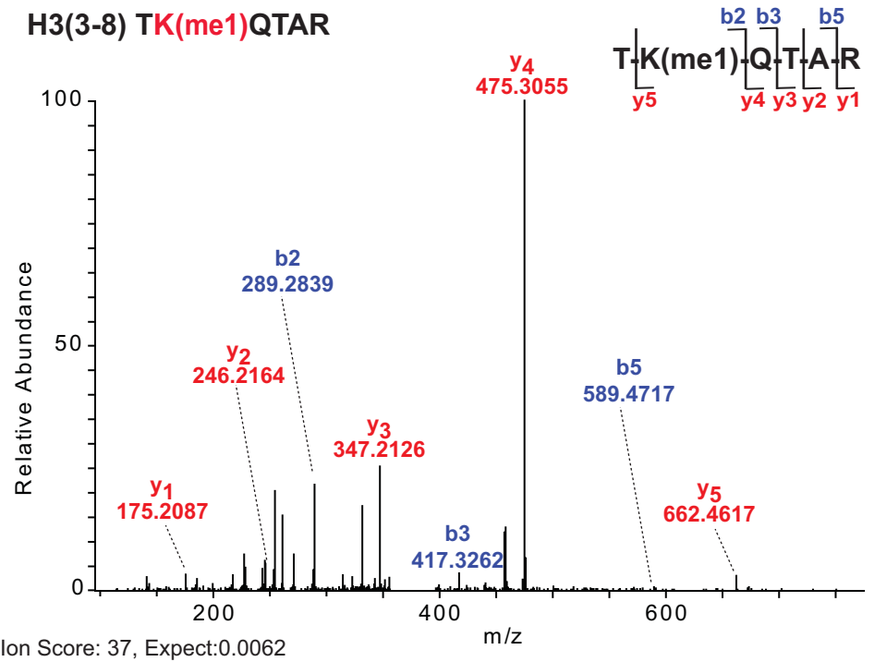
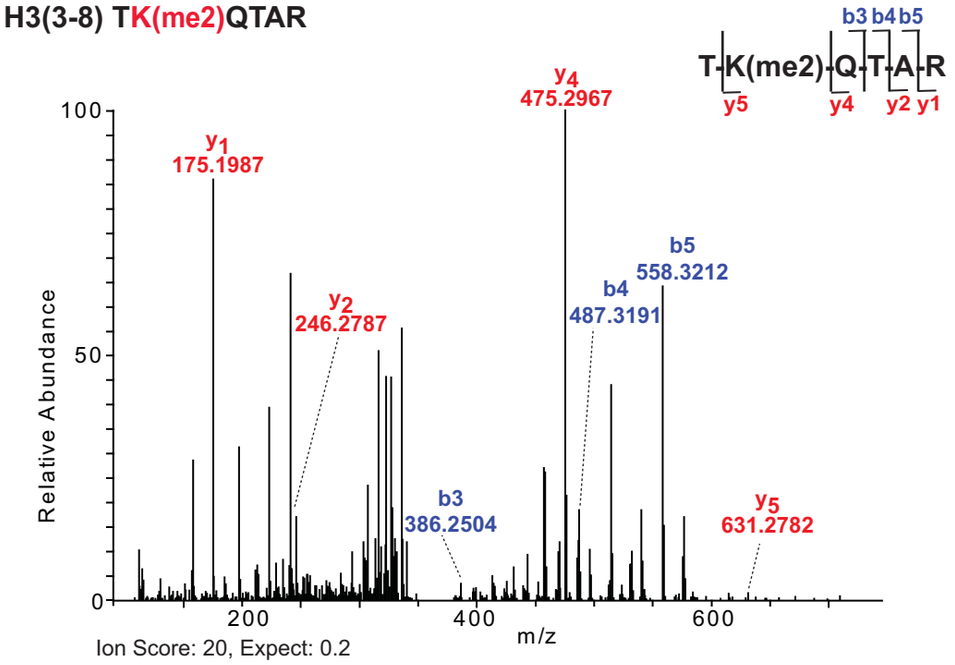
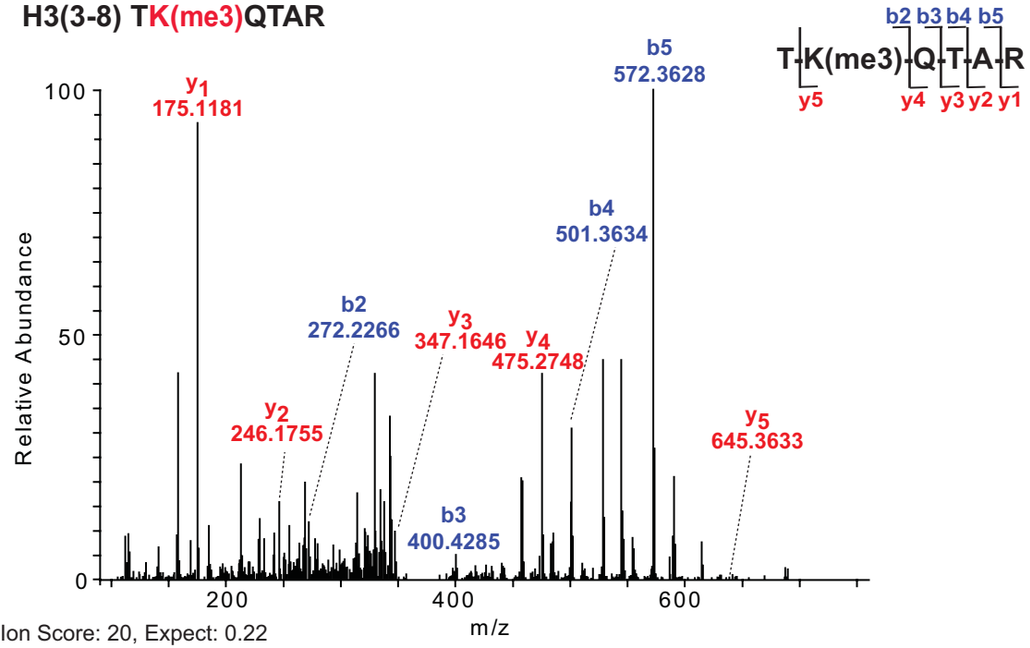
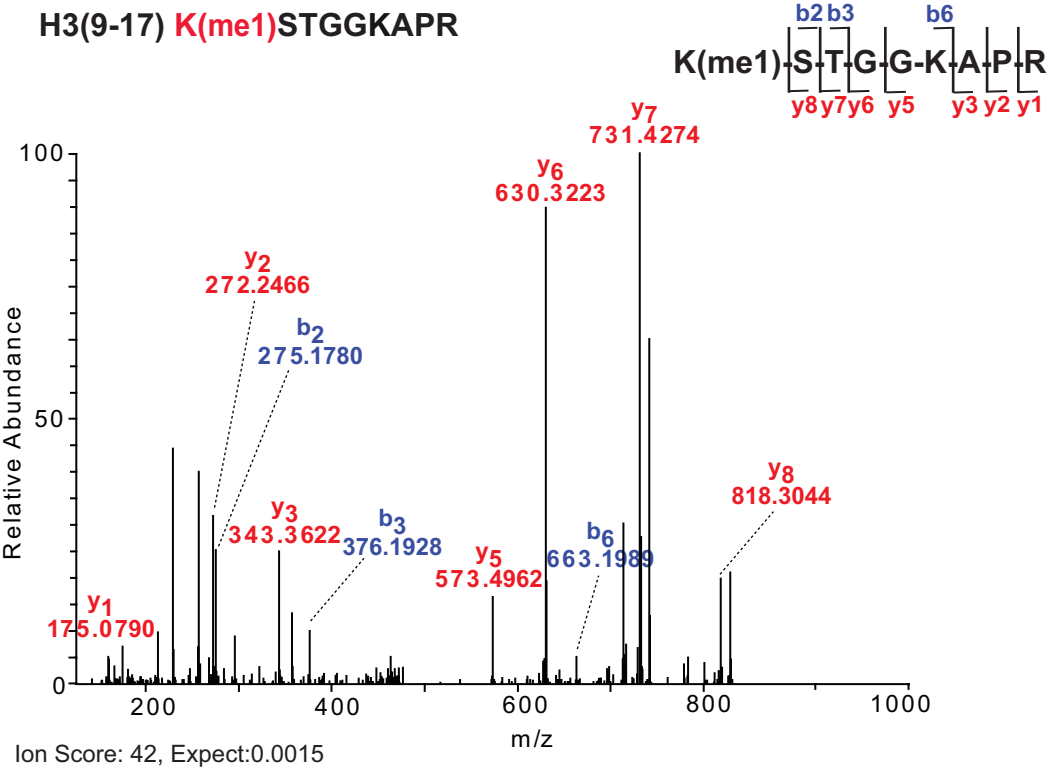
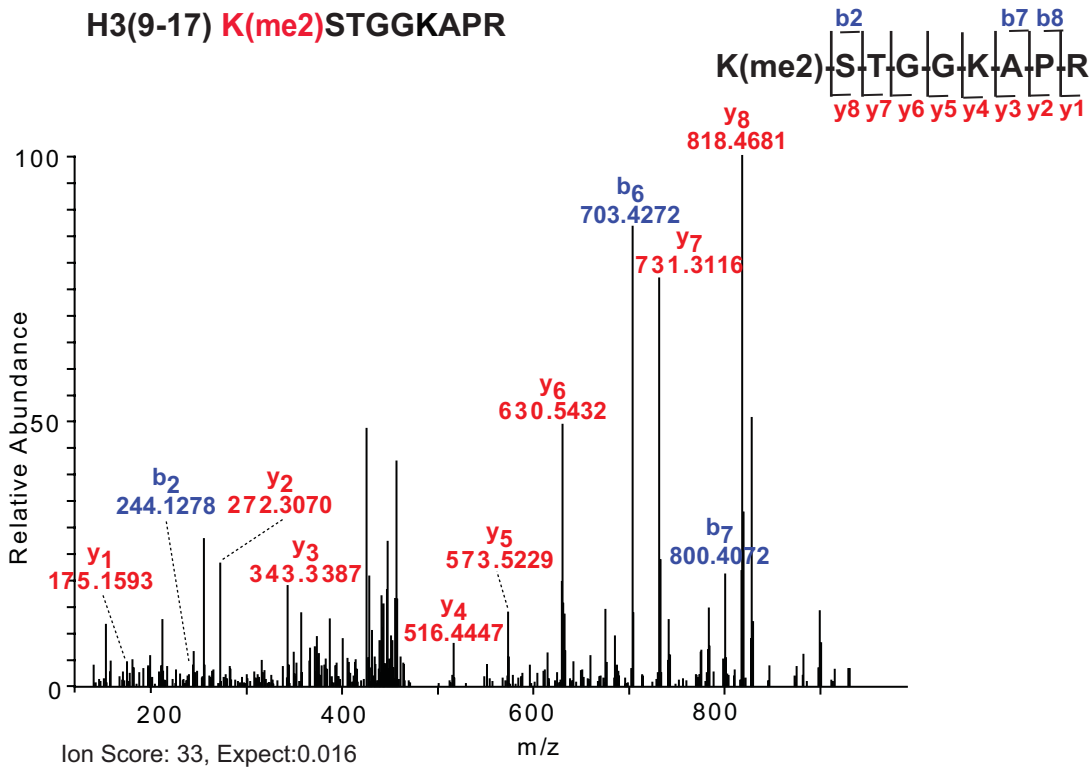
Soldi *et al.*, 2012 Figure S10

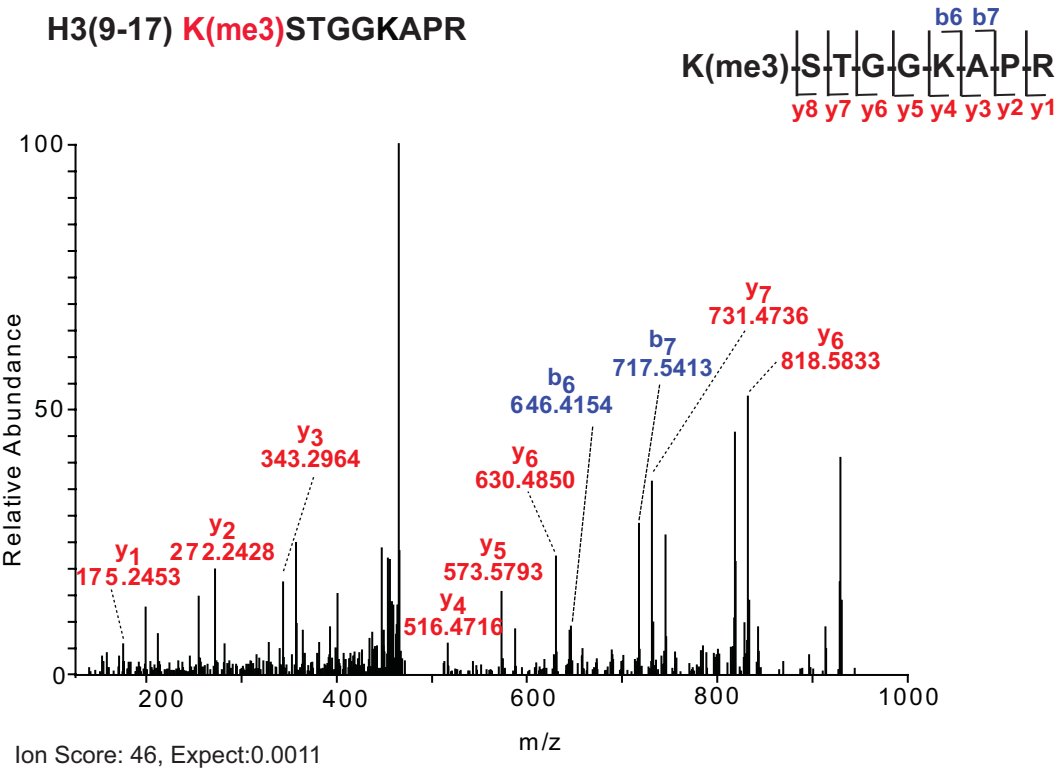


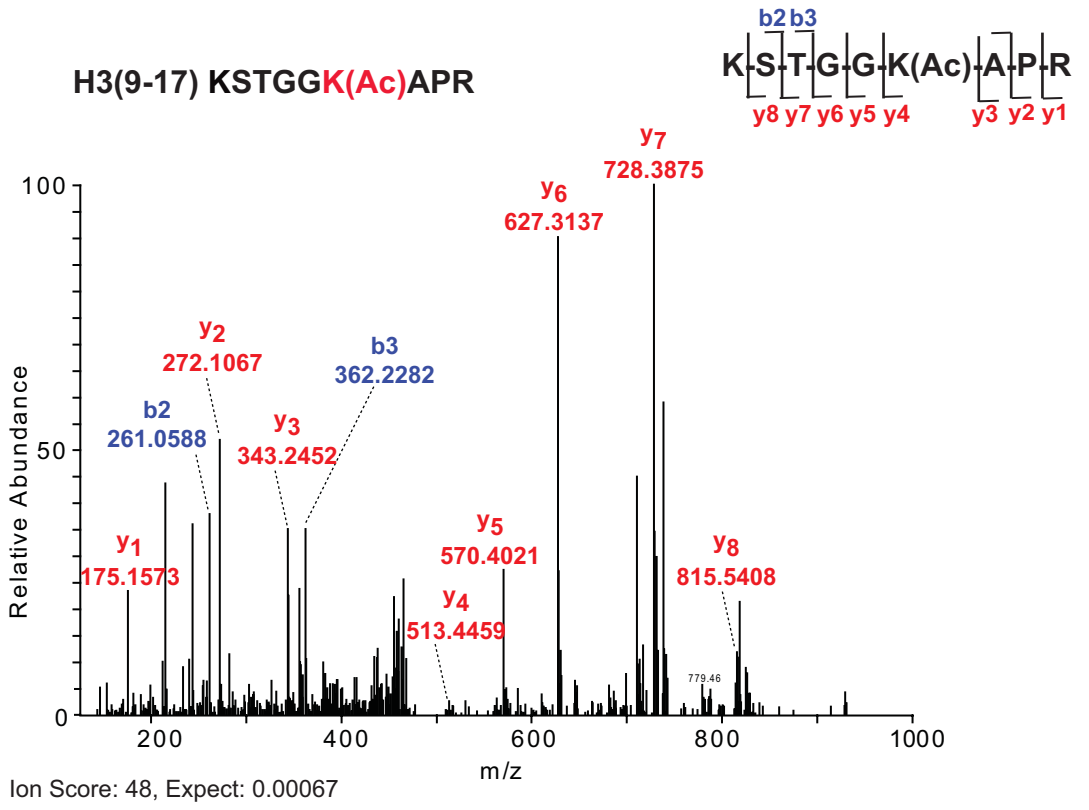


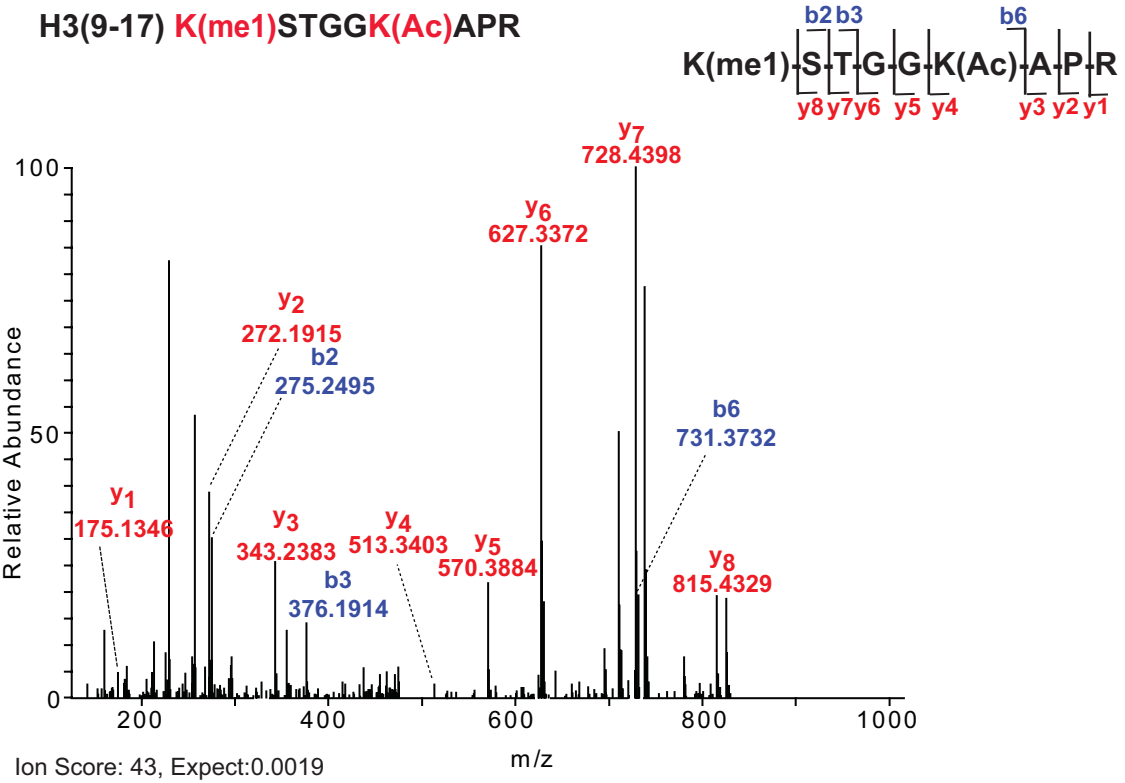


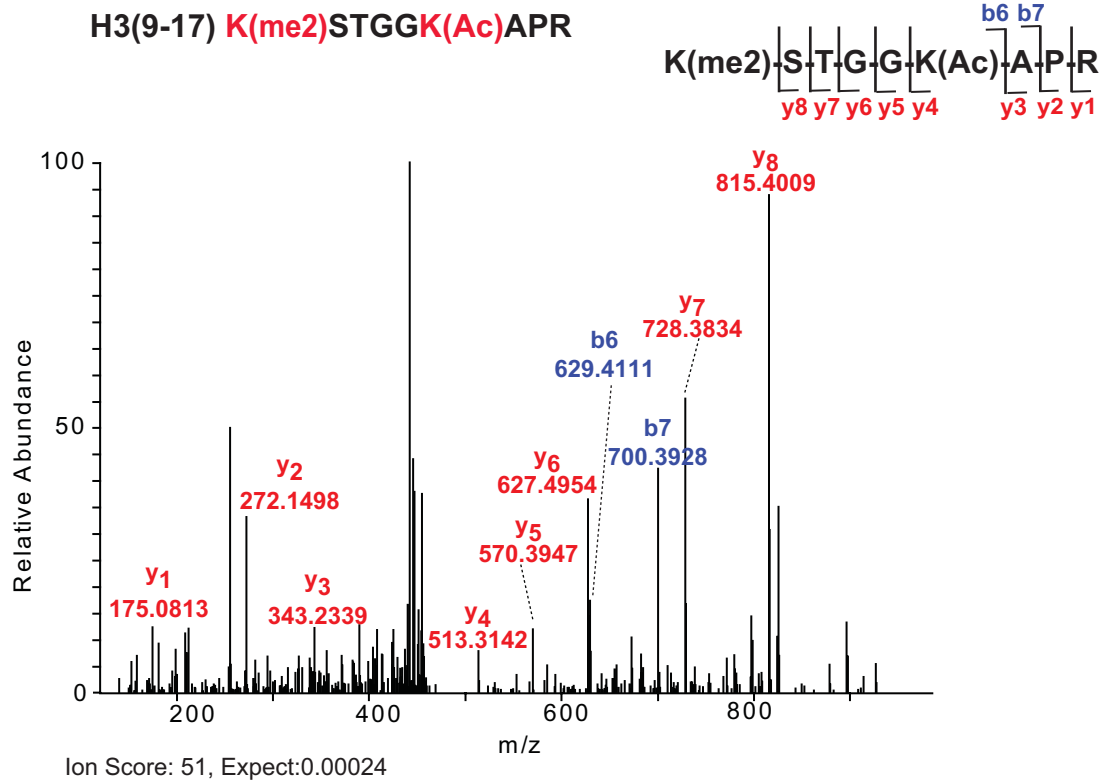

H3(9-17) K(me1)STGGKAPR
K(me1)-S-T-G-G-K-A-P-R
b2 b3
b6
y8 y7 y6 y5 y3 y2 y1
y7 731.4274
y6 630.3223
y2 272.2466
b2 275.1780
y8 818.3044
y3 343.3622
b3 376.1928
y5 573.4962
b6 663.1989
y1 175.0790
Relative Abundance
m/z
Ion Score: 42, Expect:0.0015

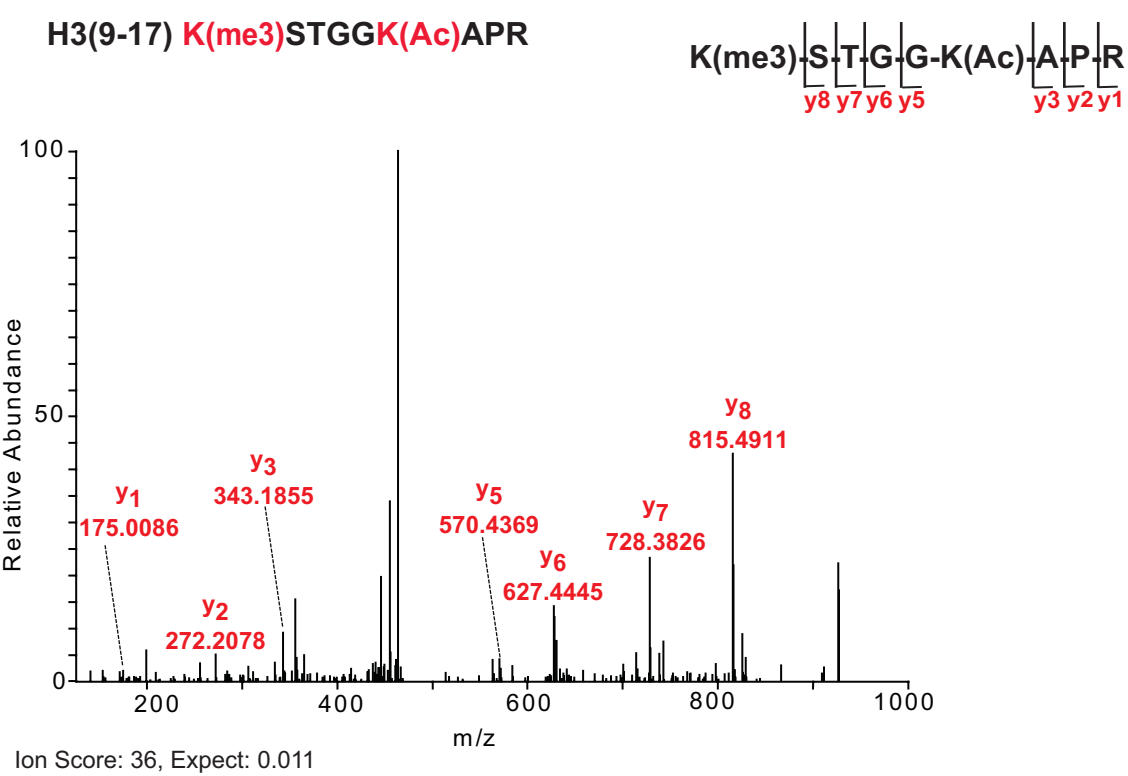

H3(9-17) K(me2)STGGKAPR
K(me2)-S-T-G-G-K-A-P-R
b2
b7 b8
y8 y7 y6 y5 y4 y3 y2 y1
y8 818.4681
b6 703.4272
y7 731.3116
y6 630.5432
b2 244.1278
y2 272.3070
y5 573.5229
b7 800.4072
y3 343.3387
y1 175.1593
y4 516.4447
Relative Abundance
m/z
Ion Score: 33, Expect:0.016

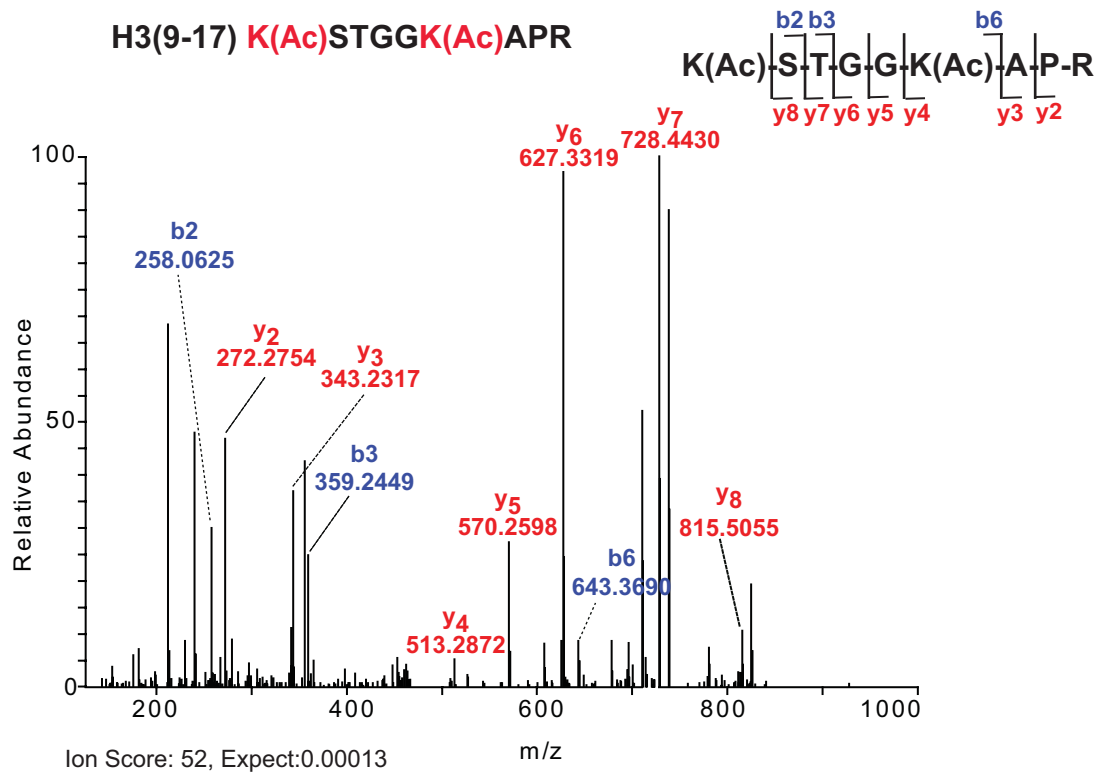

H3(9-17) K(me3)STGGKAPR
K(me3)-S-T-G-G-K-A-P-R
b6 b7
y8 y7 y6 y5 y4 y3 y2 y1
y7 731.4736
b7 717.5413
y6 818.5833
b6 646.4154
y3 343.2964
y6 630.4850
y2 272.2428
y5 573.5793
y1 175.2453
y4 516.4716
Relative Abundance
m/z
Ion Score: 46, Expect:0.0011


