Supplemental data

Supplemental Table 1

Alphabetical list of all tri-deuteroacetylated, internal peptides that were only present in the digested proteome of mouse caspase-3- and/or mouse caspase-7-treated mouse Mf4/4 lysates. Sequence, number of identified spectra (spectra no.), m/z, z, error (Da), threshold, highest Mascot ion score, Δ threshold and *e* value of the identified spectra with highest Mascot ion score are given.

Supplemental Table 2

List of unique caspase-7 and -3 processing events identified in recombinant caspase-7- or -3-treated macrophage lysates

The parent proteins are referred to by description (protein name), abbreviation (Abbr.), UniProt database accession number (accession No.), subcellular localization (subcell. local.) and molecular weight (M_r protein). Furthermore, the P6-P5' amino acids (cleavage site), the identified peptide, the molecular weight of the N- and C-terminal fragments generated upon cleavage of the parent protein (M_r fragments), the percentage of homology of the parent protein with its human ortholog, and the preservation of the cleavage site in the human ortholog are indicated. For known substrates, the reference is given, and newly identified cleavage sites are indicated as “new”. More detailed information on the human orthologous cleavage sites can be found in Supplemental Table 4.

Supplemental Table 3

List of all the neo-N-termini identified in the digested proteome of caspase-7 and -3

Peptides are classified according to the efficiency of their cleavage by caspase-7 compared to caspase-3, which is projected in the first column (statistically corrected C7/C3 ratio). The parent proteins are referred to by protein name and UniProt database accession number (Accession No.). Cleavage site, identified peptides and relevant references (for known caspase substrates) are indicated. Newly identified cleavage sites are indicated as “new.”

Supplemental Table 4

List of the 55 identified mouse caspase-7 and -3 cleavage sites and their corresponding cleavage sites in the human substrate orthologs

Protein substrates (abbreviated protein name) are listed alphabetically. UniProt entry name, cleavage sites (P1 residue is numbered) and the references for known substrates are given. Newly identified cleavage sites are indicated as “new.” Orthologous sites were extracted after performing a pairwise global alignment using the amino acid sequence of the identified substrates (Needleman-Wunsch; gap opening: 10.0, gap extension: 0.5, Blosum: 62 matrix).

Supplemental Table 1

Sequence	Spectra no.	m/z	z	Error (Da)	Threshold	Score of highest scoring spectra	Δ threshold	*e* value
AcD3-AAEDYAKER	2	574.7883	2	-0.0767	30	69	39	0.00001
AcD3-AAGVASLLTTAEAVVTEIPKEEKDPGM GAMGGMGGGMGGGMF	1	1050.2289	4	-0.0415	20	26	6	0.01258
AcD3-AAVADPDEFER	1	632.774	2	-0.0476	31	32	1	0.03973
AcD3-AAVPTNIIAAKAAEVR	1	842.903	2	-0.1875	31	47	16	0.00126
AcD3-AEAAMDISEGR	4	608.815	2	-0.0085	30	107	77	0.00000
AcD3-AGMAMAGQSPVLR	3	683.3322	2	-0.0121	30	57	27	0.00010
AcD3-AKAEEEFNIEKGR	3	831.4399	2	-0.0725	30	99	69	0.00000
AcD3-AMVKSVER	2	516.2888	2	-0.0728	31	58	27	0.00010
AcD3-ASSAVKVKR	3	543.8462	2	-0.0735	30	71	41	0.00000
AcD3-AVTEGAMPAATGKDQPPSTGKKKR	1	889.932	3	0.3576	36	41	5	0.01583
AcD3-CLPGLAKQPSFR	5	735.4077	2	-0.073	30	52	22	0.00032
AcD3-EDLENQTLR	1	582.7749	2	-0.0033	31	70	39	0.00001
AcD3-FAVEYFTR	2	542.2842	2	-0.0697	30	57	27	0.00010
AcD3-FLEGDQKPVER	1	704.444	2	0.1422	31	49	18	0.00080
AcD3-FPLSPPKKKDLSLEEIQKKLEAAEER	2	1100.6226	3	-0.0871	29	39	10	0.00501
AcD3-FSLADAINTEFKNTR	2	908.9656	2	-0.0107	30	89	59	0.00000
AcD3-FSQLLNCPEFVPR	3	826.4189	2	-0.0035	32	68	36	0.00001
AcD3-GADCIMLSGETAKGDYPLEAVR	2	820.3886	3	-0.0186	30	71	41	0.00000
AcD3-GEALSTLVLNR	4	612.3579	2	-0.0707	30	62	32	0.00003
AcD3-GEEQAEKTKGKR	2	770.881	2	-0.0808	31	52	21	0.00040
AcD3-GGDGQAGPDEGEVDSCLR	3	935.4052	2	-0.0686	27	97	70	0.00000
AcD3-GIVPDIAVGTKR	1	658.358	2	-0.0763	31	51	20	0.00050
AcD3-GKGVVVVMKR	2	612.351	2	-0.0543	30	55	25	0.00016
AcD3-GKPSASPQER	1	573.8047	2	1E-04	31	40	9	0.00631
AcD3-GKTEQKGGDKKR	1	778.968	2	0.0428	34	69	35	0.00002
AcD3-GKTLNDELEIIEGMKFDR	1	755.7221	3	-0.087	30	50	20	0.00050
AcD3-GKVESIMKR	4	599.875	2	0.0617	30	63	33	0.00003
AcD3-GKVTYGQKR	1	586.338	2	-0.0093	30	44	14	0.00200
AcD3-GKYSQVLANGLDNKLR	1	956.019	2	-0.0337	31	55	24	0.00020
AcD3-GLAVTPTPVPVVGSQMTR	5	935.941	2	-0.1387	30	53	23	0.00025
AcD3-GLLSQGYSDFINR	1	760.866	2	-0.1295	31	39	8	0.00794
AcD3-GLNASQIR	1	455.2632	2	-0.076	31	54	23	0.00025
AcD3-GPEQMELEEGKAGSGLR	1	947.4578	2	-0.0046	31	77	46	0.00000
AcD3-GQPGAFTCYLDAGLAR	3	871.426	2	0.0042	31	93	62	0.00000
AcD3-GQVITIGNER	6	569.8129	2	-0.0716	31	74	43	0.00000
AcD3-GTVEEDLGKSR	6	643.8311	2	-0.0915	30	62	32	0.00003
AcD3-GVMNGEYYQESNGPTDSYAAISEVDR	4	972.0705	3	-0.0428	23	98	75	0.00000
AcD3-IAVPKFKQR	1	611.392	2	0.0103	34	49	15	0.00159
AcD3-LFAIAKDSQKKTQR	5	907.525	2	-0.0133	31	70	39	0.00001
AcD3-LGGAVSLGDPLLLPAASESR	1	987.5508	2	-0.0761	31	59	28	0.00008
AcD3-MVNDGVEDLR	1	607.884	2	0.1087	31	54	23	0.00025

Supplemental Table 1 (continued)

Sequence	Spectra no.	m/z	z	Error (Da)	Threshold	Score of highest scoring spectra	Δ threshold	*e* value
AcD3-NGSGMCKAGFAGDDAPR	5	912.3651	2	-0.1335	25	91	66	0.00000
AcD3-NTEEKKSGLSVR	1	741.888	2	-0.0421	31	67	36	0.00001
AcD3-SFLAAAETLKER	1	716.45	2	0.0208	31	46	15	0.00159
AcD3-SGPPAKKIR	2	547.8477	2	-0.0756	30	71	41	0.00000
AcD3-SGQGPPAEEEEGEEEAAKEEAEAQGVR	1	1455.012	2	-0.3629	31	43	12	0.00316
AcD3-SLKEALTYDGALLGDR	3	906.418	2	-0.1369	31	67	36	0.00001
AcD3-SLVCKAGIIASAR	1	721.433	2	-0.0486	31	39	8	0.00794
AcD3-SQGPTPVCTPTFLER	1	867.945	2	0.0268	31	32	1	0.03973
AcD3-SSPDSKPKTR	1	619.3387	2	-0.0032	31	32	1	0.03973
AcD3-STAAQQELR	3	524.7723	2	-0.0088	31	65	34	0.00002
AcD3-STLAVQQYIQQNIR	2	856.912	2	-0.1961	31	60	29	0.00006
AcD3-TPAKNAQKSNQNGKDLKPSTPR	1	869.4599	3	-0.0349	30	69	39	0.00001
AcD3-VDGTVEEDLGKSR	2	750.771	2	-0.3071	31	45	14	0.00200
AcD3-YAKGFGGQYGIQKDR	1	911.911	2	-0.1285	31	85	54	0.00000

