

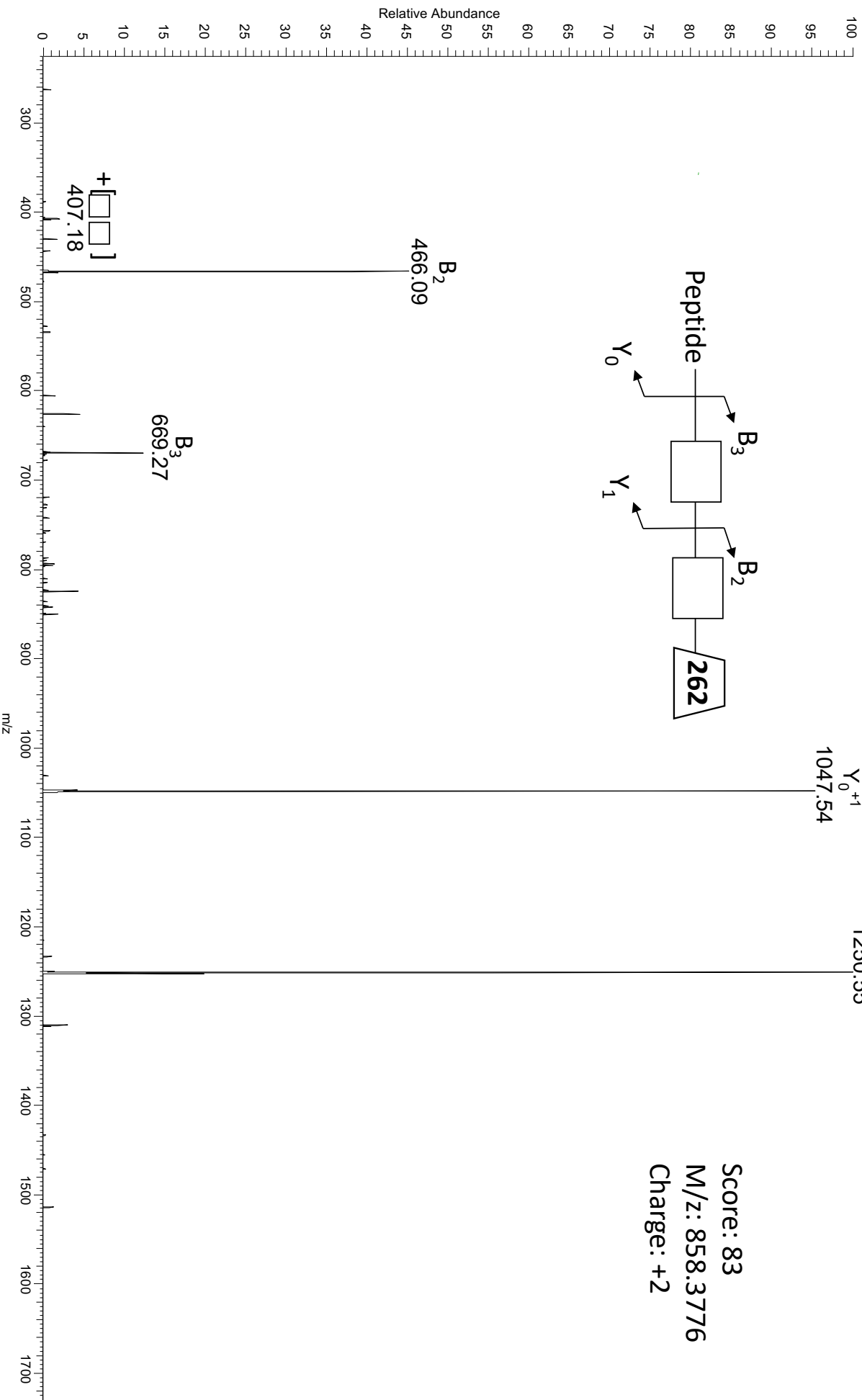
Supplementary Data 2: Identified *Burkholderia gladioli* MDU1 (AUSMDU00013928) glycopeptides

Gene	Protein name	Uniprot accession	m/z	Charge	MH+	Peptide mass	Glycan mass	Peptide sequence	MASCOT ion Score	Page
bgla_1g02560	Uncharacterized protein	F2LHM5	858.37762	2	1715.7544	1047.5065	668.247946	AAAASAAGTNDK	83	3 and 4
bgla_1g03670	ABC transporter, periplasmic substrate-binding protein	F2LHY4	1009.9695	2	2018.9382	1450.7033	568.234866	AADAGGAKPAAASGAGAH	113	5 and 6
bgla_1g31160	Bifunctional uroporphyrinogen-III synthetase/uroporphyrin-III C-methyltransferase	F2LG73	763.36084	3	2288.0809	1719.8409	568.240032	AAHPGDIASEAAATGQPR	86	7 and 8
bgla_1g32320	Uncharacterized protein	F2LGU6	895.93744	2	1790.8741	1222.6426	568.231486	APAAAPEAASAPAK	88	9 and 10
bgla_1g32320	Uncharacterized protein	F2LGU6	945.94543	2	1890.8901	1222.6426	668.247466	APAAAPEAASAPAK	80	11 and 12
bgla_1g32320	Uncharacterized protein	F2LGU6	915.75739	3	2745.2706	1508.8067	1236.463882 (2* 568.23)	ASAPAAAPEAASAPAKK	68	13 and 14
bgla_1g02400	Adhesin/hemolysin	F2LHK9	808.86163	2	1616.7225	948.5109	668.211566	ASGAKASASAK	55	15 and 16
bgla_1g28150	Uncharacterized protein	F2LBQ5	885.3573	2	1769.7138	1201.4725	568.241306	ASGAM(+16)SNDAM(+16)SK	48	17 and 18
bgla_1g28150	Uncharacterized protein	F2LBQ5	869.36279	2	1737.7248	1169.4925	568.232286	ASGAMSNDAMSK	77	19 and 20
bgla_1g28150	Uncharacterized protein	F2LBQ5	919.37048	2	1837.7402	1169.4925	668.247666	ASGAMSNDAMSK	82	21 and 22
bgla_1g37560	Uncharacterized protein	F2LG07	968.98877	2	1936.9767	1268.7321	668.244646	EASIVA AVKPQR	55	23 and 24
bgla_1g09460	Uncharacterized protein	F2LC05	786.6925	3	2358.0759	1789.8326	568.243312	FNEHPQM QFAASAPSK	68	25 and 26
bgla_1g09460	Uncharacterized protein	F2LC05	820.0296	3	2458.0872	1789.8326	668.254612	FNEHPQM QFAASAPSK	68	27 and 28
bgla_1g09460	Uncharacterized protein	F2LC05	825.36267	3	2474.0864	1805.8226	668.263822	FNEHPQM(+16)QFAASAPSK	56	29 and 30

lolA	Outer-membrane lipoprotein carrier protein	F2L9H3	827.89001	4	3308.5577	2640.2786	668.279058	GASGAMPTVKPTDNSSGTFVFSRPGR	47	31 and 32
bgla_1g28150	Uncharacterized protein	F2LBQ5	1087.9504	2	2174.9001	1606.6658	568.234286	HDAMGMSPAASDAMSK	110	33 and 34
bgla_1g28150	Uncharacterized protein	F2LBQ5	1095.9493	2	2190.8979	1622.6558	568.242086	HDAMGMSPAASDAMSK	82	35 and 36
bgla_1g35490	Periplasmic protease	F2LE35	939.47168	2	1877.9426	1309.711	568.231566	PLTAGAAAPSASAPK	28	37 and 38
bgla_1g23600	Ankyrin repeat protein	F2LDR2	704.33496	3	2111.0033	1542.7619	568.241392	IGDGRPASGAGGQNSAK	45	39 and 40
bgla_1g28150	Uncharacterized protein	F2LBQ5	801.67279	3	2403.0168	1734.7608	668.255982	KHDAMGMSPAASDAMSK	138	41 and 42
bgla_1g28150	Uncharacterized protein	F2LBQ5	1151.9988	2	2302.9968	1734.7608	568.235966	KHDAMGMSPAASDAMSK	108	43 and 44
bgla_1g22150	Uncharacterized protein	F2LA58	988.47693	2	1975.9531	1407.7227	568.230366	KPAAPAADAASAPAAQ	66	45 and 46
bgla_1g22150	Uncharacterized protein	F2LA58	1038.4868	2	2075.9728	1407.7227	668.250146	KPAAPAADAASAPAAQ	38	47 and 48
bgla_1g35490	Periplasmic protease	F2LE35	989.48334	2	1977.9659	1309.711	668.254886	PLTAGAAAPSASAPK	53	49 and 50
bgla_1g09580	Uncharacterized protein	F2LC16	888.78162	3	2664.3433	2096.0982	568.245072	SLSNQAPAASAVAAAPIDADKK	92	51 and 52
bgla_1g09580	Uncharacterized protein	F2LC16	922.12	3	2764.3584	2096.0982	668.260212	SLSNQAPAASAVAAAPIDADKK	110	53 and 54
bgla_1g09580	Uncharacterized protein	F2LC16	822.07099	3	2464.2114	1895.9821	568.229285	SNQAPAASAVAAAPIDADKK	86	55 and 56
bgla_2g17040	Uncharacterized protein	F2LPV7	885.414	3	2654.2404	1985.9774	668.263012	TDAAAPGADAAAAASTPTKAEK	86	57 and 58
bgla_1g22150	Uncharacterized protein	F2LA58	797.04413	3	2389.1308	1720.8725	668.258302	TPASAAAAAASPAAHAAR	104	59 and 60

Supplementary Data 2. Identified *Burkholderia gladioli* MDU1 (AUSMDU00013928) Glycopeptides. A total of 29 unique glycopeptides were observed within whole cell proteome samples of *B. gladioli* MDU1. 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.

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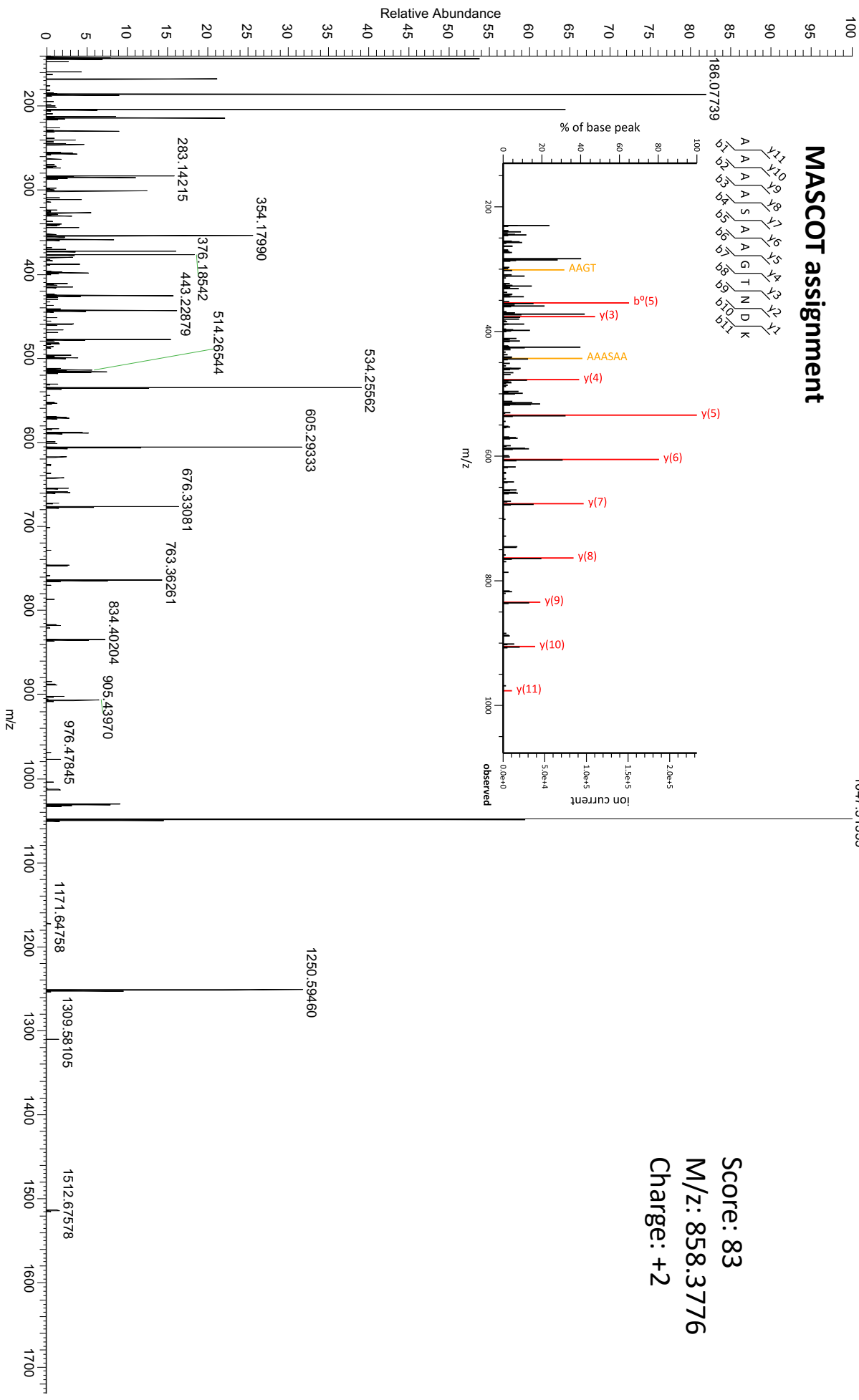
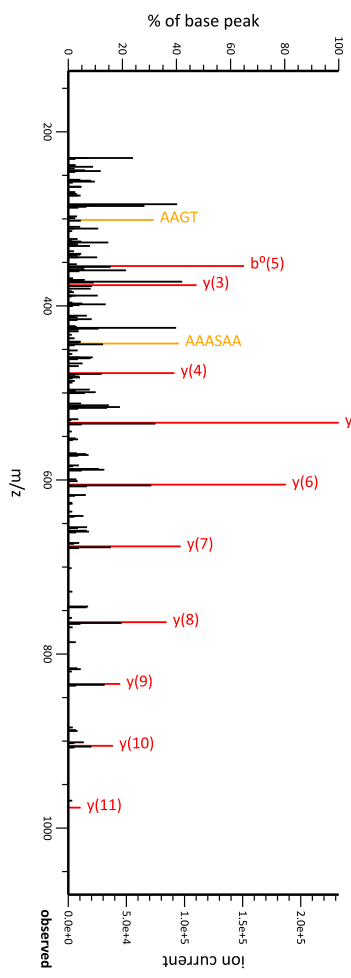
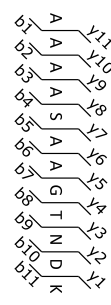
Score: 83

M/z: 858.3776

Charge: +2

1047.51355

MASCOT assignment

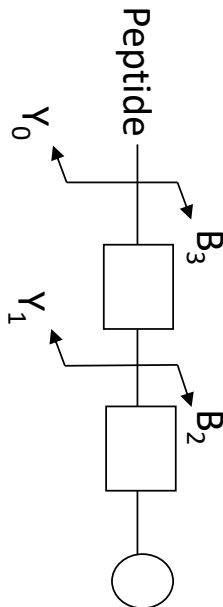
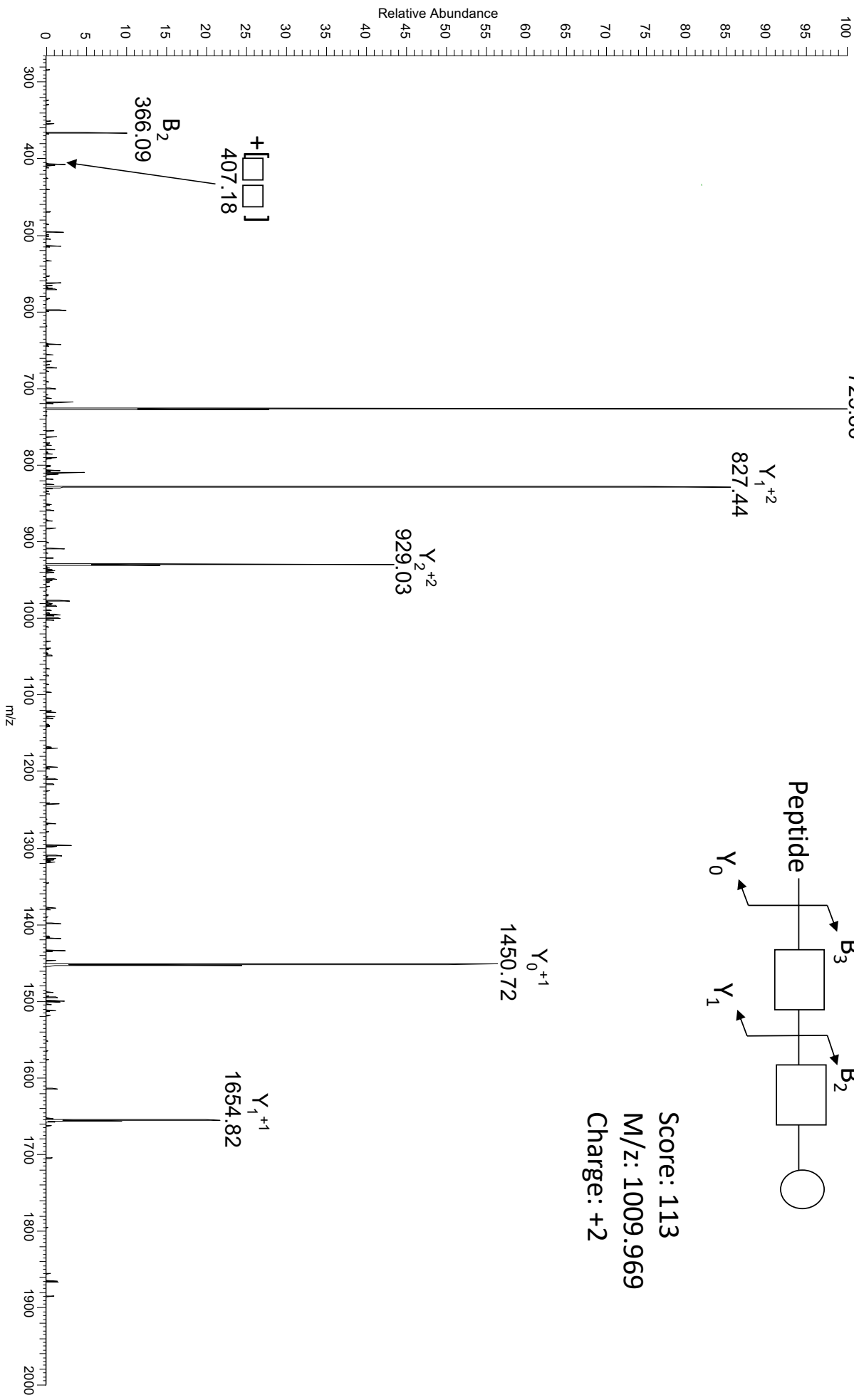


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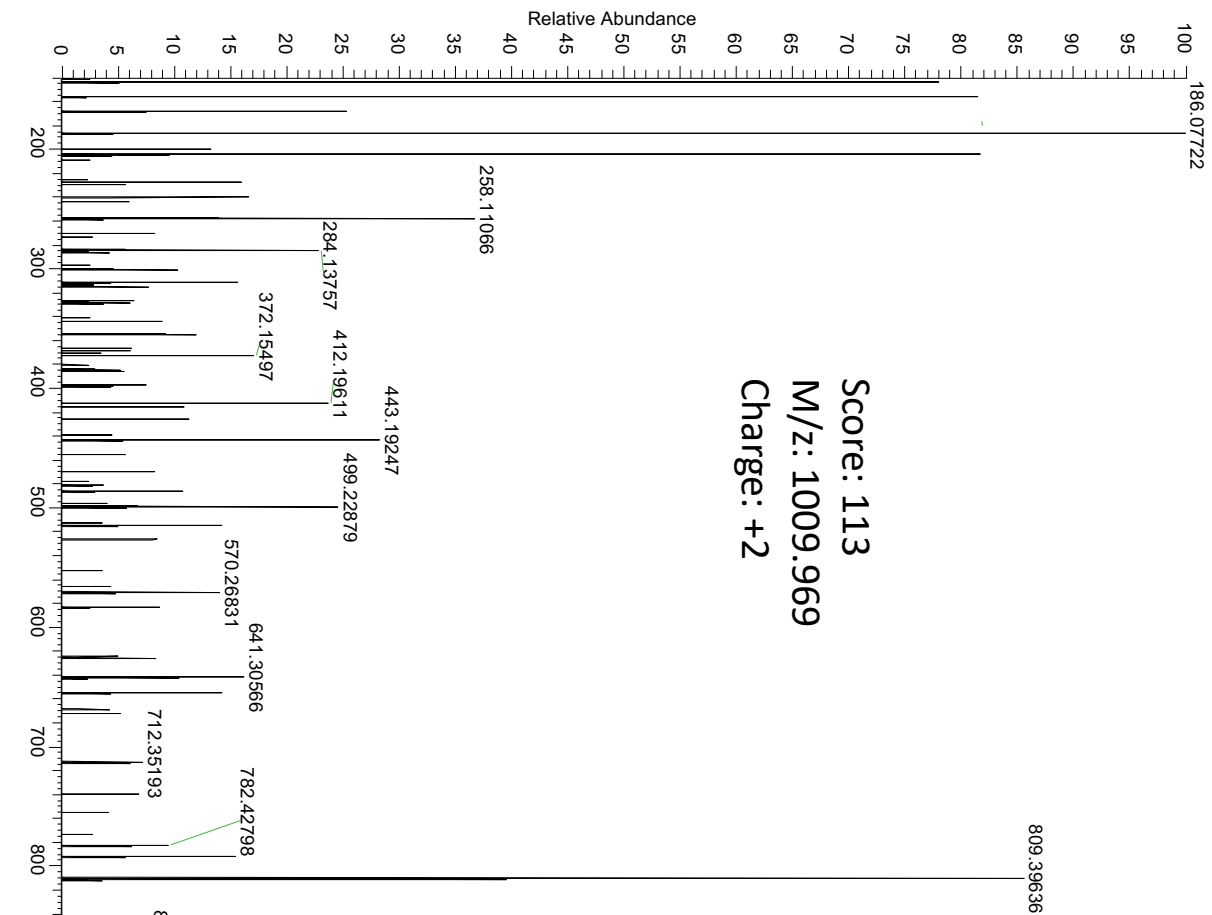
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Charge: +2

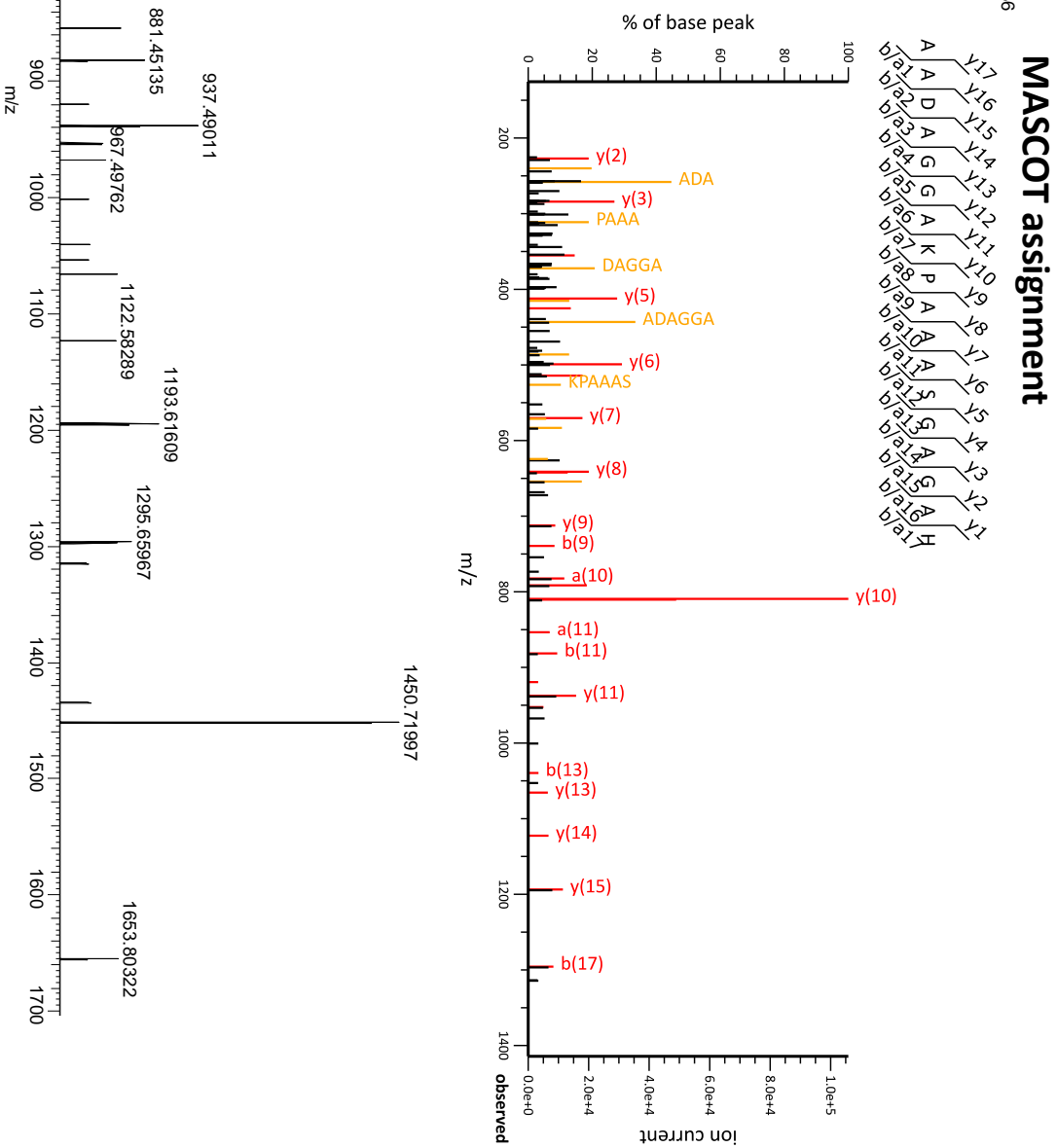
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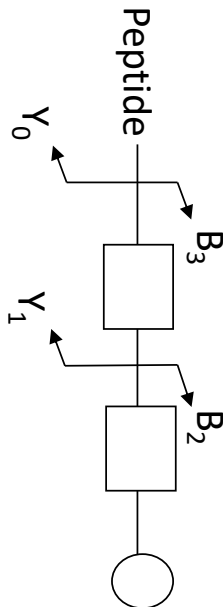
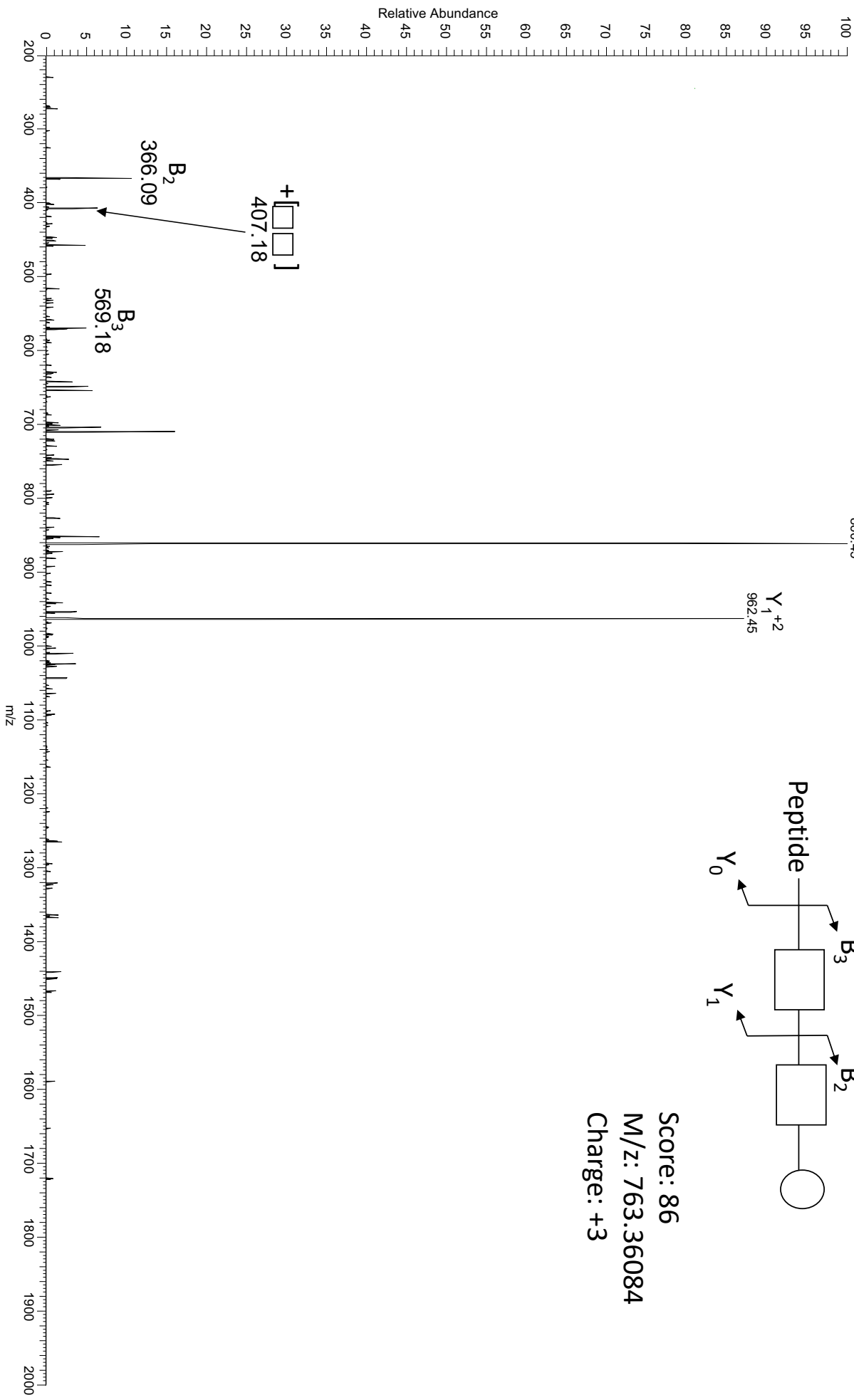
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Charge: +2



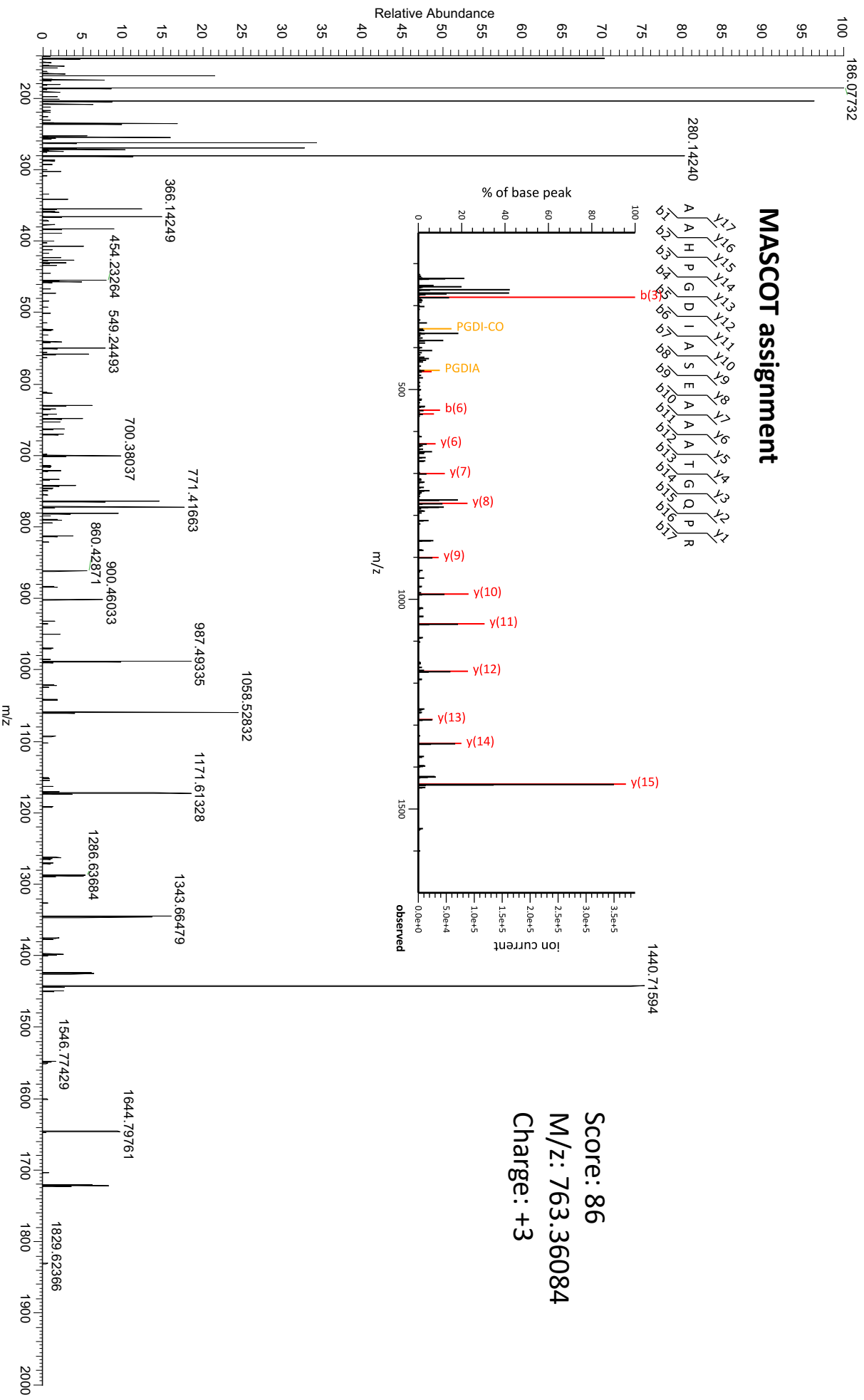
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M/z: 1009.969
Charge: +2