H3(9-17) KSTGGK(Ac)APR
K-S-T-G-G-K(Ac)-A-P-R
b2 b3
y8 y7 y6 y5 y4
y3 y2 y1
y7 728.3875
y6 627.3137
y2 272.1067
b3 362.2282
b2 261.0588
y3 343.2452
y5 570.4021
y8 815.5408
y1 175.1573
y4 513.4459
779.46
Relative Abundance
m/z
Ion Score: 48, Expect: 0.00067


H3(9-17) K(me1)STGGK(Ac)APR
K(me1)-S-T-G-G-K(Ac)-A-P-R
b2 b3 b6
y8 y7 y6 y5 y4 y3 y2 y1
y7 728.4398
y6 627.3372
y2 272.1915
b2 275.2495
b6 731.3732
y1 175.1346
y3 343.2383
y4 513.3403
y5 570.3884
y8 815.4329
b3 376.1914
Relative Abundance
m/z
Ion Score: 43, Expect:0.0019


H3(9-17) K(me2)STGGK(Ac)APR
K(me2)-S-T-G-G-K(Ac)-A-P-R
b6 b7
y8 y7 y6 y5 y4 y3 y2 y1
y8 815.4009
y7 728.3834
b6 629.4111
b7 700.3928
y2 272.1498
y6 627.4954
y5 570.3947
y1 175.0813
y3 343.2339
y4 513.3142
Relative Abundance
m/z
Ion Score: 51, Expect:0.00024


H3(9-17) K(me3)STGGK(Ac)APR
K(me3)-S-T-G-G-K(Ac)-A-P-R
y8 y7 y6 y5 y3 y2 y1
y8 815.4911
y3 343.1855
y1 175.0086
y5 570.4369
y7 728.3826
y6 627.4445
y2 272.2078
Relative Abundance
m/z
Ion Score: 36, Expect: 0.011

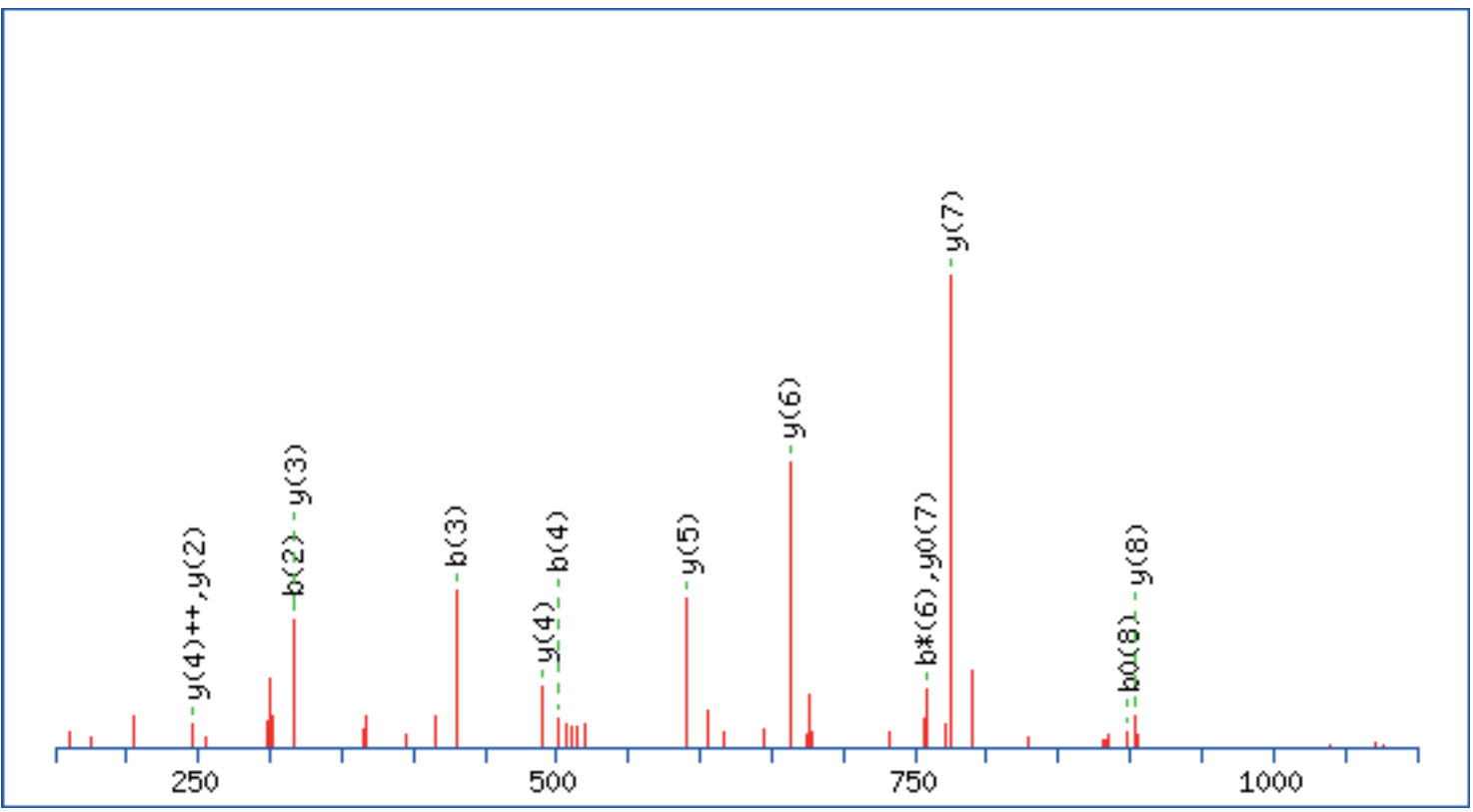

H3(9-17) K(Ac)STGGK(Ac)APR
K(Ac)-S-T-G-G-K(Ac)-A-P-R
b2 b3 b6
y8 y7 y6 y5 y4 y3 y2
y6 627.3319
y7 728.4430
b2 258.0625
y2 272.2754
y3 343.2317
b3 359.2449
y5 570.2598
y8 815.5055
b6 643.3690
y4 513.2872
Relative Abundance
m/z
Ion Score: 52, Expect:0.00013

Match to Query 3883: 1089.676092 from(545.845322,2+)
1 cycles: 1 precIntensity: 773781.4 FinneganScanNumber: 2966

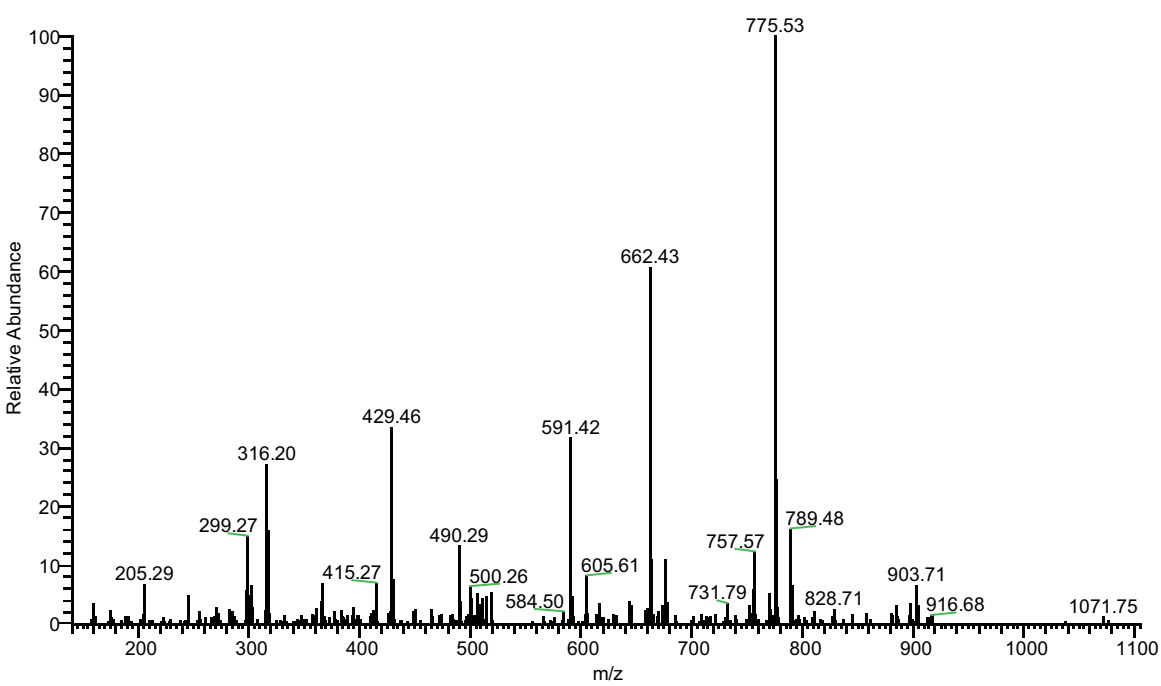
(18-26) H3:
K(me1)QLATKAAR

Monoisotopic mass of neutral peptide Mr(calc): 1089.6777
Variable modifications:
K1 : Methyl+Acetyl:2H(3) (K)
K6 : Acetyl:2H(3) (K)
Ions Score: 55 Expect: 6.4e-05
Matches : 14/80 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	188.1473	94.5773	171.1207	86.064			K							9
2	316.2059	158.6066	299.1793	150.0933			Q	903.545	452.2761	886.5184	443.7629	885.5344	443.2708	8
3	429.2899	215.1486	412.2634	206.6353			L	775.4864	388.2468	758.4598	379.7336	757.4758	379.2416	7
4	500.327	250.6672	483.3005	242.1539			A	662.4023	331.7048	645.3758	323.1915	644.3918	322.6995	6
5	601.3747	301.191	584.3482	292.6777	583.3642	292.1857	T	591.3652	296.1862	574.3387	287.673	573.3547	287.181	5
6	774.4991	387.7532	757.4725	379.2399	756.4885	378.7479	K	490.3175	245.6624	473.291	237.1491			4
7	845.5362	423.2717	828.5096	414.7585	827.5256	414.2665	A	317.1932	159.1002	300.1666	150.587			3
8	916.5733	458.7903	899.5468	450.277	898.5627	449.785	A	246.1561	123.5817	229.1295	115.0684			2
9							R	175.119	88.0631	158.0924	79.5498			1



#2966 RT: 45.34
T: ITMS + c NSI d w Full ms2 545.85@cid35.00 [140.00-1105.00]

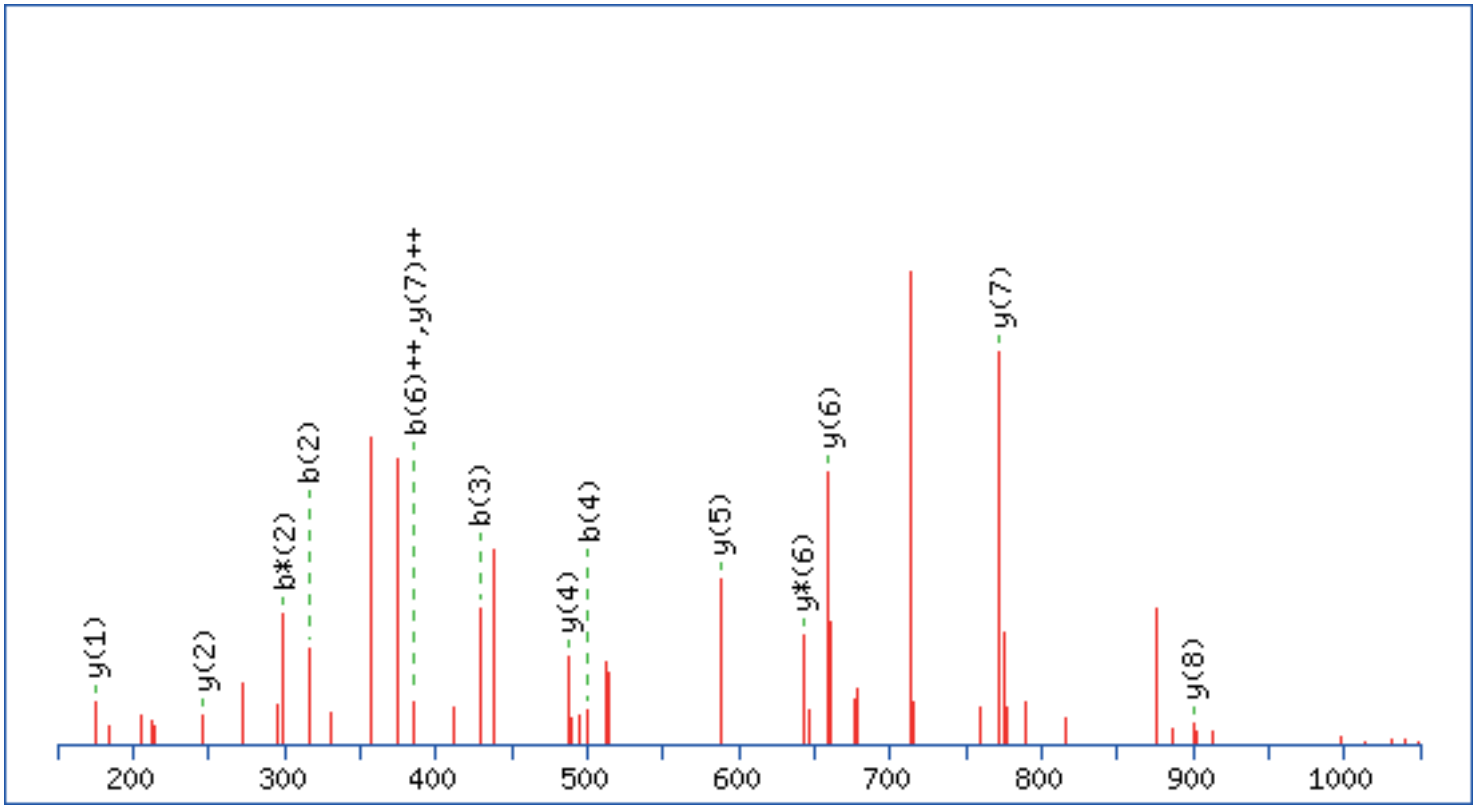


Match to Query 6224: 1086.658876 from(544.336714,2+)
1 cycles: 1 precIntensity: 3292436.8 FinneganScanNumber: 3894

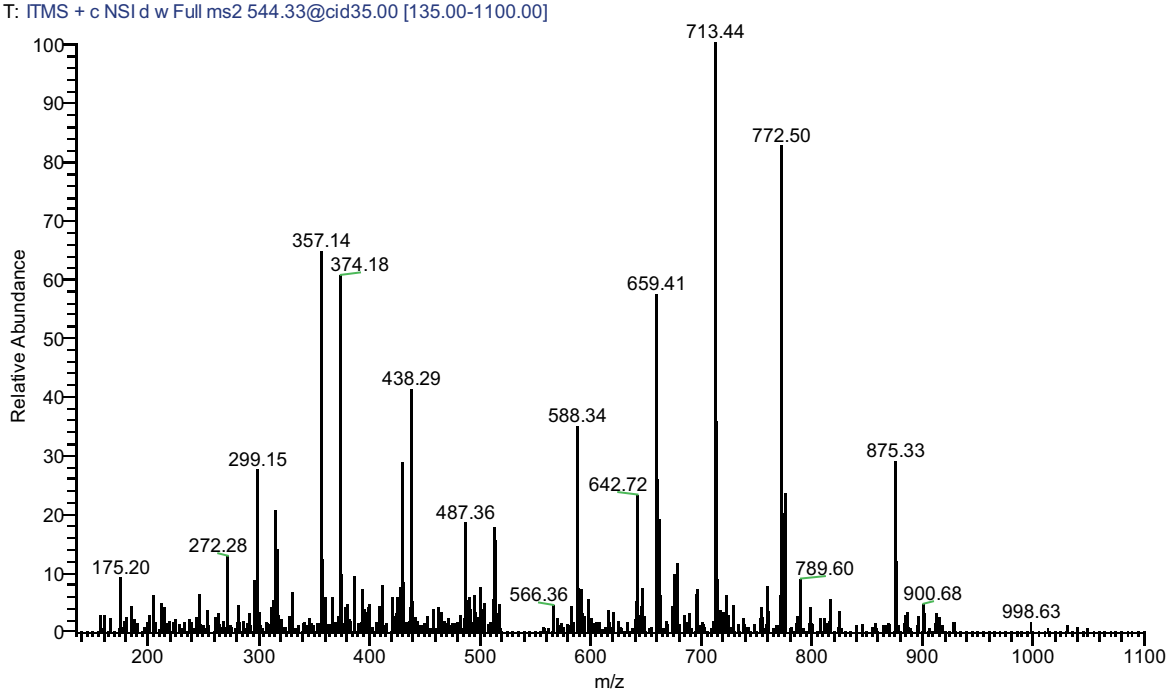
(18-26) H3:
K(me1)QLAT**K(Ac)**AAR

Monoisotopic mass of neutral peptide Mr(calc): 1086.6588
Variable modifications:
K1 : Methyl+Acetyl:2H(3) (K)
K6 : Acetyl (K)
Ions Score: 31 Expect: 0.0076
Matches : 14/80 fragment ions using 36 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	188.1473	94.5773	171.1207	86.064			K							9
2	316.2059	158.6066	299.1793	150.0933			Q	900.5261	450.7667	883.4996	442.2534	882.5156	441.7614	8
3	429.2899	215.1486	412.2634	206.6353			L	772.4676	386.7374	755.441	378.2241	754.457	377.7321	7
4	500.327	250.6672	483.3005	242.1539			A	659.3835	330.1954	642.357	321.6821	641.3729	321.1901	6
5	601.3747	301.191	584.3482	292.6777	583.3642	292.1857	T	588.3464	294.6768	571.3198	286.1636	570.3358	285.6715	5
6	771.4802	386.2438	754.4537	377.7305	753.4697	377.2385	K	487.2987	244.153	470.2722	235.6397			4
7	842.5174	421.7623	825.4908	413.249	824.5068	412.757	A	317.1932	159.1002	300.1666	150.587			3
8	913.5545	457.2809	896.5279	448.7676	895.5439	448.2756	A	246.1561	123.5817	229.1295	115.0684			2
9							R	175.119	88.0631	158.0924	79.5498			1



#3894 RT: 46.44
T: ITMS + c NSI d w Full ms2 544.33@cid35.00 [135.00-1100.00]

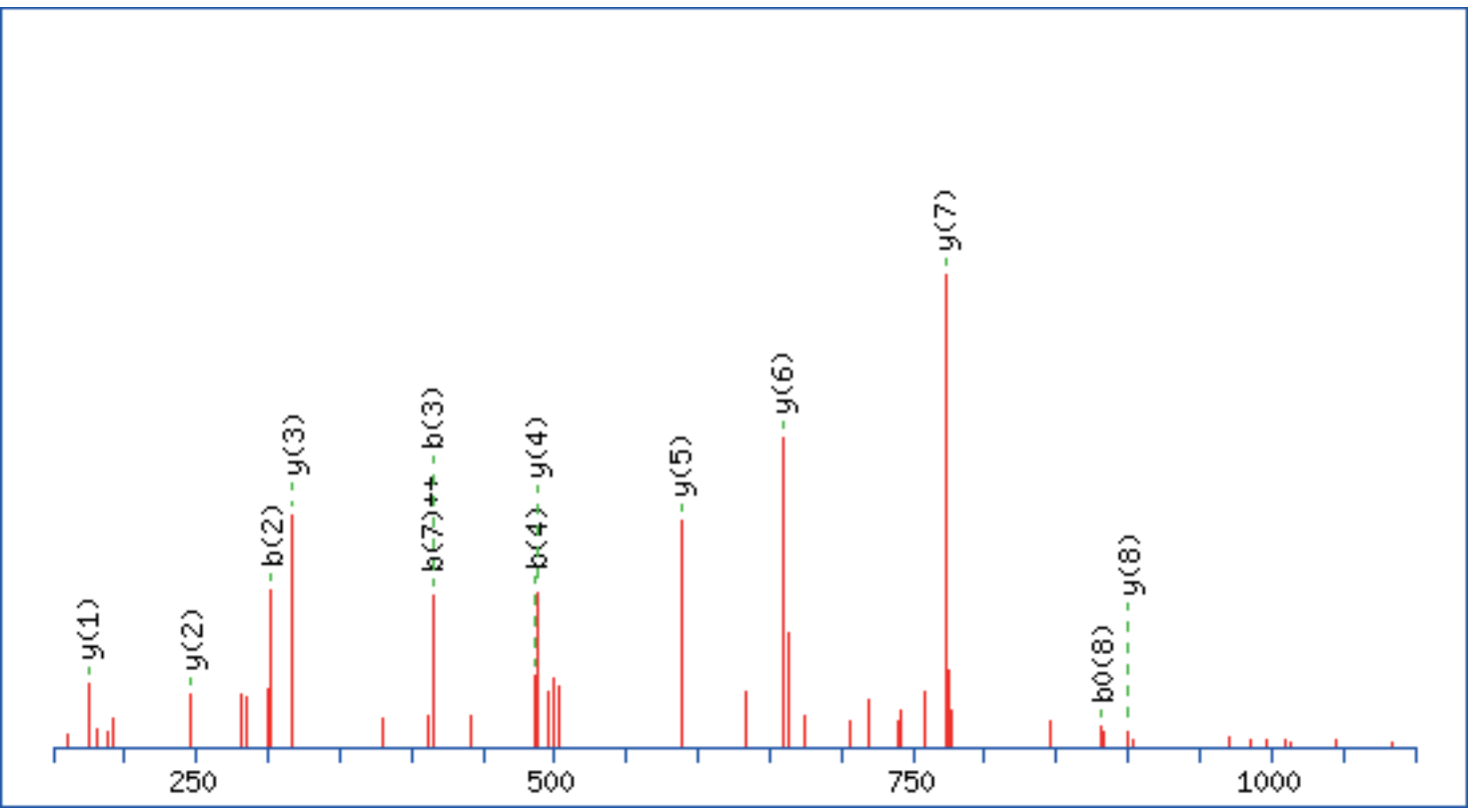


Match to Query 6089: 1072.643042 from(537.328797,2+)
1 cycles: 1 precIntensity: 1960211.0 FinneganScanNumber: 3213

(18-26) H3:
KQLAT**K(Ac)**AAR

Monoisotopic mass of neutral peptide Mr(calc): 1072.6432
Variable modifications:
K1 : Acetyl:2H(3) (K)
K6 : Acetyl (K)
Ions Score: 69 Expect: 4.1e-06
Matches : 13/80 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	174.1316	87.5695	157.1051	79.0562			K							9
2	302.1902	151.5987	285.1637	143.0855			Q	900.5261	450.7667	883.4996	442.2534	882.5156	441.7614	8
3	415.2743	208.1408	398.2477	199.6275			L	772.4676	386.7374	755.441	378.2241	754.457	377.7321	7
4	486.3114	243.6593	469.2848	235.1461			A	659.3835	330.1954	642.357	321.6821	641.3729	321.1901	6
5	587.3591	294.1832	570.3325	285.6699	569.3485	285.1779	T	588.3464	294.6768	571.3198	286.1636	570.3358	285.6715	5
6	757.4646	379.2359	740.438	370.7227	739.454	370.2307	K	487.2987	244.153	470.2722	235.6397			4
7	828.5017	414.7545	811.4752	406.2412	810.4911	405.7492	A	317.1932	159.1002	300.1666	150.587			3
8	899.5388	450.2731	882.5123	441.7598	881.5283	441.2678	A	246.1561	123.5817	229.1295	115.0684			2
9							R	175.119	88.0631	158.0924	79.5498			1