Supplemental Table 2

Caspase-7

Protein name	Abbr.	Accession Nr.	Subcell. Local.	M_r protein (kDa)	Cleavage site	Identified peptide	M_r fragments (kDa)	Protein homology with human orthologue	Cleavage site preserved in human orthologue	Status
40S ribosomal protein S18	Rps18	P62270	Cytoplasm	18	QKDVKD$_{92}$GKYSQ	GKYSQVLANGLDNKLR	11-7	100%	Yes	New
60S ribosomal protein L28	Rpl28	P41105	Cytoplasm	16	VEPAAD$_{56}$GKGVV	GKGVVVVMKR	9-7	98%	Yes	New
MKI67 FHA domain-interacting nucleolar phosphoprotein	Mki67ip	Q91VE6	Nucleus Nucleolus	36	KKSSVD$_{252}$SQGPT	SQGPTPVCTPTFLER	29-7	61%	No*	New
Nucleophosmin	Npm1	Q61937	Nucleus Nucleolus	33	KKSVRD$_{197}$TPAKN	TPAKNAQKSNQNGKDLKPSTPR	22-11	94%	No*	(1)
Probable rRNA-processing protein EBP2	Ebp2	Q9D903	Nucleus Nucleolus	35	FSDKLD$_{211}$FLEGD	FLEGDQKPVER	24-11	83%	Yes	New
Myb-binding protein 1A	Mybbp1a	Q7TPV4	Nucleolus Cytoplasm	152	AASQQD$_{1201}$AVTEG	AVTEGAMPAATGKDQPPSTGKKKR	137-15	69%	No*	New

Caspase-3

Protein name	Abbr.	Accession Nr.	Subcell. Local.	M_r protein (kDa)	Cleavage site	Identified peptide	M_r fragments (kDa)	Protein homology with human orthologue	Cleavage site preserved in human orthologue	Status
Hepatoma-derived growth factor	Hdgf	P51859	Cytoplasm	26	TPSEPD$_{205}$SGQGP	SGQGPPAEEEEGEEEAAKEEAEAQGVR	16-10	89%	No*	New
Nuclear ubiquitous casein and cyclin-dependent kinases substrate	Nucks1	Q80XU3	Nucleus	26	EDYGRD$_{29}$SGPPA	SGPPAKKIR	23-3	95%	Yes	(2, 3)
Glutathione S-transferase P1	Gstp1	P19157	Cytoplasm	24	EAAQMD$_{91}$MVNDG	MVNDGVEDLR	11-13	85%	No*	New

Supplemental Table 3

C7/C3 ratio	Protein name	Abbr.	Accession Nr.	Cleavage site	Identified peptide	Status
4.5/1	Coiled-coil domain-containing protein 137	CCDC137	Q8R0K4	KGEEPD$_{108}$IAVPK	IAVPKFKQR	New
4.0/1	Kinesin-associated protein 3	Kifap3	P70188	KKKAVD$_{249}$EDLEN	EDLENQTLR	New
3.8/1	WW domain-binding protein 11	Wbp11	Q923D5	EDSERD$_{297}$NTEEK	NTEEKKSGLSVR	New
3.2/1	Short isoform of heterogeneous nuclear ribonucleoprotein U	Hnrnpu	O88568	QQAGGD$_{206}$GKTEQ	GKTEQKGGDKKR	(4)
2.7/1	Heat shock protein 60	Hsp60	P63038	RTALLD$_{531}$AAGVA	AAGVASLLTTAEAVVTEIPKEEKD PGMGAMGGMGGGMGGGMF	(2, 3, 5)
1.9/1	60S ribosomal protein L5	Rpl5	P47962	NVESID$_{135}$GQPGA	GQPGAFTCYLDAGLAR	New
1.9/1	Vacuolar ATP synthase subunit H	VATH	Q8BVE3	IRGAVD$_{11}$AAVPT	AAVPTNIIAAKAAEVR	New
1.9/1	Hypothetical RNA-binding protein Lupus Lal	Larp1	Q6ZQ58	DYSQTD$_{472}$FSQLL	FSQLLNCPEFVPR	New
1.6/1	Serine/arginine repetitive matrix protein 2	Srrm2	Q8BTI8	ERSESD$_{1516}$SSPDS	SSPDSKPKTR	New
1.2/1	Pyruvate kinase isozymes M1/M2	Pkm2	P52480	ANAVLD$_{354}$GADCI	GADCIMLSGETAKGDYPLEAVR	New
1.2/1	ATP-dependent RNA helicase DDX1	Ddx1	Q91VR5	PVDEFD$_{685}$GKVTY	GKVTYGQKR	(2)
1.2/1	Cytosolic phospholipase A2	cPLA2	P47713	FDDELD$_{521}$AAVAD	AAVADPDEFER	(4-8)
1.1/1	Craniofacial development protein 1	Cfdp1	O88271	KEDEVD$_{40}$GEEQA	GEEQAEKTKGKR	New
1.1/1	Clathrin light chain A	Clta	O08585	GPDAVD$_{75}$GVMNG	GVMNGEYYQESNGPTDSYAAISEVDR	New
1/1.1	26S protease regulatory subunit 8	PRS8	P62196	xxMALD$_{4}$GPEQM	GPEQMELEEGKAGSGLR	New
1/1.1	Actin, aortic smooth muscle	Acta2	P62737	SYELPD$_{246}$GQVIT	GQVITIGNER	(5, 9, 10)
1/1.1	Protein FAM21	Fam21	Q6PGL7	DDDEVD$_{668}$LFAIA	LFAIAKDSQKKTQR	New
1/1.1	Polypyrimidine tract-binding protein 1	Ptbp1	P17225	xxxxMD$_{2}$GIVPD	GIVPDIAVGTKR	(2, 11)
1/1.2	TAR DNA-binding protein 43	Tardbp	Q921F2	KMDETD$_{89}$ASSAV	ASSAVKVKR	(2, 4)
1/1.3	Splicing factor U2AF 65 kDa subunit	U2af2	P26369	PTMTPD$_{128}$GLAVT	GLAVTPTPVPVVGSQMTR	(2, 4)
1/1.3	Serine/arginine repetitive matrix protein 2	Srrm2	Q8BTI8	SSQELD$_{1502}$GKPSA	GKPSASPQER	New
1/1.6	Heat shock protein 60	Hsp60	P63038	VITVKD$_{203}$GKTLN	GKTLNDELEIIEGMKFDR	(2, 3, 5)
1/2.1	Polypyrimidine tract-binding protein 1	Ptbp1	P17225	SAAAVD$_{171}$AGMAM	AGMAMAGQSPVLR	(2, 3, 11)
1/2.2	Vimentin	Vim	P20152	LQDSVD$_{85}$FSLAD	FSLADAINTEFKNTR	(2-4)
1/2.6	Protein FAM136A	Fam136a	Q9CR98	VQEAVD$_{14}$AMVKS	AMVKSVER	New
1/2.7	Myosin-9	Myh9	Q8VDD5	LEDTLD$_{1153}$STAAQ	STAAQQELR	(2, 4, 12, 13)
1/2.7	Lysosomal protective protein	Ppgb	P16675	DQDEID$_{31}$CLPGL	CLPGLAKQPSFR	New
1/2.8	Vacuolar ATP synthase subunit E 1	Atp6v1e1	P50518	KAEEID$_{31}$AKAEE	AKAEEEFNIEKGR	New
1/2.9	Eukaryotic translation initiation factor 4H	Eif4h	Q9WUK2	EFDEVD$_{92}$SLKEA	SLKEALTYDGALLGDR	(2, 3, 5)
1/2.9	Vacuolar ATP synthase catalytic subunit A	Atp6v1a	P50516	LTMEVD$_{299}$GKVES	GKVESIMKR	New
1/3.3	Aspartyl-tRNA synthetase, cytoplasmic	Dars	Q922B2	PREIVD$_{19}$AAEDY	AAEDYAKER	New
1/3.1	Phosphoribosyl pyrophosphate synthetase-associated protein 2	Prpsap2	Q8R574	IIDDVD$_{276}$SFLAA	SFLAAAETLKER	New
1/3.7	HS1 binding protein 3	Hs1bp3	Q3TC93	LFDDPD$_{274}$LGGAV	LGGAVSLGDPLLLPAASESR	New
1/4.0	Actin-related protein 2/3 complex subunit 5	Arpc5	Q9CPW4	FVDEED$_{29}$GGDGQ	GGDGQAGPDEGEVDSCLR	New
1/4.8	Hematopoietic lineage cell-specific protein	Hcls1	P49710	HESQRD$_{189}$YAKGF	YAKGFGGQYGIQKDR	(2)
1/4.8	Actin, cytoplasmic 1	Actb	P60710	AALVVD$_{11}$NGSGM	NGSGMCKAGFAGDDAPR	(5, 9, 10)
1/5.0	Endoplasmin	Hsp90b1	P08113	DEVDVD$_{28}$GTVEE	GTVEEDLGKSR	(2, 4)
1/5.6	Heat shock protein 60	Hsp60	P63038	IAEDVD$_{279}$GEALS	GEALSTLVLNR	(2, 3, 5)
1/5.6	Preimplantation protein 3	Mobkl3	Q6PEB6	SFDEMD$_{34}$STLAV	STLAVQQYIQQNIR	New
1/5.9	cAMP-dependent protein kinase type II-alpha regulatory subunit	Prkar2a	P12367	PPDLVD$_{30}$FAVEY	FAVEYFTR	New
1/6.3	Stathmin	Stmn1	P54227	KESVPD$_{34}$FPLSP	FPLSPPKKKDLSLEEIQKKLEAAEER	New
1/6.7	Endoplasmin	Hsp90b1	P08113	EAIQLD$_{59}$GLNAS	GLNASQIR	(2)
1/7.7	ATP-dependent RNA helicase DDX1	Ddx1	Q91VR5	VLDEAD$_{373}$GLLSQ	GLLSQGYSDFINR	(2)
1/9.1	Ubiquitin carboxyl-terminal hydrolase 5	Usp5	P56399	HIDDLD$_{767}$AEAAM	AEAAMDISEGR	New
1/11.1	Endoplasmin	Hsp90b1	P08113	ADDEVD$_{26}$VDGTV	VDGTVEEDLGKSR	(2, 4, 5)
1/12.5	Elongation factor 2	Eef2	P58252	KSTLTD$_{37}$SLVCK	SLVCKAGIIASAR	New

