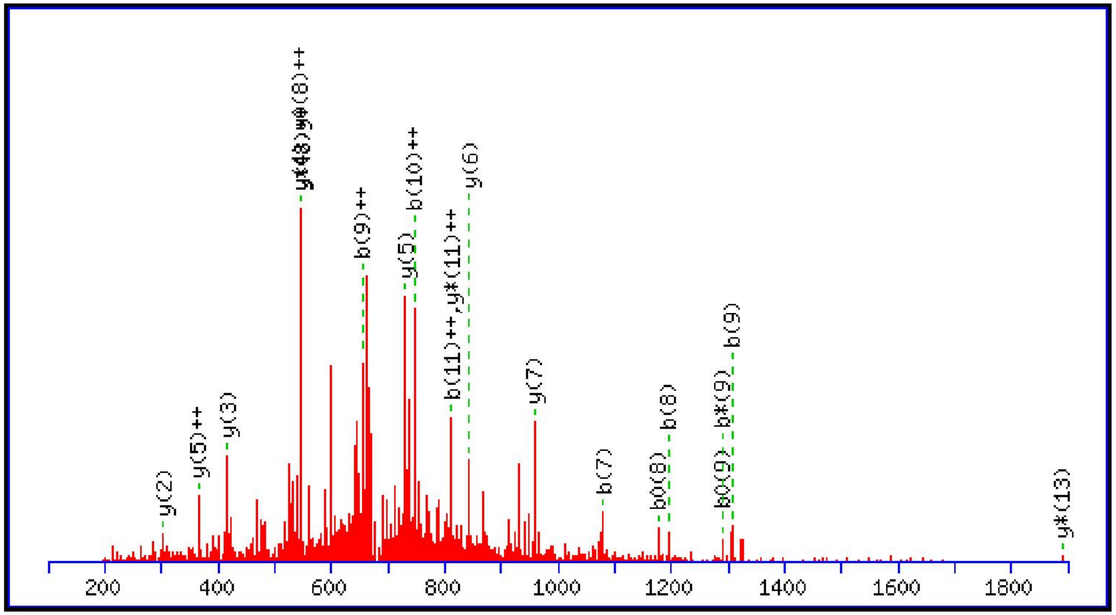


#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							12
2	226.1186	113.5629	209.0921	105.0497			P	***1292.6696***	646.8385	1275.6431	638.3252	1274.6591	637.8332	11
3	313.1506	157.0790	296.1241	148.5657	295.1401	148.0737	S	1195.6169	598.3121	1178.5903	589.7988	1177.6063	589.3068	10
4	400.1827	200.5950	383.1561	192.0817	382.1721	191.5897	S	***1108.5848***	554.7961	1091.5583	546.2828	1090.5743	545.7908	9
5	602.3417	301.6745	585.3151	293.1612	584.3311	292.6692	K	***1021.5528***	511.2800	1004.5263	502.7668	1003.5422	502.2748	8
6	737.4044	369.2058	720.3778	360.6925	719.3938	360.2005	M	***819.3938***	410.2005	802.3673	401.6873	801.3832	401.1953	7
7	866.4470	433.7271	849.4204	425.2138	848.4364	424.7218	E	684.3311	342.6692	667.3046	334.1559	666.3206	333.6639	6
8	995.4895	498.2484	978.4630	489.7351	977.4790	489.2431	E	***555.2885***	278.1479	538.2620	269.6346	537.2780	269.1426	5
9	1092.5423	546.7748	1075.5158	538.2615	1074.5317	537.7695	P	426.2459	213.6266	409.2194	205.1133			4
10	1149.5638	575.2855	1132.5372	566.7722	1131.5532	566.2802	G	329.1932	165.1002	312.1666	156.5870			3
11	1246.6165	623.8119	1229.5900	615.2986	1228.6060	614.8066	P	***272.1717***	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of ENRKYYMDLKENQR
Found in Q00577, Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2

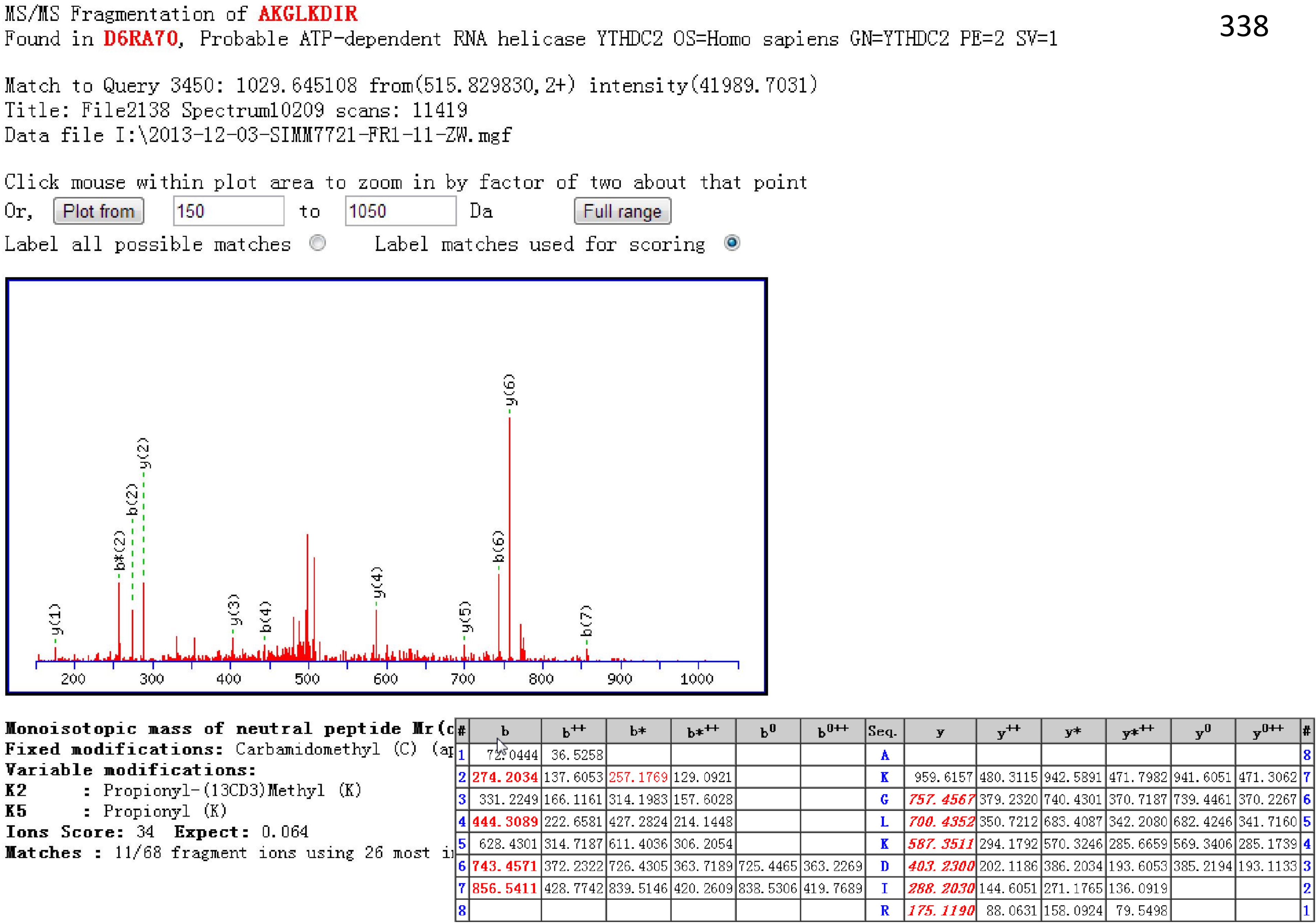
Match to Query 16507: 2036.032602 from(679.684810,3+) intensity(31246.3711)
Title: File2138 Spectrum11727 scans: 13000
Data file I:\2013-12-03-SIMM7721-FR1-11-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2036.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
M7 : Label:13C(1)2H(3)+Oxidation (M)
K10 : Propionyl (K)
Ions Score: 24 **Expect:** 2.5
Matches : 20/148 fragment ions using 31 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	N	1907.9825	954.4949	1890.9560	945.9816	1889.9720	945.4896	13
3	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	R	1793.9396	897.4734	1776.9131	888.9602	1775.9290	888.4682	12
4	602.3529	301.6801	585.3264	293.1668	584.3424	292.6748	K	1637.8385	819.4229	1620.8119	810.9096	1619.8279	810.4176	11
5	765.4162	383.2118	748.3897	374.6985	747.4057	374.2065	Y	1435.6795	718.3434	1418.6529	709.8301	1417.6689	709.3381	10
6	928.4796	464.7434	911.4530	456.2302	910.4690	455.7381	Y	1272.6161	636.8117	1255.5896	628.2984	1254.6056	627.8064	9
7	**1079.5372**	540.2722	1062.5106	531.7589	1061.5266	531.2669	M	1109.5528	555.2800	1092.5263	546.7668	1091.5423	546.2748	8
8	**1194.5641**	597.7857	1177.5376	589.2724	1176.5535	588.7804	D	***958.4952***	479.7513	941.4687	471.2380	940.4847	470.7460	7
9	**1307.6482**	**654.3277**	1290.6216	645.8144	1289.6376	645.3224	L	***843.4683***	422.2378	826.4417	413.7245	825.4577	413.2325	6
10	1491.7693	**746.3883**	1474.7428	737.8750	1473.7588	737.3830	K	***730.3842***	365.6958	713.3577	357.1825	712.3737	356.6905	5
11	1620.8119	**810.9096**	1603.7854	802.3963	1602.8014	801.9043	E	***546.2631***	273.6352	529.2365	265.1219	528.2525	264.6299	4
12	1734.8549	867.9311	1717.8283	859.4178	1716.8443	858.9258	N	***417.2205***	209.1139	400.1939	200.6006			3
13	1862.9134	931.9604	1845.8869	923.4471	1844.9029	922.9551	Q	***303.1775***	152.0924	286.1510	143.5791			2
14							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKGLKDIR**
Found in **D6RA70**, Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=2 SV=1

Match to Query 3450: 1029.645108 from(515.829830,2+) intensity(41989.7031)
Title: File2138 Spectrum10209 scans: 11419
Data file I:\2013-12-03-SIMM7721-FR1-11-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

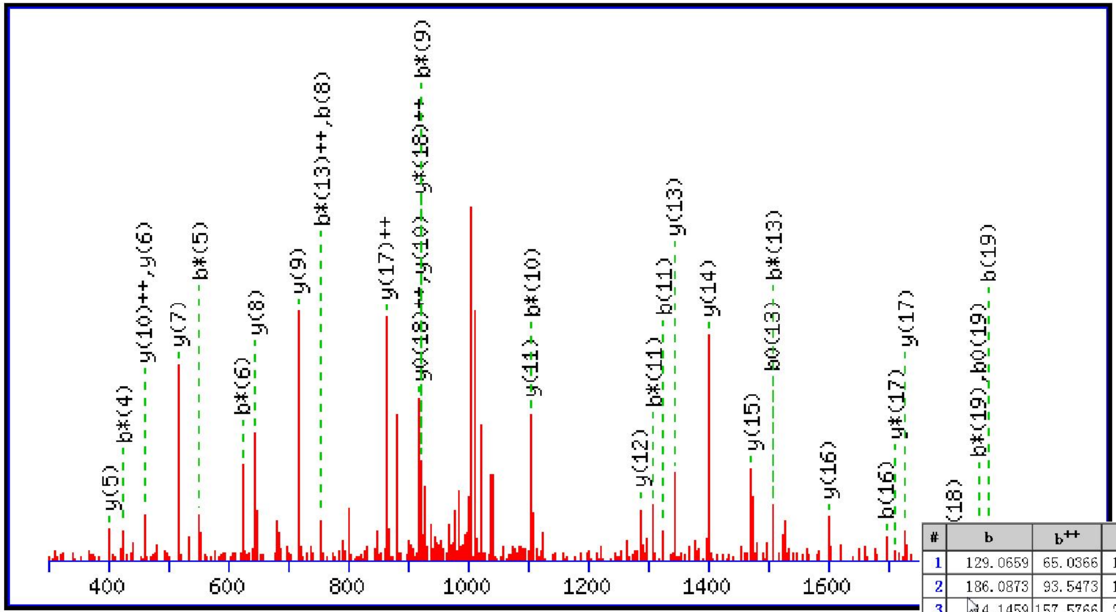
Monoisotopic mass of neutral peptide Mr(c
Fixed modifications: Carbamidomethyl (C) (ap
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
Ions Score: 34 **Expect:** 0.064
Matches : 11/68 fragment ions using 26 most i

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	72.0444	36.5258					A							8
2	**274.2034**	137.6053	257.1769	129.0921			K	959.6157	480.3115	942.5891	471.7982	941.6051	471.3062	7
3	331.2249	166.1161	314.1983	157.6028			G	***757.4567***	379.2320	740.4301	370.7187	739.4461	370.2267	6
4	**444.3089**	222.6581	427.2824	214.1448			L	***700.4352***	350.7212	683.4087	342.2080	682.4246	341.7160	5
5	628.4301	314.7187	611.4036	306.2054			K	***587.3511***	294.1792	570.3246	285.6659	569.3406	285.1739	4
6	**743.4571**	372.2322	726.4305	363.7189	725.4465	363.2269	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
7	**856.5411**	428.7742	839.5146	420.2609	838.5306	419.7689	I	***288.2030***	144.6051	271.1765	136.0919			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **QGQQQAGGKKKAEGGGGGGR**
Found in **Q00839**, Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6

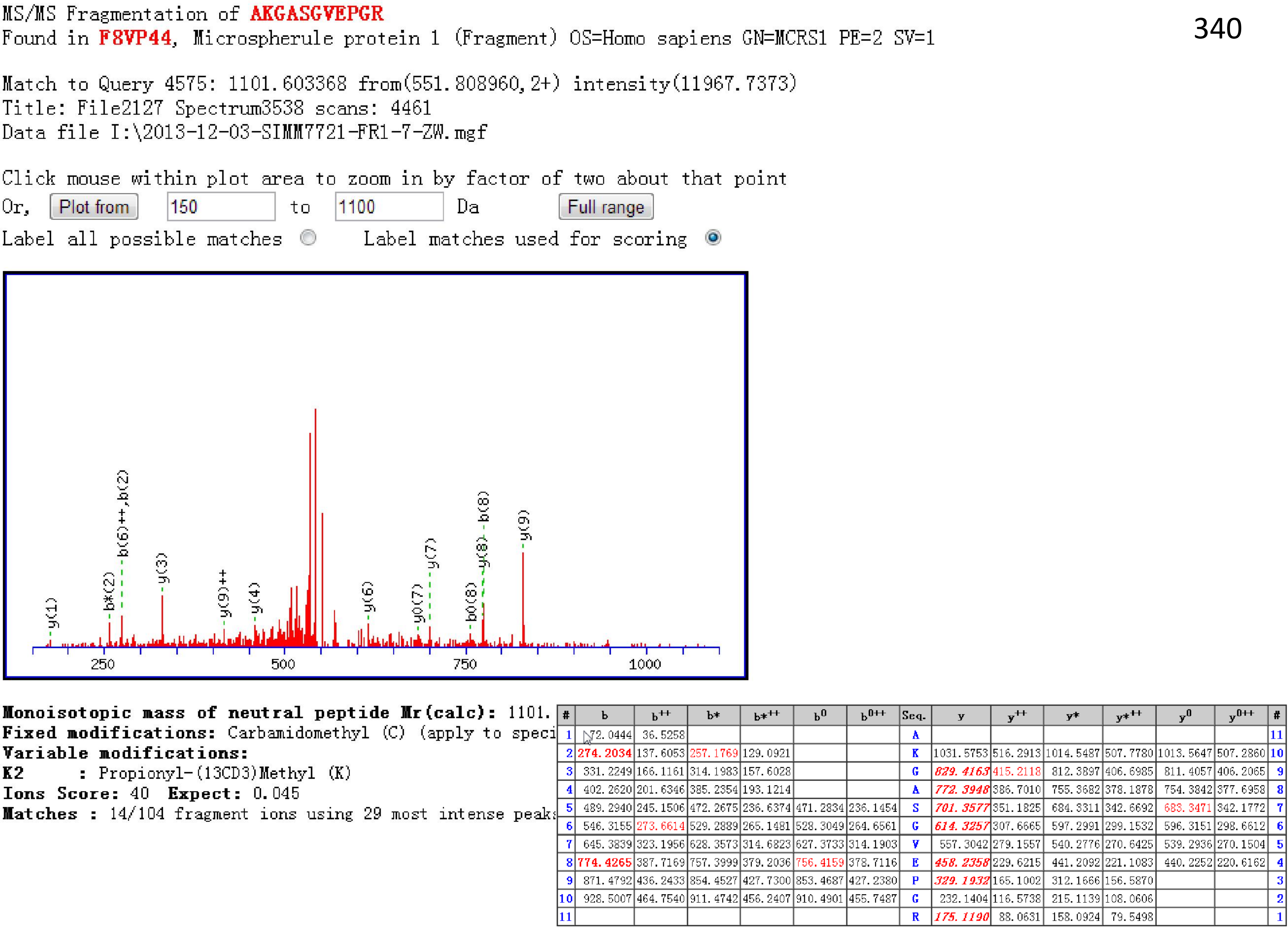
Match to Query 13876: 2041.058208 from(1021.536380,2+) intensity(36121.1484)
Title: File2127 Spectrum4467 scans: 5468
Data file I:\2013-12-03-SIMM7721-FR1-7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2041.0574
Fixed modifications: Carbamidomethyl (C) (apply to specified re
Variable modifications:
K9 : Propionyl (K)
K10 : Propionyl (K)
K11 : Propionyl-(13CD3)Methyl (K)
Ions Score: 88 **Expect:** 1e-006
Matches : 34/190 fragment ions using 51 most intense peaks (he

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							20
2	186.0873	93.5473	169.0608	85.0340			G	1914.0061	957.5067	1896.9795	948.9934	1895.9955	948.5014	19
3	314.1459	157.5766	297.1193	149.0633			Q	1856.9846	928.9959	1839.9580	920.4827	1838.9740	919.9906	18
4	442.2045	221.6059	425.1779	213.0926			Q	***1728.9260***	864.9666	1711.8995	856.4534	1710.9154	855.9614	17
5	570.2631	285.6352	553.2365	277.1219			Q	***1600.8674***	800.9374	1583.8409	792.4241	1582.8569	791.9321	16
6	641.3002	321.1537	624.2736	312.6404			A	***1472.8089***	736.9081	1455.7823	728.3948	1454.7983	727.9028	15
7	698.3216	349.6645	681.2951	341.1512			G	***1401.7717***	701.3895	1384.7452	692.8762	1383.7612	692.3842	14
8	**755.3431**	378.1752	738.3165	369.6619			G	***1344.7503***	672.8788	1327.7237	664.3655	1326.7397	663.8735	13
9	939.4643	470.2358	922.4377	461.7225			K	***1287.7288***	644.3680	1270.7023	635.8548	1269.7182	635.3628	12
10	1123.5855	562.2964	1106.5589	553.7831			K	***1103.6076***	552.3075	1086.5811	543.7942	1085.5971	543.3022	11
11	**1325.7445**	663.3759	1308.7179	654.8626			K	***919.4865***	460.2469	902.4599	451.7336	901.4759	451.2416	10
12	1396.7816	698.8944	1379.7550	690.3812			A	***717.3274***	359.1674	700.3009	350.6541	699.3169	350.1621	9
13	1525.8242	763.4157	1508.7976	754.9024	1507.8136	754.4104	E	***646.2903***	323.6488	629.2638	315.1355	628.2798	314.6435	8
14	1582.8456	791.9265	1565.8191	783.4132	1564.8351	782.9212	G	***517.2477***	259.1275	500.2212	250.6142			7
15	1639.8671	820.4372	1622.8405	811.9239	1621.8565	811.4319	G	***460.2263***	230.6168	443.1997	222.1035			6
16	**1696.8886**	848.9479	1679.8620	840.4346	1678.8780	839.9426	G	***403.2048***	202.1060	386.1783	193.5928			5
17	1753.9100	877.4587	1736.8835	868.9454	1735.8995	868.4534	G	346.1833	173.5953	329.1568	165.0820			4
18	**1810.9315**	905.9694	1793.9049	897.4561	1792.9209	896.9641	G	289.1619	145.0846	272.1353	136.5713			3
19	**1867.9530**	934.4801	1850.9264	925.9668	1849.9424	925.4748	G	232.1404	116.5738	215.1139	108.0606			2
20							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKGASGVEPGR**
Found in **F8VP44**, Microspherule protein 1 (Fragment) OS=Homo sapiens GN=MCRS1 PE=2 SV=1

Match to Query 4575: 1101.603368 from(551.808960,2+) intensity(11967.7373)
Title: File2127 Spectrum3538 scans: 4461
Data file I:\2013-12-03-SIMM7721-FR1-7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●

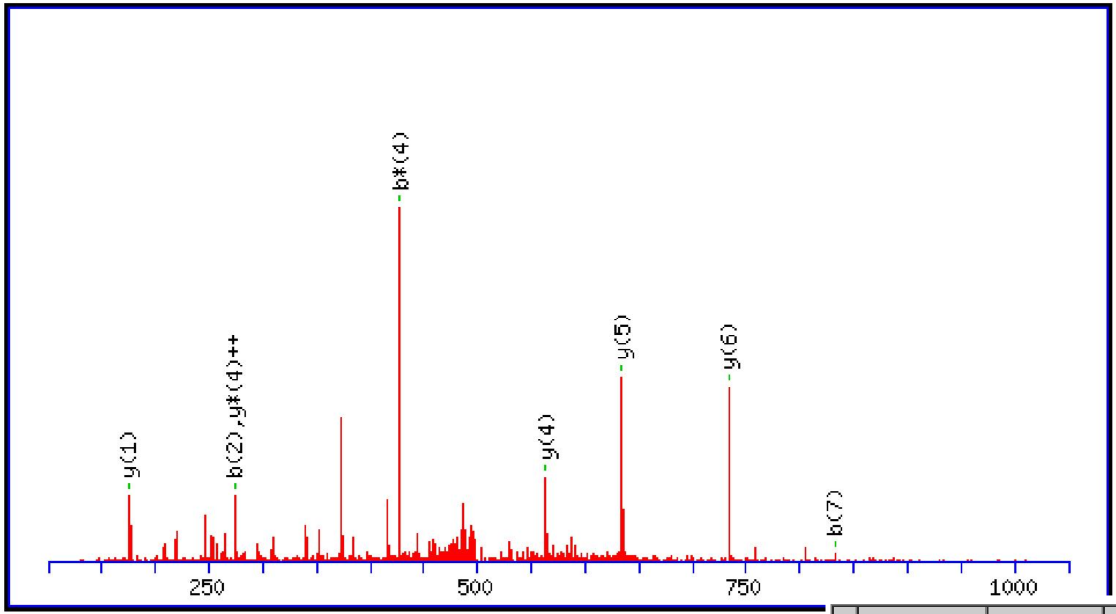
Monoisotopic mass of neutral peptide Mr(calc): 1101.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 40 **Expect:** 0.045
Matches : 14/104 fragment ions using 29 most intense peak

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							11
2	**274.2034**	137.6053	257.1769	129.0921			K	1031.5753	516.2913	1014.5487	507.7780	1013.5647	507.2860	10
3	331.2249	166.1161	314.1983	157.6028			G	***829.4163***	415.2118	812.3897	406.6985	811.4057	406.2065	9
4	402.2620	201.6346	385.2354	193.1214			A	***772.3948***	386.7010	755.3682	378.1878	754.3842	377.6958	8
5	489.2940	245.1506	472.2675	236.6374	471.2834	236.1454	S	***701.3577***	351.1825	684.3311	342.6692	683.3471	342.1772	7
6	546.3155	273.6614	529.2889	265.1481	528.3049	264.6561	G	***614.3257***	307.6665	597.2991	299.1532	596.3151	298.6612	6
7	645.3839	323.1956	628.3573	314.6823	627.3733	314.1903	V	557.3042	279.1557	540.2776	270.6425	539.2936	270.1504	5
8	**774.4265**	387.7169	757.3999	379.2036	756.4159	378.7116	E	***458.2358***	229.6215	441.2092	221.1083	440.2252	220.6162	4
9	871.4792	436.2433	854.4527	427.7300	853.4687	427.2380	P	***329.1932***	165.1002	312.1666	156.5870			3
10	928.5007	464.7540	911.4742	456.2407	910.4901	455.7487	G	232.1404	116.5738	215.1139	108.0606			2
11							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAVAFGKR**
Found in **Q5VTI5**, Pleckstrin homology domain-containing family A member 6 OS=Homo sapiens GN=PLEKHA6 PE=2 SV=1

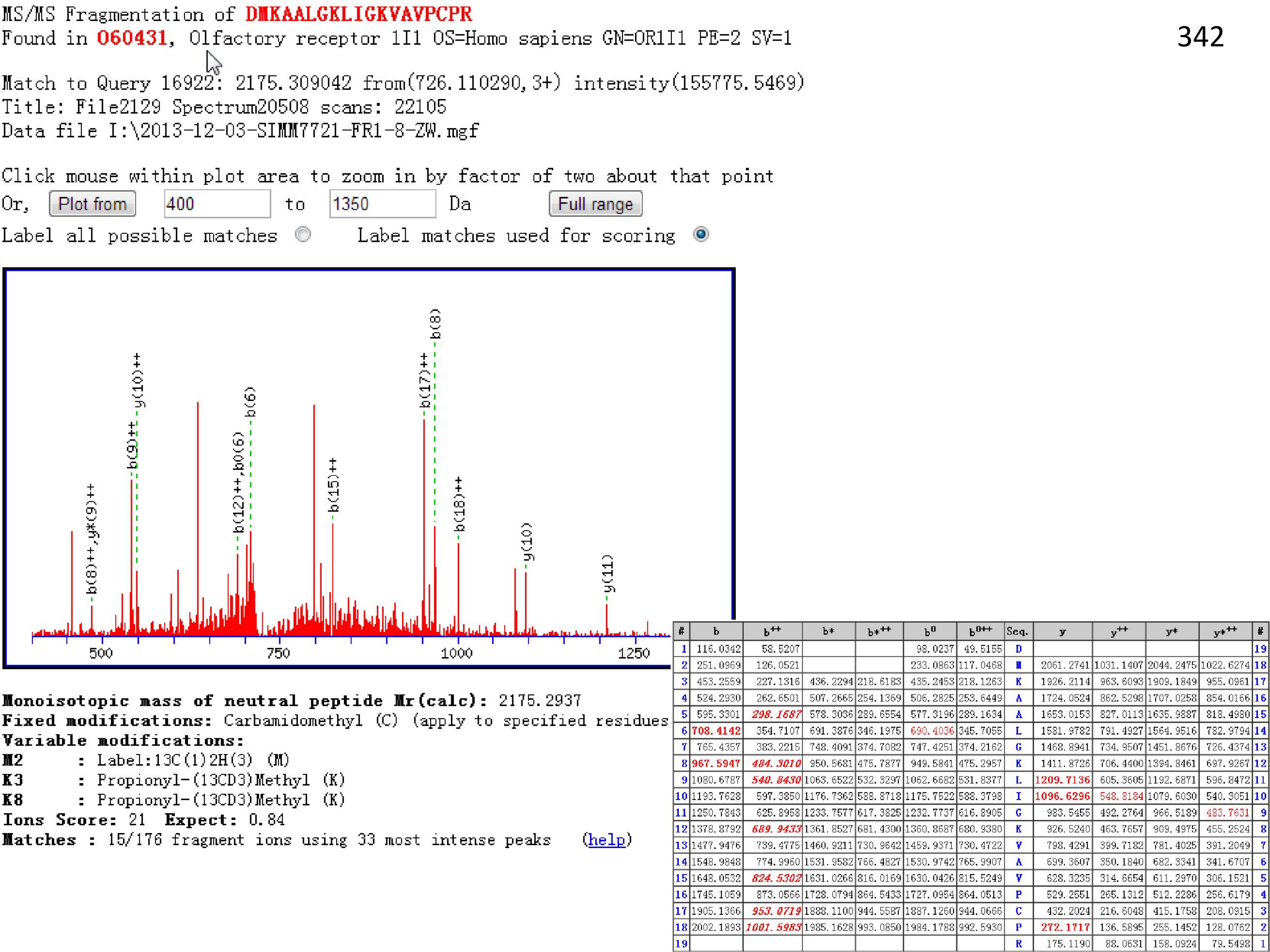
Match to Query 3845: 1005.625348 from(503.819950,2+) intensity(84494.7266)
Title: File2129 Spectrum9966 scans: 11045
Data file I:\2013-12-03-SIMM7721-FR1-8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1005.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 33 **Expect:** 0.097
Matches : 8/56 fragment ions using 9 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	203.1663	102.0868	186.1397	93.5735	K					8
2	**274.2034**	137.6053	257.1769	129.0921	A	804.4727	402.7400	787.4461	394.2267	7
3	373.2718	187.1395	356.2453	178.6263	V	***733.4355***	367.2214	716.4090	358.7081	6
4	444.3089	222.6581	427.2824	214.1448	A	***634.3671***	317.6872	617.3406	309.1739	5
5	591.3773	296.1923	574.3508	287.6790	F	***563.3300***	282.1686	546.3035	273.6554	4
6	648.3988	324.7030	631.3723	316.1898	G	416.2616	208.6344	399.2350	200.1212	3
7	**832.5200**	416.7636	815.4934	408.2504	K	359.2401	180.1237	342.2136	171.6104	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **DMKAALGKLIGKVAVPCPR**
Found in **O60431**, Olfactory receptor 1I1 OS=Homo sapiens GN=OR1I1 PE=2 SV=1

Match to Query 16922: 2175.309042 from(726.110290,3+) intensity(155775.5469)
Title: File2129 Spectrum20508 scans: 22105
Data file I:\2013-12-03-SIMM7721-FR1-8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1350 Da Full range
Label all possible matches ○ Label matches used for scoring ●

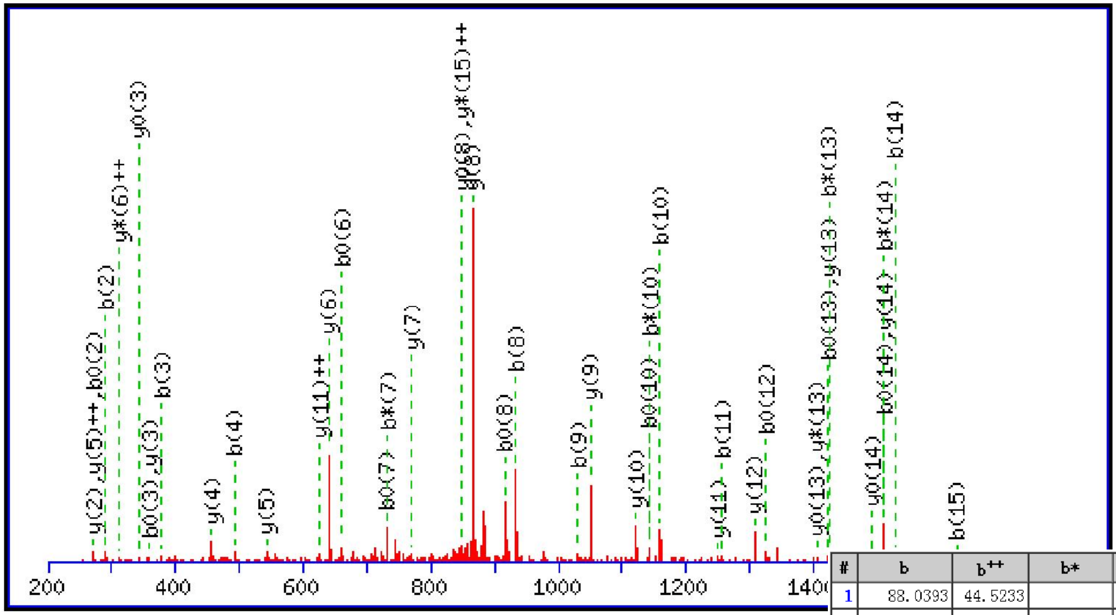
Monoisotopic mass of neutral peptide Mr(calc): 2175.2937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues
Variable modifications:
M2 : Label:13C(1)2H(3) (M)
K3 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl-(13CD3)Methyl (K)
Ions Score: 21 **Expect:** 0.84
Matches : 15/176 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	116.0342	58.5207			98.0237	49.5155	D					19
2	251.0969	126.0521			233.0863	117.0468	M	2061.2741	1031.1407	2044.2475	1022.6274	18
3	453.2559	227.1316	436.2294	218.6183	435.2453	218.1263	K	1926.2114	963.6093	1909.1849	955.0961	17
4	524.2930	262.6501	507.2665	254.1369	506.2825	253.6449	A	1724.0524	862.5298	1707.0258	854.0166	16
5	595.3301	***298.1687***	578.3036	289.6554	577.3196	289.1634	A	1653.0153	827.0113	1635.9887	818.4980	15
6	**708.4142**	354.7107	691.3876	346.1975	690.4036	345.7055	L	1581.9782	791.4927	1564.9516	782.9794	14
7	765.4357	383.2215	748.4091	374.7082	747.4251	374.2162	G	1468.8941	734.9507	1451.8676	726.4374	13
8	**967.5947**	***484.3010***	950.5681	475.7877	949.5841	475.2957	K	1411.8726	706.4400	1394.8461	697.9267	12
9	1080.6787	***540.8430***	1063.6522	532.3297	1062.6682	531.8377	L	**1209.7136**	605.3605	1192.6871	596.8472	11
10	1193.7628	597.3850	1176.7362	588.8718	1175.7522	588.3798	I	**1096.6296**	548.8184	1079.6030	540.3051	10
11	1250.7843	625.8958	1233.7577	617.3825	1232.7737	616.8905	G	983.5455	492.2764	966.5189	483.7631	9
12	1378.8792	***689.9433***	1361.8527	681.4300	1360.8687	680.9380	K	926.5240	463.7657	909.4975	455.2524	8
13	1477.9476	739.4775	1460.9211	730.9642	1459.9371	730.4722	V	798.4291	399.7182	781.4025	391.2049	7
14	1548.9848	774.9960	1531.9582	766.4827	1530.9742	765.9907	A	699.3607	350.1840	682.3341	341.6707	6
15	1648.0532	***824.5302***	1631.0266	816.0169	1630.0426	815.5249	V	628.3235	314.6654	611.2970	306.1521	5
16	1745.1059	873.0566	1728.0794	864.5433	1727.0954	864.0513	P	529.2551	265.1312	512.2286	256.6179	4
17	1905.1366	***953.0719***	1888.1100	944.5587	1887.1260	944.0666	C	432.2024	216.6048	415.1758	208.0915	3
18	2002.1893	***1001.5983***	1985.1628	993.0850	1984.1788	992.5930	P	**272.1717**	136.5895	255.1452	128.0762	2
19							R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of SKSDGEAKPEPSPSPR
Found in K7EJL0, DNA (cytosine-5)-methyltransferase 1 (Fragment) OS=Homo sapiens GN=DNMT1 PE=4 SV=1

Match to Query 13991: 1797.905608 from(899.960080,2+) intensity(36378.1719)
Title: File2129 Spectrum6164 scans: 7079
Data file I:\2013-12-03-SIMM7721-FR1-8-ZW.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 ●



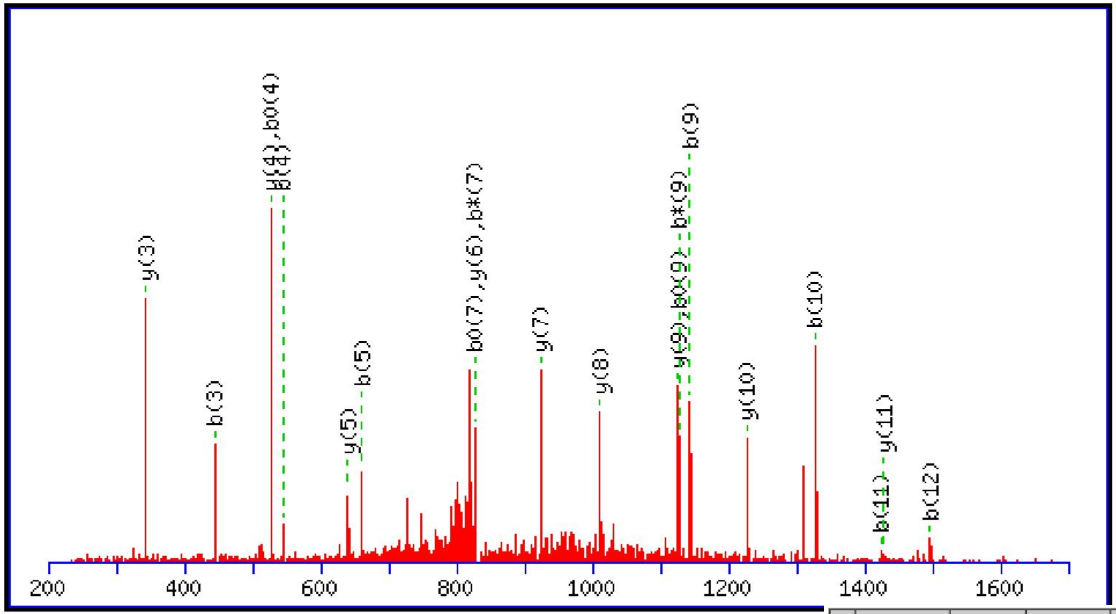
Monoisotopic mass of neutral peptide Mr(calc): 1797.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 78 **Expect:** 6.8e-006
Matches : 44/174 fragment ions using 72 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	K	1711.8770	856.4421	1694.8504	847.9289	1693.8664	847.4369	15
3	**377.2303**	189.1188	360.2038	180.6055	359.2198	180.1135	S	***1509.7180***	755.3626	1492.6914	746.8494	1491.7074	746.3573	14
4	**492.2573**	246.6323	475.2307	238.1190	474.2467	237.6270	D	***1422.6859***	711.8466	1405.6594	703.3333	1404.6754	702.8413	13
5	549.2788	275.1430	532.2522	266.6297	531.2682	266.1377	G	***1307.6590***	654.3331	1290.6325	645.8199	1289.6484	645.3279	12
6	678.3213	339.6643	661.2948	331.1510	660.3108	330.6590	E	***1250.6375***	625.8224	1233.6110	617.3091	1232.6270	616.8171	11
7	749.3585	375.1829	732.3319	366.6696	731.3479	366.1776	A	***1121.5949***	561.3011	1104.5684	552.7878	1103.5844	552.2958	10
8	**933.4796**	467.2435	916.4531	458.7302	915.4691	458.2382	K	***1050.5578***	525.7826	1033.5313	517.2693	1032.5473	516.7773	9
9	**1030.5324**	515.7698	1013.5059	507.2566	1012.5218	506.7646	P	***866.4367***	433.7220	849.4101	425.2087	848.4261	424.7167	8
10	**1159.5750**	580.2911	1142.5484	571.7779	1141.5644	571.2859	E	***769.3839***	385.1956	752.3573	376.6823	751.3733	376.1903	7
11	**1256.6278**	628.8175	1239.6012	620.3042	1238.6172	619.8122	P	***640.3413***	320.6743	623.3148	312.1610	622.3307	311.6690	6
12	1343.6598	672.3335	1326.6332	663.8203	1325.6492	663.3282	S	***543.2885***	272.1479	526.2620	263.6346	525.2780	263.1426	5
13	1440.7126	720.8599	1423.6860	712.3466	1422.7020	711.8546	P	***456.2565***	228.6319	439.2300	220.1186	438.2459	219.6266	4
14	**1527.7446**	764.3759	1510.7180	755.8627	1509.7340	755.3706	S	***359.2037***	180.1055	342.1772	171.5922	341.1932	171.1002	3
15	**1624.7973**	812.9023	1607.7708	804.3890	1606.7868	803.8970	P	***272.1717***	136.5895	255.1452	128.0762			2
16							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KGKTDSPWIKPAR**
Found in **Q9H9B1**, Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens GN=EHMT1 PE=1 SV=4

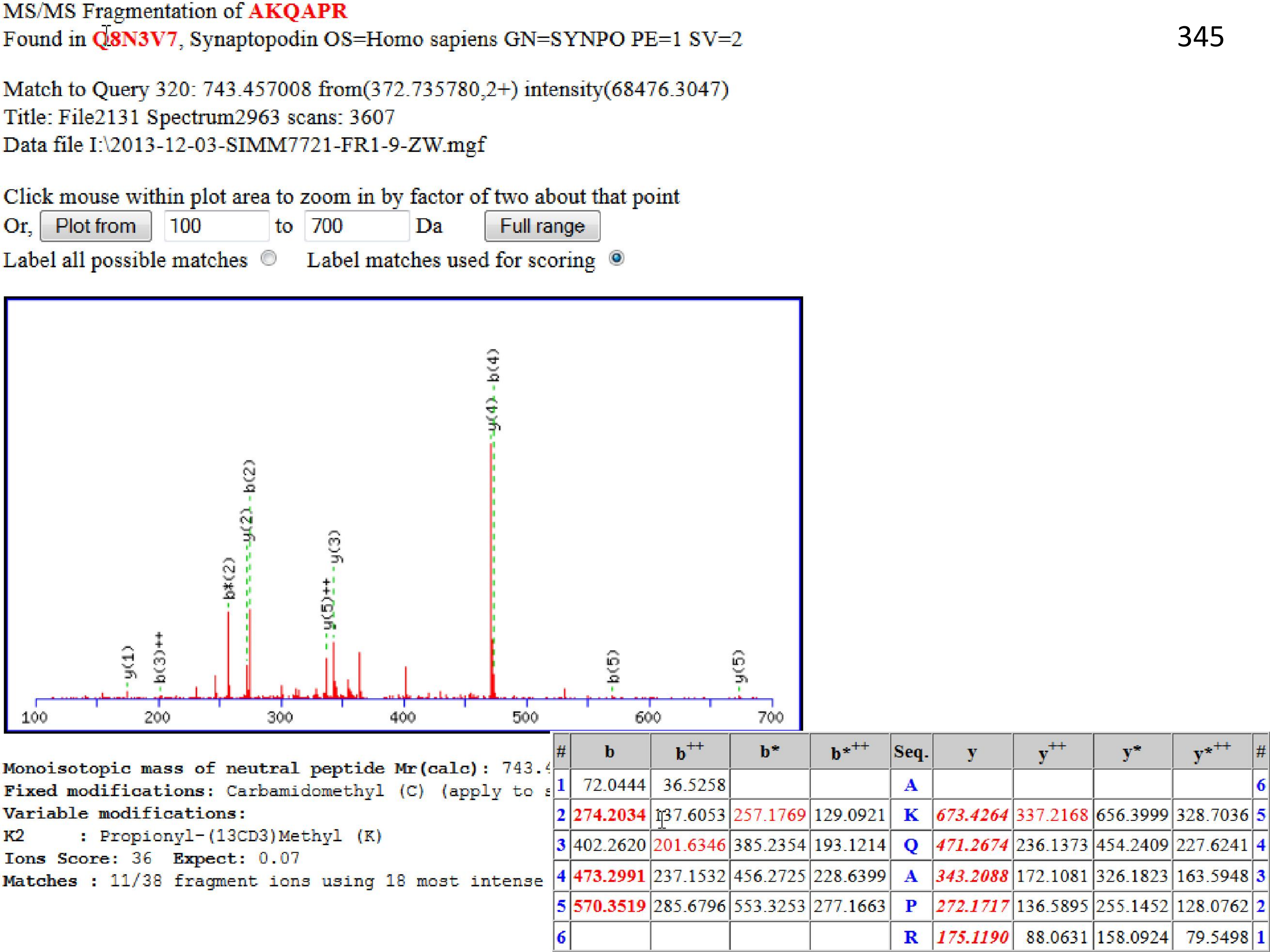
Match to Query 12342: 1668.949068 from(835.481810,2+) intensity(71590.4922)
Title: File2129 Spectrum13072 scans: 14280
Data file I:\2013-12-03-SIMM7721-FR1-8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 200 to 1700 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1668.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 60 **Expect:** 0.00051
Matches : 21/124 fragment ions using 29 most intense peak:

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							13
2	242.1499	121.5786	225.1234	113.0653			G	1485.8333	743.4203	1468.8067	734.9070	1467.8227	734.4150	12
3	**444.3089**	222.6581	427.2824	214.1448			K	***1428.8118***	714.9095	1411.7853	706.3963	1410.8012	705.9043	11
4	**545.3566**	273.1819	528.3301	264.6687	527.3460	264.1767	T	***1226.6528***	613.8300	1209.6263	605.3168	1208.6422	604.8248	10
5	**660.3836**	330.6954	643.3570	322.1821	642.3730	321.6901	D	***1125.6051***	563.3062	1108.5786	554.7929	1107.5946	554.3009	9
6	747.4156	374.2114	730.3890	365.6982	729.4050	365.2061	S	***1010.5782***	505.7927	993.5516	497.2795	992.5676	496.7874	8
7	844.4683	422.7378	827.4418	414.2245	826.4578	413.7325	P	***923.5461***	462.2767	906.5196	453.7634			7
8	1030.5477	515.7775	1013.5211	507.2642	1012.5371	506.7722	W	***826.4934***	413.7503	809.4668	405.2371			6
9	**1143.6317**	572.3195	1126.6052	563.8062	1125.6212	563.3142	I	***640.4141***	320.7107	623.3875	312.1974			5
10	**1327.7529**	664.3801	1310.7264	655.8668	1309.7423	655.3748	K	***527.3300***	264.1686	510.3035	255.6554			4
11	**1424.8057**	712.9065	1407.7791	704.3932	1406.7951	703.9012	P	***343.2088***	172.1081	326.1823	163.5948			3
12	**1495.8428**	748.4250	1478.8162	739.9118	1477.8322	739.4197	A	246.1561	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKQAPR**

Found in **Q8N3V7**, Synaptopodin OS=Homo sapiens GN=SYNPO PE=1 SV=2

Match to Query 320: 743.457008 from(372.735780,2+) intensity(68476.3047)

Title: File2131 Spectrum2963 scans: 3607

Data file I:\2013-12-03-SIMM7721-FR1-9-ZW.mgf

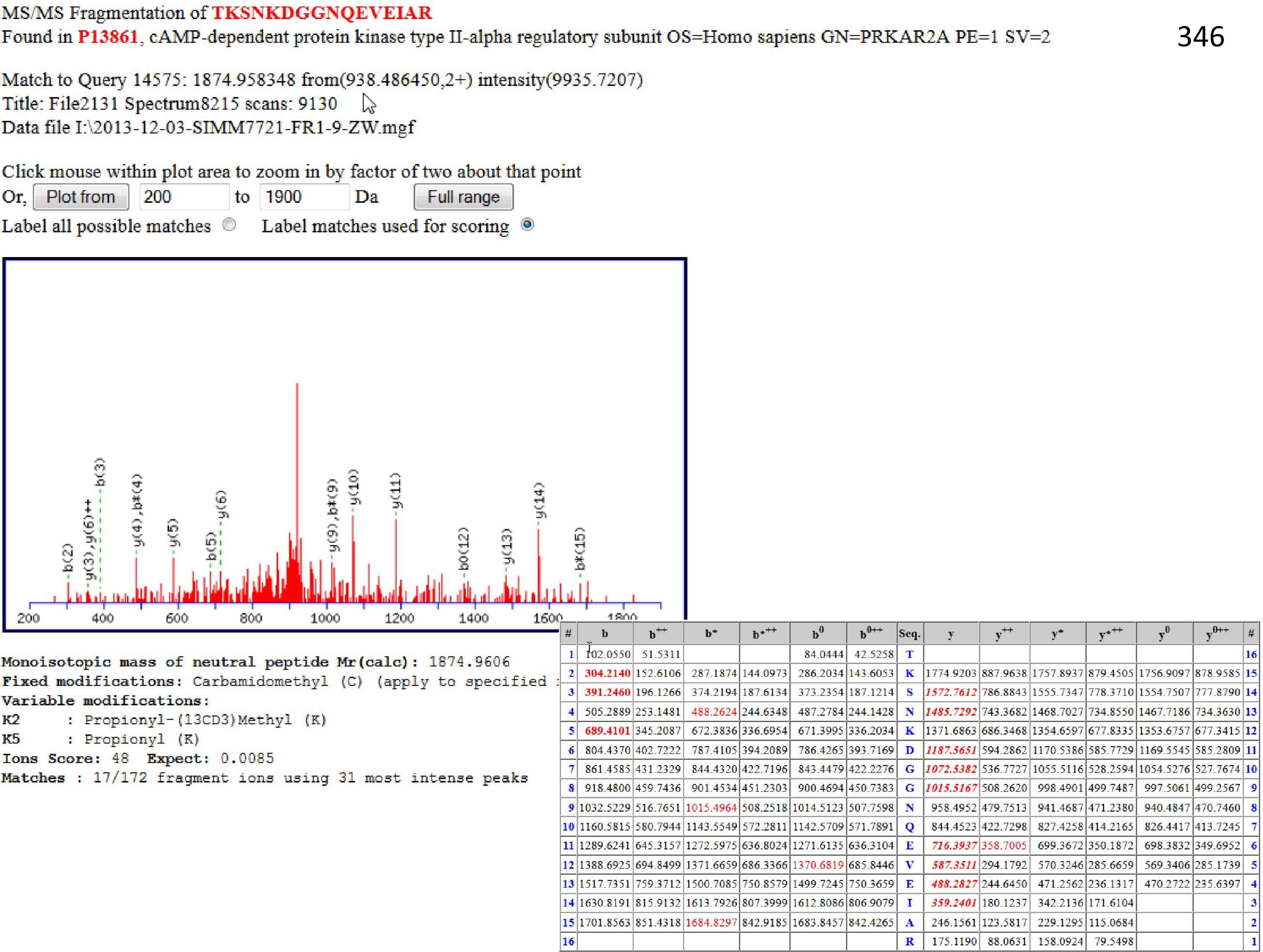
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 743.4
Fixed modifications: Carbamidomethyl (C) (apply to s
Variable modifications:
K2     : Propionyl-(13CD3)Methyl (K)
Ions Score: 36   Expect: 0.07
Matches : 11/38 fragment ions using 18 most intense
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.0444	36.5258			A					6
2	**274.2034**	137.6053	257.1769	129.0921	K	***673.4264***	337.2168	656.3999	328.7036	5
3	402.2620	201.6346	385.2354	193.1214	Q	***471.2674***	236.1373	454.2409	227.6241	4
4	**473.2991**	237.1532	456.2725	228.6399	A	***343.2088***	172.1081	326.1823	163.5948	3
5	**570.3519**	285.6796	553.3253	277.1663	P	***272.1717***	136.5895	255.1452	128.0762	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **TKSNKDGGNQEVEIAR**

Found in **P13861**, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2

Match to Query 14575: 1874.958348 from(938.486450,2+) intensity(9935.7207)

Title: File2131 Spectrum8215 scans: 9130

Data file I:\2013-12-03-SIMM7721-FR1-9-ZW.mgf

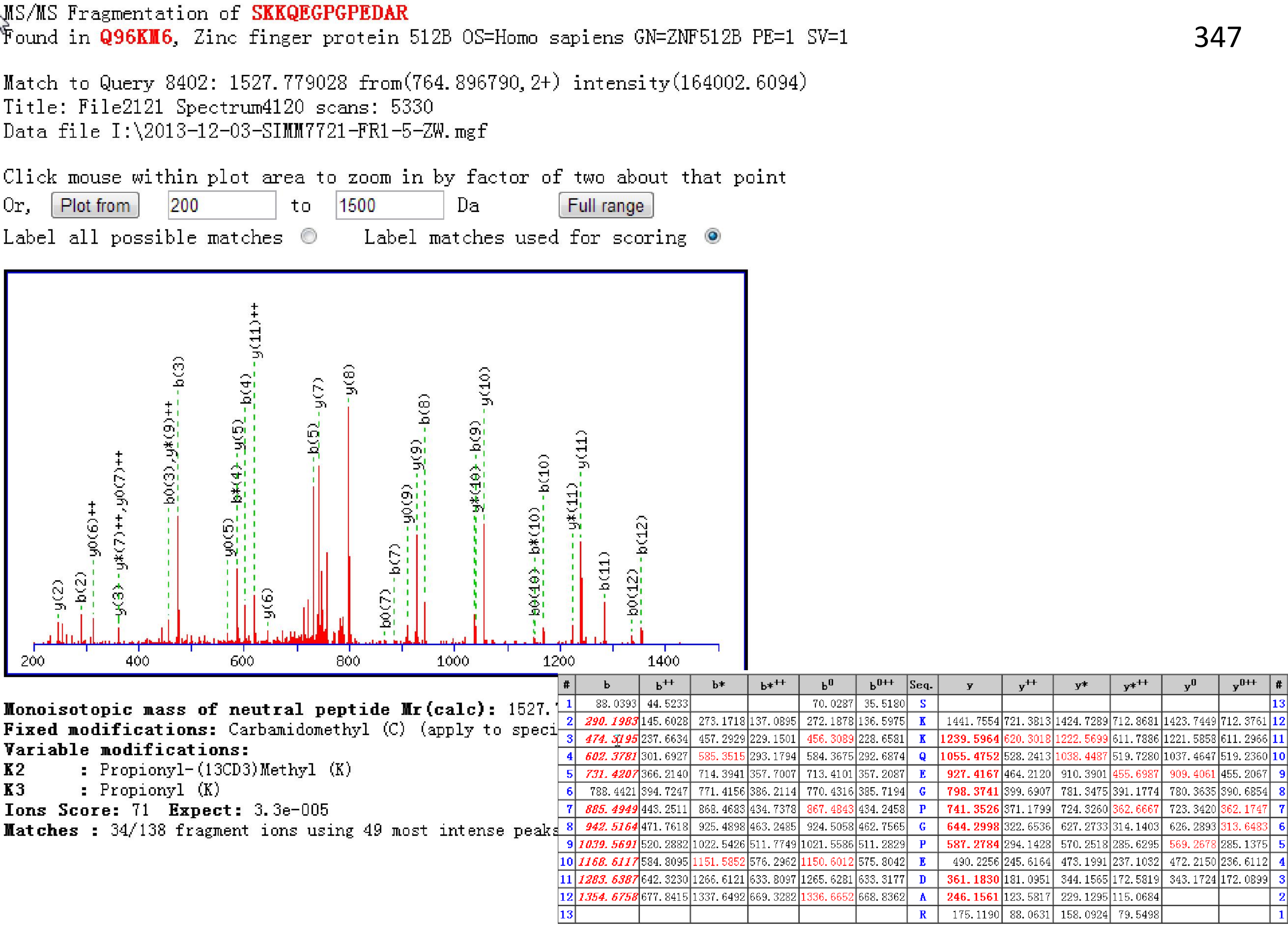
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1900 Da Full range

Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1874.9606
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
K5      : Propionyl (K)
Ions Score: 48  Expect: 0.0085
Matches : 17/172 fragment ions using 31 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							16
2	**304.2140**	152.6106	287.1874	144.0973	286.2034	143.6053	K	1774.9203	887.9638	1757.8937	879.4505	1756.9097	878.9585	15
3	**391.2460**	196.1266	374.2194	187.6134	373.2354	187.1214	S	***1572.7612***	786.8843	1555.7347	778.3710	1554.7507	777.8790	14
4	505.2889	253.1481	488.2624	244.6348	487.2784	244.1428	N	***1485.7292***	743.3682	1468.7027	734.8550	1467.7186	734.3630	13
5	**689.4101**	345.2087	672.3836	336.6954	671.3995	336.2034	K	1371.6863	686.3468	1354.6597	677.8335	1353.6757	677.3415	12
6	804.4370	402.7222	787.4105	394.2089	786.4265	393.7169	D	***1187.5651***	594.2862	1170.5386	585.7729	1169.5545	585.2809	11
7	861.4585	431.2329	844.4320	422.7196	843.4479	422.2276	G	***1072.5382***	536.7727	1055.5116	528.2594	1054.5276	527.7674	10
8	918.4800	459.7436	901.4534	451.2303	900.4694	450.7383	G	***1015.5167***	508.2620	998.4901	499.7487	997.5061	499.2567	9
9	1032.5229	516.7651	1015.4964	508.2518	1014.5123	507.7598	N	958.4952	479.7513	941.4687	471.2380	940.4847	470.7460	8
10	1160.5815	580.7944	1143.5549	572.2811	1142.5709	571.7891	Q	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	7
11	1289.6241	645.3157	1272.5975	636.8024	1271.6135	636.3104	E	***716.3937***	358.7005	699.3672	350.1872	698.3832	349.6952	6
12	1388.6925	694.8499	1371.6659	686.3366	1370.6819	685.8446	V	***587.3511***	294.1792	570.3246	285.6659	569.3406	285.1739	5
13	1517.7351	759.3712	1500.7085	750.8579	1499.7245	750.3659	E	***488.2827***	244.6450	471.2562	236.1317	470.2722	235.6397	4
14	1630.8191	815.9132	1613.7926	807.3999	1612.8086	806.9079	I	***359.2401***	180.1237	342.2136	171.6104			3
15	1701.8563	851.4318	1684.8297	842.9185	1683.8457	842.4265	A	246.1561	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **SKKQEGPGPEDAR**

Found in **Q96KM6**, Zinc finger protein 512B OS=Homo sapiens GN=ZNF512B PE=1 SV=1

Match to Query 8402: 1527.779028 from(764.896790,2+) intensity(164002.6094)

Title: File2121 Spectrum4120 scans: 5330

Data file I:\2013-12-03-SIMM7721-FR1-5-ZW.mgf

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

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1527.

