

Supplementary Data 3

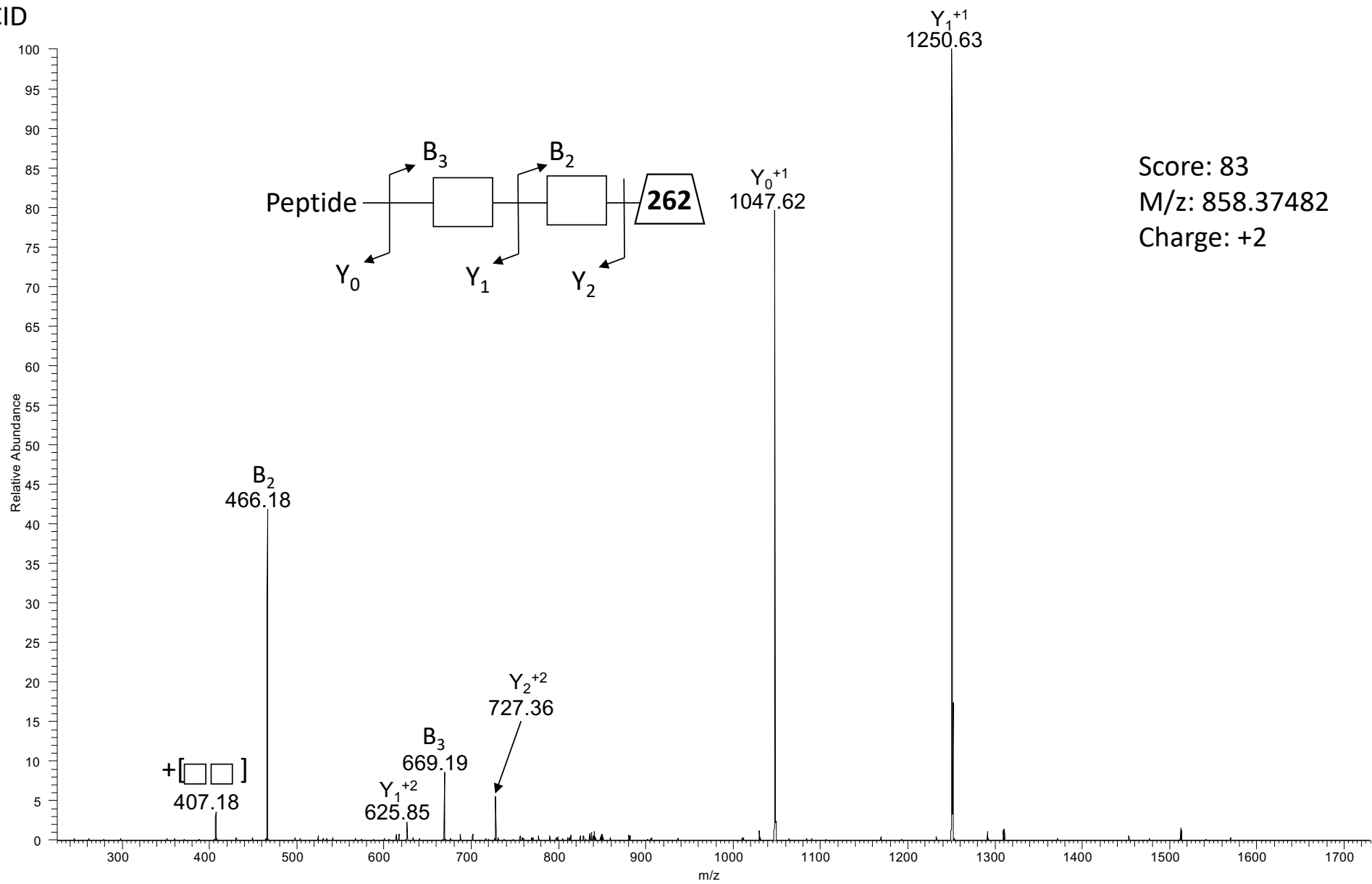
Supplementary Data: Identified *Burkholderia gladioli* MDU2 (AUSMDU00013929) glycopeptides

Gene	Protein name	Uniprot accession	m/z	Charge	MH+	Peptide mass	Glycan mass	Peptide sequence	MASCOT ion Score	Page
bgla_1g02560	Uncharacterized protein	F2LHM5	858.37482	2	1715.74	1047.51	668.24	AAAASAAGTNDK	83	3 and 4
bgla_1g31160	Bifunctional uroporphyrinogen-III synthetase/uroporphyrin-III C-methyltransferase	F2LG73	763.3587	3	2288.06	1719.84	568.22	AAHPGDIASEAAATGQPR	84	5 and 6
bgla_1g32320	Uncharacterized protein	F2LGU6	945.94171	2	1890.88	1222.64	668.23	APAAAPEAASAPAK	74	7 and 8
bgla_1g32320	Uncharacterized protein	F2LGU6	1359.09094	2	2717.17	1380.71	1336.46214 (2*668.2311)	ASAPAAPEAASAPAK	70	9 and 10
bgla_1g28150	Uncharacterized protein	F2LBQ5	877.35632	2	1753.70	1185.48	568.22	ASGAM(+16)SNDAMSK	64	11 and 12
bgla_1g28150	Uncharacterized protein	F2LBQ5	869.37994	2	1737.75	1169.49	568.26	ASGAMSNDAMSK	56	13 and 14
bgla_1g28150	Uncharacterized protein	F2LBQ5	919.38995	2	1837.77	1169.49	668.28	ASGAMSNDAMSK	72	15 and 16
bgla_1g35490	Periplasmic protease	F2LE35	1119.00671	2	2237.01	1000.51	1236.49968 (2*568.2445)	ASSAKPASAPN	51	17 and 18
bgla_1g09280	Putative lipoprotein	F2LAW2	980.5174	2	1960.03	1391.76	568.26	AVPAAPASGAAPAAAK	76	19 and 20
bgla_1g09460	Uncharacterized protein	F2LC05	820.04755	3	2458.13	1789.83	668.29	FNEHPQMQFAASAPSK	80	21 and 22
lolA	Outer-membrane lipoprotein carrier protein	F2L9H3	798.88324	4	3192.51	2624.29	568.22	GASGAMPTVKPTDNSSGTFVFSRPGR	27	23 and 24
bgla_1g28150	Uncharacterized protein	F2LBQ5	1095.94482	2	2190.88	1622.66	568.23	HDAMGM(+16)SPAASDAMSK	84	25 and 26
bgla_1g28150	Uncharacterized protein	F2LBQ5	1087.97119	2	2174.93	1606.67	568.27	HDAMGMSPAASDAMSK	118	27 and 28
bgla_1g23600	Ankyrin repeat protein	F2LDR2	704.34857	3	2111.03	1542.76	568.27	IGDGRPASGAGGQNSAK	57	29 and 30
bgla_1g23600	Ankyrin repeat protein	F2LDR2	737.68756	3	2211.05	1542.76	668.28	IGDGRPASGAGGQNSAK	33	31 and 32

bgla_1g28150	Uncharacterized protein	F2LBQ5	779.01428	3	2335.03	1766.74	568.29	KHDAM(+16)GM(+16)SPAASDAMSK	52	33 and 34
bgla_1g28150	Uncharacterized protein	F2LBQ5	768.34943	3	2303.03	1734.76	568.27	KHDAMGMSPAASDAMSK	103	35 and 36
bgla_1g28150	Uncharacterized protein	F2LBQ5	801.68872	3	2403.05	1734.76	668.29	KHDAMGMSPAASDAMSK	20	37 and 38
bgla_1g28150	Uncharacterized protein	F2LBQ5	807.02075	3	2419.05	1750.75	668.30	KHDAMGM(+16)SPAASDAMSK	73	39 and 40
bgla_1g22150	Uncharacterized protein	F2LA58	1038.50659	2	2076.01	1407.72	668.28	KPAAPAADAASAPAAQ	89	41 and 42
bgla_1g35490	Periplasmic protease	F2LE35	939.46844	2	1877.93	1309.71	568.22	PLTAGAAAPSASAPK	42	43 and 44
bgla_1g35490	Periplasmic protease	F2LE35	989.48029	2	1977.95	1309.71	668.24	PLTAGAAAPSASAPK	80	45 and 46
bgla_1g09580	Uncharacterized protein	F2LC16	922.13824	3	2764.40	2096.10	668.30	SLSNQAPAASAVAAAPIDADKK	116	47 and 48
bgla_1g22150	Uncharacterized protein	F2LA58	986.46613	3	2957.38	1720.87	1236.51001 (2*568.2550)	TPASAAAAASTPGAHAAR	76	49 and 50

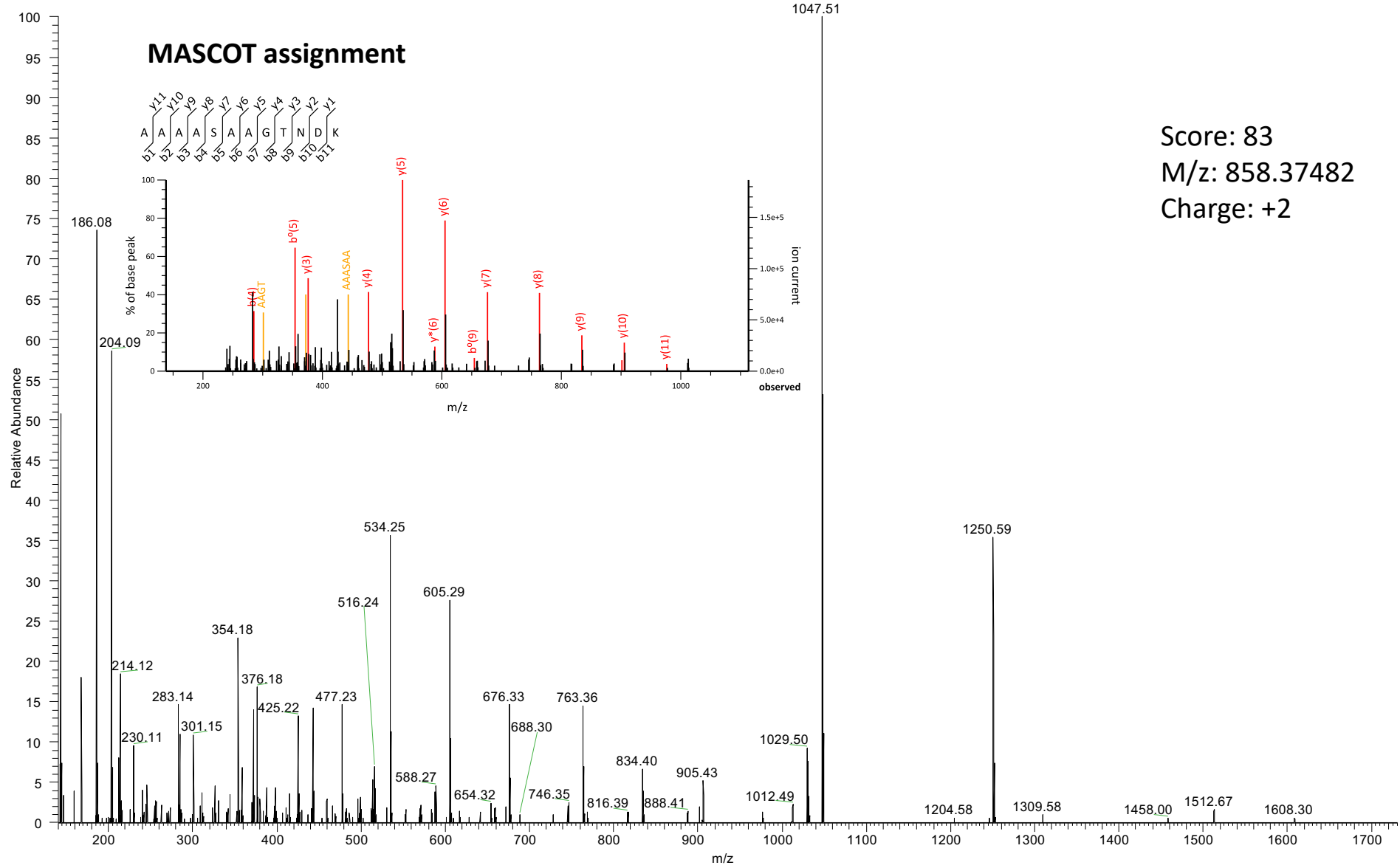
Supplementary Data 3. Identified *Burkholderia gladioli* MDU2 (AUSMDU00013929) Glycopeptides. A total of 24 unique glycopeptides were observed within whole cell proteome samples of *B. gladioli* MDU2. For assigned glycopeptides the gene, protein name, uniprot accession (mapped to *B. gladioli* BSR3), observed m/z, charge state, MH+ mass, peptide mass, glycan, peptide sequence, MASCOT ion score and containing annotated CID and HCD data are provided.

ITMS-CID



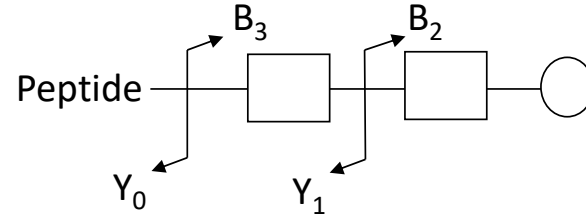
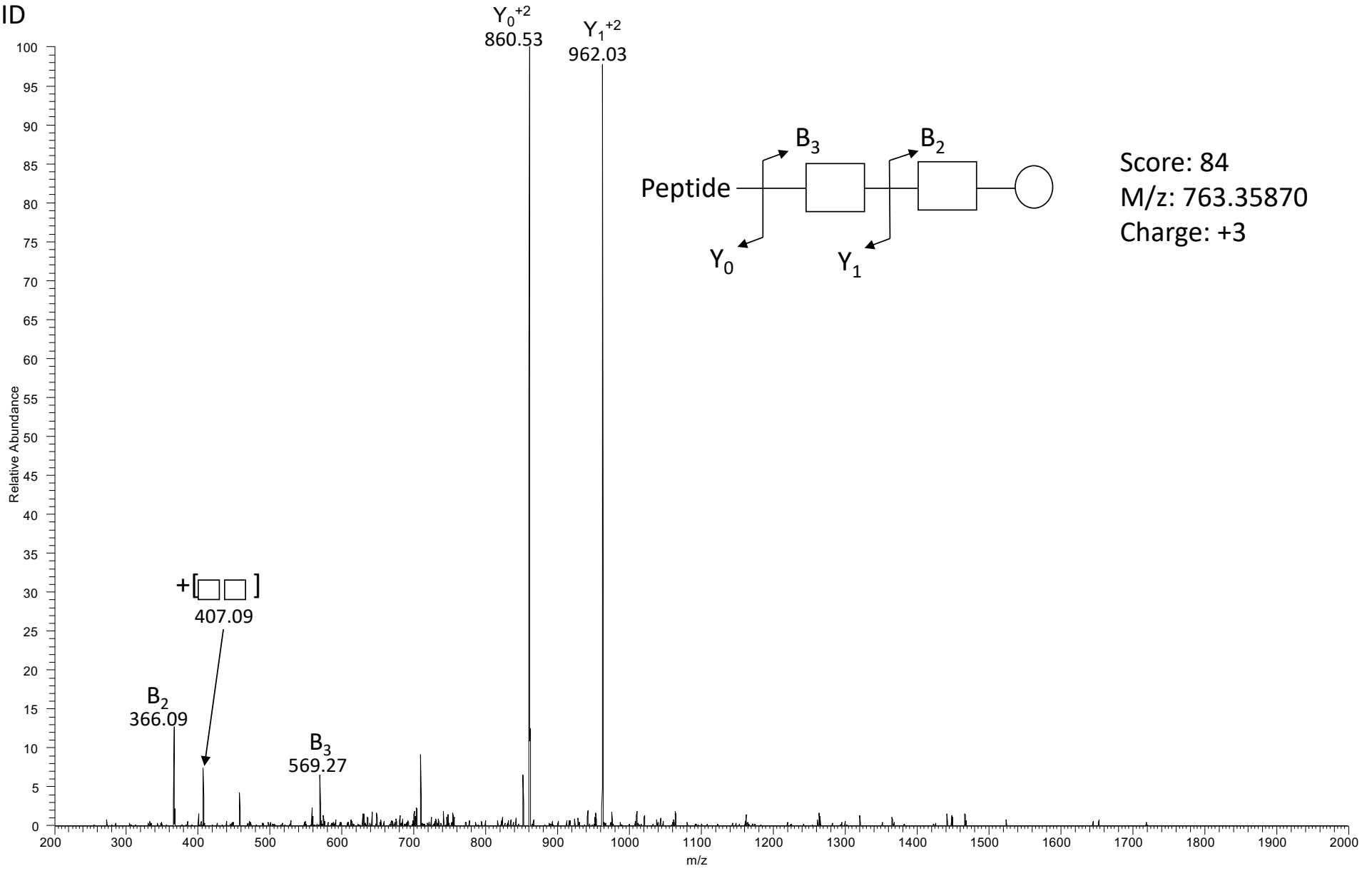
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M/z: 858.37482
Charge: +2

FTMS-HCD



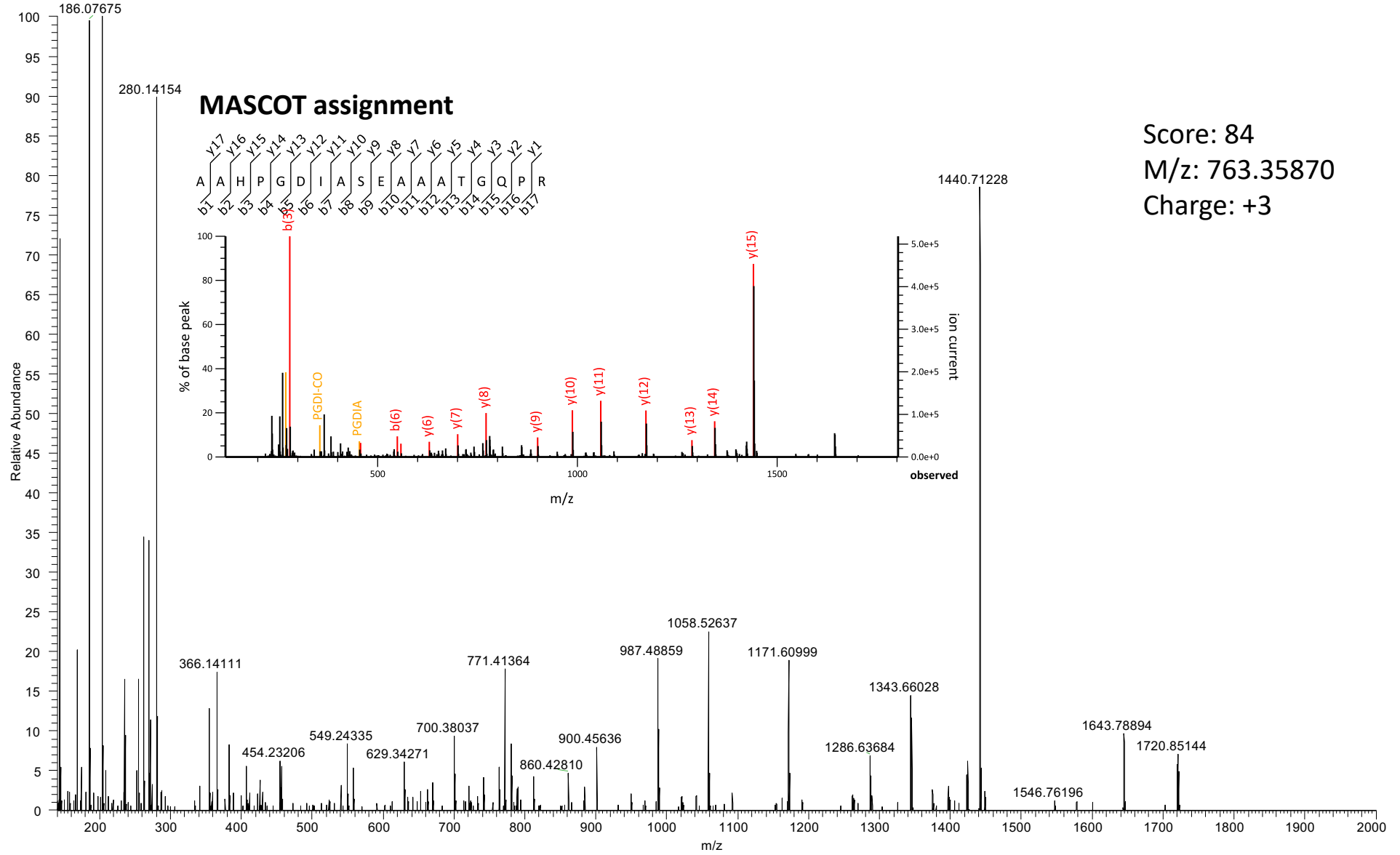
Score: 83
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Charge: +2

