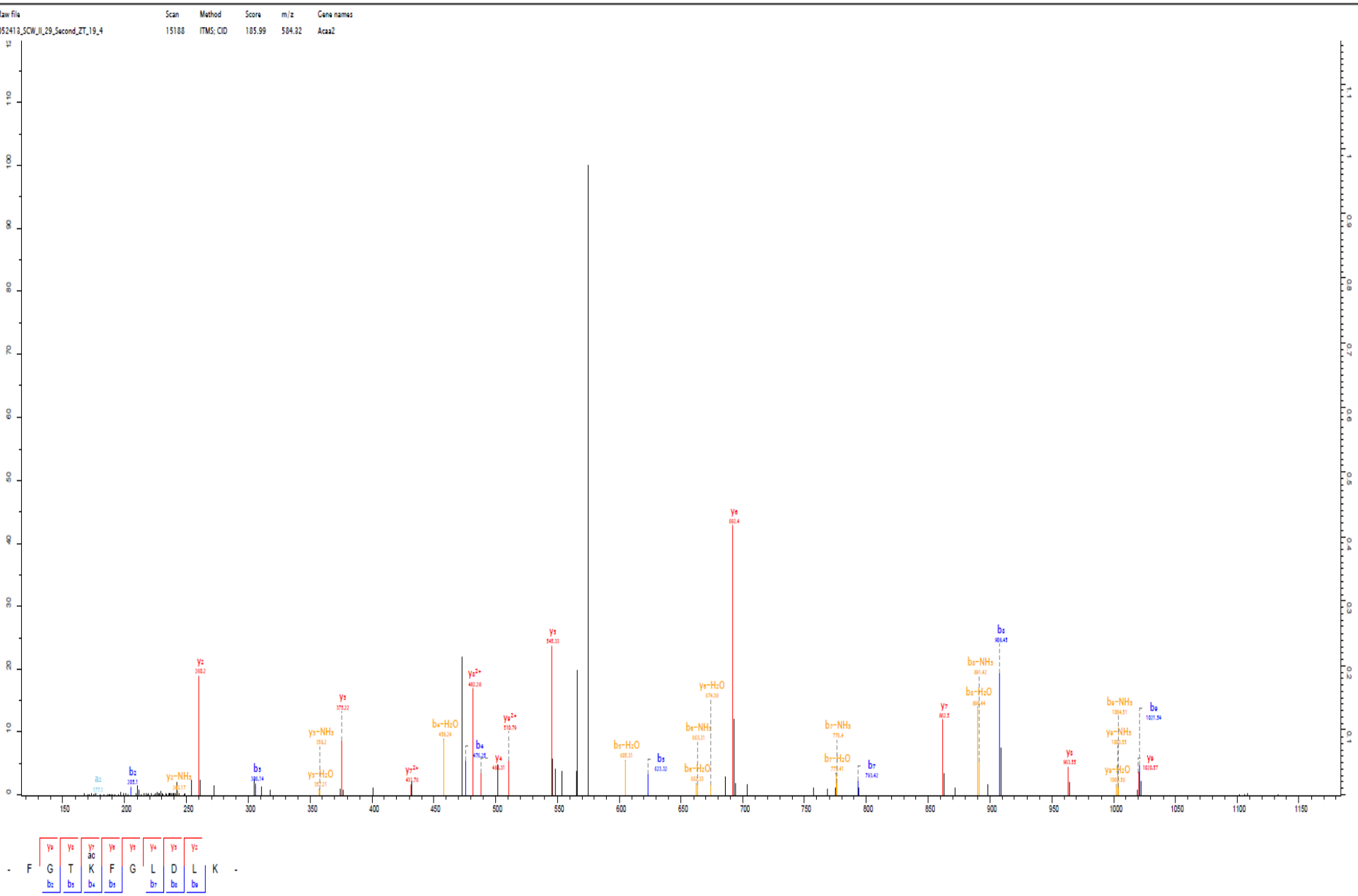
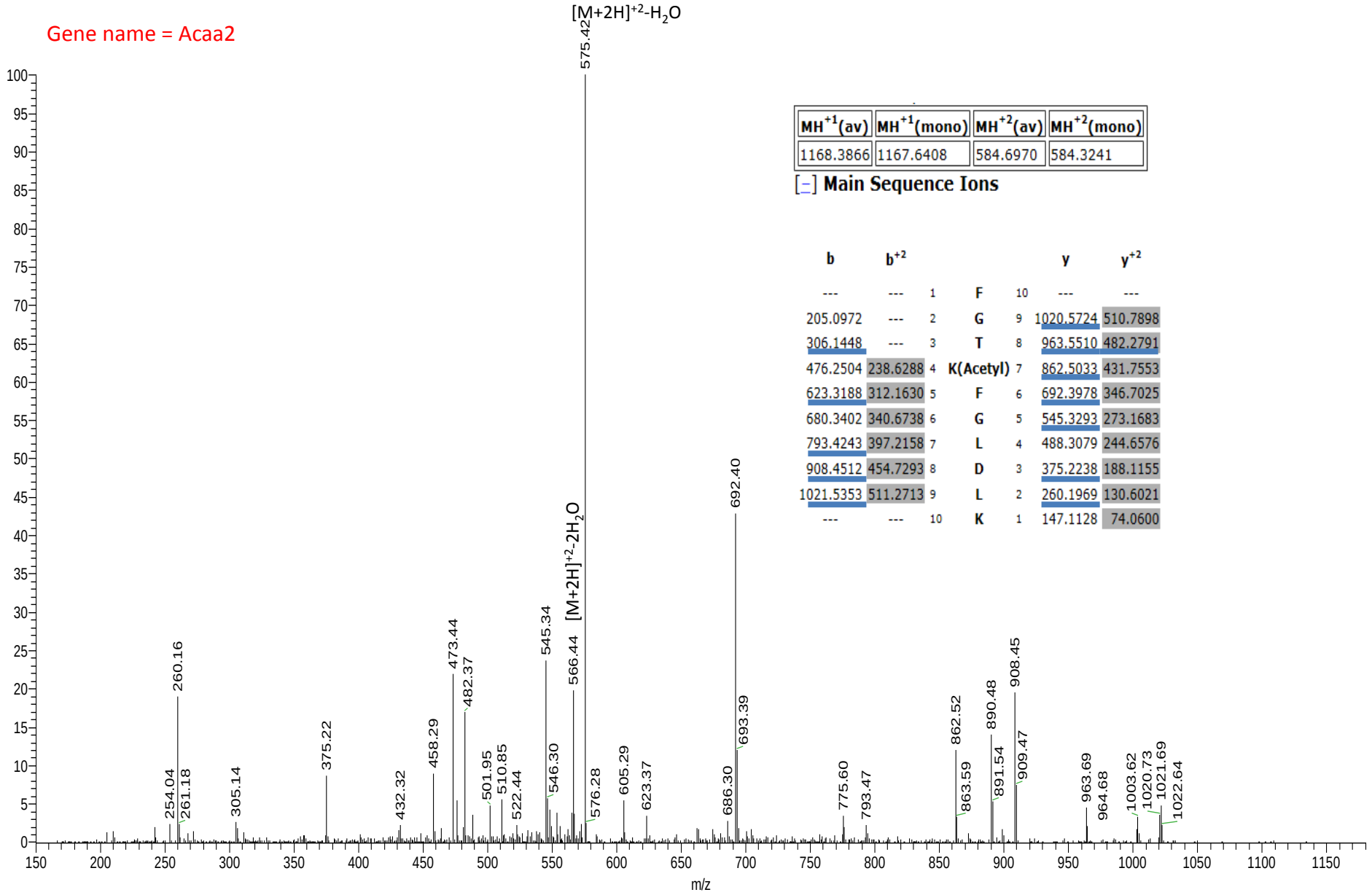
Raw file	Scan	Method	Score	m/z	Gene names
052418_SCW_II_29_Second_ZT_19_4	15188	ITMS; CID	185.99	584.32	Acaa2



- F G T K F G L D L K -

052413_SCW_II_29_Second_ZT_19_4 #15188 RT: 82.56 AV: 1 NL: 9.74E3
T: ITMS + c NSI d Full ms2 584.32@cid35.00 [150.00-1180.00]

Gene name = Acaa2

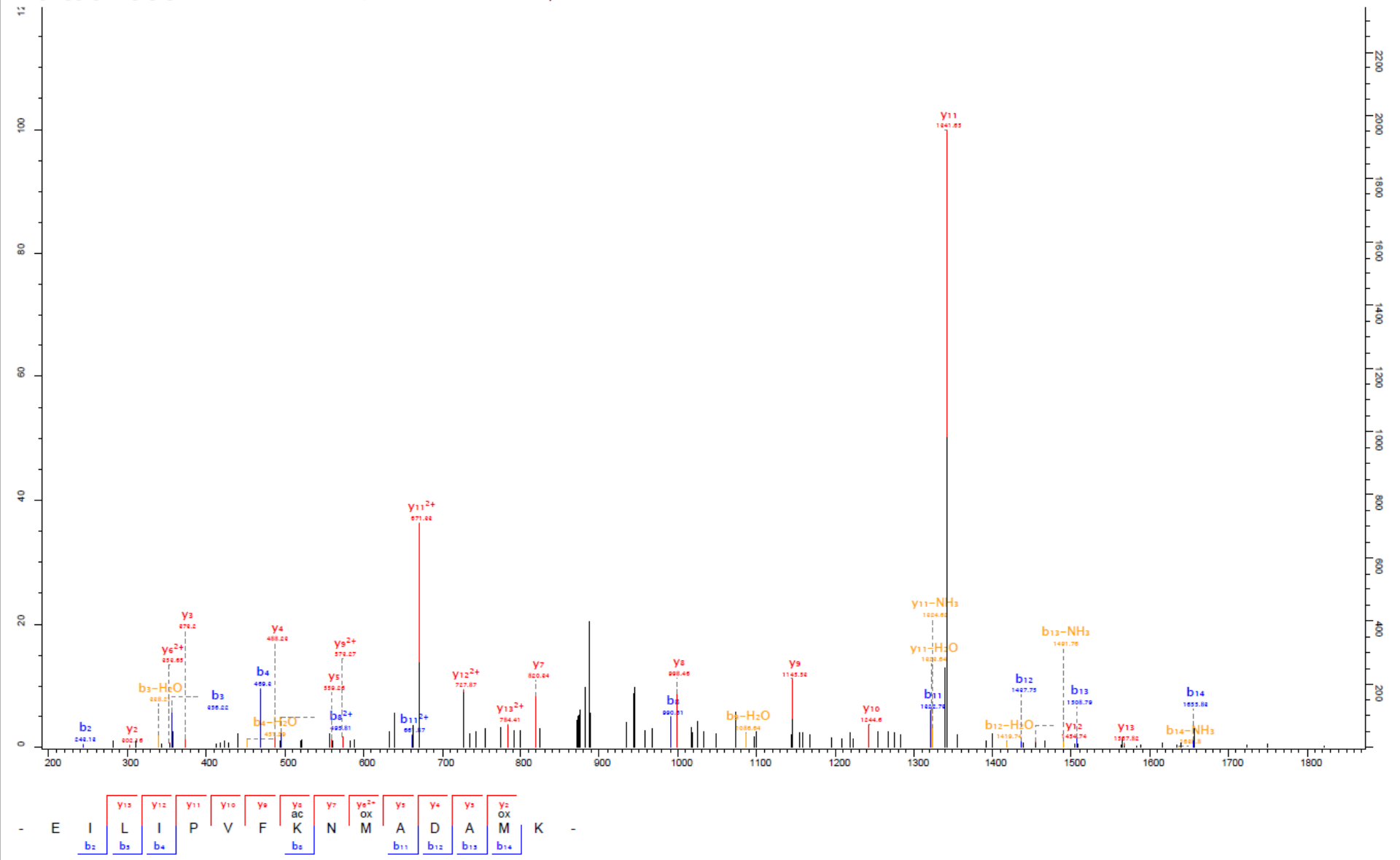


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)
1168.3866	1167.6408	584.6970	584.3241

[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	F	10	---	---
205.0972	---	2	G	9	1020.5724	510.7898
306.1448	---	3	T	8	963.5510	482.2791
476.2504	238.6288	4	K(Acetyl)	7	862.5033	431.7553
623.3188	312.1630	5	F	6	692.3978	346.7025
680.3402	340.6738	6	G	5	545.3293	273.1683
793.4243	397.2158	7	L	4	488.3079	244.6576
908.4512	454.7293	8	D	3	375.2238	188.1155
1021.5353	511.2713	9	L	2	260.1969	130.6021
---	---	10	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
052413_SCW_II_29_Second_ZT_16_3	13965	ITMS; CID	148.7	905.48	Acly



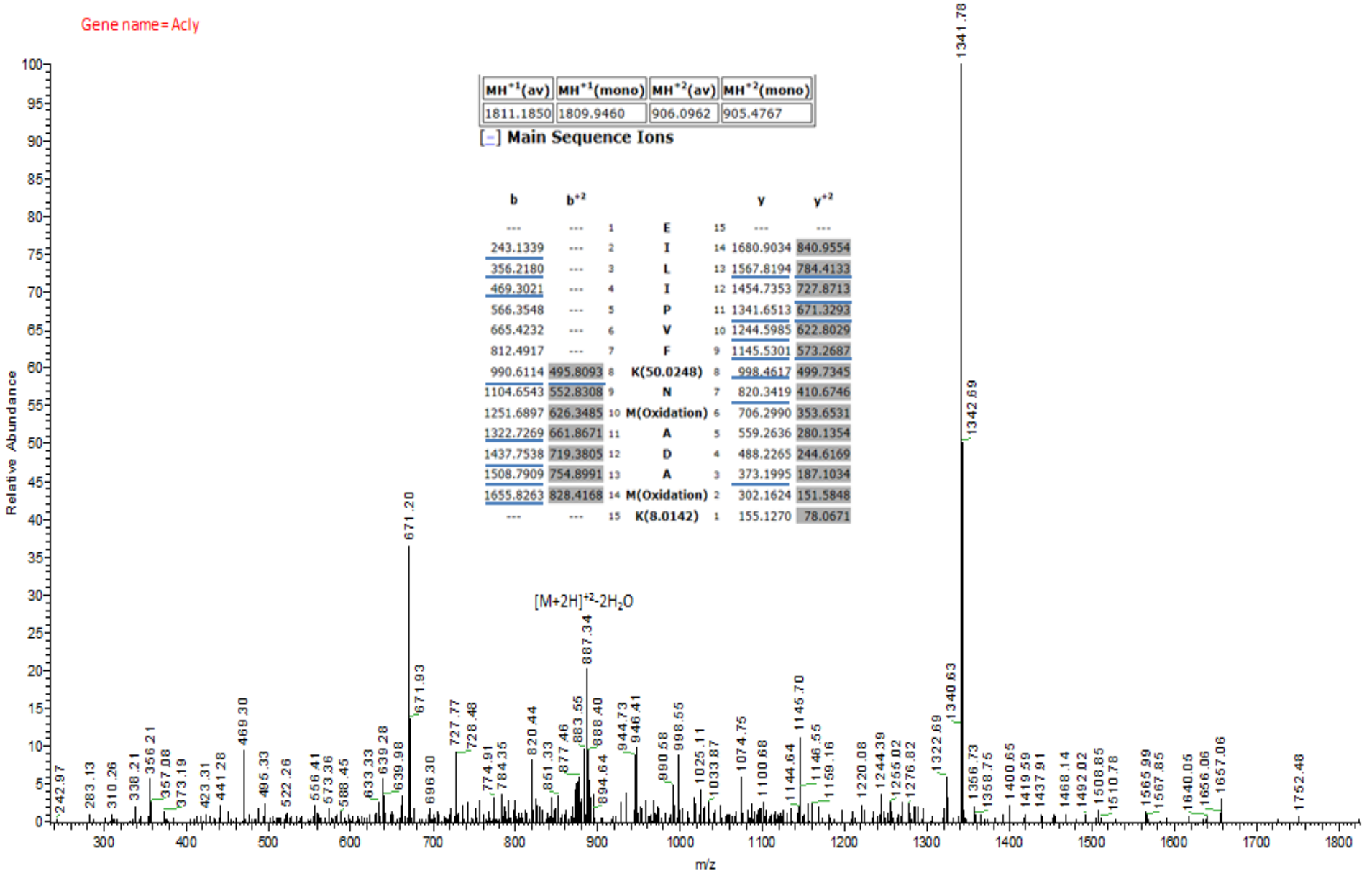
052413_SCW_II_29_Second_ZT_16_3 #13965 RT: 85.47 AV: 1 NL: 1.96E3
T: ITMS + c NSI d Full ms2 905.48@cid35.00 [235.00-1825.00]

Gene name = Acly

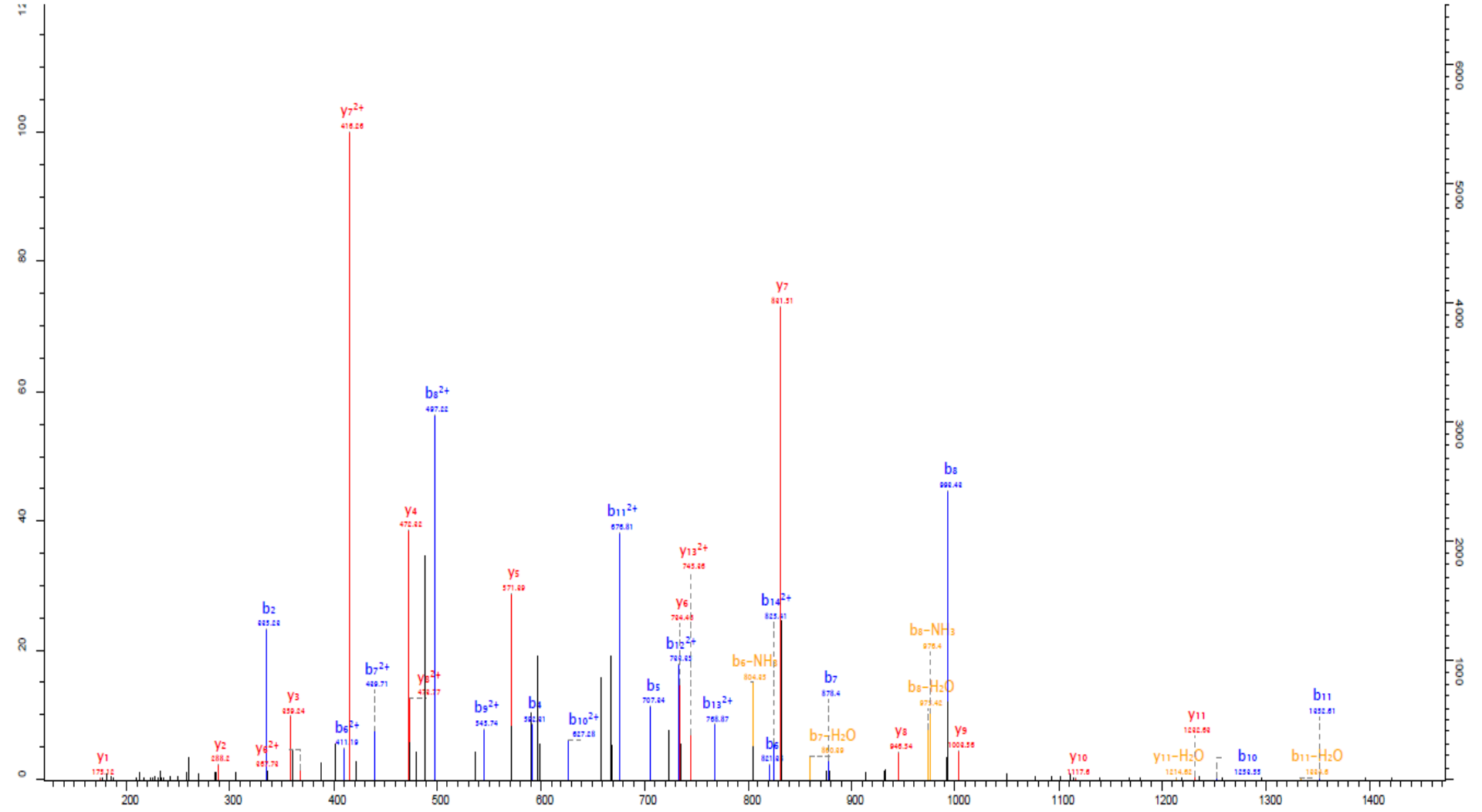
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1811.1850	1809.9460	906.0962	905.4767

[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	E	15	---	---
243.1339	---	2	I	14	1680.9034	840.9554
356.2180	---	3	L	13	1567.8194	784.4133
469.3021	---	4	I	12	1454.7353	727.8713
566.3548	---	5	P	11	1341.6513	671.3293
665.4232	---	6	V	10	1244.5985	622.8029
812.4917	---	7	F	9	1145.5301	573.2687
990.6114	495.8093	8	K(50.0248)	8	998.4617	499.7345
1104.6543	552.8308	9	N	7	820.3419	410.6746
1251.6897	626.3485	10	M(Oxidation)	6	706.2990	353.6531
1322.7269	661.8671	11	A	5	559.2636	280.1354
1437.7538	719.3805	12	D	4	488.2265	244.6169
1508.7909	754.8991	13	A	3	373.1995	187.1034
1655.8263	828.4168	14	M(Oxidation)	2	302.1624	151.5848
---	---	15	K(8.0142)	1	155.1270	78.0671

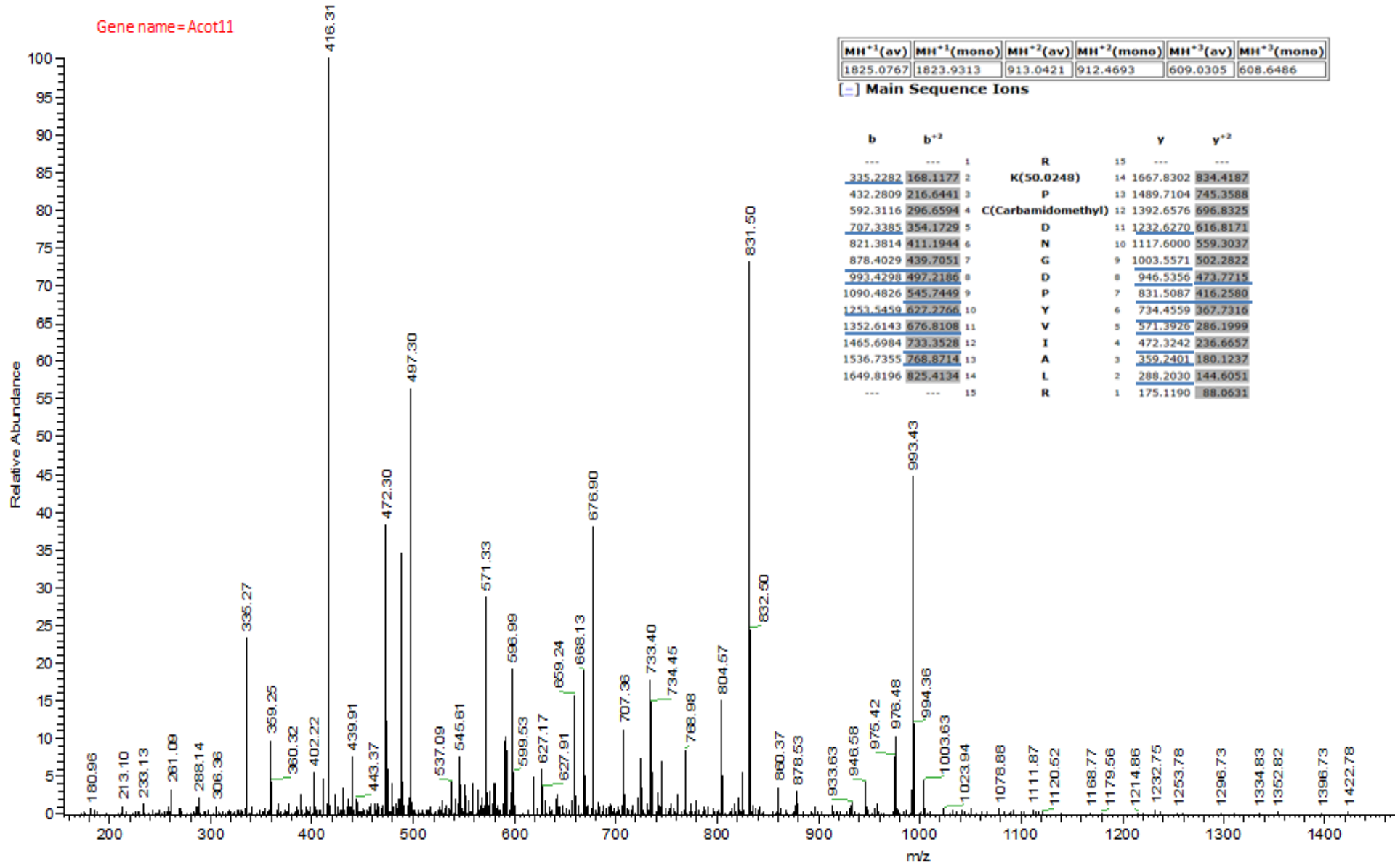


Raw file	Scan	Method	Score	m/z	Gene names
052413_SCW_II_29_Second_ZT_35_9	11568	ITMS; CID	178.67	608.65	Acot11



052413_SCW_II_29_Second_ZT_35_9 #11568 RT: 70.86 AV: 1 NL: 5.43E3
T: ITMS + c NSI d Full ms2 608.65@cid35.00 [155.00-1840.00]

Gene name = Acot11

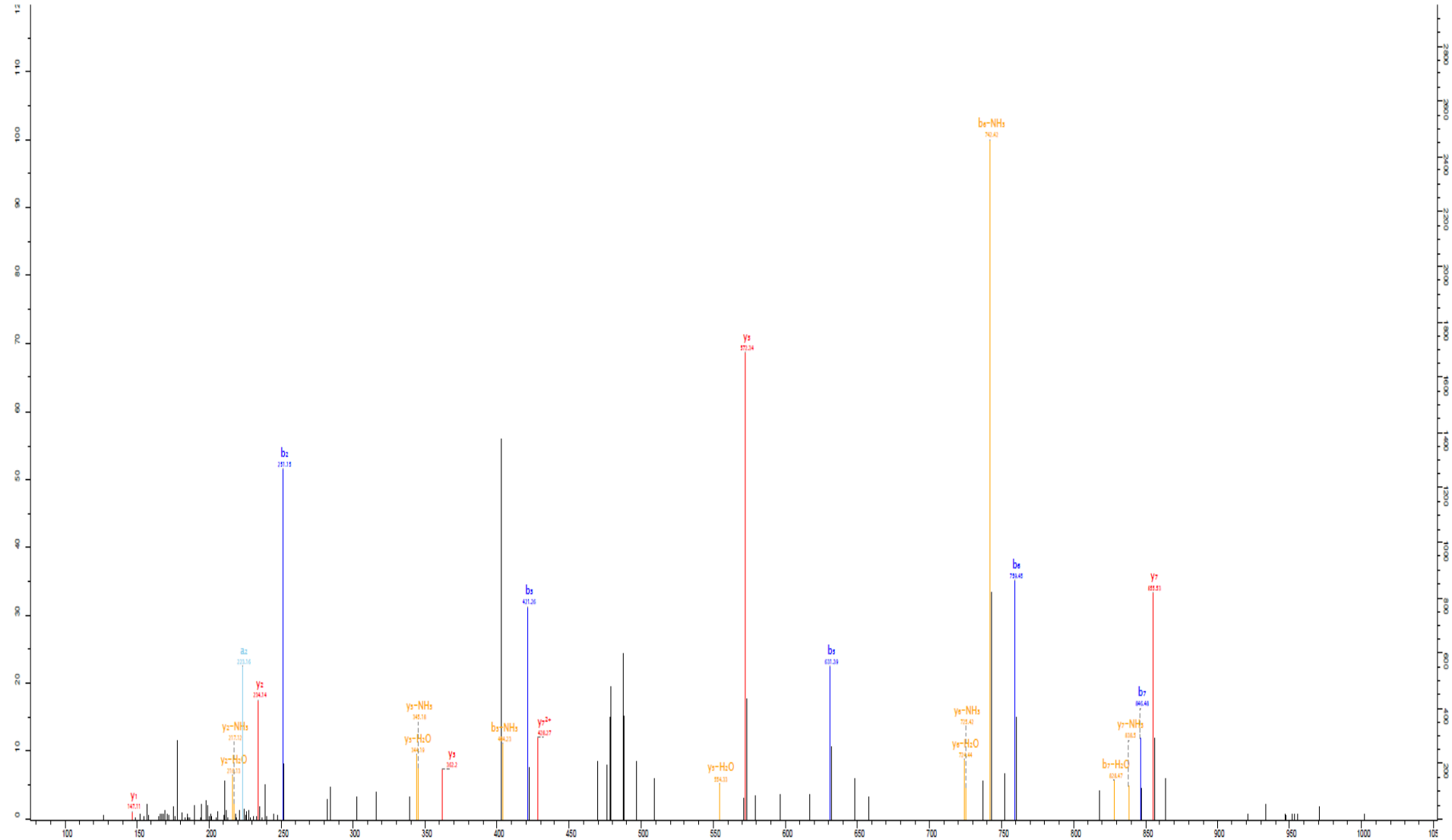


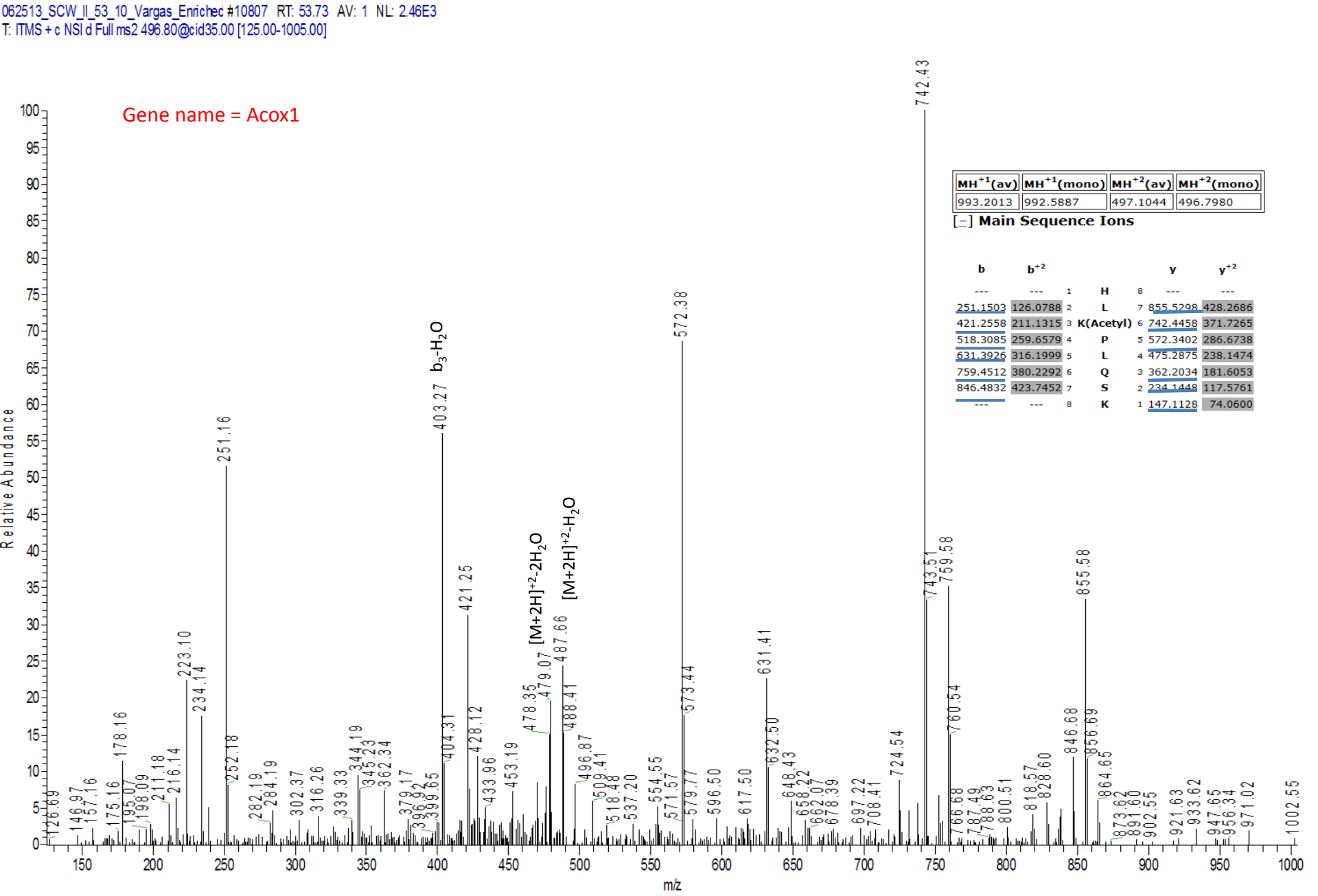
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1825.0767	1823.9313	913.0421	912.4693	609.0305	608.6486

[–] **Main Sequence Ions**

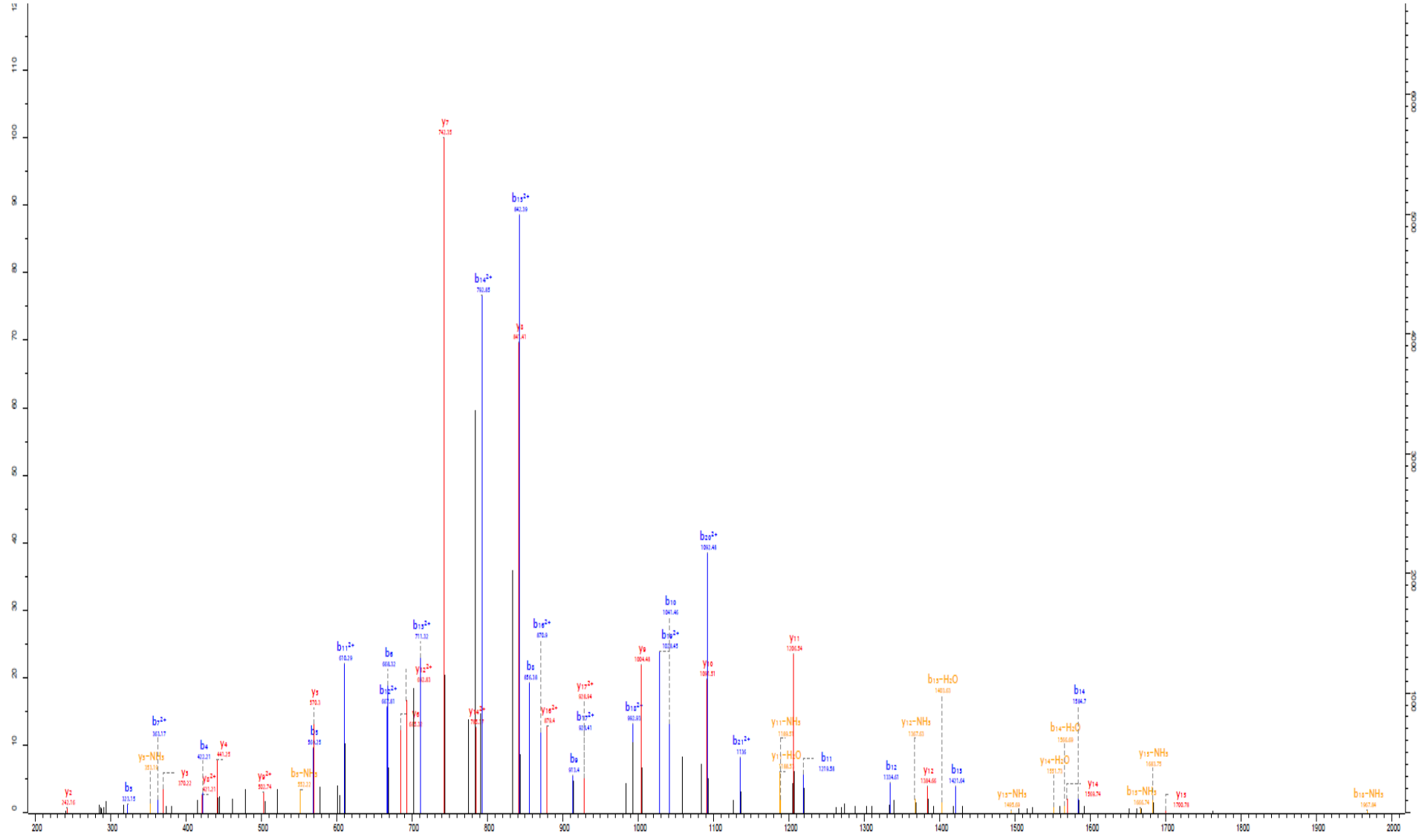
b	b^{+2}				y	y^{+2}
---	---	1	R	15	---	---
335.2282	168.1177	2	K(50.0248)	14	1667.8302	834.4187
432.2809	216.6441	3	P	13	1489.7104	745.3588
592.3116	296.6594	4	C(Carbamidomethyl)	12	1392.6576	696.8325
707.3385	354.1729	5	D	11	1232.6270	616.8171
821.3814	411.1944	6	N	10	1117.6000	559.3037
878.4029	439.7051	7	G	9	1003.5571	502.2822
993.4298	497.2186	8	D	8	946.5356	473.7715
1090.4826	545.7449	9	P	7	831.5087	416.2580
1253.5459	627.2766	10	Y	6	734.4559	367.7316
1352.6143	676.8108	11	V	5	571.3926	286.1999
1465.6984	733.3528	12	I	4	472.3242	236.6657
1536.7355	768.8714	13	A	3	359.2401	180.1237
1649.8196	825.4134	14	L	2	288.2030	144.6051
---	---	15	R	1	175.1190	88.0631

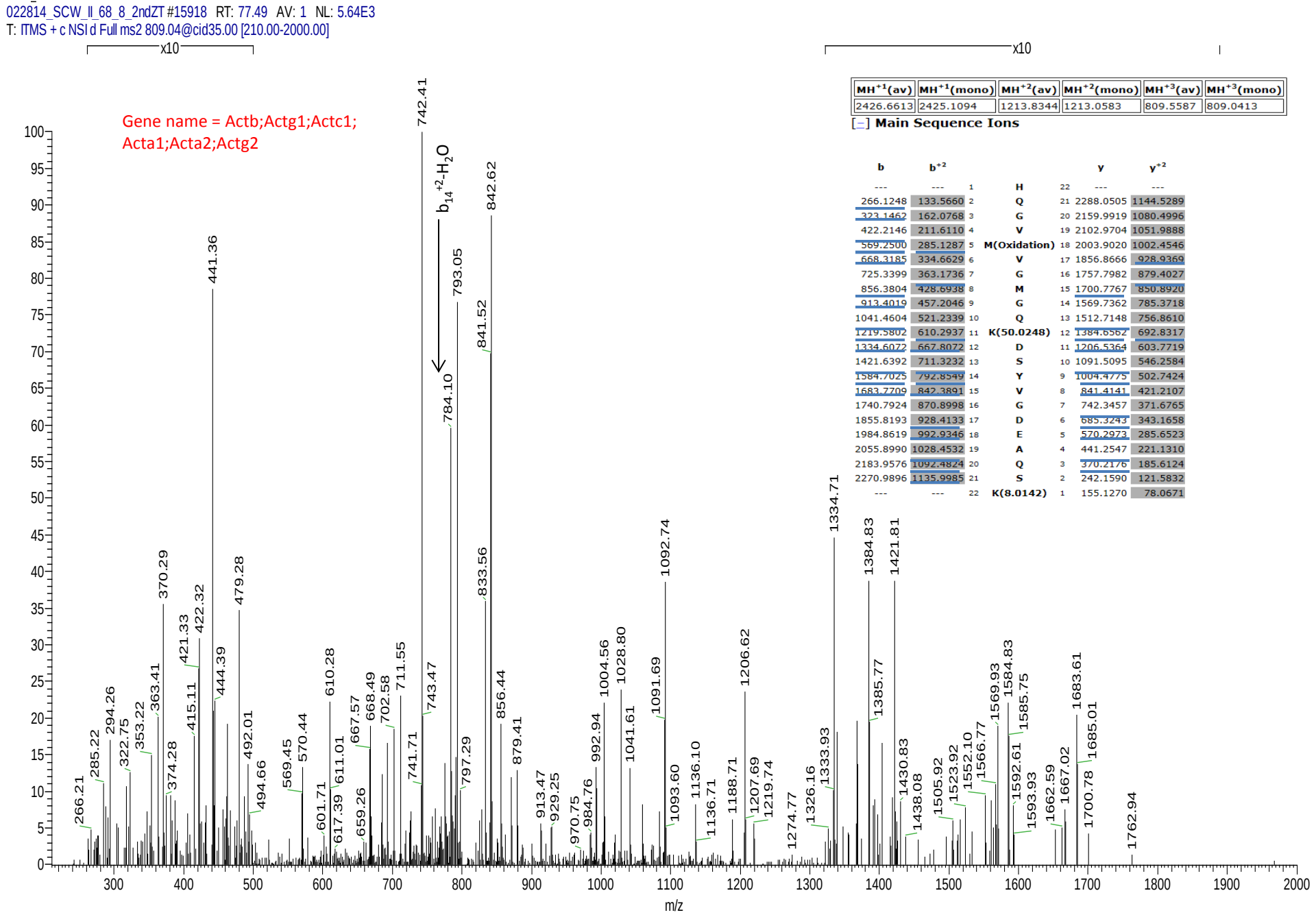
Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_10_Vargas_Enriched	10807	ITMS; CID	126.24	496.8	Acox1



