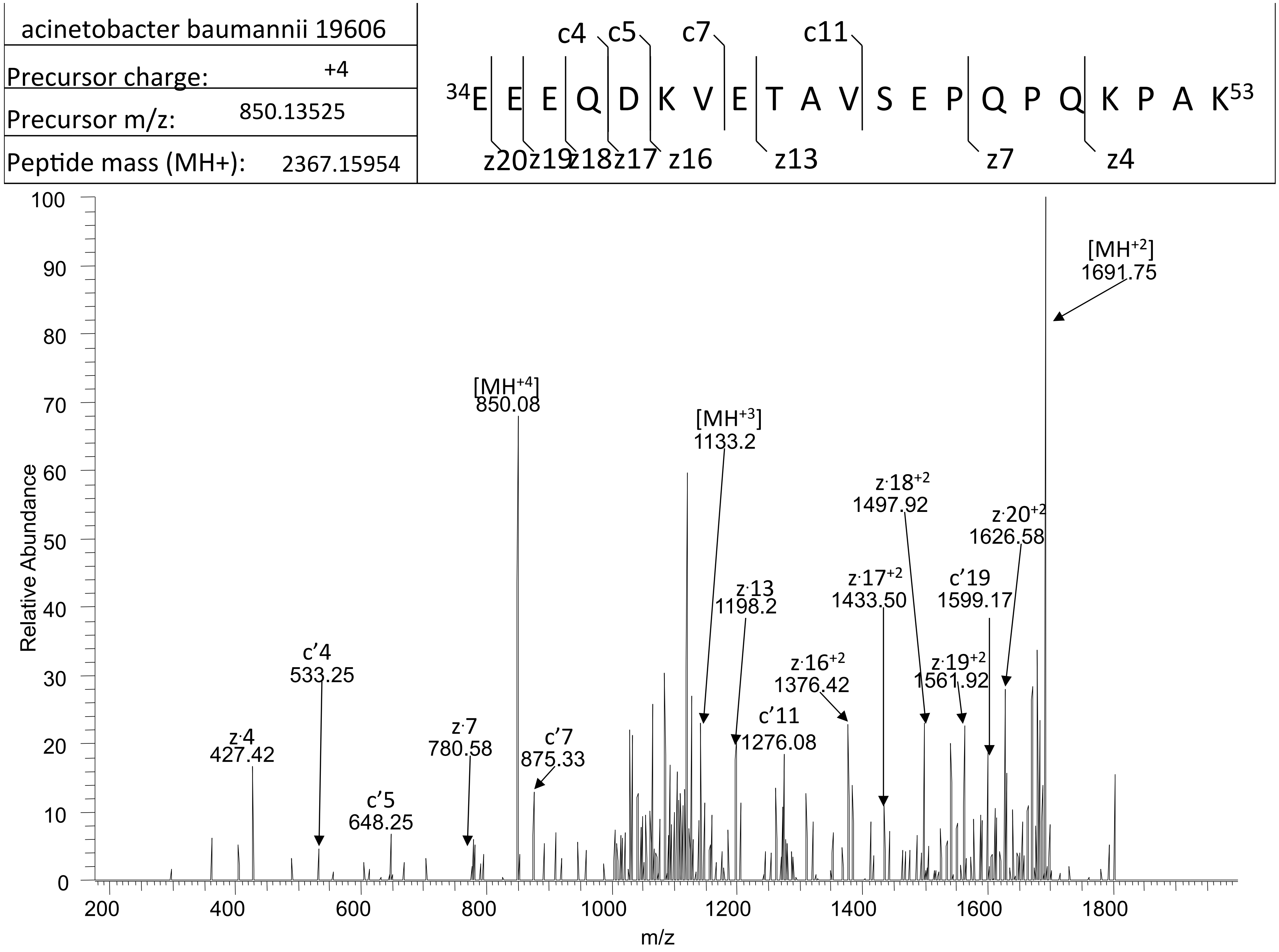
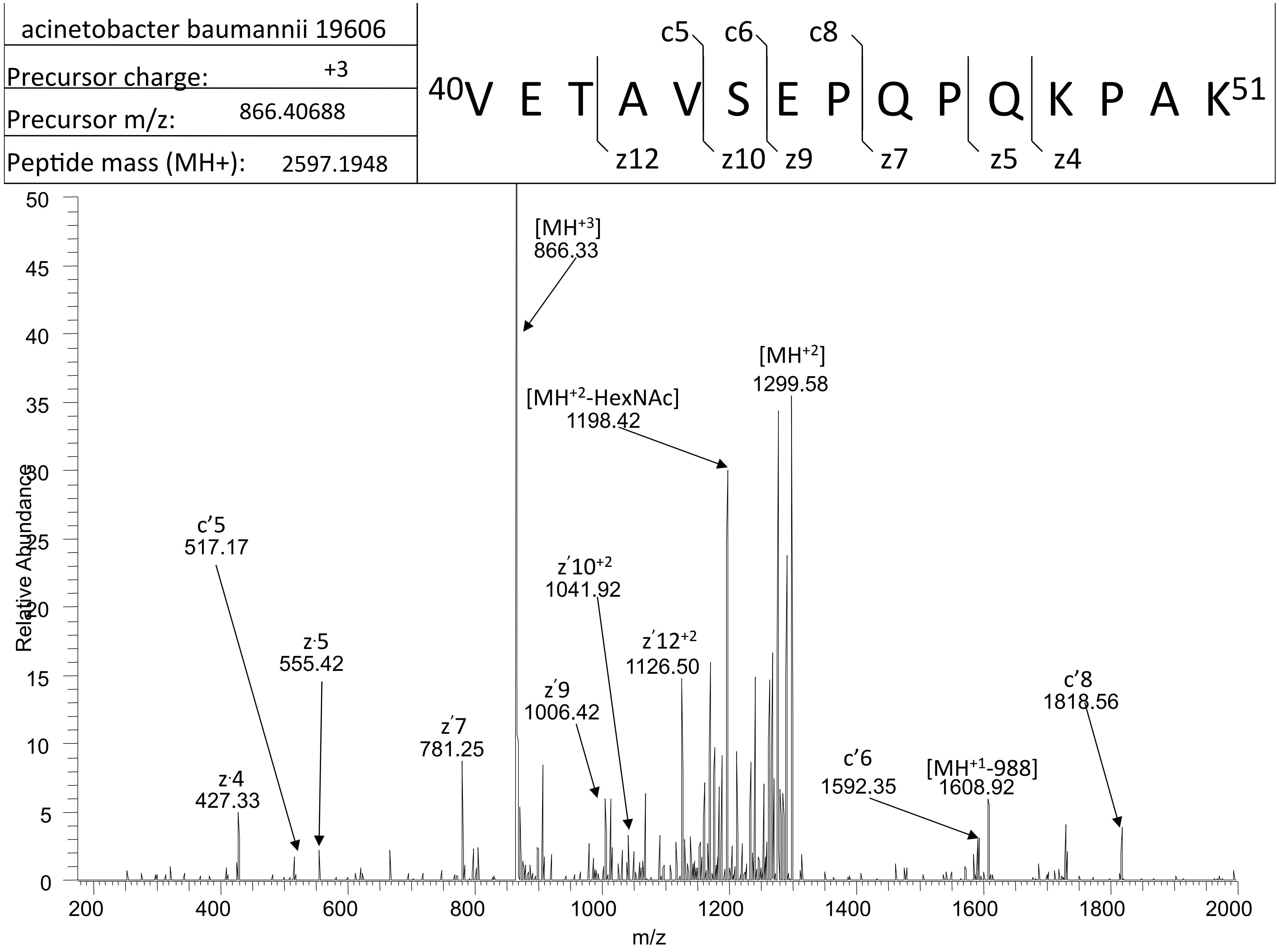
Supplementary table 10A: Glycopeptides identified using ETD in *Acinetobacter baumannii* (strain ATCC19606)