Supplemental Table 4

Protein	Uniprot ID	Cleavage site	P1	Status
Acta2	ACTA_MOUSE	SLEKSYELPD$_{246}$GQVITIGNER	D	(5)
	ACTA_HUMAN	SLEKSYELPD$_{246}$GQVITIGNER	D	
Actb	ACTB_MOUSE	DDDIAALVVD$_{11}$NGSGMCKAGF	D	(5)
	ACTB_HUMAN	DDDIAALVVD$_{11}$NGSGMCKAGF	D	
Arpc5	ARPC5_MOUSE	DENKFVDEED$_{29}$GGDGQAGPDE	D	New
	ARPC5_HUMAN	DENKFVDEED$_{29}$GGDGQAGPDE	D	
Atp6v1a	VATA_MOUSE	DFPELTMEVD$_{299}$GKVESIMKRT	D	New
	VATA_HUMAN	DFPELTMEVD$_{299}$GKVESIMKRT	D	
Atp6v1e1	VATE1_MOUSE	EANEKAEEID$_{31}$AKAEEEFNIE	D	New
	VATE1_HUMAN	EANEKAEEID$_{31}$AKAEEEFNIE	D	
CCDC137	CC137_MOUSE	EKEAKGEEPD$_{108}$IAVPKFKQRK	D	New
	CC137_HUMAN	EKEAKGEEPD$_{108}$IAVPKFKQRK	D	
Cfdp1	CFDP1_MOUSE	NELVKEDEVD$_{40}$GEEQAEKTKG	D	New
	CFDP1_HUMAN	NELVKEDEVD$_{40}$GEEQTQKTQG	D	
Clta	CLCA_MOUSE	RAGGGPDAVD$_{75}$GVMNGEYYQE	D	New
	CLCA_HUMAN	EPPGGPDAVD$_{76}$GVMNGEYYQE	D	
cPLA2	PA24A_MOUSE	QDSFDD-ELD$_{521}$AAVADPDEFE	D	(5)
	PA24A_HUMAN	QDSFDDDELD$_{522}$AAVADPDEFE	D	(4)
Dars	SYDC_MOUSE	GQEKPREIVD$_{19}$AAEDYAKERY	D	New
	SYDC_HUMAN	SQEKPREIMD$_{19}$AAEDYAKERY	D	
Ddx1	DDX1_MOUSE	DIKVPVDEFD$_{685}$GKVTYGQKRA	D	New
	DDX1_HUMAN	DIKVPVDEFD$_{685}$GKVTYGQKRA	D	(2)
	DDX1_MOUSE	VRFLVLDEAD$_{373}$GLLSQGYSDF	D	New
	DDX1_HUMAN	VRFLVLDEAD$_{373}$GLLSQGYSDF	D	
Ebp2	EBP2_MOUSE	YQKGFSDKLD$_{211}$FLEGDQKPV-	D	New
	EBP2_HUMAN	YQKGFSDKLD$_{211}$FLEGDQKPLA	D	
Eef2	EF2_MOUSE	VDHGKSTLTD$_{37}$SLVCKAGIIA	D	New
	EF2_HUMAN	VDHGKSTLTD$_{37}$SLVCKAGIIA	D	
Eif4h	IF4H_MOUSE	FCYVEFDEVD$_{92}$SLKEALTYDG	D	(5)
	IF4H_HUMAN	FCYVEFDEVD$_{93}$SLKEALTYDG	D	(2, 3)
Fam21	FAM21_MOUSE	FEDDDDDEVD$_{668}$LFAIAKDSQK	D	New
	FAM21_HUMAN	SLFEEDKEDD$_{664}$LFAIAKDSQK	D	
Fam136a	F136A_MOUSE	QQLRVQEAVD$_{14}$AMVKSVEREN	D	New
	F136A_HUMAN	QQLRVQEAVE$_{14}$SMVKSLEREN	E	
Gstp1	GSTP1_MOUSE	KNQREAAQMD$_{91}$MVNDGVEDLR	D	New
	GSTP1_HUMAN	KDQQEAALVD$_{91}$MVNDGVEDLR	D	
Hcls1	HCLS1_MOUSE	ETEKHESQRD$_{189}$YAKGFGGQYG	D	New
	HCLS1_HUMAN	ETEKHESQRD$_{189}$YAKGFGGQYG	D	(2)
Hdgf	HDGF_MOUSE	EKNSTPSEPD$_{205}$SGQGPPAEEE	D	New
	HDGF_HUMAN	EKNSTPSEPG$_{205}$SGRGPPQEEE	G	
Hnrnpu	O88568_MOUSE	RQGQQQAGGD$_{206}$GKTEQKGGDK	D	New
	HNRPU_HUMAN	GGRPGAPAGD$_{231}$GKTEQKGGDK	D	(4)
Hs1bp3	H1BP3_MOUSE	DSLKLFDDPD$_{274}$LGGAVSLGDP	D	New
	H1BP3_HUMAN	DPLKLFDDPD$_{270}$LGGAIPLGDS	D	
Hsp60	CH60_MOUSE	GRKGVITVKD$_{203}$GKTLNDELEI	D	New
	CH60_HUMAN	GRKGVITVKD$_{203}$GKTLNDELEI	D	
	CH60_MOUSE	PLVIIAEDVD$_{279}$GEALSTLVLN	D	New
	CH60_HUMAN	PLVIIAEDVD$_{279}$GEALSTLVLN	D	
	CH60_MOUSE	TKVVRTALLD$_{531}$AAGVASLLTT	D	New
	CH60_HUMAN	TKVVRTALLD$_{531}$AAGVASLLTT	D	

Supplemental Table 4 (continued)

