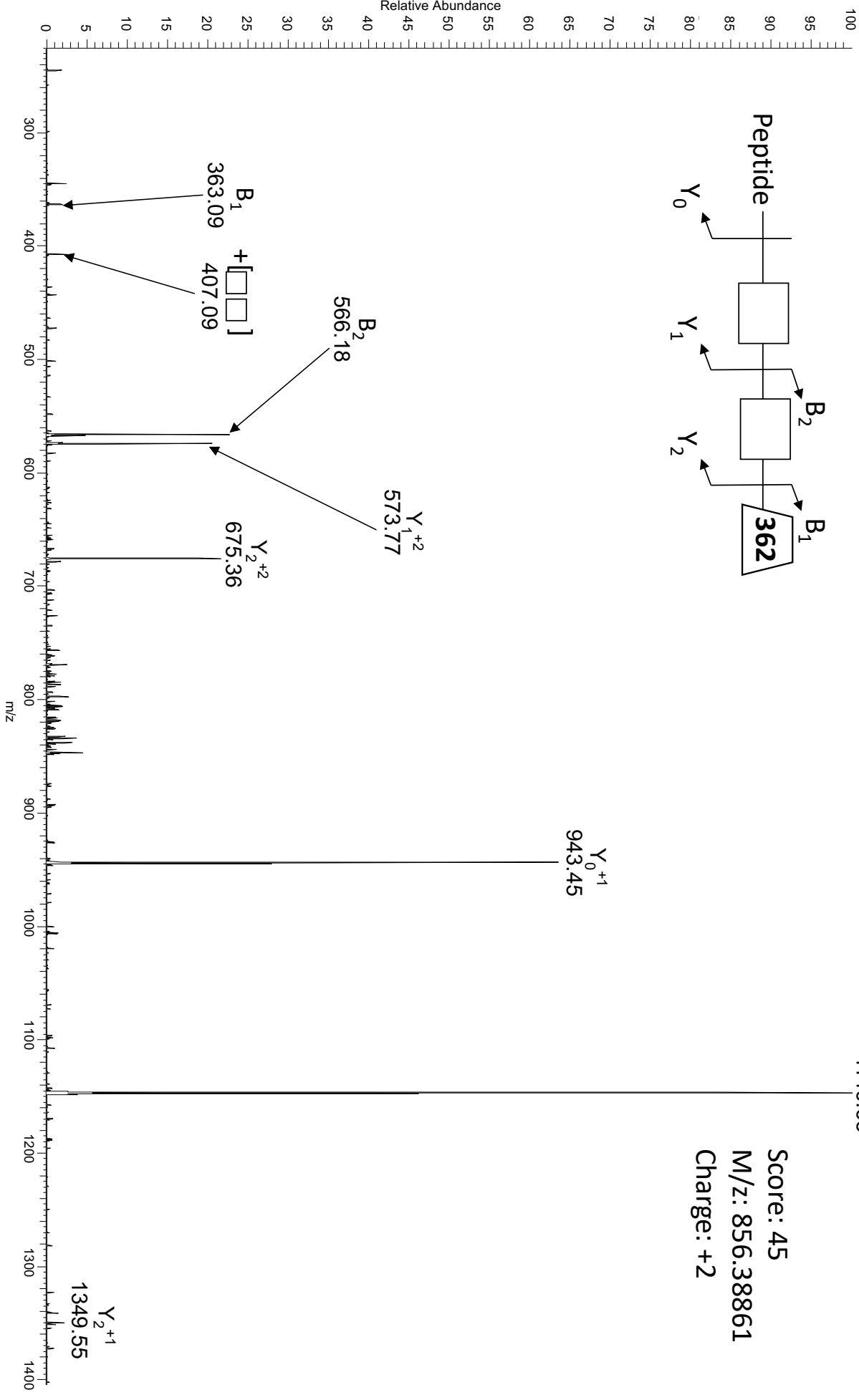
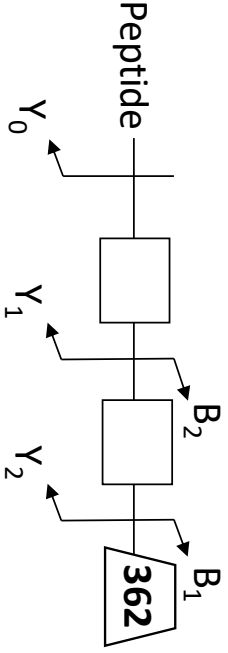


Supplementary Data 1: Identified *Burkholderia thailandensis* E264 glycopeptides

Gene	Protein name	Uniprot accession	m/z	Charge	MH+	peptide mass	Glycan mass	Peptide sequence	Mascot Ion Score	Page
unannotated, chromosome 1 (871694:872364)	unannotated ORF	N/A	856.3886	2	1711.769	943.52	768.25	AEAASAPAKK	45	2 and 3
unannotated, chromosome 1 (871694:872364)	unannotated ORF	N/A	792.3414	2	1583.675	815.42	768.25	AEAASAPAK	37	4 and 5
BTH_I3002	ABC transporter, periplasmic substrate-binding protein	Q2SU93	1007.4660	2	2013.924	1445.71	568.21	PAAASGAPAPAASGAAAH	47	6 and 7
BTH_I12165	Uncharacterized protein	Q2T396	826.41028	3	2477.215	1909.00	568.21	DASGKEIPLTPQAASQAK	41	8 and 9
unannotated, chromosome 1 (871694:872364)	unannotated ORF	N/A	806.39978	2	1611.792	943.52	668.27	AEAASAPAKK	38	10 and 11
unannotated, chromosome 1 (871694:872364)	unannotated ORF	N/A	742.35083	2	1483.694	815.42	668.27	AEAASAPAK	49	12 and 13
DR63_725	Uncharacterized protein	A0A096YKY7	957.47852	2	1913.949	1345.69	568.26	AVPAAPASGAASAPAH	60	14 and 15
BTH_I1626	Uncharacterized protein	Q2SY35	780.030017	3	2338.074	1769.86	568.21	LNEHPQMQFAASAPTK	36	16 and 17

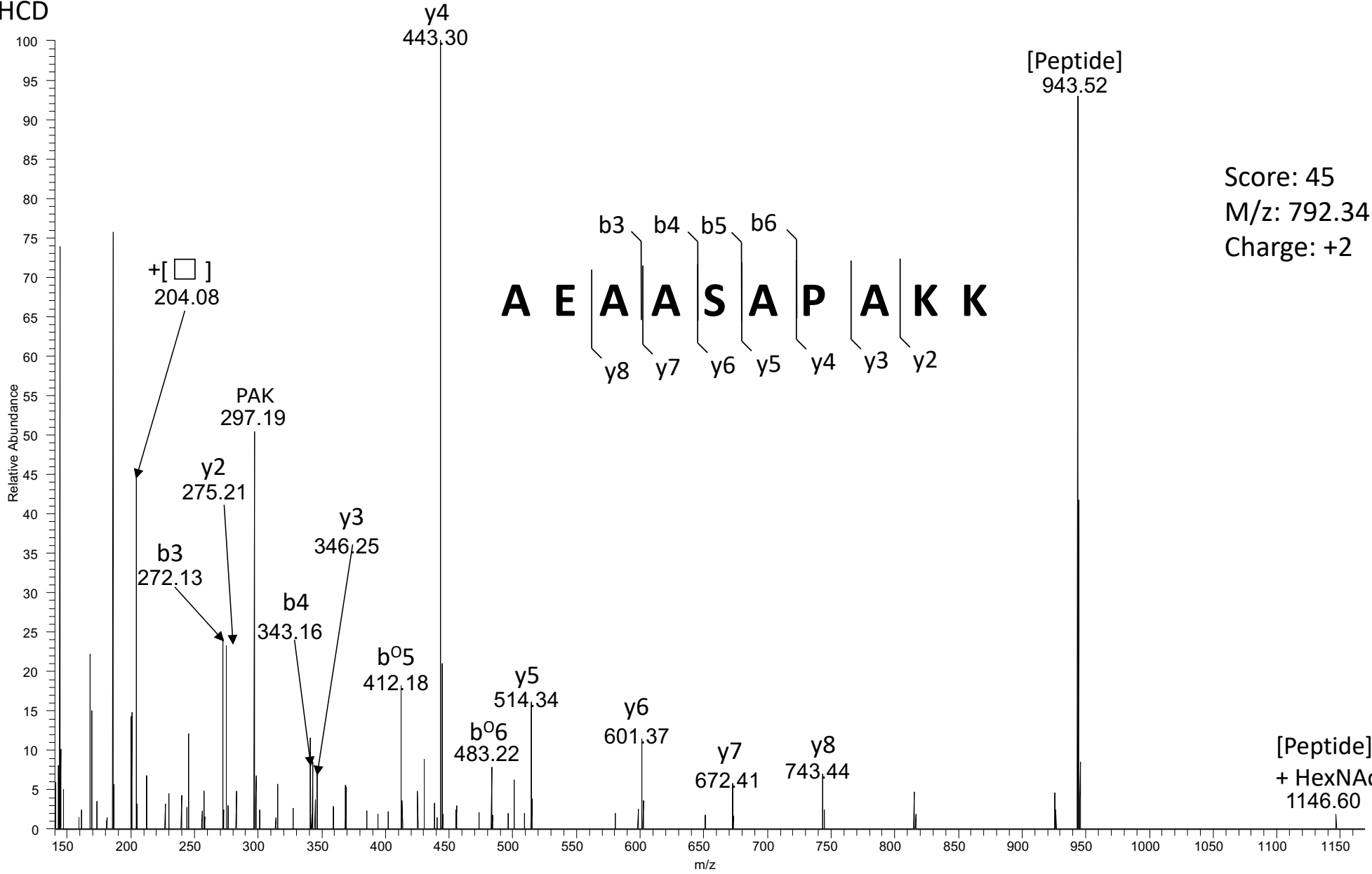
Supplementary Data 1. Identified *Burkholderia thailandensis* E264 Glycopeptides. A total of 8 unique glycopeptides were observed within whole cell proteome samples of *B. thailandensis* E264. For assigned glycopeptides the gene, protein name, uniprot accession (mapped to *B. thailandensis* E264), observed 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