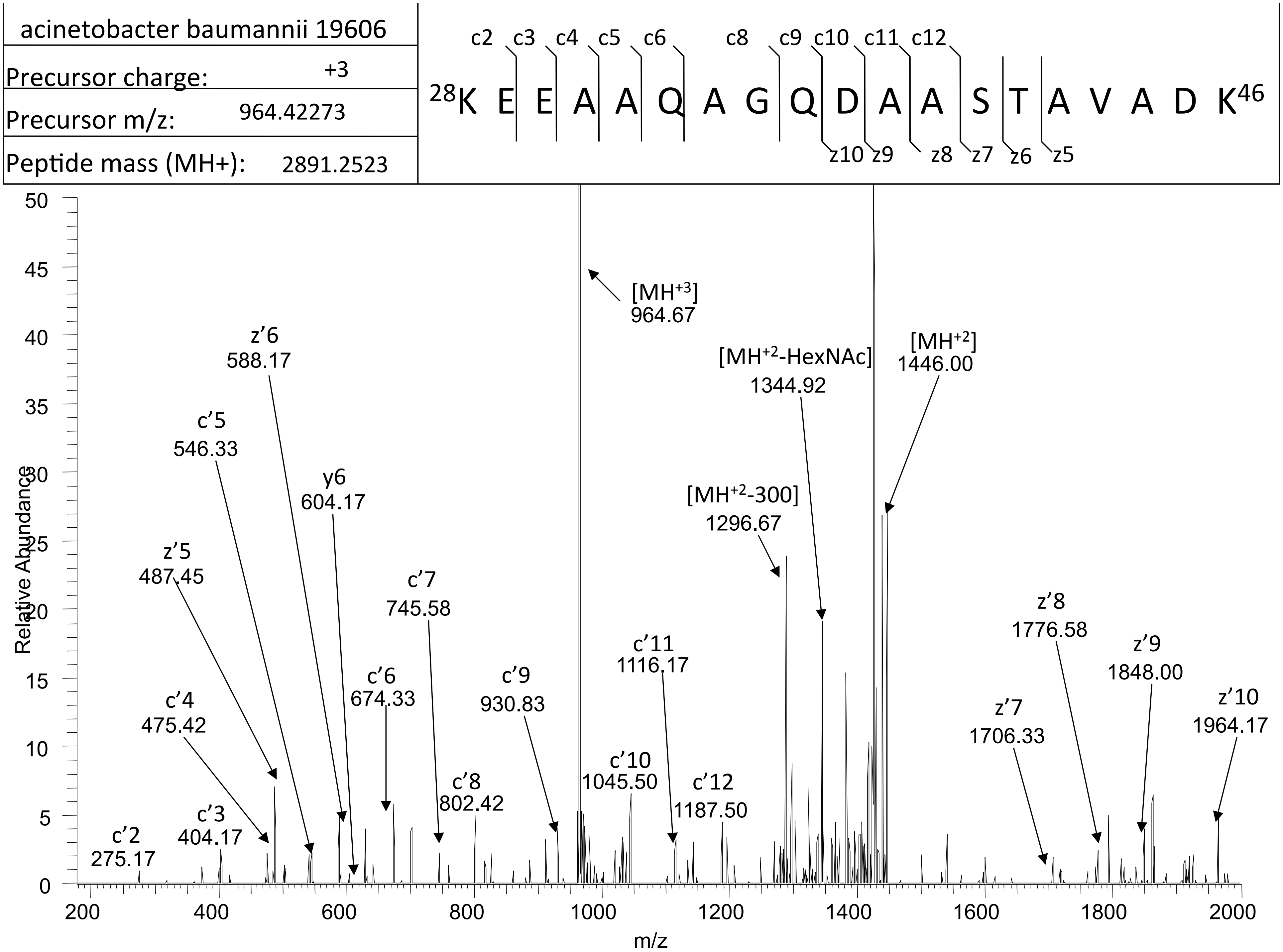
Uniprot accession number	Protein name	parent mass	charge	Precursor MH+	glycan mass	glycan composition	peptide mass	peptide	Site localisation	Page
D0C6Q2_ ACIBA	Putative uncharacterized protein [HMPREF0010_00432] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]"	850.14	4	3397.52	1030.36	HexNAc-Hex$_2$-HexNAc-300	2367.160	^{34}EEEQDKVETAVSEPQPQKPAK^{53}	S^{45+}	3
D0C6Q2_ ACIBA	Putative uncharacterized protein [HMPREF0010_00432] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]"	866.41	3	2597.19	988.34	HexNAc-Hex$_2$-HexNAc-258	1608.859	^{40}VETAVSEPQPQKPAK^{51}	S^{45+}	4
D0C7T4_ ACIBA	Putative uncharacterized protein [HMPREF0010_00814] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	964.42	3	2891.25	1030.36	HexNAc-Hex$_2$-HexNAc-300	1860.893	^{28}KEEAAQAGQDAASTAVADK^{46}	S^{40+}	5
D0C8B9_ ACIBA	Uncharacterized protein [F911_02370] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	1007.05	3	3019.13	1030.36	HexNAc-Hex$_2$-HexNAc-300	1988.766	^{28}NDGM(+16)HEASDPATSHDM(+16)NK^{45}	S^{35+}	6
D0C8B9_ ACIBA	Uncharacterized protein [F911_02370] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	755.78	4	3020.11	1030.36	HexNAc-Hex$_2$-HexNAc-300	1989.753	^{28}N(+1)DGM(+16)HEASDPATSHDM(+16)NK^{45}	S^{35+}	7
D0C8B9_ ACIBA	Uncharacterized protein [F911_02370] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	755.04	4	3017.15	1044.38	HexNAc-Hex$_2$-HexNAc-314	1972.765	^{28}NDGM(+16)HEASDPATSHDMNK^{45}	S^{35+}	8
D0CAB8_ ACIBA	Uncharacterized protein [F911_03368] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	657.32	3	1969.94	1030.36	HexNAc-Hex$_2$-HexNAc-300	939.562	^{302}AKPASAPAVK^{311}	S^{306+}	9

D0CAB8_ACIBA	Uncharacterized protein [F911_03368] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	643.31	3	1927.91	988.35	HexNAc-Hex$_2$-HexNAc-258	939.562	^{302}AKPASAPAVK^{311}	S^{306+}	10
D0CAB8_ACIBA	Uncharacterized protein [F911_03368] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	1128.16	3	3382.47	1030.36	HexNAc-Hex$_2$-HexNAc-300	2352.114	^{116}KTEASAAAATEQQDSFDAQVQR^{136}	S^{120}	11
D0CDQ9_ACIBA	Uncharacterized protein [F911_00789] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	846.38	3	2536.10	1030.36	HexNAc-Hex$_2$-HexNAc-300	1505.744	^{40}STAKDEQPASSASVK^{54}	S$^{51/50+}$	12
D0CEI7_ACIBA	TolA (Uncharacterized protein) [F911_02604] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	855.70	3	2565.10	1030.36	HexNAc-Hex$_2$-HexNAc-300	1534.734	^{52}QAASDIATATDNASAK^{67}	S^{55+}	13
D0CEI7_ACIBA	TolA (Uncharacterized protein) [F911_02604] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	951.74	3	2853.20	988.35	HexNAc-Hex$_2$-HexNAc-300	1864.848	^{48}SAGDQAASDIATATDNASAK^{67}	S^{55+}	14
D0CEI7_ACIBA	TolA (Uncharacterized protein) [F911_02604] [Acinetobacter baumannii ATCC 19606 = CIP 70.34]	965.74	3	2895.21	1030.36	HexNAc-Hex$_2$-HexNAc-300	1864.852	^{48}SAGDQAASDIATATDNASAK^{67}	S^{55+}	15

Supplementary table 10A: Identifications are labeled according to the corresponding Uniprot accession number and protein name. The parent m/z, charge state, deconvoluted mas mass, glycan mass, peptide mass, peptide sequence and glycan site attachment are provided for each identified glycopeptide. All identified glycopeptide ETD spectra are provided on the corresponding pages


acinetobacter baumannii 19606
Precursor charge: +4
Precursor m/z: 850.13525
Peptide mass (MH+): 2367.15954
c4 c5 c7 c11
34E E E Q D K V E T A V S E P Q P Q K P A K53
z20 z19 z18 z17 z16 z13 z7 z4
Relative Abundance
100
90
80
70
60
50
40
30
20
10
0
200
400
600
800
1000
1200
1400
1600
1800
m/z
[MH+2]
1691.75
[MH+4]
850.08
[MH+3]
1133.2
z·18+2
1497.92
z·20+2
1626.58
z·13
1198.2
z·17+2
1433.50
c’19
1599.17
z·16+2
1376.42
z·19+2
1561.92
c’11
1276.08
c’4
533.25
z·4
427.42
c’5
648.25
z·7
780.58
c’7
875.33


acinetobacter baumannii 19606
Precursor charge: +3
Precursor m/z: 866.40688
Peptide mass (MH+): 2597.1948
40V E T A V S E P Q P Q K P A K51
c5
c6
c8
z12
z10
z9
z7
z5
z4
[MH+3]
866.33
[MH+2]
1299.58
[MH+2-HexNAc]
1198.42
c'5
517.17
z·5
555.42
z·4
427.33
z'7
781.25
z'9
1006.42
z'10+2
1041.92
z'12+2
1126.50
c'6
1592.35
[MH+1-988]
1608.92
c'8
1818.56
Relative Abundance
m/z
0
5
10
15
20
25
30
35
40
45
50
200
400
600
800
1000
1200
1400
1600
1800
2000