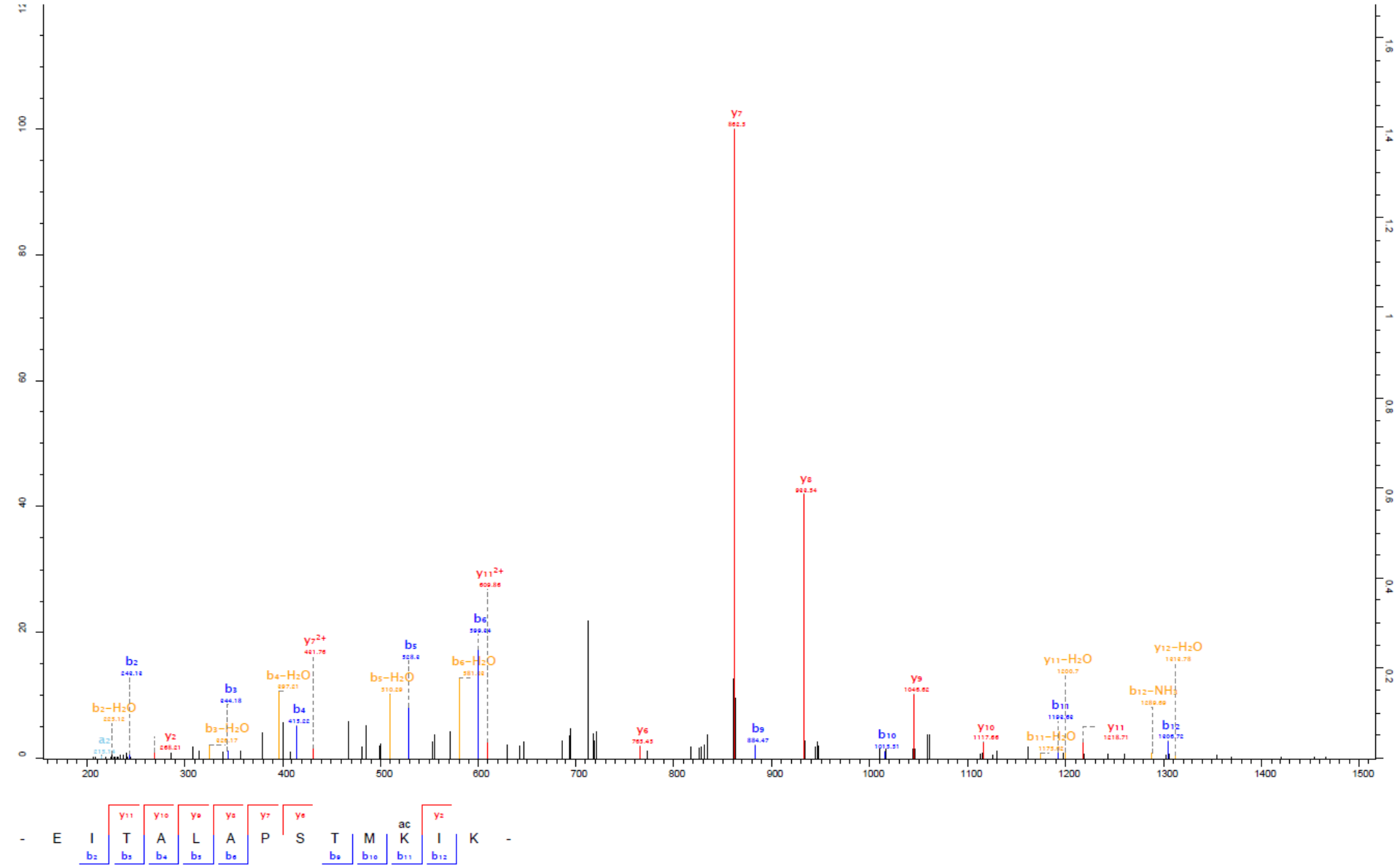

062513_SCW_II_53_10_Vargas_Enriched #10807 RT: 53.73 AV: 1 NL: 2.46E3
T: ITMS + c NSI d Full ms2 496.80@cid35.00 [125.00-1005.00]
Gene name = Acox1
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
993.2013 992.5887 497.1044 496.7980
[–] Main Sequence Ions
b b+2 y y+2
--- --- 1 H 8 --- ---
251.1503 126.0788 2 L 7 855.5298 428.2686
421.2558 211.1315 3 K(Acetyl) 6 742.4458 371.7265
518.3085 259.6579 4 P 5 572.3402 286.6738
631.3926 316.1999 5 L 4 475.2875 238.1474
759.4512 380.2292 6 Q 3 362.2034 181.6053
846.4832 423.7452 7 S 2 234.1448 117.5761
--- --- 8 K 1 147.1128 74.0600
Relative Abundance
m/z
b3-H2O
[M+2H]+2-2H2O
[M+2H]+2-H2O

Raw file	Scan	Method	Score	m/z	Gene names
022814_SCW_JI_68_8_2ndZT	15918	ITMS; CID	260.49	809.04	Actb;Actg1;Actc1;Acta1;Acta2;Actg2




022814_SCW_II_68_8_2ndZT #15918 RT: 77.49 AV: 1 NL: 5.64E3
T: ITMS + c NSI d Full ms2 809.04@cid35.00 [210.00-2000.00]
x10
x10
Gene name = Actb;Actg1;Actc1;
Acta1;Acta2;Actg2
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono) MH+3(av) MH+3(mono)
2426.6613 2425.1094 1213.8344 1213.0583 809.5587 809.0413
[–] Main Sequence Ions
b b+2 y y+2
--- --- 1 H 22 --- ---
266.1248 133.5660 2 Q 21 2288.0505 1144.5289
323.1462 162.0768 3 G 20 2159.9919 1080.4996
422.2146 211.6110 4 V 19 2102.9704 1051.9888
569.2500 285.1287 5 M(Oxidation) 18 2003.9020 1002.4546
668.3185 334.6629 6 V 17 1856.8666 928.9369
725.3399 363.1736 7 G 16 1757.7982 879.4027
856.3804 428.6938 8 M 15 1700.7767 850.8920
913.4019 457.2046 9 G 14 1569.7362 785.3718
1041.4604 521.2339 10 Q 13 1512.7148 756.8610
1219.5802 610.2937 11 K(50.0248) 12 1384.6562 692.8317
1334.6072 667.8072 12 D 11 1206.5364 603.7719
1421.6392 711.3232 13 S 10 1091.5095 546.2584
1584.7025 792.8549 14 Y 9 1004.4775 502.7424
1683.7709 842.3891 15 V 8 841.4141 421.2107
1740.7924 870.8998 16 G 7 742.3457 371.6765
1855.8193 928.4133 17 D 6 685.3243 343.1658
1984.8619 992.9346 18 E 5 570.2973 285.6523
2055.8990 1028.4532 19 A 4 441.2547 221.1310
2183.9576 1092.4824 20 Q 3 370.2176 185.6124
2270.9896 1135.9985 21 S 2 242.1590 121.5832
--- --- 22 K(8.0142) 1 155.1270 78.0671
b14+2-H2O
m/z

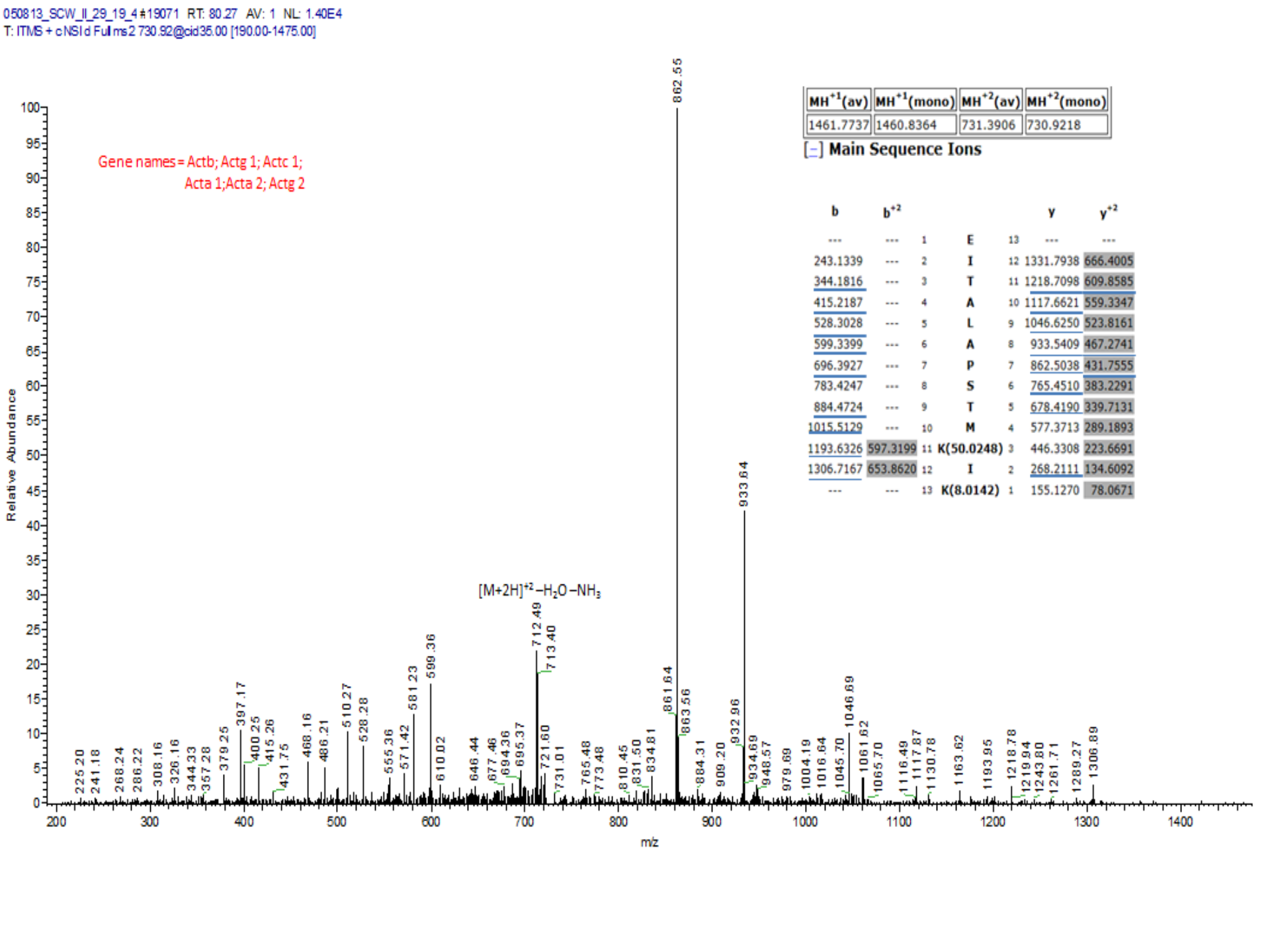
Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	19071	ITMS; CID	111.72	730.92	Actb;Actg1;Actc1;Acta1;Acta2;Actg2



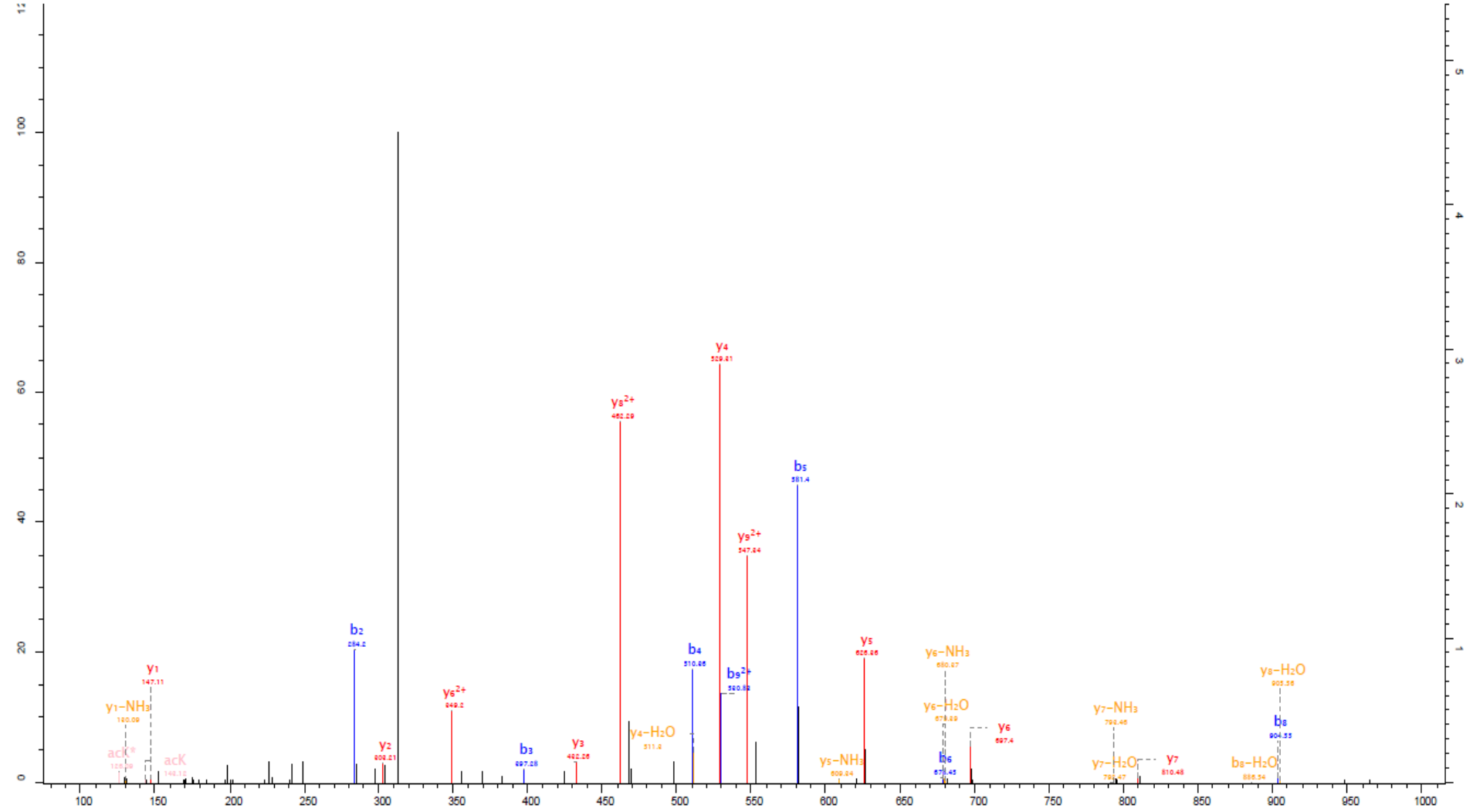
- E I T A L A P S T M ac K I K -

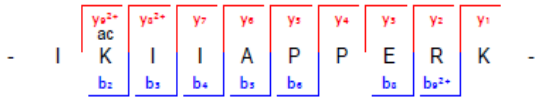
b2 b3 b4 b5 b6 b9 b10 b11 b12

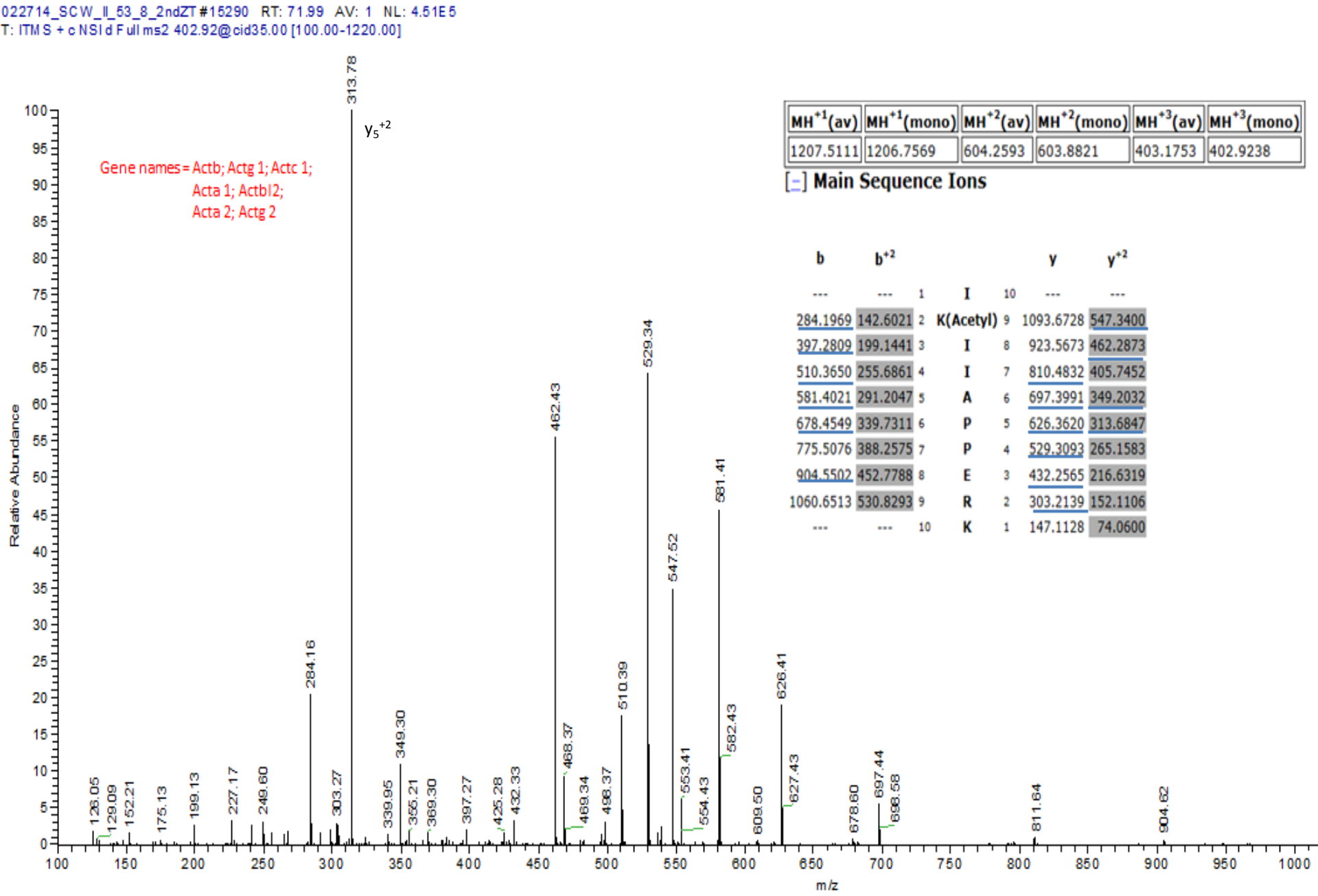
y11 y10 y9 y8 y7 y6 y2


050813_SCW_II_29_19_4 #19071 RT: 80.27 AV: 1 NL: 1.40E4
T: ITMS + c NSI d Full ms2 730.92@cid35.00 [190.00-1475.00]
Gene names = Actb; Actg 1; Actc 1;
Acta 1;Acta 2; Actg 2
MH+1(av) 1461.7737
MH+1(mono) 1460.8364
MH+2(av) 731.3906
MH+2(mono) 730.9218
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 E 13 --- ---
243.1339 --- 2 I 12 1331.7938 666.4005
344.1816 --- 3 T 11 1218.7098 609.8585
415.2187 --- 4 A 10 1117.6621 559.3347
528.3028 --- 5 L 9 1046.6250 523.8161
599.3399 --- 6 A 8 933.5409 467.2741
696.3927 --- 7 P 7 862.5038 431.7555
783.4247 --- 8 S 6 765.4510 383.2291
884.4724 --- 9 T 5 678.4190 339.7131
1015.5129 --- 10 M 4 577.3713 289.1893
1193.6326 597.3199 11 K(50.0248) 3 446.3308 223.6691
1306.7167 653.8620 12 I 2 268.2111 134.6092
--- --- 13 K(8.0142) 1 155.1270 78.0671
[M+2H]+2 –H2O –NH3
862.55
933.64
712.49
713.40
599.36
581.23
510.27
528.28
397.17
400.25
415.26
468.16
486.21
379.25
431.75
555.36
571.42
610.02
646.44
677.46
694.36
695.37
721.60
731.01
765.48
773.48
810.45
831.50
834.81
861.64
863.56
884.31
909.20
932.96
934.69
948.57
979.69
1004.19
1016.64
1045.70
1046.69
1061.62
1065.70
1116.49
1117.87
1130.78
1163.62
1193.95
1218.78
1219.94
1243.80
1261.71
1289.27
1306.89
225.20
241.18
268.24
286.22
308.16
326.16
344.33
357.28
Relative Abundance
m/z

Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_8_2ndZT	15290	ITMS; CID	139.15	402.92	Actb;Actg1;Actc1;Acta1;Actbl2;Acta2;Actg2





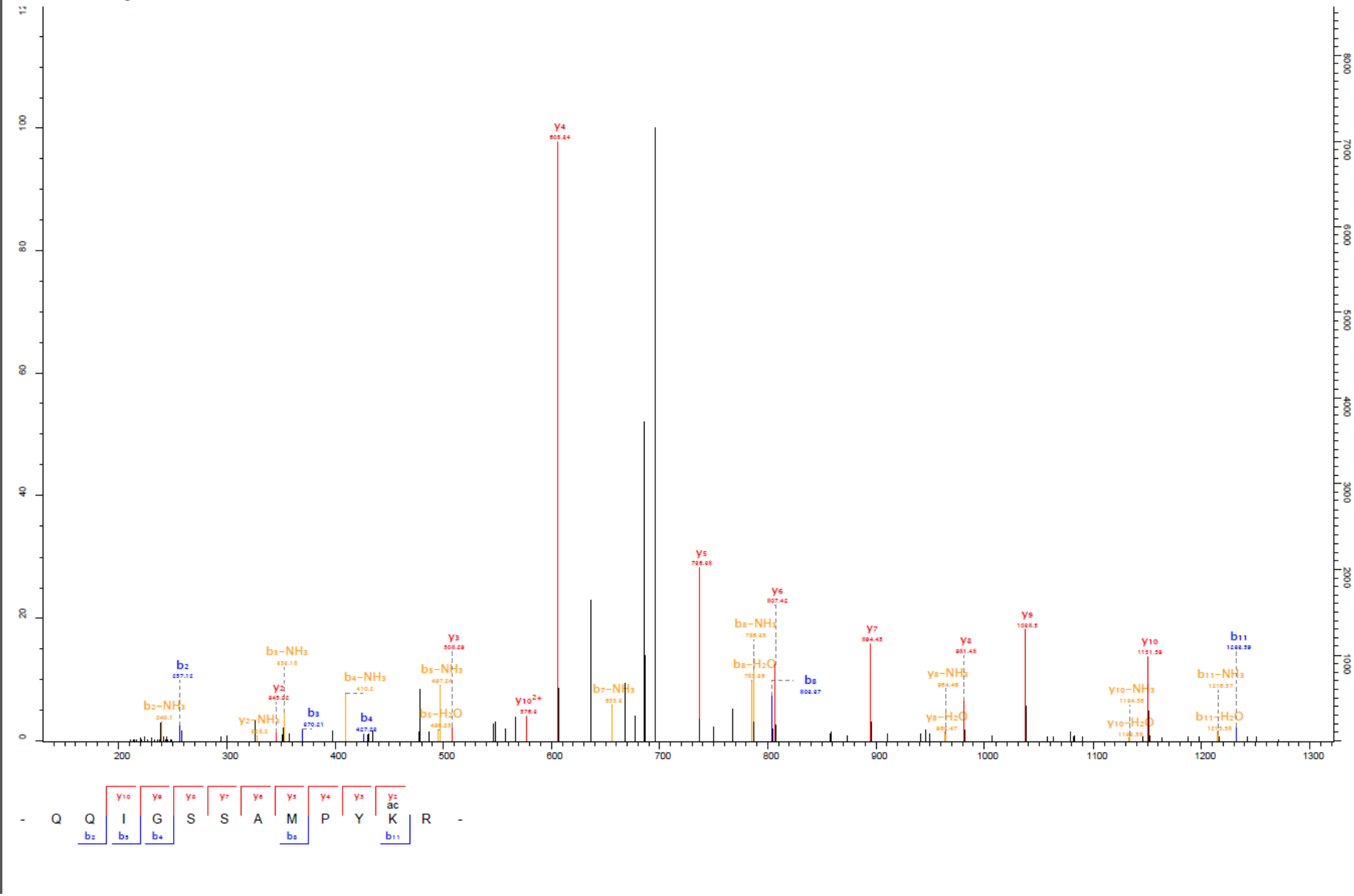


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1207.5111	1206.7569	604.2593	603.8821	403.1753	402.9238

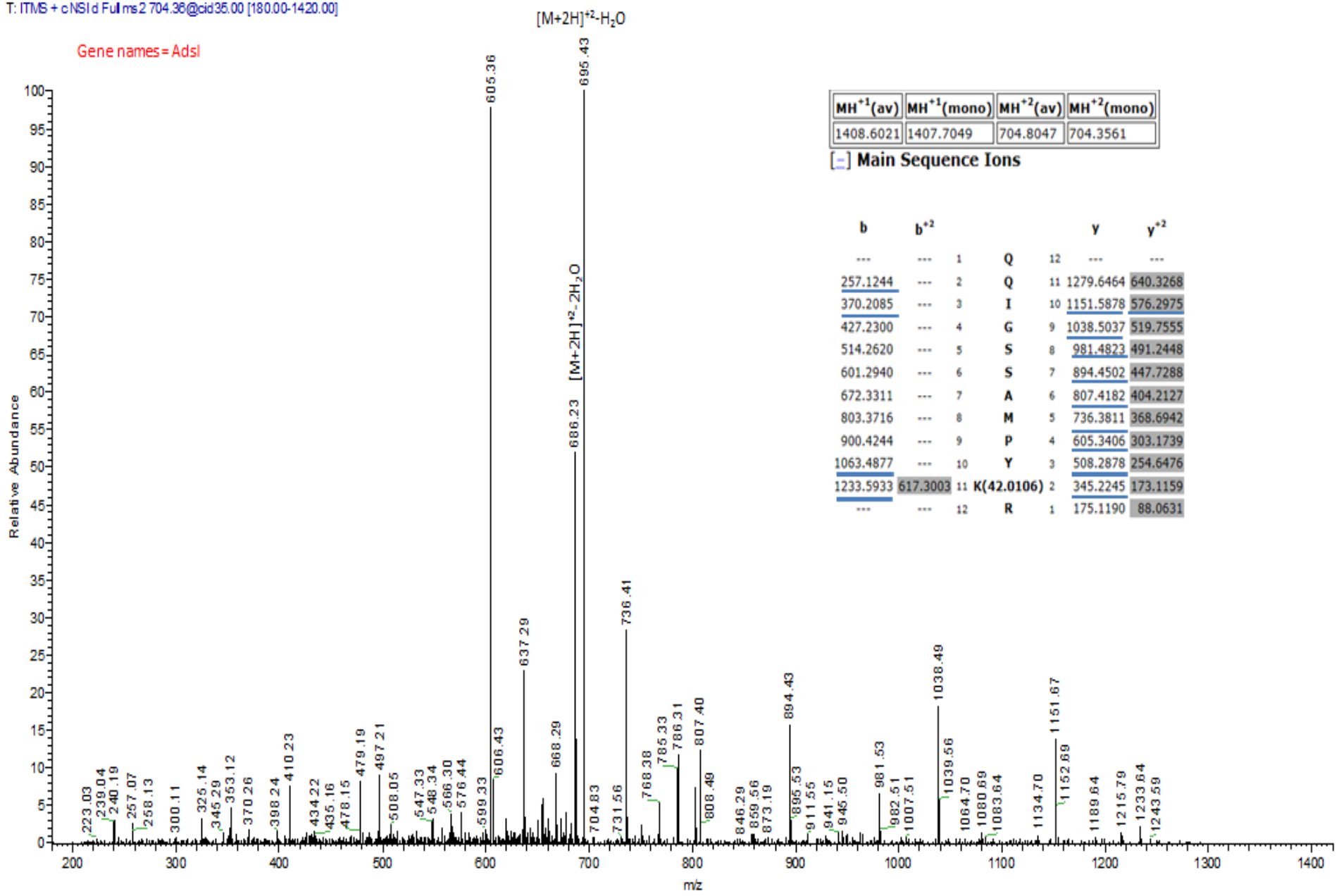
[-] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	I	10	---	---
284.1969	142.6021	2	K(Acetyl)	9	1093.6728	547.3400
397.2809	199.1441	3	I	8	923.5673	462.2873
510.3650	255.6861	4	I	7	810.4832	405.7452
581.4021	291.2047	5	A	6	697.3991	349.2032
678.4549	339.7311	6	P	5	626.3620	313.6847
775.5076	388.2575	7	P	4	529.3093	265.1583
904.5502	452.7788	8	E	3	432.2565	216.6319
1060.6513	530.8293	9	R	2	303.2139	152.1106
---	---	10	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_5_Vargas_Enriched	16139	ITMS; CID	140.14	704.36	Adsl



062513_SCW_II_53_5_Vargas_Enrichec #16139 RT: 69.65 AV: 1 NL: 7.15E3
T: ITMS + c NSI d Full ms2 704.36@cid35.00 [180.00-1420.00]

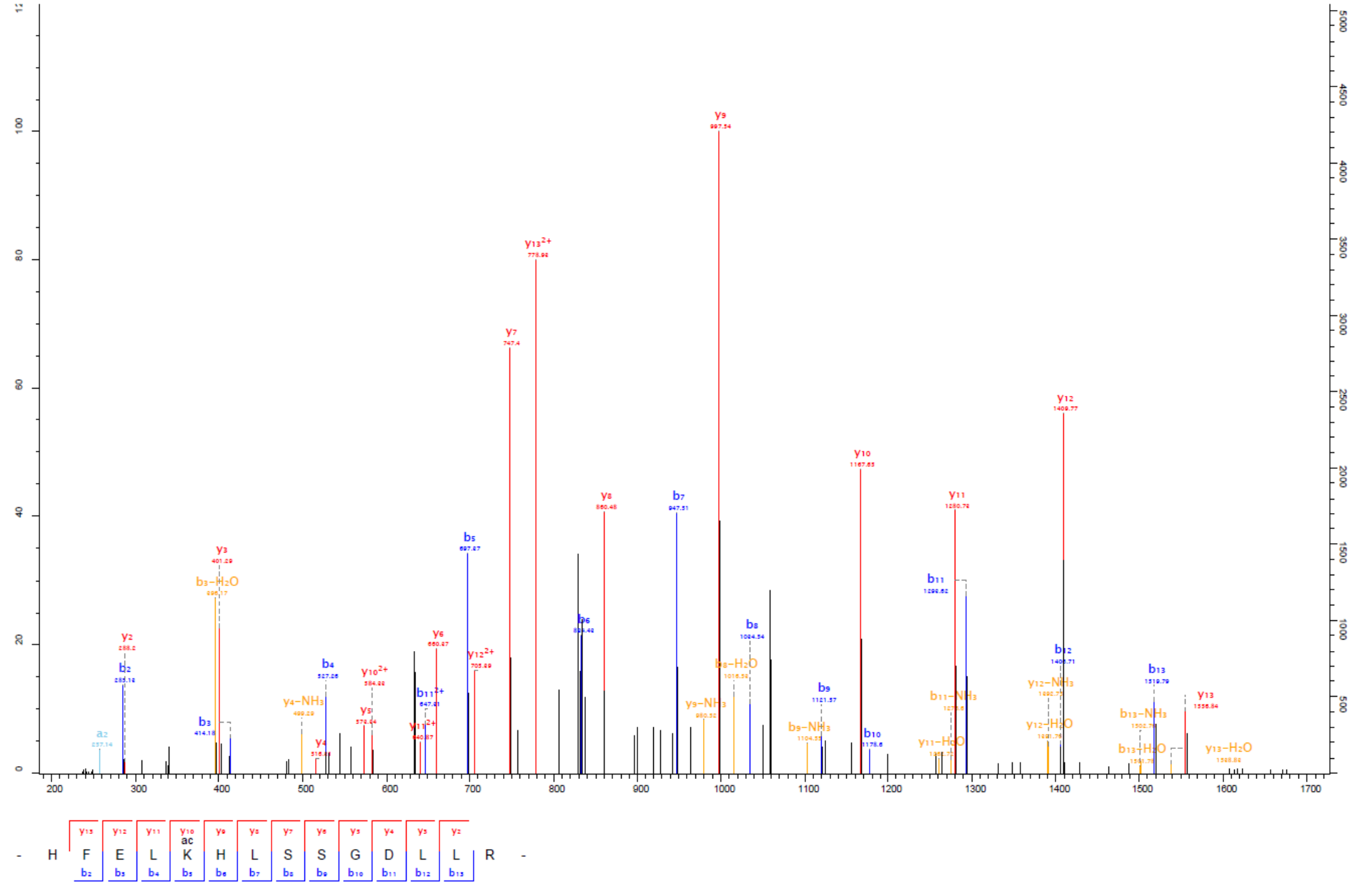


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1408.6021	1407.7049	704.8047	704.3561

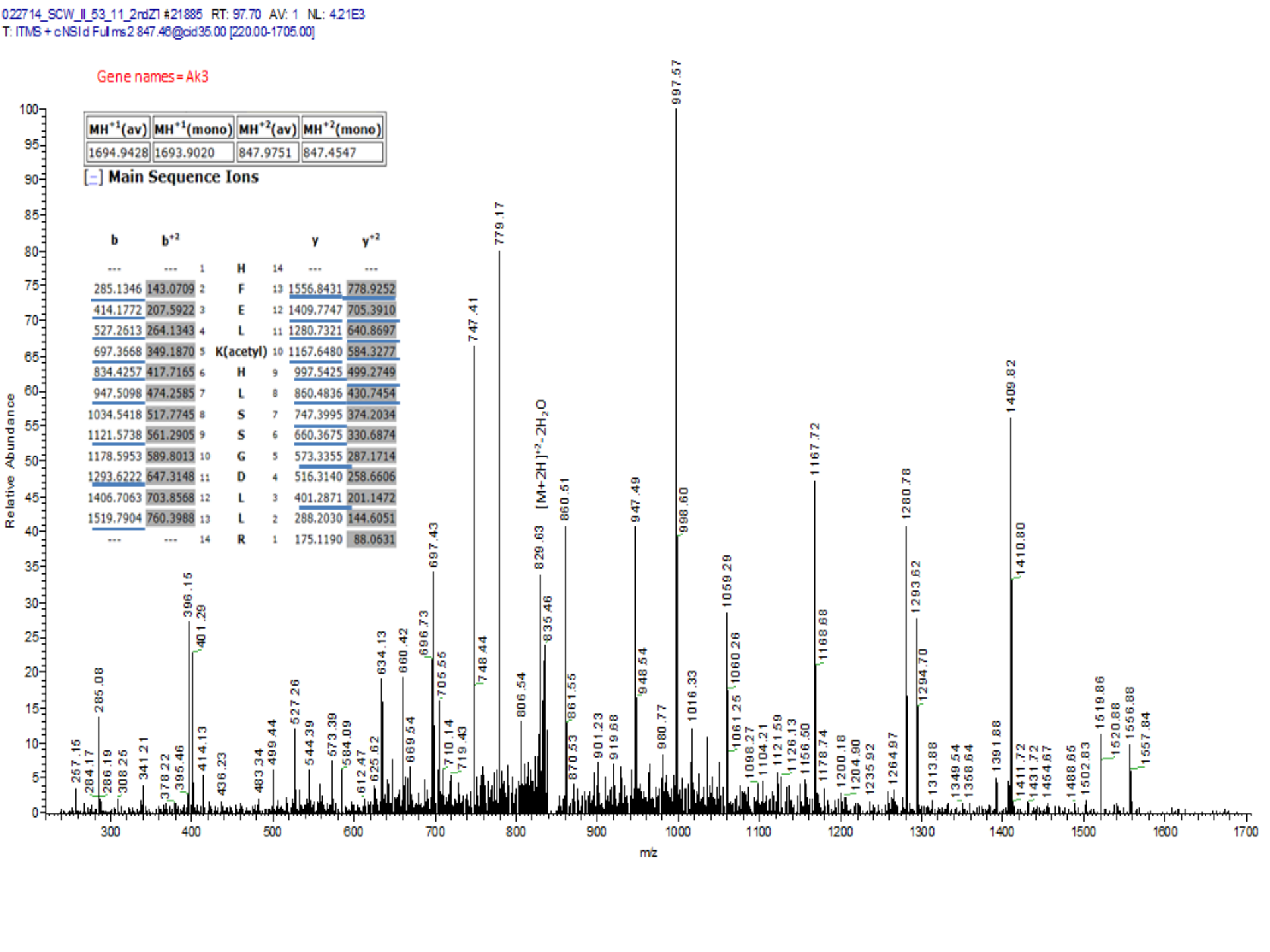
[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	Q	12	---	---
257.1244	---	2	Q	11	1279.6464	640.3268
370.2085	---	3	I	10	1151.5878	576.2975
427.2300	---	4	G	9	1038.5037	519.7555
514.2620	---	5	S	8	981.4823	491.2448
601.2940	---	6	S	7	894.4502	447.7288
672.3311	---	7	A	6	807.4182	404.2127
803.3716	---	8	M	5	736.3811	368.6942
900.4244	---	9	P	4	605.3406	303.1739
1063.4877	---	10	Y	3	508.2878	254.6476
1233.5933	617.3003	11	K(42.0106)	2	345.2245	173.1159
---	---	12	R	1	175.1190	88.0631