Protein	Uniprot ID	Cleavage site	P1	Status
Hsp90b1	ENPL_MOUSE	GFVRADDEVD$_{26}$VDGTVEEDLG	D	(5)
	ENPL_HUMAN	GSVRADDEVD$_{26}$VDGTVEEDLG	D	(4)
	ENPL_MOUSE	VRADDEVDVD$_{28}$GTVEEDLGKS	D	New
	ENPL_HUMAN	VRADDEVDVD$_{28}$GTVEEDLGKS	D	(2, 4)
	ENPL_MOUSE	QREEEAIQLD$_{59}$GLNASQIREL	D	New
	ENPL_HUMAN	QREEEAIQLD$_{59}$GLNASQIREL	D	
Kifap3	KIFA3_MOUSE	ELSKKKKAVD$_{249}$EDLENQTLRK	D	New
	KIFA3_HUMAN	ELSKKKKAVD$_{249}$EDPENQTLRK	D	
Larp1	LARP1_MOUSE	PPIVDYSQTD$_{472}$FSQLLNCPEF	D	New
	LARP1_HUMAN	PPIVDYSQTD$_{495}$FSQLLNCPEF	D	
Mki67ip	MK67I_MOUSE	RSRRKKSSVD$_{252}$SQGPTPVCTP	D	New
	MK67I_HUMAN	-T-PEK-TVD$_{229}$SQGPTPVCTP	D	
Mobkl3	MOBL3_MOUSE	WPDESFDEMD$_{34}$STLAVQQYIQ	D	New
	MOBL3_HUMAN	WPDESFDEMD$_{34}$STLAVQQYIQ	D	
Mybbp1a	MBB1A_MOUSE	PEKNAASQQD$_{1201}$AVTEGAMPAA	D	New
	MBB1A_HUMAN	P----A--ED$_{1194}$----GT-PAA	D	
Myh9	MYH9_MOUSE	LKTELEDTLD$_{1153}$STAAQQELRS	D	New
	MYH9_HUMAN	LKTELEDTLD$_{1153}$STAAQQELRS	D	(2, 4)
Npm1	NPM_MOUSE	KVPVKKSVRD$_{197}$TPAKNAQKSN	D	New
	NPM_HUMAN	KAPVKKSIRD$_{198}$TPAKNAQKSN	D	
Nucks1	NUCKS_MOUSE	DDADEDYGRD$_{29}$SGPPAKKIRS	D	New
	NUCKS_HUMAN	DDADEDYGRD$_{29}$SGPPTKKIRS	D	(2, 3)
Pkm2	KPYM_MOUSE	GSDVANAVLD$_{354}$GADCIMLSGE	D	New
	KPYM_HUMAN	GSDVANAVLD$_{354}$GADCIMLSGE	D	
Ppgb	PPGB_MOUSE	EAAPDQDEID$_{31}$CLPGLAKQPS	D	New
	PPGB_HUMAN	EAAPDQDEIQ$_{36}$RLPGLAKQPS	Q	
Prkar2a	KAP2_MOUSE	-GQQPPDLVD$_{30}$FAVEYFTRLR	D	New
	KAP2_HUMAN	LRQQPPDLVE$_{31}$FAVEYFTRLR	D	
Prpsap2	KPRB_MOUSE	IVDDIIDDVD$_{276}$SFLAAAETLK	D	New
	KPRB_HUMAN	IVDDIIDDVD$_{276}$SFLAAAETLK	D	
PRS8	PRS8_MOUSE	xxxxxxMALD$_{4}$GPEQMELEEG	D	New
	PRS8_HUMAN	xxxxxxMALD$_{4}$GPEQMELEEG	D	
Ptbp1	PTBP1_MOUSE	xxxxxxxxMD$_{2}$GIVPDIAVGT	D	New
	PTBP1_HUMAN	xxxxxxxxMD$_{2}$GIVPDIAVGT	D	(2)
	PTBP1_MOUSE	ALAASAAAVD$_{171}$AGMAMAGQSP	D	New
	PTBP1_HUMAN	ALAASAAAVD$_{172}$AGMAMAGQSP	D	(2, 3)
Rpl5	RL5_MOUSE	NGGEYNVESID$_{136}$DGQPGAFTCY	D	New
	RL5_HUMAN	TGDEYNVESID$_{136}$DGQPGAFTCY	D	
Rpl28	RL28_MOUSE	KTVGVEPAAD$_{56}$GKGVVVVMKR	D	New
	RL28_HUMAN	KTVGVEPAAD$_{56}$GKGVVVVIKR	D	
Rps18	RS18_MOUSE	FLNRQKDVKD$_{92}$GKYSQVLANG	D	New
	RS18_HUMAN	FLNRQKDVKD$_{92}$GKYSQVLANG	D	
Srrm2	SRRM2_MOUSE	SRSGSSQELD$_{1502}$GKPSASPQER	D	New
	SRRM2_HUMAN	SRSGSSQELD$_{1546}$VKPSASPQER	D	
	SRRM2_MOUSE	ASPQERSESD$_{1516}$SSPDSKPKTR	D	New
	SRRM2_HUMAN	ASPQERSESD$_{1560}$SSPDSKAKTR	D	
Stmn1	STMN1_MOUSE	SPRSKESVPD$_{34}$FPLSPPKKKD	D	New
	STMN1_HUMAN	SPRSKESVPE$_{34}$FPLSPPKKKD	E	
Tardbp	TADBP_MOUSE	DNKRKMDETD$_{89}$ASSAVKVKRA	D	New
	TADBP_HUMAN	DNKRKMDETD$_{89}$ASSAVKVKRA	D	(2, 4)

Supplemental Table 4 (continued)

Protein	Uniprot ID	Cleavage site	P1	Status
U2af2	U2AF2_MOUSE	TALLPTMTPD$_{128}$GLAVTPTPVP	D	New
	U2AF2_HUMAN	TALLPTMTPD$_{128}$GLAVTPTPVP	D	(2, 4)
Usp5	UBP5_MOUSE	WIFSHIDDLD$_{767}$AEAAMDISEG	D	New
	UBP5_HUMAN	WIFSHIDDLD$_{767}$AEAAMDISEG	D	
VATH	VATH_MOUSE	TKMDIRGAVD$_{11}$AAVPTNIIAA	D	New
	VATH_HUMAN	TKMDIRGAVD$_{11}$AAVPTNIIAA	D	
Vim	VIME_MOUSE	GVRLLQDSVD$_{85}$FSLADAINTE	D	New
	VIME_HUMAN	GVRLLQDSVD$_{85}$FSLADAINTE	D	(2-4)
Wbp11	WBP11_MOUSE	FGHREDSERD$_{297}$NTEEKKSGLS	D	New
	WBP11_HUMAN	FVHRDNGERD$_{297}$NNEEKKSGLS	D	

References of Supplemental Tables

1. Thiede, B., et al., *Shotgun proteome analysis of protein cleavage in apoptotic cells.* Proteomics, 2005. **5**(8): p. 2123-30.
2. Van Damme, P., et al., *Caspase-specific and nonspecific in vivo protein processing during Fas-induced apoptosis.* Nat Methods, 2005. **2**(10): p. 771-7.
3. Impens, F., et al., *Mechanistic insight into taxol-induced cell death.* Oncogene, 2008. **27**(33): p. 4580-91.
4. Gausdal, G., et al., *Abolition of stress-induced protein synthesis sensitizes leukemia cells to anthracycline-induced death.* Blood, 2008. **111**(5): p. 2866-77.
5. Lamkanfi, M., et al., *Targeted peptidecentric proteomics reveals caspase-7 as a substrate of the caspase-1 inflammasomes.* Mol Cell Proteomics, 2008. **7**(12): p. 2350-63.
6. Adam-Klages, S., et al., *Caspase-mediated inhibition of human cytosolic phospholipase A2 during apoptosis.* J Immunol, 1998. **161**(10): p. 5687-94.
7. Atsumi, G., et al., *Fas-induced arachidonic acid release is mediated by Ca2+-independent phospholipase A2 but not cytosolic phospholipase A2, which undergoes proteolytic inactivation.* J Biol Chem, 1998. **273**(22): p. 13870-7.
8. Luschen, S., et al., *Cleavage of human cytosolic phospholipase A2 by caspase-1 (ICE) and caspase-8 (FLICE).* Biochem Biophys Res Commun, 1998. **253**(1): p. 92-8.
9. Kayalar, C., et al., *Cleavage of actin by interleukin 1 beta-converting enzyme to reverse DNase I inhibition.* Proc Natl Acad Sci U S A, 1996. **93**(5): p. 2234-8.