#3213 RT: 40.19
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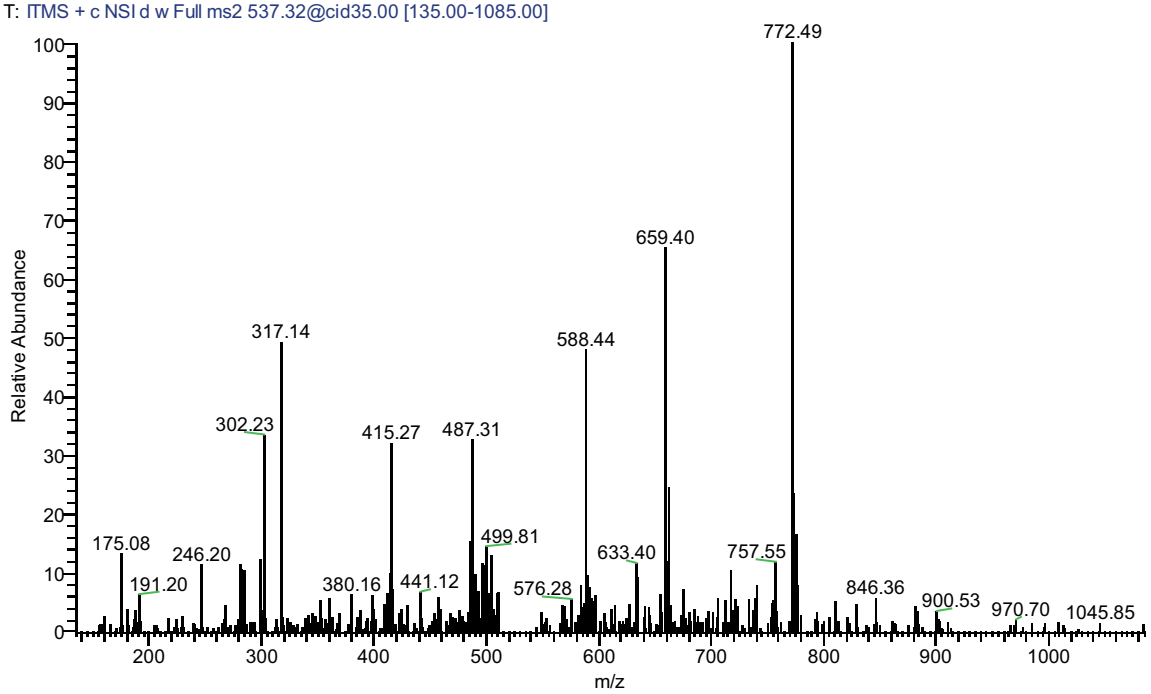
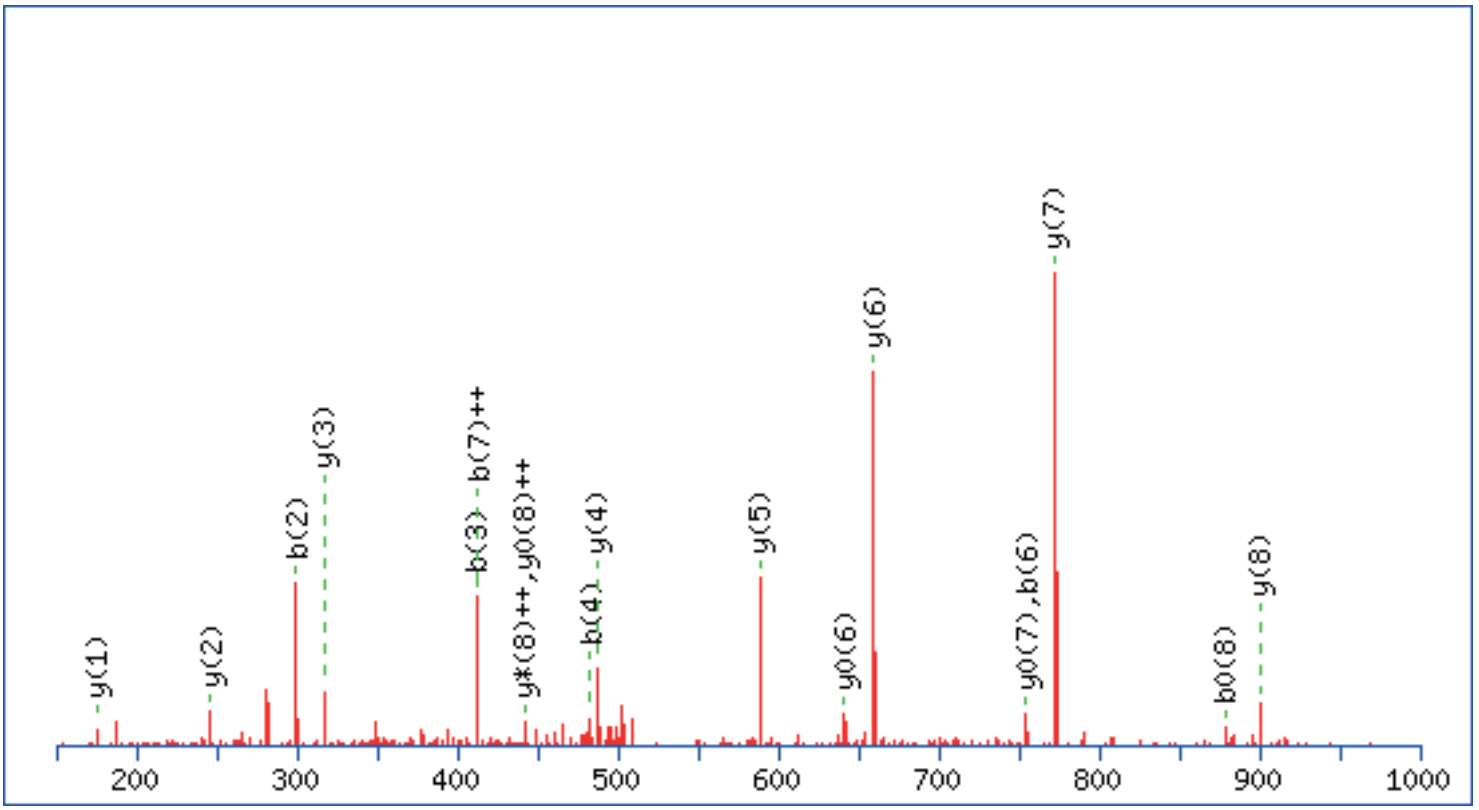


Match to Query 6191: 1069.620370 from(535.817461,2+)
1 cycles: 1 precIntensity: 46889152.2 FinneganScanNumber: 4653

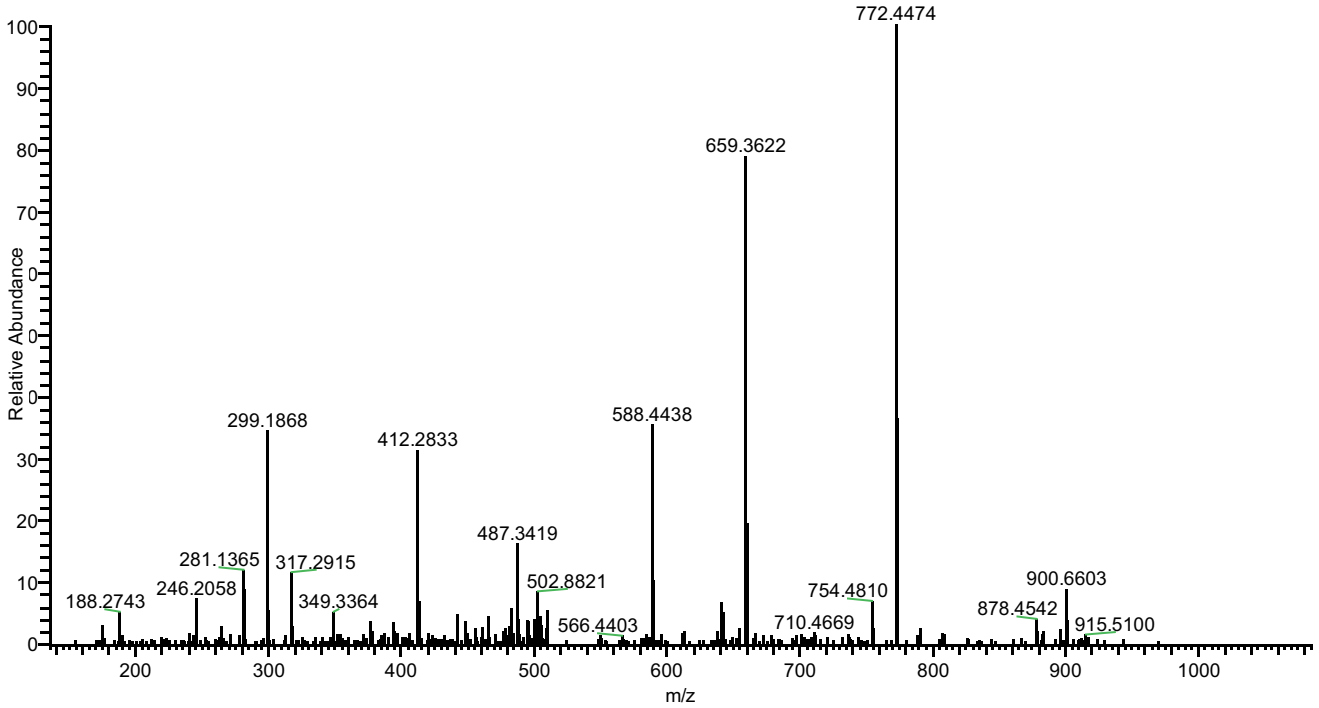
(18-26) H3:
K(Ac)QLAT**K(Ac)**AAR

Monoisotopic mass of neutral peptide Mr(calc): 1069.6243
Variable modifications:
K1 : Acetyl (K)
K6 : Acetyl (K)
Ions Score: 63 Expect: 6.1e-06
Matches : 18/80 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	171.1128	86.06	154.0863	77.5468			K							9
2	**299.171**	150.0893	282.1448	141.5761			Q	***900.526***	450.7667	883.4996	442.2534	882.5156	441.7614	8
3	**412.255**	206.6314	395.2289	198.1181			L	***772.468***	386.7374	755.441	378.2241	754.457	377.7321	7
4	**483.293**	242.1499	466.266	233.6366			A	***659.384***	330.1954	642.357	321.6821	641.3729	321.1901	6
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	T	***588.346***	294.6768	571.3198	286.1636	570.3358	285.6715	5
6	**754.446**	377.7265	737.4192	369.2132	736.4352	368.7212	K	***487.299***	244.153	470.2722	235.6397			4
7	825.4829	413.2451	808.4563	404.7318	807.4723	404.2398	A	***317.193***	159.1002	300.1666	150.587			3
8	896.52	448.7636	879.4934	440.2504	878.5094	439.7584	A	***246.156***	123.5817	229.1295	115.0684			2
9							R	***175.119***	88.0631	158.0924	79.5498			1



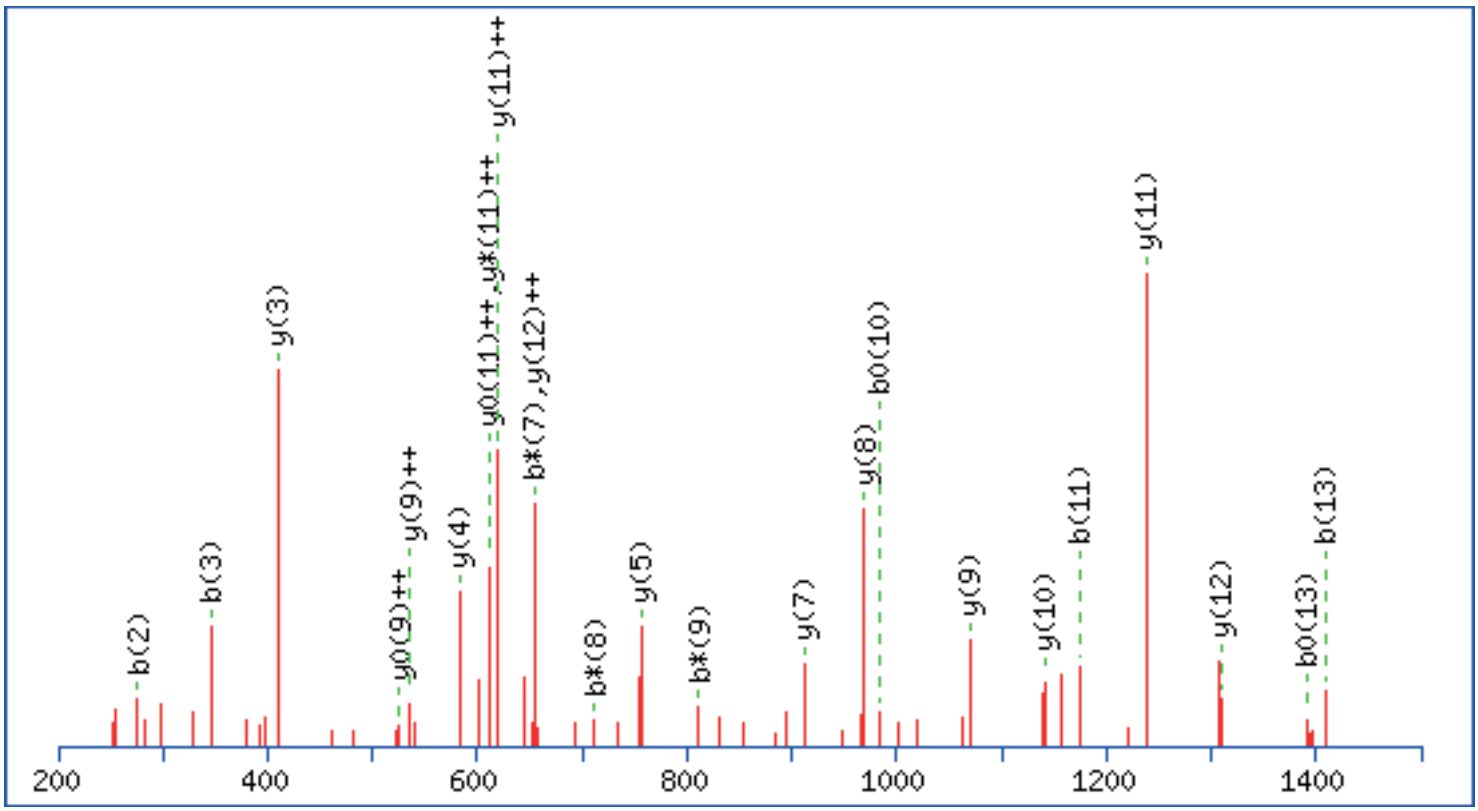
#4653 RT: 45.32
T: ITMS + c NSI d w Full ms2 535.82@cid35.00 [135.00-1085.00]



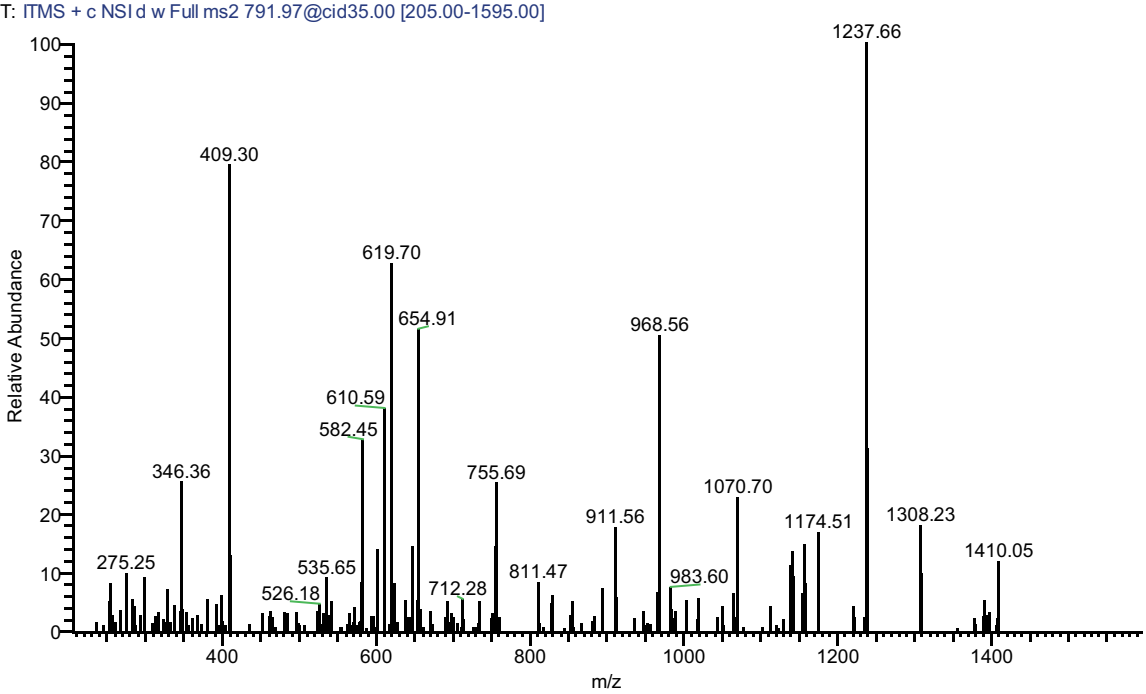
Match to Query 6918: 1581.934028 from(791.974290,2+)
1 cycles: 1 precIntensity: 7858579.2 FinneganScanNumber: 3174
Monoisotopic mass of neutral peptide Mr(calc): 1581.9301
Variable modifications:
K1 : Methyl+Acetyl:2H(3) (K) K11 : Acetyl:2H(3) (K)
K10 : Acetyl:2H(3) (K)
Ions Score: 59 Expect: 9.2e-06
Matches : 24/138 fragment ions using 36 most intense peaks

(27-40) H3:
K(me1)SAPATGGVKKPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	188.1473	94.5773	171.1207	86.064			K							14
2	275.1793	138.0933	258.1528	129.58	257.1687	129.088	S	1395.797	698.4023	1378.771	689.8891	1377.787	689.397	13
3	346.2164	173.6119	329.1899	165.0986	328.2059	164.6066	A	1308.765	654.8863	1291.739	646.373	1290.755	645.881	12
4	443.2692	222.1382	426.2426	213.625	425.2586	213.133	P	1237.728	619.3678	1220.702	610.8545	1219.718	610.3625	11
5	514.3063	257.6568	497.2798	249.1435	496.2957	248.6515	A	1140.676	570.8414	1123.649	562.3281	1122.665	561.8361	10
6	615.354	308.1806	598.3274	299.6674	597.3434	299.1753	T	1069.638	535.3228	1052.612	526.8095	1051.628	526.3175	9
7	672.3754	336.6914	655.3489	328.1781	654.3649	327.6861	G	968.5907	484.799	951.5641	476.2857			8
8	729.3969	365.2021	712.3704	356.6888	711.3863	356.1968	G	911.5692	456.2882	894.5427	447.775			7
9	828.4653	414.7363	811.4388	406.223	810.4548	405.731	V	854.5478	427.7775	837.5212	419.2642			6
10	1001.59	501.2985	984.5631	492.7852	983.5791	492.2932	K	755.4793	378.2433	738.4528	369.73			5
11	1174.714	587.8607	1157.688	579.3474	1156.704	578.8554	K	582.355	291.6811	565.3284	283.1679			4
12	1271.767	636.387	1254.74	627.8738	1253.756	627.3818	P	409.2306	205.119	392.2041	196.6057			3
13	1408.826	704.9165	1391.799	696.4032	1390.815	695.9112	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



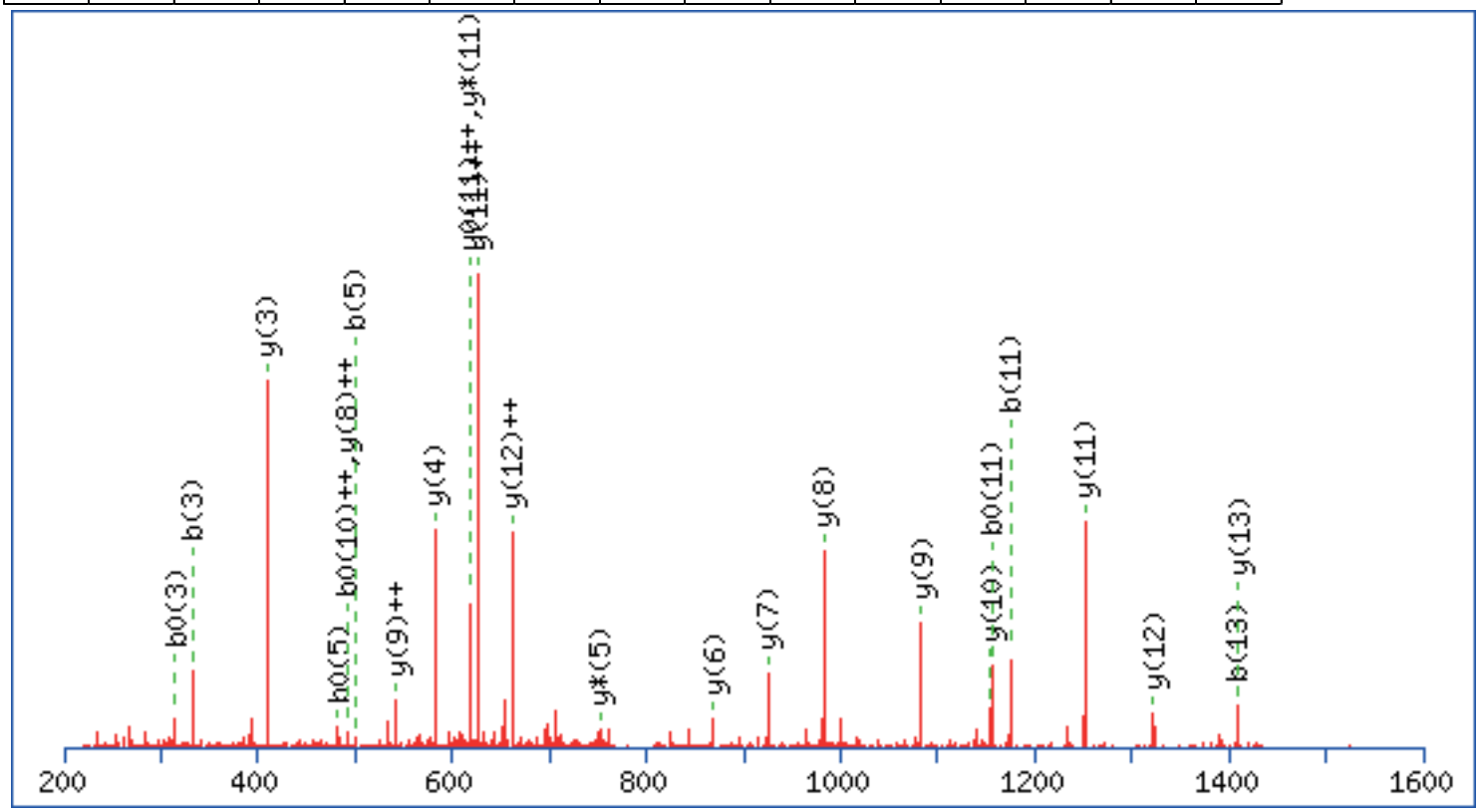
#3174 RT: 46.32
T: ITMS + c NSI d w Full ms2 791.97@cid35.00 [205.00-1595.00]



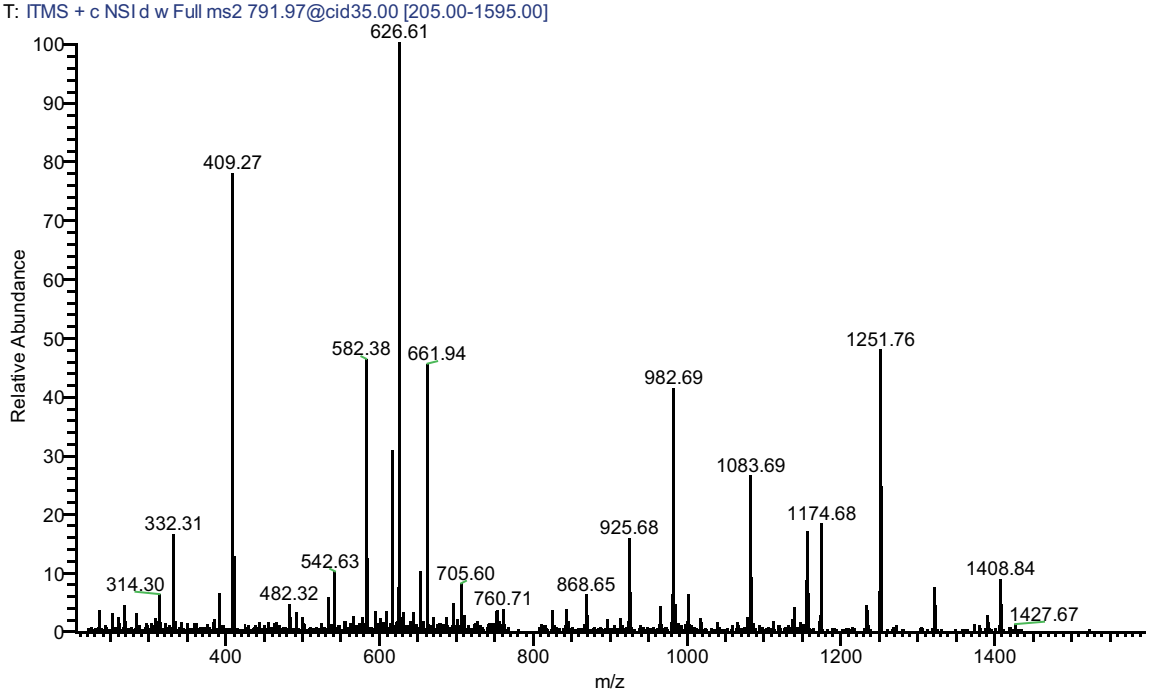
Match to Query 4870: 1581.928834 from(791.971693,2+)
1 cycles: 1 precIntensity: 2934398.2 FinneganScanNumber: 2470
Monoisotopic mass of neutral peptide Mr(calc): 1581.9301
Variable modifications:
K1 : Acetyl:2H(3) (K) K11 : Acetyl:2H(3) (K)
K10 : Methyl+Acetyl:2H(3) (K)
Ions Score: 66 Expect: 5.7e-06
Matches : 25/138 fragment ions using 40 most intense peaks

(27-40) H3:
KSAPATGGV**K(me1)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	174.1316	87.5695	157.1051	79.0562			K							14
2	261.1637	131.0855	244.1371	122.5722	243.1531	122.0802	S	1409.813	705.4102	1392.787	696.8969	1391.803	696.4049	13
3	332.2008	166.604	315.1742	158.0908	314.1902	157.5987	A	1322.781	661.8941	1305.755	653.3809	1304.77	652.8889	12
4	429.2535	215.1304	412.227	206.6171	411.243	206.1251	P	1251.744	626.3756	1234.717	617.8623	1233.733	617.3703	11
5	500.2907	250.649	483.2641	242.1357	482.2801	241.6437	A	1154.691	577.8492	1137.665	569.3359	1136.681	568.8439	10
6	601.3383	301.1728	584.3118	292.6595	583.3278	292.1675	T	1083.654	542.3306	1066.628	533.8174	1065.643	533.3254	9
7	658.3598	329.6835	641.3332	321.1703	640.3492	320.6783	G	982.6063	491.8068	965.5798	483.2935			8
8	715.3813	358.1943	698.3547	349.681	697.3707	349.189	G	925.5849	463.2961	908.5583	454.7828			7
9	814.4497	407.7285	797.4231	399.2152	796.4391	398.7232	V	868.5634	434.7853	851.5369	426.2721			6
10	1001.59	501.2985	984.5631	492.7852	983.5791	492.2932	K	769.495	385.2511	752.4684	376.7379			5
11	1174.714	587.8607	1157.688	579.3474	1156.704	578.8554	K	582.355	291.6811	565.3284	283.1679			4
12	1271.767	636.387	1254.74	627.8738	1253.756	627.3818	P	409.2306	205.119	392.2041	196.6057			3
13	1408.826	704.9165	1391.799	696.4032	1390.815	695.9112	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



#2470 RT: 46.80
T: ITMS + c NSI d w Full ms2 791.97@cid35.00 [205.00-1595.00]



Match to Query 6698: 1550.920012 from(776.467282,2+)

1 cycles: 1 precIntensity: 6201700.9 FinneganScanNumber: 1995

Monoisotopic mass of neutral peptide Mr(calc): 1550.9163

Variable modifications:

K1 : Dimethyl (K) K11 : Acetyl:2H(3) (K)