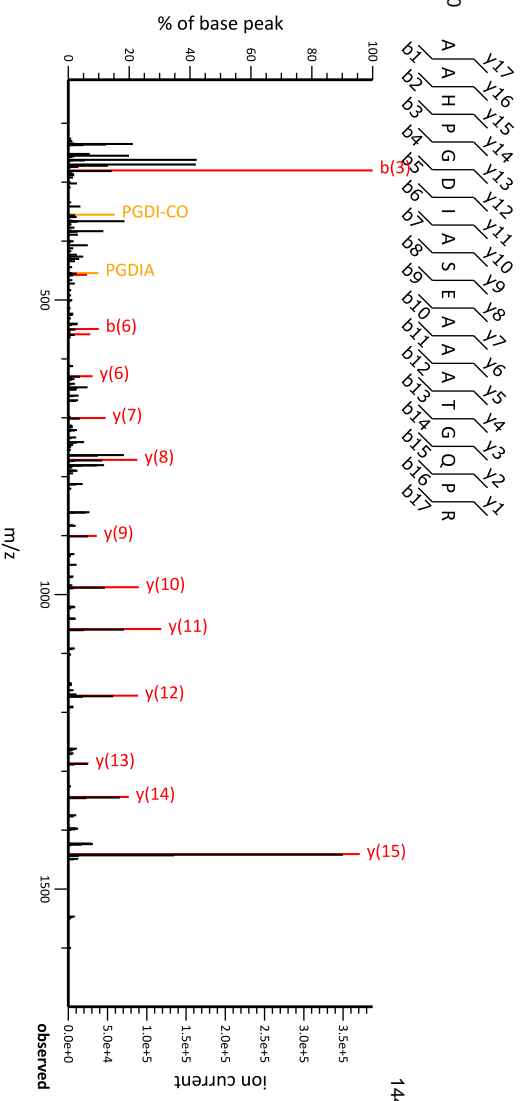
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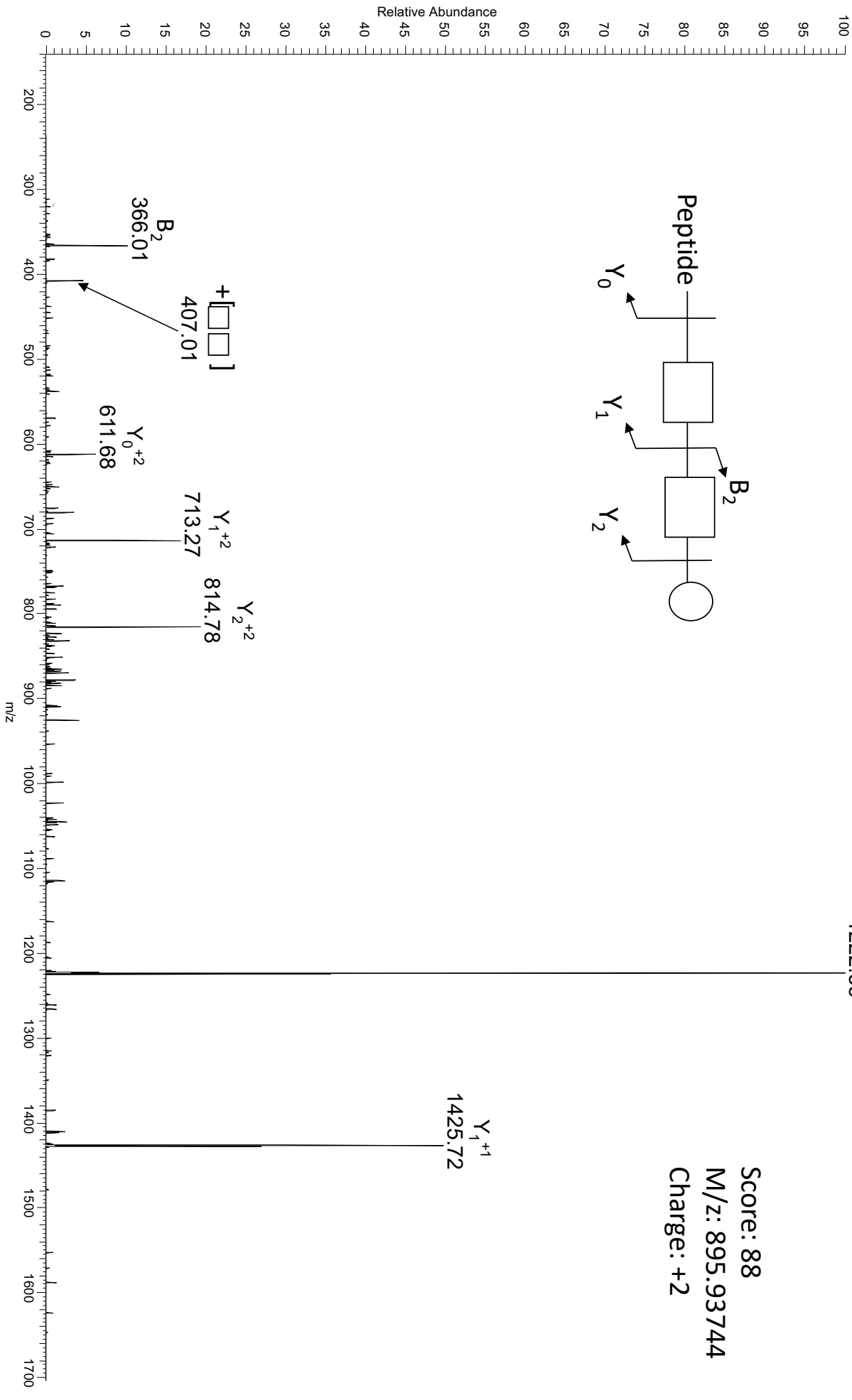
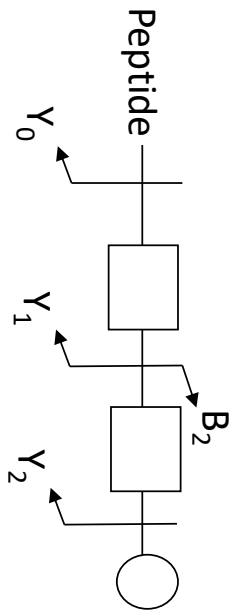
Score: 86
M/z: 763.36084
Charge: +3



MASCOT assignment

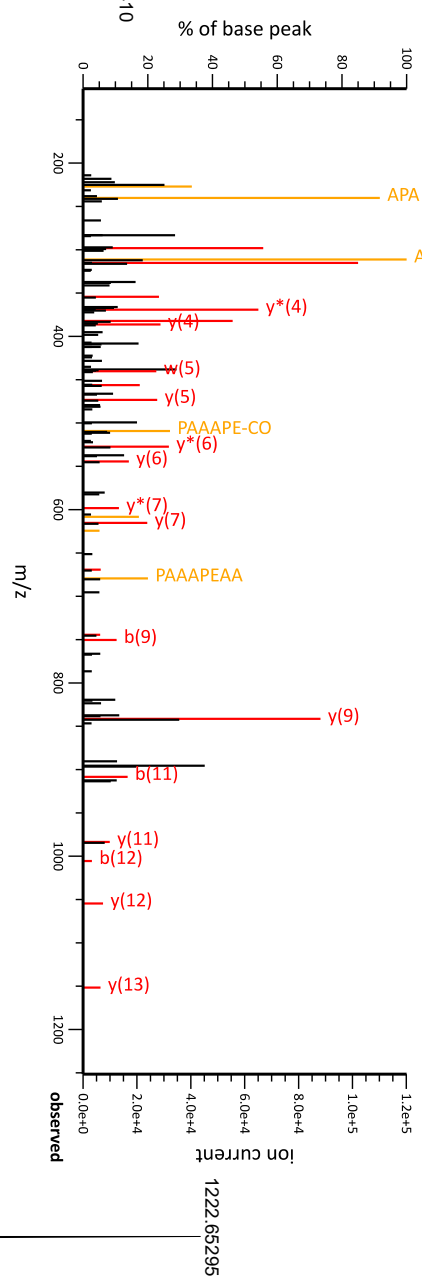


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Charge: +3

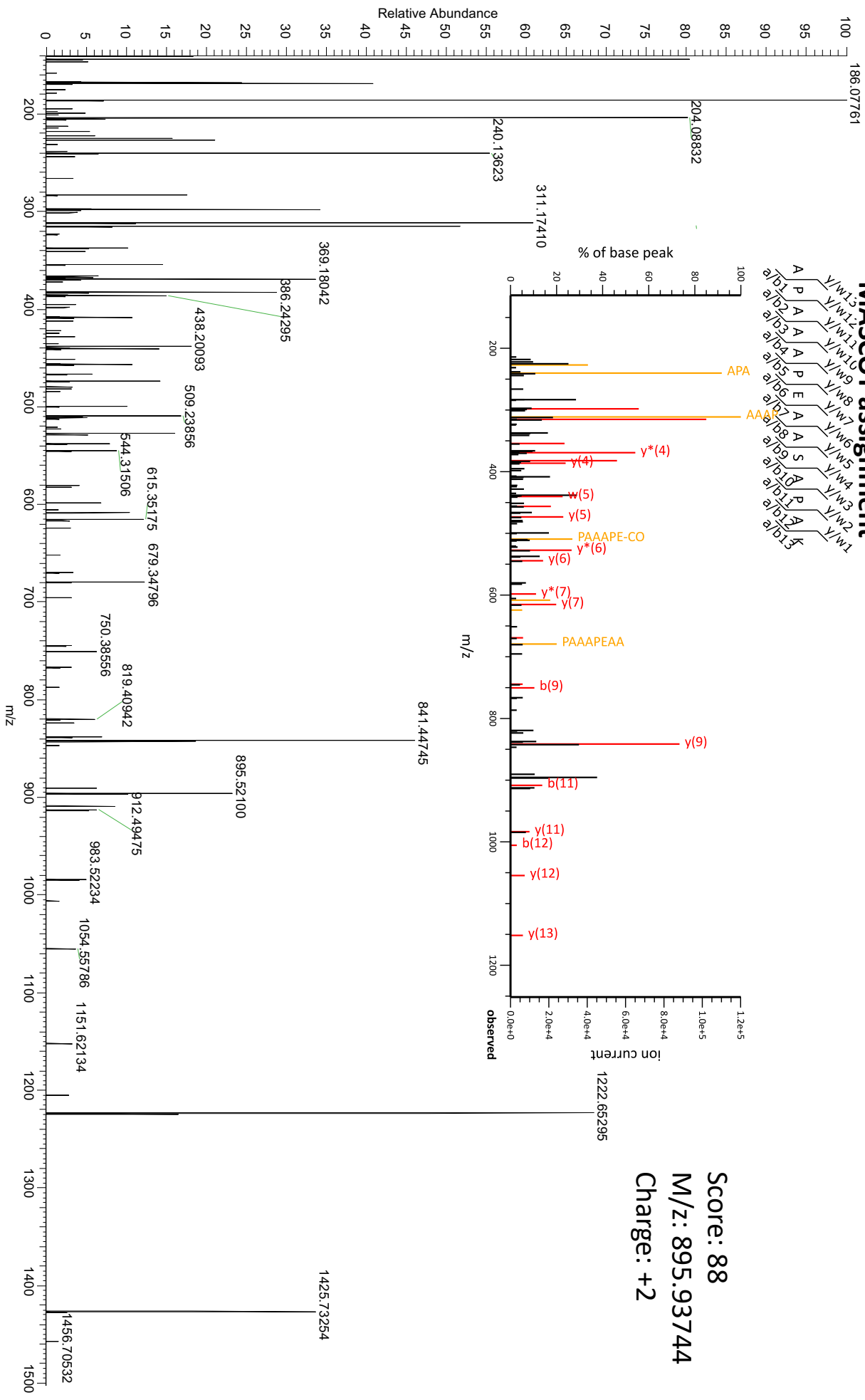


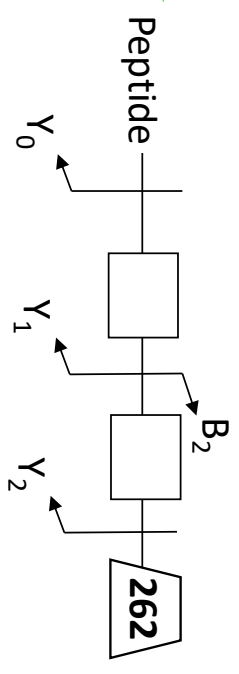
MASCOT assignment

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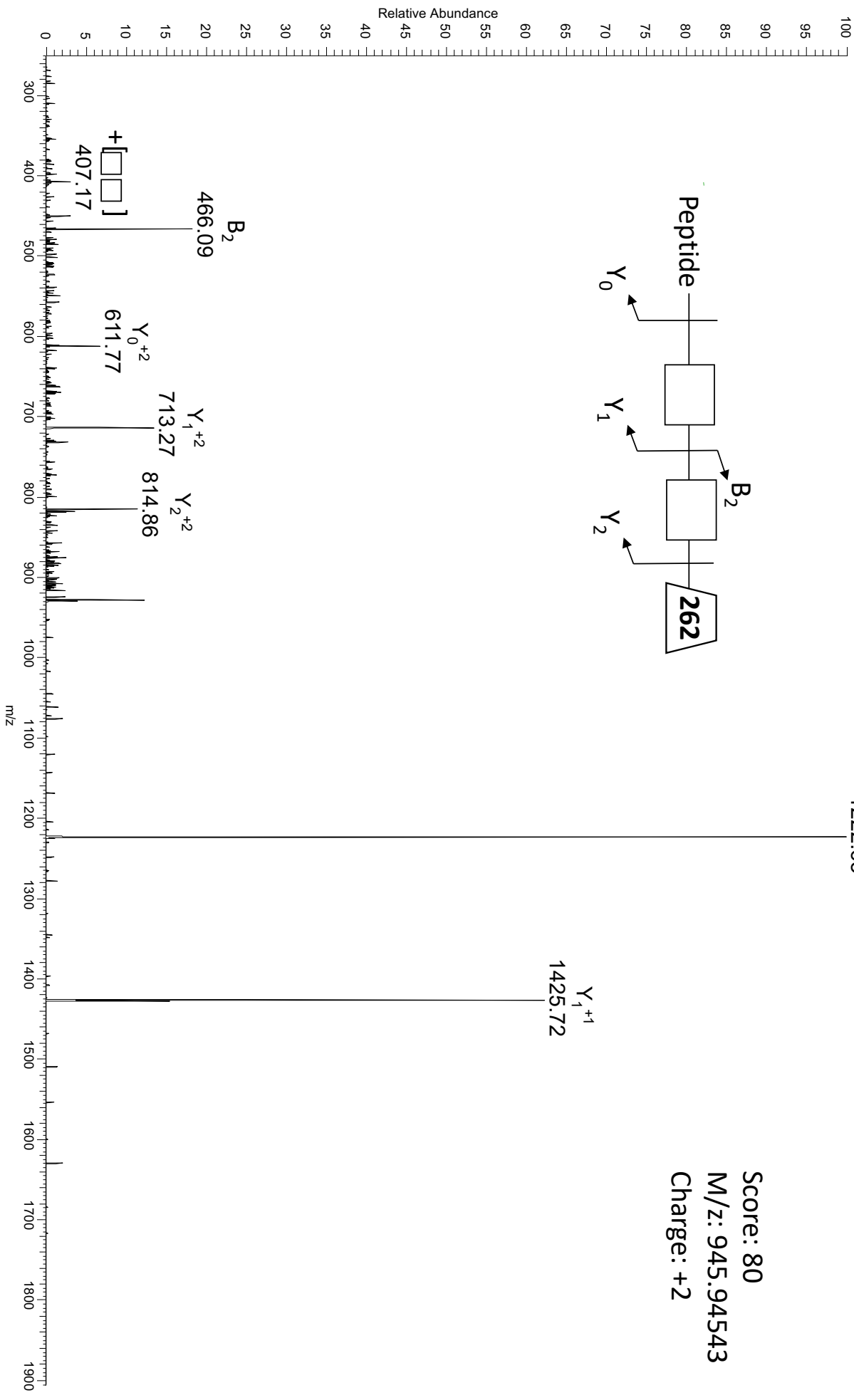


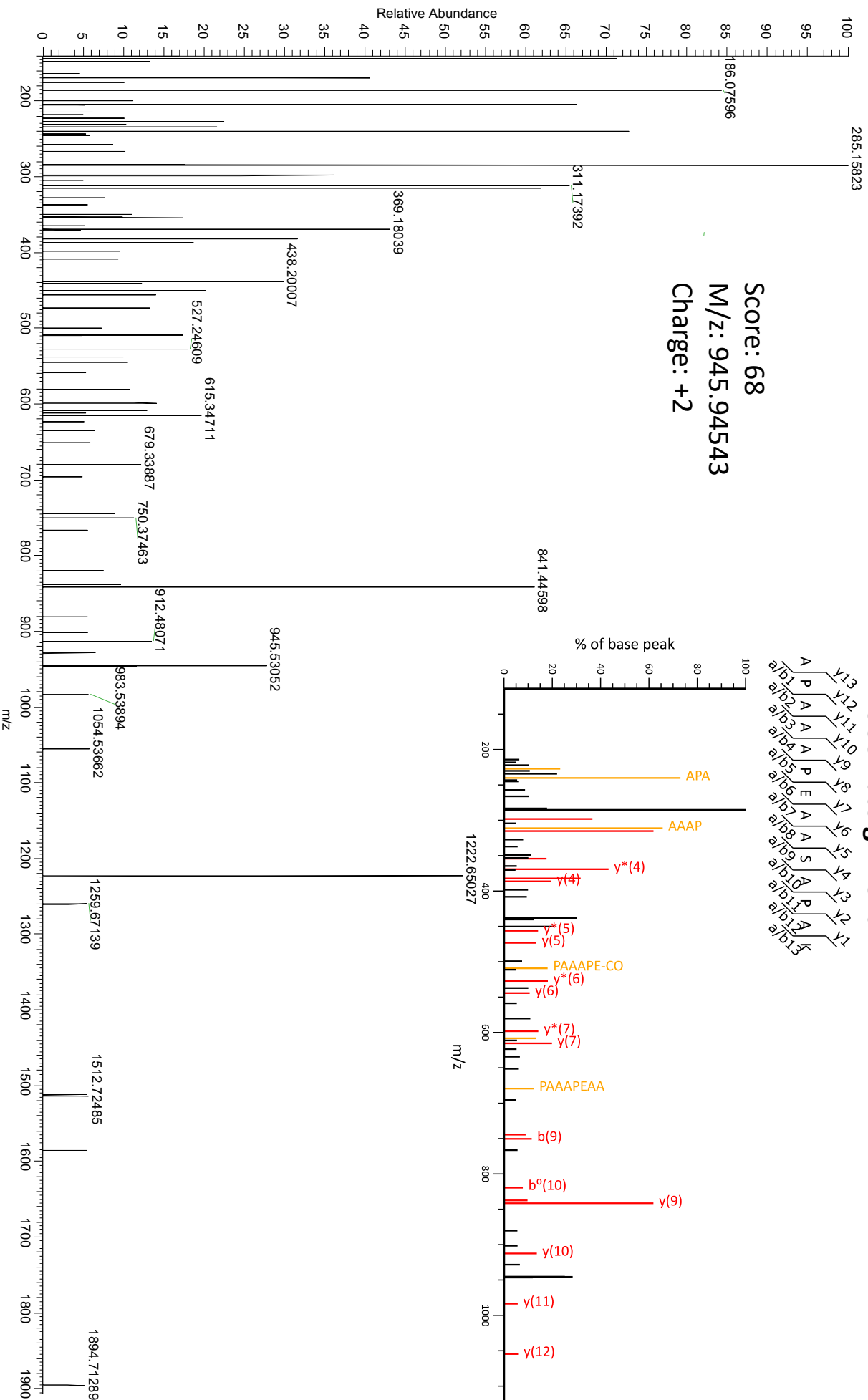
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Charge: +2



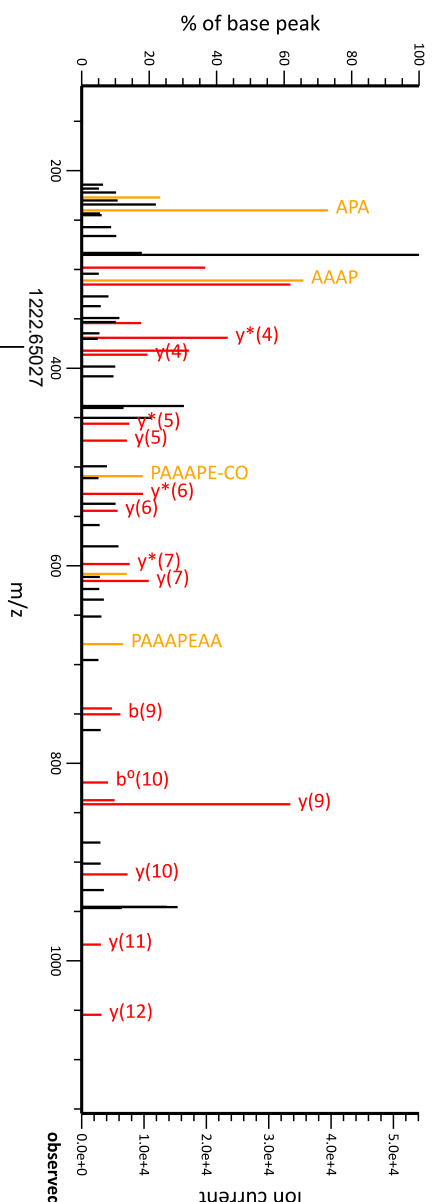
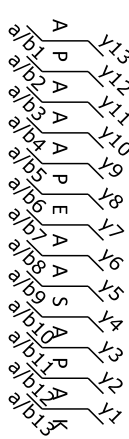


Score: 80
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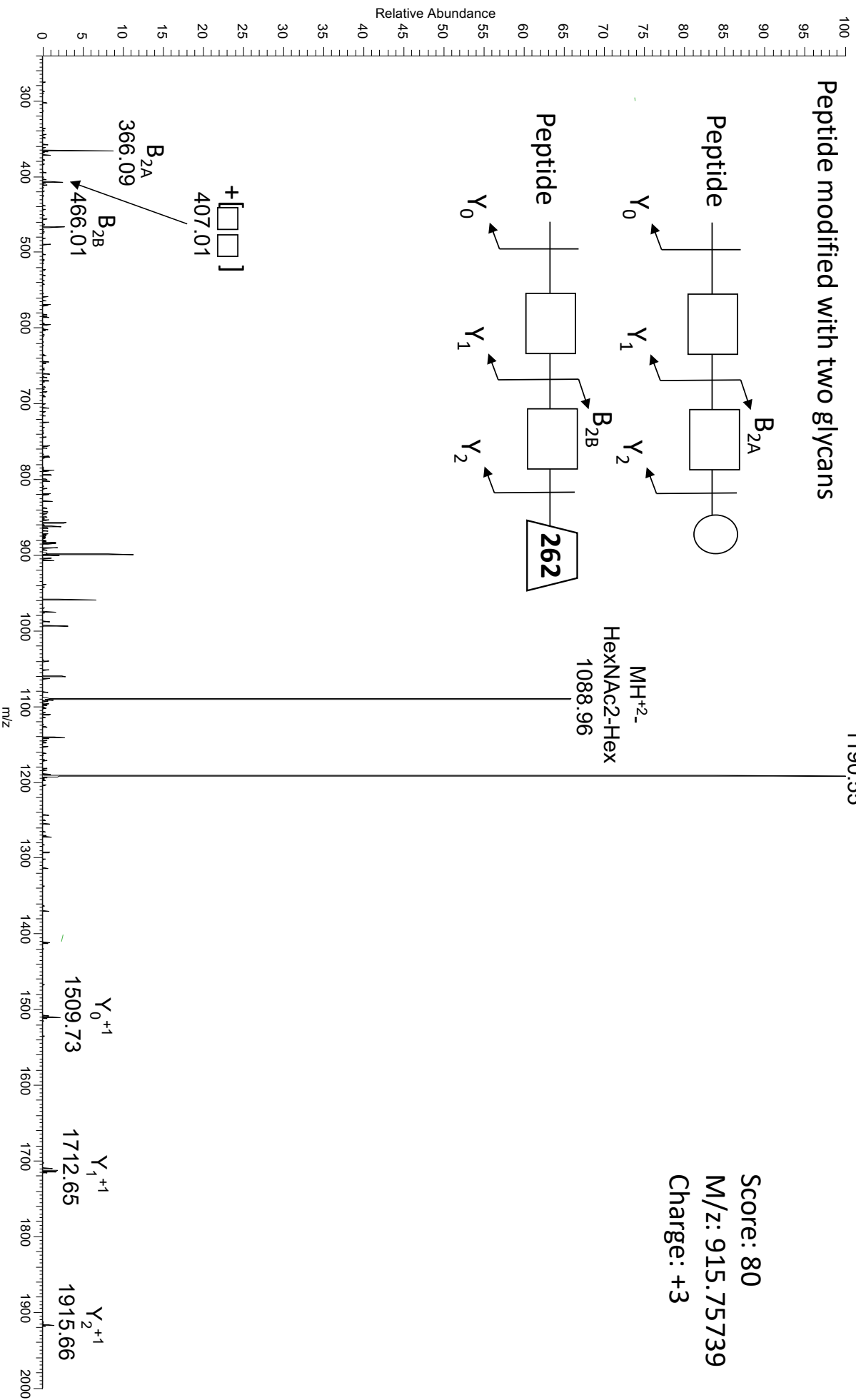
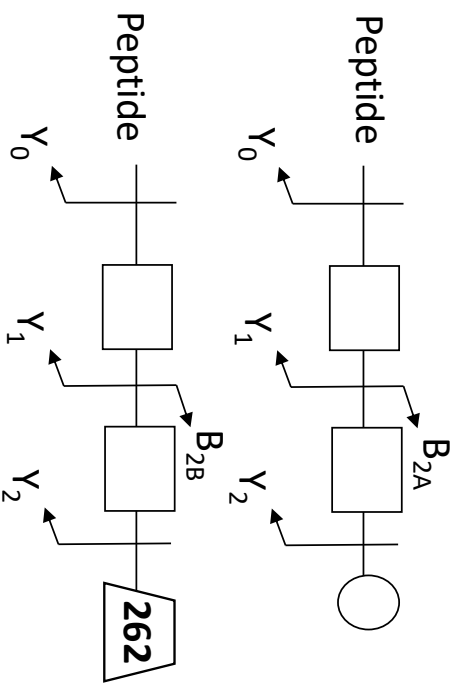




MASCOT assignment



Peptide modified with two glycans



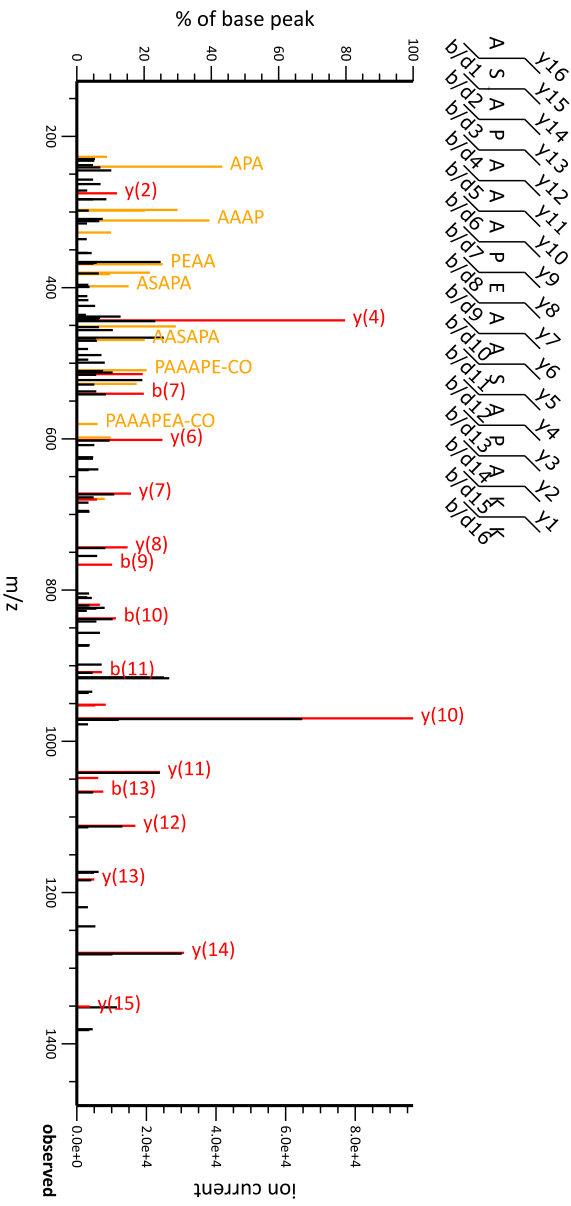
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M/z: 915.75739

Charge: +3

186.07759

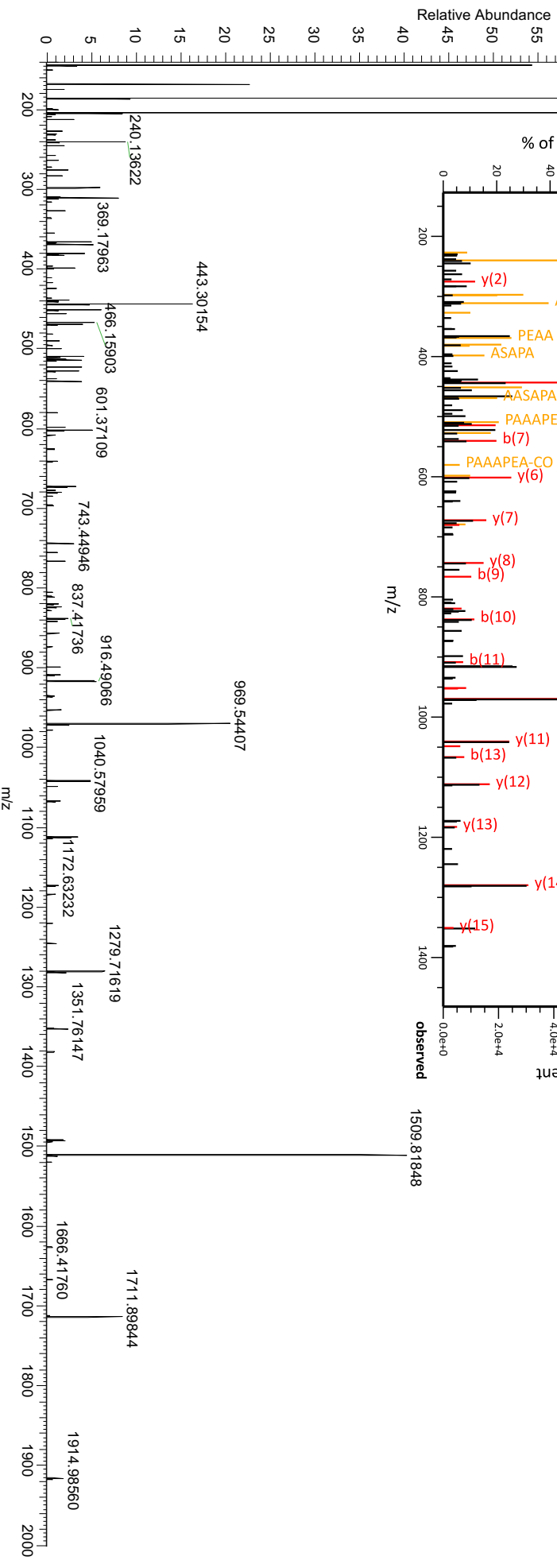
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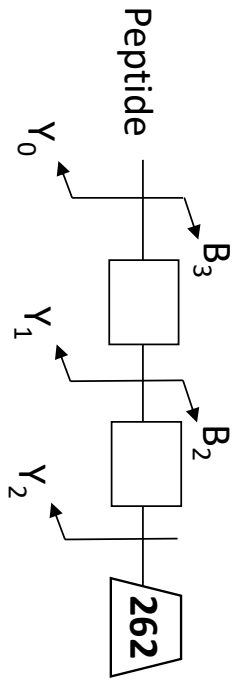
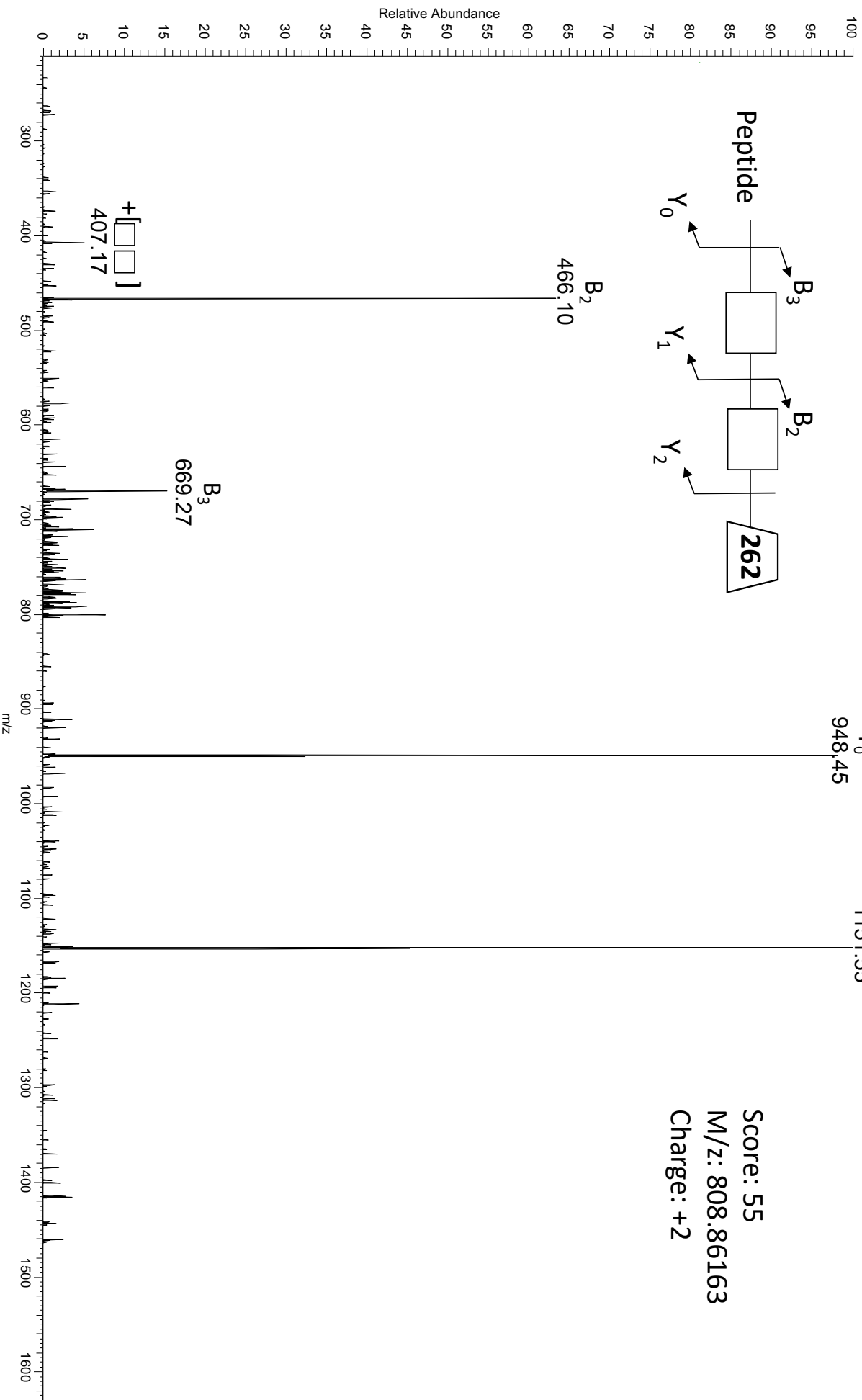
Score: 68