10. Mashima, T., et al., *Actin cleavage by CPP-32/apopain during the development of apoptosis.* Oncogene, 1997. **14**(9): p. 1007-12.
11. Back, S.H., S. Shin, and S.K. Jang, *Polypyrimidine tract-binding proteins are cleaved by caspase-3 during apoptosis.* J Biol Chem, 2002. **277**(30): p. 27200-9.
12. Enoksson, M., et al., *Identification of proteolytic cleavage sites by quantitative proteomics.* J Proteome Res, 2007. **6**(7): p. 2850-8.
13. Gerner, C., et al., *The Fas-induced apoptosis analyzed by high throughput proteome analysis.* J Biol Chem, 2000. **275**(50): p. 39018-26.

Supplemental Figure 1

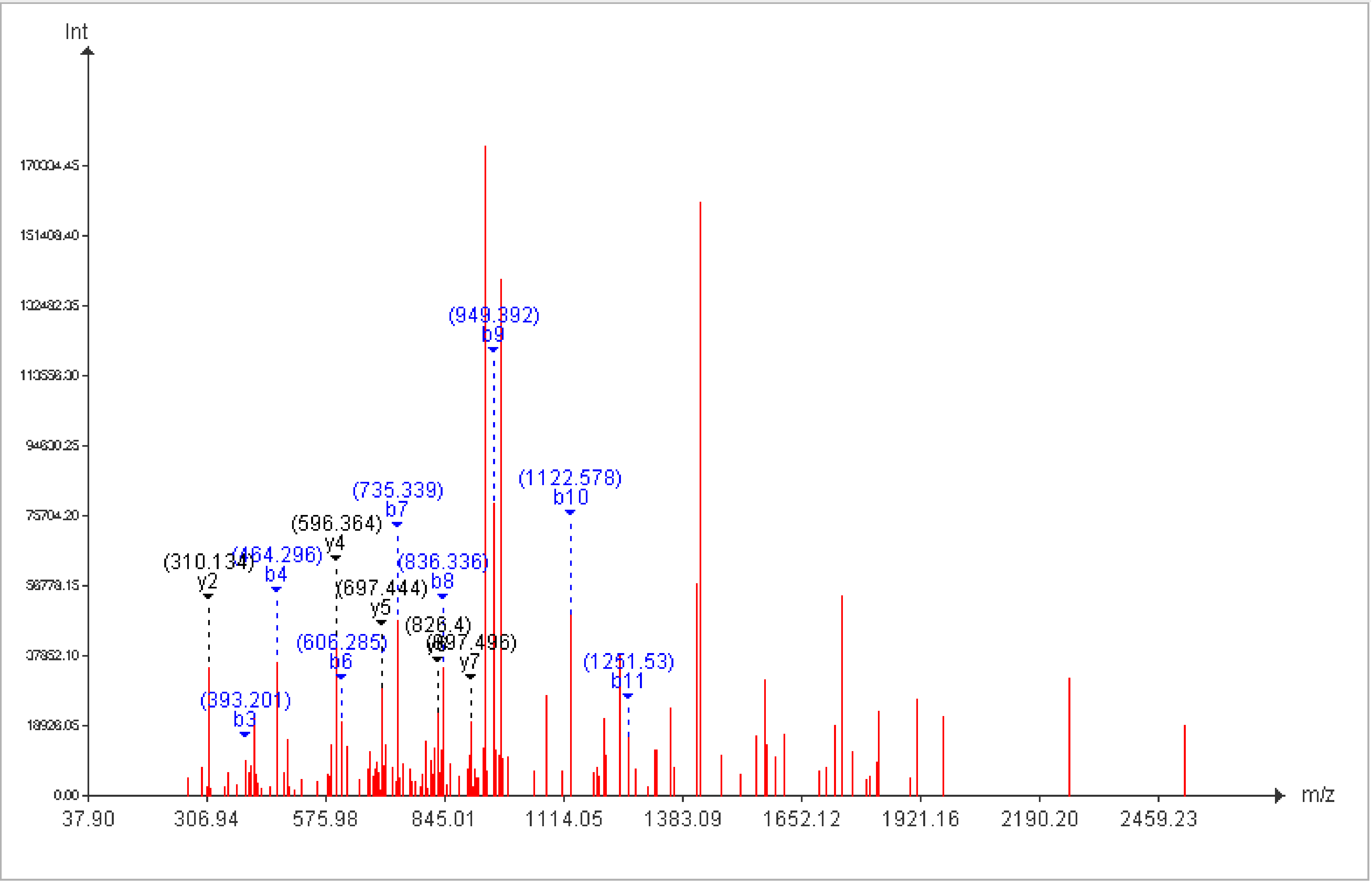
List of identified high scoring MS/MS spectra (n=55)

AcD3-SFLAAAETLK(AcD3K)ER(C13*)-COOH*

precursor mass: 716.4500 Da (charge: +2) protein: Q8R574 (277-288)

score (threshold): 46.0 (31.0)

instrument: Bruker Esquire HCT

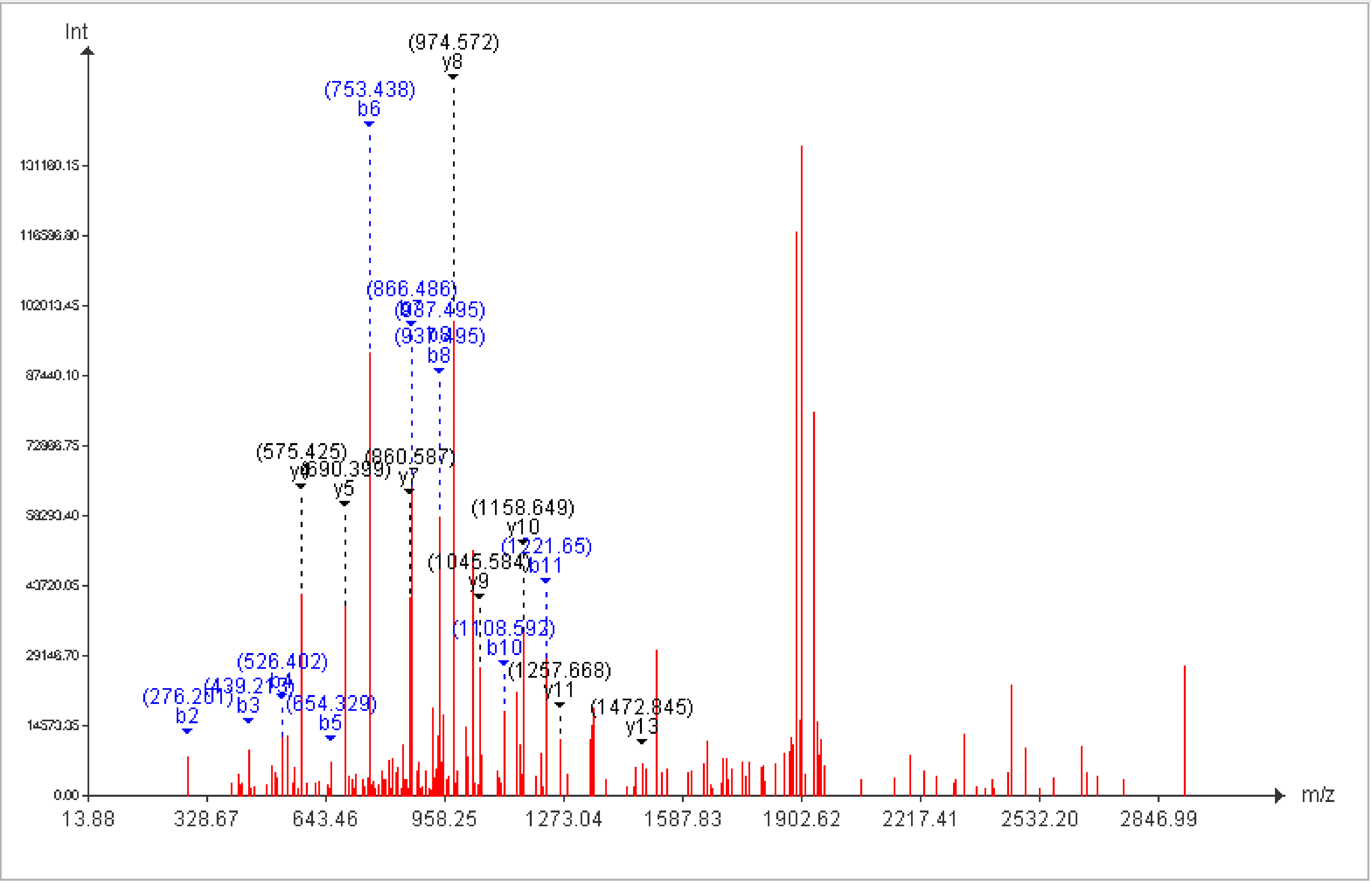


AcD3-GK(AcD3K)YSQVLANGLDNK(AcD3K*)LR-COOH*

precursor mass: 956.0190 Da (charge: +2) protein: P62270 (93-108)