Fixed modifications: Carbamidomethyl (C) (apply to speci

Variable modifications:

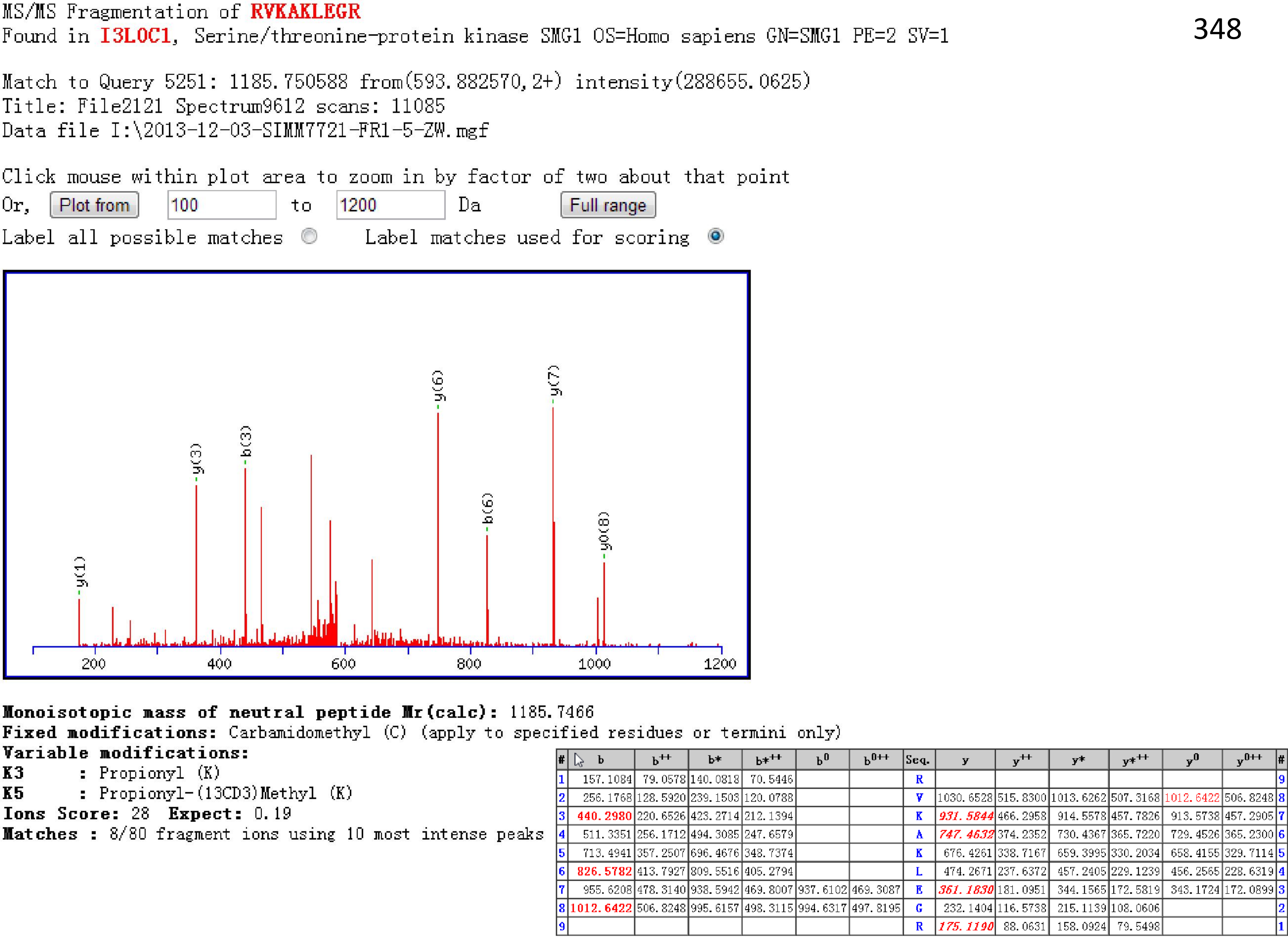
K2 : Propionyl-(13CD3)Methyl (K)

K3 : Propionyl (K)

Ions Score: 71 **Expect:** 3.3e-005

Matches : 34/138 fragment ions using 49 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	***290.1983***	145.6028	273.1718	137.0895	272.1878	136.5975	K	1441.7554	721.3813	1424.7289	712.8681	1423.7449	712.3761	12
3	***474.3195***	237.6634	457.2929	229.1501	456.3089	228.6581	K	**1239.5964**	620.3018	1222.5699	611.7886	1221.5858	611.2966	11
4	***602.3781***	301.6927	585.3515	293.1794	584.3675	292.6874	Q	**1055.4752**	528.2413	1038.4487	519.7280	1037.4647	519.2360	10
5	***731.4207***	366.2140	714.3941	357.7007	713.4101	357.2087	E	**927.4167**	464.2120	910.3901	455.6987	909.4061	455.2067	9
6	788.4421	394.7247	771.4156	386.2114	770.4316	385.7194	G	**798.3741**	399.6907	781.3475	391.1774	780.3635	390.6854	8
7	***885.4949***	443.2511	868.4683	434.7378	867.4843	434.2458	P	**741.3526**	371.1799	724.3260	362.6667	723.3420	362.1747	7
8	***942.5164***	471.7618	925.4898	463.2485	924.5058	462.7565	G	**644.2998**	322.6536	627.2733	314.1403	626.2893	313.6483	6
9	***1039.5691***	520.2882	1022.5426	511.7749	1021.5586	511.2829	P	**587.2784**	294.1428	570.2518	285.6295	569.2678	285.1375	5
10	***1168.6117***	584.8095	1151.5852	576.2962	1150.6012	575.8042	E	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
11	***1283.6387***	642.3230	1266.6121	633.8097	1265.6281	633.3177	D	**361.1830**	181.0951	344.1565	172.5819	343.1724	172.0899	3
12	***1354.6758***	677.8415	1337.6492	669.3282	1336.6652	668.8362	A	**246.1561**	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **RVKAKLEGR**
Found in **I3L0C1**, Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1 PE=2 SV=1

Match to Query 5251: 1185.750588 from(593.882570,2+) intensity(288655.0625)
Title: File2121 Spectrum9612 scans: 11085
Data file I:\2013-12-03-SIMM7721-FR1-5-ZW.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 ●

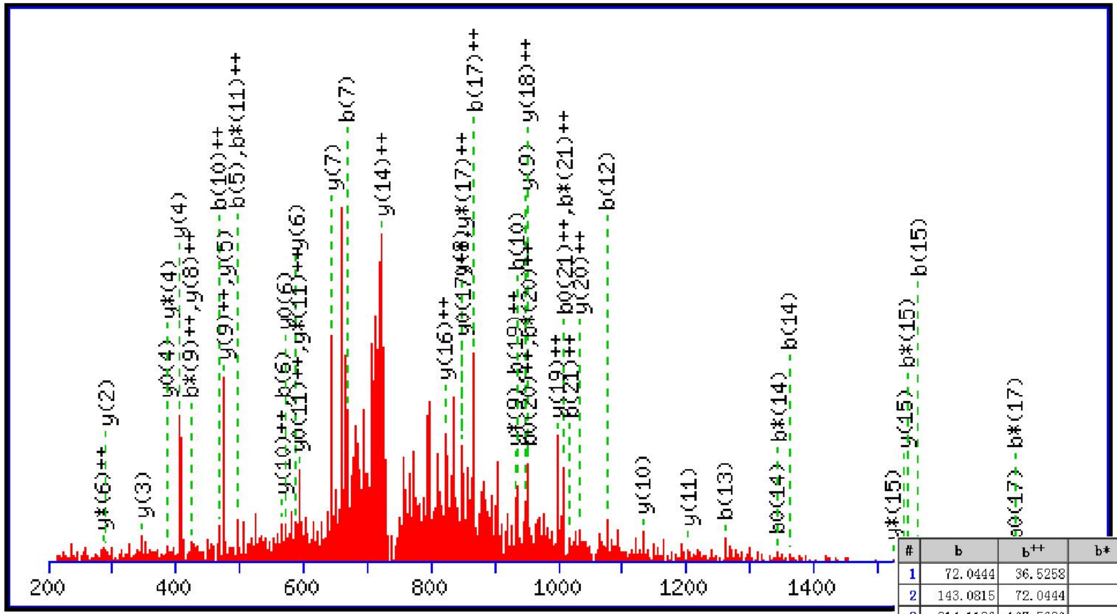
Monoisotopic mass of neutral peptide Mr(calc): 1185.7466
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
Ions Score: 28 **Expect:** 0.19
Matches : 8/80 fragment ions using 10 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							9
2	256.1768	128.5920	239.1503	120.0788			V	1030.6528	515.8300	1013.6262	507.3168	1012.6422	506.8248	8
3	**440.2980**	220.6526	423.2714	212.1394			K	***931.5844***	466.2958	914.5578	457.7826	913.5738	457.2905	7
4	511.3351	256.1712	494.3085	247.6579			A	***747.4632***	374.2352	730.4367	365.7220	729.4526	365.2300	6
5	713.4941	357.2507	696.4676	348.7374			K	676.4261	338.7167	659.3995	330.2034	658.4155	329.7114	5
6	**826.5782**	413.7927	809.5516	405.2794			L	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	955.6208	478.3140	938.5942	469.8007	937.6102	469.3087	E	***361.1830***	181.0951	344.1565	172.5819	343.1724	172.0899	3
8	**1012.6422**	506.8248	995.6157	498.3115	994.6317	497.8195	G	232.1404	116.5738	215.1139	108.0606			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AAAPKATPVAAAKTKGLAGGDR**
Found in **B4DH53**, MAP1S light chain OS=Homo sapiens GN=MAP1S PE=2 SV=1

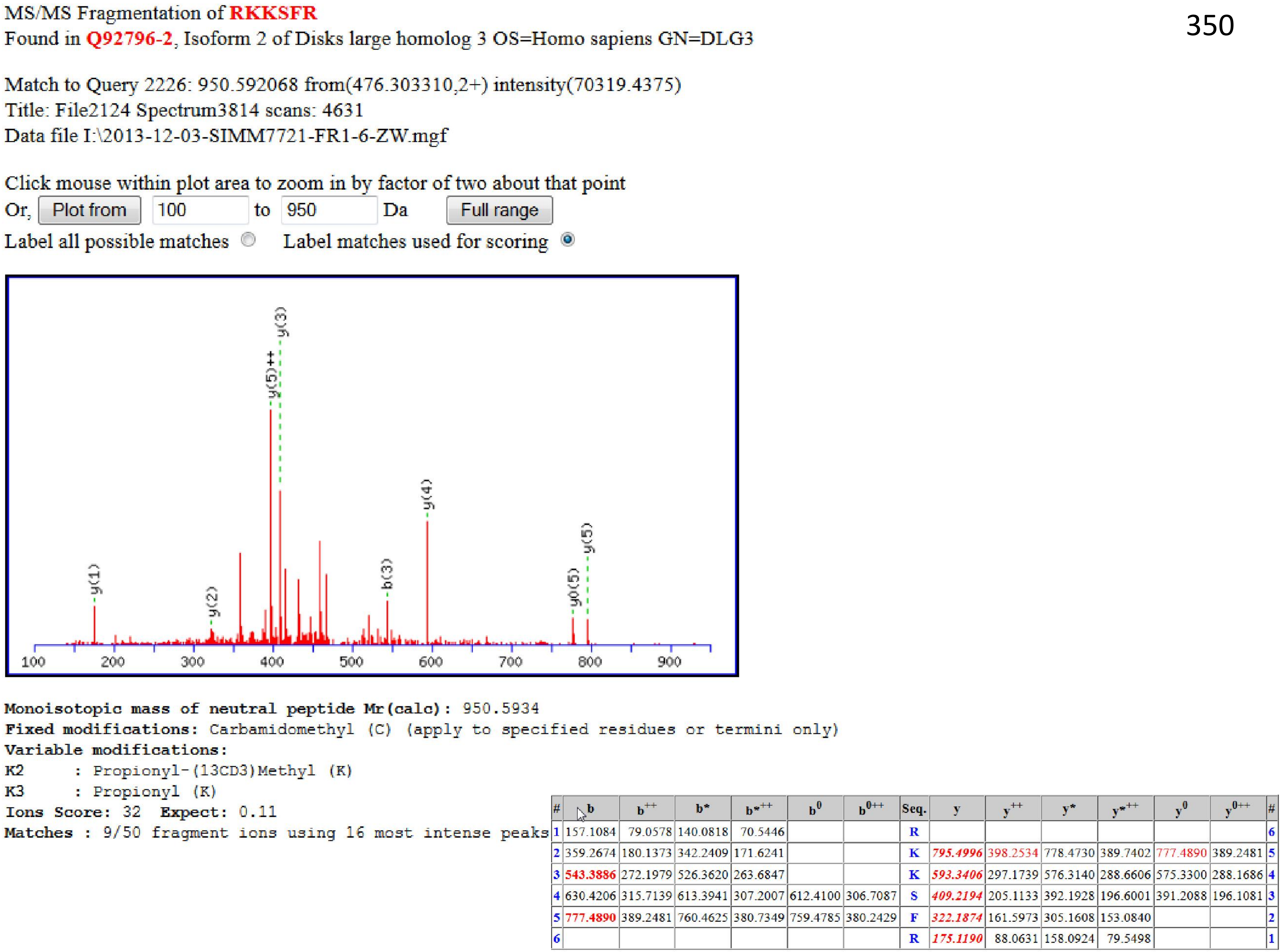
Match to Query 15266: 2207.252532 from(736.758120,3+) intensity(24746.5586)
Title: File2121 Spectrum10944 scans: 12472
Data file I:\2013-12-03-SIMM7721-FR1-5-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2207.2546
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K5 : Propionyl (K)
K13 : Propionyl (K)
K15 : Propionyl-(13CD3)Methyl (K)
Ions Score: 26 **Expect:** 1.1
Matches : 52/230 fragment ions using 145 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							22
2	143.0815	72.0444					A	2137.2248	1069.1160	2120.1983	1060.6028	2119.2143	1060.1108	21
3	214.1186	107.5629					A	2066.1877	1033.5975	2049.1612	1025.0842	2048.1771	1024.5922	20
4	311.1714	156.0893					P	1995.1506	998.0789	1978.1240	989.5657	1977.1400	989.0737	19
5	**495.2926**	248.1499	478.2660	239.6366			K	1898.0978	949.5526	1881.0713	941.0393	1880.0873	940.5473	18
6	**566.3297**	283.6685	549.3031	275.1552			A	1713.9766	857.4920	1696.9501	848.9787	1695.9661	848.4867	17
7	**667.3774**	334.1923	650.3508	325.6790	649.3668	325.1870	T	1642.9395	821.9734	1625.9130	813.4601	1624.9290	812.9681	16
8	764.4301	382.7187	747.4036	374.2054	746.4196	373.7134	P	**1541.8919**	771.4496	1524.8653	762.9363	1523.8813	762.4443	15
9	863.4985	432.2529	846.4720	423.7396	845.4880	423.2476	V	1444.8391	722.9232	1427.8125	714.4099	1426.8285	713.9179	14
10	**934.5356**	467.7715	917.5091	459.2582	916.5251	458.7662	A	1345.7707	673.3890	1328.7441	664.8757	1327.7601	664.3837	13
11	1005.5728	503.2900	988.5462	494.7767	987.5622	494.2847	A	1274.7336	637.8704	1257.7070	629.3571	1256.7230	628.8651	12
12	**1076.6099**	538.8086	1059.5833	530.2953	1058.5993	529.8033	A	**1203.6964**	602.3519	1186.6699	593.8386	1185.6859	593.3466	11
13	**1260.7311**	630.8692	1243.7045	622.3559	1242.7205	621.8639	K	**1132.6593**	566.8333	1115.6328	558.3200	1114.6488	557.8280	10
14	**1361.7787**	681.3930	1344.7522	672.8797	1343.7682	672.3877	T	**948.5382**	474.7727	931.5116	466.2594	930.5276	465.7674	9
15	**1563.9377**	782.4725	1546.9112	773.9592	1545.9272	773.4672	K	**847.4905**	424.2489	830.4639	415.7356	829.4799	415.2436	8
16	1620.9592	810.9832	1603.9327	802.4700	1602.9486	801.9780	G	**645.3315**	323.1694	628.3049	314.6561	627.3209	314.1641	7
17	1734.0433	867.5253	1717.0167	859.0120	1716.0327	858.5200	L	**588.3100**	294.6586	571.2835	286.1454	570.2994	285.6534	6
18	1805.0804	903.0438	1788.0538	894.5306	1787.0698	894.0385	A	**475.2259**	238.1166	458.1994	229.6033	457.2154	229.1113	5
19	1862.1018	931.5546	1845.0753	923.0413	1844.0913	922.5493	G	**404.1888**	202.5980	387.1623	194.0848	386.1783	193.5928	4
20	1919.1233	960.0653	1902.0968	951.5520	1901.1127	951.0600	G	**347.1674**	174.0873	330.1408	165.5740	329.1568	165.0820	3
21	2034.1503	1017.5788	2017.1237	1009.0655	2016.1397	1008.5735	D	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	2
22							R	175.1190	88.0631	158.0924	79.5498			1



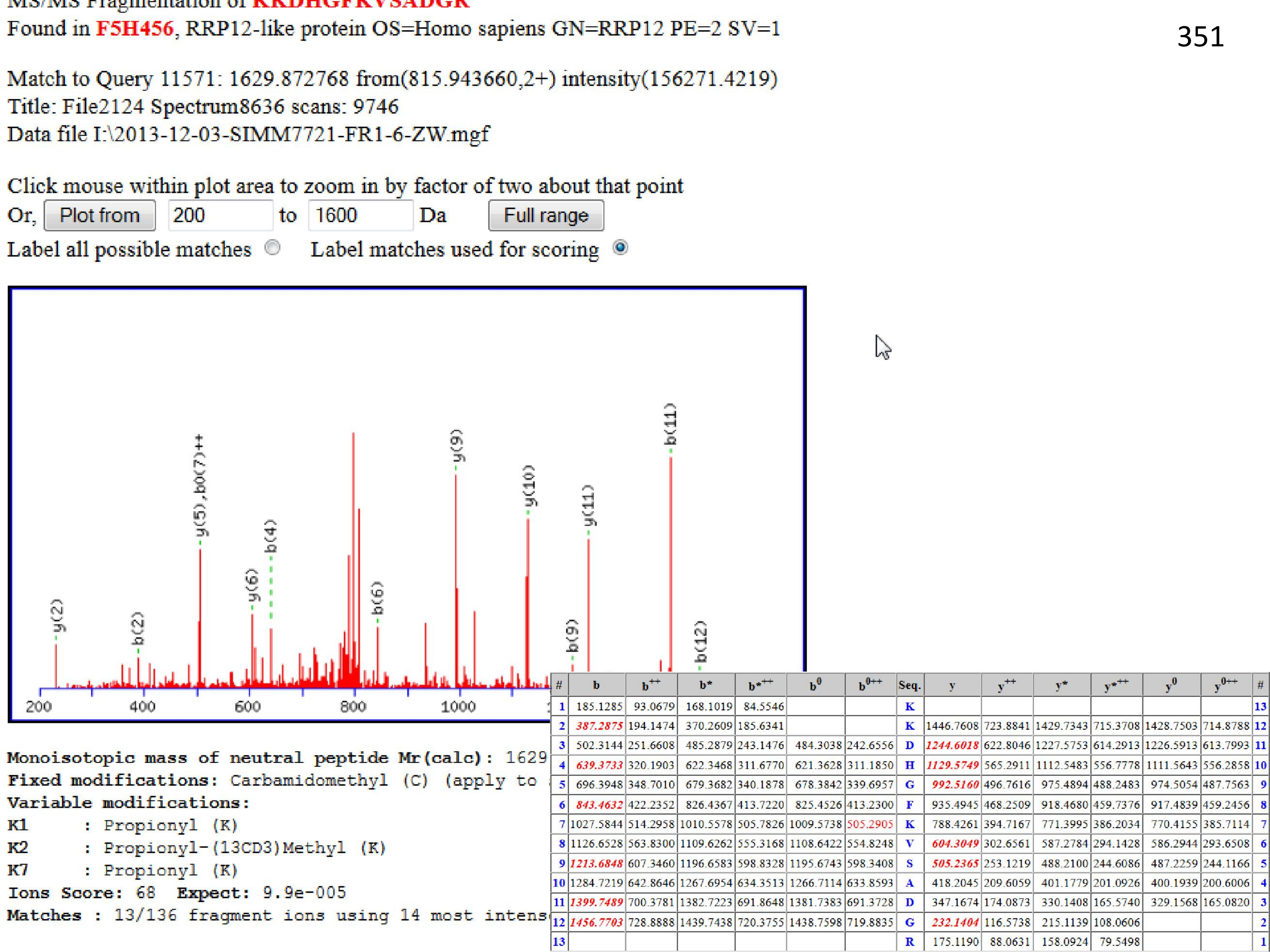
MS/MS Fragmentation of **RKKSFR**
Found in **Q92796-2**, Isoform 2 of Disks large homolog 3 OS=Homo sapiens GN=DLG3

Match to Query 2226: 950.592068 from(476.303310,2+) intensity(70319.4375)
Title: File2124 Spectrum3814 scans: 4631
Data file I:\2013-12-03-SIMM7721-FR1-6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 950.5934
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 32 **Expect:** 0.11
Matches : 9/50 fragment ions using 16 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							6
2	359.2674	180.1373	342.2409	171.6241			K	***795.4996***	398.2534	778.4730	389.7402	777.4890	389.2481	5
3	**543.3886**	272.1979	526.3620	263.6847			K	***593.3406***	297.1739	576.3140	288.6606	575.3300	288.1686	4
4	630.4206	315.7139	613.3941	307.2007	612.4100	306.7087	S	***409.2194***	205.1133	392.1928	196.6001	391.2088	196.1081	3
5	**777.4890**	389.2481	760.4625	380.7349	759.4785	380.2429	F	***322.1874***	161.5973	305.1608	153.0840			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KKDHGFKVSADGK**

Found in **F5H456**, RRP12-like protein OS=Homo sapiens GN=RRP12 PE=2 SV=1

Match to Query 11571: 1629.872768 from(815.943660,2+) intensity(156271.4219)
Title: File2124 Spectrum8636 scans: 9746
Data file I:\2013-12-03-SIMM7721-FR1-6-ZW.mgf

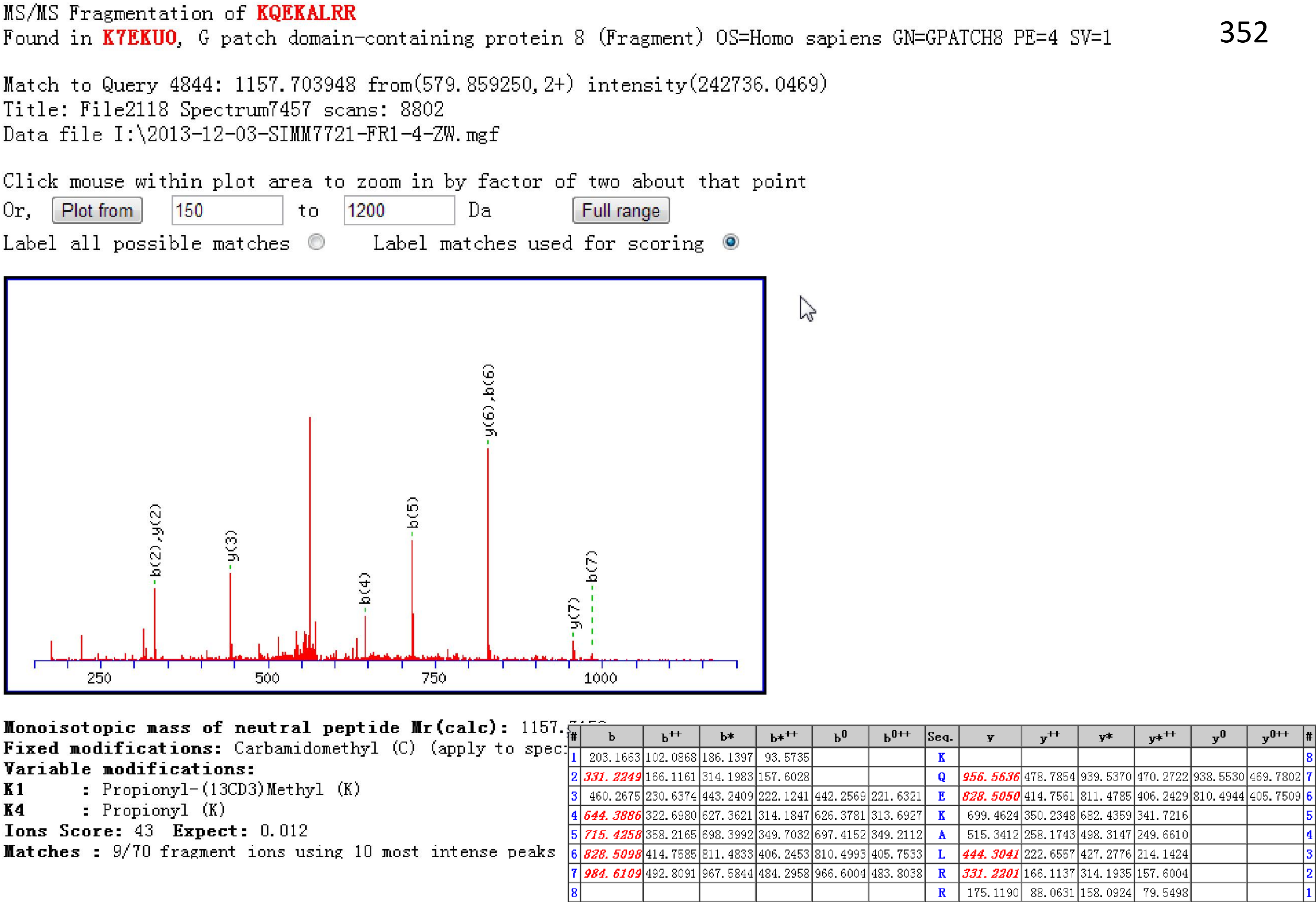
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1629
Fixed modifications: Carbamidomethyl (C) (apply to
Variable modifications:
K1     : Propionyl (K)
K2     : Propionyl-(13CD3)Methyl (K)
K7     : Propionyl (K)
Ions Score: 68  Expect: 9.9e-005
Matches : 13/136 fragment ions using 14 most intens
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							13
2	***387.2875***	194.1474	370.2609	185.6341			K	1446.7608	723.8841	1429.7343	715.3708	1428.7503	714.8788	12
3	502.3144	251.6608	485.2879	243.1476	484.3038	242.6556	D	***1244.6018***	622.8046	1227.5753	614.2913	1226.5913	613.7993	11
4	***639.3733***	320.1903	622.3468	311.6770	621.3628	311.1850	H	***1129.5749***	565.2911	1112.5483	556.7778	1111.5643	556.2858	10
5	696.3948	348.7010	679.3682	340.1878	678.3842	339.6957	G	***992.5160***	496.7616	975.4894	488.2483	974.5054	487.7563	9
6	***843.4632***	422.2352	826.4367	413.7220	825.4526	413.2300	F	935.4945	468.2509	918.4680	459.7376	917.4839	459.2456	8
7	1027.5844	514.2958	1010.5578	505.7826	1009.5738	505.2905	K	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	7
8	1126.6528	563.8300	1109.6262	555.3168	1108.6422	554.8248	V	***604.3049***	302.6561	587.2784	294.1428	586.2944	293.6508	6
9	***1213.6848***	607.3460	1196.6583	598.8328	1195.6743	598.3408	S	***505.2365***	253.1219	488.2100	244.6086	487.2259	244.1166	5
10	1284.7219	642.8646	1267.6954	634.3513	1266.7114	633.8593	A	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	4
11	***1399.7489***	700.3781	1382.7223	691.8648	1381.7383	691.3728	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
12	***1456.7703***	728.8888	1439.7438	720.3755	1438.7598	719.8835	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KQEKALRR**

Found in **K7EKU0**, G patch domain-containing protein 8 (Fragment) OS=Homo sapiens GN=GPATCH8 PE=4 SV=1

Match to Query 4844: 1157.703948 from(579.859250,2+) intensity(242736.0469)

Title: File2118 Spectrum7457 scans: 8802

Data file I:\2013-12-03-SIMM7721-FR1-4-ZW.mgf

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

Or, Plot from 150 to 1200 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1157.

Fixed modifications: Carbamidomethyl (C) (apply to spec

Variable modifications:

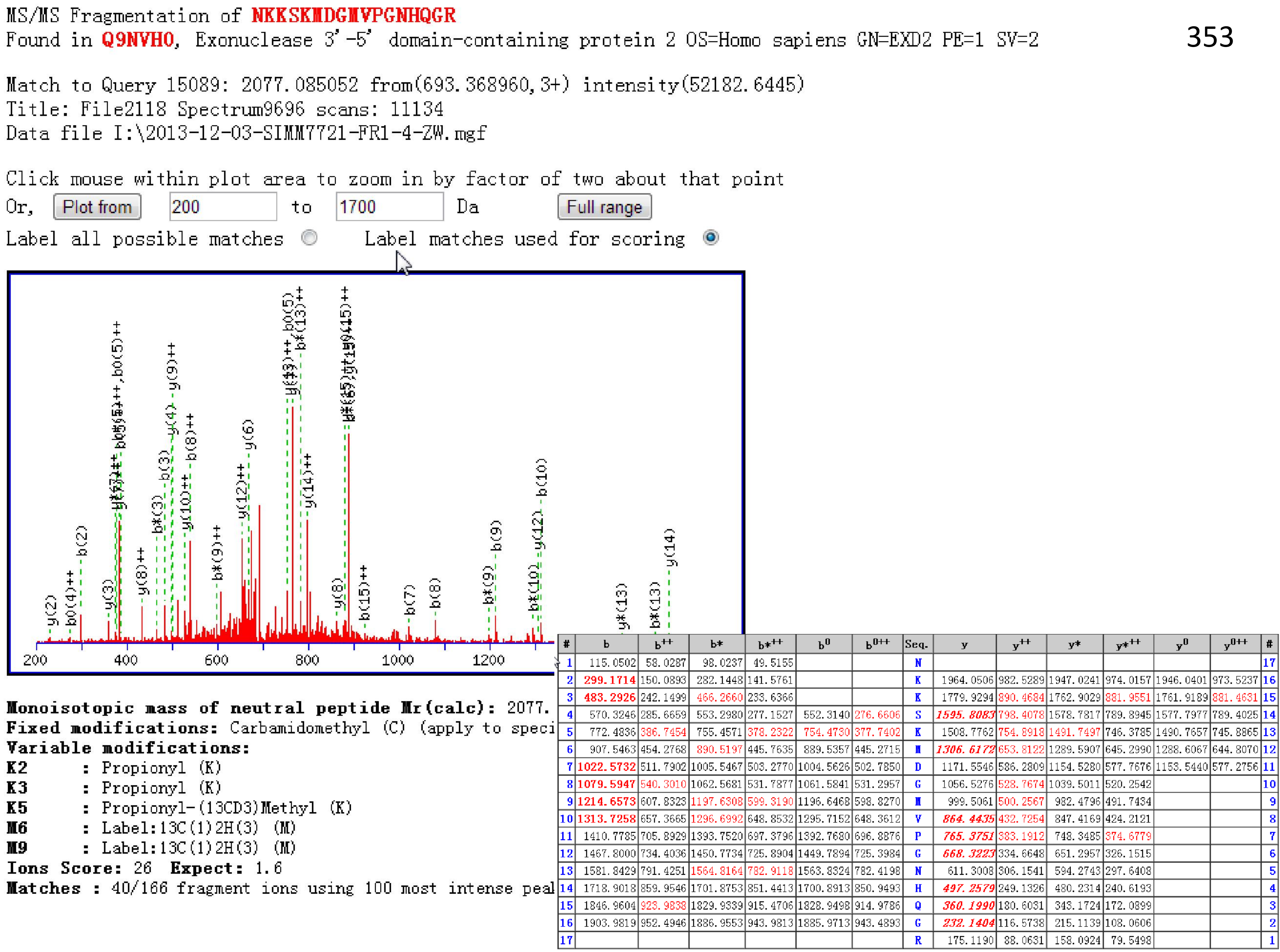
K1 : Propionyl-(13CD3)Methyl (K)

K4 : Propionyl (K)

Ions Score: 43 **Expect:** 0.012

Matches : 9/70 fragment ions using 10 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	***331.2249***	166.1161	314.1983	157.6028			Q	***956.5636***	478.7854	939.5370	470.2722	938.5530	469.7802	7
3	460.2675	230.6374	443.2409	222.1241	442.2569	221.6321	E	***828.5050***	414.7561	811.4785	406.2429	810.4944	405.7509	6
4	***644.3886***	322.6980	627.3621	314.1847	626.3781	313.6927	K	699.4624	350.2348	682.4359	341.7216			5
5	***715.4258***	358.2165	698.3992	349.7032	697.4152	349.2112	A	515.3412	258.1743	498.3147	249.6610			4
6	***828.5098***	414.7585	811.4833	406.2453	810.4993	405.7533	L	***444.3041***	222.6557	427.2776	214.1424			3
7	***984.6109***	492.8091	967.5844	484.2958	966.6004	483.8038	R	***331.2201***	166.1137	314.1935	157.6004			2
8							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **NKKSKMDGMVPGNHQGR**
Found in **Q9NVH0**, Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2

Match to Query 15089: 2077.085052 from(693.368960,3+) intensity(52182.6445)
Title: File2118 Spectrum9696 scans: 11134
Data file I:\2013-12-03-SIMM7721-FR1-4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

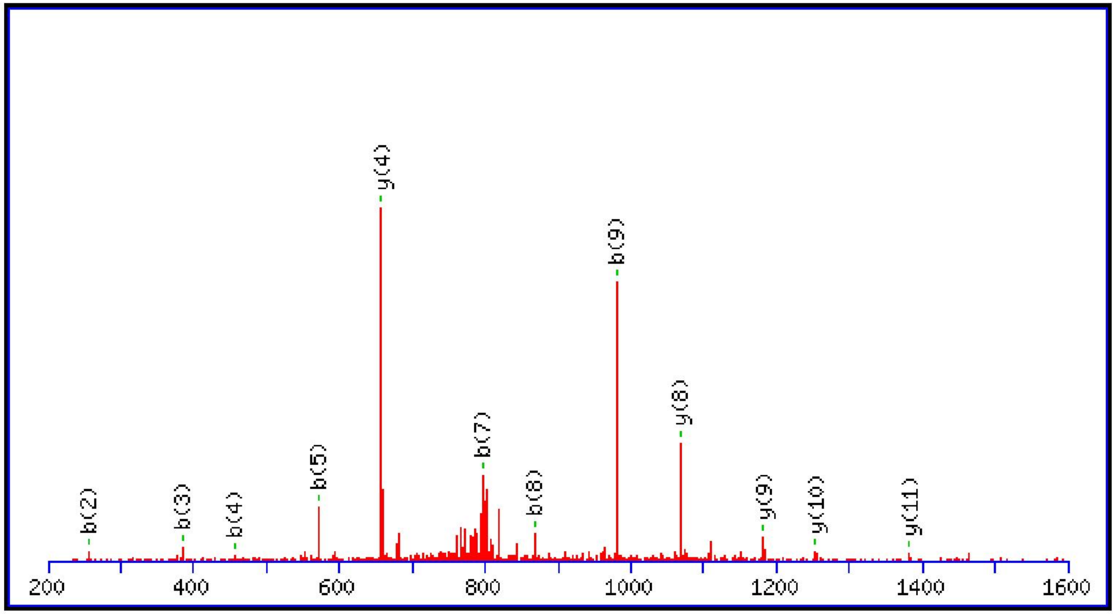
Monoisotopic mass of neutral peptide Mr(calc): 2077.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K2 : Propionyl (K)
K3 : Propionyl (K)
K5 : Propionyl-(13CD3)Methyl (K)
M6 : Label:13C(1)2H(3) (M)
M9 : Label:13C(1)2H(3) (M)
Ions Score: 26 **Expect:** 1.6
Matches : 40/166 fragment ions using 100 most intense peal

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155			N							17
2	**299.1714**	150.0893	282.1448	141.5761			K	1964.0506	982.5289	1947.0241	974.0157	1946.0401	973.5237	16
3	**483.2926**	242.1499	466.2660	233.6366			K	1779.9294	890.4684	1762.9029	881.9551	1761.9189	881.4631	15
4	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	S	***1595.8083***	798.4078	1578.7817	789.8945	1577.7977	789.4025	14
5	772.4836	386.7454	755.4571	378.2322	754.4730	377.7402	K	1508.7762	754.8918	1491.7497	746.3785	1490.7657	745.8865	13
6	907.5463	454.2768	890.5197	445.7635	889.5357	445.2715	M	***1306.6172***	653.8122	1289.5907	645.2990	1288.6067	644.8070	12
7	**1022.5732**	511.7902	1005.5467	503.2770	1004.5626	502.7850	D	1171.5546	586.2809	1154.5280	577.7676	1153.5440	577.2756	11
8	**1079.5947**	540.3010	1062.5681	531.7877	1061.5841	531.2957	G	1056.5276	528.7674	1039.5011	520.2542			10
9	**1214.6573**	607.8323	1197.6308	599.3190	1196.6468	598.8270	M	999.5061	500.2567	982.4796	491.7434			9
10	**1313.7258**	657.3665	1296.6992	648.8532	1295.7152	648.3612	V	***864.4435***	432.7254	847.4169	424.2121			8
11	1410.7785	705.8929	1393.7520	697.3796	1392.7680	696.8876	P	***765.3751***	383.1912	748.3485	374.6779			7
12	1467.8000	734.4036	1450.7734	725.8904	1449.7894	725.3984	G	***668.3223***	334.6648	651.2957	326.1515			6
13	1581.8429	791.4251	1564.8164	782.9118	1563.8324	782.4198	N	611.3008	306.1541	594.2743	297.6408			5
14	1718.9018	859.9546	1701.8753	851.4413	1700.8913	850.9493	H	***497.2579***	249.1326	480.2314	240.6193			4
15	1846.9604	923.9838	1829.9339	915.4706	1828.9498	914.9786	Q	***360.1990***	180.6031	343.1724	172.0899			3
16	1903.9819	952.4946	1886.9553	943.9813	1885.9713	943.4893	G	***232.1404***	116.5738	215.1139	108.0606			2
17							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAEADPQAIPKKR**
Found in **P51608**, Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1

Match to Query 11184: 1636.942848 from(819.478700,2+) intensity(50295.8867)
Title: File2115 Spectrum8551 scans: 9683
Data file I:\2013-12-03-SIMM7721-FR1-3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



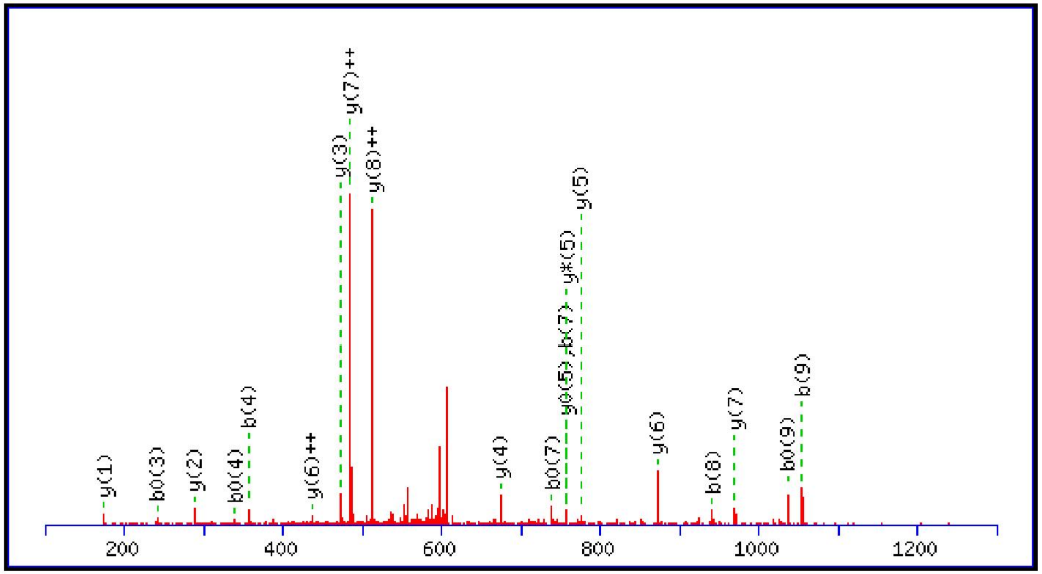
Monoisotopic mass of neutral peptide Mr(calc): 1636.9420
Fixed modifications: Carbamidomethyl (C) (apply to spec
Variable modifications:
K1 : Propionyl (K)
K11 : Propionyl (K)
K12 : Propionyl-(13CD3)Methyl (K)
Ions Score: 59 **Expect:** 0.00046
Matches : 12/124 fragment ions using 14 most intense peak

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							13
2	***256.1656***	128.5864	239.1390	120.0731			A	1453.8282	727.4177	1436.8016	718.9045	1435.8176	718.4125	12
3	***385.2082***	193.1077	368.1816	184.5944	367.1976	184.1024	E	**1382.7911**	691.8992	1365.7645	683.3859	1364.7805	682.8939	11
4	***456.2453***	228.6263	439.2187	220.1130	438.2347	219.6210	A	**1253.7485**	627.3779	1236.7219	618.8646	1235.7379	618.3726	10
5	***571.2722***	286.1397	554.2457	277.6265	553.2617	277.1345	D	**1182.7114**	591.8593	1165.6848	583.3460	1164.7008	582.8540	9
6	668.3250	334.6661	651.2984	326.1529	650.3144	325.6608	P	**1067.6844**	534.3459	1050.6579	525.8326			8
7	***796.3836***	398.6954	779.3570	390.1821	778.3730	389.6901	Q	970.6317	485.8195	953.6051	477.3062			7
8	***867.4207***	434.2140	850.3941	425.7007	849.4101	425.2087	A	842.5731	421.7902	825.5465	413.2769			6
9	***980.5047***	490.7560	963.4782	482.2427	962.4942	481.7507	I	771.5360	386.2716	754.5094	377.7583			5
10	1077.5575	539.2824	1060.5310	530.7691	1059.5469	530.2771	P	**658.4519**	329.7296	641.4254	321.2163			4
11	1261.6787	631.3430	1244.6521	622.8297	1243.6681	622.3377	K	561.3991	281.2032	544.3726	272.6899			3
12	1463.8377	732.4225	1446.8111	723.9092	1445.8271	723.4172	K	377.2780	189.1426	360.2514	180.6293			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **DSGPPTKKIR**
Found in **Q9H1E3**, Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1

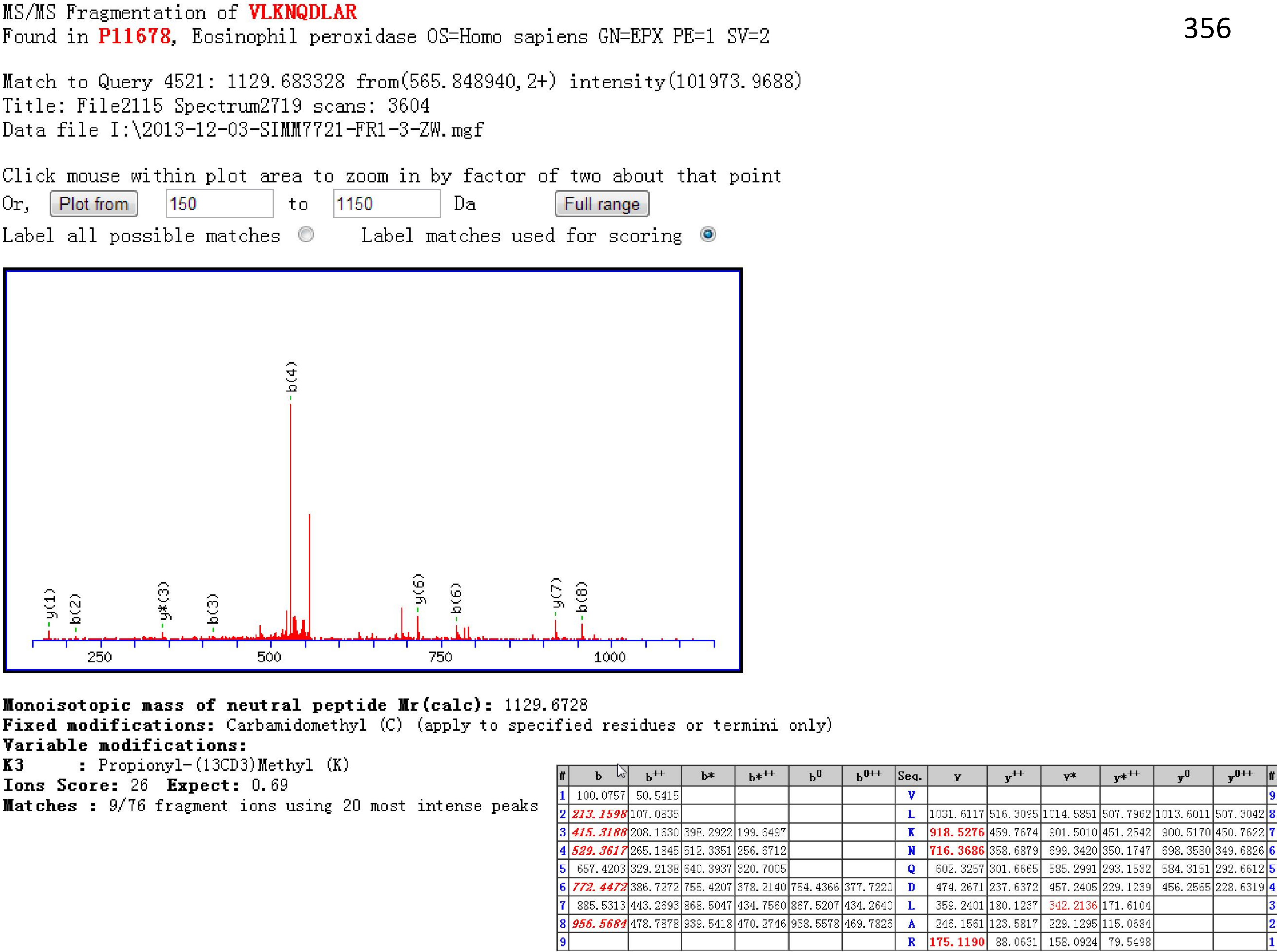
Match to Query 5873: 1227.709088 from(614.861820,2+) intensity(208671.0000)
Title: File2115 Spectrum7255 scans: 8333
Data file I:\2013-12-03-SIMM7721-FR1-3-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1227.7096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
K8 : Propionyl (K)
Ions Score: 51 **Expect:** 0.0032
Matches : 20/88 fragment ions using 31 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							10
2	203.0662	102.0368			185.0557	93.0315	S	1113.6899	557.3486	1096.6634	548.8353	1095.6793	548.3433	9
3	260.0877	130.5475			242.0771	121.5422	G	1026.6579	513.8326	1009.6313	505.3193	1008.6473	504.8273	8
4	**357.1405**	179.0739			339.1299	170.0686	P	***969.6364***	485.3218	952.6099	476.8086	951.6258	476.3166	7
5	454.1932	227.6003			436.1827	218.5950	P	***872.5836***	436.7955	855.5571	428.2822	854.5731	427.7902	6
6	555.2409	278.1241			537.2304	269.1188	T	***775.5309***	388.2691	758.5043	379.7558	757.5203	379.2638	5
7	**757.3999**	379.2036	740.3734	370.6903	739.3894	370.1983	K	***674.4832***	337.7452	657.4567	329.2320			4
8	**941.5211**	471.2642	924.4946	462.7509	923.5105	462.2589	K	***472.3242***	236.6657	455.2976	228.1525			3
9	**1054.6052**	527.8062	1037.5786	519.2930	1036.5946	518.8009	I	***288.2030***	144.6051	271.1765	136.0919			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1



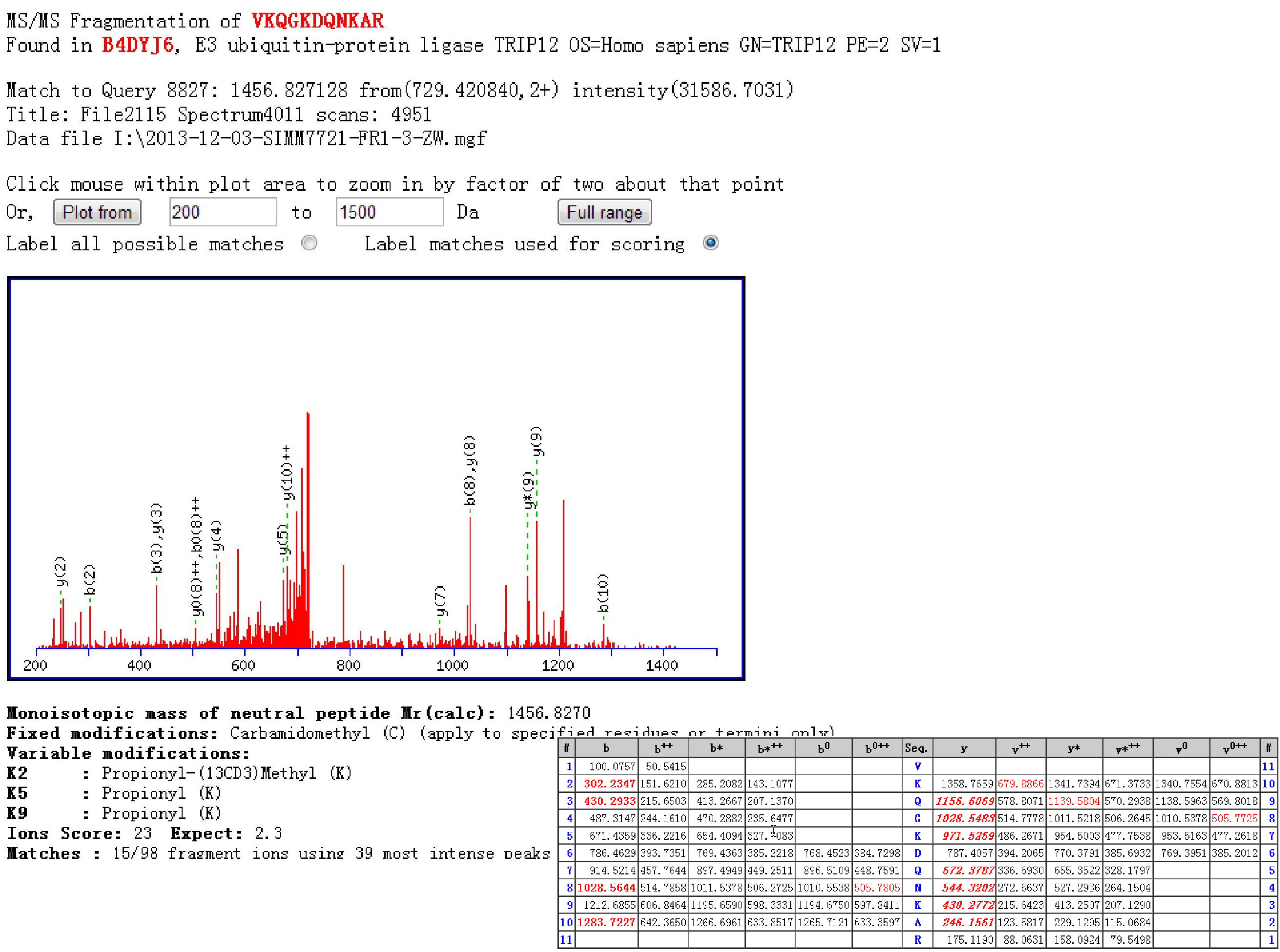
MS/MS Fragmentation of **VLKNQDLAR**
Found in **P11678**, Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2

Match to Query 4521: 1129.683328 from(565.848940,2+) intensity(101973.9688)
Title: File2115 Spectrum2719 scans: 3604
Data file I:\2013-12-03-SIMM7721-FR1-3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, 150 to 1150 Da
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1129.6728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 26 **Expect:** 0.69
Matches : 9/76 fragment ions using 20 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	100.0757	50.5415					V							9
2	***213.1598***	107.0835					L	1031.6117	516.3095	1014.5851	507.7962	1013.6011	507.3042	8
3	***415.3188***	208.1630	398.2922	199.6497			K	**918.5276**	459.7674	901.5010	451.2542	900.5170	450.7622	7
4	***529.3617***	265.1845	512.3351	256.6712			N	**716.3686**	358.6879	699.3420	350.1747	698.3580	349.6826	6
5	657.4203	329.2138	640.3937	320.7005			Q	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	5
6	***772.4472***	386.7272	755.4207	378.2140	754.4366	377.7220	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	885.5313	443.2693	868.5047	434.7560	867.5207	434.2640	L	359.2401	180.1237	342.2136	171.6104			3
8	***956.5684***	478.7878	939.5418	470.2746	938.5578	469.7826	A	246.1561	123.5817	229.1295	115.0684			2
9							R	**175.1190**	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **VKQGKDQNKAR**

Found in **B4DYJ6**, E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=2 SV=1

Match to Query 8827: 1456.827128 from(729.420840,2+) intensity(31586.7031)

Title: File2115 Spectrum4011 scans: 4951

Data file I:\2013-12-03-SIMM7721-FR1-3-ZW.mgf

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

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1456.8270

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

Variable modifications:

K2 : Propionyl-(13CD3)Methyl (K)

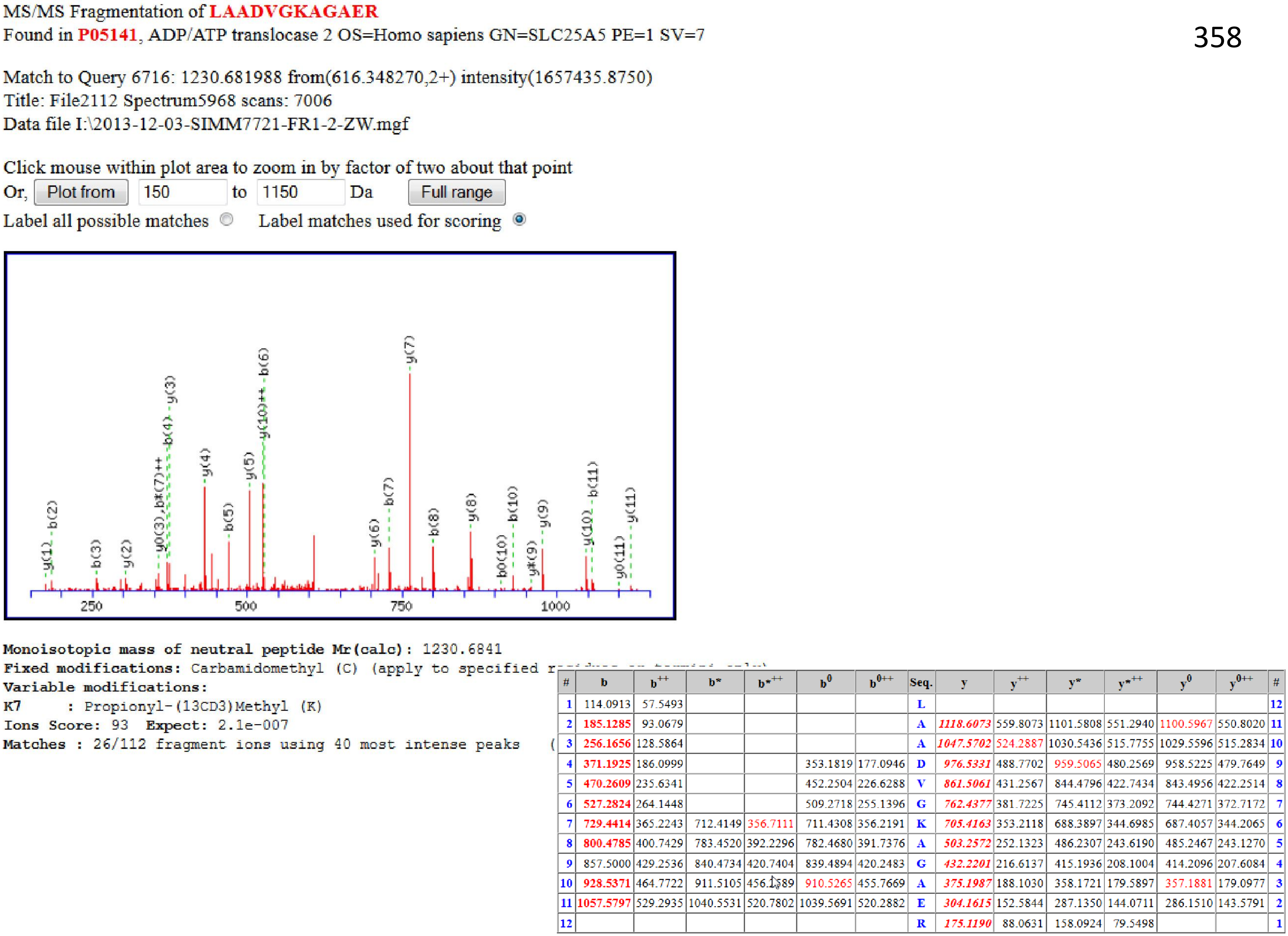
K5 : Propionyl (K)

K9 : Propionyl (K)

Ions Score: 23 **Expect:** 2.3

Matches : 15/98 fragment ions using 39 most intense peaks

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	100.0757	50.5415					V							11
2	**302.2347**	151.6210	285.2082	143.1077			K	1358.7659	679.8866	1341.7394	671.3733	1340.7554	670.8813	10
3	**430.2933**	215.6503	413.2667	207.1370			Q	***1156.6069***	578.8071	1139.5804	570.2938	1138.5963	569.8018	9
4	487.3147	244.1610	470.2882	235.6477			G	***1028.5483***	514.7778	1011.5218	506.2645	1010.5378	505.7725	8
5	671.4359	336.2216	654.4094	327.7083			K	***971.5269***	486.2671	954.5003	477.7538	953.5163	477.2618	7
6	786.4629	393.7351	769.4363	385.2218	768.4523	384.7298	D	787.4057	394.2065	770.3791	385.6932	769.3951	385.2012	6
7	914.5214	457.7644	897.4949	449.2511	896.5109	448.7591	Q	***672.3787***	336.6930	655.3522	328.1797			5
8	**1028.5644**	514.7858	1011.5378	506.2725	1010.5538	505.7805	N	***544.3202***	272.6637	527.2936	264.1504			4
9	1212.6855	606.8464	1195.6590	598.3331	1194.6750	597.8411	K	***430.2772***	215.6423	413.2507	207.1290			3
10	**1283.7227**	642.3650	1266.6961	633.8517	1265.7121	633.3597	A	***246.1561***	123.5817	229.1295	115.0684			2
11							R	175.1190	88.0631	158.0924	79.5498			1



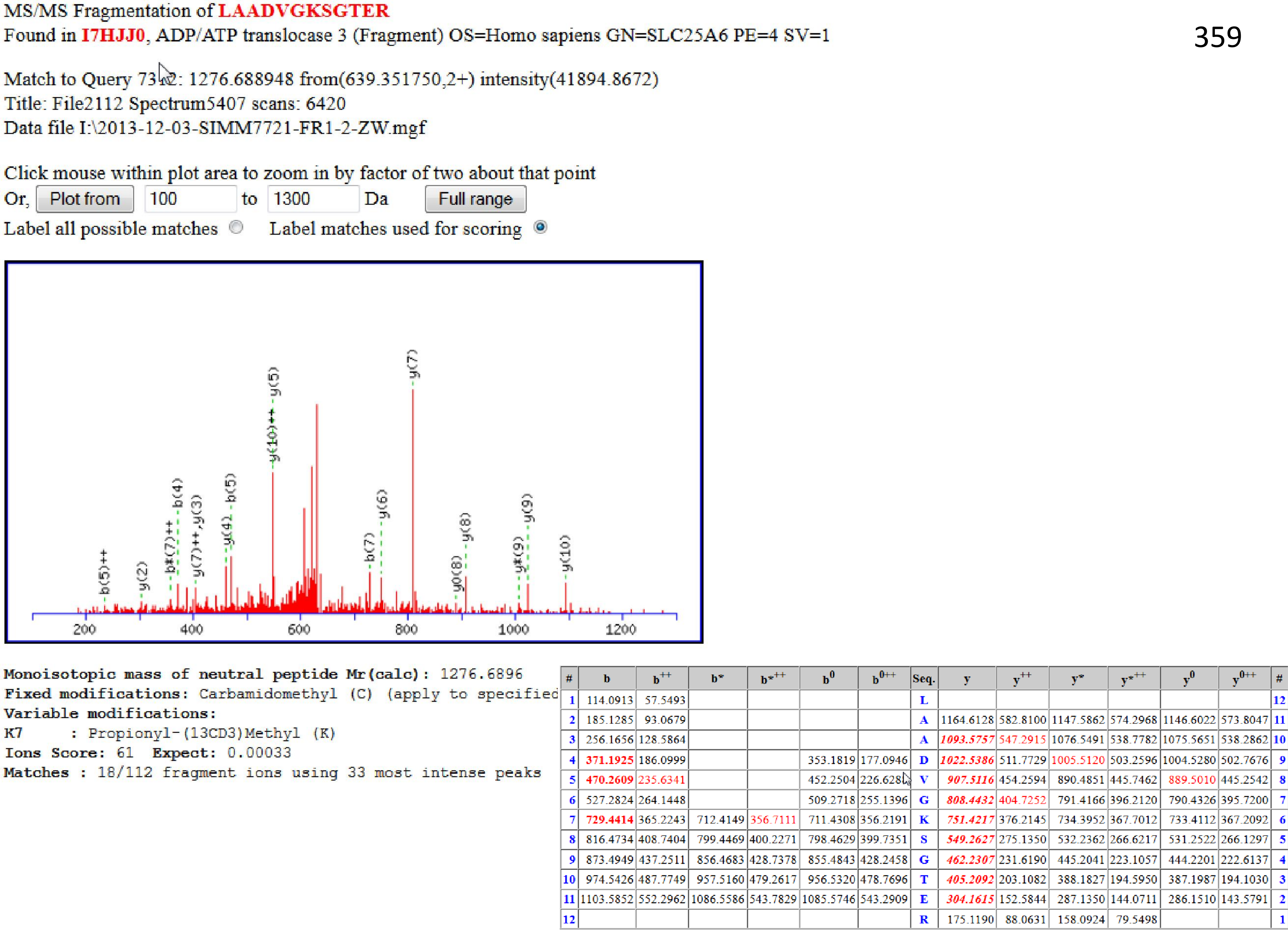
MS/MS Fragmentation of **LAADVGKAGAER**
Found in **P05141**, ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7

Match to Query 6716: 1230.681988 from(616.348270,2+) intensity(1657435.8750)
Title: File2112 Spectrum5968 scans: 7006
Data file I:\2013-12-03-SIMM7721-FR1-2-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1230.6841
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 93 **Expect:** 2.1e-007
Matches : 26/112 fragment ions using 40 most intense peaks (

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493					L							12
2	**185.1285**	93.0679					A	***1118.6073***	559.8073	1101.5808	551.2940	1100.5967	550.8020	11
3	**256.1656**	128.5864					A	***1047.5702***	524.2887	1030.5436	515.7755	1029.5596	515.2834	10
4	**371.1925**	186.0999			353.1819	177.0946	D	***976.5331***	488.7702	959.5065	480.2569	958.5225	479.7649	9
5	**470.2609**	235.6341			452.2504	226.6288	V	***861.5061***	431.2567	844.4796	422.7434	843.4956	422.2514	8
6	**527.2824**	264.1448			509.2718	255.1396	G	***762.4377***	381.7225	745.4112	373.2092	744.4271	372.7172	7
7	**729.4414**	365.2243	712.4149	356.7111	711.4308	356.2191	K	***705.4163***	353.2118	688.3897	344.6985	687.4057	344.2065	6
8	**800.4785**	400.7429	783.4520	392.2296	782.4680	391.7376	A	***503.2572***	252.1323	486.2307	243.6190	485.2467	243.1270	5
9	857.5000	429.2536	840.4734	420.7404	839.4894	420.2483	G	***432.2201***	216.6137	415.1936	208.1004	414.2096	207.6084	4
10	**928.5371**	464.7722	911.5105	456.[illegible]589	910.5265	455.7669	A	***375.1987***	188.1030	358.1721	179.5897	357.1881	179.0977	3
11	**1057.5797**	529.2935	1040.5531	520.7802	1039.5691	520.2882	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LAADVGKSGTER**

Found in **I7HJJ0**, ADP/ATP translocase 3 (Fragment) OS=Homo sapiens GN=SLC25A6 PE=4 SV=1

Match to Query 73: 1276.688948 from(639.351750,2+) intensity(41894.8672)

Title: File2112 Spectrum5407 scans: 6420

Data file I:\2013-12-03-SIMM7721-FR1-2-ZW.mgf

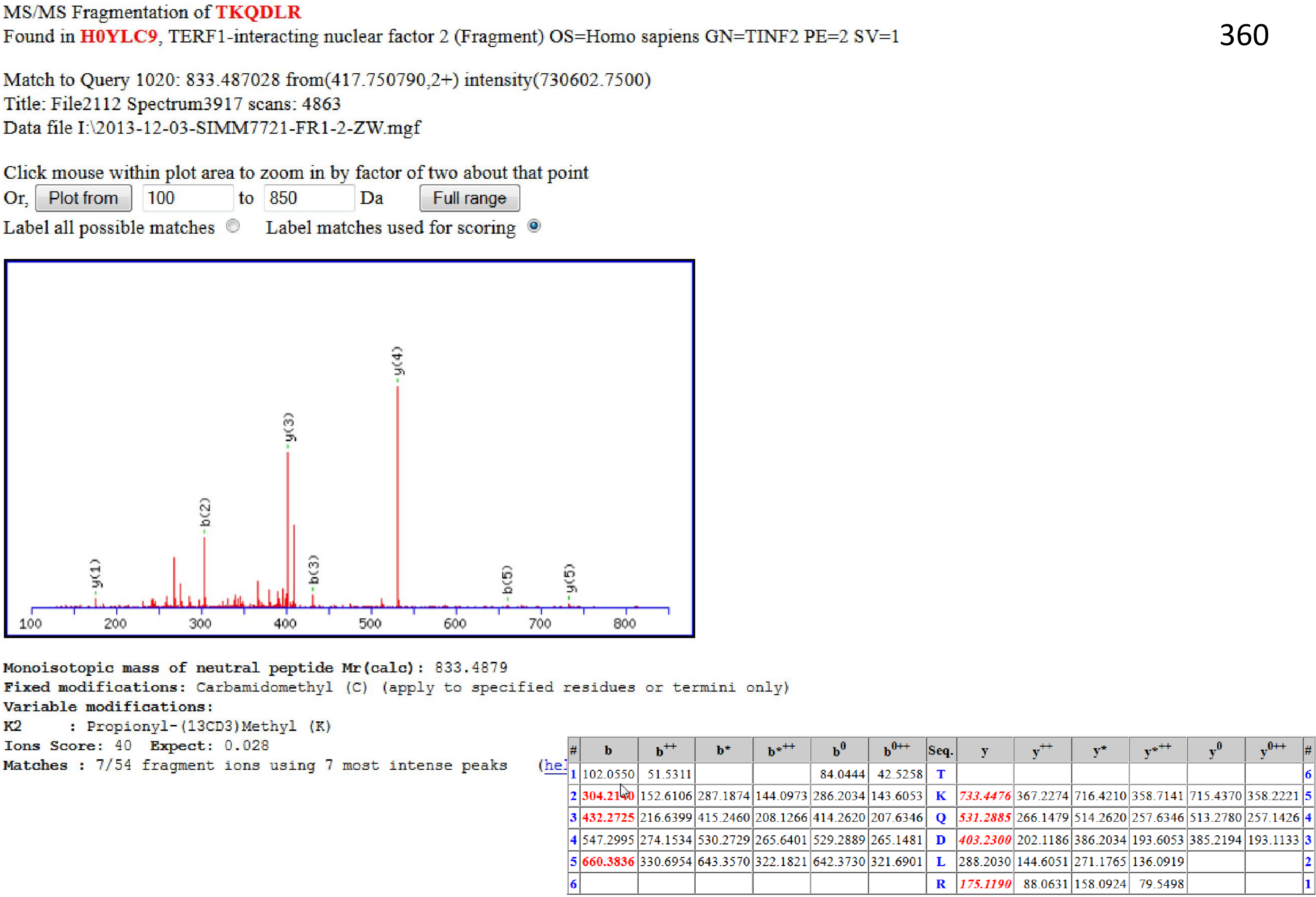
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1300 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1276.6896
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K7 : Propionyl-(13CD3)Methyl (K)
Ions Score: 61 **Expect:** 0.00033
Matches : 18/112 fragment ions using 33 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							12
2	185.1285	93.0679					A	1164.6128	582.8100	1147.5862	574.2968	1146.6022	573.8047	11
3	256.1656	128.5864					A	***1093.5757***	547.2915	1076.5491	538.7782	1075.5651	538.2862	10
4	**371.1925**	186.0999			353.1819	177.0946	D	***1022.5386***	511.7729	1005.5120	503.2596	1004.5280	502.7676	9
5	**470.2609**	235.6341			452.2504	226.628	V	***907.5116***	454.2594	890.4851	445.7462	889.5010	445.2542	8
6	527.2824	264.1448			509.2718	255.1396	G	***808.4432***	404.7252	791.4166	396.2120	790.4326	395.7200	7
7	**729.4414**	365.2243	712.4149	356.7111	711.4308	356.2191	K	***751.4217***	376.2145	734.3952	367.7012	733.4112	367.2092	6
8	816.4734	408.7404	799.4469	400.2271	798.4629	399.7351	S	***549.2627***	275.1350	532.2362	266.6217	531.2522	266.1297	5
9	873.4949	437.2511	856.4683	428.7378	855.4843	428.2458	G	***462.2307***	231.6190	445.2041	223.1057	444.2201	222.6137	4
10	974.5426	487.7749	957.5160	479.2617	956.5320	478.7696	T	***405.2092***	203.1082	388.1827	194.5950	387.1987	194.1030	3
11	1103.5852	552.2962	1086.5586	543.7829	1085.5746	543.2909	E	***304.1615***	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