M/z: 915.75739

Charge: +3

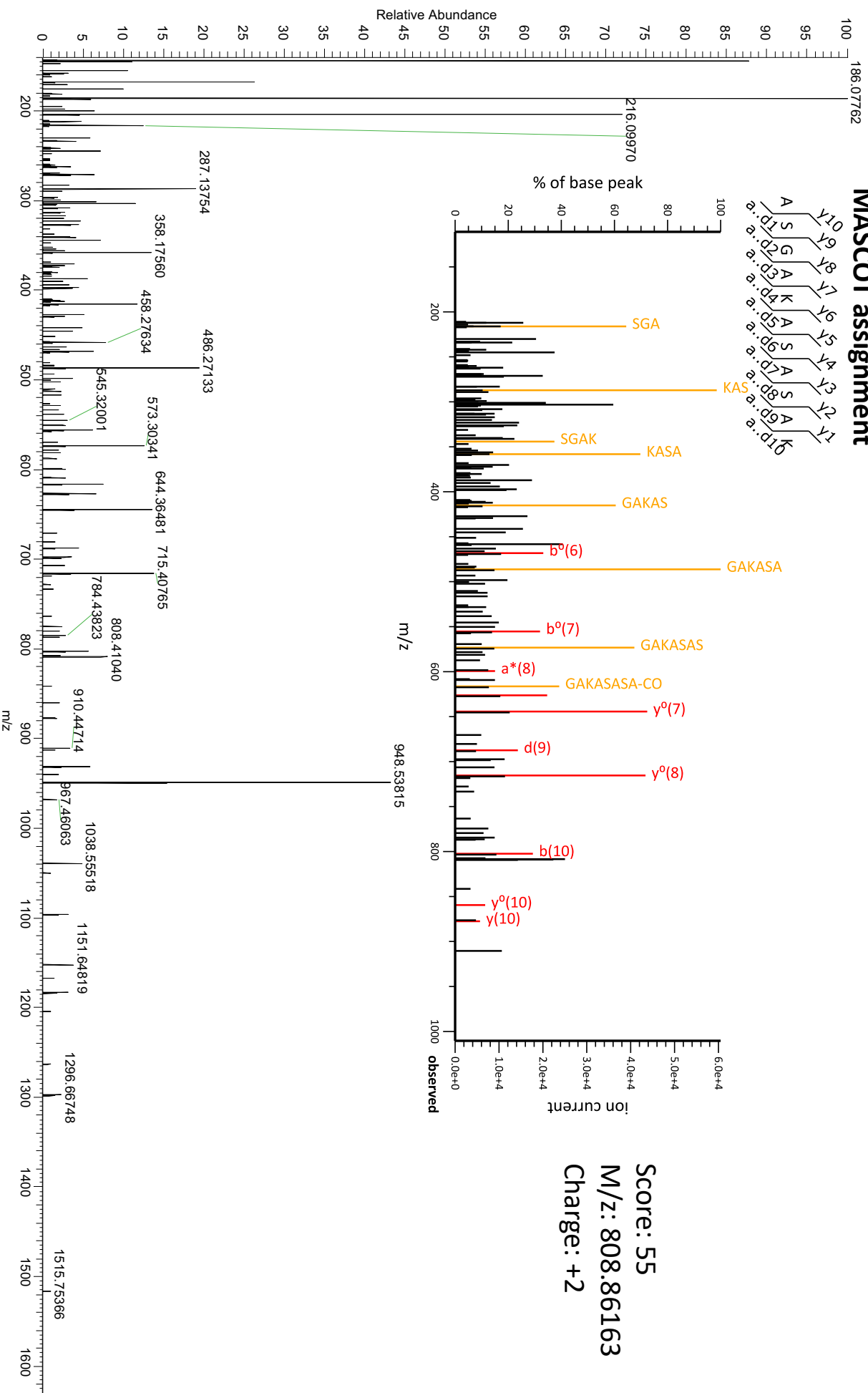


ITMS-CID



Score: 55
M/z: 808.86163
Charge: +2

MASCOT assignment

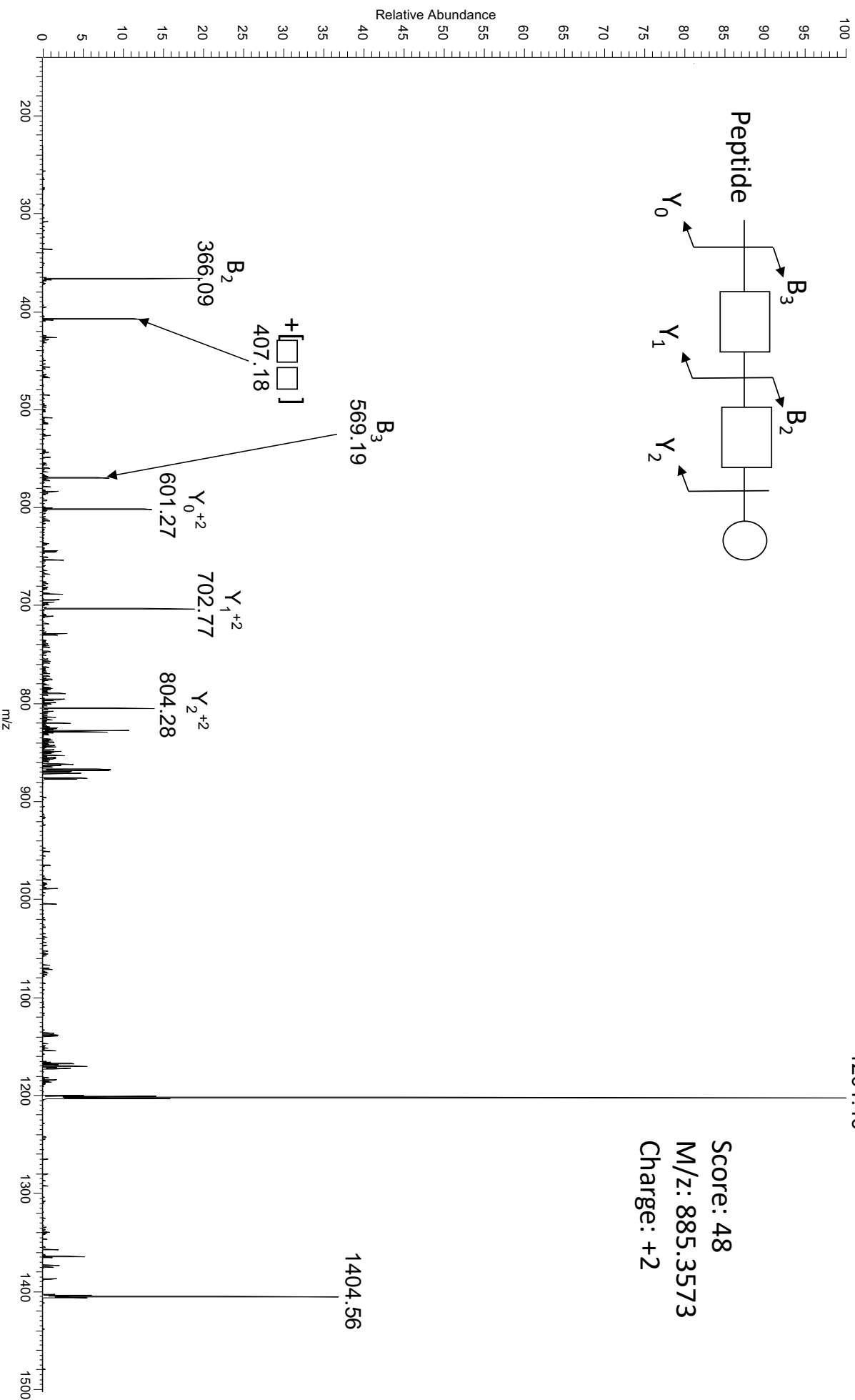
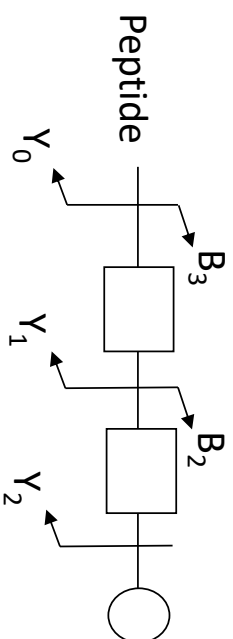


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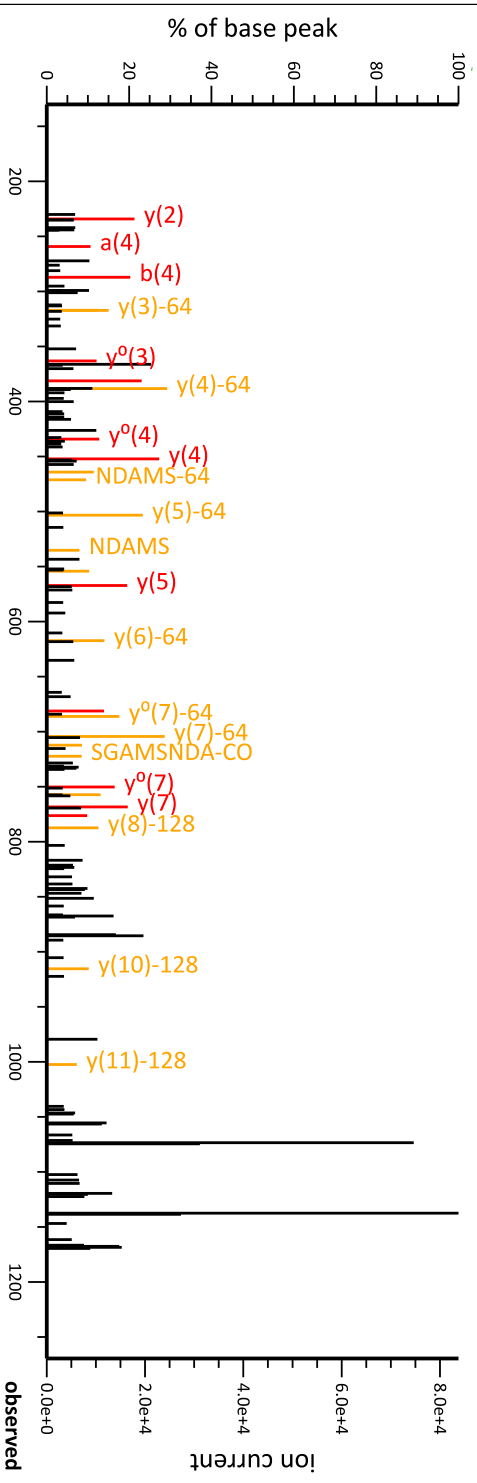
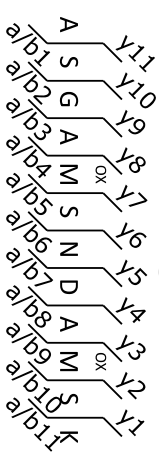
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Charge: +2

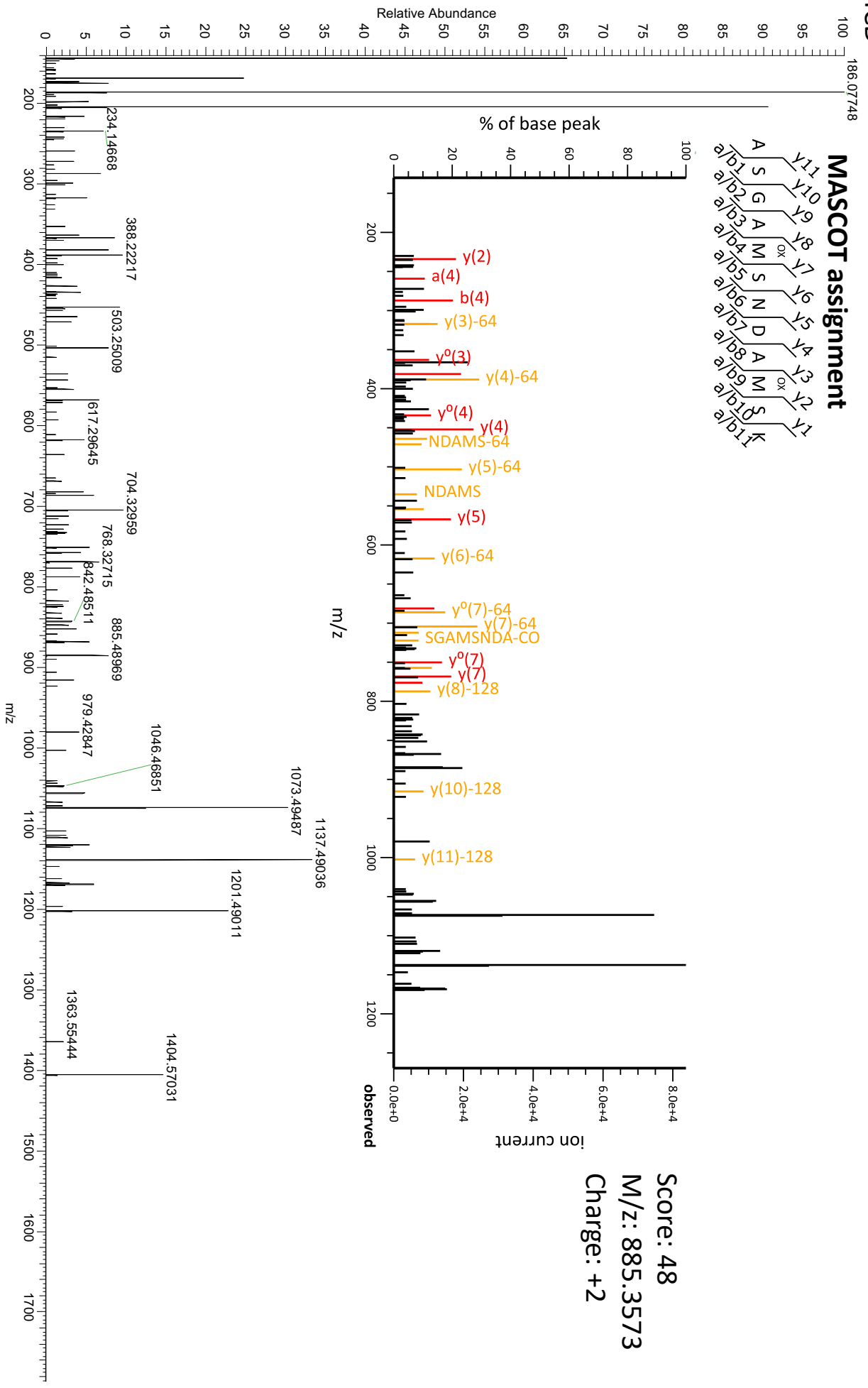
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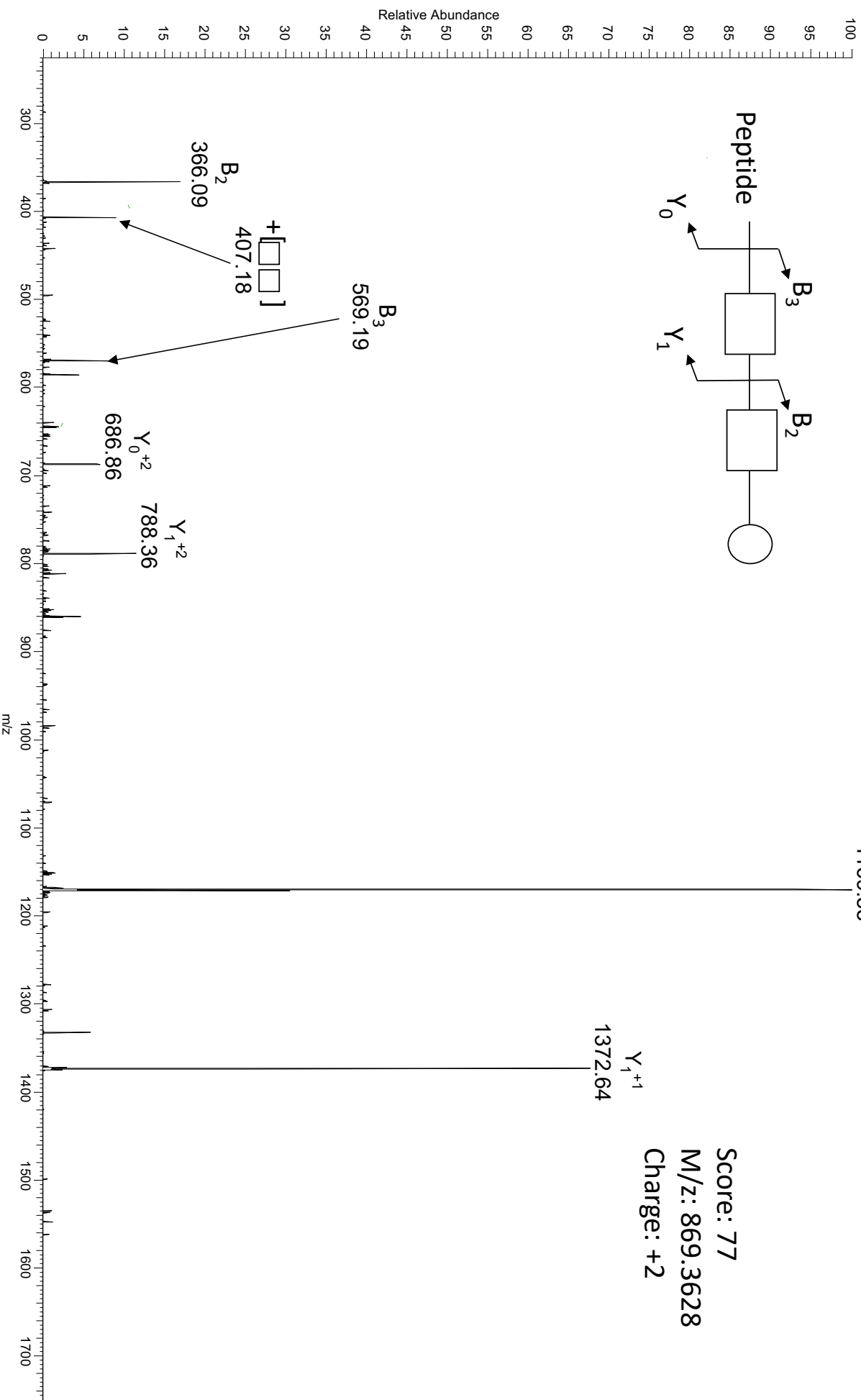
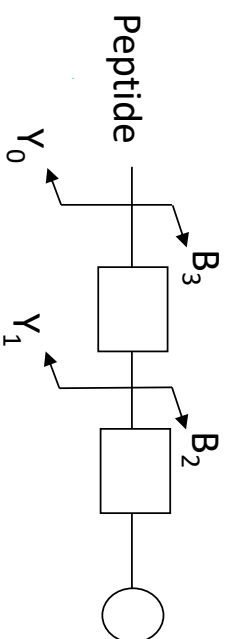
MASCOT assignment



Score: 48
M/z: 885.3573
Charge: +2

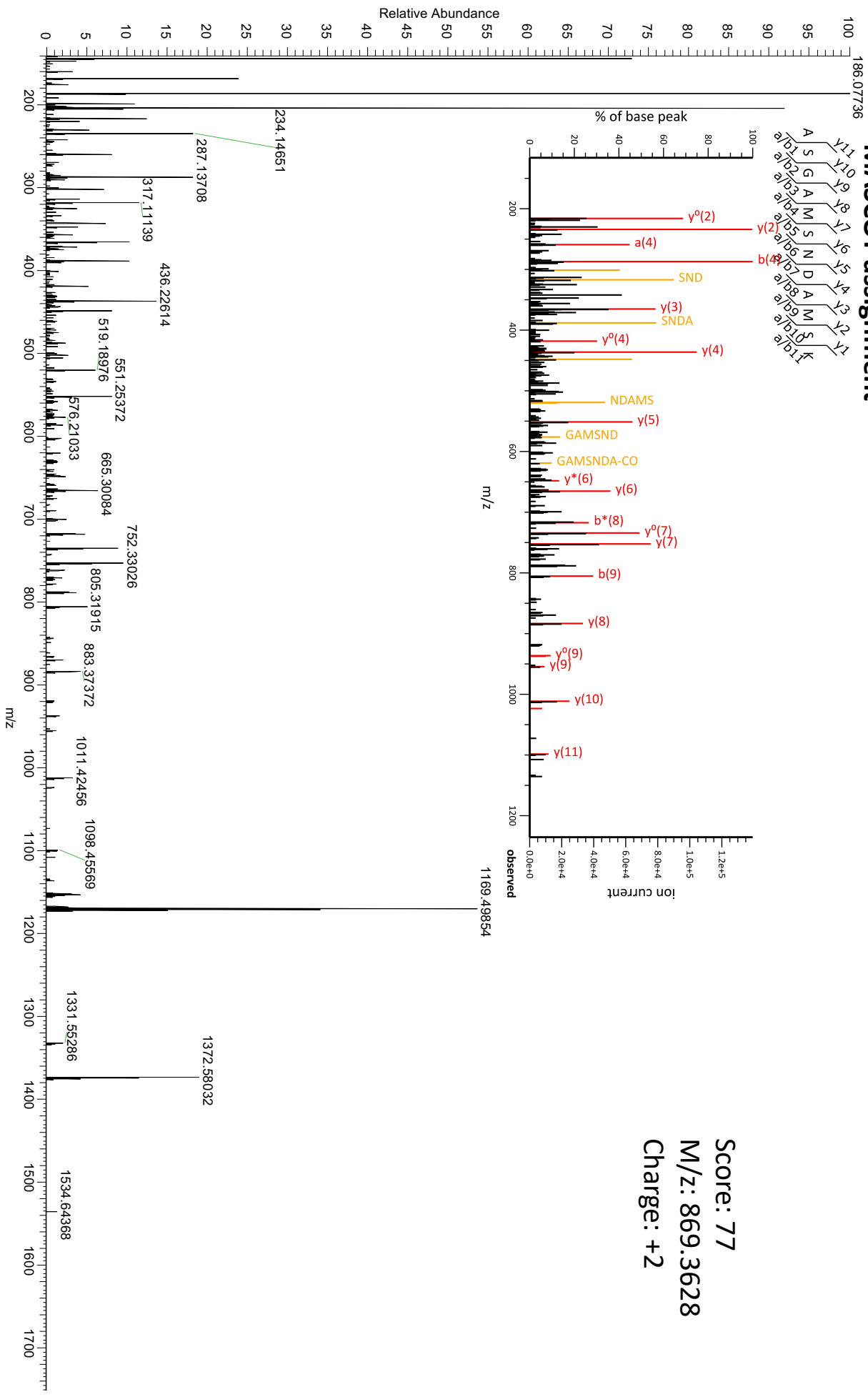
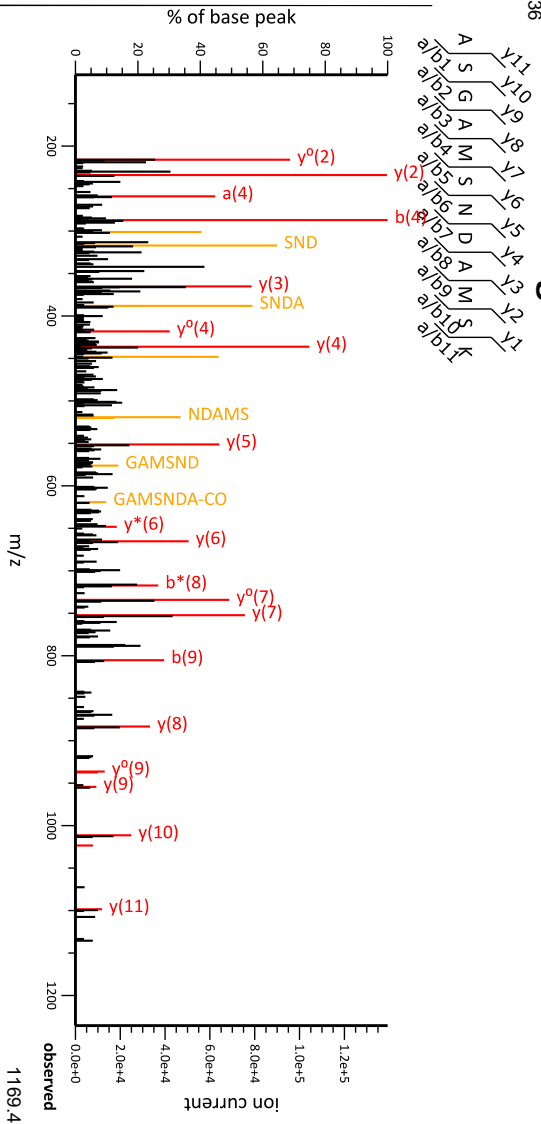


ITMS-CID



Score: 77
M/z: 869.3628
Charge: +2

MASCOT assignment

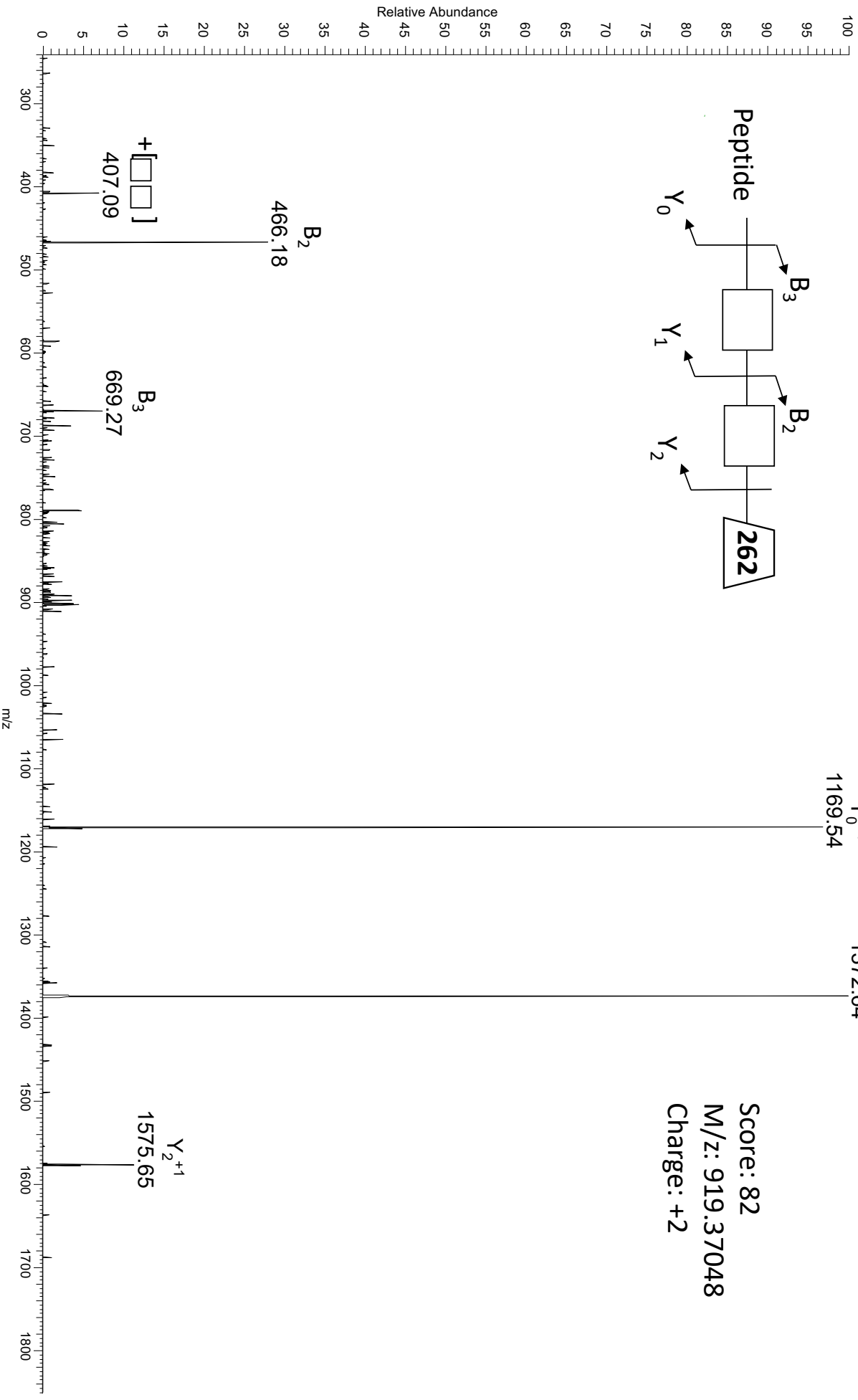
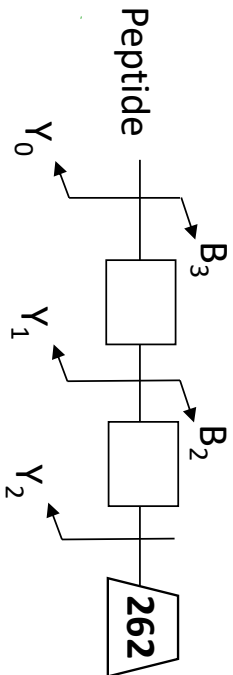


Score: 77

M/z: 869.3628

Charge: +2

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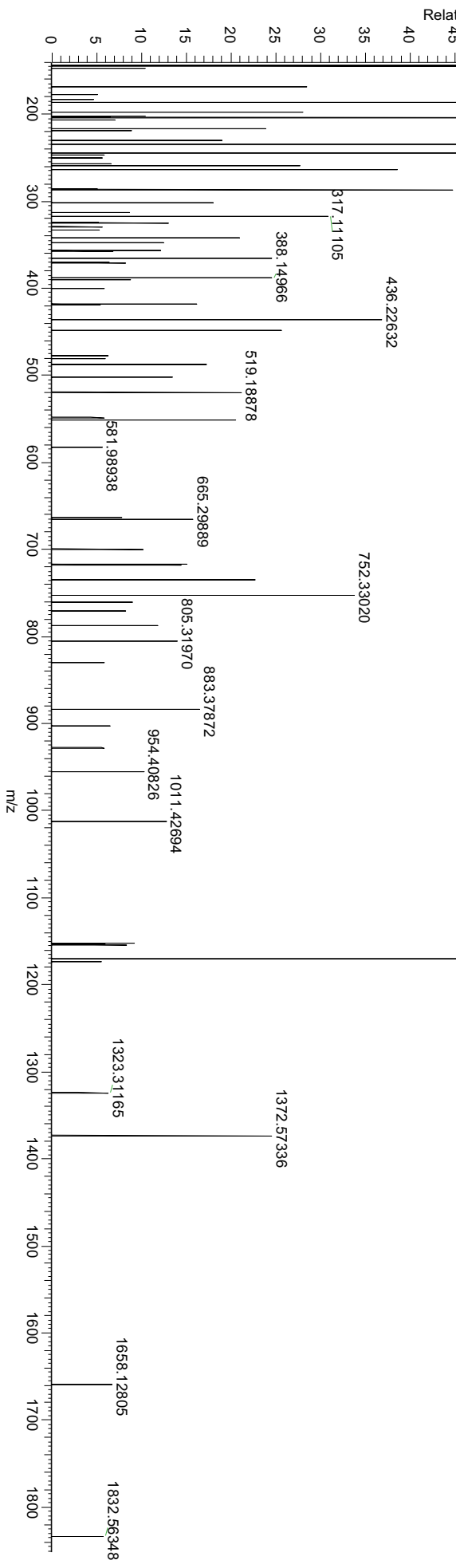
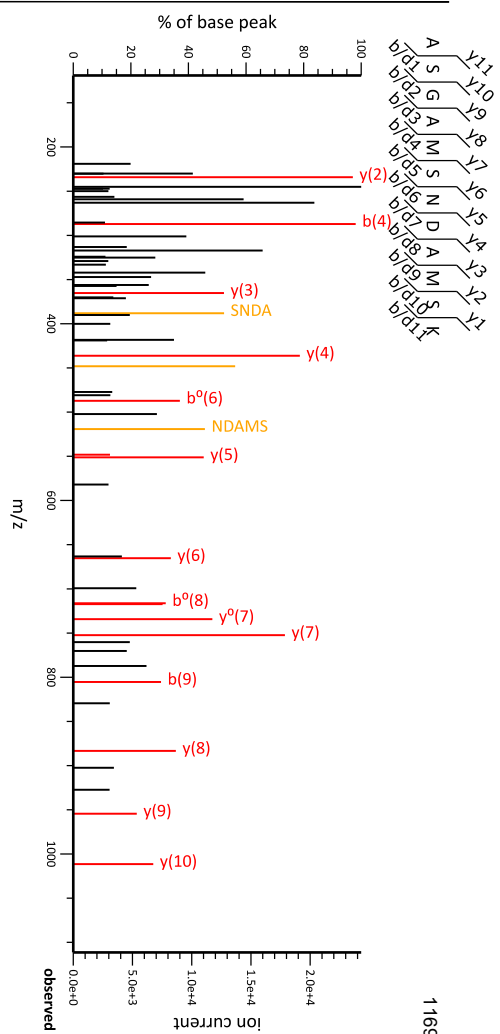