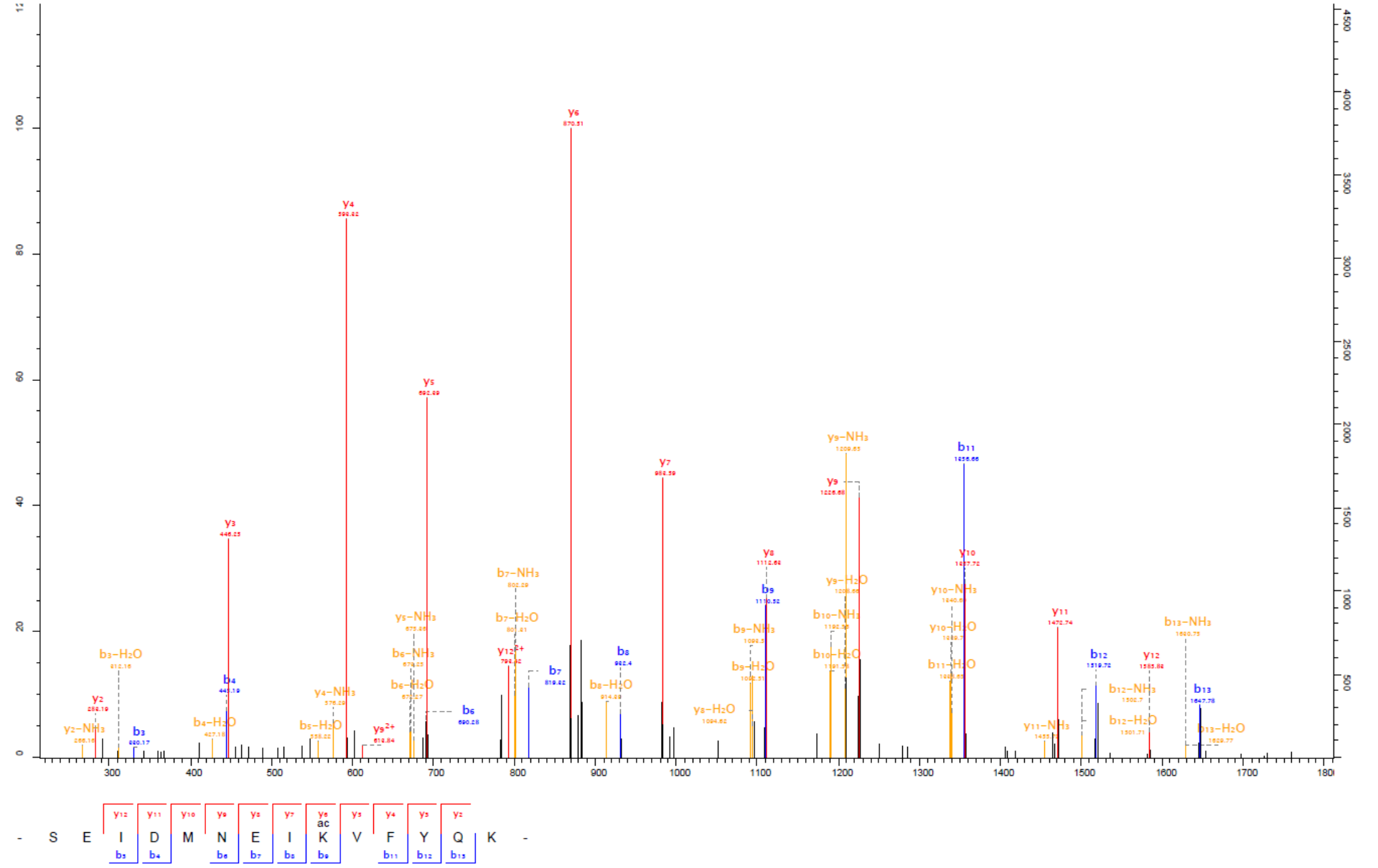
Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_11_2ndZT	21885	ITMS; CID	218.2	847.46	Ak3



- H F E L K(ac) H L S S G D L L R -


022714_SCW_II_53_11_2ndZT #21885 RT: 97.70 AV: 1 NL: 4.21E3
T: ITMS + c NSI d Full ms2 847.46@cid35.00 [220.00-1705.00]
Gene names = Ak3
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1694.9428 1693.9020 847.9751 847.4547
[–] Main Sequence Ions
b b+2 y y+2
--- --- 1 H 14 --- ---
285.1346 143.0709 2 F 13 1556.8431 778.9252
414.1772 207.5922 3 E 12 1409.7747 705.3910
527.2613 264.1343 4 L 11 1280.7321 640.8697
697.3668 349.1870 5 K(acetyl) 10 1167.6480 584.3277
834.4257 417.7165 6 H 9 997.5425 499.2749
947.5098 474.2585 7 L 8 860.4836 430.7454
1034.5418 517.7745 8 S 7 747.3995 374.2034
1121.5738 561.2905 9 S 6 660.3675 330.6874
1178.5953 589.8013 10 G 5 573.3355 287.1714
1293.6222 647.3148 11 D 4 516.3140 258.6606
1406.7063 703.8568 12 L 3 401.2871 201.1472
1519.7904 760.3988 13 L 2 288.2030 144.6051
--- --- 14 R 1 175.1190 88.0631
Relative Abundance
m/z
[M+2H]+2-2H2O

Raw file	Scan	Method	Score	m/z	Gene names
022814_SCW_II_68_1_2ndZT	26349	ITMS; CID	281.6	901.45	Anxa1



- S E I D M N E I K V F Y Q K -

y12 y11 y10 y9 y8 y7 y6 ac y5 y4 y3 y2

b3 b4 b5 b6 b7 b8 b9 b11 b12 b13

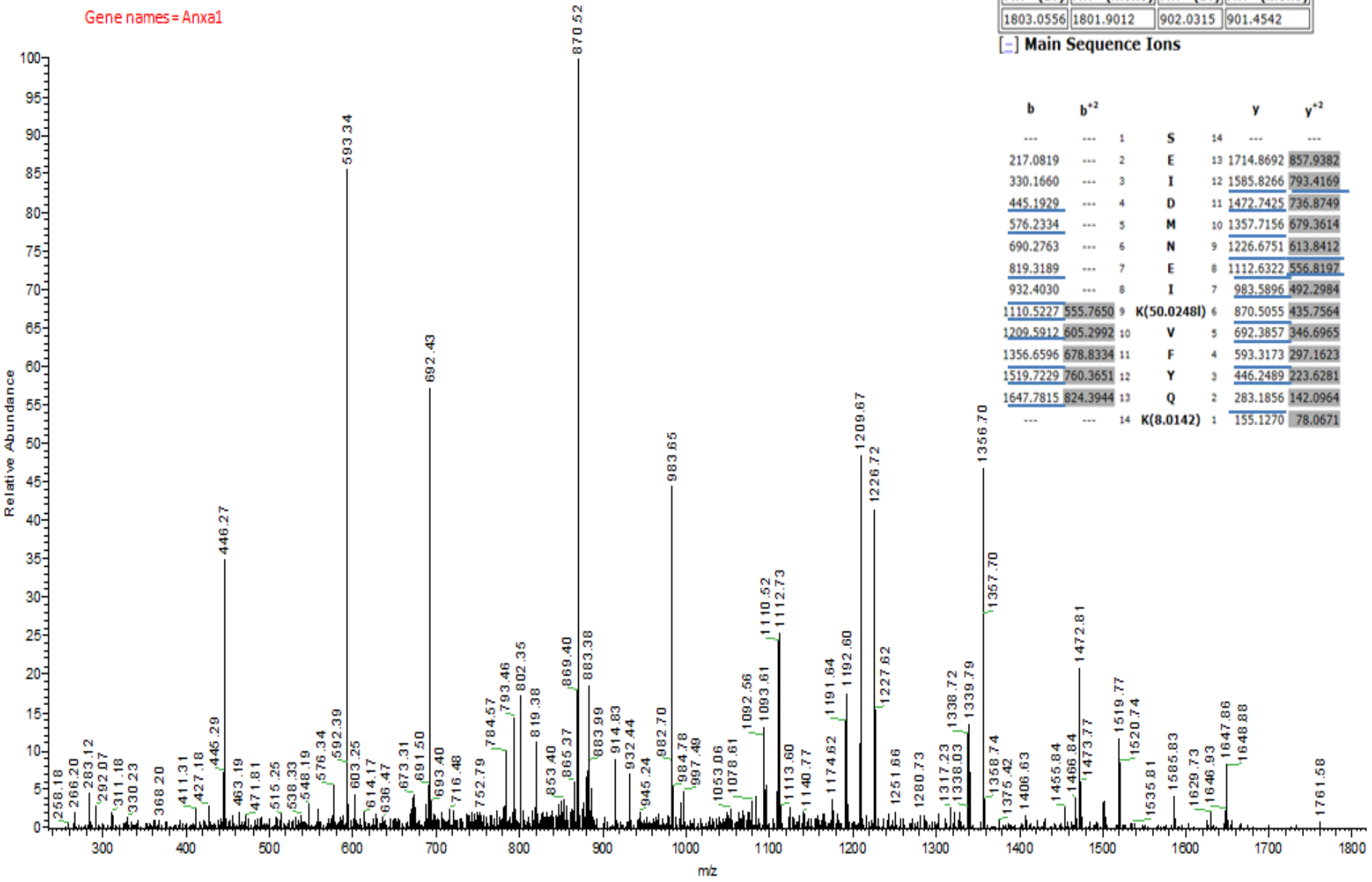
022814_SCW_II_68_1_2ndZ1#26349 RT: 116.17 AV: 1 NL: 3.78E3
T: ITMS + cNSI d Full ms2 901.45@cid35.00 [235.00-1815.00]

Gene names = Anxa1

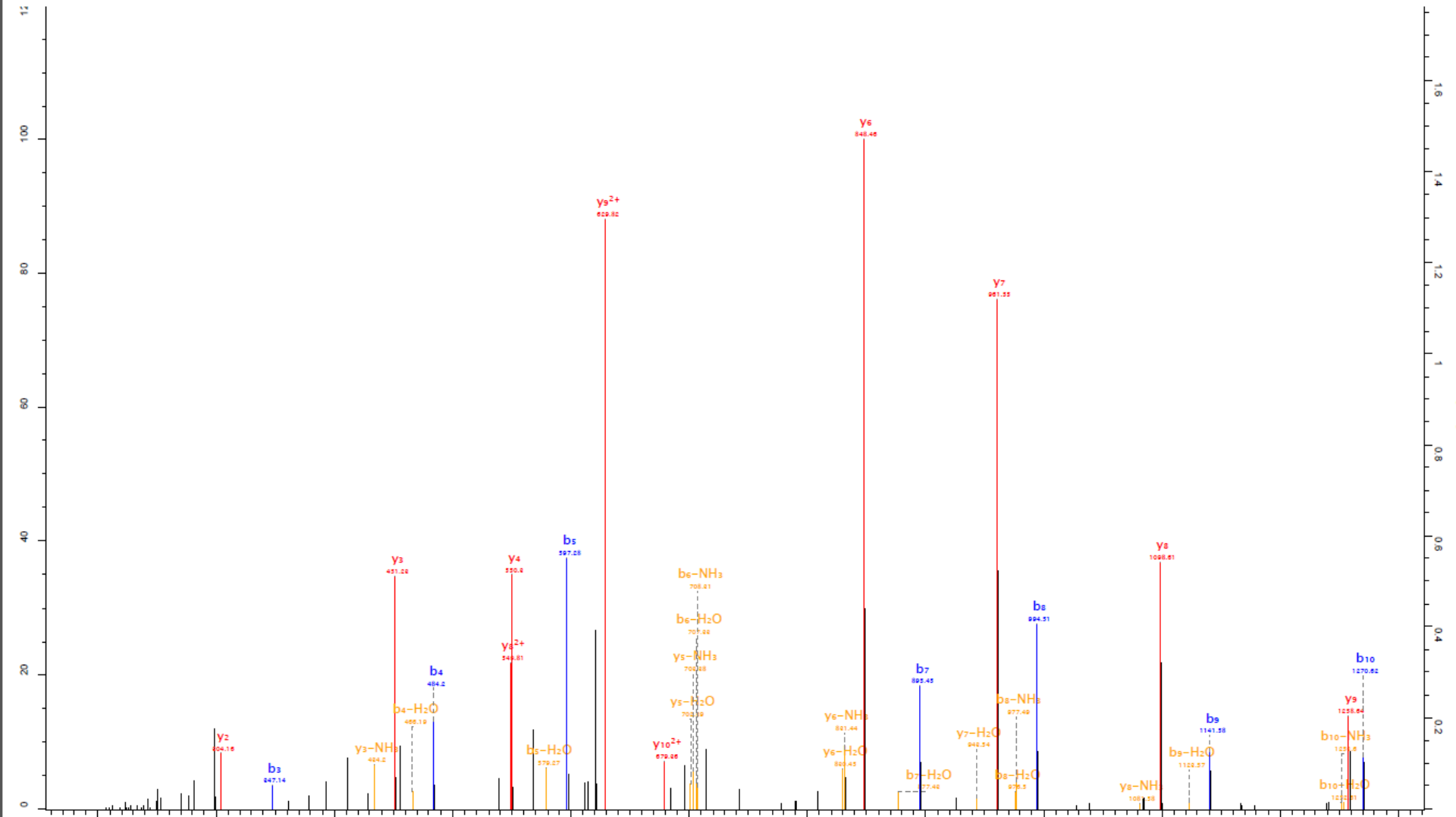
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1803.0556	1801.9012	902.0315	901.4542

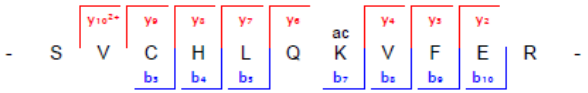
[-] Main Sequence Ions

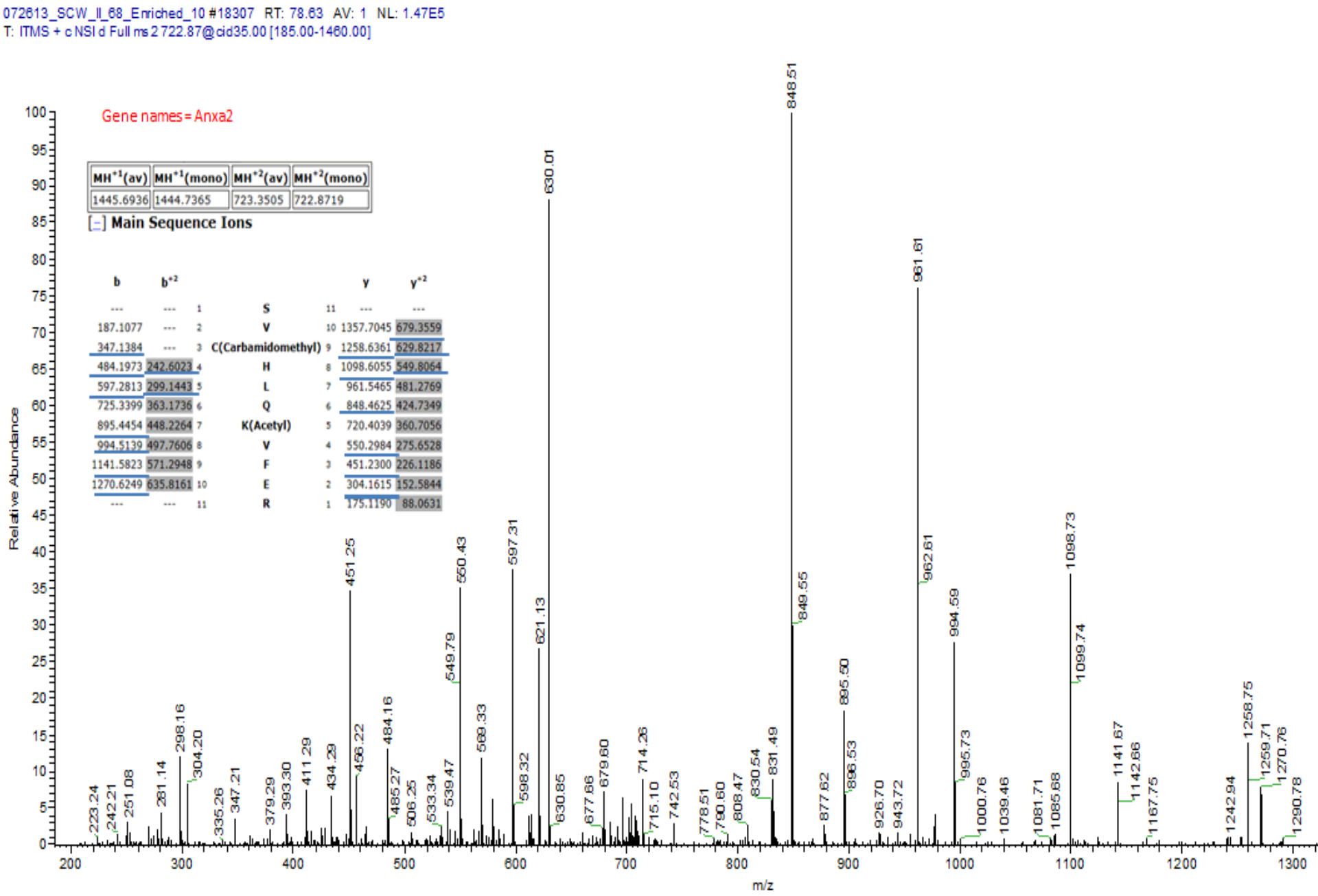
b	b^{+2}			y	y^{+2}
---	---	1	S	---	---
217.0819	---	2	E	1714.8692	857.9382
330.1660	---	3	I	1585.8266	793.4169
445.1929	---	4	D	1472.7425	736.8749
576.2334	---	5	M	1357.7156	679.3614
690.2763	---	6	N	1226.6751	613.8412
819.3189	---	7	E	1112.6322	556.8197
932.4030	---	8	I	983.5896	492.2984
1110.5227	555.7650	9	K(50.0248l)	870.5055	435.7564
1209.5912	605.2992	10	V	692.3857	346.6965
1356.6596	678.8334	11	F	593.3173	297.1623
1519.7229	760.3651	12	Y	446.2489	223.6281
1647.7815	824.3944	13	Q	283.1856	142.0964
---	---	14	K(8.0142)	155.1270	78.0671



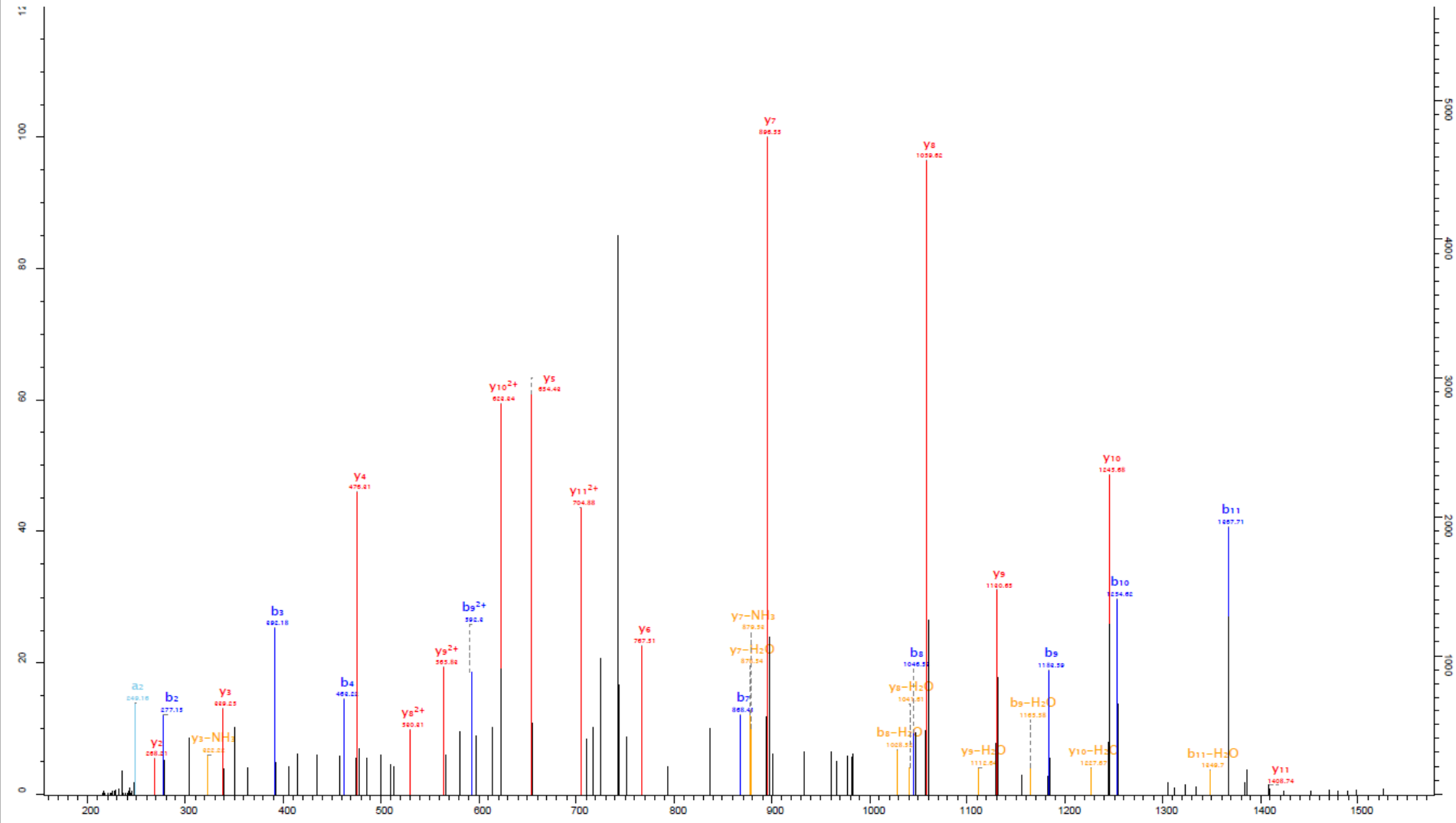
Raw file	Scan	Method	Score	m/z	Gene names
072613_SCW_II_68_Enriched_10	18307	ITMS; CID	170.4	722.87	Anxa2



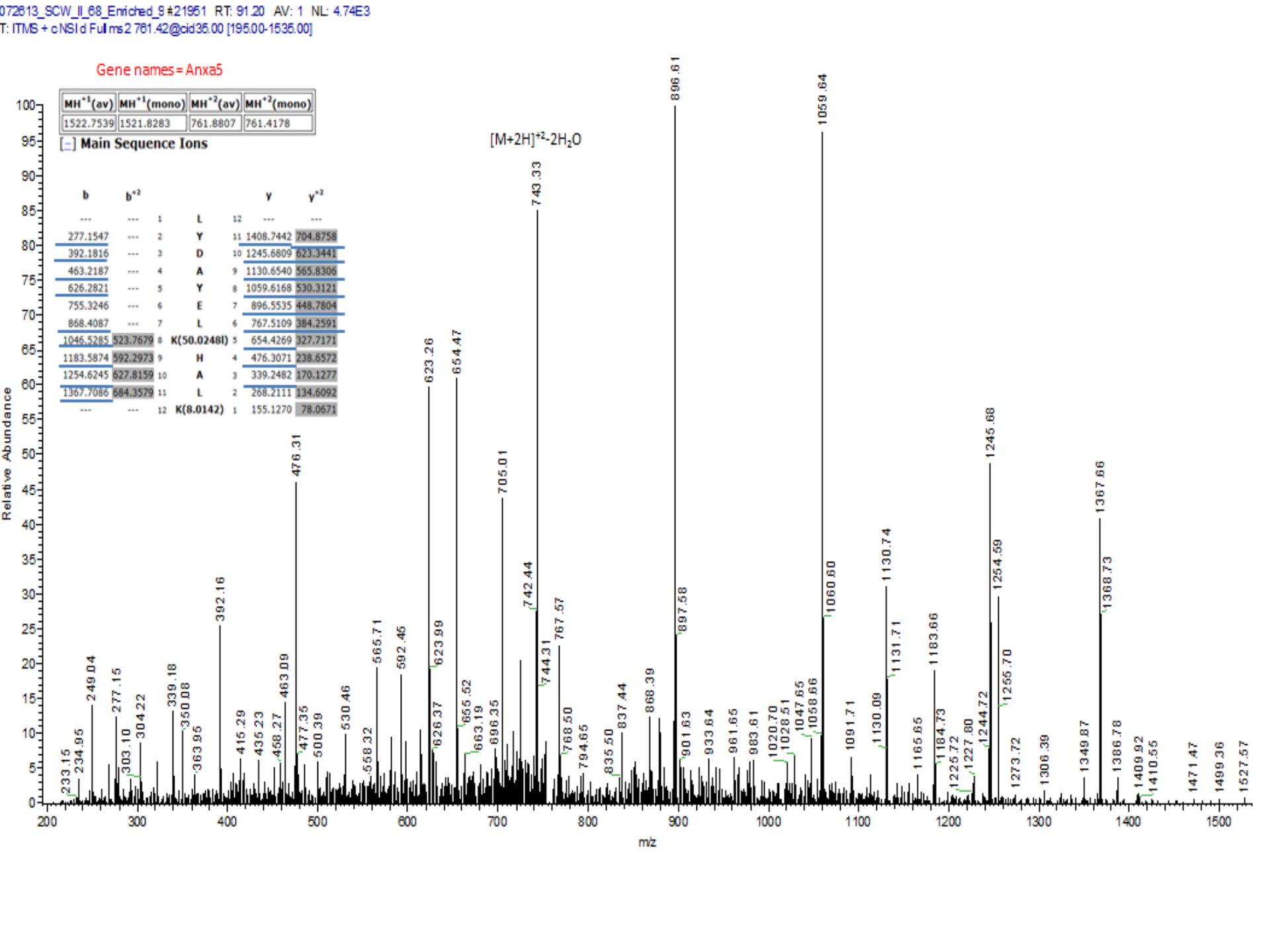



072613_SCW_II_68_Enriched_10 #18307 RT: 78.63 AV: 1 NL: 1.47E5
T: ITMS + c NSI d Full ms2 722.87@cid35.00 [185.00-1460.00]
Gene names = Anxa2
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1445.6936 1444.7365 723.3505 722.8719
[–] Main Sequence Ions
b b+2 y y+2
--- --- 1 S 11 --- ---
187.1077 --- 2 V 10 1357.7045 679.3559
347.1384 --- 3 C(Carbamidomethyl) 9 1258.6361 629.8217
484.1973 242.6023 4 H 8 1098.6055 549.8064
597.2813 299.1443 5 L 7 961.5465 481.2769
725.3399 363.1736 6 Q 6 848.4625 424.7349
895.4454 448.2264 7 K(Acetyl) 5 720.4039 360.7056
994.5139 497.7606 8 V 4 550.2984 275.6528
1141.5823 571.2948 9 F 3 451.2300 226.1186
1270.6249 635.8161 10 E 2 304.1615 152.5844
--- --- 11 R 1 175.1190 88.0631
Relative Abundance
m/z

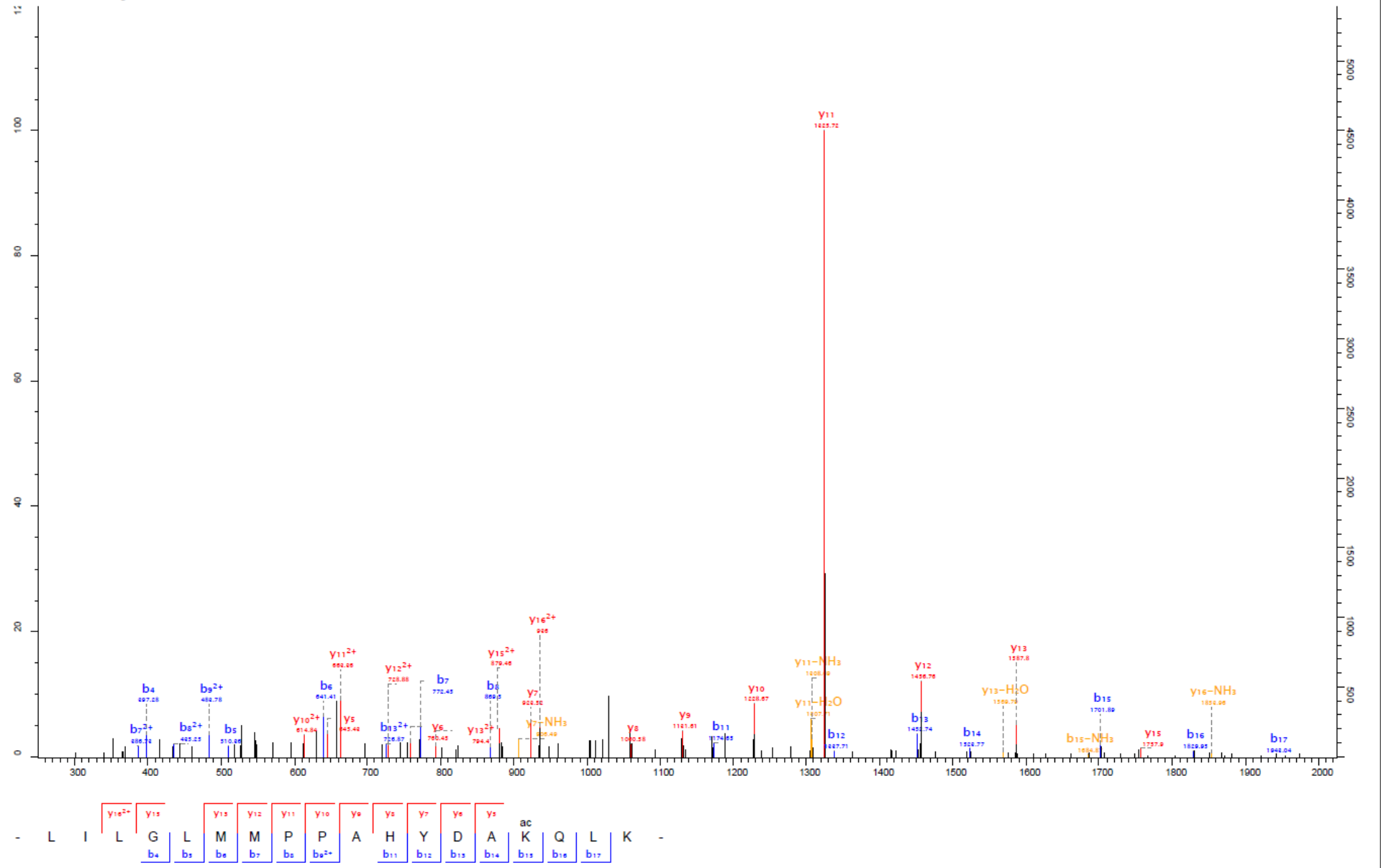
Raw file	Scan	Method	Score	m/z	Gene names
072613_SCW_II_68_Enriched_9	21951	ITMS; CID	186.76	761.42	Anxa5



- L Y D A Y E L K(ac) H A L K -


072613_SCW_II_68_Enriched_9 #21961 RT: 91.20 AV: 1 NL: 4.74E3
T: ITMS + cNSI d Full ms2 761.42@cid35.00 [195.00-1535.00]
Gene names = Anxa5
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1522.7539 1521.8283 761.8807 761.4178
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 L 12 --- ---
277.1547 --- 2 Y 11 1408.7442 704.8758
392.1816 --- 3 D 10 1245.6809 623.3441
463.2187 --- 4 A 9 1130.6540 565.8306
626.2821 --- 5 Y 8 1059.6168 530.3121
755.3246 --- 6 E 7 896.5535 448.7804
868.4087 --- 7 L 6 767.5109 384.2591
1046.5285 523.7679 8 K(50.0248l) 5 654.4269 327.7171
1183.5874 592.2973 9 H 4 476.3071 238.6572
1254.6245 627.8159 10 A 3 339.2482 170.1277
1367.7086 684.3579 11 L 2 268.2111 134.6092
--- --- 12 K(8.0142) 1 155.1270 78.0671
[M+2H]+2-2H2O
Relative Abundance
m/z

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_6_Vargas_Enriched	23417	ITMS; CID	169.64	1049.08	Anxa6



- L I L G L M M P P A H Y D A K Q L K -

ac

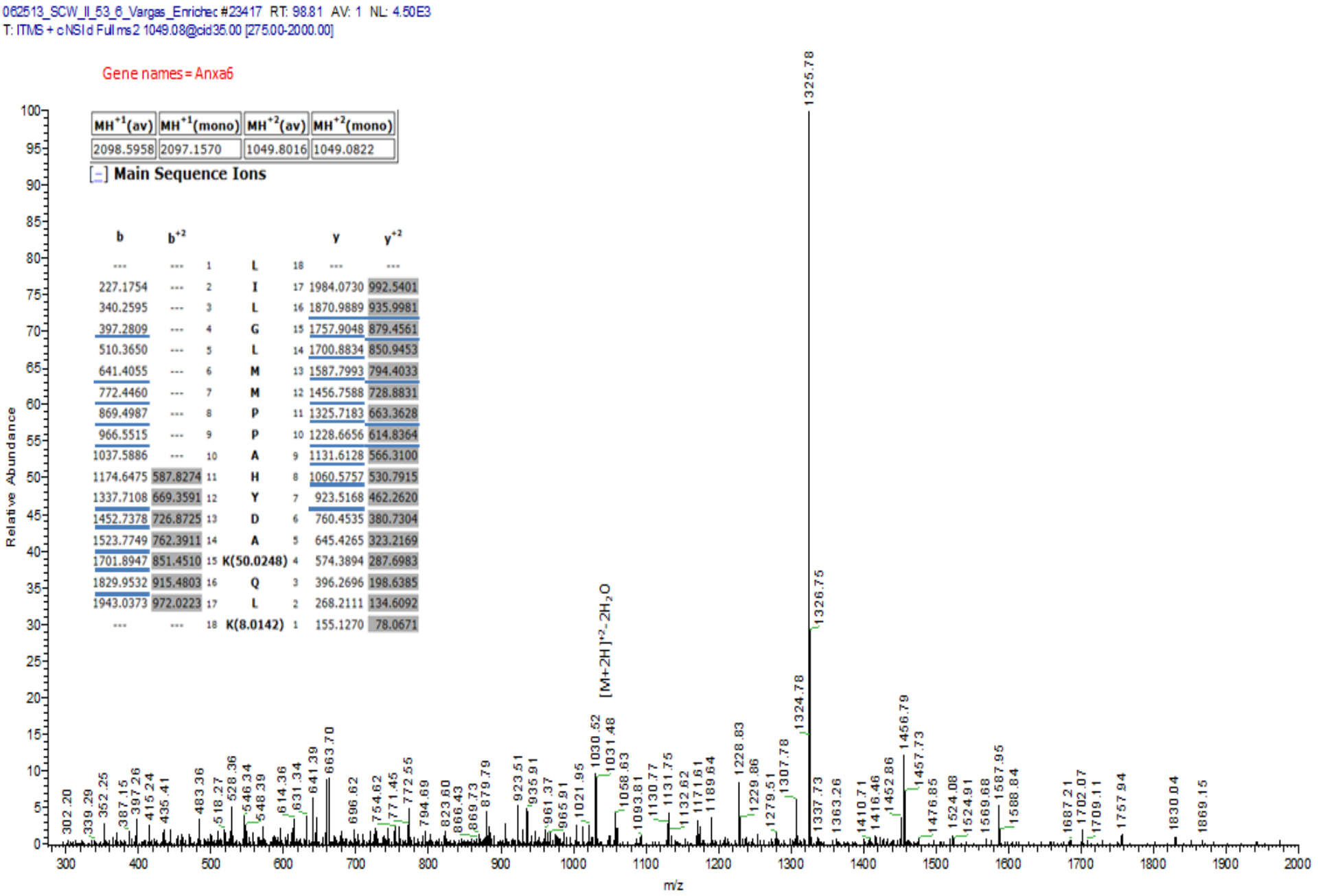
062513_SCW_II_53_6_Vargas_Enrichec #23417 RT: 98.81 AV: 1 NL: 4.50E3
T: ITMS + cNSI d Full ms2 1049.08@cid35.00 [275.00-2000.00]

Gene names = Anxa6

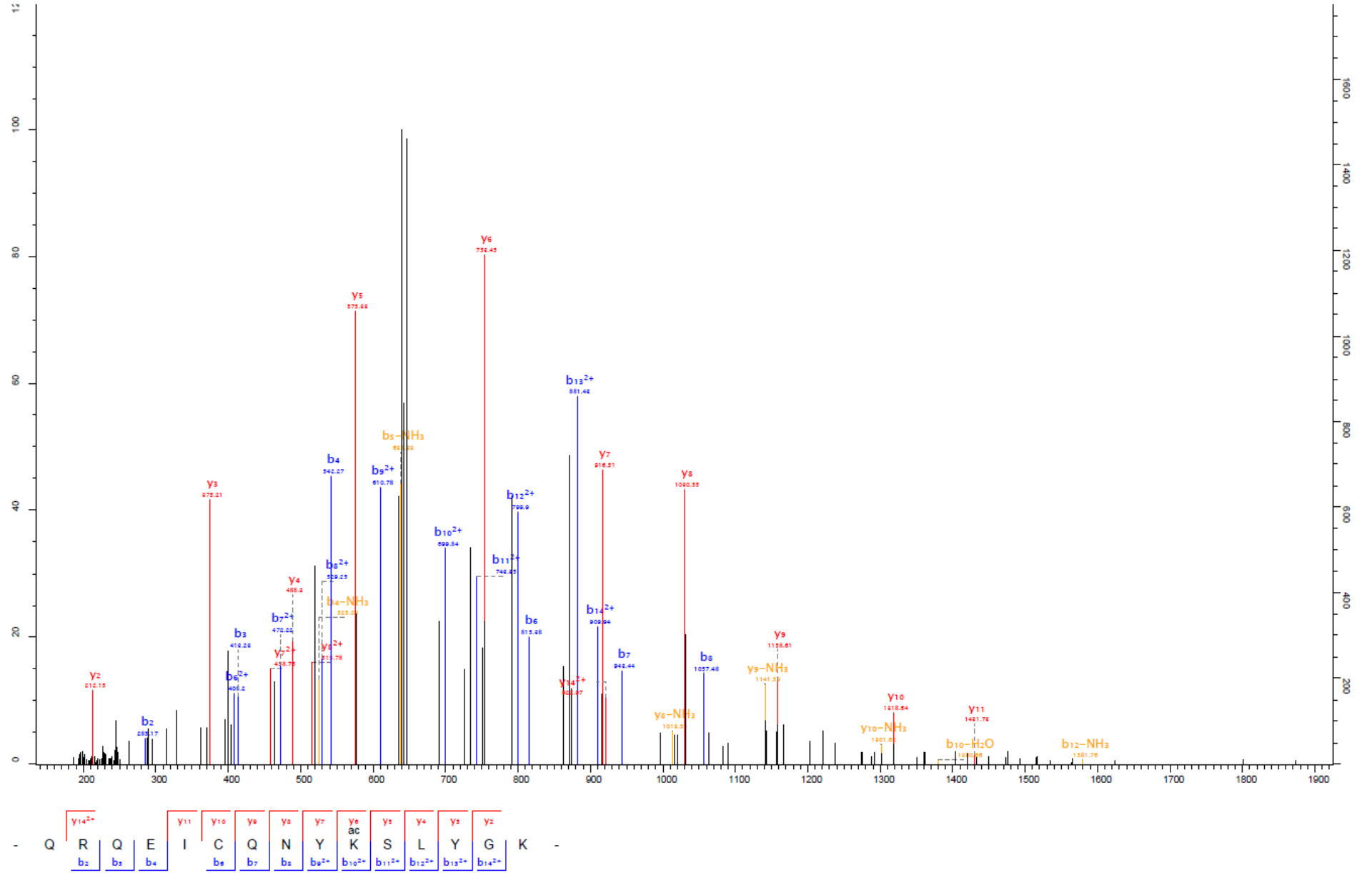
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
2098.5958	2097.1570	1049.8016	1049.0822

[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	L	18	---	---
227.1754	---	2	I	17	1984.0730	992.5401
340.2595	---	3	L	16	1870.9889	935.9981
397.2809	---	4	G	15	1757.9048	879.4561
510.3650	---	5	L	14	1700.8834	850.9453
641.4055	---	6	M	13	1587.7993	794.4033
772.4460	---	7	M	12	1456.7588	728.8831
869.4987	---	8	P	11	1325.7183	663.3628
966.5515	---	9	P	10	1228.6656	614.8364
1037.5886	---	10	A	9	1131.6128	566.3100
1174.6475	587.8274	11	H	8	1060.5757	530.7915
1337.7108	669.3591	12	Y	7	923.5168	462.2620
1452.7378	726.8725	13	D	6	760.4535	380.7304
1523.7749	762.3911	14	A	5	645.4265	323.2169
1701.8947	851.4510	15	K(50.0248)	4	574.3894	287.6983
1829.9532	915.4803	16	Q	3	396.2696	198.6385
1943.0373	972.0223	17	L	2	268.2111	134.6092
---	---	18	K(8.0142)	1	155.1270	78.0671