ITMS-CID



Score: 84
M/z: 763.35870
Charge: +3

FTMS-HCD

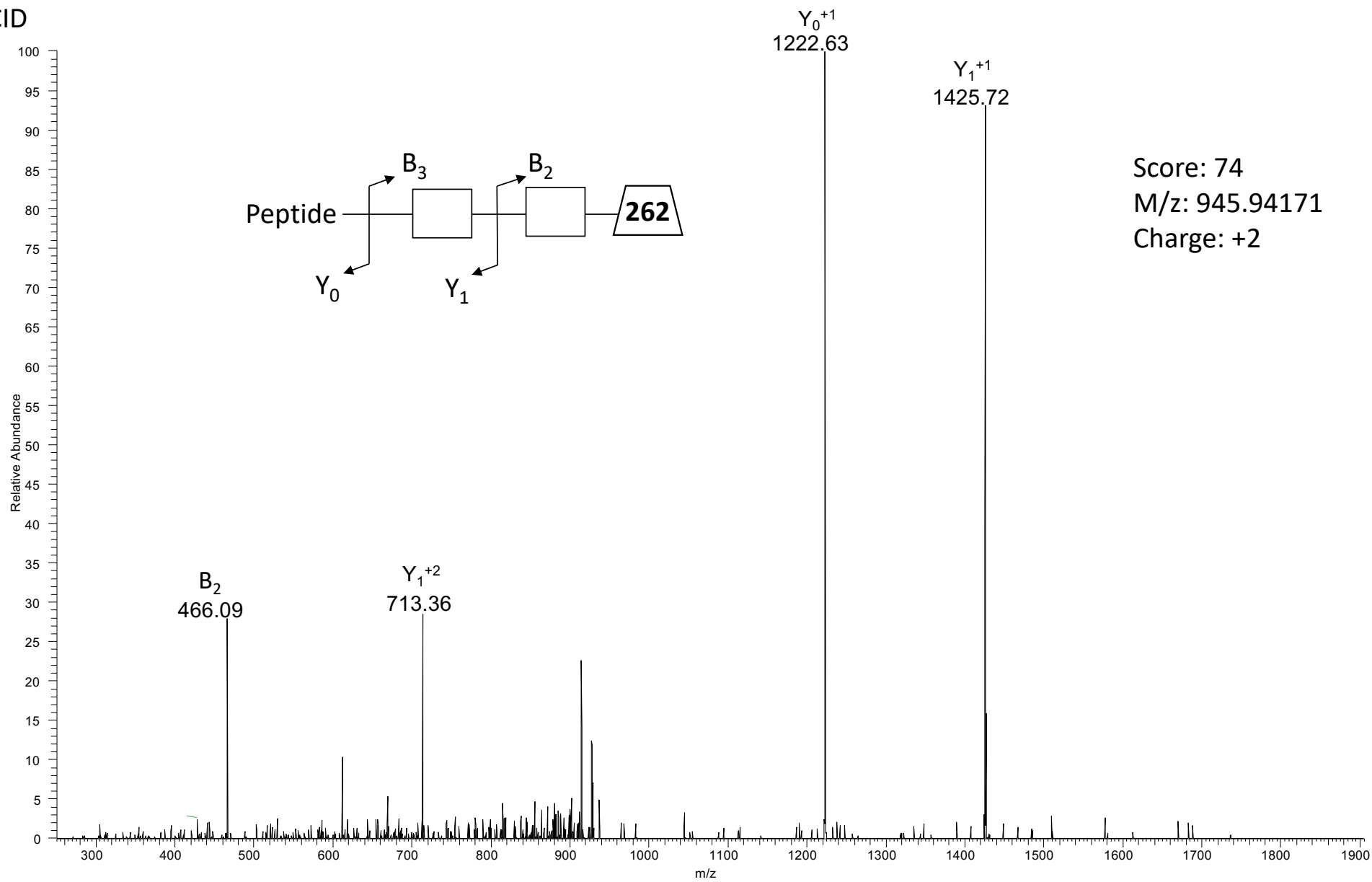


Score: 84

M/z: 763.35870

Charge: +3

ITMS-CID

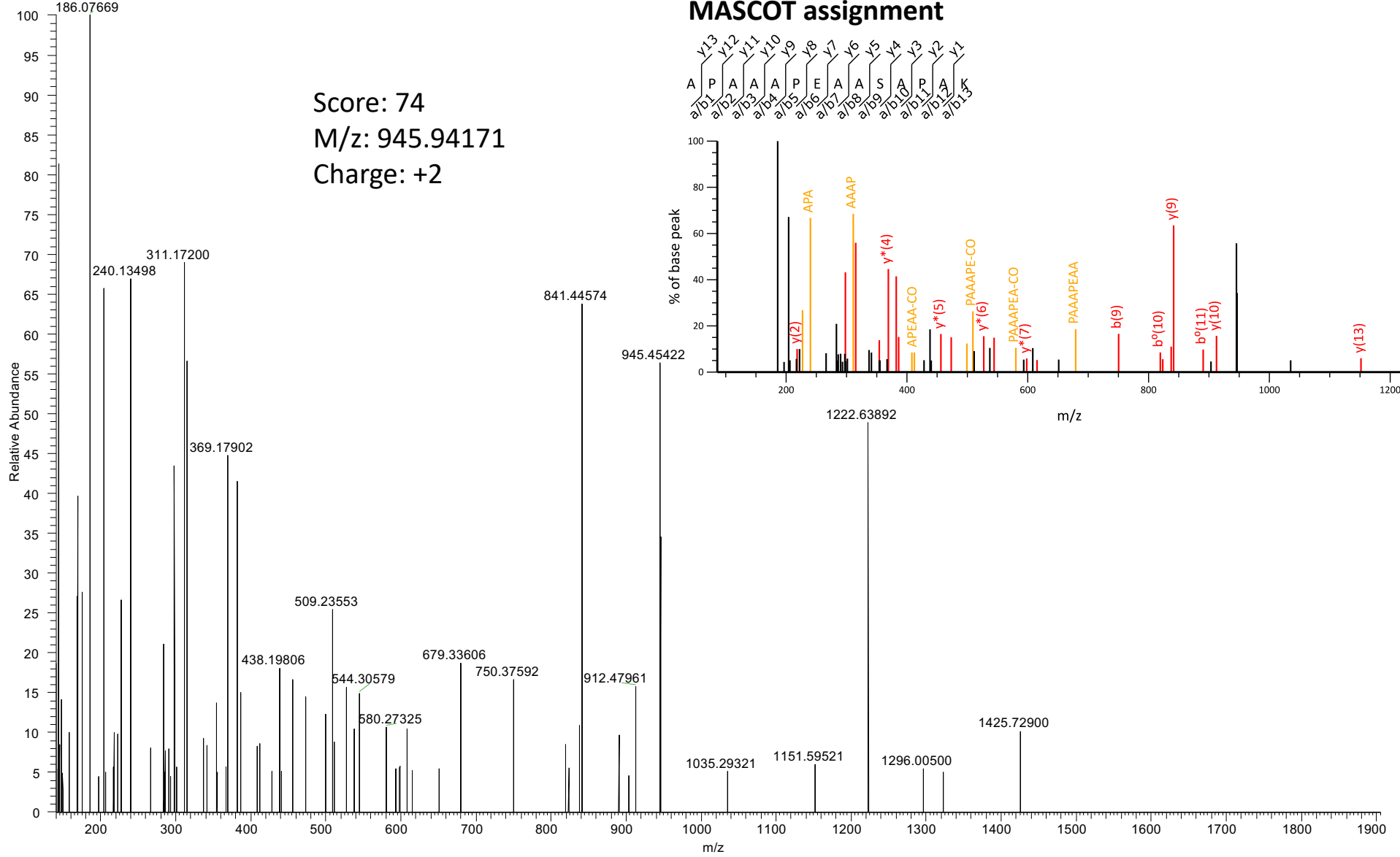


Score: 74

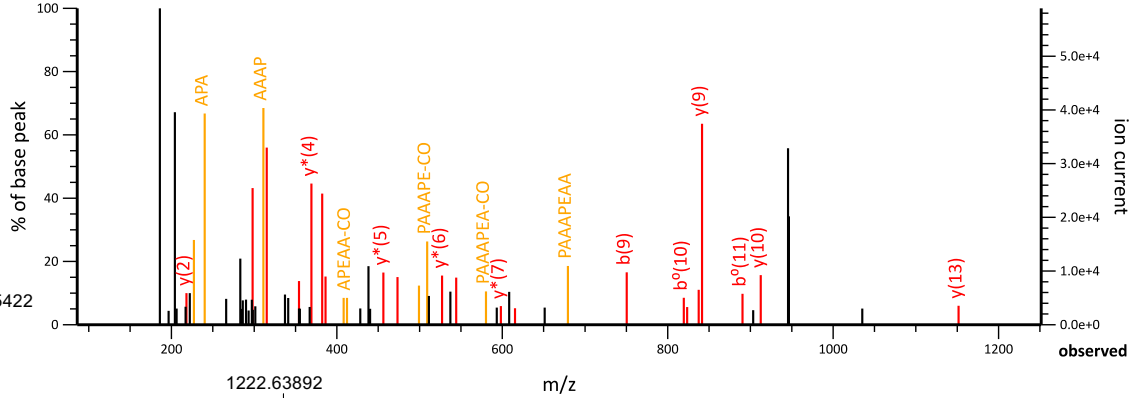
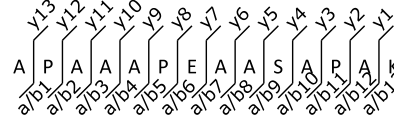
M/z: 945.94171

Charge: +2

FTMS-HCD

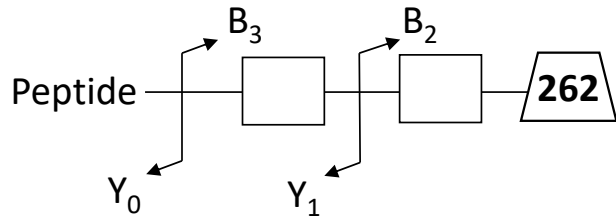
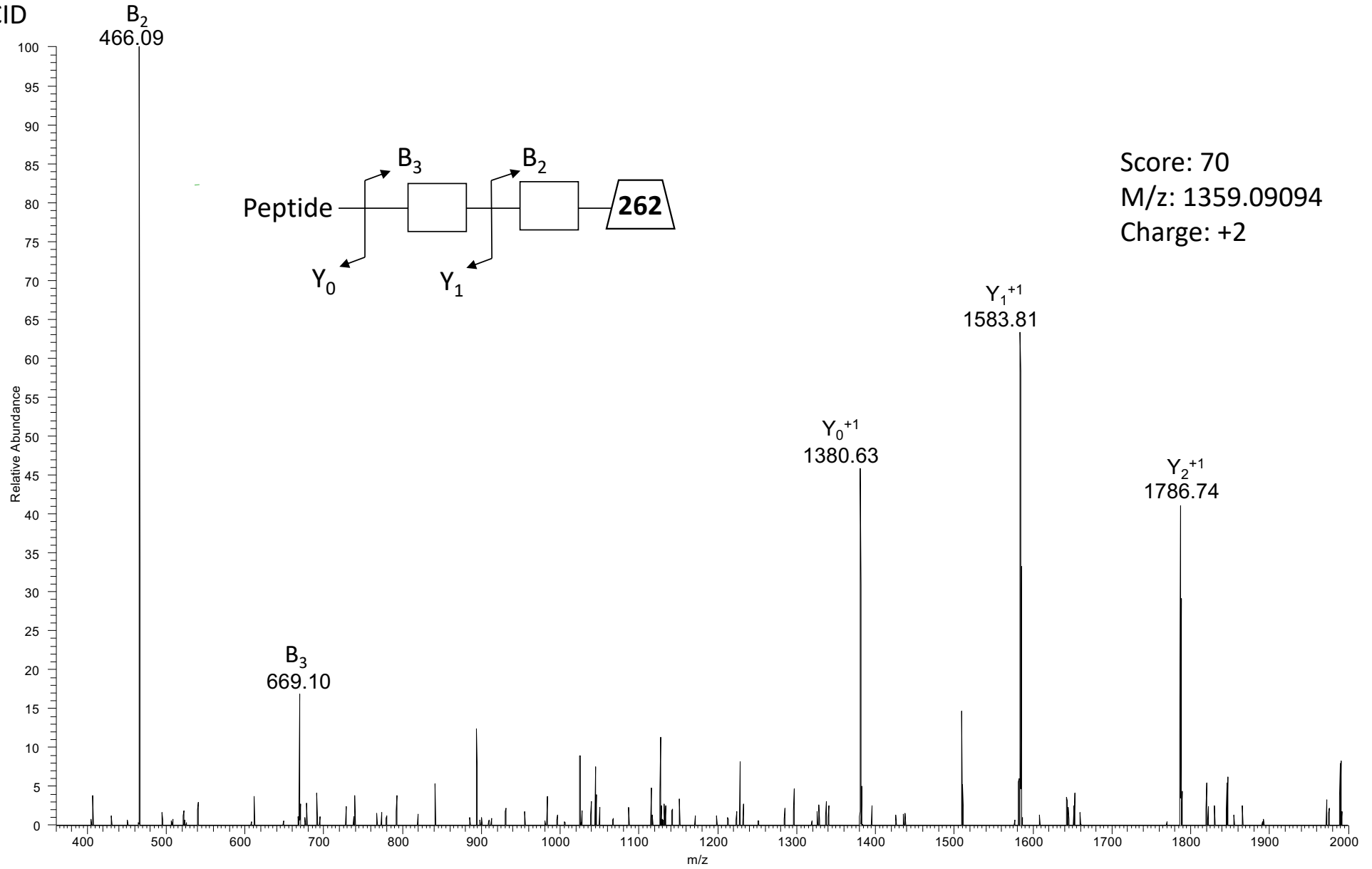


MASCOT assignment



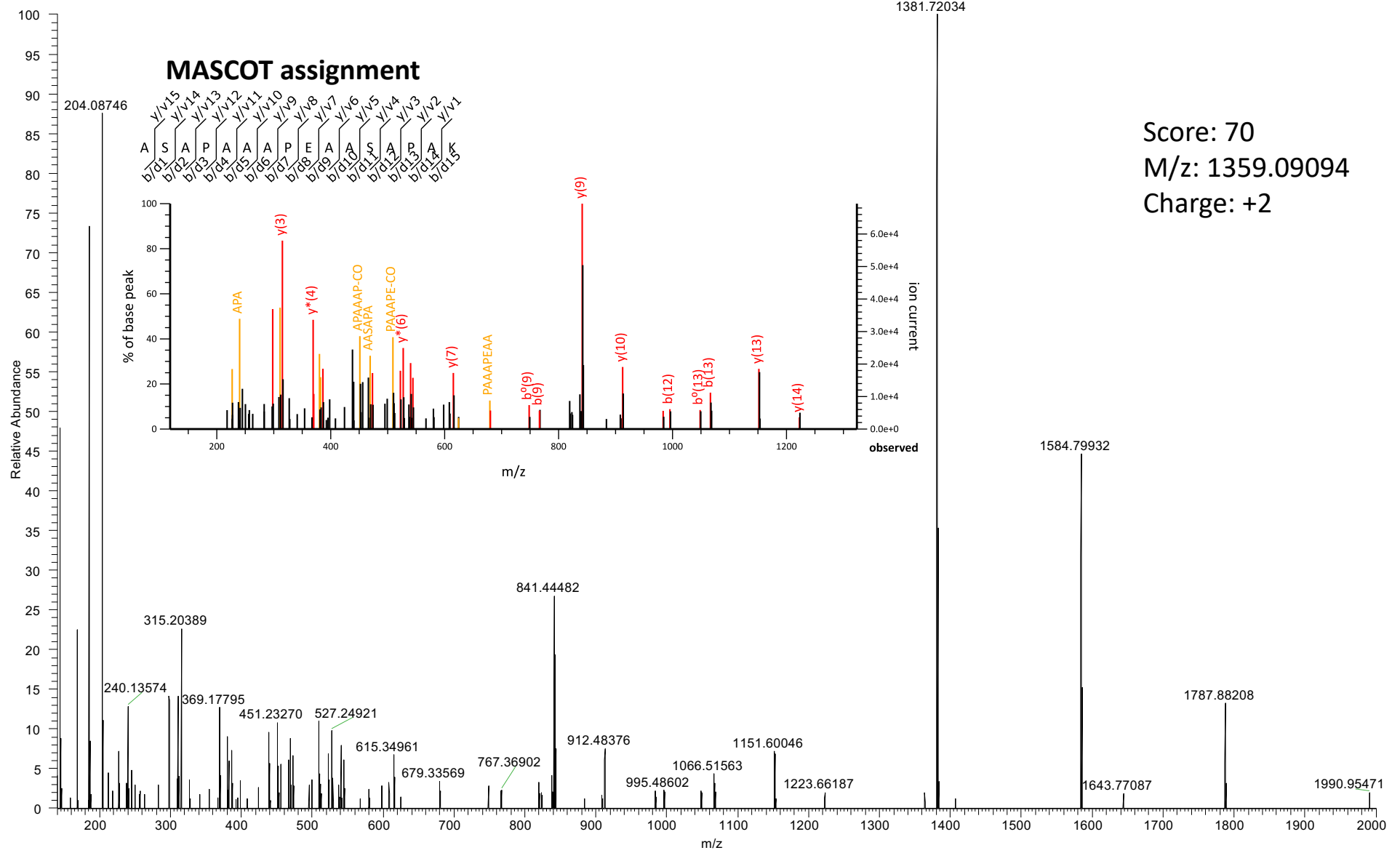
ion current
5.0e+4
4.0e+4
3.0e+4
2.0e+4
1.0e+4
0.0e+0
observed

ITMS-CID

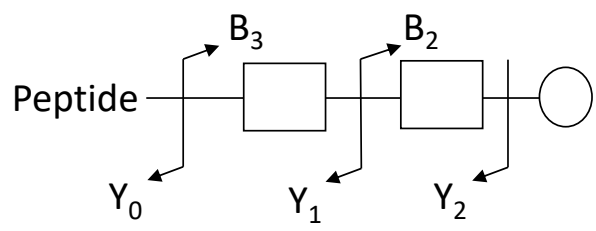
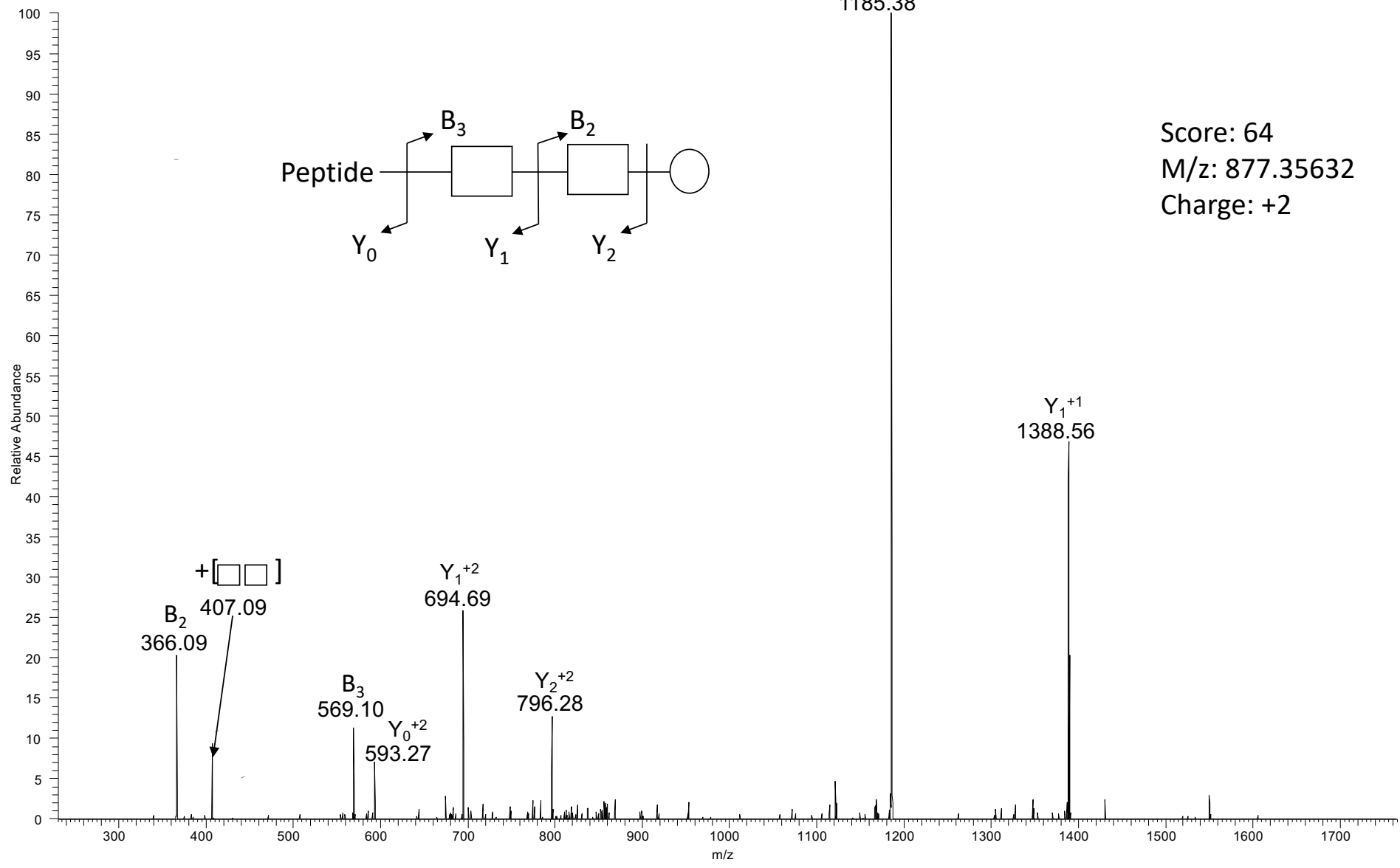


Score: 70
M/z: 1359.09094
Charge: +2

FTMS-HCD

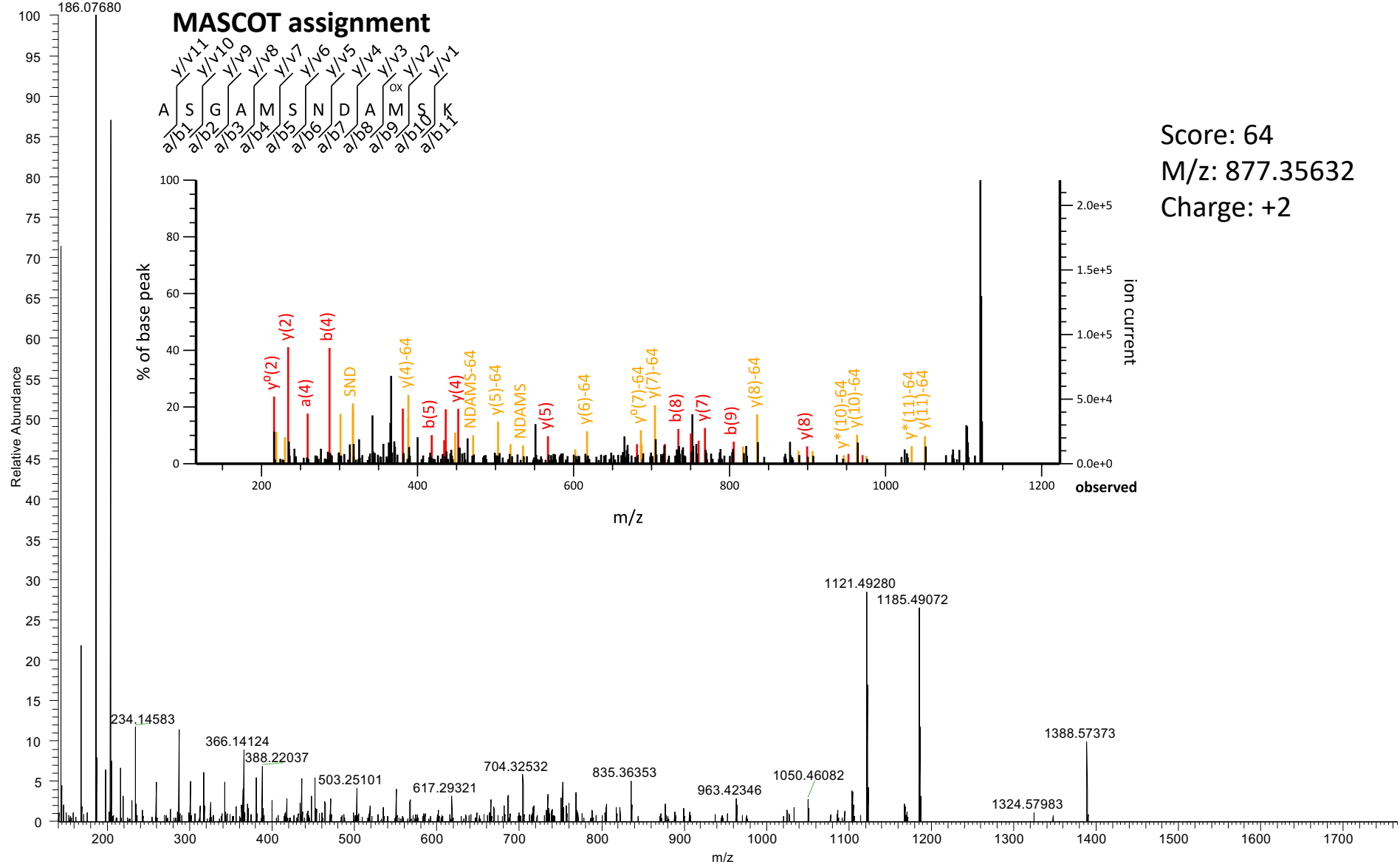


ITMS-CID

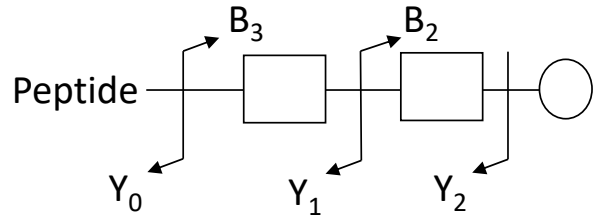
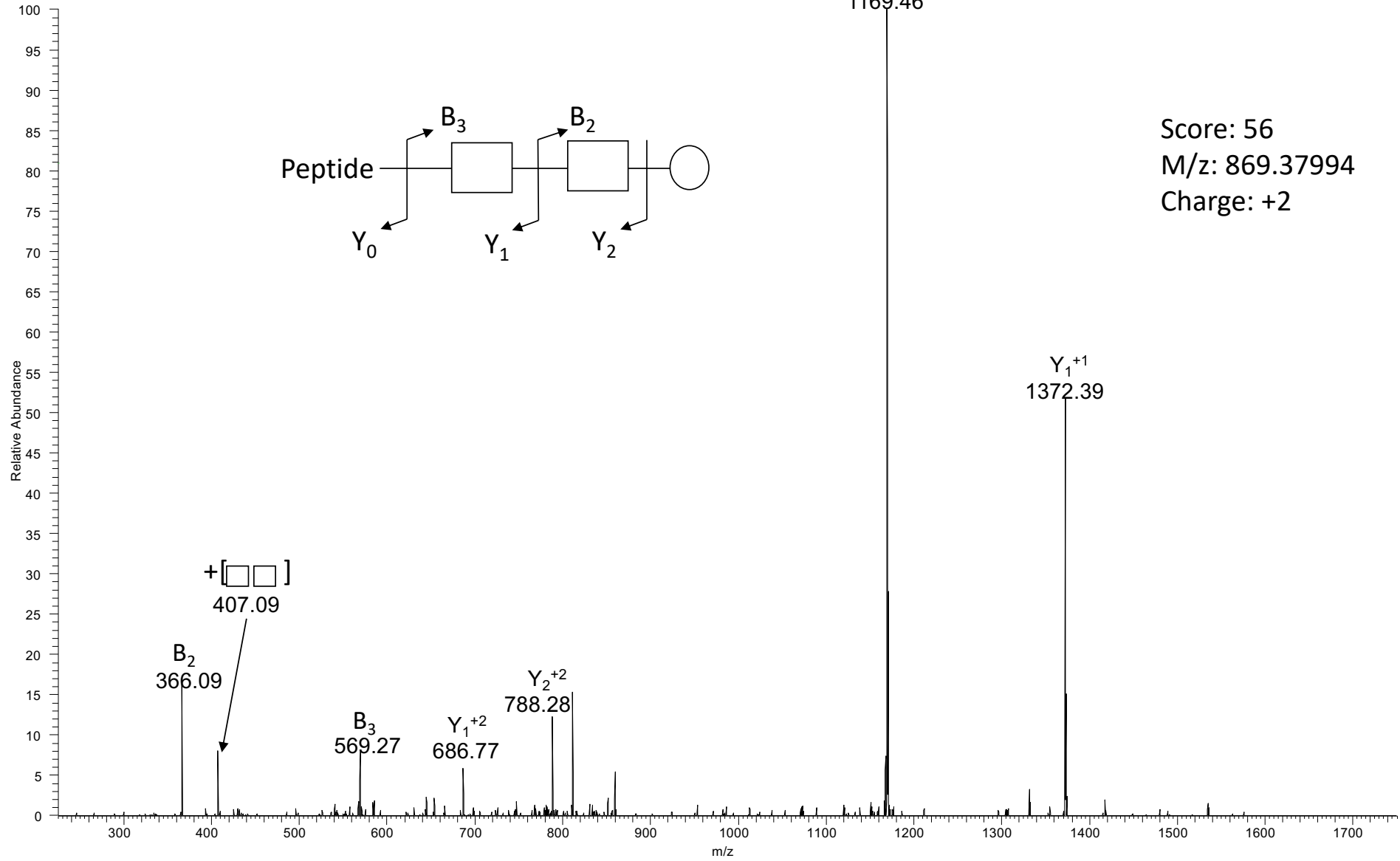