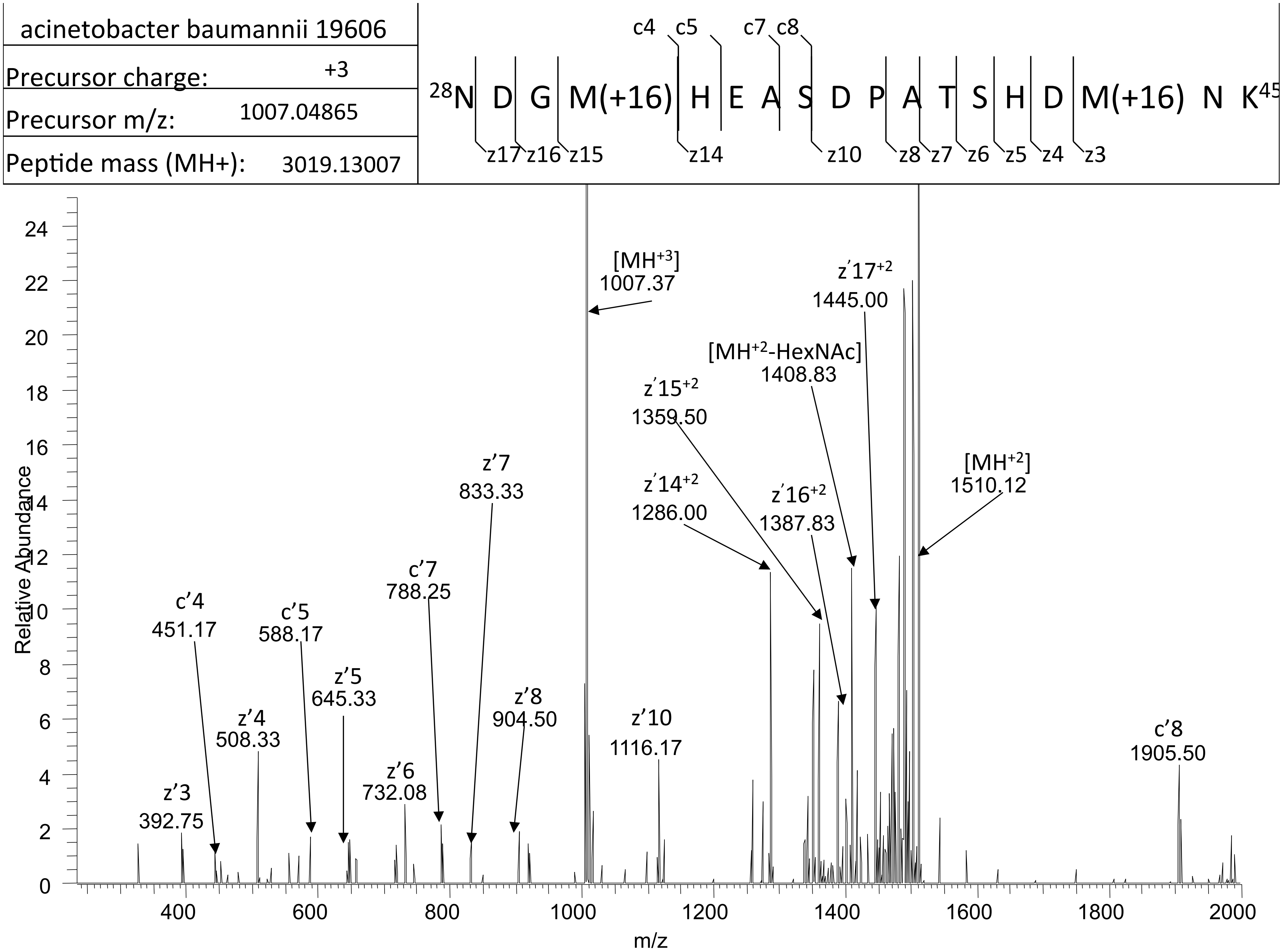


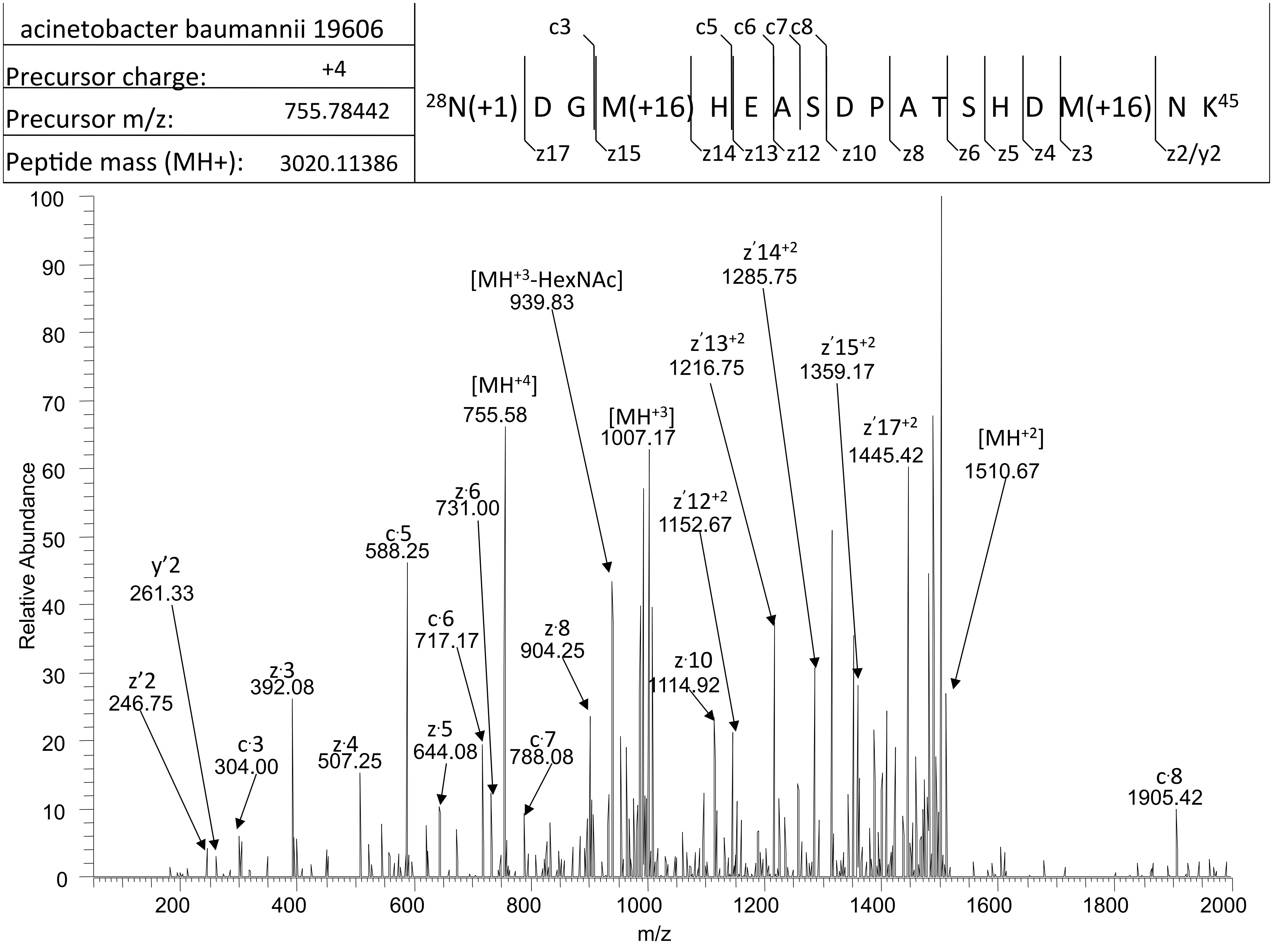
acinetobacter baumannii 19606

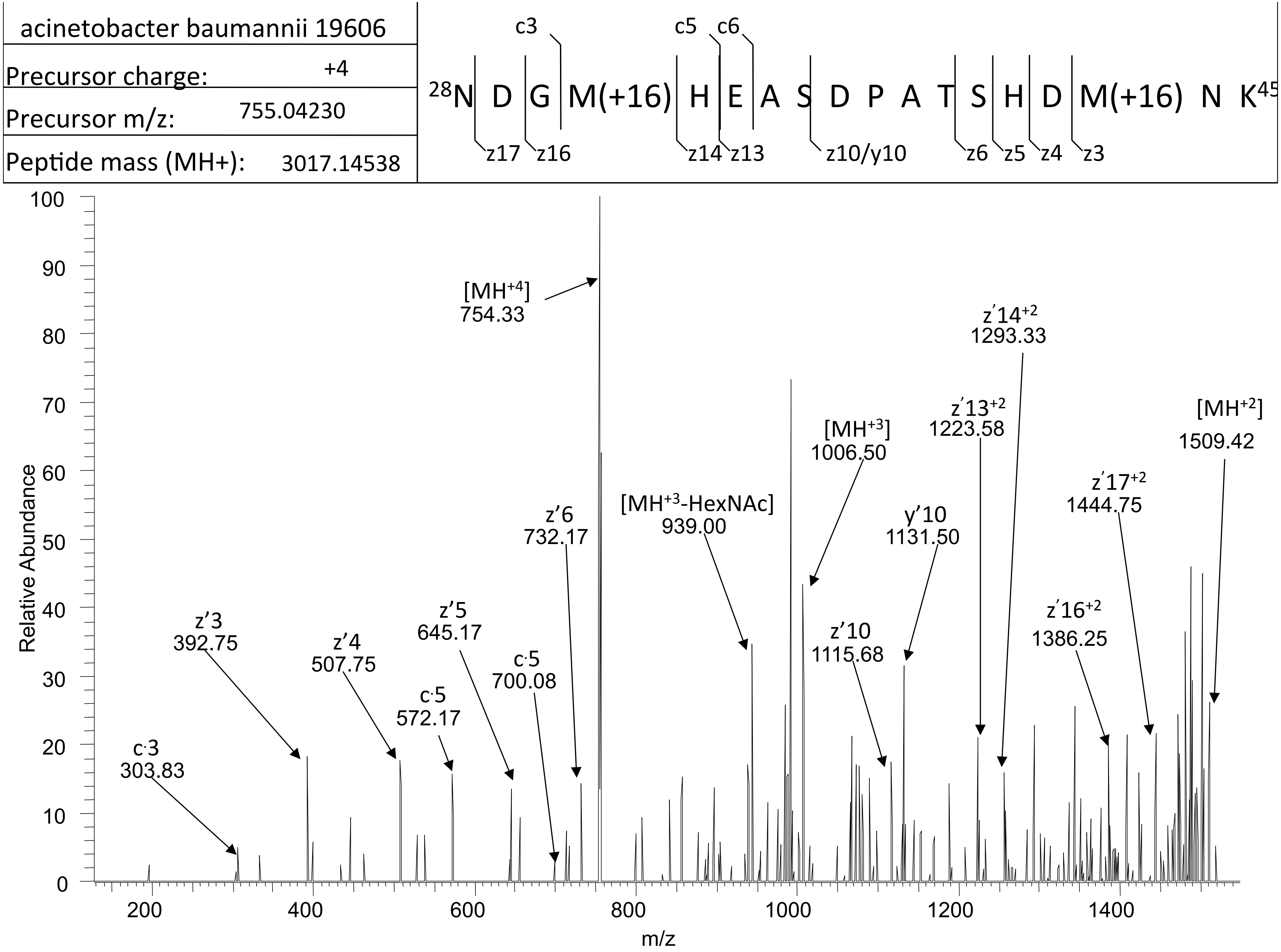
Precursor charge: +3

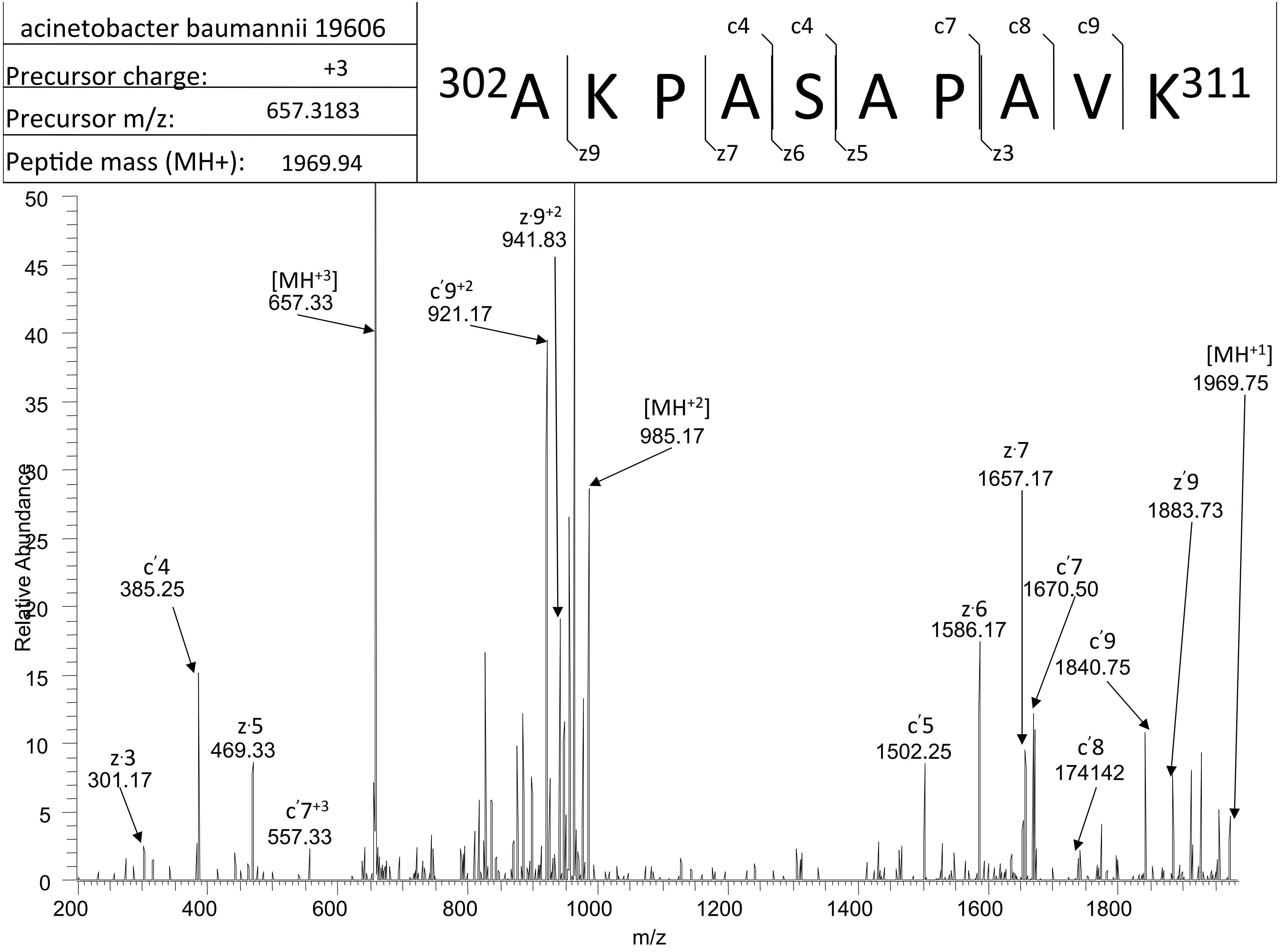
Precursor m/z: 964.42273

Peptide mass (MH+): 2891.2523


acinetobacter baumannii 19606
Precursor charge: +3
Precursor m/z: 1007.04865
Peptide mass (MH+): 3019.13007
c4 c5 c7 c8
28N D G M(+16) H E A S D P A T S H D M(+16) N K45
z17 z16 z15 z14 z10 z8 z7 z6 z5 z4 z3
[MH+3]
1007.37
z′17+2
1445.00
[MH+2-HexNAc]
1408.83
z′15+2
1359.50
[MH+2]
1510.12
z′14+2
1286.00
z′16+2
1387.83
z′7
833.33
c′7
788.25
c′4
451.17
c′5
588.17
z′5
645.33
z′4
508.33
z′6
732.08
z′8
904.50
z′10
1116.17
z′3
392.75
c′8
1905.50
Relative Abundance
0
2
4
6
8
10
12
14
16
18
20
22
24
400
600
800
1000
1200
1400
1600
1800
2000
m/z