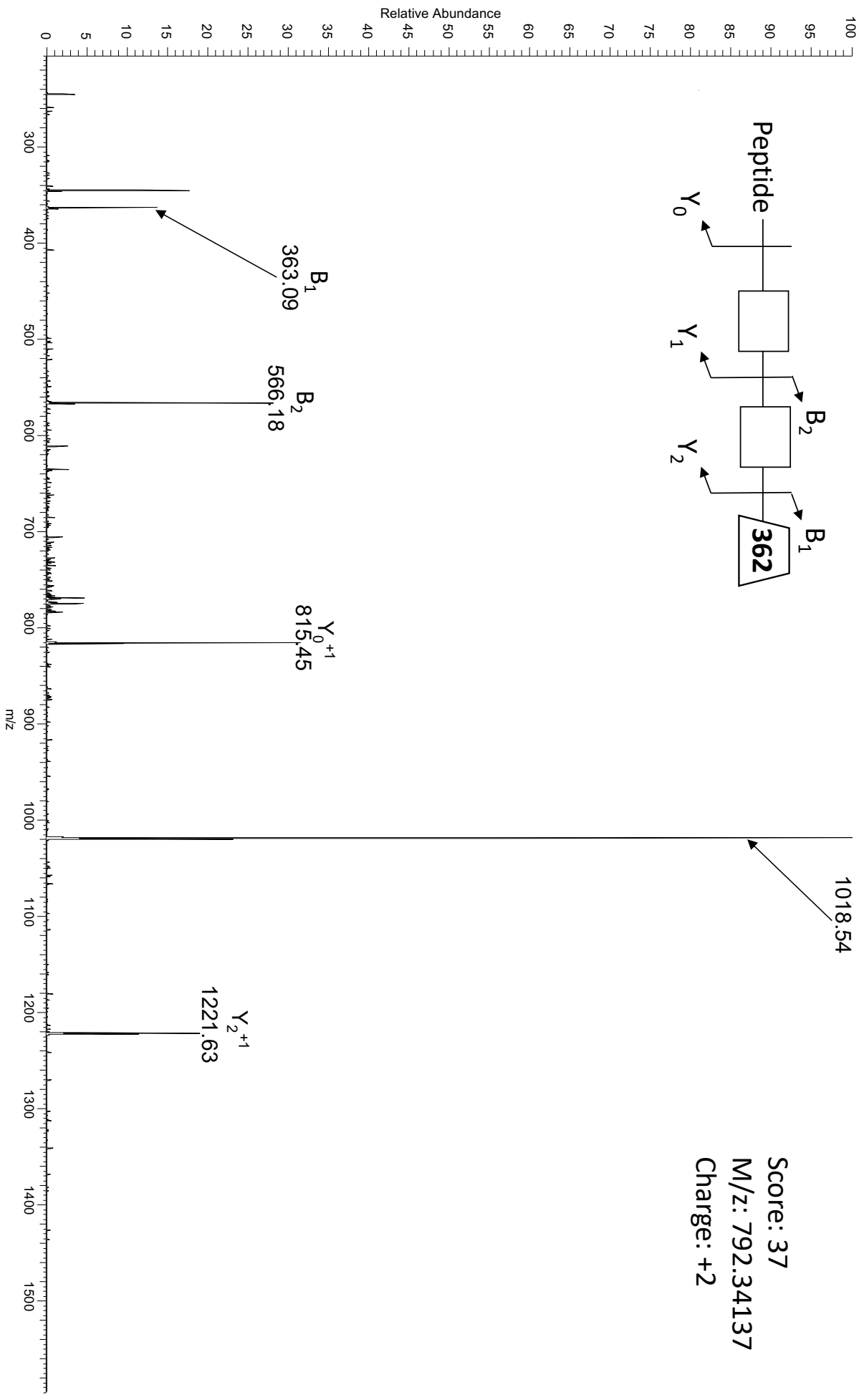
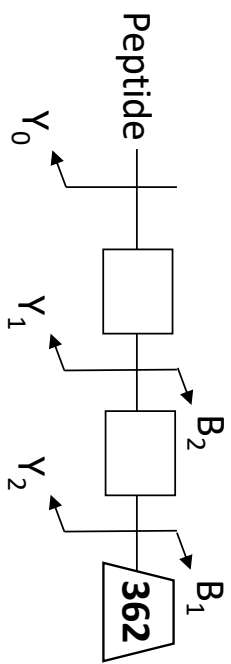
Score: 45
M/z: 856.38861
Charge: +2