Score: 64
M/z: 877.35632
Charge: +2

FTMS-HCD

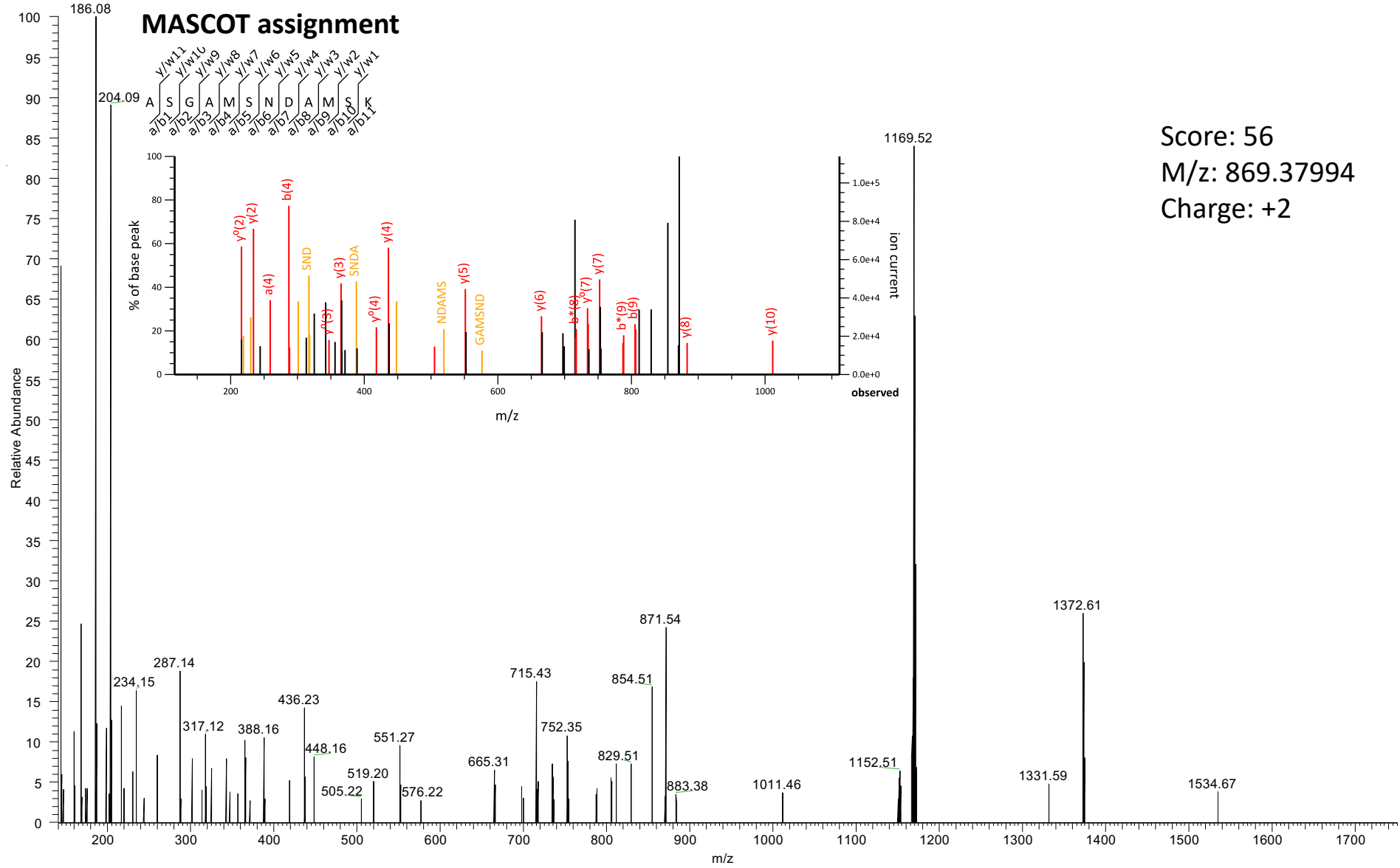


ITMS-CID



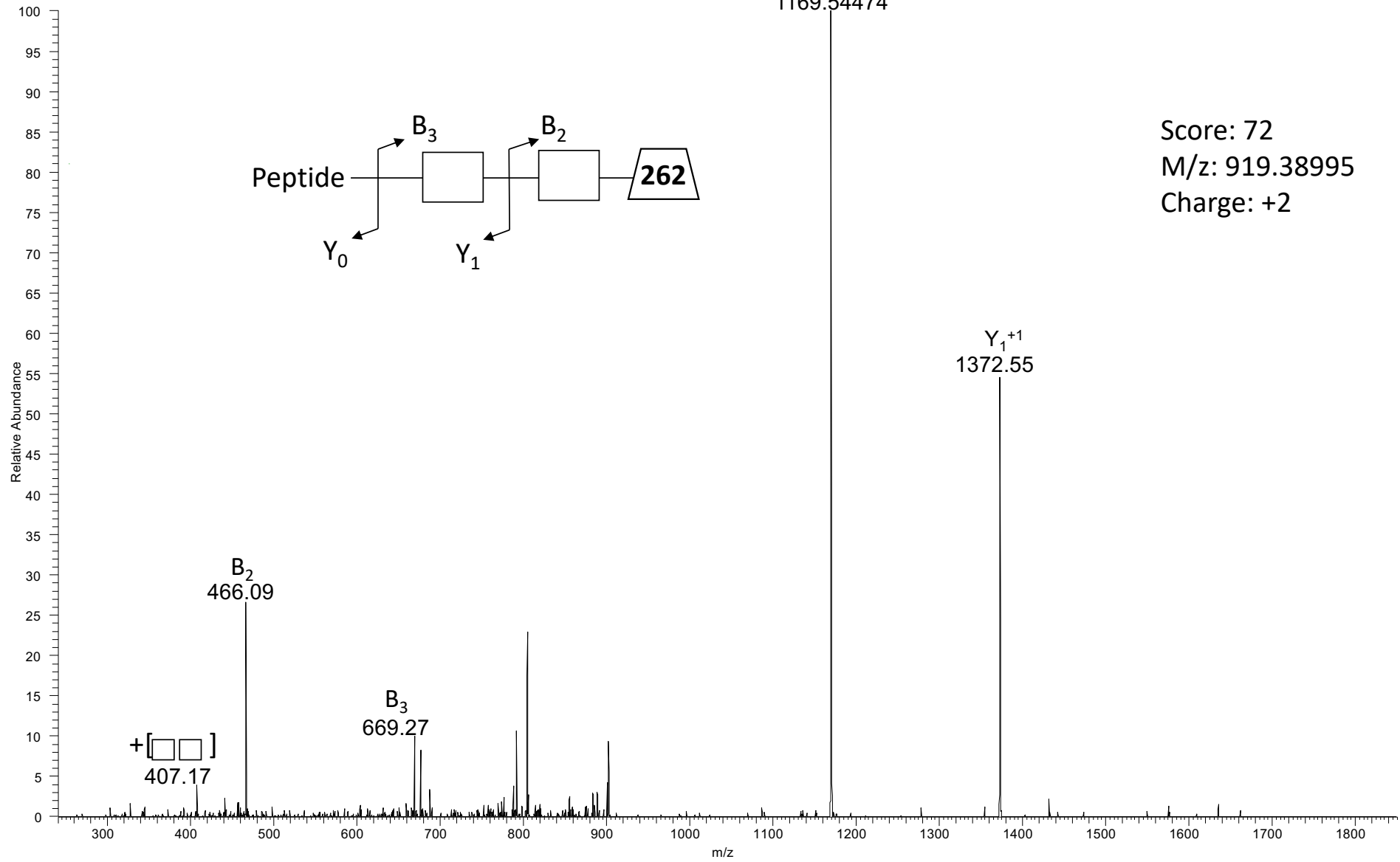
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Charge: +2

FTMS-HCD



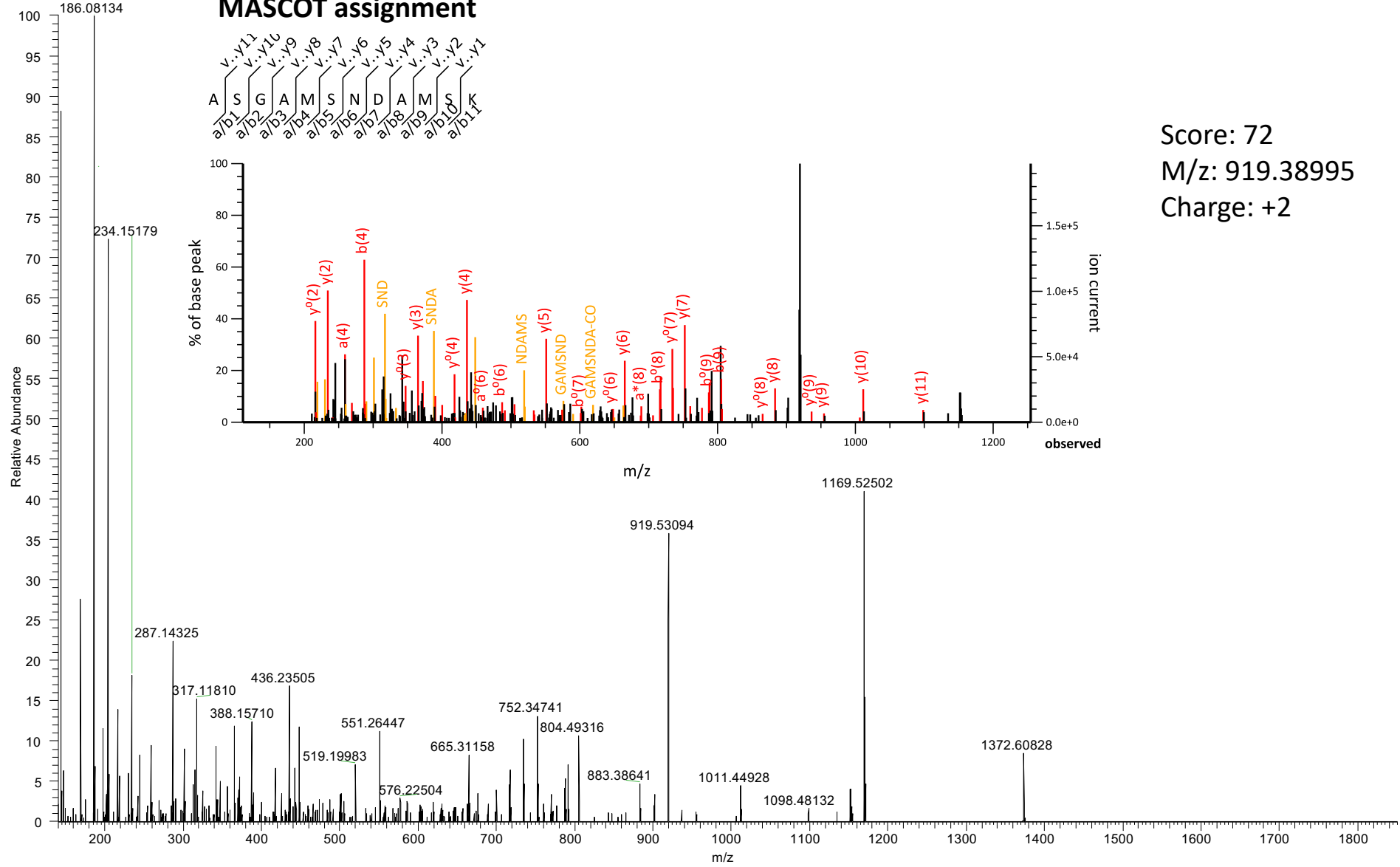
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M/z: 869.37994
Charge: +2