Score: 82

M/z: 919.37048

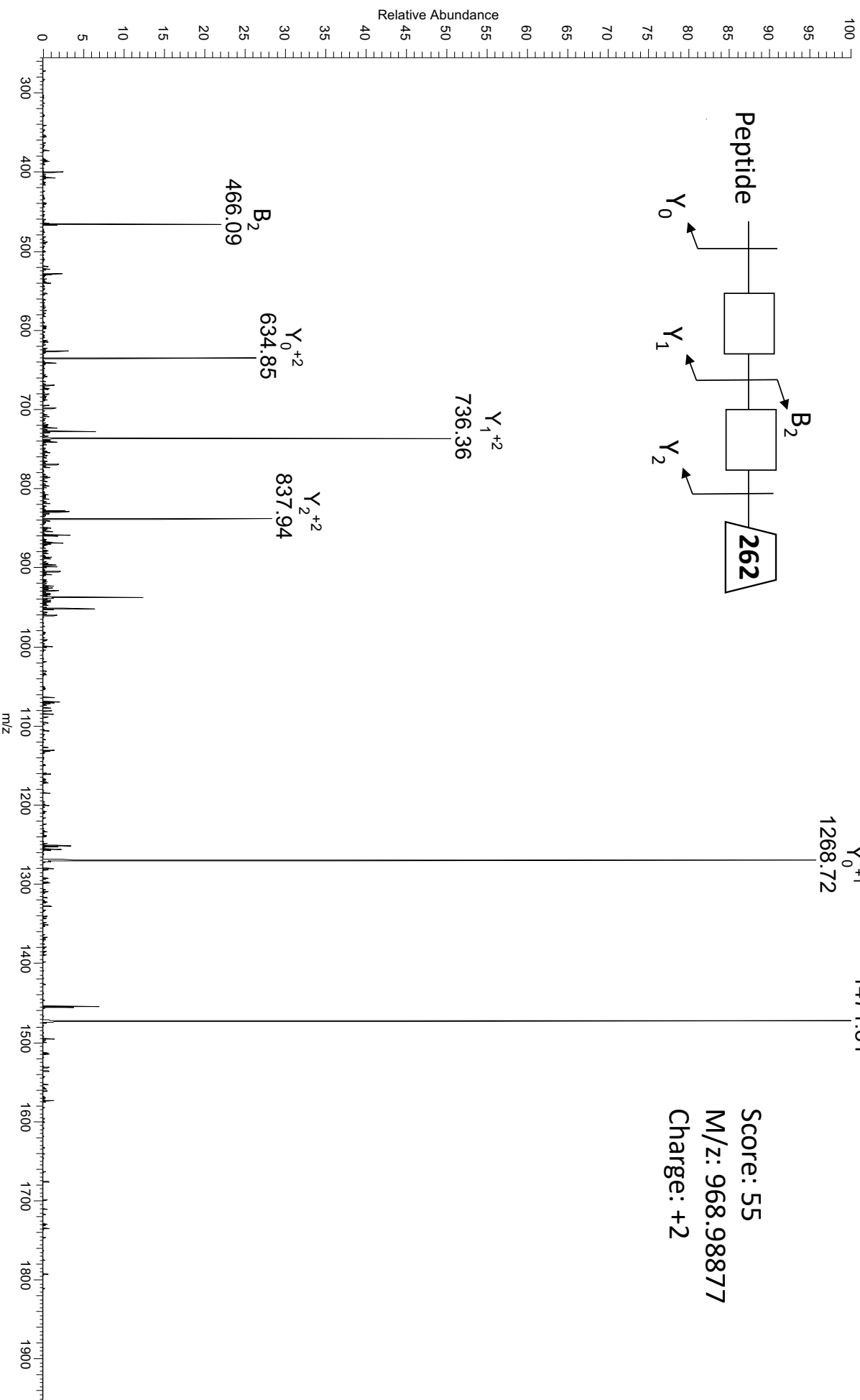
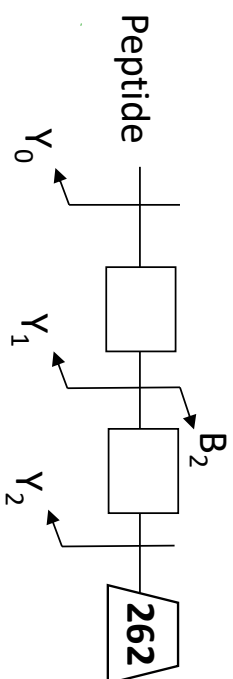
Charge: +2

MASCOT assignment



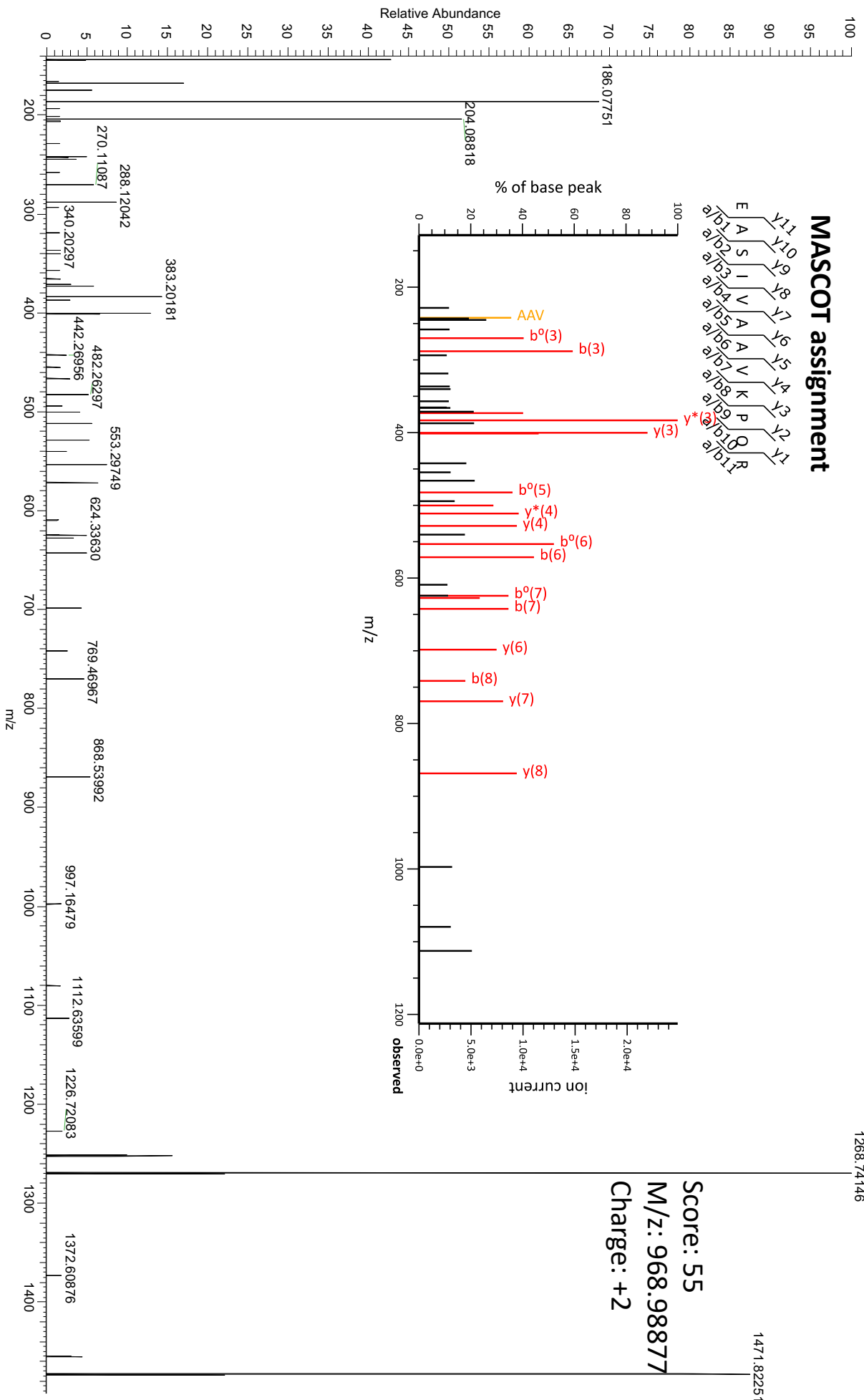
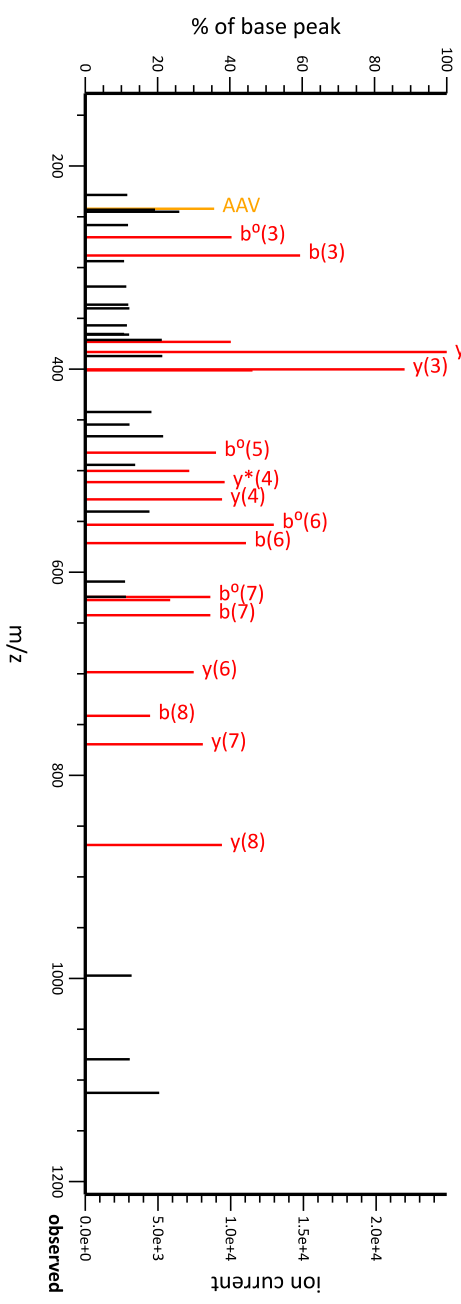
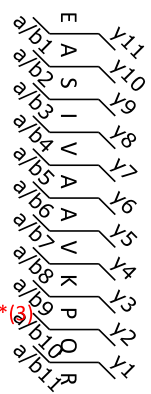
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Charge: +2

ITMS-CID



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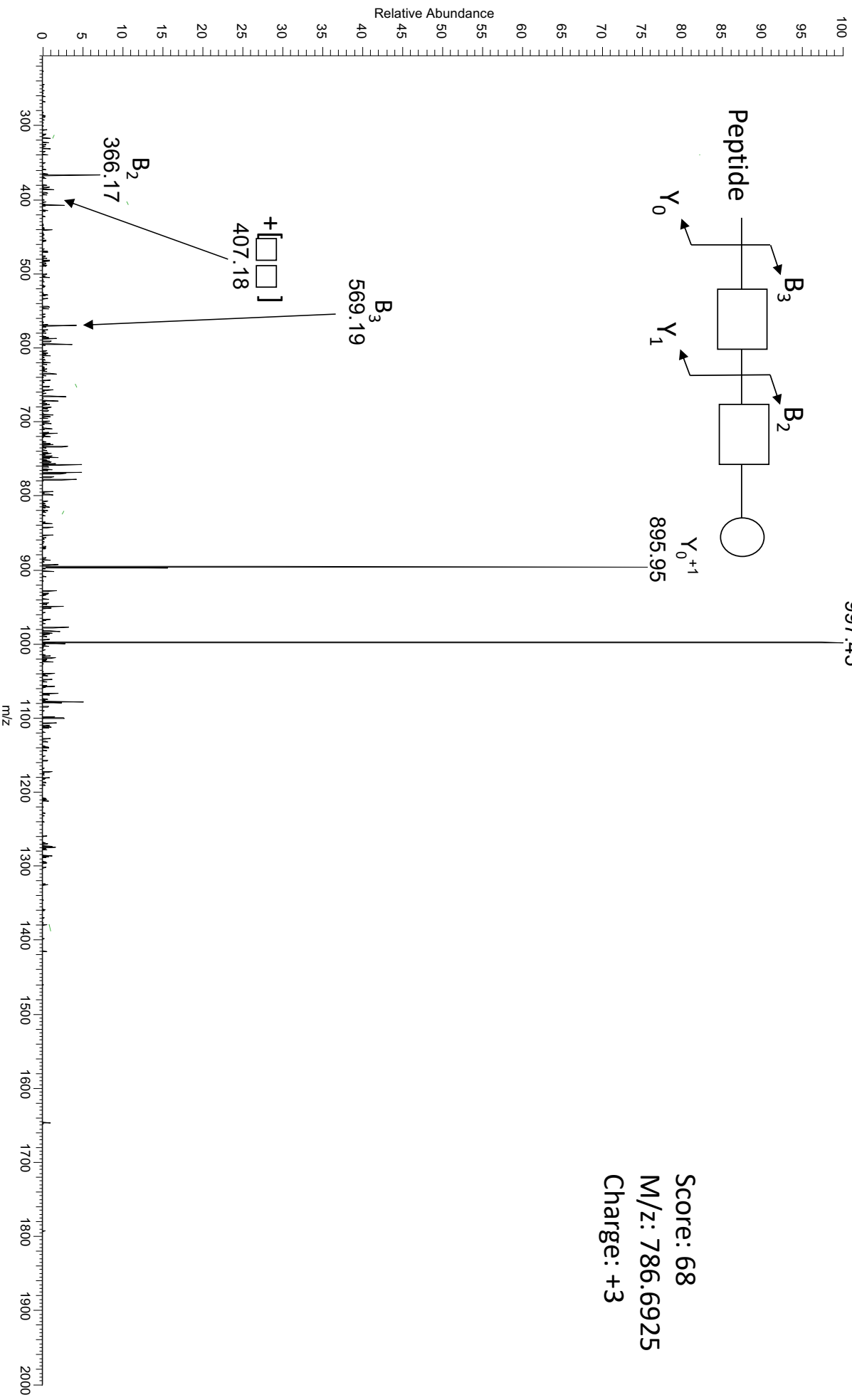
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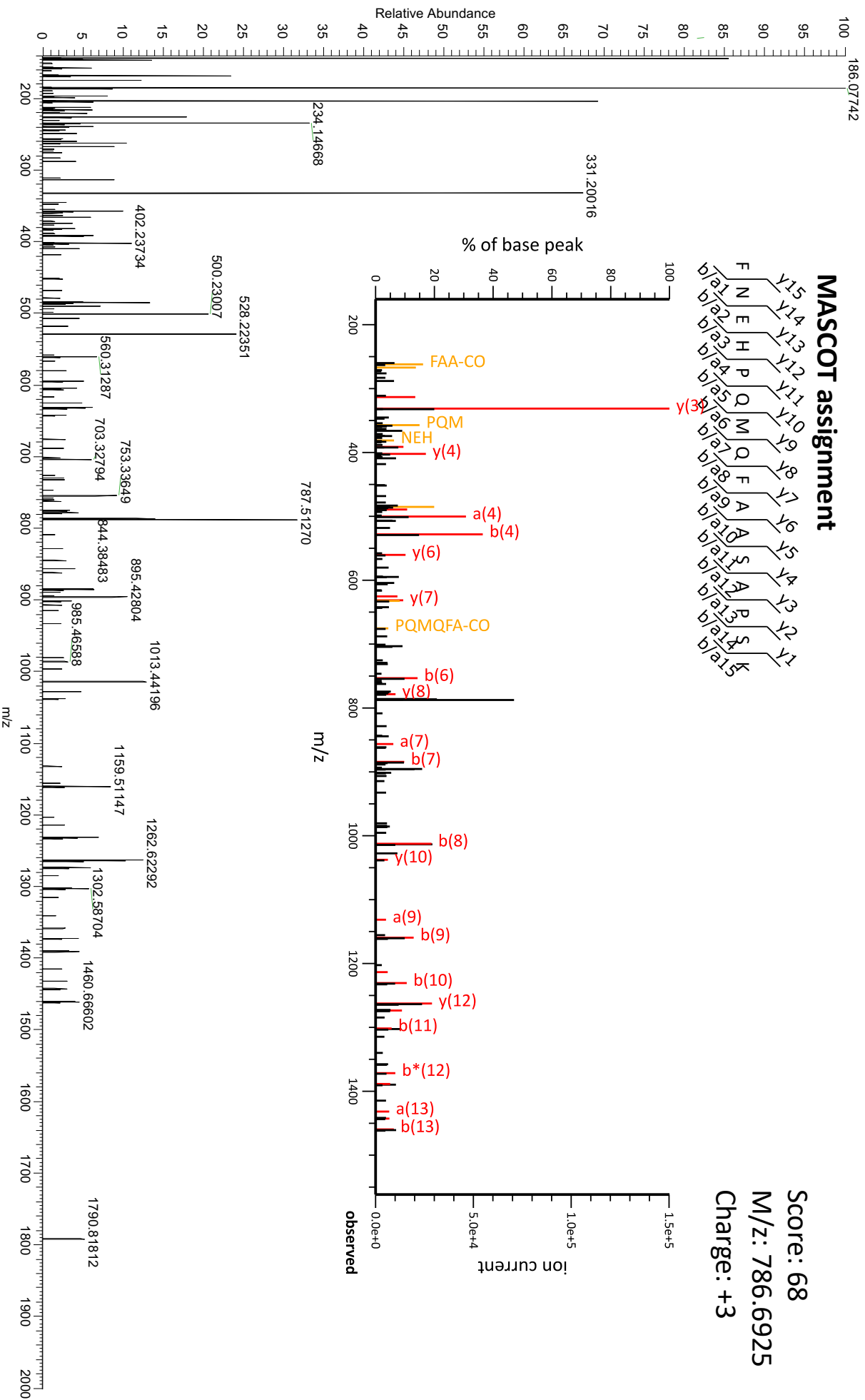
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Score: 55
M/z: 968.98877
Charge: +2

ITMS-CID

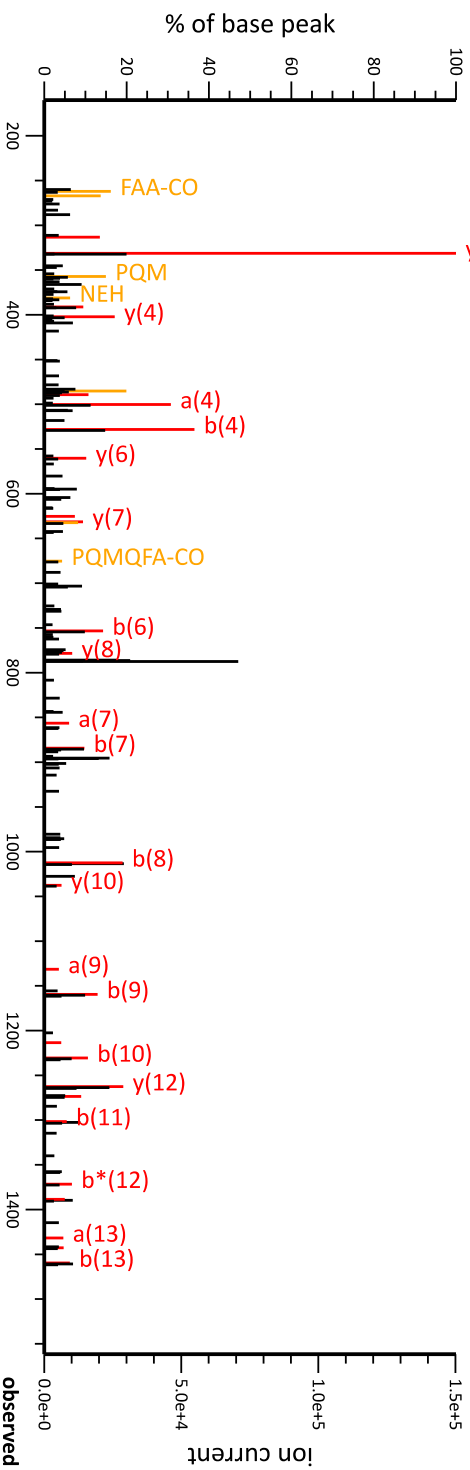


Score: 68
M/z: 786.6925
Charge: +3



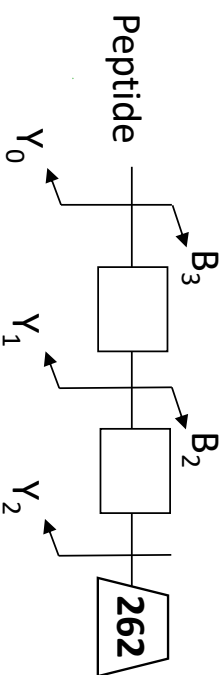
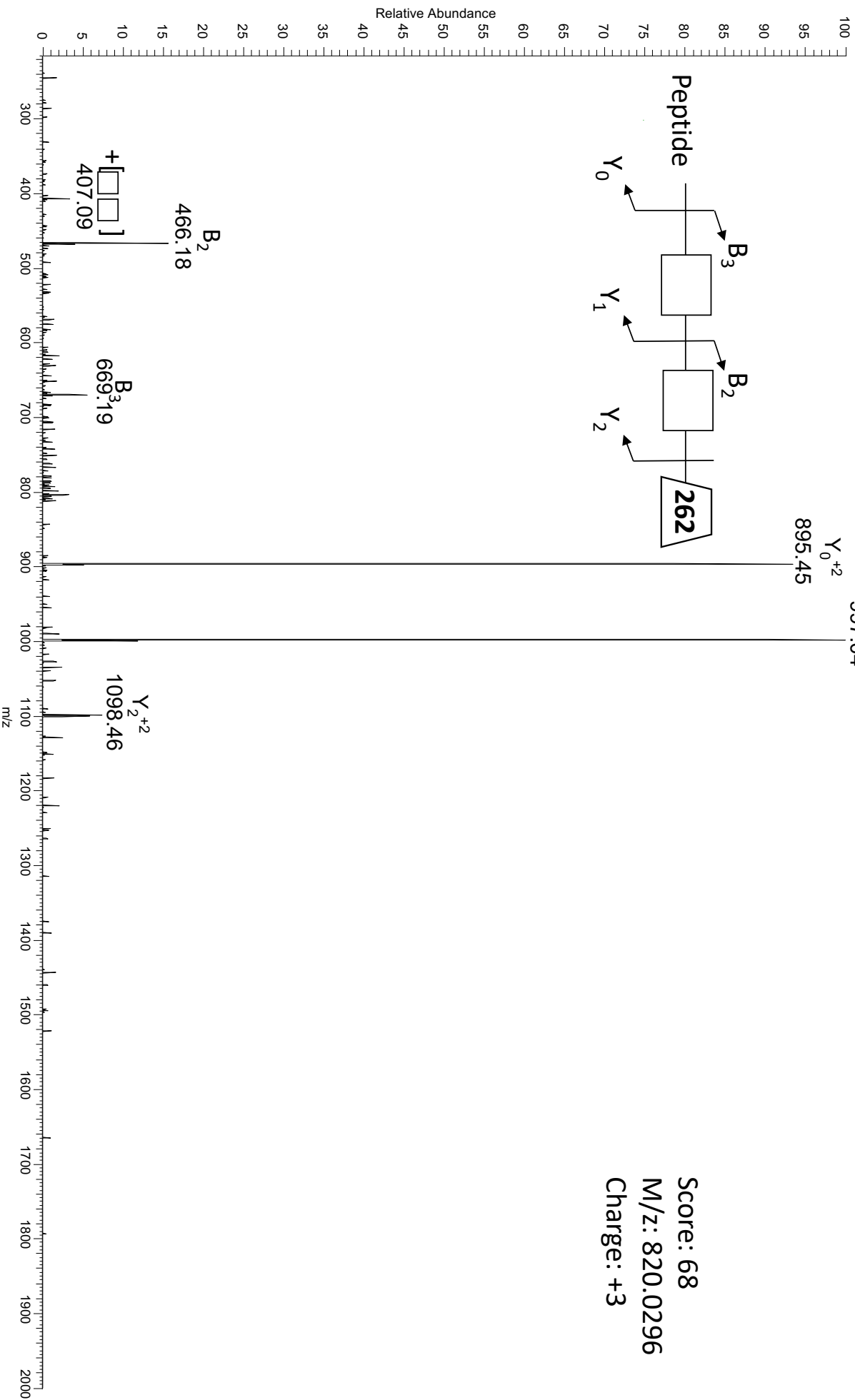
MASCOT assignment

F y15
N y14
E y13
H y12
P y11
Q y10
M y9
Q y8
F y7
A y6
A y5
S y4
P y3
S y2
K y1



Score: 68
M/z: 786.6925
Charge: +3

ITMS-CID

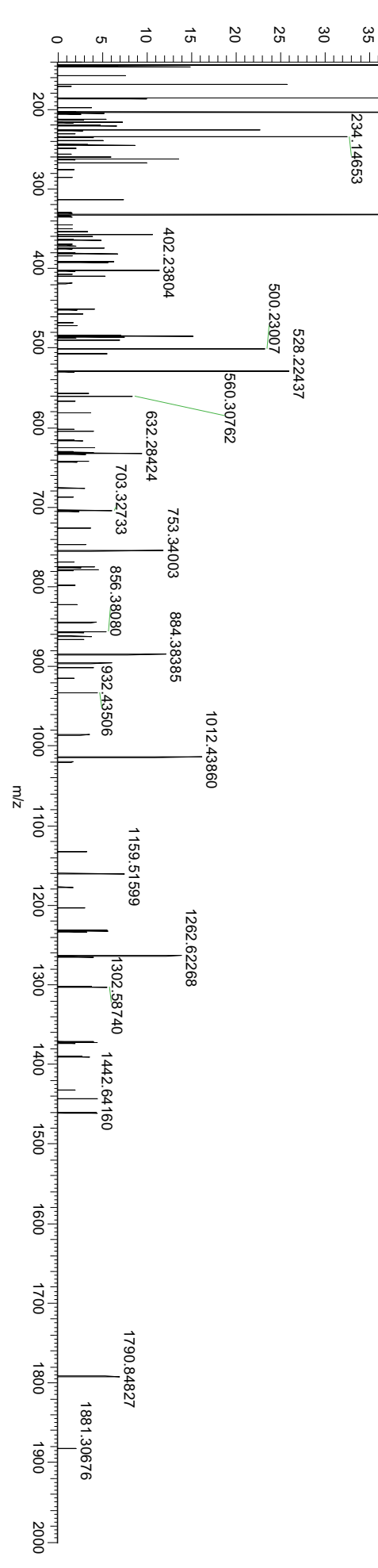
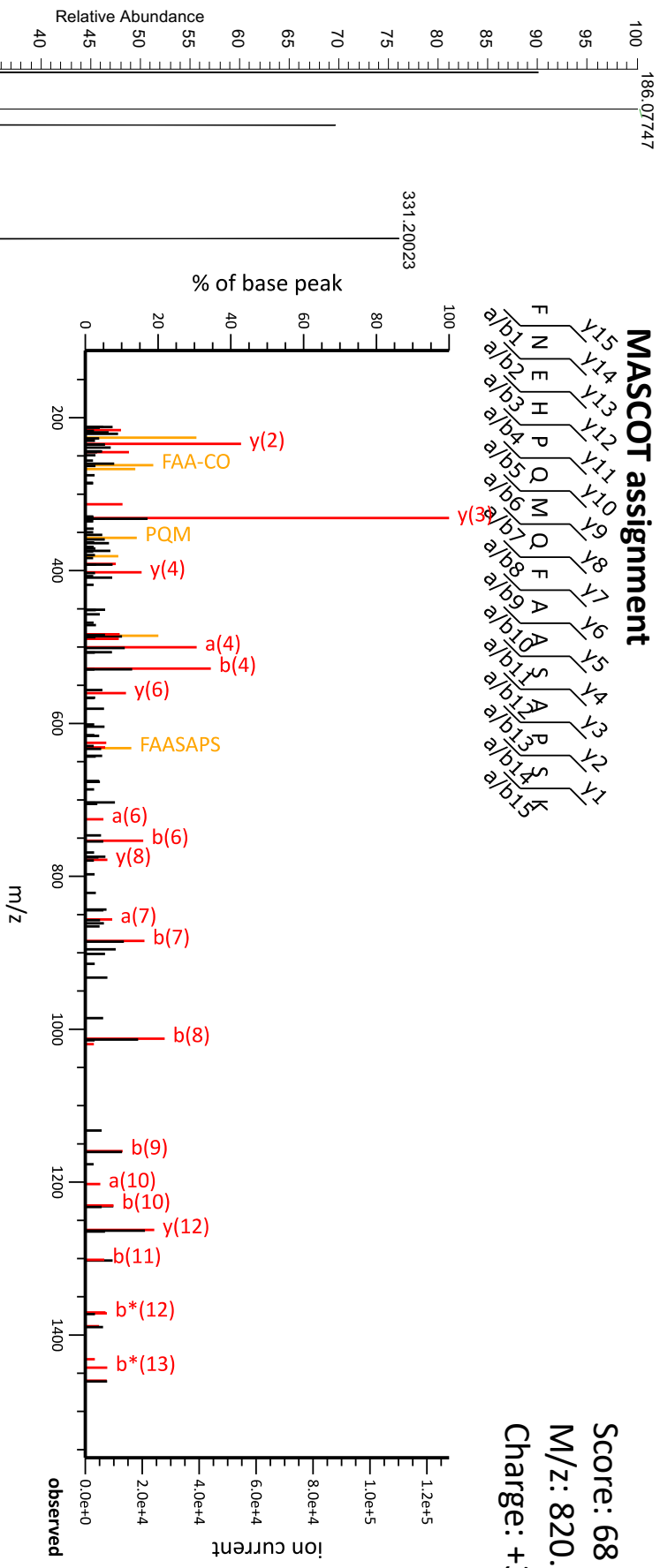


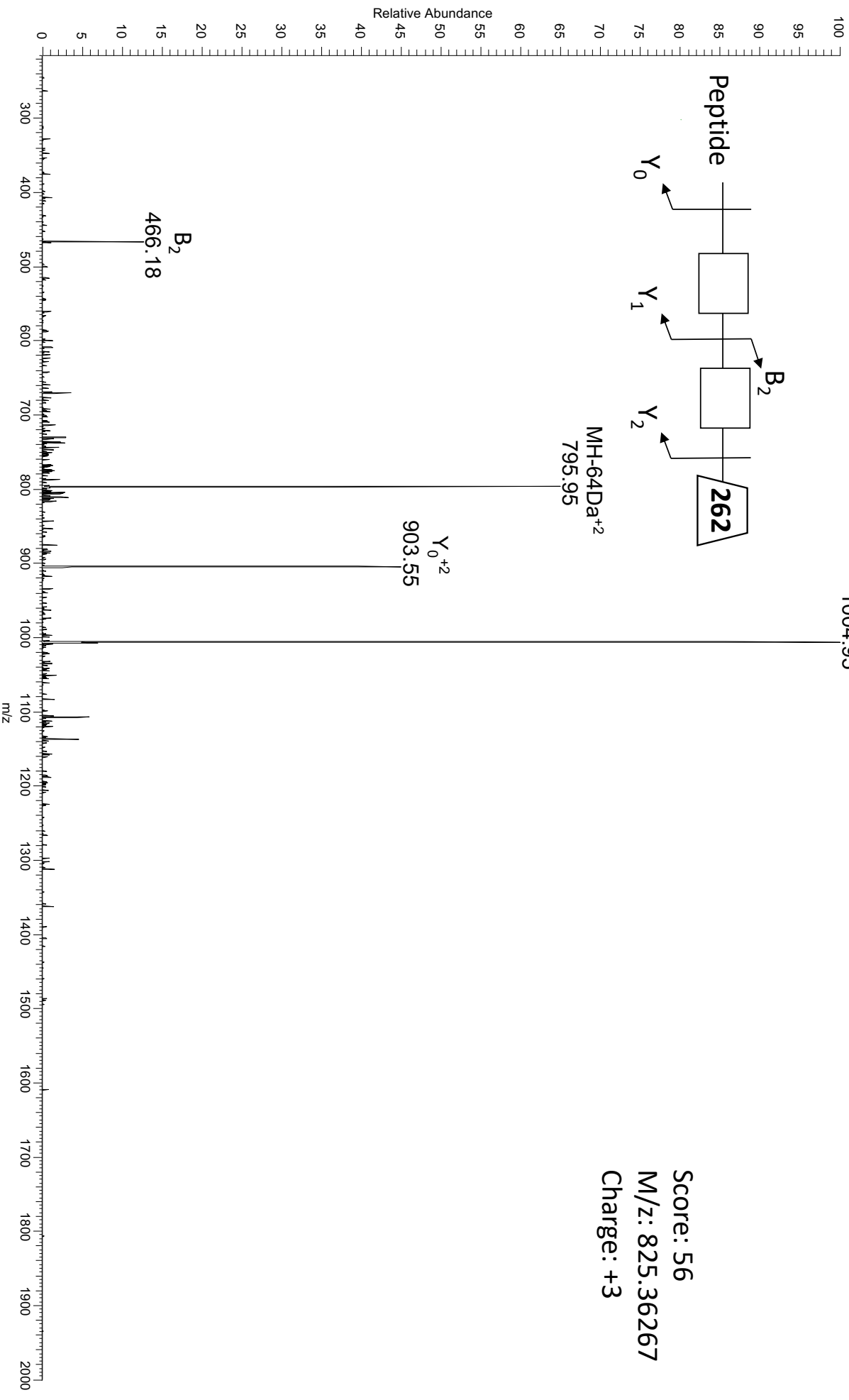
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Charge: +3