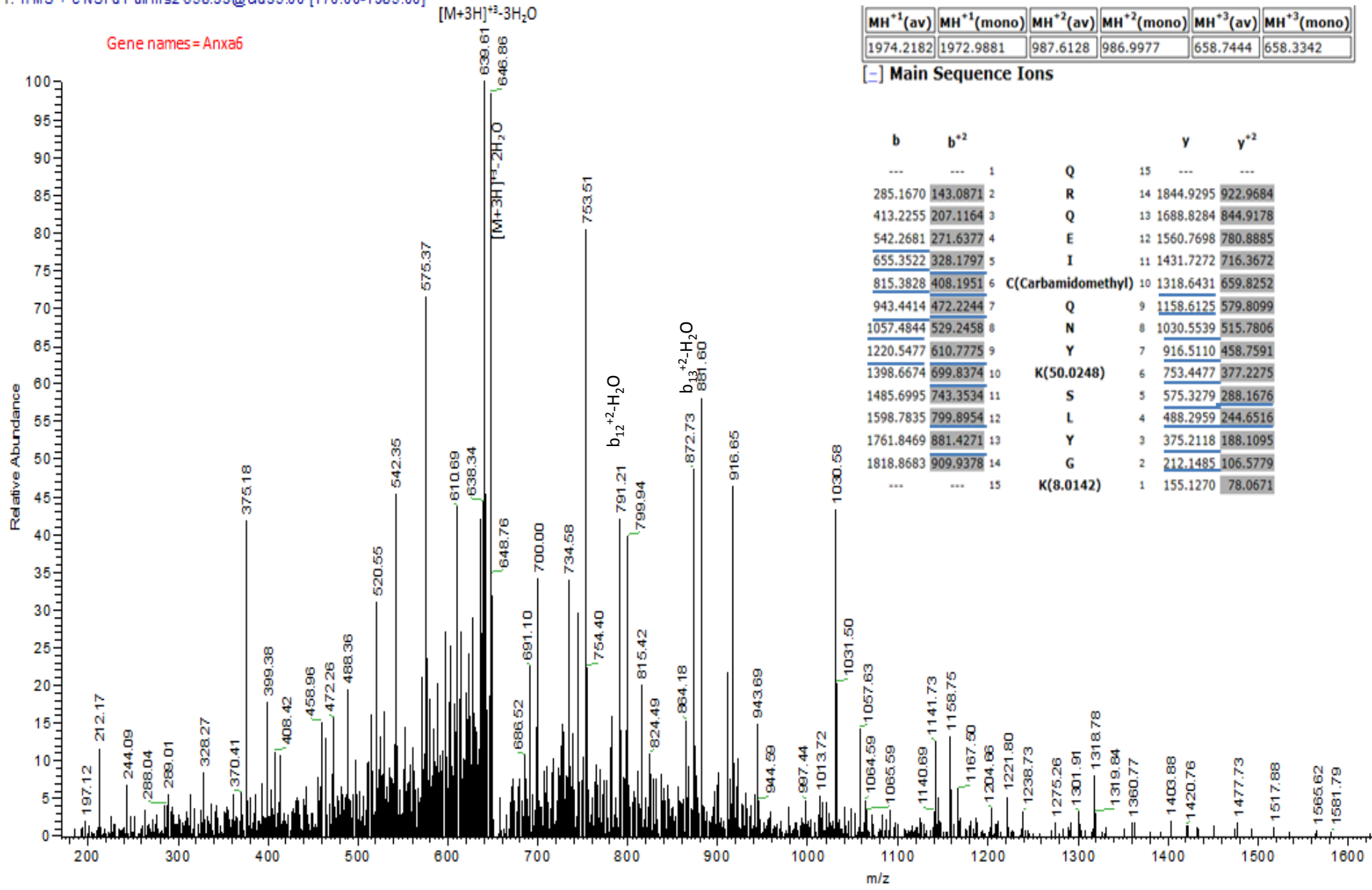
Raw file	Scan	Method	Score	m/z	Gene names
050713_SCW_II_29_35_9	14427	ITMS; CID	144.88	658.33	Anxa6



- Q R Q E I C Q N Y K(ac) S L Y G K -

050713_SCW_II_29_35_9 #14427 RT: 67.81 AV: 1 NL: 1.48E3
T: ITMS + c NSI d Full ms2 658.33@cid35.00 [170.00-1985.00]

Gene names = Anxa6

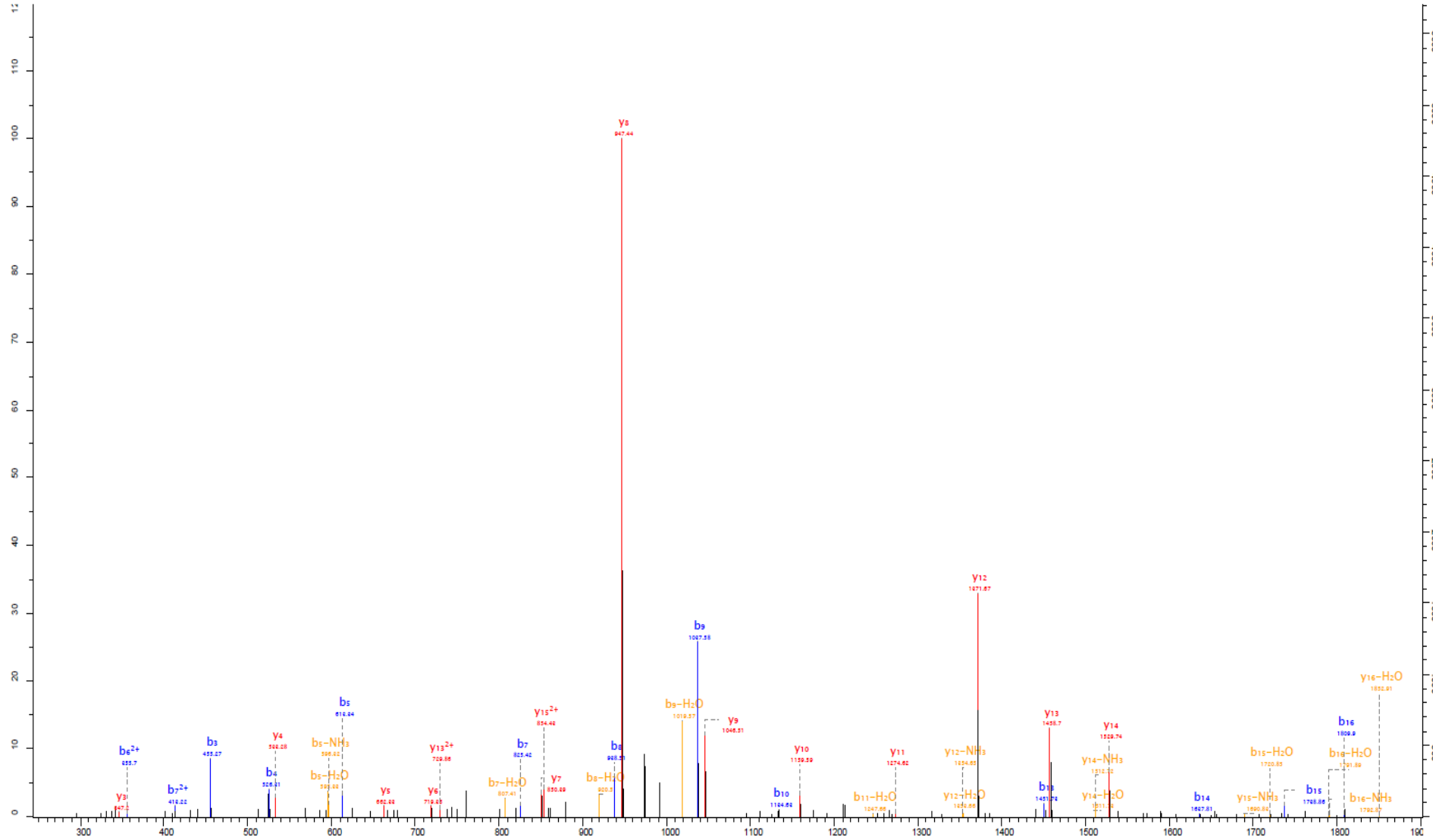


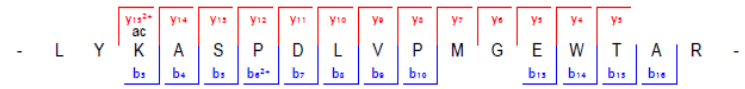
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1974.2182	1972.9881	987.6128	986.9977	658.7444	658.3342

[-] Main Sequence Ions

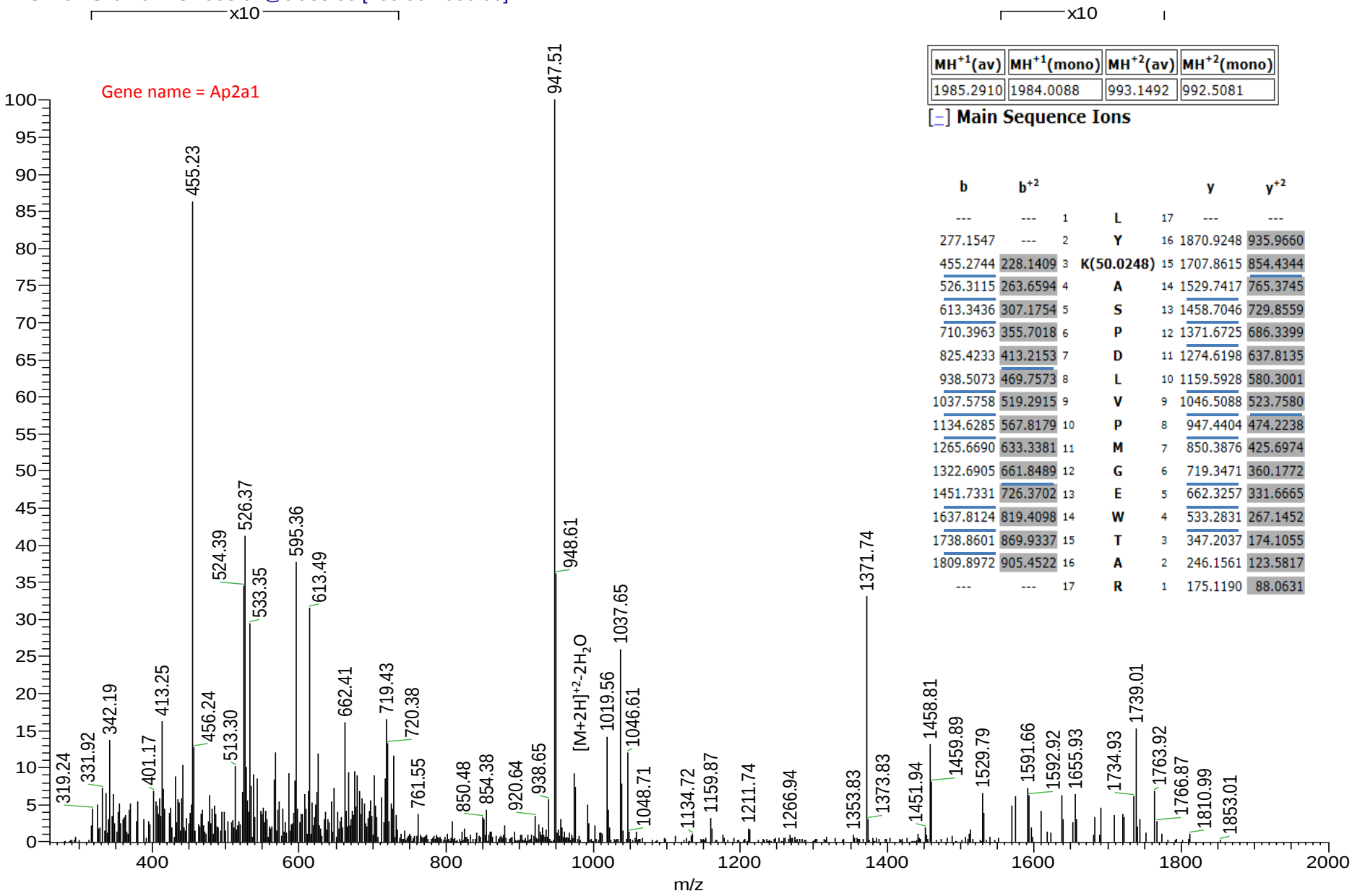
b	b^{+2}				y	y^{+2}
---	---	1	Q	15	---	---
285.1670	143.0871	2	R	14	1844.9295	922.9684
413.2255	207.1164	3	Q	13	1688.8284	844.9178
542.2681	271.6377	4	E	12	1560.7698	780.8885
655.3522	328.1797	5	I	11	1431.7272	716.3672
815.3828	408.1951	6	C(Carbamidomethyl)	10	1318.6431	659.8252
943.4414	472.2244	7	Q	9	1158.6125	579.8099
1057.4844	529.2458	8	N	8	1030.5539	515.7806
1220.5477	610.7775	9	Y	7	916.5110	458.7591
1398.6674	699.8374	10	K(50.0248)	6	753.4477	377.2275
1485.6995	743.3534	11	S	5	575.3279	288.1676
1598.7835	799.8954	12	L	4	488.2959	244.6516
1761.8469	881.4271	13	Y	3	375.2118	188.1095
1818.8683	909.9378	14	G	2	212.1485	106.5779
---	---	15	K(8.0142)	1	155.1270	78.0671

Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	22702	ITMS; CID	180.32	993.01	Ap2a1





062513_SCW_II_53_4_Vargas_Enriched #22702 RT: 97.73 AV: 1 NL: 4.76E3
T: ITMS + c NSI d Full ms2 993.01@cid35.00 [260.00-2000.00]

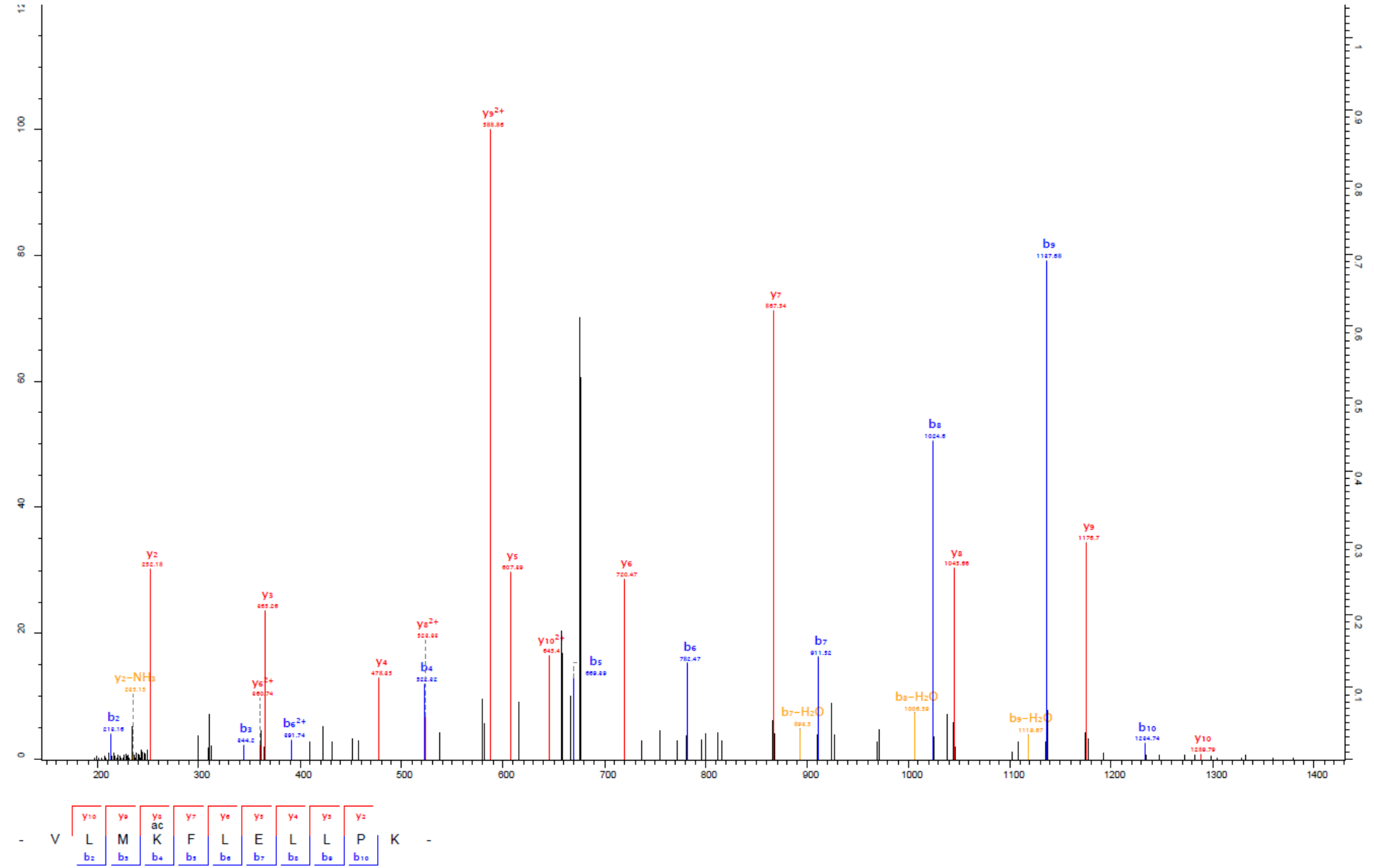


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1985.2910	1984.0088	993.1492	992.5081

[–] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	L	17	---	---
277.1547	---	2	Y	16	1870.9248	935.9660
455.2744	228.1409	3	K(50.0248)	15	1707.8615	854.4344
526.3115	263.6594	4	A	14	1529.7417	765.3745
613.3436	307.1754	5	S	13	1458.7046	729.8559
710.3963	355.7018	6	P	12	1371.6725	686.3399
825.4233	413.2153	7	D	11	1274.6198	637.8135
938.5073	469.7573	8	L	10	1159.5928	580.3001
1037.5758	519.2915	9	V	9	1046.5088	523.7580
1134.6285	567.8179	10	P	8	947.4404	474.2238
1265.6690	633.3381	11	M	7	850.3876	425.6974
1322.6905	661.8489	12	G	6	719.3471	360.1772
1451.7331	726.3702	13	E	5	662.3257	331.6665
1637.8124	819.4098	14	W	4	533.2831	267.1452
1738.8601	869.9337	15	T	3	347.2037	174.1055
1809.8972	905.4522	16	A	2	246.1561	123.5817
---	---	17	R	1	175.1190	88.0631

Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	29089	ITMS; CID	156.14	694.93	Ap2b1



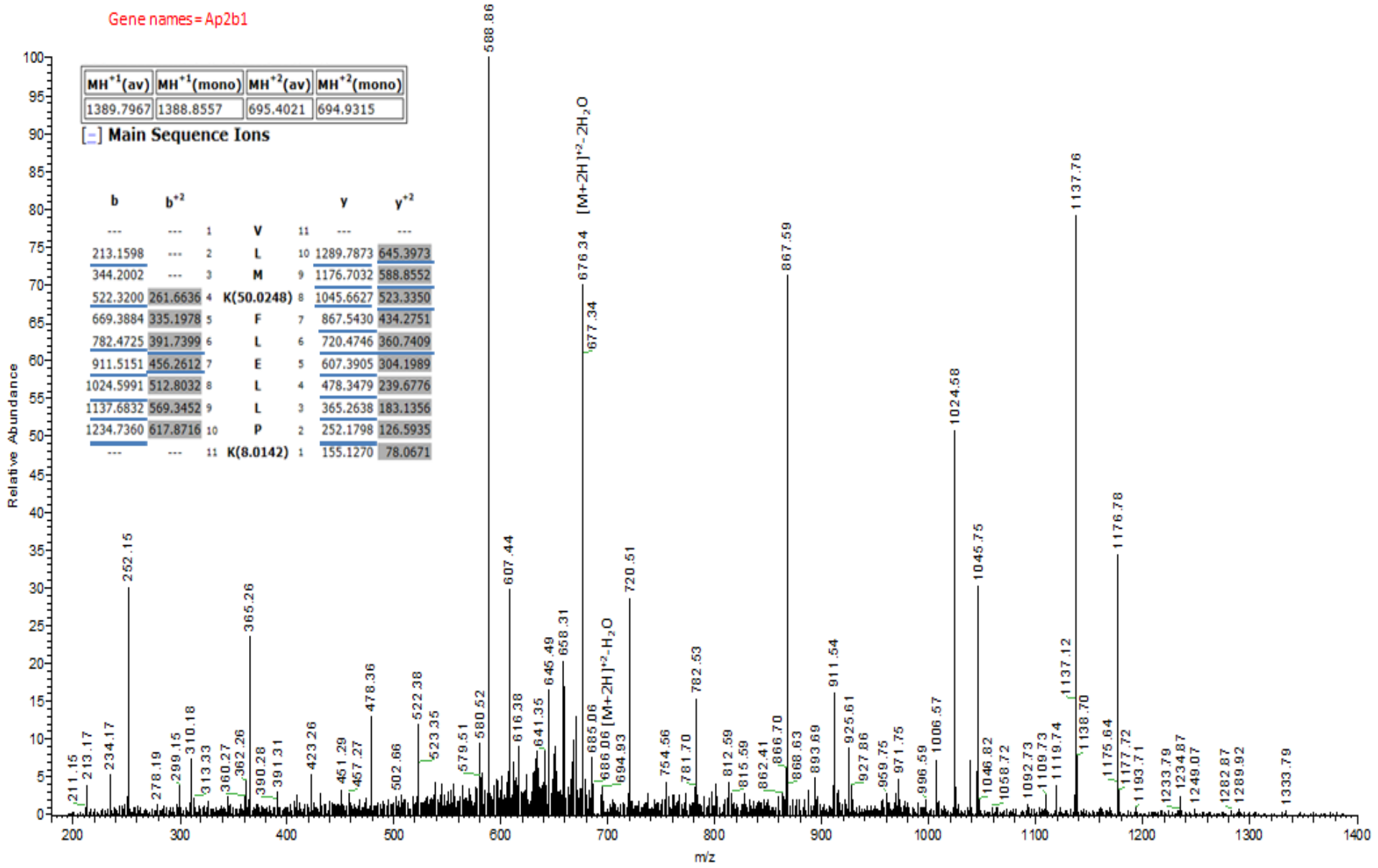
050813_SCW_II_29_19_4 #29089 RT: 111.51 AV: 1 NL: 8.72E3
T: ITMS + c NSI d Full ms2 694.93@cid35.00 [180.00-1400.00]

Gene names = Ap2b1

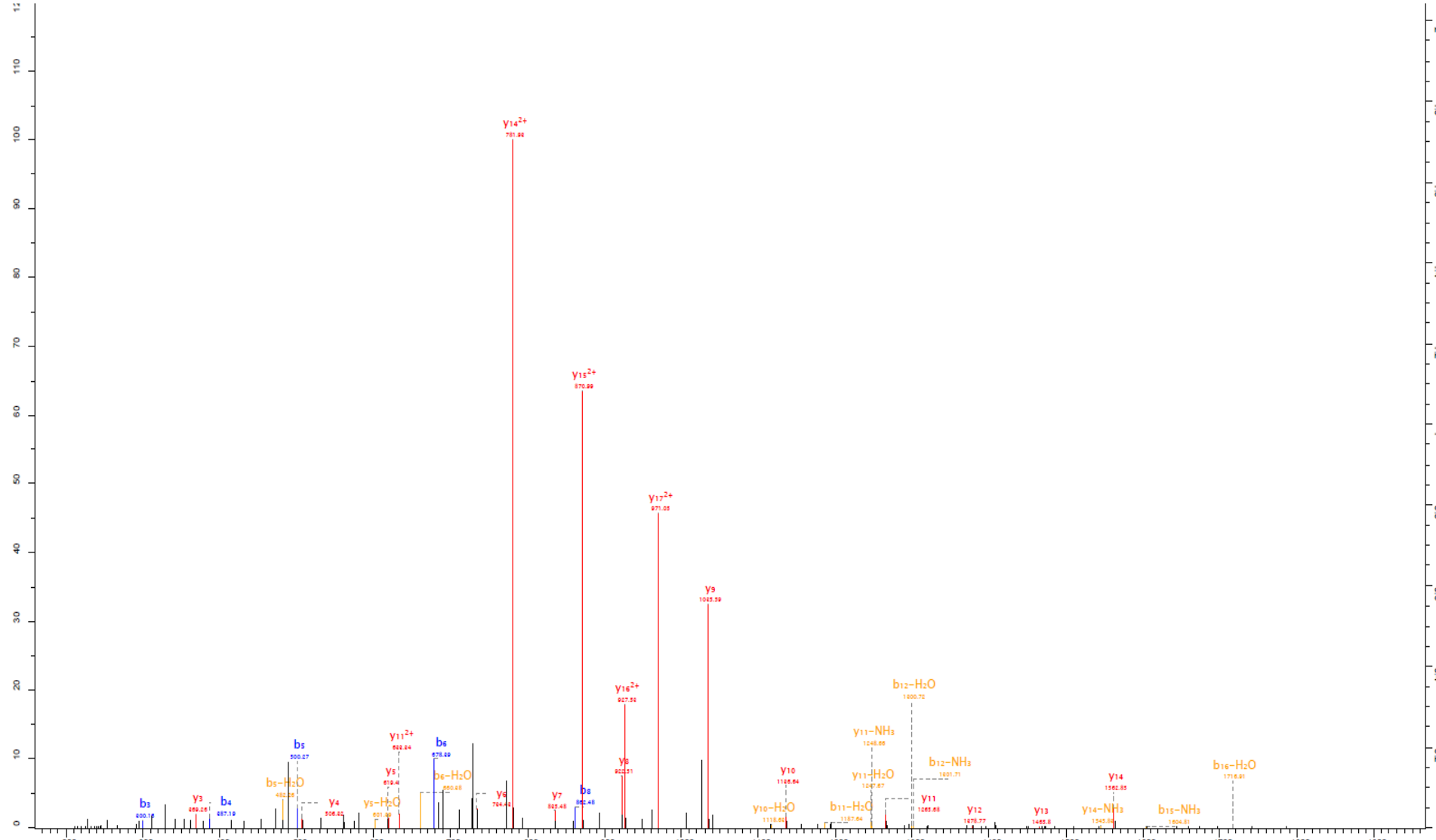
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1389.7967	1388.8557	695.4021	694.9315

[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	V	11	---	---
213.1598	---	2	L	10	1289.7873	645.3973
344.2002	---	3	M	9	1176.7032	588.8552
522.3200	261.6636	4	K(50.0248)	8	1045.6627	523.3350
669.3884	335.1978	5	F	7	867.5430	434.2751
782.4725	391.7399	6	L	6	720.4746	360.7409
911.5151	456.2612	7	E	5	607.3905	304.1989
1024.5991	512.8032	8	L	4	478.3479	239.6776
1137.6832	569.3452	9	L	3	365.2638	183.1356
1234.7360	617.8716	10	P	2	252.1798	126.5935
---	---	11	K(8.0142)	1	155.1270	78.0671



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_6_Vargas_Enriched	23981	ITMS; CID	94.63	747.42	Asap2



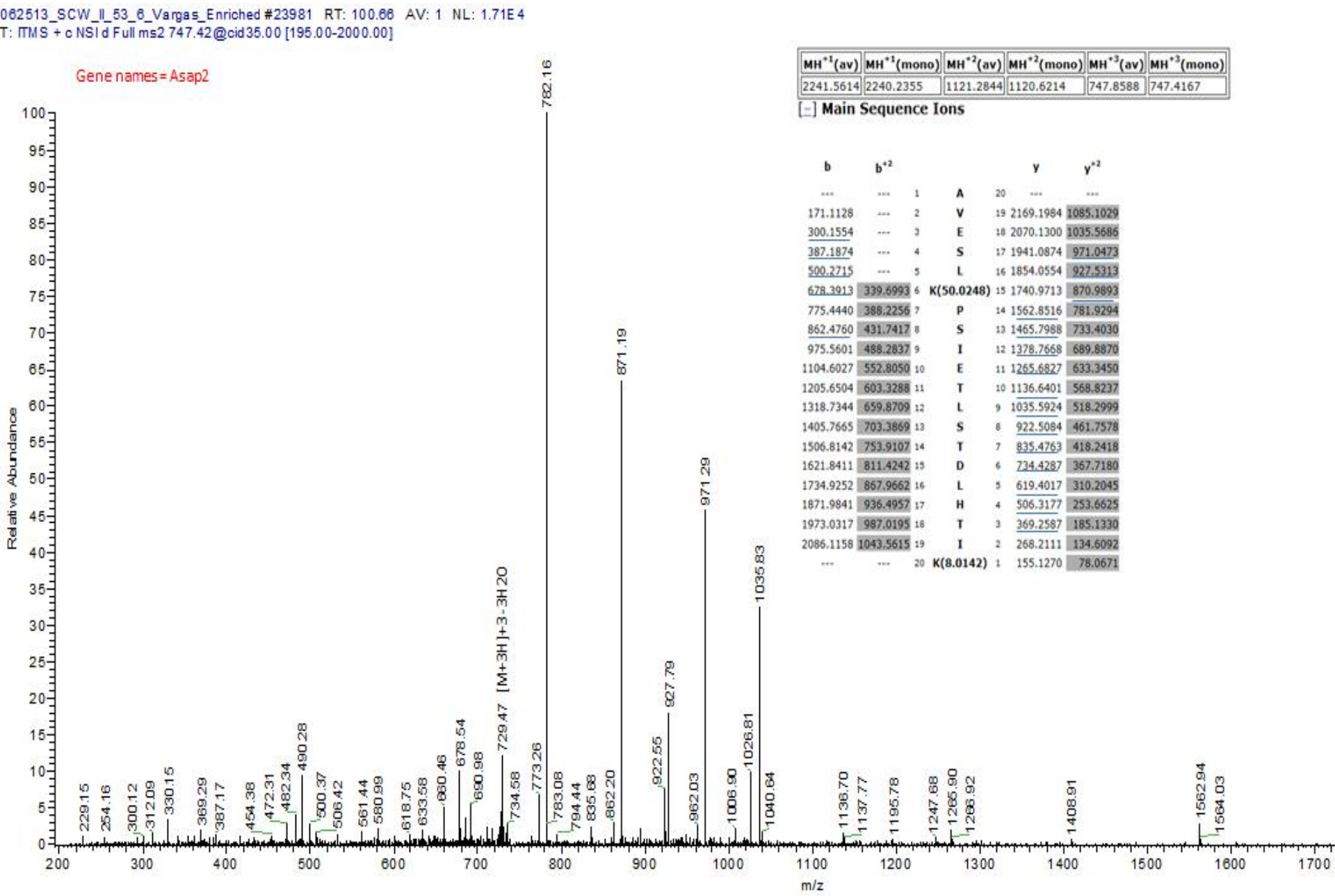
062513_SCW_II_53_6_Vargas_Enriched #23981 RT: 100.66 AV: 1 NL: 1.71E4
T: ITMS + c NSI d Full ms2 747.42@cid35.00 [195.00-2000.00]

Gene names = Asap2

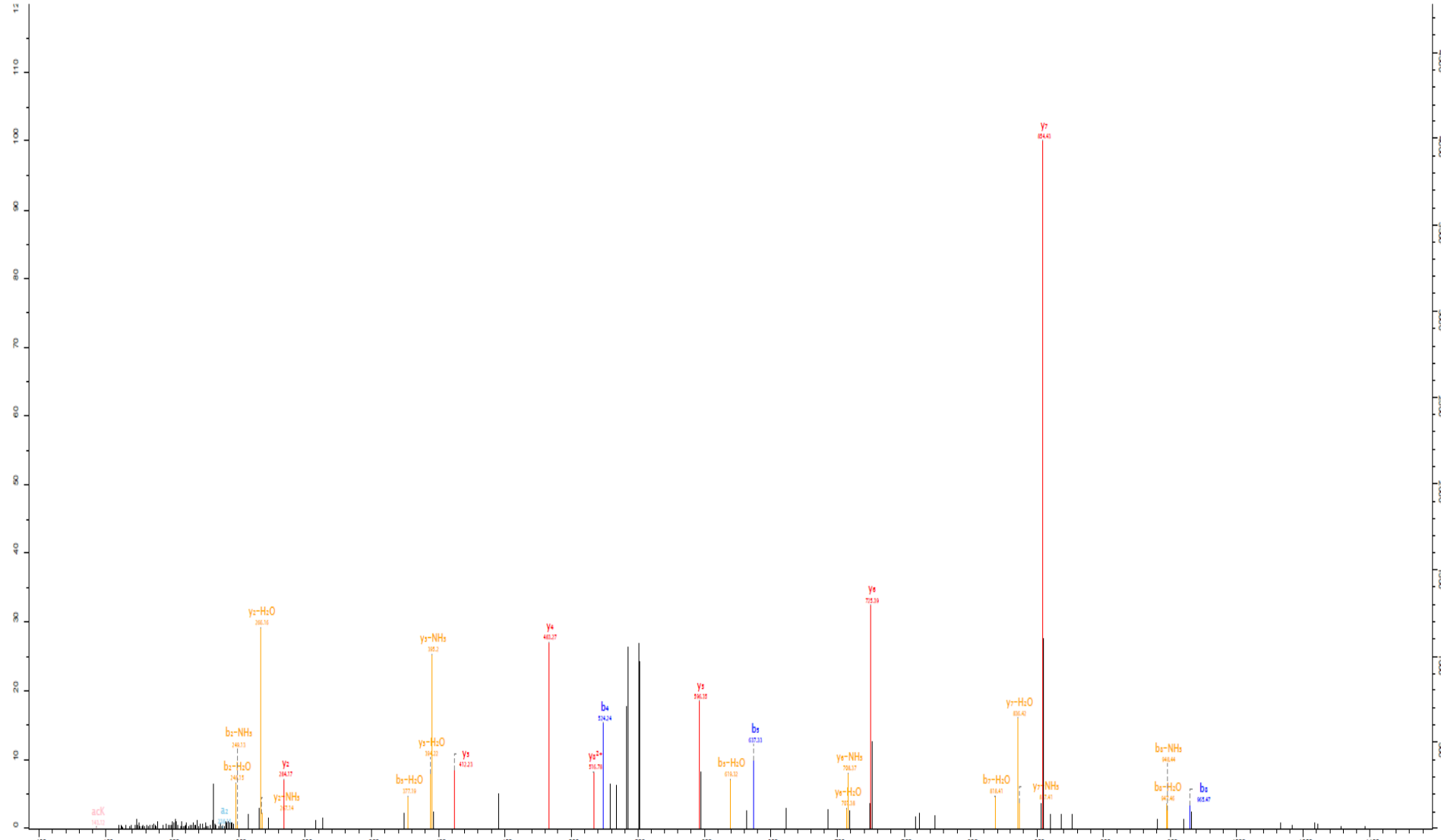
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
2241.5614	2240.2355	1121.2844	1120.6214	747.8588	747.4167

[−] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	A	20	---	---
171.1128	---	2	V	19	2169.1984	1085.1029
300.1554	---	3	E	18	2070.1300	1035.5686
387.1874	---	4	S	17	1941.0874	971.0473
500.2715	---	5	L	16	1854.0554	927.5313
678.3913	339.6993	6	K(50.0248)	15	1740.9713	870.9893
775.4440	388.2256	7	P	14	1562.8516	781.9294
862.4760	431.7417	8	S	13	1465.7988	733.4030
975.5601	488.2837	9	I	12	1378.7668	689.8870
1104.6027	552.8050	10	E	11	1265.6827	633.3450
1205.6504	603.3288	11	T	10	1136.6401	568.8237
1318.7344	659.8709	12	L	9	1035.5924	518.2999
1405.7665	703.3869	13	S	8	922.5084	461.7578
1506.8142	753.9107	14	T	7	835.4763	418.2418
1621.8411	811.4242	15	D	6	734.4287	367.7180
1734.9252	867.9662	16	L	5	619.4017	310.2045
1871.9841	936.4957	17	H	4	506.3177	253.6625
1973.0317	987.0195	18	T	3	369.2587	185.1330
2086.1158	1043.5615	19	I	2	268.2111	134.6092
---	---	20	K(8.0142)	1	155.1270	78.0671



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_JI_53_5_Vargas_Enriched	12159	ITMS; CID	125.72	560.3	Brd3



- S K E E L A Q E K -

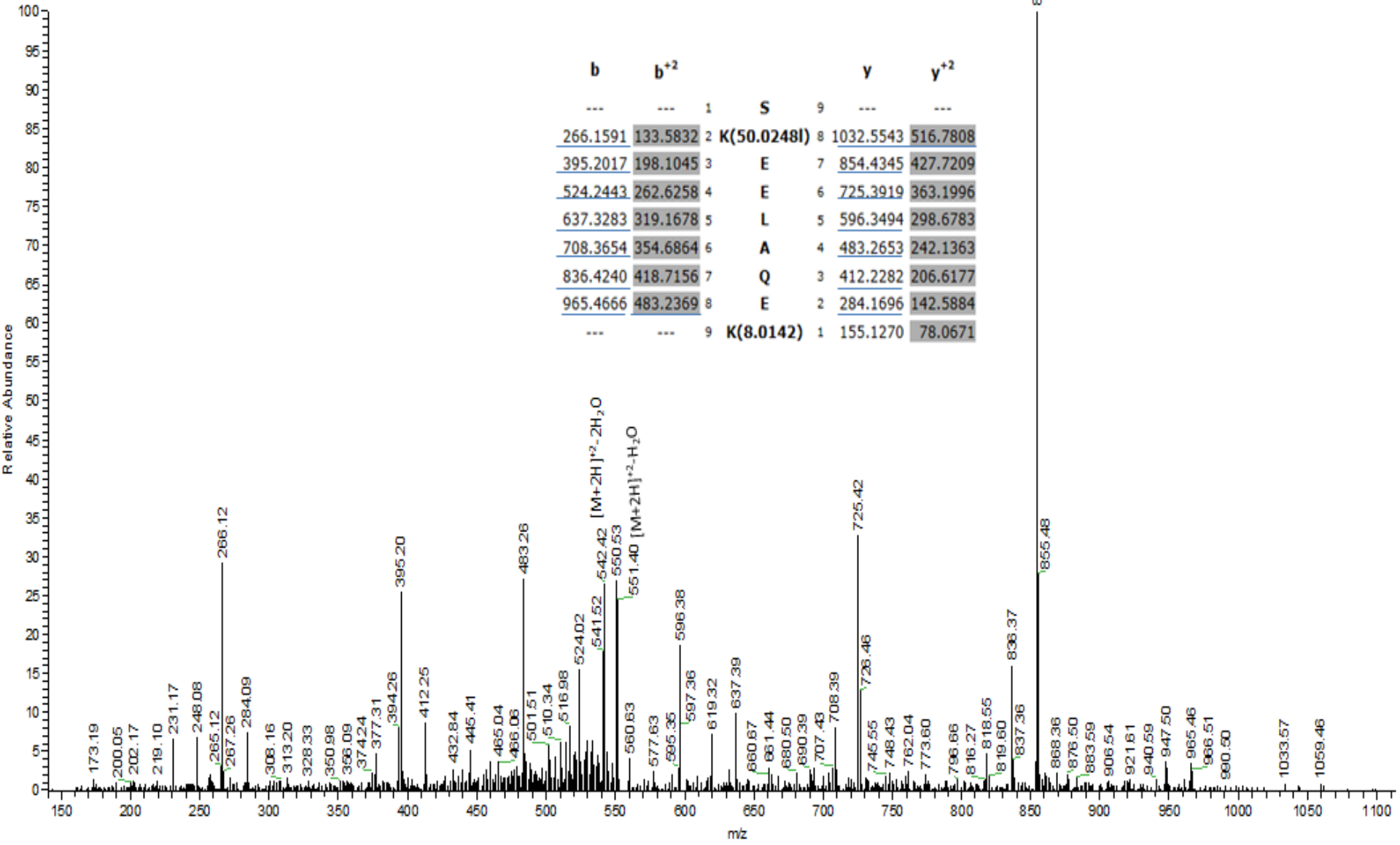
062513_SCW_II_53_5_Vargas_Enriched #12159 RT: 56.13 AV: 1 NL: 3.99E3
T: ITMS + c NSI d Full ms2 560.30@cid35.00 [140.00-1135.00]