ITMS-CID

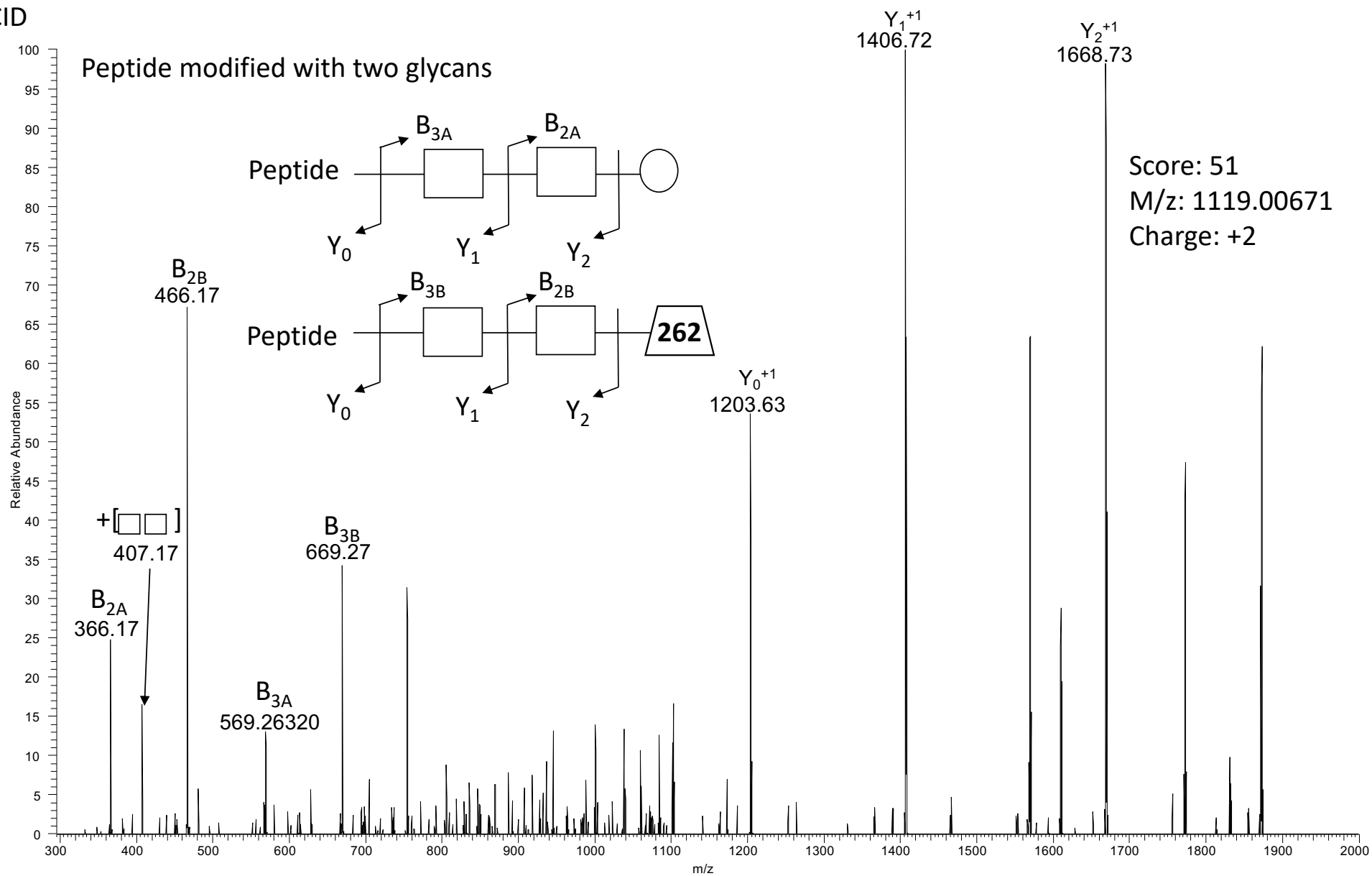


Score: 72
M/z: 919.38995
Charge: +2

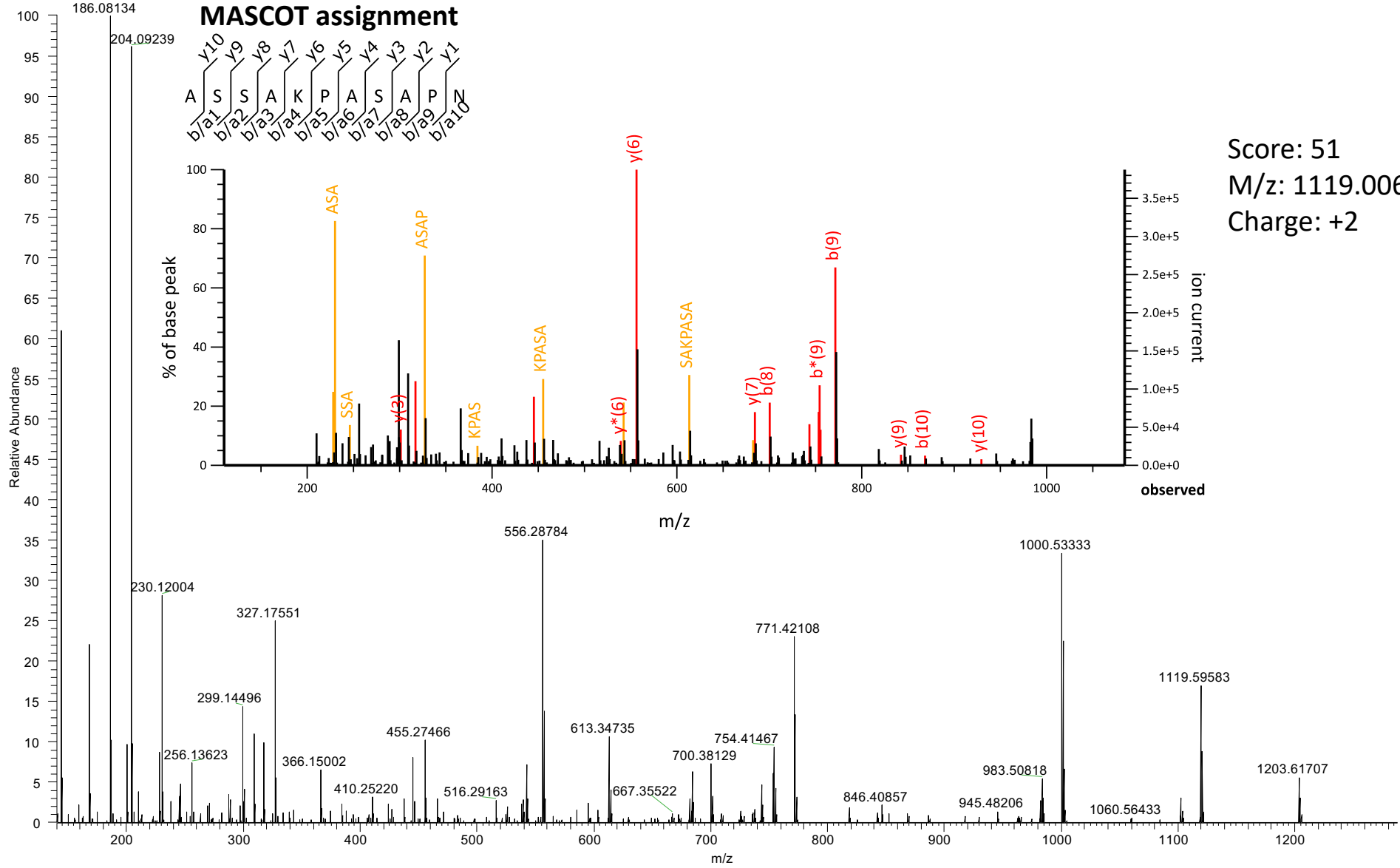
FTMS-HCD



ITMS-CID

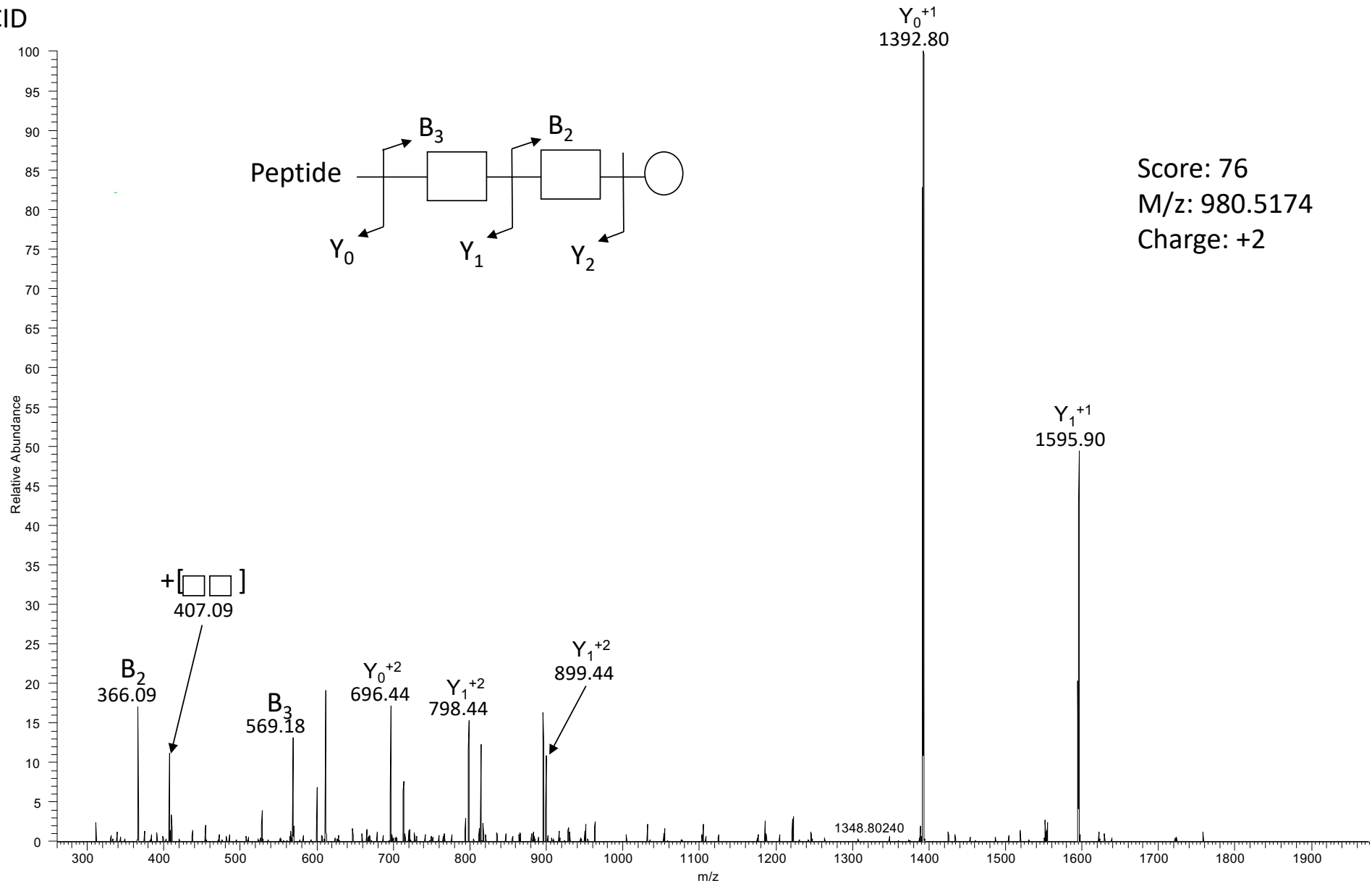


FTMS-HCD



Score: 51
M/z: 1119.00671
Charge: +2

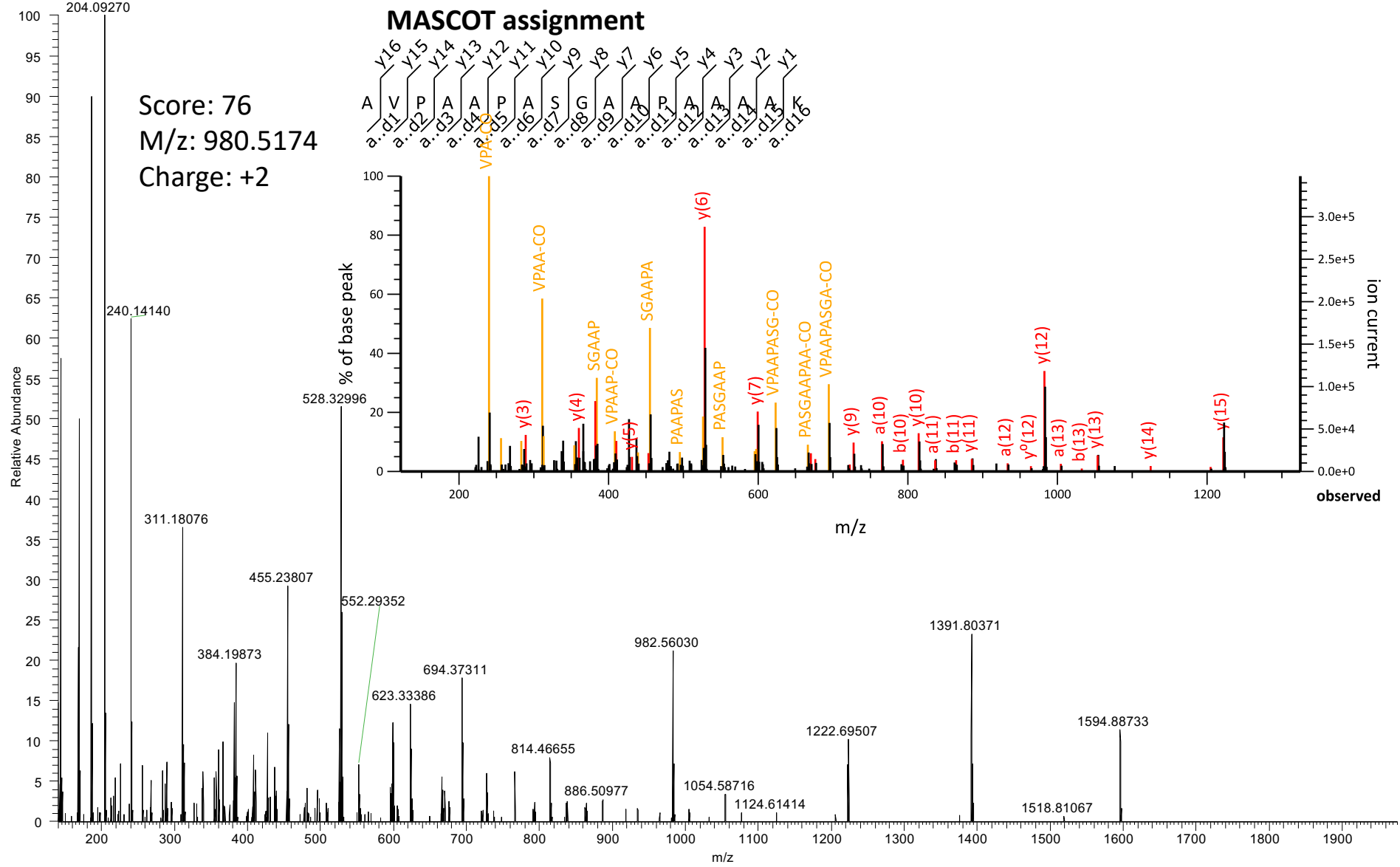
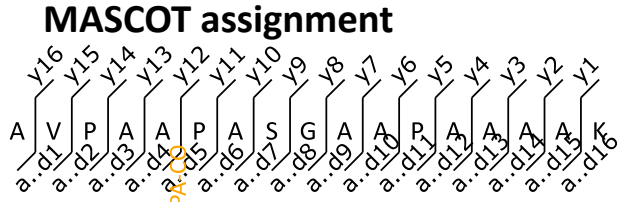
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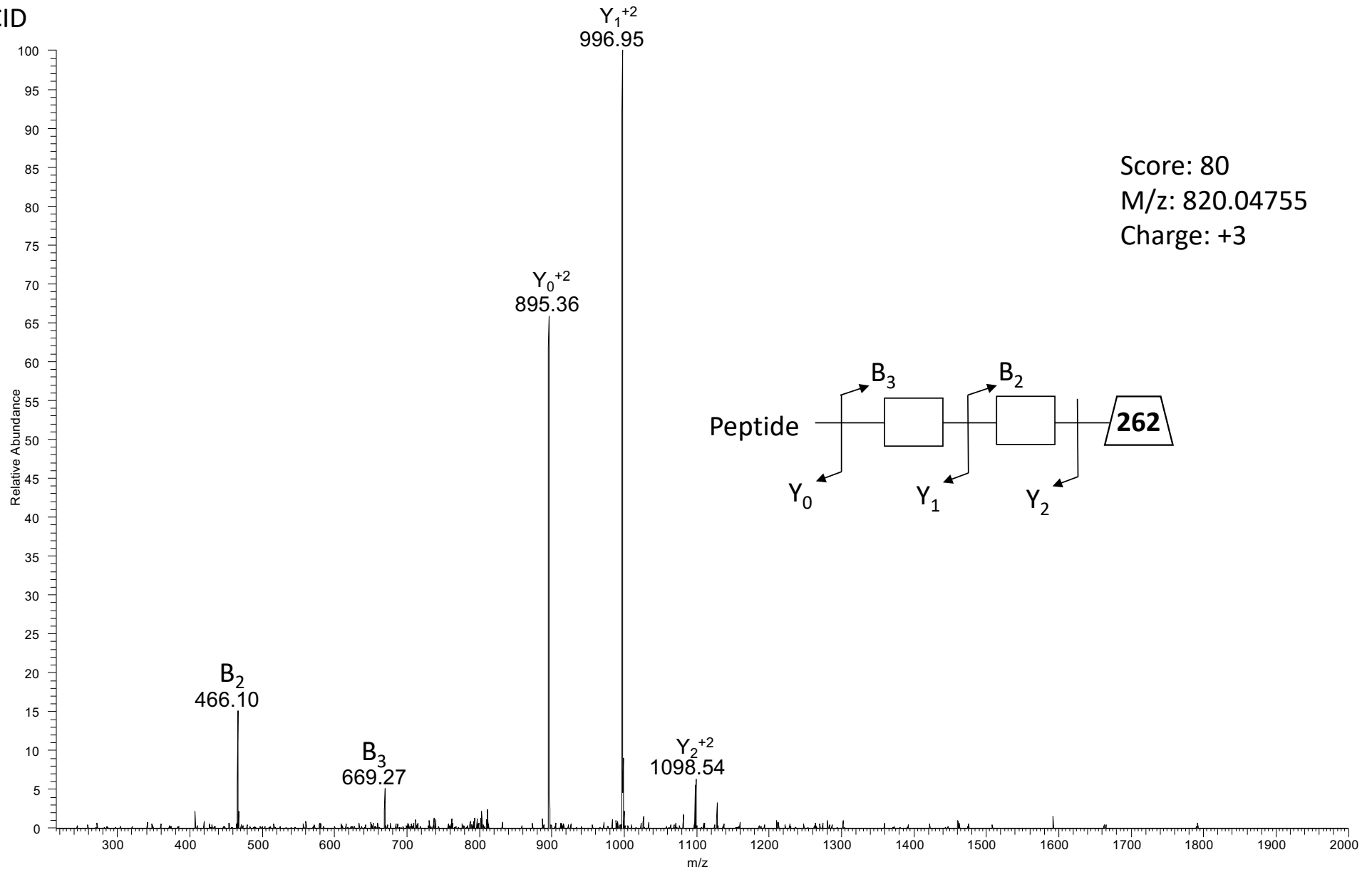
Score: 76
M/z: 980.5174
Charge: +2

FTMS-HCD

Score: 76
M/z: 980.5174
Charge: +2



ITMS-CID

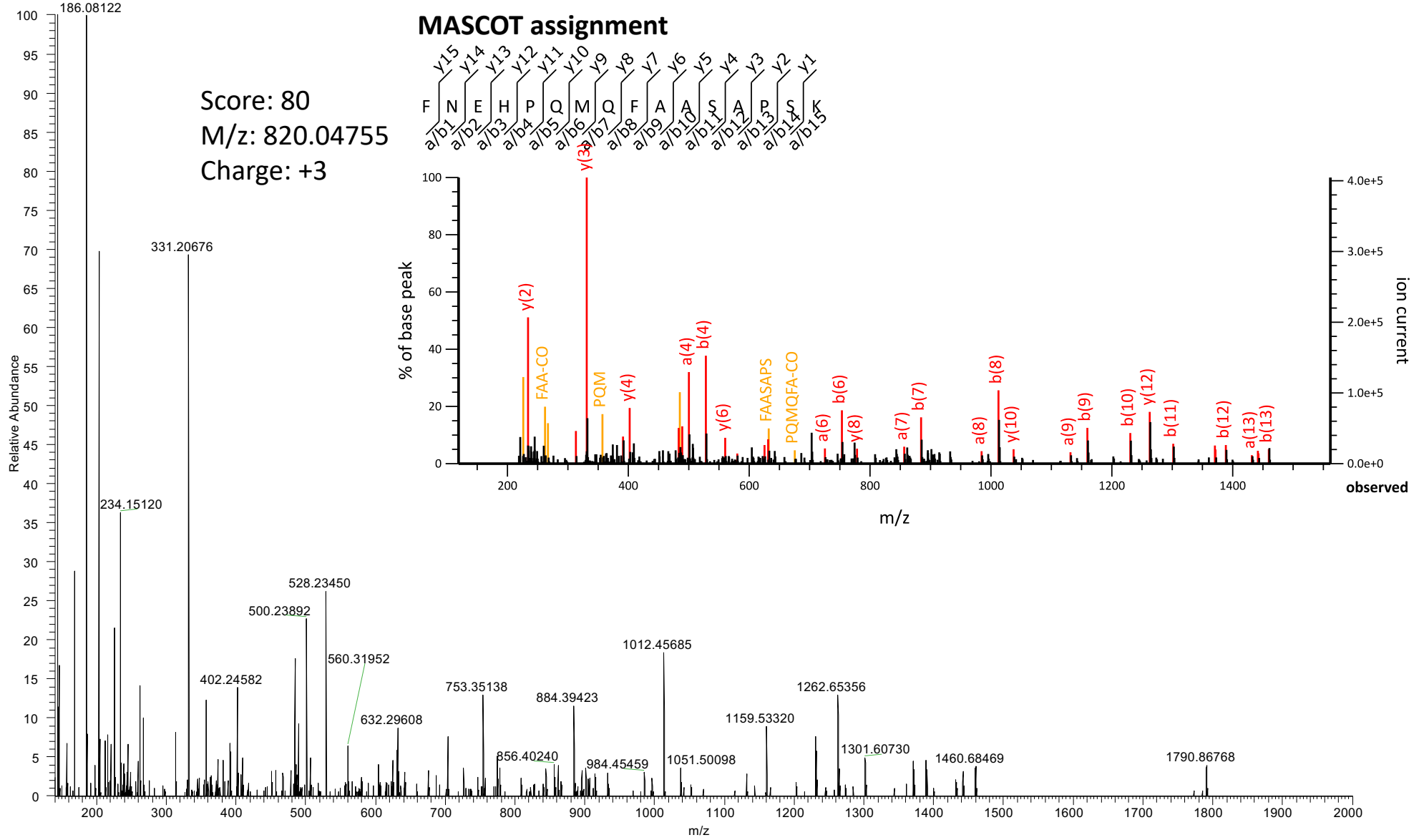


Score: 80

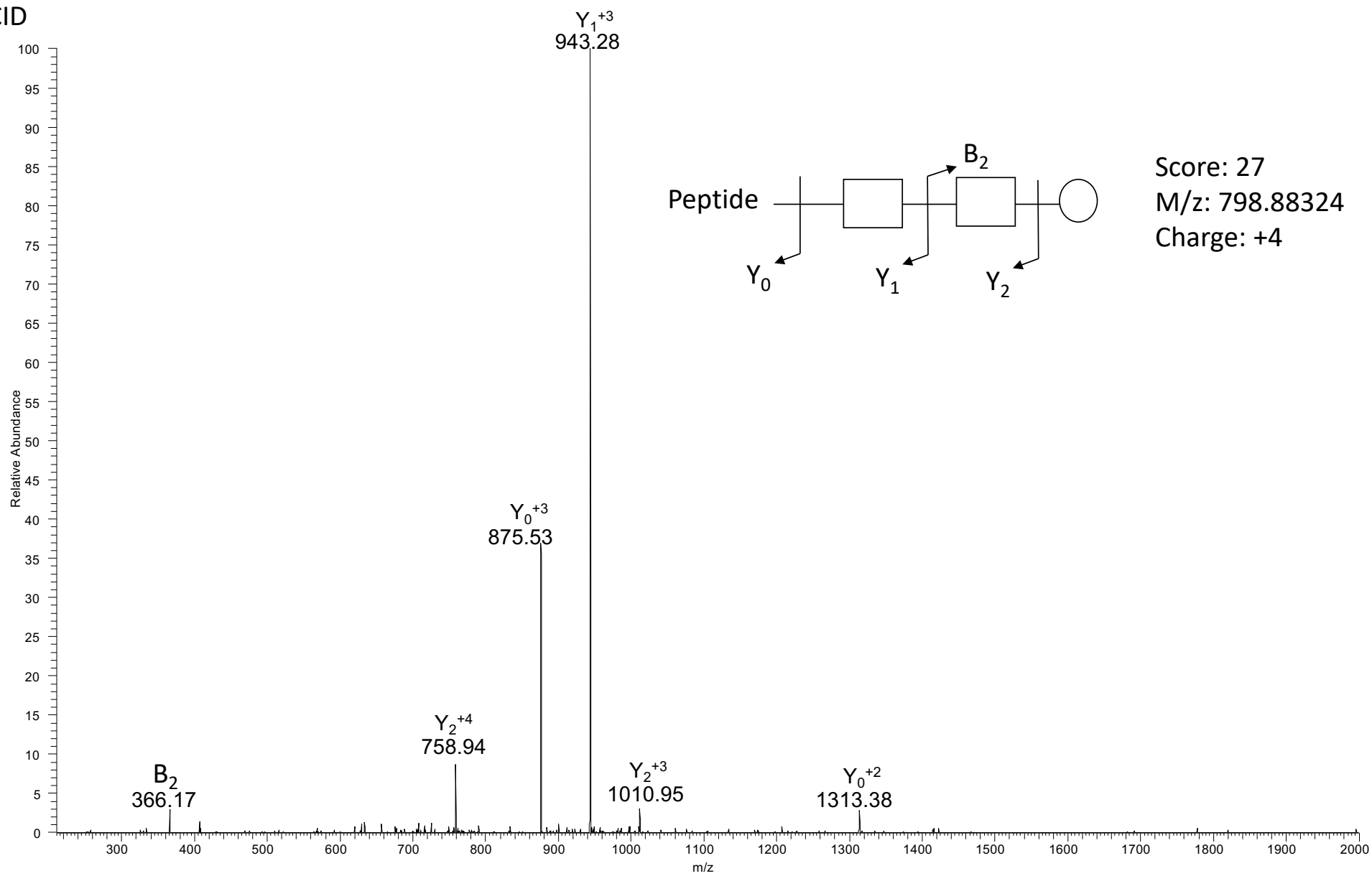
M/z: 820.04755

Charge: +3

FTMS-HCD



ITMS-CID

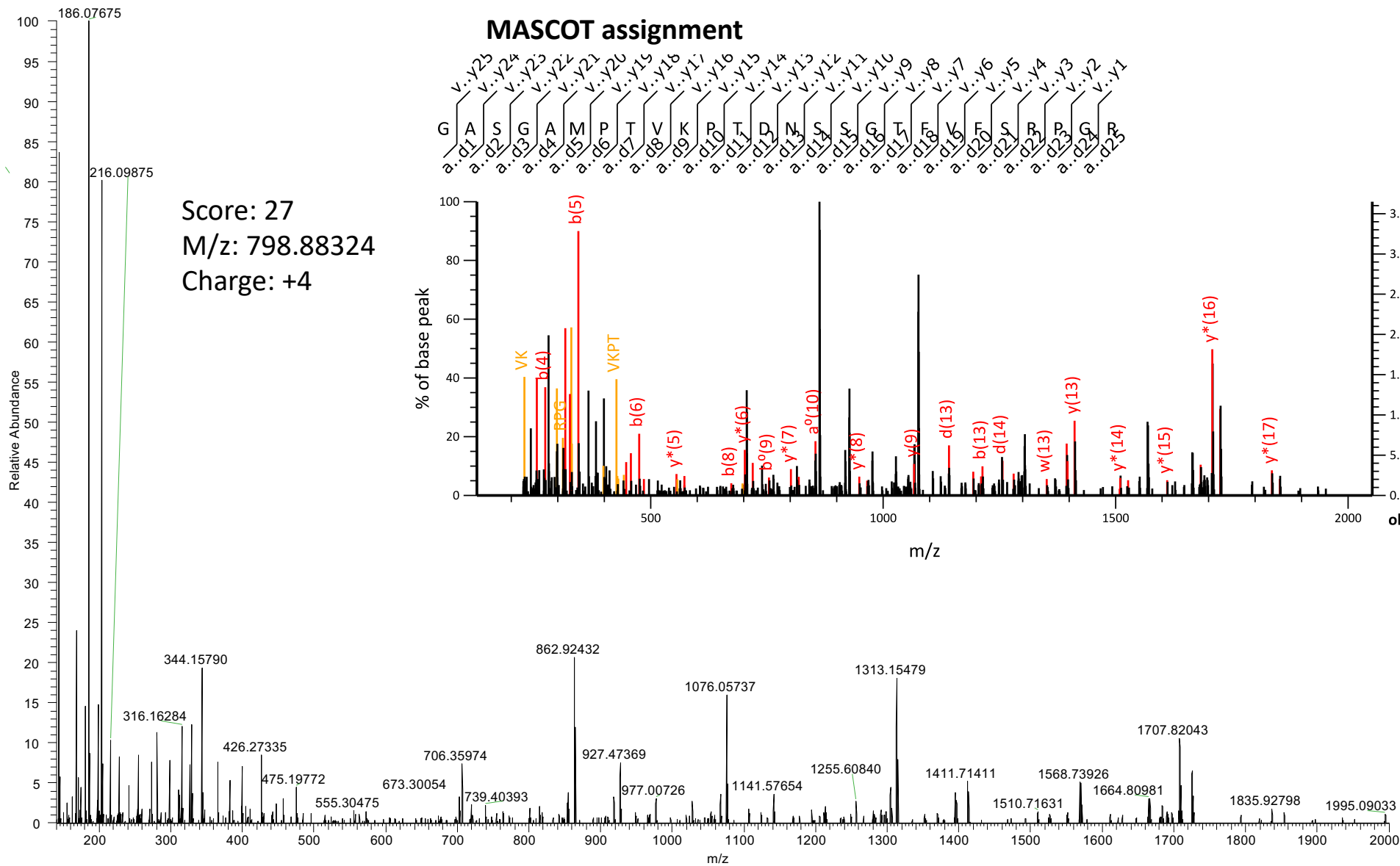


Score: 27

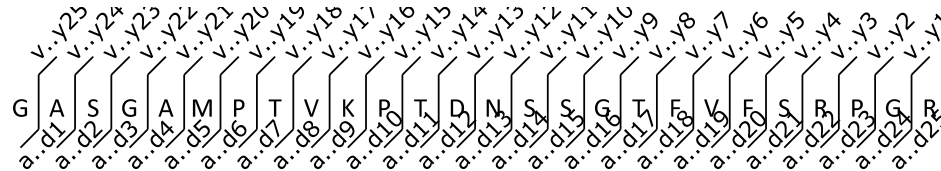
M/z: 798.88324

Charge: +4

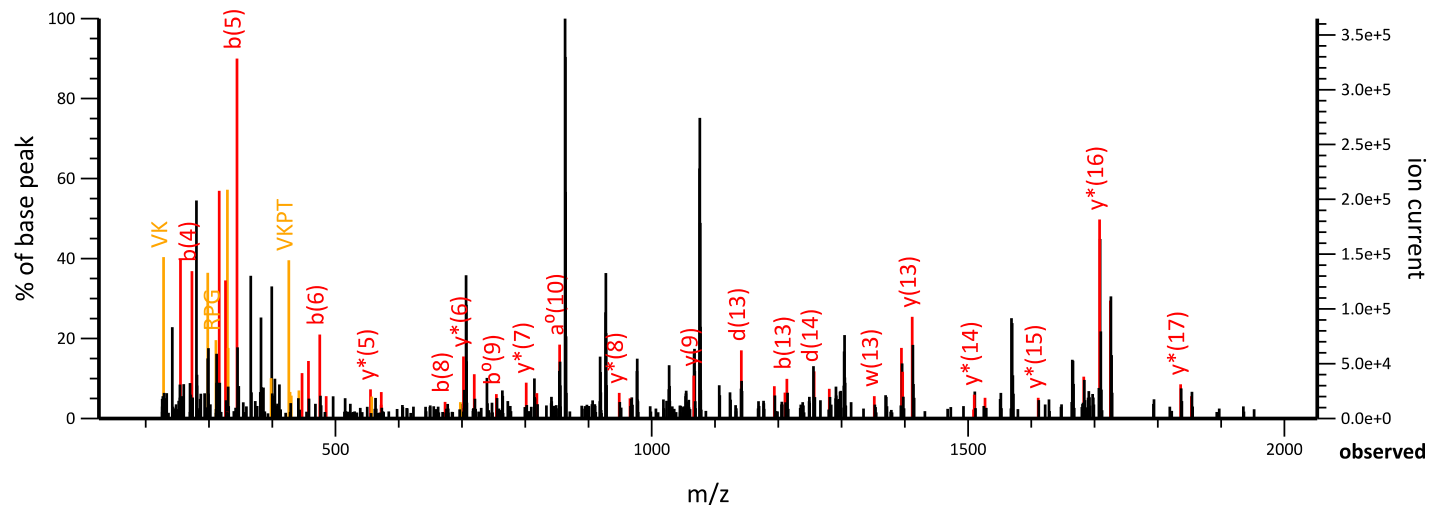
FTMS-HCD



MASCOT assignment



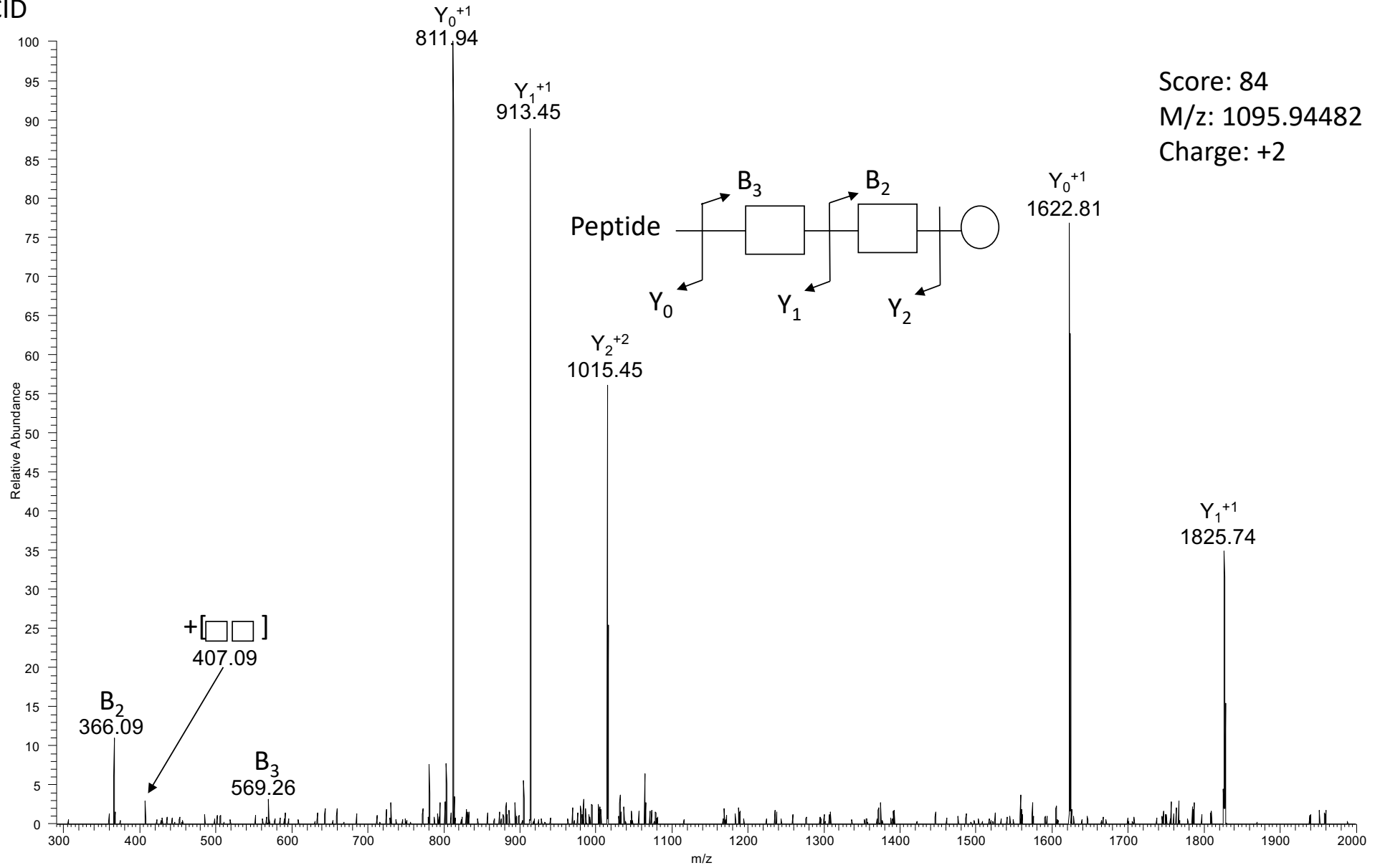
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Charge: +4



observed

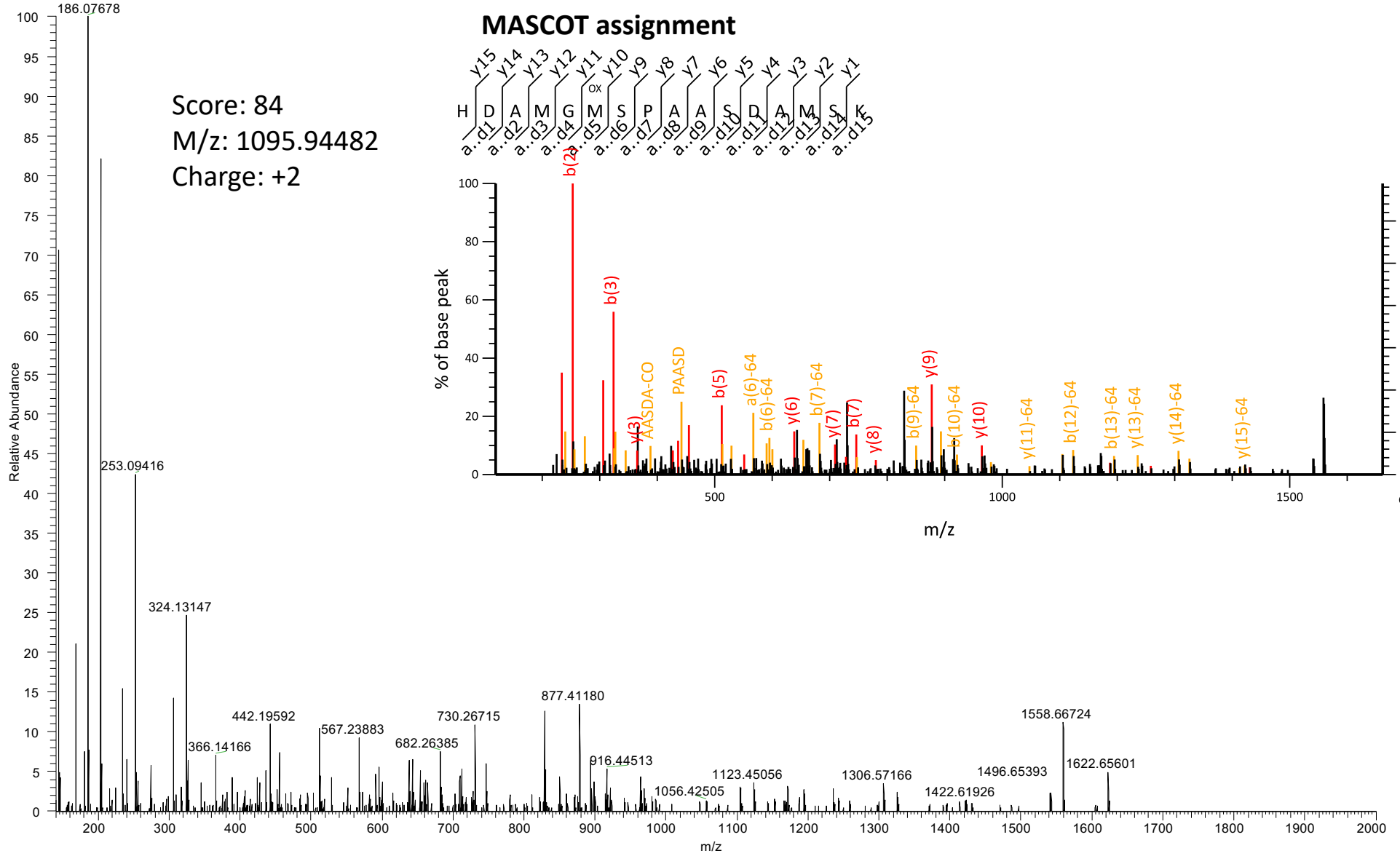
ion current

ITMS-CID

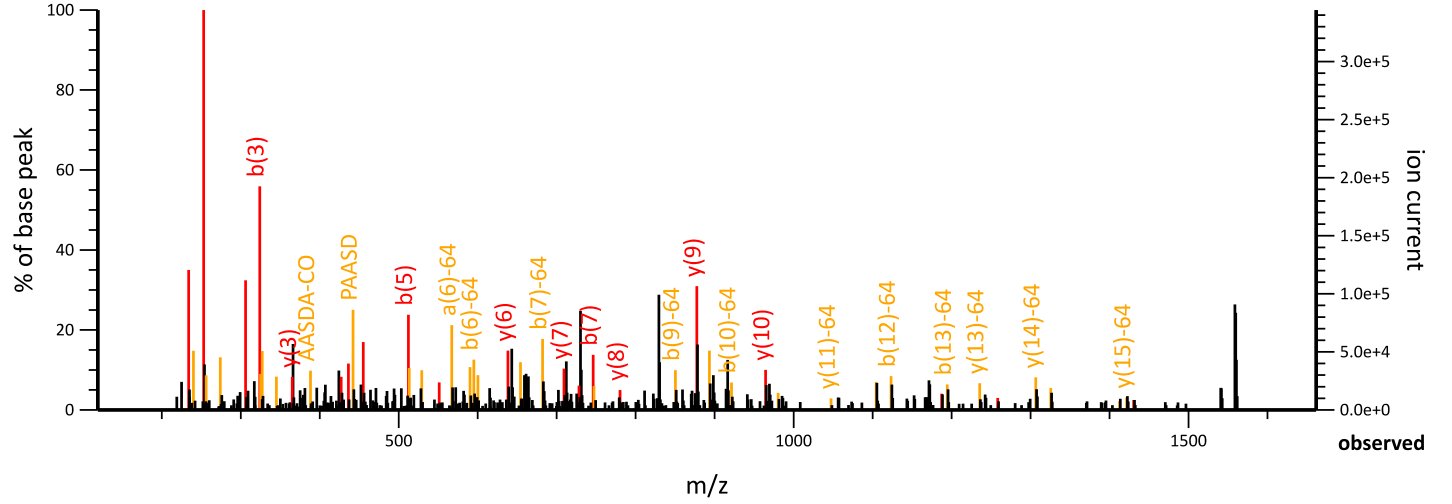
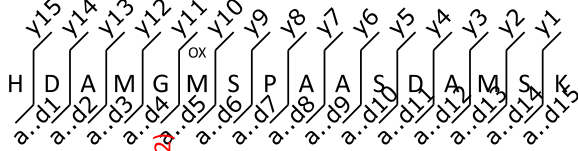