MASCOT assignment

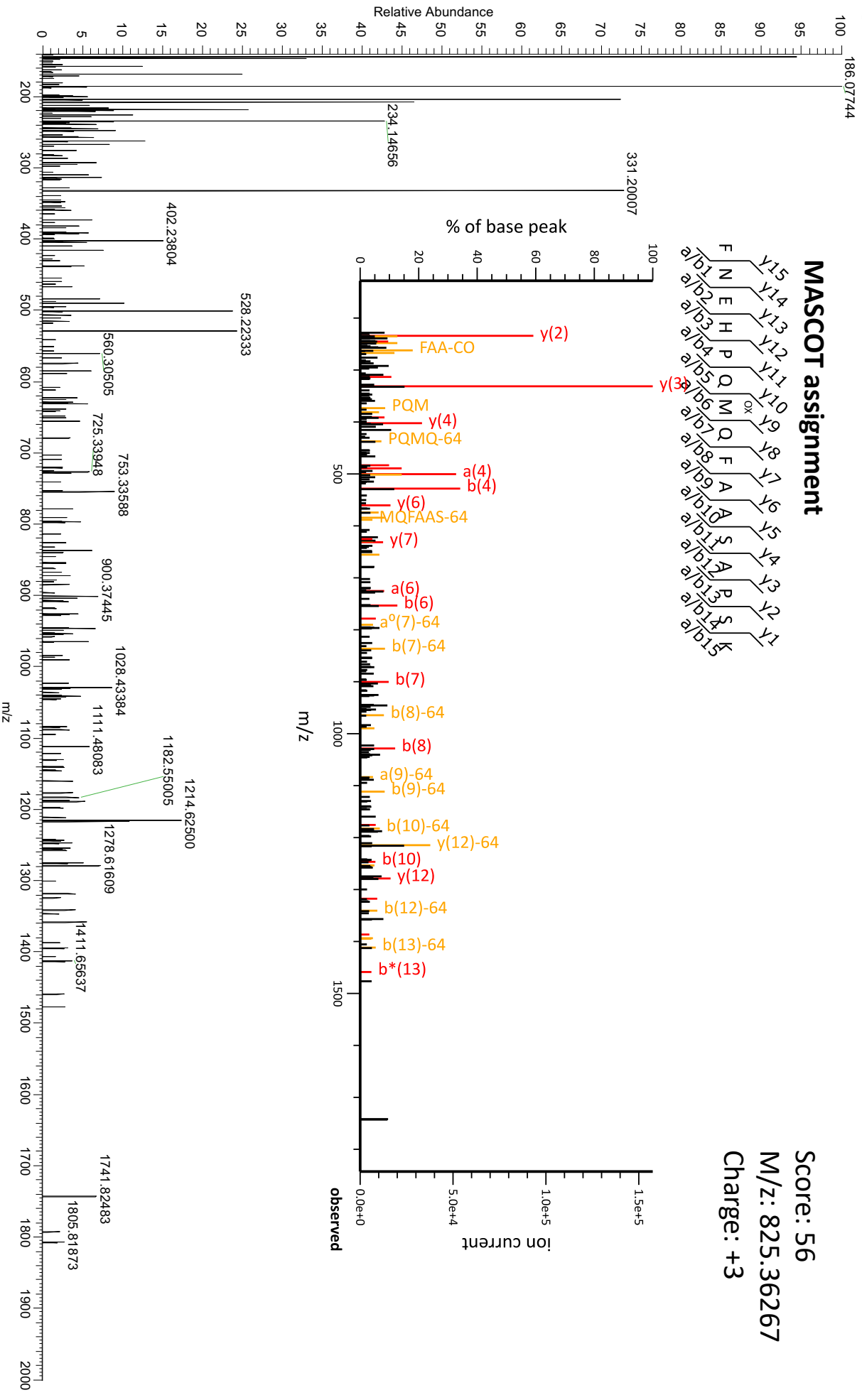
- F y15
- N y14
- E y13
- H y12
- P y11
- Q y10
- M y9
- O y8
- F y7
- A y6
- A y5
- S y4
- A y3
- P y2
- S y1
- r
- a/b1
- a/b2
- a/b3
- a/b4
- a/b5
- a/b6
- a/b7
- a/b8
- a/b9
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- a/b13
- a/b14
- a/b15

Score: 68
M/z: 820.0296
Charge: +3



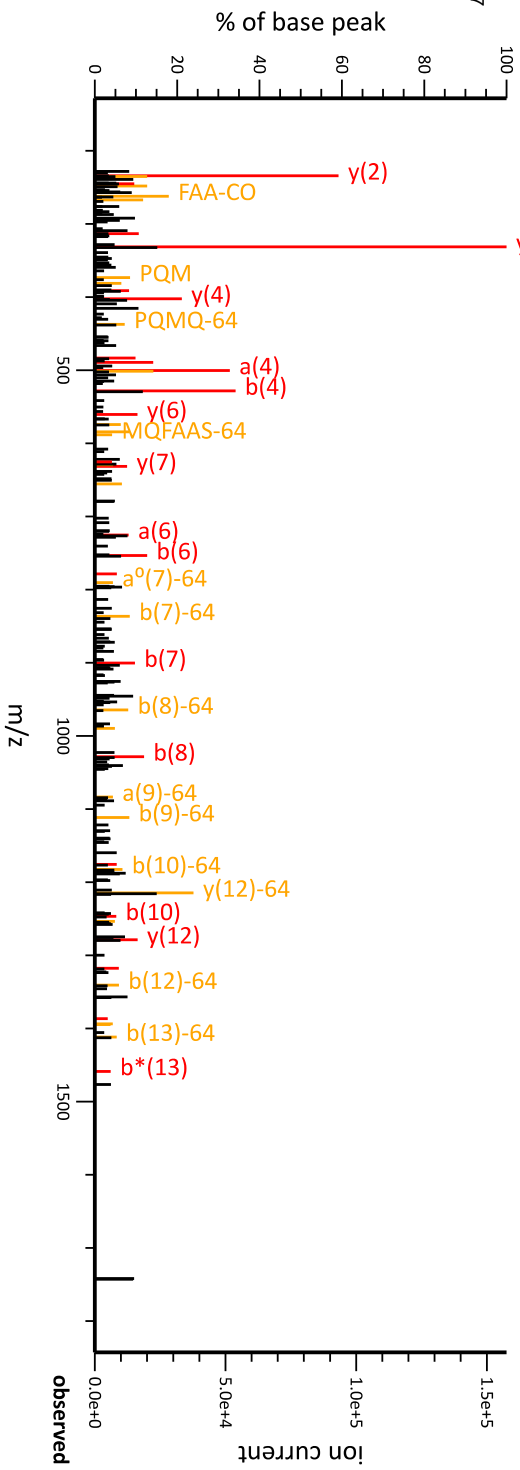


Score: 56
M/z: 825.36267
Charge: +3



MASCOT assignment

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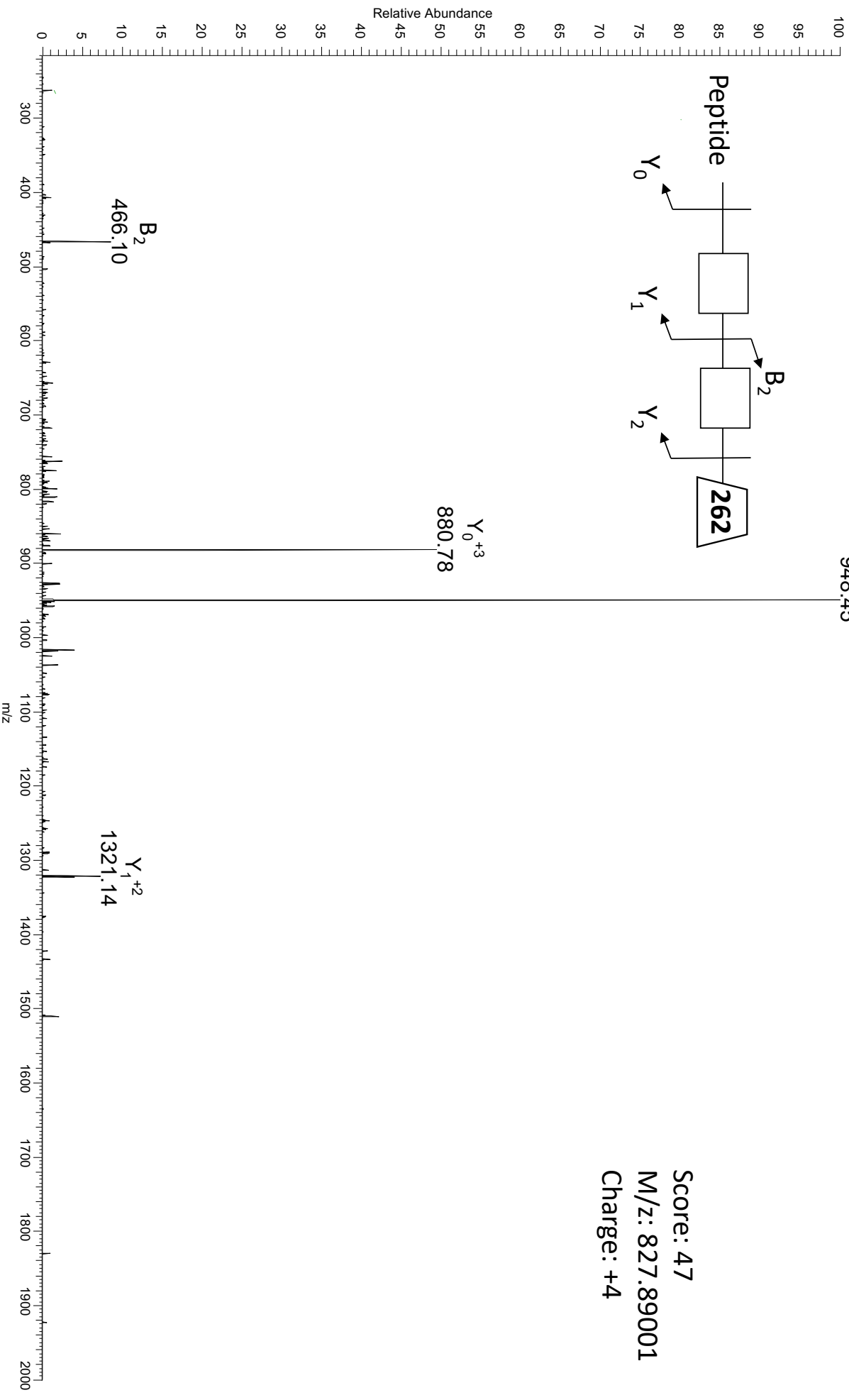


Score: 56

M/z: 825.36267

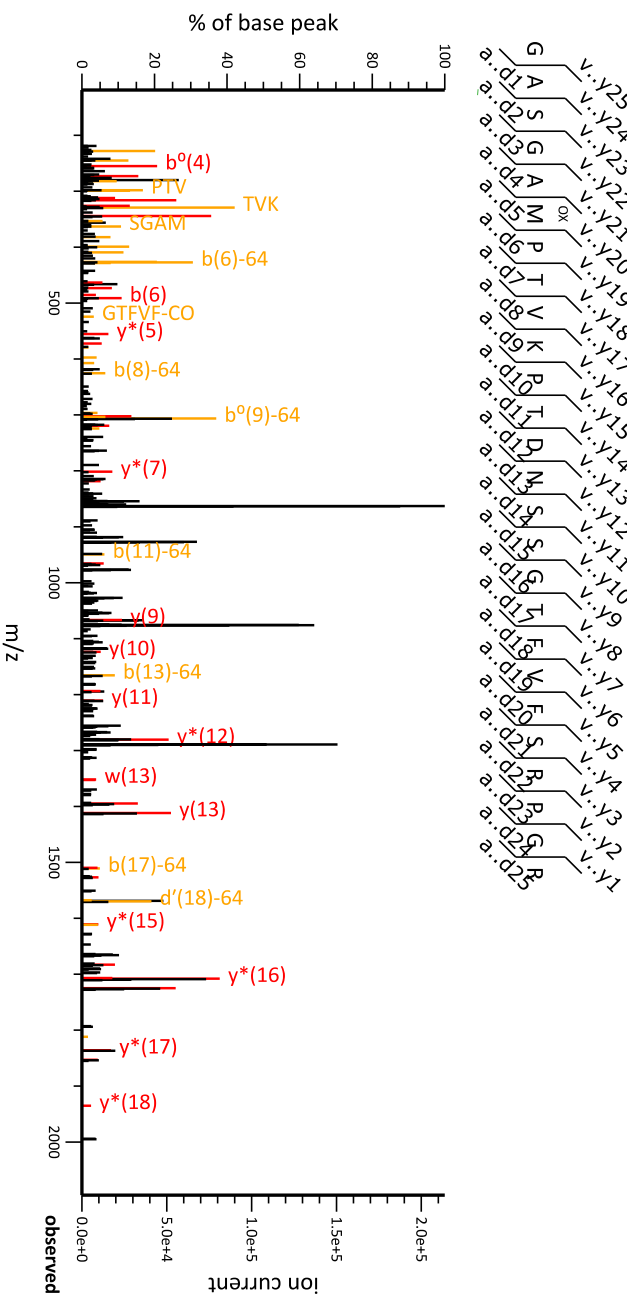
Charge: +3

ITMS-CID



Score: 47
M/z: 827.89001
Charge: +4

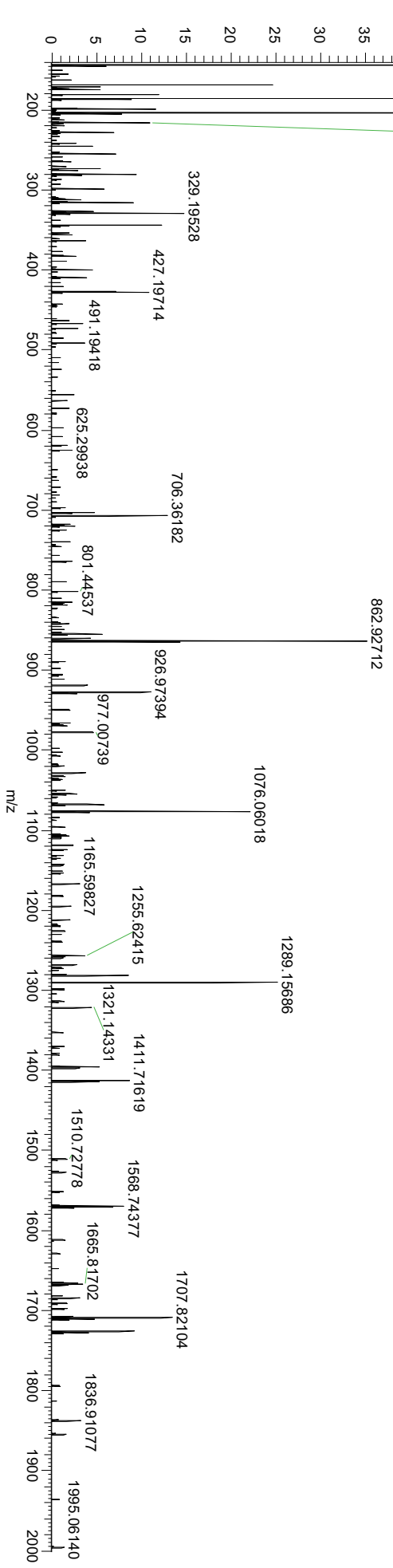
MASCOT assignment

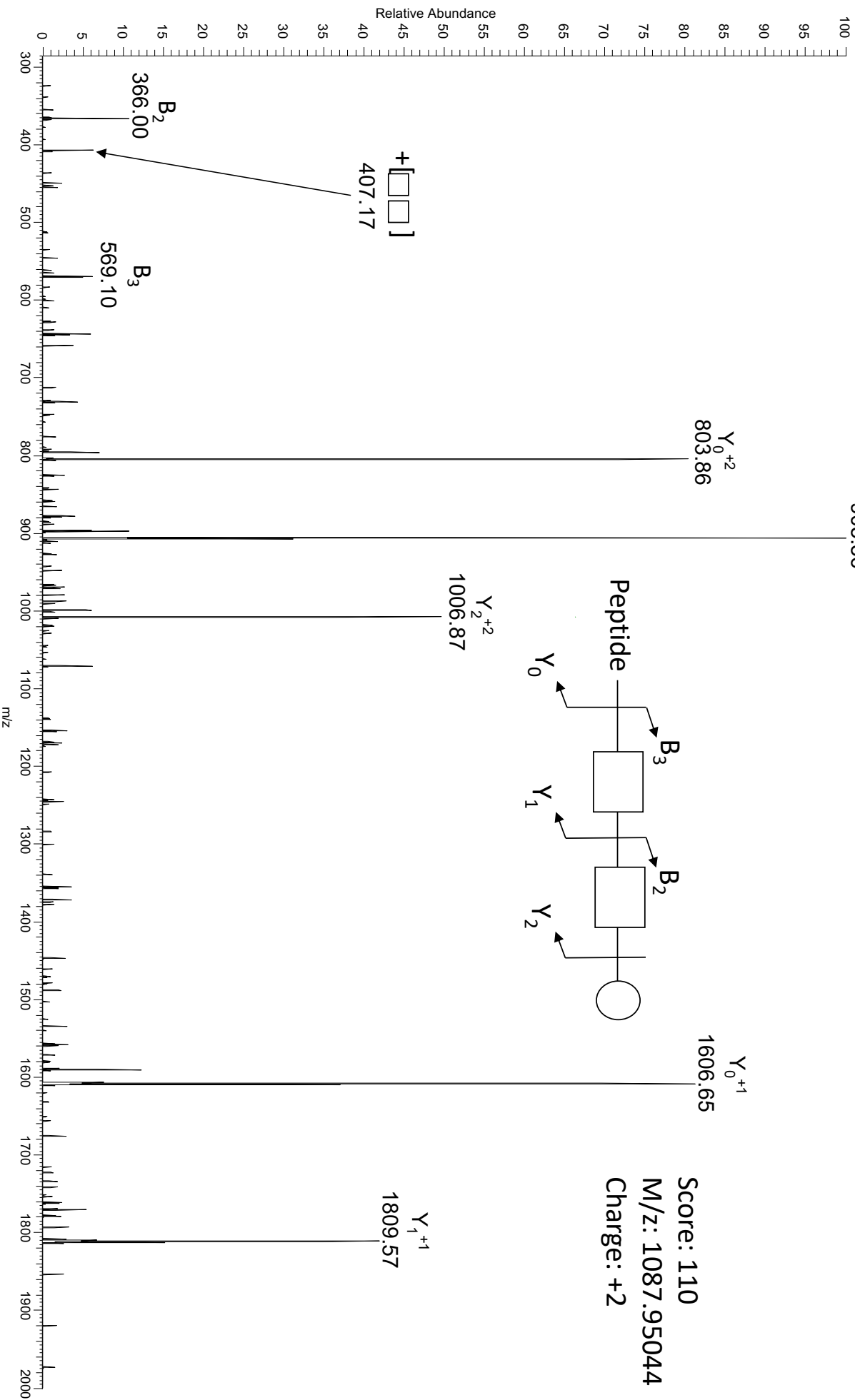


Score: 47

M/z: 827.89001

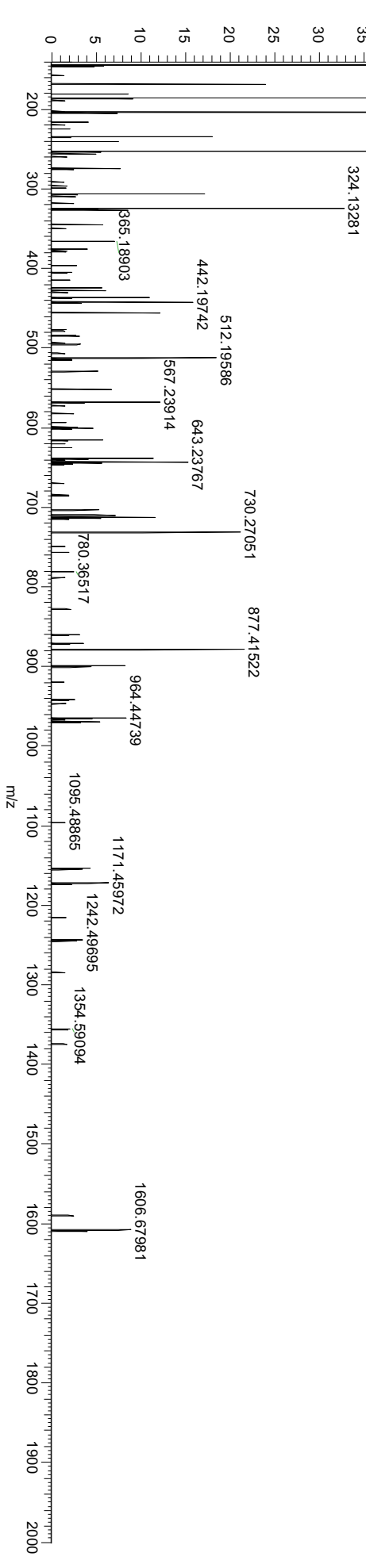
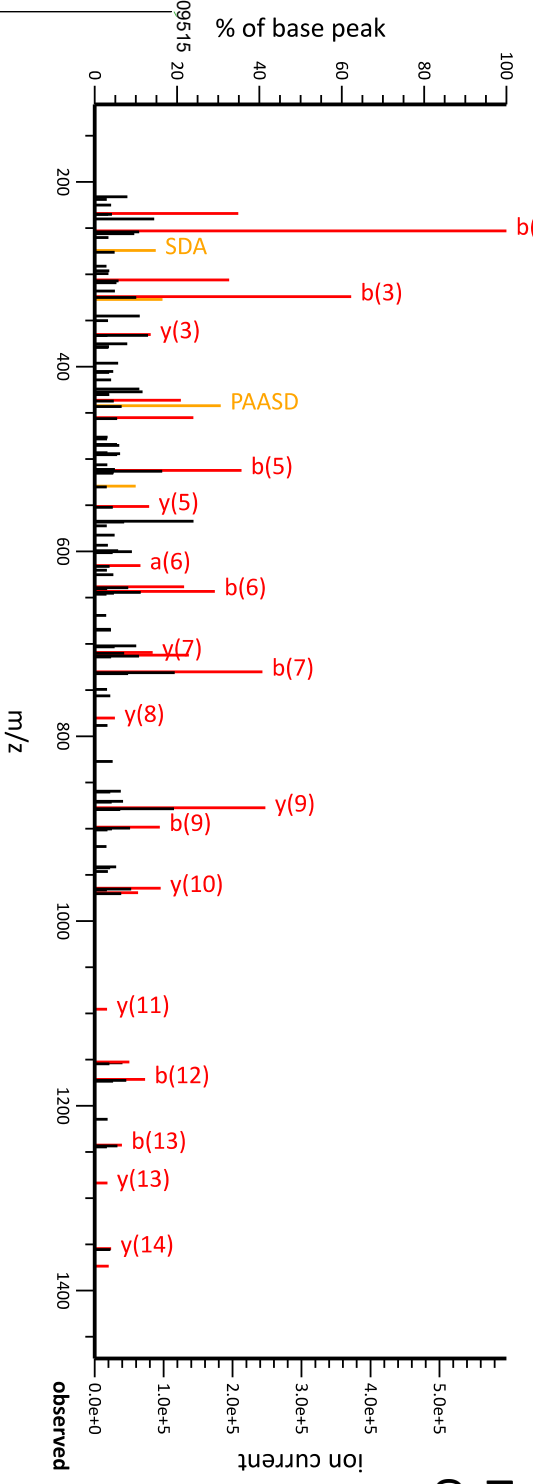
Charge: +4





MASCOT assignment

H y15
D y14
A y13
M y12
G y11
M y10
S y9
P y8
A y7
A y6
S y5
P y4
A y3
M y2
S y1
F y0

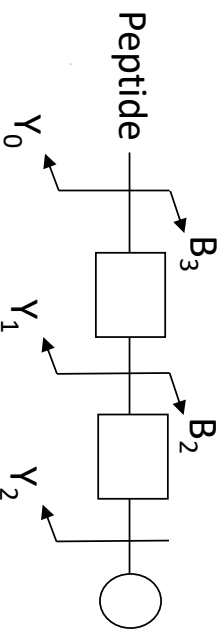
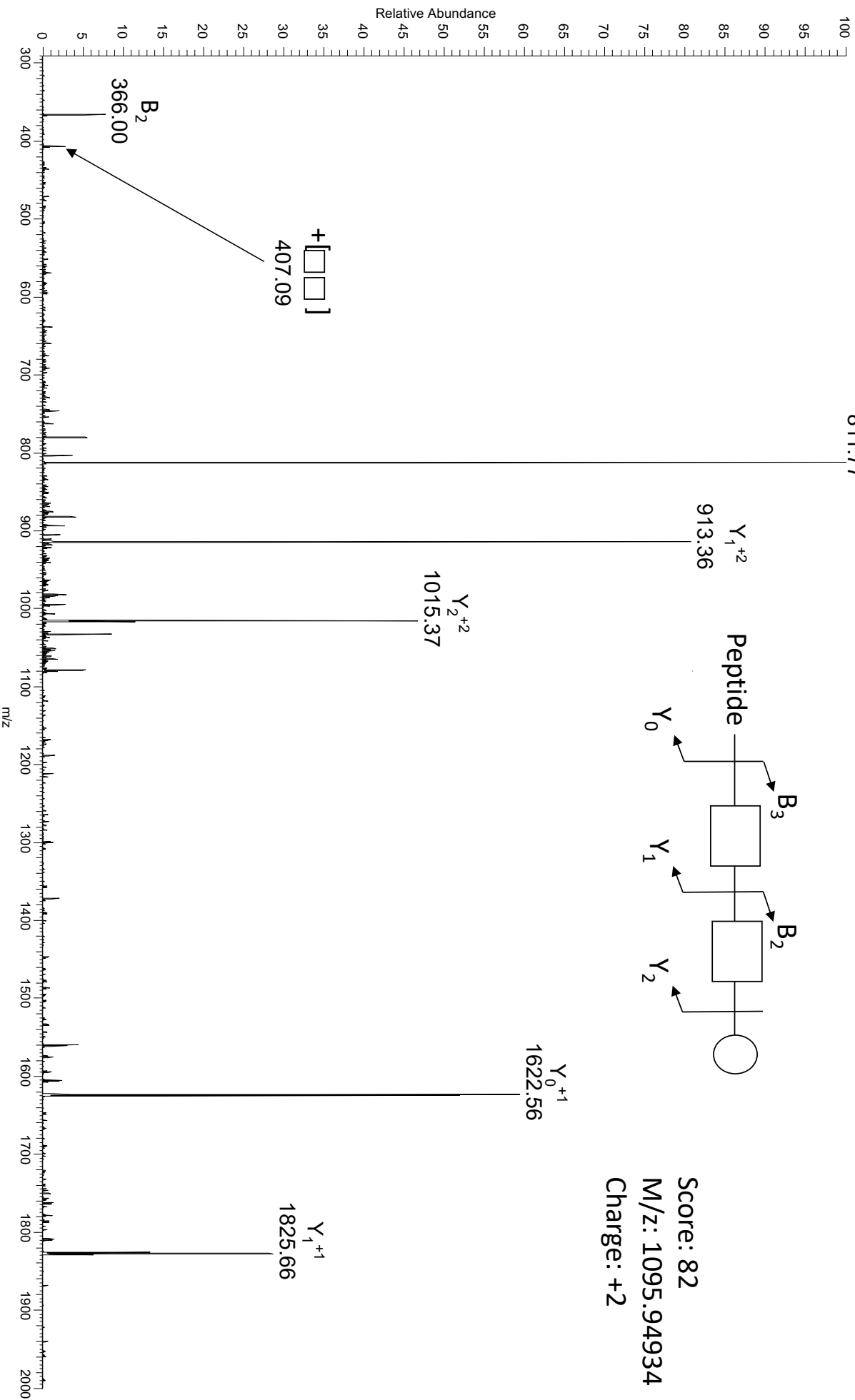


Score: 110

M/z: 1087.95044

Charge: +2

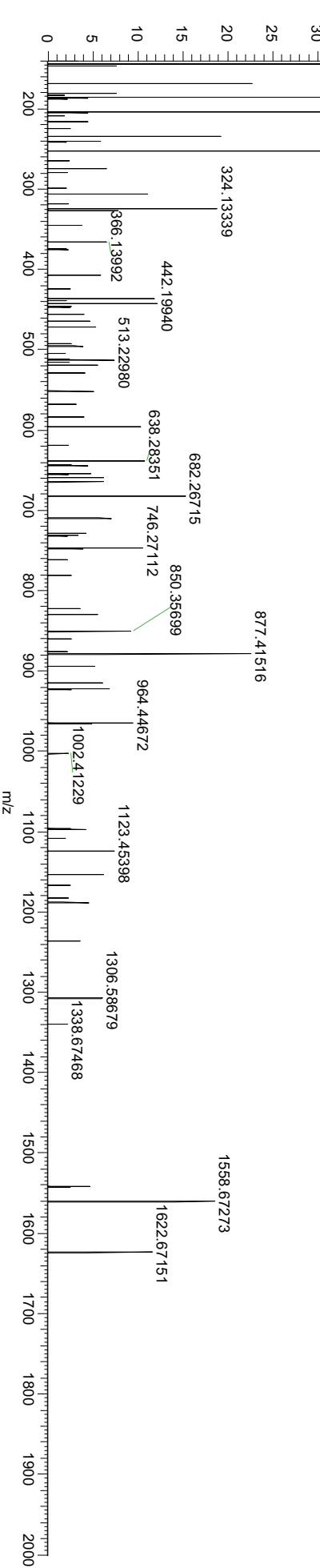
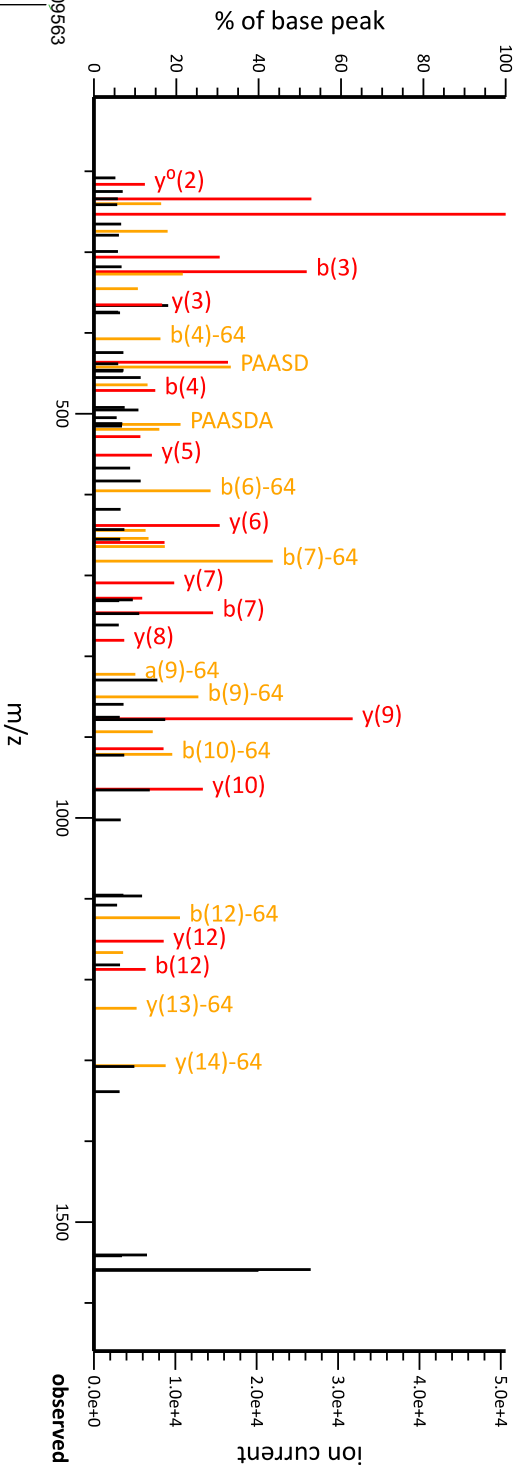
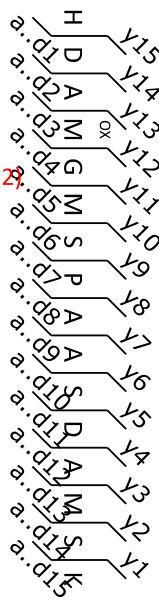
ITMS-CID