FTMS-HCD

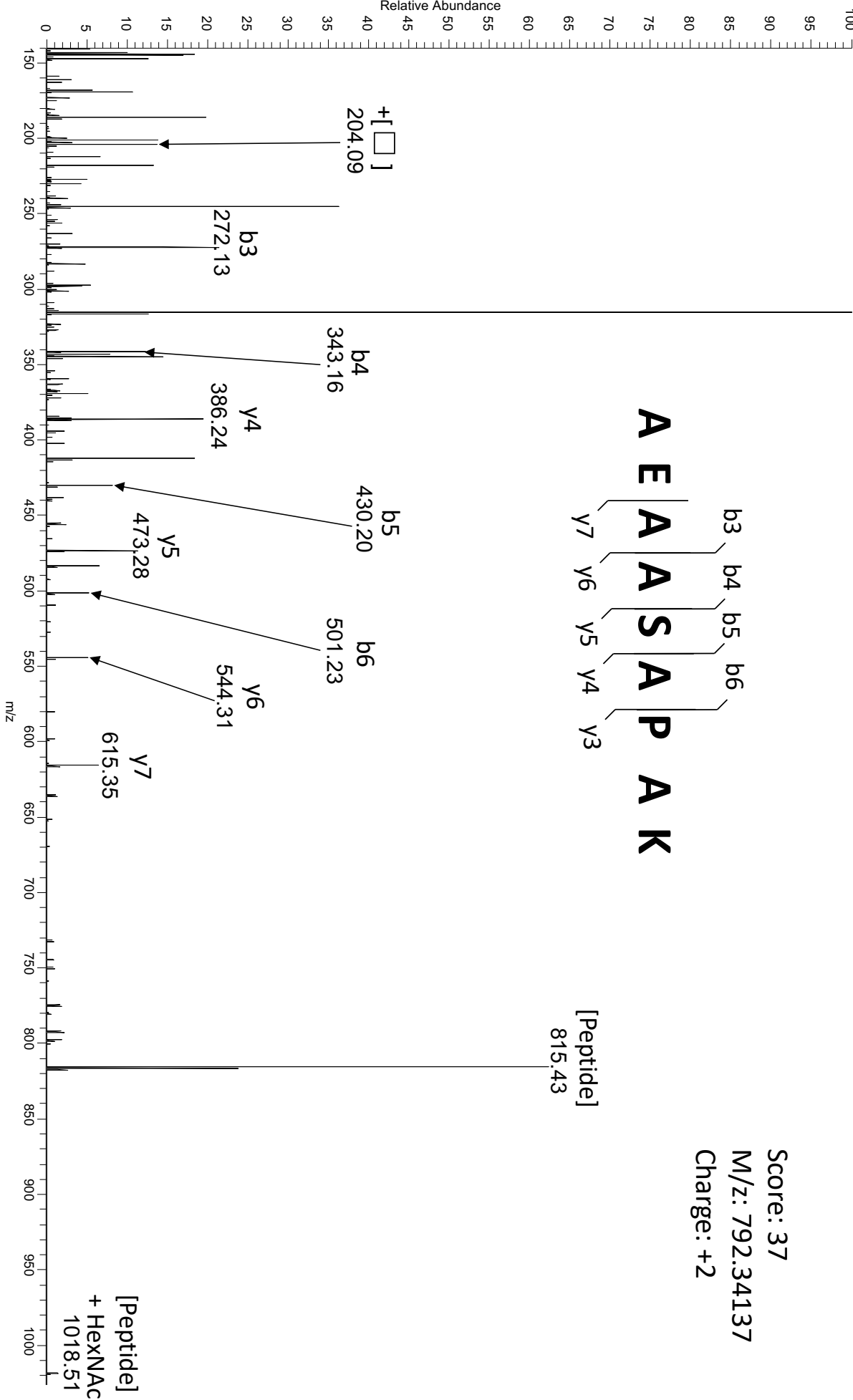


Score: 45
M/z: 792.34137
Charge: +2

ITMS-CID



Score: 37
M/z: 792.34137
Charge: +2

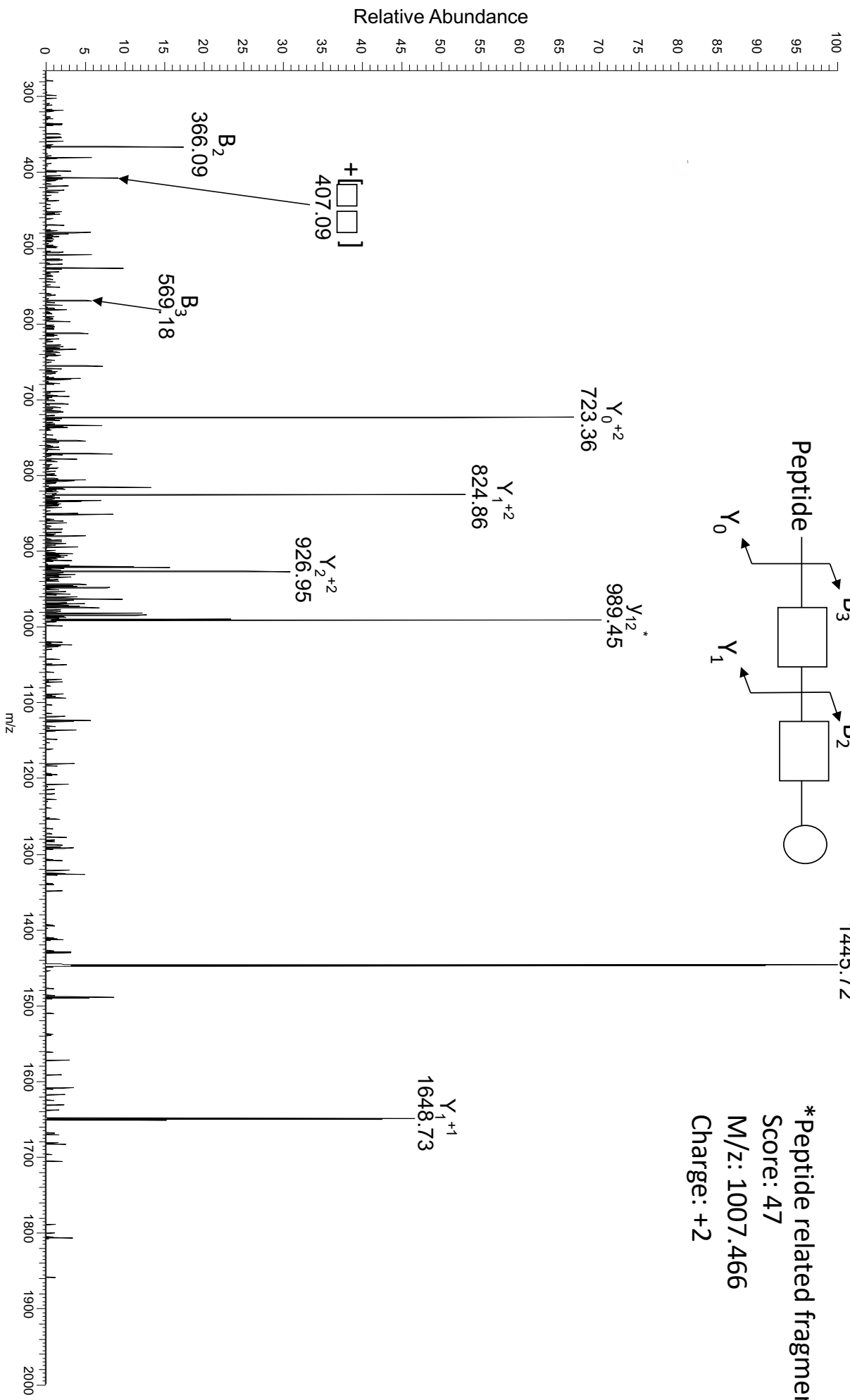


Score: 37

M/z: 792.34137

Charge: +2

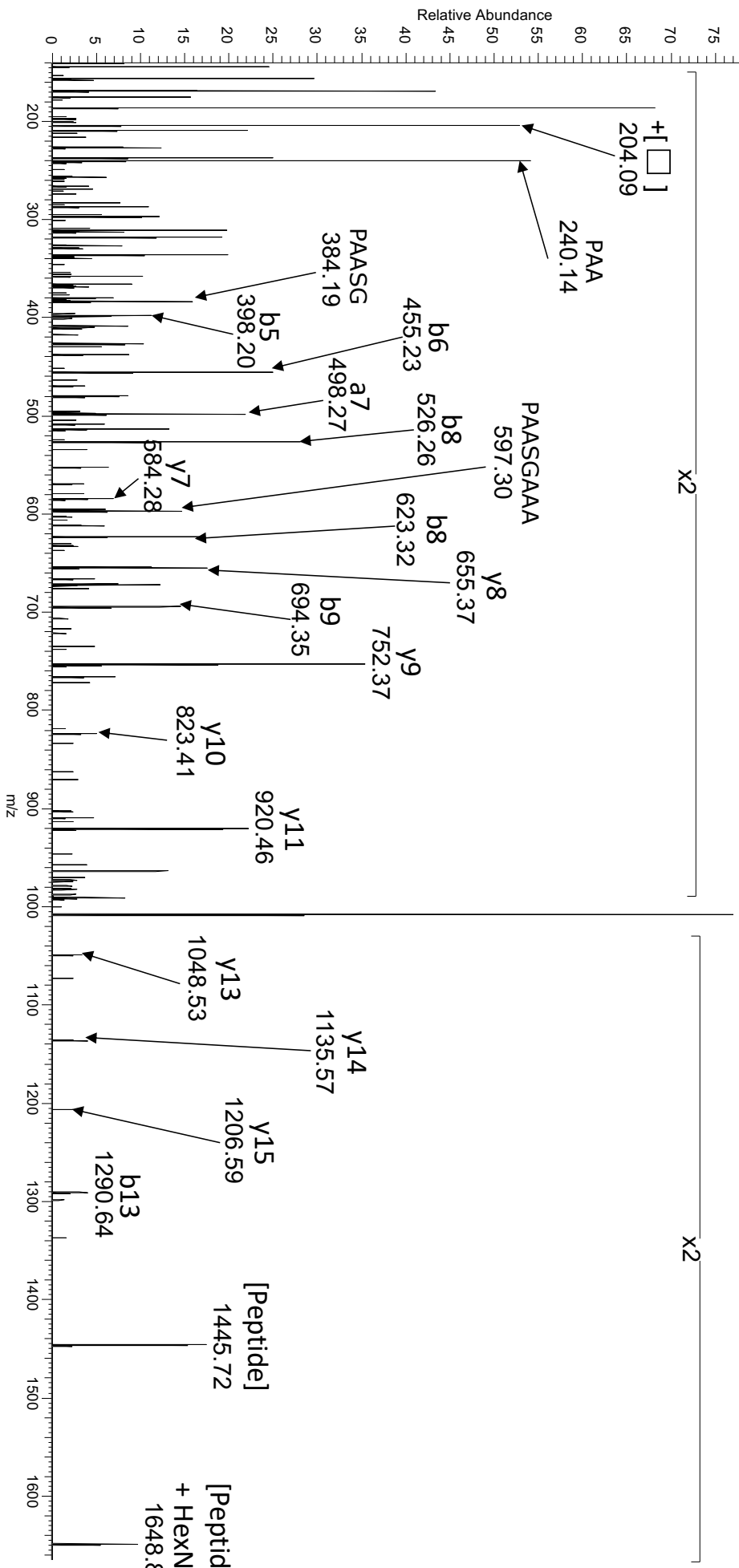
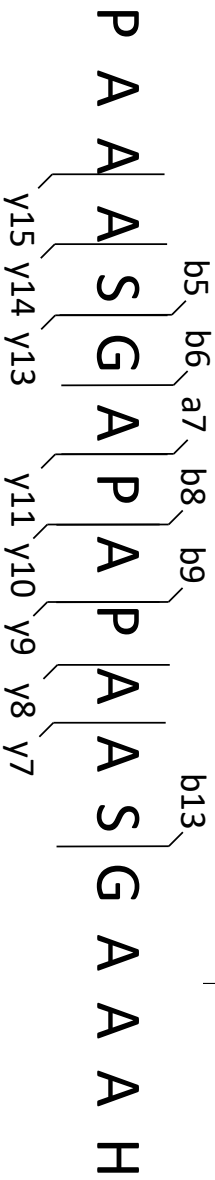
ITMS-CID