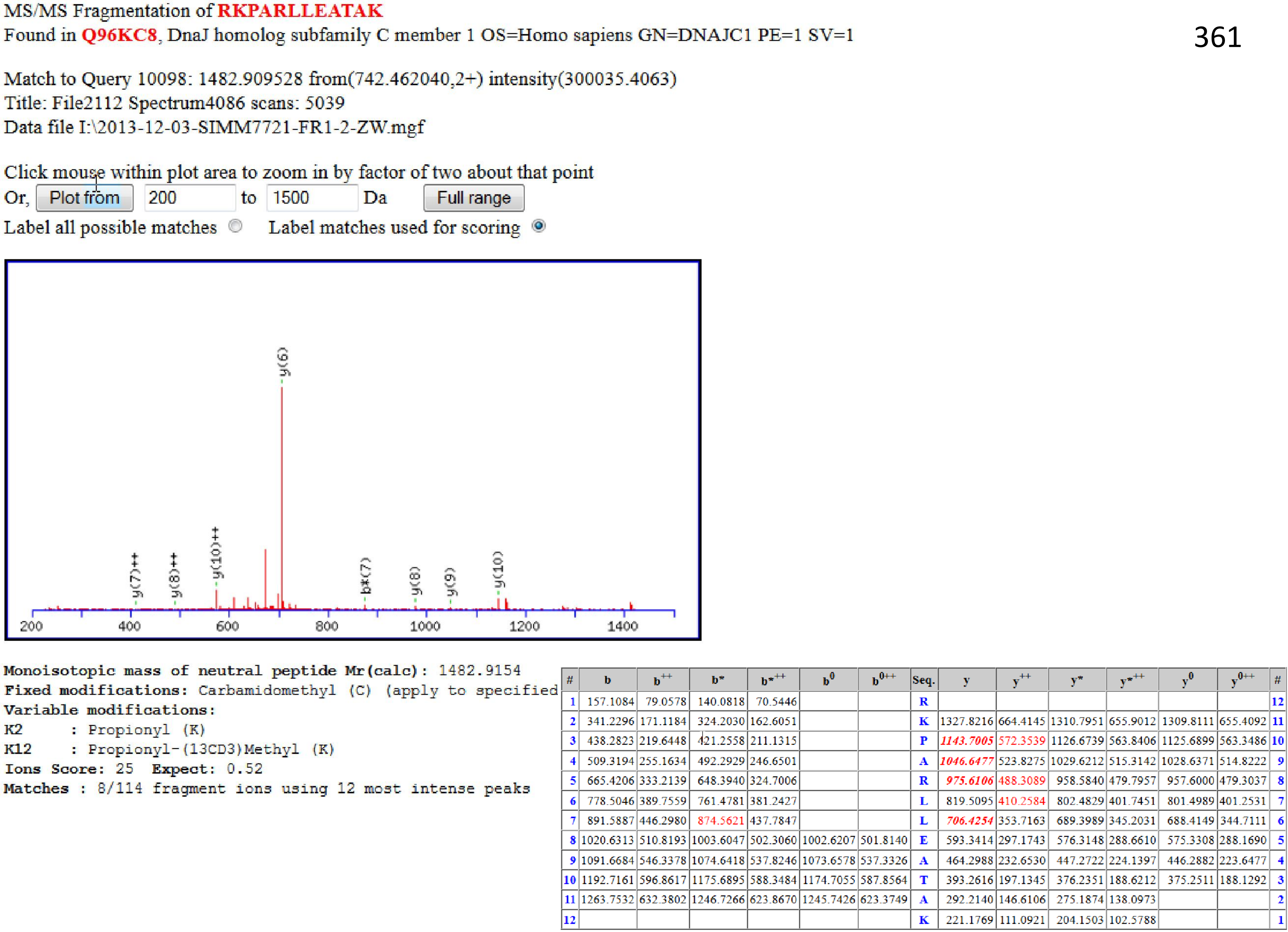
MS/MS Fragmentation of **TKQDLR**
Found in **H0YLC9**, TERF1-interacting nuclear factor 2 (Fragment) OS=Homo sapiens GN=TINF2 PE=2 SV=1

Match to Query 1020: 833.487028 from(417.750790,2+) intensity(730602.7500)
Title: File2112 Spectrum3917 scans: 4863
Data file I:\2013-12-03-SIMM7721-FR1-2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 833.4879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2      : Propionyl-(13CD3)Methyl (K)
Ions Score: 40  Expect: 0.028
Matches : 7/54 fragment ions using 7 most intense peaks  (hel
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							6
2	**304.2140**	152.6106	287.1874	144.0973	286.2034	143.6053	K	***733.4476***	367.2274	716.4210	358.7141	715.4370	358.2221	5
3	**432.2725**	216.6399	415.2460	208.1266	414.2620	207.6346	Q	***531.2885***	266.1479	514.2620	257.6346	513.2780	257.1426	4
4	547.2995	274.1534	530.2729	265.6401	529.2889	265.1481	D	***403.2300***	202.1186	386.2034	193.6053	385.2194	193.1133	3
5	**660.3836**	330.6954	643.3570	322.1821	642.3730	321.6901	L	288.2030	144.6051	271.1765	136.0919			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **RKPARLLEATAK**

Found in **Q96KC8**, DnaJ homolog subfamily C member 1 OS=Homo sapiens GN=DNAJC1 PE=1 SV=1

Match to Query 10098: 1482.909528 from(742.462040,2+) intensity(300035.4063)

Title: File2112 Spectrum4086 scans: 5039

Data file I:\2013-12-03-SIMM7721-FR1-2-ZW.mgf

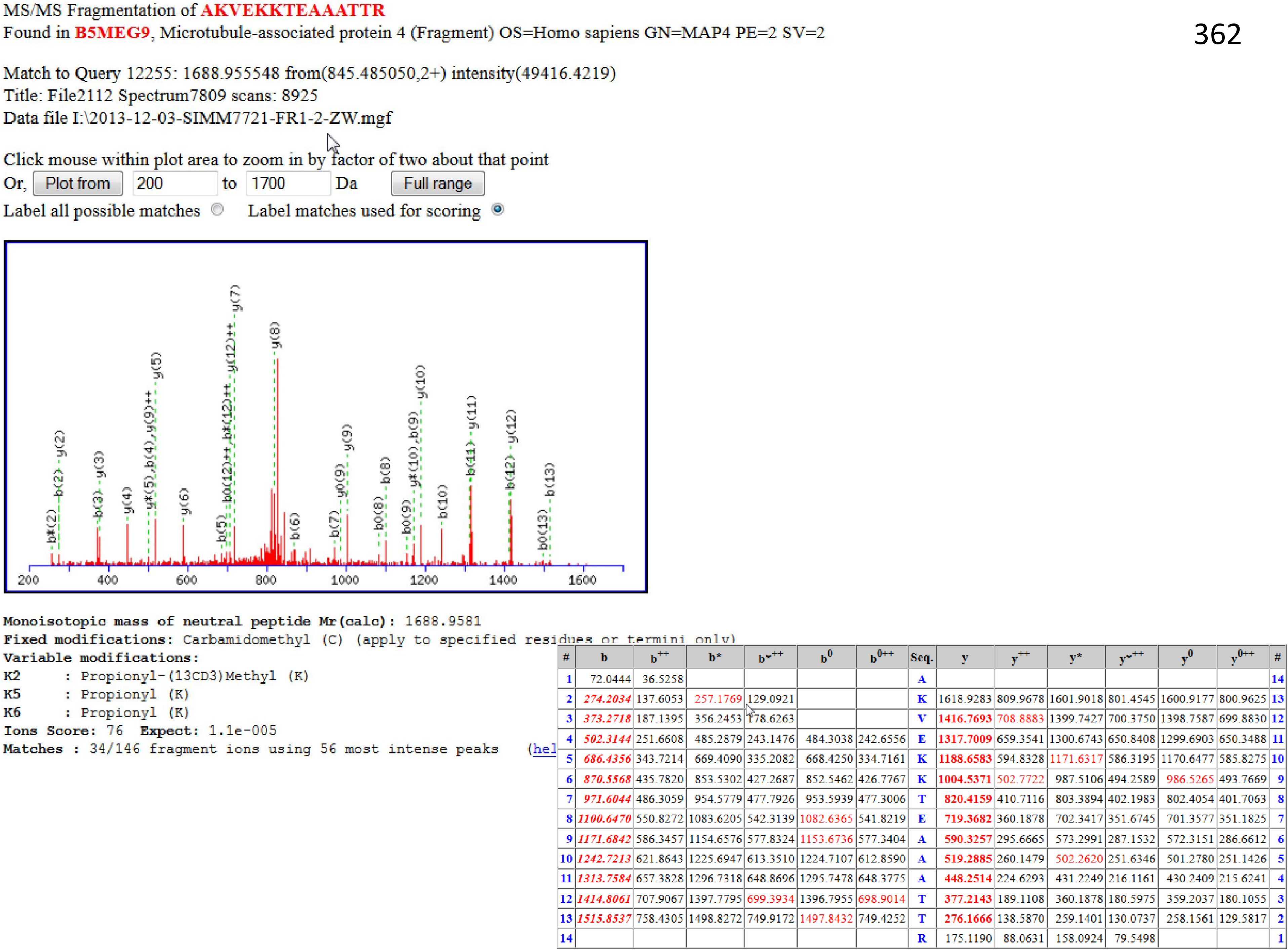
Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 200 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1482.9154
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K2      : Propionyl (K)
K12     : Propionyl-(13CD3)Methyl (K)
Ions Score: 25  Expect: 0.52
Matches : 8/114 fragment ions using 12 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	341.2296	171.1184	324.2030	162.6051			K	1327.8216	664.4145	1310.7951	655.9012	1309.8111	655.4092	11
3	438.2823	219.6448	421.2558	211.1315			P	***1143.7005***	572.3539	1126.6739	563.8406	1125.6899	563.3486	10
4	509.3194	255.1634	492.2929	246.6501			A	***1046.6477***	523.8275	1029.6212	515.3142	1028.6371	514.8222	9
5	665.4206	333.2139	648.3940	324.7006			R	***975.6106***	488.3089	958.5840	479.7957	957.6000	479.3037	8
6	778.5046	389.7559	761.4781	381.2427			L	819.5095	410.2584	802.4829	401.7451	801.4989	401.2531	7
7	891.5887	446.2980	874.5621	437.7847			L	***706.4254***	353.7163	689.3989	345.2031	688.4149	344.7111	6
8	1020.6313	510.8193	1003.6047	502.3060	1002.6207	501.8140	E	593.3414	297.1743	576.3148	288.6610	575.3308	288.1690	5
9	1091.6684	546.3378	1074.6418	537.8246	1073.6578	537.3326	A	464.2988	232.6530	447.2722	224.1397	446.2882	223.6477	4
10	1192.7161	596.8617	1175.6895	588.3484	1174.7055	587.8564	T	393.2616	197.1345	376.2351	188.6212	375.2511	188.1292	3
11	1263.7532	632.3802	1246.7266	623.8670	1245.7426	623.3749	A	292.2140	146.6106	275.1874	138.0973			2
12							K	221.1769	111.0921	204.1503	102.5788			1



MS/MS Fragmentation of **AKVEKKTEAAATTR**

Found in **B5MEG9**, Microtubule-associated protein 4 (Fragment) OS=Homo sapiens GN=MAP4 PE=2 SV=2

Match to Query 12255: 1688.955548 from(845.485050,2+) intensity(49416.4219)

Title: File2112 Spectrum7809 scans: 8925

Data file I:\2013-12-03-SIMM7721-FR1-2-ZW.mgf

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

Or, Plot from 200 to 1700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1688.9581

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

Variable modifications:

K2 : Propionyl-(13CD3)Methyl (K)

K5 : Propionyl (K)

K6 : Propionyl (K)

Ions Score: 76 **Expect:** 1.1e-005

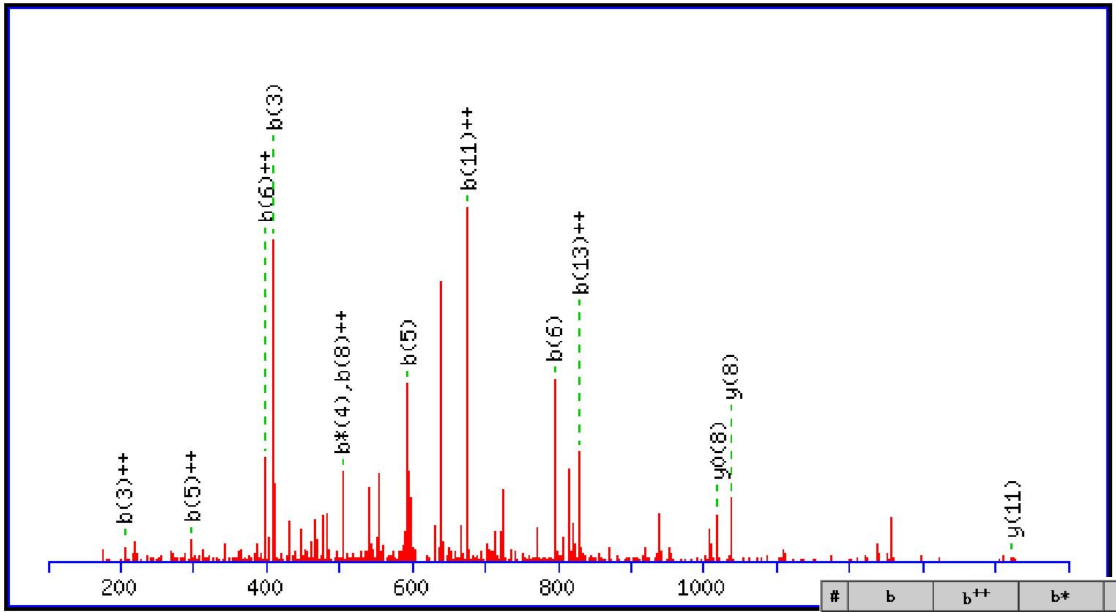
Matches : 34/146 fragment ions using 56 most intense peaks (hel

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							14
2	*274.2034*	137.6053	257.1769	129.0921			K	1618.9283	809.9678	1601.9018	801.4545	1600.9177	800.9625	13
3	*373.2718*	187.1395	356.2453	178.6263			V	**1416.7693**	708.8883	1399.7427	700.3750	1398.7587	699.8830	12
4	*502.3144*	251.6608	485.2879	243.1476	484.3038	242.6556	E	**1317.7009**	659.3541	1300.6743	650.8408	1299.6903	650.3488	11
5	*686.4356*	343.7214	669.4090	335.2082	668.4250	334.7161	K	**1188.6583**	594.8328	1171.6317	586.3195	1170.6477	585.8275	10
6	*870.5568*	435.7820	853.5302	427.2687	852.5462	426.7767	K	**1004.5371**	502.7722	987.5106	494.2589	986.5265	493.7669	9
7	*971.6044*	486.3059	954.5779	477.7926	953.5939	477.3006	T	**820.4159**	410.7116	803.3894	402.1983	802.4054	401.7063	8
8	*1100.6470*	550.8272	1083.6205	542.3139	1082.6365	541.8219	E	**719.3682**	360.1878	702.3417	351.6745	701.3577	351.1825	7
9	*1171.6842*	586.3457	1154.6576	577.8324	1153.6736	577.3404	A	**590.3257**	295.6665	573.2991	287.1532	572.3151	286.6612	6
10	*1242.7213*	621.8643	1225.6947	613.3510	1224.7107	612.8590	A	**519.2885**	260.1479	502.2620	251.6346	501.2780	251.1426	5
11	*1313.7584*	657.3828	1296.7318	648.8696	1295.7478	648.3775	A	**448.2514**	224.6293	431.2249	216.1161	430.2409	215.6241	4
12	*1414.8061*	707.9067	1397.7795	699.3934	1396.7955	698.9014	T	**377.2143**	189.1108	360.1878	180.5975	359.2037	180.1055	3
13	*1515.8537*	758.4305	1498.8272	749.9172	1497.8432	749.4252	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FFNIAKDPRVSMRR**
Found in **J3QSX2**, Neurofascin OS=Homo sapiens GN=NFASC PE=4 SV=1

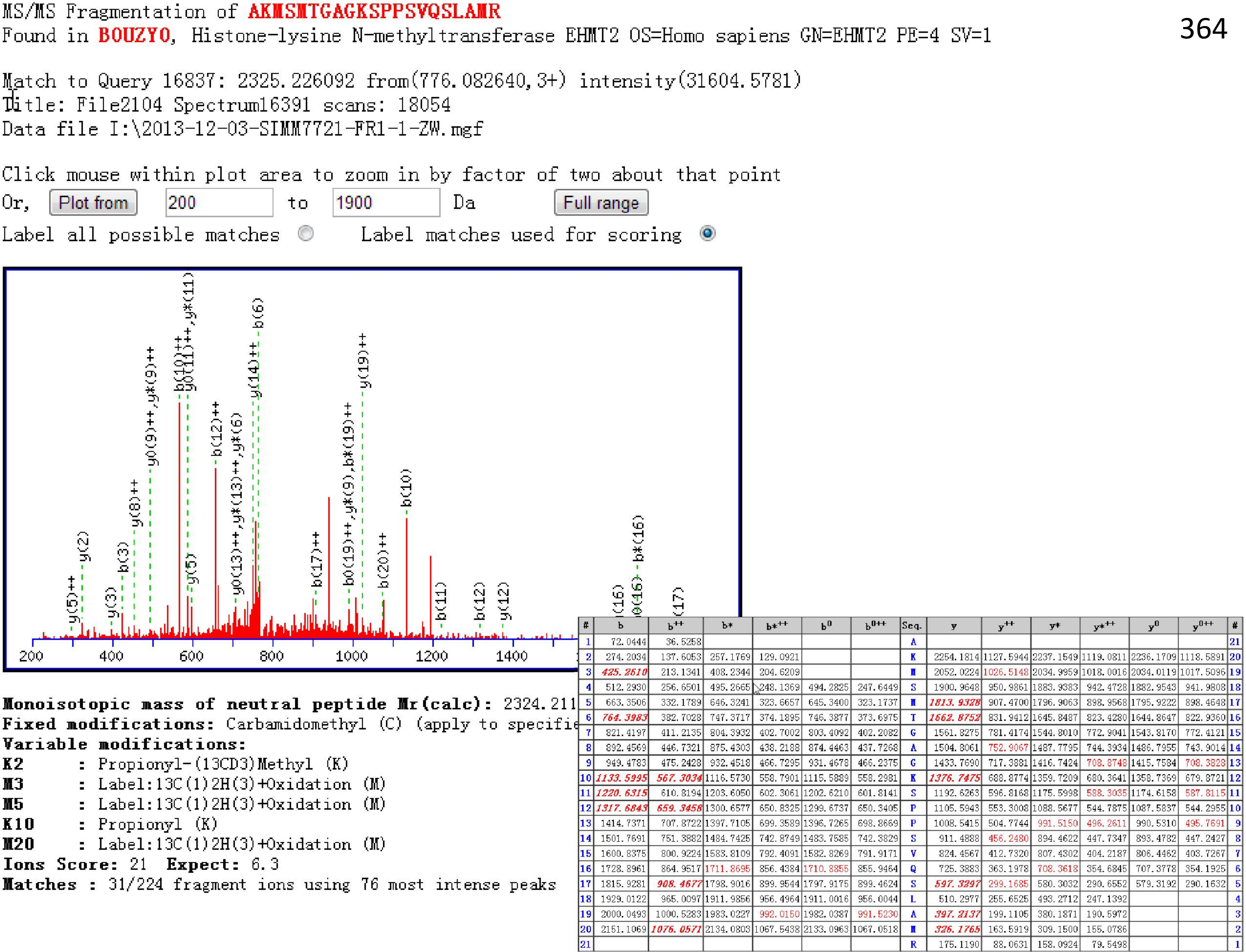
Match to Query 13482: 1829.997222 from(611.006350,3+) intensity(2895879.0000)
Title: File2104 Spectrum6401 scans: 7647
Data file I:\2013-12-03-SIMM7721-FR1-1-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1830.
Fixed modifications: Carbamidomethyl (C) (apply to spec
Variable modifications:
K6 : Propionyl-(13CD3)Methyl (K)
M12 : Label:13C(1)2H(3)+Oxidation (M)
Ions Score: 24 **Expect:** 2.5
Matches : 13/134 fragment ions using 26 most intense peak

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							14
2	295.1441	148.0757					F	1683.9504	842.4789	1666.9239	833.9656	1665.9399	833.4736	13
3	**409.1870**	***205.0972***	392.1605	196.5839			N	1536.8820	768.9447	1519.8555	760.4314	1518.8715	759.9394	12
4	522.2711	261.6392	505.2445	253.1259			I	**1422.8391**	711.9232	1405.8126	703.4099	1404.8285	702.9179	11
5	**593.3082**	***297.1577***	576.2817	288.6445			A	1309.7550	655.3812	1292.7285	646.8679	1291.7445	646.3759	10
6	**795.4672**	***398.2372***	778.4407	389.7240			K	1238.7179	619.8626	1221.6914	611.3493	1220.7074	610.8573	9
7	910.4942	455.7507	893.4676	447.2374	892.4836	446.7454	D	**1036.5589**	518.7831	1019.5324	510.2698	1018.5483	509.7778	8
8	1007.5469	***504.2771***	990.5204	495.7638	989.5364	495.2718	P	921.5320	461.2696	904.5054	452.7563	903.5214	452.2643	7
9	1163.6480	582.3277	1146.6215	573.8144	1145.6375	573.3224	R	824.4792	412.7432	807.4527	404.2300	806.4686	403.7380	6
10	1262.7165	631.8619	1245.6899	623.3486	1244.7059	622.8566	V	668.3781	334.6927	651.3515	326.1794	650.3675	325.6874	5
11	1349.7485	***675.3779***	1332.7219	666.8646	1331.7379	666.3726	S	569.3097	285.1585	552.2831	276.6452	551.2991	276.1532	4
12	1500.8061	750.9067	1483.7795	742.3934	1482.7955	741.9014	M	482.2776	241.6425	465.2511	233.1292			3
13	1656.9072	***828.9572***	1639.8806	820.4440	1638.8966	819.9519	R	331.2201	166.1137	314.1935	157.6004			2
14							R	175.1190	88.0631	158.0924	79.5498			1



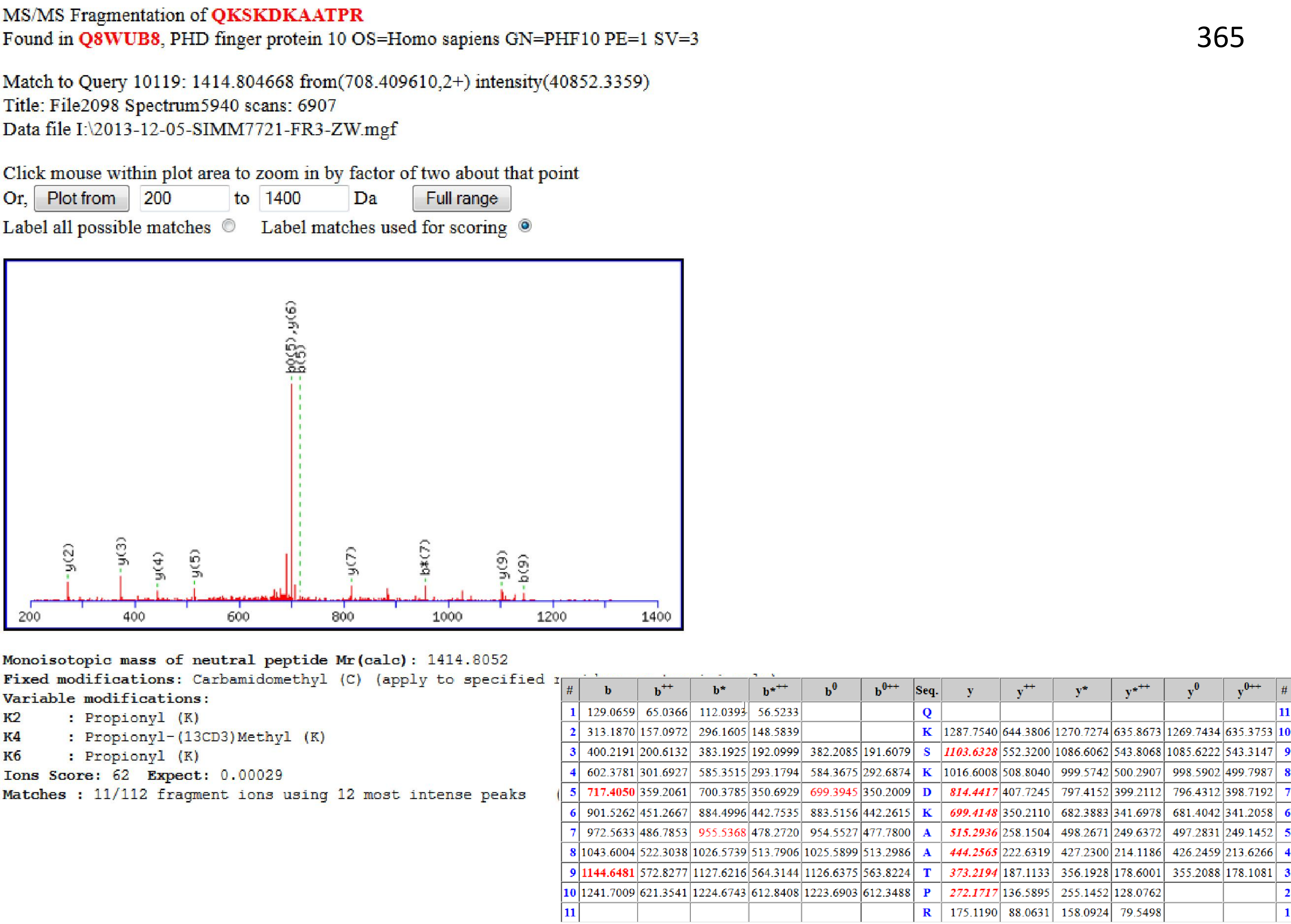
MS/MS Fragmentation of **AKMSMTGAGKSPPSVQSLAMR**
Found in **BOUZYO**, Histone-lysine N-methyltransferase EHMT2 OS=Homo sapiens GN=EHMT2 PE=4 SV=1

Match to Query 16837: 2325.226092 from(776.082640,3+) intensity(31604.5781)
Title: File2104 Spectrum16391 scans: 18054
Data file I:\2013-12-03-SIMM7721-FR1-1-ZW.mgf

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

Monoisotopic mass of neutral peptide Mr(calc): 2324.211
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
M3 : Label:13C(1)2H(3)+Oxidation (M)
M5 : Label:13C(1)2H(3)+Oxidation (M)
K10 : Propionyl (K)
M20 : Label:13C(1)2H(3)+Oxidation (M)
Ions Score: 21 **Expect:** 6.3
Matches : 31/224 fragment ions using 76 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258					A							21
2	274.2034	137.6053	257.1769	129.0921			K	2254.1814	1127.5944	2237.1549	1119.0811	2236.1709	1118.5891	20
3	**425.2610**	213.1341	408.2344	204.6209			M	2052.0224	1026.5148	2034.9959	1018.0016	2034.0119	1017.5096	19
4	512.2930	256.6501	495.2665	248.1369	494.2825	247.6449	S	1900.9648	950.9861	1883.9383	942.4728	1882.9543	941.9808	18
5	663.3506	332.1789	646.3241	323.6657	645.3400	323.1737	M	**1813.9328**	907.4700	1796.9063	898.9568	1795.9222	898.4648	17
6	**764.3983**	382.7028	747.3717	374.1895	746.3877	373.6975	T	**1662.8752**	831.9412	1645.8487	823.4280	1644.8647	822.9360	16
7	821.4197	411.2135	804.3932	402.7002	803.4092	402.2082	G	1561.8275	781.4174	1544.8010	772.9041	1543.8170	772.4121	15
8	892.4569	446.7321	875.4303	438.2188	874.4463	437.7268	A	1504.8061	752.9067	1487.7795	744.3934	1486.7955	743.9014	14
9	949.4783	475.2428	932.4518	466.7295	931.4678	466.2375	G	1433.7690	717.3881	1416.7424	708.8748	1415.7584	708.3828	13
10	**1133.5995**	**567.3034**	1116.5730	558.7901	1115.5889	558.2981	K	**1376.7475**	688.8774	1359.7209	680.3641	1358.7369	679.8721	12
11	**1220.6315**	610.8194	1203.6050	602.3061	1202.6210	601.8141	S	1192.6263	596.8168	1175.5998	588.3035	1174.6158	587.8115	11
12	**1317.6843**	**659.3458**	1300.6577	650.8325	1299.6737	650.3405	P	1105.5943	553.3008	1088.5677	544.7875	1087.5837	544.2955	10
13	1414.7371	707.8722	1397.7105	699.3589	1396.7265	698.8669	P	1008.5415	504.7744	991.5150	496.2611	990.5310	495.7691	9
14	1501.7691	751.3882	1484.7425	742.8749	1483.7585	742.3829	S	911.4888	456.2480	894.4622	447.7347	893.4782	447.2427	8
15	1600.8375	800.9224	1583.8109	792.4091	1582.8269	791.9171	V	824.4567	412.7320	807.4302	404.2187	806.4462	403.7267	7
16	1728.8961	864.9517	1711.8695	856.4384	1710.8855	855.9464	Q	725.3883	363.1978	708.3618	354.6845	707.3778	354.1925	6
17	1815.9281	**908.4677**	1798.9016	899.9544	1797.9175	899.4624	S	**597.3297**	299.1685	580.3032	290.6552	579.3192	290.1632	5
18	1929.0122	965.0097	1911.9856	956.4964	1911.0016	956.0044	L	510.2977	255.6525	493.2712	247.1392			4
19	2000.0493	1000.5283	1983.0227	992.0150	1982.0387	991.5230	A	**397.2137**	199.1105	380.1871	190.5972			3
20	2151.1069	**1076.0571**	2134.0803	1067.5438	2133.0963	1067.0518	M	**326.1765**	163.5919	309.1500	155.0786			2
21							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **QKSKDKAATPR**
Found in **Q8WUB8**, PHD finger protein 10 OS=Homo sapiens GN=PHF10 PE=1 SV=3

Match to Query 10119: 1414.804668 from(708.409610,2+) intensity(40852.3359)
Title: File2098 Spectrum5940 scans: 6907
Data file I:\2013-12-05-SIMM7721-FR3-ZW.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 ●