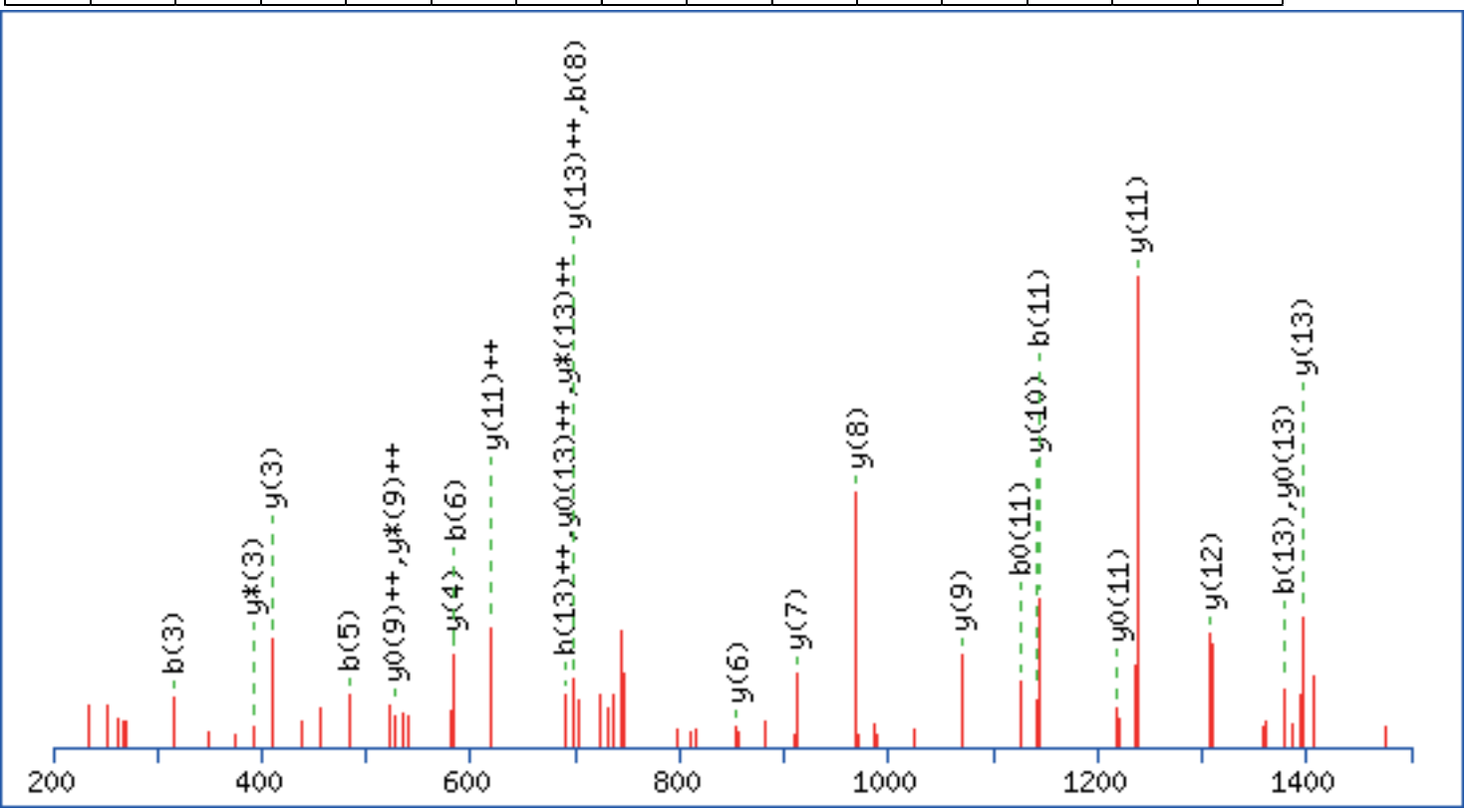
K10 : Acetyl:2H(3) (K)

Ions Score: 55 Expect: 9.2e-06

Matches : 27/138 fragment ions using 48 most intense peaks

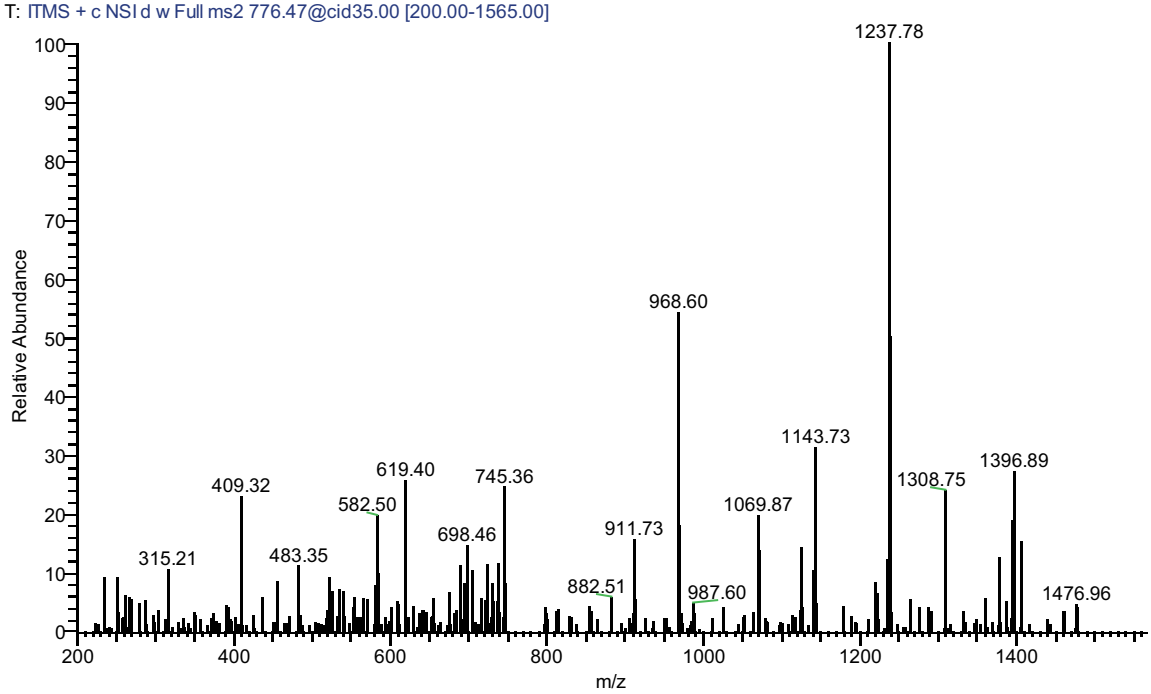
(27-40) H3: K**(me2)**SAPATGGVKKPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.1335	79.0704	140.107	70.5571			K							14
2	244.1656	122.5864	227.139	114.0731	226.155	113.5811	S	***1395.797***	698.4023	1378.771	689.8891	1377.787	689.397	13
3	315.2027	158.105	298.1761	149.5917	297.1921	149.0997	A	***1308.765***	654.8863	1291.739	646.373	1290.755	645.881	12
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	P	***1237.728***	619.3678	1220.702	610.8545	1219.718	610.3625	11
5	483.2926	242.1499	466.266	233.6366	465.282	233.1446	A	***1140.676***	570.8414	1123.649	562.3281	1122.665	561.8361	10
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	T	***1069.638***	535.3228	1052.612	526.8095	1051.628	526.3175	9
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	G	***968.5907***	484.799	951.5641	476.2857			8
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	G	***911.5692***	456.2882	894.5427	447.775			7
9	797.4516	399.2294	780.425	390.7162	779.441	390.2241	V	***854.5478***	427.7775	837.5212	419.2642			6
10	970.5759	485.7916	953.5494	477.2783	952.5654	476.7863	K	755.4793	378.2433	738.4528	369.73			5
11	1143.7	572.3538	1126.674	563.8405	1125.69	563.3485	K	***582.355***	291.6811	565.3284	283.1679			4
12	1240.753	620.8802	1223.727	612.3669	1222.743	611.8749	P	***409.2306***	205.119	392.2041	196.6057			3
13	1377.812	689.4096	1360.785	680.8963	1359.801	680.4043	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



#1995 RT: 36.91

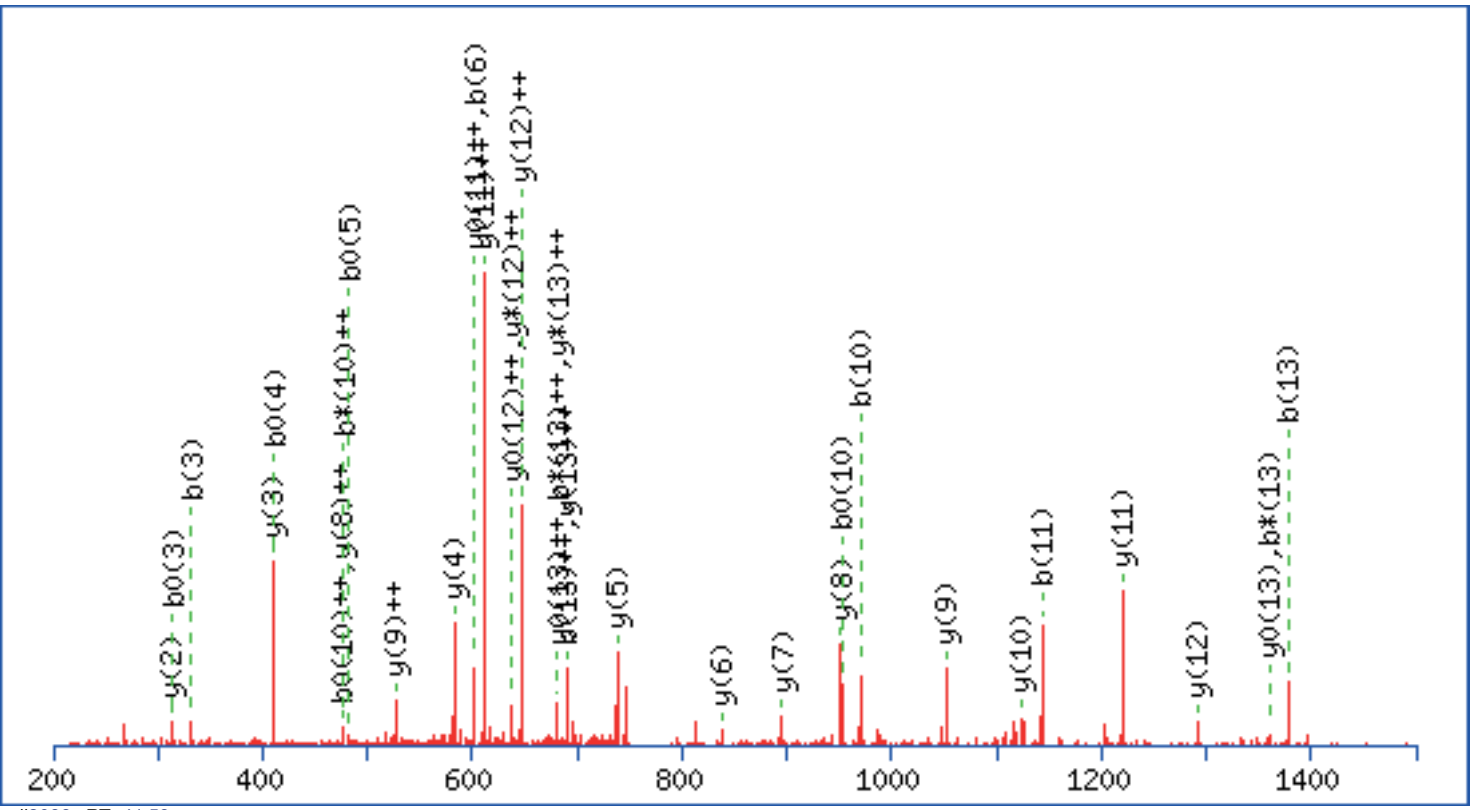
T: ITMS + c NSI d w Full ms2 776.47@cid35.00 [200.00-1565.00]



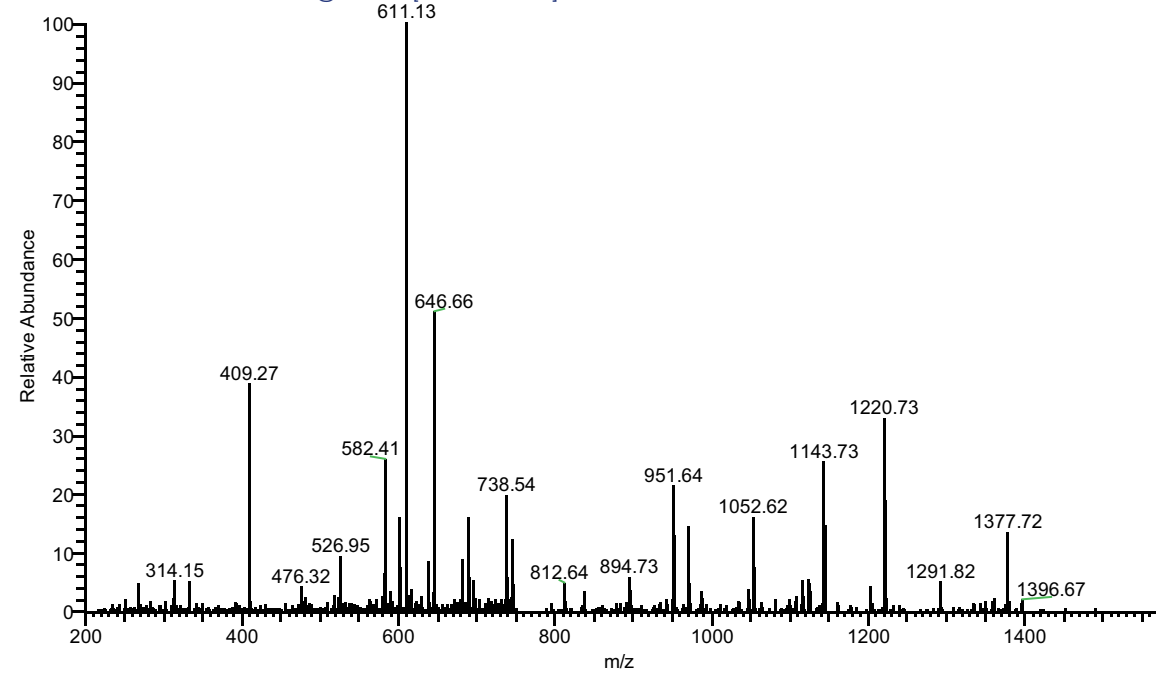
Match to Query 4746: 1550.915270 from(776.464911,2+)
1 cycles: 1 precIntensity: 418128.8 FinneganScanNumber: 2088
Monoisotopic mass of neutral peptide Mr(calc): 1550.9163
Variable modifications:
K1 : Acetyl:2H(3) (K) K11 : Acetyl:2H(3) (K)
K10 : Dimethyl (K)
Ions Score: 76 Expect: 1.1e-06
Matches : 36/138 fragment ions using 52 most intense peaks

(27-40) H3:
KSAPATGGV**K(me2)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	174.1316	87.5695	157.1051	79.0562			K							14
2	261.1637	131.0855	244.1371	122.5722	243.1531	122.0802	S	1378.799	689.9033	1361.773	681.39	1360.789	680.898	13
3	332.2008	166.604	315.1742	158.0908	314.1902	157.5987	A	1291.767	646.3873	1274.741	637.874	1273.757	637.382	12
4	429.2535	215.1304	412.227	206.6171	411.243	206.1251	P	1220.73	610.8687	1203.704	602.3554	1202.72	601.8634	11
5	500.2907	250.649	483.2641	242.1357	482.2801	241.6437	A	1123.677	562.3423	1106.651	553.8291	1105.667	553.337	10
6	601.3383	301.1728	584.3118	292.6595	583.3278	292.1675	T	1052.64	526.8238	1035.614	518.3105	1034.63	517.8185	9
7	658.3598	329.6835	641.3332	321.1703	640.3492	320.6783	G	951.5926	476.2999	934.566	467.7867			8
8	715.3813	358.1943	698.3547	349.681	697.3707	349.189	G	894.5711	447.7892	877.5446	439.2759			7
9	814.4497	407.7285	797.4231	399.2152	796.4391	398.7232	V	837.5497	419.2785	820.5231	410.7652			6
10	970.5759	485.7916	953.5494	477.2783	952.5654	476.7863	K	738.4812	369.7443	721.4547	361.231			5
11	1143.7	572.3538	1126.674	563.8405	1125.69	563.3485	K	582.355	291.6811	565.3284	283.1679			4
12	1240.753	620.8802	1223.727	612.3669	1222.743	611.8749	P	409.2306	205.119	392.2041	196.6057			3
13	1377.812	689.4096	1360.785	680.8963	1359.801	680.4043	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



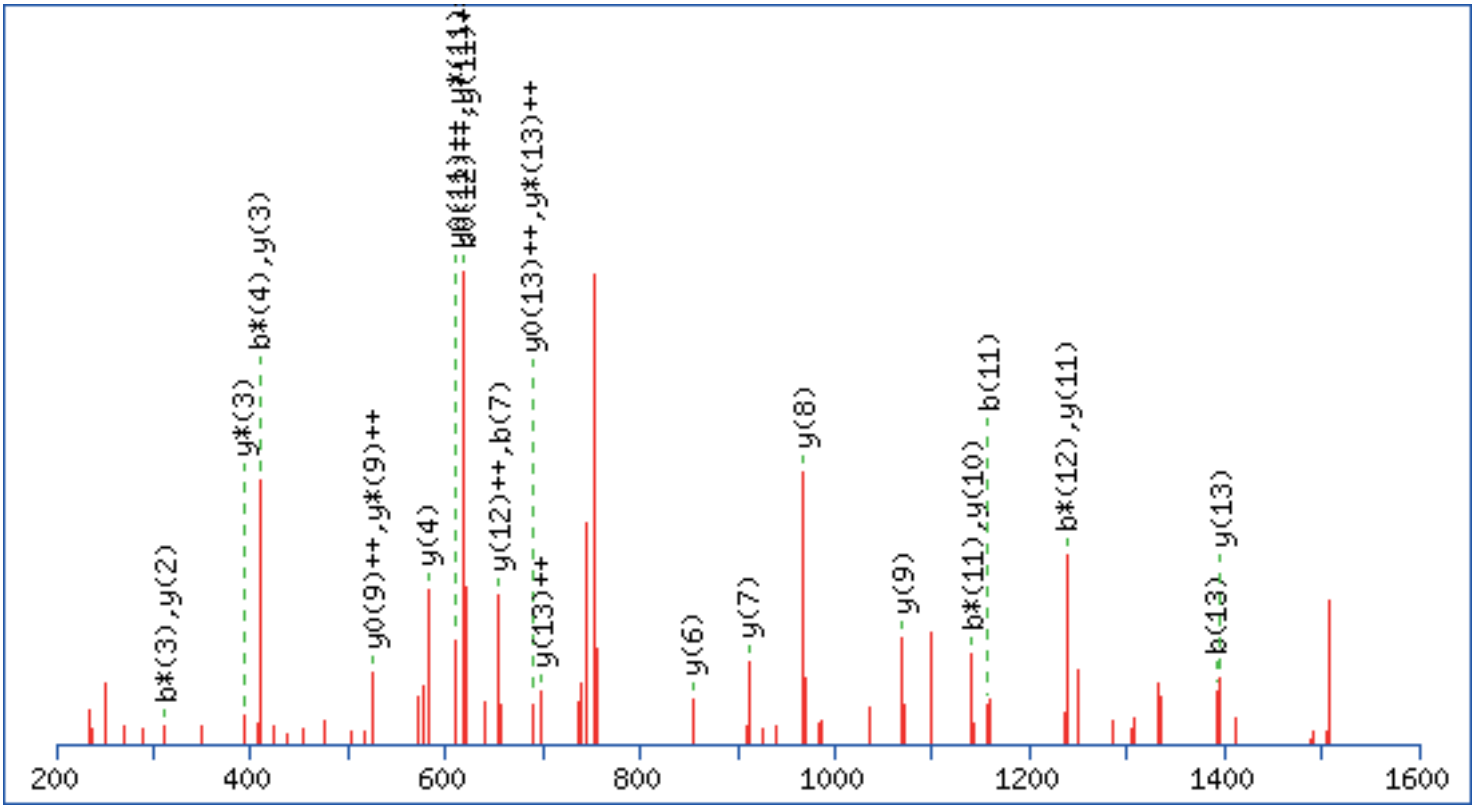
#2088 RT: 41.58
T: ITMS + c NSI d w Full ms2 776.47@cid35.00 [200.00-1565.00]



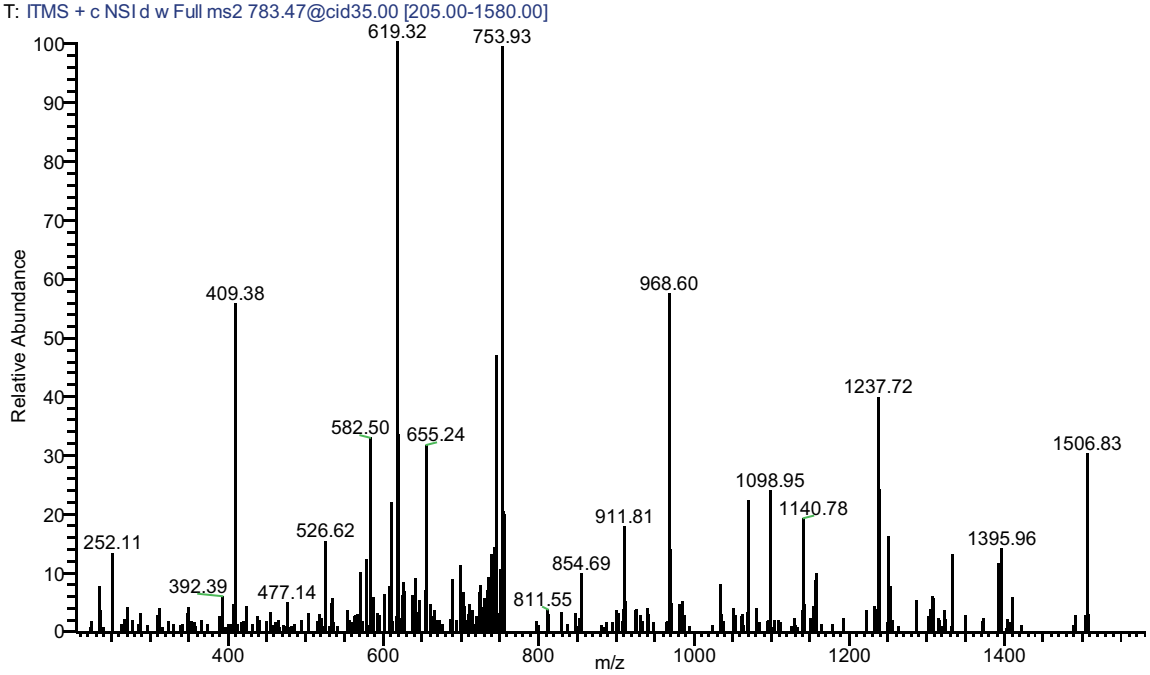
Match to Query 6794: 1564.938410 from(783.476481,2+)
1 cycles: 1 precIntensity: 1630580.3 FinneganScanNumber: 1919
Monoisotopic mass of neutral peptide Mr(calc): 1564.9320
Variable modifications:
K1 : Trimethyl (K)
K10 : Acetyl:2H(3) (K)
K11 : Acetyl:2H(3) (K)
Ions Score: 45 Expect: 0.00015
Matches : 29/138 fragment ions using 52 most intense peaks

(27-40) H3:
K**(me3)**SAPATGGVKKPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	171.1492	86.0782	154.1226	77.565			K							14
2	258.1812	129.5942	241.1547	121.081	240.1707	120.589	S	***1395.797***	698.4023	1378.771	689.8891	1377.787	689.397	13
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	A	1308.765	654.8863	1291.739	646.373	1290.755	645.881	12
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	P	***1237.728***	619.3678	1220.702	610.8545	1219.718	610.3625	11
5	497.3082	249.1577	480.2817	240.6445	479.2976	240.1525	A	***1140.676***	570.8414	1123.649	562.3281	1122.665	561.8361	10
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	T	***1069.638***	535.3228	1052.612	526.8095	1051.628	526.3175	9
7	**655.3774**	328.1923	638.3508	319.679	637.3668	319.187	G	***968.5907***	484.799	951.5641	476.2857			8
8	712.3988	356.703	695.3723	348.1898	694.3883	347.6978	G	***911.5692***	456.2882	894.5427	447.775			7
9	811.4672	406.2373	794.4407	397.724	793.4567	397.232	V	***854.5478***	427.7775	837.5212	419.2642			6
10	984.5916	492.7994	967.565	484.2862	966.581	483.7941	K	755.4793	378.2433	738.4528	369.73			5
11	**1157.716**	579.3616	1140.689	570.8483	1139.705	570.3563	K	***582.355***	291.6811	565.3284	283.1679			4
12	1254.769	627.888	1237.742	619.3747	1236.758	618.8827	P	***409.2306***	205.119	392.2041	196.6057			3
13	**1391.828**	696.4174	1374.801	687.9042	1373.817	687.4122	H	***312.1779***	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



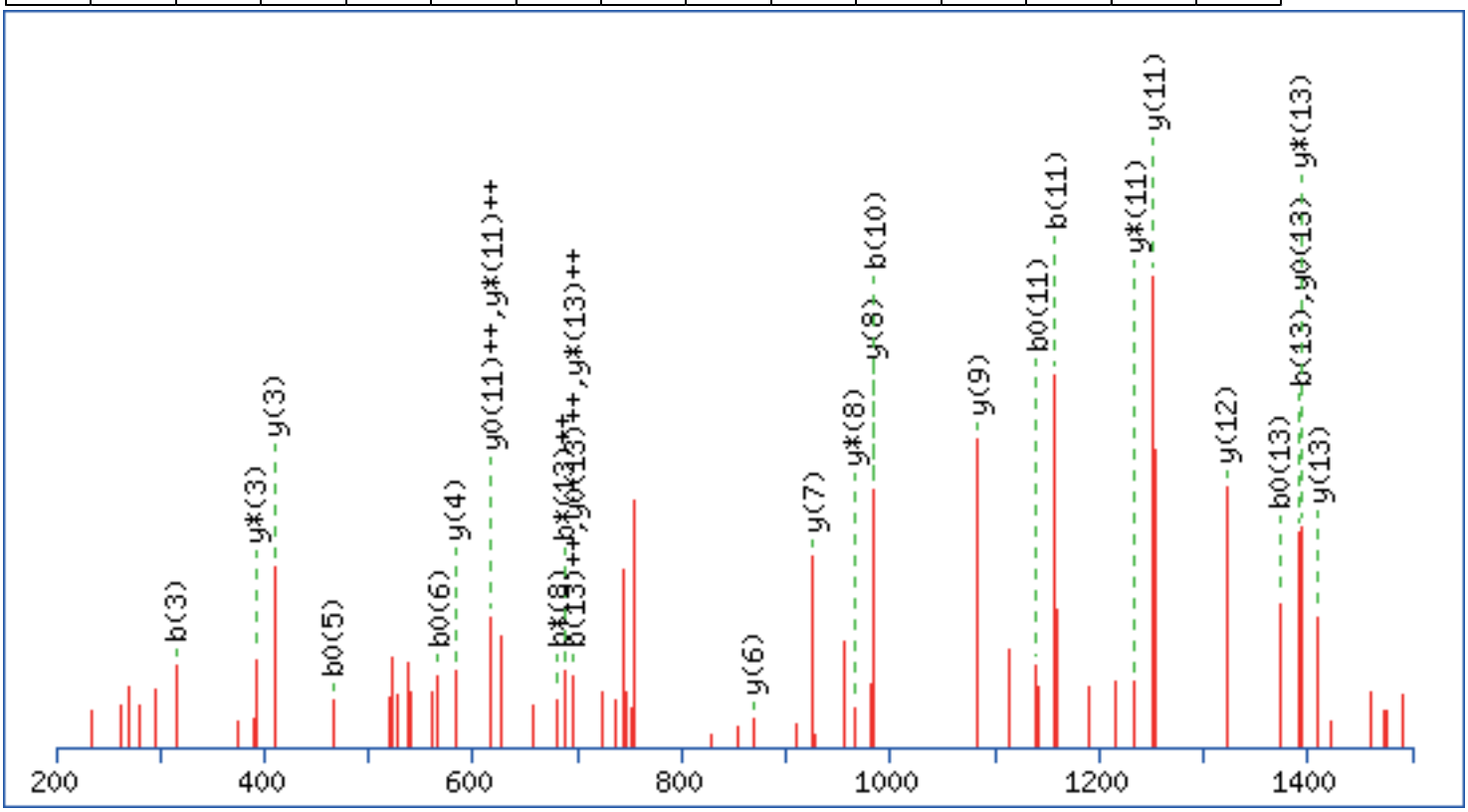
#1919 RT: 36.26
T: ITMS + c NSI d w Full ms2 783.47@cid35.00 [205.00-1580.00]