Score: 84
M/z: 1095.94482
Charge: +2

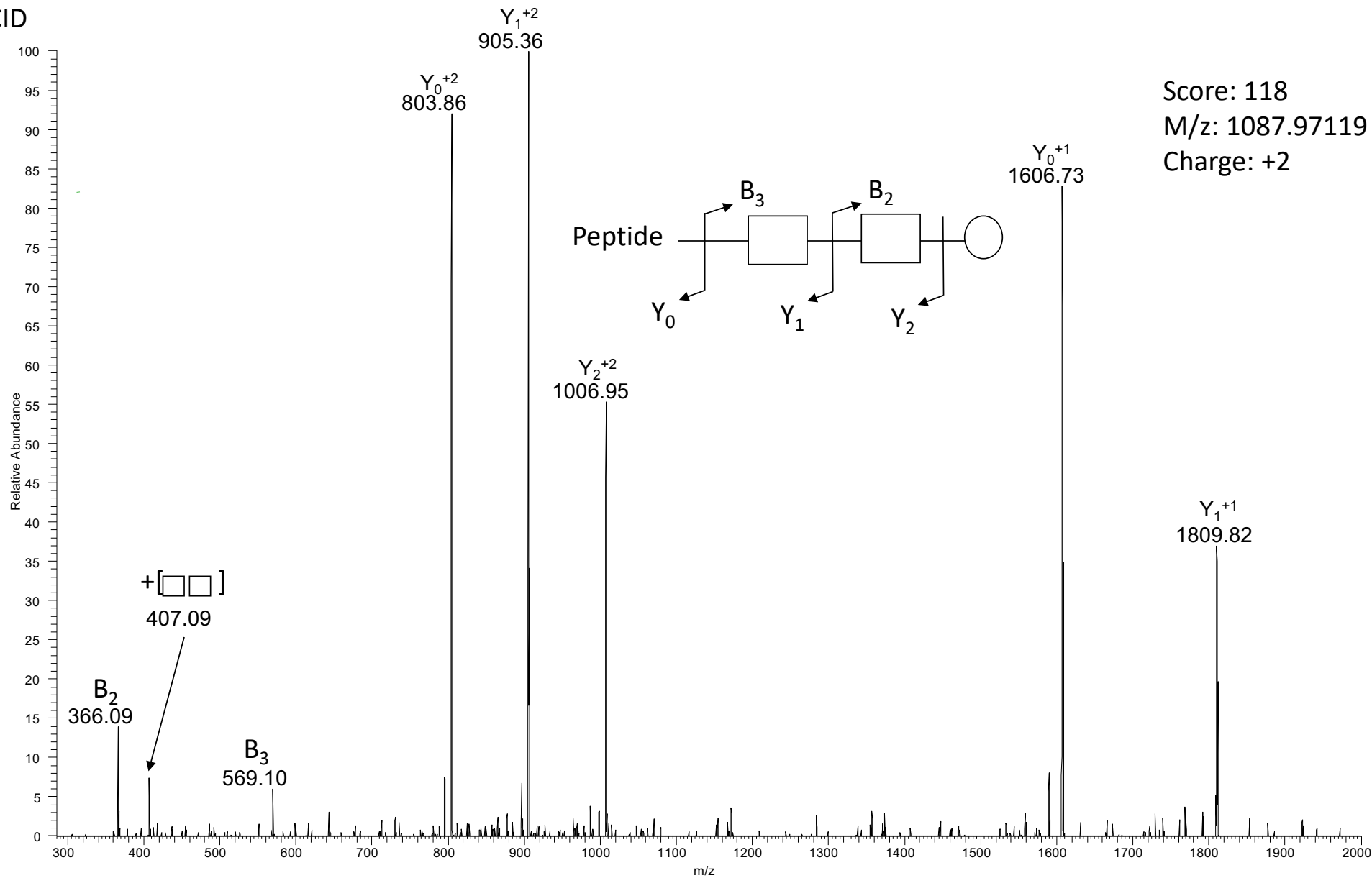
FTMS-HCD



MASCOT assignment

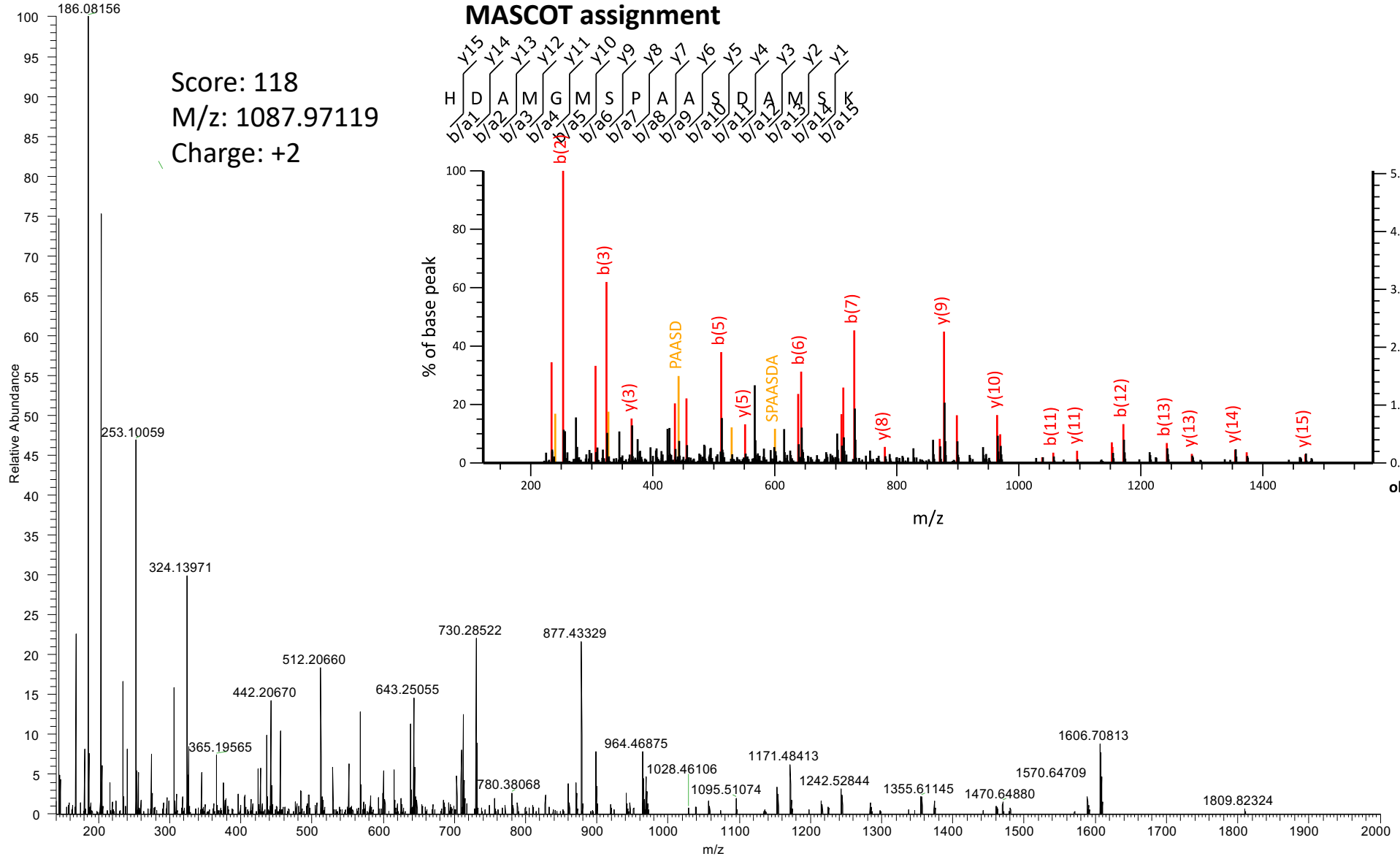


ITMS-CID



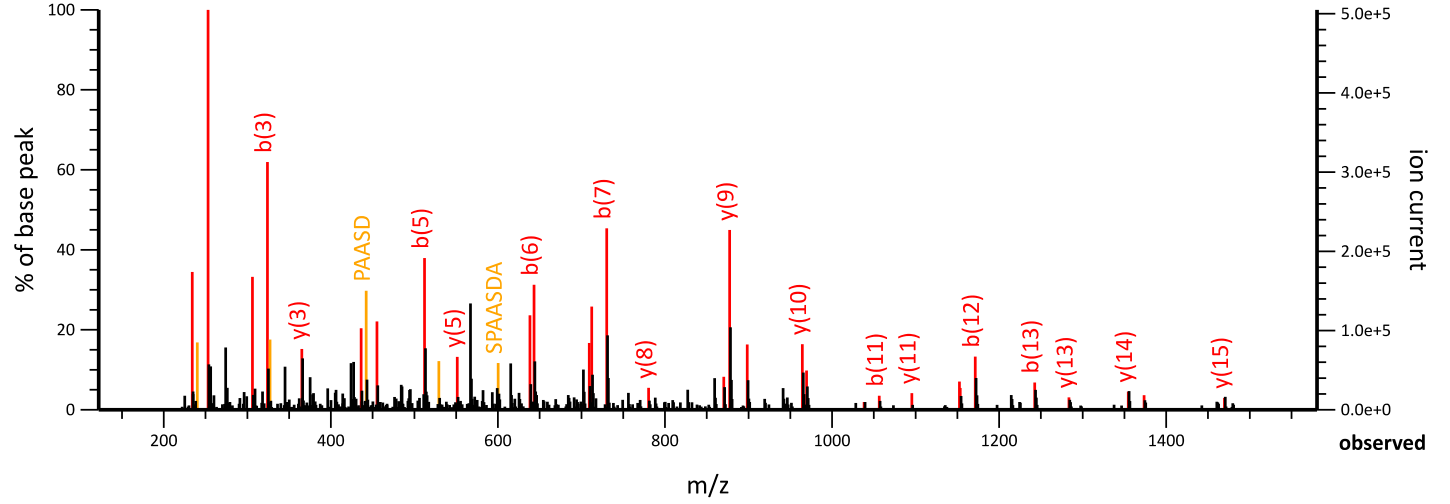
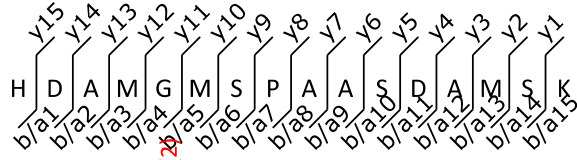
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M/z: 1087.97119
Charge: +2

FTMS-HCD

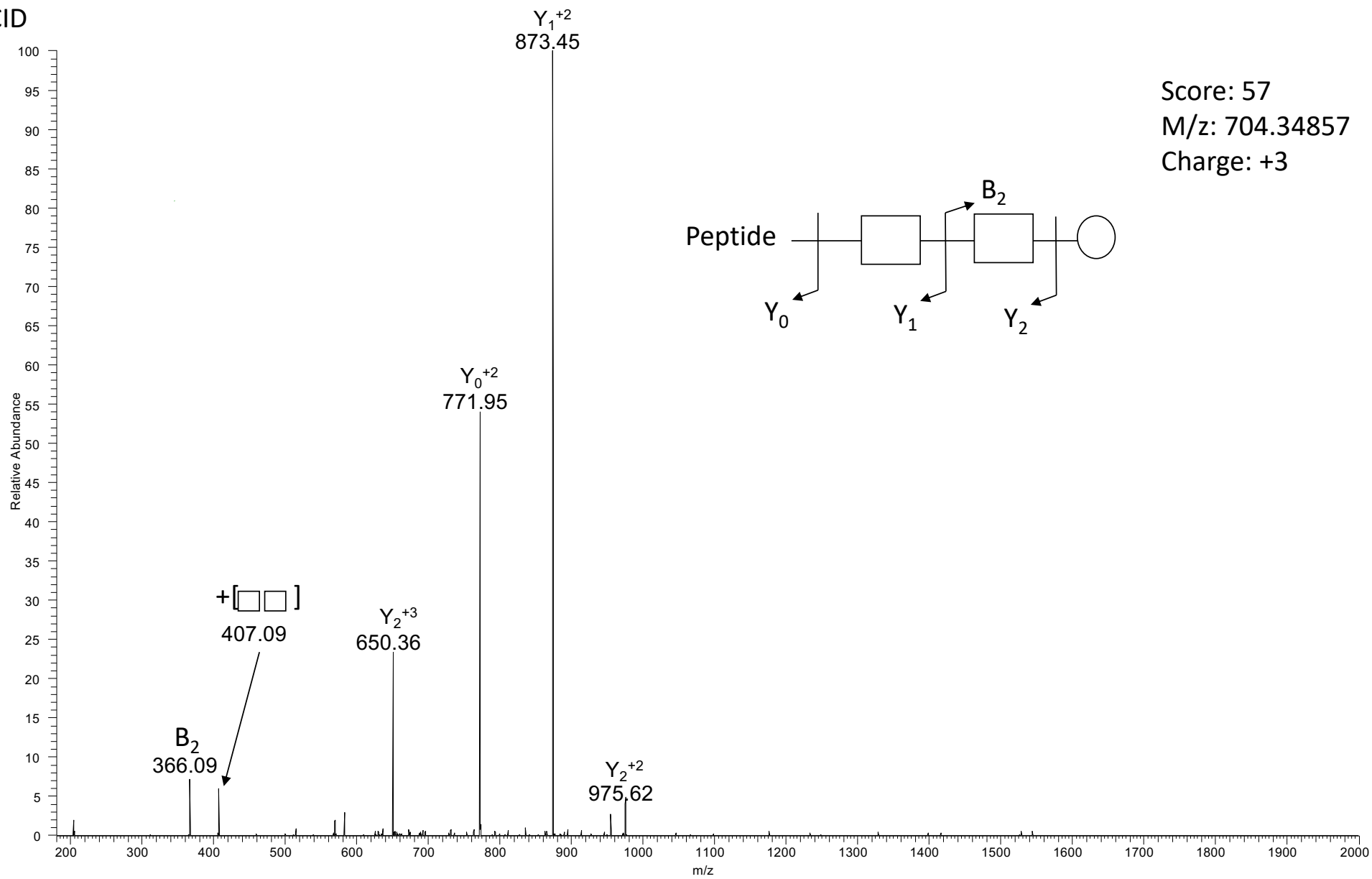


Score: 118
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Charge: +2

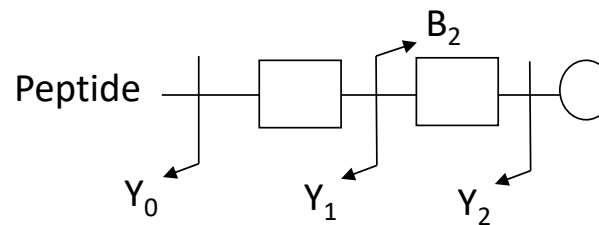
MASCOT assignment



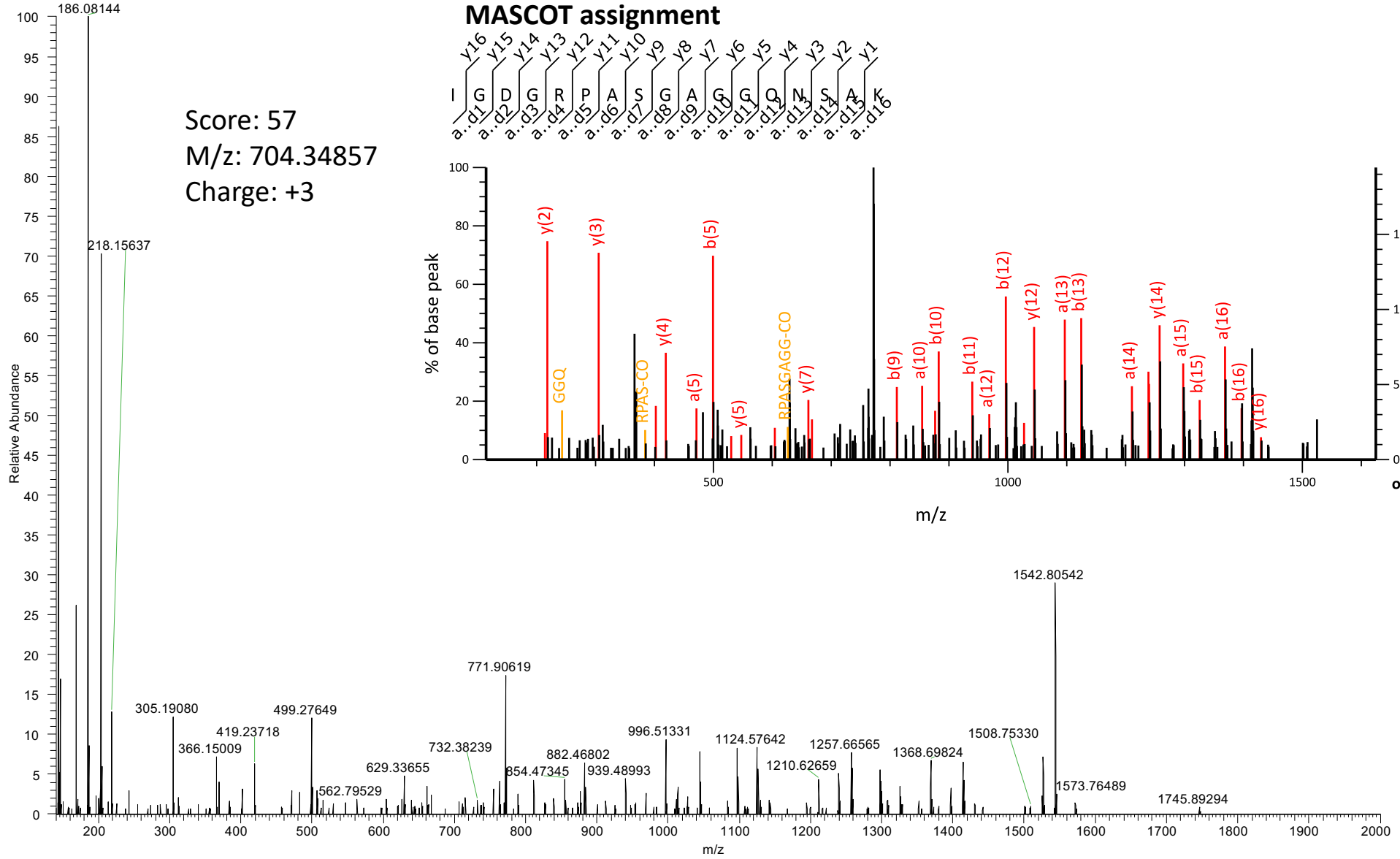
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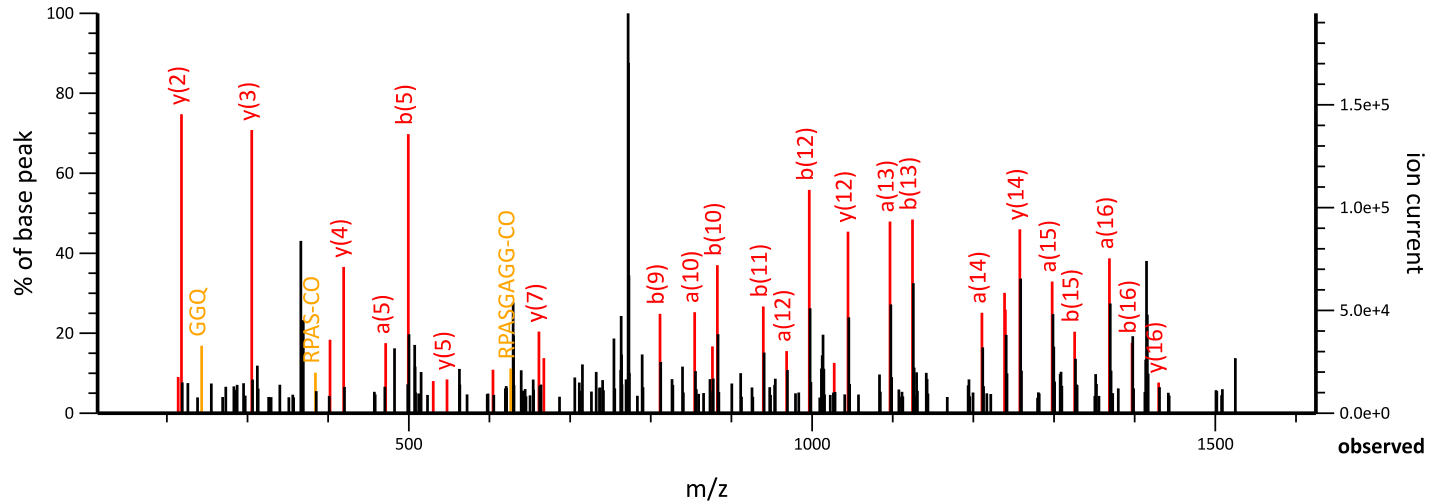
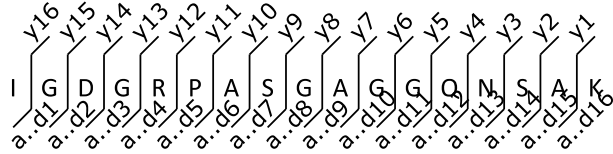
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M/z: 704.34857
Charge: +3