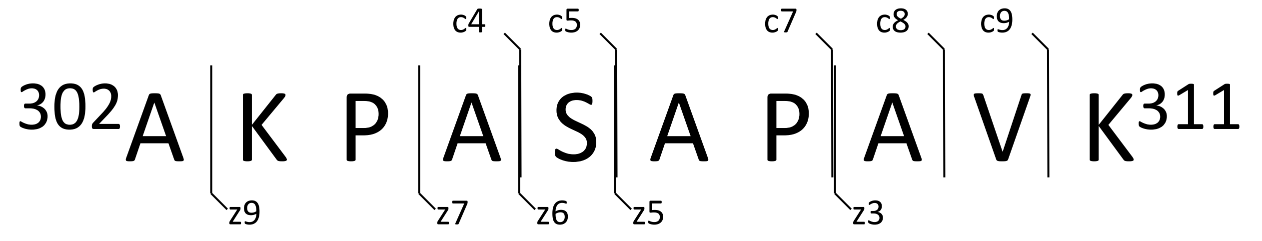

acinetobacter baumannii 19606
Precursor charge: +4
Precursor m/z: 755.78442
Peptide mass (MH+): 3020.11386
c3 c5 c6 c7 c8
28N(+1) D G M(+16) H E A S D P A T S H D M(+16) N K45
z17 z15 z14 z13 z12 z10 z8 z6 z5 z4 z3 z2/y2
Relative Abundance
m/z
z′2 246.75
y′2 261.33
c·3 304.00
z·3 392.08
z·4 507.25
c·5 588.25
z·5 644.08
c·6 717.17
z·6 731.00
[MH+4] 755.58
c·7 788.08
z·8 904.25
[MH+3-HexNAc] 939.83
[MH+3] 1007.17
z·10 1114.92
z′12+2 1152.67
z′13+2 1216.75
z′14+2 1285.75
z′15+2 1359.17
z′17+2 1445.42
[MH+2] 1510.67
c·8 1905.42
0
10
20
30
40
50
60
70
80
90
100
200
400
600
800
1000
1200
1400
1600
1800
2000

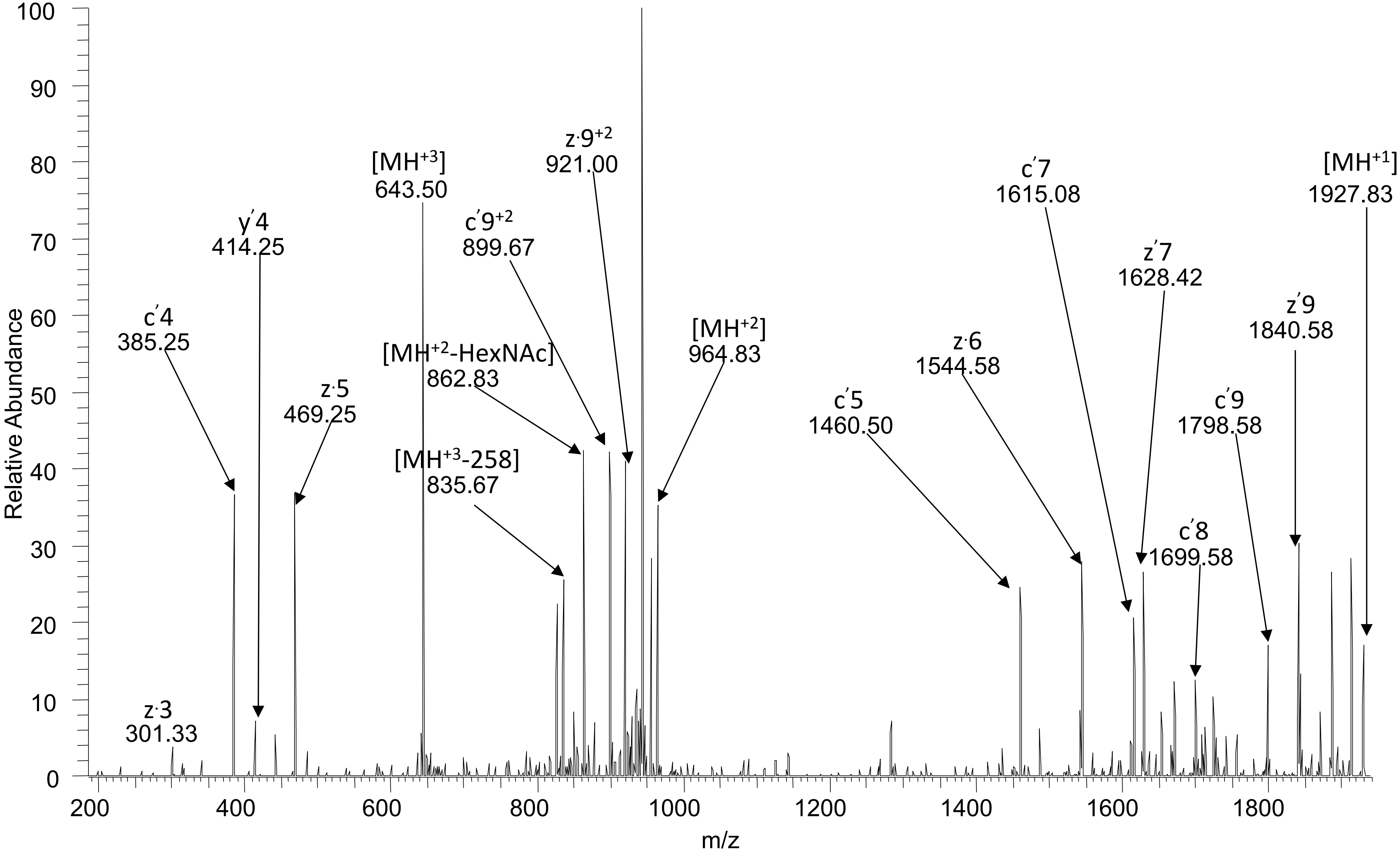

acinetobacter baumannii 19606
Precursor charge: +4
Precursor m/z: 755.04230
Peptide mass (MH+): 3017.14538
28N D G M(+16) H E A S D P A T S H D M(+16) N K45
c3
c5
c6
z17
z16
z14
z13
z10/y10
z6
z5
z4
z3
[MH+4] 754.33
[MH+3-HexNAc] 939.00
[MH+3] 1006.50
z′14+2 1293.33
z′13+2 1223.58
[MH+2] 1509.42
z′17+2 1444.75
y′10 1131.50
z′6 732.17
z′10 1115.68
z′16+2 1386.25
z′5 645.17
c·5 700.08
z′3 392.75
z′4 507.75
c·5 572.17
c·3 303.83
Relative Abundance
0
10
20
30
40
50
60
70
80
90
100
200
400
600
800
1000
1200
1400
m/z