Gene names = Brd3

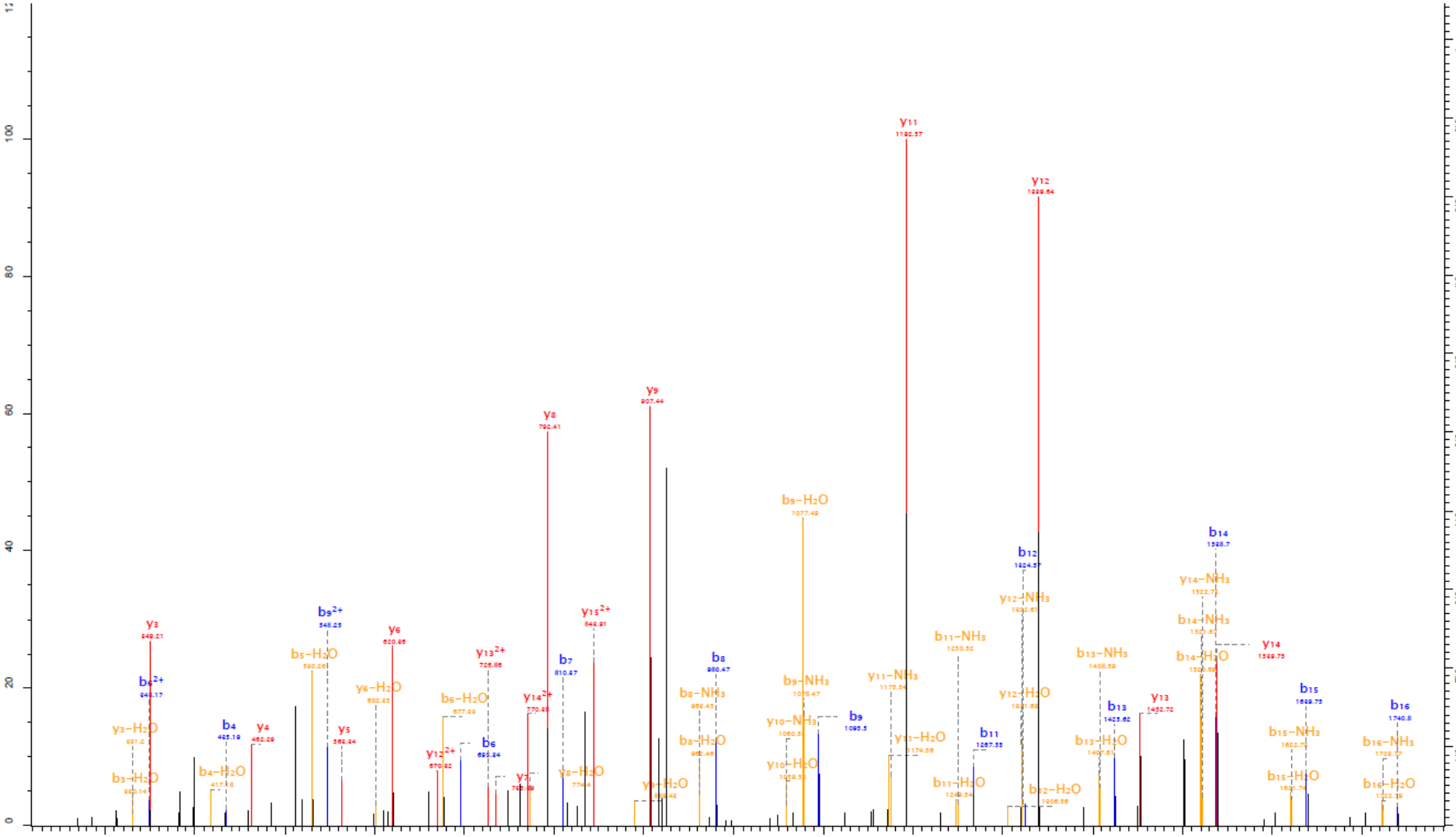
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1120.2107	1119.5863	560.6091	560.2968

[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	S	9	---	---
266.1591	133.5832	2	K(50.0248l)	8	1032.5543	516.7808
395.2017	198.1045	3	E	7	854.4345	427.7209
524.2443	262.6258	4	E	6	725.3919	363.1996
637.3283	319.1678	5	L	5	596.3494	298.6783
708.3654	354.6864	6	A	4	483.2653	242.1363
836.4240	418.7156	7	Q	3	412.2282	206.6177
965.4666	483.2369	8	E	2	284.1696	142.5884
---	---	9	K(8.0142)	1	155.1270	78.0671



Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_4_2ndZT	24781	ITMS; CID	339.81	944.45	Calm1



- E A F S L F D ac K D G D G T I T T K -

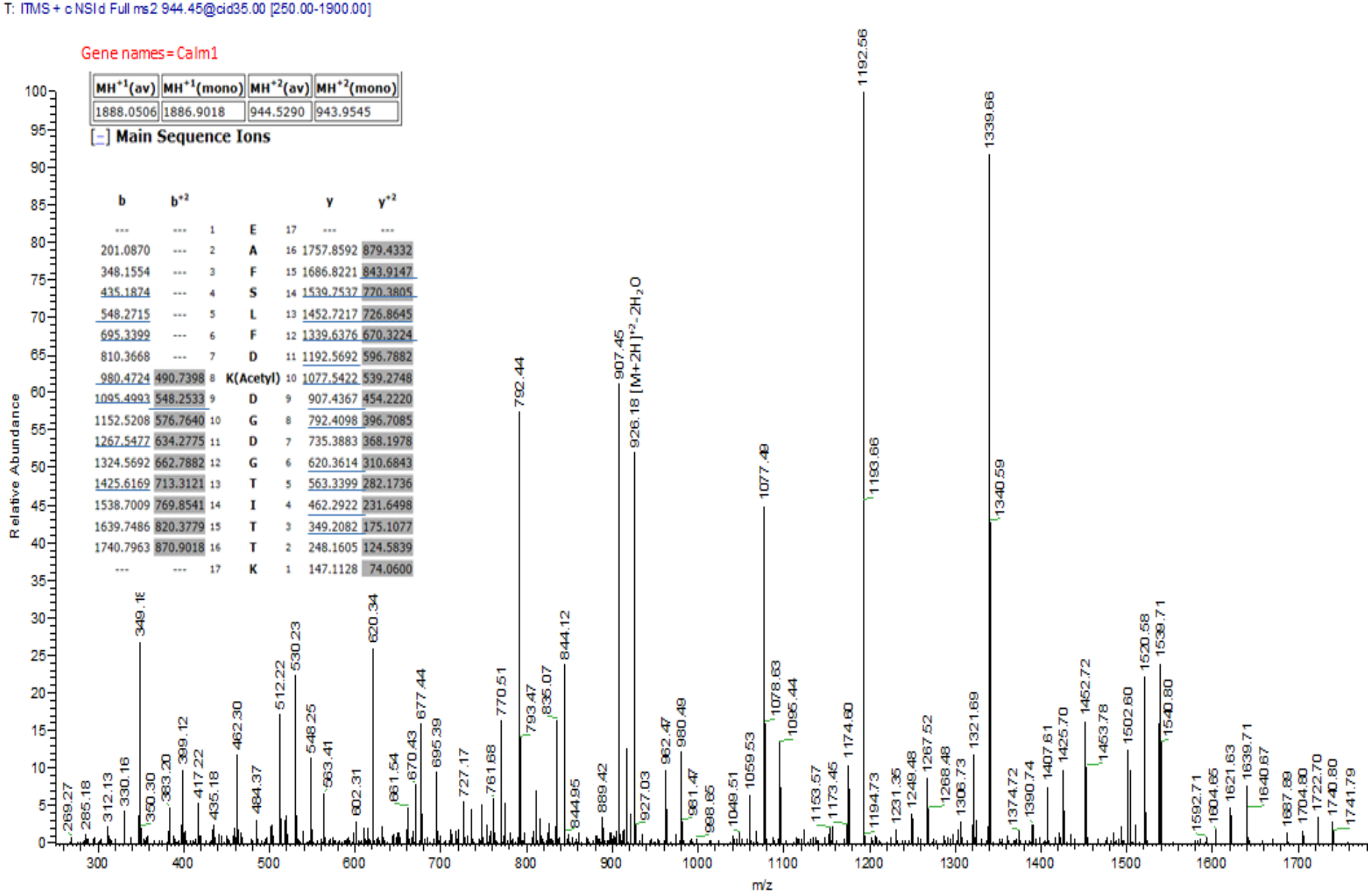
022714_SCW_II_53_4_2ndZT#24781 RT: 110.84 AV: 1 NL: 8.73E3
T: ITMS + c NSI d Full ms2 944.45@cid35.00 [250.00-1900.00]

Gene names = Calm1

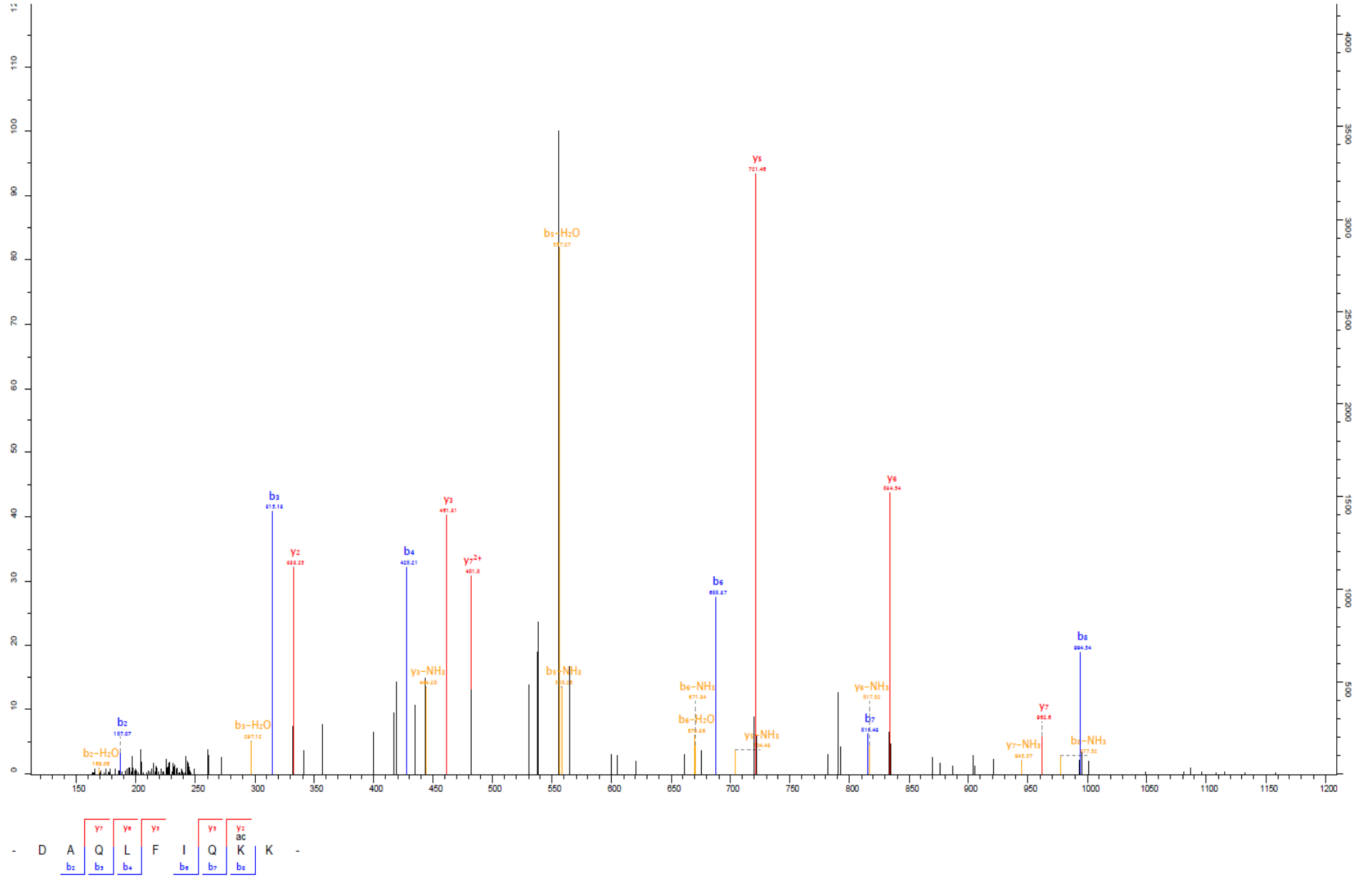
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1888.0506	1886.9018	944.5290	943.9545

[−] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	E	17	---	---
201.0870	---	2	A	16	1757.8592	879.4332
348.1554	---	3	F	15	1686.8221	843.9147
435.1874	---	4	S	14	1539.7537	770.3805
548.2715	---	5	L	13	1452.7217	726.8645
695.3399	---	6	F	12	1339.6376	670.3224
810.3668	---	7	D	11	1192.5692	596.7882
980.4724	490.7398	8	K(Acetyl)	10	1077.5422	539.2748
1095.4993	548.2533	9	D	9	907.4367	454.2220
1152.5208	576.7640	10	G	8	792.4098	396.7085
1267.5477	634.2775	11	D	7	735.3883	368.1978
1324.5692	662.7882	12	G	6	620.3614	310.6843
1425.6169	713.3121	13	T	5	563.3399	282.1736
1538.7009	769.8541	14	I	4	462.2922	231.6498
1639.7486	820.3779	15	T	3	349.2082	175.1077
1740.7963	870.9018	16	T	2	248.1605	124.5839
---	---	17	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	17448	ITMS; CID	125.57	574.84	Cat

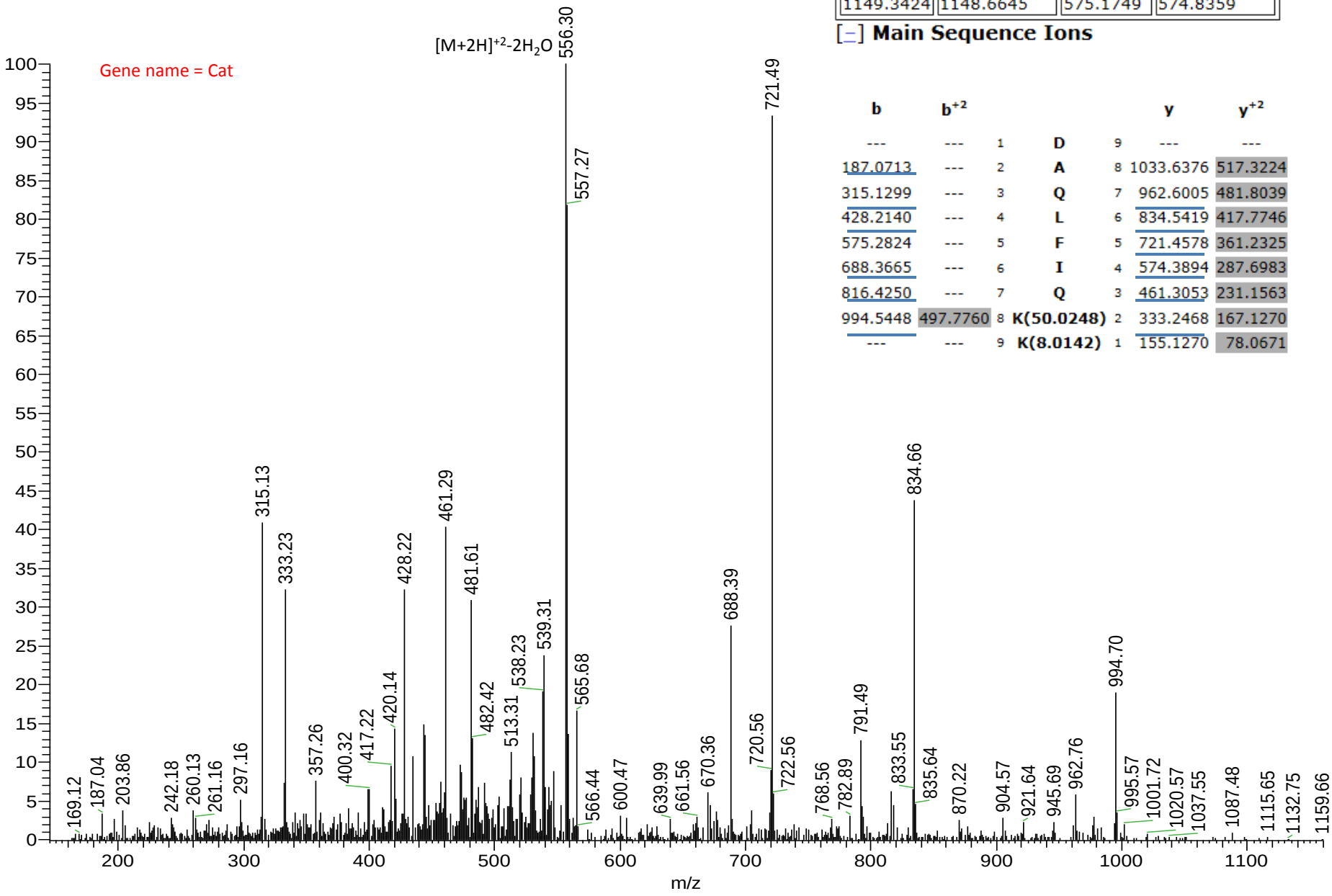


062513_SCW_II_53_4_Vargas_Enriched #17448 RT: 78.57 AV: 1 NL: 3.47E3
T: ITMS + c NSI d Full ms2 574.84@cid35.00 [145.00-1160.00]

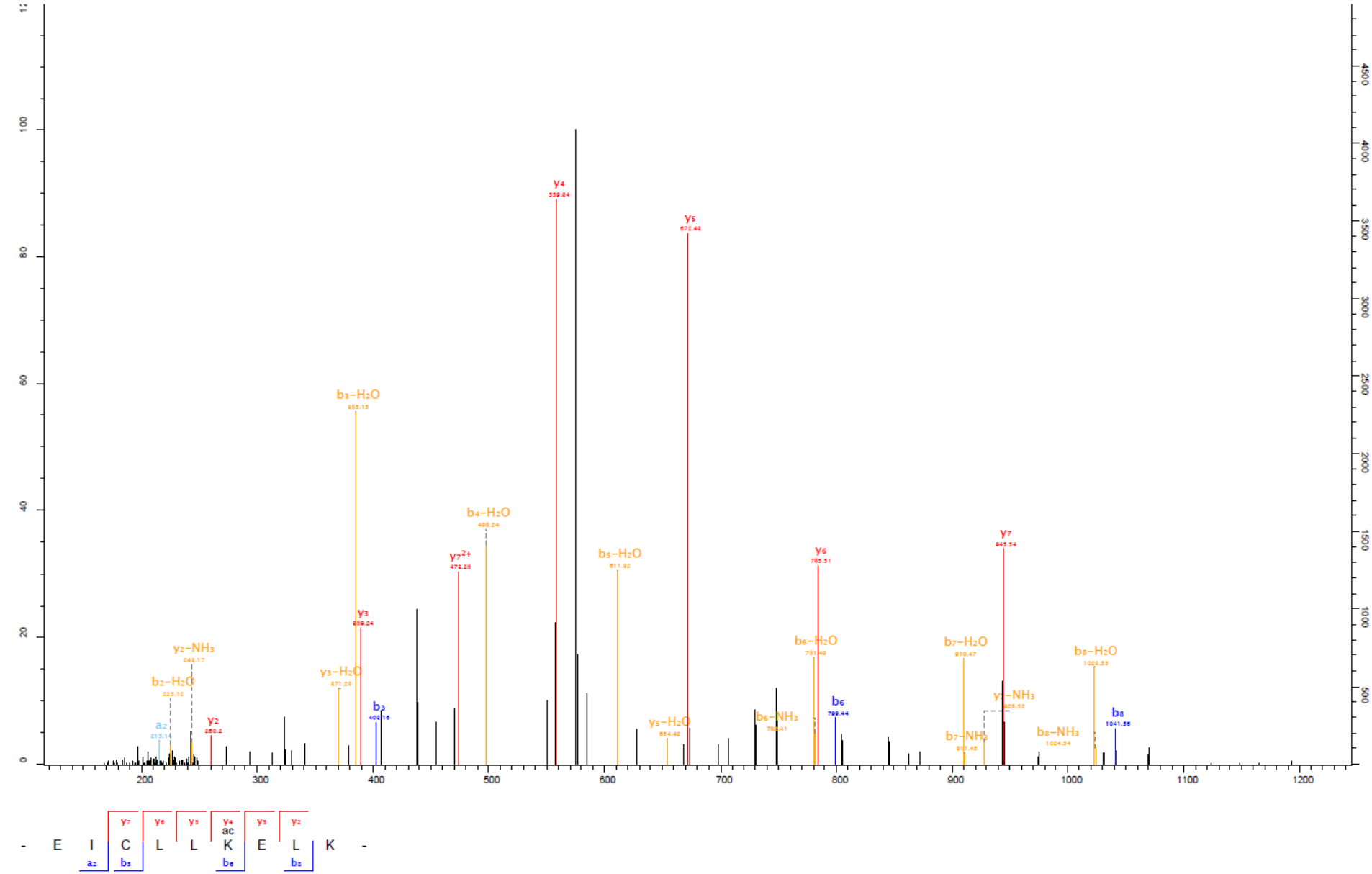
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1149.3424	1148.6645	575.1749	574.8359

[–] **Main Sequence Ions**

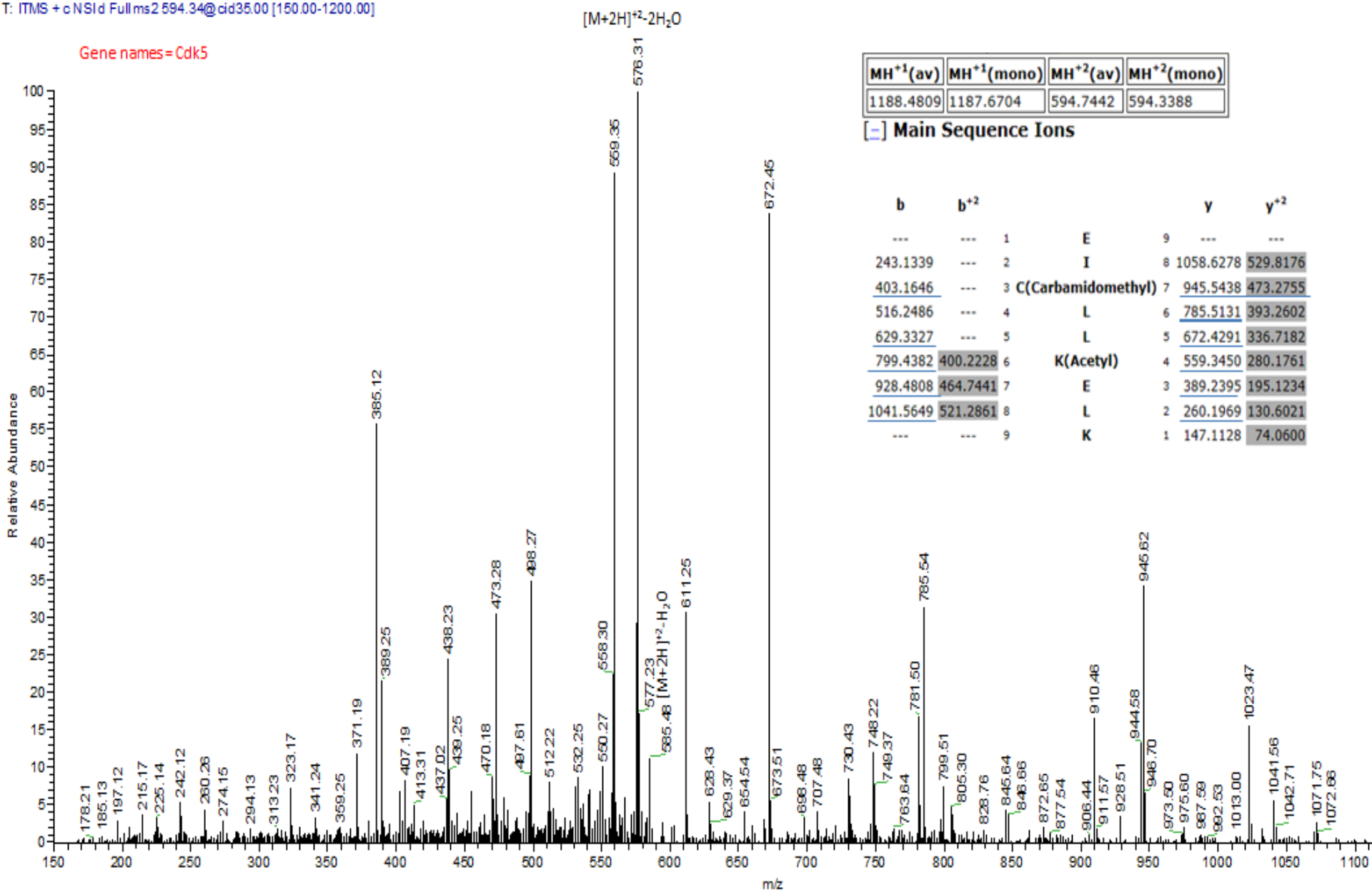
b	b^{+2}				y	y^{+2}
---	---	1	D	9	---	---
187.0713	---	2	A	8	1033.6376	517.3224
315.1299	---	3	Q	7	962.6005	481.8039
428.2140	---	4	L	6	834.5419	417.7746
575.2824	---	5	F	5	721.4578	361.2325
688.3665	---	6	I	4	574.3894	287.6983
816.4250	---	7	Q	3	461.3053	231.1563
994.5448	497.7760	8	K(50.0248)	2	333.2468	167.1270
---	---	9	K(8.0142)	1	155.1270	78.0671



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	21862	ITMS; CID	157.66	594.34	Cdk5



062513_SCW_II_53_4_Vargas_Enrichec #21862 RT: 94.61 AV: 1 NL: 4.09E3
T: ITMS + c NSI d Full ms2 594.34@cid35.00 [150.00-1200.00]

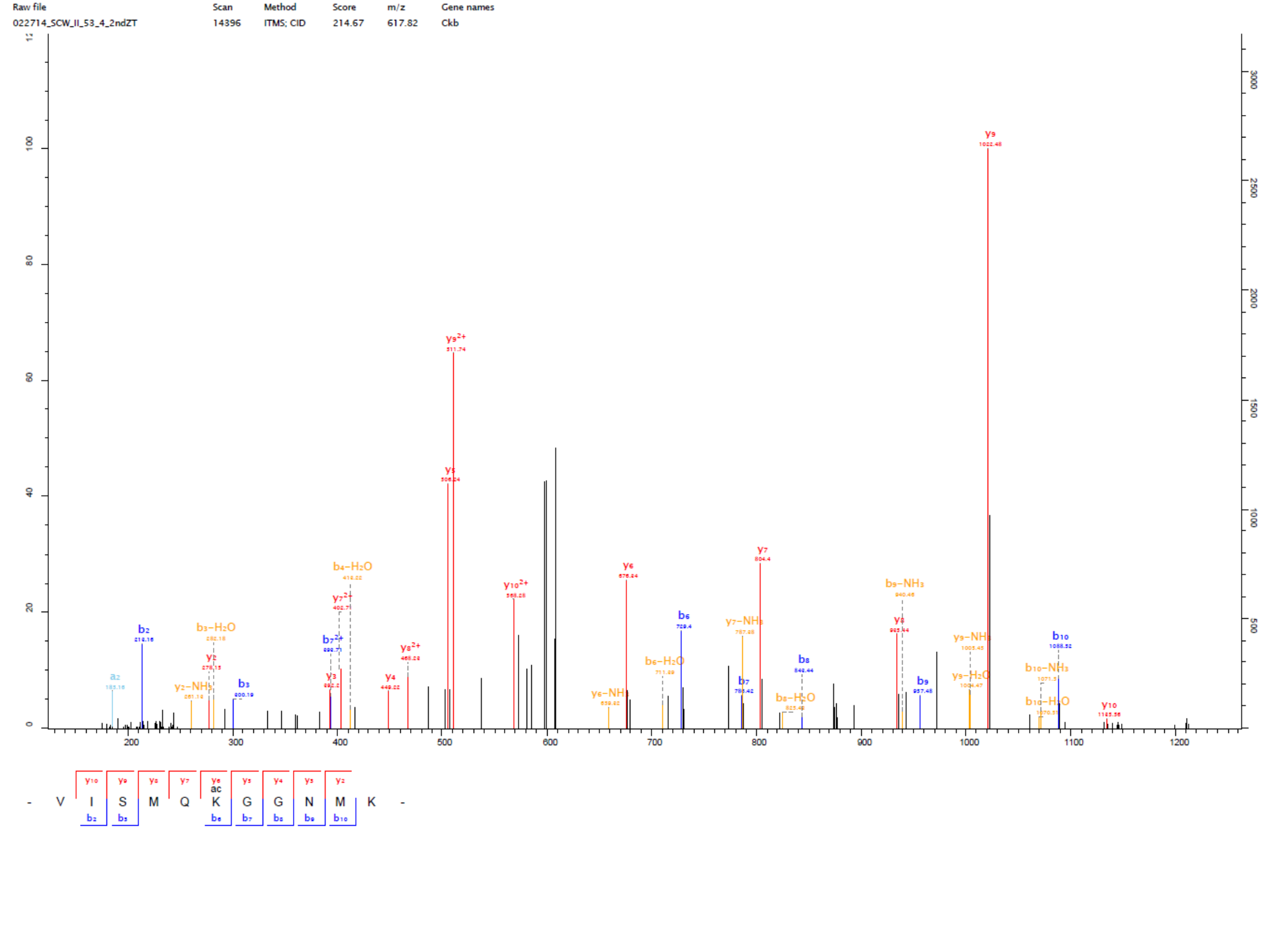


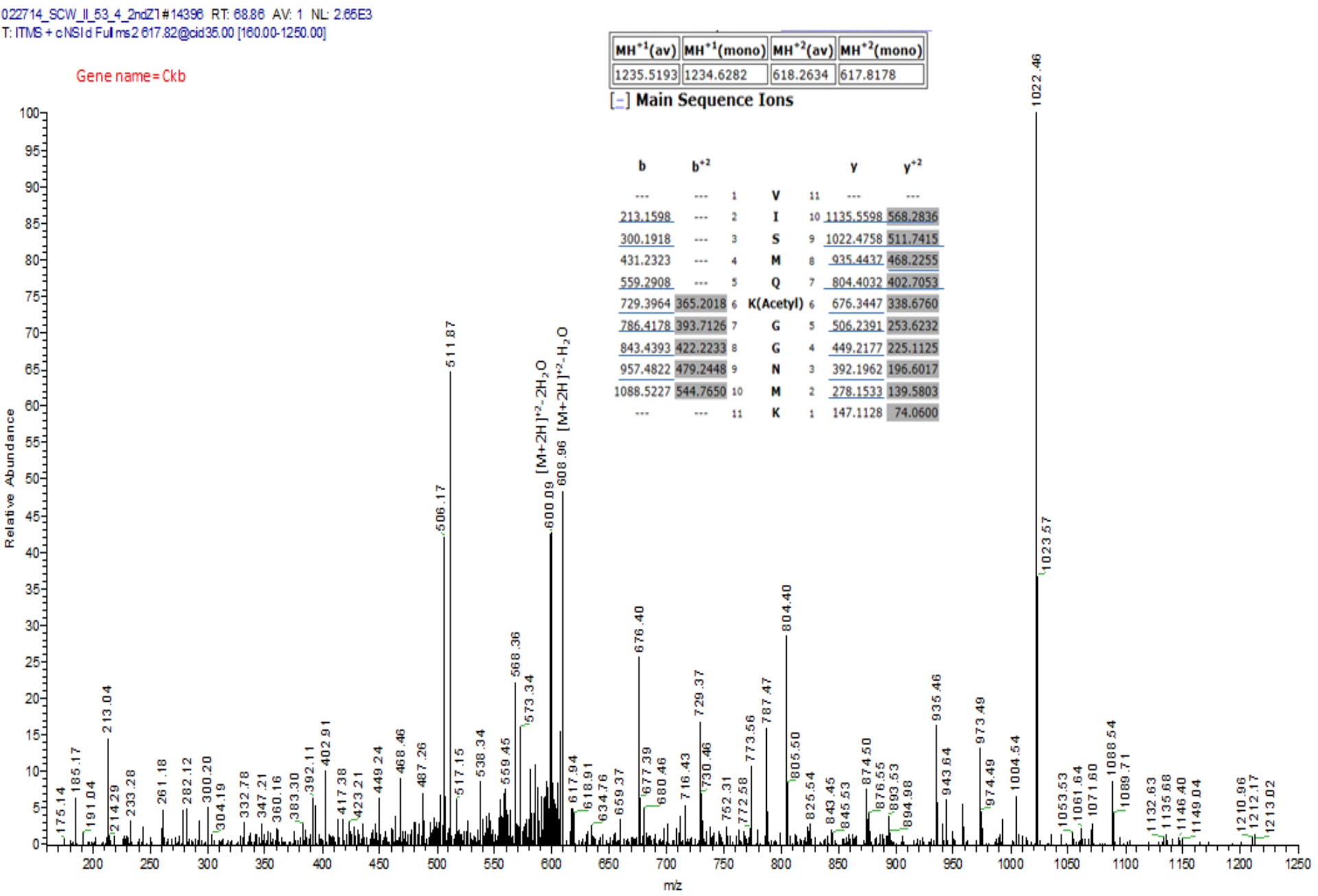
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1188.4809	1187.6704	594.7442	594.3388

[-] Main Sequence Ions

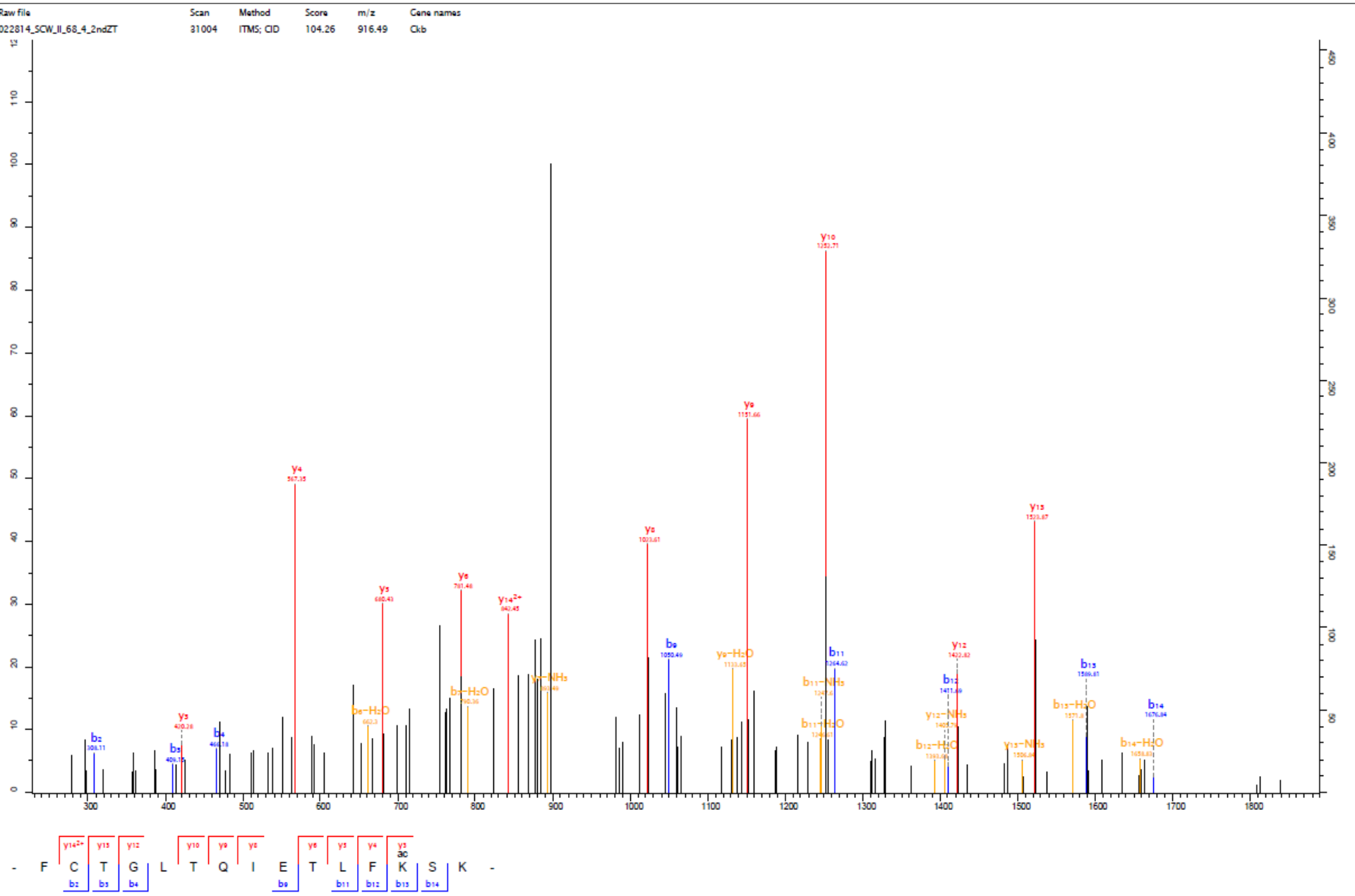
b	b^{+2}				y	y^{+2}
---	---	1	E	9	---	---
243.1339	---	2	I	8	1058.6278	529.8176
403.1646	---	3	C(Carbamidomethyl)	7	945.5438	473.2755
516.2486	---	4	L	6	785.5131	393.2602
629.3327	---	5	L	5	672.4291	336.7182
799.4382	400.2228	6	K(Acetyl)	4	559.3450	280.1761
928.4808	464.7441	7	E	3	389.2395	195.1234
1041.5649	521.2861	8	L	2	260.1969	130.6021
---	---	9	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_4_2ndZT	14396	ITMS; CID	214.67	617.82	Ckb




022714_SCW_II_53_4_2ndZ1#14396 RT: 68.86 AV: 1 NL: 2.65E3
T: ITMS + c NSI d Full ms2 617.82@cid35.00 [160.00-1250.00]
Gene name=Ckb
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1235.5193 1234.6282 618.2634 617.8178
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 V 11 --- ---
213.1598 --- 2 I 10 1135.5598 568.2836
300.1918 --- 3 S 9 1022.4758 511.7415
431.2323 --- 4 M 8 935.4437 468.2255
559.2908 --- 5 Q 7 804.4032 402.7053
729.3964 365.2018 6 K(Acetyl) 6 676.3447 338.6760
786.4178 393.7126 7 G 5 506.2391 253.6232
843.4393 422.2233 8 G 4 449.2177 225.1125
957.4822 479.2448 9 N 3 392.1962 196.6017
1088.5227 544.7650 10 M 2 278.1533 139.5803
--- --- 11 K 1 147.1128 74.0600
Relative Abundance
m/z
[M+2H]+2-2H2O
[M+2H]+2-H2O
1022.46
1023.57
511.87
506.17
600.09
608.96
804.40
676.40
729.37
568.36
573.34
787.47
935.46
973.49
213.04
1004.54
1088.54