score (threshold): 55.0 (31.0)

instrument: Bruker Esquire HCT

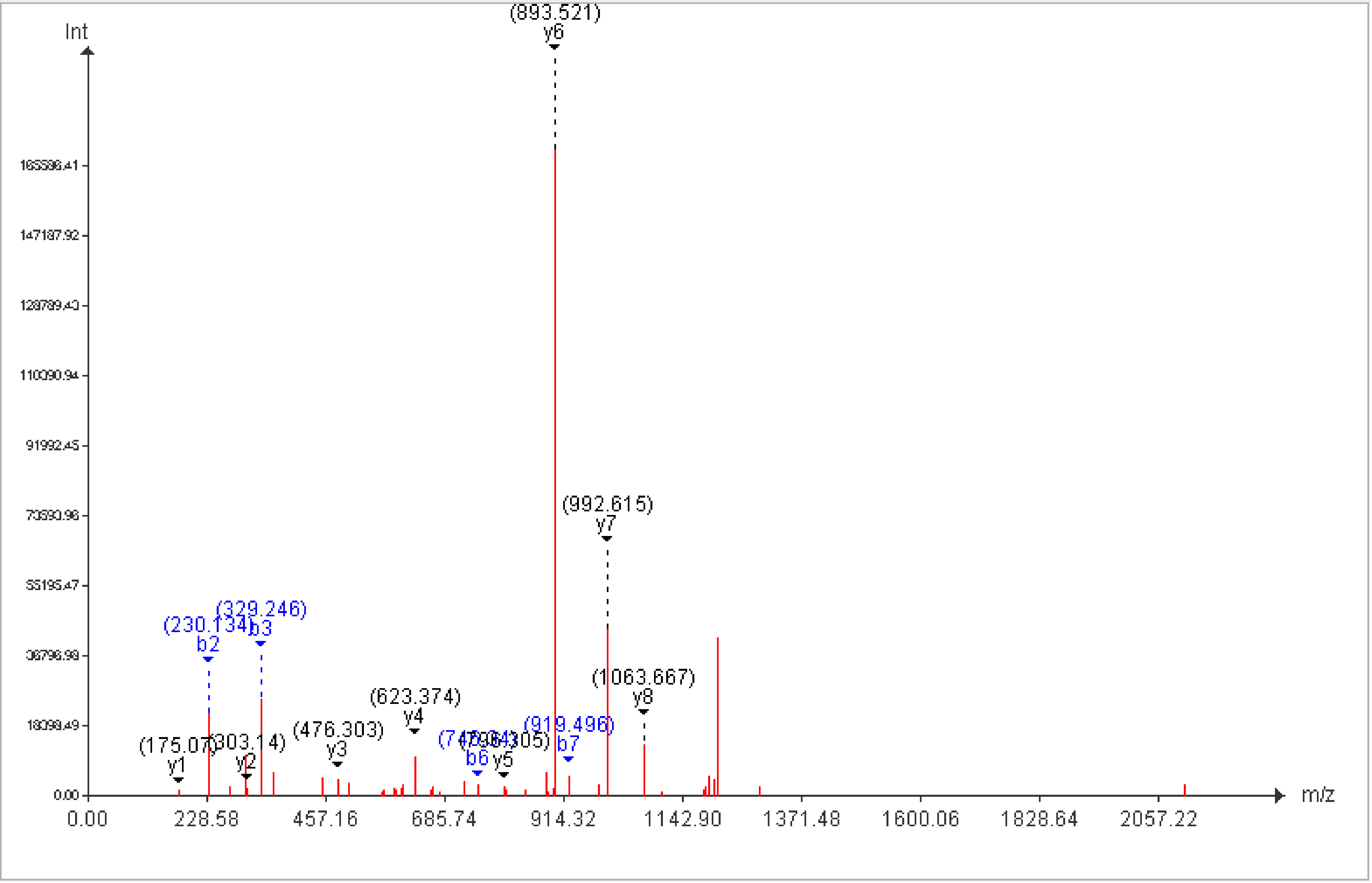


AcD3-IAVPK(AcD3K)FK(AcD3K*)QR-COOH*

precursor mass: 611.3920 Da (charge: +2) protein: IPI00401962.2 (109-117)

score (threshold): 49.0 (34.0)

instrument: Bruker Esquire HCT

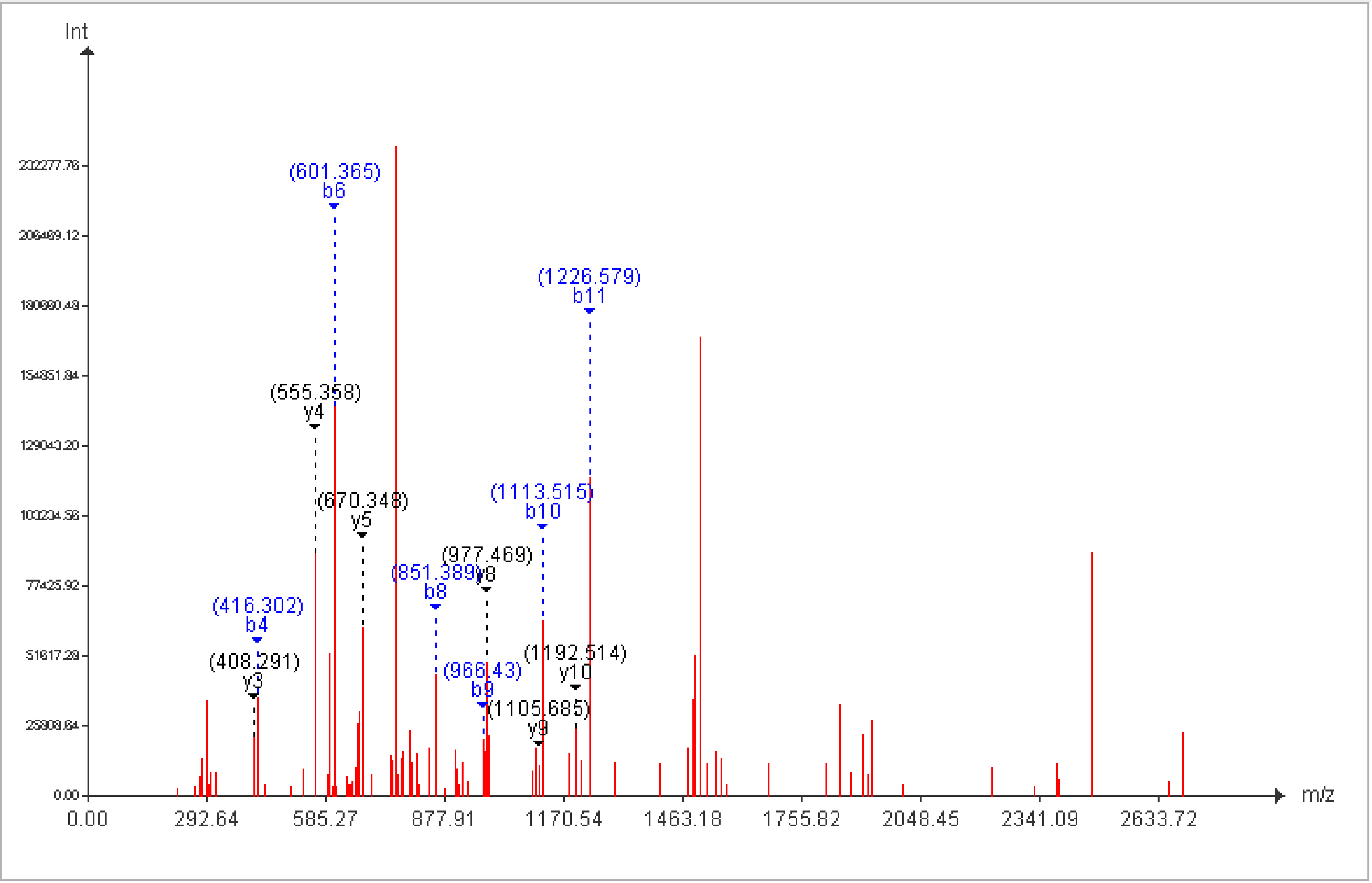


AcD3-GLLSQGYSDFINR(C13)-COOH*

precursor mass: 760.8660 Da (charge: +2) protein: Q91VR5 (374-386)