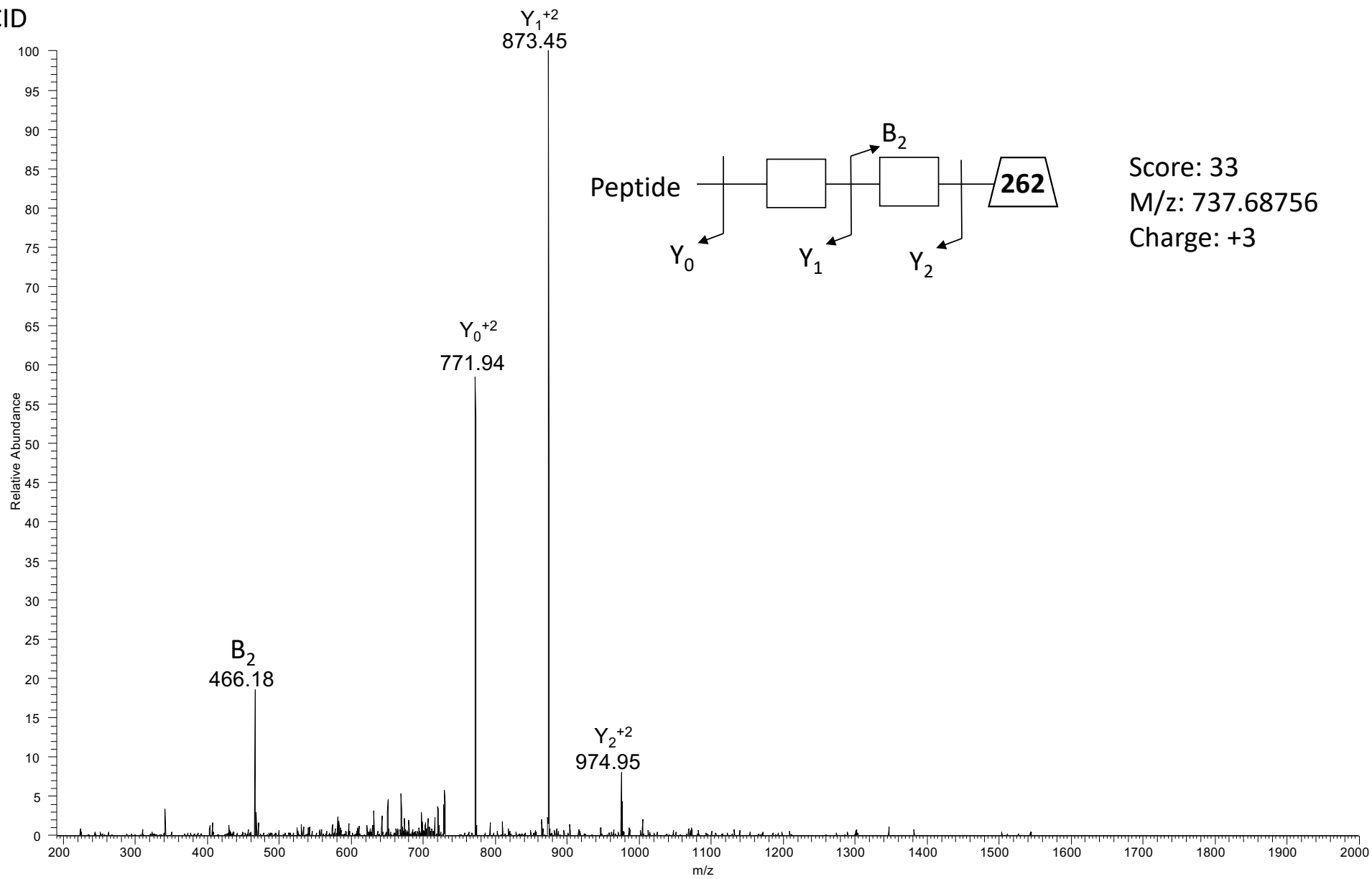
FTMS-HCD



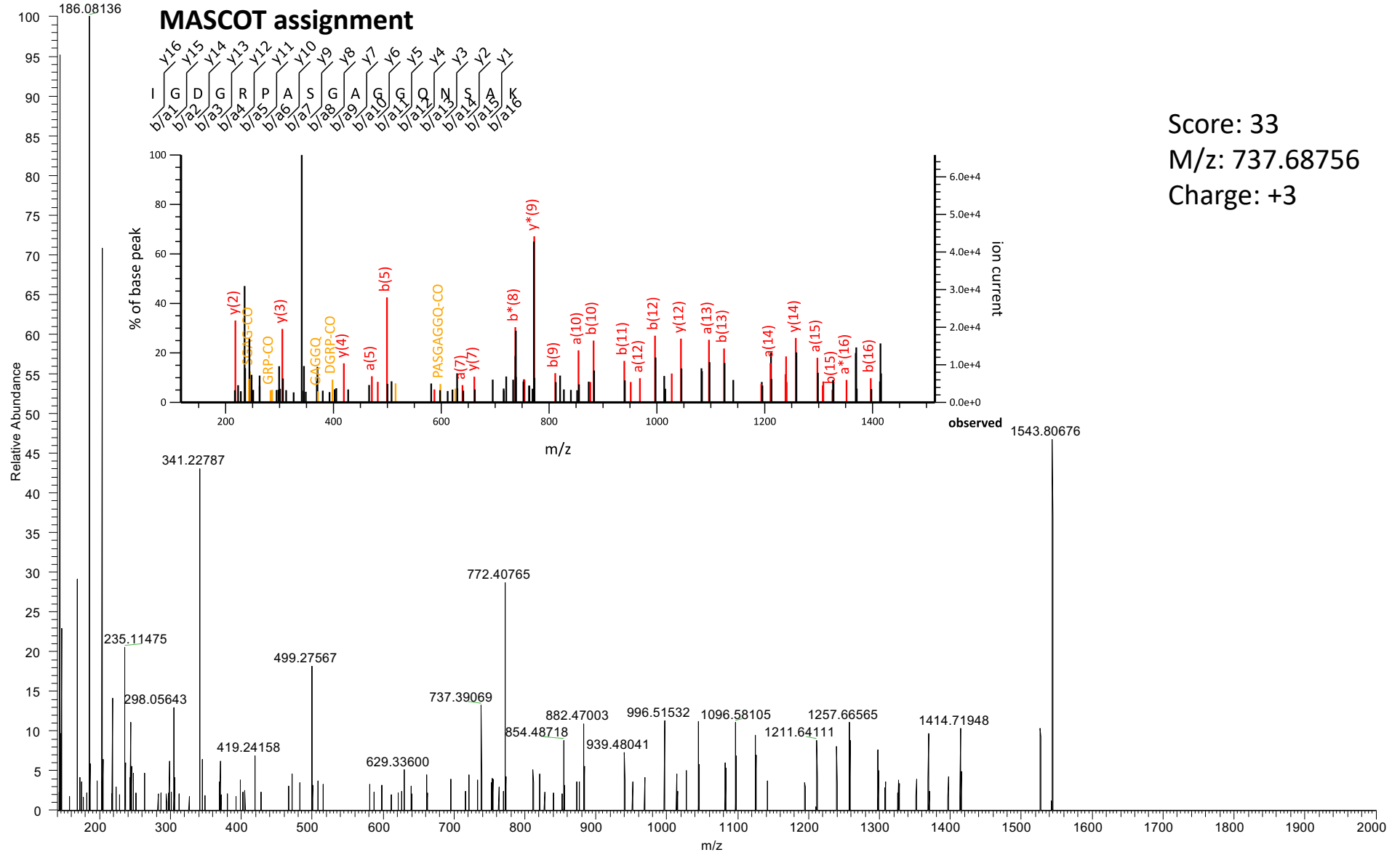
MASCOT assignment



ITMS-CID

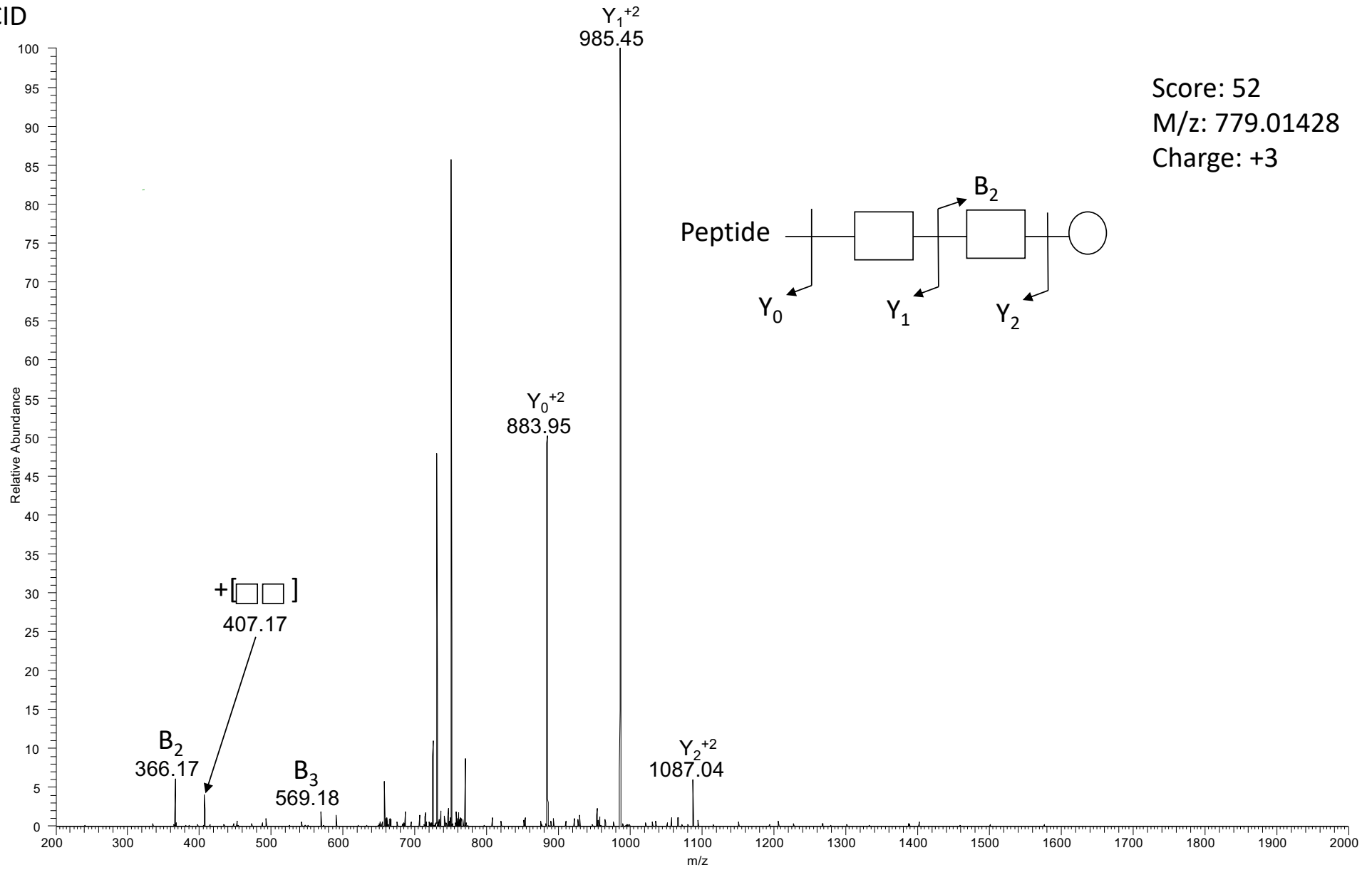


FTMS-HCD

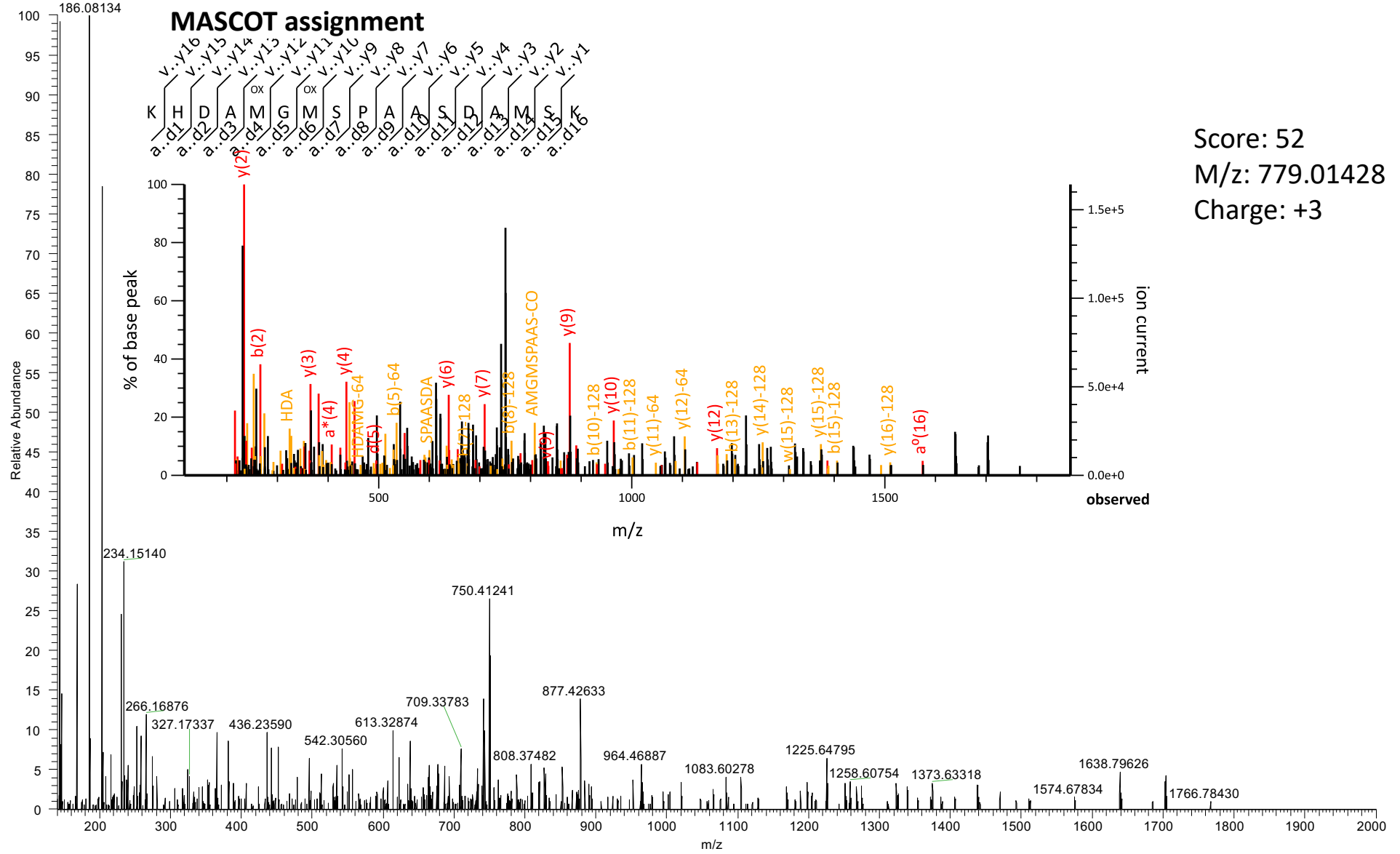


ITMS-CID

Score: 52
M/z: 779.01428
Charge: +3

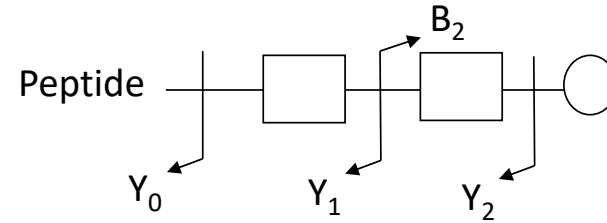
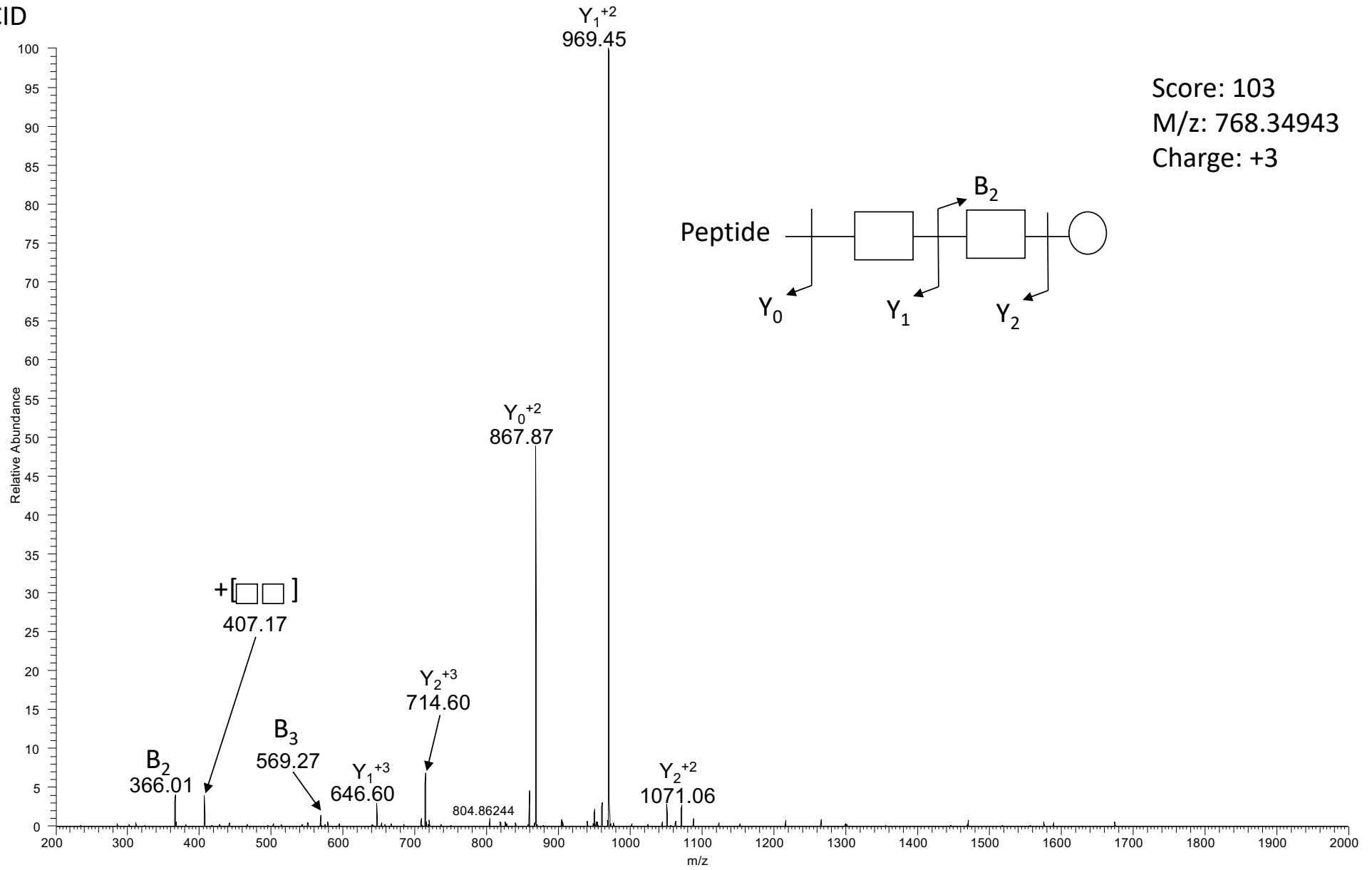