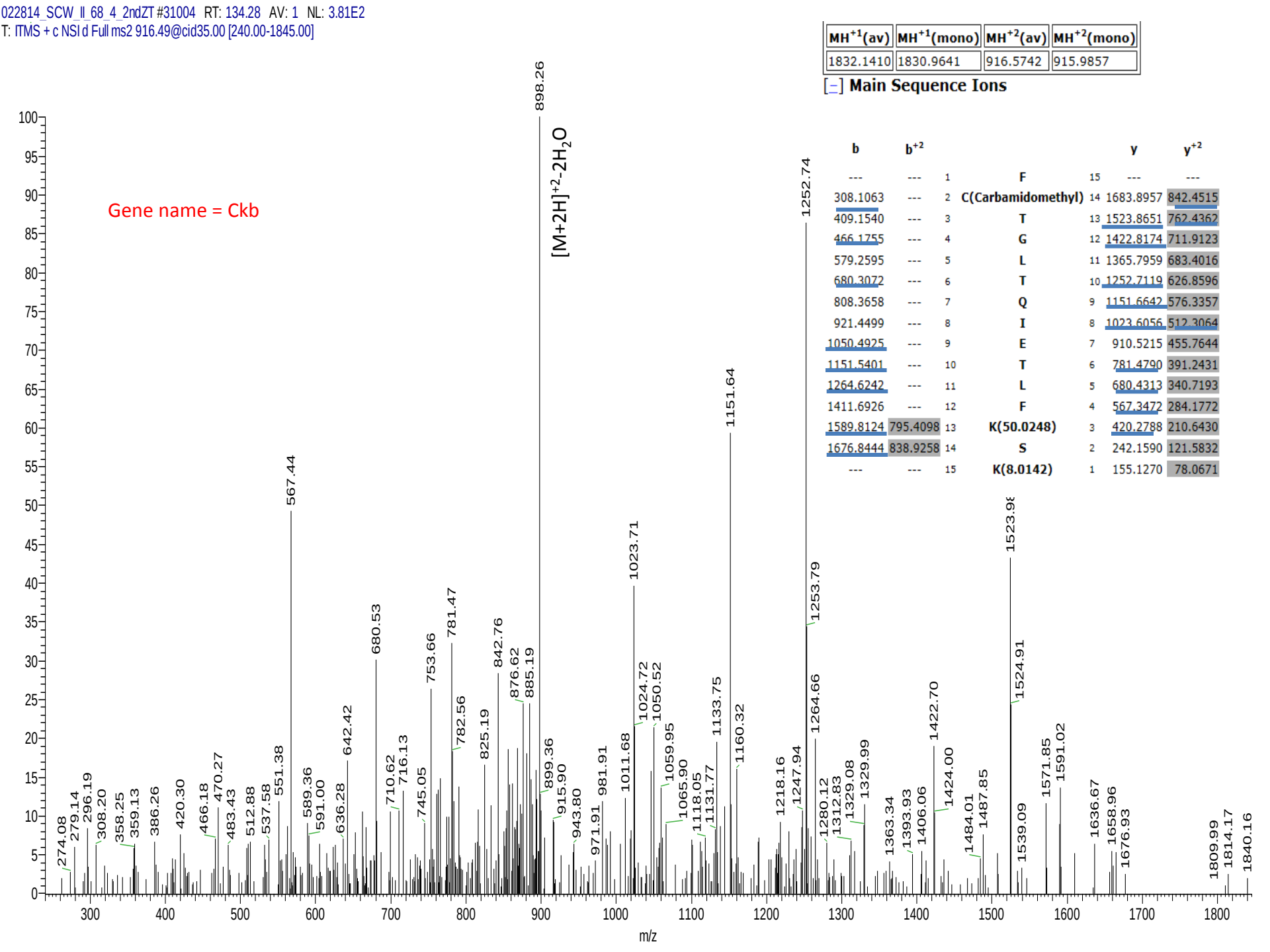
Raw file	Scan	Method	Score	m/z	Gene names
022814_SCW_II_68_4_2ndZT	31004	ITMS; CID	104.26	916.49	Ckb



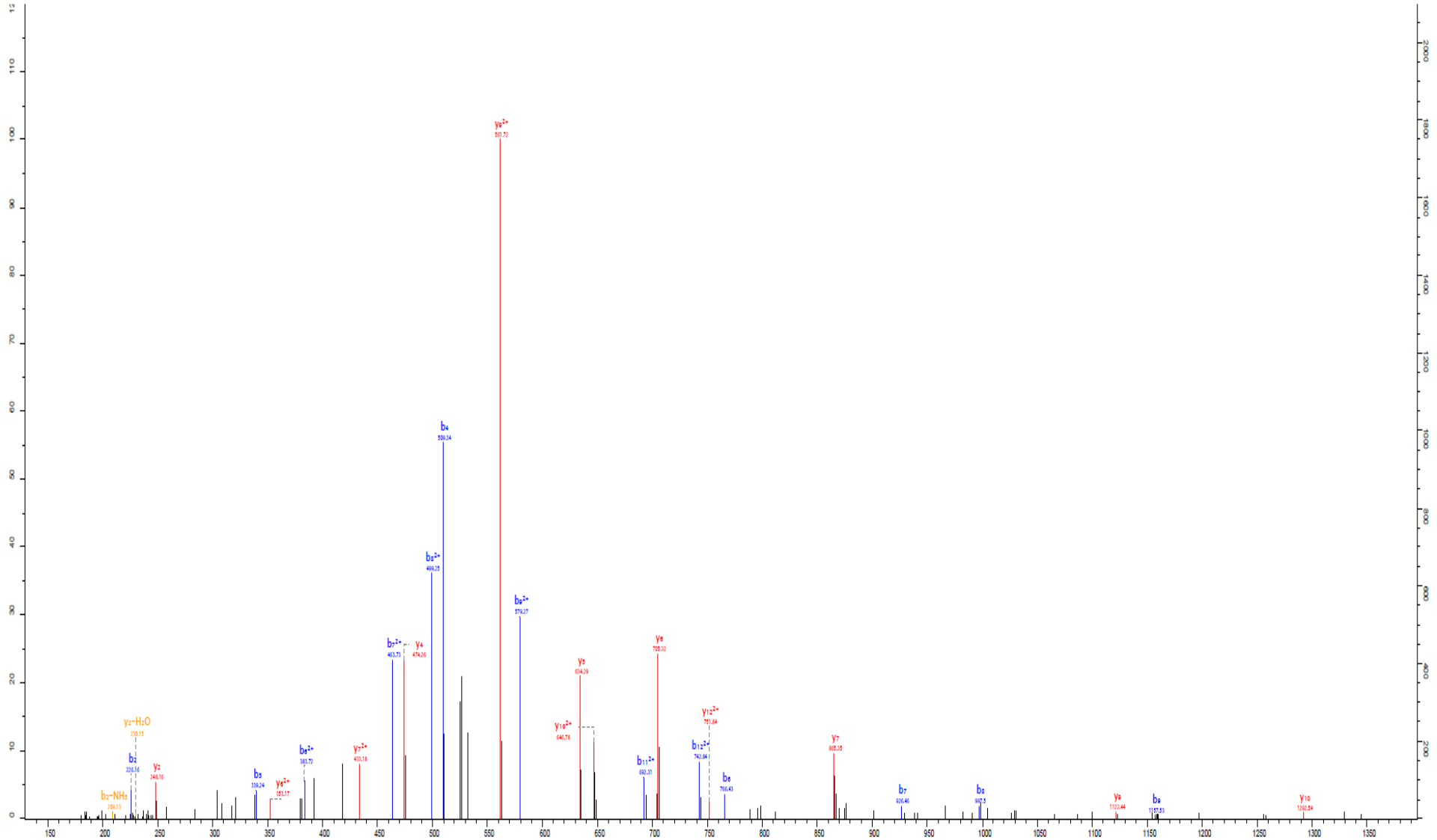
- F C T G L T Q I E T L F K S K -

y14 2+ y13 y12 y10 y9 y8 y6 y5 y4 y3 ac

b2 b3 b4 b9 b11 b12 b13 b14


022814_SCW_II_68_4_2ndZT #31004 RT: 134.28 AV: 1 NL: 3.81E2
T: ITMS + c NSI d Full ms2 916.49@cid35.00 [240.00-1845.00]
Gene name = Ckb
[M+2H]+2-2H2O
m/z
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1832.1410 1830.9641 916.5742 915.9857
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 F 15 --- ---
308.1063 --- 2 C(Carbamidomethyl) 14 1683.8957 842.4515
409.1540 --- 3 T 13 1523.8651 762.4362
466.1755 --- 4 G 12 1422.8174 711.9123
579.2595 --- 5 L 11 1365.7959 683.4016
680.3072 --- 6 T 10 1252.7119 626.8596
808.3658 --- 7 Q 9 1151.6642 576.3357
921.4499 --- 8 I 8 1023.6056 512.3064
1050.4925 --- 9 E 7 910.5215 455.7644
1151.5401 --- 10 T 6 781.4790 391.2431
1264.6242 --- 11 L 5 680.4313 340.7193
1411.6926 --- 12 F 4 567.3472 284.1772
1589.8124 795.4098 13 K(50.0248) 3 420.2788 210.6430
1676.8444 838.9258 14 S 2 242.1590 121.5832
--- --- 15 K(8.0142) 1 155.1270 78.0671

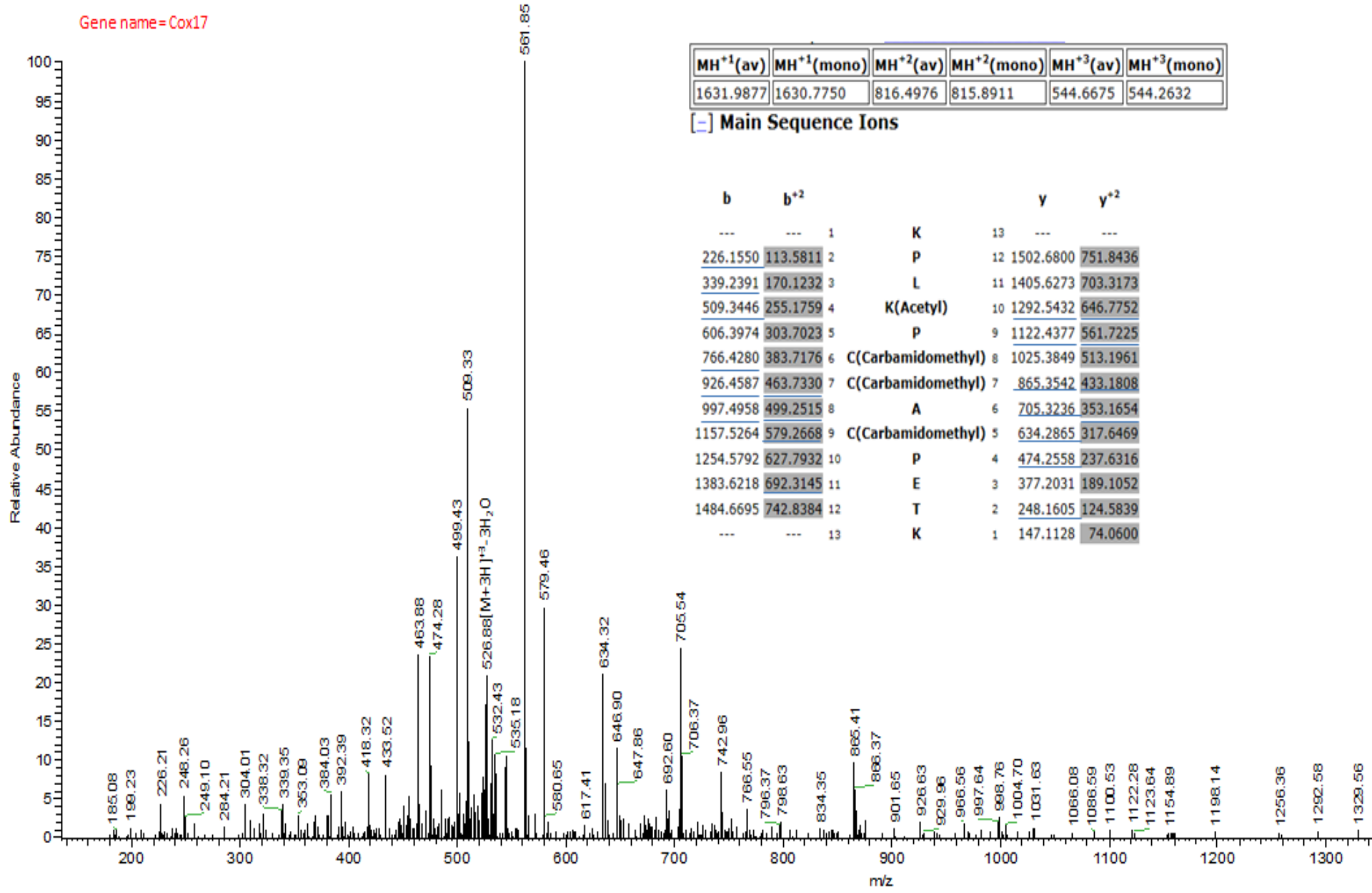
Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_9_2ndZT	10898	ITMS; CID	120.84	544.6	Cox17



- K P L K P C C A C P E T K -

022714_SCW_II_53_9_2ndZT #10898 RT: 54.38 AV: 1 NL: 1.75E3
T: ITMS + c NSI d Full ms2 544.60@cid35.00 [135.00-1645.00]

Gene name=Cox17

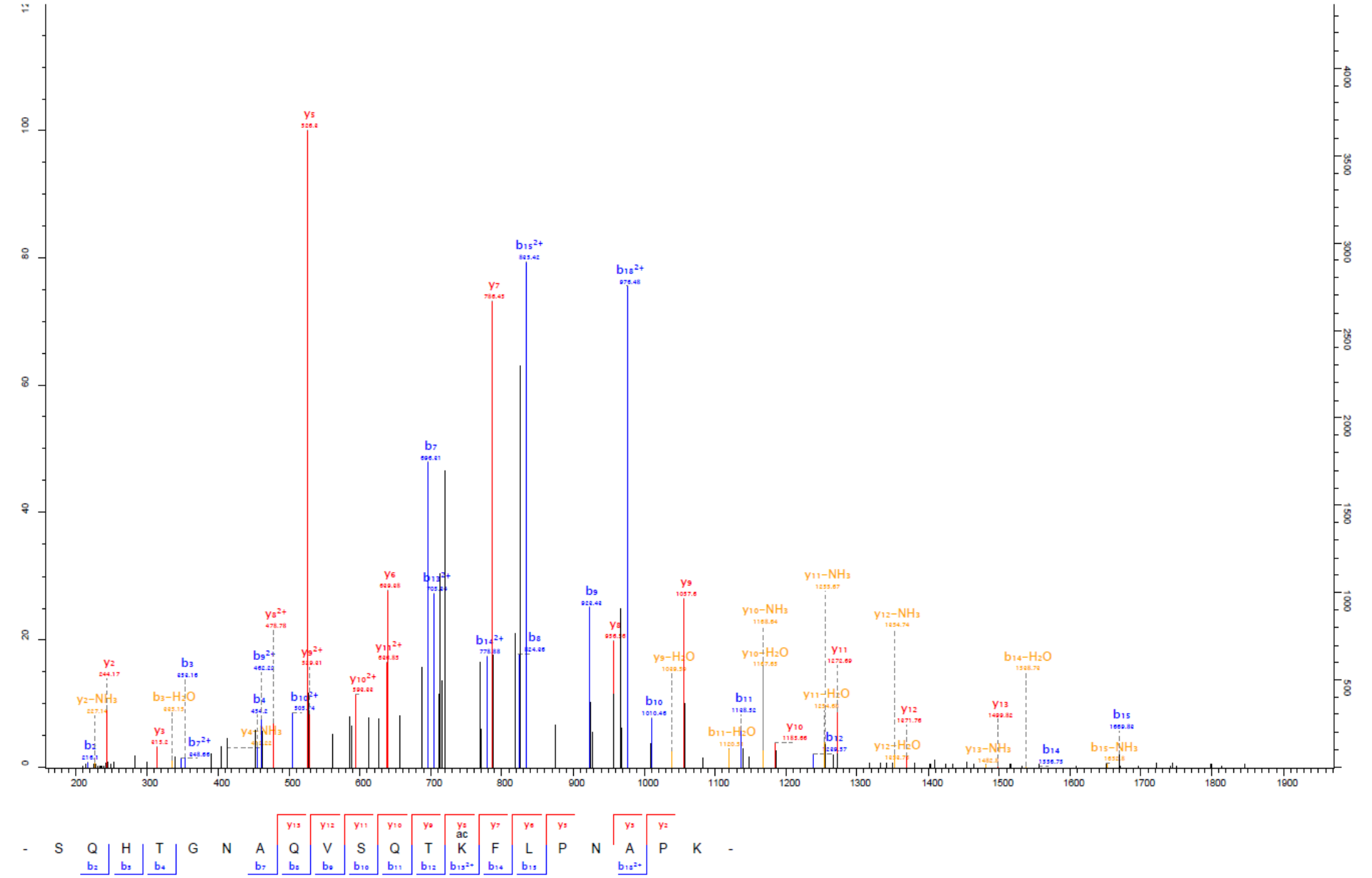


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1631.9877	1630.7750	816.4976	815.8911	544.6675	544.2632

[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	K	13	---	---
226.1550	113.5811	2	P	12	1502.6800	751.8436
339.2391	170.1232	3	L	11	1405.6273	703.3173
509.3446	255.1759	4	K(Acetyl)	10	1292.5432	646.7752
606.3974	303.7023	5	P	9	1122.4377	561.7225
766.4280	383.7176	6	C(Carbamidomethyl)	8	1025.3849	513.1961
926.4587	463.7330	7	C(Carbamidomethyl)	7	865.3542	433.1808
997.4958	499.2515	8	A	6	705.3236	353.1654
1157.5264	579.2668	9	C(Carbamidomethyl)	5	634.2865	317.6469
1254.5792	627.7932	10	P	4	474.2558	237.6316
1383.6218	692.3145	11	E	3	377.2031	189.1052
1484.6695	742.8384	12	T	2	248.1605	124.5839
---	---	13	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_8_2ndZT	17064	ITMS; CID	185.2	732.38	Ddx1

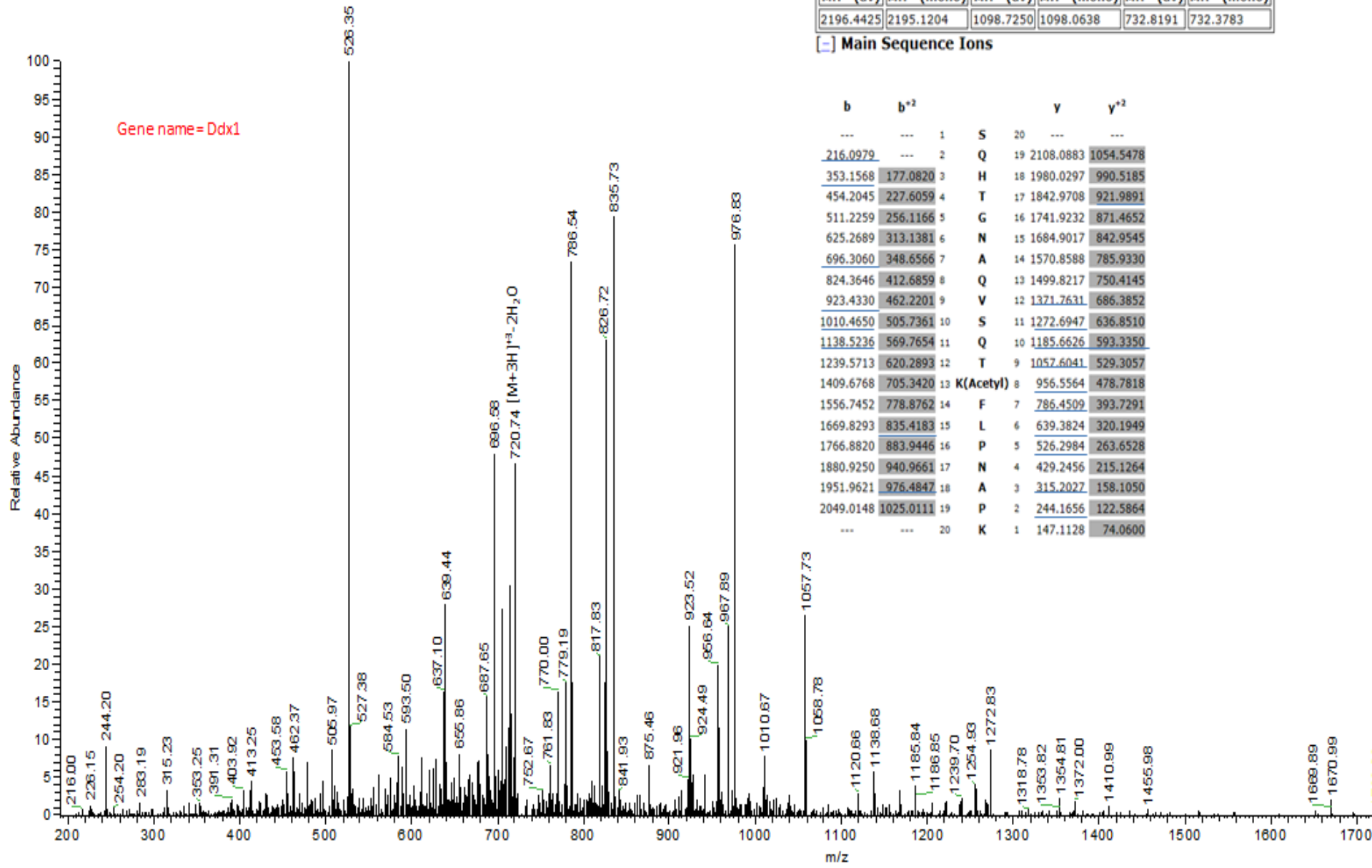


022714_SCW_II_53_8_2ndZT #17064 RT: 79.32 AV: 1 NL: 3.64E3
T: ITMS + c NSId Full ms2 732.38@cid35.00 [190.00-2000.00]

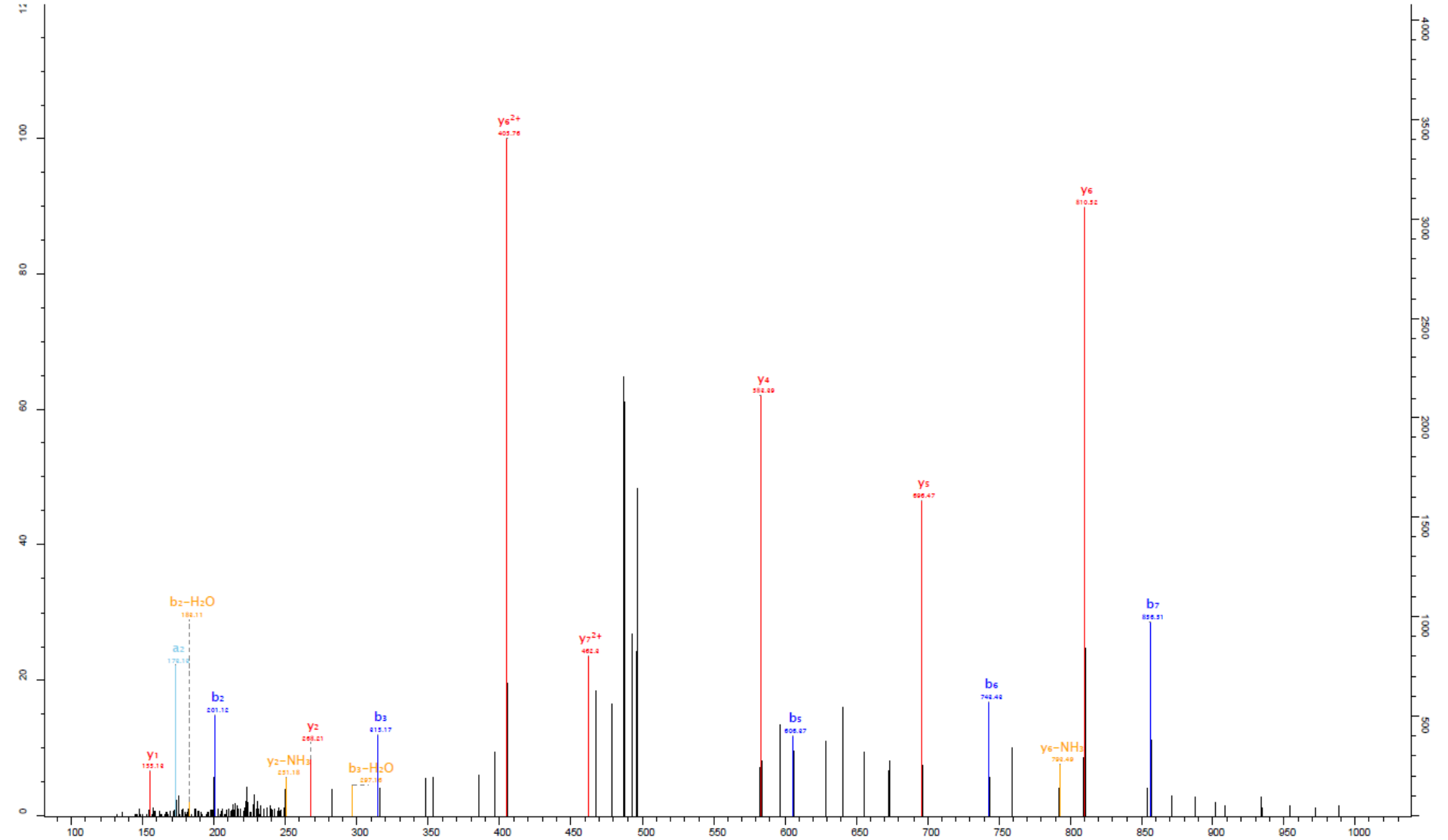
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
2196.4425	2195.1204	1098.7250	1098.0638	732.8191	732.3783

[-] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	S	20	---	---
216.0979	---	2	Q	19	2108.0883	1054.5478
353.1568	177.0820	3	H	18	1980.0297	990.5185
454.2045	227.6059	4	T	17	1842.9708	921.9891
511.2259	256.1166	5	G	16	1741.9232	871.4652
625.2689	313.1381	6	N	15	1684.9017	842.9545
696.3060	348.6566	7	A	14	1570.8588	785.9330
824.3646	412.6859	8	Q	13	1499.8217	750.4145
923.4330	462.2201	9	V	12	1371.7631	686.3852
1010.4650	505.7361	10	S	11	1272.6947	636.8510
1138.5236	569.7654	11	Q	10	1185.6626	593.3350
1239.5713	620.2893	12	T	9	1057.6041	529.3057
1409.6768	705.3420	13	K(Acetyl)	8	956.5564	478.7818
1556.7452	778.8762	14	F	7	786.4509	393.7291
1669.8293	835.4183	15	L	6	639.3824	320.1949
1766.8820	883.9446	16	P	5	526.2984	263.6528
1880.9250	940.9661	17	N	4	429.2456	215.1264
1951.9621	976.4847	18	A	3	315.2027	158.1050
2049.0148	1025.0111	19	P	2	244.1656	122.5864
---	---	20	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
050713_SCW_II_29_40_10	13282	ITMS; CID	116.05	505.82	Ddx39b

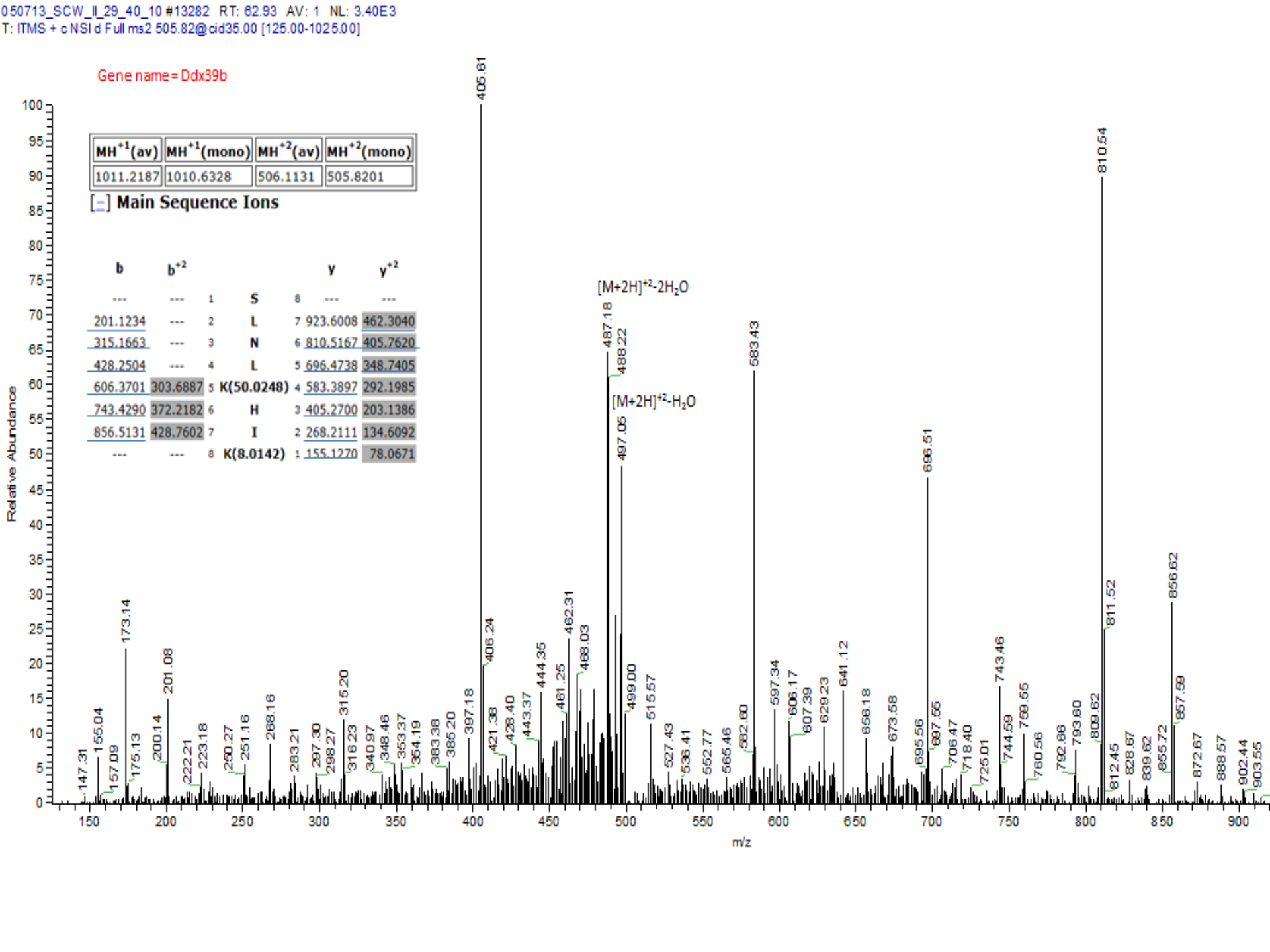


- S L N L K H I K -

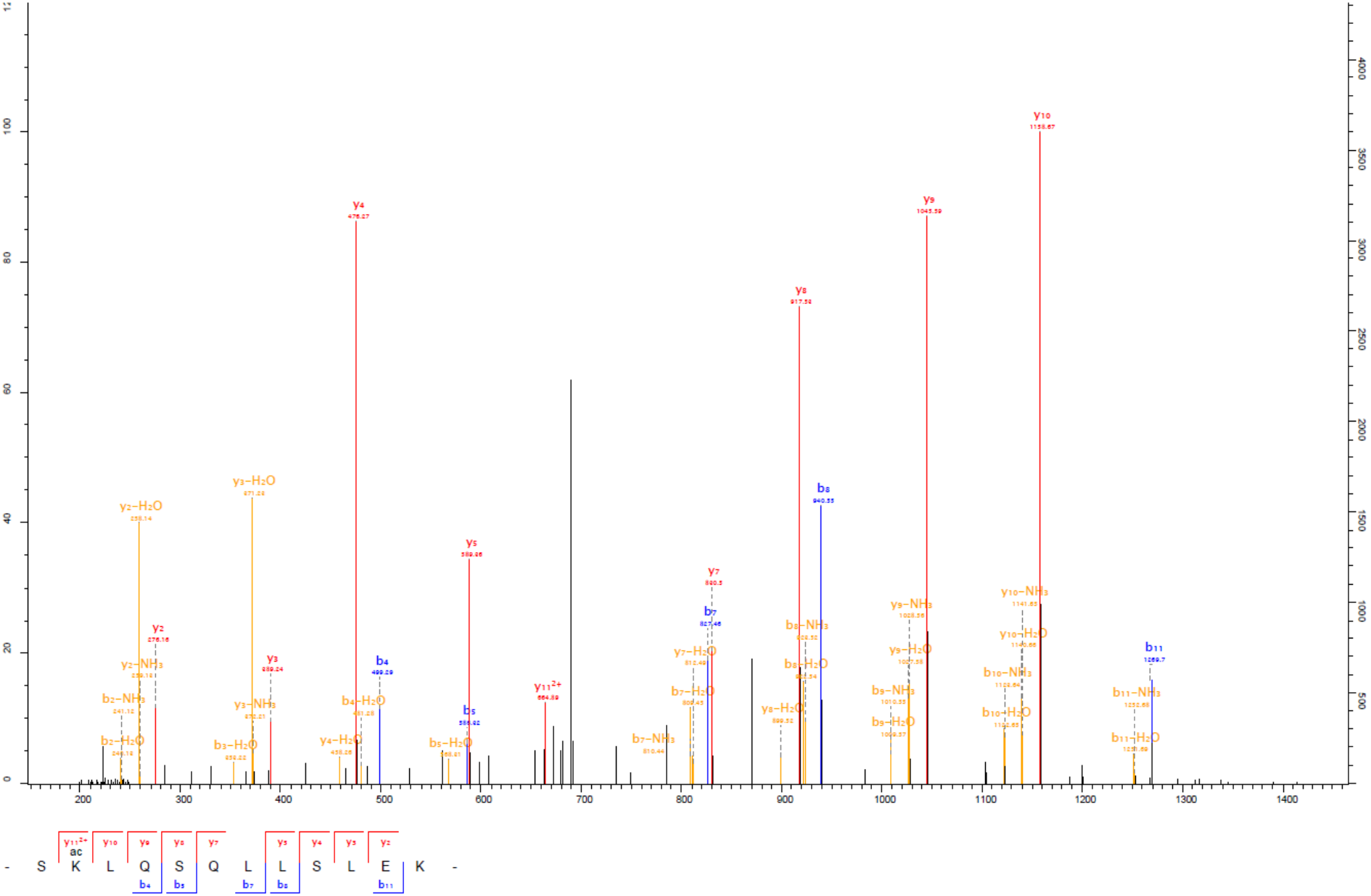
y7 2+ y6 y5 y4 ac y2 y1

b2 b3 b5 b6 b7

050713_SCW_II_29_40_10 #13282 RT: 62.93 AV: 1 NL: 3.40E3
T: ITMS + c NSI d Full ms2 505.82@cid35.00 [125.00-1025.00]



Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_4_Vargas_Enriched	20362	ITMS; CID	240.18	708.41	Dnm2



- S K L Q S Q L L S L E K -

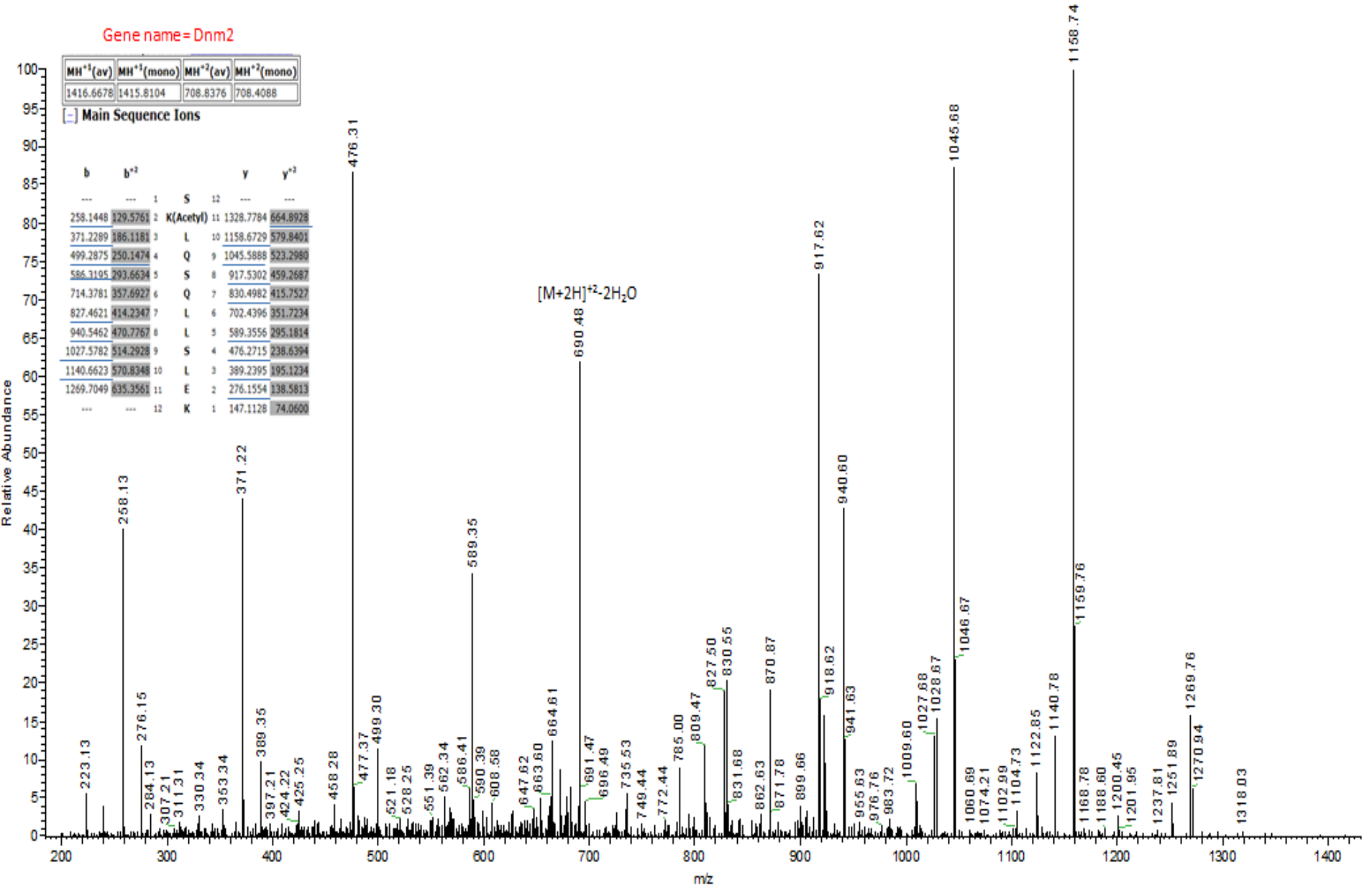
062513_SCW_II_53_4_Vargas_Enrichec #20362 RT: 89.15 AV: 1 NL: 3.60E3
T: ITMS + cNSI d Full ms2 708.41@cid35.00 [185.00-1430.00]