score (threshold): 39.0 (31.0)

instrument: Bruker Esquire HCT

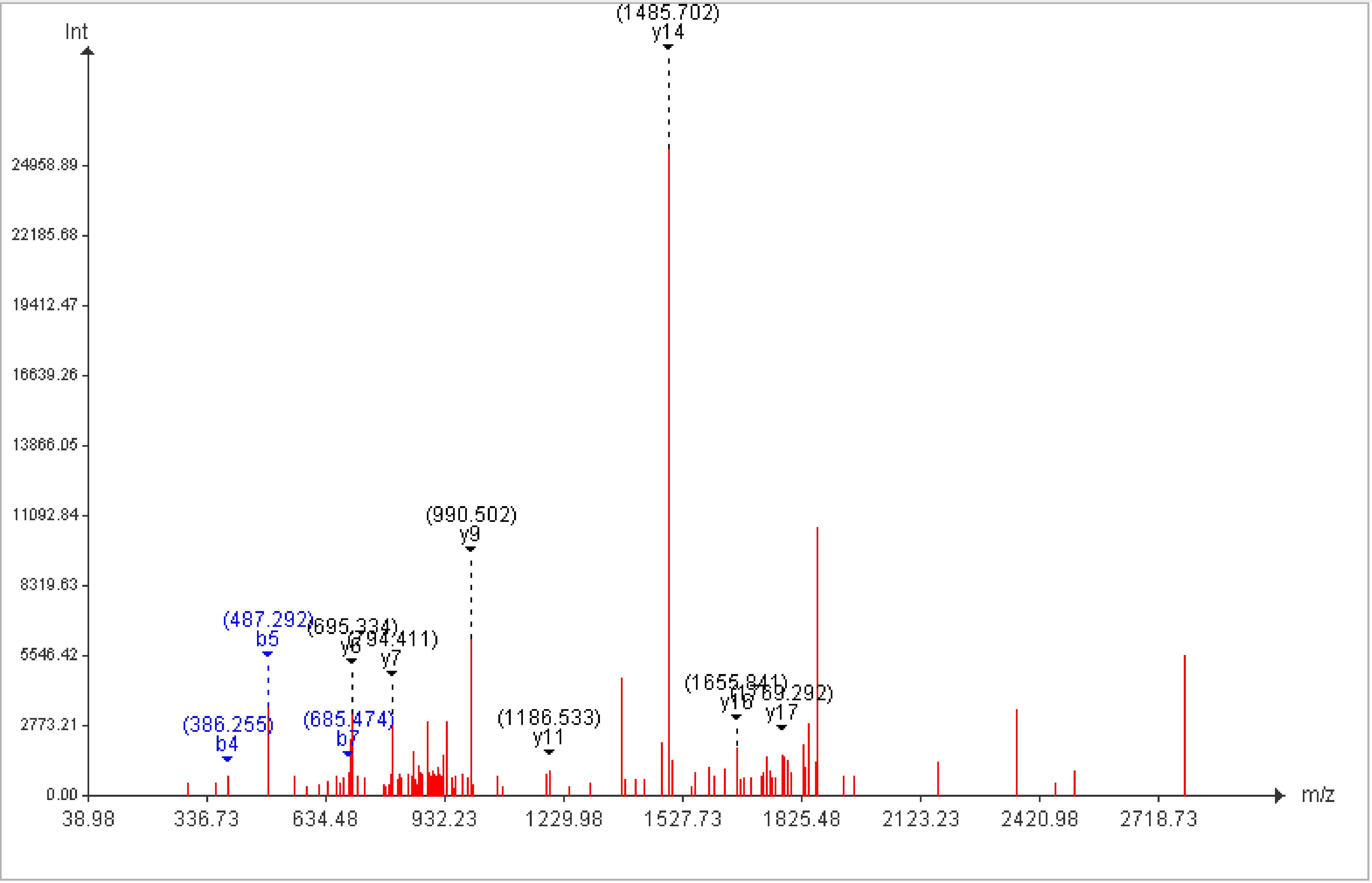


AcD3-GLAVTPTPVPVVGSQM(Mox)TR-COOH

precursor mass: 935.9410 Da (charge: +2) protein: P26369 (129-146)

score (threshold): 53.0 (31.0)

instrument: Bruker Esquire HCT

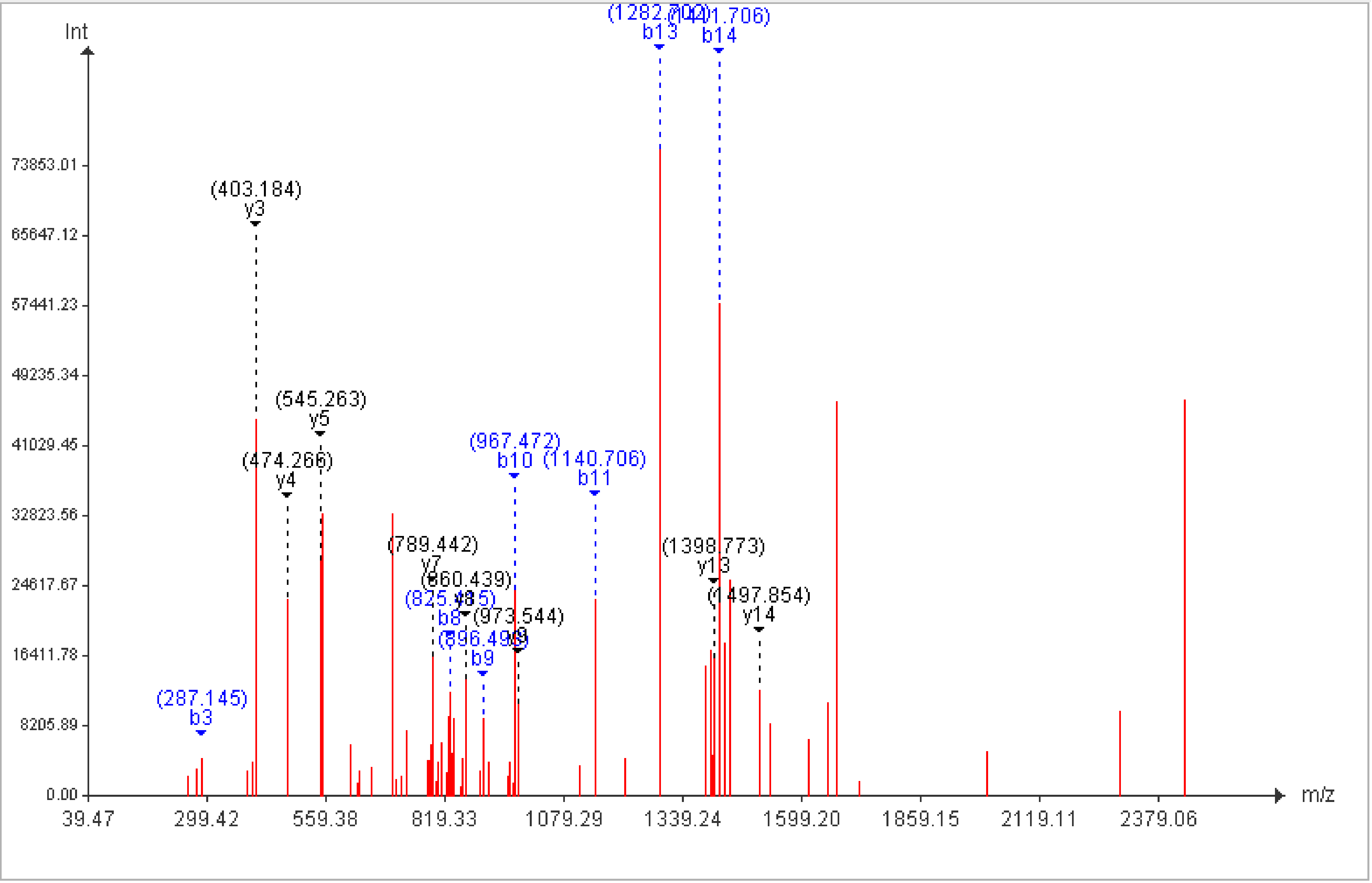


AcD3-AAVPTNIIAAK(AcD3K)AAEVR-COOH*

precursor mass: 842.9030 Da (charge: +2) protein: Q8BVE3 (12-27)