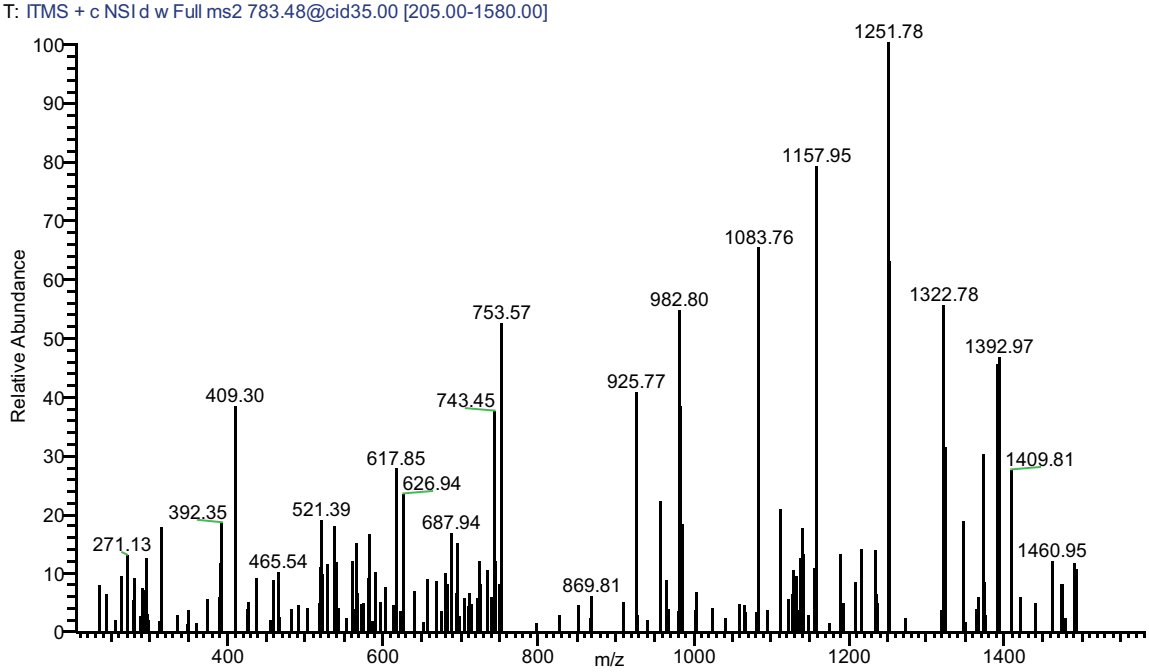
Match to Query 6791: 1564.937474 from(783.476013,2+)
1 cycles: 1 precIntensity: 1812948.0 FinneganScanNumber: 2129
Monoisotopic mass of neutral peptide Mr(calc): 1564.9320
Variable modifications:
K1 : Dimethyl (K)
K10 : Methyl+Acetyl:2H(3) (K)
K11 : Acetyl:2H(3) (K)
Ions Score: 34 Expect: 0.0015
Matches : 29/138 fragment ions using 69 most intense peaks

(27-40) H3:
K**(me2)**SAPATGGVK**(me1)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.1335	79.0704	140.107	70.5571			K							14
2	244.1656	122.5864	227.139	114.0731	226.155	113.5811	S	1409.813	705.4102	1392.787	696.8969	1391.803	696.4049	13
3	315.2027	158.105	298.1761	149.5917	297.1921	149.0997	A	1322.781	661.8941	1305.755	653.3809	1304.77	652.8889	12
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	P	1251.744	626.3756	1234.717	617.8623	1233.733	617.3703	11
5	483.2926	242.1499	466.266	233.6366	465.282	233.1446	A	1154.691	577.8492	1137.665	569.3359	1136.681	568.8439	10
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	T	1083.654	542.3306	1066.628	533.8174	1065.644	533.3254	9
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	G	982.6063	491.8068	965.5798	483.2935			8
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	G	925.5849	463.2961	908.5583	454.7828			7
9	797.4516	399.2294	780.425	390.7162	779.441	390.2241	V	868.5634	434.7853	851.5369	426.2721			6
10	984.5916	492.7994	967.565	484.2862	966.581	483.7941	K	769.495	385.2511	752.4684	376.7379			5
11	1157.716	579.3616	1140.689	570.8483	1139.705	570.3563	K	582.355	291.6811	565.3284	283.1679			4
12	1254.769	627.888	1237.742	619.3747	1236.758	618.8827	P	409.2306	205.119	392.2041	196.6057			3
13	1391.828	696.4174	1374.801	687.9042	1373.817	687.4122	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



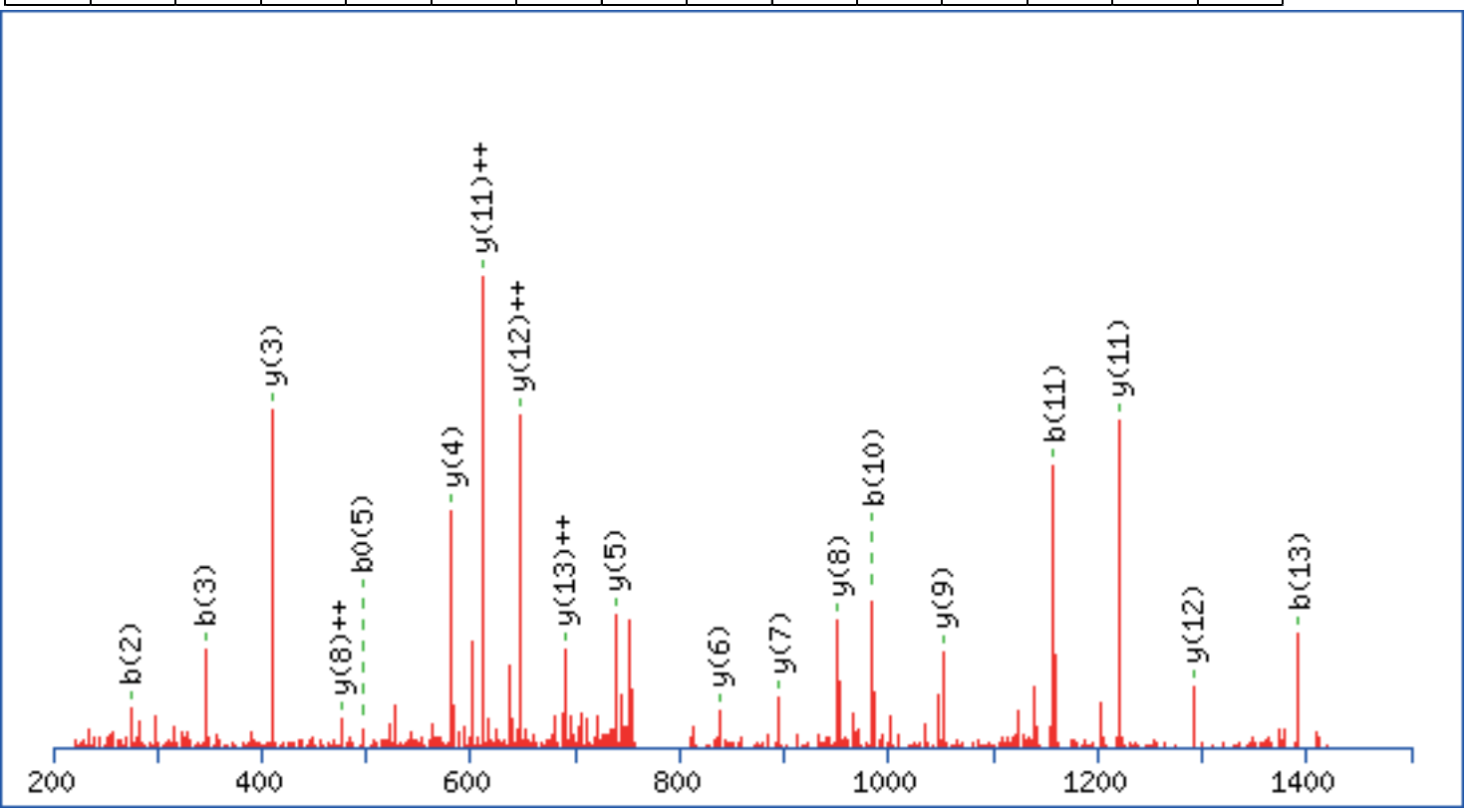
#2129 RT: 38.08
T: ITMS + c NSI d w Full ms2 783.48@cid35.00 [205.00-1580.00]



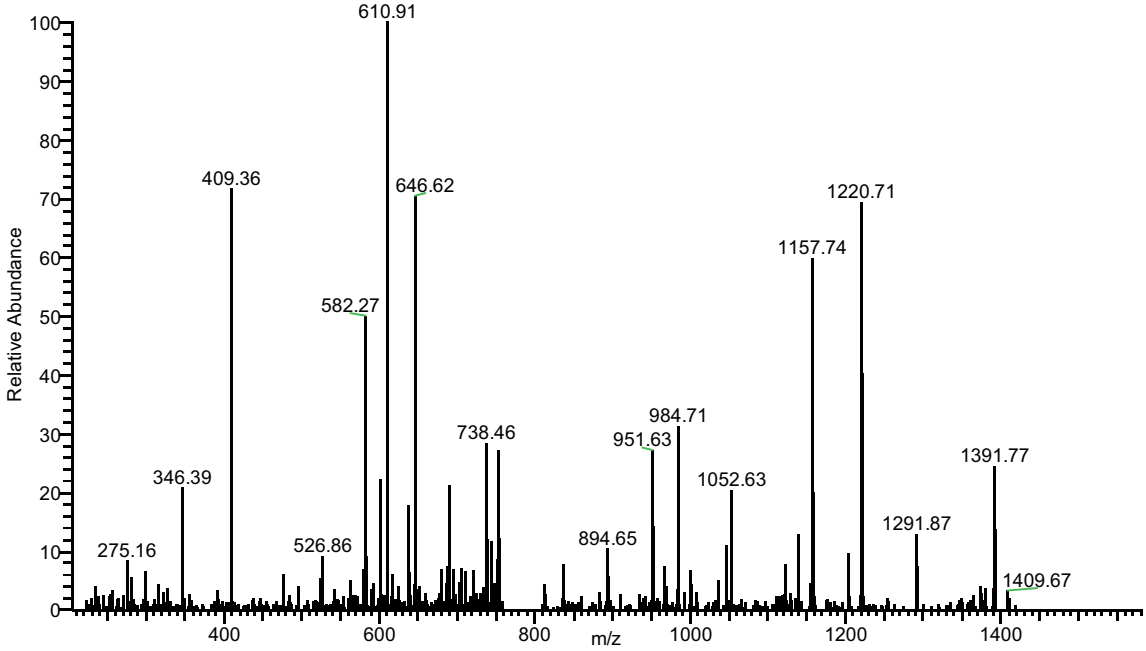
Match to Query 4803: 1564.933912 from(783.474232,2+)
1 cycles: 1 precIntensity: 93701.7 FinneganScanNumber: 2258
Monoisotopic mass of neutral peptide Mr(calc): 1564.9320
Variable modifications:
K1 : Methyl+Acetyl:2H(3) (K)
K10 : Dimethyl (K)
K11 : Acetyl:2H(3) (K)
Ions Score: 75 Expect: 1.4e-06
Matches : 19/138 fragment ions using 24 most intense peaks

(27-40) H3:
K**(me1)**SAPATGGVK**(me2)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	188.1473	94.5773	171.1207	86.064			K							14
2	275.1793	138.0933	258.1528	129.58	257.1687	129.088	S	1378.799	689.9033	1361.773	681.39	1360.789	680.898	13
3	346.2164	173.6119	329.1899	165.0986	328.2059	164.6066	A	1291.767	646.3873	1274.741	637.874	1273.757	637.382	12
4	443.2692	222.1382	426.2426	213.625	425.2586	213.133	P	1220.73	610.8687	1203.704	602.3554	1202.72	601.8634	11
5	514.3063	257.6568	497.2798	249.1435	496.2957	248.6515	A	1123.677	562.3423	1106.651	553.8291	1105.667	553.337	10
6	615.354	308.1806	598.3274	299.6674	597.3434	299.1753	T	1052.64	526.8238	1035.614	518.3105	1034.63	517.8185	9
7	672.3754	336.6914	655.3489	328.1781	654.3649	327.6861	G	951.5926	476.2999	934.566	467.7867			8
8	729.3969	365.2021	712.3704	356.6888	711.3863	356.1968	G	894.5711	447.7892	877.5446	439.2759			7
9	828.4653	414.7363	811.4388	406.223	810.4548	405.731	V	837.5497	419.2785	820.5231	410.7652			6
10	984.5916	492.7994	967.565	484.2862	966.581	483.7941	K	738.4812	369.7443	721.4547	361.231			5
11	1157.716	579.3616	1140.689	570.8483	1139.705	570.3563	K	582.355	291.6811	565.3284	283.1679			4
12	1254.769	627.888	1237.742	619.3747	1236.758	618.8827	P	409.2306	205.119	392.2041	196.6057			3
13	1391.828	696.4174	1374.801	687.9042	1373.817	687.4122	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



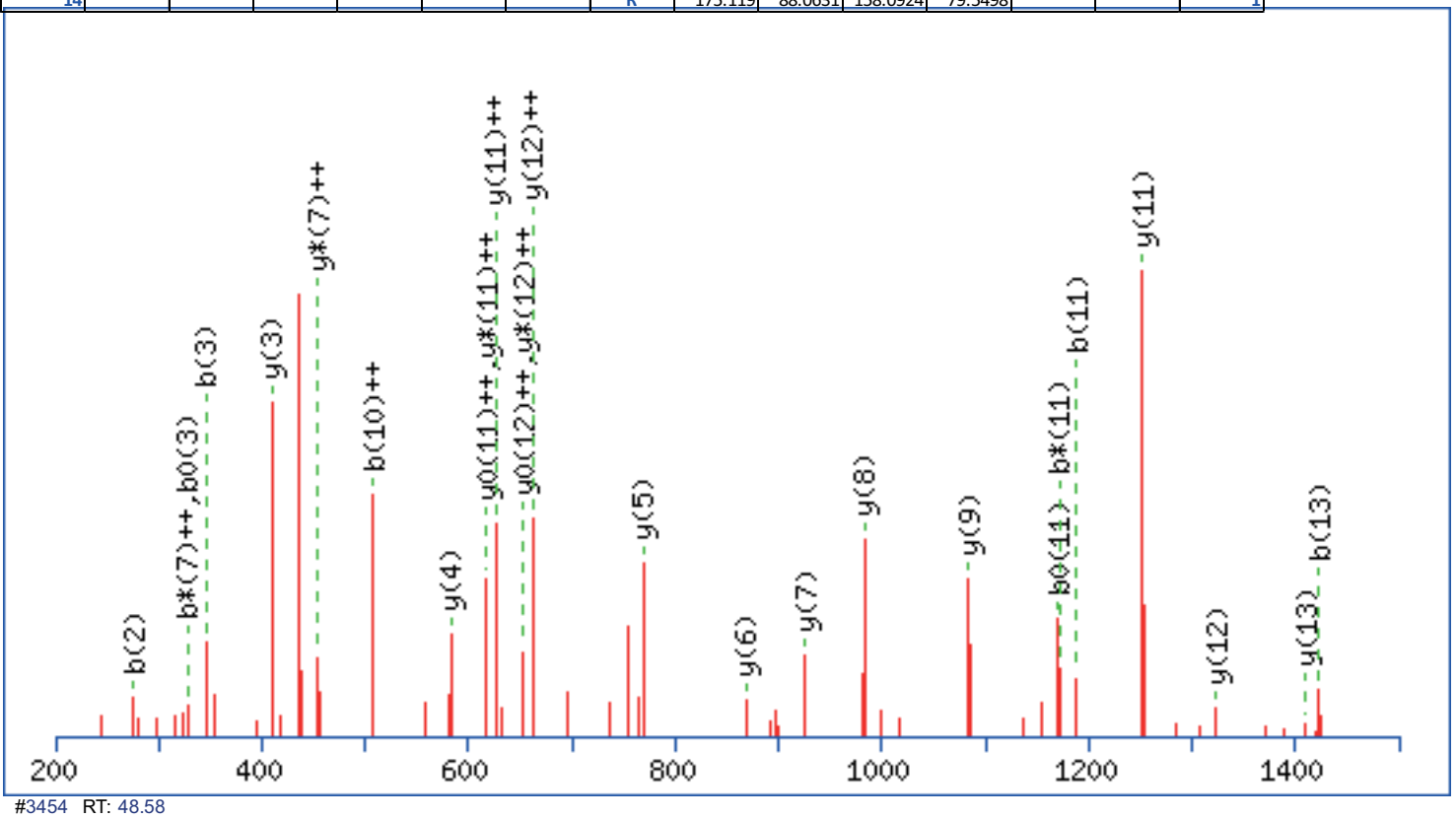
#2258 RT: 43.94
T: ITMS + c NSI d w Full ms2 783.47@cid35.00 [205.00-1580.00]



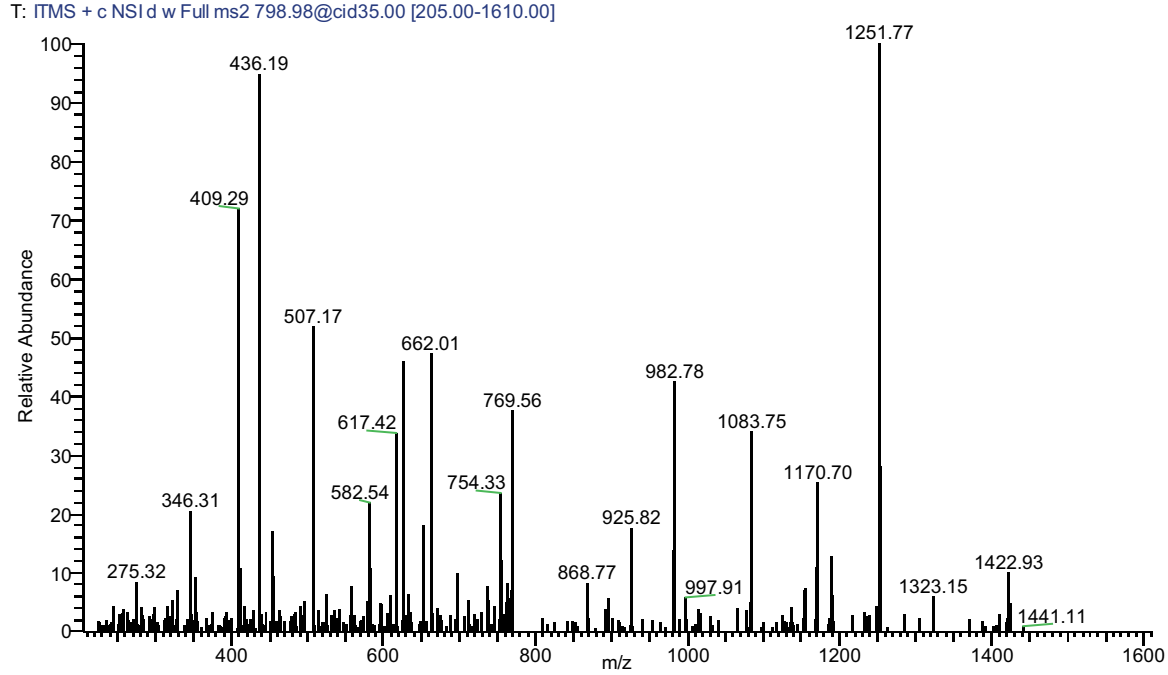
Match to Query 7041: 1595.947628 from(798.981090,2+)
1 cycles: 1 precIntensity: 1192017.5 FinneganScanNumber: 3454
Monoisotopic mass of neutral peptide Mr(calc): 1595.9457
Variable modifications:
K1 : Methyl+Acetyl:2H(3) (K)
K10 : Methyl+Acetyl:2H(3) (K)
K11 : Acetyl:2H(3) (K)
Ions Score: 70 Expect: 7e-07
Matches : 26/138 fragment ions using 36 most intense peaks

(27-40) H3:
K(me1)SAPATGGV**K(me1)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	188.1473	94.5773	171.1207	86.064			K							14
2	275.1793	138.0933	258.1528	129.58	257.1687	129.088	S	1409.813	705.4102	1392.787	696.8969	1391.803	696.4049	13
3	346.2164	173.6119	329.1899	165.0986	328.2059	164.6066	A	1322.781	661.8941	1305.755	653.3809	1304.77	652.8889	12
4	443.2692	222.1382	426.2426	213.625	425.2586	213.133	P	1251.744	626.3756	1234.717	617.8623	1233.733	617.3703	11
5	514.3063	257.6568	497.2798	249.1435	496.2957	248.6515	A	1154.691	577.8492	1137.665	569.3359	1136.681	568.8439	10
6	615.354	308.1806	598.3274	299.6674	597.3434	299.1753	T	1083.654	542.3306	1066.628	533.8174	1065.644	533.3254	9
7	672.3754	336.6914	655.3489	328.1781	654.3649	327.6861	G	982.6063	491.8068	965.5798	483.2935			8
8	729.3969	365.2021	712.3704	356.6888	711.3863	356.1968	G	925.5849	463.2961	908.5583	454.7828			7
9	828.4653	414.7363	811.4388	406.223	810.4548	405.731	V	868.5634	434.7853	851.5369	426.2721			6
10	1015.605	508.3063	998.5788	499.793	997.5948	499.301	K	769.495	385.2511	752.4684	376.7379			5
11	1188.73	594.8685	1171.703	586.3552	1170.719	585.8632	K	582.355	291.6811	565.3284	283.1679			4
12	1285.783	643.3949	1268.756	634.8816	1267.772	634.3896	P	409.2306	205.119	392.2041	196.6057			3
13	1422.841	711.9243	1405.815	703.411	1404.831	702.919	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



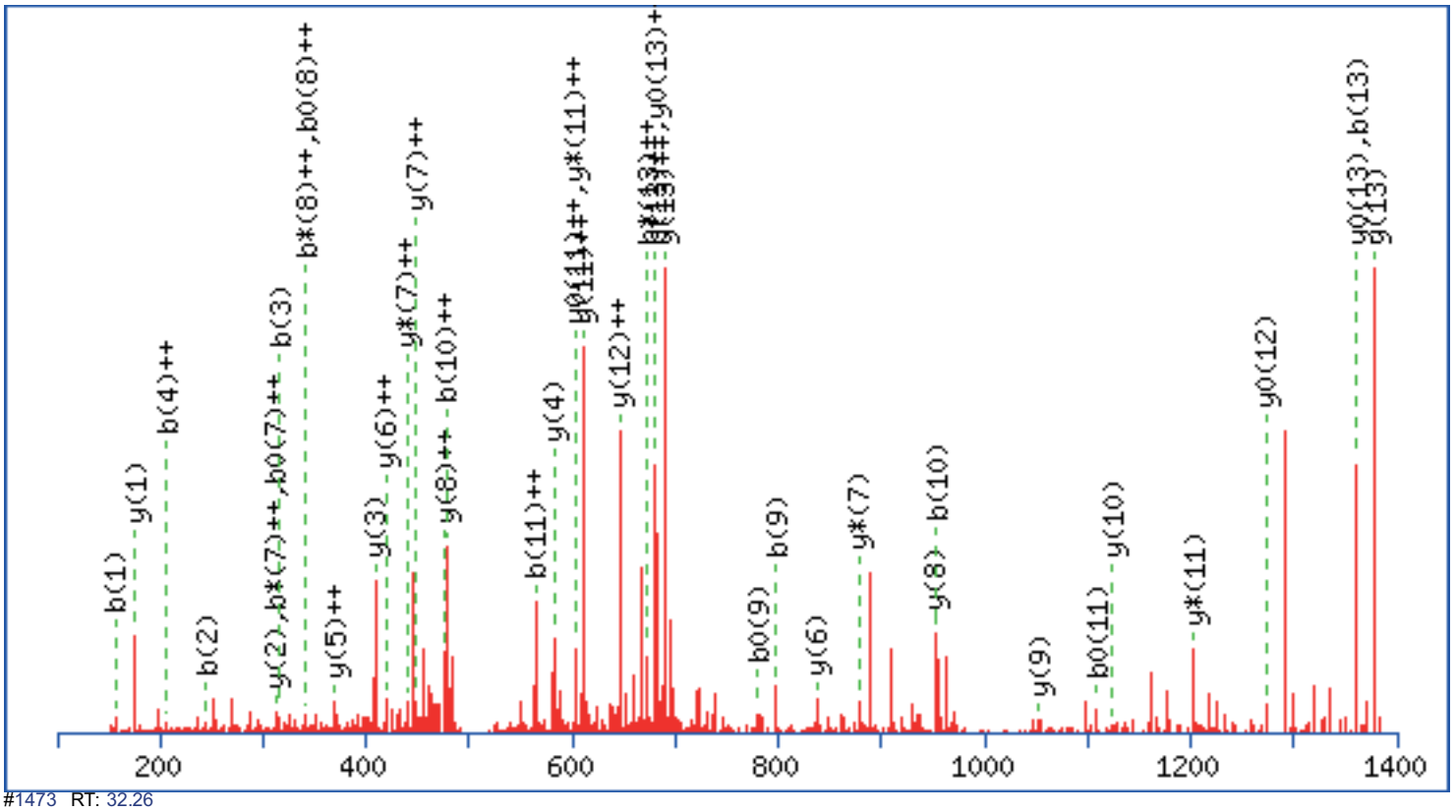
#3454 RT: 48.58
T: ITMS + c NSI d w Full ms2 798.98@cid35.00 [205.00-1610.00]



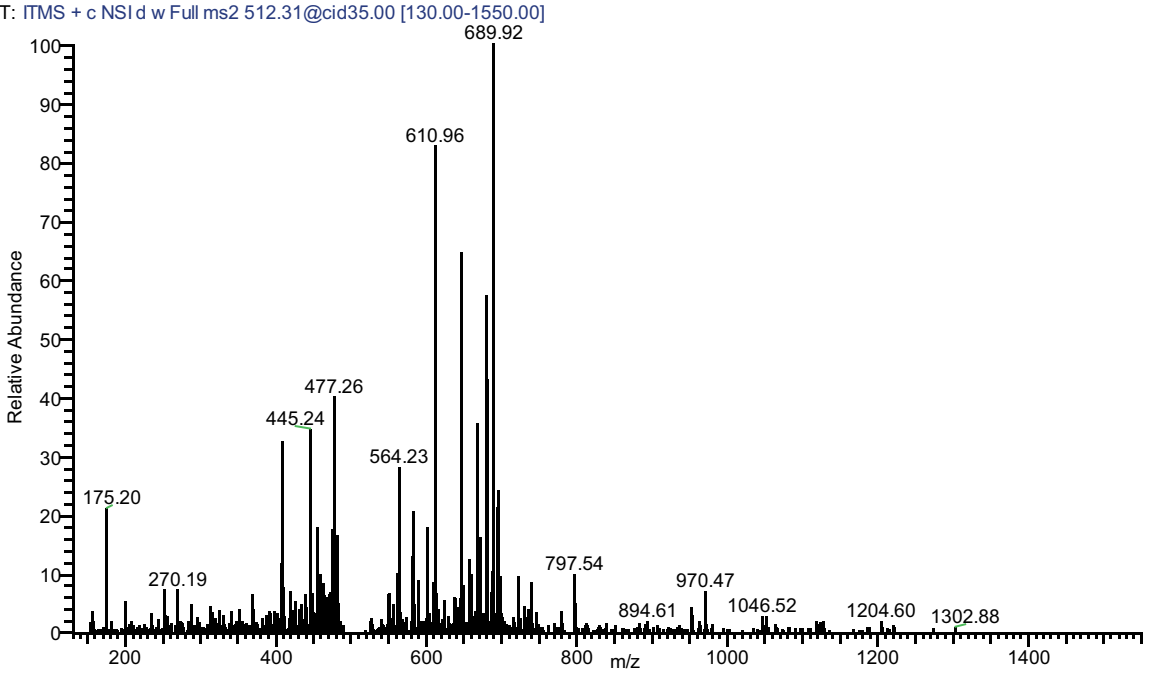
Match to Query 4665: 1533.913701 from(512.311843,3+)
1 cycles: 1 precIntensity: 487216.6 FinneganScanNumber: 1473
Monoisotopic mass of neutral peptide Mr(calc): 1533.9182
Variable modifications:
K1 : Dimethyl (K)
K10 : Dimethyl (K)
K11 : Acetyl:2H(3) (K)
Ions Score: 41 Expect: 0.00065
Matches : 43/138 fragment ions using 103 most intense peaks