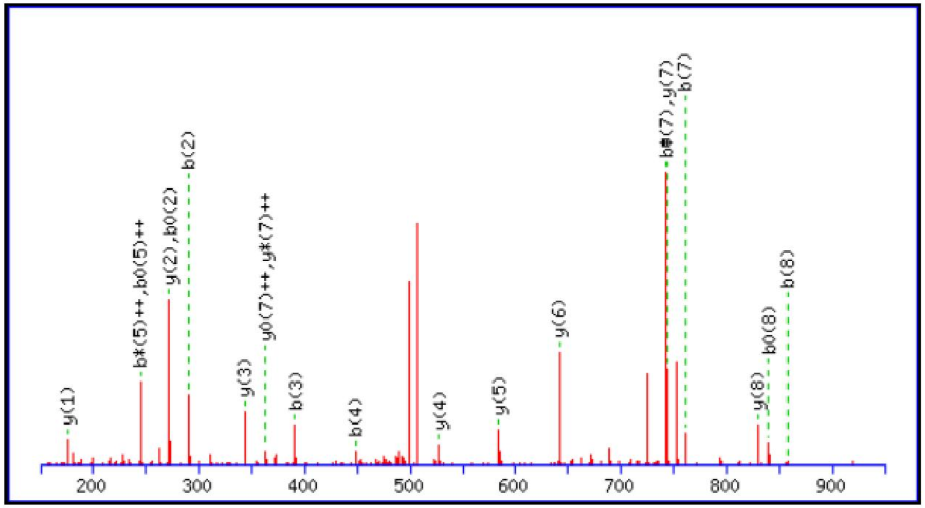
```
Monoisotopic mass of neutral peptide Mr(calc): 1414.8052
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K2      : Propionyl (K)
K4      : Propionyl-(13CD3)Methyl (K)
K6      : Propionyl (K)
Ions Score: 62  Expect: 0.00029
Matches : 11/112 fragment ions using 12 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	313.1870	157.0972	296.1605	148.5839			K	1287.7540	644.3806	1270.7274	635.8673	1269.7434	635.3753	10
3	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	S	***1103.6328***	552.3200	1086.6062	543.8068	1085.6222	543.3147	9
4	602.3781	301.6927	585.3515	293.1794	584.3675	292.6874	K	1016.6008	508.8040	999.5742	500.2907	998.5902	499.7987	8
5	**717.4050**	359.2061	700.3785	350.6929	699.3945	350.2009	D	***814.4417***	407.7245	797.4152	399.2112	796.4312	398.7192	7
6	901.5262	451.2667	884.4996	442.7535	883.5156	442.2615	K	***699.4148***	350.2110	682.3883	341.6978	681.4042	341.2058	6
7	972.5633	486.7853	955.5368	478.2720	954.5527	477.7800	A	***515.2936***	258.1504	498.2671	249.6372	497.2831	249.1452	5
8	1043.6004	522.3038	1026.5739	513.7906	1025.5899	513.2986	A	***444.2565***	222.6319	427.2300	214.1186	426.2459	213.6266	4
9	**1144.6481**	572.8277	1127.6216	564.3144	1126.6375	563.8224	T	***373.2194***	187.1133	356.1928	178.6001	355.2088	178.1081	3
10	1241.7009	621.3541	1224.6743	612.8408	1223.6903	612.3488	P	***272.1717***	136.5895	255.1452	128.0762			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KSTGGKAPR**
Found in **Q71DI3**, Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3

Match to Query 3734: 1030.605328 from(516.309940,2+) intensity(1718561.0000)
Title: File2098 Spectrum1118 scans: 1738
Data file I:\2013-12-05-SIMM7721-FR3-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



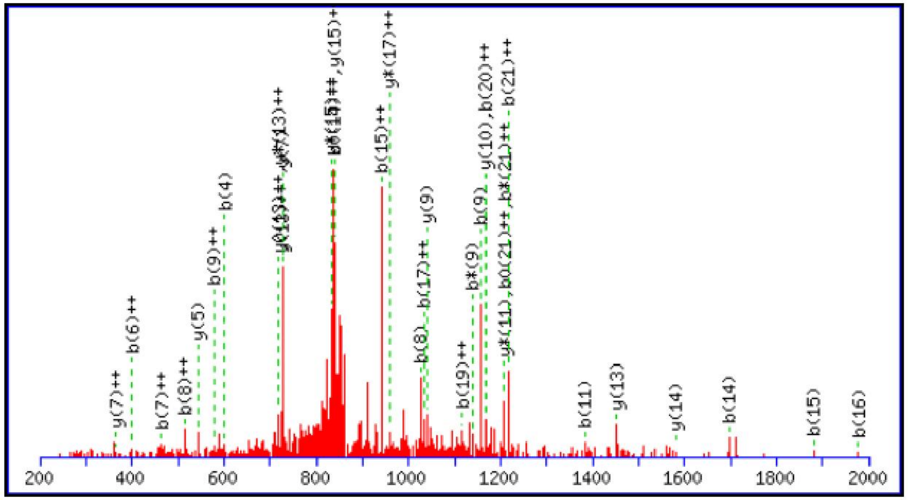
Monoisotopic mass of neutral peptide Mr(calc): 1030.6044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
Ions Score: 78 **Expect:** 5.4e-006
Matches : 21/82 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	S	***829.4526***	415.2300	812.4261	406.7167	811.4421	406.2247	8
3	**391.2460**	196.1266	374.2194	187.6134	373.2354	187.1214	T	***742.4206***	371.7139	725.3941	363.2007	724.4100	362.7087	7
4	**448.2675**	224.6374	431.2409	216.1241	430.2569	215.6321	G	***641.3729***	321.1901	624.3464	312.6768			6
5	505.2889	253.1481	488.2624	244.6348	487.2784	244.1428	G	***584.3515***	292.6794	567.3249	284.1661			5
6	689.4101	345.2087	672.3836	336.6954	671.3995	336.2034	K	***527.3300***	264.1686	510.3035	255.6554			4
7	**760.4472**	380.7272	743.4207	372.2140	742.4367	371.7220	A	***343.2088***	172.1081	326.1823	163.5948			3
8	**857.5000**	429.2536	840.4734	420.7404	839.4894	420.2483	P	***272.1717***	136.5895	255.1452	128.0762			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KVKDAQQVEPEGQEKPSPATVR**
Found in **E7EPN9**, Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=2 SV=1

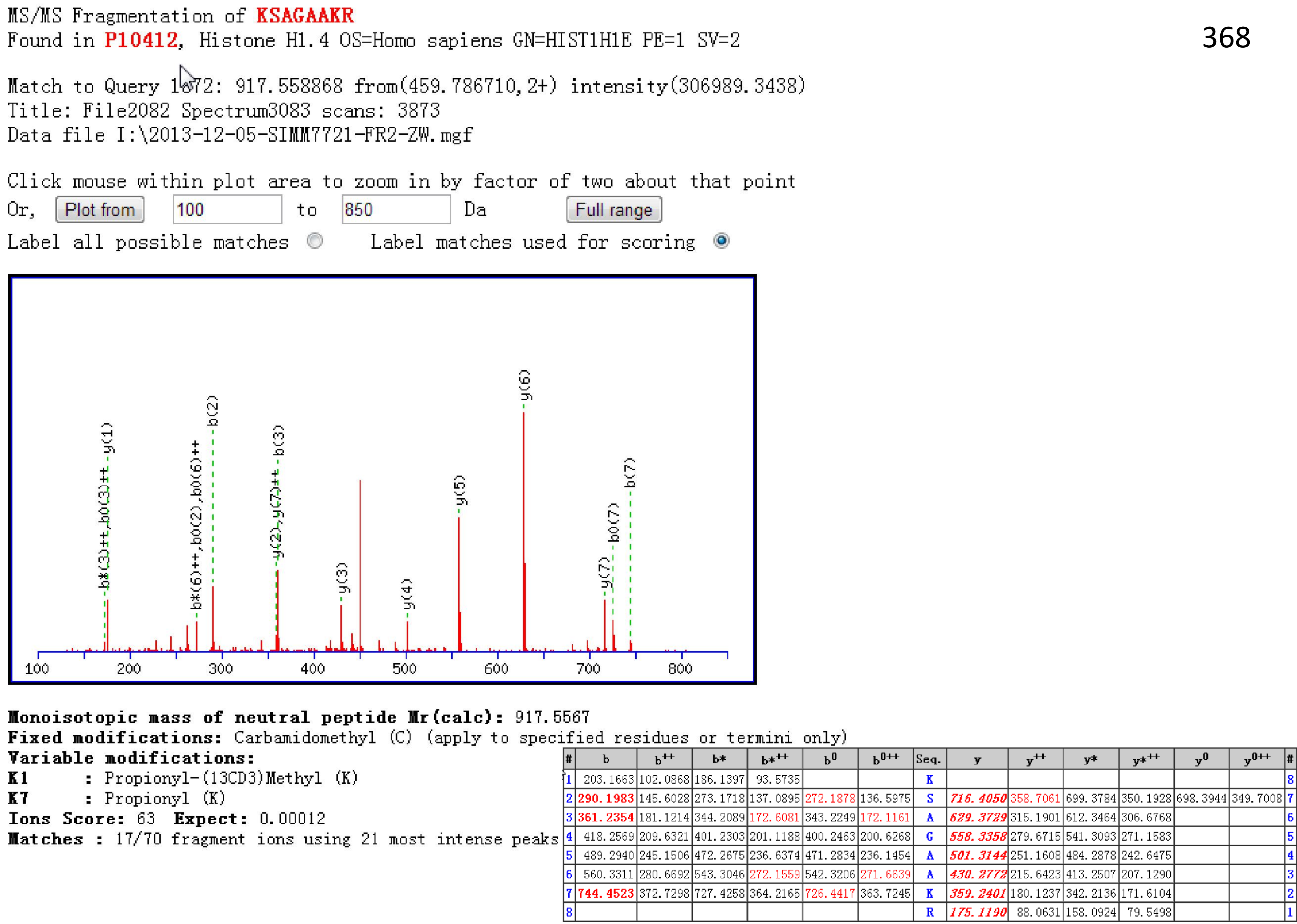
Match to Query 18785: 2606.383092 from(869.801640,3+) intensity(51321.1563)
Title: File2098 Spectrum9005 scans: 10134
Data file I:\2013-12-05-SIMM7721-FR3-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2606.3824
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
K15 : Propionyl (K)
Ions Score: 31 **Expect:** 0.61
Matches : 35/242 fragment ions using 79 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	185.1285	93.0679	168.1019	84.5546			K							22
2	284.1969	142.6021	267.1703	134.0888			V	2423.2685	1212.1379	2406.2420	1203.6246	2405.2580	1203.1326	21
3	486.3559	243.6816	469.3293	235.1683			K	2324.2001	1162.6037	2307.1736	1154.0904	2306.1896	1153.5984	20
4	***601.3828***	301.1951	584.3563	292.6818	583.3723	292.1898	D	2122.0411	1061.5242	2105.0146	1053.0109	2104.0305	1052.5189	19
5	672.4199	336.7136	655.3934	328.2003	654.4094	327.7083	A	2007.0142	1004.0107	1989.9876	995.4974	1989.0036	995.0054	18
6	800.4785	***400.7429***	783.4520	392.2296	782.4680	391.7376	Q	1935.9770	968.4922	1918.9505	959.9789	1917.9665	959.4869	17
7	928.5371	***464.7722***	911.5105	456.2589	910.5265	455.7669	Q	1807.9185	904.4629	1790.8919	895.9496	1789.9079	895.4576	16
8	***1027.6055***	***514.3064***	1010.5790	505.7931	1009.5949	505.3011	V	1679.8599	840.4336	1662.8333	831.9203	1661.8493	831.4283	15
9	***1156.6481***	***578.8277***	1139.6216	570.3144	1138.6375	569.8224	E	**1580.7915**	790.8994	1563.7649	782.3861	1562.7809	781.8941	14
10	1253.7009	627.3541	1236.6743	618.8408	1235.6903	618.3488	P	**1451.7489**	726.3781	1434.7223	717.8648	1433.7383	717.3728	13
11	***1382.7435***	691.8754	1365.7169	683.3621	1364.7329	682.8701	E	1354.6961	677.8517	1337.6696	669.3384	1336.6856	668.8464	12
12	1439.7649	720.3861	1422.7384	711.8728	1421.7544	711.3808	G	1225.6535	613.3304	1208.6270	604.8171	1207.6430	604.3251	11
13	1567.8235	784.4154	1550.7970	775.9021	1549.8129	775.4101	Q	**1168.6321**	584.8197	1151.6055	576.3064	1150.6215	575.8144	10
14	***1696.8661***	848.9367	1679.8395	840.4234	1678.8555	839.9314	E	**1040.5735**	520.7904	1023.5469	512.2771	1022.5629	511.7851	9
15	***1880.9873***	***940.9973***	1863.9607	932.4840	1862.9767	931.9920	K	911.5309	456.2691	894.5043	447.7558	893.5203	447.2638	8
16	***1978.0400***	989.5237	1961.0135	981.0104	1960.0295	980.5184	P	**727.4097**	364.2085	710.3832	355.6952	709.3991	355.2032	7
17	2065.0721	***1033.0397***	2048.0455	1024.5264	2047.0615	1024.0344	S	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	6
18	2162.1248	1081.5661	2145.0983	1073.0528	2144.1143	1072.5608	P	**543.3249**	272.1661	526.2984	263.6528	525.3144	263.1608	5
19	2233.1619	***1117.0846***	2216.1354	1108.5713	2215.1514	1108.0793	A	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
20	2334.2096	***1167.6084***	2317.1831	1159.0952	2316.1991	1158.6032	T	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2433.2780	***1217.1427***	2416.2515	1208.6294	2415.2675	1208.1374	V	274.1874	137.5973	257.1608	129.0840			2
22							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KSAGAAKR**
Found in **P10412**, Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2

Match to Query 1872: 917.558868 from(459.786710,2+) intensity(306989.3438)
Title: File2082 Spectrum3083 scans: 3873
Data file I:\2013-12-05-SIMM7721-FR2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range
Label all possible matches ○ Label matches used for scoring ●

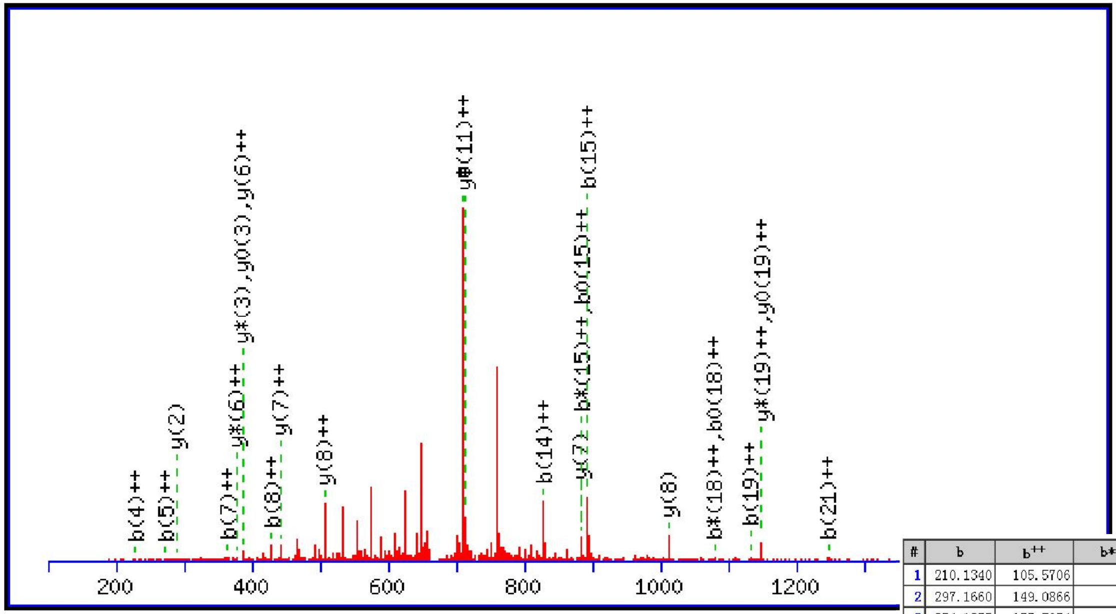
Monoisotopic mass of neutral peptide Mr(calc): 917.5567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K7 : Propionyl (K)
Ions Score: 63 **Expect:** 0.00012
Matches : 17/70 fragment ions using 21 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	**290.1983**	145.6028	273.1718	137.0895	272.1878	136.5975	S	***716.4050***	358.7061	699.3784	350.1928	698.3944	349.7008	7
3	**361.2354**	181.1214	344.2089	172.6081	343.2249	172.1161	A	***629.3729***	315.1901	612.3464	306.6768			6
4	418.2569	209.6321	401.2303	201.1188	400.2463	200.6268	G	***558.3358***	279.6715	541.3093	271.1583			5
5	489.2940	245.1506	472.2675	236.6374	471.2834	236.1454	A	***501.3144***	251.1608	484.2878	242.6475			4
6	560.3311	280.6692	543.3046	272.1559	542.3206	271.6639	A	***430.2772***	215.6423	413.2507	207.1290			3
7	**744.4523**	372.7298	727.4258	364.2165	726.4417	363.7245	K	***359.2401***	180.1237	342.2136	171.6104			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **MSGTSSPEAVKKLLENMQSDLR**
Found in **Q7Z3U7**, Protein MON2 homolog OS=Homo sapiens GN=MON2 PE=1 SV=2

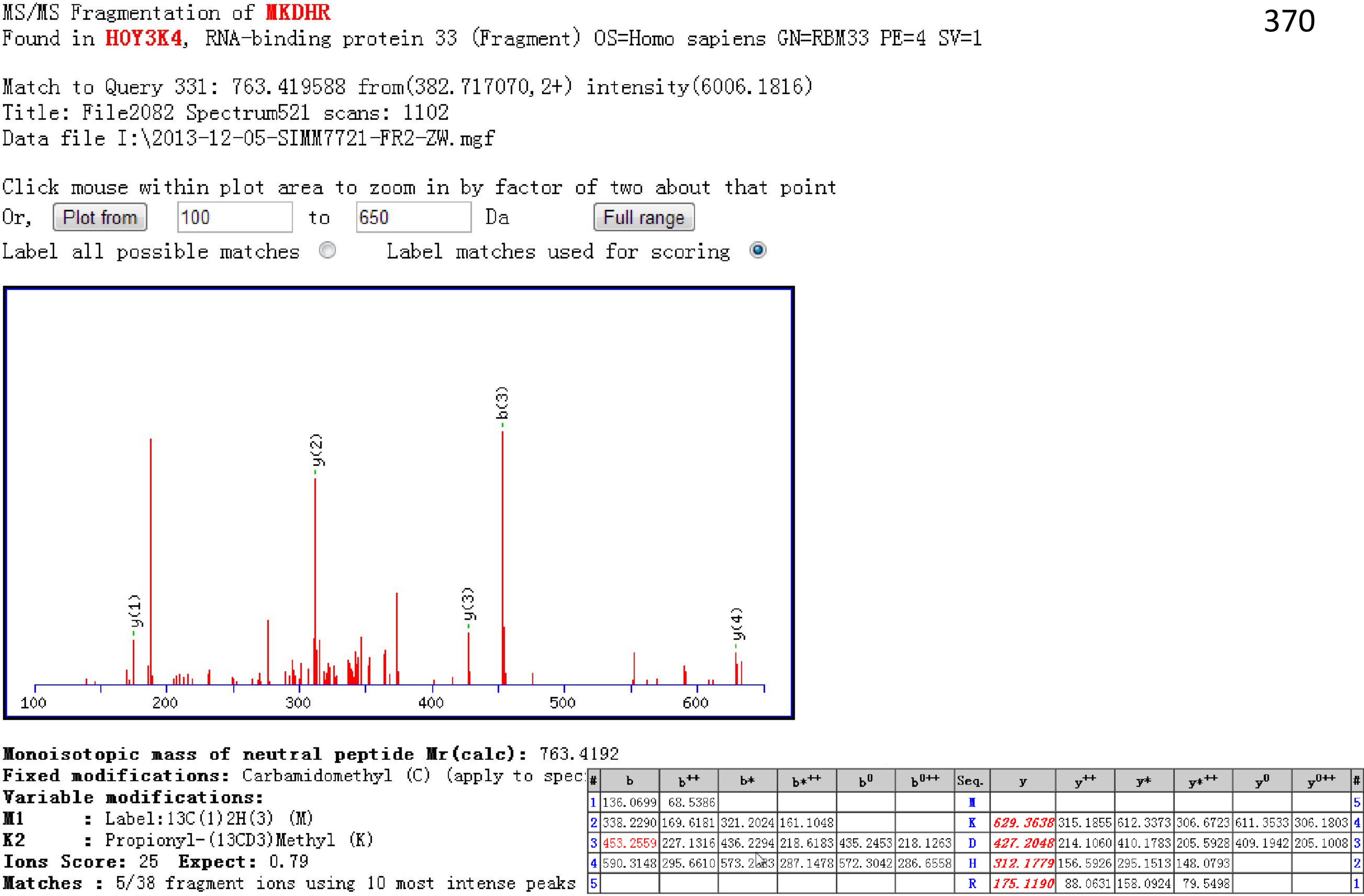
Match to Query 17939: 2666.420096 from(667.612300,4+) intensity(304631.7500)
Title: File2082 Spectrum19148 scans: 20680
Data file I:\2013-12-05-SIMM7721-FR2-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 2666.4353
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
N-term : Propionyl-(13CD3)Methyl (Protein N-term)
M1 : Label:13C(1)2H(3) (M)
K11 : Propionyl-(13CD3)Methyl (K)
K12 : Propionyl-(13CD3)Methyl (K)
M17 : Label:13C(1)2H(3)+Oxidation (M)
Ions Score: 22 **Expect:** 4.5
Matches : 25/226 fragment ions using 53 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	210.1340	105.5706					M							22
2	297.1660	149.0866			279.1555	140.0814	S	2458.3159	1229.6616	2441.2894	1221.1483	2440.3054	1220.6563	21
3	354.1875	177.5974			336.1769	168.5921	G	2371.2839	1186.1456	2354.2574	1177.6323	2353.2733	1177.1403	20
4	455.2352	***228.1212***			437.2246	219.1159	T	2314.2624	1157.6349	2297.2359	1149.1216	2296.2519	1148.6296	19
5	542.26[illegible]2	***271.6372***			524.2566	262.6320	S	2213.2148	1107.1110	2196.1882	1098.5977	2195.2042	1098.1057	18
6	629.2992	315.1532			611.2887	306.1480	S	2126.1827	1063.5950	2109.1562	1055.0817	2108.1722	1054.5897	17
7	726.3520	***363.6796***			708.3414	354.6743	P	2039.1507	1020.0790	2022.1242	1011.5657	2021.1401	1011.0737	16
8	855.3946	***428.2009***			837.3840	419.1956	E	1942.0979	971.5526	1925.0714	963.0393	1924.0874	962.5473	15
9	926.4317	463.7195			908.4211	454.7142	A	1813.0554	907.0313	1796.0288	898.5180	1795.0448	898.0260	14
10	1025.5001	513.2537			1007.4895	504.2484	V	1742.0182	871.5128	1724.9917	862.9995	1724.0077	862.5075	13
11	1227.6591	614.3332	1210.6326	605.8199	1209.6486	605.3279	K	1642.9498	821.9786	1625.9233	813.4653	1624.9393	812.9733	12
12	1429.8181	715.4127	1412.7916	706.8994	1411.8076	706.4074	K	1440.7908	720.8990	1423.7643	712.3858	1422.7802	711.8938	11
13	1542.9022	771.9547	1525.8756	763.4415	1524.8916	762.9495	L	1238.6318	619.8195	1221.6052	611.3063	1220.6212	610.8143	10
14	1655.9863	***828.4968***	1638.9597	819.9835	1637.9757	819.4915	L	1125.5477	563.2775	1108.5212	554.7642	1107.5372	554.2722	9
15	1785.0289	***893.0181***	1768.0023	884.5048	1767.0183	884.0128	E	**1012.4637**	506.7355	995.4371	498.2222	994.4531	497.7302	8
16	1899.0718	950.0395	1882.0452	941.5263	1881.0612	941.0342	N	**883.4211**	442.2142	866.3945	433.7009	865.4105	433.2089	7
17	2050.1294	1025.5683	2033.1028	1017.0550	2032.1188	1016.5630	M	769.3782	385.1927	752.3516	376.6794	751.3676	376.1874	6
18	2178.1879	1089.5976	2161.1614	1081.0843	2160.1774	1080.5923	Q	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
19	2265.2200	***1133.1136***	2248.1934	1124.6003	2247.2094	1124.1083	S	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
20	2380.2469	1190.6271	2363.2204	1182.1138	2362.2364	1181.6218	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
21	2493.3310	***1247.1691***	2476.3044	1238.6559	2475.3204	1238.1638	L	**288.2030**	144.6051	271.1765	136.0919			2
22							R	175.1190	88.0631	158.0924	79.5498			1



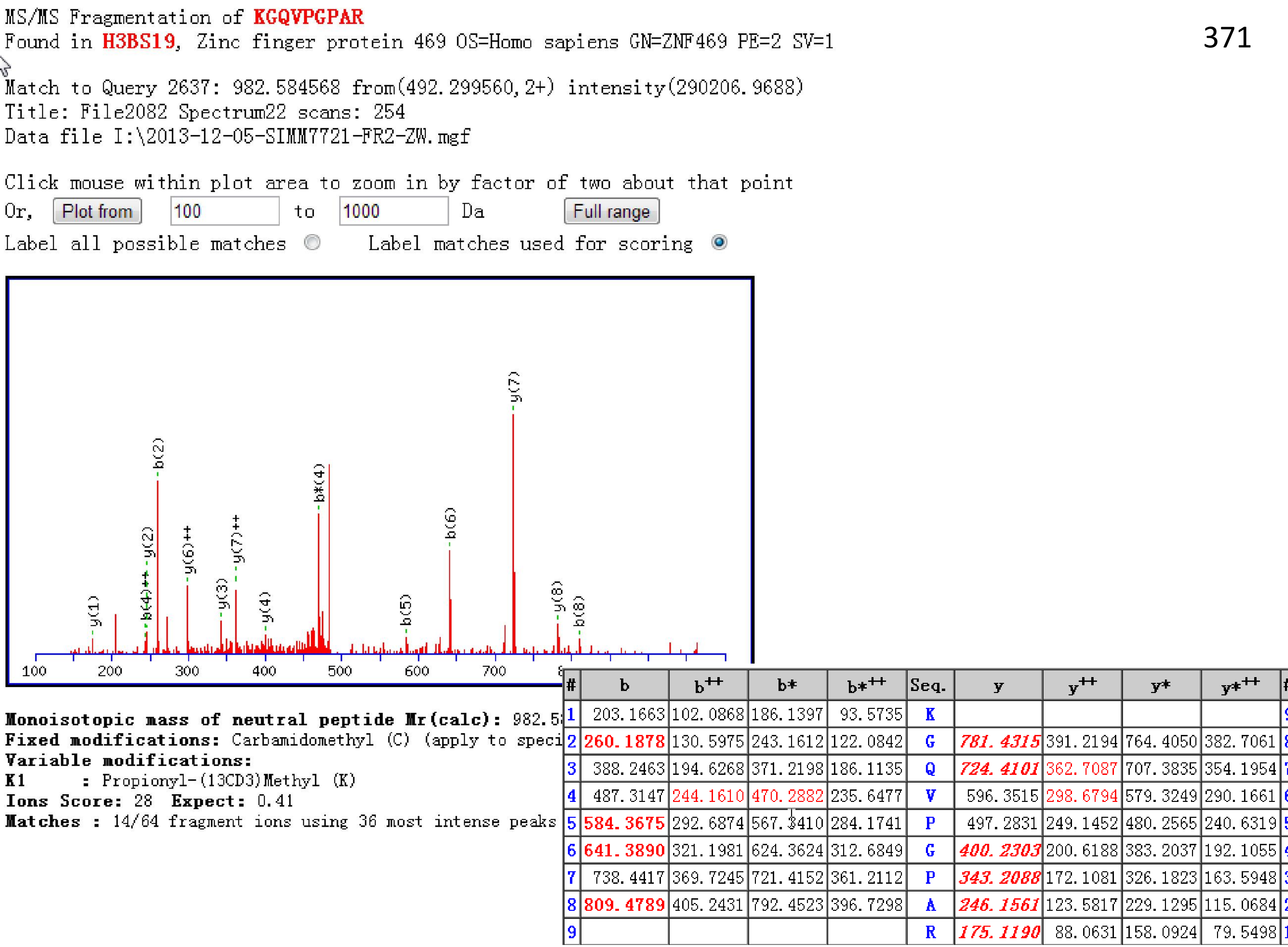
MS/MS Fragmentation of **MKDHR**
Found in **H0Y3K4**, RNA-binding protein 33 (Fragment) OS=Homo sapiens GN=RBM33 PE=4 SV=1

Match to Query 331: 763.419588 from(382.717070,2+) intensity(6006.1816)
Title: File2082 Spectrum521 scans: 1102
Data file I:\2013-12-05-SIMM7721-FR2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 650 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 763.4192
Fixed modifications: Carbamidomethyl (C) (apply to spec
Variable modifications:
M1 : Label:13C(1)2H(3) (M)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 25 **Expect:** 0.79
Matches : 5/38 fragment ions using 10 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	136.0699	68.5386					M							5
2	338.2290	169.6181	321.2024	161.1048			K	***629.3638***	315.1855	612.3373	306.6723	611.3533	306.1803	4
3	453.2559	227.1316	436.2294	218.6183	435.2453	218.1263	D	***427.2048***	214.1060	410.1783	205.5928	409.1942	205.1008	3
4	590.3148	295.6610	573.2[illegible]3	287.1478	572.3042	286.6558	H	***312.1779***	156.5926	295.1513	148.0793			2
5							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KGQVPGPAR**

Found in **H3BS19**, Zinc finger protein 469 OS=Homo sapiens GN=ZNF469 PE=2 SV=1

Match to Query 2637: 982.584568 from(492.299560,2+) intensity(290206.9688)

Title: File2082 Spectrum22 scans: 254

Data file I:\2013-12-05-SIMM7721-FR2-ZW.mgf

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

Or, Plot from 100 to 1000 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 982.5

Fixed modifications: Carbamidomethyl (C) (apply to speci

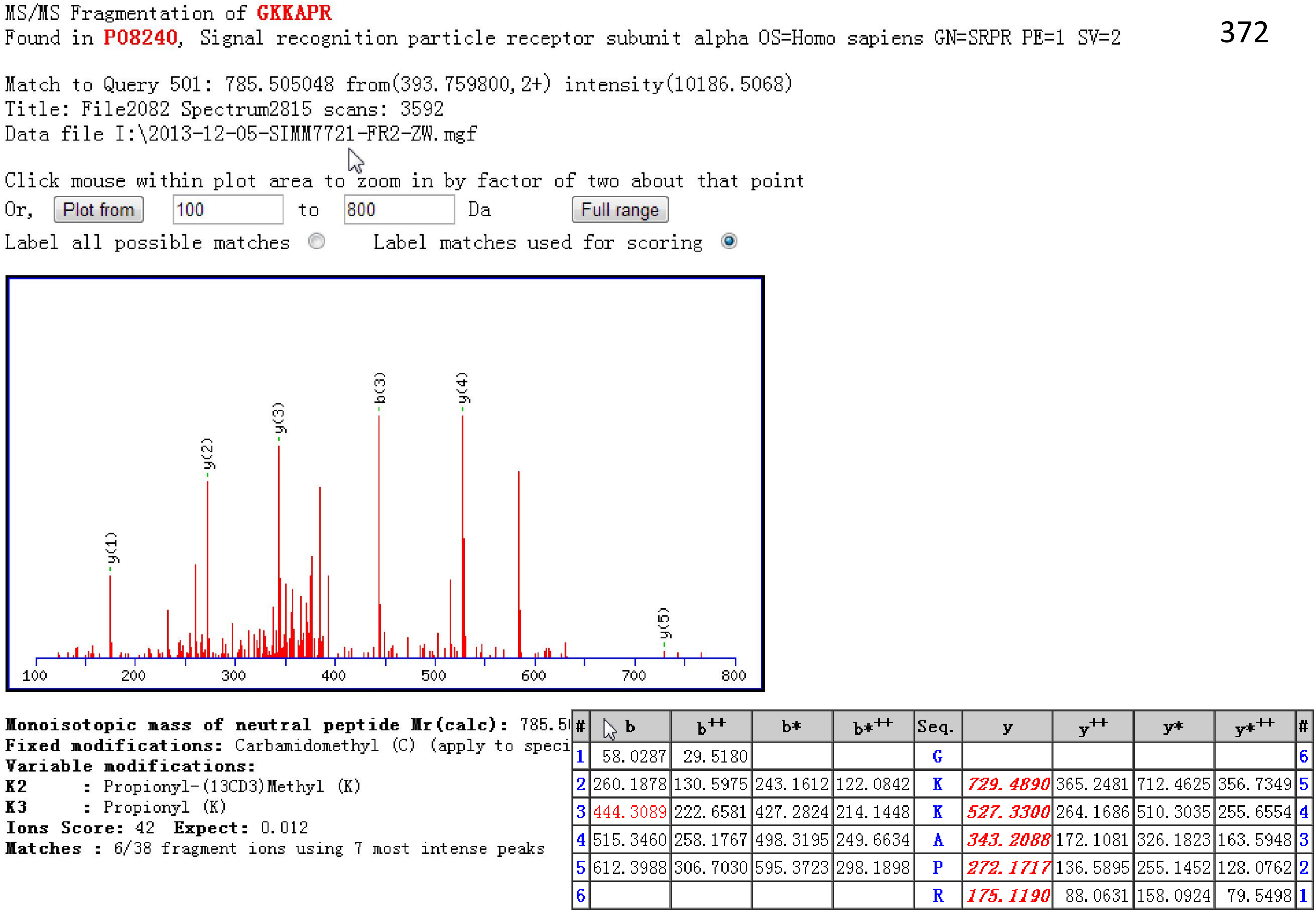
Variable modifications:

K1 : Propionyl-(13CD3)Methyl (K)

Ions Score: 28 **Expect:** 0.41

Matches : 14/64 fragment ions using 36 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	Seq.	y	y^{++}	y*	$y*^{++}$	#
1	203.1663	102.0868	186.1397	93.5735	K					9
2	**260.1878**	130.5975	243.1612	122.0842	G	***781.4315***	391.2194	764.4050	382.7061	8
3	388.2463	194.6268	371.2198	186.1135	Q	***724.4101***	362.7087	707.3835	354.1954	7
4	487.3147	244.1610	470.2882	235.6477	V	596.3515	298.6794	579.3249	290.1661	6
5	**584.3675**	292.6874	567.3410	284.1741	P	497.2831	249.1452	480.2565	240.6319	5
6	**641.3890**	321.1981	624.3624	312.6849	G	***400.2303***	200.6188	383.2037	192.1055	4
7	738.4417	369.7245	721.4152	361.2112	P	***343.2088***	172.1081	326.1823	163.5948	3
8	**809.4789**	405.2431	792.4523	396.7298	A	***246.1561***	123.5817	229.1295	115.0684	2
9					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **GKKAPR**

Found in **P08240**, Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2

Match to Query 501: 785.505048 from(393.759800,2+) intensity(10186.5068)

Title: File2082 Spectrum2815 scans: 3592

Data file I:\2013-12-05-SIMM7721-FR2-ZW.mgf

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

Or, Plot from 100 to 800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 785.5

Fixed modifications: Carbamidomethyl (C) (apply to speci

Variable modifications:

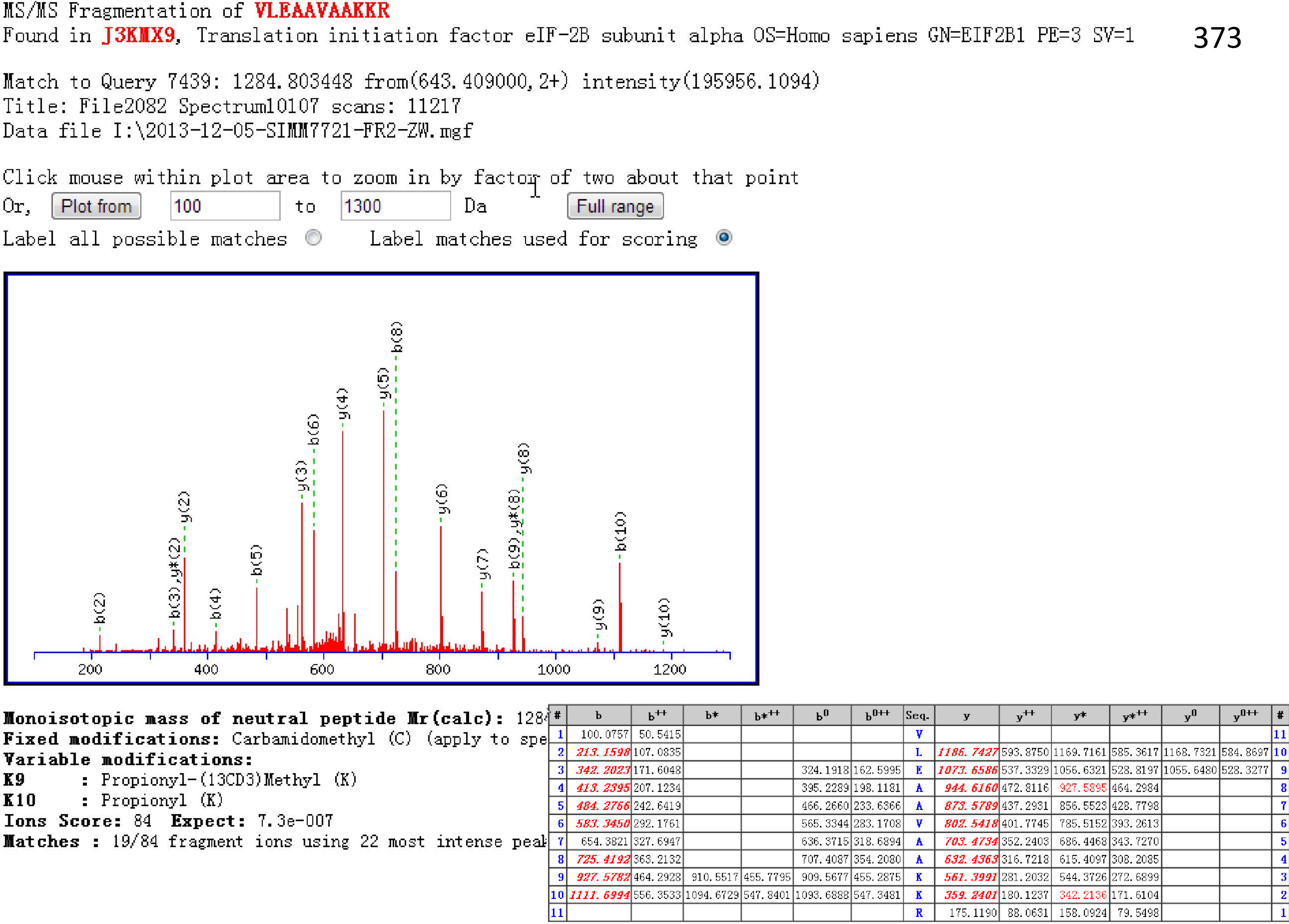
K2 : Propionyl-(13CD3)Methyl (K)

K3 : Propionyl (K)

Ions Score: 42 **Expect:** 0.012

Matches : 6/38 fragment ions using 7 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	58.0287	29.5180			G					6
2	260.1878	130.5975	243.1612	122.0842	K	***729.4890***	365.2481	712.4625	356.7349	5
3	444.3089	222.6581	427.2824	214.1448	K	***527.3300***	264.1686	510.3035	255.6554	4
4	515.3460	258.1767	498.3195	249.6634	A	***343.2088***	172.1081	326.1823	163.5948	3
5	612.3988	306.7030	595.3723	298.1898	P	***272.1717***	136.5895	255.1452	128.0762	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **VLEAAVAAKKR**
Found in **J3KMX9**, Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=3 SV=1

Match to Query 7439: 1284.803448 from(643.409000,2+) intensity(195956.1094)
Title: File2082 Spectrum10107 scans: 11217
Data file I:\2013-12-05-SIMM7721-FR2-ZW.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 ●

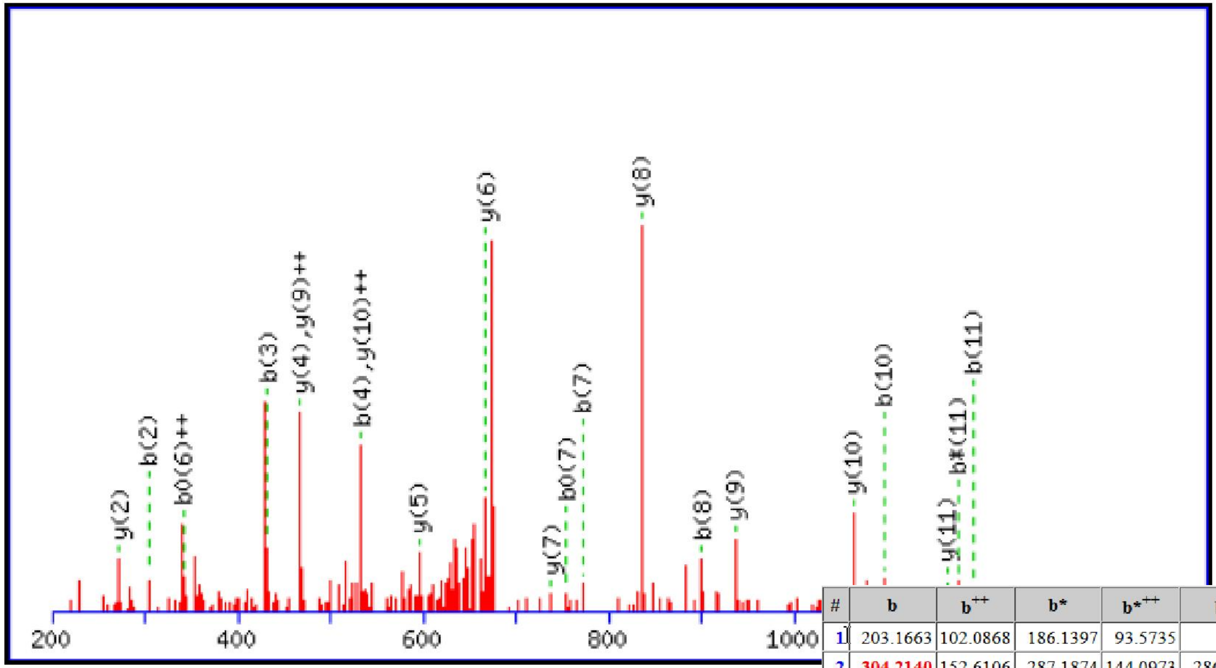
Monoisotopic mass of neutral peptide Mr(calc): 128
Fixed modifications: Carbamidomethyl (C) (apply to spe
Variable modifications:
K9 : Propionyl-(13CD3)Methyl (K)
K10 : Propionyl (K)
Ions Score: 84 **Expect:** 7.3e-007
Matches : 19/84 fragment ions using 22 most intense peak

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							11
2	***213.1598***	107.0835					L	***1186.7427***	593.8750	1169.7161	585.3617	1168.7321	584.8697	10
3	***342.2023***	171.6048			324.1918	162.5995	E	***1073.6586***	537.3329	1056.6321	528.8197	1055.6480	528.3277	9
4	***413.2395***	207.1234			395.2289	198.1181	A	***944.6160***	472.8116	927.5895	464.2984			8
5	***484.2766***	242.6419			466.2660	233.6366	A	***873.5789***	437.2931	856.5523	428.7798			7
6	***583.3450***	292.1761			565.3344	283.1708	V	***802.5418***	401.7745	785.5152	393.2613			6
7	654.3821	327.6947			636.3715	318.6894	A	***703.4734***	352.2403	686.4468	343.7270			5
8	***725.4192***	363.2132			707.4087	354.2080	A	***632.4363***	316.7218	615.4097	308.2085			4
9	***927.5782***	464.2928	910.5517	455.7795	909.5677	455.2875	K	***561.3991***	281.2032	544.3726	272.6899			3
10	***1111.6994***	556.3533	1094.6729	547.8401	1093.6888	547.3481	K	***359.2401***	180.1237	342.2136	171.6104			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KTQTPAAQPVPR**
Found in **Q6P1J9**, Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1

Match to Query 8100: 1366.784148 from(684.399350,2+) intensity(13853.9492)
Title: File2079 Spectrum3458 scans: 4218
Data file I:\2013-12-05-SIMM7721-FR4-ZW.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 ●



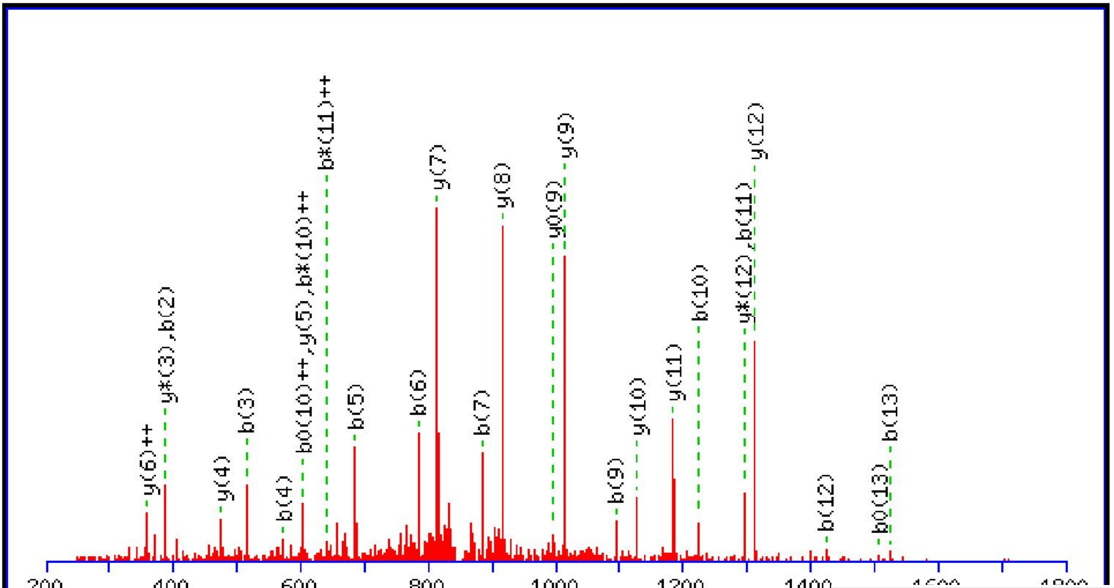
Monoisotopic mass of neutral peptide Mr(calc): 1366
Fixed modifications: Carbamidomethyl (C) (apply to
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 68 **Expect:** 5.7e-005
Matches : 21/114 fragment ions using 31 most intens

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							12
2	**304.2140**	152.6106	287.1874	144.0973	286.2034	143.6053	T	***1165.6324***	583.3198	1148.6059	574.8066	1147.6218	574.3146	11
3	**432.2725**	216.6399	415.2460	208.1266	414.2620	207.6346	Q	***1064.5847***	532.7960	1047.5582	524.2827	1046.5742	523.7907	10
4	**533.3202**	267.1638	516.2937	258.6505	515.3097	258.1585	T	***936.5261***	468.7667	919.4996	460.2534	918.5156	459.7614	9
5	630.3730	315.6901	613.3464	307.1769	612.3624	306.6849	P	***835.4785***	418.2429	818.4519	409.7296			8
6	701.4101	351.2087	684.3836	342.6954	683.3995	342.2034	A	***738.4257***	369.7165	721.3992	361.2032			7
7	**772.4472**	386.7272	755.4207	378.2140	754.4367	377.7220	A	***667.3886***	334.1979	650.3620	325.6847			6
8	**900.5058**	450.7565	883.4792	442.2433	882.4952	441.7513	Q	***596.3515***	298.6794	579.3249	290.1661			5
9	997.5586	499.2829	980.5320	490.7696	979.5480	490.2776	P	***468.2929***	234.6501	451.2663	226.1368			4
10	**1096.6270**	548.8171	1079.6004	540.3039	1078.6164	539.8118	V	371.2401	186.1237	354.2136	177.6104			3
11	**1193.6797**	597.3435	1176.6532	588.8302	1175.6692	588.3382	P	***272.1717***	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1

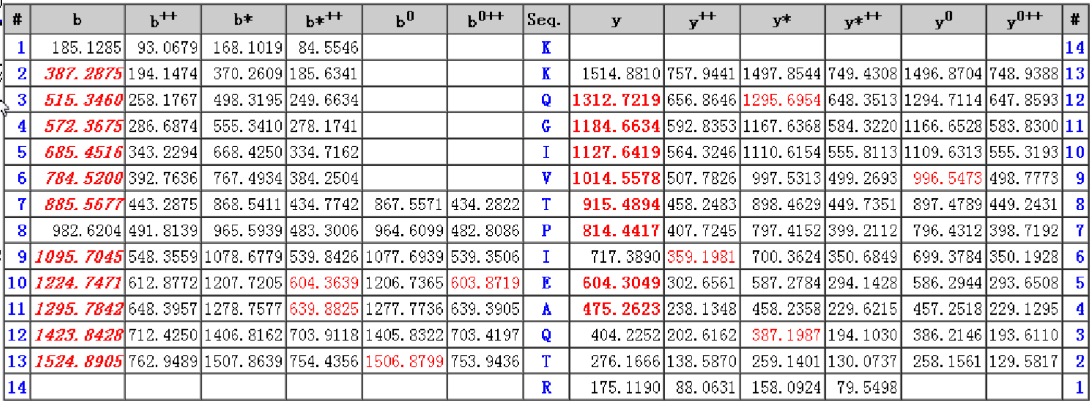
MS/MS Fragmentation of **KKQGIVTPIEAQTR**
Found in **P98175**, RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3

Match to Query 9778: 1697.994488 from(850.004520,2+) intensity(87675.4375)
Title: File2076 Spectrum9627 scans: 10873
Data file I:\2013-12-05-SIMM7721-FR14-ZW.mgf

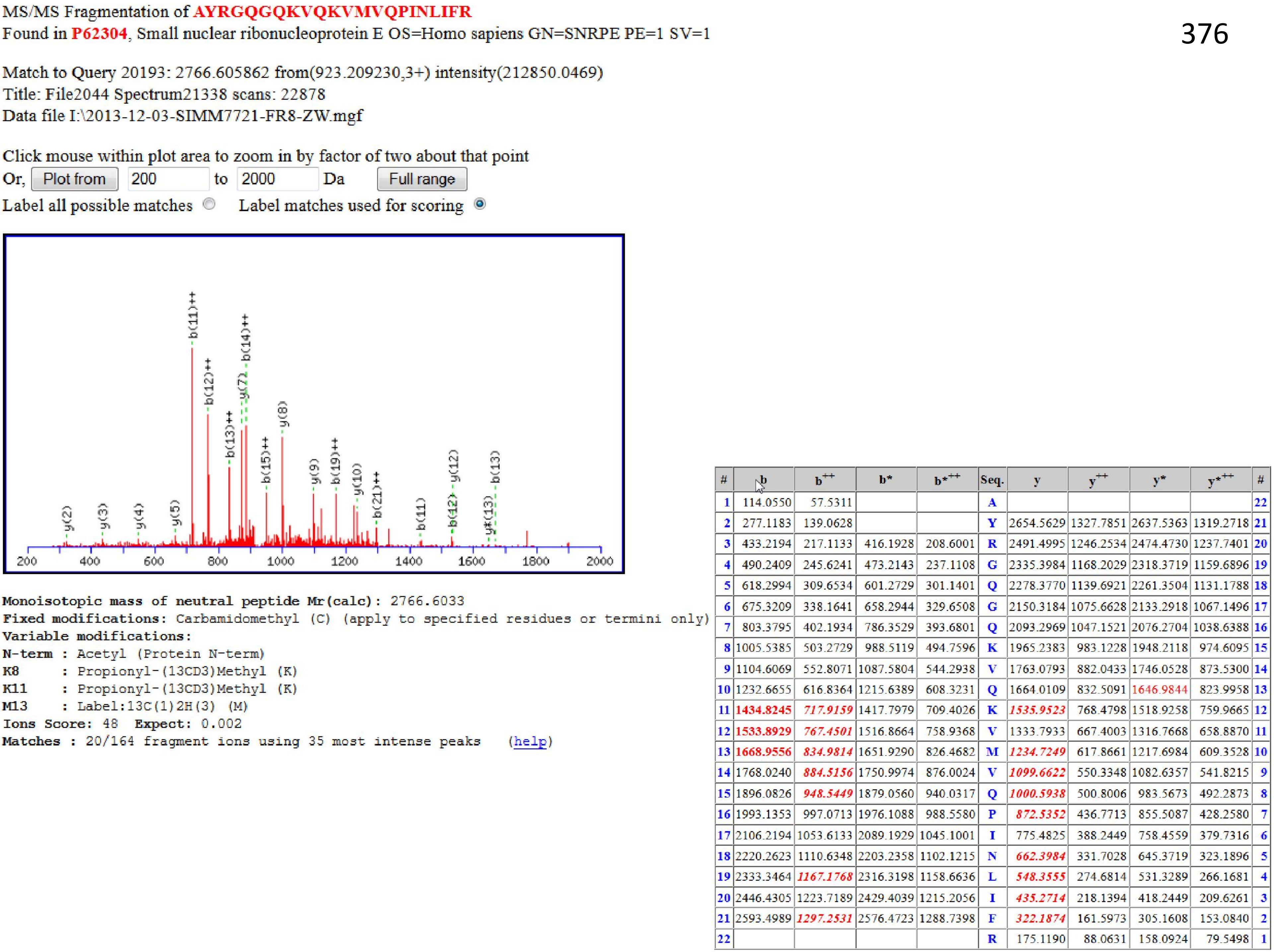
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1697.9
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K1 : Propionyl (K)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 72 **Expect:** 1.9e-005
Matches : 27/142 fragment ions using 40 most intense peaks



#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							14
2	***387.2875***	194.1474	370.2609	185.6341			K	1514.8810	757.9441	1497.8544	749.4308	1496.8704	748.9388	13
3	***515.3460***	258.1767	498.3195	249.6634			Q	**1312.7219**	656.8646	1295.6954	648.3513	1294.7114	647.8593	12
4	***572.3675***	286.6874	555.3410	278.1741			G	**1184.6634**	592.8353	1167.6368	584.3220	1166.6528	583.8300	11
5	***685.4516***	343.2294	668.4250	334.7162			I	**1127.6419**	564.3246	1110.6154	555.8113	1109.6313	555.3193	10
6	***784.5200***	392.7636	767.4934	384.2504			V	**1014.5578**	507.7826	997.5313	499.2693	996.5473	498.7773	9
7	***885.5677***	443.2875	868.5411	434.7742	867.5571	434.2822	T	**915.4894**	458.2483	898.4629	449.7351	897.4789	449.2431	8
8	982.6204	491.8139	965.5939	483.3006	964.6099	482.8086	P	**814.4417**	407.7245	797.4152	399.2112	796.4312	398.7192	7
9	***1095.7045***	548.3559	1078.6779	539.8426	1077.6939	539.3506	I	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	6
10	***1224.7471***	612.8772	1207.7205	604.3639	1206.7365	603.8719	E	**604.3049**	302.6561	587.2784	294.1428	586.2944	293.6508	5
11	***1295.7842***	648.3957	1278.7577	639.8825	1277.7736	639.3905	A	**475.2623**	238.1348	458.2358	229.6215	457.2518	229.1295	4
12	***1423.8428***	712.4250	1406.8162	703.9118	1405.8322	703.4197	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
13	***1524.8905***	762.9489	1507.8639	754.4356	1506.8799	753.9436	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
14							R	175.1190	88.0631	158.0924	79.5498			1



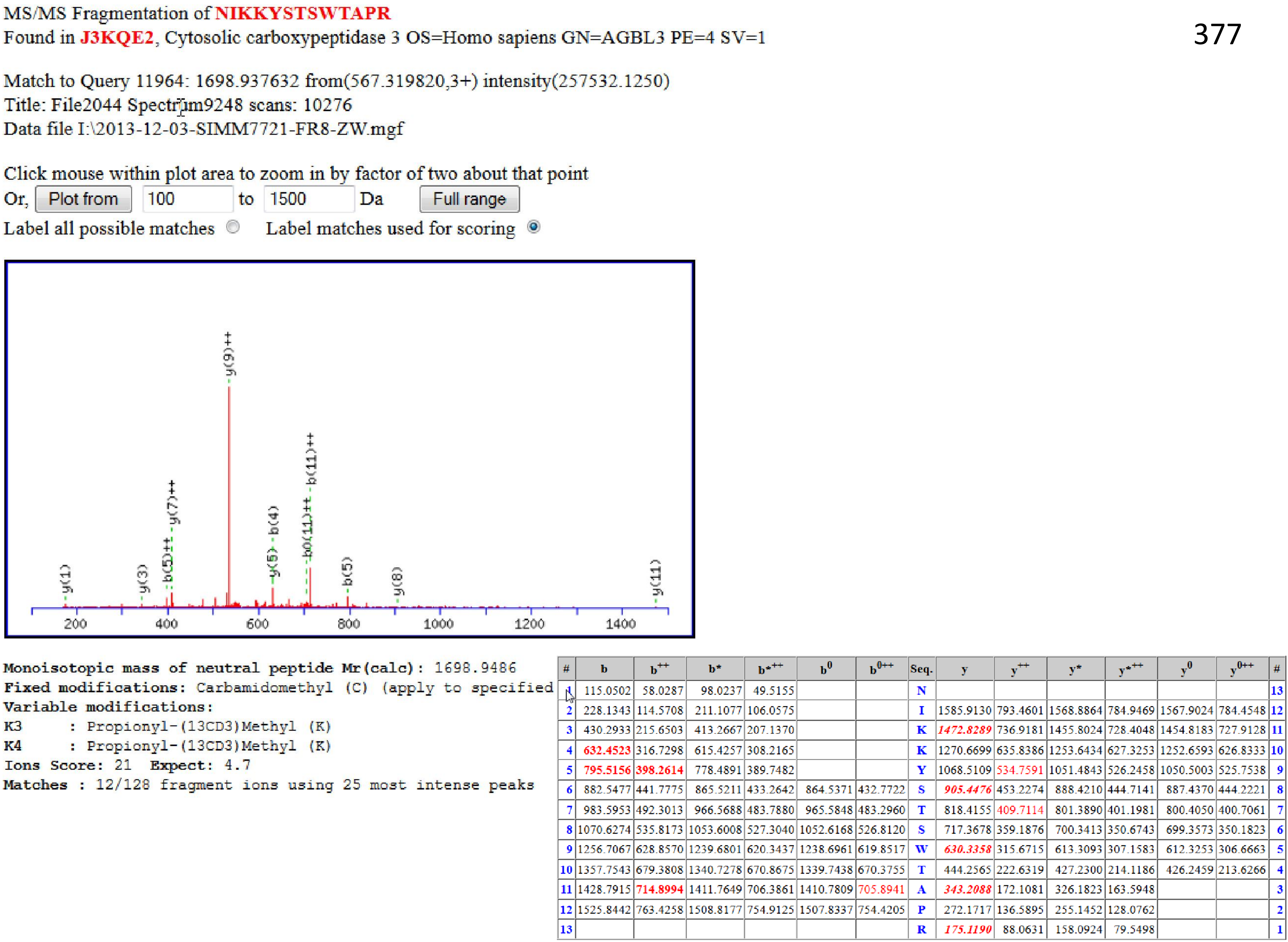
MS/MS Fragmentation of **AYRGQGQKVQKVMVQPINLIFR**
Found in **P62304**, Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1

Match to Query 20193: 2766.605862 from(923.209230,3+) intensity(212850.0469)
Title: File2044 Spectrum21338 scans: 22878
Data file I:\2013-12-03-SIMM7721-FR8-ZW.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 ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2766.6033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Acetyl (Protein N-term)
K8     : Propionyl-(13CD3)Methyl (K)
K11    : Propionyl-(13CD3)Methyl (K)
M13    : Label:13C(1)2H(3) (M)
Ions Score: 48  Expect: 0.002
Matches : 20/164 fragment ions using 35 most intense peaks   (help)
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	114.0550	57.5311			A					22
2	277.1183	139.0628			Y	2654.5629	1327.7851	2637.5363	1319.2718	21
3	433.2194	217.1133	416.1928	208.6001	R	2491.4995	1246.2534	2474.4730	1237.7401	20
4	490.2409	245.6241	473.2143	237.1108	G	2335.3984	1168.2029	2318.3719	1159.6896	19
5	618.2994	309.6534	601.2729	301.1401	Q	2278.3770	1139.6921	2261.3504	1131.1788	18
6	675.3209	338.1641	658.2944	329.6508	G	2150.3184	1075.6628	2133.2918	1067.1496	17
7	803.3795	402.1934	786.3529	393.6801	Q	2093.2969	1047.1521	2076.2704	1038.6388	16
8	1005.5385	503.2729	988.5119	494.7596	K	1965.2383	983.1228	1948.2118	974.6095	15
9	1104.6069	552.8071	1087.5804	544.2938	V	1763.0793	882.0433	1746.0528	873.5300	14
10	1232.6655	616.8364	1215.6389	608.3231	Q	1664.0109	832.5091	1646.9844	823.9958	13
11	**1434.8245**	***717.9159***	1417.7979	709.4026	K	***1535.9523***	768.4798	1518.9258	759.9665	12
12	**1533.8929**	***767.4501***	1516.8664	758.9368	V	1333.7933	667.4003	1316.7668	658.8870	11
13	**1668.9556**	***834.9814***	1651.9290	826.4682	M	***1234.7249***	617.8661	1217.6984	609.3528	10
14	1768.0240	***884.5156***	1750.9974	876.0024	V	***1099.6622***	550.3348	1082.6357	541.8215	9
15	1896.0826	***948.5449***	1879.0560	940.0317	Q	***1000.5938***	500.8006	983.5673	492.2873	8
16	1993.1353	997.0713	1976.1088	988.5580	P	***872.5352***	436.7713	855.5087	428.2580	7
17	2106.2194	1053.6133	2089.1929	1045.1001	I	775.4825	388.2449	758.4559	379.7316	6
18	2220.2623	1110.6348	2203.2358	1102.1215	N	***662.3984***	331.7028	645.3719	323.1896	5
19	2333.3464	***1167.1768***	2316.3198	1158.6636	L	***548.3555***	274.6814	531.3289	266.1681	4
20	2446.4305	1223.7189	2429.4039	1215.2056	I	***435.2714***	218.1394	418.2449	209.6261	3
21	2593.4989	***1297.2531***	2576.4723	1288.7398	F	***322.1874***	161.5973	305.1608	153.0840	2
22					R	175.1190	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **NIKKYSTSWTAPR**

Found in **J3KQE2**, Cytosolic carboxypeptidase 3 OS=Homo sapiens GN=AGBL3 PE=4 SV=1

Match to Query 11964: 1698.937632 from(567.319820,3+) intensity(257532.1250)

Title: File2044 Spectrum9248 scans: 10276

Data file I:\2013-12-03-SIMM7721-FR8-ZW.mgf

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

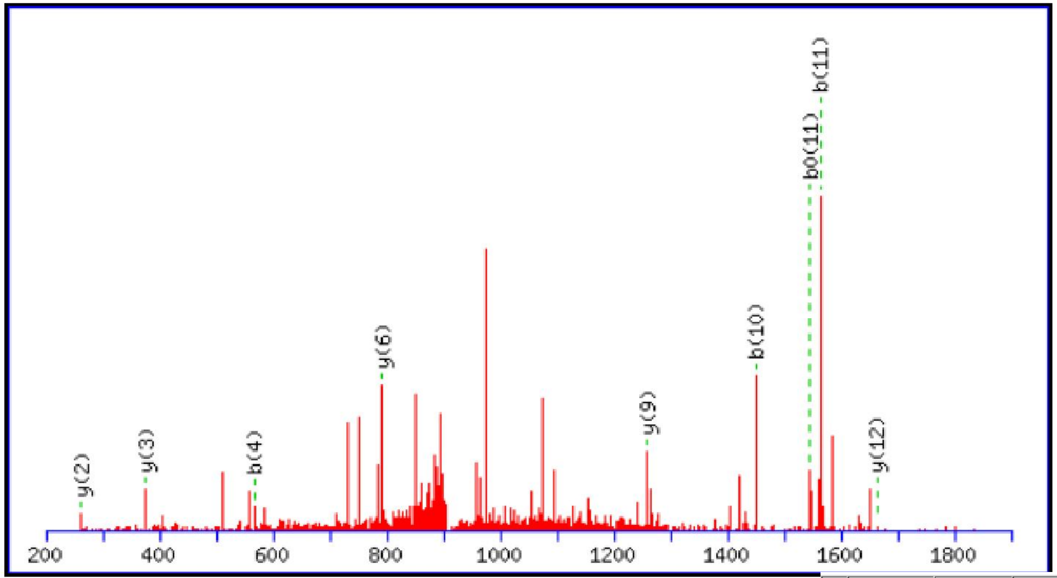
```
Monoisotopic mass of neutral peptide Mr(calc): 1698.9486
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K3      : Propionyl-(13CD3)Methyl (K)
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 21  Expect: 4.7
Matches : 12/128 fragment ions using 25 most intense peaks
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	228.1343	114.5708	211.1077	106.0575			I	1585.9130	793.4601	1568.8864	784.9469	1567.9024	784.4548	12
3	430.2933	215.6503	413.2667	207.1370			K	***1472.8289***	736.9181	1455.8024	728.4048	1454.8183	727.9128	11
4	**632.4523**	316.7298	615.4257	308.2165			K	1270.6699	635.8386	1253.6434	627.3253	1252.6593	626.8333	10
5	**795.5156**	**398.2614**	778.4891	389.7482			Y	1068.5109	534.7591	1051.4843	526.2458	1050.5003	525.7538	9
6	882.5477	441.7775	865.5211	433.2642	864.5371	432.7722	S	***905.4476***	453.2274	888.4210	444.7141	887.4370	444.2221	8
7	983.5953	492.3013	966.5688	483.7880	965.5848	483.2960	T	818.4155	409.7114	801.3890	401.1981	800.4050	400.7061	7
8	1070.6274	535.8173	1053.6008	527.3040	1052.6168	526.8120	S	717.3678	359.1876	700.3413	350.6743	699.3573	350.1823	6
9	1256.7067	628.8570	1239.6801	620.3437	1238.6961	619.8517	W	***630.3358***	315.6715	613.3093	307.1583	612.3253	306.6663	5
10	1357.7543	679.3808	1340.7278	670.8675	1339.7438	670.3755	T	444.2565	222.6319	427.2300	214.1186	426.2459	213.6266	4
11	1428.7915	**714.8994**	1411.7649	706.3861	1410.7809	705.8941	A	***343.2088***	172.1081	326.1823	163.5948			3
12	1525.8442	763.4258	1508.8177	754.9125	1507.8337	754.4205	P	272.1717	136.5895	255.1452	128.0762			2
13							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **CGKFFRYRCTLSR**
Found in **O43361**, Zinc finger protein 749 OS=Homo sapiens GN=ZNF749 PE=1 SV=2

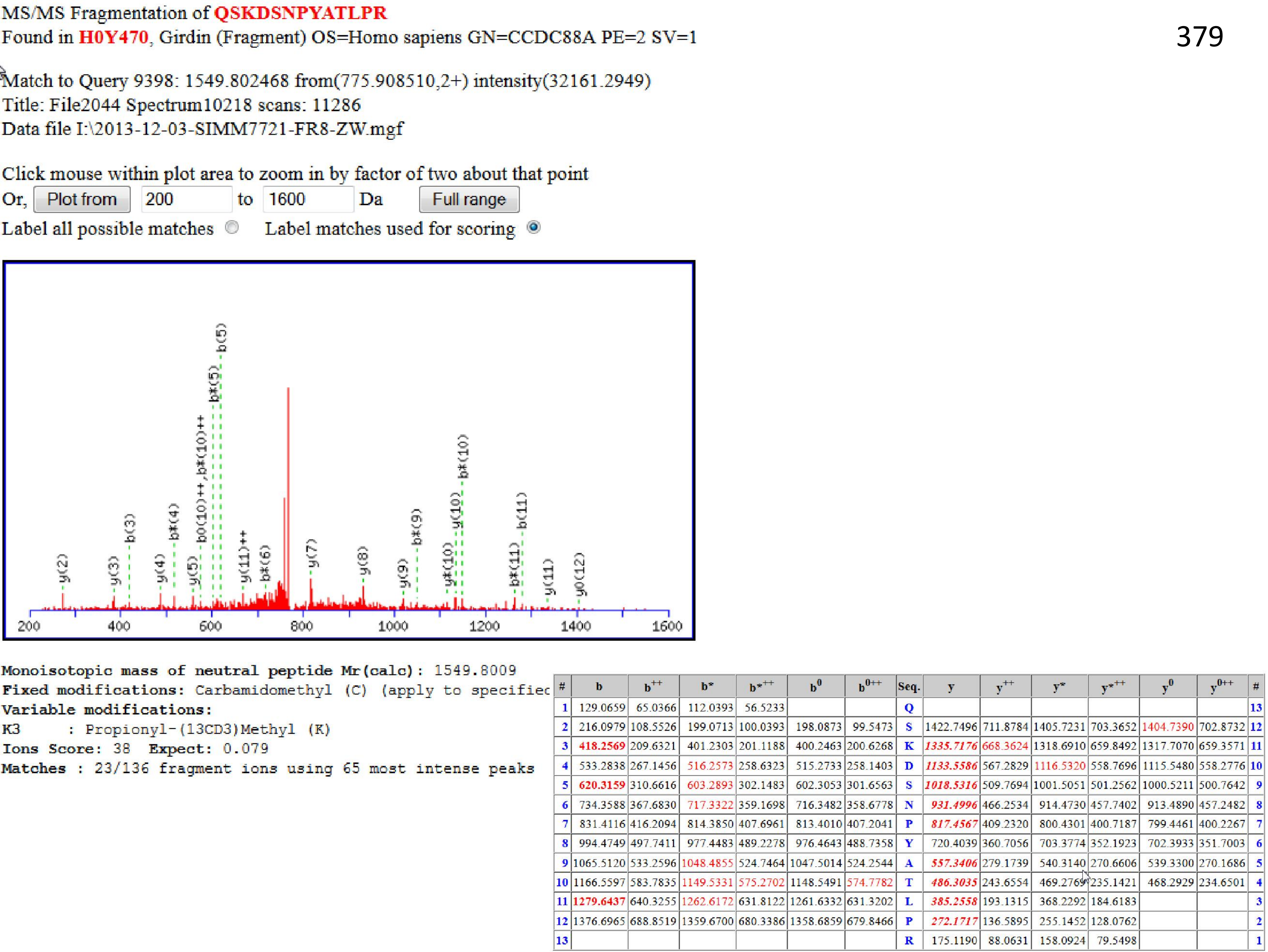
Match to Query 13490: 1823.930388 from(912.972470,2+) intensity(331487.7500)
Title: File2044 Spectrum15015 scans: 16283
Data file I:\2013-12-03-SIMM7721-FR8-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1823.9196
Fixed modifications: Carbamidomethyl (C) (apply to specifie
Variable modifications:
K3     : Propionyl-(13CD3)Methyl (K)
Ions Score: 24  Expect: 2.4
Matches : 9/120 fragment ions using 16 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0379	81.0226					C							13
2	218.0594	109.5333					G	***1664.8962***	832.9518	1647.8697	824.4385	1646.8857	823.9465	12
3	420.2184	210.6128	403.1919	202.0996			K	1607.8748	804.4410	1590.8482	795.9277	1589.8642	795.4357	11
4	**567.2868**	284.1470	550.2603	275.6338			F	1405.7158	703.3615	1388.6892	694.8482	1387.7052	694.3562	10
5	714.3552	357.6813	697.3287	349.1680			F	***1258.6473***	629.8273	1241.6208	621.3140	1240.6368	620.8220	9
6	870.4563	435.7318	853.4298	427.2185			R	1111.5789	556.2931	1094.5524	547.7798	1093.5684	547.2878	8
7	1033.5197	517.2635	1016.4931	508.7502			Y	955.4778	478.2425	938.4513	469.7293	937.4672	469.2373	7
8	1189.6208	595.3140	1172.5942	586.8008			R	***792.4145***	396.7109	775.3879	388.1976	774.4039	387.7056	6
9	1349.6514	675.3294	1332.6249	666.8161			C	636.3134	318.6603	619.2868	310.1470	618.3028	309.6550	5
10	**1450.6991**	725.8532	1433.6726	717.3399	1432.6885	716.8479	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
11	**1563.7832**	782.3952	1546.7566	773.8820	1545.7726	773.3899	L	***375.2350***	188.1212	358.2085	179.6079	357.2245	179.1159	3
12	1650.8152	825.9112	1633.7887	817.3980	1632.8046	816.9060	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



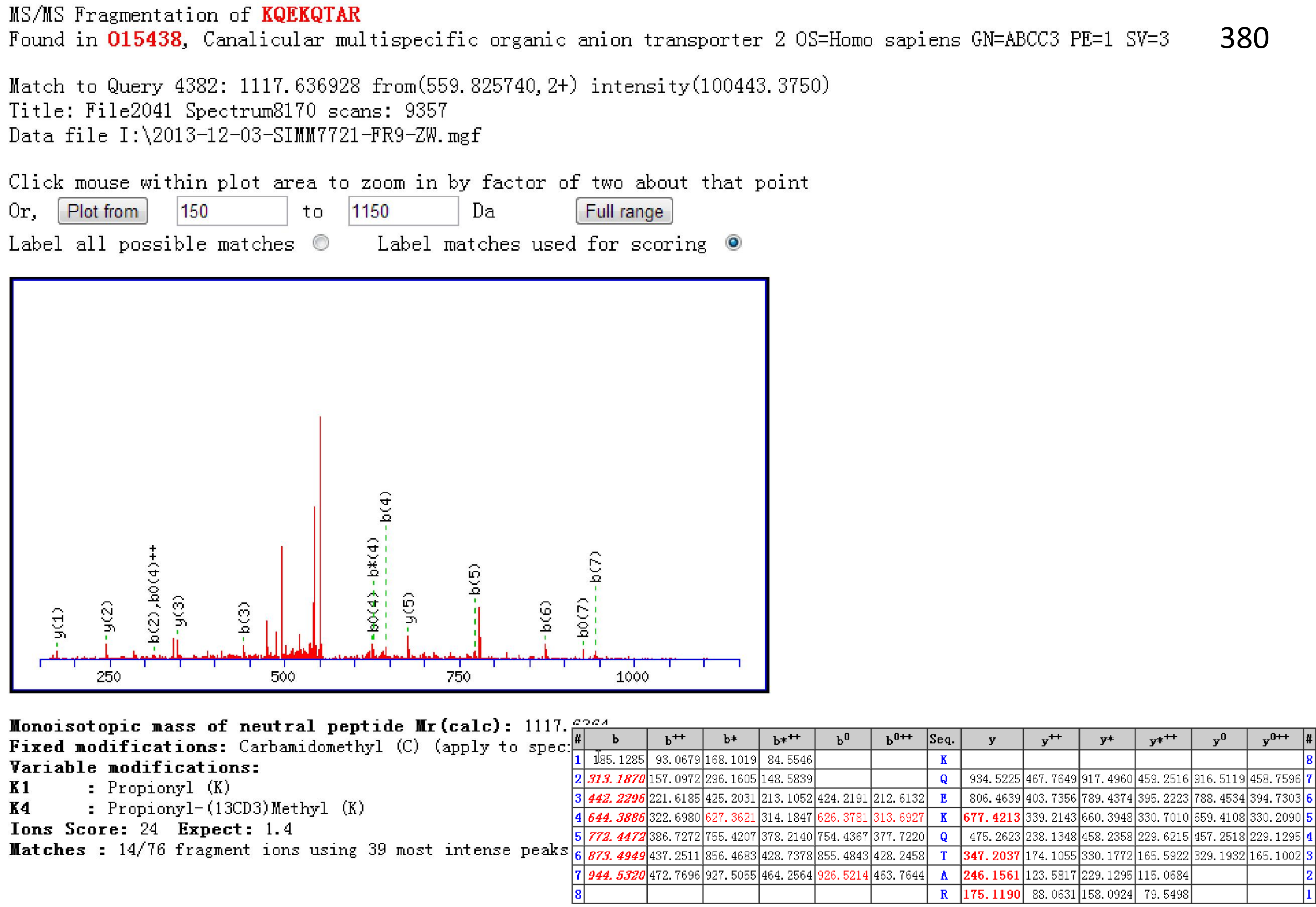
MS/MS Fragmentation of **QSKDSNPYATLPR**
Found in **H0Y470**, Girdin (Fragment) OS=Homo sapiens GN=CCDC88A PE=2 SV=1

Match to Query 9398: 1549.802468 from(775.908510,2+) intensity(32161.2949)
Title: File2044 Spectrum10218 scans: 11286
Data file I:\2013-12-03-SIMM7721-FR8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1549.8009
Fixed modifications: Carbamidomethyl (C) (apply to specifiec
Variable modifications:
K3      : Propionyl-(13CD3)Methyl (K)
Ions Score: 38  Expect: 0.079
Matches : 23/136 fragment ions using 65 most intense peaks
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233			Q							13
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	S	1422.7496	711.8784	1405.7231	703.3652	1404.7390	702.8732	12
3	**418.2569**	209.6321	401.2303	201.1188	400.2463	200.6268	K	***1335.7176***	668.3624	1318.6910	659.8492	1317.7070	659.3571	11
4	533.2838	267.1456	516.2573	258.6323	515.2733	258.1403	D	***1133.5586***	567.2829	1116.5320	558.7696	1115.5480	558.2776	10
5	**620.3159**	310.6616	603.2893	302.1483	602.3053	301.6563	S	***1018.5316***	509.7694	1001.5051	501.2562	1000.5211	500.7642	9
6	734.3588	367.6830	717.3322	359.1698	716.3482	358.6778	N	***931.4996***	466.2534	914.4730	457.7402	913.4890	457.2482	8
7	831.4116	416.2094	814.3850	407.6961	813.4010	407.2041	P	***817.4567***	409.2320	800.4301	400.7187	799.4461	400.2267	7
8	994.4749	497.7411	977.4483	489.2278	976.4643	488.7358	Y	720.4039	360.7056	703.3774	352.1923	702.3933	351.7003	6
9	1065.5120	533.2596	1048.4855	524.7464	1047.5014	524.2544	A	***557.3406***	279.1739	540.3140	270.6606	539.3300	270.1686	5
10	1166.5597	583.7835	1149.5331	575.2702	1148.5491	574.7782	T	***486.3035***	243.6554	469.2769	235.1421	468.2929	234.6501	4
11	**1279.6437**	640.3255	1262.6172	631.8122	1261.6332	631.3202	L	***385.2558***	193.1315	368.2292	184.6183			3
12	1376.6965	688.8519	1359.6700	680.3386	1358.6859	679.8466	P	***272.1717***	136.5895	255.1452	128.0762			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KQEKQTAR**

Found in **O15438**, Canalicular multispecific organic anion transporter 2 OS=Homo sapiens GN=ABCC3 PE=1 SV=3

Match to Query 4382: 1117.636928 from(559.825740,2+) intensity(100443.3750)

Title: File2041 Spectrum8170 scans: 9357

Data file I:\2013-12-03-SIMM7721-FR9-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1117.

Fixed modifications: Carbamidomethyl (C) (apply to spec

Variable modifications:

K1 : Propionyl (K)

K4 : Propionyl-(13CD3)Methyl (K)

Ions Score: 24 **Expect:** 1.4

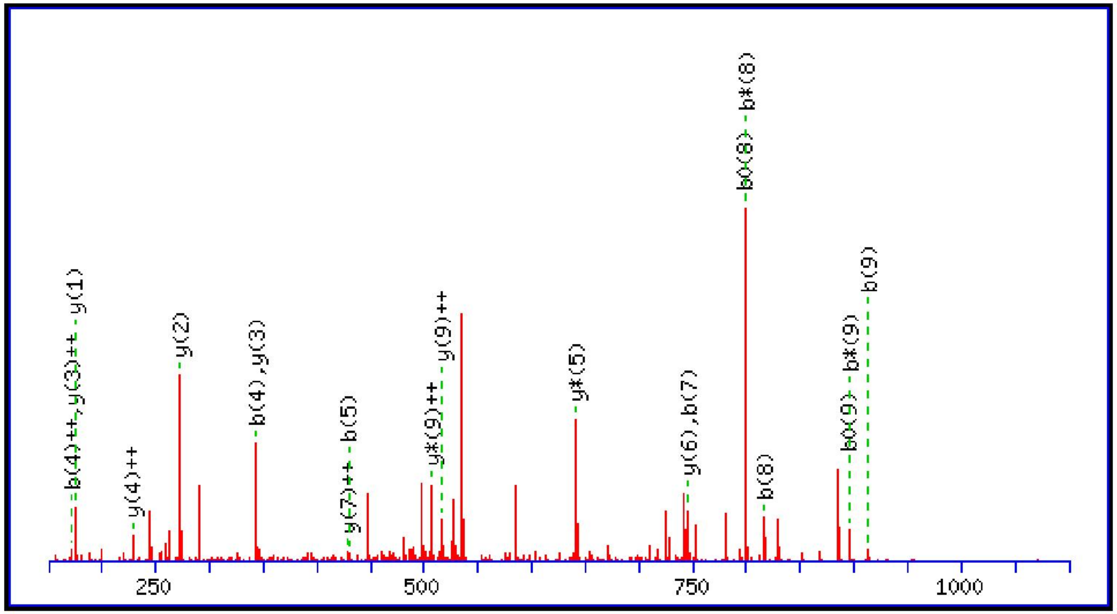
Matches : 14/76 fragment ions using 39 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	***313.1870***	157.0972	296.1605	148.5839			Q	934.5225	467.7649	917.4960	459.2516	916.5119	458.7596	7
3	***442.2296***	221.6185	425.2031	213.1052	424.2191	212.6132	E	806.4639	403.7356	789.4374	395.2223	788.4534	394.7303	6
4	***644.3886***	322.6980	627.3621	314.1847	626.3781	313.6927	K	**677.4213**	339.2143	660.3948	330.7010	659.4108	330.2090	5
5	***772.4472***	386.7272	755.4207	378.2140	754.4367	377.7220	Q	475.2623	238.1348	458.2358	229.6215	457.2518	229.1295	4
6	***873.4949***	437.2511	856.4683	428.7378	855.4843	428.2458	T	**347.2037**	174.1055	330.1772	165.5922	329.1932	165.1002	3
7	***944.5320***	472.7696	927.5055	464.2564	926.5214	463.7644	A	**246.1561**	123.5817	229.1295	115.0684			2
8							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GGDISKIAPR**
Found in **Q5T3P9**, Galectin-8 (Fragment) OS=Homo sapiens GN=LGALS8 PE=2 SV=1

Match to Query 3909: 1086.630468 from(544.322510,2+) intensity(1937397.2500)
Title: File2041 Spectrum7088 scans: 8230
Data file I:\2013-12-03-SIMM7721-FR9-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



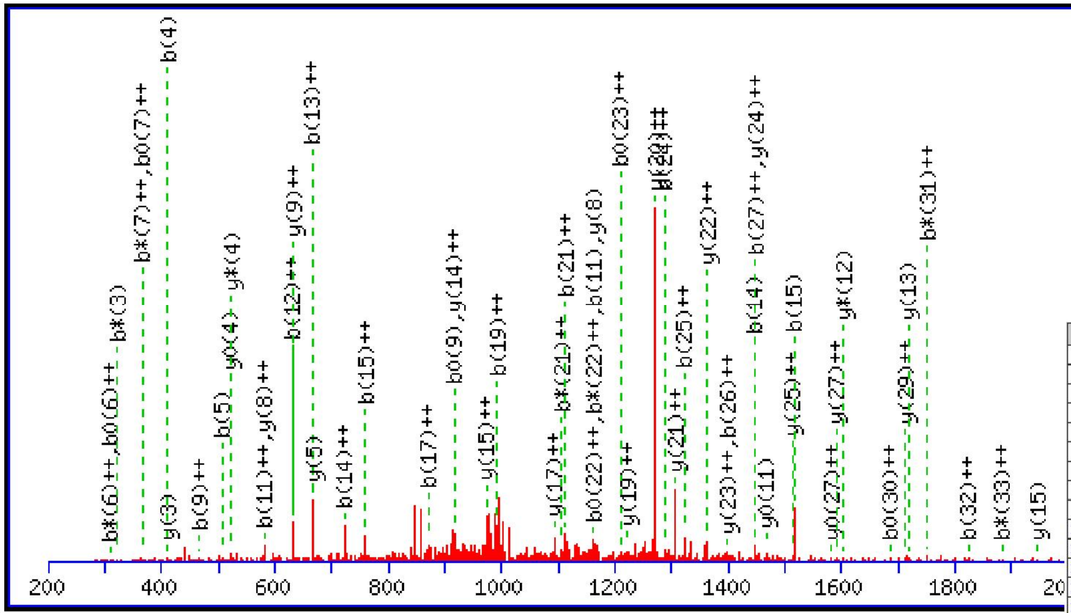
Monoisotopic mass of neutral peptide Mr(calc): 1086.6306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : Propionyl-(13CD3)Methyl (K)
Ions Score: 30 **Expect:** 0.32
Matches : 20/84 fragment ions using 41 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	115.0502	58.0287					G	1030.6164	515.8118	1013.5899	507.2986	1012.6058	506.8066	9
3	230.0771	115.5422			212.0666	106.5369	D	973.5949	487.3011	956.5684	478.7878	955.5844	478.2958	8
4	***343.1612***	172.0842			325.1506	163.0790	I	858.5680	429.7876	841.5414	421.2744	840.5574	420.7824	7
5	***430.1932***	215.6003			412.1827	206.5950	S	**745.4839**	373.2456	728.4574	364.7323	727.4734	364.2403	6
6	632.3523	316.6798	615.3257	308.1665	614.3417	307.6745	K	658.4519	329.7296	641.4254	321.2163			5
7	***745.4363***	373.2218	728.4098	364.7085	727.4258	364.2165	I	456.2929	228.6501	439.2663	220.1368			4
8	***816.4734***	408.7404	799.4469	400.2271	798.4629	399.7351	A	**343.2088**	172.1081	326.1823	163.5948			3
9	***913.5262***	457.2667	896.4996	448.7535	895.5156	448.2615	P	**272.1717**	136.5895	255.1452	128.0762			2
10							R	**175.1190**	88.0631	158.0924	79.5498			1

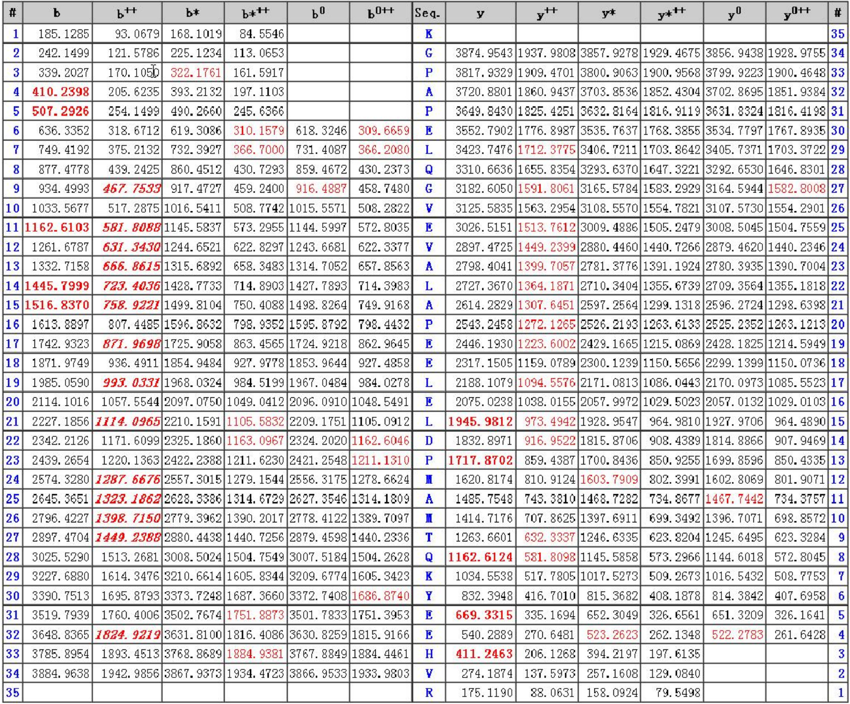
MS/MS Fragmentation of **KGPAPELQGVEVALAPEELELDPMAMTQKYEEHVR**
Found in **H0YEX5**, Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens GN=SF3B2 PE=4 SV=1

Match to Query 23420: 4058.043896 from(1015.518250,4+) intensity(0.0000)
Title: File2041 Spectrum17436 scans: 19010
Data file I:\2013-12-03-SIMM7721-FR9-ZW.mgf