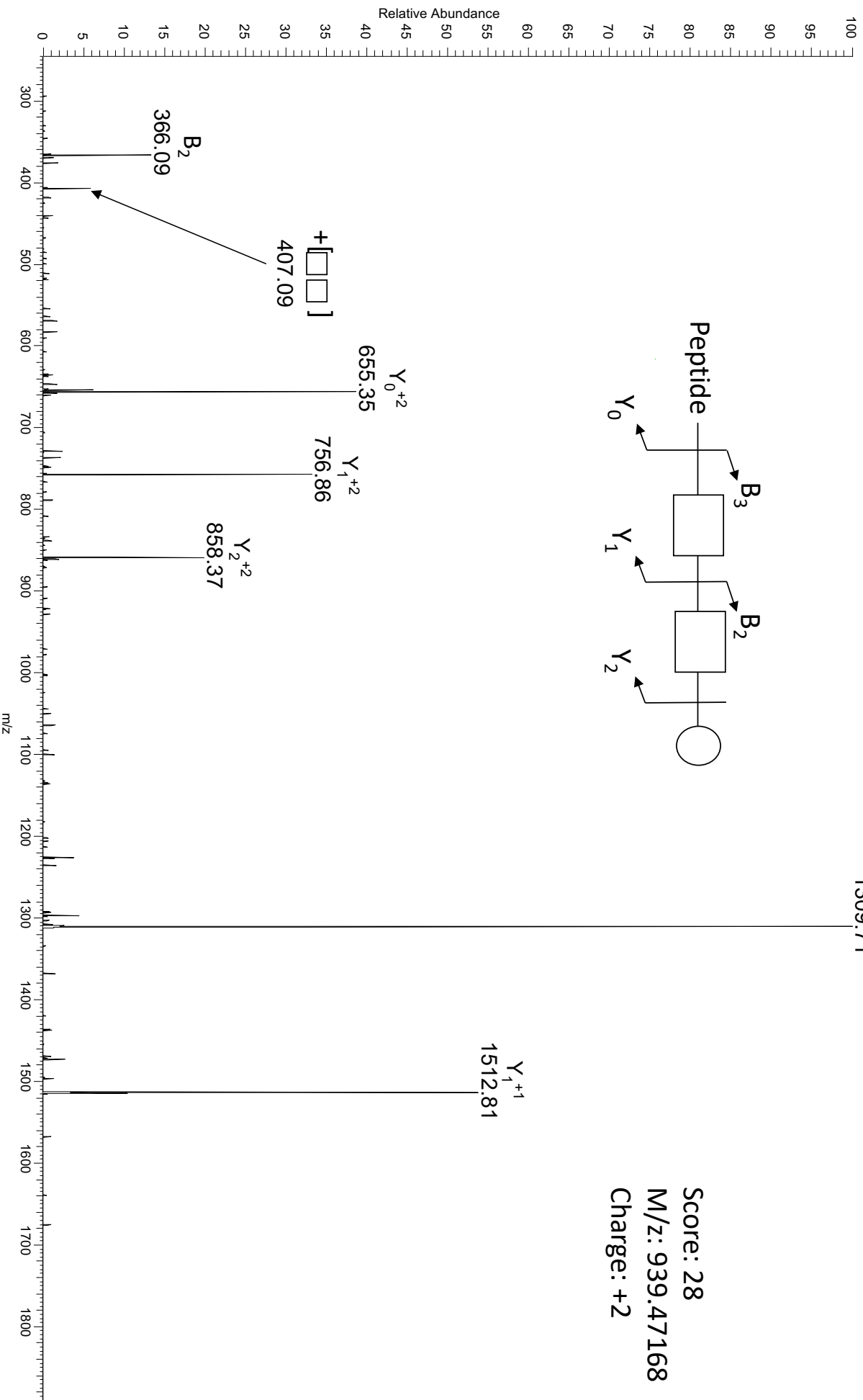
Score: 82
M/z: 1095.94934
Charge: +2

186.07767

MASCOT assignment



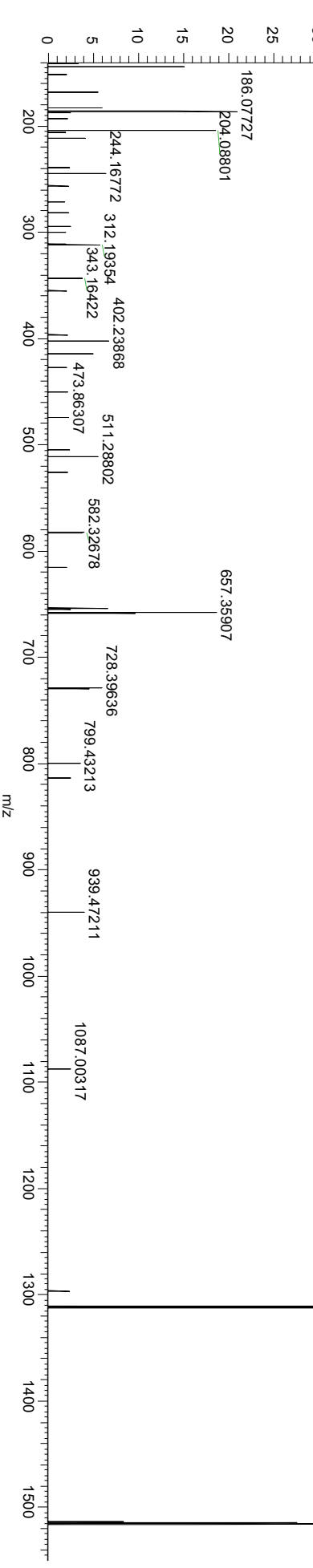
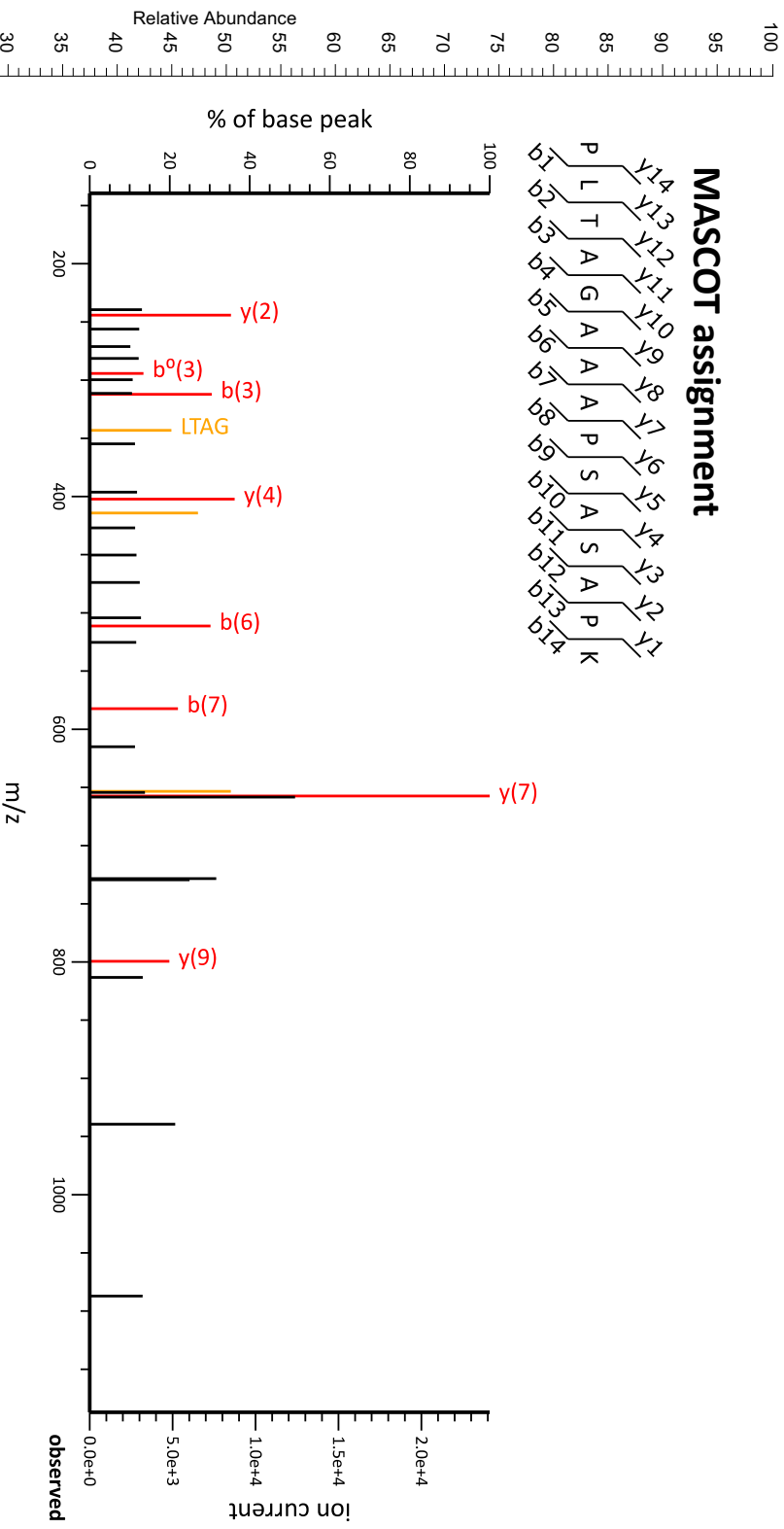
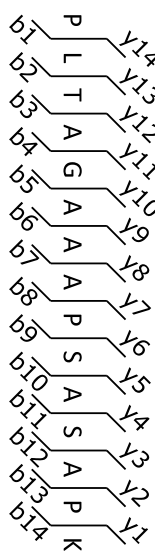
Score: 82
M/z: 1095.94934
Charge: +2



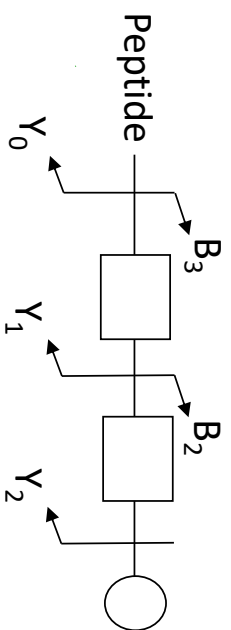
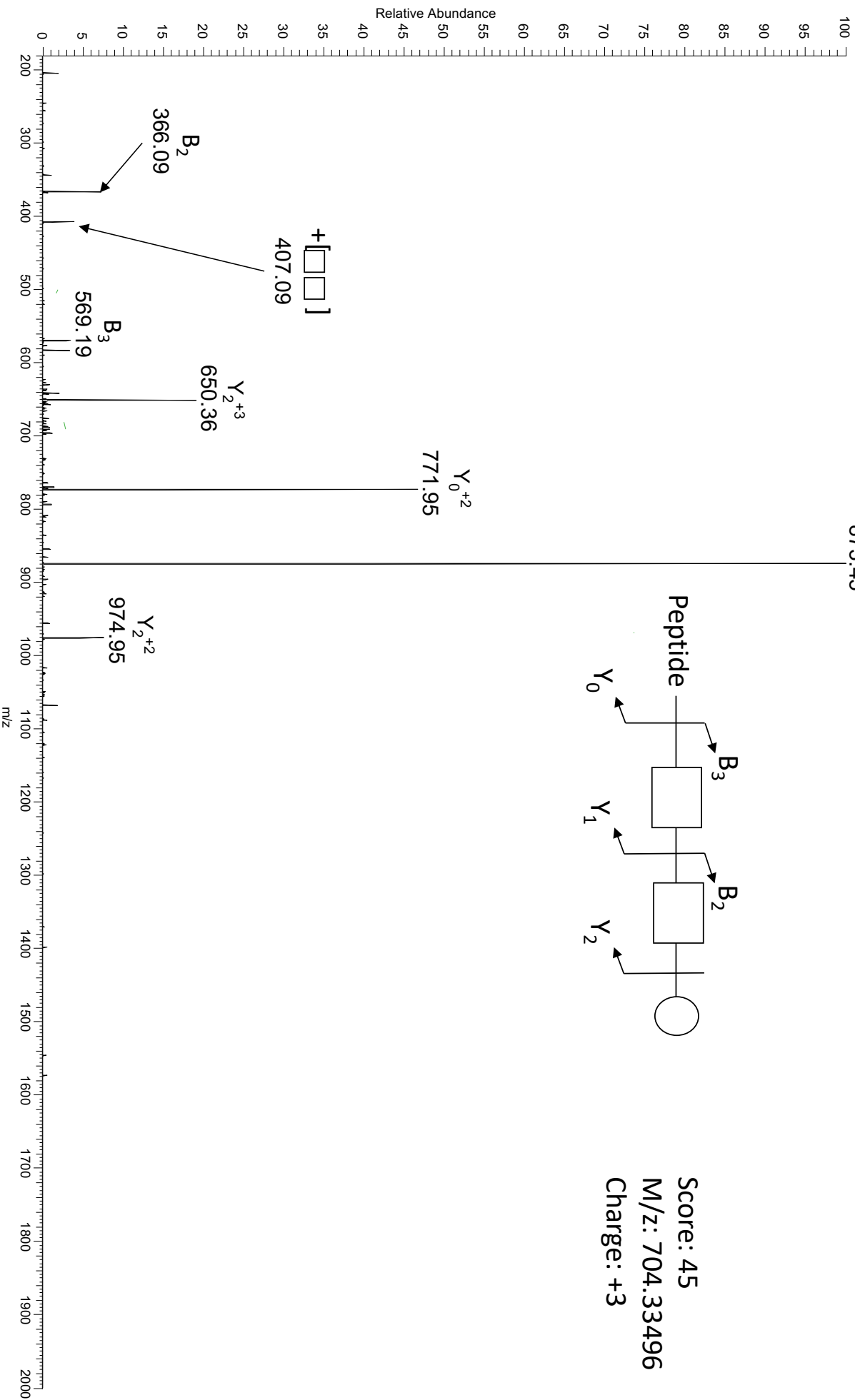
1310.72241

Score: 28
M/z: 939.47168
Charge: +2

MASCOT assignment



ITMS-CID

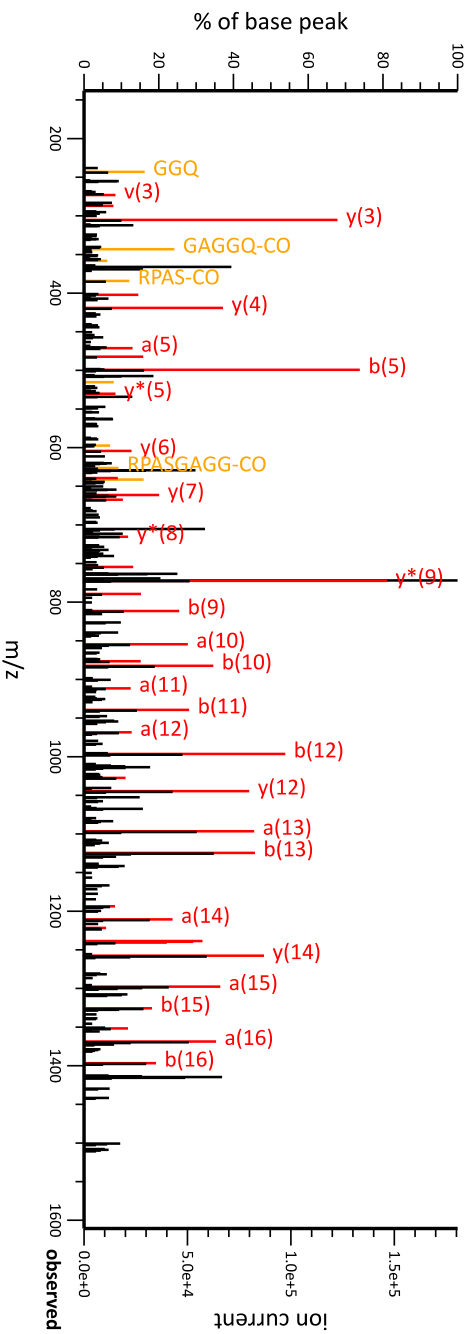


Score: 45
M/z: 704.33496
Charge: +3

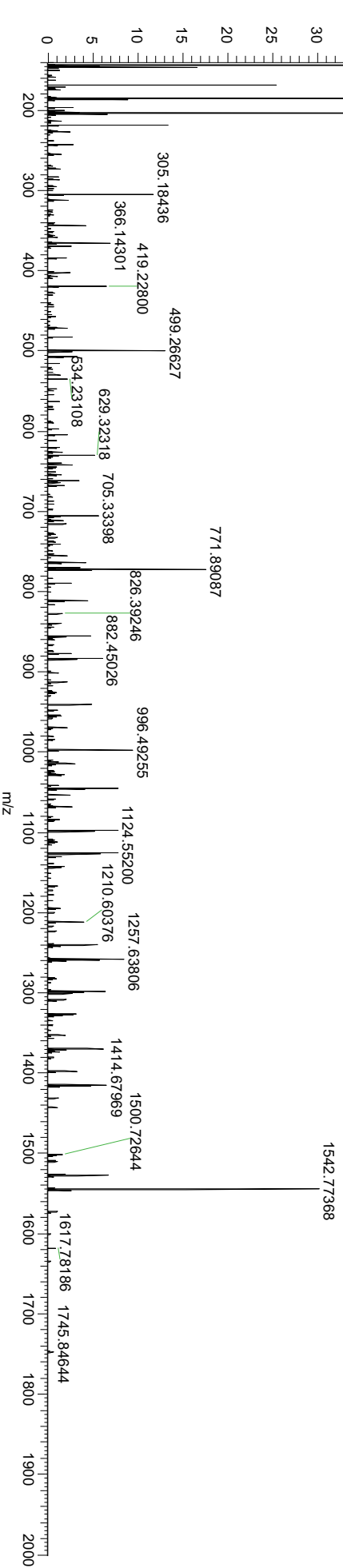
186.07753

MASCOT assignment

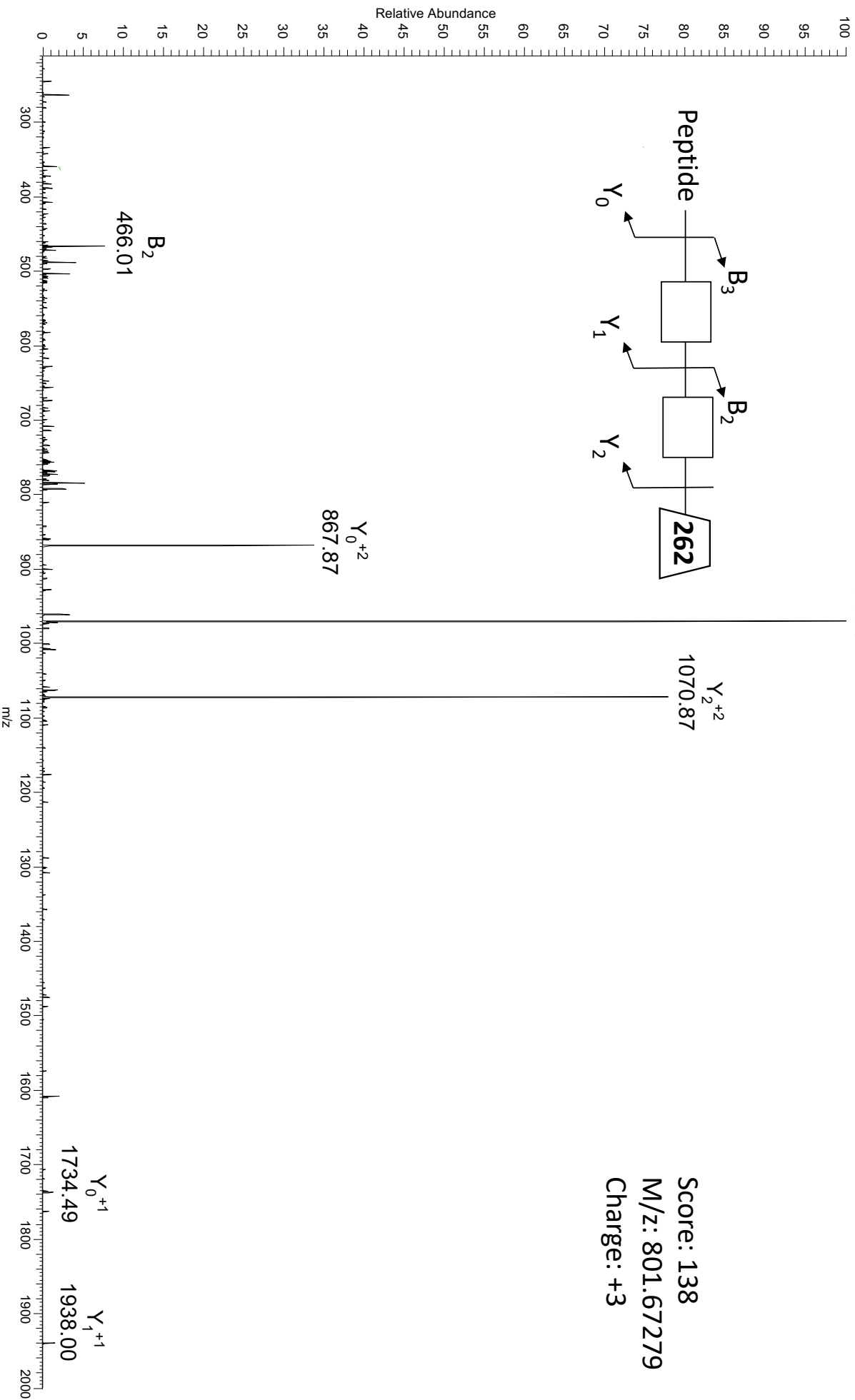
I
V/V16
V/V15
V/V14
V/V13
V/V12
V/V11
V/V10
V/V9
V/V8
V/V7
V/V6
V/V5
V/V4
V/V3
V/V2
V/V1
K
I
G
D
G
R
P
A
S
G
A
G
G
Q
C
O
P
E
L
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P
E
L
E



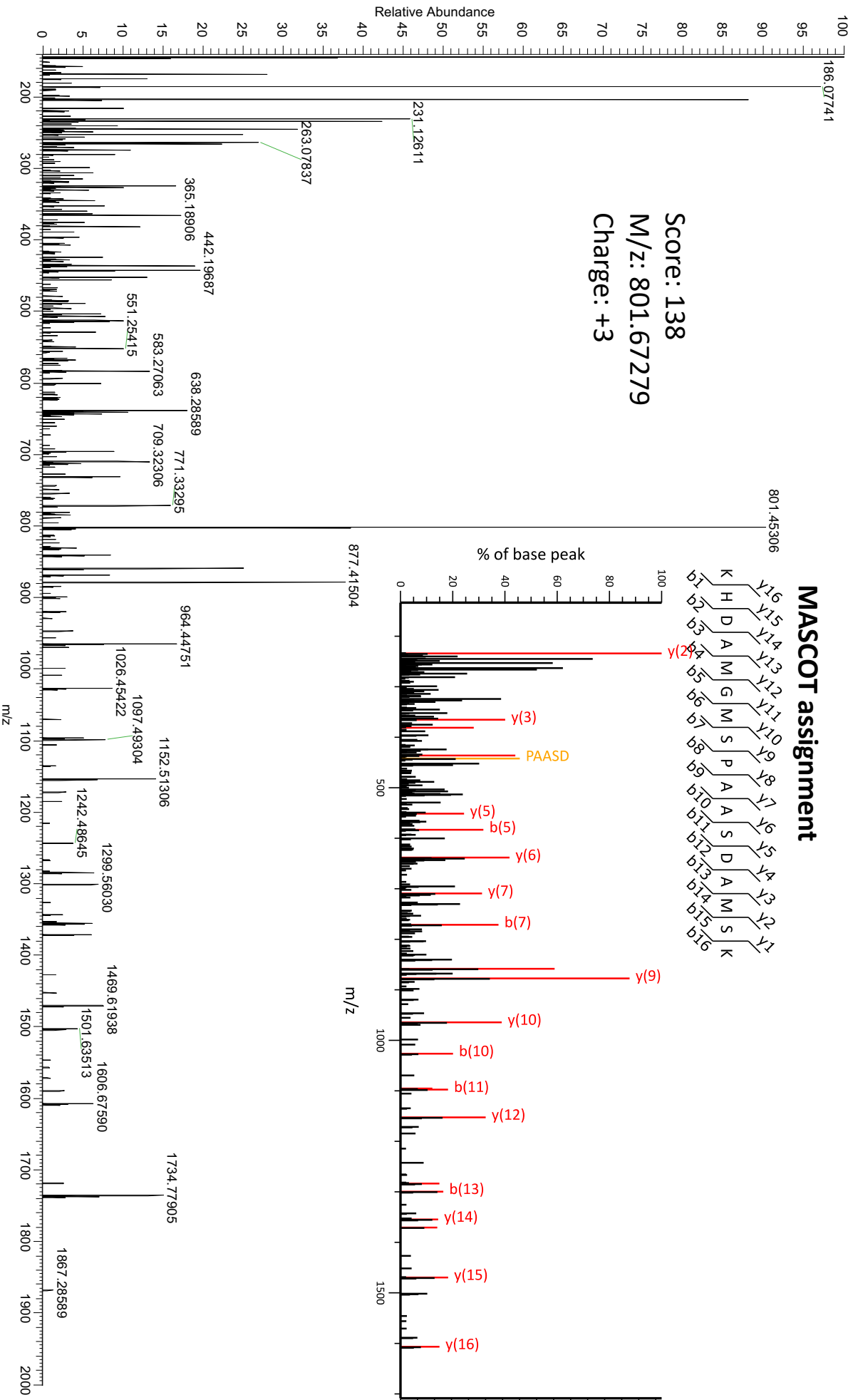
Score: 45
M/z: 704.33496
Charge: +3



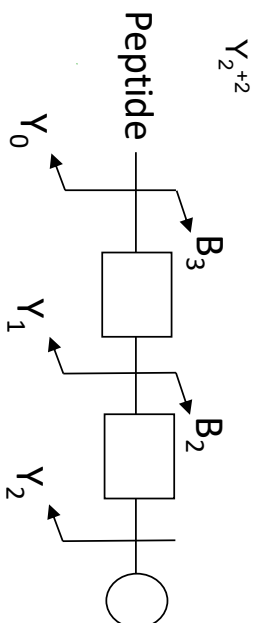
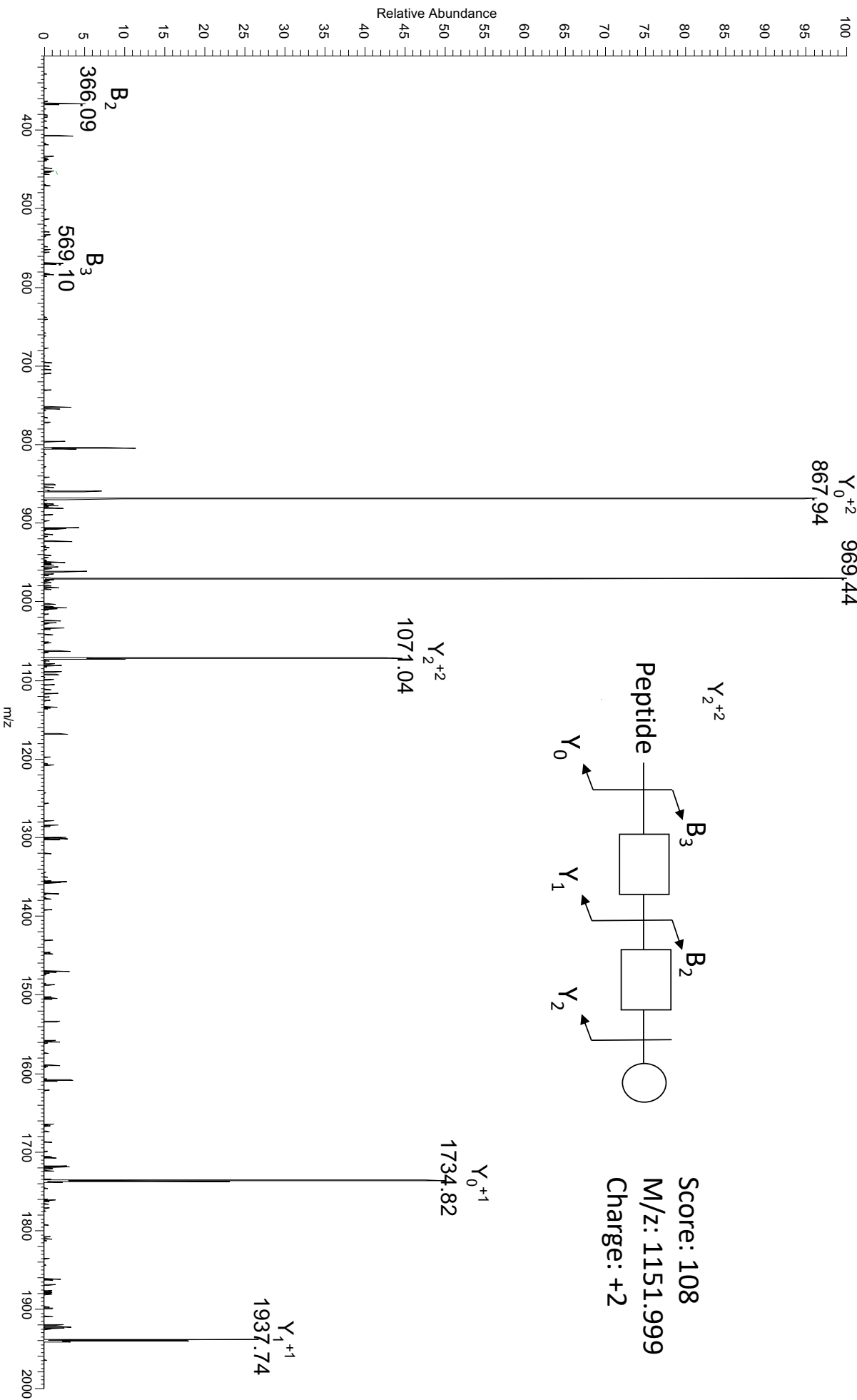
ITMS-CID



Score: 138
M/z: 801.67279
Charge: +3



ITMS-CID

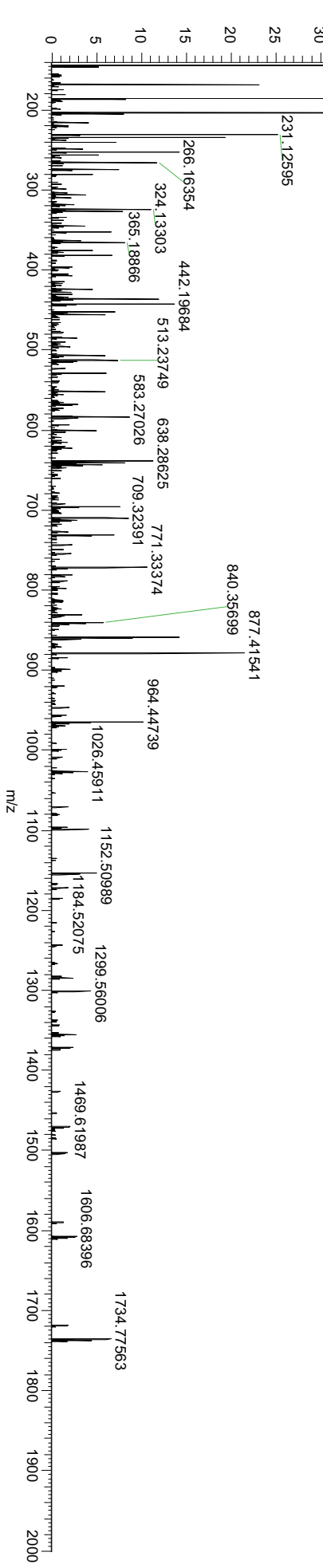
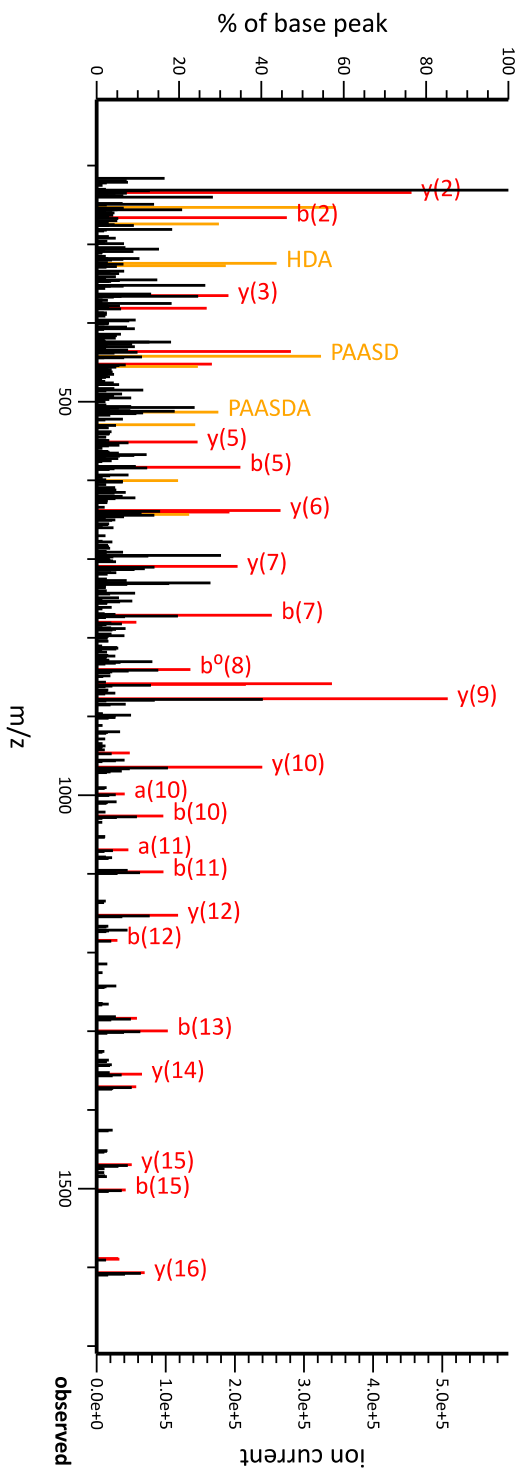


Score: 108
M/z: 1151.999
Charge: +2

186.07764

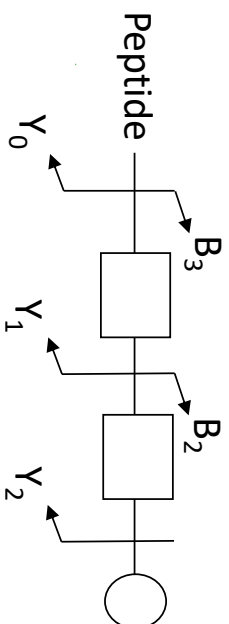
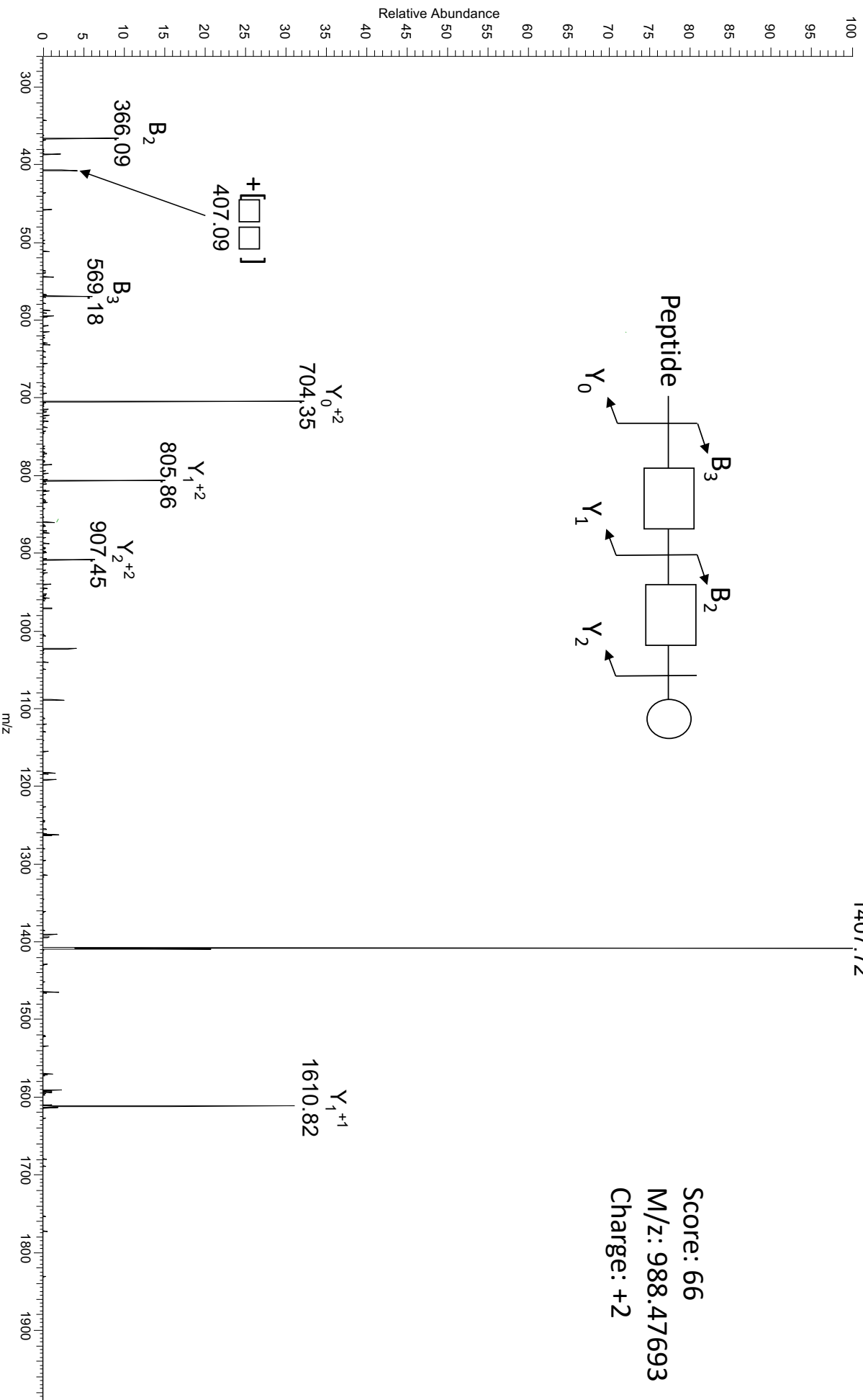
MASCOT assignment

- y16
- y15
- y14
- y13
- y12
- y11
- y10
- y9
- y8
- y7
- y6
- y5
- y4
- y3
- y2
- y1
- b/a1
- b/a2
- b/a3
- b/a4
- b/a5
- b/a6
- b/a7
- b/a8
- b/a9
- b/a10
- b/a11
- b/a12
- b/a13
- b/a14
- b/a15
- b/a16