(27-40) H3:
K(me2)SAPATGGV**K(me2)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.1335	79.0704	140.107	70.5571			K							14
2	244.1656	122.5864	227.139	114.0731	226.155	113.5811	S	1378.799	689.9033	1361.773	681.39	1360.789	680.898	13
3	315.2027	158.105	298.1761	149.5917	297.1921	149.0997	A	1291.767	646.3873	1274.741	637.874	1273.757	637.382	12
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	P	1220.73	610.8687	1203.704	602.3554	1202.72	601.8634	11
5	483.2926	242.1499	466.266	233.6366	465.282	233.1446	A	1123.677	562.3423	1106.651	553.8291	1105.667	553.337	10
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	T	1052.64	526.8238	1035.614	518.3105	1034.63	517.8185	9
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	G	951.5926	476.2999	934.566	467.7867			8
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	G	894.5711	447.7892	877.5446	439.2759			7
9	797.4516	399.2294	780.425	390.7162	779.441	390.2241	V	837.5497	419.2785	820.5231	410.7652			6
10	953.5778	477.2926	936.5513	468.7793	935.5673	468.2873	K	738.4812	369.7443	721.4547	361.231			5
11	1126.702	563.8547	1109.676	555.3415	1108.692	554.8495	K	582.355	291.6811	565.3284	283.1679			4
12	1223.755	612.3811	1206.728	603.8678	1205.744	603.3758	P	409.2306	205.119	392.2041	196.6057			3
13	1360.814	680.9106	1343.787	672.3973	1342.803	671.9053	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.119	88.0631	158.0924	79.5498			1



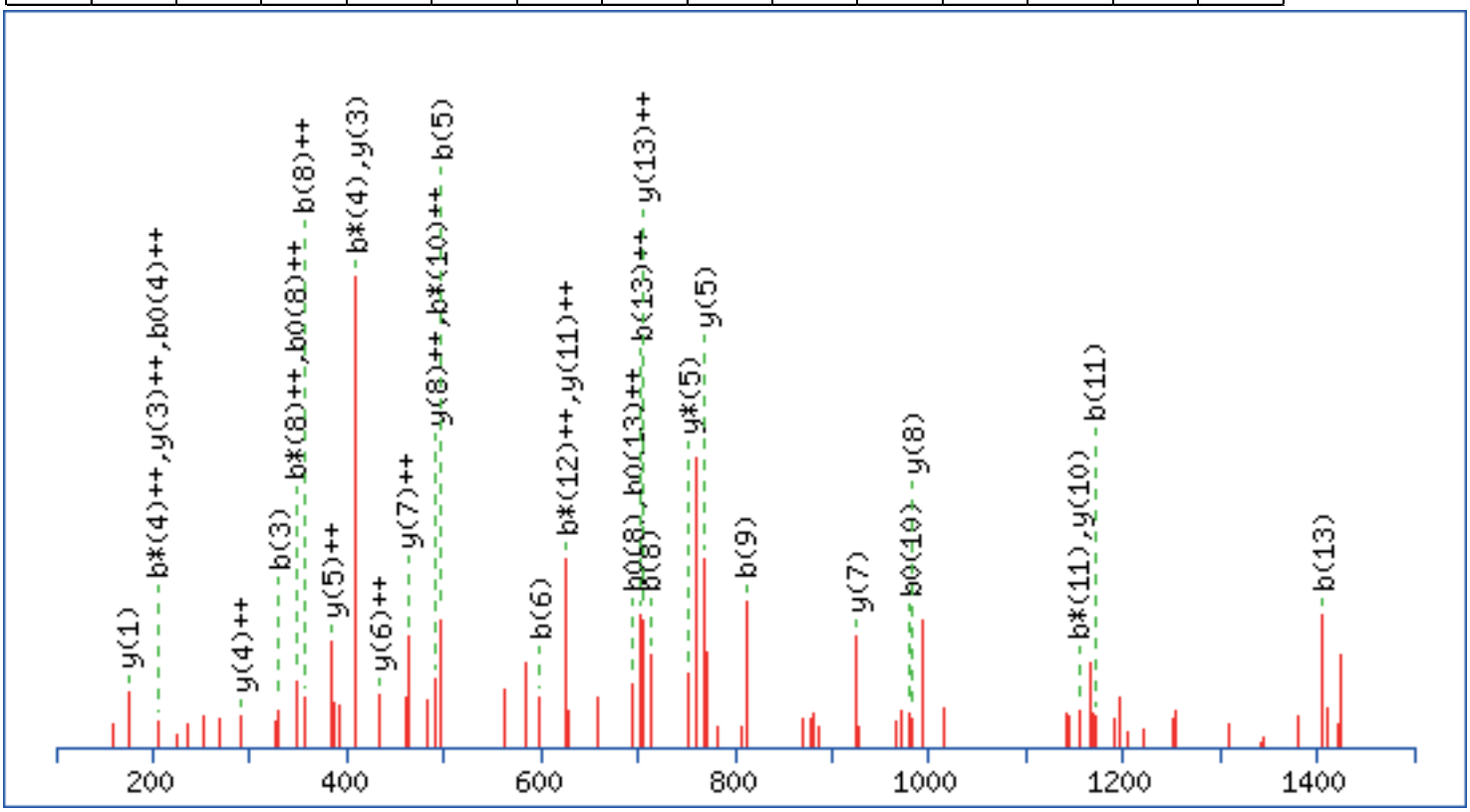
#1473 RT: 32.26
T: ITMS + c NSI d w Full ms2 512.31@cid35.00 [130.00-1550.00]



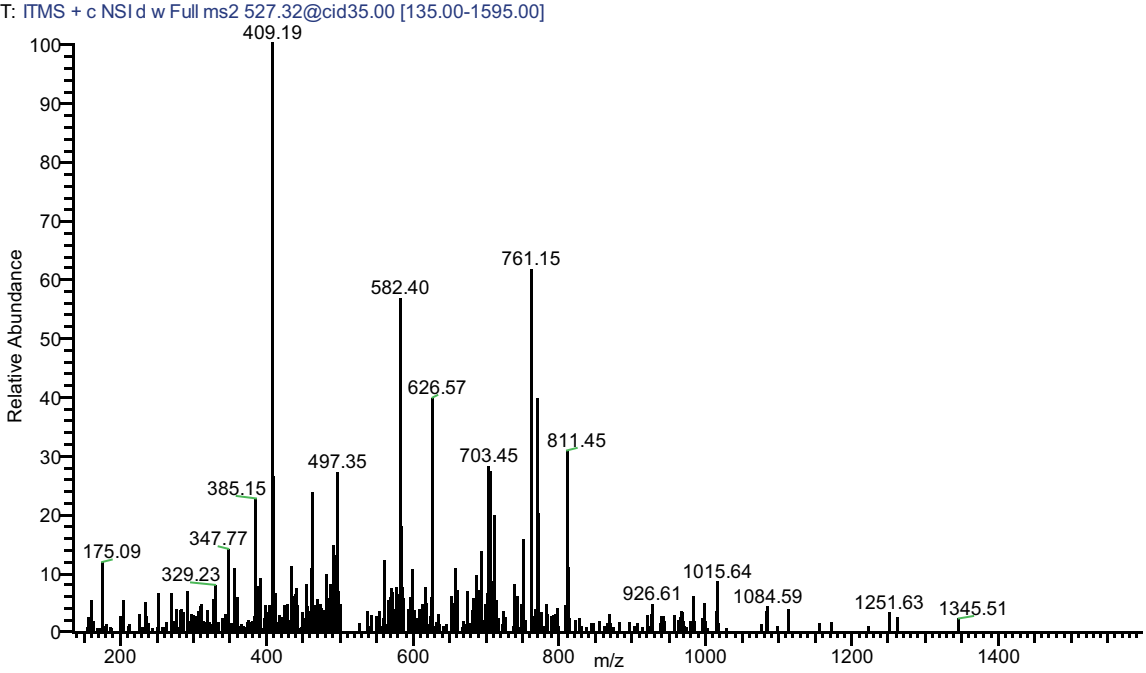
Match to Query 7219: 1578.946857 from(527.322895,3+)
1 cycles: 1 precIntensity: 6788125.4 FinneganScanNumber: 2819
Monoisotopic mass of neutral peptide Mr(calc): 1578.9476
Variable modifications:
K1 : Trimethyl (K)
K10 : Methyl+Acetyl:2H(3) (K)
K11 : Acetyl:2H(3) (K)
Ions Score: 35 Expect: 0.0088
Matches : 35/138 fragment ions using 61 most intense peaks

(27-40) H3:
K(me3)SAPATGGV**K(me1)**KPHR

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	171.1492	86.0782	154.1226	77.565			K							14
2	258.1812	129.5942	241.1547	121.081	240.1707	120.589	S	1409.813	705.4102	1392.787	696.8969	1391.803	696.4049	13
3	***329.2183***	165.1128	312.1918	156.5995	311.2078	156.1075	A	1322.781	661.8941	1305.755	653.3809	1304.77	652.8889	12
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	P	1251.744	626.3756	1234.717	617.8623	1233.733	617.3703	11
5	***497.3082***	249.1577	480.2817	240.6445	479.2976	240.1525	A	**1154.691**	577.8492	1137.665	569.3359	1136.681	568.8439	10
6	***598.3559***	299.6816	581.3293	291.1683	580.3453	290.6763	T	1083.654	542.3306	1066.628	533.8174	1065.644	533.3254	9
7	655.3774	328.1923	638.3508	319.679	637.3668	319.187	G	**982.6063**	491.8068	965.5798	483.2935			8
8	***712.3988***	356.703	695.3723	348.1898	694.3883	347.6978	G	**925.5849**	463.2961	908.5583	454.7828			7
9	***811.4672***	406.2373	794.4407	397.724	793.4567	397.232	V	868.5634	434.7853	851.5369	426.2721			6
10	998.6072	499.8073	981.5807	491.294	980.5967	490.802	K	**769.495**	385.2511	752.4684	376.7379			5
11	***1171.732***	586.3694	1154.705	577.8562	1153.721	577.3642	K	582.355	291.6811	565.3284	283.1679			4
12	1268.784	634.8958	1251.758	626.3825	1250.774	625.8905	P	**409.2306**	205.119	392.2041	196.6057			3
13	***1405.843***	703.4253	1388.817	694.912	1387.833	694.42	H	312.1779	156.5926	295.1513	148.0793			2
14							R	**175.119**	88.0631	158.0924	79.5498			1



#2819 RT: 39.31
T: ITMS + c NSI d w Full ms2 527.32@cid35.00 [135.00-1595.00]

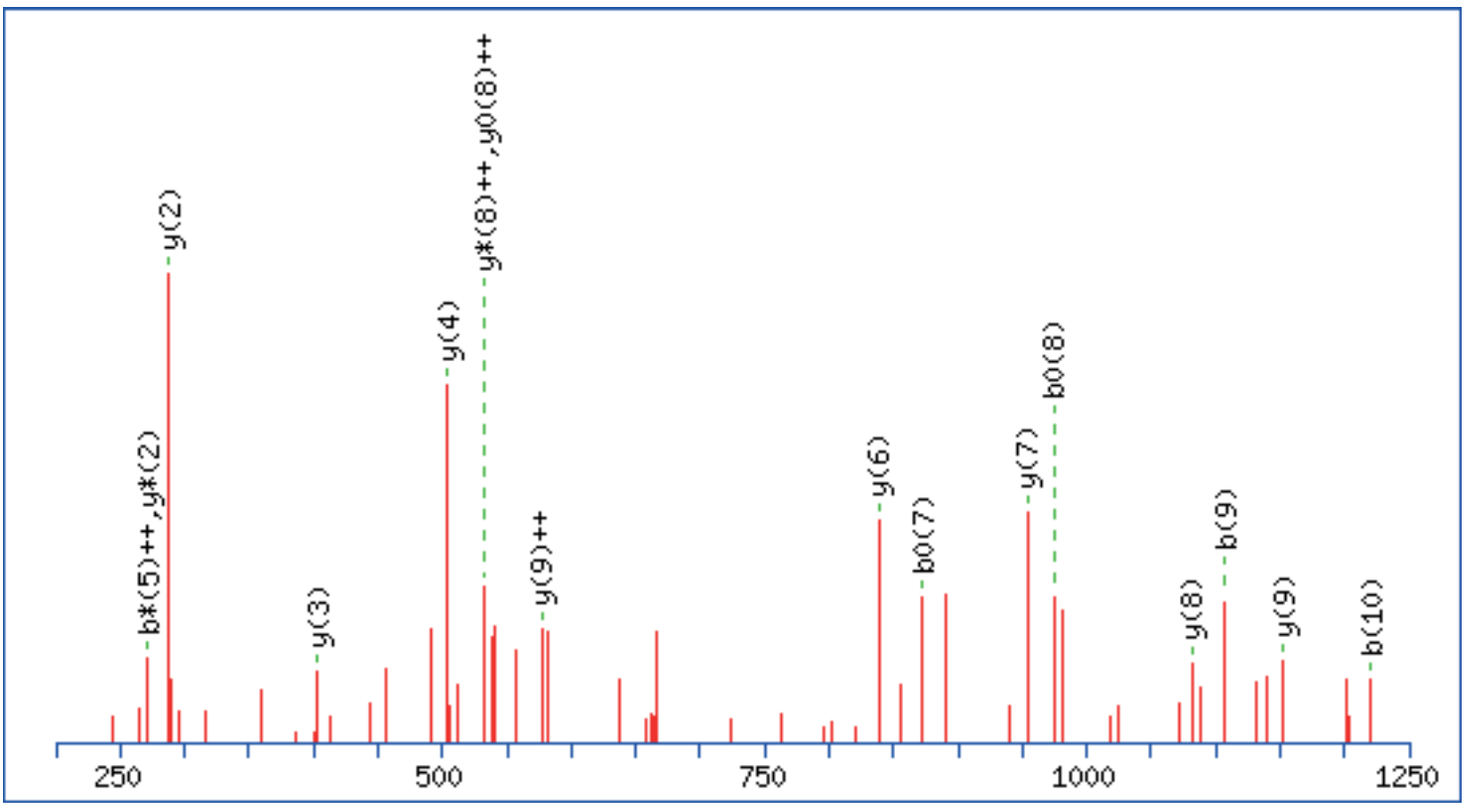


Match to Query 5712: 1393.732630 from(697.873591,2+)
1 cycles: 1 precIntensity: 326052.5 FinneganScanNumber: 6769

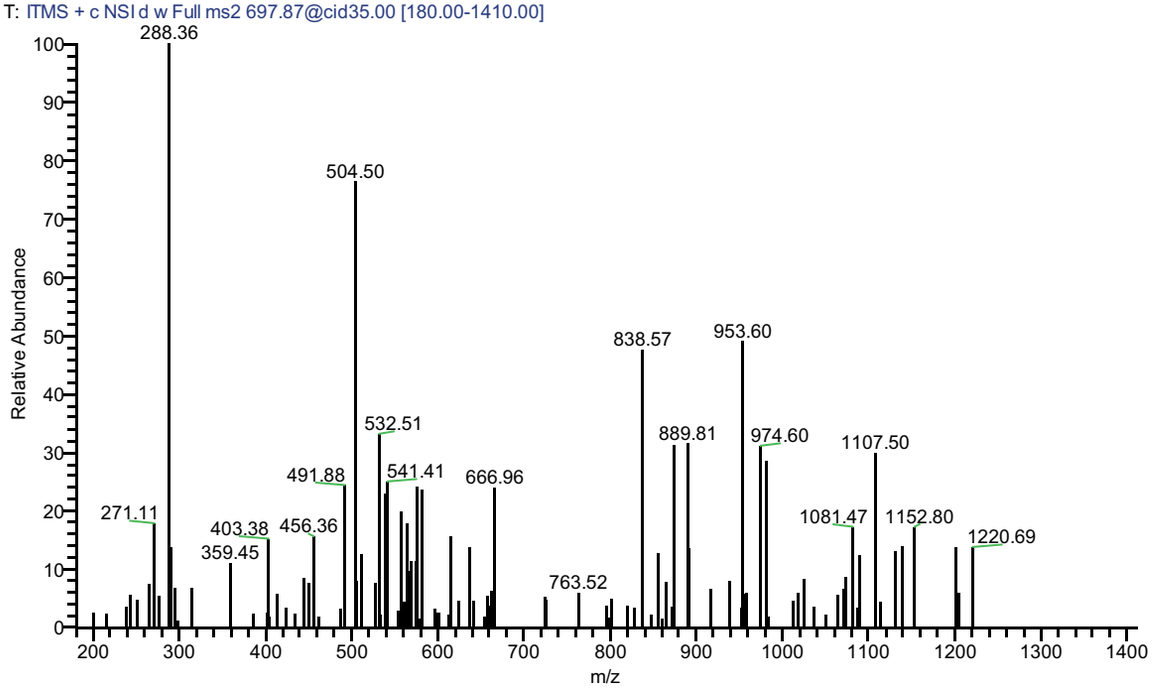
(73-83) H3:
EIAQDF**K(me1)**TDLR

Monoisotopic mass of neutral peptide Mr(calc): 1393.7281
Variable modifications:
K7 : Methyl+Acetyl:2H(3) (K)
Ions Score: 49 Expect: 0.00047
Matches : 16/110 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	130.0499	65.5286			112.0393	56.5233	E							11
2	243.1339	122.0706			225.1234	113.0653	I	1265.693	633.35	1248.666	624.8367	1247.682	624.3447	10
3	314.171	157.5892			296.1605	148.5839	A	***1152.609***	576.808	1135.582	568.2947	1134.598	567.8027	9
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	Q	***1081.572***	541.2894	1064.545	532.7762	1063.561	532.2841	8
5	557.2566	279.1319	540.23	270.6186	539.246	270.1266	D	***953.513***	477.2601	936.4865	468.7469	935.5024	468.2549	7
6	704.325	352.6661	687.2984	344.1529	686.3144	343.6608	F	***838.4861***	419.7467	821.4595	411.2334	820.4755	410.7414	6
7	891.465	446.2361	874.4384	437.7229	873.4544	437.2309	K	691.4176	346.2125	674.3911	337.6992	673.4071	337.2072	5
8	992.5127	496.76	975.4861	488.2467	974.5021	487.7547	T	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
9	1107.54	554.2734	1090.513	545.7602	1089.529	545.2682	D	***403.23***	202.1186	386.2034	193.6053	385.2194	193.1133	3
10	1220.624	610.8155	1203.597	602.3022	1202.613	601.8102	L	***288.203***	144.6051	271.1765	136.0919			2
11							R	175.119	88.0631	158.0924	79.5498			1



#6769 RT: 79.31
T: ITMS + c NSI d w Full ms2 697.87@cid35.00 [180.00-1410.00]

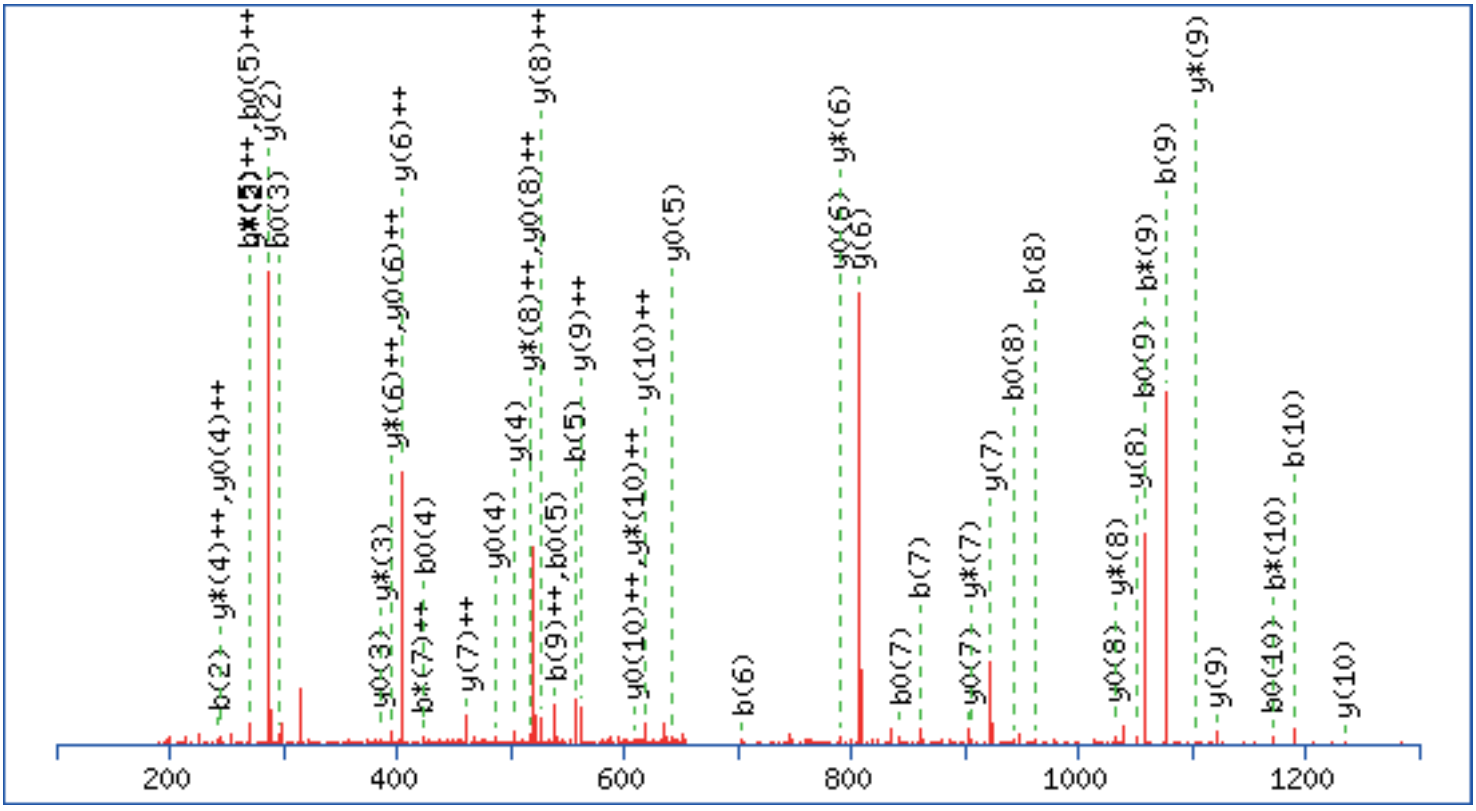


Match to Query 3954: 1362.710200 from(682.362376,2+)
1 cycles: 1 precIntensity: 24651262.1 FinneganScanNumber: 3300

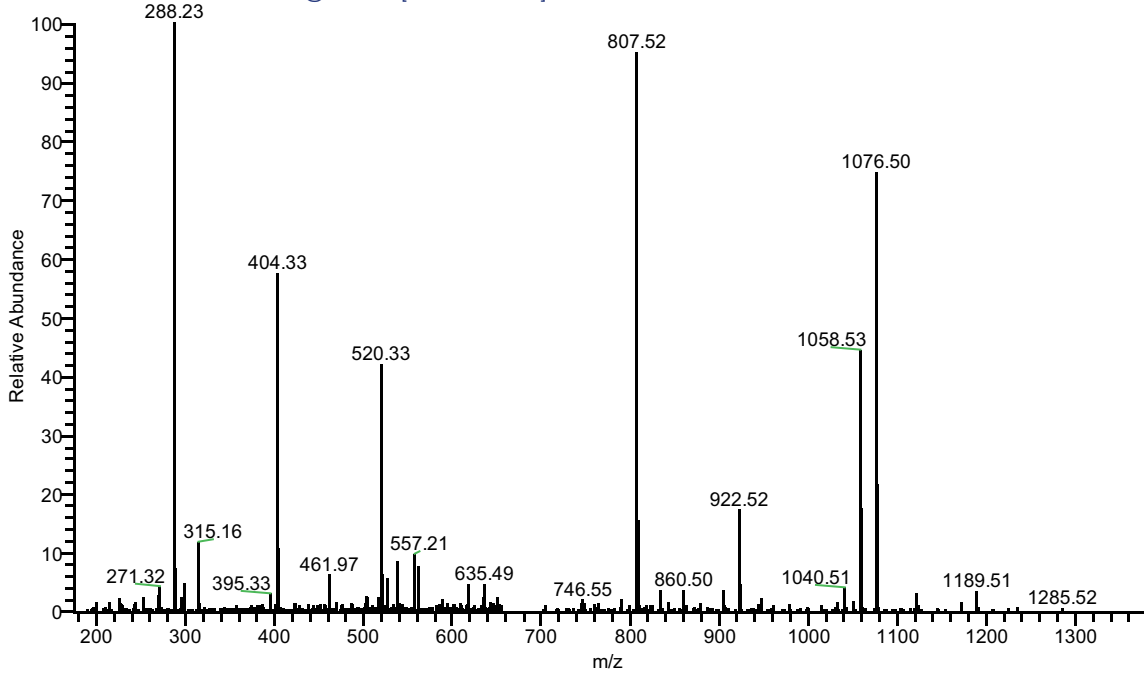
(73-83) H3:
EIAQDF**K(me2)**TDLR

Monoisotopic mass of neutral peptide Mr(calc): 1362.7143
Variable modifications:
K7 : Dimethyl (K)
Ions Score: 32 Expect: 0.0096
Matches : 52/110 fragment ions using 105 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	***243.1339***	122.0706			225.1234	113.0653	I	***1234.679***	617.8431	1217.653	609.3299	1216.668	608.8379	10
3	314.171	157.5892			296.1605	148.5839	A	***1121.595***	561.3011	1104.568	552.7878	1103.584	552.2958	9
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	Q	***1050.558***	525.7826	1033.531	517.2693	1032.547	516.7773	8
5	***557.2566***	279.1319	540.23	270.6186	539.246	270.1266	D	***922.4993***	461.7533	905.4727	453.24	904.4887	452.748	7
6	***704.325***	352.6661	687.2984	344.1529	686.3144	343.6608	F	***807.4723***	404.2398	790.4458	395.7265	789.4617	395.2345	6
7	***860.4512***	430.7293	843.4247	422.216	842.4407	421.724	K	660.4039	330.7056	643.3774	322.1923	642.3933	321.7003	5
8	***961.4989***	481.2531	944.4724	472.7398	943.4884	472.2478	T	***504.2776***	252.6425	487.2511	244.1292	486.2671	243.6372	4
9	***1076.526***	538.7666	1059.499	530.2533	1058.515	529.7613	D	403.23	202.1186	386.2034	193.6053	385.2194	193.1133	3
10	***1189.61***	595.3086	1172.583	586.7953	1171.599	586.3033	L	***288.203***	144.6051	271.1765	136.0919			2
11							R	175.119	88.0631	158.0924	79.5498			1