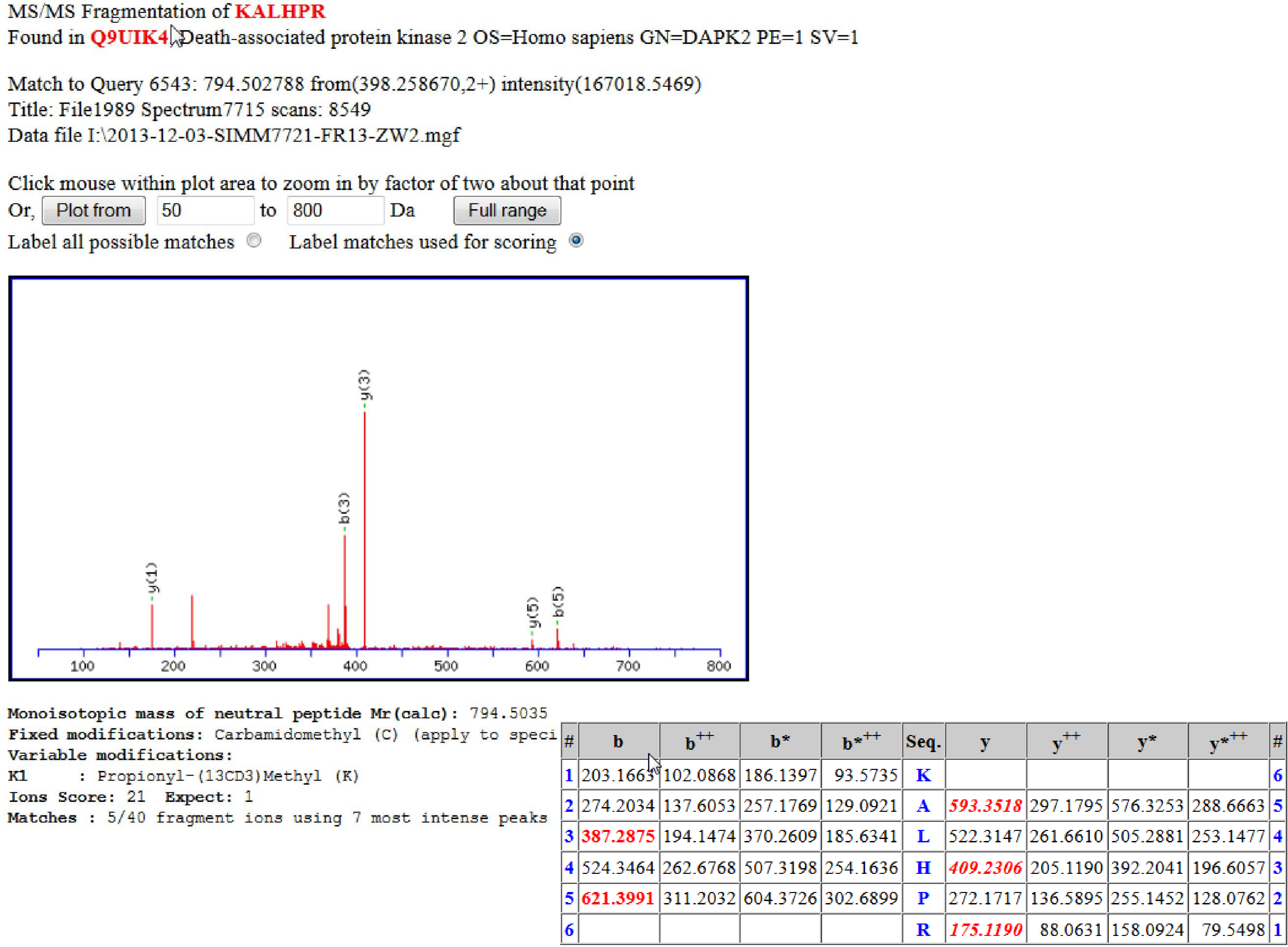
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 4058.0682
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K1 : Propionyl (K)
M24 : Label:13C(1)2H(3) (M)
M26 : Label:13C(1)2H(3)+Oxidation (M)
K29 : Propionyl-(13CD3)Methyl (K)
Ions Score: 34 **Expect:** 0.35
Matches : 56/392 fragment ions using 170 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							35
2	242.1499	121.5786	225.1234	113.0653			G	3874.9543	1937.9808	3857.9278	1929.4675	3856.9438	1928.9755	34
3	339.2027	170.1050	322.1761	161.5917			P	3817.9329	1909.4701	3800.9063	1900.9568	3799.9223	1900.4648	33
4	410.2398	205.6235	393.2132	197.1103			A	3720.8801	1860.9437	3703.8536	1852.4304	3702.8695	1851.9384	32
5	507.2926	254.1499	490.2660	245.6366			P	3649.8430	1825.4251	3632.8164	1816.9119	3631.8324	1816.4198	31
6	636.3352	318.6712	619.3086	310.1579	618.3246	309.6659	E	3552.7902	1776.8987	3535.7637	1768.3855	3534.7797	1767.8935	30
7	749.4192	375.2132	732.3927	366.7000	731.4087	366.2080	L	3423.7476	1712.3775	3406.7211	1703.8642	3405.7371	1703.3722	29
8	877.4778	439.2425	860.4512	430.7293	859.4672	430.2373	Q	3310.6636	1655.8354	3293.6370	1647.3221	3292.6530	1646.8301	28
9	934.4993	467.7533	917.4727	459.2400	916.4887	458.7480	G	3182.6050	1591.8061	3165.5784	1583.2929	3164.5944	1582.8008	27
10	1033.5677	517.2875	1016.5411	508.7742	1015.5571	508.2822	V	3125.5835	1563.2954	3108.5570	1554.7821	3107.5730	1554.2901	26
11	1162.6103	581.8088	1145.5837	573.2955	1144.5997	572.8035	E	3026.5151	1513.7612	3009.4886	1505.2479	3008.5045	1504.7559	25
12	1261.6787	631.3430	1244.6521	622.8297	1243.6681	622.3377	V	2897.4725	1449.2399	2880.4460	1440.7266	2879.4620	1440.2346	24
13	1332.7158	666.8615	1315.6892	658.3483	1314.7052	657.8563	A	2798.4041	1399.7057	2781.3776	1391.1924	2780.3935	1390.7004	23
14	1445.7999	723.4036	1428.7733	714.8903	1427.7893	714.3983	L	2727.3670	1364.1871	2710.3404	1355.6739	2709.3564	1355.1818	22
15	1516.8370	758.9221	1499.8104	750.4088	1498.8264	749.9168	A	2614.2829	1307.6451	2597.2564	1299.1318	2596.2724	1298.6398	21
16	1613.8897	807.4485	1596.8632	798.9352	1595.8792	798.4432	P	2543.2458	1272.1265	2526.2193	1263.6133	2525.2352	1263.1213	20
17	1742.9323	871.9698	1725.9058	863.4565	1724.9218	862.9645	E	2446.1930	1223.6002	2429.1665	1215.0869	2428.1825	1214.5949	19
18	1871.9749	936.4911	1854.9484	927.9778	1853.9644	927.4858	E	2317.1505	1159.0789	2300.1239	1150.5656	2299.1399	1150.0736	18
19	1985.0590	993.0331	1968.0324	984.5199	1967.0484	984.0278	L	2188.1079	1094.5576	2171.0813	1086.0443	2170.0973	1085.5523	17
20	2114.1016	1057.5544	2097.0750	1049.0412	2096.0910	1048.5491	E	2075.0238	1038.0155	2057.9972	1029.5023	2057.0132	1029.0103	16
21	2227.1856	1114.0965	2210.1591	1105.5832	2209.1751	1105.0912	L	1945.9812	973.4942	1928.9547	964.9810	1927.9706	964.4890	15
22	2342.2126	1171.6099	2325.1860	1163.0967	2324.2020	1162.6046	D	1832.8971	916.9522	1815.8706	908.4389	1814.8866	907.9469	14
23	2439.2654	1220.1363	2422.2388	1211.6230	2421.2548	1211.1310	P	1717.8702	859.4387	1700.8436	850.9255	1699.8596	850.4335	13
24	2574.3280	1287.6676	2557.3015	1279.1544	2556.3175	1278.6624	M	1620.8174	810.9124	1603.7909	802.3991	1602.8069	801.9071	12
25	2645.3651	1323.1862	2628.3386	1314.6729	2627.3546	1314.1809	A	1485.7548	743.3810	1468.7282	734.8677	1467.7442	734.3757	11
26	2796.4227	1398.7150	2779.3962	1390.2017	2778.4122	1389.7097	M	1414.7176	707.8625	1397.6911	699.3492	1396.7071	698.8572	10
27	2897.4704	1449.2388	2880.4438	1440.7256	2879.4598	1440.2336	T	1263.6601	632.3337	1246.6335	623.8204	1245.6495	623.3284	9
28	3025.5290	1513.2681	3008.5024	1504.7549	3007.5184	1504.2628	Q	1162.6124	581.8098	1145.5858	573.2966	1144.6018	572.8045	8
29	3227.6880	1614.3476	3210.6614	1605.8344	3209.6774	1605.3423	K	1034.5538	517.7805	1017.5273	509.2673	1016.5432	508.7753	7
30	3390.7513	1695.8793	3373.7248	1687.3660	3372.7408	1686.8740	Y	832.3948	416.7010	815.3682	408.1878	814.3842	407.6958	6
31	3519.7939	1760.4006	3502.7674	1751.8873	3501.7833	1751.3953	E	669.3315	335.1694	652.3049	326.6561	651.3209	326.1641	5
32	3648.8365	1824.9219	3631.8100	1816.4086	3630.8259	1815.9166	E	540.2889	270.6481	523.2623	262.1348	522.2783	261.6428	4
33	3785.8954	1893.4513	3768.8689	1884.9381	3767.8849	1884.4461	H	411.2463	206.1268	394.2197	197.6135			3
34	3884.9638	1942.9856	3867.9373	1934.4723	3866.9533	1933.9803	V	274.1874	137.5973	257.1608	129.0840			2
35							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KALHPR**

Found in **Q9UIK4** Death-associated protein kinase 2 OS=Homo sapiens GN=DAPK2 PE=1 SV=1

Match to Query 6543: 794.502788 from(398.258670,2+) intensity(167018.5469)

Title: File1989 Spectrum7715 scans: 8549

Data file I:\2013-12-03-SIMM7721-FR13-ZW2.mgf

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

Or, Plot from 50 to 800 Da Full range

Label all possible matches ○ Label matches used for scoring ●

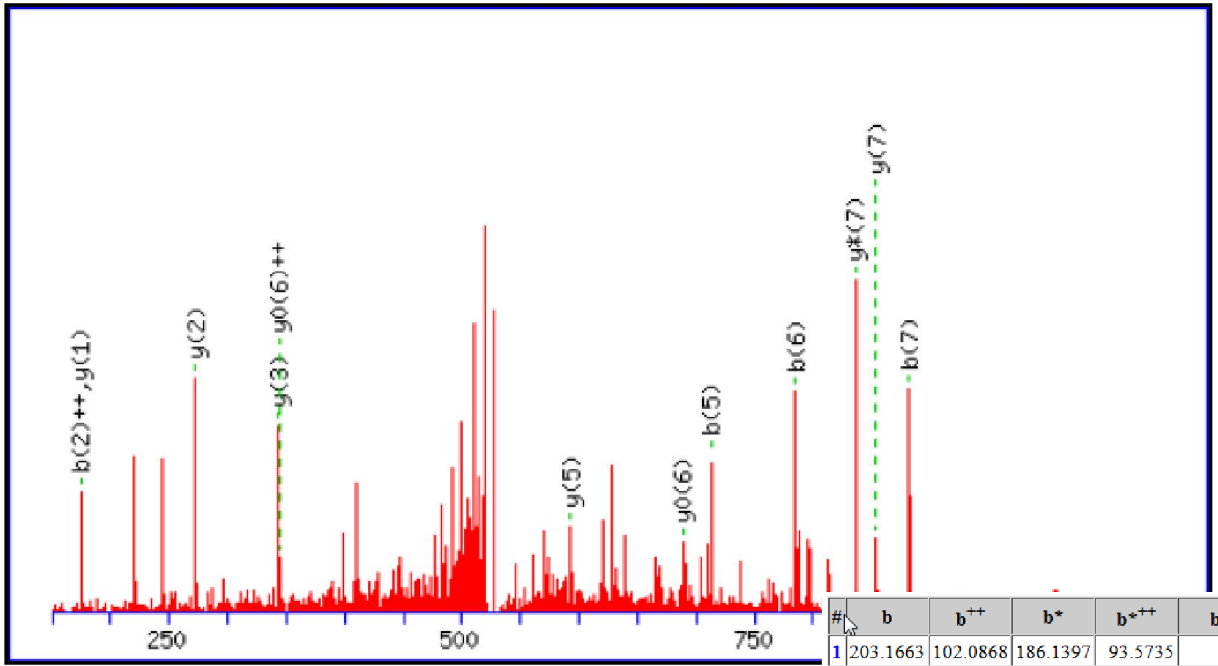
```
Monoisotopic mass of neutral peptide Mr(calc): 794.5035
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
Ions Score: 21  Expect: 1
Matches : 5/40 fragment ions using 7 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	203.1663	102.0868	186.1397	93.5735	K					6
2	274.2034	137.6053	257.1769	129.0921	A	*593.3518*	297.1795	576.3253	288.6663	5
3	**387.2875**	194.1474	370.2609	185.6341	L	522.3147	261.6610	505.2881	253.1477	4
4	524.3464	262.6768	507.3198	254.1636	H	*409.2306*	205.1190	392.2041	196.6057	3
5	**621.3991**	311.2032	604.3726	302.6899	P	272.1717	136.5895	255.1452	128.0762	2
6					R	*175.1190*	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KFLYSAPR**
Found in **Q9UK61**, Protein FAM208A OS=Homo sapiens GN=FAM208A PE=1 SV=3

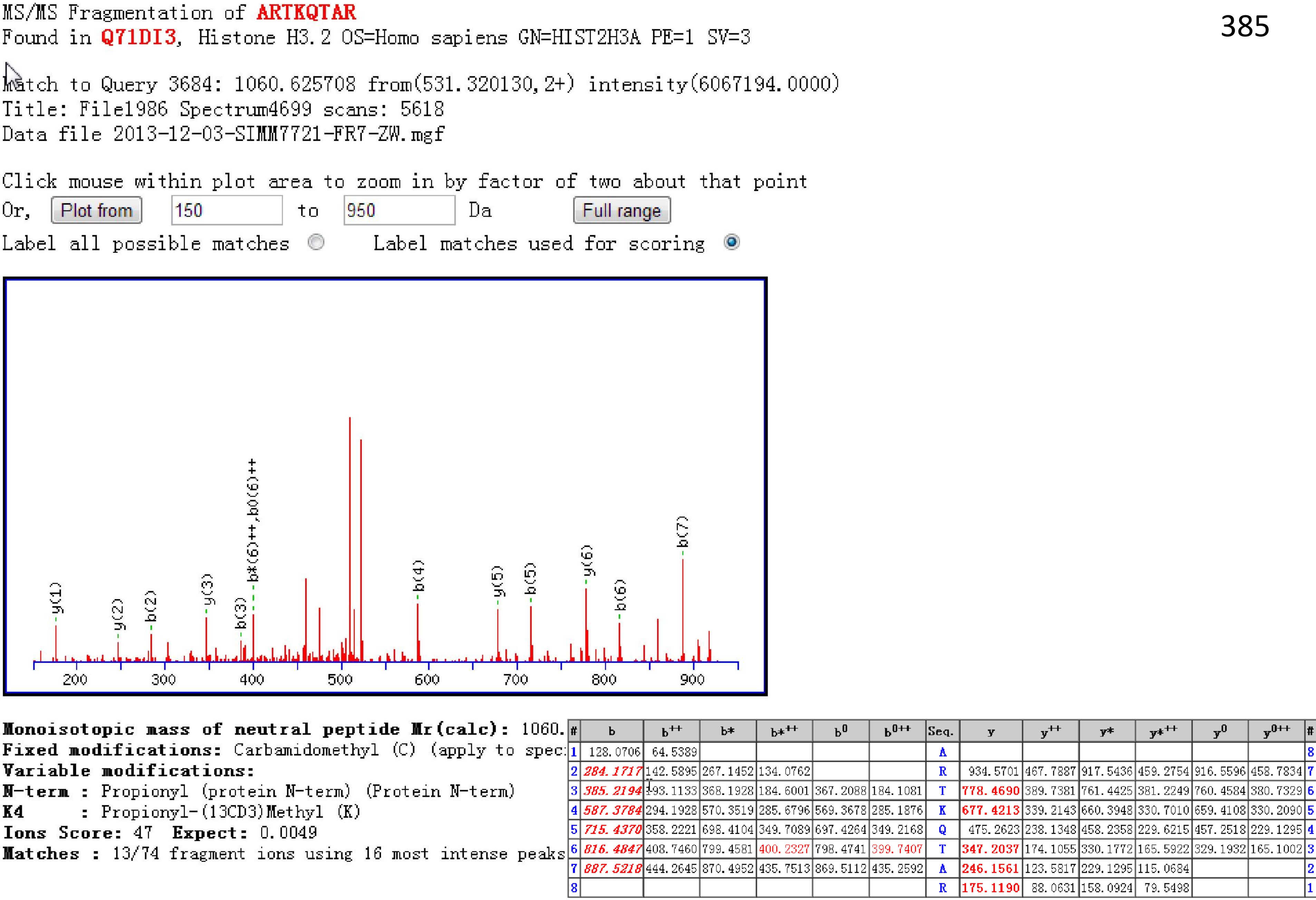
Match to Query 9354: 1054.603248 from(528.308900,2+) intensity(92075.4531)
Title: File1989 Spectrum9020 scans: 9941
Data file I:\2013-12-03-SIMM7721-FR13-ZW2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1054
Fixed modifications: Carbamidomethyl (C) (apply to
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
Ions Score: 23  Expect: 1.9
Matches : 12/70 fragment ions using 27 most intense
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							8
2	350.2347	175.6210	333.2082	167.1077			F	***853.4567***	427.2320	836.4301	418.7187	835.4461	418.2267	7
3	463.3188	232.1630	446.2922	223.6497			L	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
4	626.3821	313.6947	609.3555	305.1814			Y	***593.3042***	297.1557	576.2776	288.6425	575.2936	288.1504	5
5	**713.4141**	357.2107	696.3876	348.6974	695.4036	348.2054	S	430.2409	215.6241	413.2143	207.1108	412.2303	206.6188	4
6	**784.4512**	392.7293	767.4247	384.2160	766.4407	383.7240	A	***343.2088***	172.1081	326.1823	163.5948			3
7	**881.5040**	441.2556	864.4775	432.7424	863.4934	432.2504	P	***272.1717***	136.5895	255.1452	128.0762			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



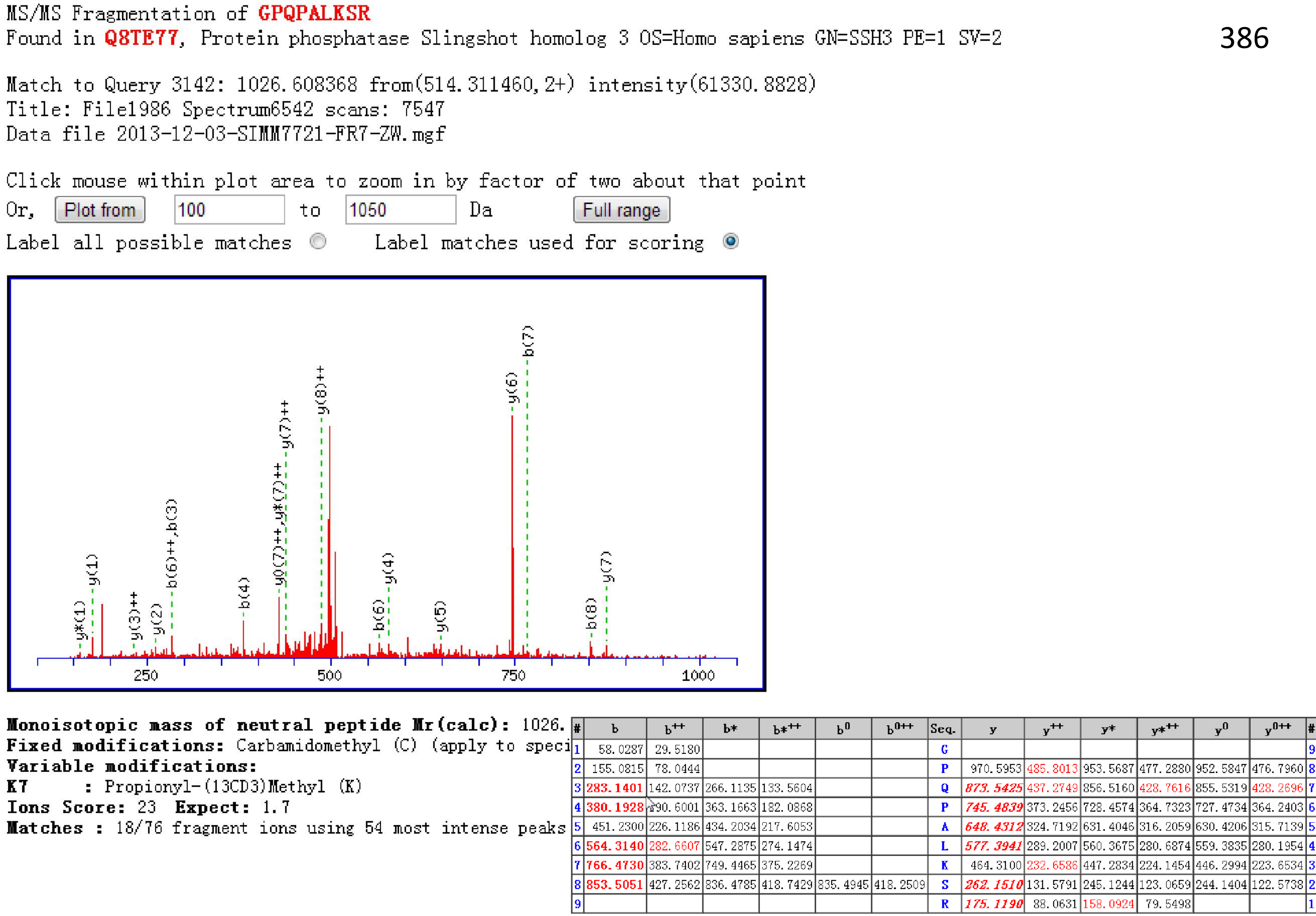
MS/MS Fragmentation of **ARTKQTAR**
Found in **Q71DI3**, Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3

Match to Query 3684: 1060.625708 from(531.320130,2+) intensity(6067194.0000)
Title: File1986 Spectrum4699 scans: 5618
Data file 2013-12-03-SIMM7721-FR7-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1060.
Fixed modifications: Carbamidomethyl (C) (apply to spec:
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 47 **Expect:** 0.0049
Matches : 13/74 fragment ions using 16 most intense peaks

#	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	128.0706	64.5389					A							8
2	284.1717	142.5895	267.1452	134.0762			R	934.5701	467.7887	917.5436	459.2754	916.5596	458.7834	7
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	T	778.4690	389.7381	761.4425	381.2249	760.4584	380.7329	6
4	587.3784	294.1928	570.3519	285.6796	569.3678	285.1876	K	677.4213	339.2143	660.3948	330.7010	659.4108	330.2090	5
5	715.4370	358.2221	698.4104	349.7089	697.4264	349.2168	Q	475.2623	238.1348	458.2358	229.6215	457.2518	229.1295	4
6	816.4847	408.7460	799.4581	400.2327	798.4741	399.7407	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
7	887.5218	444.2645	870.4952	435.7513	869.5112	435.2592	A	246.1561	123.5817	229.1295	115.0684			2
8							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **GPQPALKSR**

Found in **Q8TE77**, Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2

Match to Query 3142: 1026.608368 from(514.311460,2+) intensity(61330.8828)

Title: File1986 Spectrum6542 scans: 7547

Data file 2013-12-03-SIMM7721-FR7-ZW.mgf

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

Or, Plot from 100 to 1050 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1026.

Fixed modifications: Carbamidomethyl (C) (apply to speci

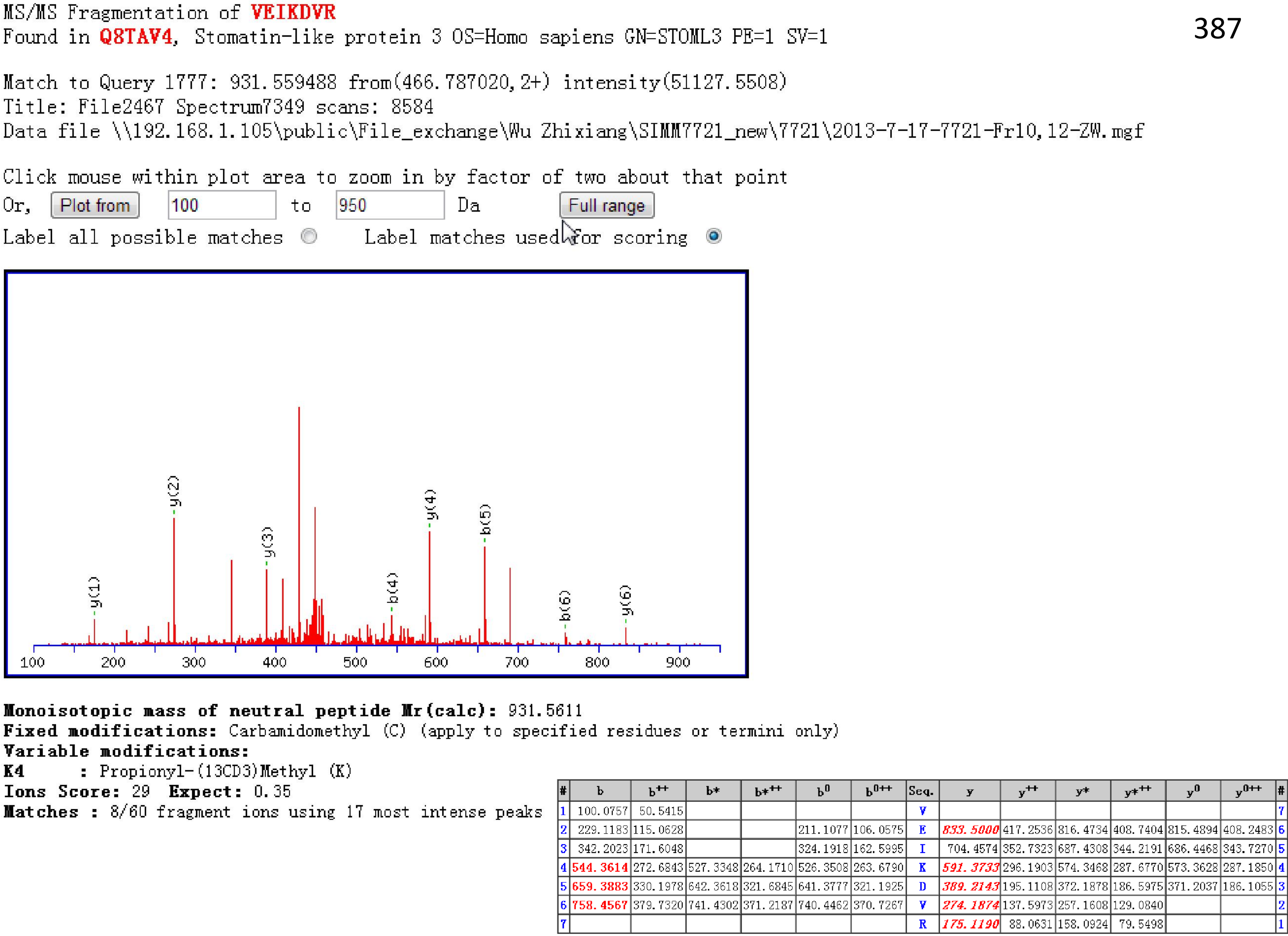
Variable modifications:

K7 : Propionyl-(13CD3)Methyl (K)

Ions Score: 23 **Expect:** 1.7

Matches : 18/76 fragment ions using 54 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180					G							9
2	155.0815	78.0444					P	970.5953	485.8013	953.5687	477.2880	952.5847	476.7960	8
3	**283.1401**	142.0737	266.1135	133.5604			Q	***873.5425***	437.2749	856.5160	428.7616	855.5319	428.2696	7
4	**380.1928**	190.6001	363.1663	182.0868			P	***745.4839***	373.2456	728.4574	364.7323	727.4734	364.2403	6
5	451.2300	226.1186	434.2034	217.6053			A	***648.4312***	324.7192	631.4046	316.2059	630.4206	315.7139	5
6	**564.3140**	282.6607	547.2875	274.1474			L	***577.3941***	289.2007	560.3675	280.6874	559.3835	280.1954	4
7	**766.4730**	383.7402	749.4465	375.2269			K	464.3100	232.6586	447.2834	224.1454	446.2994	223.6534	3
8	**853.5051**	427.2562	836.4785	418.7429	835.4945	418.2509	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



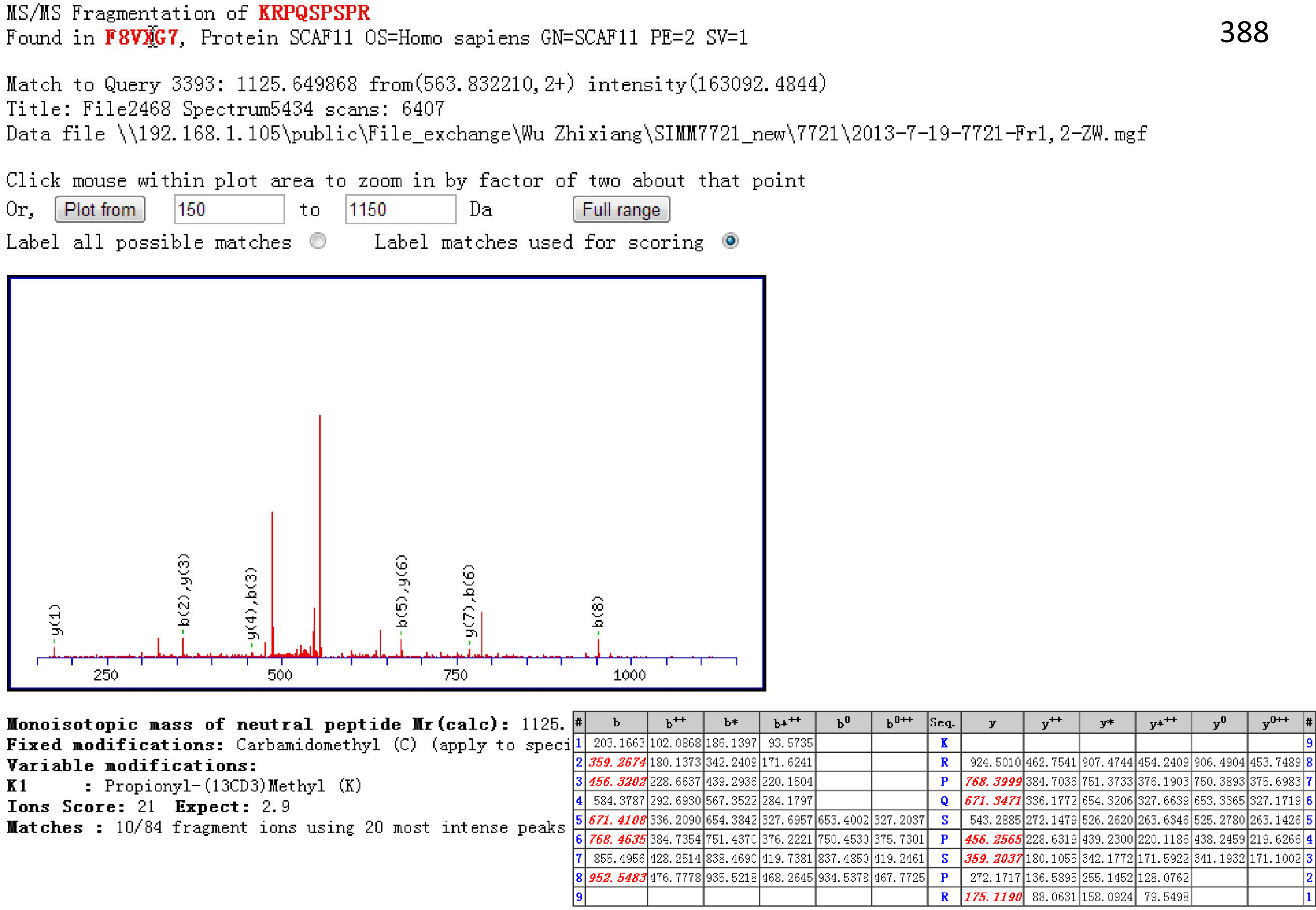
MS/MS Fragmentation of **VEIKDVR**
Found in **Q8TAV4**, Stomatin-like protein 3 OS=Homo sapiens GN=STOML3 PE=1 SV=1

Match to Query 1777: 931.559488 from(466.787020,2+) intensity(51127.5508)
Title: File2467 Spectrum7349 scans: 8584
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-17-7721-Fr10,12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 931.5611
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 29 **Expect:** 0.35
Matches : 8/60 fragment ions using 17 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							7
2	229.1183	115.0628			211.1077	106.0575	E	*833.5000*	417.2536	816.4734	408.7404	815.4894	408.2483	6
3	342.2023	171.6048			324.1918	162.5995	I	704.4574	352.7323	687.4308	344.2191	686.4468	343.7270	5
4	**544.3614**	272.6843	527.3348	264.1710	526.3508	263.6790	K	*591.3733*	296.1903	574.3468	287.6770	573.3628	287.1850	4
5	**659.3883**	330.1978	642.3618	321.6845	641.3777	321.1925	D	*389.2143*	195.1108	372.1878	186.5975	371.2037	186.1055	3
6	**758.4567**	379.7320	741.4302	371.2187	740.4462	370.7267	V	*274.1874*	137.5973	257.1608	129.0840			2
7							R	*175.1190*	88.0631	158.0924	79.5498			1



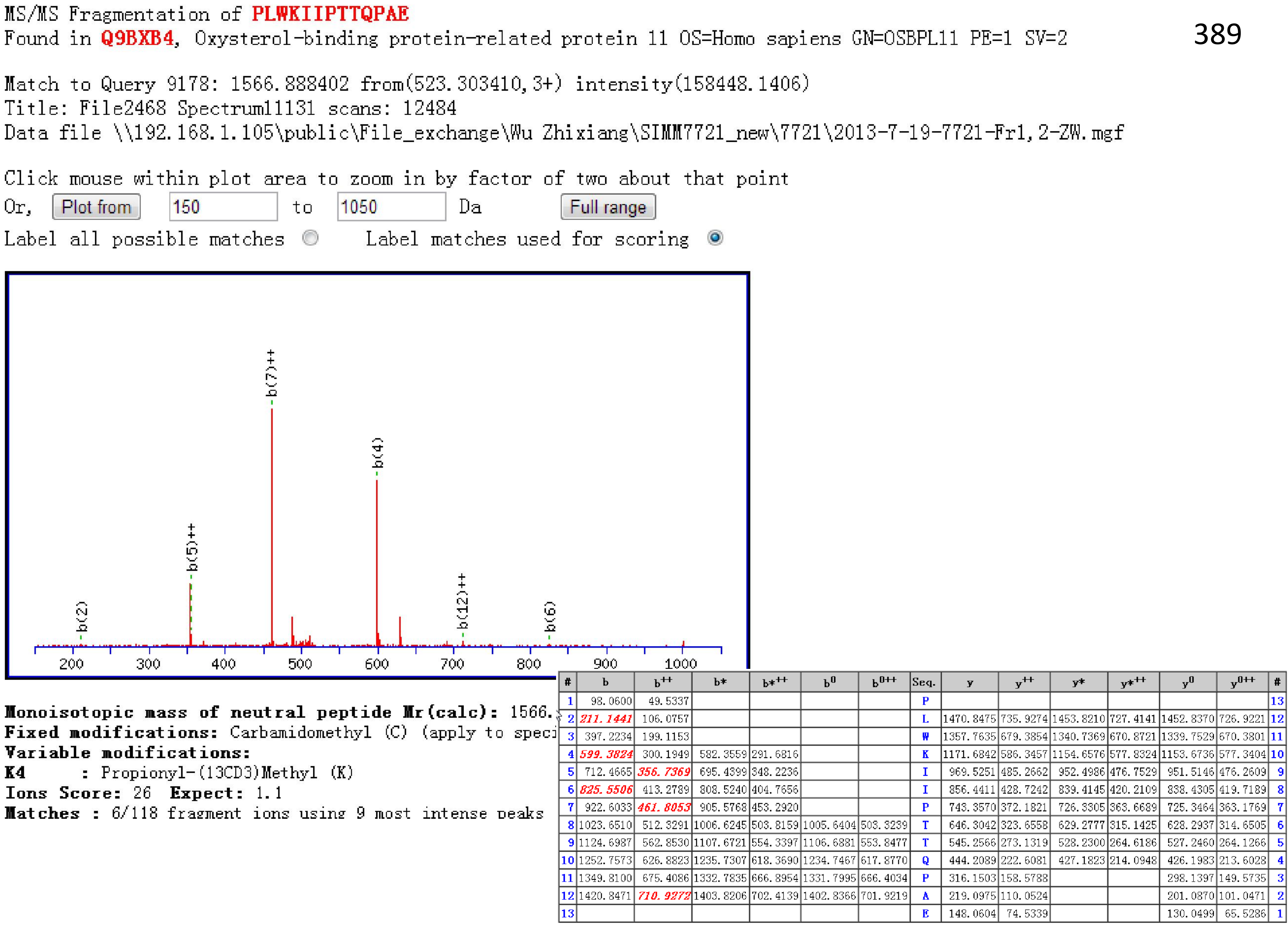
MS/MS Fragmentation of **KRPQSPSPR**
Found in **F8VXG7**, Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=2 SV=1

Match to Query 3393: 1125.649868 from(563.832210,2+) intensity(163092.4844)
Title: File2468 Spectrum5434 scans: 6407
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr1,2-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1125.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 21 **Expect:** 2.9
Matches : 10/84 fragment ions using 20 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							9
2	***359.2674***	180.1373	342.2409	171.6241			R	924.5010	462.7541	907.4744	454.2409	906.4904	453.7489	8
3	***456.3202***	228.6637	439.2936	220.1504			P	***768.3999***	384.7036	751.3733	376.1903	750.3893	375.6983	7
4	584.3787	292.6930	567.3522	284.1797			Q	***671.3471***	336.1772	654.3206	327.6639	653.3365	327.1719	6
5	***671.4108***	336.2090	654.3842	327.6957	653.4002	327.2037	S	543.2885	272.1479	526.2620	263.6346	525.2780	263.1426	5
6	***768.4635***	384.7354	751.4370	376.2221	750.4530	375.7301	P	***456.2565***	228.6319	439.2300	220.1186	438.2459	219.6266	4
7	855.4956	428.2514	838.4690	419.7381	837.4850	419.2461	S	***359.2037***	180.1055	342.1772	171.5922	341.1932	171.1002	3
8	***952.5483***	476.7778	935.5218	468.2645	934.5378	467.7725	P	272.1717	136.5895	255.1452	128.0762			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



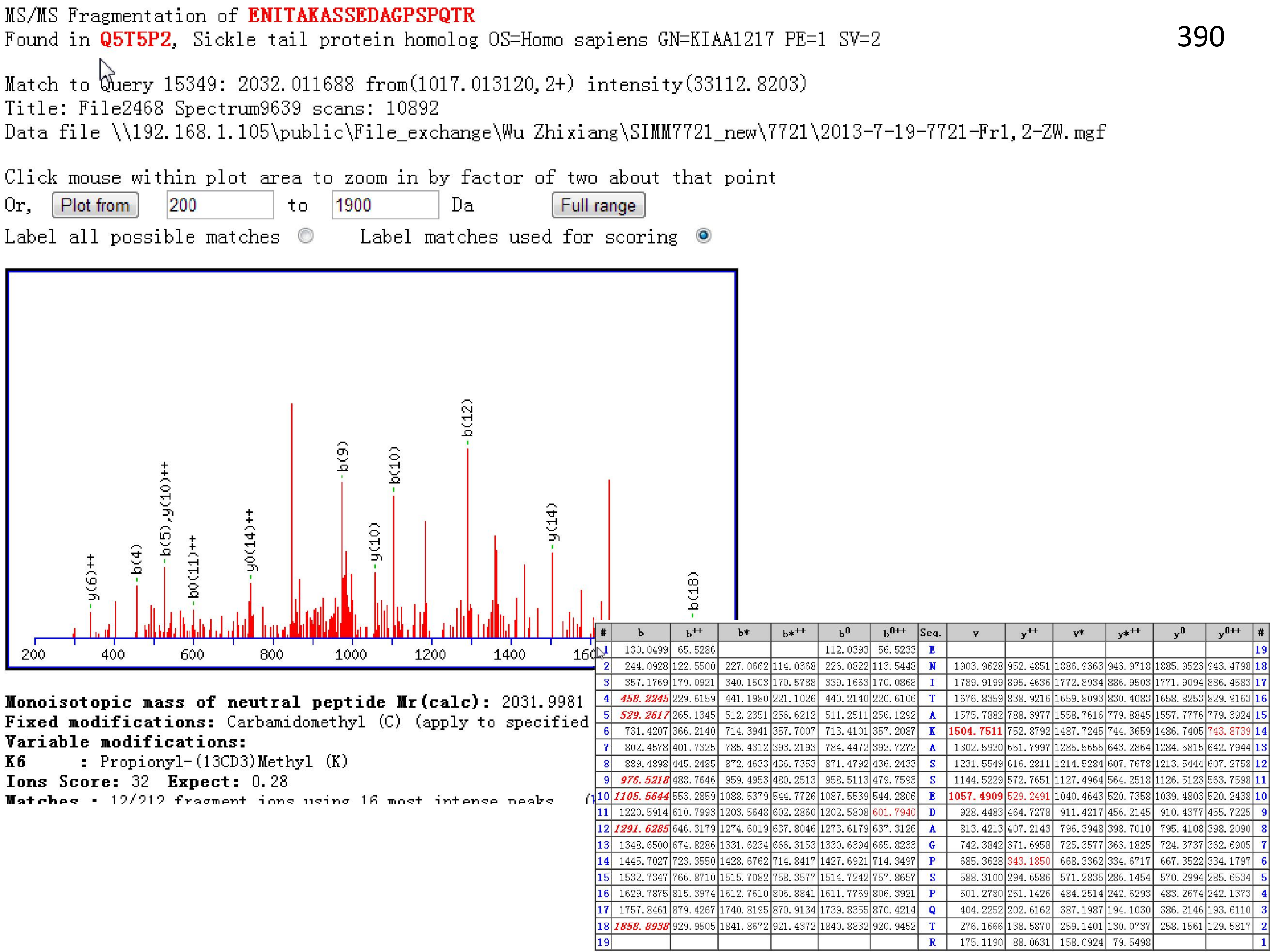
MS/MS Fragmentation of PLWKIIPTTQPAE
Found in Q9BXB4, Oxysterol-binding protein-related protein 11 OS=Homo sapiens GN=OSBPL11 PE=1 SV=2

Match to Query 9178: 1566.888402 from(523.303410,3+) intensity(158448.1406)
Title: File2468 Spectrum11131 scans: 12484
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr1,2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1566.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
Ions Score: 26 **Expect:** 1.1
Matches : 6/118 fragment ions using 9 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.0600	49.5337					P							13
2	***211.1441***	106.0757					L	1470.8475	735.9274	1453.8210	727.4141	1452.8370	726.9221	12
3	397.2234	199.1153					W	1357.7635	679.3854	1340.7369	670.8721	1339.7529	670.3801	11
4	***599.3824***	300.1949	582.3559	291.6816			K	1171.6842	586.3457	1154.6576	577.8324	1153.6736	577.3404	10
5	712.4665	***356.7369***	695.4399	348.2236			I	969.5251	485.2662	952.4986	476.7529	951.5146	476.2609	9
6	***825.5506***	413.2789	808.5240	404.7656			I	856.4411	428.7242	839.4145	420.2109	838.4305	419.7189	8
7	922.6033	***461.8053***	905.5768	453.2920			P	743.3570	372.1821	726.3305	363.6689	725.3464	363.1769	7
8	1023.6510	512.3291	1006.6245	503.8159	1005.6404	503.3239	T	646.3042	323.6558	629.2777	315.1425	628.2937	314.6505	6
9	1124.6987	562.8530	1107.6721	554.3397	1106.6881	553.8477	T	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	5
10	1252.7573	626.8823	1235.7307	618.3690	1234.7467	617.8770	Q	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	4
11	1349.8100	675.4086	1332.7835	666.8954	1331.7995	666.4034	P	316.1503	158.5788			298.1397	149.5735	3
12	1420.8471	***710.9272***	1403.8206	702.4139	1402.8366	701.9219	A	219.0975	110.0524			201.0870	101.0471	2
13							E	148.0604	74.5339			130.0499	65.5286	1



MS/MS Fragmentation of **ENITAKASSEDAGPSPQTR**

Found in **Q5T5P2**, Sickle tail protein homolog OS=Homo sapiens GN=KIAA1217 PE=1 SV=2

Match to Query 15349: 2032.011688 from(1017.013120,2+) intensity(33112.8203)

Title: File2468 Spectrum9639 scans: 10892

Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr1,2-ZW.mgf

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

Or, 200 to 1900 Da

Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 2031.9981

Fixed modifications: Carbamidomethyl (C) (apply to specified

Variable modifications:

K6 : Propionyl-(13CD3)Methyl (K)

Ions Score: 32 **Expect:** 0.28

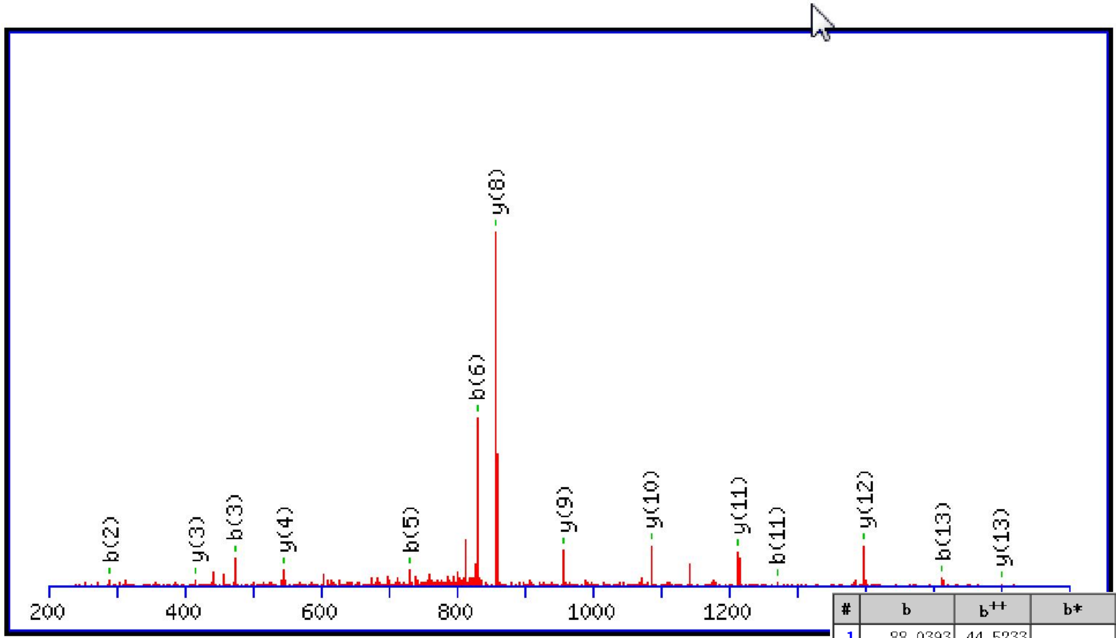
Matches : 12/212 fragment ions using 16 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							19
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	N	1903.9628	952.4851	1886.9363	943.9718	1885.9523	943.4798	18
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	I	1789.9199	895.4636	1772.8934	886.9503	1771.9094	886.4583	17
4	***458.2245***	229.6159	441.1980	221.1026	440.2140	220.6106	T	1676.8359	838.9216	1659.8093	830.4083	1658.8253	829.9163	16
5	***529.2617***	265.1345	512.2351	256.6212	511.2511	256.1292	A	1575.7882	788.3977	1558.7616	779.8845	1557.7776	779.3924	15
6	731.4207	366.2140	714.3941	357.7007	713.4101	357.2087	K	**1504.7511**	752.8792	1487.7245	744.3659	1486.7405	743.8739	14
7	802.4578	401.7325	785.4312	393.2193	784.4472	392.7272	A	1302.5920	651.7997	1285.5655	643.2864	1284.5815	642.7944	13
8	889.4898	445.2485	872.4633	436.7353	871.4792	436.2433	S	1231.5549	616.2811	1214.5284	607.7678	1213.5444	607.2758	12
9	***976.5218***	488.7646	959.4953	480.2513	958.5113	479.7593	S	1144.5229	572.7651	1127.4964	564.2518	1126.5123	563.7598	11
10	***1105.5644***	553.2859	1088.5379	544.7726	1087.5539	544.2806	E	**1057.4909**	529.2491	1040.4643	520.7358	1039.4803	520.2438	10
11	1220.5914	610.7993	1203.5648	602.2860	1202.5808	601.7940	D	928.4483	464.7278	911.4217	456.2145	910.4377	455.7225	9
12	***1291.6285***	646.3179	1274.6019	637.8046	1273.6179	637.3126	A	813.4213	407.2143	796.3948	398.7010	795.4108	398.2090	8
13	1348.6500	674.8286	1331.6234	666.3153	1330.6394	665.8233	G	742.3842	371.6958	725.3577	363.1825	724.3737	362.6905	7
14	1445.7027	723.3550	1428.6762	714.8417	1427.6921	714.3497	P	685.3628	343.1850	668.3362	334.6717	667.3522	334.1797	6
15	1532.7347	766.8710	1515.7082	758.3577	1514.7242	757.8657	S	588.3100	294.6586	571.2835	286.1454	570.2994	285.6534	5
16	1629.7875	815.3974	1612.7610	806.8841	1611.7769	806.3921	P	501.2780	251.1426	484.2514	242.6293	483.2674	242.1373	4
17	1757.8461	879.4267	1740.8195	870.9134	1739.8355	870.4214	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
18	***1858.8938***	929.9505	1841.8672	921.4372	1840.8832	920.9452	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SKKEQVPSGAELER**
Found in **J3KP06**, LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=4 SV=1

Match to Query 10535: 1686.906348 from(844.460450,2+) intensity(147791.4844)
Title: File2468 Spectrum8789 scans: 9986
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr1,2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



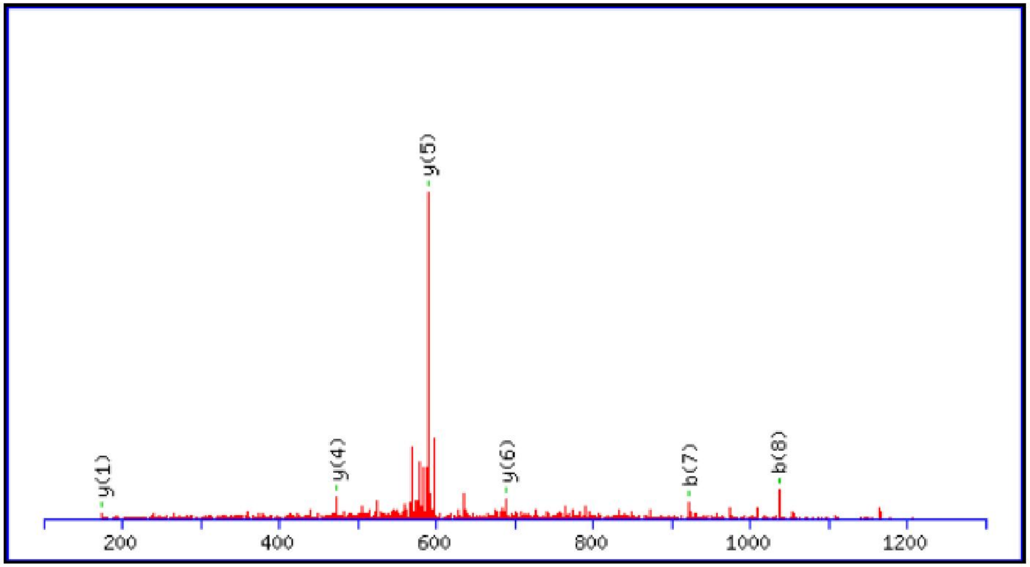
Monoisotopic mass of neutral peptide Mr(calc): 1686.
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
Ions Score: 83 **Expect:** 2.9e-006
Matches : 14/152 fragment ions using 14 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	***290.1983***	145.6028	273.1718	137.0895	272.1878	136.5975	K	***1600.8813***	800.9443	1583.8548	792.4310	1582.8708	791.9390	13
3	***474.3195***	237.6634	457.2929	229.1501	456.3089	228.6581	K	***1398.7223***	699.8648	1381.6958	691.3515	1380.7118	690.8595	12
4	603.3621	302.1847	586.3355	293.6714	585.3515	293.1794	E	***1214.6012***	607.8042	1197.5746	599.2909	1196.5906	598.7989	11
5	***731.4207***	366.2140	714.3941	357.7007	713.4101	357.2087	Q	***1085.5586***	543.2829	1068.5320	534.7696	1067.5480	534.2776	10
6	***830.4891***	415.7482	813.4625	407.2349	812.4785	406.7429	V	***957.5000***	479.2536	940.4734	470.7404	939.4894	470.2483	9
7	927.5418	464.2746	910.5153	455.7613	909.5313	455.2693	P	***858.4316***	429.7194	841.4050	421.2061	840.4210	420.7141	8
8	1014.5739	507.7906	997.5473	499.2773	996.5633	498.7853	S	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	7
9	1071.5953	536.3013	1054.5688	527.7880	1053.5848	527.2960	G	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	6
10	1142.6325	571.8199	1125.6059	563.3066	1124.6219	562.8146	A	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	5
11	***1271.6750***	636.3412	1254.6485	627.8279	1253.6645	627.3359	E	***546.2882***	273.6477	529.2617	265.1345	528.2776	264.6425	4
12	1384.7591	692.8832	1367.7326	684.3699	1366.7485	683.8779	L	***417.2456***	209.1264	400.2191	200.6132	399.2350	200.1212	3
13	***1513.8017***	757.4045	1496.7752	748.8912	1495.7911	748.3992	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **MKLTDSVLR**
Found in **Q6UXN9**, WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1

Match to Query 5340: 1210.725188 from(606.369870,2+) intensity(59204.6523)
Title: File2474 Spectrum12217 scans: 13685
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr3,4-ZW.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 ●



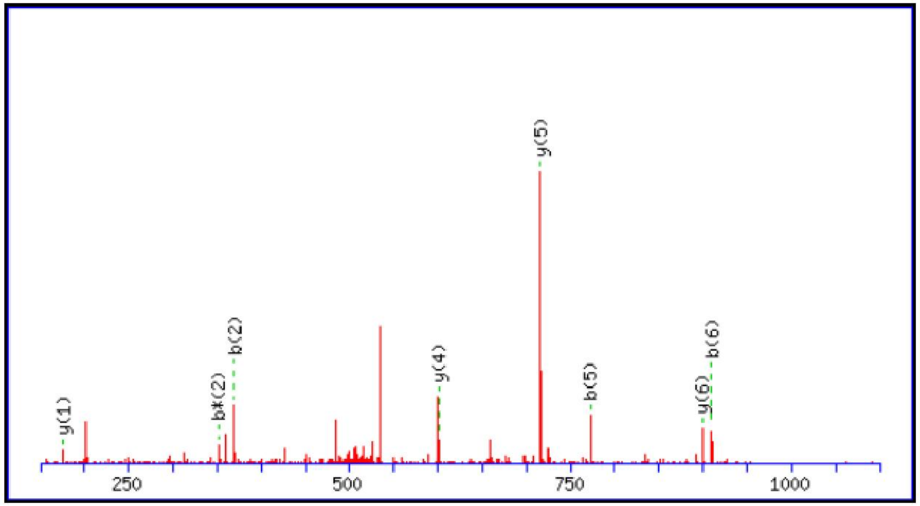
Monoisotopic mass of neutral peptide Mr(calc): 1209.7184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl-(13CD3)Methyl (Protein N-term)
K2 : Propionyl-(13CD3)Methyl (K)
Ions Score: 20 **Expect:** 2.7
Matches : 6/82 fragment ions using 11 most intense peaks (h

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	206.1118	103.5595					M							9
2	408.2708	204.6390	391.2443	196.1258			K	1005.6212	503.3142	988.5946	494.8009	987.6106	494.3089	8
3	521.3549	261.1811	504.3283	252.6678			L	803.4621	402.2347	786.4356	393.7214	785.4516	393.2294	7
4	622.4026	311.7049	605.3760	303.1916	604.3920	302.6996	T	***690.3781***	345.6927	673.3515	337.1794	672.3675	336.6874	6
5	737.4295	369.2184	720.4030	360.7051	719.4189	360.2131	D	***589.3304***	295.1688	572.3039	286.6556	571.3198	286.1636	5
6	824.4615	412.7344	807.4350	404.2211	806.4510	403.7291	S	***474.3035***	237.6554	457.2769	229.1421	456.2929	228.6501	4
7	**923.5300**	462.2686	906.5034	453.7553	905.5194	453.2633	V	387.2714	194.1394	370.2449	185.6261			3
8	**1036.6140**	518.8106	1019.5875	510.2974	1018.6035	509.8054	L	288.2030	144.6051	271.1765	136.0919			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KKNKSHR**
Found in **H7BZ93**, Histone-lysine N-methyltransferase SETD2 (Fragment) OS=Homo sapiens GN=SETD2 PE=4 SV=1

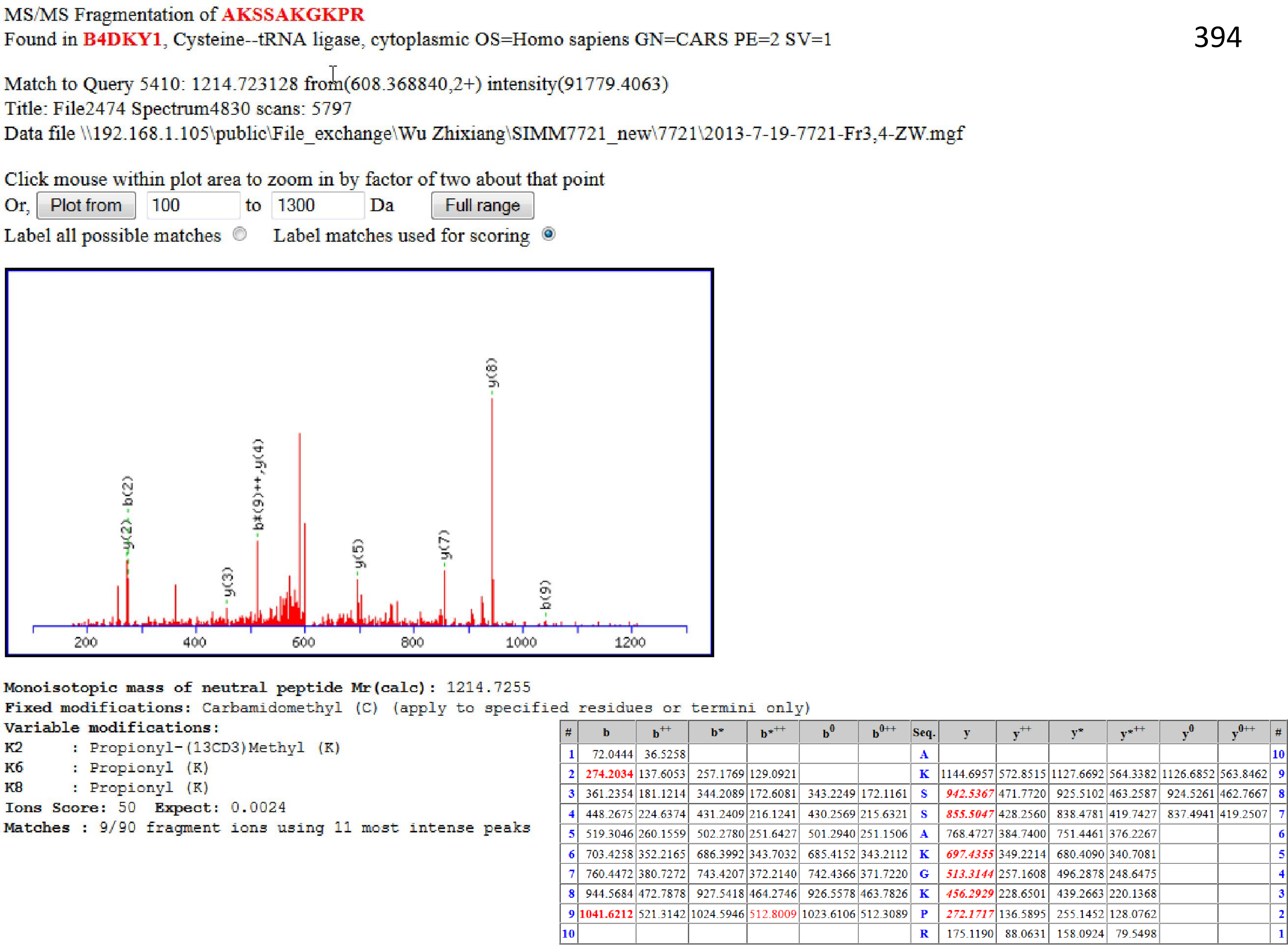
Match to Query 3595: 1082.644868 from(542.329710,2+) intensity(422100.2500)
Title: File2474 Spectrum3905 scans: 4809
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr3,4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1082.6469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl (K)
K2      : Propionyl (K)
K4      : Propionyl-(13CD3)Methyl (K)
Ions Score: 22  Expect: 1.9
Matches : 8/60 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			**K**							7
2	***369.2496***	185.1285	352.2231	176.6152			**K**	***899.5330***	450.2701	882.5065	441.7569	881.5224	441.2649	6
3	483.2926	242.1499	466.2660	233.6366			**N**	***715.4118***	358.2096	698.3853	349.6963	697.4013	349.2043	5
4	685.4516	343.2294	668.4250	334.7161			**K**	***601.3689***	301.1881	584.3424	292.6748	583.3583	292.1828	4
5	***772.4836***	386.7454	755.4571	378.2322	754.4730	377.7402	**S**	399.2099	200.1086	382.1833	191.5953	381.1993	191.1033	3
6	***909.5425***	455.2749	892.5160	446.7616	891.5319	446.2696	**H**	312.1779	156.5926	295.1513	148.0793			2
7							**R**	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AKSSAKGKPR**
Found in **B4DKY1**, Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=2 SV=1

Match to Query 5410: 1214.723128 from(608.368840,2+) intensity(91779.4063)
Title: File2474 Spectrum4830 scans: 5797
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr3,4-ZW.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 ●

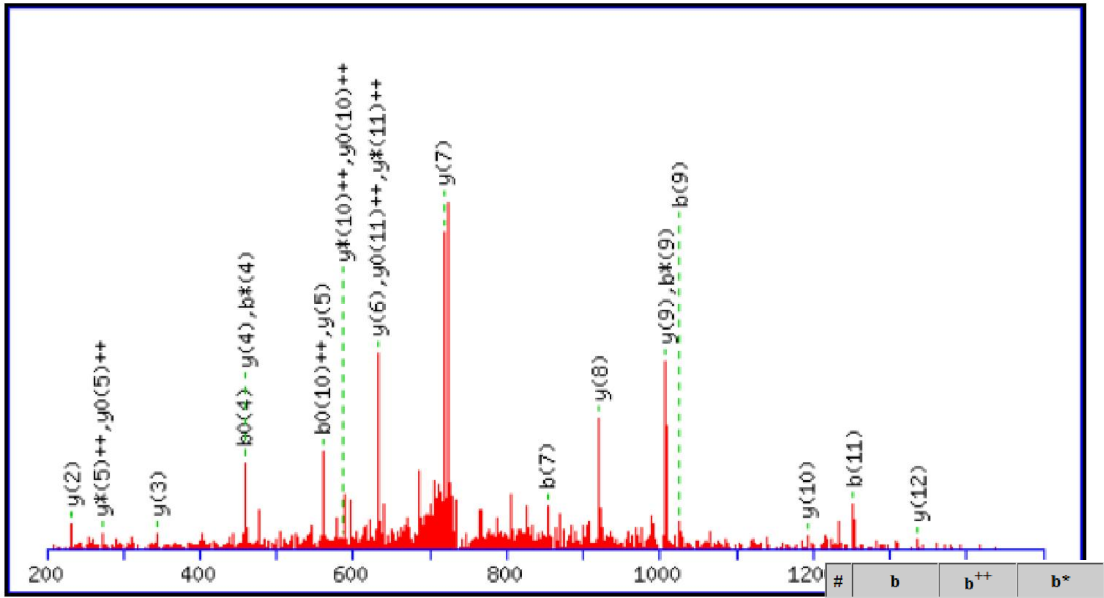
Monoisotopic mass of neutral peptide Mr(calc): 1214.7255
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Propionyl-(13CD3)Methyl (K)
K6 : Propionyl (K)
K8 : Propionyl (K)
Ions Score: 50 **Expect:** 0.0024
Matches : 9/90 fragment ions using 11 most intense peaks

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					A							10
2	**274.2034**	137.6053	257.1769	129.0921			K	1144.6957	572.8515	1127.6692	564.3382	1126.6852	563.8462	9
3	361.2354	181.1214	344.2089	172.6081	343.2249	172.1161	S	***942.5367***	471.7720	925.5102	463.2587	924.5261	462.7667	8
4	448.2675	224.6374	431.2409	216.1241	430.2569	215.6321	S	***855.5047***	428.2560	838.4781	419.7427	837.4941	419.2507	7
5	519.3046	260.1559	502.2780	251.6427	501.2940	251.1506	A	768.4727	384.7400	751.4461	376.2267			6
6	703.4258	352.2165	686.3992	343.7032	685.4152	343.2112	K	***697.4355***	349.2214	680.4090	340.7081			5
7	760.4472	380.7272	743.4207	372.2140	742.4366	371.7220	G	***513.3144***	257.1608	496.2878	248.6475			4
8	944.5684	472.7878	927.5418	464.2746	926.5578	463.7826	K	***456.2929***	228.6501	439.2663	220.1368			3
9	**1041.6212**	521.3142	1024.5946	512.8009	1023.6106	512.3089	P	***272.1717***	136.5895	255.1452	128.0762			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FGSKSKSATNLGR**
Found in **Q9H0H5**, Rac GTPase-activating protein 1 OS=Homo sapiens GN=RACGAP1 PE=1 SV=1

Match to Query 8290: 1481.813088 from(741.913820,2+) intensity(55957.7969)
Title: File2470 Spectrum8755 scans: 9996
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr13,14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



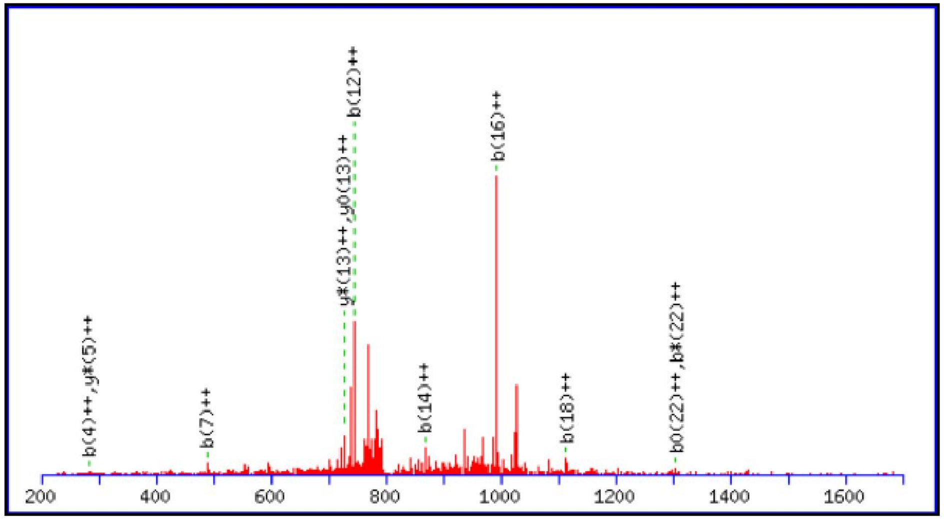
```
Monoisotopic mass of neutral peptide Mr(calc): 1481.8111
Fixed modifications: Carbamidomethyl (C) (apply to specif
Variable modifications:
K4      : Propionyl (K)
K6      : Propionyl-(13CD3)Methyl (K)
Ions Score: 78  Expect: 7.6e-006
Matches : 23/126 fragment ions using 26 most intense peak
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							13
2	205.0972	103.0522					G	***1335.7499***	668.3786	1318.7234	659.8653	1317.7394	659.3733	12
3	292.1292	146.5682			274.1186	137.5629	S	1278.7285	639.8679	1261.7019	631.3546	1260.7179	630.8626	11
4	476.2504	238.6288	459.2238	230.1155	458.2398	229.6235	K	***1191.6964***	596.3519	1174.6699	587.8386	1173.6859	587.3466	10
5	563.2824	282.1448	546.2558	273.6316	545.2718	273.1395	S	***1007.5753***	504.2913	990.5487	495.7780	989.5647	495.2860	9
6	765.4414	383.2243	748.4149	374.7111	747.4308	374.2191	K	***920.5432***	460.7753	903.5167	452.2620	902.5327	451.7700	8
7	**852.4734**	426.7404	835.4469	418.2271	834.4629	417.7351	S	***718.3842***	359.6958	701.3577	351.1825	700.3737	350.6905	7
8	923.5105	462.2589	906.4840	453.7456	905.5000	453.2536	A	***631.3522***	316.1797	614.3257	307.6665	613.3416	307.1745	6
9	**1024.5582**	512.7827	1007.5317	504.2695	1006.5477	503.7775	T	***560.3151***	280.6612	543.2885	272.1479	542.3045	271.6559	5
10	1138.6011	569.8042	1121.5746	561.2909	1120.5906	560.7989	N	***459.2674***	230.1373	442.2409	221.6241			4
11	**1251.6852**	626.3462	1234.6587	617.8330	1233.6746	617.3410	L	***345.2245***	173.1159	328.1979	164.6026			3
12	1308.7067	654.8570	1291.6801	646.3437	1290.6961	645.8517	G	***232.1404***	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KVDFDIKGDDLIVFLHIQKTGGTTFGR**
Found in **J3KP99**, Heparan-sulfate 6-O-sulfotransferase 2 OS=Homo sapiens GN=HS6ST2 PE=4 SV=1