Score: 108
M/z: 1151.999
Charge: +2

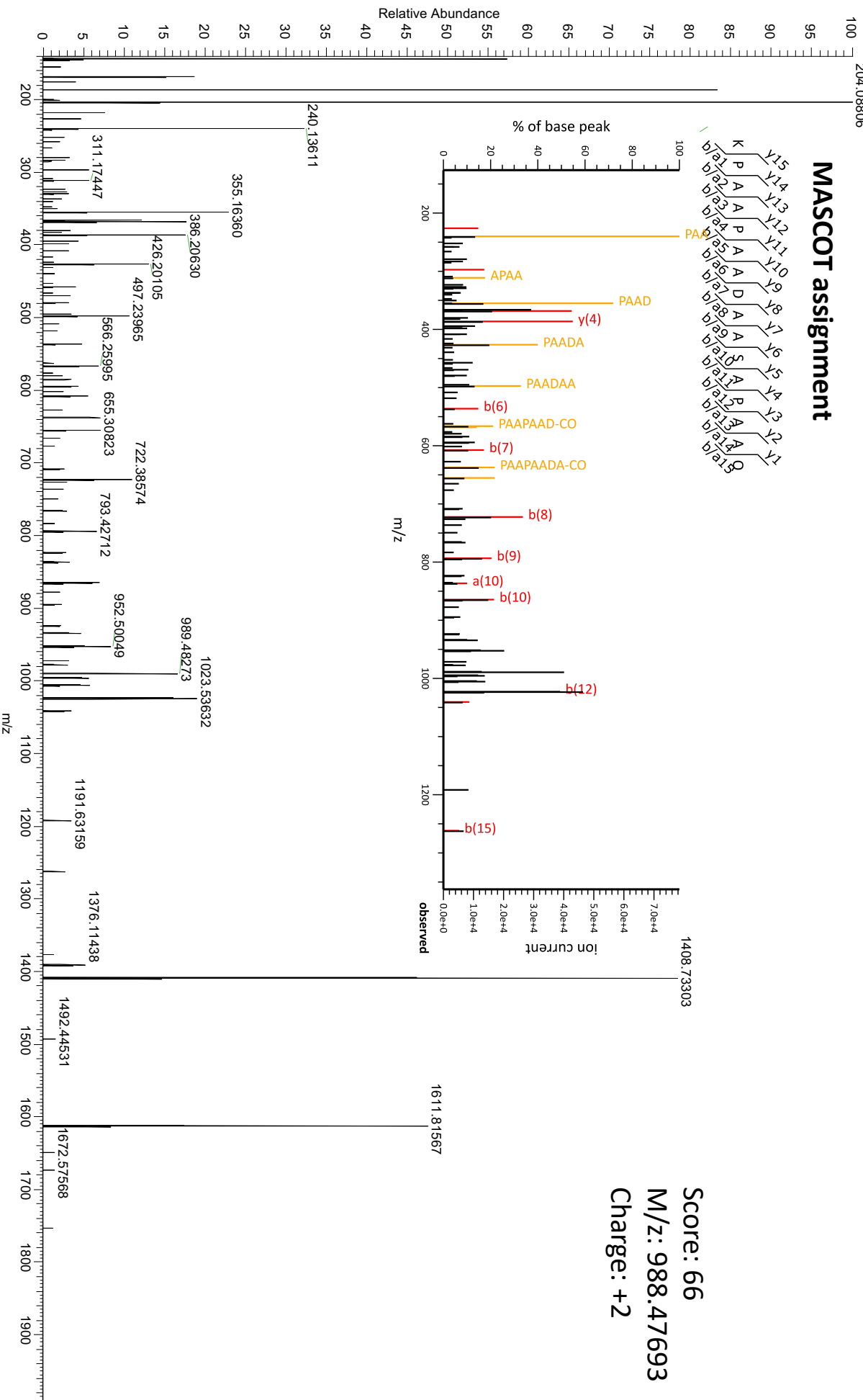
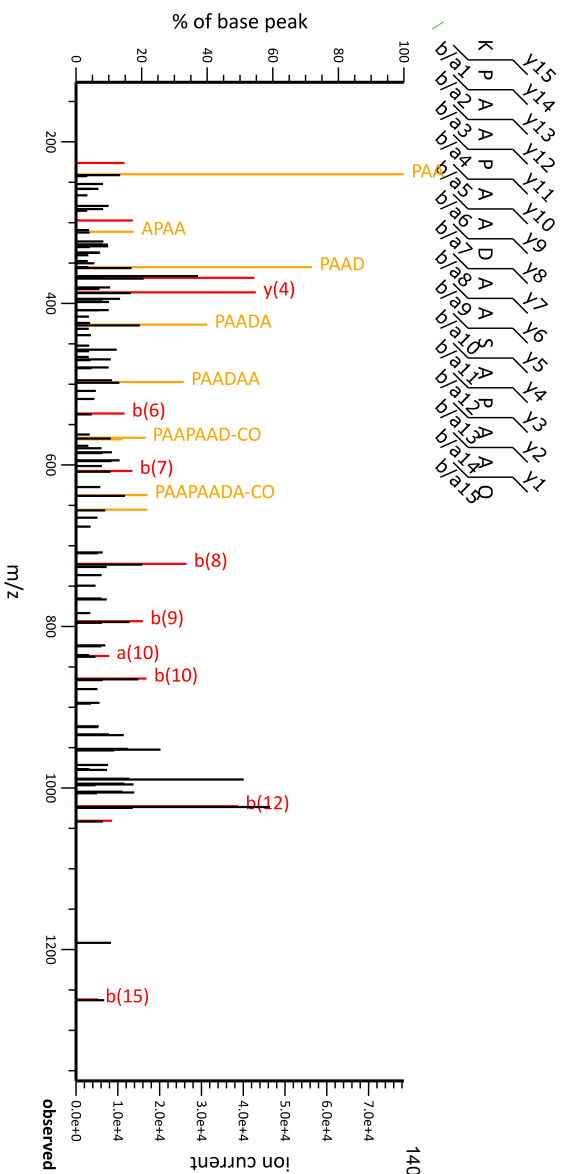
ITMS-CID



Score: 66
M/z: 988.47693
Charge: +2

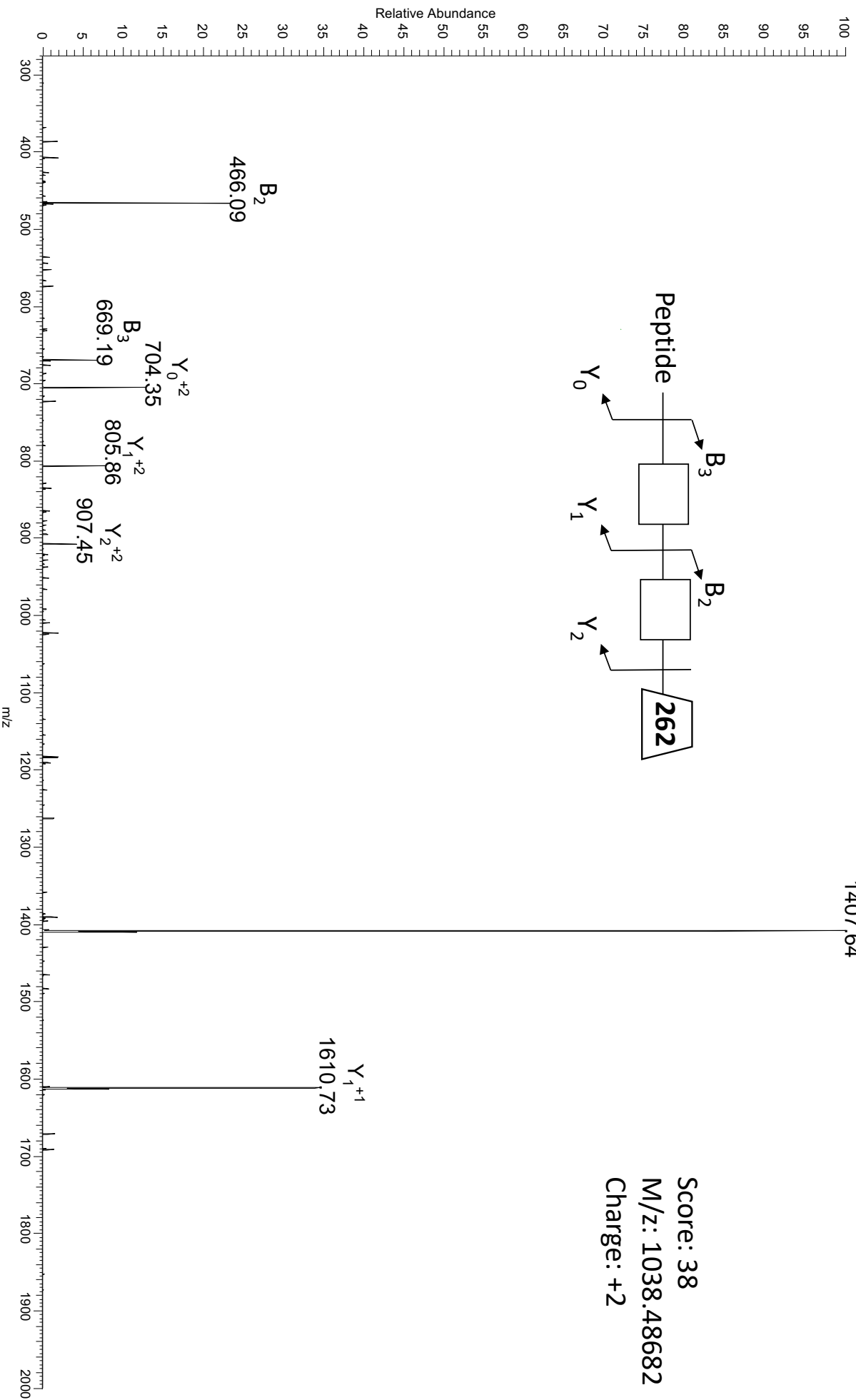
204.08806

MASCOT assignment

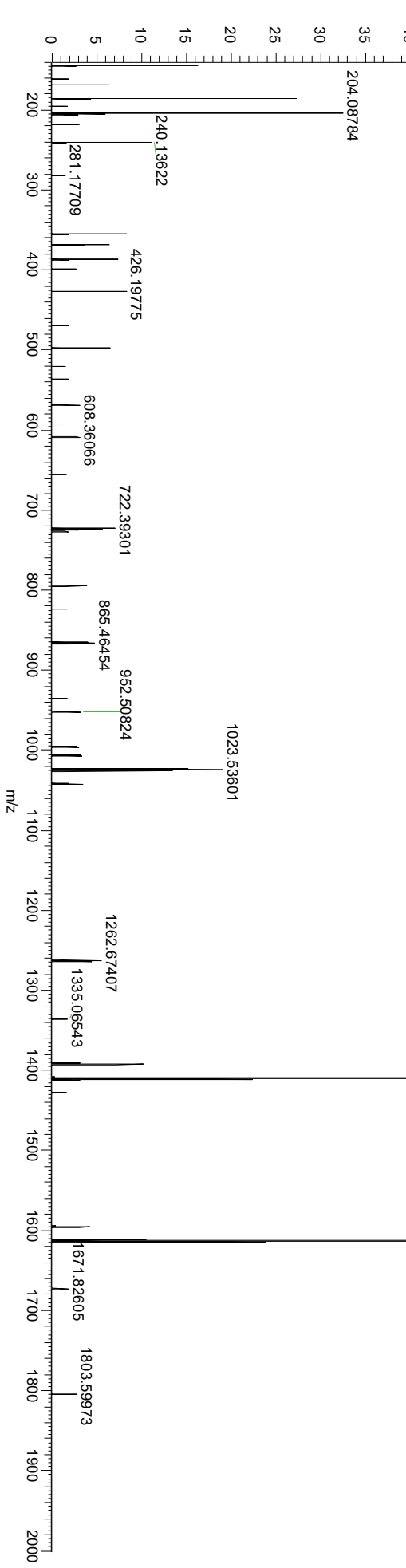
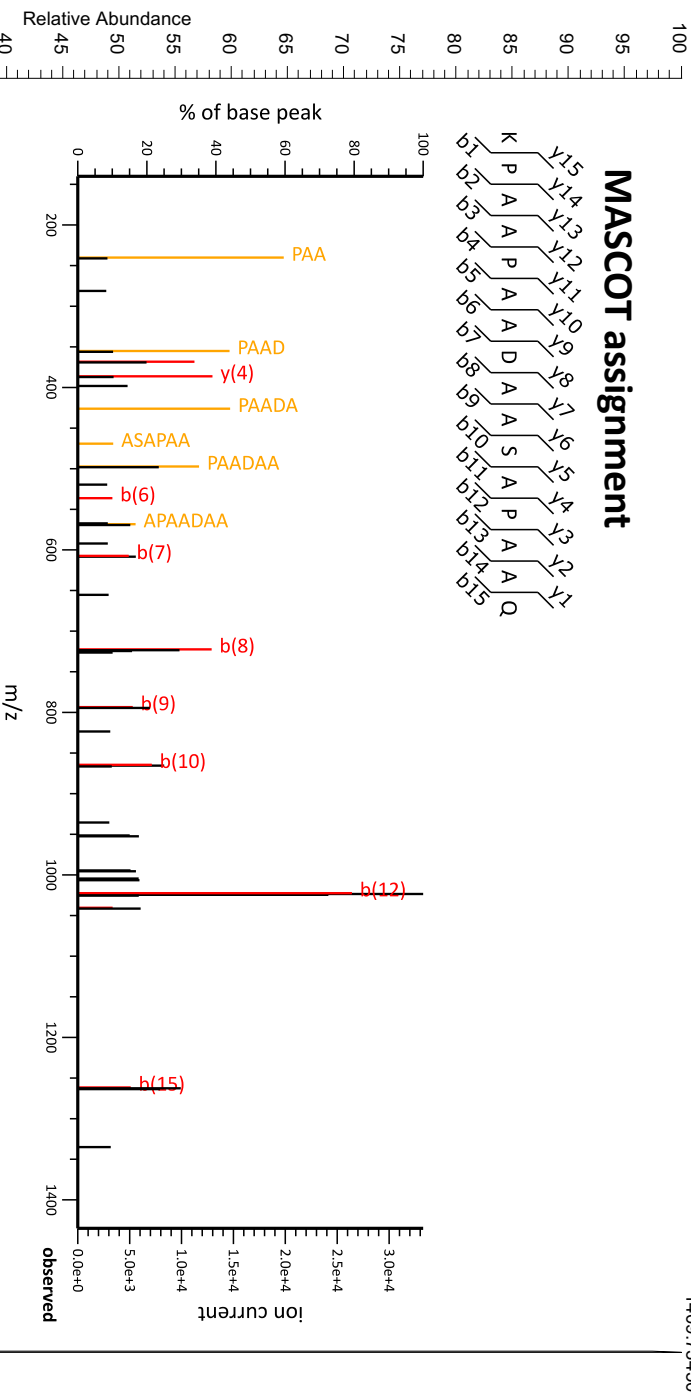
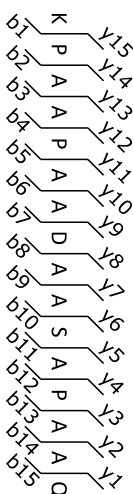


Score: 66
M/z: 988.47693
Charge: +2

ITMS-CID

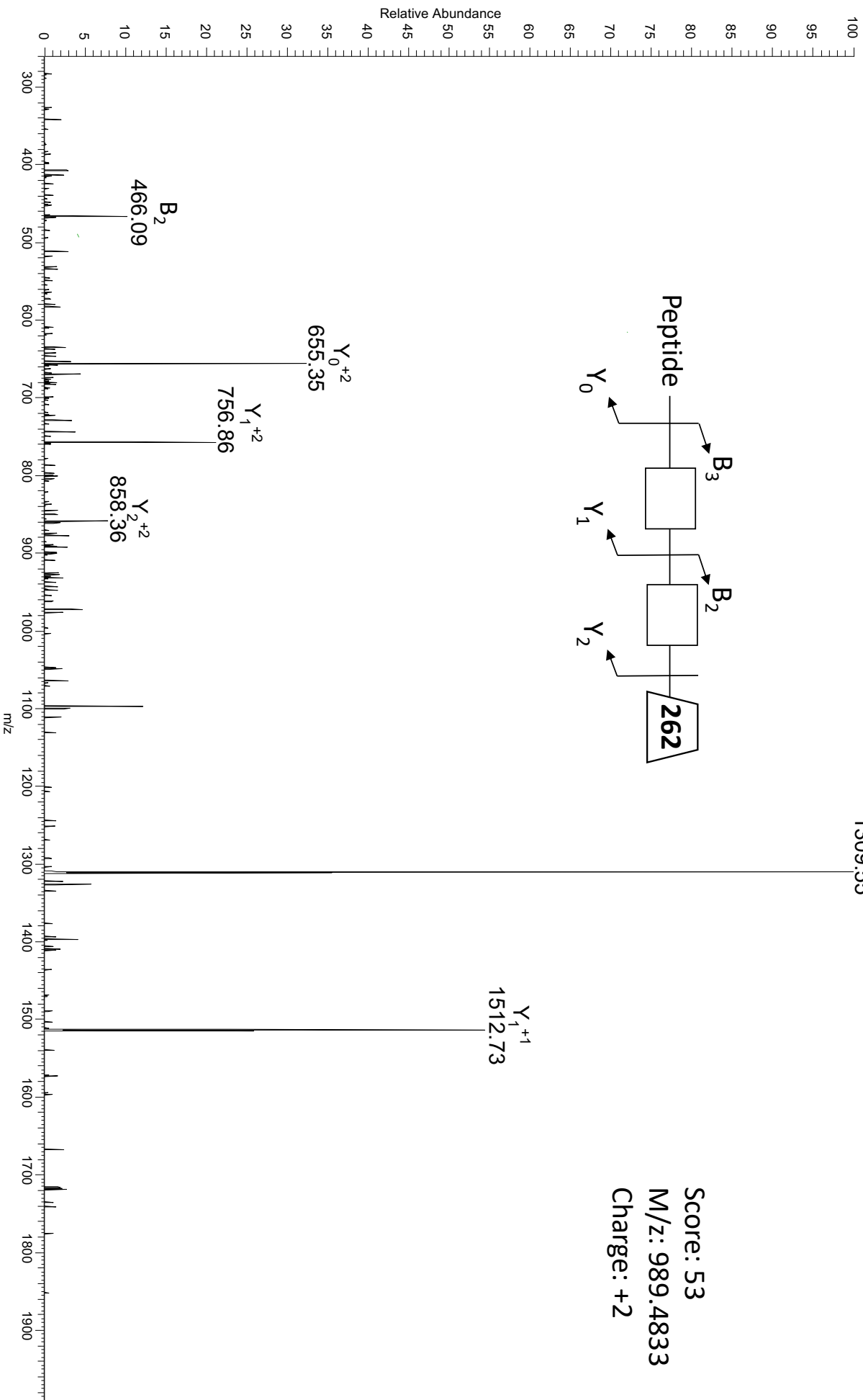


MASCOT assignment



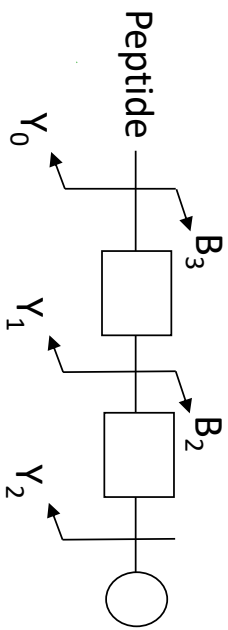
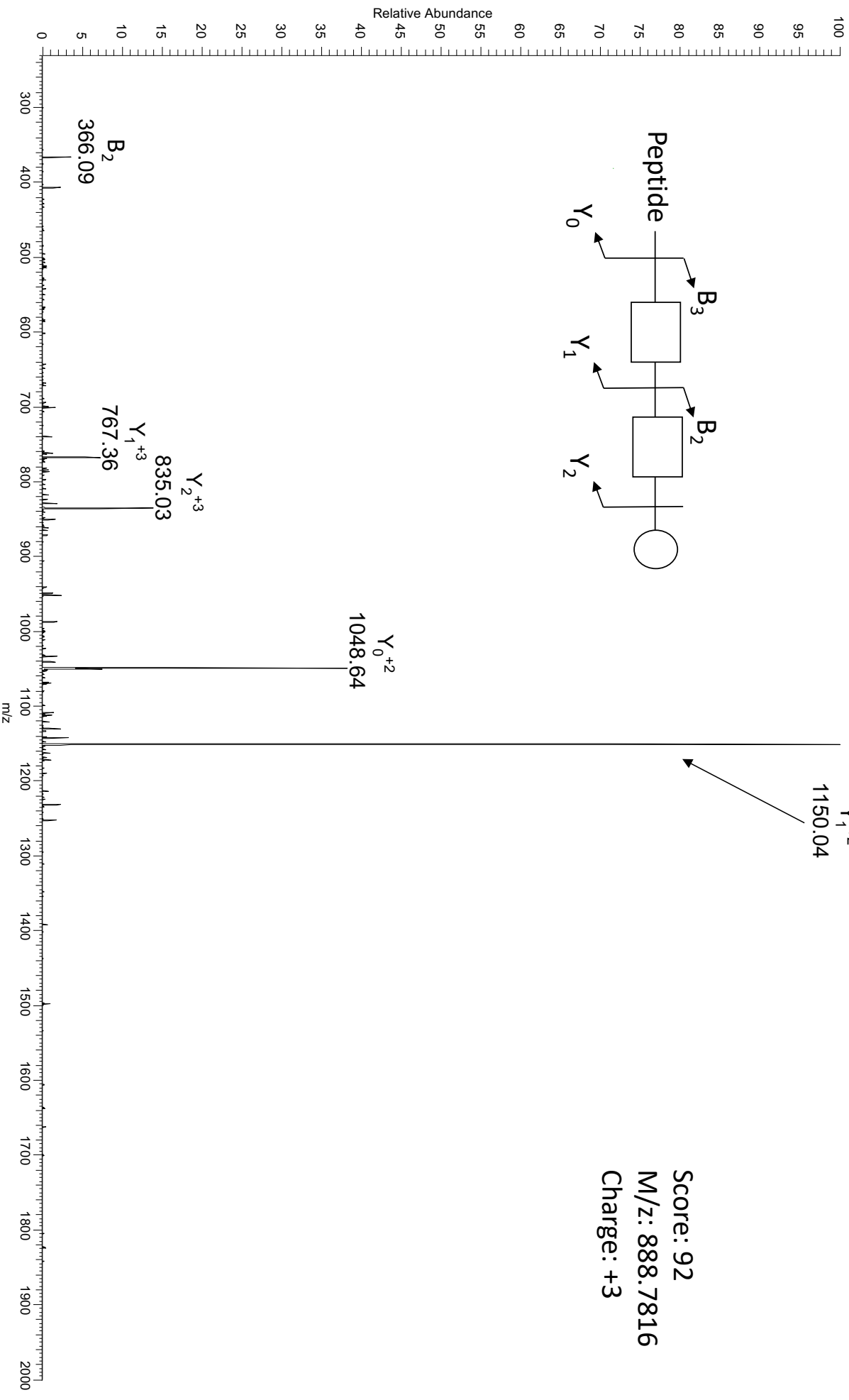
Score: 38
M/z: 1038.48682
Charge: +2