FTMS-HCD

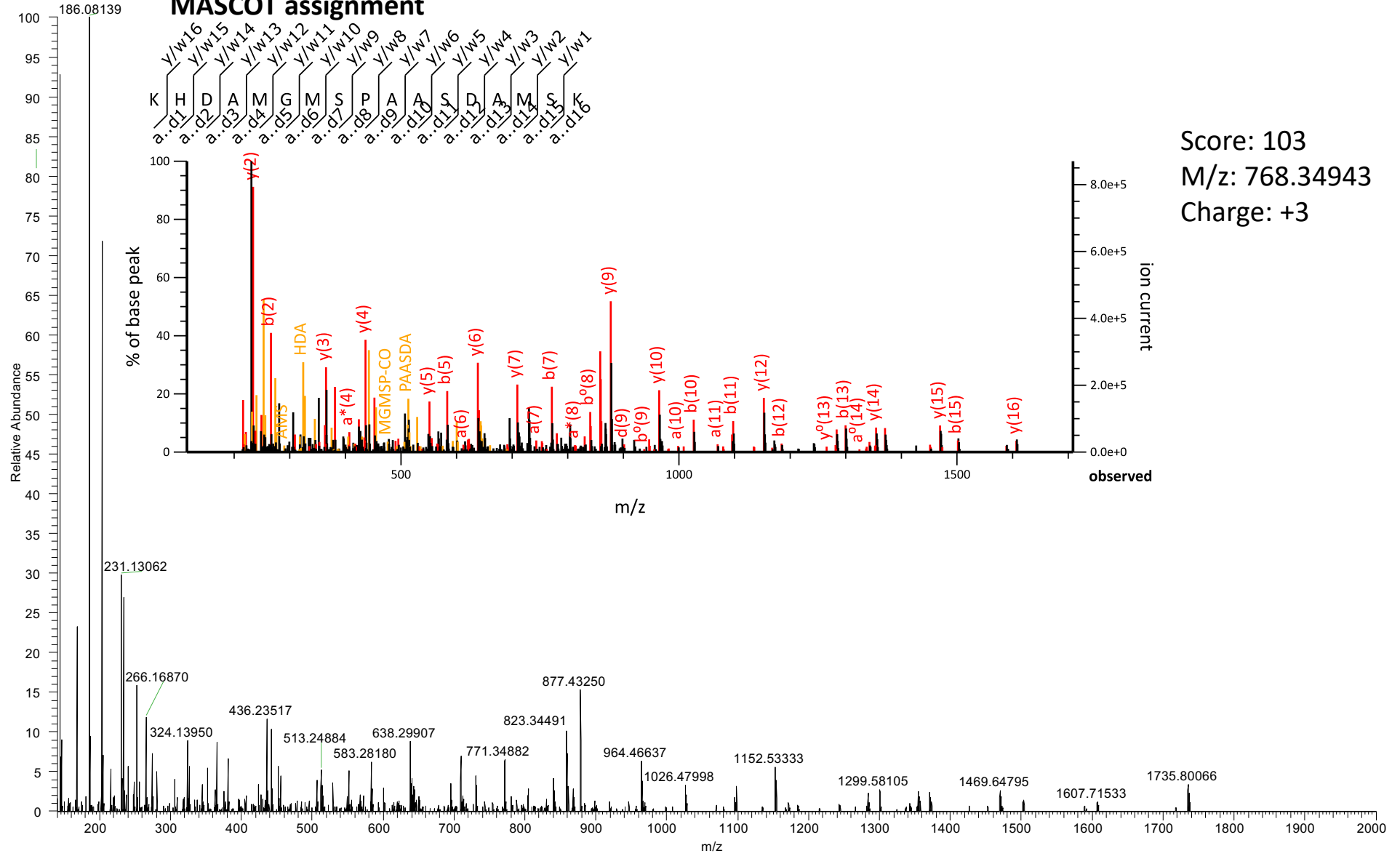


ITMS-CID

Score: 103
M/z: 768.34943
Charge: +3

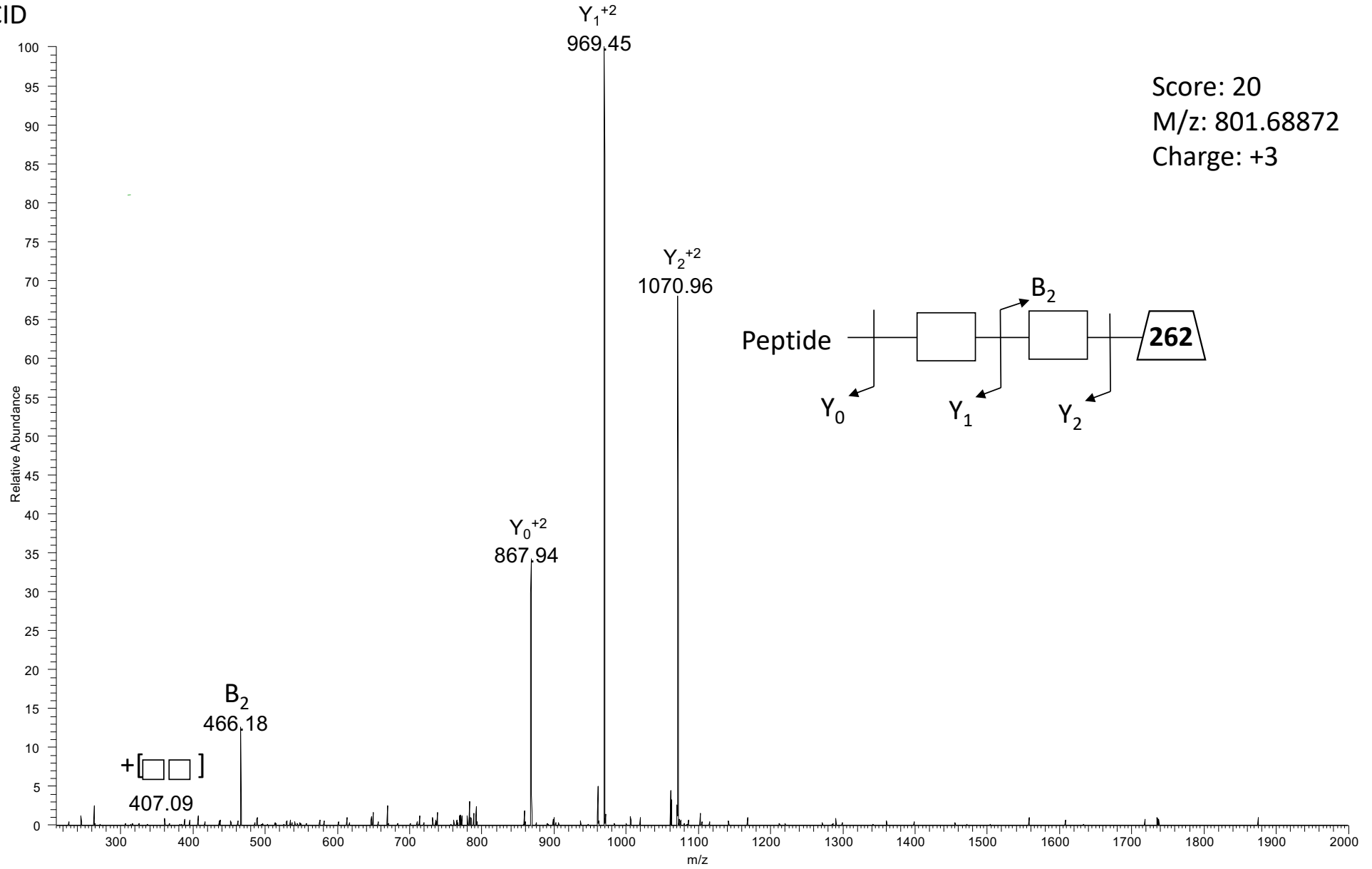


FTMS-HCD



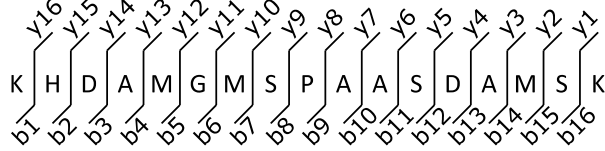
ITMS-CID

Score: 20
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Charge: +3

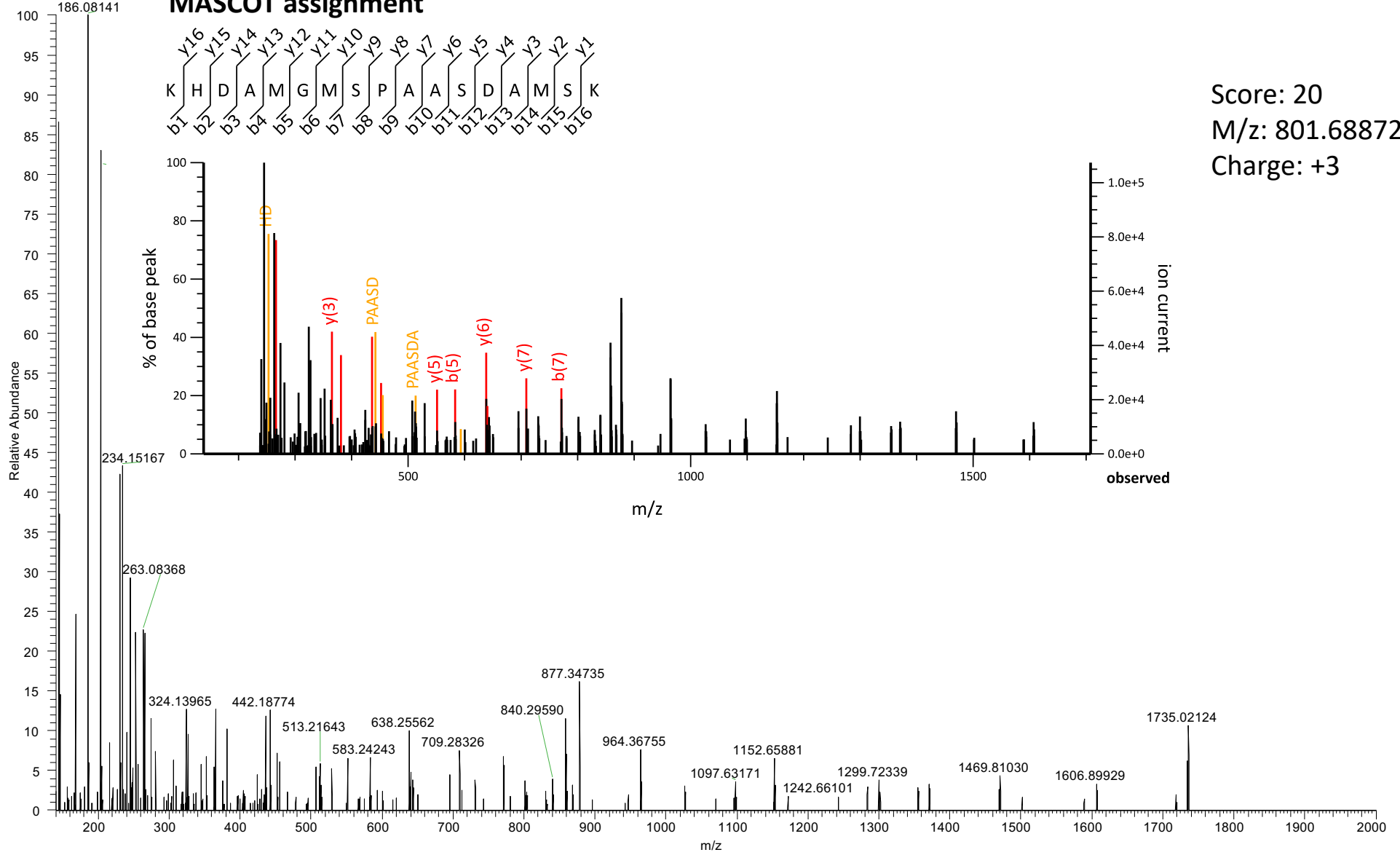


FTMS-HCD

MASCOT assignment

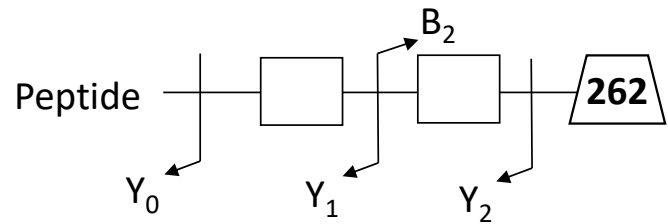
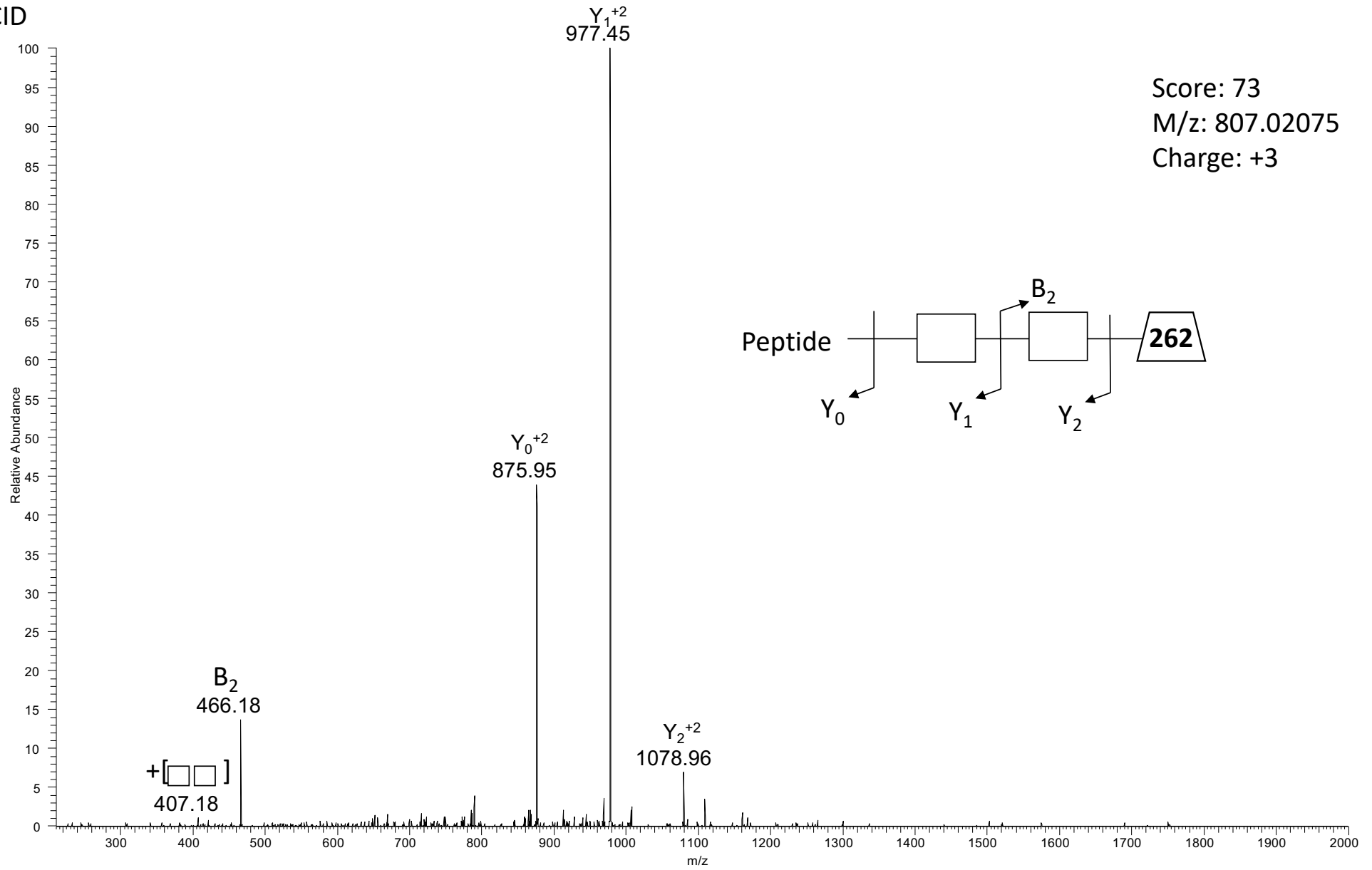


Score: 20
M/z: 801.68872
Charge: +3



ITMS-CID

Score: 73
M/z: 807.02075
Charge: +3



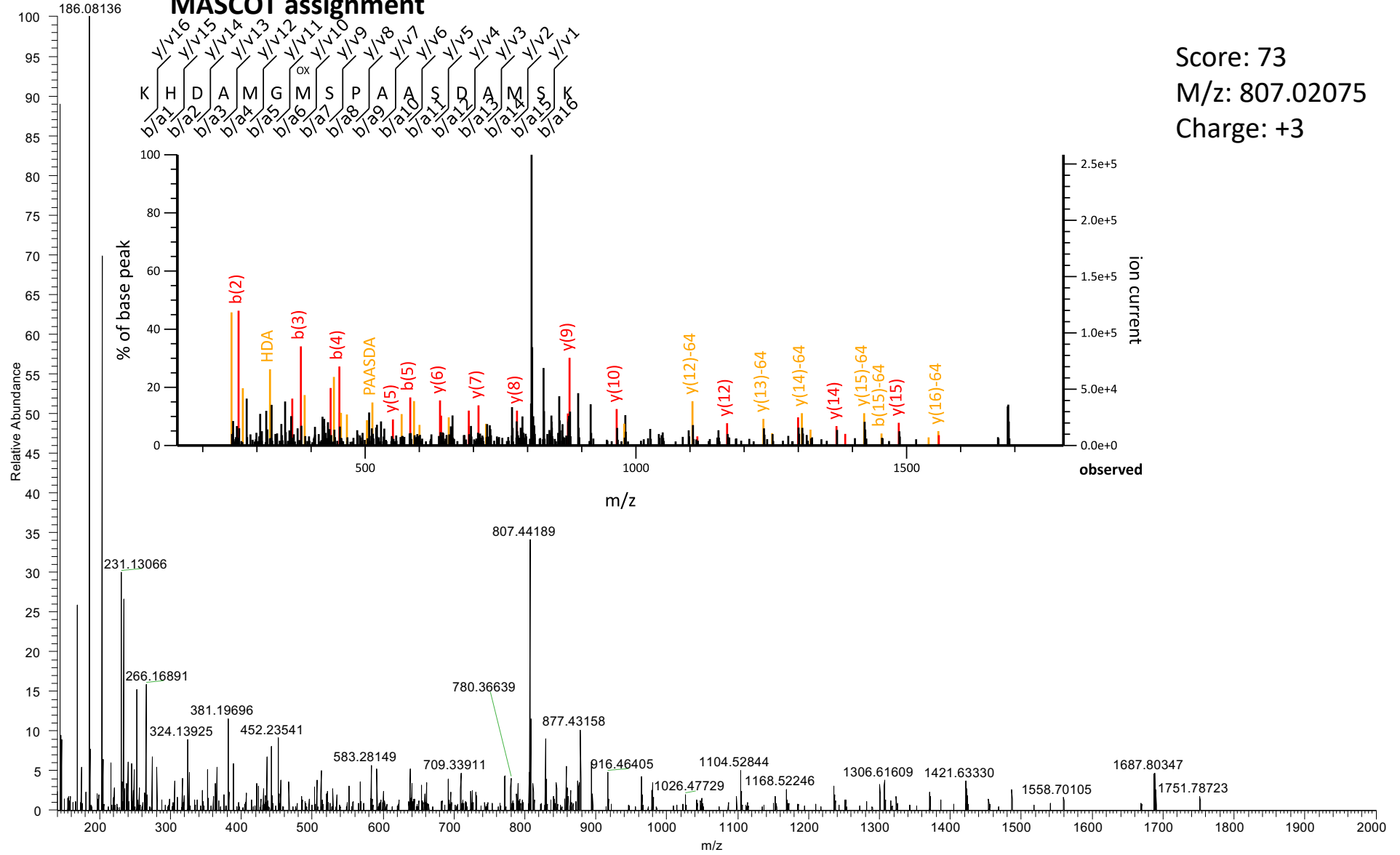
FTMS-HCD

MASCOT assignment

Score: 73

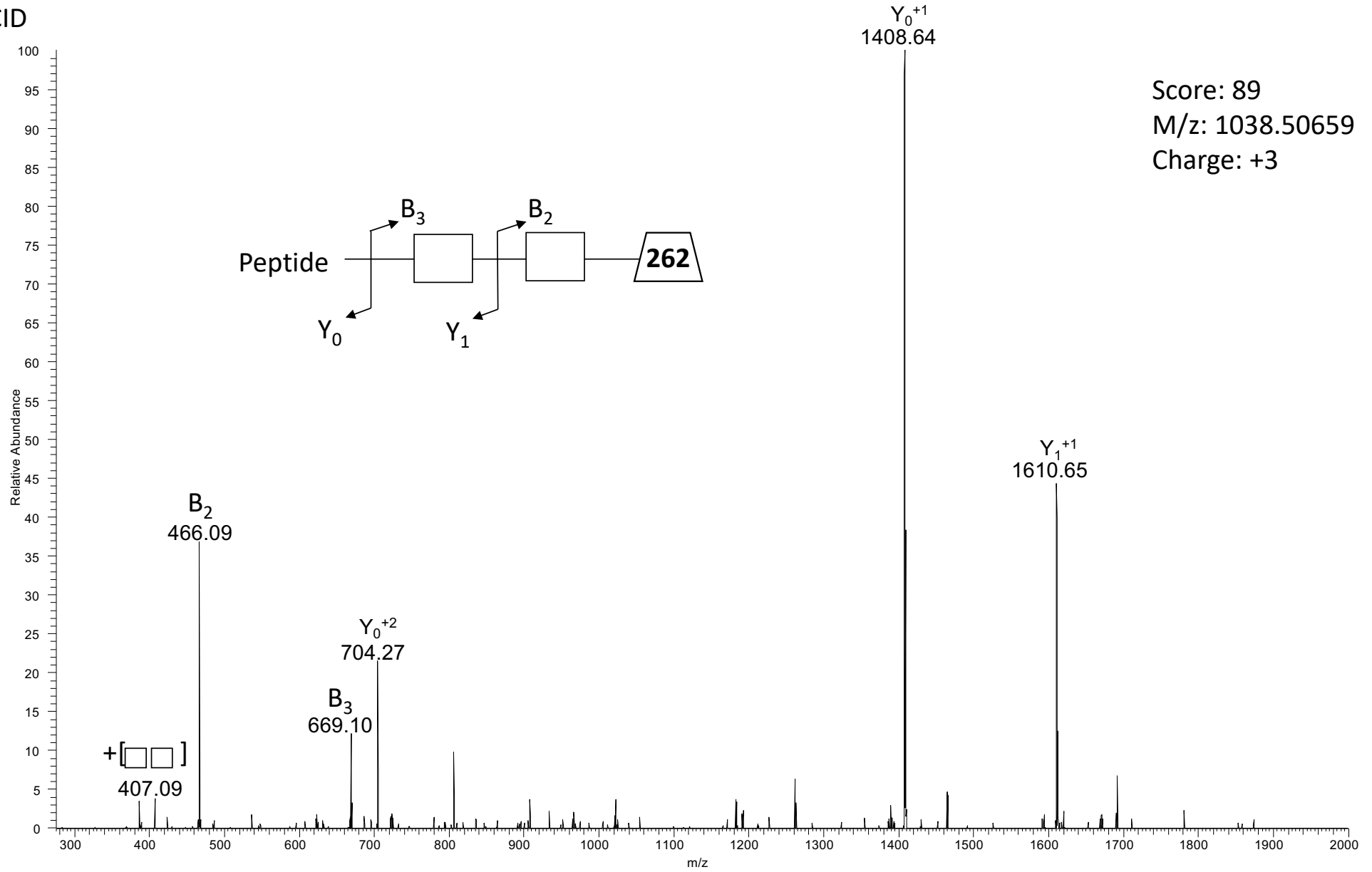
M/z: 807.02075

Charge: +3



ITMS-CID

Score: 89
M/z: 1038.50659
Charge: +3



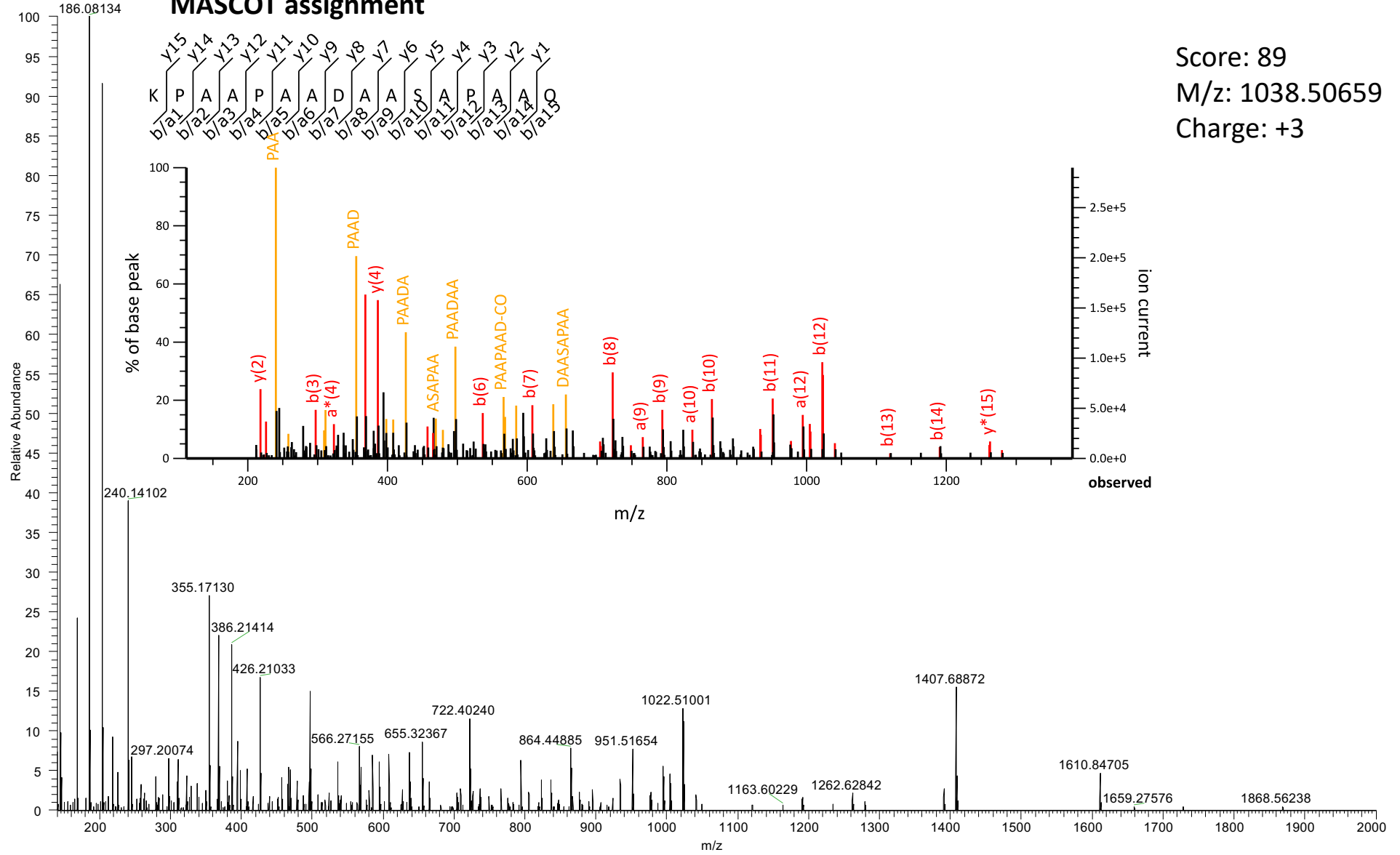
FTMS-HCD

MASCOT assignment

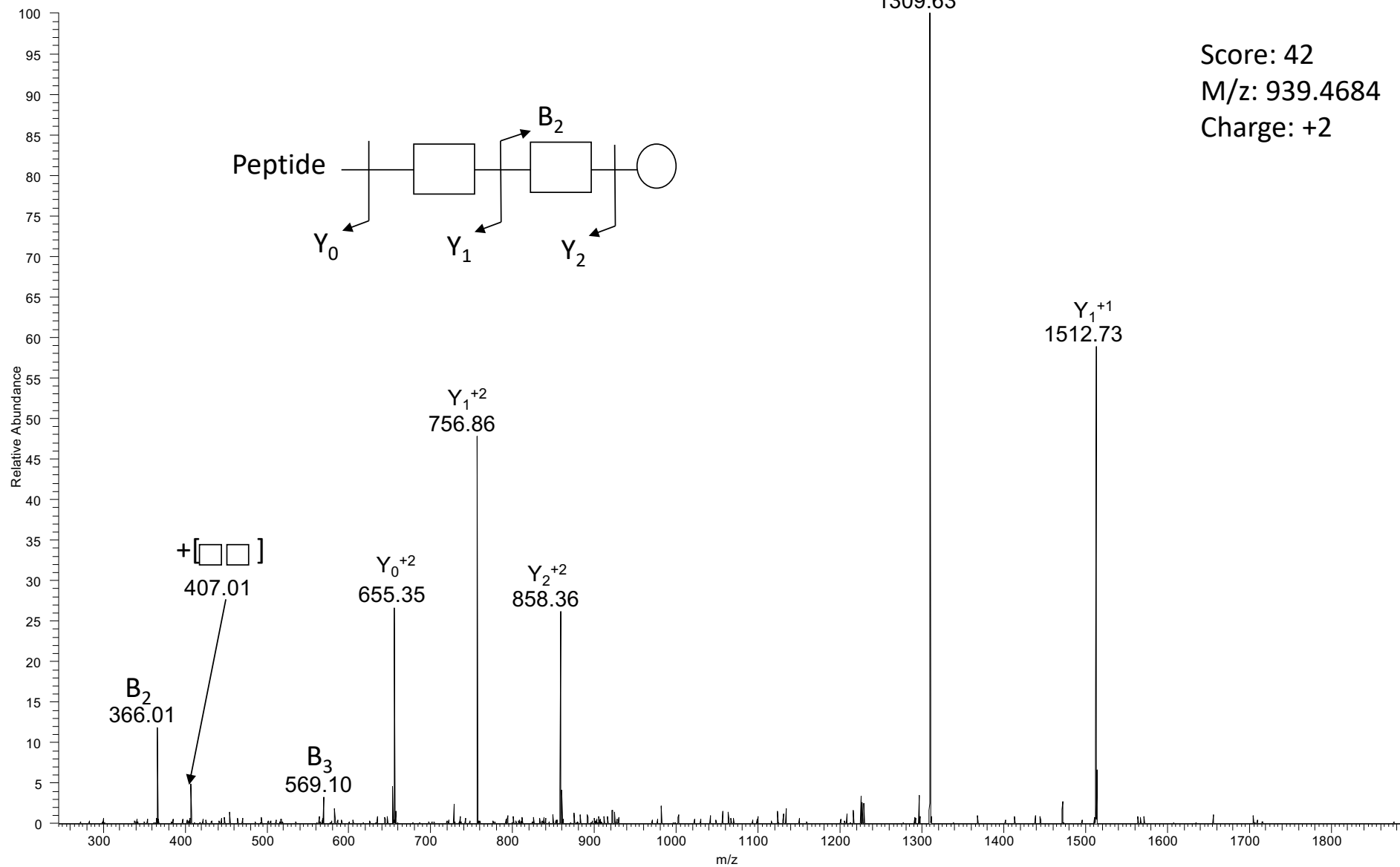
Score: 89

M/z: 1038.50659

Charge: +3



ITMS-CID



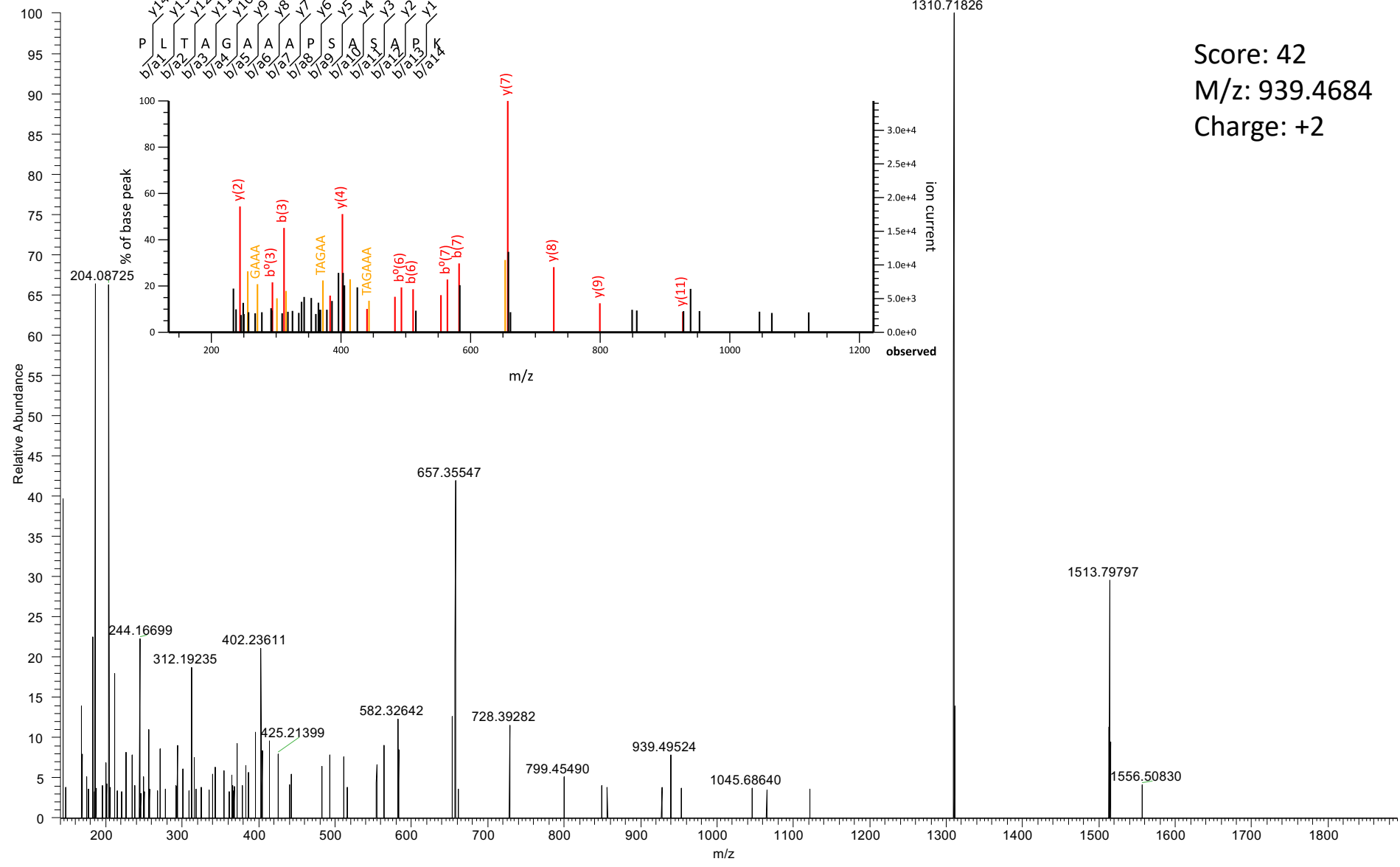
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M/z: 939.4684
Charge: +2