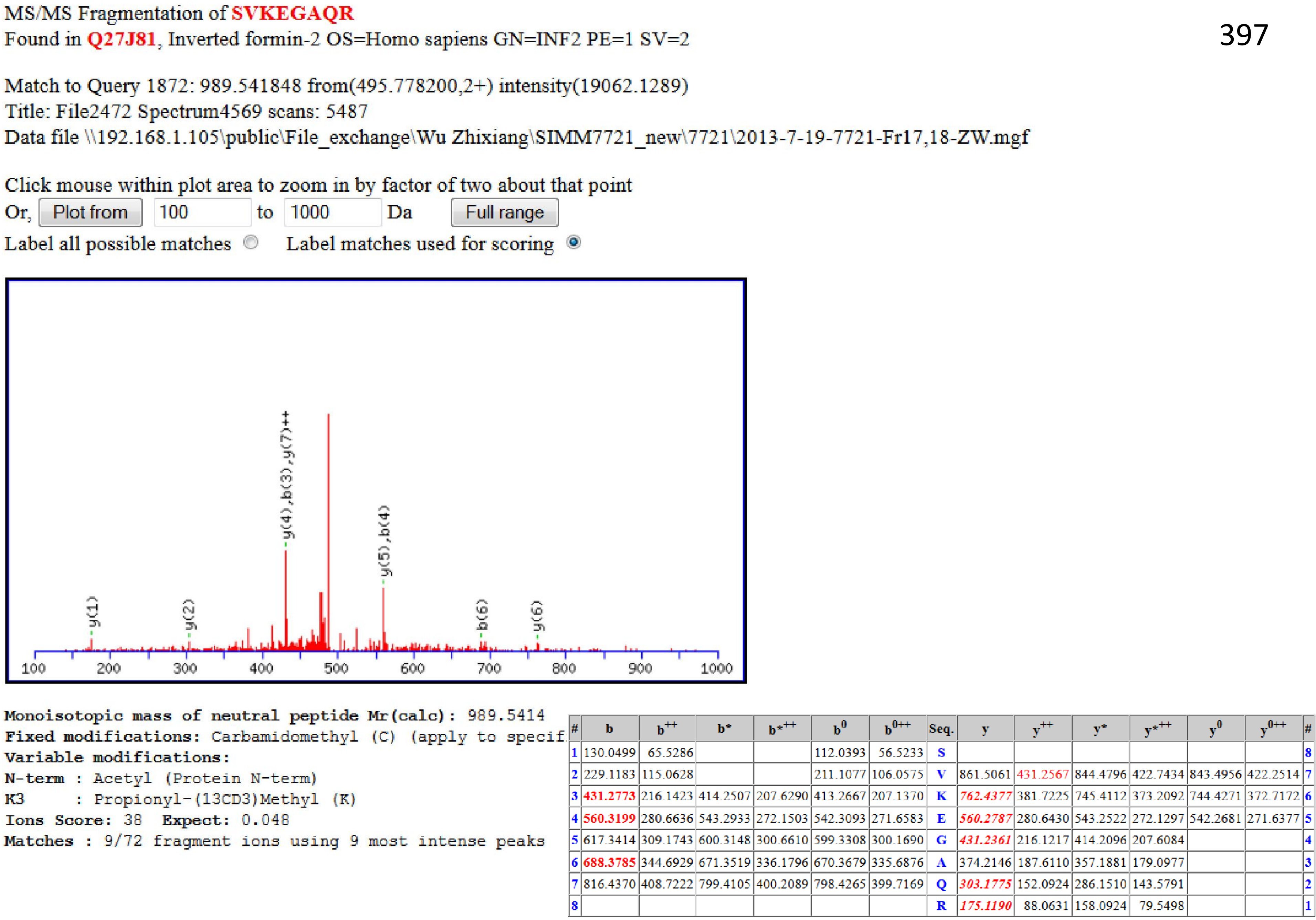
Match to Query 20874: 3205.751176 from(802.445070,4+) intensity(46632.4727)
Title: File2473 Spectrum15088 scans: 16639
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr19,20ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3205.7296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini or
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
K7      : Propionyl (K)
K19     : Propionyl (K)
Ions Score: 21  Expect: 4.2
Matches : 11/302 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							27
2	302.2347	151.6210	285.2082	143.1077			V	3004.5779	1502.7926	2987.5513	1494.2793	2986.5673	1493.7873	26
3	417.2616	209.1345	400.2351	200.6212	399.2511	200.1292	D	2905.5094	1453.2584	2888.4829	1444.7451	2887.4989	1444.2531	25
4	564.3301	***282.6687***	547.3035	274.1554	546.3195	273.6634	F	2790.4825	1395.7449	2773.4559	1387.2316	2772.4719	1386.7396	24
5	679.3570	340.1821	662.3305	331.6689	661.3464	331.1769	D	2643.4141	1322.2107	2626.3875	1313.6974	2625.4035	1313.2054	23
6	792.4411	396.7242	775.4145	388.2109	774.4305	387.7189	I	2528.3871	1264.6972	2511.3606	1256.1839	2510.3766	1255.6919	22
7	976.5622	***488.7848***	959.5357	480.2715	958.5517	479.7795	K	2415.3031	1208.1552	2398.2765	1199.6419	2397.2925	1199.1499	21
8	1033.5837	517.2955	1016.5572	508.7822	1015.5731	508.2902	G	2231.1819	1116.0946	2214.1553	1107.5813	2213.1713	1107.0893	20
9	1148.6107	574.8090	1131.5841	566.2957	1130.6001	565.8037	D	2174.1604	1087.5839	2157.1339	1079.0706	2156.1499	1078.5786	19
10	1263.6376	632.3224	1246.6110	623.8092	1245.6270	623.3172	D	2059.1335	1030.0704	2042.1069	1021.5571	2041.1229	1021.0651	18
11	1376.7217	688.8645	1359.6951	680.3512	1358.7111	679.8592	L	1944.1065	972.5569	1927.0800	964.0436	1926.0960	963.5516	17
12	1489.8057	***745.4065***	1472.7792	736.8932	1471.7952	736.4012	I	1831.0225	916.0149	1813.9959	907.5016	1813.0119	907.0096	16
13	1588.8741	794.9407	1571.8476	786.4274	1570.8636	785.9354	V	1717.9384	859.4728	1700.9119	850.9596	1699.9279	850.4676	15
14	1735.9426	***868.4749***	1718.9160	859.9616	1717.9320	859.4696	F	1618.8700	809.9386	1601.8435	801.4254	1600.8594	800.9334	14
15	1849.0266	925.0169	1832.0001	916.5037	1831.0161	916.0117	L	1471.8016	736.4044	1454.7750	727.8912	1453.7910	727.3992	13
16	1986.0855	***993.5464***	1969.0590	985.0331	1968.0750	984.5411	H	1358.7175	679.8624	1341.6910	671.3491	1340.7070	670.8571	12
17	2099.1696	1050.0884	2082.1430	1041.5752	2081.1590	1041.0832	I	1221.6586	611.3329	1204.6321	602.8197	1203.6480	602.3277	11
18	2227.2282	***1114.1177***	2210.2016	1105.6044	2209.2176	1105.1124	Q	1108.5746	554.7909	1091.5480	546.2776	1090.5640	545.7856	10
19	2411.3493	1206.1783	2394.3228	1197.6650	2393.3388	1197.1730	K	980.5160	490.7616	963.4894	482.2483	962.5054	481.7563	9
20	2512.3970	1256.7022	2495.3705	1248.1889	2494.3865	1247.6969	T	796.3948	398.7010	779.3682	390.1878	778.3842	389.6958	8
21	2569.4185	1285.2129	2552.3919	1276.6996	2551.4079	1276.2076	G	695.3471	348.1772	678.3206	339.6639	677.3366	339.1719	7
22	2626.4400	1313.7236	2609.4134	1305.2103	2608.4294	1304.7183	G	638.3257	319.6665	621.2991	311.1532	620.3151	310.6612	6
23	2727.4876	1364.2475	2710.4611	1355.7342	2709.4771	1355.2422	T	581.3042	291.1557	564.2776	282.6425	563.2936	282.1504	5
24	2828.5353	1414.7713	2811.5088	1406.2580	2810.5247	1405.7660	T	480.2565	240.6319	463.2300	232.1186	462.2459	231.6266	4
25	2975.6037	1488.3055	2958.5772	1479.7922	2957.5932	1479.3002	F	379.2088	190.1081	362.1823	181.5948			3
26	3032.6252	1516.8162	3015.5986	1508.3030	3014.6146	1507.8110	G	232.1404	116.5738	215.1139	108.0606			2
27							R	175.1190	88.0631	158.0924	79.5498			1



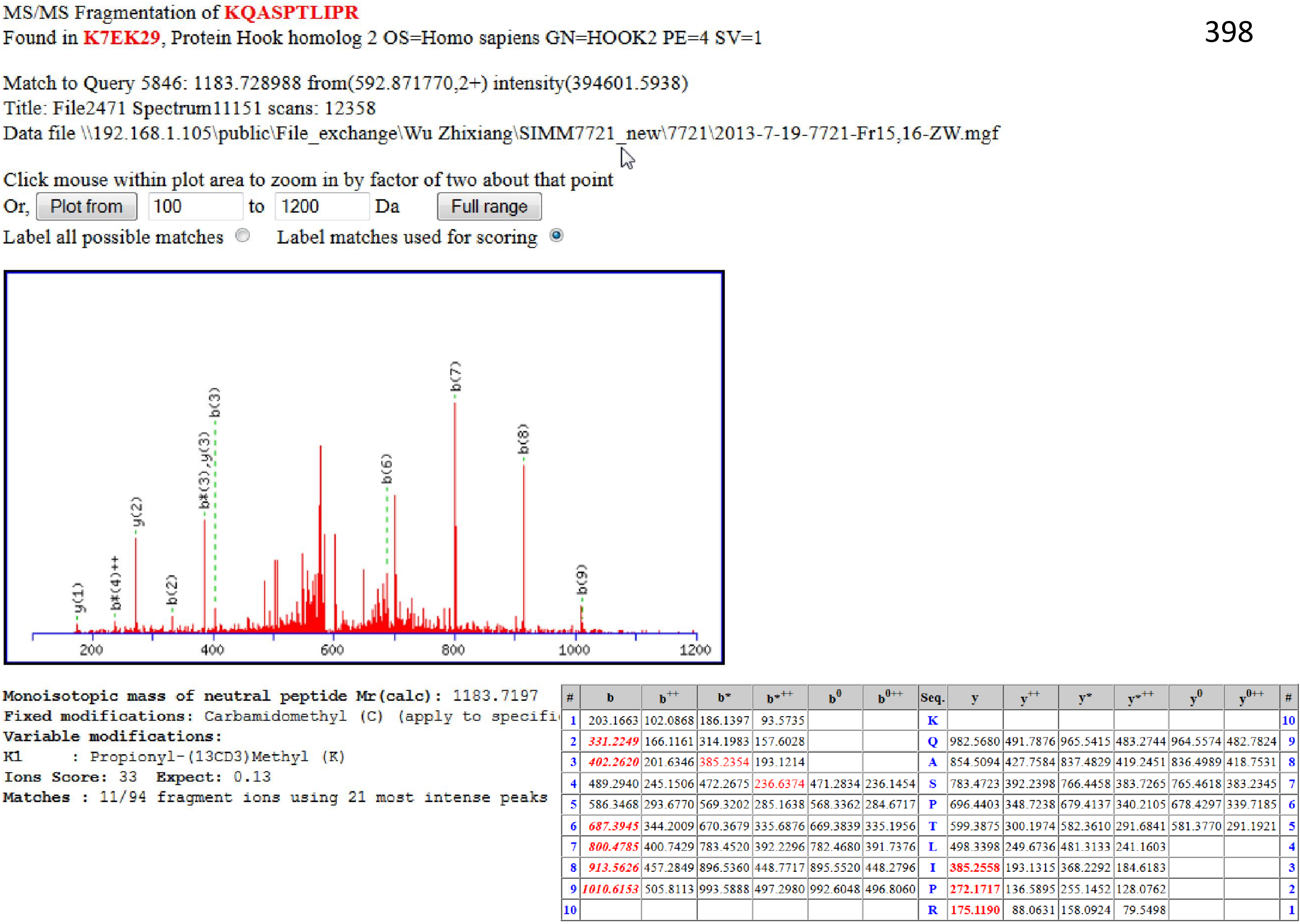
MS/MS Fragmentation of SVKEGAQR
Found in Q27J81, Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2

Match to Query 1872: 989.541848 from(495.778200,2+) intensity(19062.1289)
Title: File2472 Spectrum4569 scans: 5487
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr17,18-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 989.5414
Fixed modifications: Carbamidomethyl (C) (apply to specif
Variable modifications:
N-term : Acetyl (Protein N-term)
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 38 **Expect:** 0.048
Matches : 9/72 fragment ions using 9 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	S							8
2	229.1183	115.0628			211.1077	106.0575	V	861.5061	431.2567	844.4796	422.7434	843.4956	422.2514	7
3	**431.2773**	216.1423	414.2507	207.6290	413.2667	207.1370	K	***762.4377***	381.7225	745.4112	373.2092	744.4271	372.7172	6
4	**560.3199**	280.6636	543.2933	272.1503	542.3093	271.6583	E	***560.2787***	280.6430	543.2522	272.1297	542.2681	271.6377	5
5	617.3414	309.1743	600.3148	300.6610	599.3308	300.1690	G	***431.2361***	216.1217	414.2096	207.6084			4
6	**688.3785**	344.6929	671.3519	336.1796	670.3679	335.6876	A	374.2146	187.6110	357.1881	179.0977			3
7	816.4370	408.7222	799.4105	400.2089	798.4265	399.7169	Q	***303.1775***	152.0924	286.1510	143.5791			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KQASPTLIPR**
Found in **K7EK29**, Protein Hook homolog 2 OS=Homo sapiens GN=HOOK2 PE=4 SV=1

Match to Query 5846: 1183.728988 from(592.871770,2+) intensity(394601.5938)
Title: File2471 Spectrum11151 scans: 12358
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr15,16-ZW.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 ●

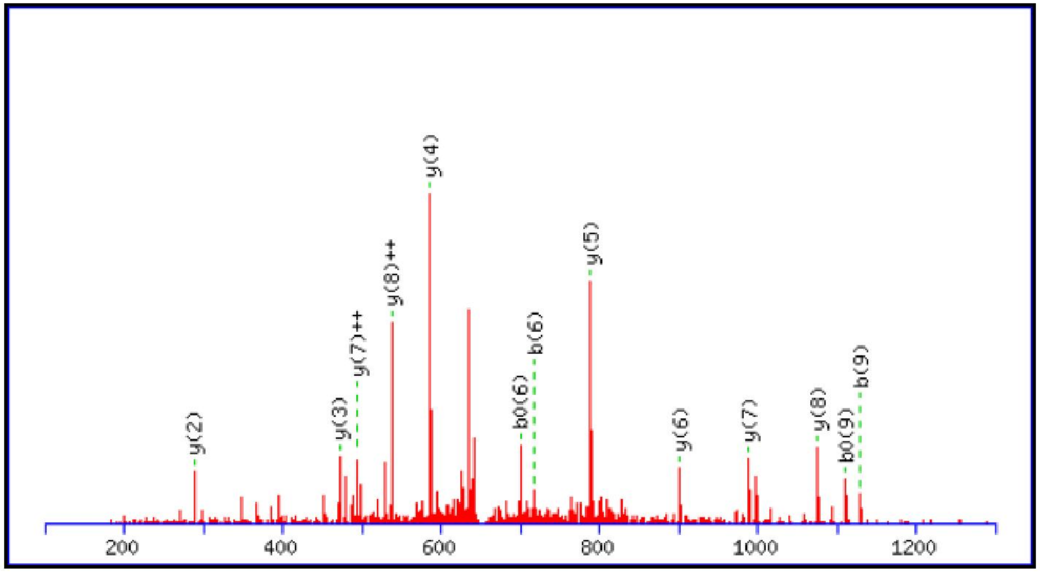
Monoisotopic mass of neutral peptide Mr(calc): 1183.7197
Fixed modifications: Carbamidomethyl (C) (apply to specifi
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
Ions Score: 33 **Expect:** 0.13
Matches : 11/94 fragment ions using 21 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	203.1663	102.0868	186.1397	93.5735			K							10
2	***331.2249***	166.1161	314.1983	157.6028			Q	982.5680	491.7876	965.5415	483.2744	964.5574	482.7824	9
3	***402.2620***	201.6346	385.2354	193.1214			A	854.5094	427.7584	837.4829	419.2451	836.4989	418.7531	8
4	489.2940	245.1506	472.2675	236.6374	471.2834	236.1454	S	783.4723	392.2398	766.4458	383.7265	765.4618	383.2345	7
5	586.3468	293.6770	569.3202	285.1638	568.3362	284.6717	P	696.4403	348.7238	679.4137	340.2105	678.4297	339.7185	6
6	***687.3945***	344.2009	670.3679	335.6876	669.3839	335.1956	T	599.3875	300.1974	582.3610	291.6841	581.3770	291.1921	5
7	***800.4785***	400.7429	783.4520	392.2296	782.4680	391.7376	L	498.3398	249.6736	481.3133	241.1603			4
8	***913.5626***	457.2849	896.5360	448.7717	895.5520	448.2796	I	**385.2558**	193.1315	368.2292	184.6183			3
9	***1010.6153***	505.8113	993.5888	497.2980	992.6048	496.8060	P	**272.1717**	136.5895	255.1452	128.0762			2
10							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **EVSSLKNKLR**
Found in **P35579**, Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

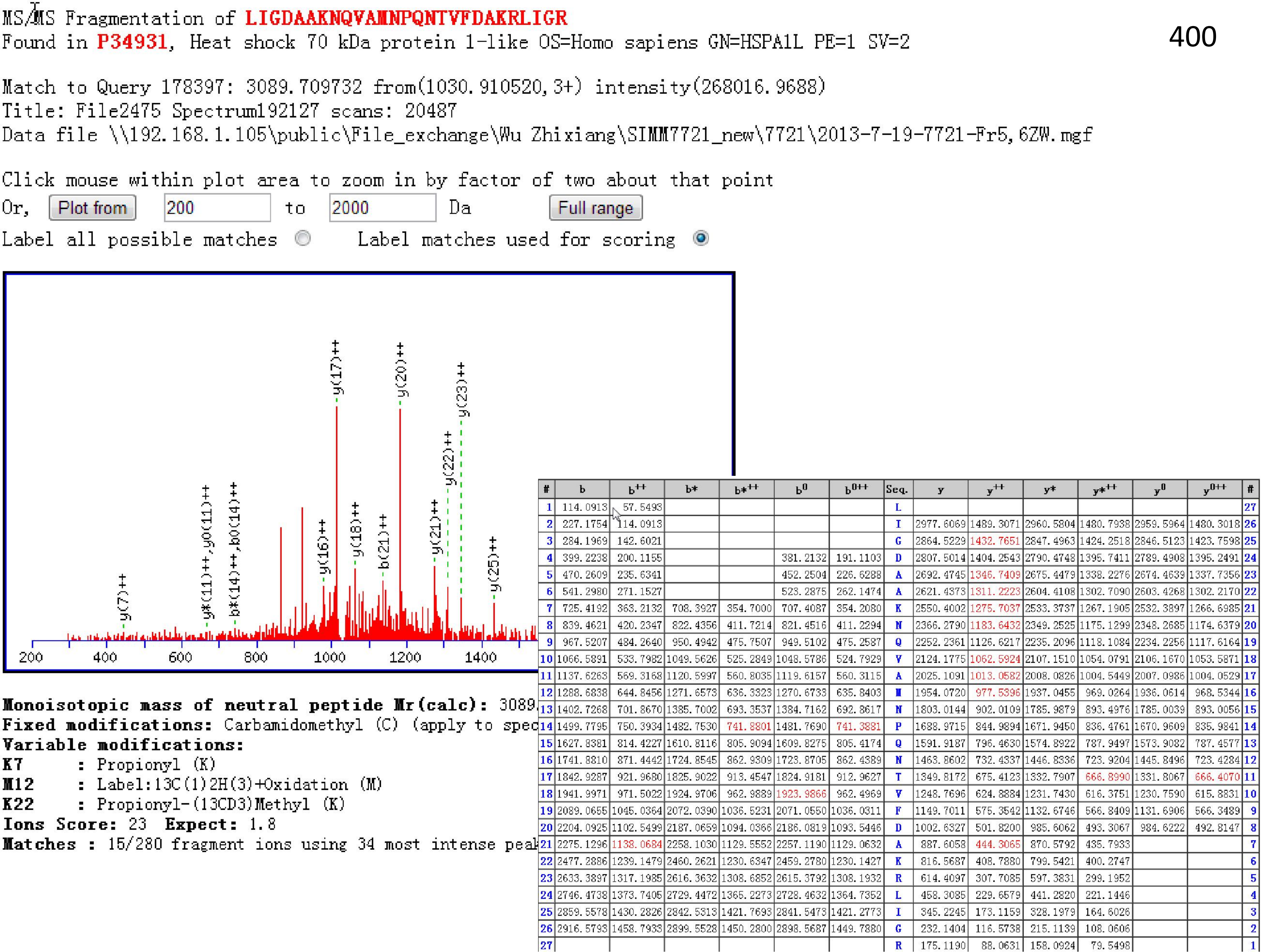
Match to Query 7849: 1302.779768 from(652.397160,2+) intensity(1046549.3750)
Title: File2471 Spectrum13819 scans: 15204
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr15,16-ZW.mgf

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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1302.7780
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K6      : Propionyl-(13CD3)Methyl (K)
K8      : Propionyl (K)
Ions Score: 47  Expect: 0.0061
Matches : 13/86 fragment ions using 23 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	229.1183	115.0628			211.1077	106.0575	V	1174.7427	587.8750	1157.7161	579.3617	1156.7321	578.8697	9
3	316.1503	158.5788			298.1397	149.5735	S	***1075.6743***	538.3408	1058.6477	529.8275	1057.6637	529.3355	8
4	403.1823	202.0948			385.1718	193.0895	S	***988.6422***	494.8248	971.6157	486.3115	970.6317	485.8195	7
5	516.2664	258.6368			498.2558	249.6316	L	***901.6102***	451.3087	884.5836	442.7955			6
6	**718.4254**	359.7163	701.3989	351.2031	700.4149	350.7111	K	***788.5261***	394.7667	771.4996	386.2534			5
7	832.4683	416.7378	815.4418	408.2245	814.4578	407.7325	N	***586.3671***	293.6872	569.3406	285.1739			4
8	1016.5895	508.7984	999.5630	500.2851	998.5790	499.7931	K	***472.3242***	236.6657	455.2976	228.1525			3
9	**1129.6736**	565.3404	1112.6470	556.8272	1111.6630	556.3351	L	***288.2030***	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LIGDAAKNQVAMNPQNTVFDAKRLIGR**
Found in **P34931**, Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2

Match to Query 178397: 3089.709732 from(1030.910520,3+) intensity(268016.9688)
Title: File2475 Spectrum192127 scans: 20487
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr5,6ZW.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 ●

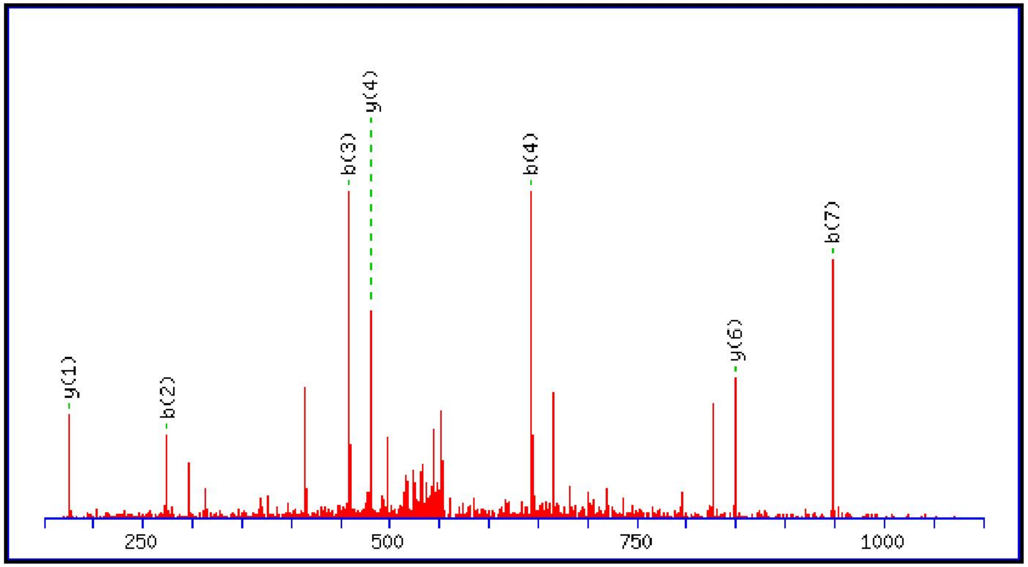
Monoisotopic mass of neutral peptide Mr(calc): 3089.
Fixed modifications: Carbamidomethyl (C) (apply to spec
Variable modifications:
K7 : Propionyl (K)
M12 : Label:13C(1)2H(3)+Oxidation (M)
K22 : Propionyl-(13CD3)Methyl (K)
Ions Score: 23 **Expect:** 1.8
Matches : 15/280 fragment ions using 34 most intense peak

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							27
2	227.1754	114.0913					I	2977.6069	1489.3071	2960.5804	1480.7938	2959.5964	1480.3018	26
3	284.1969	142.6021					G	2864.5229	1432.7651	2847.4963	1424.2518	2846.5123	1423.7598	25
4	399.2238	200.1155			381.2132	191.1103	D	2807.5014	1404.2543	2790.4748	1395.7411	2789.4908	1395.2491	24
5	470.2609	235.6341			452.2504	226.6288	A	2692.4745	1346.7409	2675.4479	1338.2276	2674.4639	1337.7356	23
6	541.2980	271.1527			523.2875	262.1474	A	2621.4373	1311.2223	2604.4108	1302.7090	2603.4268	1302.2170	22
7	725.4192	363.2132	708.3927	354.7000	707.4087	354.2080	K	2550.4002	1275.7037	2533.3737	1267.1905	2532.3897	1266.6985	21
8	839.4621	420.2347	822.4356	411.7214	821.4516	411.2294	N	2366.2790	1183.6432	2349.2525	1175.1299	2348.2685	1174.6379	20
9	967.5207	484.2640	950.4942	475.7507	949.5102	475.2587	Q	2252.2361	1126.6217	2235.2096	1118.1084	2234.2256	1117.6164	19
10	1066.5891	533.7982	1049.5626	525.2849	1048.5786	524.7929	V	2124.1775	1062.5924	2107.1510	1054.0791	2106.1670	1053.5871	18
11	1137.6263	569.3168	1120.5997	560.8035	1119.6157	560.3115	A	2025.1091	1013.0582	2008.0826	1004.5449	2007.0986	1004.0529	17
12	1288.6838	644.8456	1271.6573	636.3323	1270.6733	635.8403	M	1954.0720	977.5396	1937.0455	969.0264	1936.0614	968.5344	16
13	1402.7268	701.8670	1385.7002	693.3537	1384.7162	692.8617	N	1803.0144	902.0109	1785.9879	893.4976	1785.0039	893.0056	15
14	1499.7795	750.3934	1482.7530	741.8801	1481.7690	741.3881	P	1688.9715	844.9894	1671.9450	836.4761	1670.9609	835.9841	14
15	1627.8381	814.4227	1610.8116	805.9094	1609.8275	805.4174	Q	1591.9187	796.4630	1574.8922	787.9497	1573.9082	787.4577	13
16	1741.8810	871.4442	1724.8545	862.9309	1723.8705	862.4389	N	1463.8602	732.4337	1446.8336	723.9204	1445.8496	723.4284	12
17	1842.9287	921.9680	1825.9022	913.4547	1824.9181	912.9627	T	1349.8172	675.4123	1332.7907	666.8990	1331.8067	666.4070	11
18	1941.9971	971.5022	1924.9706	962.9889	1923.9866	962.4969	V	1248.7696	624.8884	1231.7430	616.3751	1230.7590	615.8831	10
19	2089.0655	1045.0364	2072.0390	1036.5231	2071.0550	1036.0311	F	1149.7011	575.3542	1132.6746	566.8409	1131.6906	566.3489	9
20	2204.0925	1102.5499	2187.0659	1094.0366	2186.0819	1093.5446	D	1002.6327	501.8200	985.6062	493.3067	984.6222	492.8147	8
21	2275.1296	1138.0684	2258.1030	1129.5552	2257.1190	1129.0632	A	887.6058	444.3065	870.5792	435.7933			7
22	2477.2886	1239.1479	2460.2621	1230.6347	2459.2780	1230.1427	K	816.5687	408.7880	799.5421	400.2747			6
23	2633.3897	1317.1985	2616.3632	1308.6852	2615.3792	1308.1932	R	614.4097	307.7085	597.3831	299.1952			5
24	2746.4738	1373.7405	2729.4472	1365.2273	2728.4632	1364.7352	L	458.3085	229.6579	441.2820	221.1446			4
25	2859.5578	1430.2826	2842.5313	1421.7693	2841.5473	1421.2773	I	345.2245	173.1159	328.1979	164.6026			3
26	2916.5793	1458.7933	2899.5528	1450.2800	2898.5687	1449.7880	G	232.1404	116.5738	215.1139	108.0606			2
27							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KAKKAHPR**
Found in **E9PL73**, Protein FAM9B OS=Homo sapiens GN=FAM9B PE=2 SV=1

Match to Query 34632: 1120.697488 from(561.356020,2+) intensity(202018.6406)
Title: File2475 Spectrum181455 scans: 8846
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr5,6ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



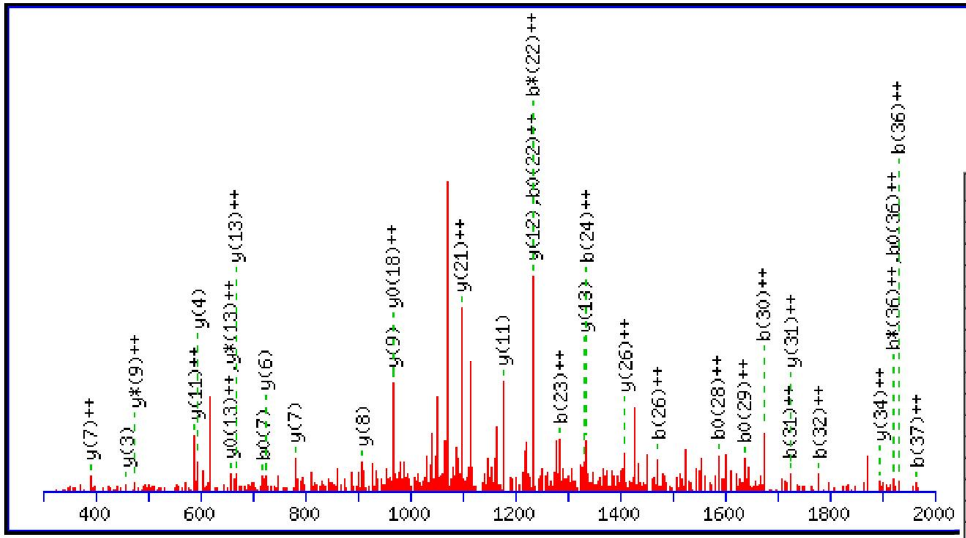
Monoisotopic mass of neutral peptide Mr(calc): 1120.6989
Fixed modifications: Carbamidomethyl (C) (apply to specified
Variable modifications:
K1 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
K4 : Propionyl (K)
Ions Score: 26 **Expect:** 0.47
Matches : 7/56 fragment ions using 10 most intense peaks (hel

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	203.1663	102.0868	186.1397	93.5735	K					8
2	***274.2034***	137.6053	257.1769	129.0921	A	919.5472	460.2772	902.5207	451.7640	7
3	***458.3246***	229.6659	441.2980	221.1527	K	**848.5101**	424.7587	831.4835	416.2454	6
4	***642.4458***	321.7265	625.4192	313.2132	K	664.3889	332.6981	647.3624	324.1848	5
5	713.4829	357.2451	696.4563	348.7318	A	**480.2677**	240.6375	463.2412	232.1242	4
6	850.5418	425.7745	833.5152	417.2613	H	409.2306	205.1190	392.2041	196.6057	3
7	***947.5945***	474.3009	930.5680	465.7876	P	272.1717	136.5895	255.1452	128.0762	2
8					R	**175.1190**	88.0631	158.0924	79.5498	1

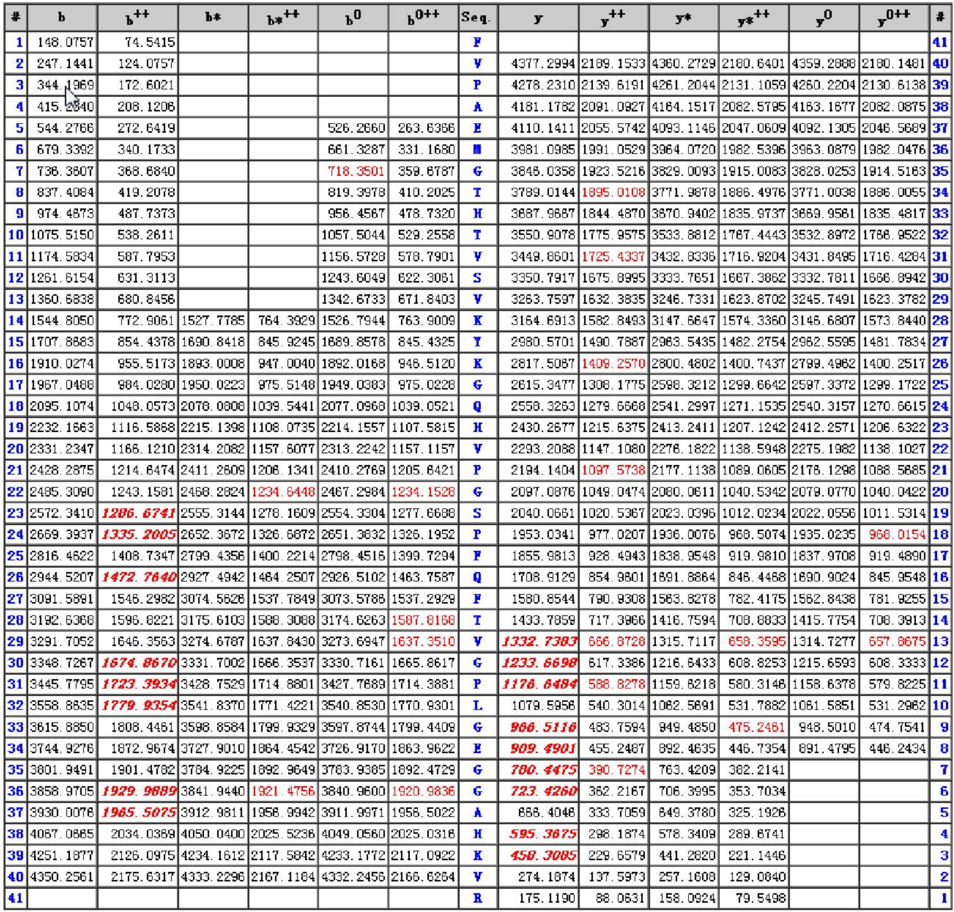
MS/MS Fragmentation of **FVPAEMGTHTVSVKYKGQHVPGSPFQFTVGPLGEGGAHKVR**
Found in **Q5HY54**, Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1

Match to Query 191879: 4523.332696 from(1131.840450,4+) intensity(0.0000)
Title: File2475 Spectrum188372 scans: 16226
Data file \\192.168.1.105\public\File_exchange\Wu Zhixiang\SIMM7721_new\7721\2013-7-19-7721-Fr5,6ZW.mgf

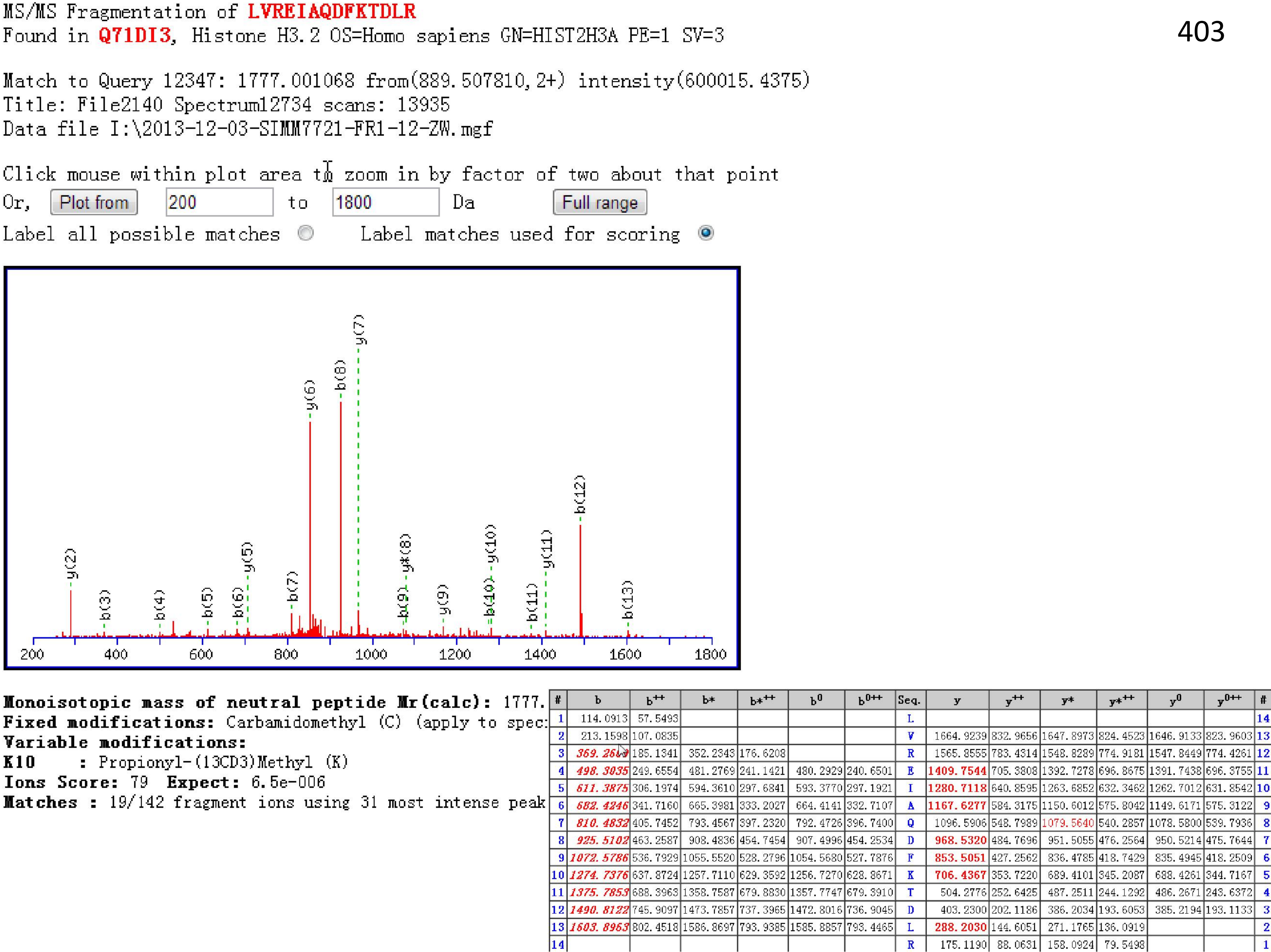
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 4523.3606
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or te
Variable modifications:
M6 : Label:13C(1)2H(3) (M)
K14 : Propionyl (K)
K16 : Propionyl-(13CD3)Methyl (K)
K39 : Propionyl (K)
Ions Score: 43 **Expect:** 0.034
Matches : 35/432 fragment ions using 51 most intense peaks (help)



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							41
2	247.1441	124.0757					V	4377.2994	2189.1533	4360.2729	2180.6401	4359.2888	2180.1481	40
3	344.1969	172.6021					P	4278.2310	2139.6191	4261.2044	2131.1059	4260.2204	2130.6138	39
4	415.2340	208.1206					A	4181.1782	2091.0927	4164.1517	2082.5795	4163.1677	2082.0875	38
5	544.2766	272.6419			526.2660	263.6366	E	4110.1411	2055.5742	4093.1146	2047.0609	4092.1305	2046.5689	37
6	679.3392	340.1733			661.3287	331.1680	M	3981.0985	1991.0529	3964.0720	1982.5396	3963.0879	1982.0476	36
7	736.3607	368.6840			718.3501	359.6787	G	3846.0358	1923.5216	3829.0093	1915.0083	3828.0253	1914.5163	35
8	837.4084	419.2078			819.3978	410.2025	T	3789.0144	1895.0108	3771.9878	1886.4976	3771.0038	1886.0055	34
9	974.4673	487.7373			956.4567	478.7320	H	3687.9667	1844.4870	3670.9402	1835.9737	3669.9561	1835.4817	33
10	1075.5150	538.2611			1057.5044	529.2558	T	3550.9078	1775.9575	3533.8812	1767.4443	3532.8972	1766.9522	32
11	1174.5834	587.7953			1156.5728	578.7901	V	3449.8601	1725.4337	3432.8336	1716.9204	3431.8495	1716.4284	31
12	1261.6154	631.3113			1243.6049	622.3061	S	3350.7917	1675.8995	3333.7651	1667.3862	3332.7811	1666.8942	30
13	1360.6838	680.8456			1342.6733	671.8403	V	3263.7597	1632.3835	3246.7331	1623.8702	3245.7491	1623.3782	29
14	1544.8050	772.9061	1527.7785	764.3929	1526.7944	763.9009	K	3164.6913	1582.8493	3147.6647	1574.3360	3146.6807	1573.8440	28
15	1707.8683	854.4378	1690.8418	845.9245	1689.8578	845.4325	Y	2980.5701	1490.7887	2963.5435	1482.2754	2962.5595	1481.7834	27
16	1910.0274	955.5173	1893.0008	947.0040	1892.0168	946.5120	K	2817.5067	1409.2570	2800.4802	1400.7437	2799.4962	1400.2517	26
17	1967.0488	984.0280	1950.0223	975.5148	1949.0383	975.0228	G	2615.3477	1308.1775	2598.3212	1299.6642	2597.3372	1299.1722	25
18	2095.1074	1048.0573	2078.0808	1039.5441	2077.0968	1039.0521	Q	2558.3263	1279.6668	2541.2997	1271.1535	2540.3157	1270.6615	24
19	2232.1663	1116.5868	2215.1398	1108.0735	2214.1557	1107.5815	H	2430.2677	1215.6375	2413.2411	1207.1242	2412.2571	1206.6322	23
20	2331.2347	1166.1210	2314.2082	1157.6077	2313.2242	1157.1157	V	2293.2088	1147.1080	2276.1822	1138.5948	2275.1982	1138.1027	22
21	2428.2875	1214.6474	2411.2609	1206.1341	2410.2769	1205.6421	P	2194.1404	1097.5738	2177.1138	1089.0605	2176.1298	1088.5685	21
22	2485.3090	1243.1581	2468.2824	1234.6448	2467.2984	1234.1528	G	2097.0876	1049.0474	2080.0611	1040.5342	2079.0770	1040.0422	20
23	2572.3410	**1286.6741**	2555.3144	1278.1609	2554.3304	1277.6688	S	2040.0661	1020.5367	2023.0396	1012.0234	2022.0556	1011.5314	19
24	2669.3937	**1335.2005**	2652.3672	1326.6872	2651.3832	1326.1952	P	1953.0341	977.0207	1936.0076	968.5074	1935.0235	968.0154	18
25	2816.4622	1408.7347	2799.4356	1400.2214	2798.4516	1399.7294	F	1855.9813	928.4943	1838.9548	919.9810	1837.9708	919.4890	17
26	2944.5207	**1472.7640**	2927.4942	1464.2507	2926.5102	1463.7587	Q	1708.9129	854.9601	1691.8864	846.4468	1690.9024	845.9548	16
27	3091.5891	1546.2982	3074.5626	1537.7849	3073.5786	1537.2929	F	1580.8544	790.9308	1563.8278	782.4175	1562.8438	781.9255	15
28	3192.6368	1596.8221	3175.6103	1588.3088	3174.6263	1587.8168	T	1433.7859	717.3966	1416.7594	708.8833	1415.7754	708.3913	14
29	3291.7052	1646.3563	3274.6787	1637.8430	3273.6947	1637.3510	V	**1332.7383**	666.8728	1315.7117	658.3595	1314.7277	657.8675	13
30	3348.7267	**1674.8670**	3331.7002	1666.3537	3330.7161	1665.8617	G	**1233.6698**	617.3386	1216.6433	608.8253	1215.6593	608.3333	12
31	3445.7795	**1723.3934**	3428.7529	1714.8801	3427.7689	1714.3881	P	**1176.6484**	588.8278	1159.6218	580.3146	1158.6378	579.8225	11
32	3558.8635	**1779.9354**	3541.8370	1771.4221	3540.8530	1770.9301	L	1079.5956	540.3014	1062.5691	531.7882	1061.5851	531.2962	10
33	3615.8850	1808.4461	3598.8584	1799.9329	3597.8744	1799.4409	G	**966.5116**	483.7594	949.4850	475.2461	948.5010	474.7541	9
34	3744.9276	1872.9674	3727.9010	1864.4542	3726.9170	1863.9622	E	**909.4901**	455.2487	892.4635	446.7354	891.4795	446.2434	8
35	3801.9491	1901.4782	3784.9225	1892.9649	3783.9385	1892.4729	G	**780.4475**	390.7274	763.4209	382.2141			7
36	3858.9705	**1929.9889**	3841.9440	1921.4756	3840.9600	1920.9836	G	**723.4260**	362.2167	706.3995	353.7034			6
37	3930.0076	**1965.5075**	3912.9811	1956.9942	3911.9971	1956.5022	A	666.4046	333.7059	649.3780	325.1926			5
38	4067.0665	2034.0369	4050.0400	2025.5236	4049.0560	2025.0316	H	**595.3675**	298.1874	578.3409	289.6741			4
39	4251.1877	2126.0975	4234.1612	2117.5842	4233.1772	2117.0922	K	**458.3085**	229.6579	441.2820	221.1446			3
40	4350.2561	2175.6317	4333.2296	2167.1184	4332.2456	2166.6264	V	274.1874	137.5973	257.1608	129.0840			2
41							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LVREIAQDFKTDLR**
Found in **Q71DI3**, Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3

Match to Query 12347: 1777.001068 from(889.507810,2+) intensity(600015.4375)
Title: File2140 Spectrum12734 scans: 13935
Data file I:\2013-12-03-SIMM7721-FR1-12-ZW.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 ●

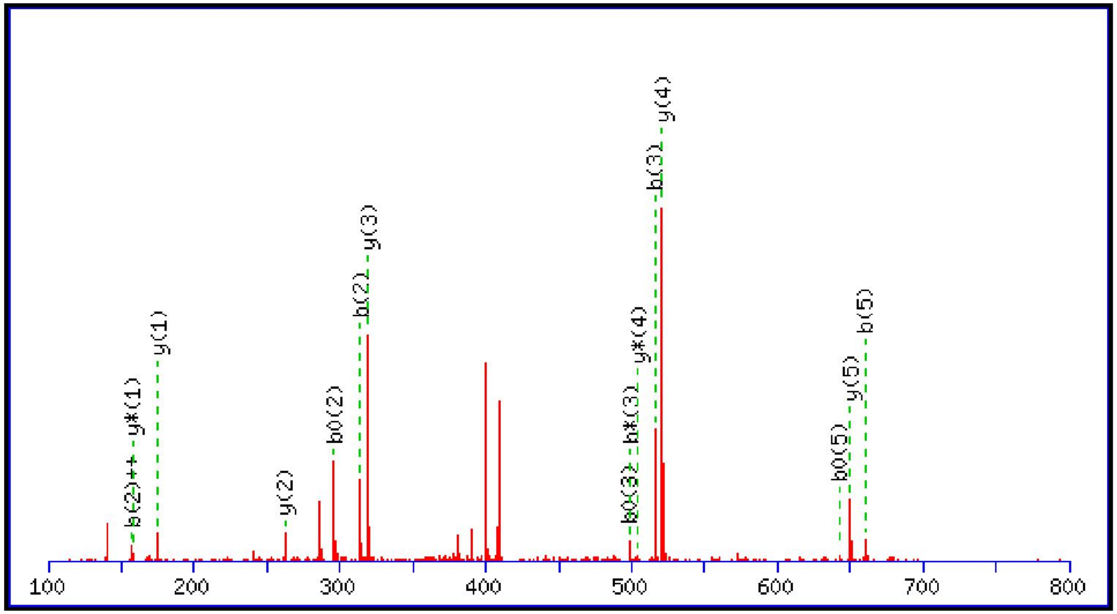
Monoisotopic mass of neutral peptide Mr(calc): 1777.
Fixed modifications: Carbamidomethyl (C) (apply to spec:
Variable modifications:
K10 : Propionyl-(13CD3)Methyl (K)
Ions Score: 79 **Expect:** 6.5e-006
Matches : 19/142 fragment ions using 31 most intense peak

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							14
2	213.1598	107.0835					V	1664.9239	832.9656	1647.8973	824.4523	1646.9133	823.9603	13
3	***369.26[illegible]***	185.1341	352.2343	176.6208			R	1565.8555	783.4314	1548.8289	774.9181	1547.8449	774.4261	12
4	***498.3035***	249.6554	481.2769	241.1421	480.2929	240.6501	E	**1409.7544**	705.3808	1392.7278	696.8675	1391.7438	696.3755	11
5	***611.3875***	306.1974	594.3610	297.6841	593.3770	297.1921	I	**1280.7118**	640.8595	1263.6852	632.3462	1262.7012	631.8542	10
6	***682.4246***	341.7160	665.3981	333.2027	664.4141	332.7107	A	**1167.6277**	584.3175	1150.6012	575.8042	1149.6171	575.3122	9
7	***810.4832***	405.7452	793.4567	397.2320	792.4726	396.7400	Q	1096.5906	548.7989	1079.5640	540.2857	1078.5800	539.7936	8
8	***925.5102***	463.2587	908.4836	454.7454	907.4996	454.2534	D	**968.5320**	484.7696	951.5055	476.2564	950.5214	475.7644	7
9	***1072.5786***	536.7929	1055.5520	528.2796	1054.5680	527.7876	F	**853.5051**	427.2562	836.4785	418.7429	835.4945	418.2509	6
10	***1274.7376***	637.8724	1257.7110	629.3592	1256.7270	628.8671	K	**706.4367**	353.7220	689.4101	345.2087	688.4261	344.7167	5
11	***1375.7853***	688.3963	1358.7587	679.8830	1357.7747	679.3910	T	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
12	***1490.8122***	745.9097	1473.7857	737.3965	1472.8016	736.9045	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
13	***1603.8963***	802.4518	1586.8697	793.9385	1585.8857	793.4465	L	**288.2030**	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **KEKGSR**
Found in **B4DTG2**, Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=2 SV=1

Match to Query 1118: 833.487948 from(417.751250,2+) intensity(336946.6563)
Title: File2140 Spectrum2369 scans: 3105
Data file I:\2013-12-03-SIMM7721-FR1-12-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



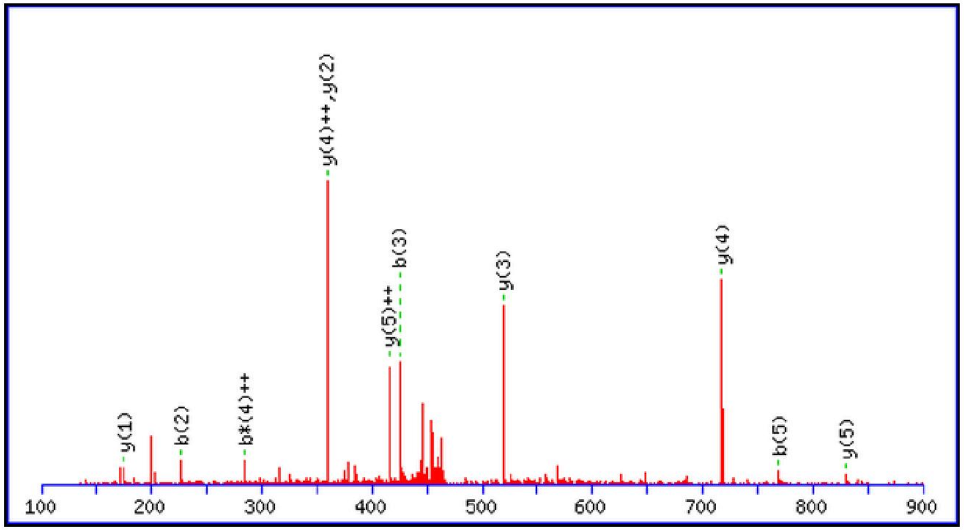
Monoisotopic mass of neutral peptide Mr(calc): 833.4879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K3 : Propionyl-(13CD3)Methyl (K)
Ions Score: 35 **Expect:** 0.098
Matches : 15/56 fragment ions using 26 most intense peak

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							6
2	**314.1710**	157.5892	297.1445	149.0759	296.1605	148.5839	E	***650.3741***	325.6907	633.3475	317.1774	632.3635	316.6854	5
3	**516.3301**	258.6687	499.3035	250.1554	498.3195	249.6634	K	***521.3315***	261.1694	504.3049	252.6561	503.3209	252.1641	4
4	573.3515	287.1794	556.3250	278.6661	555.3410	278.1741	G	***319.1724***	160.0899	302.1459	151.5766	301.1619	151.0846	3
5	**660.3836**	330.6954	643.3570	322.1821	642.3730	321.6901	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
6							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LLKCKR**
Found in **P17568|NDUB7_HUMAN** in **Uniprot_Human**, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Homo sapiens GN=NDUFB7 PE=1 SV=4

Match to Query 2324: 942.567908 from(472.291230,2+) intensity(57368.6758) rtinseconds(1352) scans(8425) index(7488)
Title: File1029 Spectrum7615 scans: 8425
Data file 2013-7-21-liver-Ca-Fr7,8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



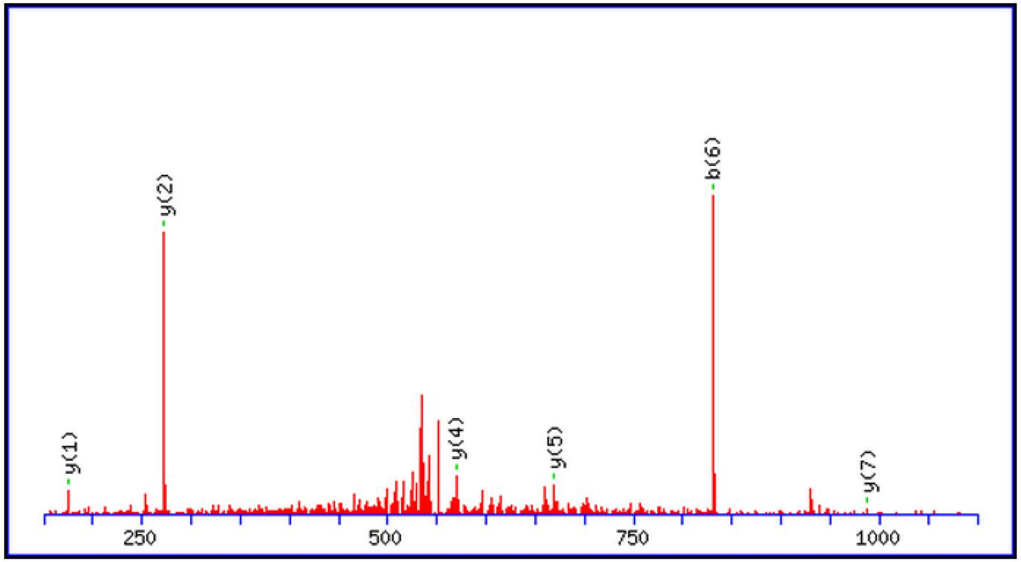
```
Monoisotopic mass of neutral peptide Mr(calc): 942.5684
Fixed modifications: Carbamidom
Variable modifications:
K3      : Propionyl-Methylation
K5      : Propionyl (K)
Ions Score: 26  Expect: 0.94
Matches : 11/36 fragment ions u
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			L					6
2	**227.1754**	114.0913			L	***830.4917***	415.7495	813.4651	407.2362	5
3	**425.3122**	213.1598	408.2857	204.6465	K	***717.4076***	359.2074	700.3811	350.6942	4
4	585.3429	293.1751	568.3163	284.6618	C	***519.2708***	260.1390	502.2442	251.6258	3
5	**769.4641**	385.2357	752.4375	376.7224	K	***359.2401***	180.1237	342.2136	171.6104	2
6					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **NRYVKVPR**
Found in **C9JQE1|C9JQE1_HUMAN** in **Uniprot_Human**, Mitochondrial inner membrane protease subunit 2 OS=Homo sapiens GN=IMMP2L PE=2 SV=1

Match to Query 4410: 1100.635708 from(551.325130,2+) intensity(18755.7891) rtinseconds(1395) scans(8723) index(7755)
Title: File1029 Spectrum7895 scans: 8723
Data file 2013-7-21-liver-Ca-Fr7,8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



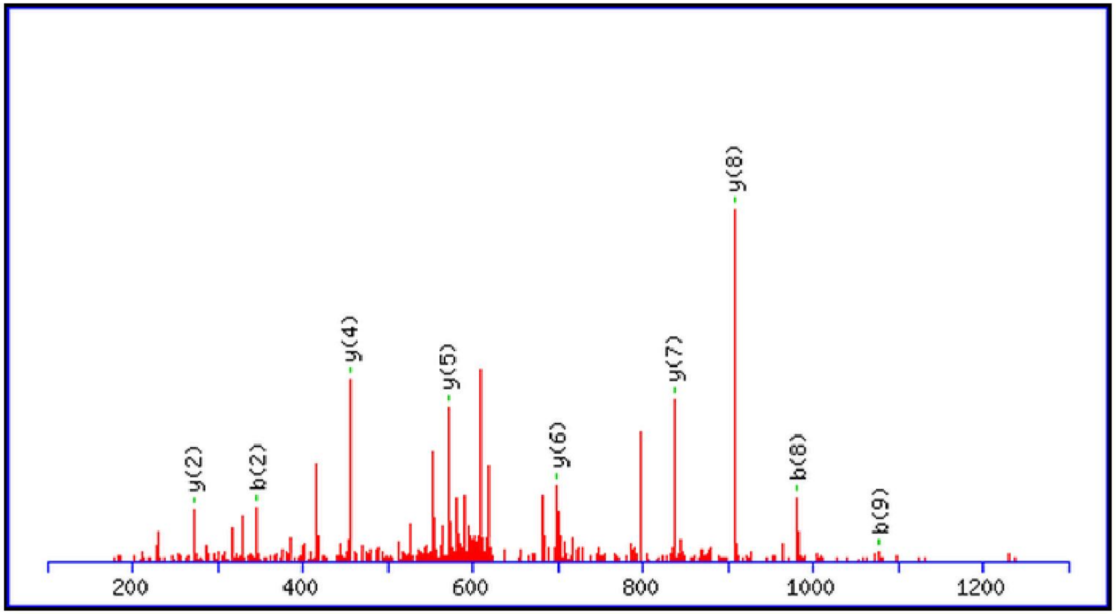
```
Monoisotopic mass of neutral peptide Mr(calc): 11
Fixed modifications: Carbamidomethyl (C) (apply t
Variable modifications:
K5      : Propionyl-Methylation (K)
Ions Score: 31  Expect: 0.39
Matches : 6/56 fragment ions using 10 most intens
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	115.0502	58.0287	98.0237	49.5155	N					8
2	271.1513	136.0793	254.1248	127.5660	R	***987.6098***	494.3085	970.5833	485.7953	7
3	434.2146	217.6110	417.1881	209.0977	Y	831.5087	416.2580	814.4822	407.7447	6
4	533.2831	267.1452	516.2565	258.6319	V	***668.4454***	334.7263	651.4188	326.2130	5
5	731.4199	366.2136	714.3933	357.7003	K	***569.3770***	285.1921	552.3504	276.6788	4
6	830.4883	415.7478	813.4618	407.2345	V	371.2401	186.1237	354.2136	177.6104	3
7	927.5411	464.2742	910.5145	455.7609	P	***272.1717***	136.5895	255.1452	128.0762	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **FKAHQDALPR**
Found in **A6PVN3|A6PVN3_HUMAN** in **Uniprot_Human**, Carnitine O-acetyltransferase OS=Homo sapiens GN=CRAT PE=2 SV=1