ITMS-CID

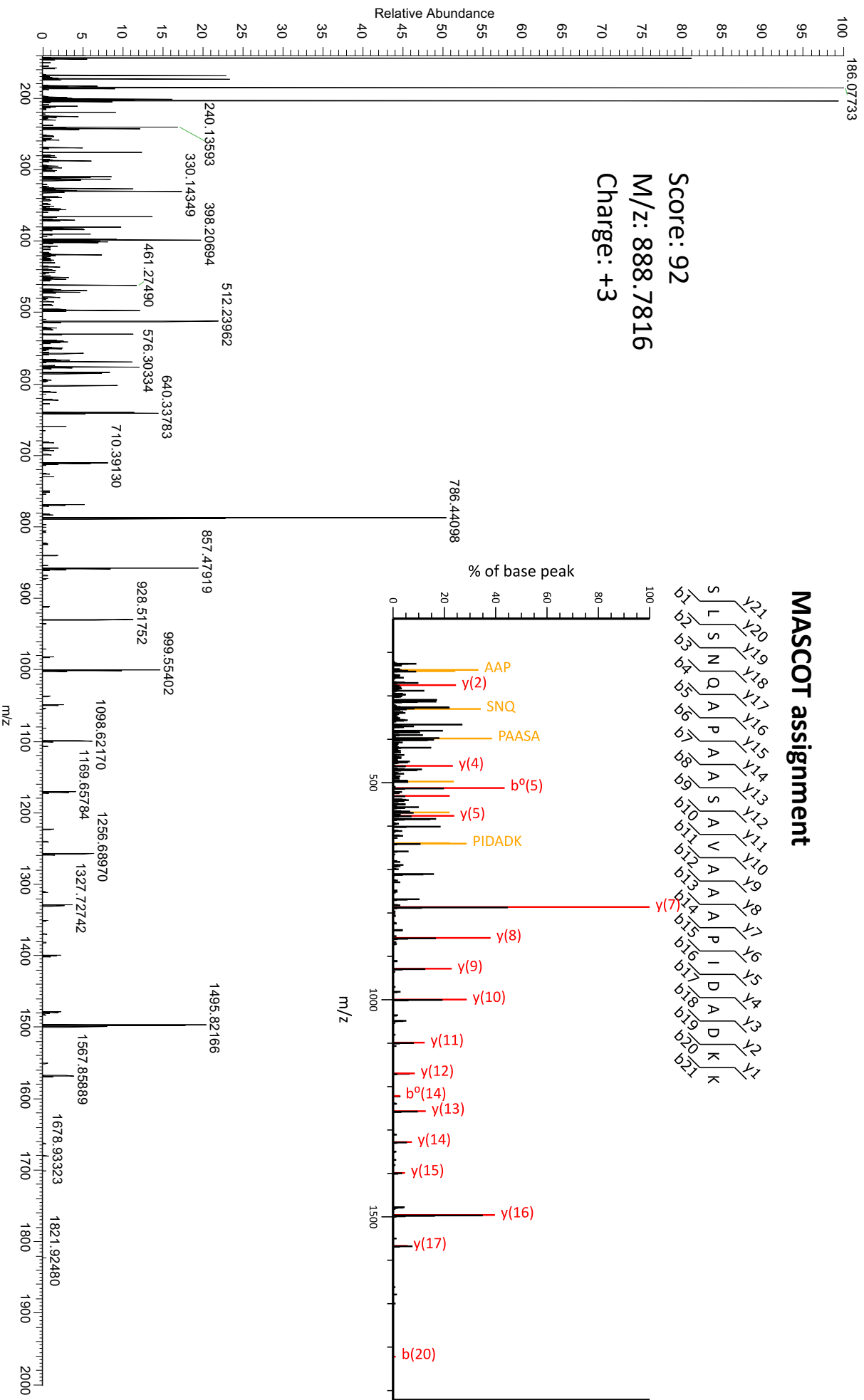


Score: 53
M/z: 989.4833
Charge: +2

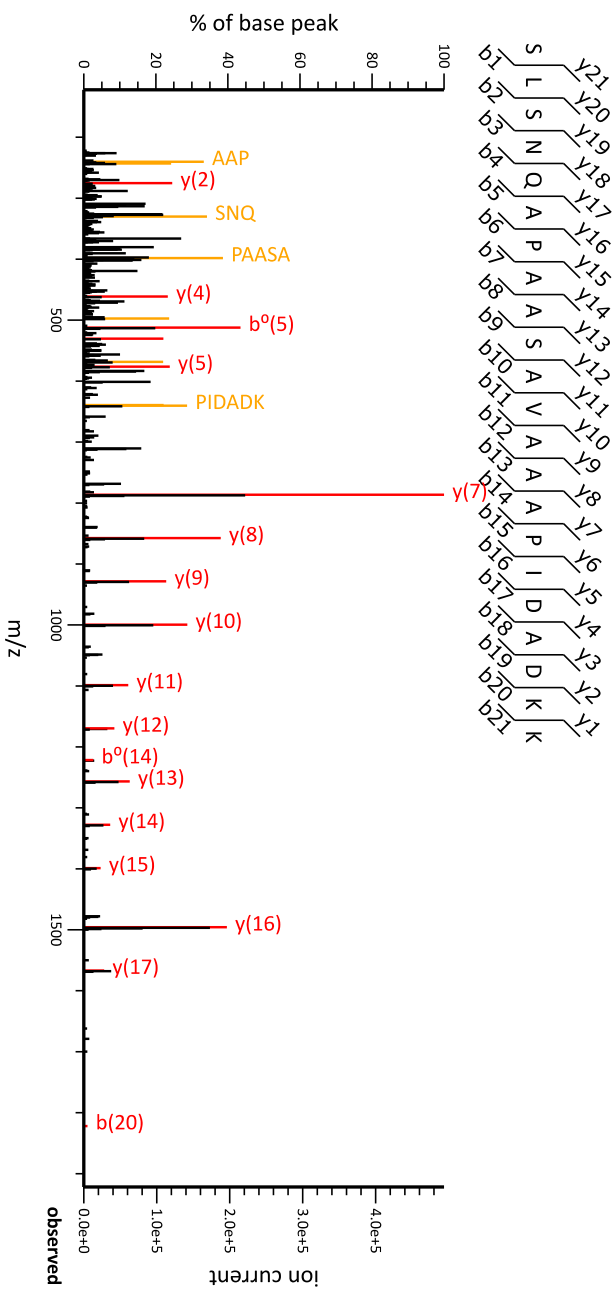
ITMS-CID



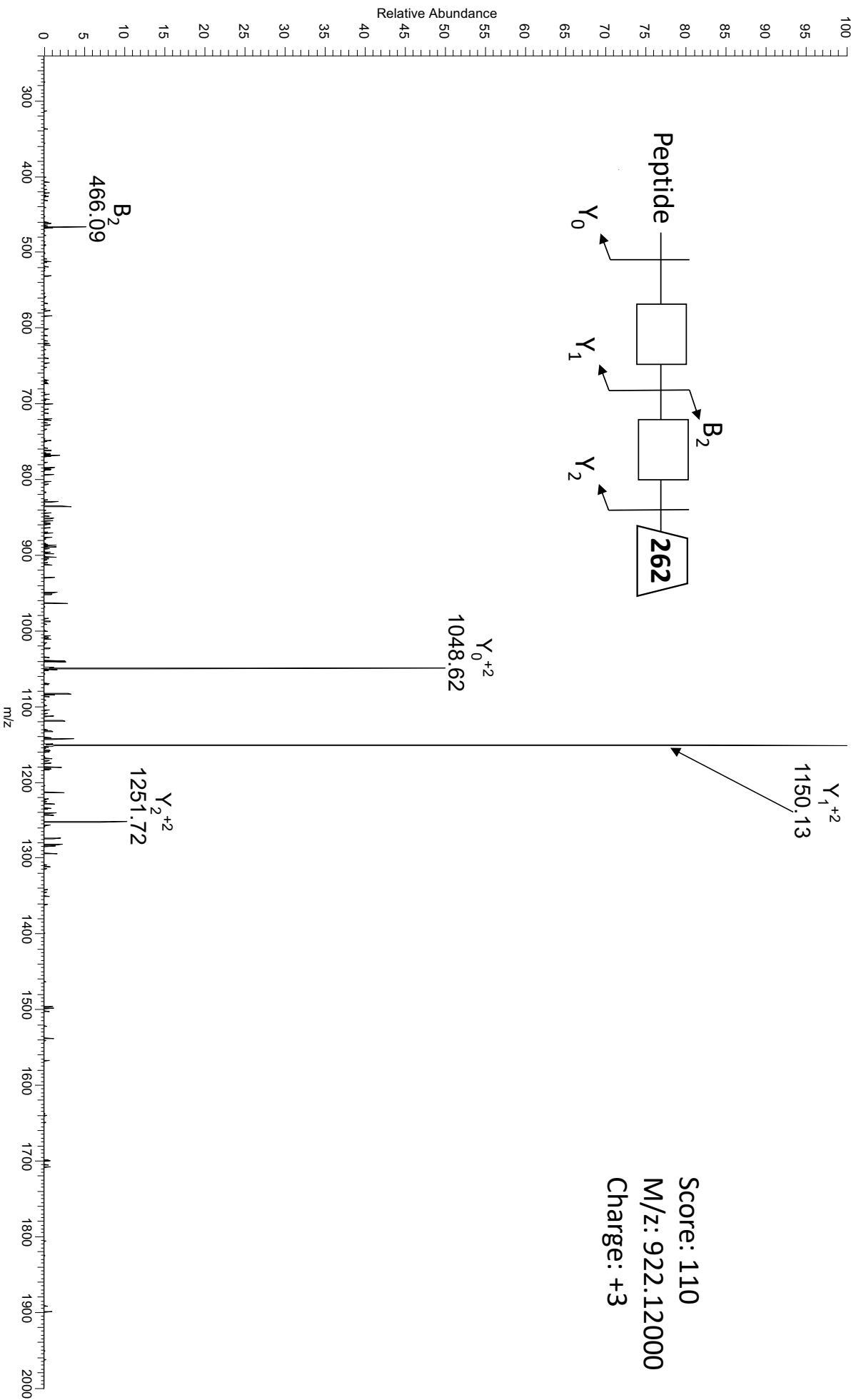
Score: 92
M/z: 888.7816
Charge: +3

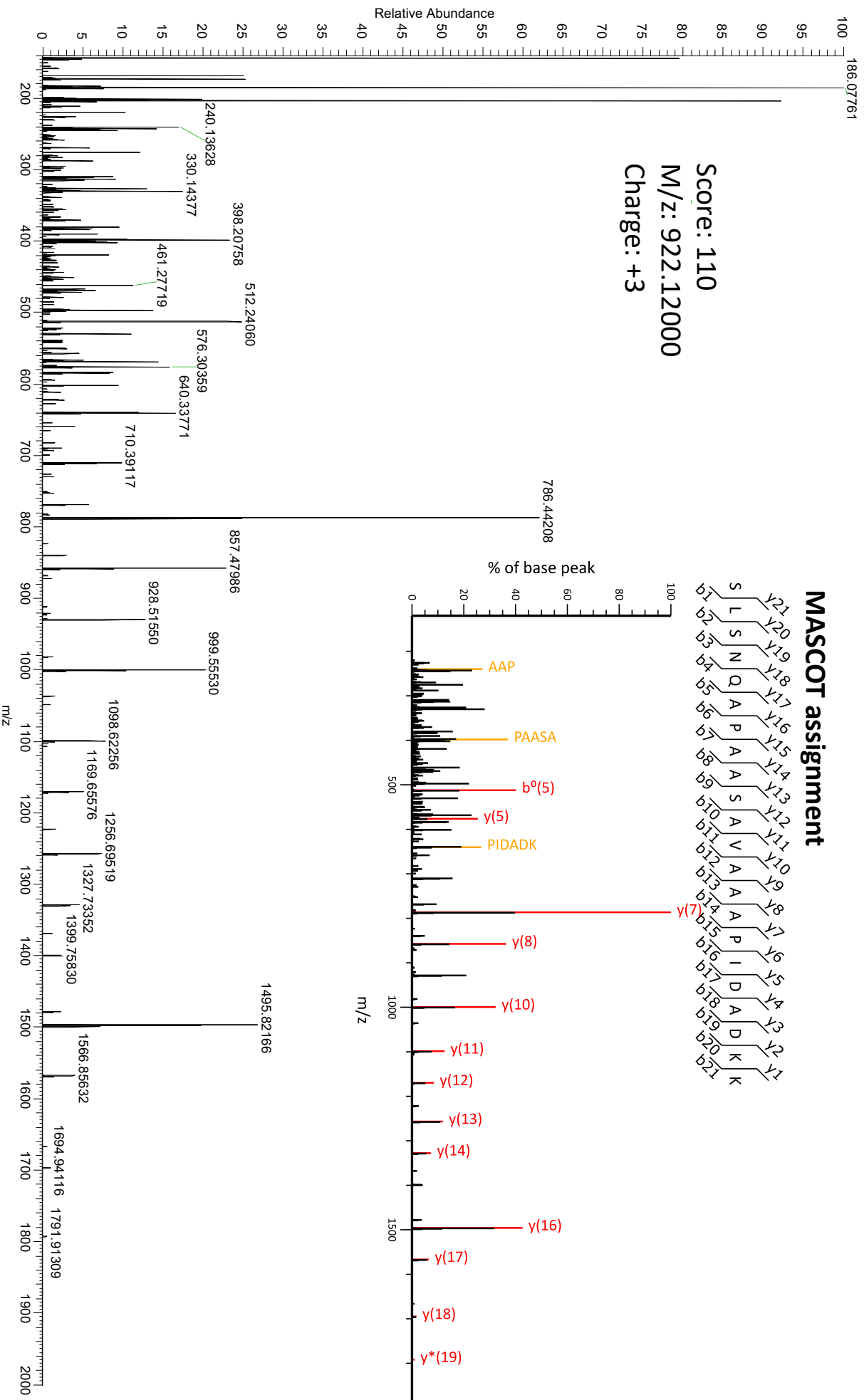


MASCOT assignment

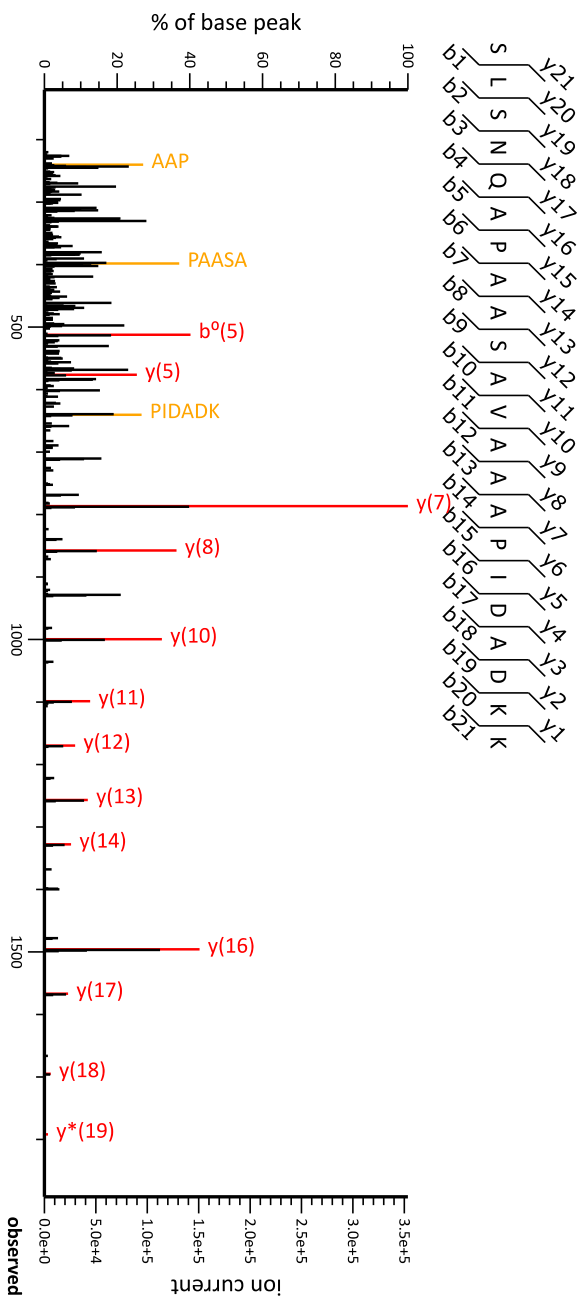


ITMS-CID

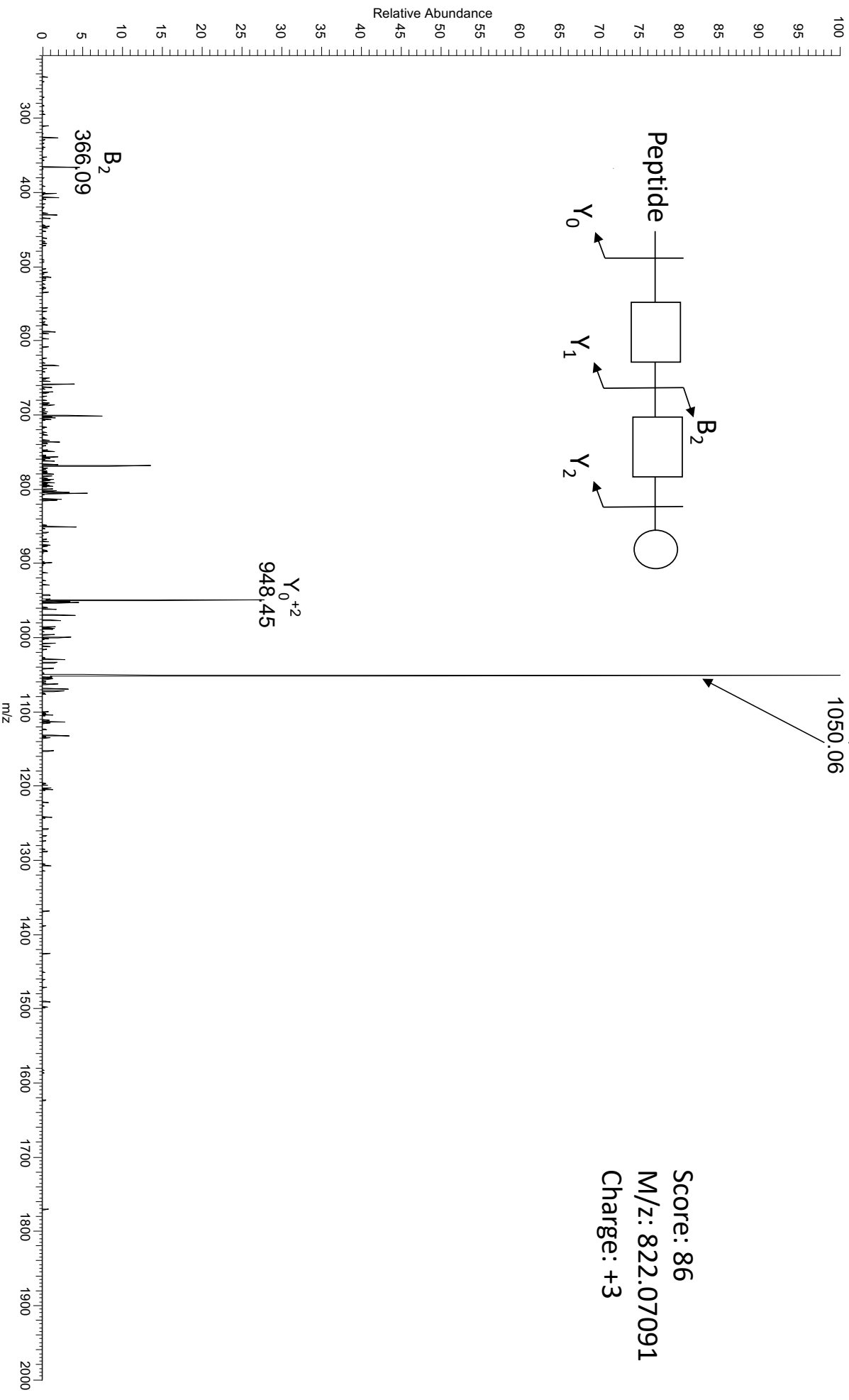


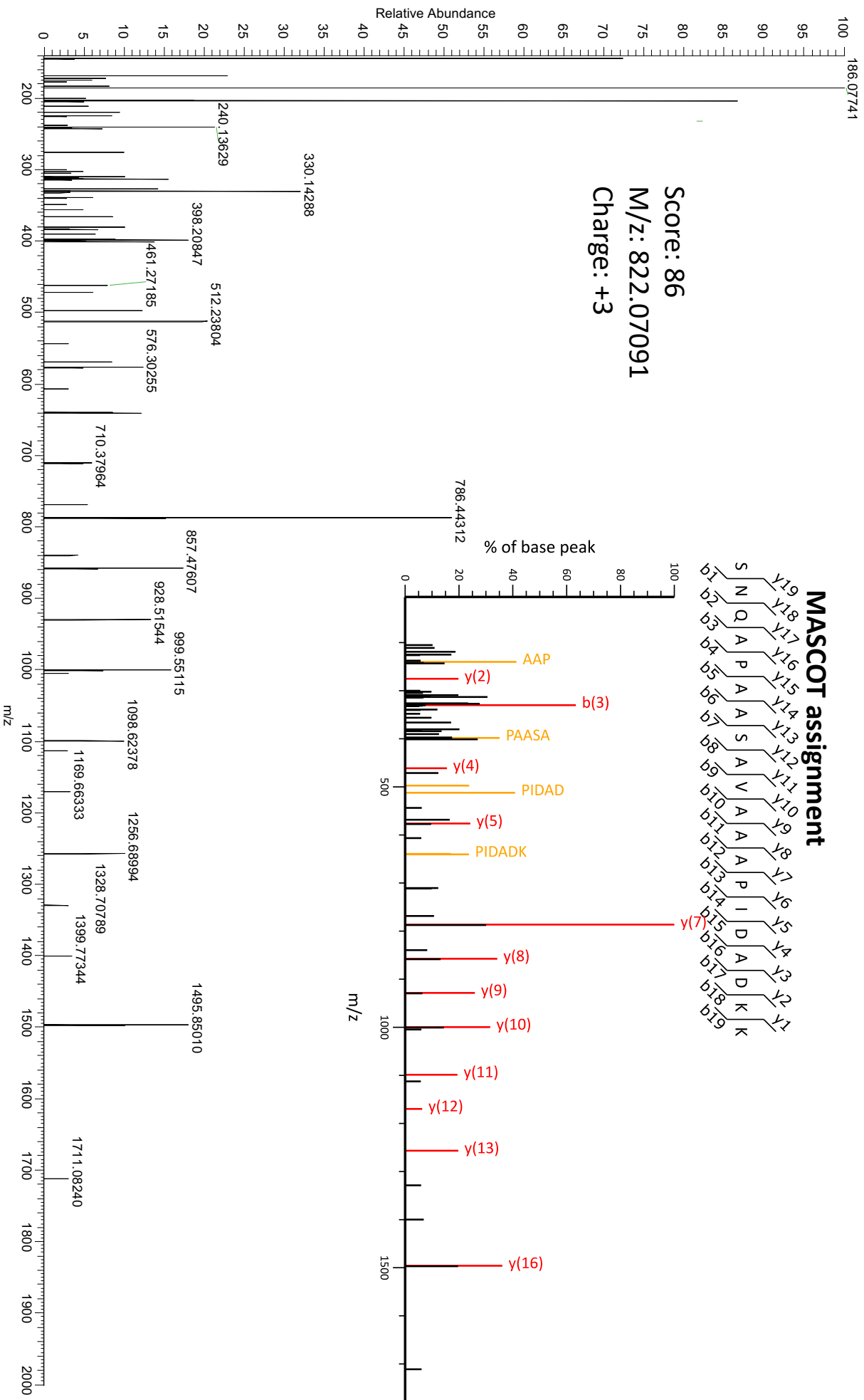


MASCOT assignment



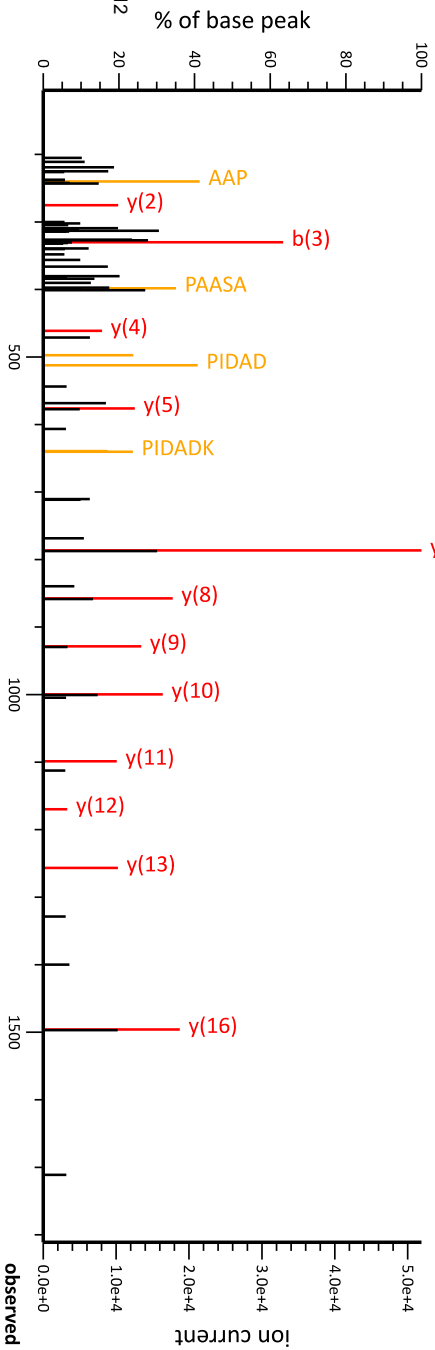
ITMS-CID





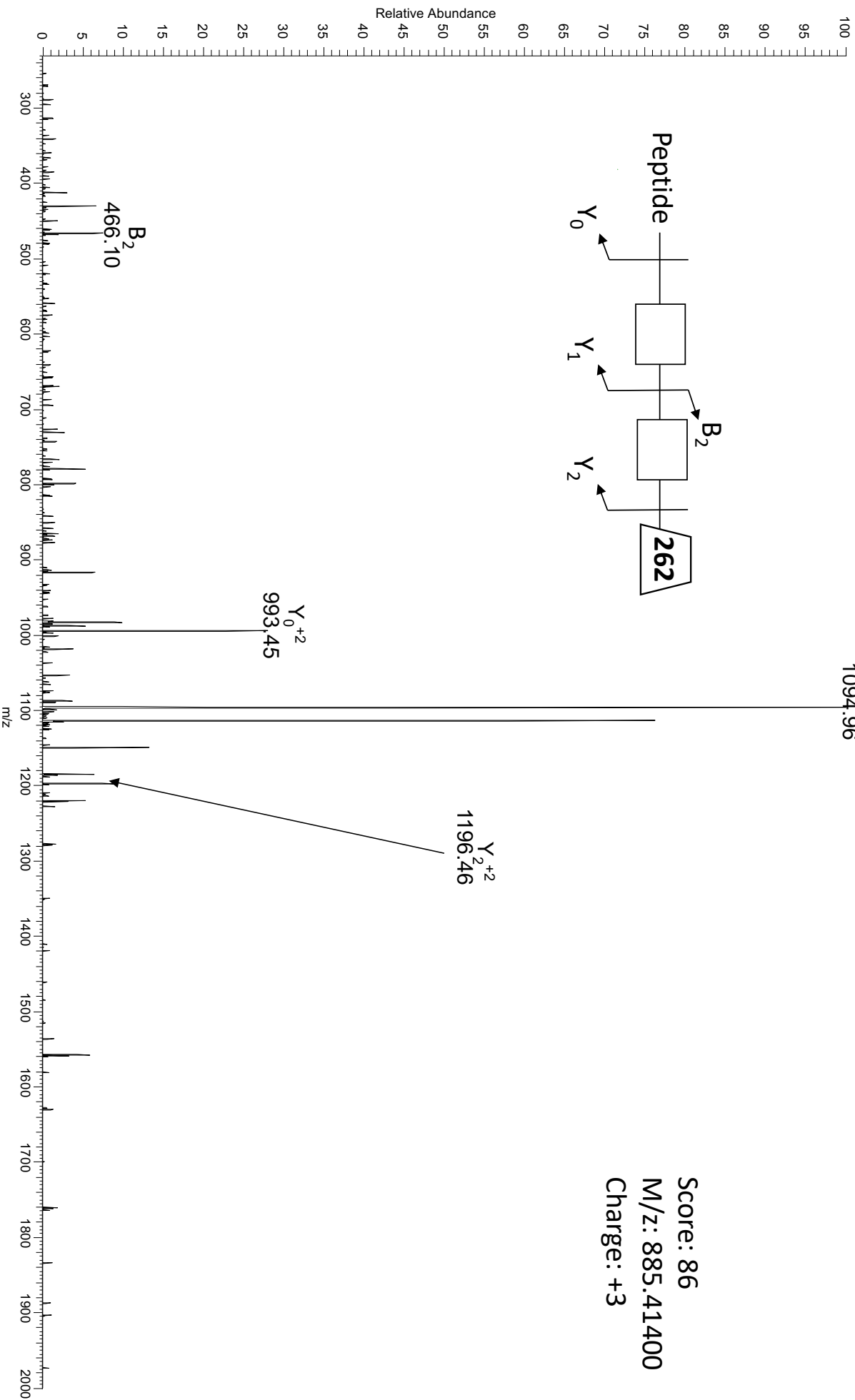
MASCOT assignment

- S
- N
- Q
- A
- P
- A
- A
- S
- A
- V
- A
- A
- A
- P
- I
- D
- A
- D
- K
- K
- y19
- y18
- y17
- y16
- y15
- y14
- y13
- y12
- y11
- y10
- y9
- y8
- y7
- y6
- y5
- y4
- y3
- y2
- y1
- b1
- b2
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- b6
- b7
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- b12
- b13
- b14
- b15
- b16
- b17
- b18
- b19



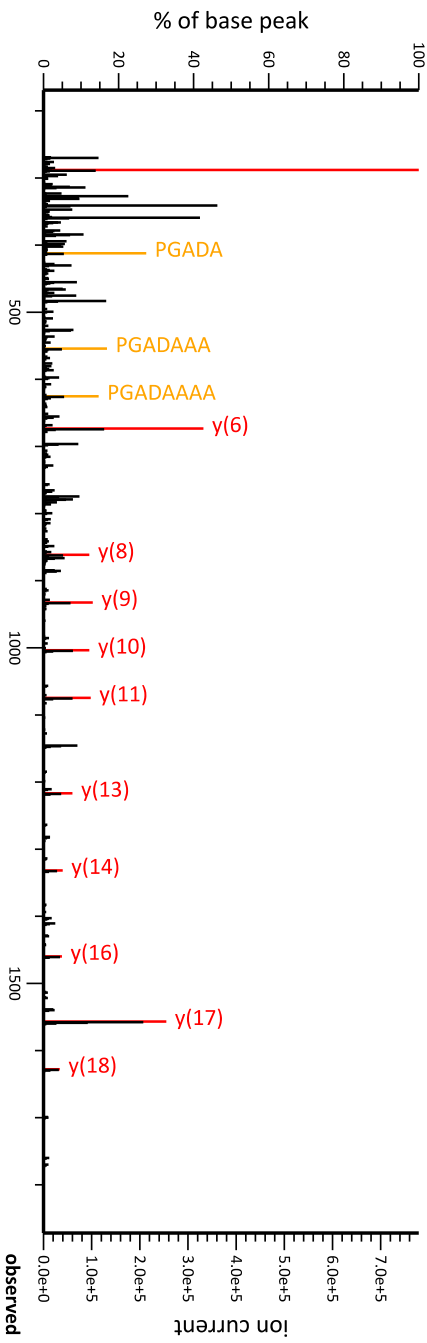
observed

ITMS-CID

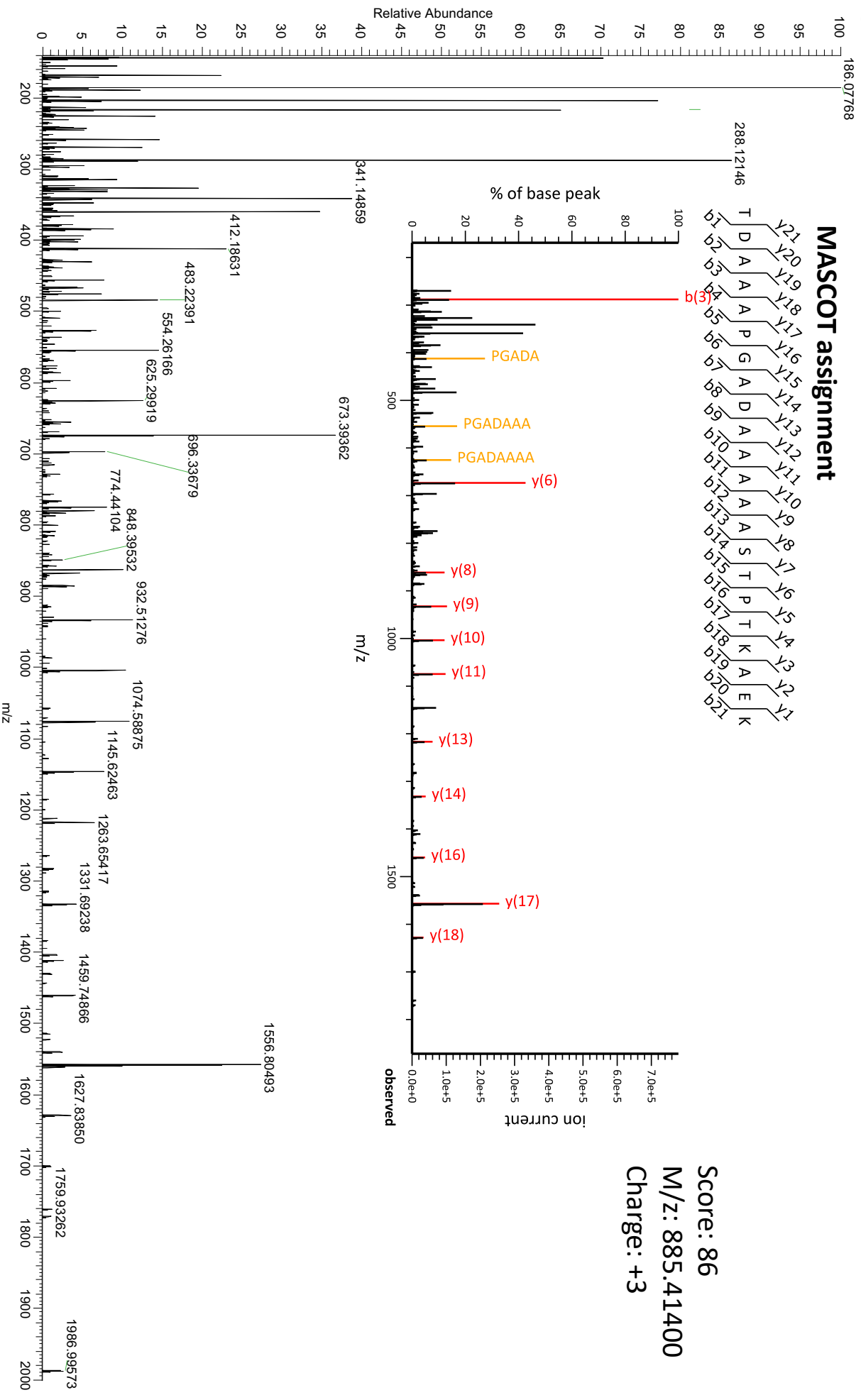


MASCOT assignment

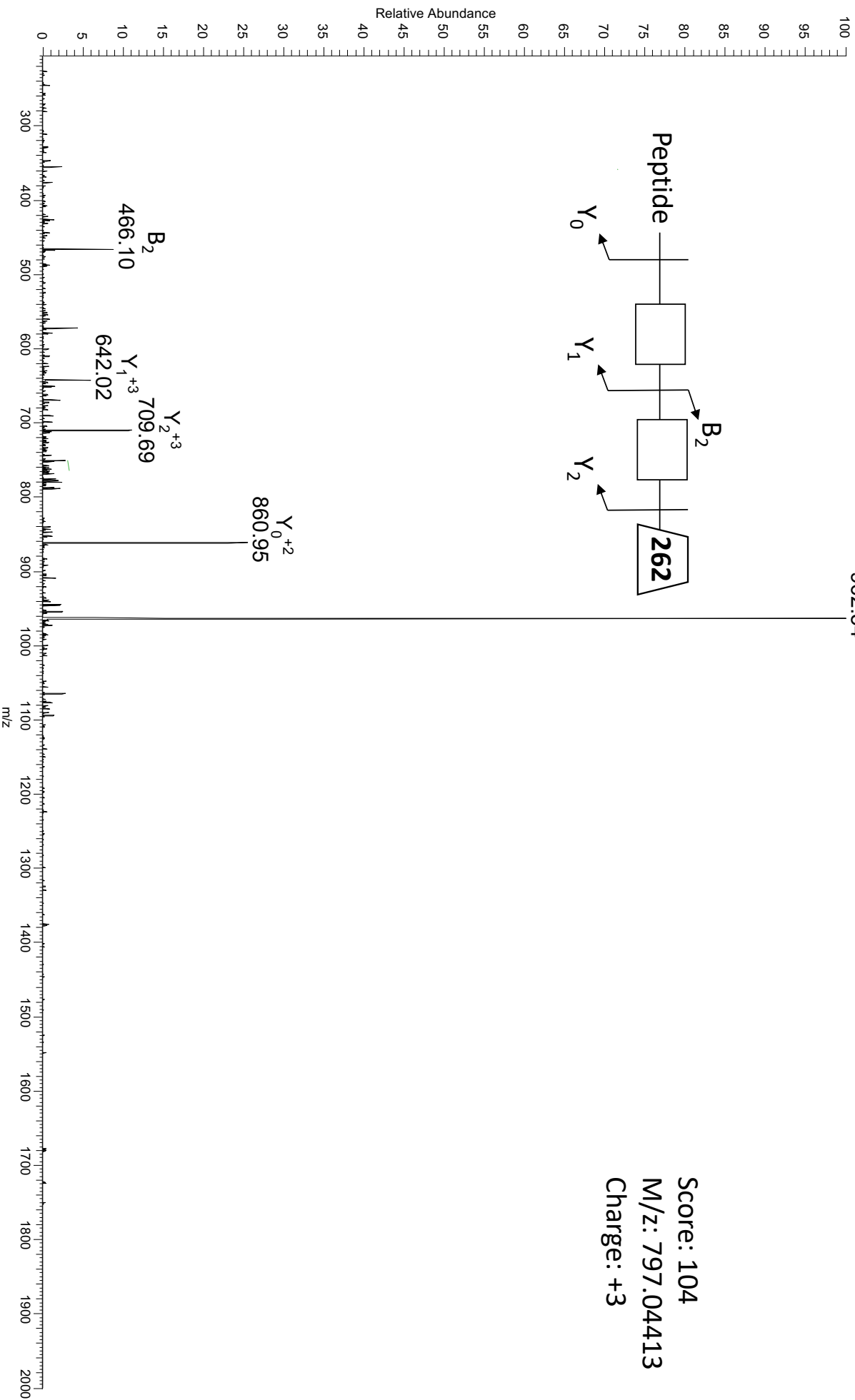
T D A A A P G A D A A A A A S T P T K A E K
Y21 Y20 Y19 Y18 Y17 Y16 Y15 Y14 Y13 Y12 Y11 Y10 Y9 Y8 Y7 Y6 Y5 Y4 Y3 Y2 Y1
b1 b2 b3 b4 b5 b6 b7 b8 b9 b10 b11 b12 b13 b14 b15 b16 b17 b18 b19 b20 b21



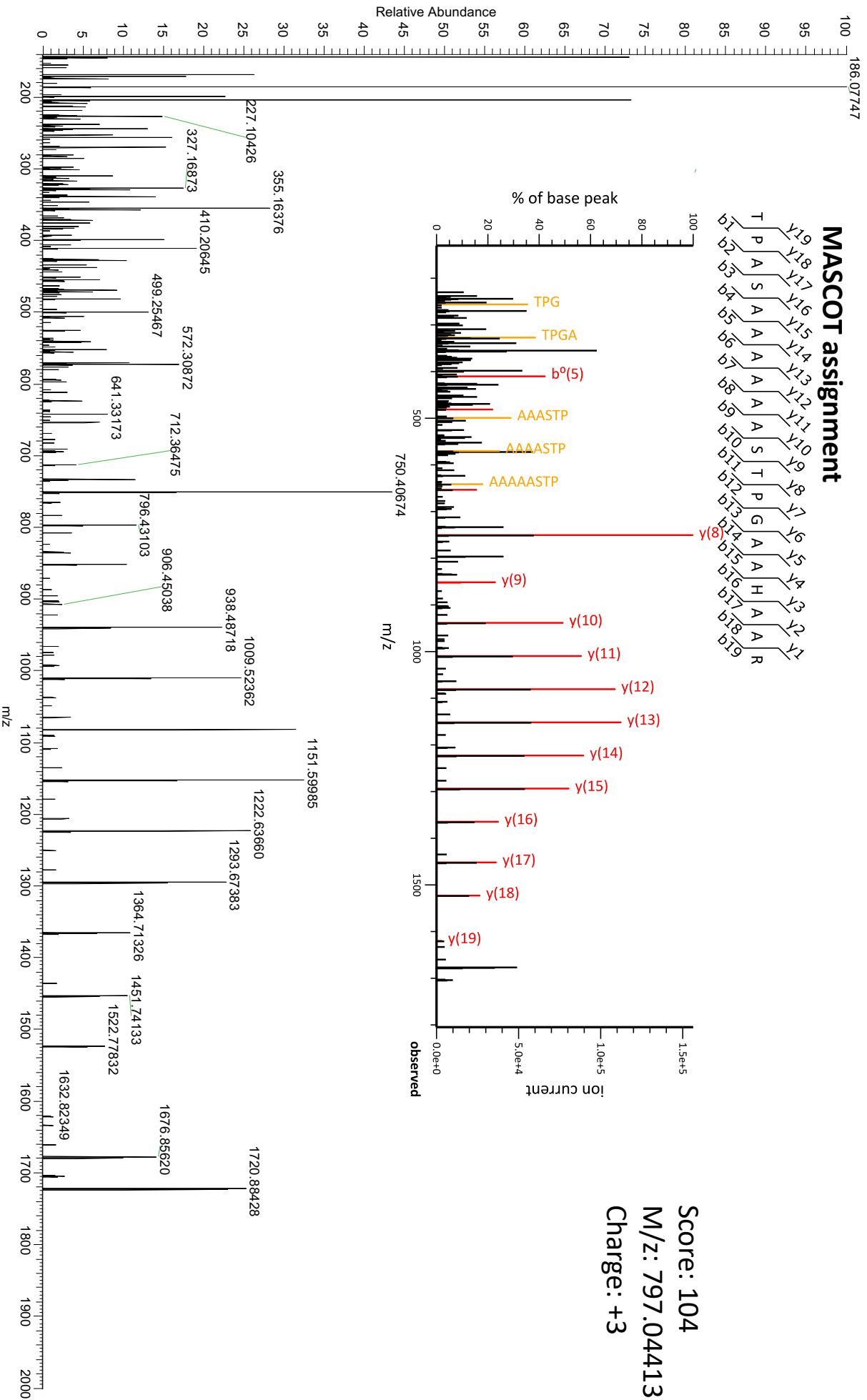
Score: 86
M/z: 885.41400
Charge: +3



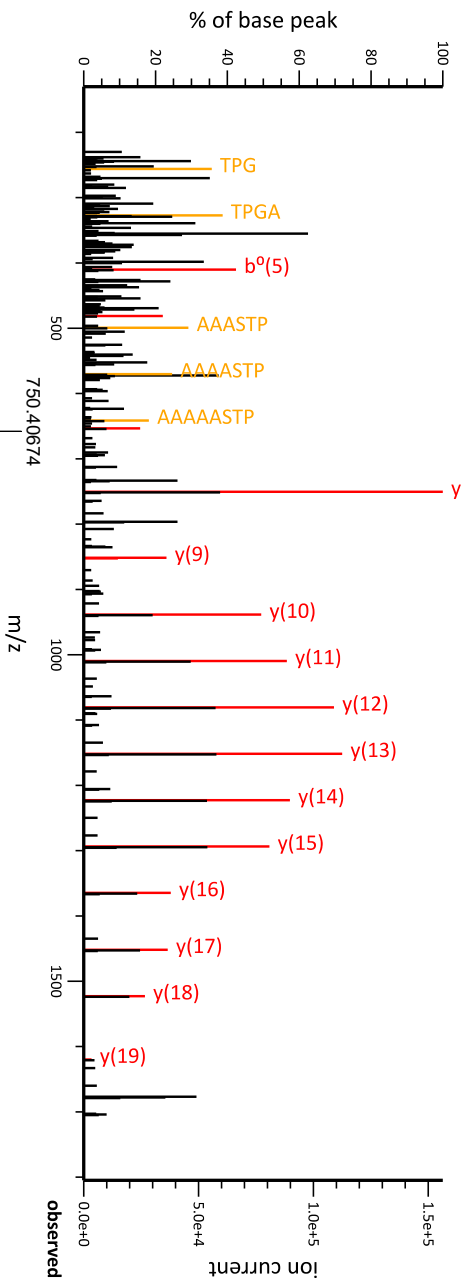
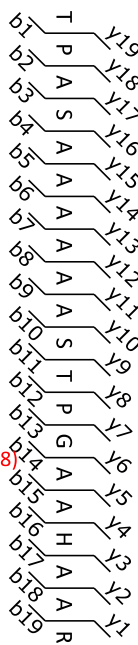
ITMS-CID



Score: 104
M/z: 797.04413
Charge: +3



MASCOT assignment



Score: 104
M/z: 797.04413
Charge: +3