Gene name = Dnm2

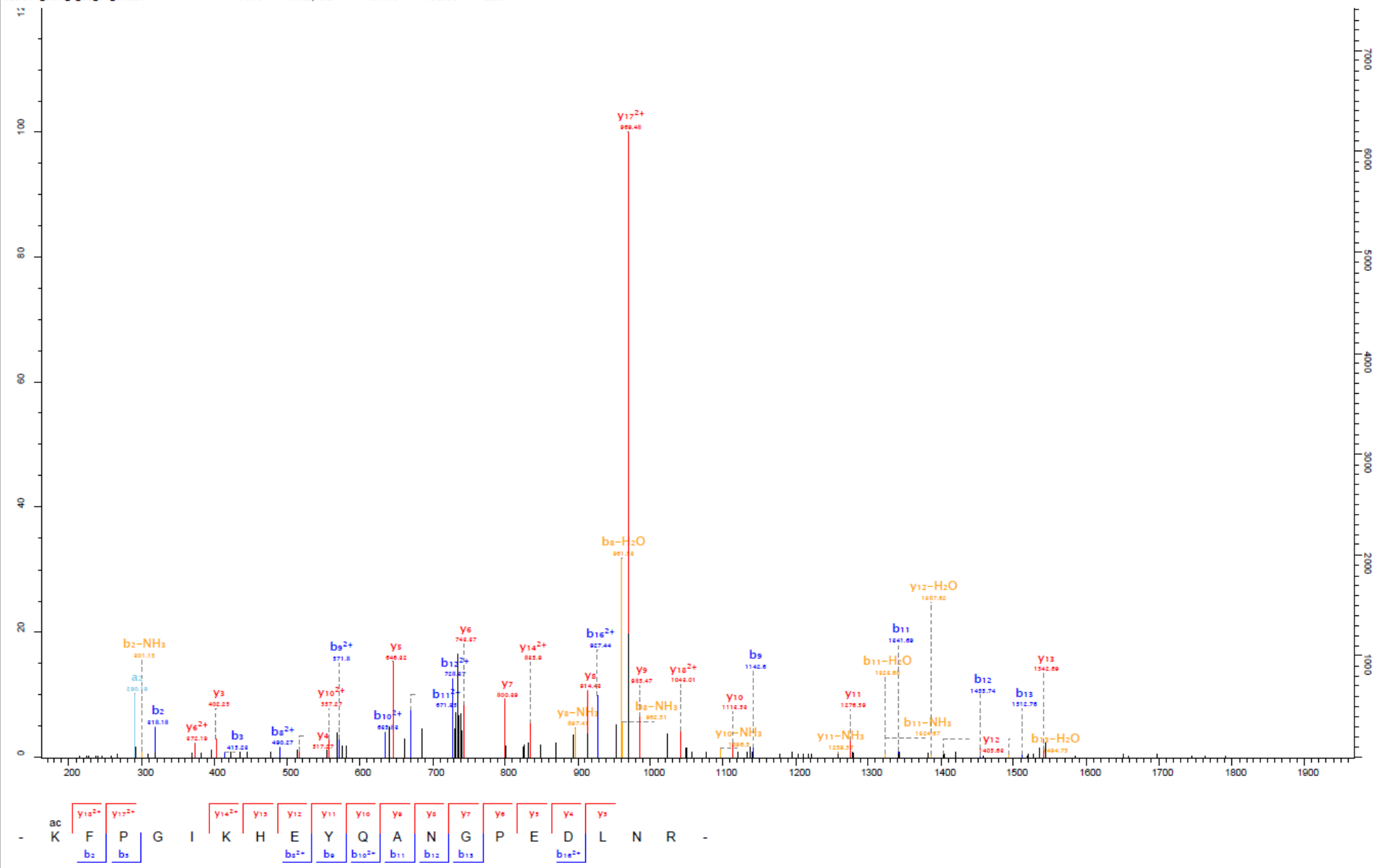
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1416.6678	1415.8104	708.8376	708.4088

[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	S	12	---	---
258.1448	129.5761	2	K(Acetyl)	11	1328.7784	664.8928
371.2289	186.1181	3	L	10	1158.6729	579.8401
499.2875	250.1474	4	Q	9	1045.5888	523.2980
586.3195	293.6634	5	S	8	917.5302	459.2687
714.3781	357.6927	6	Q	7	830.4982	415.7527
827.4621	414.2347	7	L	6	702.4396	351.7234
940.5462	470.7767	8	L	5	589.3556	295.1814
1027.5782	514.2928	9	S	4	476.2715	238.6394
1140.6623	570.8348	10	L	3	389.2395	195.1234
1269.7049	635.3561	11	E	2	276.1554	138.5813
---	---	12	K	1	147.1128	74.0600



Raw file	Scan	Method	Score	m/z	Gene names
022814_SCW_II_68_11_2ndZT	17315	ITMS; CID	161.75	752.38	Dstn



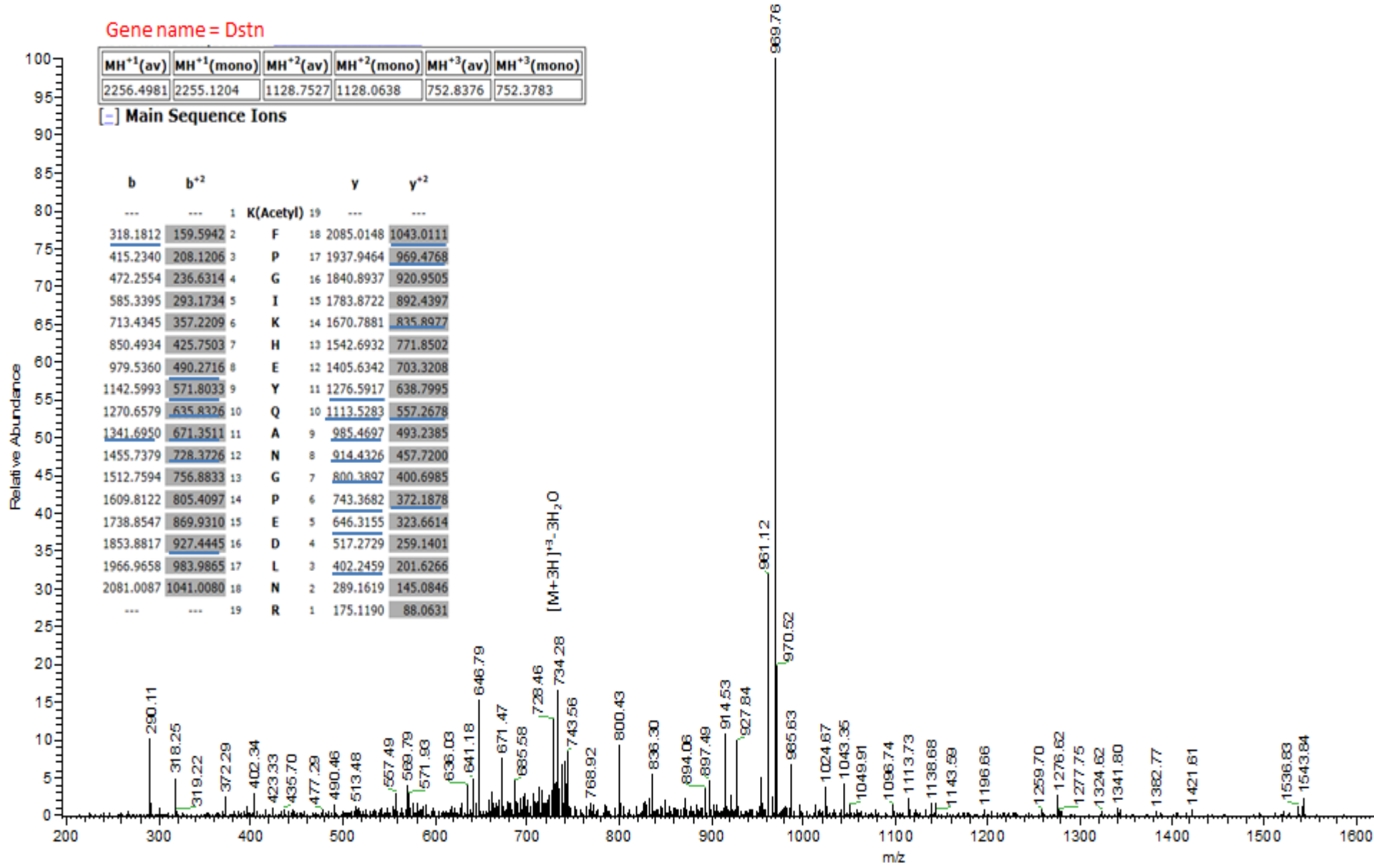
022814_SCW_II_68_11_2ndZT#17315 RT: 79.73 AV: 1 NL: 6.19E3
T: ITMS + c NSI d Full ms2 752.38@cid35.00 [195.00-2000.00]

Gene name = Dstn

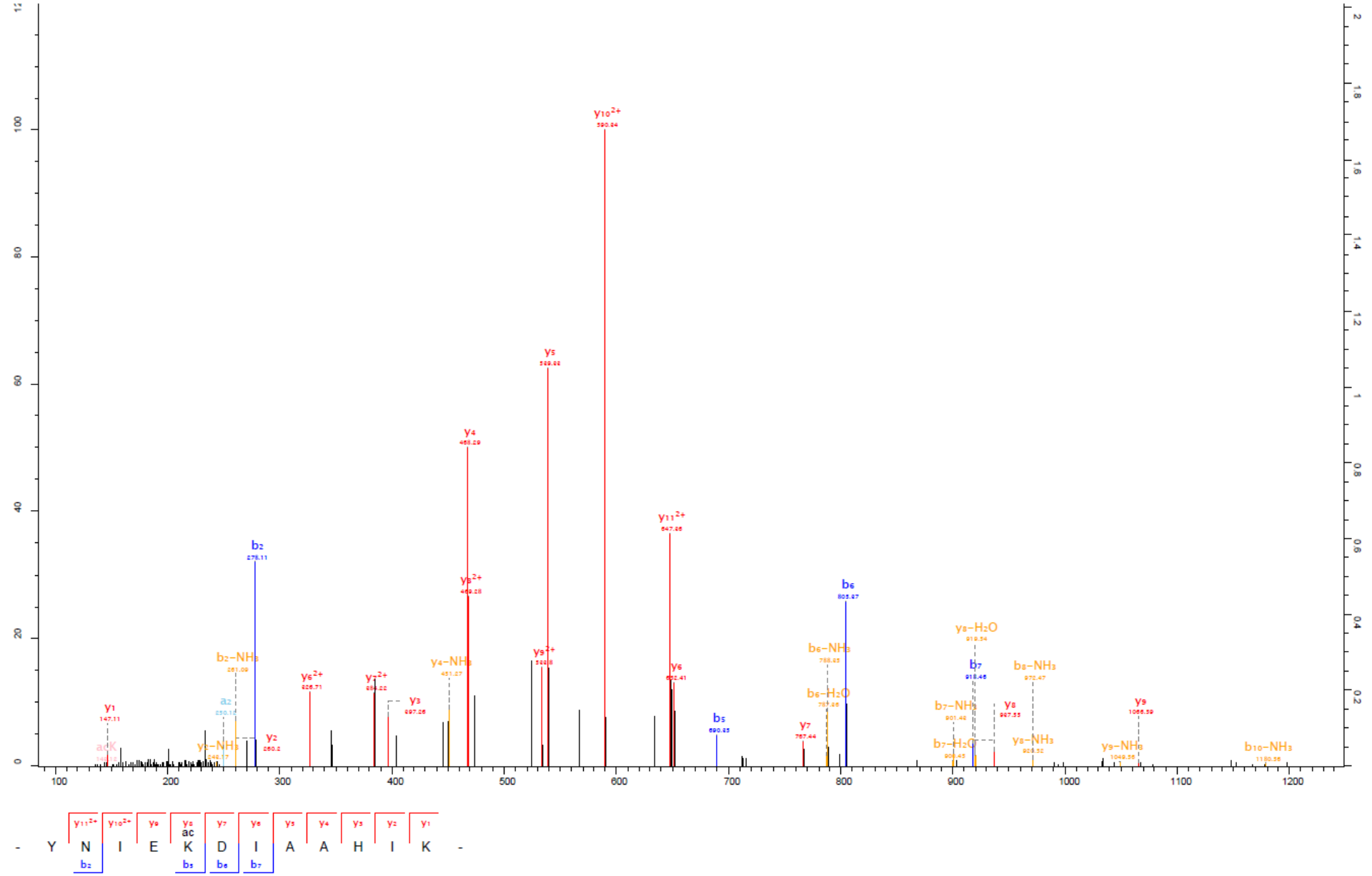
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
2256.4981	2255.1204	1128.7527	1128.0638	752.8376	752.3783

[–] Main Sequence Ions

b	b^{+2}			y	y^{+2}
---	---	1	K(Acetyl) 19	---	---
318.1812	159.5942	2	F	18 2085.0148	1043.0111
415.2340	208.1206	3	P	17 1937.9464	969.4768
472.2554	236.6314	4	G	16 1840.8937	920.9505
585.3395	293.1734	5	I	15 1783.8722	892.4397
713.4345	357.2209	6	K	14 1670.7881	835.8977
850.4934	425.7503	7	H	13 1542.6932	771.8502
979.5360	490.2716	8	E	12 1405.6342	703.3208
1142.5993	571.8033	9	Y	11 1276.5917	638.7995
1270.6579	635.8326	10	Q	10 1113.5283	557.2678
1341.6950	671.3511	11	A	9 985.4697	493.2385
1455.7379	728.3726	12	N	8 914.4326	457.7200
1512.7594	756.8833	13	G	7 800.3897	400.6985
1609.8122	805.4097	14	P	6 743.3682	372.1878
1738.8547	869.9310	15	E	5 646.3155	323.6614
1853.8817	927.4445	16	D	4 517.2729	259.1401
1966.9658	983.9865	17	L	3 402.2459	201.6266
2081.0087	1041.0080	18	N	2 289.1619	145.0846
---	---	19	R	1 175.1190	88.0631

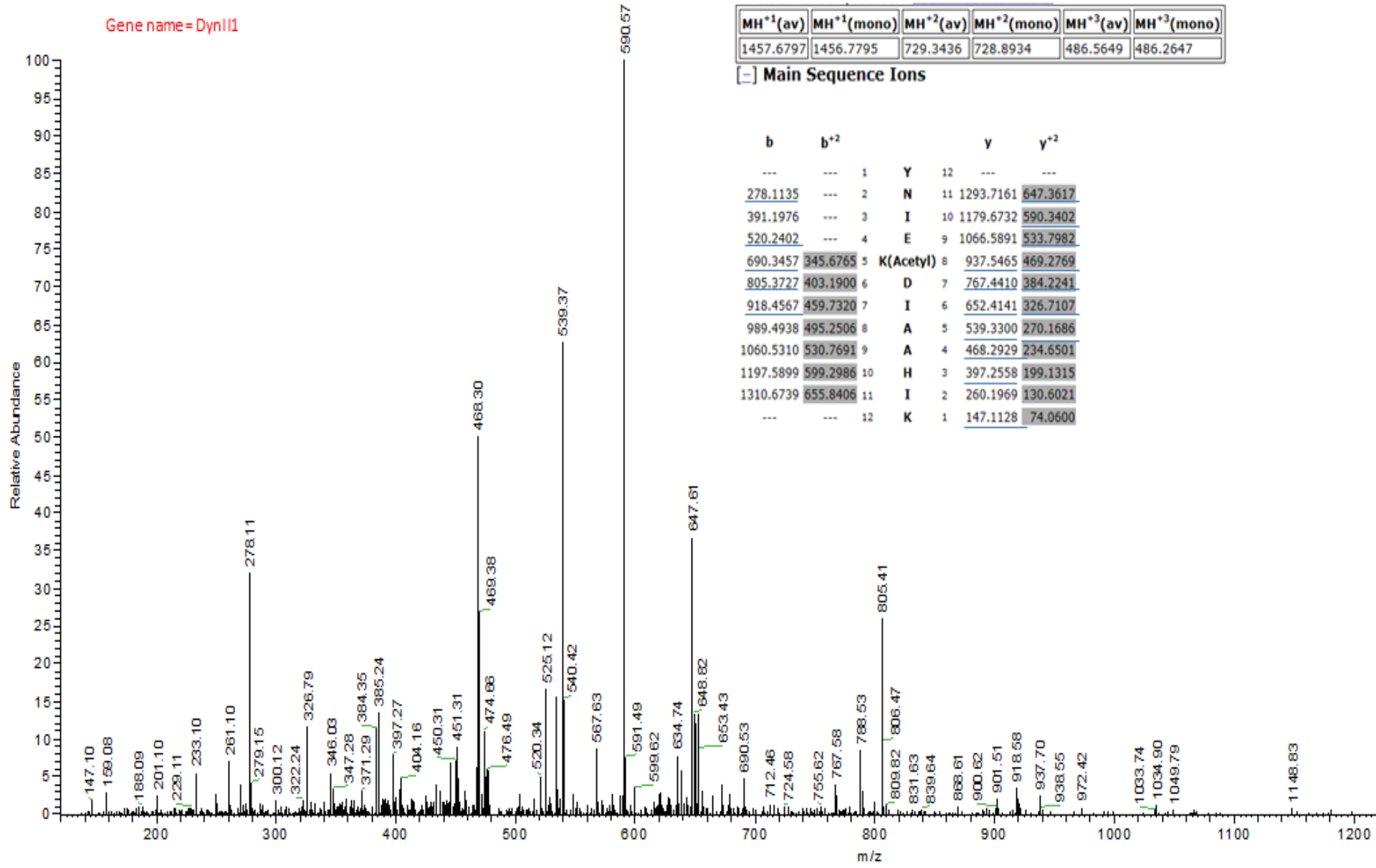


Raw file	Scan	Method	Score	m/z	Gene names
062513_SCW_II_53_9_Vargas_Enriched	19957	ITMS; CID	160.72	486.26	Dynll1



062513_SCW_II_53_9_Vargas_Enriched #19957 RT: 87.00 AV: 1 NL: 1.68E4
T: ITMS + c NSI d Full ms2 486.26@cid35.00 [120.00-1470.00]

Gene name = DynII1

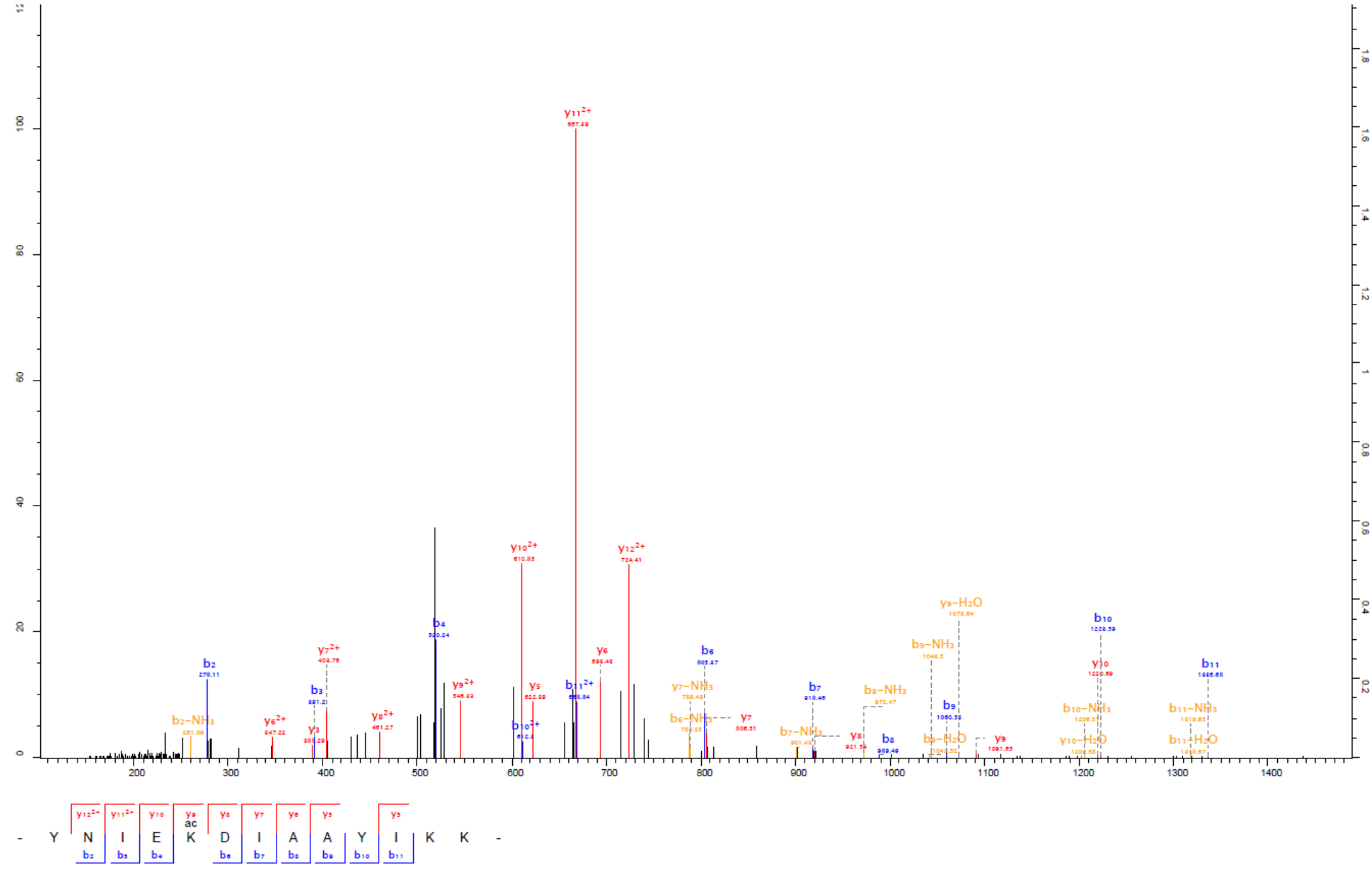


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1457.6797	1456.7795	729.3436	728.8934	486.5649	486.2647

[-] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	Y	12	---	---
278.1135	---	2	N	11	1293.7161	647.3617
391.1976	---	3	I	10	1179.6732	590.3402
520.2402	---	4	E	9	1066.5891	533.7982
690.3457	345.6765	5	K(Acetyl)	8	937.5465	469.2769
805.3727	403.1900	6	D	7	767.4410	384.2241
918.4567	459.7320	7	I	6	652.4141	326.7107
989.4938	495.2506	8	A	5	539.3300	270.1686
1060.5310	530.7691	9	A	4	468.2929	234.6501
1197.5899	599.2986	10	H	3	397.2558	199.1315
1310.6739	655.8406	11	I	2	260.1969	130.6021
---	---	12	K	1	147.1128	74.0600

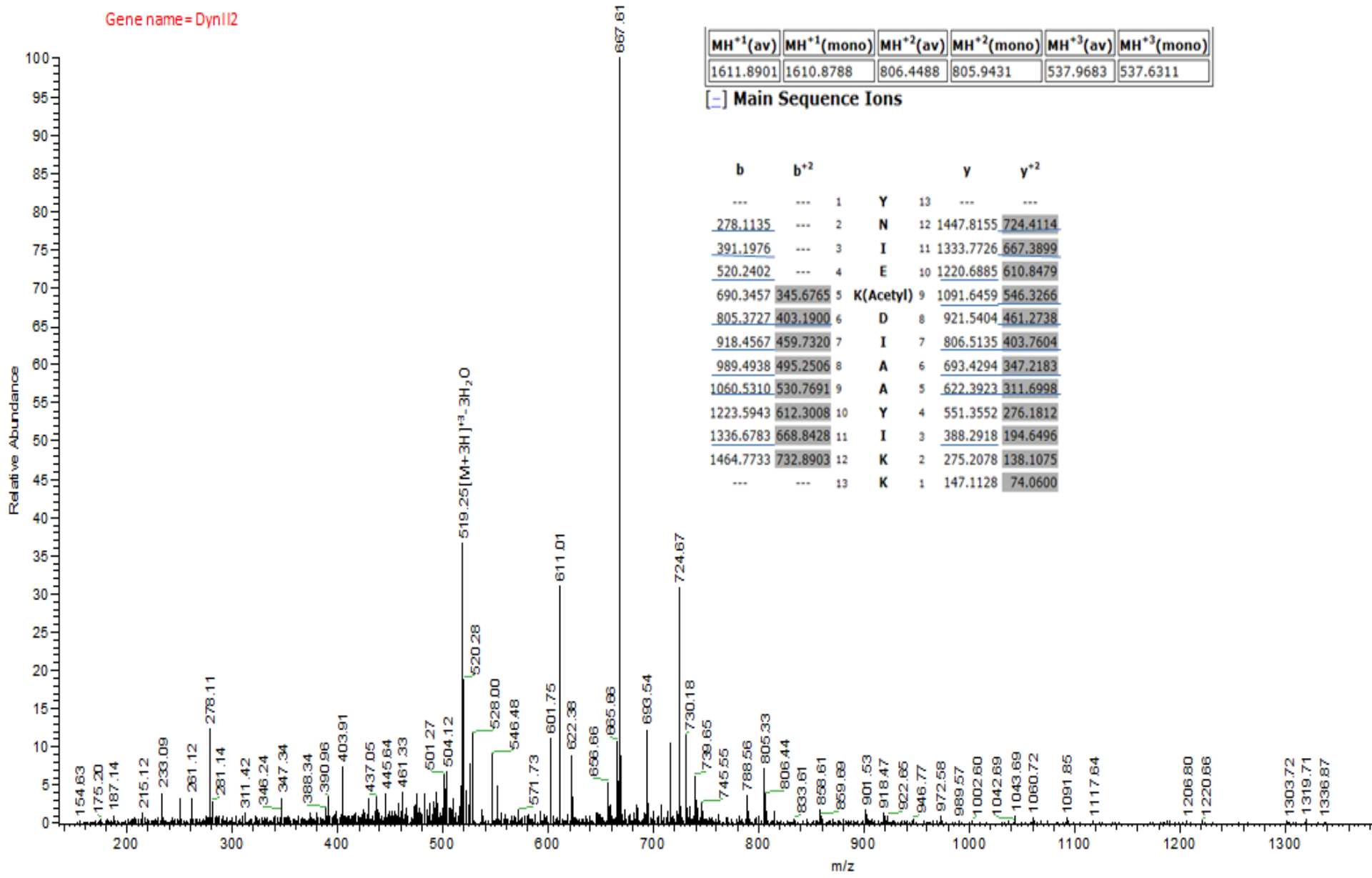
Raw file	Scan	Method	Score	m/z	Gene names
050713_SCW_II_29_31_8	20661	ITMS; CID	223.22	537.63	Dynll2



- Y N I E K D I A A Y I K K -

050713_SCW_II_29_31_8 #20661 RT: 89.37 AV: 1 NL: 1.59E4
T: ITMS + cNSI d Full ms2 537.63@cid35.00 [135.00-1625.00]

Gene name = DynII2

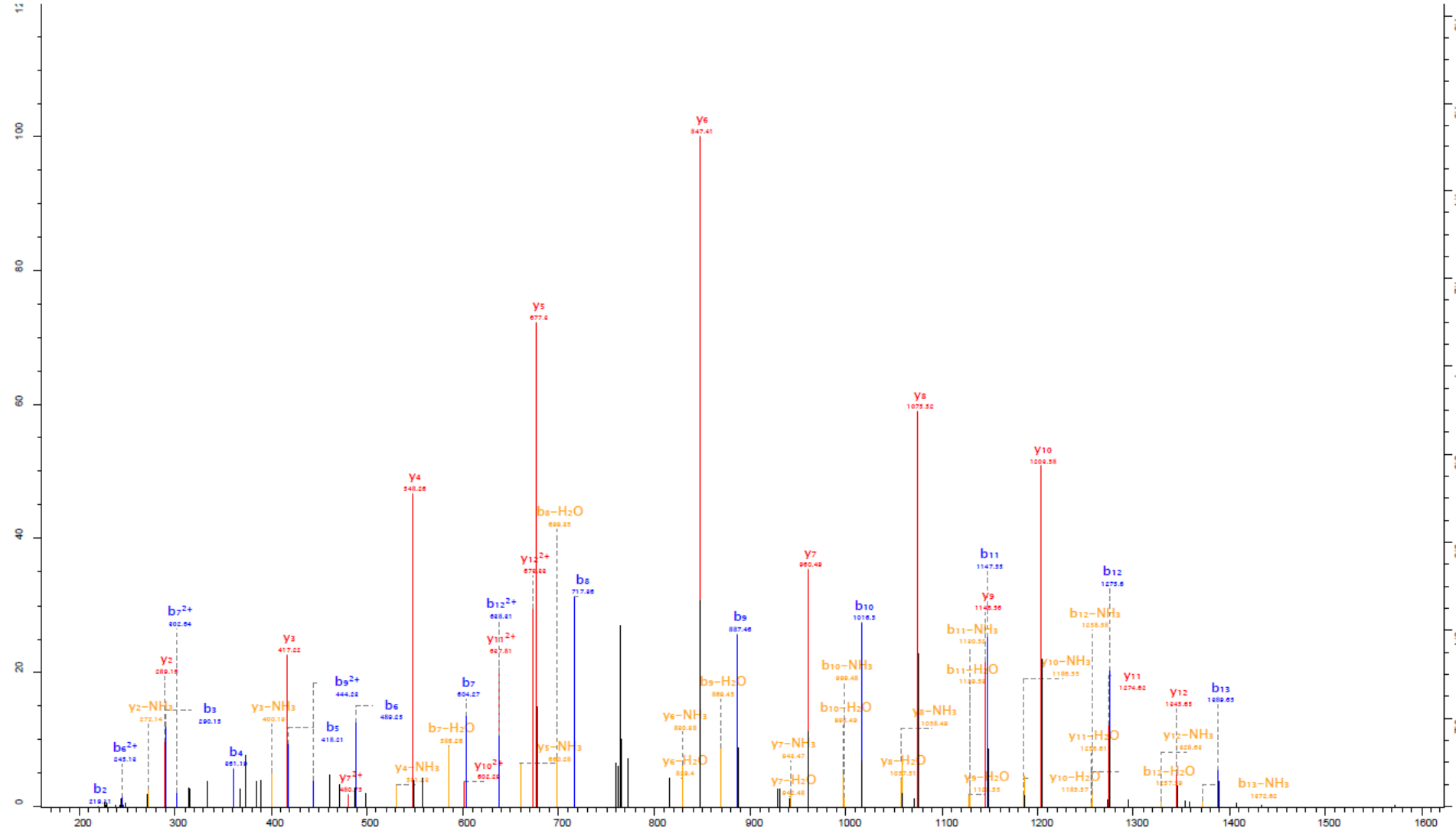


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)	MH^{+3}(av)	MH^{+3}(mono)
1611.8901	1610.8788	806.4488	805.9431	537.9683	537.6311

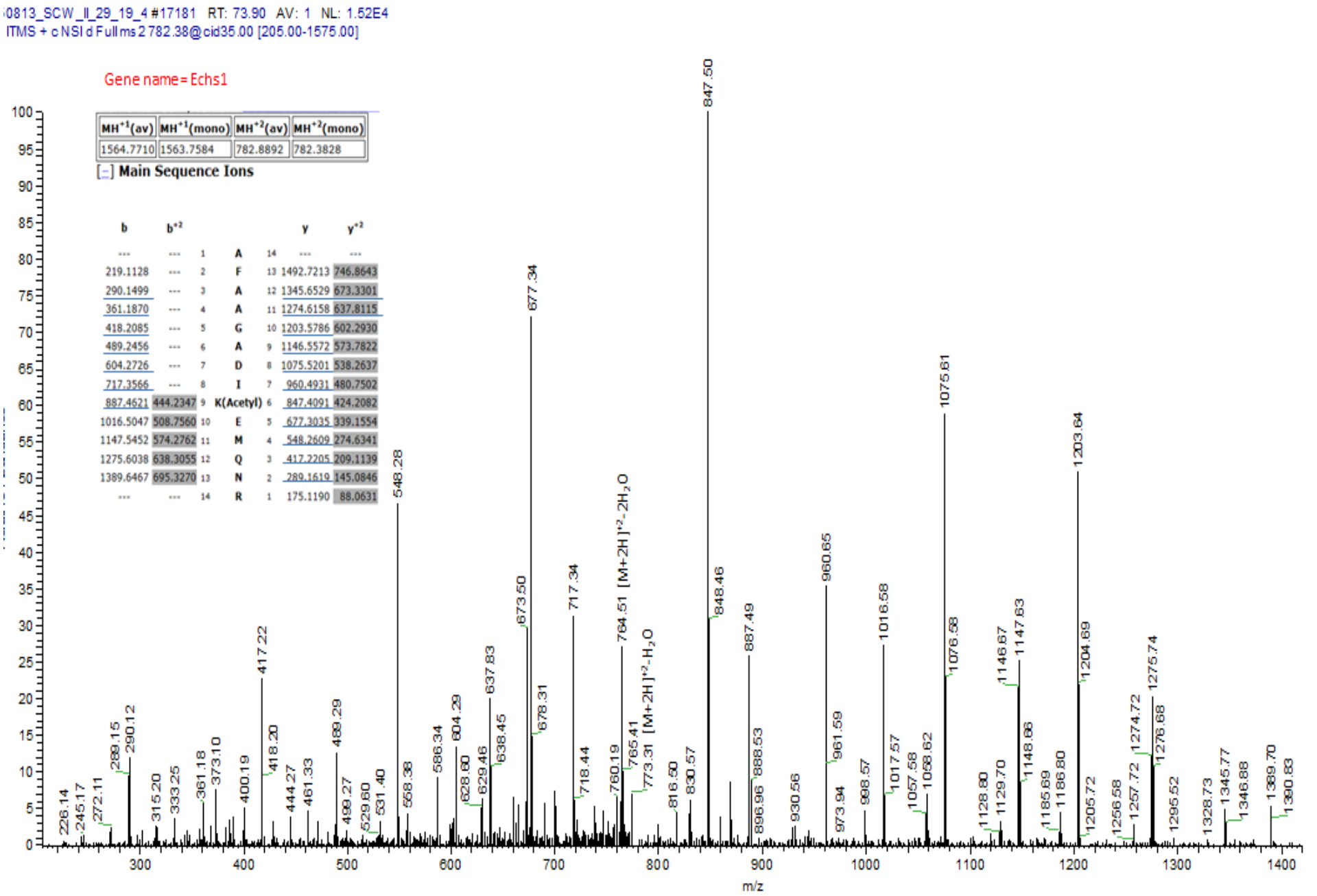
[-] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	Y	13	---	---
278.1135	---	2	N	12	1447.8155	724.4114
391.1976	---	3	I	11	1333.7726	667.3899
520.2402	---	4	E	10	1220.6885	610.8479
690.3457	345.6765	5	K(Acetyl)	9	1091.6459	546.3266
805.3727	403.1900	6	D	8	921.5404	461.2738
918.4567	459.7320	7	I	7	806.5135	403.7604
989.4938	495.2506	8	A	6	693.4294	347.2183
1060.5310	530.7691	9	A	5	622.3923	311.6998
1223.5943	612.3008	10	Y	4	551.3552	276.1812
1336.6783	668.8428	11	I	3	388.2918	194.6496
1464.7733	732.8903	12	K	2	275.2078	138.1075
---	---	13	K	1	147.1128	74.0600

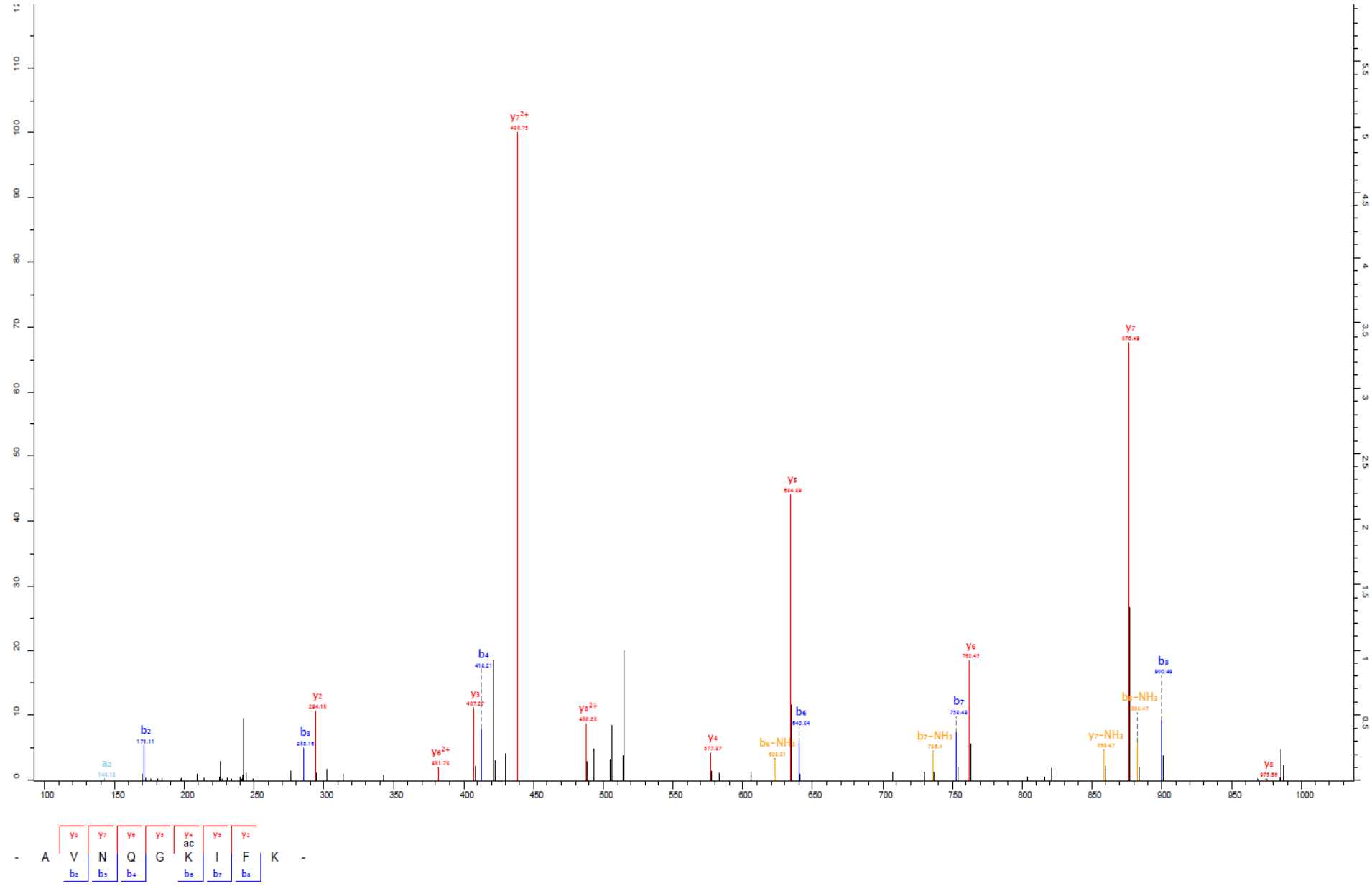
Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	17181	ITMS; CID	346.65	782.38	Echs1



		y12	y11	y10	y9	y8	y7	y6	y5	y4	y3	y2	
-	A	F	A	A	G	A	D	I	K (ac)	E	M	Q	N	R	-
		b2	b3	b4	b5	b6	b7	b8	b9	b10	b11	b12	b13		


0813_SCW_II_29_19_4 #17181 RT: 73.90 AV: 1 NL: 1.52E4
ITMS + c NSI d Full ms 2 782.38@cid35.00 [205.00-1575.00]
Gene name = Echs1
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1564.7710 1563.7584 782.8892 782.3828
[–] Main Sequence Ions
b b+2 y y+2
--- --- 1 A 14 --- ---
219.1128 --- 2 F 13 1492.7213 746.8643
290.1499 --- 3 A 12 1345.6529 673.3301
361.1870 --- 4 A 11 1274.6158 637.8115
418.2085 --- 5 G 10 1203.5786 602.2930
489.2456 --- 6 A 9 1146.5572 573.7822
604.2726 --- 7 D 8 1075.5201 538.2637
717.3566 --- 8 I 7 960.4931 480.7502
887.4621 444.2347 9 K(Acetyl) 6 847.4091 424.2082
1016.5047 508.7560 10 E 5 677.3035 339.1554
1147.5452 574.2762 11 M 4 548.2609 274.6341
1275.6038 638.3055 12 Q 3 417.2205 209.1139
1389.6467 695.3270 13 N 2 289.1619 145.0846
--- --- 14 R 1 175.1190 88.0631
m/z
[M+2H]+2-2H2O
[M+2H]+2-H2O

Raw file	Scan	Method	Score	m/z	Gene names
022814_SCW_II_68_5_2ndZT	15143	ITMS; CID	169.12	523.8	Eef1g