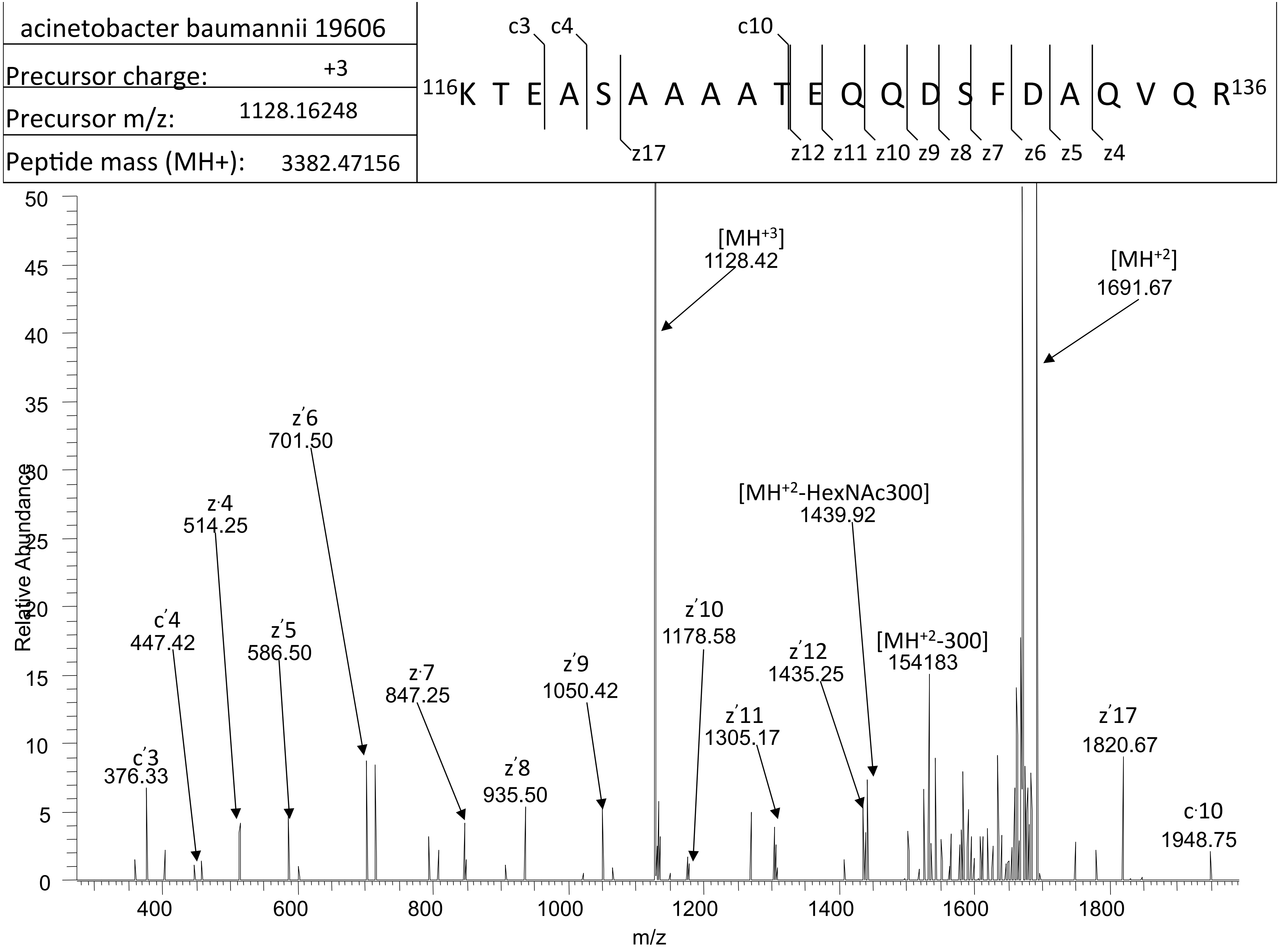


acinetobacter baumannii 19606	
Precursor charge:	+3
Precursor m/z:	657.3183
Peptide mass (MH+):	1969.94

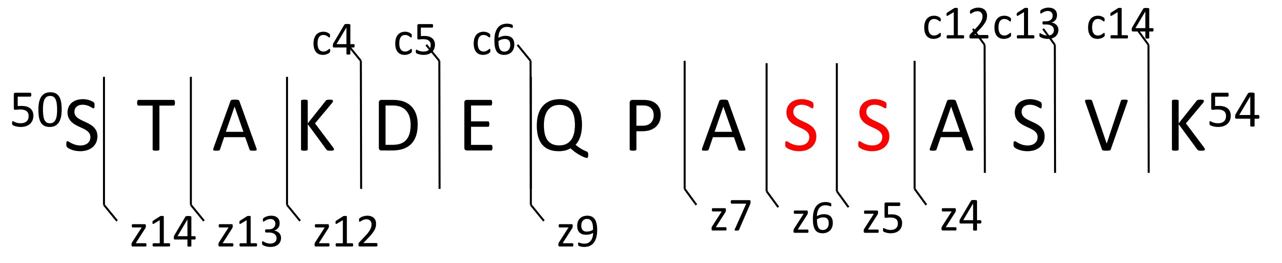
acinetobacter baumannii 19606	
Precursor charge:	+3
Precursor m/z:	643.30884
Peptide mass (MH+):	1927.91064