#3300 RT: 55.26
T: ITMS + c NSI d w Full ms2 682.37@cid35.00 [175.00-1375.00]

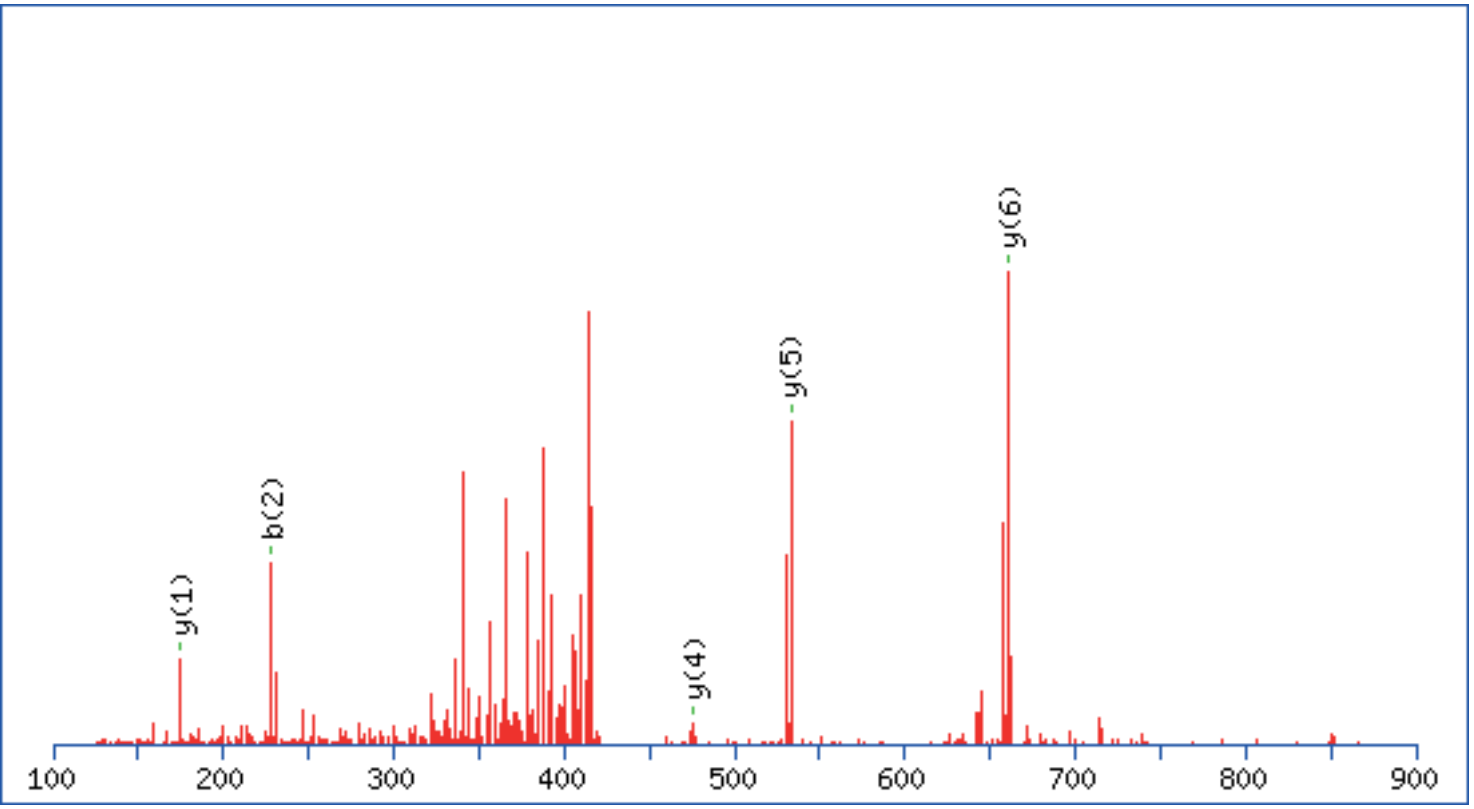


Match to Query 2358: 887.503504 from(444.759028,2+)
1 cycles: 1 precIntensity: 1832389.1 FinneganScanNumber: 680

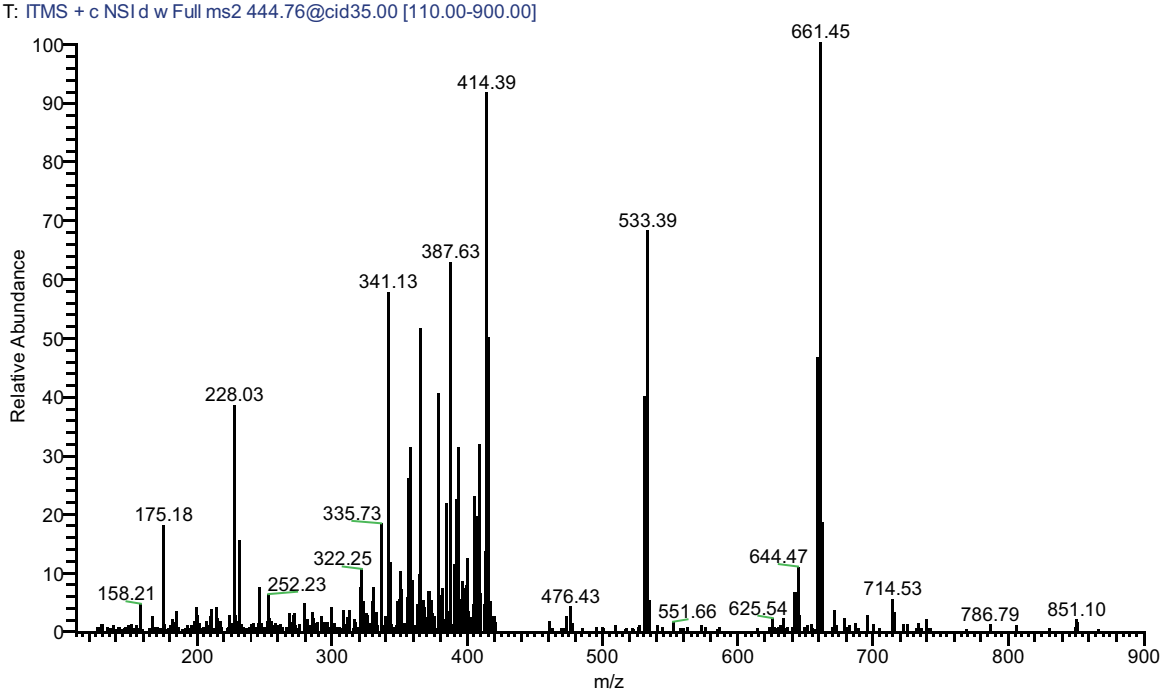
(4-11) H2A:
G**K(Ac)**QGGKAR

Monoisotopic mass of neutral peptide Mr(calc): 887.5016
Variable modifications:
K2 : Acetyl (K)
K6 : Acetyl:2H(3) (K)
Ions Score: 22 Expect: 0.071
Matches : 5/54 fragment ions using 8 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.518			G					8
2	228.1343	114.5708	211.1077	106.0575	K	831.4875	416.2474	814.4609	407.7341	7
3	356.1928	178.6001	339.1663	170.0868	Q	***661.3819***	331.1946	644.3554	322.6813	6
4	413.2143	207.1108	396.1878	198.5975	G	***533.3234***	267.1653	516.2968	258.652	5
5	470.2358	235.6215	453.2092	227.1083	G	***476.3019***	238.6546	459.2753	230.1413	4
6	643.3601	322.1837	626.3336	313.6704	K	419.2804	210.1438	402.2539	201.6306	3
7	714.3972	357.7023	697.3707	349.189	A	246.1561	123.5817	229.1295	115.0684	2
8					R	***175.119***	88.0631	158.0924	79.5498	1



#680 RT: 25.99
T: ITMS + c NSI d w Full ms2 444.76@cid35.00 [110.00-900.00]

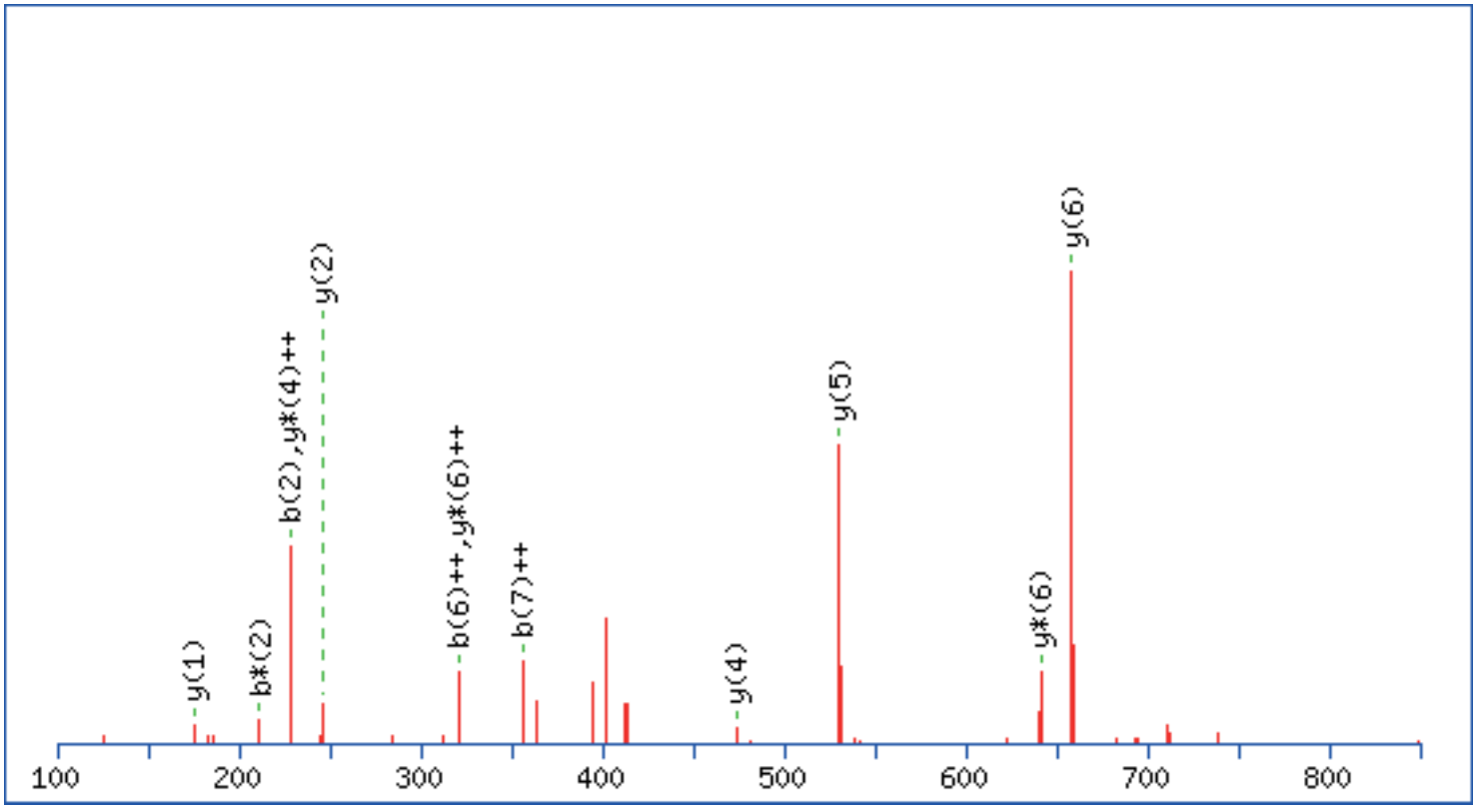


Match to Query 4588: 884.485432 from(443.249992,2+)
1 cycles: 1 precIntensity: 175756.1 FinneganScanNumber: 918

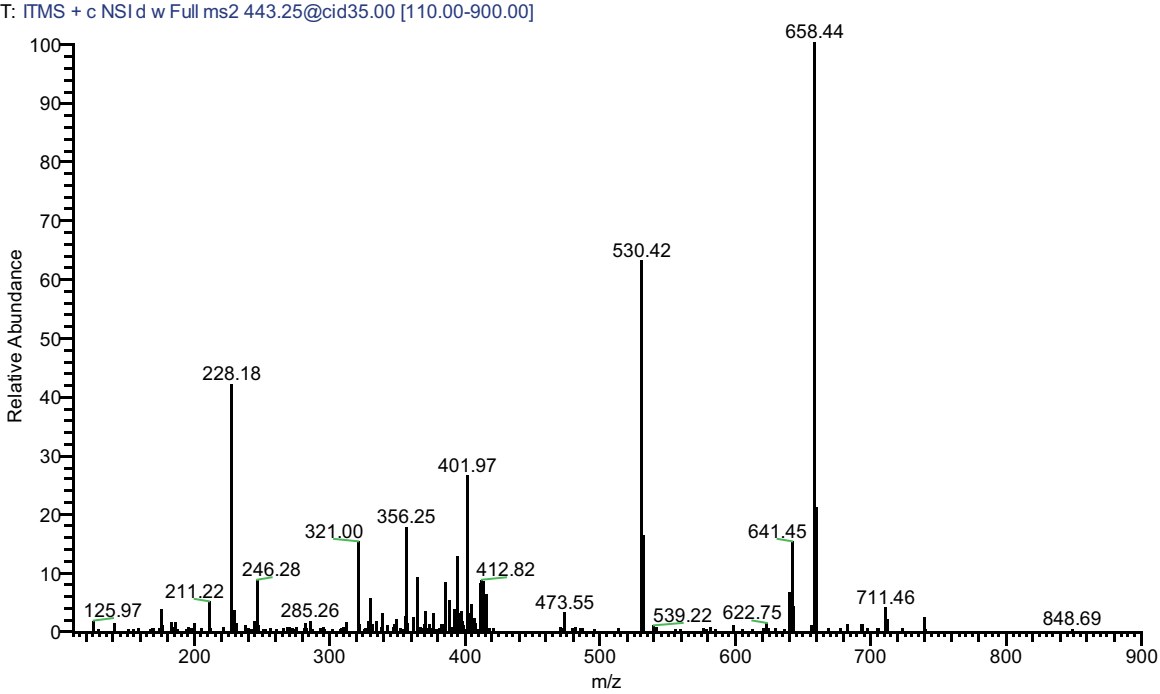
(4-11) H2A:
G**K(Ac)**QGG**K(Ac)**AR

Monoisotopic mass of neutral peptide Mr(calc): 884.4828
Variable modifications:
K2 : Acetyl (K)
K6 : Acetyl (K)
Ions Score: 32 Expect: 0.0048
Matches : 13/54 fragment ions using 19 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.518			G					8
2	**228.1343**	114.5708	211.1077	106.0575	K	828.4686	414.738	811.4421	406.2247	7
3	**356.1928**	178.6001	339.1663	170.0868	Q	***658.3631***	329.6852	641.3366	321.1719	6
4	413.2143	207.1108	396.1878	198.5975	G	***530.3045***	265.6559	513.278	257.1426	5
5	470.2358	235.6215	453.2092	227.1083	G	***473.2831***	237.1452	456.2565	228.6319	4
6	640.3413	**320.6743**	623.3148	312.161	K	416.2616	208.6344	399.235	200.1212	3
7	711.3784	**356.1928**	694.3519	347.6796	A	***246.1561***	123.5817	229.1295	115.0684	2
8					R	***175.119***	88.0631	158.0924	79.5498	1



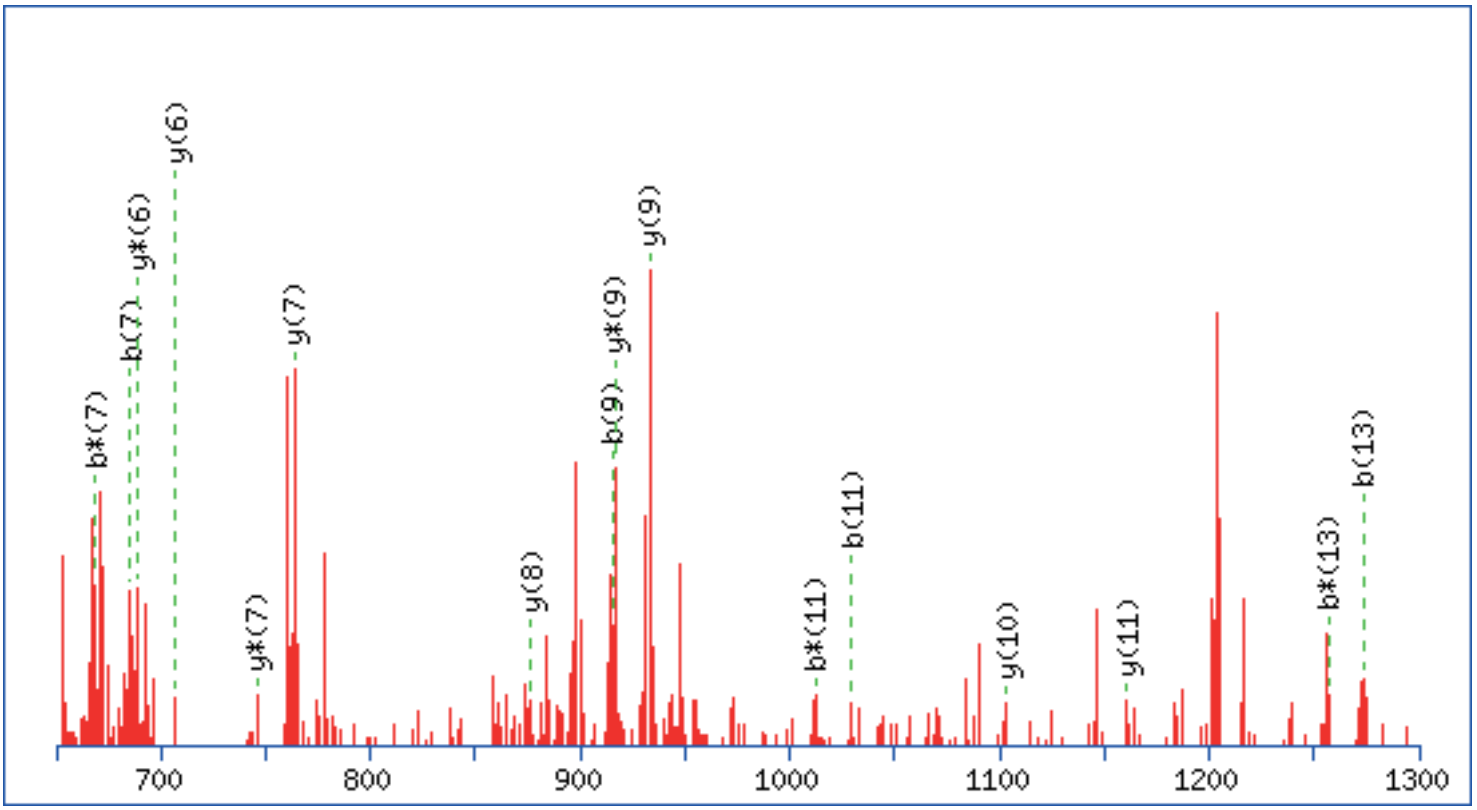
#918 RT: 25.87
T: ITMS + c NSI d w Full ms2 443.25@cid35.00 [110.00-900.00]



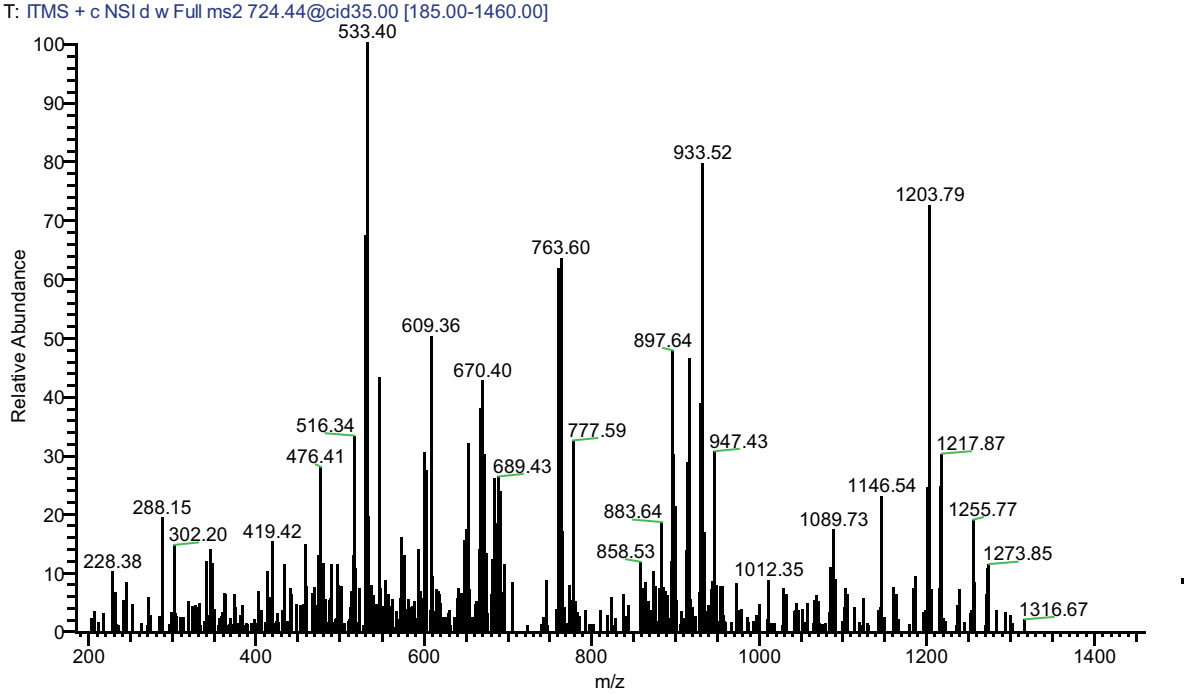
Match to Query 10349: 1446.860830 from(724.437691,2+)
1 cycles: 1 precIntensity: 869333.4 FinneganScanNumber: 4119
Monoisotopic mass of neutral peptide Mr(calc): 1446.8617
Variable modifications:
K2 : Acetyl:2H(3) (K) K9 : Acetyl:2H(3) (K)
K5 : Acetyl (K) K13 : Acetyl:2H(3) (K)
Ions Score: 32 Expect: 0.0017
Matches : 33/102 fragment ions using 101 most intense peaks

(4-17) H4:
GKGG**K(Ac)**GLGKGGAKR

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	58.0287	29.518			G					14
2	***231.1531***	116.0802	214.1265	107.5669	K	1390.848	695.9274	1373.821	687.4141	13
3	***288.1746***	144.5909	271.148	136.0776	G	1217.723	609.3652	1200.697	600.8519	12
4	***345.196***	173.1017	328.1695	164.5884	G	***1160.702***	580.8545	1143.675	572.3412	11
5	515.3016	258.1544	498.275	249.6411	K	***1103.68***	552.3438	1086.654	543.8305	10
6	572.323	286.6651	555.2965	278.1519	G	***933.5747***	467.291	916.5482	458.7777	9
7	***685.4071***	343.2072	668.3805	334.6939	L	***876.5532***	438.7803	859.5267	430.267	8
8	742.4285	371.7179	725.402	363.2046	G	***763.4692***	382.2382	746.4426	373.725	7
9	***915.5529***	458.2801	898.5264	449.7668	K	***706.4477***	353.7275	689.4212	345.2142	6
10	972.5744	486.7908	955.5478	478.2775	G	***533.3234***	267.1653	516.2968	258.652	5
11	***1029.596***	515.3016	1012.569	506.7883	G	***476.3019***	238.6546	459.2753	230.1413	4
12	1100.633	550.8201	1083.606	542.3068	A	***419.2804***	210.1438	402.2539	201.6306	3
13	***1273.757***	637.3823	1256.731	628.869	K	***348.2433***	174.6253	331.2168	166.112	2
14					R	175.119	88.0631	158.0924	79.5498	1



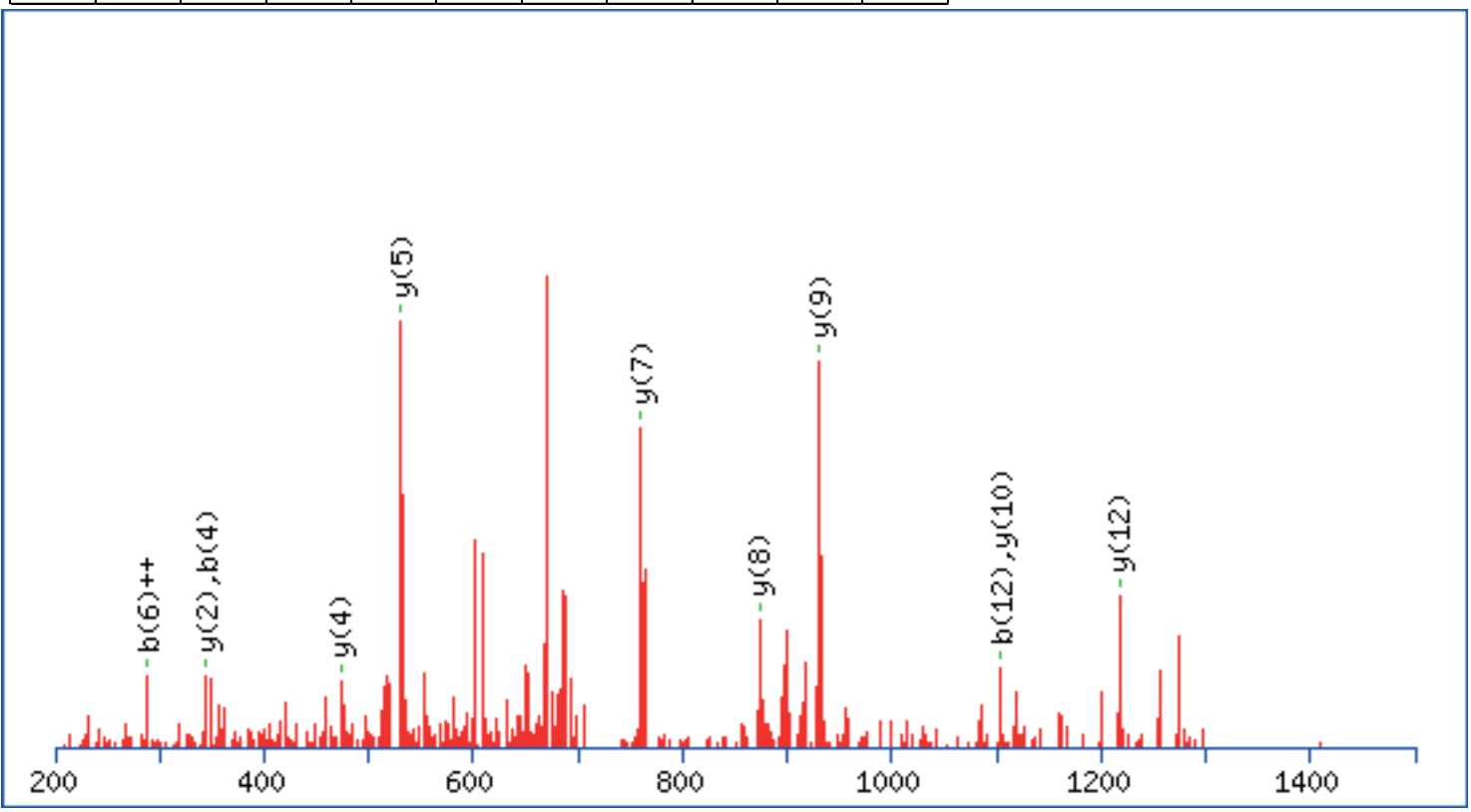
#4119 RT: 52.44
T: ITMS + c NSI d w Full ms2 724.44@cid35.00 [185.00-1460.00]