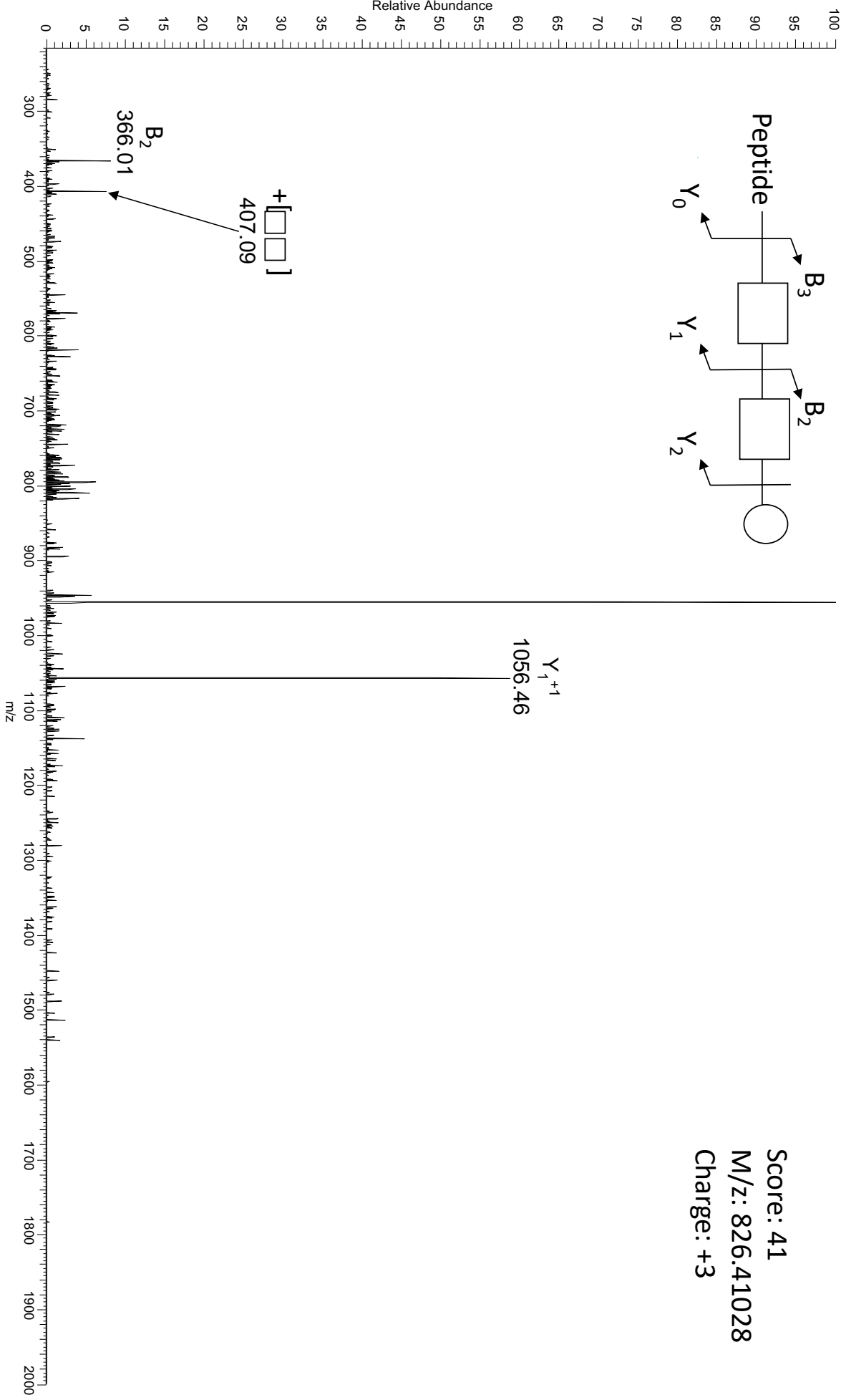
* Peptide related fragment
Score: 47
M/z: 1007.466
Charge: +2