Match to Query 5947: 1251.672088 from(626.843320,2+) intensity(31733.7090) rtinseconds(1386) scans(6589) index(5577)
Title: File969 Spectrum5592 scans: 6589
Data file 2013-7-18-liver-Ca-Fr9,10-ZW.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 ☐



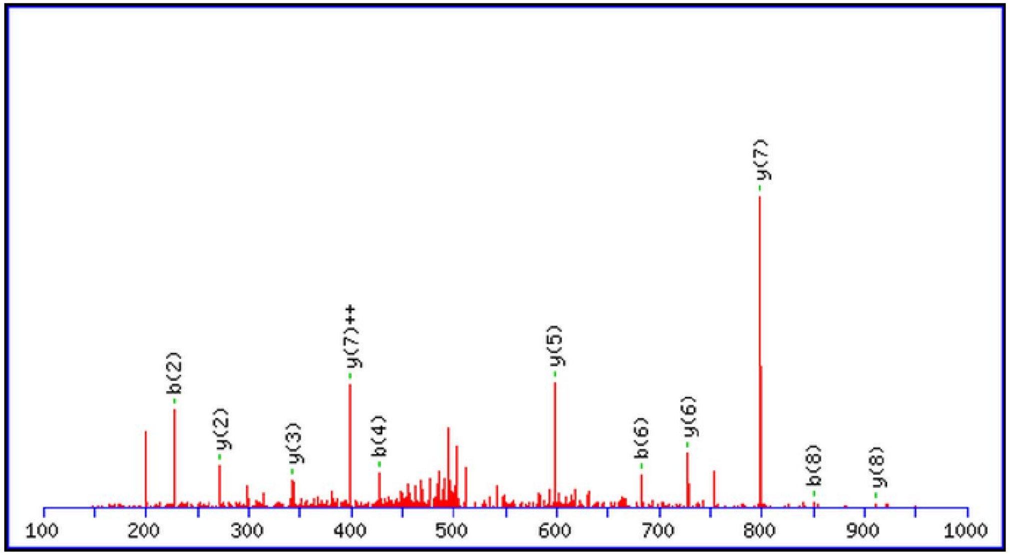
```
Monoisotopic mass of neutral peptide Mr(calc):
Fixed modifications: Carbamidomethyl (C) (apply
Variable modifications:
K2      : Propionyl-Methylation (K)
Ions Score: 54  Expect: 0.0013
Matches : 9/88 fragment ions using 11 most inte
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	**346.2125**	173.6099	329.1860	165.0966			K	1105.6113	553.3093	1088.5847	544.7960	1087.6007	544.3040	9
3	417.2496	209.1285	400.2231	200.6152			A	***907.4744***	454.2409	890.4479	445.7276	889.4639	445.2356	8
4	554.3085	277.6579	537.2820	269.1446			H	***836.4373***	418.7223	819.4108	410.2090	818.4268	409.7170	7
5	682.3671	341.6872	665.3406	333.1739			Q	***699.3784***	350.1928	682.3519	341.6796	681.3678	341.1876	6
6	797.3941	399.2007	780.3675	390.6874	779.3835	390.1954	D	***571.3198***	286.1636	554.2933	277.6503	553.3093	277.1583	5
7	868.4312	434.7192	851.4046	426.2060	850.4206	425.7139	A	***456.2929***	228.6501	439.2663	220.1368			4
8	**981.5152**	491.2613	964.4887	482.7480	963.5047	482.2560	L	385.2558	193.1315	368.2292	184.6183			3
9	**1078.5680**	539.7876	1061.5415	531.2744	1060.5574	530.7824	P	***272.1717***	136.5895	255.1452	128.0762			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LIAEGKAPR**
Found in **O75891|AL1L1_HUMAN** in **Uniprot_Human**, Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2

Match to Query 2492: 1023.609468 from(512.812010,2+) intensity(40682.7891) rtinseconds(1510) scans(7416) index(6342)
Title: File969 Spectrum6358 scans: 7416
Data file 2013-7-18-liver-Ca-Fr9,10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



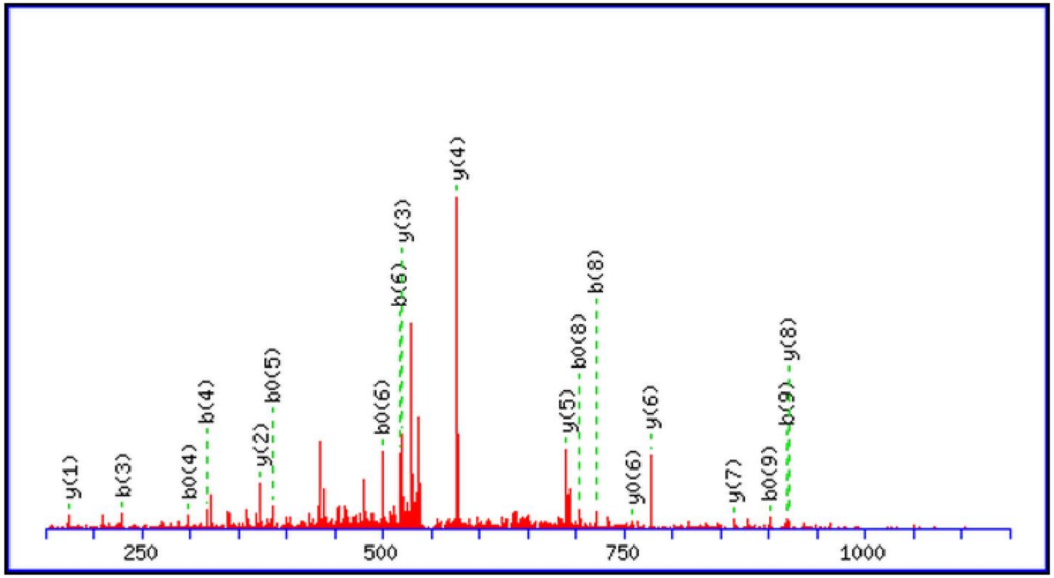
```
Monoisotopic mass of neutral peptide Mr(calc): 1023.6077
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6      : Propionyl-Methylation (K)
Ions Score: 46  Expect: 0.0035
Matches : 11/70 fragment ions using 1
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493					L							9
2	**227.1754**	114.0913					I	***911.5309***	456.2691	894.5043	447.7558	893.5203	447.2638	8
3	298.2125	149.6099					A	***798.4468***	399.7271	781.4203	391.2138	780.4363	390.7218	7
4	**427.2551**	214.1312			409.2445	205.1259	E	***727.4097***	364.2085	710.3832	355.6952	709.3992	355.2032	6
5	484.2766	242.6419			466.2660	233.6366	G	***598.3671***	299.6872	581.3406	291.1739			5
6	**682.4134**	341.7103	665.3869	333.1971	664.4028	332.7051	K	541.3457	271.1765	524.3191	262.6632			4
7	753.4505	377.2289	736.4240	368.7156	735.4400	368.2236	A	***343.2088***	172.1081	326.1823	163.5948			3
8	**850.5033**	425.7553	833.4767	417.2420	832.4927	416.7500	P	***272.1717***	136.5895	255.1452	128.0762			2
9							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **DGGSSLGFKR**
Found in **P06213-2|INSR_HUMAN** in **Uniprot_Human**, Isoform Short of Insulin receptor OS=Homo sapiens GN=INSR

Match to Query 3765: 1092.555888 from(547.285220,2+) intensity(179640.7813) rtinseconds(2030) scans(11483) index(10208)
Title: File973 Spectrum10235 scans: 11483
Data file 2013-7-21-liver-Ca-Fr19,20-ZW.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 ☐



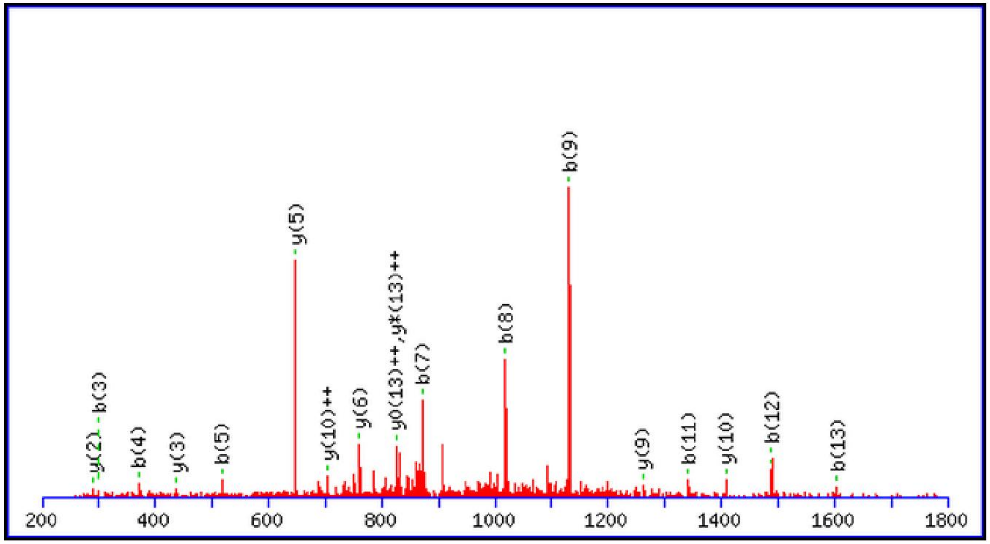
```
Monoisotopic mass of neutral pept
Fixed modifications: Carbamidometh
Variable modifications:
K9      : Propionyl-Methylation (K)
Ions Score: 39  Expect: 0.033
Matches : 19/82 fragment ions usi
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							10
2	173.0557	87.0315			155.0451	78.0262	G	978.5367	489.7720	961.5102	481.2587	960.5261	480.7667	9
3	**230.0771**	115.5422			212.0666	106.5369	G	***921.5152***	461.2613	904.4887	452.7480	903.5047	452.2560	8
4	**317.1092**	159.0582			299.0986	150.0529	S	***864.4938***	432.7505	847.4672	424.2373	846.4832	423.7452	7
5	404.1412	202.5742			386.1306	193.5690	S	***777.4618***	389.2345	760.4352	380.7212	759.4512	380.2292	6
6	**517.2253**	259.1163			499.2147	250.1110	L	***690.4297***	345.7185	673.4032	337.2052			5
7	574.2467	287.6270			556.2362	278.6217	G	***577.3457***	289.1765	560.3191	280.6632			4
8	**721.3151**	361.1612			703.3046	352.1559	F	***520.3242***	260.6657	503.2976	252.1525			3
9	**919.4520**	460.2296	902.4254	451.7164	901.4414	451.2243	K	***373.2558***	187.1315	356.2292	178.6183			2
10							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AGQAFRKFLPLFDR**
Found in **B8ZZL8|B8ZZL8_HUMAN** in **Uniprot_Human**, 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=2 SV=1

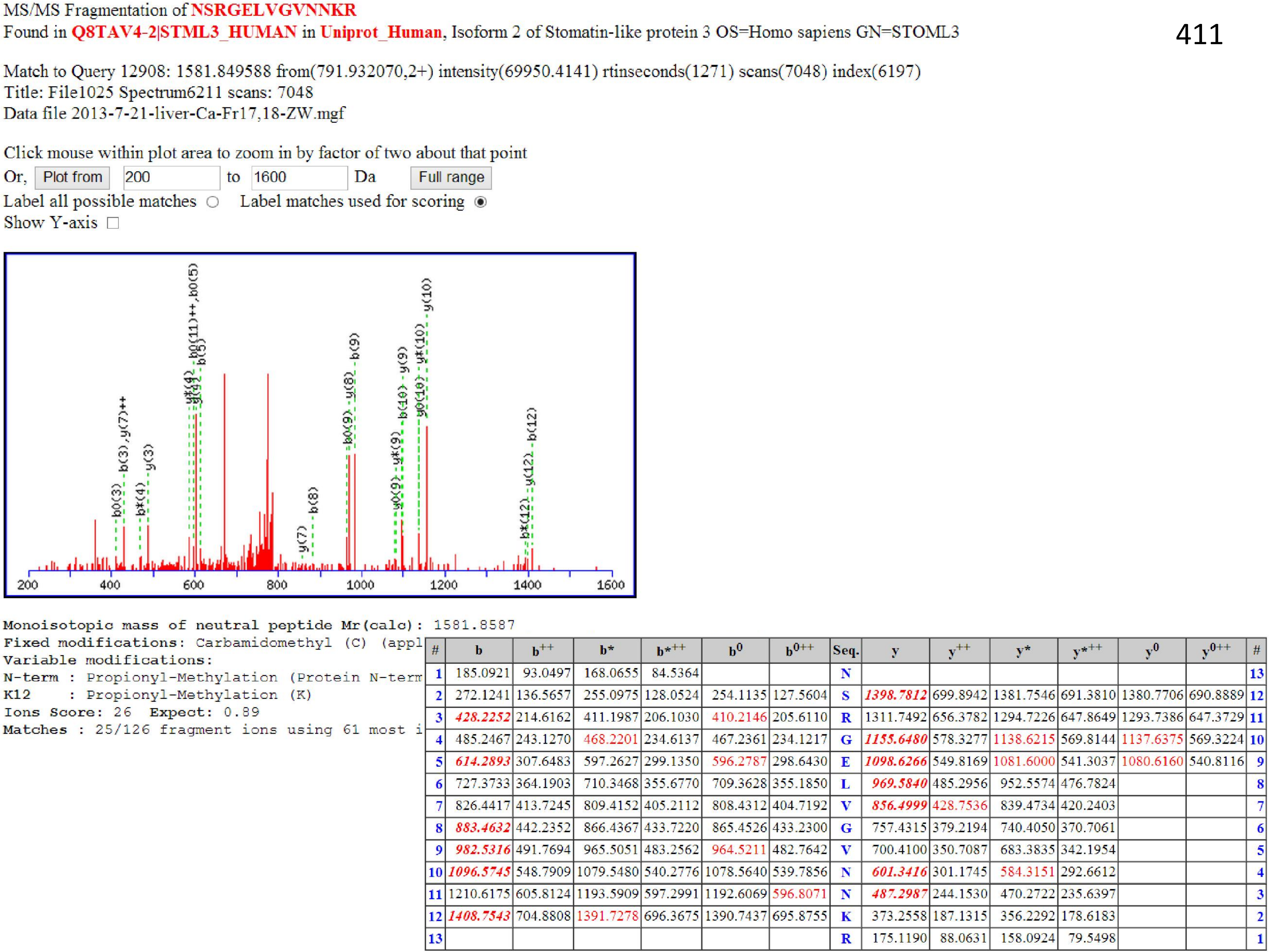
Match to Query 13326: 1776.954328 from(889.484440,2+) intensity(133526.0625) rtinseconds(3649) scans(23129) index(20952)
Title: File973 Spectrum21095 scans: 23129
Data file 2013-7-21-liver-Ca-Fr19,20-ZW.mgf

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 ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1
Fixed modifications: Carbamidomethyl (C) (apply
Variable modifications:
N-term : Acetyl (Protein N-term)
K7      : Propionyl-Methylation (K)
Ions Score: 51   Expect: 0.004
Matches : 18/126 fragment ions using 32 most int
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0550	57.5311					A							14
2	171.0764	86.0418					G	1664.9271	832.9672	1647.9006	824.4539	1646.9166	823.9619	13
3	***299.1350***	150.0711	282.1084	141.5579			Q	1607.9057	804.4565	1590.8791	795.9432	1589.8951	795.4512	12
4	***370.1721***	185.5897	353.1456	177.0764			A	1479.8471	740.4272	1462.8205	731.9139	1461.8365	731.4219	11
5	***517.2405***	259.1239	500.2140	250.6106			F	**1408.8100**	704.9086	1391.7834	696.3953	1390.7994	695.9033	10
6	673.3416	337.1745	656.3151	328.6612			R	**1261.7416**	631.3744	1244.7150	622.8611	1243.7310	622.3691	9
7	***871.4785***	436.2429	854.4519	427.7296			K	1105.6404	553.3239	1088.6139	544.8106	1087.6299	544.3186	8
8	***1018.5469***	509.7771	1001.5203	501.2638			F	907.5036	454.2554	890.4771	445.7422	889.4930	445.2502	7
9	***1131.6309***	566.3191	1114.6044	557.8058			L	**760.4352**	380.7212	743.4087	372.2080	742.4246	371.7160	6
10	1228.6837	614.8455	1211.6572	606.3322			P	**647.3511**	324.1792	630.3246	315.6659	629.3406	315.1739	5
11	***1341.7678***	671.3875	1324.7412	662.8742			L	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
12	***1488.8362***	744.9217	1471.8096	736.4085			F	**437.2143**	219.1108	420.1878	210.5975	419.2037	210.1055	3
13	***1603.8631***	802.4352	1586.8366	793.9219	1585.8526	793.4299	D	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	2
14							R	175.1190	88.0631	158.0924	79.5498			1



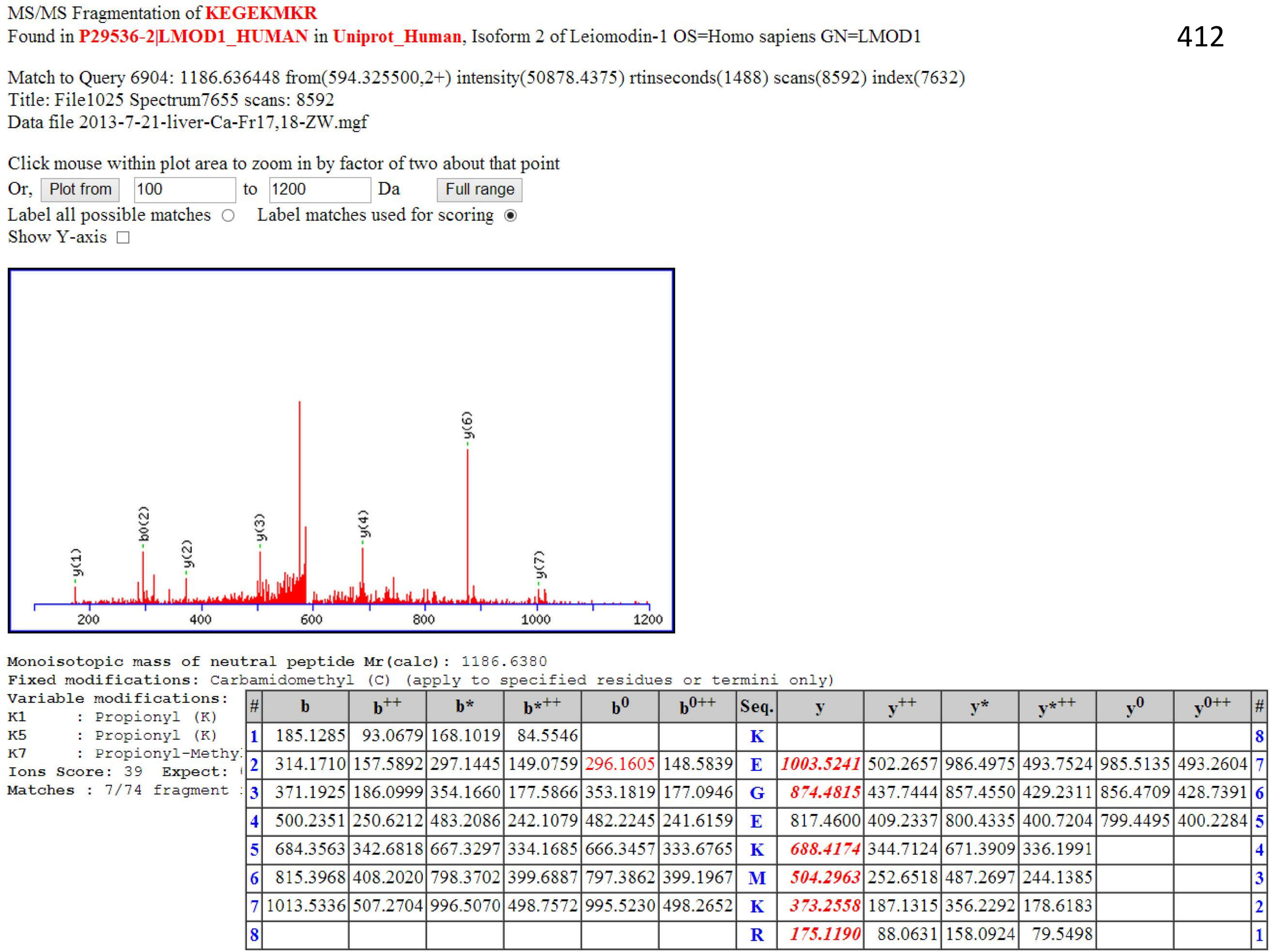
MS/MS Fragmentation of **NSRGELVGVNNKR**
Found in **Q8TAV4-2|STML3_HUMAN** in **Uniprot_Human**, Isoform 2 of Stomatin-like protein 3 OS=Homo sapiens GN=STOML3

Match to Query 12908: 1581.849588 from(791.932070,2+) intensity(69950.4141) rtinseconds(1271) scans(7048) index(6197)
Title: File1025 Spectrum6211 scans: 7048
Data file 2013-7-21-liver-Ca-Fr17,18-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

```
Monoisotopic mass of neutral peptide Mr(calc): 1581.8587
Fixed modifications: Carbamidomethyl (C) (appl
Variable modifications:
N-term : Propionyl-Methylation (Protein N-term
K12    : Propionyl-Methylation (K)
Ions Score: 26  Expect: 0.89
Matches : 25/126 fragment ions using 61 most i
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	185.0921	93.0497	168.0655	84.5364			N							13
2	272.1241	136.5657	255.0975	128.0524	254.1135	127.5604	S	***1398.7812***	699.8942	1381.7546	691.3810	1380.7706	690.8889	12
3	***428.2252***	214.6162	411.1987	206.1030	410.2146	205.6110	R	1311.7492	656.3782	1294.7226	647.8649	1293.7386	647.3729	11
4	485.2467	243.1270	468.2201	234.6137	467.2361	234.1217	G	***1155.6480***	578.3277	1138.6215	569.8144	1137.6375	569.3224	10
5	***614.2893***	307.6483	597.2627	299.1350	596.2787	298.6430	E	***1098.6266***	549.8169	1081.6000	541.3037	1080.6160	540.8116	9
6	727.3733	364.1903	710.3468	355.6770	709.3628	355.1850	L	***969.5840***	485.2956	952.5574	476.7824			8
7	826.4417	413.7245	809.4152	405.2112	808.4312	404.7192	V	***856.4999***	428.7536	839.4734	420.2403			7
8	***883.4632***	442.2352	866.4367	433.7220	865.4526	433.2300	G	757.4315	379.2194	740.4050	370.7061			6
9	***982.5316***	491.7694	965.5051	483.2562	964.5211	482.7642	V	700.4100	350.7087	683.3835	342.1954			5
10	***1096.5745***	548.7909	1079.5480	540.2776	1078.5640	539.7856	N	***601.3416***	301.1745	584.3151	292.6612			4
11	1210.6175	605.8124	1193.5909	597.2991	1192.6069	596.8071	N	***487.2987***	244.1530	470.2722	235.6397			3
12	***1408.7543***	704.8808	1391.7278	696.3675	1390.7437	695.8755	K	373.2558	187.1315	356.2292	178.6183			2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KEGEKMKR**
Found in **P29536-2|LMOD1_HUMAN** in **Uniprot_Human**, Isoform 2 of Leiomodin-1 OS=Homo sapiens GN=LMOD1

Match to Query 6904: 1186.636448 from(594.325500,2+) intensity(50878.4375) rtinseconds(1488) scans(8592) index(7632)
Title: File1025 Spectrum7655 scans: 8592
Data file 2013-7-21-liver-Ca-Fr17,18-ZW.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 ☐

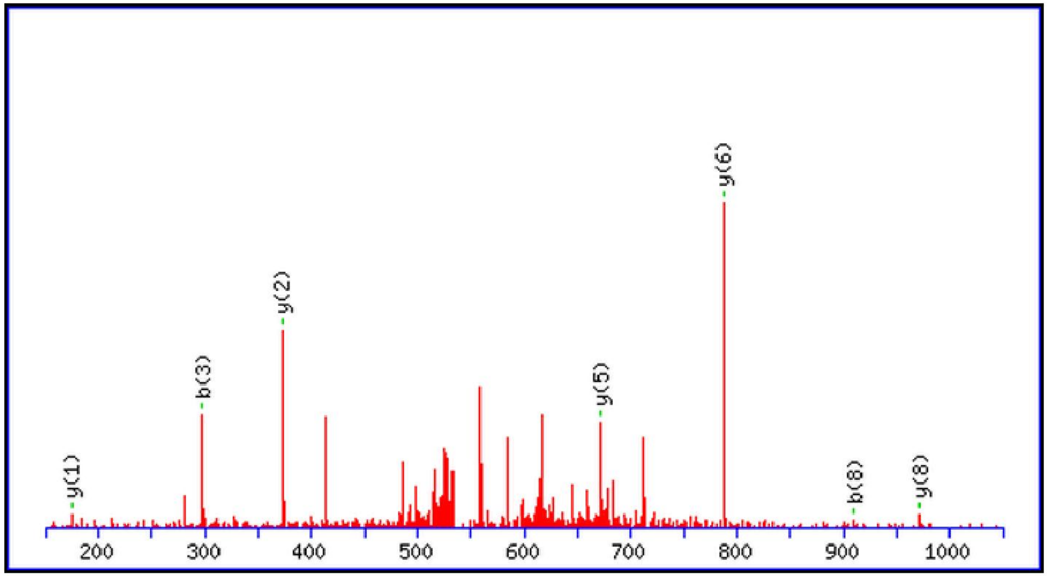
Monoisotopic mass of neutral peptide Mr(calc): 1186.6380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Propionyl (K)
K5 : Propionyl (K)
K7 : Propionyl-Methy
Ions Score: 39 Expect:
Matches : 7/74 fragment

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							8
2	314.1710	157.5892	297.1445	149.0759	296.1605	148.5839	E	***1003.5241***	502.2657	986.4975	493.7524	985.5135	493.2604	7
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	G	***874.4815***	437.7444	857.4550	429.2311	856.4709	428.7391	6
4	500.2351	250.6212	483.2086	242.1079	482.2245	241.6159	E	817.4600	409.2337	800.4335	400.7204	799.4495	400.2284	5
5	684.3563	342.6818	667.3297	334.1685	666.3457	333.6765	K	***688.4174***	344.7124	671.3909	336.1991			4
6	815.3968	408.2020	798.3702	399.6887	797.3862	399.1967	M	***504.2963***	252.6518	487.2697	244.1385			3
7	1013.5336	507.2704	996.5070	498.7572	995.5230	498.2652	K	***373.2558***	187.1315	356.2292	178.6183			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LSPDNGKKR**
Found in **B2RNG4|B2RNG4_HUMAN** in **Uniprot_Human**, Protein TRIM6-TRIM34 OS=Homo sapiens GN=TRIM6-TRIM34 PE=2 SV=1

Match to Query 4814: 1083.608368 from(542.811460,2+) intensity(212965.7344) rtinseconds(2398) scans(15090) index(13709)
Title: File1025 Spectrum13732 scans: 15090
Data file 2013-7-21-liver-Ca-Fr17,18-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



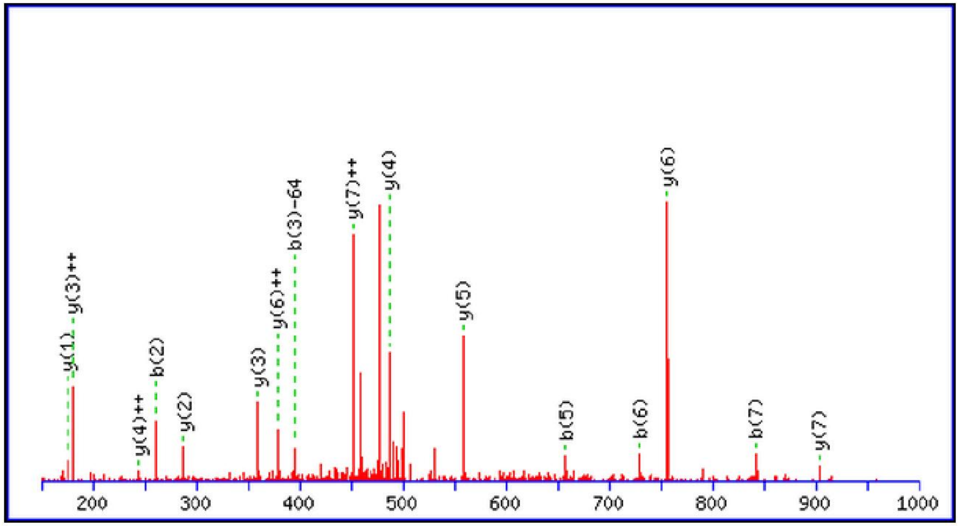
```
Monoisotopic mass of neutral peptide Mr(calc): 1083.6036
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
K8      : Propionyl-Methylation (K)
Ions Score: 43  Expect: 0.017
Matches : 7/76 fragment ions using 9 mos
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							9
2	201.1234	101.0653			183.1128	92.0600	S	*971.5269*	486.2671	954.5003	477.7538	953.5163	477.2618	8
3	298.1761	149.5917			280.1656	140.5864	P	884.4948	442.7511	867.4683	434.2378	866.4843	433.7458	7
4	413.2031	207.1052			395.1925	198.0999	D	*787.4421*	394.2247	770.4155	385.7114	769.4315	385.2194	6
5	527.2460	264.1266	510.2195	255.6134	509.2354	255.1214	N	*672.4151*	336.7112	655.3886	328.1979			5
6	584.2675	292.6374	567.2409	284.1241	566.2569	283.6321	G	558.3722	279.6897	541.3457	271.1765			4
7	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	K	501.3507	251.1790	484.3242	242.6657			3
8	910.4993	455.7533	893.4727	447.2400	892.4887	446.7480	K	*373.2558*	187.1315	356.2292	178.6183			2
9							R	*175.1190*	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IMKAQALR**
Found in **P07900-2|HS90A_HUMAN** in **Uniprot_Human**, Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1

Match to Query 2990: 1015.586708 from(508.800630,2+) intensity(289366.1875) rtinseconds(1549) scans(8352) index(7232)
Title: File1027 Spectrum7290 scans: 8352
Data file 2013-7-21-liver-Ca-Fr6-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1015.5848
Fixed modifications: Carbamidomethyl (C) (app
Variable modifications:
M2      : Oxidation (M), with neutral losses 0
K3      : Propionyl-Methylation (K)
Ions Score: 55  Expect: 0.0025
Matches : 16/78 fragment ions using 25 most i
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	114.0913	57.5493			I					8
2	**261.1267**	131.0670			M	***903.5081***	452.2577	886.4815	443.7444	7
3	459.2636	230.1354	442.2370	221.6221	K	***756.4727***	378.7400	739.4461	370.2267	6
4	530.3007	265.6540	513.2741	257.1407	A	***558.3358***	279.6715	541.3093	271.1583	5
5	**658.3593**	329.6833	641.3327	321.1700	Q	***487.2987***	244.1530	470.2722	235.6397	4
6	**729.3964**	365.2018	712.3698	356.6886	A	***359.2401***	180.1237	342.2136	171.6104	3
7	**842.4804**	421.7439	825.4539	413.2306	L	***288.2030***	144.6051	271.1765	136.0919	2
8					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KAKDDATLSGKR**

Found in **Q13442|HAP28_HUMAN** in **Uniprot_Human**, 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1

Match to Query 10700: 1470.804908 from(736.409730,2+) intensity(58645.5586) rtinseconds(1749) scans(10412) index(9337)

Title: File971 Spectrum9371 scans: 10412

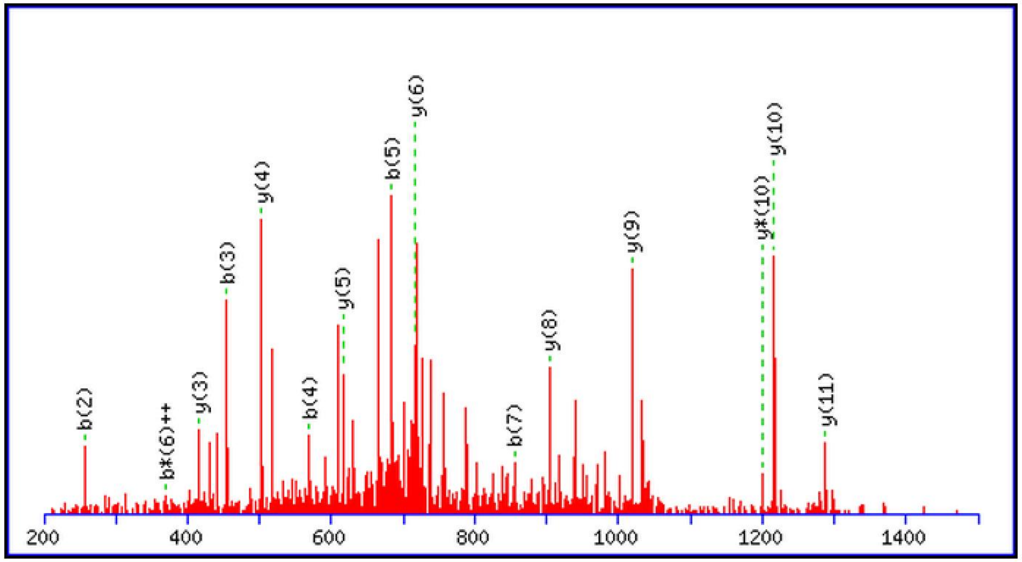
Data file 2013-7-21-liver-Ca-Fr1,2-ZW.mgf

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

Or, Plot from 200 to 1500 Da Full range

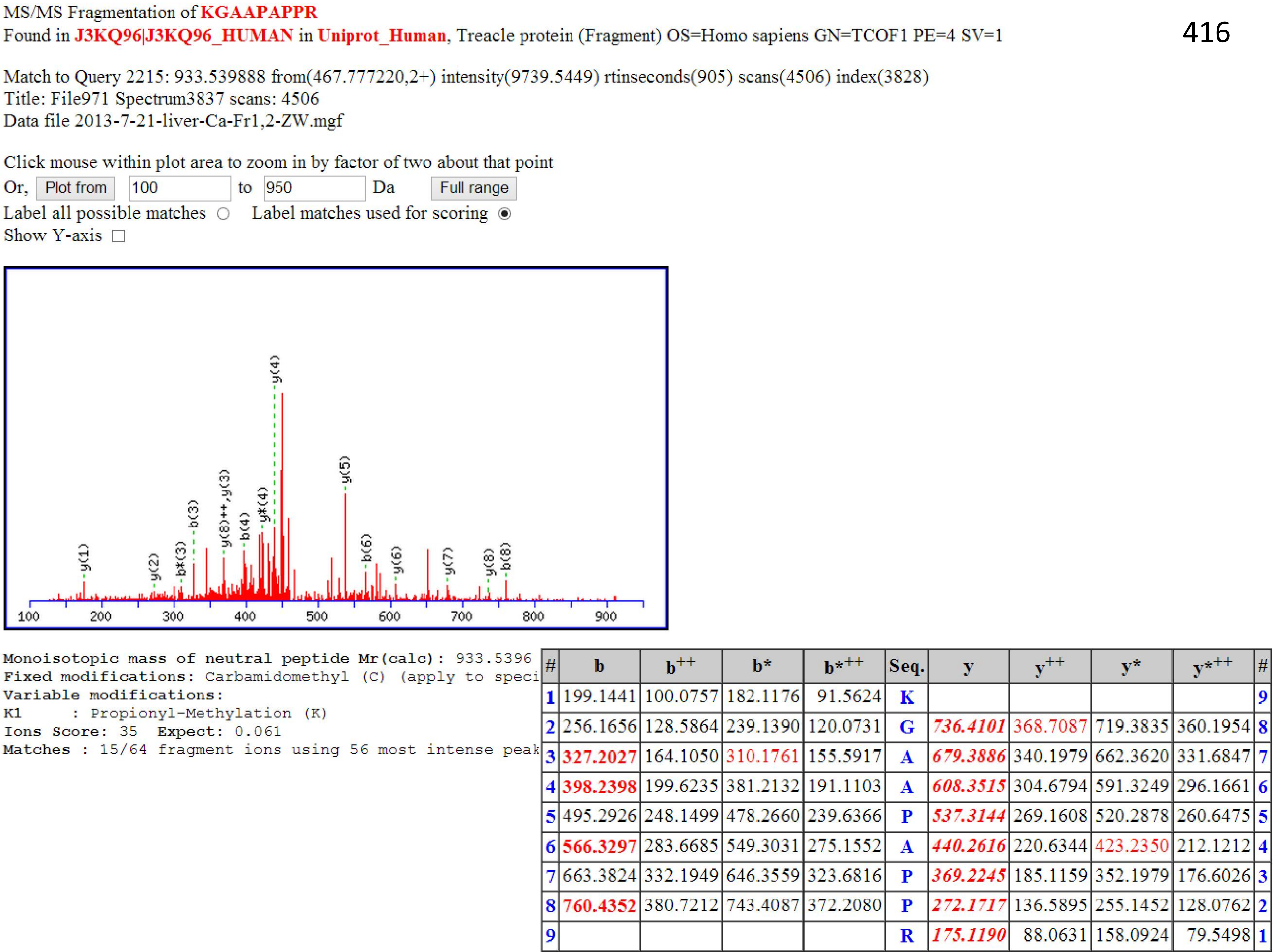
Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 1470.8042
Fixed modifications: Carbamidomethyl (C) (app
Variable modifications:
K1      : Propionyl (K)
K3      : Propionyl-Methylation (K)
K11     : Propionyl (K)
Ions Score: 35  Expect: 0.14
Matches : 15/120 fragment ions using 39 most
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	185.1285	93.0679	168.1019	84.5546			K							12
2	**256.1656**	128.5864	239.1390	120.0731			A	***1287.6903***	644.3488	1270.6638	635.8355	1269.6797	635.3435	11
3	**454.3024**	227.6548	437.2758	219.1416			K	***1216.6532***	608.8302	1199.6266	600.3170	1198.6426	599.8250	10
4	**569.3293**	285.1683	552.3028	276.6550	551.3188	276.1630	D	***1018.5164***	509.7618	1001.4898	501.2485	1000.5058	500.7565	9
5	**684.3563**	342.6818	667.3297	334.1685	666.3457	333.6765	D	***903.4894***	452.2483	886.4629	443.7351	885.4789	443.2431	8
6	755.3934	378.2003	738.3668	369.6871	737.3828	369.1951	A	788.4625	394.7349	771.4359	386.2216	770.4519	385.7296	7
7	**856.4411**	428.7242	839.4145	420.2109	838.4305	419.7189	T	***717.4254***	359.2163	700.3988	350.7030	699.4148	350.2110	6
8	969.5251	485.2662	952.4986	476.7529	951.5146	476.2609	L	***616.3777***	308.6925	599.3511	300.1792	598.3671	299.6872	5
9	1056.5572	528.7822	1039.5306	520.2689	1038.5466	519.7769	S	***503.2936***	252.1504	486.2671	243.6372	485.2831	243.1452	4
10	1113.5786	557.2930	1096.5521	548.7797	1095.5681	548.2877	G	***416.2616***	208.6344	399.2350	200.1212			3
11	1297.6998	649.3535	1280.6733	640.8403	1279.6892	640.3483	K	359.2401	180.1237	342.2136	171.6104			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KGAAPAPPR**
Found in **J3KQ96|J3KQ96_HUMAN** in **Uniprot_Human**, Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=4 SV=1

Match to Query 2215: 933.539888 from(467.777220,2+) intensity(9739.5449) rtinseconds(905) scans(4506) index(3828)
Title: File971 Spectrum3837 scans: 4506
Data file 2013-7-21-liver-Ca-Fr1,2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

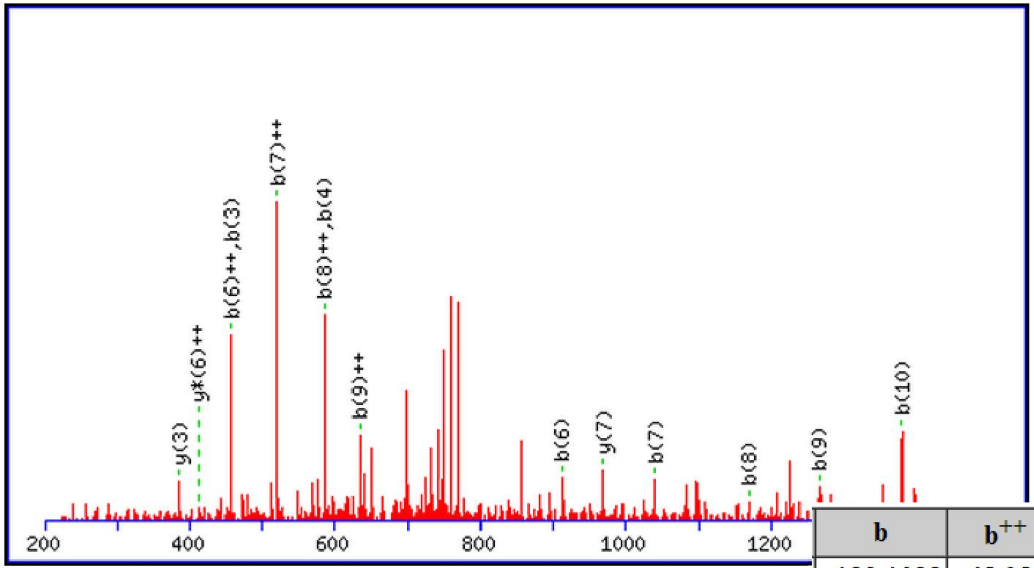
```
Monoisotopic mass of neutral peptide Mr(calc): 933.5396
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K1      : Propionyl-Methylation (K)
Ions Score: 35  Expect: 0.061
Matches : 15/64 fragment ions using 56 most intense peak
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	199.1441	100.0757	182.1176	91.5624	K					9
2	256.1656	128.5864	239.1390	120.0731	G	***736.4101***	368.7087	719.3835	360.1954	8
3	**327.2027**	164.1050	310.1761	155.5917	A	***679.3886***	340.1979	662.3620	331.6847	7
4	**398.2398**	199.6235	381.2132	191.1103	A	***608.3515***	304.6794	591.3249	296.1661	6
5	495.2926	248.1499	478.2660	239.6366	P	***537.3144***	269.1608	520.2878	260.6475	5
6	**566.3297**	283.6685	549.3031	275.1552	A	***440.2616***	220.6344	423.2350	212.1212	4
7	663.3824	332.1949	646.3559	323.6816	P	***369.2245***	185.1159	352.1979	176.6026	3
8	**760.4352**	380.7212	743.4087	372.2080	P	***272.1717***	136.5895	255.1452	128.0762	2
9					R	***175.1190***	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **KEKEQKEEPLR**
Found in **Q96M53|TBATA_HUMAN** in **Uniprot_Human**, Protein TBATA OS=Homo sapiens GN=TBATA PE=2 SV=3

Match to Query 13350: 1552.856048 from(777.435300,2+) intensity(227217.9063) rtinseconds(1951) scans(10753) index(9516)
Title: File994 Spectrum9545 scans: 10753
Data file 2013-7-18-liver-Ca-Fr3,4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



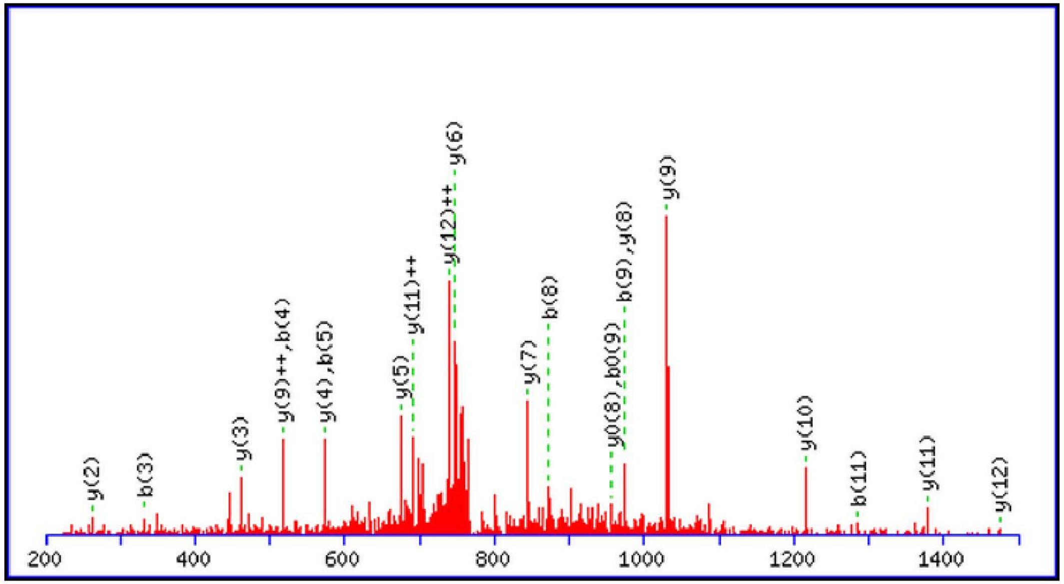
```
Monoisotopic mass of neutral peptide Mr(calc): 1552.84
Fixed modifications: Carbamidomethyl (C) (apply to spec
Variable modifications:
K3       : Propionyl-Methylation (K)
K6       : Propionyl-Methylation (K)
Ions Score: 37  Expect: 0.073
Matches : 14/120 fragment ions using 25 most intense pe
```

b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
129.1022	65.0548	112.0757	56.5415	K					11
258.1448	129.5761	241.1183	121.0628	E	1425.7584	713.3828	1408.7318	704.8696	10
456.2817	228.6445	439.2551	220.1312	K	1296.7158	648.8615	1279.6892	640.3483	9
585.3243	293.1658	568.2977	284.6525	E	1098.5790	549.7931	1081.5524	541.2798	8
713.3828	357.1951	696.3563	348.6818	Q	**969.5364**	485.2718	952.5098	476.7585	7
911.5197	**456.2635**	894.4931	447.7502	K	841.4778	421.2425	824.4512	412.7293	6
1040.5623	**520.7848**	1023.5357	512.2715	E	643.3410	322.1741	626.3144	313.6608	5
1169.6048	**585.3061**	1152.5783	576.7928	E	514.2984	257.6528	497.2718	249.1395	4
1266.6576	**633.8324**	1249.6311	625.3192	P	**385.2558**	193.1315	368.2292	184.6183	3
1379.7417	690.3745	1362.7151	681.8612	L	288.2030	144.6051	271.1765	136.0919	2
				R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **APYKGEVATLKSR**
Found in **Q14117|DPYS_HUMAN** in **Uniprot_Human**, Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1

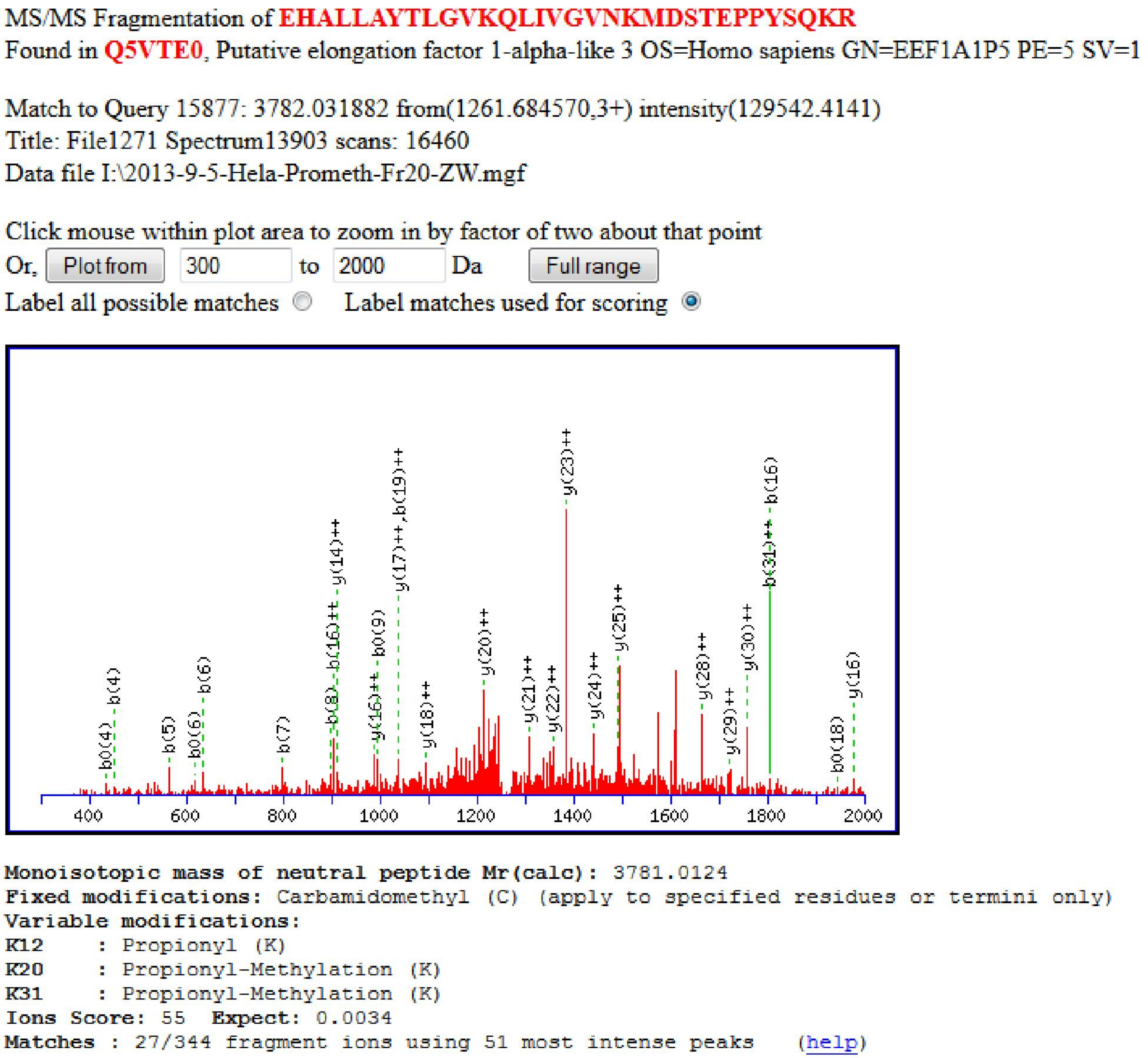
Match to Query 9695: 1545.856668 from(773.935610,2+) intensity(142534.7344) rtinseconds(2385) scans(13179) index(11610)
Title: File1038 Spectrum11670 scans: 13179
Data file 2013-7-19-Liver Ca-Fr13,14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1500] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐



```
Monoisotopic mass of neutral peptide Mr(calc): 154
Fixed modifications: Carbamidomethyl (C) (apply tc
Variable modifications:
K4      : Propionyl (K)
K11     : Propionyl-Methylation (K)
Ions Score: 93  Expect: 2e-007
Matches : 22/126 fragment ions using 26 most inter
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	72.0444	36.5258					A							13
2	169.0972	85.0522					P	***1474.8264***	737.9168	1457.7999	729.4036	1456.8158	728.9116	12
3	**332.1605**	166.5839					Y	***1377.7736***	689.3905	1360.7471	680.8772	1359.7631	680.3852	11
4	**516.2817**	258.6445	499.2551	250.1312			K	***1214.7103***	607.8588	1197.6838	599.3455	1196.6997	598.8535	10
5	**573.3031**	287.1552	556.2766	278.6419			G	***1030.5891***	515.7982	1013.5626	507.2849	1012.5786	506.7929	9
6	702.3457	351.6765	685.3192	343.1632	684.3352	342.6712	E	***973.5677***	487.2875	956.5411	478.7742	955.5571	478.2822	8
7	801.4141	401.2107	784.3876	392.6974	783.4036	392.2054	V	***844.5251***	422.7662	827.4985	414.2529	826.5145	413.7609	7
8	**872.4512**	436.7293	855.4247	428.2160	854.4407	427.7240	A	***745.4567***	373.2320	728.4301	364.7187	727.4461	364.2267	6
9	**973.4989**	487.2531	956.4724	478.7398	955.4884	478.2478	T	***674.4196***	337.7134	657.3930	329.2001	656.4090	328.7081	5
10	1086.5830	543.7951	1069.5564	535.2819	1068.5724	534.7899	L	***573.3719***	287.1896	556.3453	278.6763	555.3613	278.1843	4
11	**1284.7198**	642.8635	1267.6933	634.3503	1266.7093	633.8583	K	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	3
12	1371.7518	686.3796	1354.7253	677.8663	1353.7413	677.3743	S	***262.1510***	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **EHALLAYTLGVKQLIVGVNKMDSTEPPYSQKR**
Found in **Q5VTE0**, Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1

Match to Query 15877: 3782.031882 from(1261.684570,3+) intensity(129542.4141)
Title: File1271 Spectrum13903 scans: 16460
Data file I:\2013-9-5-Hela-Prometh-Fr20-ZW.mgf

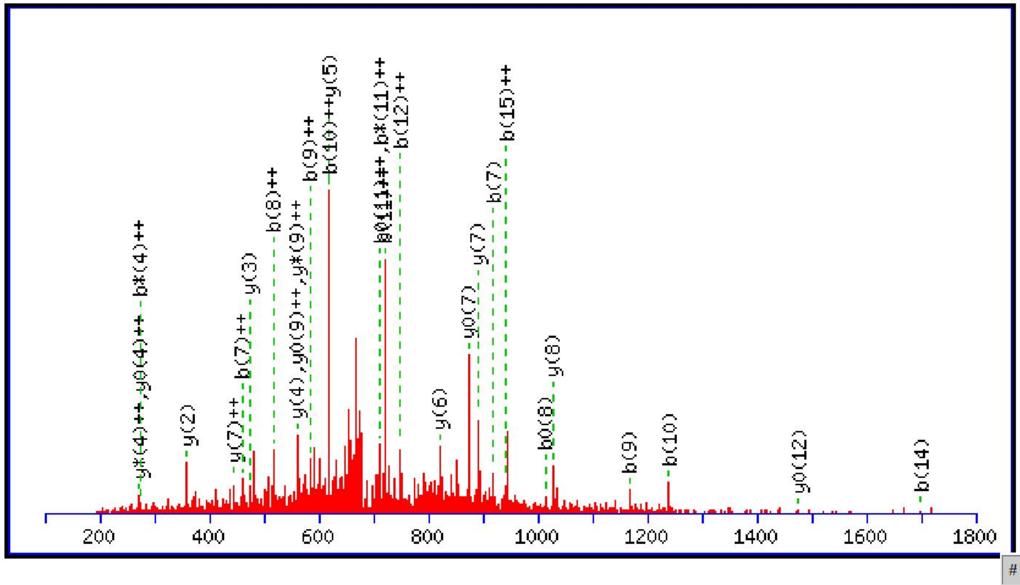
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 3781.0124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K12     : Propionyl (K)
K20     : Propionyl-Methylation (K)
K31     : Propionyl-Methylation (K)
Ions Score: 55   Expect: 0.0034
Matches : 27/344 fragment ions using 51 most intense peaks   (help)
```

MS/MS Fragmentation of **EHIKVQQLMAKGSDKR**
Found in **D3DNT2**, Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=2 SV=1

Match to Query 14176: 2057.146152 from(686.722660,3+) intensity(30272.7520)
Title: File1264 Spectrum11284 scans: 13069
Data file I:\2013-9-5-Hela-Prometh-Fr13-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



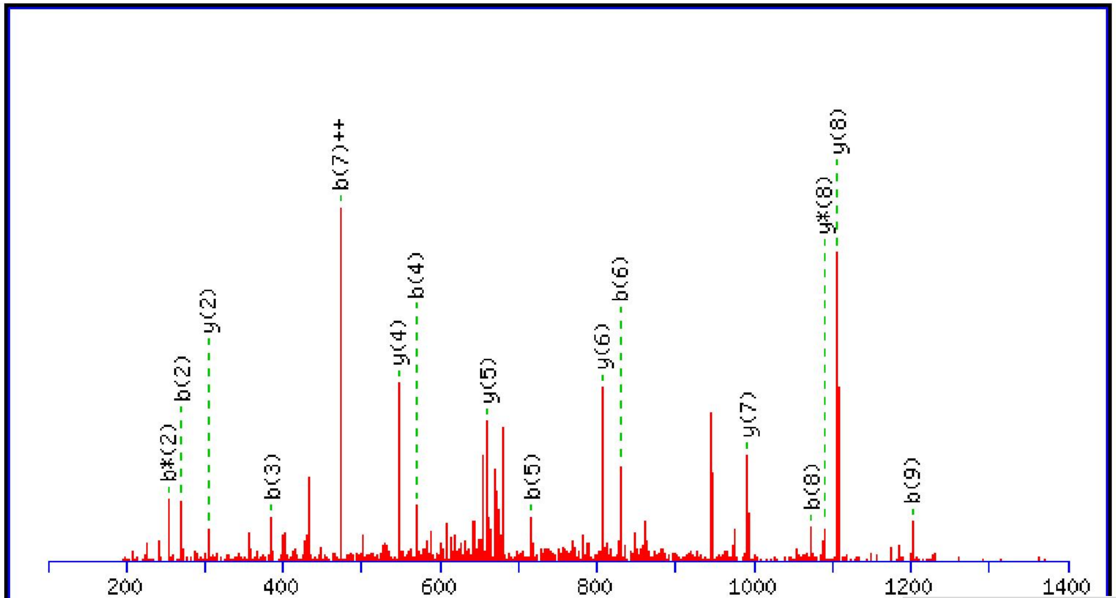
```
Monoisotopic mass of neutral peptide Mr(calc): 2057.1484
Fixed modifications: Carbamidomethyl (C) (apply to specified residue
Variable modifications:
K4      : Propionyl (K)
M9      : Label:13C(1)2H(3) (M)
K11     : Propionyl-(13CD3)Methyl (K)
K15     : Propionyl (K)
Ions Score: 23  Expect: 4.6
Matches : 29/170 fragment ions using 61 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	267.1088	134.0580			249.0982	125.0527	H	1929.1131	965.0602	1912.0866	956.5469	1911.1026	956.0549	15
3	380.1928	190.6001			362.1823	181.5948	I	1792.0542	896.5308	1775.0277	888.0175	1774.0437	887.5255	14
4	564.3140	282.6606	547.2875	274.1474	546.3035	273.6554	K	1678.9702	839.9887	1661.9436	831.4755	1660.9596	830.9834	13
5	663.3824	332.1949	646.3559	323.6816	645.3719	323.1896	V	1494.8490	747.9281	1477.8224	739.4149	1476.8384	738.9229	12
6	791.4410	396.2241	774.4145	387.7109	773.4304	387.2189	Q	1395.7806	698.3939	1378.7540	689.8807	1377.7700	689.3886	11
7	919.4996	460.2534	902.4730	451.7402	901.4890	451.2482	Q	1267.7220	634.3646	1250.6955	625.8514	1249.7114	625.3594	10
8	1032.5837	516.7955	1015.5571	508.2822	1014.5731	507.7902	L	1139.6634	570.3354	1122.6369	561.8221	1121.6529	561.3301	9
9	1167.6463	584.3268	1150.6198	575.8135	1149.6358	575.3215	M	1026.5794	513.7933	1009.5528	505.2800	1008.5688	504.7880	8
10	1238.6834	619.8454	1221.6569	611.3321	1220.6729	610.8401	A	891.5167	446.2620	874.4901	437.7487	873.5061	437.2567	7
11	1440.8425	720.9249	1423.8159	712.4116	1422.8319	711.9196	K	820.4796	410.7434	803.4530	402.2302	802.4690	401.7381	6
12	1497.8639	749.4356	1480.8374	740.9223	1479.8534	740.4303	G	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
13	1584.8959	792.9516	1567.8694	784.4383	1566.8854	783.9463	S	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	4
14	1699.9229	850.4651	1682.8963	841.9518	1681.9123	841.4598	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	3
15	1884.0441	942.5257	1867.0175	934.0124	1866.0335	933.5204	K	359.2401	180.1237	342.2136	171.6104			2
16							R	175.1190	88.0631	158.0924	79.5498			1

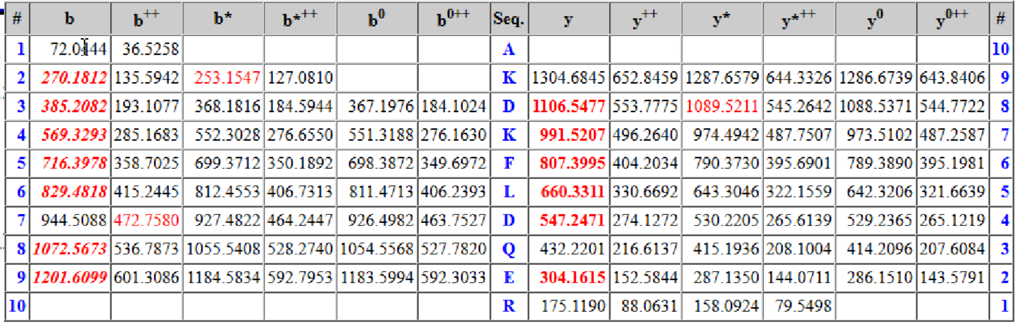
MS/MS Fragmentation of **AKDKFLDQER**
Found in **Q9H0G5**, Nuclear speckle splicing regulatory protein 1 OS=Homo sapiens GN=NSRP1 PE=1 SV=1

Match to Query 4633: 1374.713848 from(688.364200,2+) intensity(349942.2500)
Title: File1332 Spectrum10994 scans: 12239
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.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 ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1374.7143
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K2      : Propionyl-Methylation (K)
K4      : Propionyl (K)
Ions Score: 47   Expect: 0.012
Matches : 16/100 fragment ions using 24 most intense pea
```