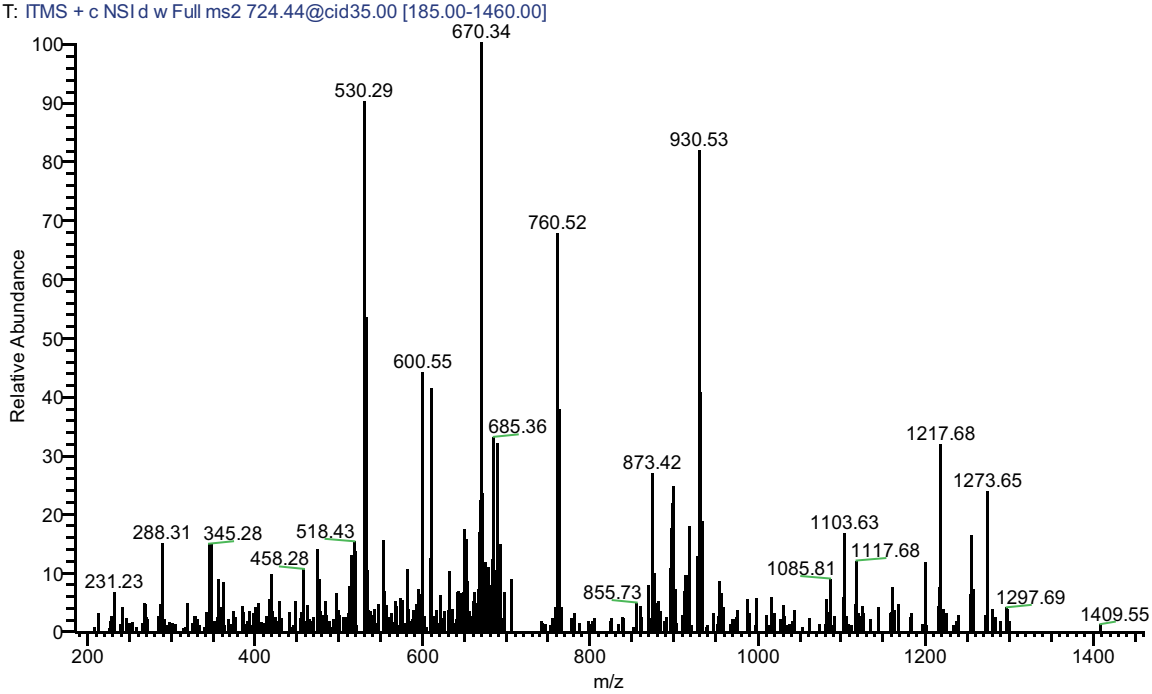
Match to Query 10342: 1446.853114 from(724.433833,2+)
1 cycles: 1 precIntensity: 681329894.1 FinneganScanNumber: 3810
Monoisotopic mass of neutral peptide Mr(calc): 1446.8617
Variable modifications:
K2 : Acetyl:2H(3) (K) K9 : Acetyl:2H(3) (K)
K5 : Acetyl:2H(3) (K) K13 : Acetyl (K)
Ions Score: 65 Expect: 3.1e-06
Matches : 12/102 fragment ions using 12 most intense peaks

(4-17) H4:
GKGGKGLGKGGA**K(Ac)**R

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.518			G					14
2	231.1531	116.0802	214.1265	107.5669	K	1390.848	695.9274	1373.821	687.4141	13
3	288.1746	144.5909	271.148	136.0776	G	1217.723	609.3652	1200.697	600.8519	12
4	345.196	173.1017	328.1695	164.5884	G	1160.702	580.8545	1143.675	572.3412	11
5	518.3204	259.6638	501.2938	251.1506	K	1103.68	552.3438	1086.654	543.8305	10
6	575.3418	288.1746	558.3153	279.6613	G	930.5559	465.7816	913.5293	457.2683	9
7	688.4259	344.7166	671.3994	336.2033	L	873.5344	437.2708	856.5079	428.7576	8
8	745.4474	373.2273	728.4208	364.7141	G	760.4503	380.7288	743.4238	372.2155	7
9	918.5717	459.7895	901.5452	451.2762	K	703.4289	352.2181	686.4023	343.7048	6
10	975.5932	488.3002	958.5666	479.787	G	530.3045	265.6559	513.278	257.1426	5
11	1032.615	516.811	1015.588	508.2977	G	473.2831	237.1452	456.2565	228.6319	4
12	1103.652	552.3295	1086.625	543.8163	A	416.2616	208.6344	399.235	200.1212	3
13	1273.757	637.3823	1256.731	628.869	K	345.2245	173.1159	328.1979	164.6026	2
14					R	175.119	88.0631	158.0924	79.5498	1



#3810 RT: 50.17
T: ITMS + c NSI d w Full ms2 724.44@cid35.00 [185.00-1460.00]



Match to Query 7926: 1443.829152 from(722.921852,2+)

1 cycles: 1 precIntensity: 2228569.7 FinneganScanNumber: 6133

Monoisotopic mass of neutral peptide Mr(calc): 1443.8428

Variable modifications:

K2 : Acetyl (K) K9 : Acetyl:2H(3) (K)

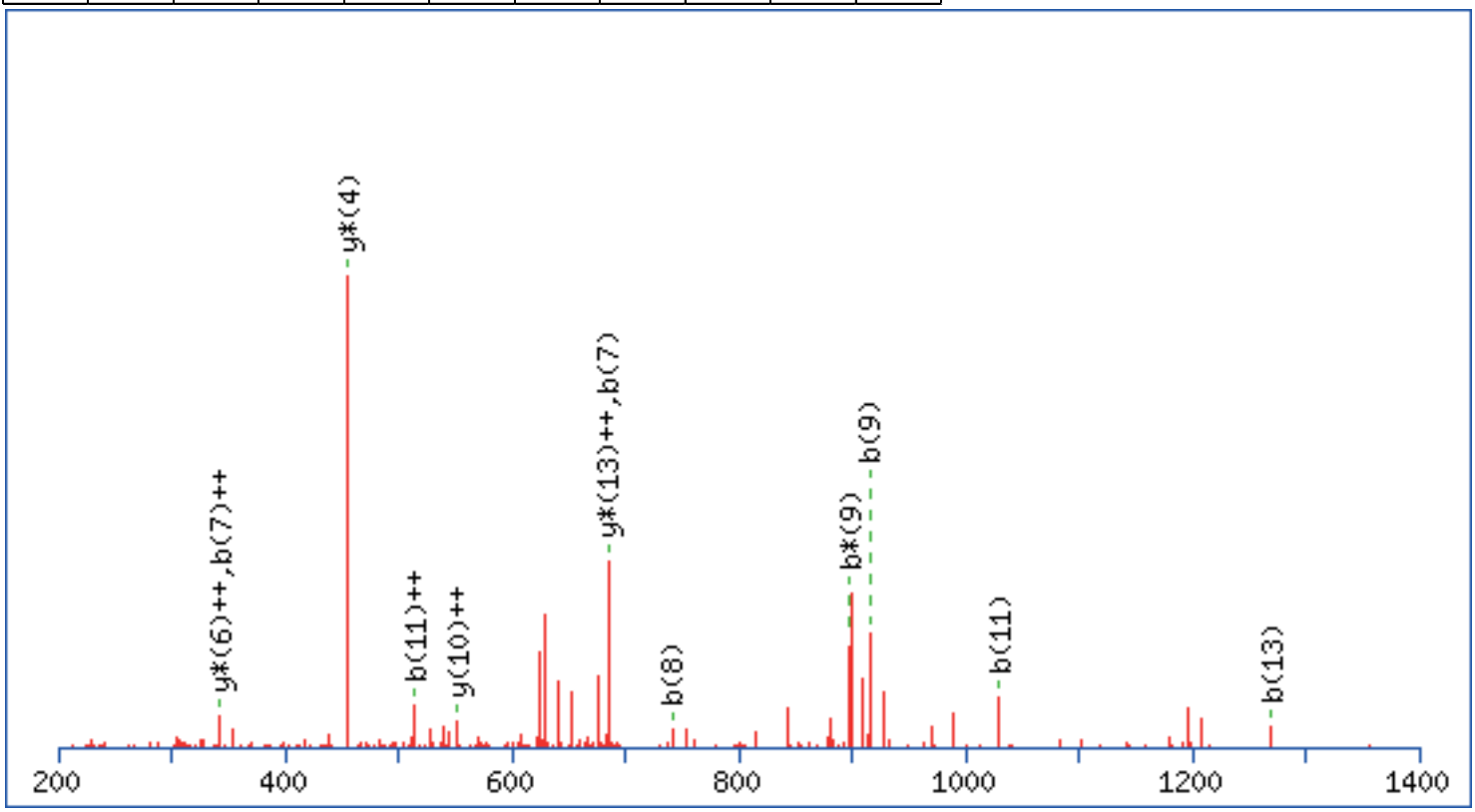
K5 : Acetyl:2H(3) (K) K13 : Acetyl (K)

Ions Score: 21 Expect: 0.05

Matches : 13/102 fragment ions using 23 most intense peaks

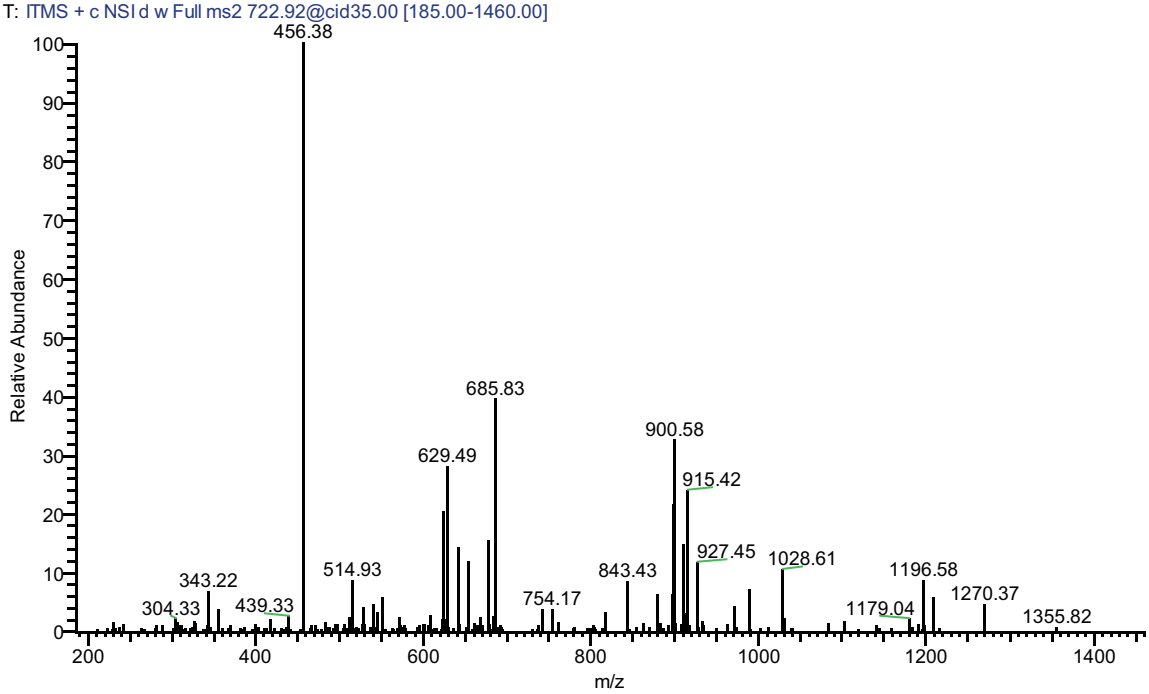
(4-17) H4: G**K(Ac)**GGKGLGKGGA**K(Ac)**R

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.518			G					14
2	228.1343	114.5708	211.1077	106.0575	K	1387.829	694.418	1370.802	685.9047	13
3	285.1557	143.0815	268.1292	134.5682	G	1217.723	609.3652	1200.697	600.8519	12
4	342.1772	171.5922	325.1506	163.079	G	1160.702	580.8545	1143.675	572.3412	11
5	***515.3016***	258.1544	498.275	249.6411	K	1103.68	552.3438	1086.654	543.8305	10
6	572.323	286.6651	555.2965	278.1519	G	930.5559	465.7816	913.5293	457.2683	9
7	***685.4071***	**343.2072**	668.3805	334.6939	L	873.5344	437.2708	856.5079	428.7576	8
8	***742.4285***	371.7179	725.402	363.2046	G	760.4503	380.7288	743.4238	372.2155	7
9	***915.5529***	458.2801	898.5264	449.7668	K	703.4289	352.2181	686.4023	343.7048	6
10	972.5744	486.7908	955.5478	478.2775	G	530.3045	265.6559	513.278	257.1426	5
11	***1029.596***	**515.3016**	1012.569	506.7883	G	473.2831	237.1452	456.2565	228.6319	4
12	1100.633	550.8201	1083.606	542.3068	A	416.2616	208.6344	399.235	200.1212	3
13	***1270.739***	635.8729	1253.712	627.3596	K	345.2245	173.1159	328.1979	164.6026	2
14					R	175.119	88.0631	158.0924	79.5498	



#6133 RT: 72.93 AV: 1

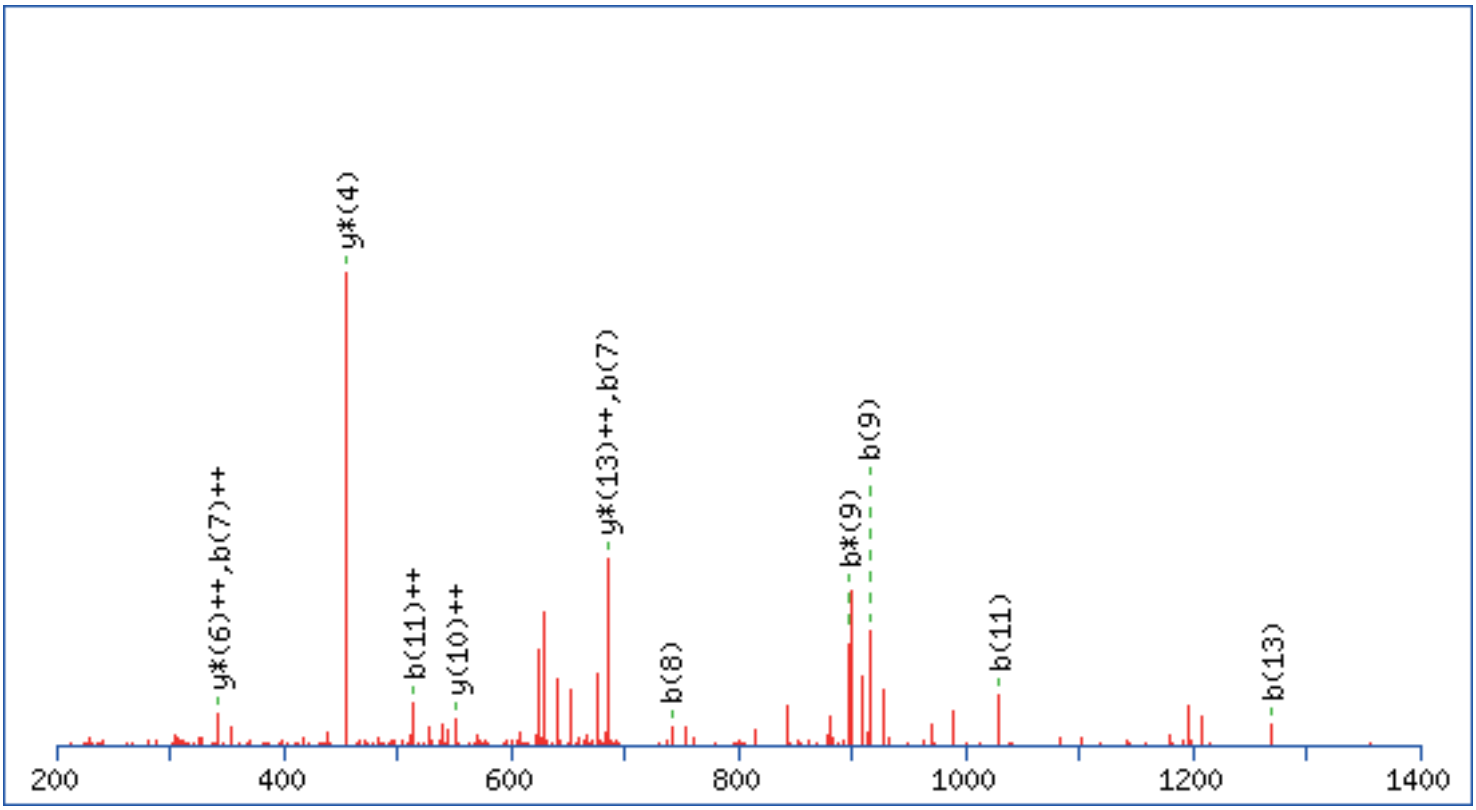
T: ITMS + c NSI d w Full ms2 722.92@cid35.00 [185.00-1460.00]



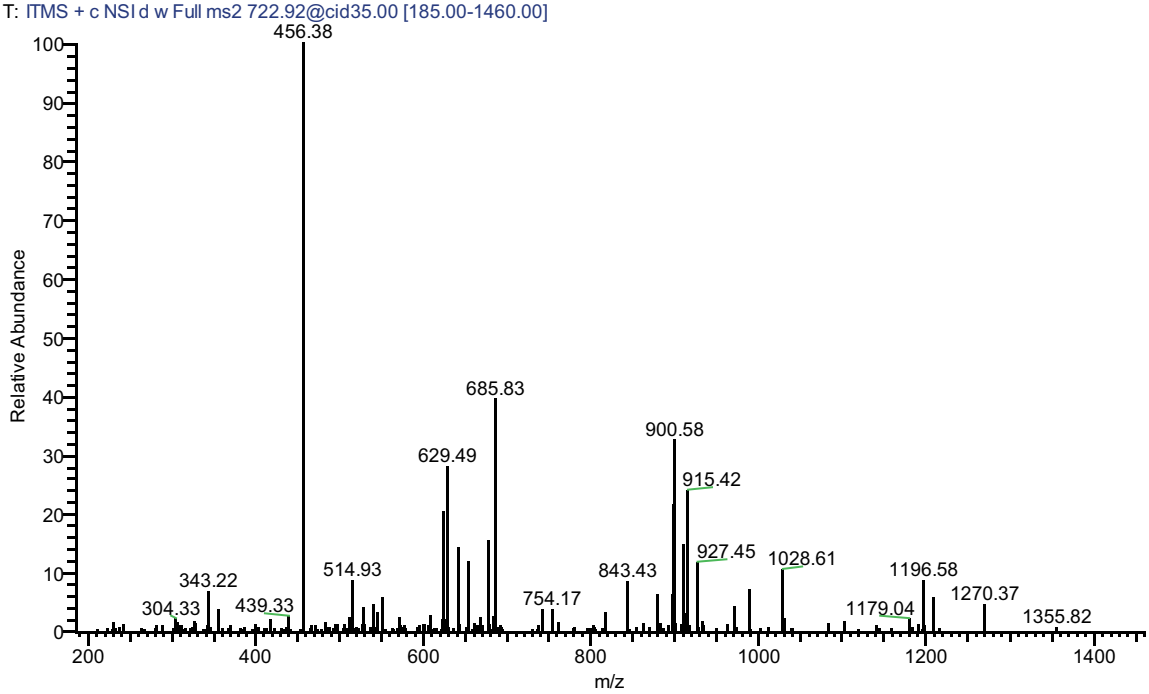
Match to Query 7926: 1443.829152 from(722.921852,2+)
1 cycles: 1 precIntensity: 2228569.7 FinneganScanNumber: 6133
Monoisotopic mass of neutral peptide Mr(calc): 1443.8428
Variable modifications:
K2 : Acetyl:2H(3) (K) K9 : Acetyl:2H(3) (K)
K5 : Acetyl (K) K13 : Acetyl (K)
Ions Score: 21 Expect: 0.052
Matches : 12/102 fragment ions using 23 most intense peaks

(4-17) H4:
GKGG**K(Ac)**GLGKGGA**K(Ac)**R

#	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	58.0287	29.518			G					14
2	231.1531	116.0802	214.1265	107.5669	K	1387.829	694.418	1370.802	685.9047	13
3	288.1746	144.5909	271.148	136.0776	G	1214.704	607.8558	1197.678	599.3425	12
4	345.196	173.1017	328.1695	164.5884	G	1157.683	579.3451	1140.656	570.8318	11
5	*515.3016*	258.1544	498.275	249.6411	K	1100.661	550.8343	1083.635	542.3211	10
6	572.323	286.6651	555.2965	278.1519	G	930.5559	465.7816	913.5293	457.2683	9
7	*685.4071*	343.2072	668.3805	334.6939	L	873.5344	437.2708	856.5079	428.7576	8
8	*742.4285*	371.7179	725.402	363.2046	G	760.4503	380.7288	743.4238	372.2155	7
9	*915.5529*	458.2801	898.5264	449.7668	K	703.4289	352.2181	686.4023	343.7048	6
10	972.5744	486.7908	955.5478	478.2775	G	530.3045	265.6559	513.278	257.1426	5
11	*1029.596*	515.3016	1012.569	506.7883	G	473.2831	237.1452	456.2565	228.6319	4
12	1100.633	550.8201	1083.606	542.3068	A	416.2616	208.6344	399.235	200.1212	3
13	*1270.739*	635.8729	1253.712	627.3596	K	345.2245	173.1159	328.1979	164.6026	2
14					R	175.119	88.0631	158.0924	79.5498	1



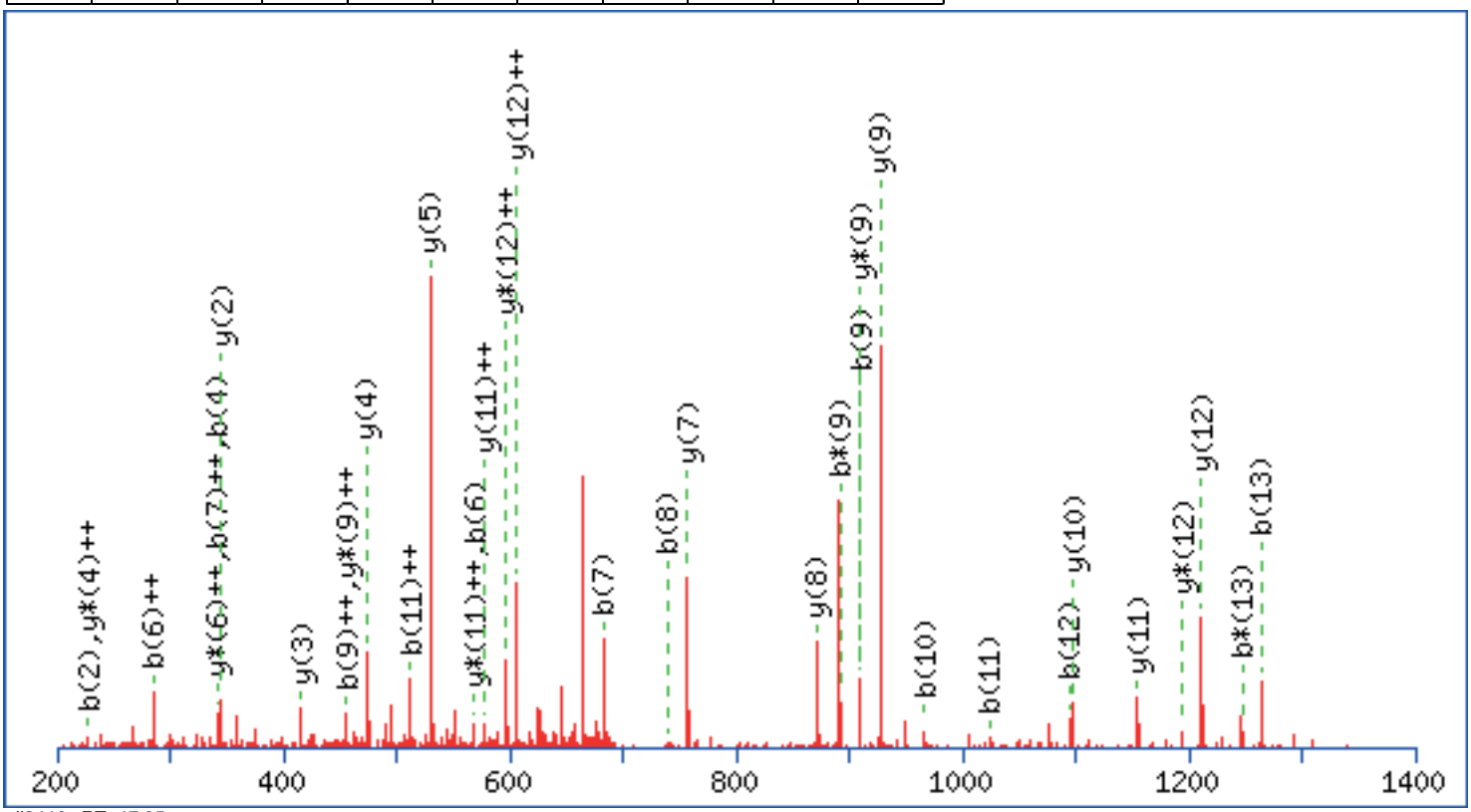
#6133 RT: 72.93 AV: 1
T: ITMS + c NSI d w Full ms2 722.92@cid35.00 [185.00-1460.00]



Match to Query 3842: 1437.804400 from(719.909476,2+)
1 cycles:1 precIntensity:2352466.7 FinneganScanNumber:2419
Monoisotopic mass of neutral peptide Mr(calc): 1437.8052
Variable modifications:
K2 : Acetyl (K) K9 : Acetyl (K)
K5 : Acetyl (K) K13 : Acetyl (K)
Ions Score: 70 Expect: 7.1e-06
Matches : 37/102 fragment ions using 68 most intense peaks

(4-17) H4:
G**K(Ac)**GG**K(Ac)**GLG**K(Ac)**GGA**K(Ac)**R

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.0287	29.518			G					14
2	228.1343	114.5708	211.1077	106.0575	K	1381.791	691.3992	1364.765	682.8859	13
3	285.1557	143.0815	268.1292	134.5682	G	1211.686	606.3464	1194.659	597.8331	12
4	342.1772	171.5922	325.1506	163.079	G	1154.664	577.8357	1137.638	569.3224	11
5	512.2827	256.645	495.2562	248.1317	K	1097.643	549.3249	1080.616	540.8116	10
6	569.3042	285.1557	552.2776	276.6425	G	927.537	464.2722	910.5105	455.7589	9
7	682.3883	341.6978	665.3617	333.1845	L	870.5156	435.7614	853.489	427.2482	8
8	739.4097	370.2085	722.3832	361.6952	G	757.4315	379.2194	740.405	370.7061	7
9	909.5152	455.2613	892.4887	446.748	K	700.4101	350.7087	683.3835	342.1954	6
10	966.5367	483.772	949.5102	475.2587	G	530.3045	265.6559	513.278	257.1426	5
11	1023.558	512.2827	1006.532	503.7694	G	473.2831	237.1452	456.2565	228.6319	4
12	1094.595	547.8013	1077.569	539.288	A	416.2616	208.6344	399.235	200.1212	3
13	1264.701	632.854	1247.674	624.3408	K	345.2245	173.1159	328.1979	164.6026	2
14					R	175.119	88.0631	158.0924	79.5498	1



#2419 RT: 47.95
T: ITMS + c NSI d w Full ms2 719.91@cid35.00 [185.00-1450.00]