[Precursor]⁺²
1007.59

Score: 47
M/z: 1007.466
Charge: +2



ITMS-CID



Score: 41

M/z: 826.41028

Charge: +3

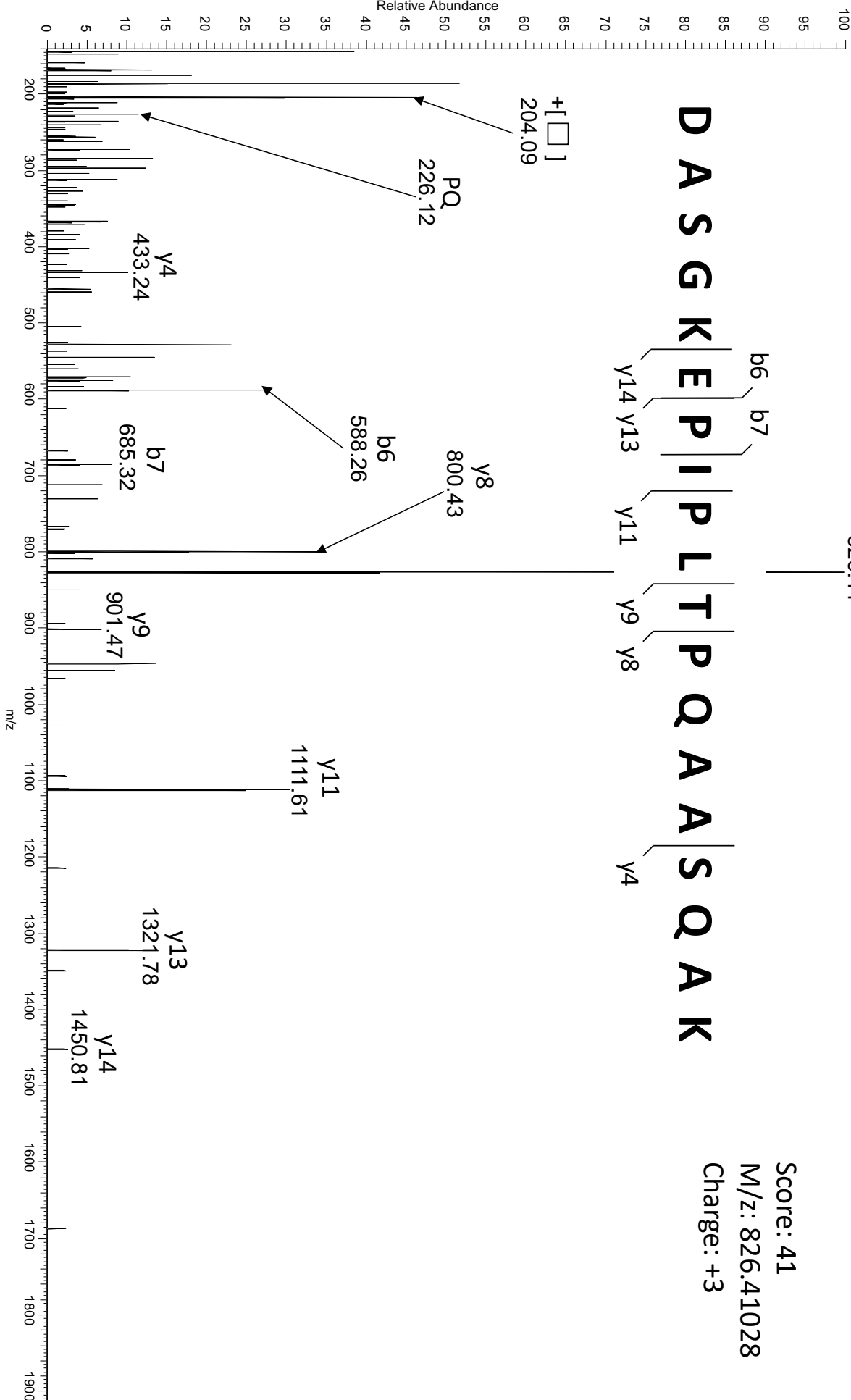
[M]⁺³
826.41

Score: 41

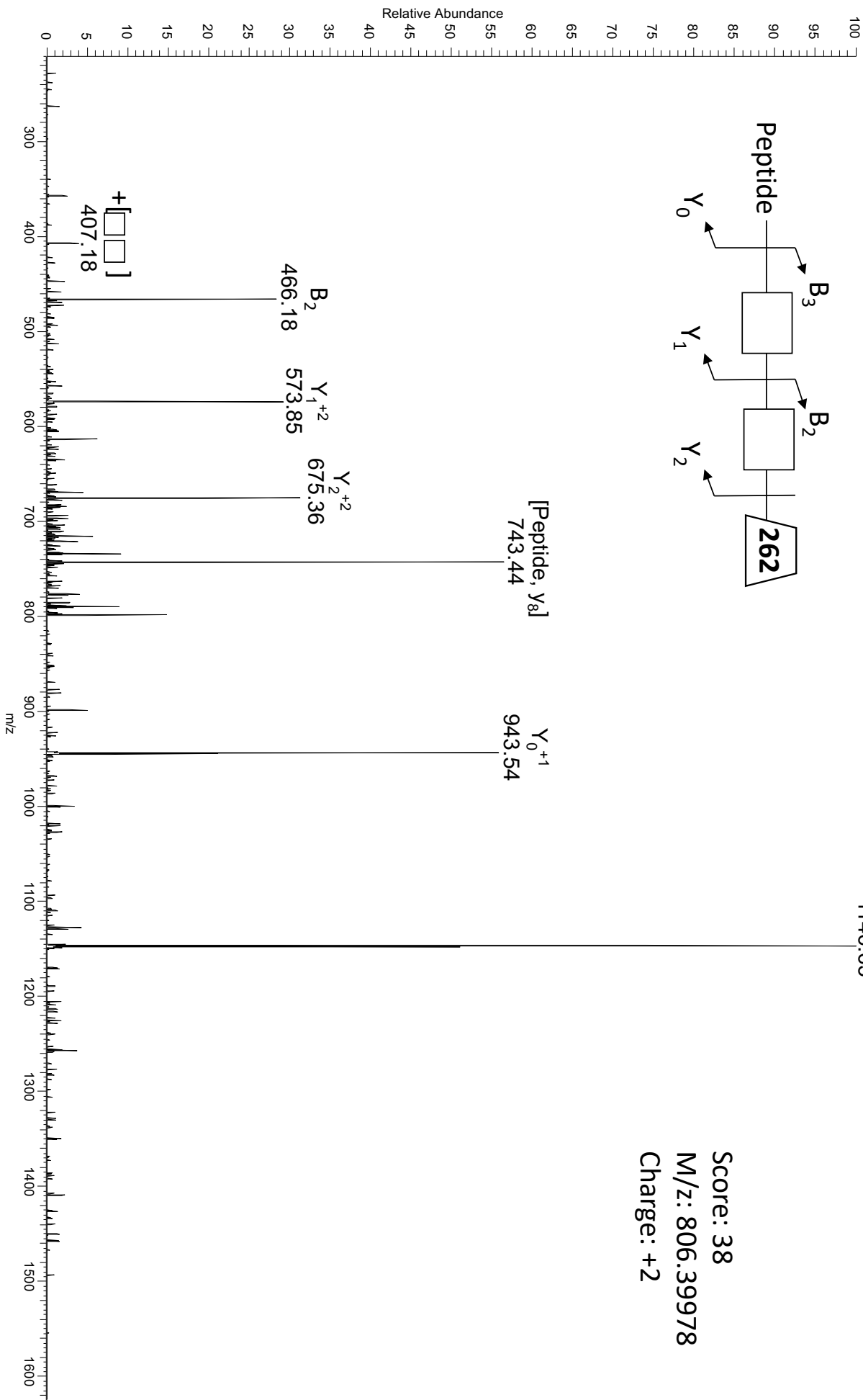
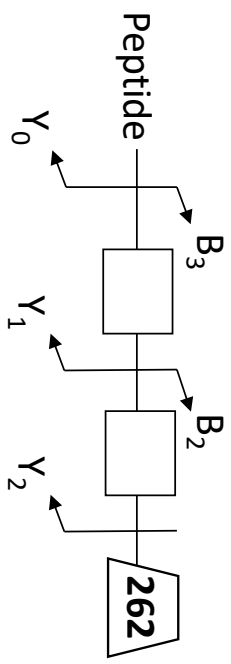
M/z: 826.41028