FTMS-HCD

MASCOT assignment

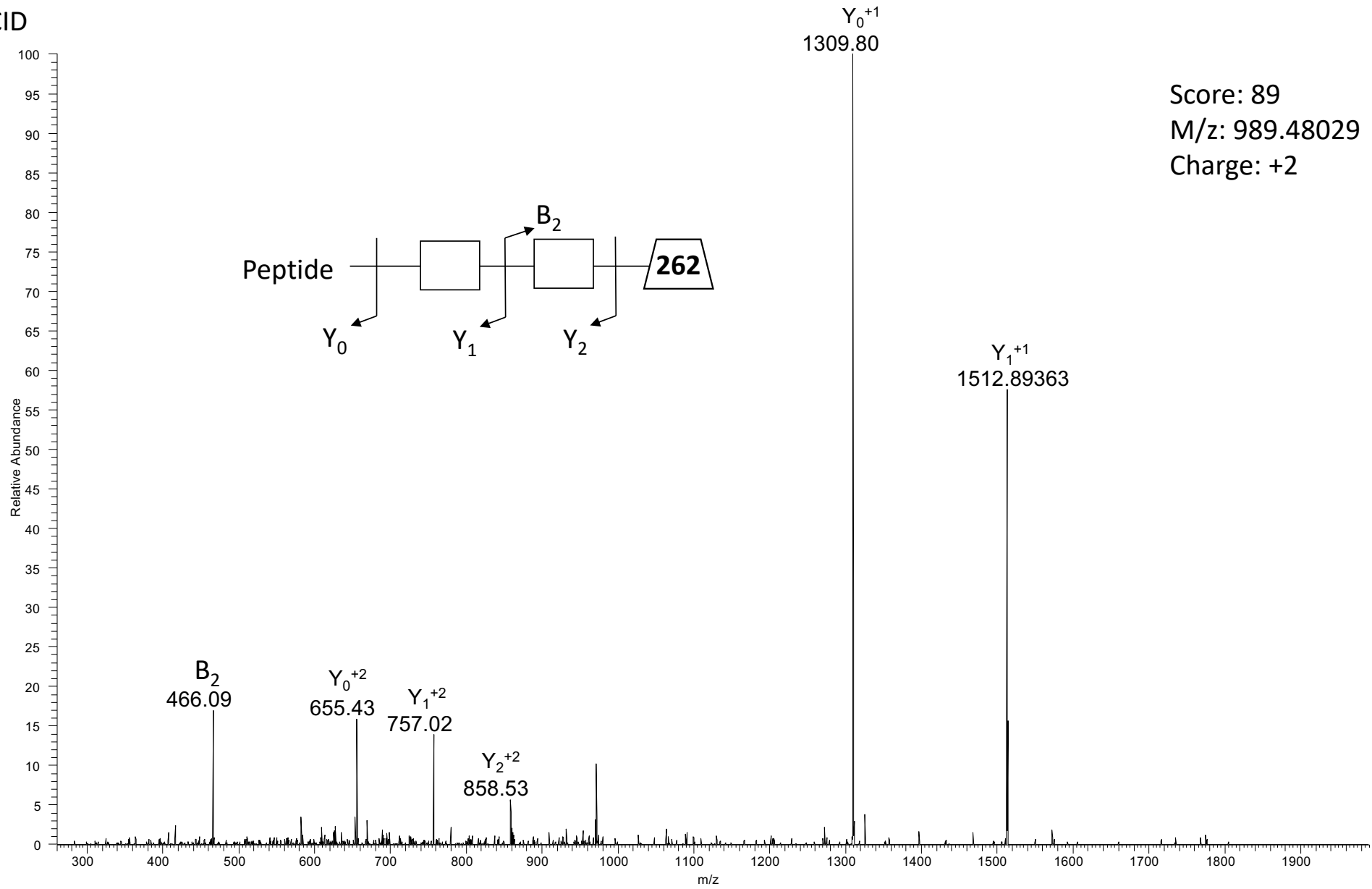
P L T A G A A A P S A S A P K
b1/r14 b1/r13 b1/r12 b1/r11 b1/r10 b1/r9 b1/r8 b1/r7 b1/r6 b1/r5 b1/r4 b1/r3 b1/r2 b1/r1

Score: 42
M/z: 939.4684
Charge: +2

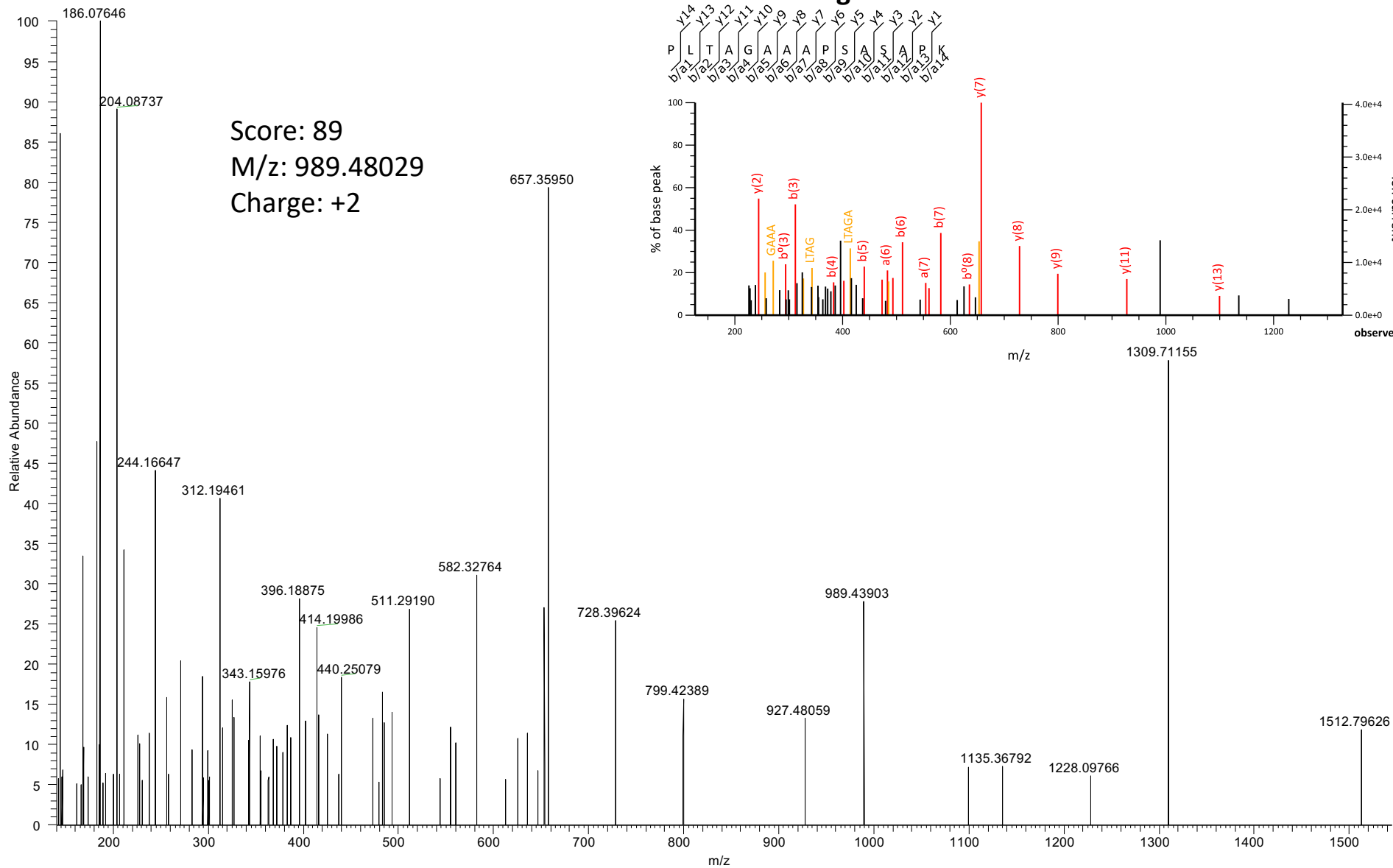


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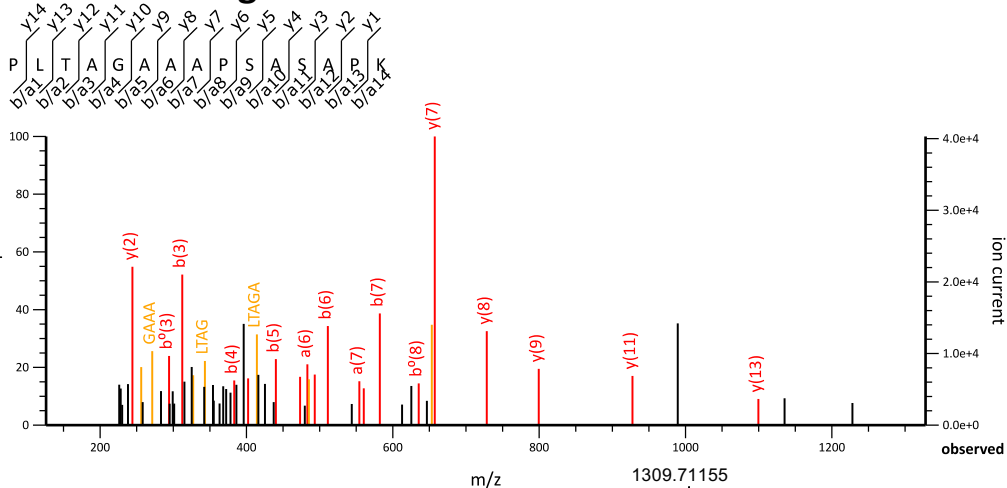
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M/z: 989.48029
Charge: +2



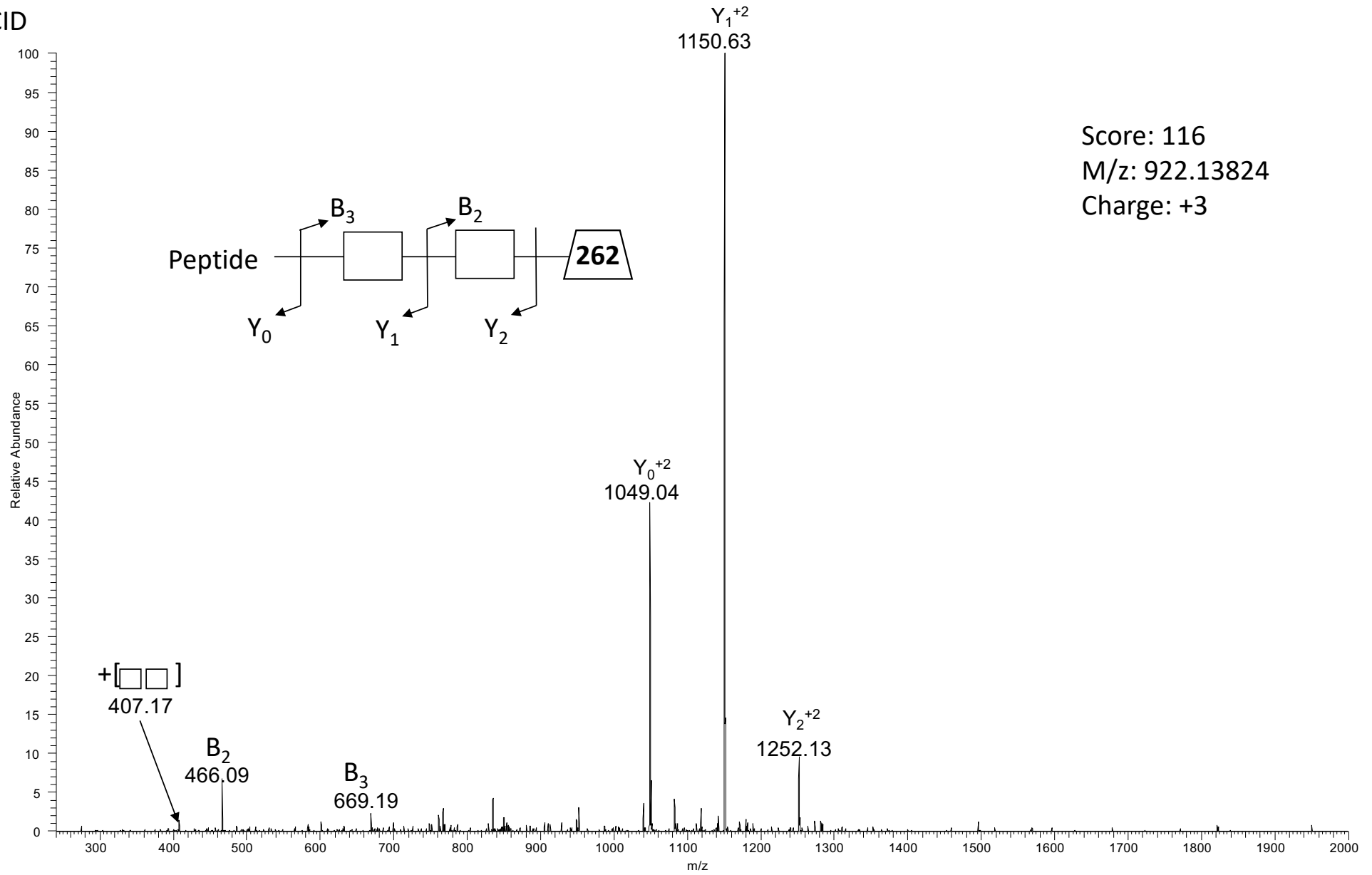
FTMS-HCD



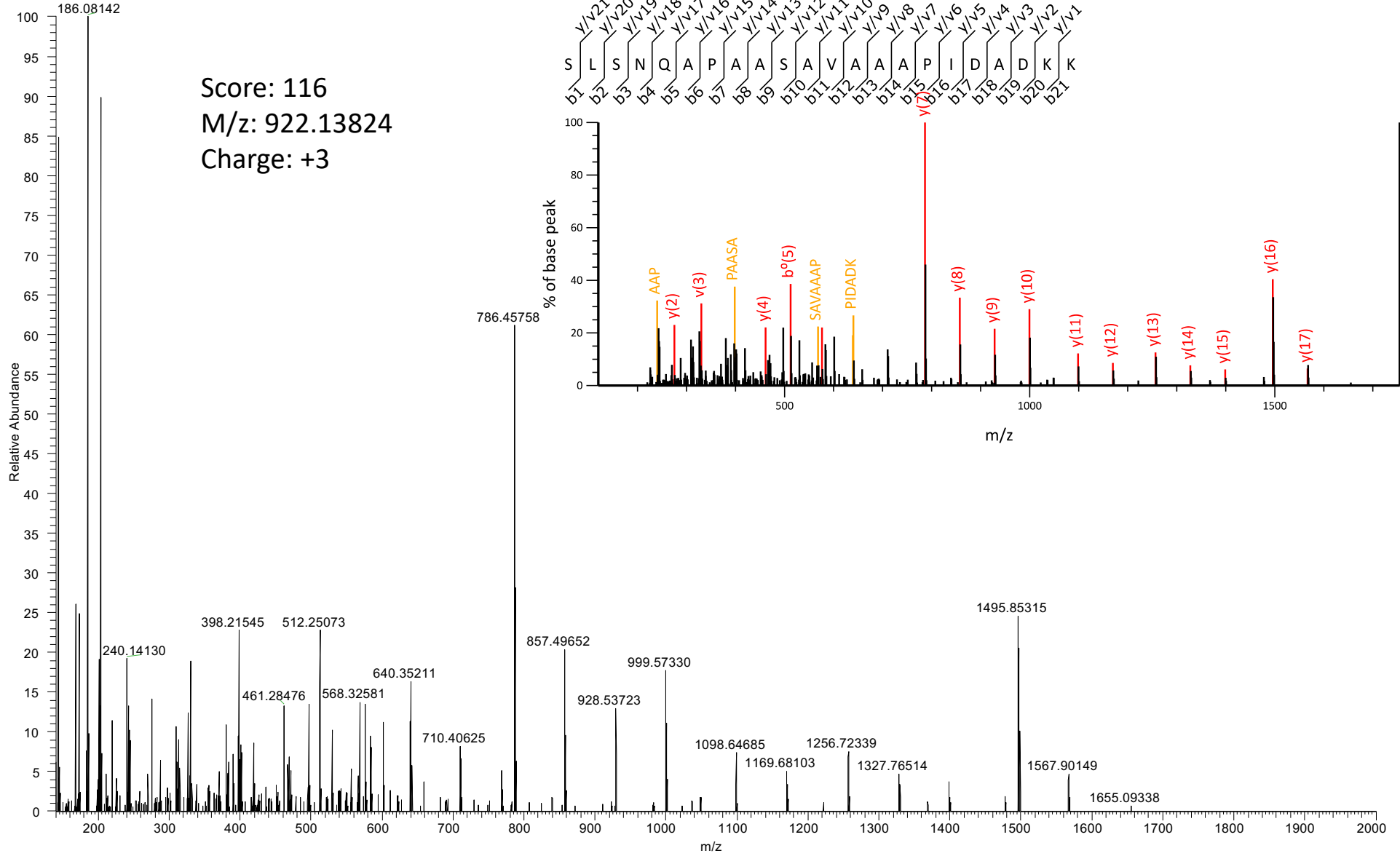
MASCOT assignment



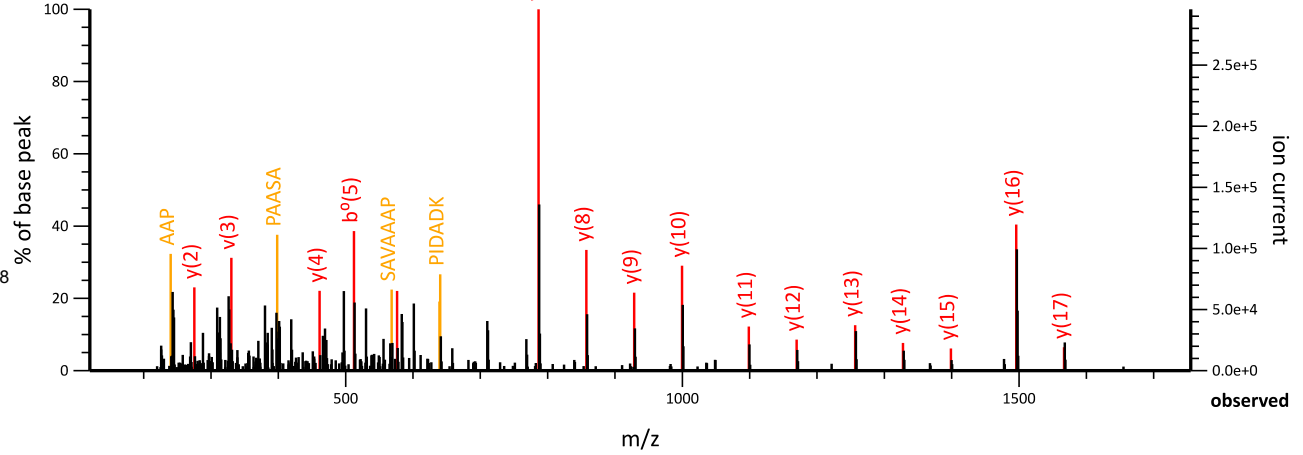
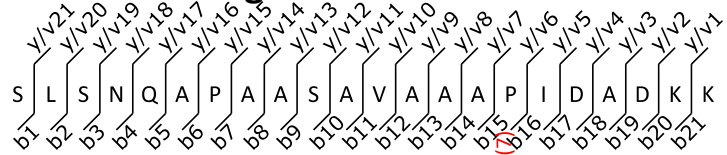
ITMS-CID



FTMS-HCD

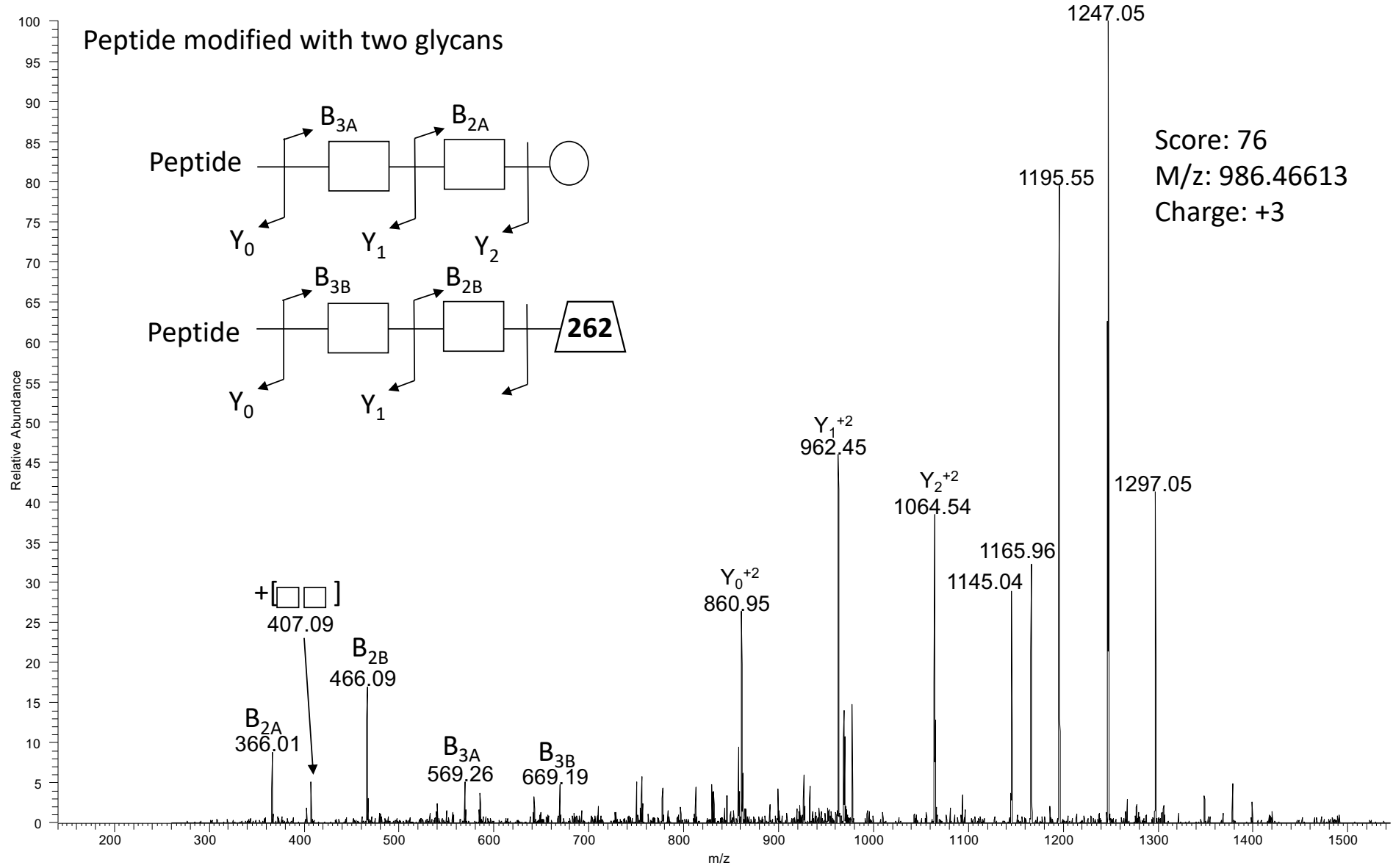


MASCOT assignment

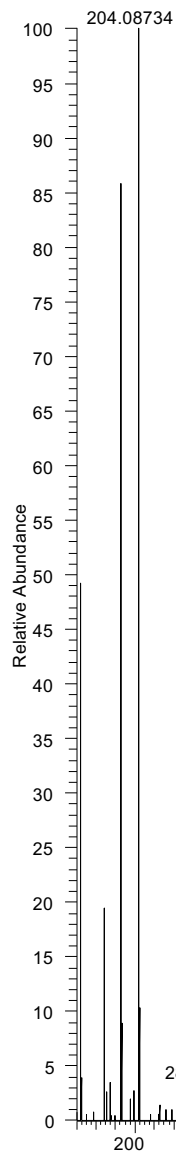


ion current
2.5e+5
2.0e+5
1.5e+5
1.0e+5
5.0e+4
0.0e+0
observed

ITMS-CID



FTMS-HCD



Score: 76
M/z: 986.46613
Charge: +3

MASCOT assignment