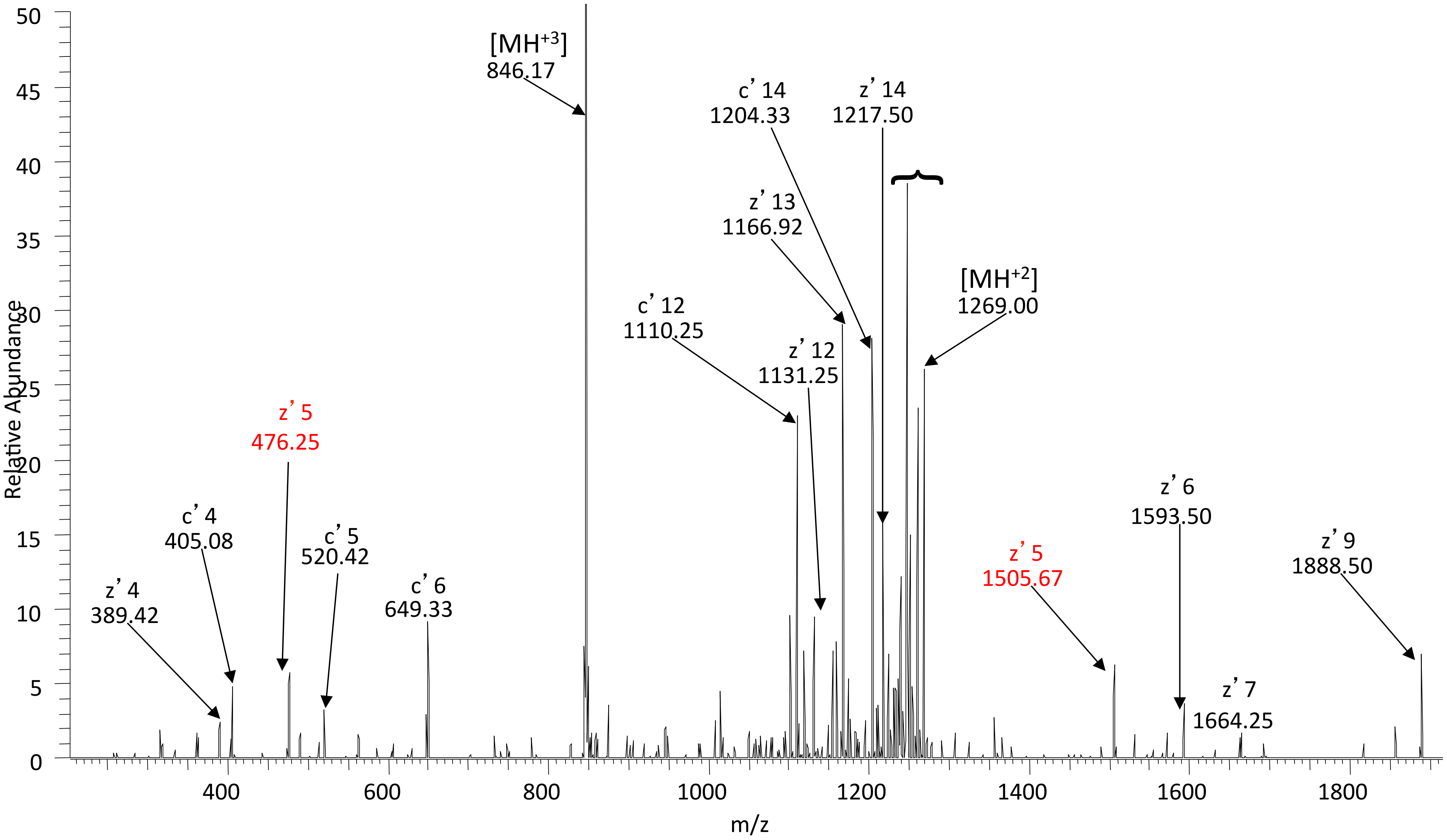


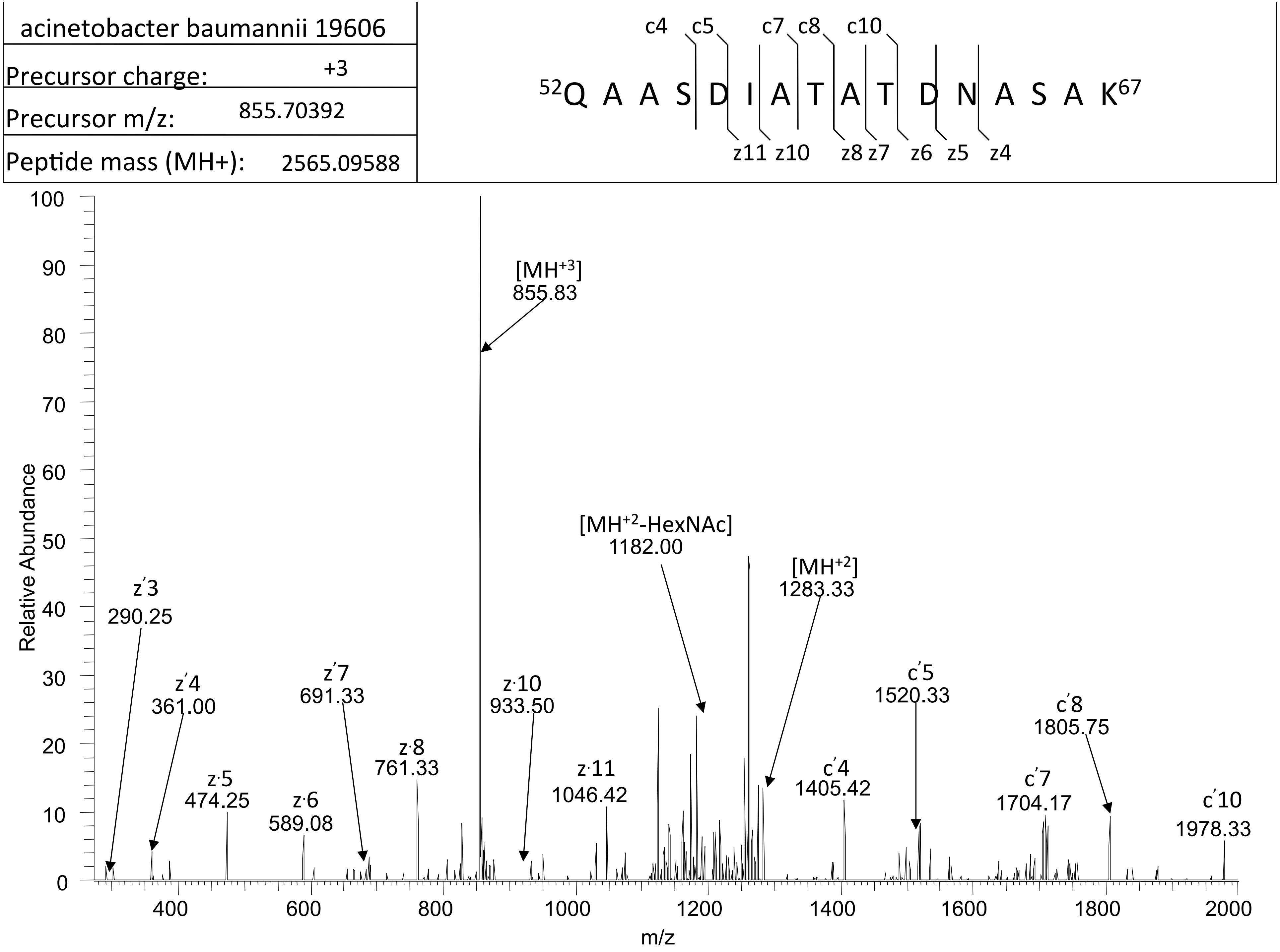


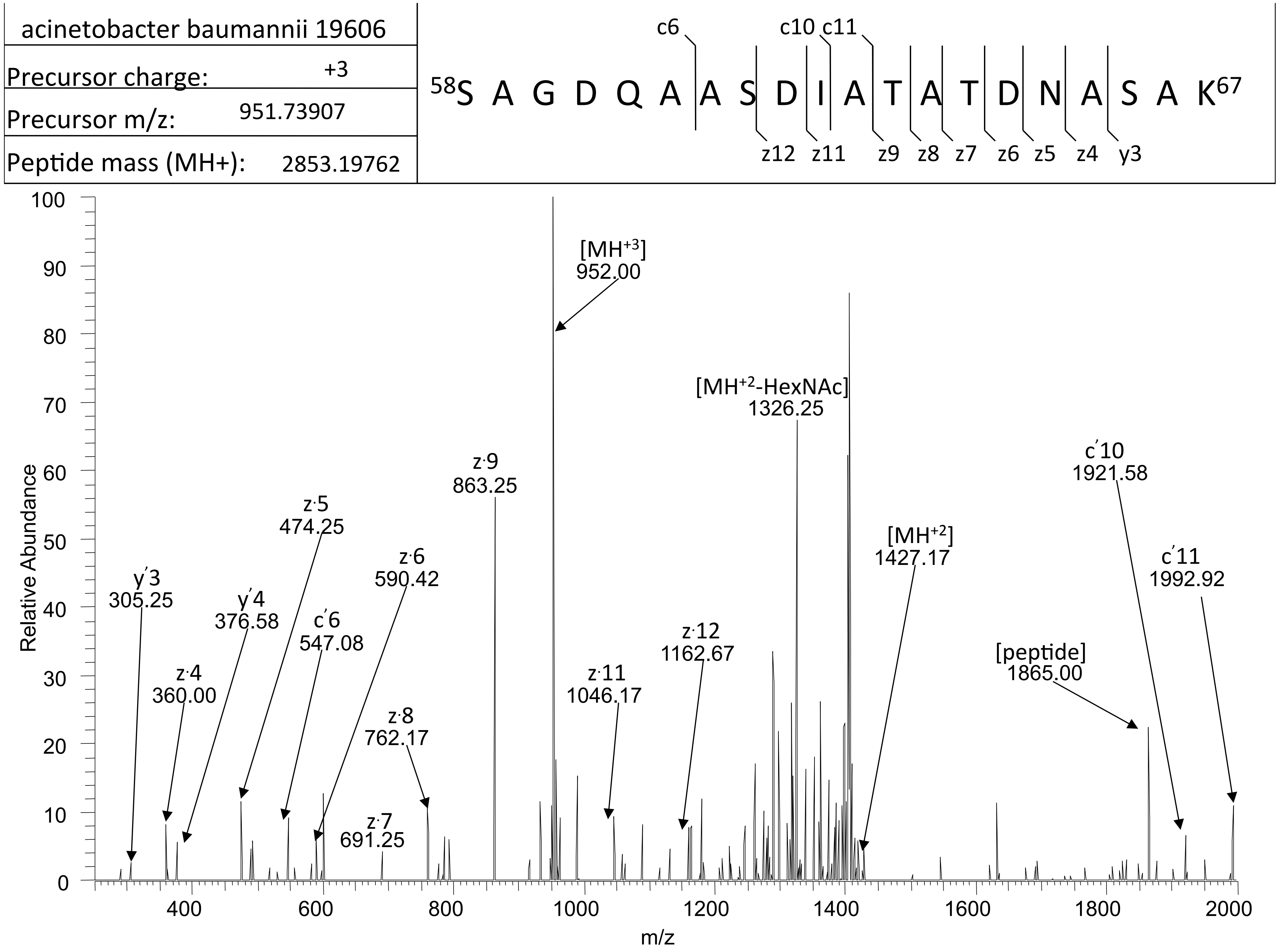

acinetobacter baumannii 19606
Precursor charge: +3
Precursor m/z: 1128.16248
Peptide mass (MH+): 3382.47156
116K T E A S A A A A T E Q Q D S F D A Q V Q R136
c3
c4
c10
z17
z12
z11
z10
z9
z8
z7
z6
z5
z4
[MH+3]
1128.42
[MH+2]
1691.67
z′6
701.50
z·4
514.25
[MH+2-HexNAc300]
1439.92
c′4
447.42
z′5
586.50
z′10
1178.58
[MH+2-300]
154183
z′12
1435.25
z·7
847.25
z′9
1050.42
z′11
1305.17
z′17
1820.67
c′3
376.33
z′8
935.50
c·10
1948.75
Relative Abundance
m/z
0
5
10
15
20
25
30
35
40
45
50
400
600
800
1000
1200
1400
1600
1800