Charge: +3

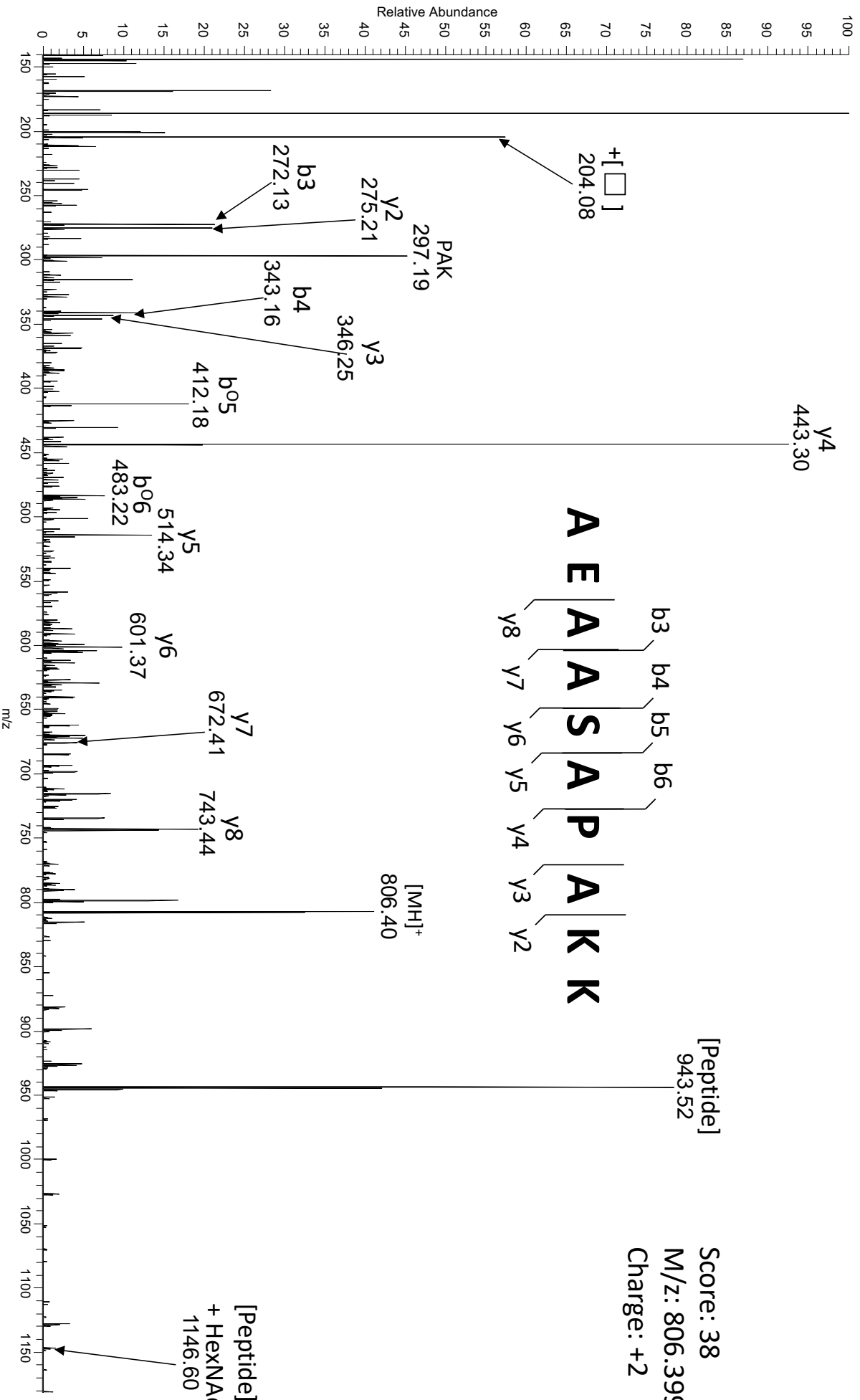
D A S G K E P I P L T P Q A A S Q A K



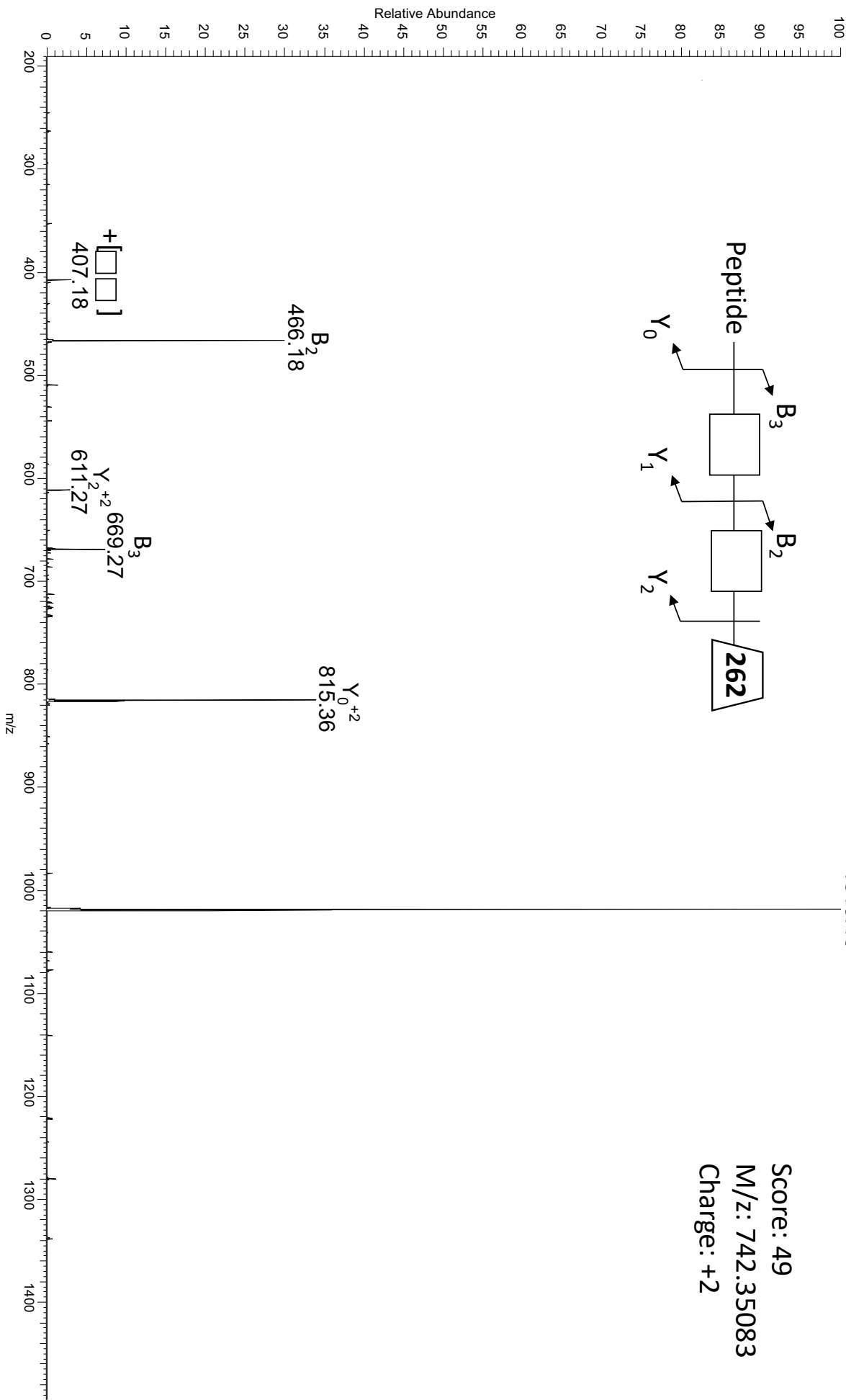
ITMS-CID



Score: 38