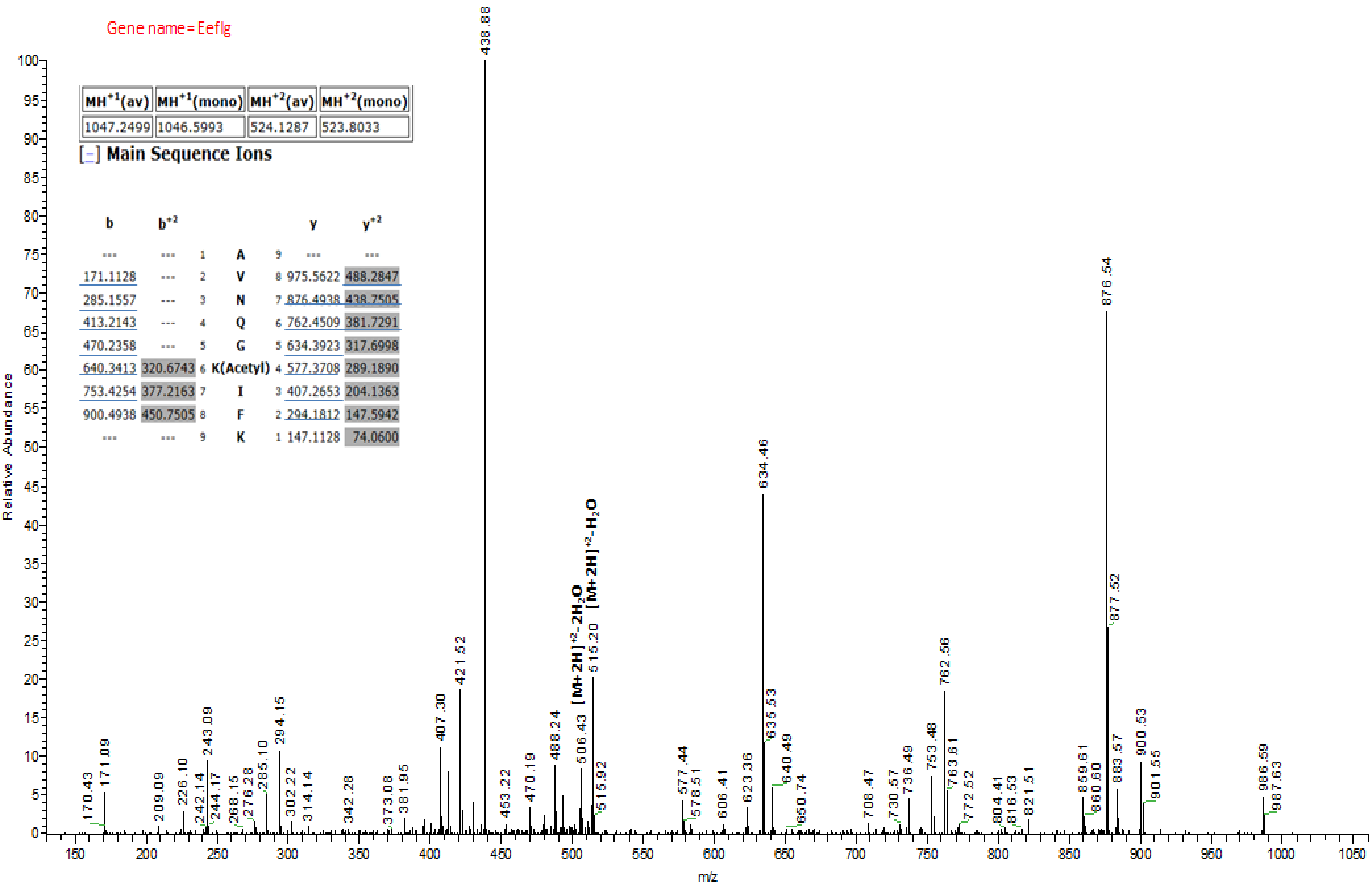


- A V N Q G K ac I F K -

y8 y7 y6 y5 y4 y3 y2
b2 b5 b4 b6 b7 b8

022814_SCW_I_68_5_2ndZI #15143 RT: 72.22 AV: 1 NL: 4.98E4
T: ITMS + c NSI d Full ms2 523.80@cid35.00 [130.00-1060.00]

Gene name= Eeflg

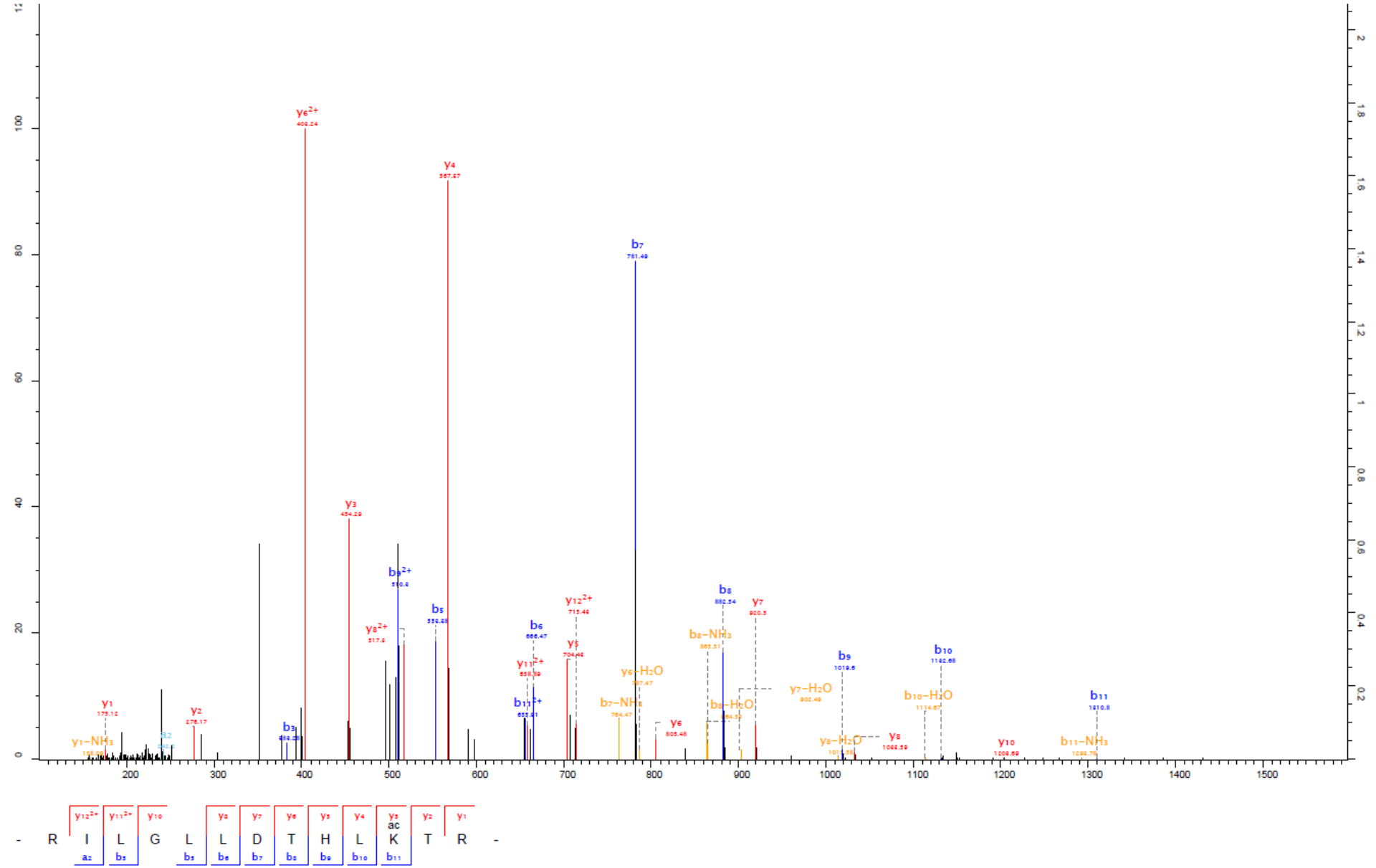


MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1047.2499	1046.5993	524.1287	523.8033

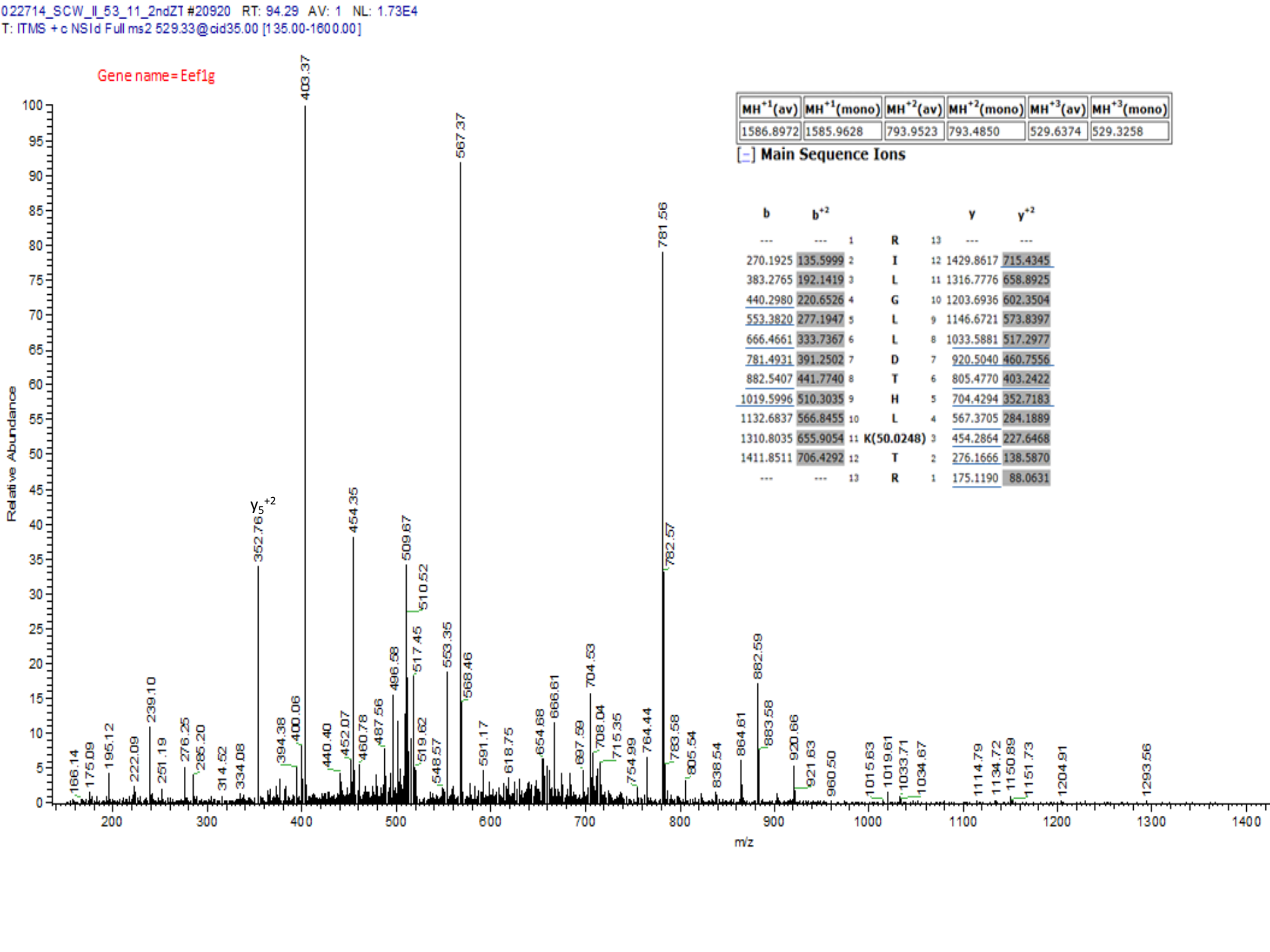
[-] **Main Sequence Ions**

b	b^{+2}				y	y^{+2}
---	---	1	A	9	---	---
171.1128	---	2	V	8	975.5622	488.2847
285.1557	---	3	N	7	876.4938	438.7505
413.2143	---	4	Q	6	762.4509	381.7291
470.2358	---	5	G	5	634.3923	317.6998
640.3413	320.6743	6	K(Acetyl)	4	577.3708	289.1890
753.4254	377.2163	7	I	3	407.2653	204.1363
900.4938	450.7505	8	F	2	294.1812	147.5942
---	---	9	K	1	147.1128	74.0600

Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_11_2ndZT	20920	ITMS; CID	151.3	529.33	Eef1g



- R I L G L L D T H L K(ac) T R -

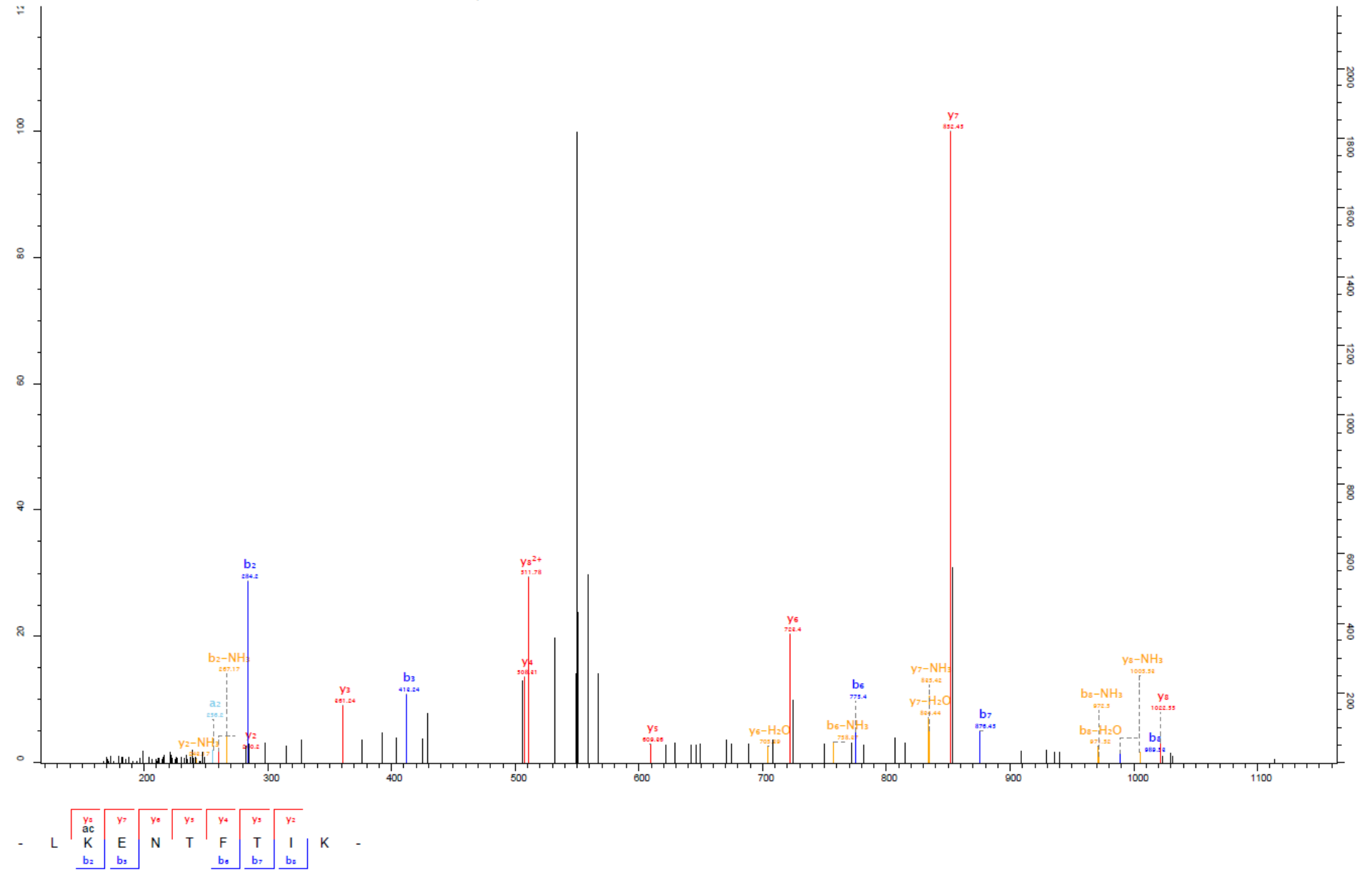


MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
1586.8972	1585.9628	793.9523	793.4850	529.6374	529.3258

[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	R	13	---	---
270.1925	135.5999	2	I	12	1429.8617	715.4345
383.2765	192.1419	3	L	11	1316.7776	658.8925
440.2980	220.6526	4	G	10	1203.6936	602.3504
553.3820	277.1947	5	L	9	1146.6721	573.8397
666.4661	333.7367	6	L	8	1033.5881	517.2977
781.4931	391.2502	7	D	7	920.5040	460.7556
882.5407	441.7740	8	T	6	805.4770	403.2422
1019.5996	510.3035	9	H	5	704.4294	352.7183
1132.6837	566.8455	10	L	4	567.3705	284.1889
1310.8035	655.9054	11	K(50.0248)	3	454.2864	227.6468
1411.8511	706.4292	12	T	2	276.1666	138.5870
---	---	13	R	1	175.1190	88.0631

Raw file	Scan	Method	Score	m/z	Gene names
022714_SCW_II_53_4_2ndZT	17926	ITMS; CID	115.57	568.32	Elp2



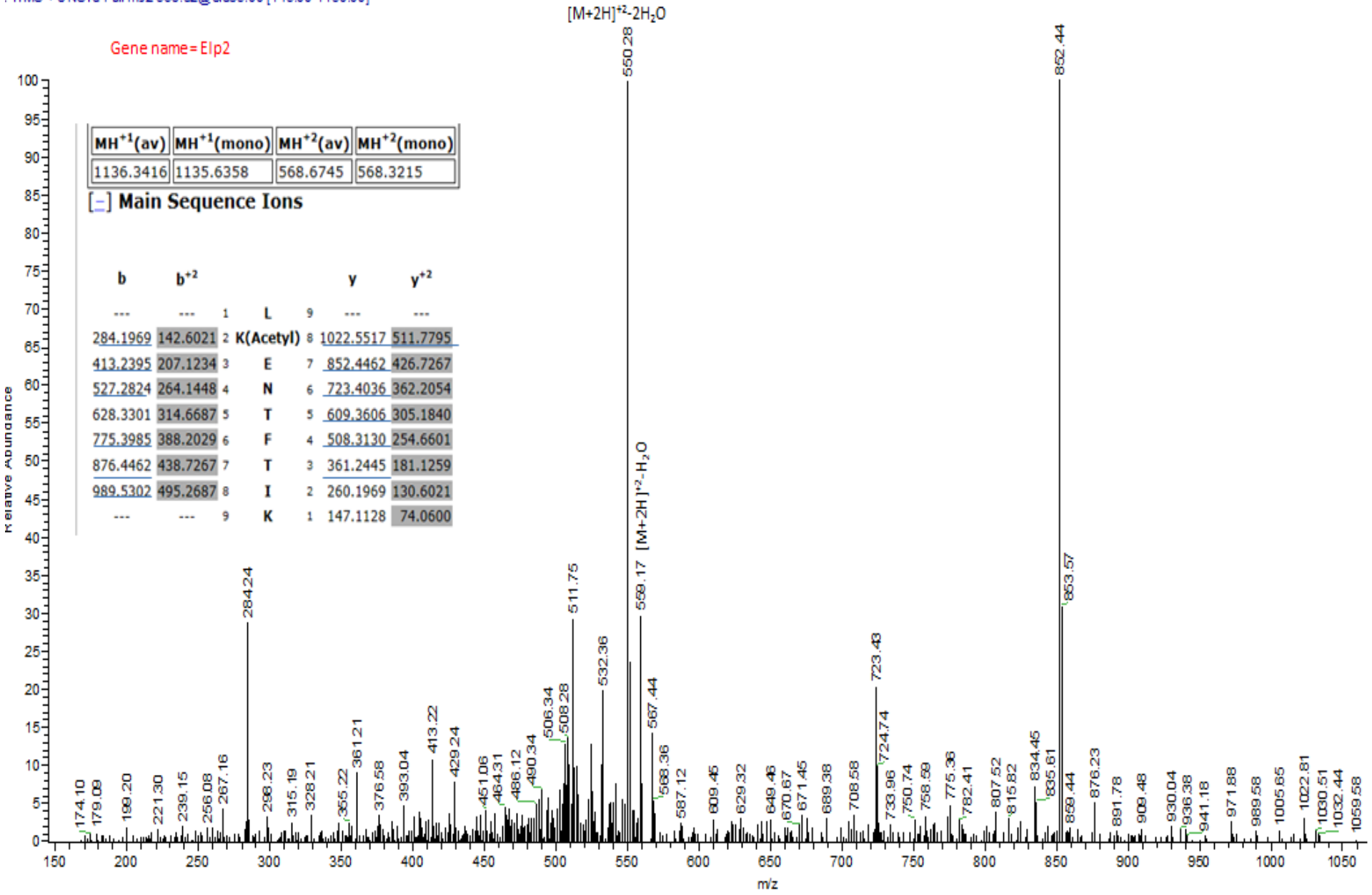
22714_SCW_II_53_4_2ndZT #17926 RT: 83.16 AV: 1 NL: 1.82E3
: ITMS + c NSI d Full ms2 568.32@cid35.00 [145.00-1150.00]

Gene name=Elp2

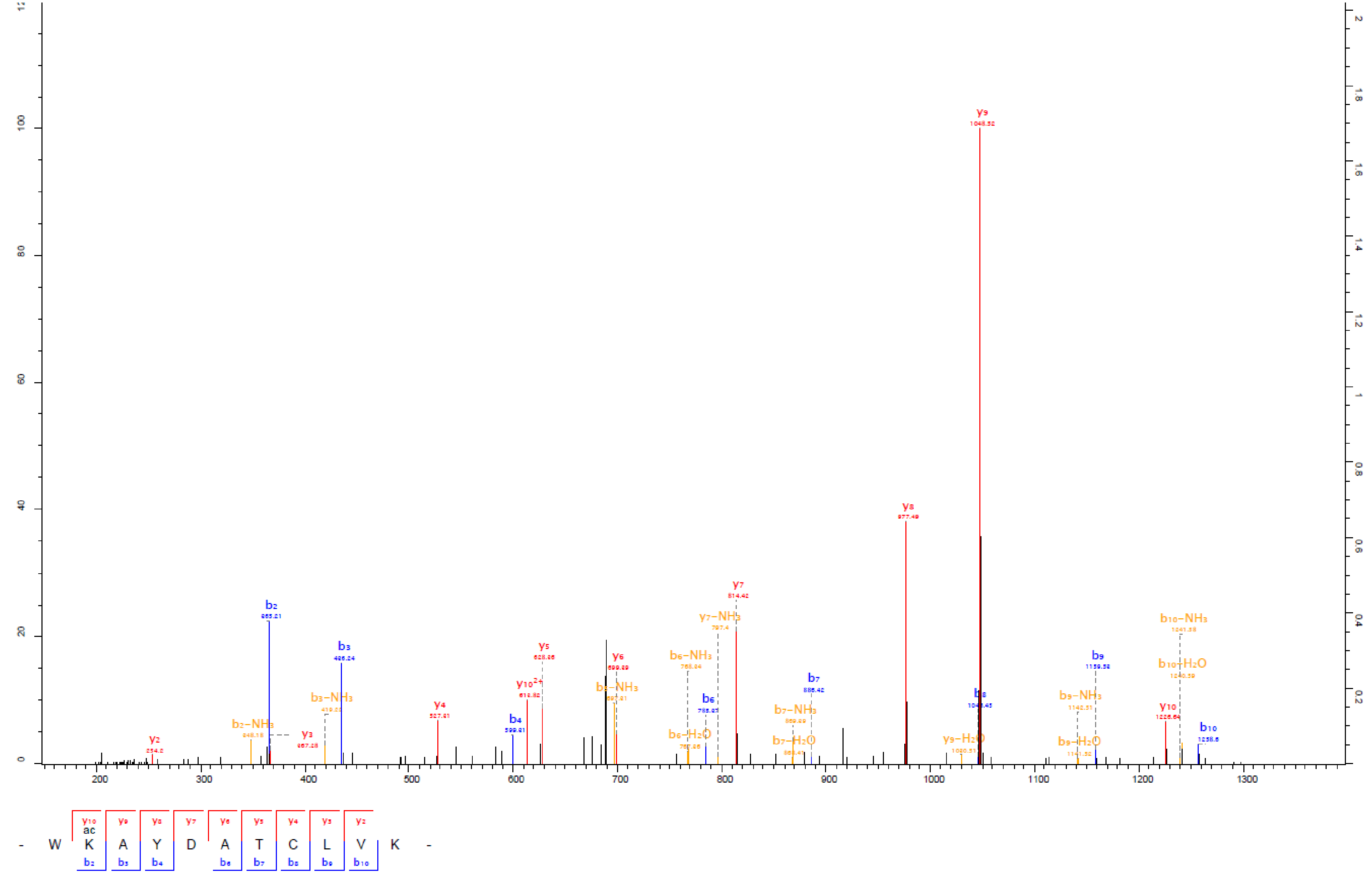
MH^{+1}(av)	MH^{+1}(mono)	MH^{+2}(av)	MH^{+2}(mono)
1136.3416	1135.6358	568.6745	568.3215

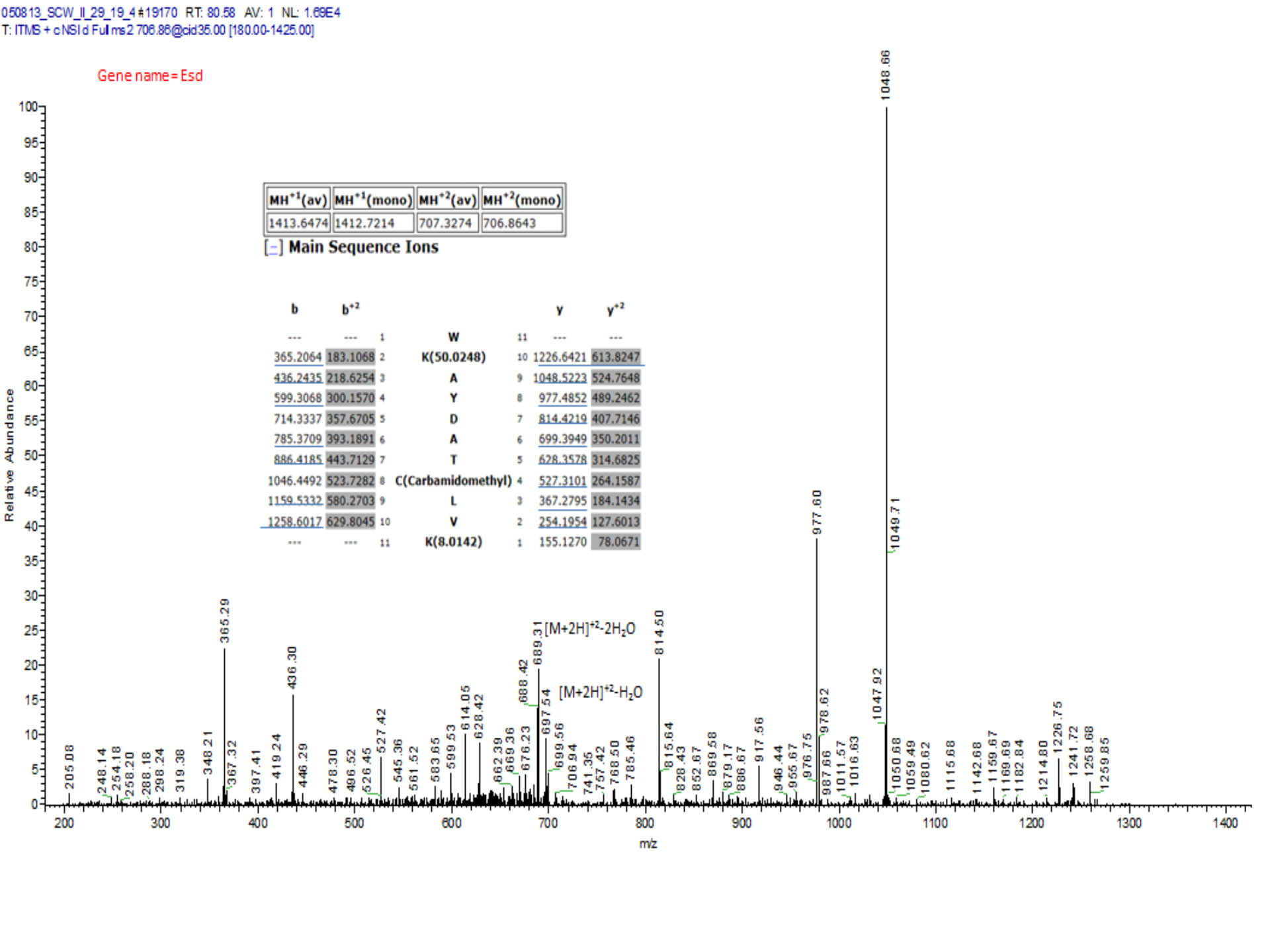
[–] Main Sequence Ions

b	b^{+2}				y	y^{+2}
---	---	1	L	9	---	---
284.1969	142.6021	2	K(Acetyl)	8	1022.5517	511.7795
413.2395	207.1234	3	E	7	852.4462	426.7267
527.2824	264.1448	4	N	6	723.4036	362.2054
628.3301	314.6687	5	T	5	609.3606	305.1840
775.3985	388.2029	6	F	4	508.3130	254.6601
876.4462	438.7267	7	T	3	361.2445	181.1259
989.5302	495.2687	8	I	2	260.1969	130.6021
---	---	9	K	1	147.1128	74.0600

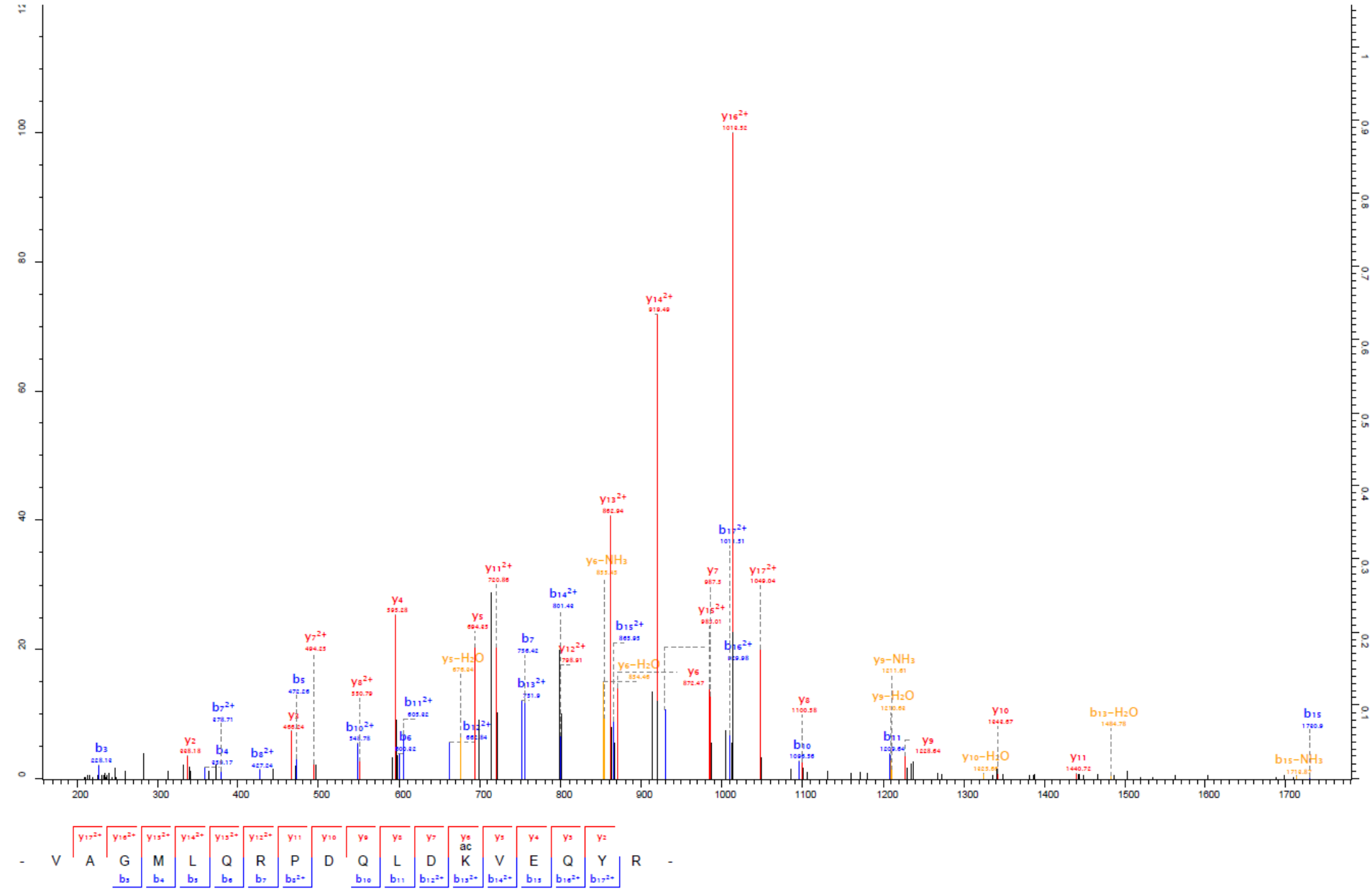


Raw file	Scan	Method	Score	m/z	Gene names
050813_SCW_II_29_19_4	19170	ITMS; CID	148.13	706.86	Esd




050813_SCW_II_29_19_4 #19170 RT: 80.58 AV: 1 NL: 1.69E4
T: ITMS + c NSI d Full ms2 706.86@cid35.00 [180.00-1425.00]
Gene name = Esd
MH+1(av) MH+1(mono) MH+2(av) MH+2(mono)
1413.6474 1412.7214 707.3274 706.8643
[-] Main Sequence Ions
b b+2 y y+2
--- --- 1 W 11 --- ---
365.2064 183.1068 2 K(50.0248) 10 1226.6421 613.8247
436.2435 218.6254 3 A 9 1048.5223 524.7648
599.3068 300.1570 4 Y 8 977.4852 489.2462
714.3337 357.6705 5 D 7 814.4219 407.7146
785.3709 393.1891 6 A 6 699.3949 350.2011
886.4185 443.7129 7 T 5 628.3578 314.6825
1046.4492 523.7282 8 C(Carbamidomethyl) 4 527.3101 264.1587
1159.5332 580.2703 9 L 3 367.2795 184.1434
1258.6017 629.8045 10 V 2 254.1954 127.6013
--- --- 11 K(8.0142) 1 155.1270 78.0671
[M+2H]+2-2H2O
[M+2H]+2-H2O
Relative Abundance
m/z

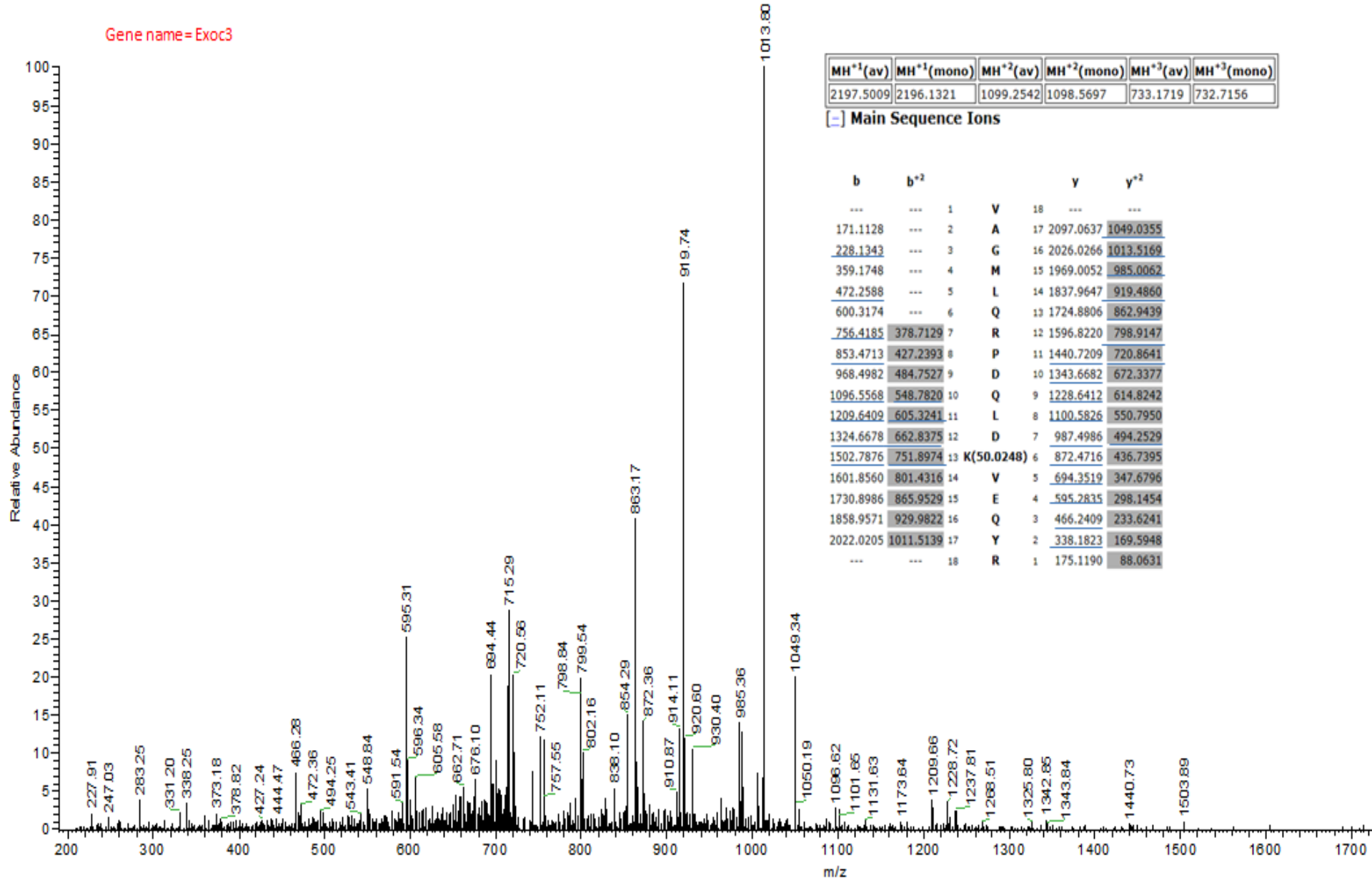
Raw file	Scan	Method	Score	m/z	Gene names
050713_SCW_II_29_28_7	17359	ITMS; CID	217.79	733.05	Exoc3



- V A G M L Q R P D Q L D K(ac) V E Q Y R -

050713_SCW_II_29_28_7 #17359 RT: 78.13 AV: 1 NL: 8.82E3
T: ITMS + c NSI d Full ms2 733.05@cid35.00 [190.00-2000.00]

Gene name = Exoc3



MH+1(av)	MH+1(mono)	MH+2(av)	MH+2(mono)	MH+3(av)	MH+3(mono)
2197.5009	2196.1321	1099.2542	1098.5697	733.1719	732.7156

[-] Main Sequence Ions

b	b+2				y	y+2
---	---	1	V	18	---	---
171.1128	---	2	A	17	2097.0637	1049.0355
228.1343	---	3	G	16	2026.0266	1013.5169
359.1748	---	4	M	15	1969.0052	985.0062
472.2588	---	5	L	14	1837.9647	919.4860
600.3174	---	6	Q	13	1724.8806	862.9439
756.4185	378.7129	7	R	12	1596.8220	798.9147
853.4713	427.2393	8	P	11	1440.7209	720.8641
968.4982	484.7527	9	D	10	1343.6682	672.3377
1096.5568	548.7820	10	Q	9	1228.6412	614.8242
1209.6409	605.3241	11	L	8	1100.5826	550.7950
1324.6678	662.8375	12	D	7	987.4986	494.2529
1502.7876	751.8974	13	K(50.0248)	6	872.4716	436.7395
1601.8560	801.4316	14	V	5	694.3519	347.6796
1730.8986	865.9529	15	E	4	595.2835	298.1454
1858.9571	929.9822	16	Q	3	466.2409	233.6241
2022.0205	1011.5139	17	Y	2	338.1823	169.5948
---	---	18	R	1	175.1190	88.0631