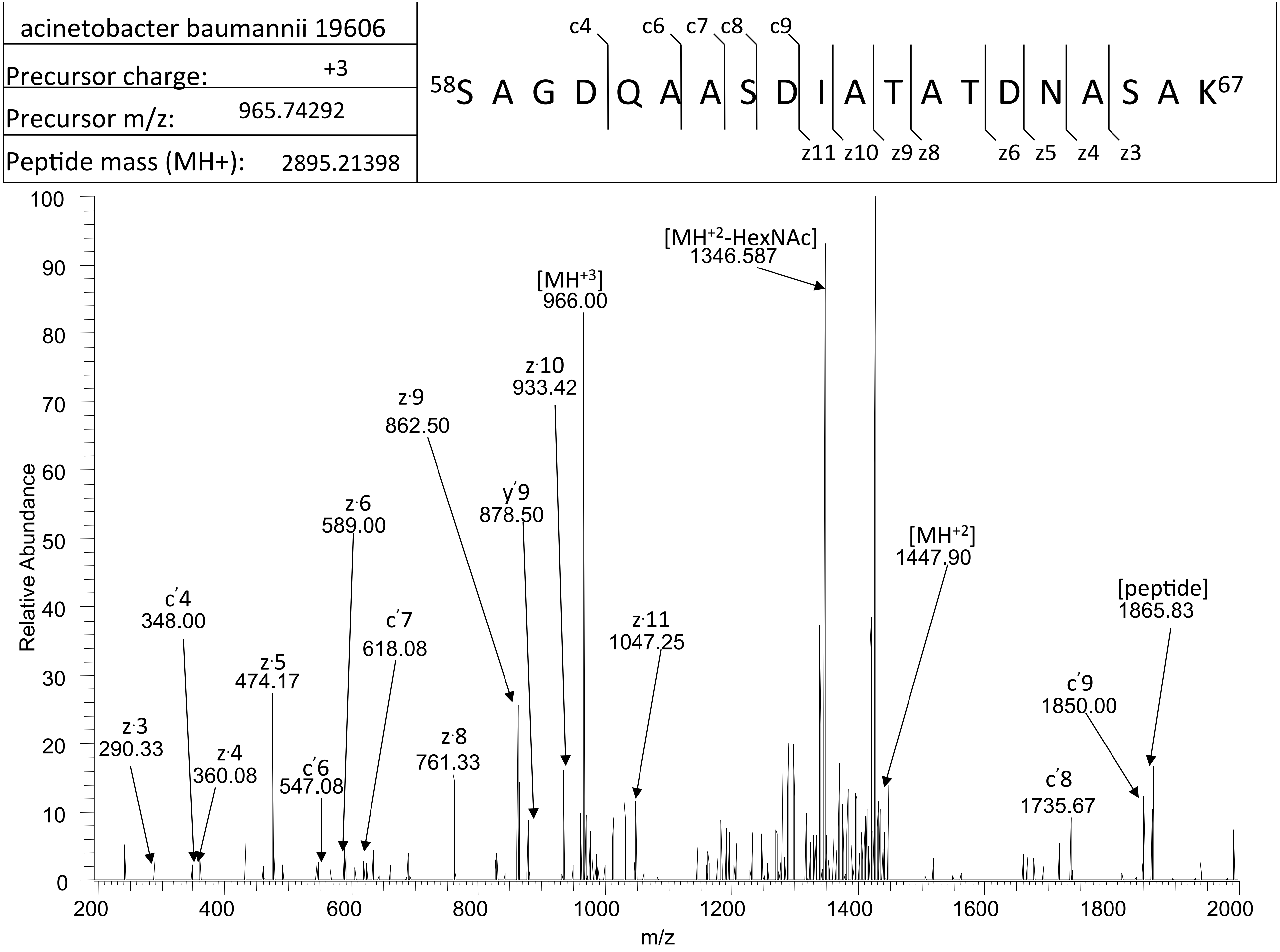
acinetobacter baumannii 19606	
Precursor charge:	+3
Precursor m/z:	846.37618
Peptide mass (MH+):	2536.1046





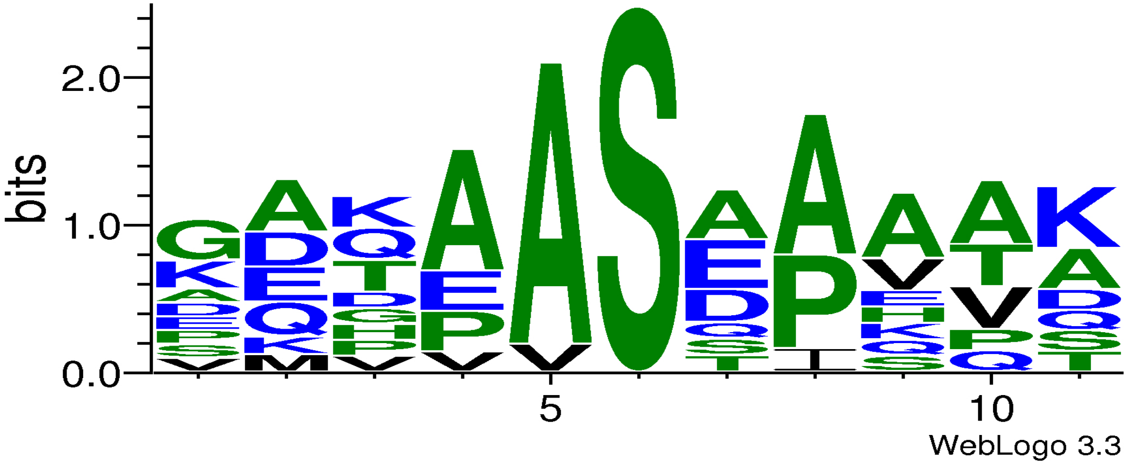

acinetobacter baumannii 19606
Precursor charge: +3
Precursor m/z: 855.70392
Peptide mass (MH+): 2565.09588
c4 c5 c7 c8 c10
^{52}Q A A S D I A T A T D N A S A K^{67}
z11 z10 z8 z7 z6 z5 z4
Relative Abundance
m/z
0
10
20
30
40
50
60
70
80
90
100
400
600
800
1000
1200
1400
1600
1800
2000
[MH^{+3}] 855.83
[MH^{+2}-HexNAc] 1182.00
[MH^{+2}] 1283.33
z′3 290.25
z′4 361.00
z·5 474.25
z·6 589.08
z′7 691.33
z·8 761.33
z·10 933.50
z·11 1046.42
c′4 1405.42
c′5 1520.33
c′7 1704.17
c′8 1805.75
c′10 1978.33


acinetobacter baumannii 19606
Precursor charge: +3
Precursor m/z: 951.73907
Peptide mass (MH+): 2853.19762
58S A G D Q A A S D I A T A T D N A S A K67
c6
c10
c11
z12
z11
z9
z8
z7
z6
z5
z4
y3
Relative Abundance
m/z
0
10
20
30
40
50
60
70
80
90
100
400
600
800
1000
1200
1400
1600
1800
2000
y′3 305.25
z·4 360.00
y′4 376.58
z·5 474.25
c′6 547.08
z·6 590.42
z·7 691.25
z·8 762.17
z·9 863.25
[MH+3] 952.00
z·11 1046.17
z·12 1162.67
[MH+2-HexNAc] 1326.25
[MH+2] 1427.17
[peptide] 1865.00
c′10 1921.58
c′11 1992.92


acinetobacter baumannii 19606
Precursor charge: +3
Precursor m/z: 965.74292
Peptide mass (MH+): 2895.21398
c4
c6
c7
c8
c9
58SAGDQAASDIATATDNASAK67
z11
z10
z9
z8
z6
z5
z4
z3
Relative Abundance
m/z
0
10
20
30
40
50
60
70
80
90
100
200
400
600
800
1000
1200
1400
1600
1800
2000
z·3 290.33
c′4 348.00
z·4 360.08
z·5 474.17
c′6 547.08
z·6 589.00
c′7 618.08
z·8 761.33
z·9 862.50
y′9 878.50
z·10 933.42
[MH+3] 966.00
z·11 1047.25
[MH+2-HexNAc] 1346.587
[MH+2] 1447.90
c′8 1735.67
c′9 1850.00
[peptide] 1865.83

Supplementary Table 10B: Glycosylation site localisation in *Acinetobacter baumannii* (strain ATCC19606)

Uniprot accession number	Site localisation	five amino acid each side of the site
D0C6C0_ACIBA	S_{186}	EQKAASEPEQK
D0C6Q2_ACIBA	S_{45}^{+}	VETAVSEPQPQ
D0C7T4_ACIBA	S_{40}^{+}	GQDAASTAVAD
D0C8B9_ACIBA	S_{35}^{+}	GMHEASDPATS
D0CAB8_ACIBA	S_{306}^{+}	KAKPASAPAVK
D0CA69_ACIBA	S_{34}	AAGAASEAVAA
D0CA69_ACIBA	S_{78}	SDVAASAAH--
D0CAB8_ACIBA	S_{120}^{+}	KKTEASAAAAT
D0CDA9_ACIBA	S_{123}	PAPVASQAK--
D0CDQ9_ACIBA	S_{49}^{+}	DEQPASSASVK
D0CEI7_ACIBA	S_{55}^{+}	GDQAASDIATA



Supplementary table 10B: Glycosylation site localization in *A. baumannii* ATCC19606. Identifications are labeled according to the corresponding Uniprot accession number within strain ATCC19606. The site and residue of localization are denoted with + indicating sites localized by ETD. To enable assessment of the local environment of glycosylation five amino acids either side of the site of modification are provided.