M/z: 806.39978
Charge: +2

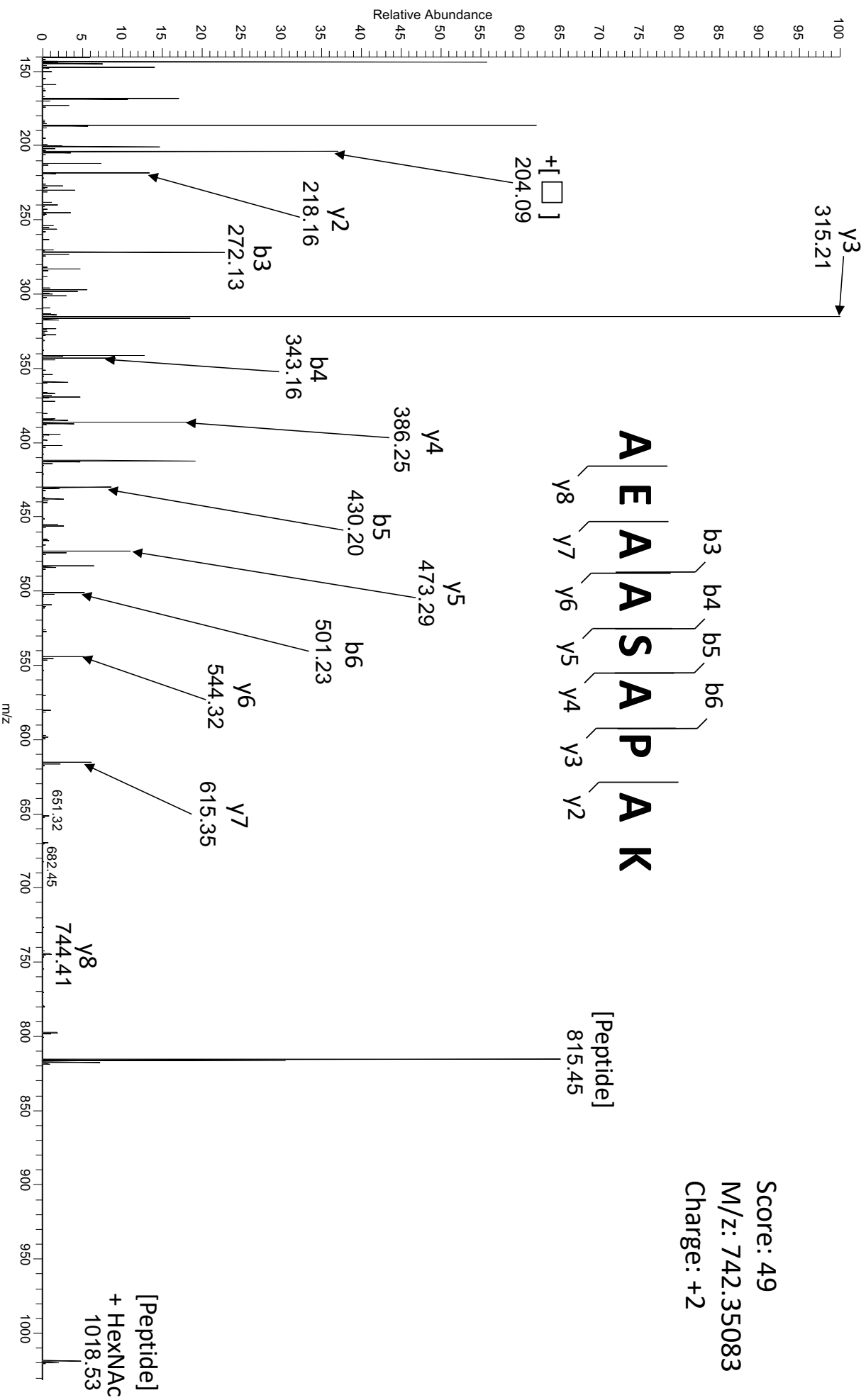


ITMS-CID

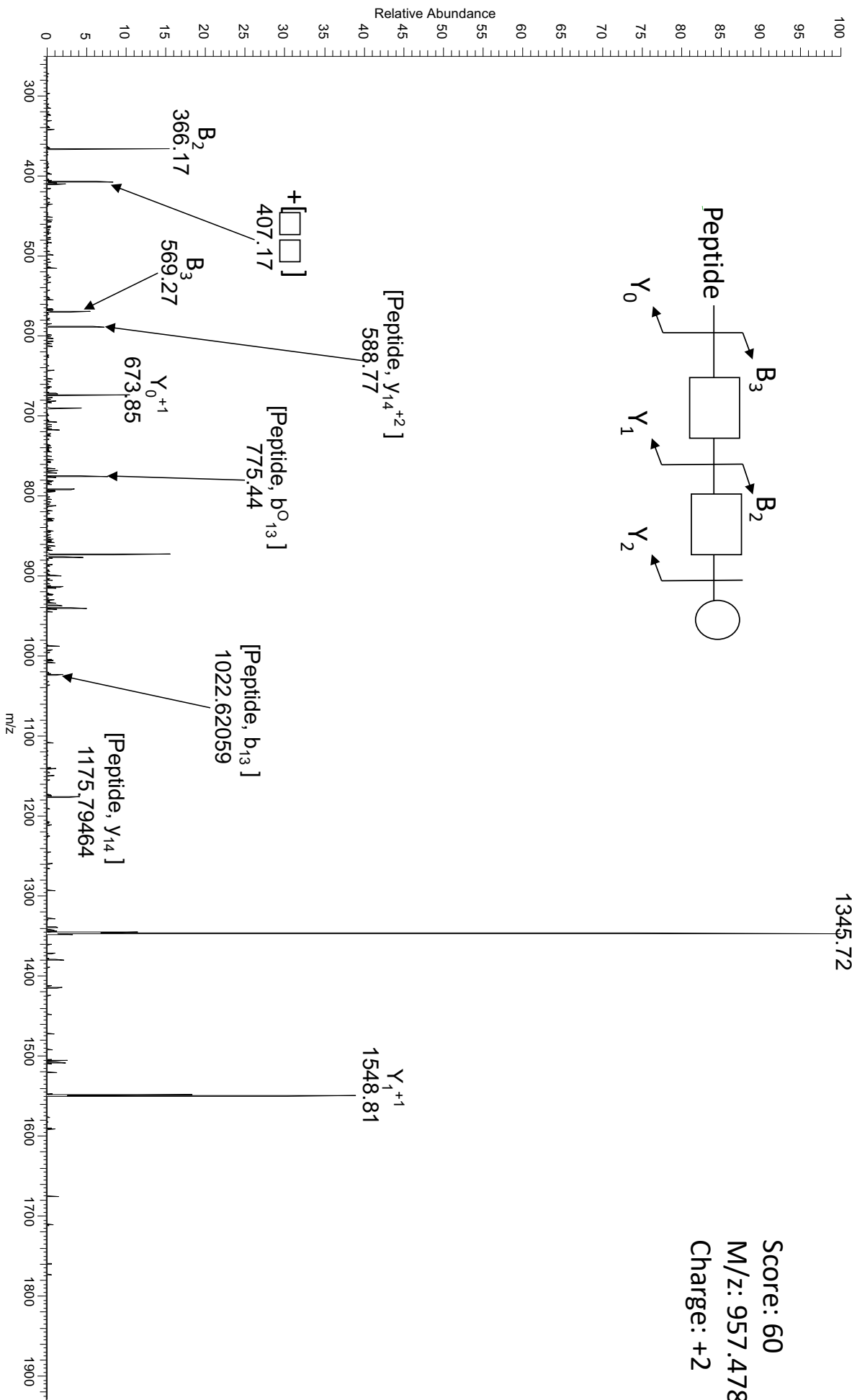
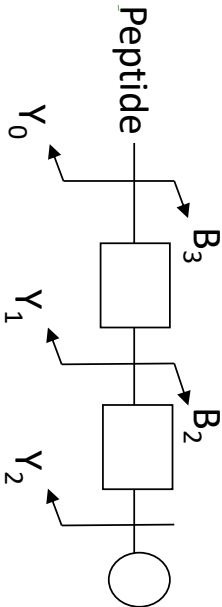