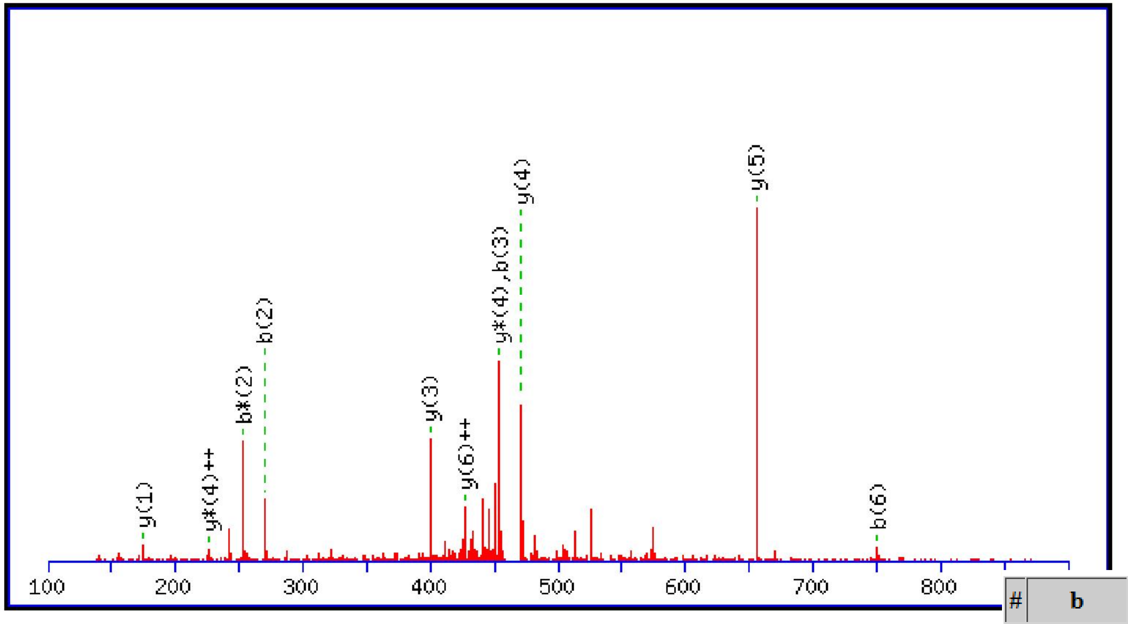


#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0[illegible]44	36.5258					A							10
2	***270.1812***	135.5942	253.1547	127.0810			K	1304.6845	652.8459	1287.6579	644.3326	1286.6739	643.8406	9
3	***385.2082***	193.1077	368.1816	184.5944	367.1976	184.1024	D	**1106.5477**	553.7775	1089.5211	545.2642	1088.5371	544.7722	8
4	***569.3293***	285.1683	552.3028	276.6550	551.3188	276.1630	K	**991.5207**	496.2640	974.4942	487.7507	973.5102	487.2587	7
5	***716.3978***	358.7025	699.3712	350.1892	698.3872	349.6972	F	**807.3995**	404.2034	790.3730	395.6901	789.3890	395.1981	6
6	***829.4818***	415.2445	812.4553	406.7313	811.4713	406.2393	L	**660.3311**	330.6692	643.3046	322.1559	642.3206	321.6639	5
7	944.5088	472.7580	927.4822	464.2447	926.4982	463.7527	D	**547.2471**	274.1272	530.2205	265.6139	529.2365	265.1219	4
8	***1072.5673***	536.7873	1055.5408	528.2740	1054.5568	527.7820	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
9	***1201.6099***	601.3086	1184.5834	592.7953	1183.5994	592.3033	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AKKAPQR**
Found in **A6PW79**, Cyclic GMP-AMP synthase OS=Homo sapiens GN=MB21D1 PE=2 SV=1

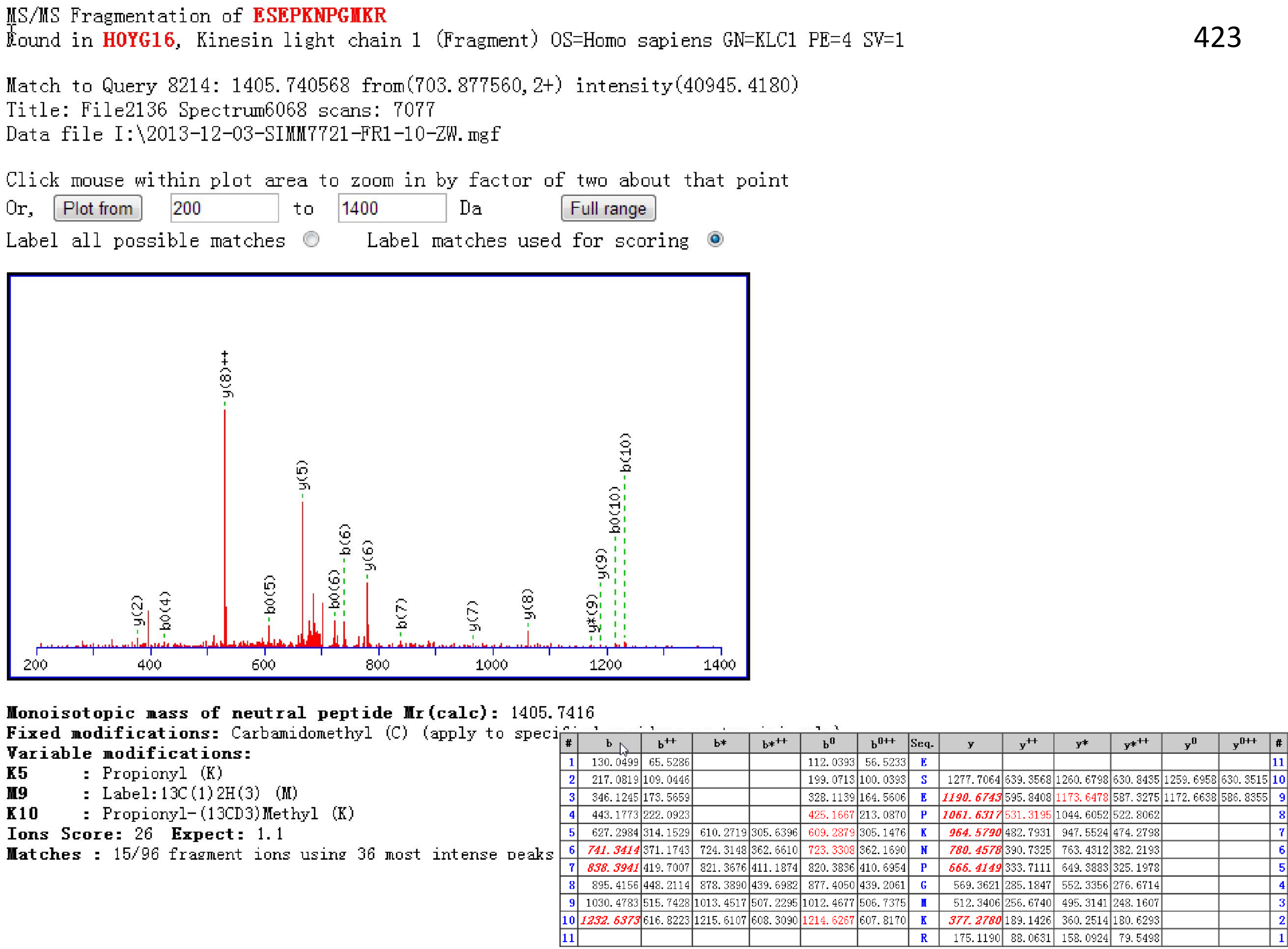
Match to Query 1841: 923.556128 from(462.785340,2+) intensity(1239225.8750)
Title: File1335 Spectrum3633 scans: 4254
Data file I:\2013-9-14-Hela-Prometh-Fr8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 923.5552
Fixed modifications: Carbamidomethyl (C) (apply to specified re
Variable modifications:
K2      : Propionyl-Methylation (K)
K3      : Propionyl (K)
Ions Score: 23  Expect: 1.4
Matches : 11/46 fragment ions using 16 most intense peaks    (he
```

#	b	b++	b*	b*++	Seq.	y	y++	y*	y*++	#
1	72.0444	36.5258			A					7
2	**270.1812**	135.5942	253.1547	127.0810	K	853.5254	427.2663	836.4989	418.7531	6
3	**454.3024**	227.6548	437.2758	219.1416	K	***655.3886***	328.1979	638.3620	319.6847	5
4	525.3395	263.1734	508.3130	254.6601	A	***471.2674***	236.1373	454.2409	227.6241	4
5	622.3923	311.6998	605.3657	303.1865	P	***400.2303***	200.6188	383.2037	192.1055	3
6	**750.4509**	375.7291	733.4243	367.2158	Q	303.1775	152.0924	286.1510	143.5791	2
7					R	***175.1190***	88.0631	158.0924	79.5498	1



MS/MS Fragmentation of **ESEPKNPGMKR**
Found in **H0YG16**, Kinesin light chain 1 (Fragment) OS=Homo sapiens GN=KLC1 PE=4 SV=1

Match to Query 8214: 1405.740568 from(703.877560,2+) intensity(40945.4180)
Title: File2136 Spectrum6068 scans: 7077
Data file I:\2013-12-03-SIMM7721-FR1-10-ZW.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 ●

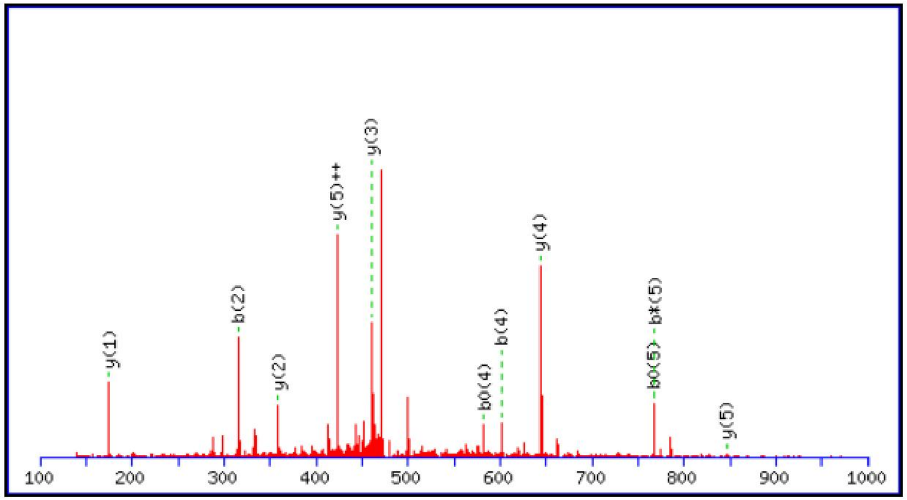
Monoisotopic mass of neutral peptide Mr(calc): 1405.7416
Fixed modifications: Carbamidomethyl (C) (apply to speci
Variable modifications:
K5 : Propionyl (K)
M9 : Label:13C(1)2H(3) (M)
K10 : Propionyl-(13CD3)Methyl (K)
Ions Score: 26 **Expect:** 1.1
Matches : 15/96 fragment ions using 36 most intense peaks

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	217.0819	109.0446			199.0713	100.0393	S	1277.7064	639.3568	1260.6798	630.8435	1259.6958	630.3515	10
3	346.1245	173.5659			328.1139	164.5606	E	***1190.6743***	595.8408	1173.6478	587.3275	1172.6638	586.8355	9
4	443.1773	222.0923			425.1667	213.0870	P	***1061.6317***	531.3195	1044.6052	522.8062			8
5	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	K	***964.5790***	482.7931	947.5524	474.2798			7
6	***741.3414***	371.1743	724.3148	362.6610	723.3308	362.1690	N	***780.4578***	390.7325	763.4312	382.2193			6
7	***838.3941***	419.7007	821.3676	411.1874	820.3836	410.6954	P	***666.4149***	333.7111	649.3883	325.1978			5
8	895.4156	448.2114	878.3890	439.6982	877.4050	439.2061	G	569.3621	285.1847	552.3356	276.6714			4
9	1030.4783	515.7428	1013.4517	507.2295	1012.4677	506.7375	M	512.3406	256.6740	495.3141	248.1607			3
10	***1232.6373***	616.8223	1215.6107	608.3090	1214.6267	607.8170	K	***377.2780***	189.1426	360.2514	180.6293			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GKKTKR**
Found in **G3V1X9**, Chromobox homolog 5 (HP1 alpha homolog, Drosophila), isoform CRA_a OS=Homo sapiens GN=CBX5 PE=2 SV=1

Match to Query 2116: 958.607888 from(480.311220,2+) intensity(122317.9688)
Title: File2044 Spectrum8587 scans: 9583
Data file I:\2013-12-03-SIMM7721-FR8-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



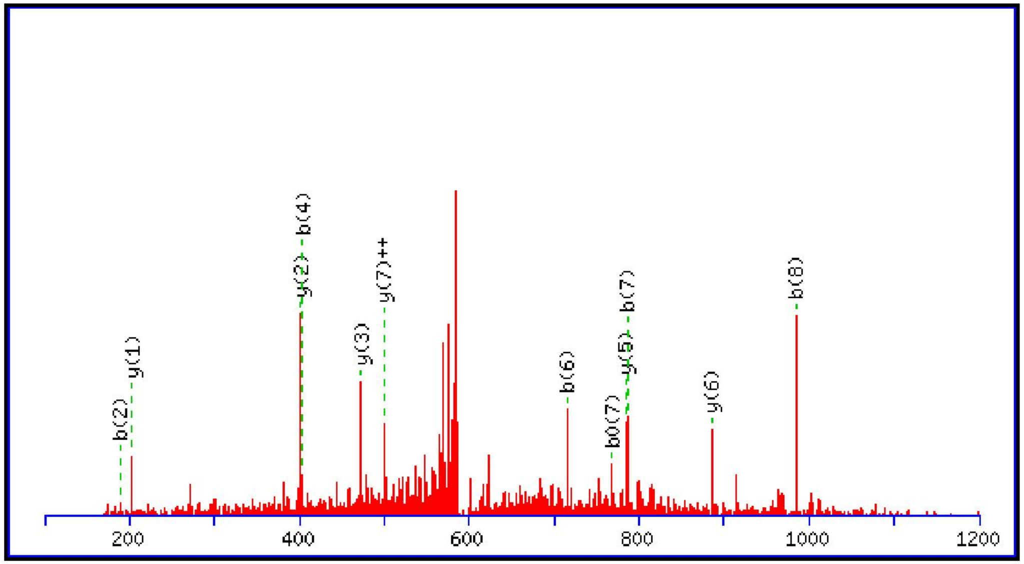
Monoisotopic mass of neutral peptide Mr(calc): 958.6084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
K2 : Propionyl-(13CD3)Methyl (K)
K3 : Propionyl (K)
K5 : Propionyl (K)
Ions Score: 37 **Expect:** 0.033
Matches : 11/48 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0550	57.5311					G							6
2	**316.2140**	158.6106	299.1874	150.0973			K	***846.5680***	423.7876	829.5415	415.2744	828.5574	414.7824	5
3	500.3351	250.6712	483.3086	242.1579			K	***644.4090***	322.7081	627.3824	314.1949	626.3984	313.7028	4
4	**601.3828**	301.1951	584.3563	292.6818	583.3723	292.1898	T	***460.2878***	230.6475	443.2613	222.1343	442.2772	221.6423	3
5	785.5040	393.2556	768.4775	384.7424	767.4934	384.2504	K	***359.2401***	180.1237	342.2136	171.6104			2
6							R	***175.1190***	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GMITKQAKK**
Found in **B4DNE3**, Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=2 SV=1

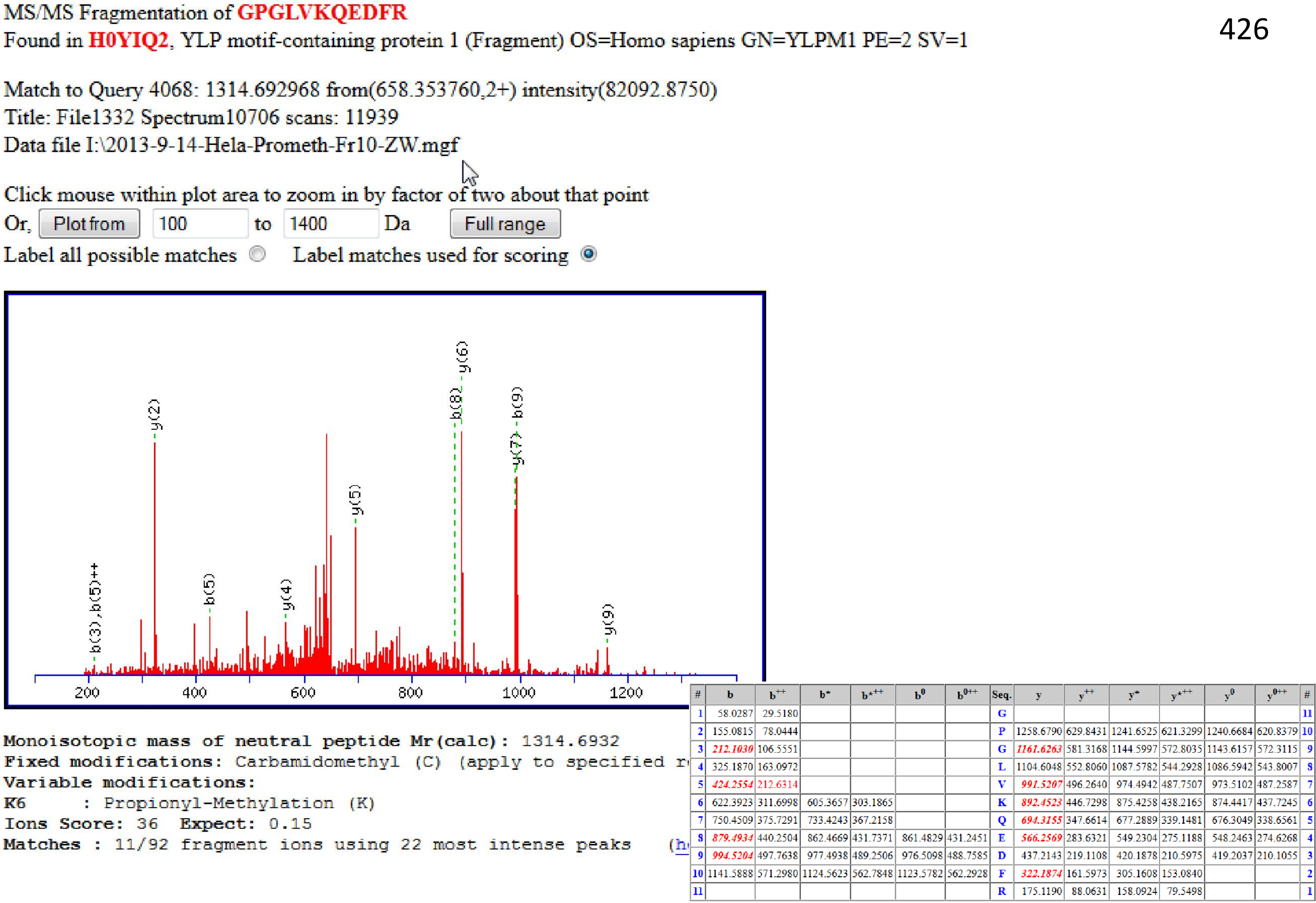
Match to Query 4149: 1185.678568 from(593.846560,2+) intensity(237169.2656)
Title: File1319 Spectrum12309 scans: 13093
Data file I:\2013-9-13-Hela-Prometh-Fr2-ZW.mgf

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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1185.6791
Fixed modifications: Carbamidomethyl (C) (apply to specified residue
Variable modifications:
K5 : Propionyl (K)
K8 : Propionyl-Methylation (K)
K9 : Propionyl (K)
Ions Score: 35 **Expect:** 0.23
Matches : 12/72 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							9
2	***189.0692***	95.0383					M	1129.6649	565.3361	1112.6384	556.8228	1111.6544	556.3308	8
3	302.1533	151.5803					I	998.6245	499.8159	981.5979	491.3026	980.6139	490.8106	7
4	***403.2010***	202.1041			385.1904	193.0988	T	***885.5404***	443.2738	868.5138	434.7606	867.5298	434.2686	6
5	587.3221	294.1647	570.2956	285.6514	569.3116	285.1594	K	***784.4927***	392.7500	767.4662	384.2367			5
6	***715.3807***	358.1940	698.3542	349.6807	697.3702	349.1887	Q	600.3715	300.6894	583.3450	292.1761			4
7	***786.4178***	393.7126	769.3913	385.1993	768.4073	384.7073	A	***472.3130***	236.6601	455.2864	228.1468			3
8	***984.5547***	492.7810	967.5281	484.2677	966.5441	483.7757	K	***401.2758***	201.1416	384.2493	192.6283			2
9							K	***203.1390***	102.0731	186.1125	93.5599			1



MS/MS Fragmentation of **GPGLVKQEDFR**

Found in **H0YIQ2**, YLP motif-containing protein 1 (Fragment) OS=Homo sapiens GN=YLPM1 PE=2 SV=1

Match to Query 4068: 1314.692968 from(658.353760,2+) intensity(82092.8750)

Title: File1332 Spectrum10706 scans: 11939

Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.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 ●

Monoisotopic mass of neutral peptide Mr(calc): 1314.6932

Fixed modifications: Carbamidomethyl (C) (apply to specified r

Variable modifications:

K6 : Propionyl-Methylation (K)

Ions Score: 36 **Expect:** 0.15

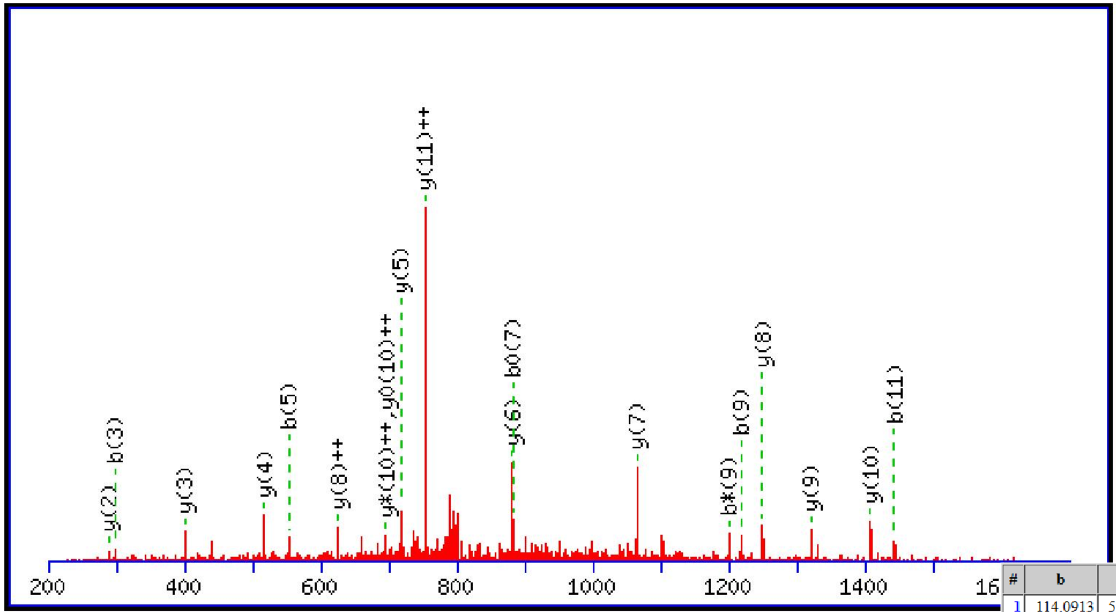
Matches : 11/92 fragment ions using 22 most intense peaks (h

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							11
2	155.0815	78.0444					P	1258.6790	629.8431	1241.6525	621.3299	1240.6684	620.8379	10
3	***212.1030***	106.5551					G	***1161.6263***	581.3168	1144.5997	572.8035	1143.6157	572.3115	9
4	325.1870	163.0972					L	1104.6048	552.8060	1087.5782	544.2928	1086.5942	543.8007	8
5	***424.2554***	212.6314					V	***991.5207***	496.2640	974.4942	487.7507	973.5102	487.2587	7
6	622.3923	311.6998	605.3657	303.1865			K	***892.4523***	446.7298	875.4258	438.2165	874.4417	437.7245	6
7	750.4509	375.7291	733.4243	367.2158			Q	***694.3155***	347.6614	677.2889	339.1481	676.3049	338.6561	5
8	***879.4934***	440.2504	862.4669	431.7371	861.4829	431.2451	E	***566.2569***	283.6321	549.2304	275.1188	548.2463	274.6268	4
9	***994.5204***	497.7638	977.4938	489.2506	976.5098	488.7585	D	437.2143	219.1108	420.1878	210.5975	419.2037	210.1055	3
10	1141.5888	571.2980	1124.5623	562.7848	1123.5782	562.2928	F	***322.1874***	161.5973	305.1608	153.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IPSAKKYKDIIR**
Found in **B1AKZ3**, Astrocytic phosphoprotein PEA-15 OS=Homo sapiens GN=PEA15 PE=2 SV=1

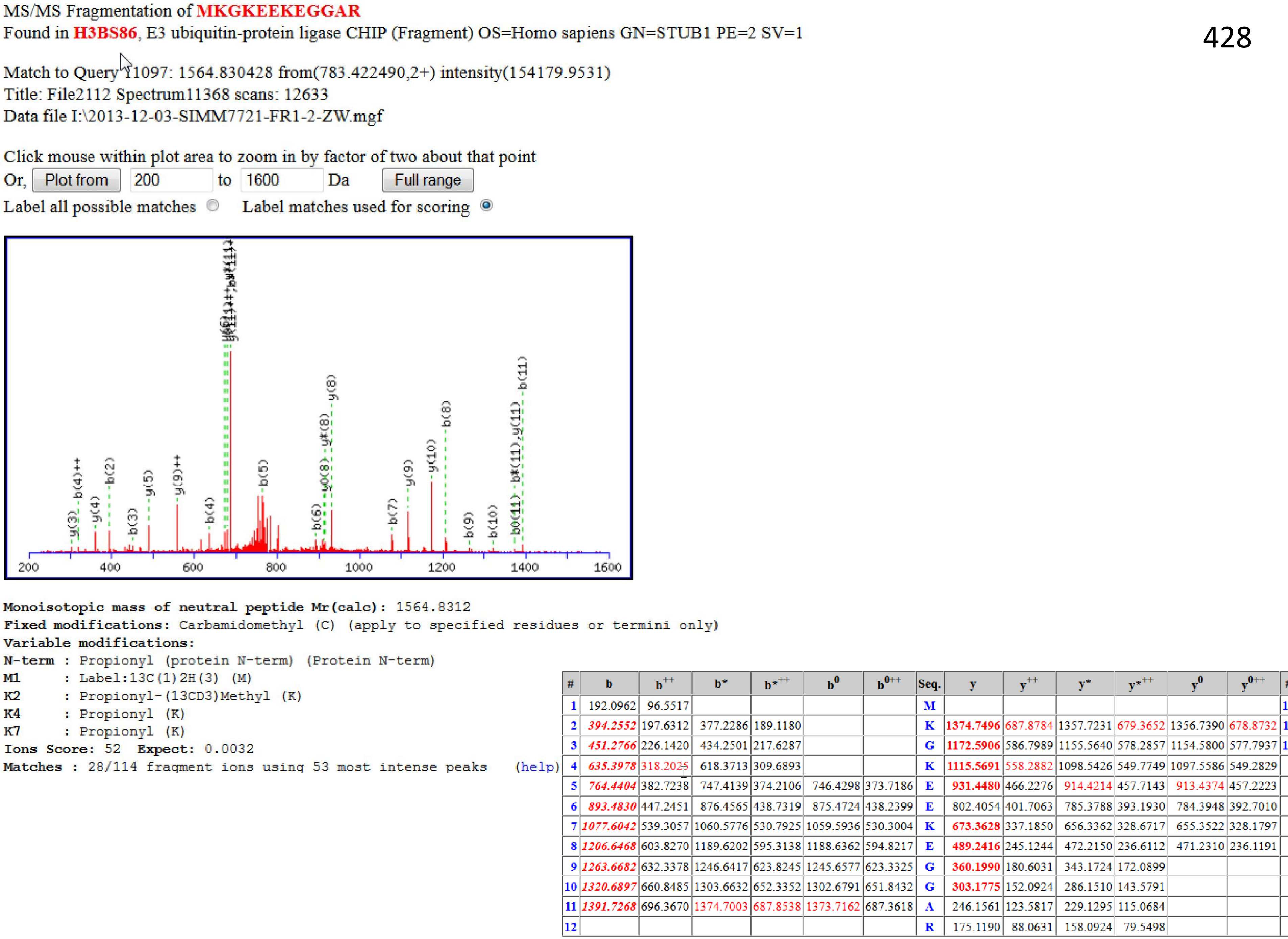
Match to Query 6766: 1616.978728 from(809.496640,2+) intensity(103500.7734)
Title: File1296 Spectrum11928 scans: 13586
Data file I:\2013-9-12-Hela-Prometh-Fr14-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1616.9774
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K5      : Propionyl (K)
K6      : Propionyl (K)
K8      : Propionyl-(13CD3)Methyl (K)
Ions Score: 65  Expect: 9.8e-005
Matches : 19/114 fragment ions using 28 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							12
2	211.1441	106.0757					P	1504.9006	752.9540	1487.8741	744.4407	1486.8901	743.9487	11
3	**298.1761**	149.5917			280.1656	140.5864	S	***1407.8479***	704.4276	1390.8213	695.9143	1389.8373	695.4223	10
4	369.2132	185.1103			351.2027	176.1050	A	***1320.8158***	660.9116	1303.7893	652.3983	1302.8053	651.9063	9
5	**553.3344**	277.1709	536.3079	268.6576	535.3239	268.1656	K	***1249.7787***	625.3930	1232.7522	616.8797	1231.7682	616.3877	8
6	737.4556	369.2314	720.4291	360.7182	719.4450	360.2262	K	***1065.6575***	533.3324	1048.6310	524.8191	1047.6470	524.3271	7
7	900.5189	450.7631	883.4924	442.2498	882.5084	441.7578	Y	***881.5364***	441.2718	864.5098	432.7585	863.5258	432.2665	6
8	1102.6779	551.8426	1085.6514	543.3293	1084.6674	542.8373	K	***718.4730***	359.7402	701.4465	351.2269	700.4625	350.7349	5
9	**1217.7049**	609.3561	1200.6783	600.8428	1199.6943	600.3508	D	***516.3140***	258.6606	499.2875	250.1474	498.3035	249.6554	4
10	1330.7890	665.8981	1313.7624	657.3848	1312.7784	656.8928	I	***401.2871***	201.1472	384.2605	192.6339			3
11	**1443.8730**	722.4401	1426.8465	713.9269	1425.8624	713.4349	I	***288.2030***	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1



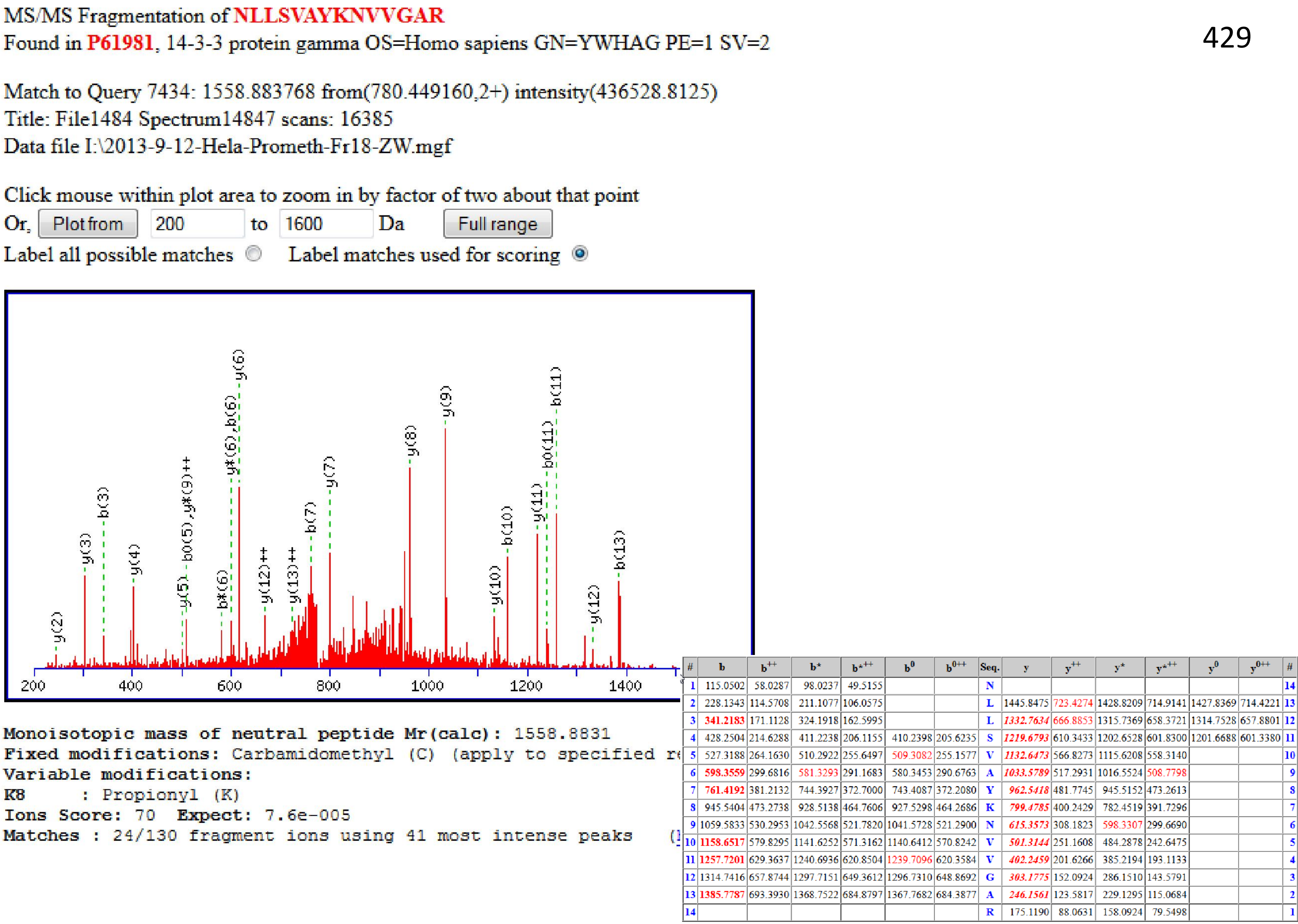
MS/MS Fragmentation of **MKGKEEKEGGAR**
Found in **H3BS86**, E3 ubiquitin-protein ligase CHIP (Fragment) OS=Homo sapiens GN=STUB1 PE=2 SV=1

Match to Query 11097: 1564.830428 from(783.422490,2+) intensity(154179.9531)
Title: File2112 Spectrum11368 scans: 12633
Data file I:\2013-12-03-SIMM7721-FR1-2-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

Monoisotopic mass of neutral peptide Mr(calc): 1564.8312
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N-term : Propionyl (protein N-term) (Protein N-term)
M1 : Label:13C(1)2H(3) (M)
K2 : Propionyl-(13CD3)Methyl (K)
K4 : Propionyl (K)
K7 : Propionyl (K)
Ions Score: 52 **Expect:** 0.0032
Matches : 28/114 fragment ions using 53 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	192.0962	96.5517					M							12
2	394.2552	197.6312	377.2286	189.1180			K	1374.7496	687.8784	1357.7231	679.3652	1356.7390	678.8732	11
3	451.2766	226.1420	434.2501	217.6287			G	1172.5906	586.7989	1155.5640	578.2857	1154.5800	577.7937	10
4	635.3978	318.2025	618.3713	309.6893			K	1115.5691	558.2882	1098.5426	549.7749	1097.5586	549.2829	9
5	764.4404	382.7238	747.4139	374.2106	746.4298	373.7186	E	931.4480	466.2276	914.4214	457.7143	913.4374	457.2223	8
6	893.4830	447.2451	876.4565	438.7319	875.4724	438.2399	E	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	7
7	1077.6042	539.3057	1060.5776	530.7925	1059.5936	530.3004	K	673.3628	337.1850	656.3362	328.6717	655.3522	328.1797	6
8	1206.6468	603.8270	1189.6202	595.3138	1188.6362	594.8217	E	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	5
9	1263.6682	632.3378	1246.6417	623.8245	1245.6577	623.3325	G	360.1990	180.6031	343.1724	172.0899			4
10	1320.6897	660.8485	1303.6632	652.3352	1302.6791	651.8432	G	303.1775	152.0924	286.1510	143.5791			3
11	1391.7268	696.3670	1374.7003	687.8538	1373.7162	687.3618	A	246.1561	123.5817	229.1295	115.0684			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of NLLSVAYKNVVGAR

Found in P61981, 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2

Match to Query 7434: 1558.883768 from(780.449160,2+) intensity(436528.8125)

Title: File1484 Spectrum14847 scans: 16385

Data file I:\2013-9-12-Hela-Prometh-Fr18-ZW.mgf

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

Or, Plot from 200 to 1600 Da Full range

Label all possible matches ○ Label matches used for scoring ●

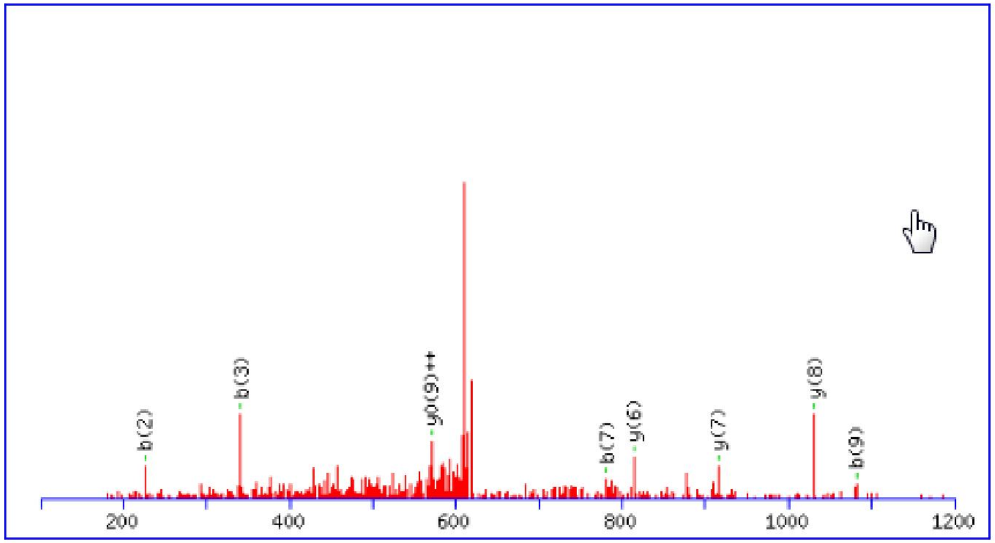
```
Monoisotopic mass of neutral peptide Mr(calc): 1558.8831
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K8      : Propionyl (K)
Ions Score: 70   Expect: 7.6e-005
Matches : 24/130 fragment ions using 41 most intense peaks
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							14
2	228.1343	114.5708	211.1077	106.0575			L	1445.8475	723.4274	1428.8209	714.9141	1427.8369	714.4221	13
3	**341.2183**	171.1128	324.1918	162.5995			L	***1332.7634***	666.8853	1315.7369	658.3721	1314.7528	657.8801	12
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	***1219.6793***	610.3433	1202.6528	601.8300	1201.6688	601.3380	11
5	527.3188	264.1630	510.2922	255.6497	509.3082	255.1577	V	***1132.6473***	566.8273	1115.6208	558.3140			10
6	**598.3559**	299.6816	581.3293	291.1683	580.3453	290.6763	A	***1033.5789***	517.2931	1016.5524	508.7798			9
7	**761.4192**	381.2132	744.3927	372.7000	743.4087	372.2080	Y	***962.5418***	481.7745	945.5152	473.2613			8
8	945.5404	473.2738	928.5138	464.7606	927.5298	464.2686	K	***799.4785***	400.2429	782.4519	391.7296			7
9	1059.5833	530.2953	1042.5568	521.7820	1041.5728	521.2900	N	***615.3573***	308.1823	598.3307	299.6690			6
10	**1158.6517**	579.8295	1141.6252	571.3162	1140.6412	570.8242	V	***501.3144***	251.1608	484.2878	242.6475			5
11	**1257.7201**	629.3637	1240.6936	620.8504	1239.7096	620.3584	V	***402.2459***	201.6266	385.2194	193.1133			4
12	1314.7416	657.8744	1297.7151	649.3612	1296.7310	648.8692	G	***303.1775***	152.0924	286.1510	143.5791			3
13	**1385.7787**	693.3930	1368.7522	684.8797	1367.7682	684.3877	A	***246.1561***	123.5817	229.1295	115.0684			2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **PQDTKPGVKR**
Found in **H0Y3K4**, RNA-binding protein 33 (Fragment) OS=Homo sapiens GN=RBM33 PE=4 SV=1

Match to Query 7071: 1254.719448 from(628.367000,2+) intensity(35620.6836)
Title: File320 Spectrum6206 scans: 7243
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\k562\2013-5-23-562-Kpropio-methyl-IP-Fr5-ZW.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 ●



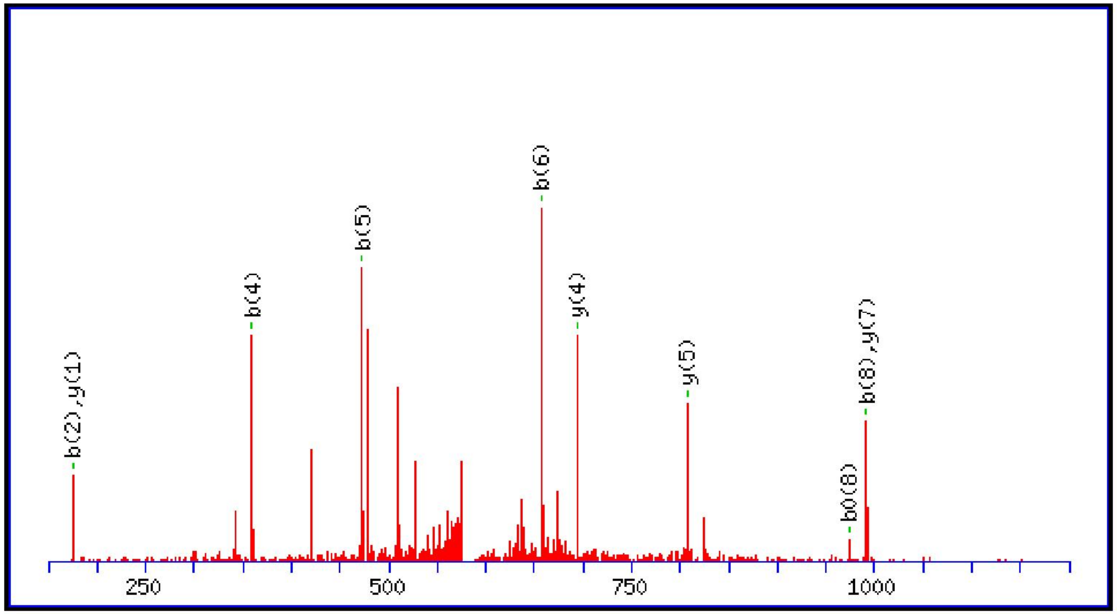
```
Monoisotopic mass of neutral peptide Mr(calc): 1254.7205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K5     : Propionyl (K)
K9     : Propionyl-(13CD3)Methyl (K)
Ions Score: 29  Expect: 0.47
Matches : 8/90 fragment ions using 11 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	98.0600	49.5337					P							10
2	***226.1186***	113.5629	209.0921	105.0497			Q	1158.6750	579.8411	1141.6484	571.3279	1140.6644	570.8358	9
3	***341.1456***	171.0764	324.1190	162.5631	323.1350	162.0711	D	***1030.6164***	515.8118	1013.5899	507.2986	1012.6058	506.8066	8
4	442.1932	221.6003	425.1667	213.0870	424.1827	212.5950	T	***915.5895***	458.2984	898.5629	449.7851	897.5789	449.2931	7
5	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	K	***814.5418***	407.7745	797.5152	399.2613			6
6	723.3672	362.1872	706.3406	353.6740	705.3566	353.1819	P	630.4206	315.7139	613.3941	307.2007			5
7	***780.3886***	390.6980	763.3621	382.1847	762.3781	381.6927	G	533.3678	267.1876	516.3413	258.6743			4
8	879.4571	440.2322	862.4305	431.7189	861.4465	431.2269	V	476.3464	238.6768	459.3198	230.1636			3
9	***1081.6161***	541.3117	1064.5895	532.7984	1063.6055	532.3064	K	377.2780	189.1426	360.2514	180.6293			2
10							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of SSALIKHKR
Found in Q5TEG9, Zinc finger protein 436 OS=Homo sapiens GN=ZNF436 PE=2 SV=1

Match to Query 2760: 1164.686628 from(583.350590,2+) intensity(358703.2813)
Title: File1332 Spectrum11041 scans: 12288
Data file I:\2013-9-14-Hela-Prometh-Fr10-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



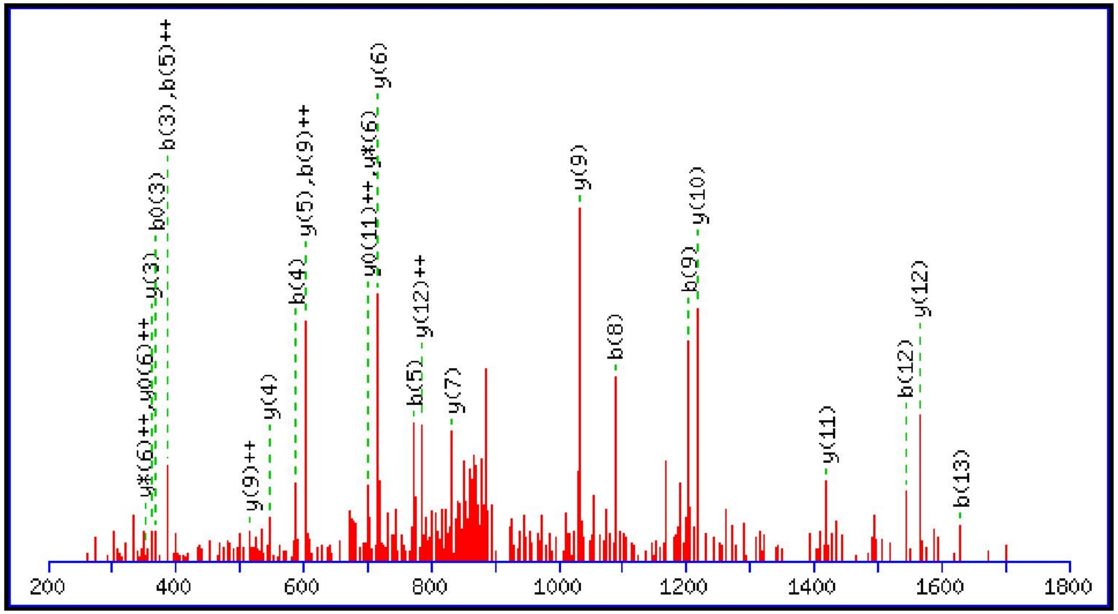
Monoisotopic mass of neutral peptide Mr(calc): 1164.6979
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K6 : Propionyl (K)
K8 : Propionyl-Methylation (K)
Ions Score: 39 **Expect:** 0.056
Matches : 10/72 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	175.0713	88.0393			157.0608	79.0340	S	1078.6731	539.8402	1061.6466	531.3269	1060.6626	530.8349	8
3	246.1084	123.5579			228.0979	114.5526	A	991.6411	496.3242	974.6146	487.8109			7
4	359.1925	180.0999			341.1819	171.0946	L	920.6040	460.8056	903.5774	452.2924			6
5	472.2766	236.6419			454.2660	227.6366	I	807.5199	404.2636	790.4934	395.7503			5
6	656.3978	328.7025	639.3712	320.1892	638.3872	319.6972	K	694.4359	347.7216	677.4093	339.2083			4
7	793.4567	397.2320	776.4301	388.7187	775.4461	388.2267	H	510.3147	255.6610	493.2881	247.1477			3
8	991.5935	496.3004	974.5669	487.7871	973.5829	487.2951	K	373.2558	187.1315	356.2292	178.6183			2
9							R	175.1190	88.0631	158.0924	79.5498			1

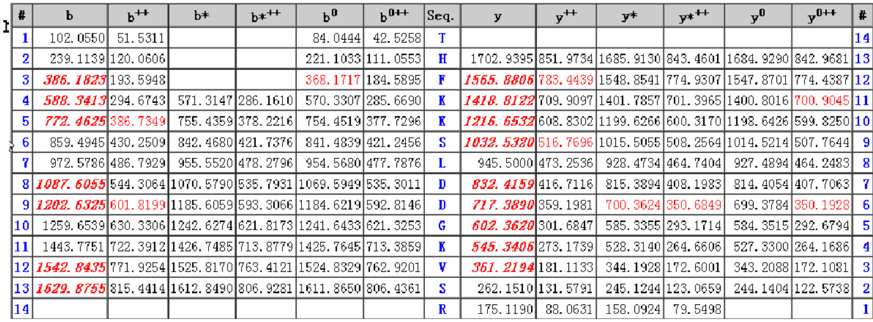
MS/MS Fragmentation of THFKKSLDDGKVSR
Found in F5H0L8, SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=2 SV=1

Match to Query 12640: 1802.979348 from(902.496950,2+) intensity(32097.1836)
Title: File394 Spectrum10127 scans: 11437
Data file \\192.168.1.104\public\raw data\Elite_01\methylation_ZW\SW620\2013-5-16-620-Kpropio-methyl-IP-Fr8-ZW.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 ●



Monoisotopic mass of neutral peptide Mr(calc): 1802.9799
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or
Variable modifications:
K4 : Propionyl-(13CD3)Methyl (K)
K5 : Propionyl (K)
K11 : Propionyl (K)
Ions Score: 45 **Expect:** 0.017
Matches : 25/148 fragment ions using 44 most intense peaks (help)

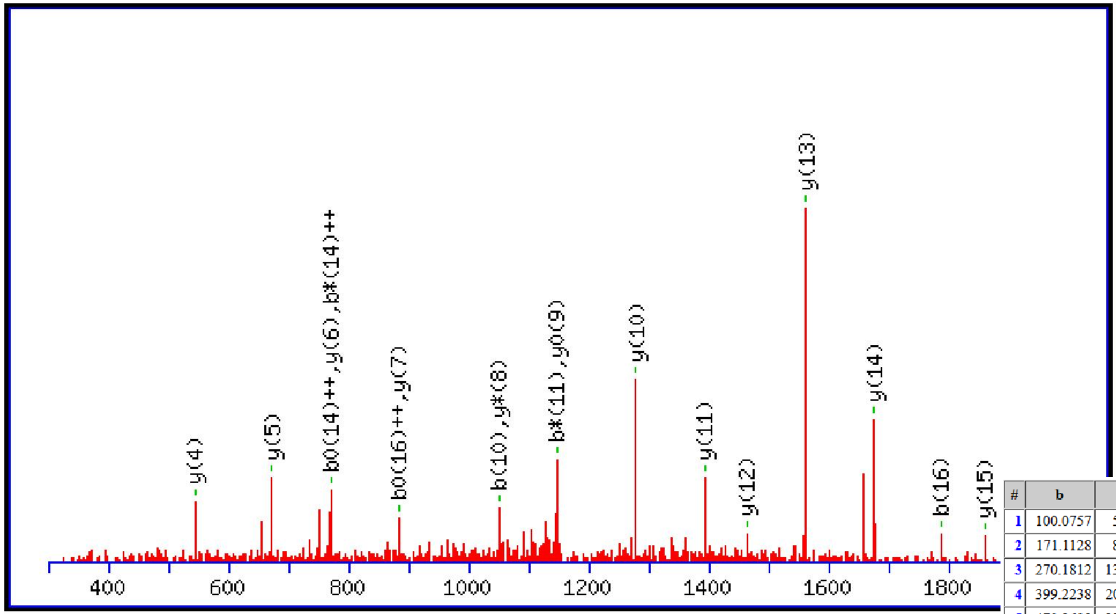


#	b	b^{++}	b*	$b*^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^0	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	239.1139	120.0606			221.1033	111.0553	H	1702.9395	851.9734	1685.9130	843.4601	1684.9290	842.9681	13
3	**386.1823**	193.5948			368.1717	184.5895	F	**1565.8806**	783.4439	1548.8541	774.9307	1547.8701	774.4387	12
4	**588.3413**	294.6743	571.3147	286.1610	570.3307	285.6690	K	**1418.8122**	709.9097	1401.7857	701.3965	1400.8016	700.9045	11
5	**772.4625**	386.7349	755.4359	378.2216	754.4519	377.7296	K	**1216.6532**	608.8302	1199.6266	600.3170	1198.6426	599.8250	10
6	859.4945	430.2509	842.4680	421.7376	841.4839	421.2456	S	**1032.5320**	516.7696	1015.5055	508.2564	1014.5214	507.7644	9
7	972.5786	486.7929	955.5520	478.2796	954.5680	477.7876	L	945.5000	473.2536	928.4734	464.7404	927.4894	464.2483	8
8	**1087.6055**	544.3064	1070.5790	535.7931	1069.5949	535.3011	D	**832.4159**	416.7116	815.3894	408.1983	814.4054	407.7063	7
9	**1202.6325**	601.8199	1185.6059	593.3066	1184.6219	592.8146	D	**717.3890**	359.1981	700.3624	350.6849	699.3784	350.1928	6
10	1259.6539	630.3306	1242.6274	621.8173	1241.6433	621.3253	G	**602.3620**	301.6847	585.3355	293.1714	584.3515	292.6794	5
11	1443.7751	722.3912	1426.7485	713.8779	1425.7645	713.3859	K	**545.3406**	273.1739	528.3140	264.6606	527.3300	264.1686	4
12	**1542.8435**	771.9254	1525.8170	763.4121	1524.8329	762.9201	V	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
13	**1629.8755**	815.4414	1612.8490	806.9281	1611.8650	806.4361	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VAVEAKNPADLPKLVEGLKR**
Found in **P13639**, Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

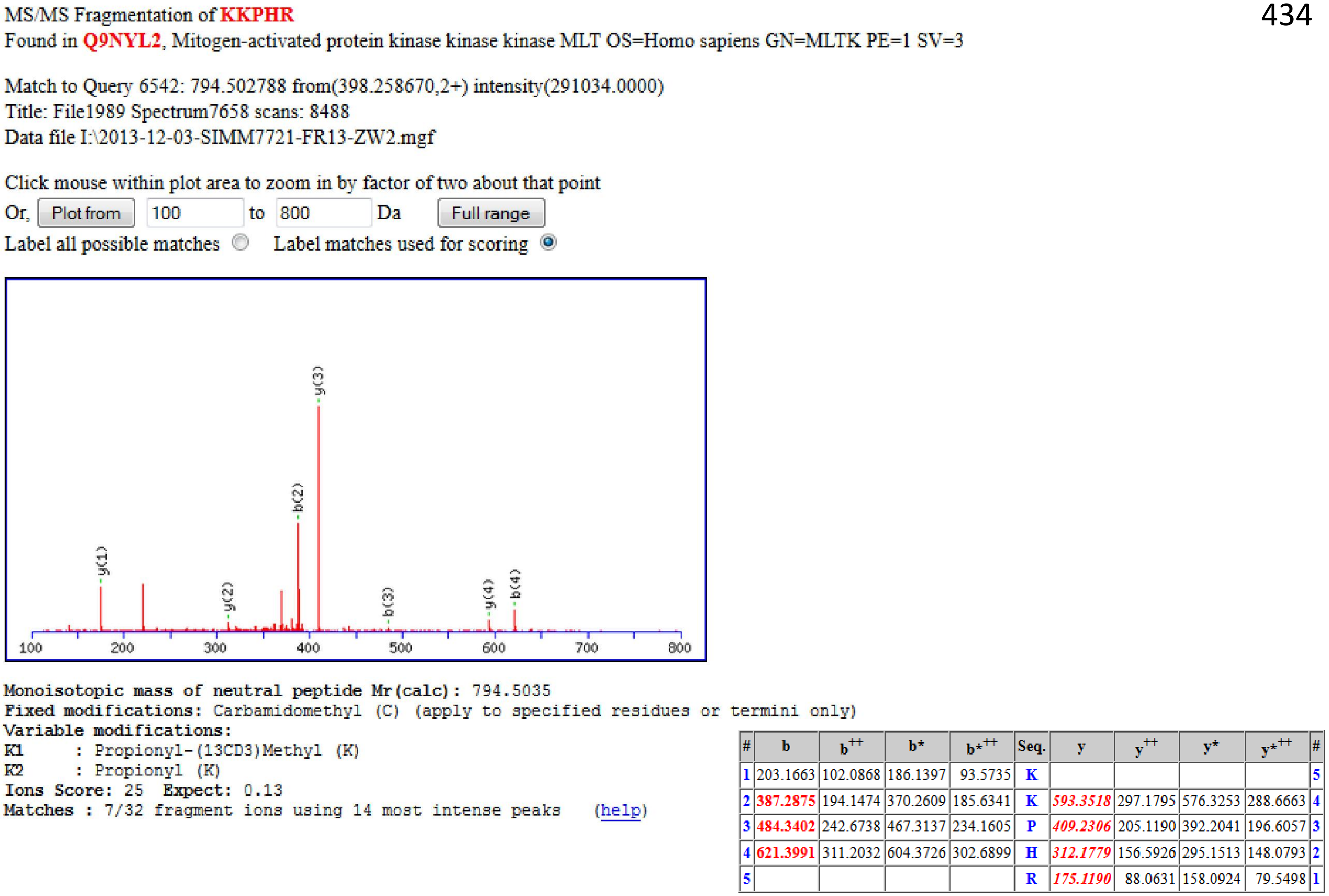
Match to Query 14960: 2328.340908 from(1165.177730,2+) intensity(69909.9141)
Title: File1308 Spectrum18902 scans: 20356
Data file I:\2013-9-12-Hela-Prometh-Fr4-ZW.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 300 to 2000 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2328.3416
Fixed modifications: Carbamidomethyl (C) (apply to specified r
Variable modifications:
K6      : Propionyl (K)
K13     : Propionyl (K)
K19     : Propionyl-Methylation (K)
Ions Score: 78  Expect: 7.5e-006
Matches : 18/204 fragment ions using 17 most intense peaks   (
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							20
2	171.1128	86.0600					A	2230.2805	1115.6439	2213.2540	1107.1306	2212.2700	1106.6386	19
3	270.1812	135.5942					V	2159.2434	1080.1254	2142.2169	1071.6121	2141.2329	1071.1201	18
4	399.2238	200.1155			381.2132	191.1103	E	2060.1750	1030.5911	2043.1485	1022.0779	2042.1645	1021.5859	17
5	470.2609	235.6341			452.2504	226.6288	A	1931.1324	966.0699	1914.1059	957.5566	1913.1219	957.0646	16
6	654.3821	327.6947	637.3556	319.1814	636.3715	318.6894	K	***1860.0953***	930.5513	1843.0688	922.0380	1842.0847	921.5460	15
7	768.4250	384.7162	751.3985	376.2029	750.4145	375.7109	N	***1675.9741***	838.4907	1658.9476	829.9774	1657.9636	829.4854	14
8	865.4778	433.2425	848.4512	424.7293	847.4672	424.2373	P	***1561.9312***	781.4692	1544.9047	772.9560	1543.9206	772.4640	13
9	936.5149	468.7611	919.4884	460.2478	918.5043	459.7558	A	***1464.8784***	732.9429	1447.8519	724.4296	1446.8679	723.9376	12
10	**1051.5419**	526.2746	1034.5153	517.7613	1033.5313	517.2693	D	***1393.8413***	697.4243	1376.8148	688.9110	1375.8308	688.4190	11
11	1164.6259	582.8166	1147.5994	574.3033	1146.6153	573.8113	L	***1278.8144***	639.9108	1261.7878	631.3976	1260.8038	630.9055	10
12	1261.6787	631.3430	1244.6521	622.8297	1243.6681	622.3377	P	1165.7303	583.3688	1148.7038	574.8555	1147.7198	574.3635	9
13	1445.7999	723.4036	1428.7733	714.8903	1427.7893	714.3983	K	1068.6776	534.8424	1051.6510	526.3291	1050.6670	525.8371	8
14	1558.8839	779.9456	1541.8574	771.4323	1540.8734	770.9403	L	***884.5564***	442.7818	867.5298	434.2686	866.5458	433.7765	7
15	1657.9523	829.4798	1640.9258	820.9665	1639.9418	820.4745	V	***771.4723***	386.2398	754.4458	377.7265	753.4617	377.2345	6
16	**1786.9949**	894.0011	1769.9684	885.4878	1768.9844	884.9958	E	***672.4039***	336.7056	655.3774	328.1923	654.3933	327.7003	5
17	1844.0164	922.5118	1826.9898	913.9986	1826.0058	913.5066	G	***543.3613***	272.1843	526.3348	263.6710			4
18	1957.1005	979.0539	1940.0739	970.5406	1939.0899	970.0486	L	486.3398	243.6736	469.3133	235.1603			3
19	2155.2373	1078.1223	2138.2107	1069.6090	2137.2267	1069.1170	K	373.2558	187.1315	356.2292	178.6183			2
20							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KKPHR**
Found in **Q9NYL2**, Mitogen-activated protein kinase kinase kinase MLT OS=Homo sapiens GN=MLTK PE=1 SV=3

Match to Query 6542: 794.502788 from(398.258670,2+) intensity(291034.0000)
Title: File1989 Spectrum7658 scans: 8488
Data file I:\2013-12-03-SIMM7721-FR13-ZW2.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 794.5035
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Propionyl-(13CD3)Methyl (K)
K2      : Propionyl (K)
Ions Score: 25  Expect: 0.13
Matches : 7/32 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	203.1663	102.0868	186.1397	93.5735	K					5
2	**387.2875**	194.1474	370.2609	185.6341	K	*593.3518*	297.1795	576.3253	288.6663	4
3	**484.3402**	242.6738	467.3137	234.1605	P	*409.2306*	205.1190	392.2041	196.6057	3
4	**621.3991**	311.2032	604.3726	302.6899	H	*312.1779*	156.5926	295.1513	148.0793	2
5					R	*175.1190*	88.0631	158.0924	79.5498	1