Score: 49
M/z: 742.35083
Charge: +2

Score: 49
M/z: 742.35083
Charge: +2



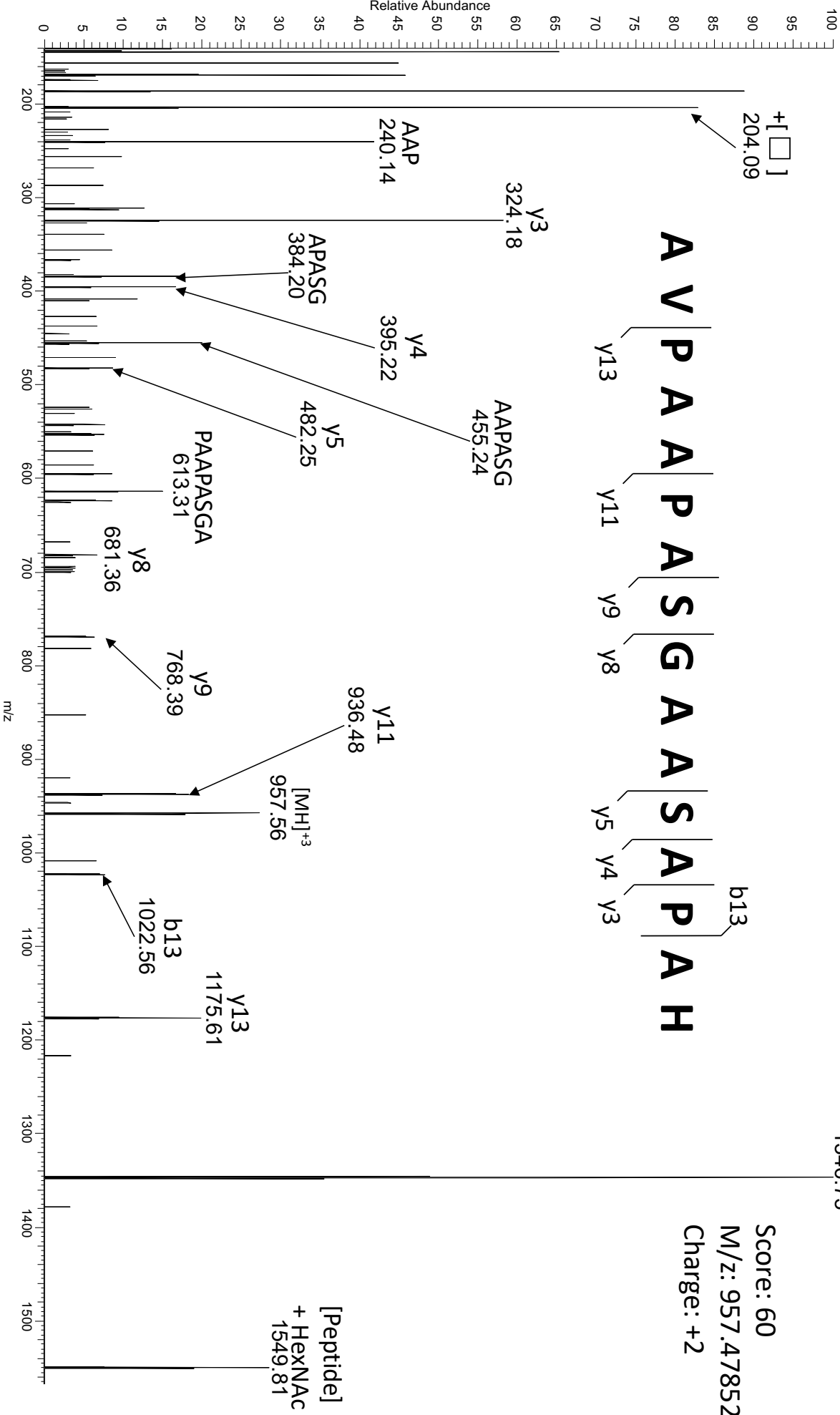
ITMS-CID



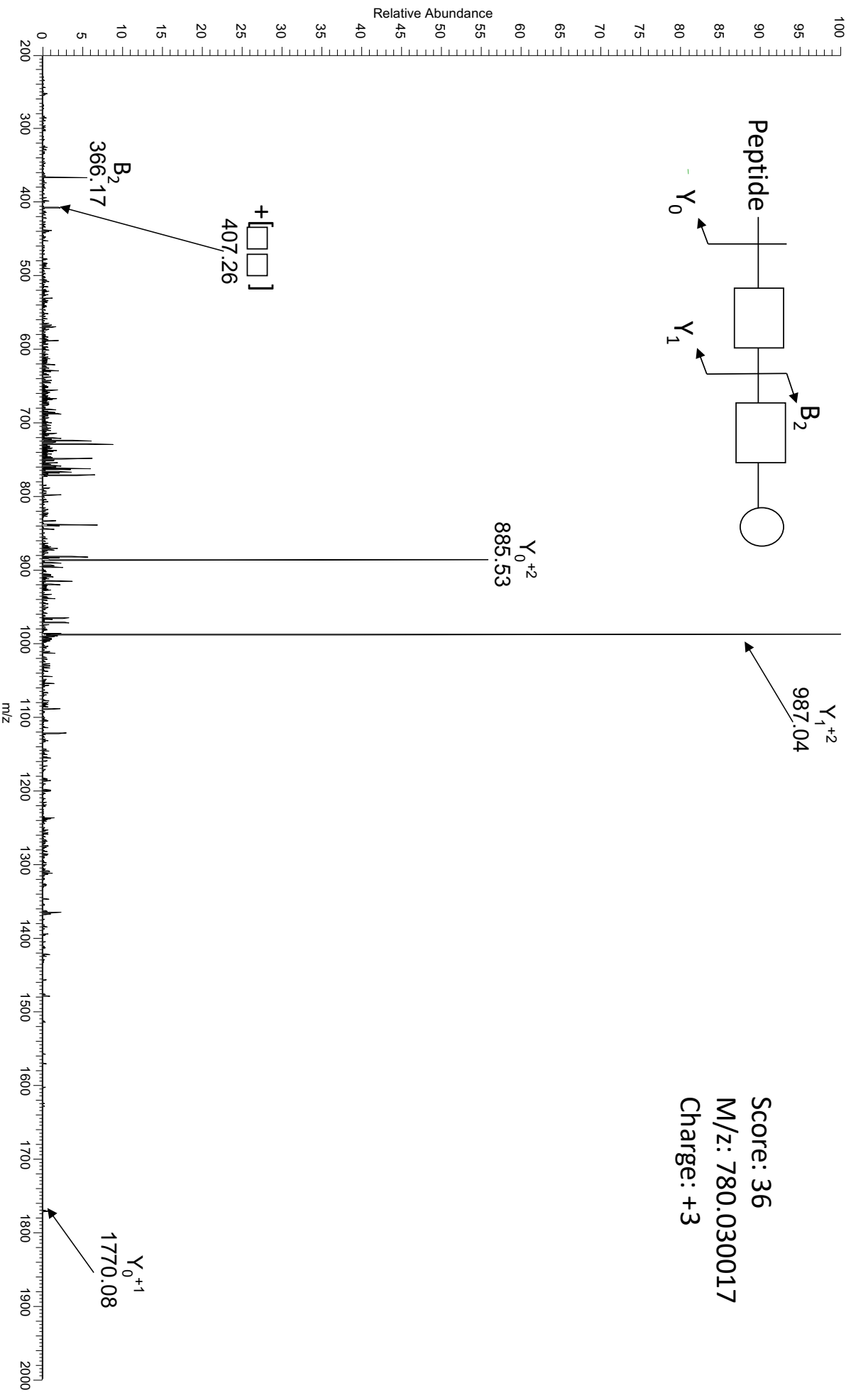
Score: 60
M/z: 957.47852
Charge: +2

[Peptide]
1346.73

Score: 60
M/z: 957.47852
Charge: +2

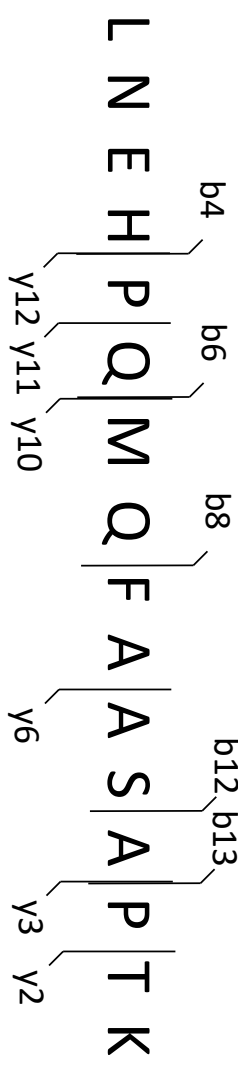
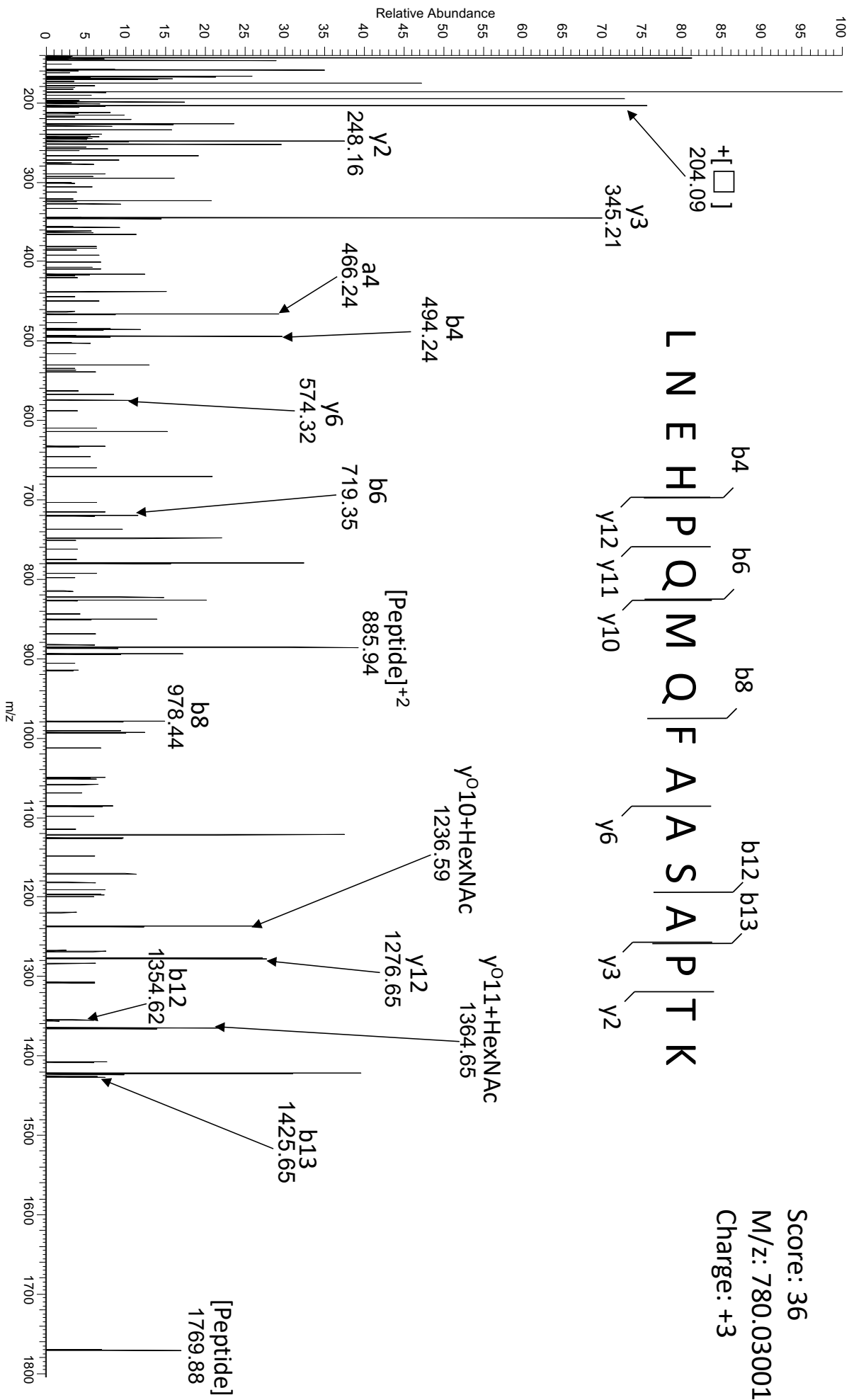


ITMS-CID



Score: 36
M/z: 780.030017
Charge: +3

FTMS-HCD



Score: 36
M/z: 780.030017
Charge: +3