score (threshold): 47.0 (31.0)

instrument: Bruker Esquire HCT

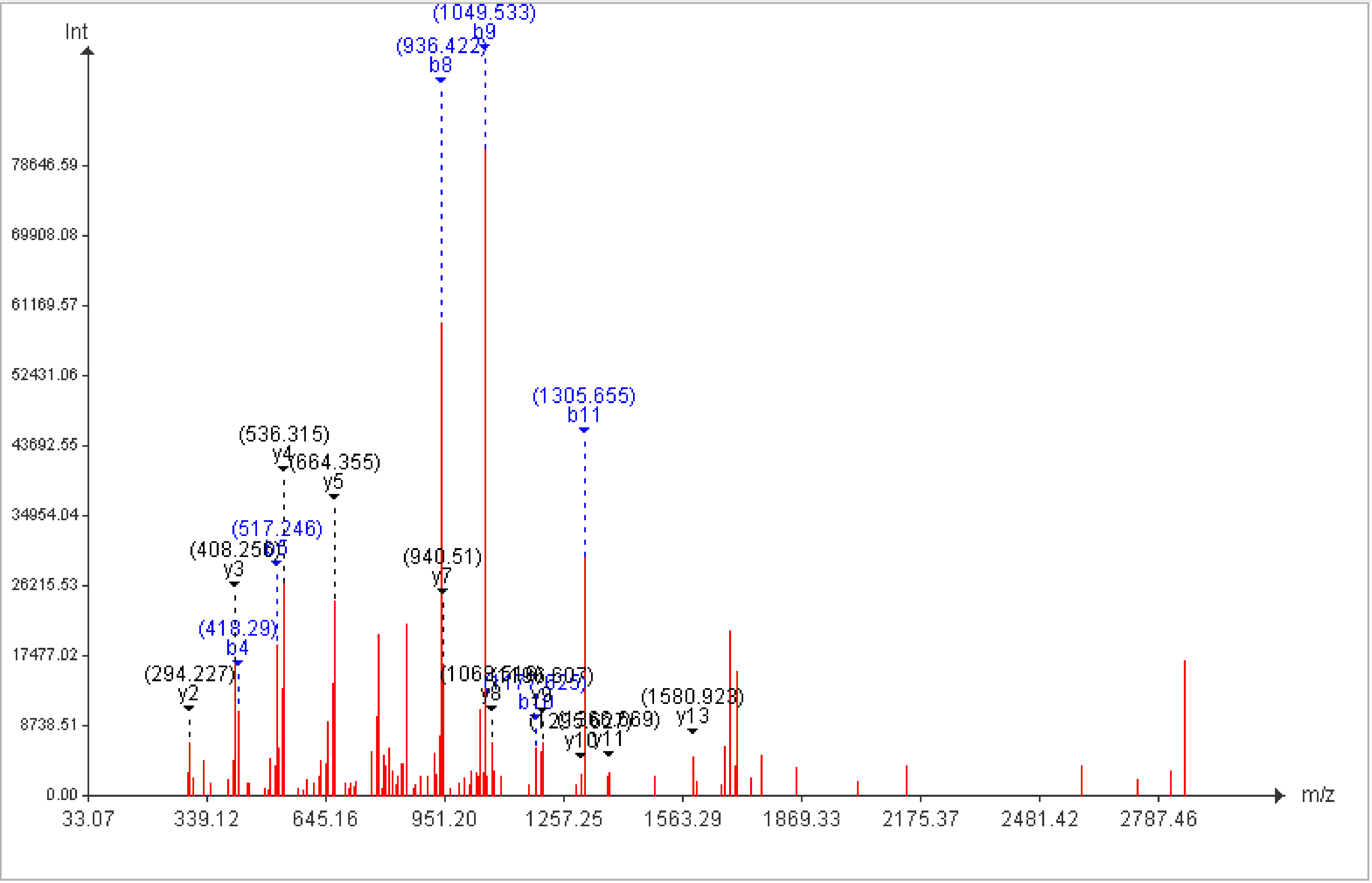


AcD3-STLAVQQYIQQNIR(C13*)-COOH

precursor mass: 856.9120 Da (charge: +2) protein: Q6PEB6 (35-48)

score (threshold): 60.0 (31.0)

instrument: Bruker Esquire HCT

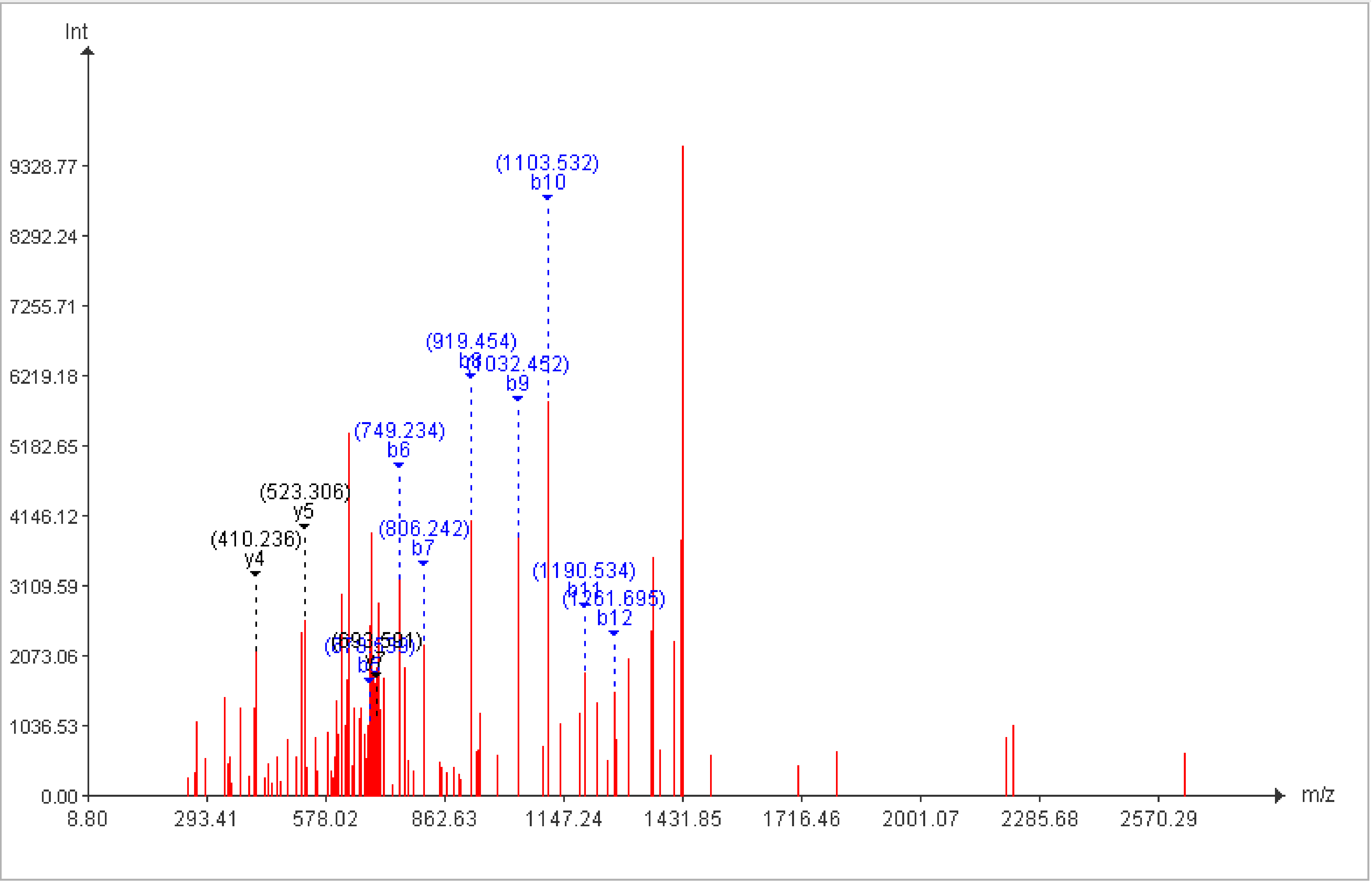


AcD3-SLVC(Cmm)K(AcD3K*)AGIIASAR(C13*)-COOH*

precursor mass: 721.4330 Da (charge: +2) protein: P58252 (37-49)

score (threshold): 39.0 (31.0)

instrument: Bruker Esquire HCT

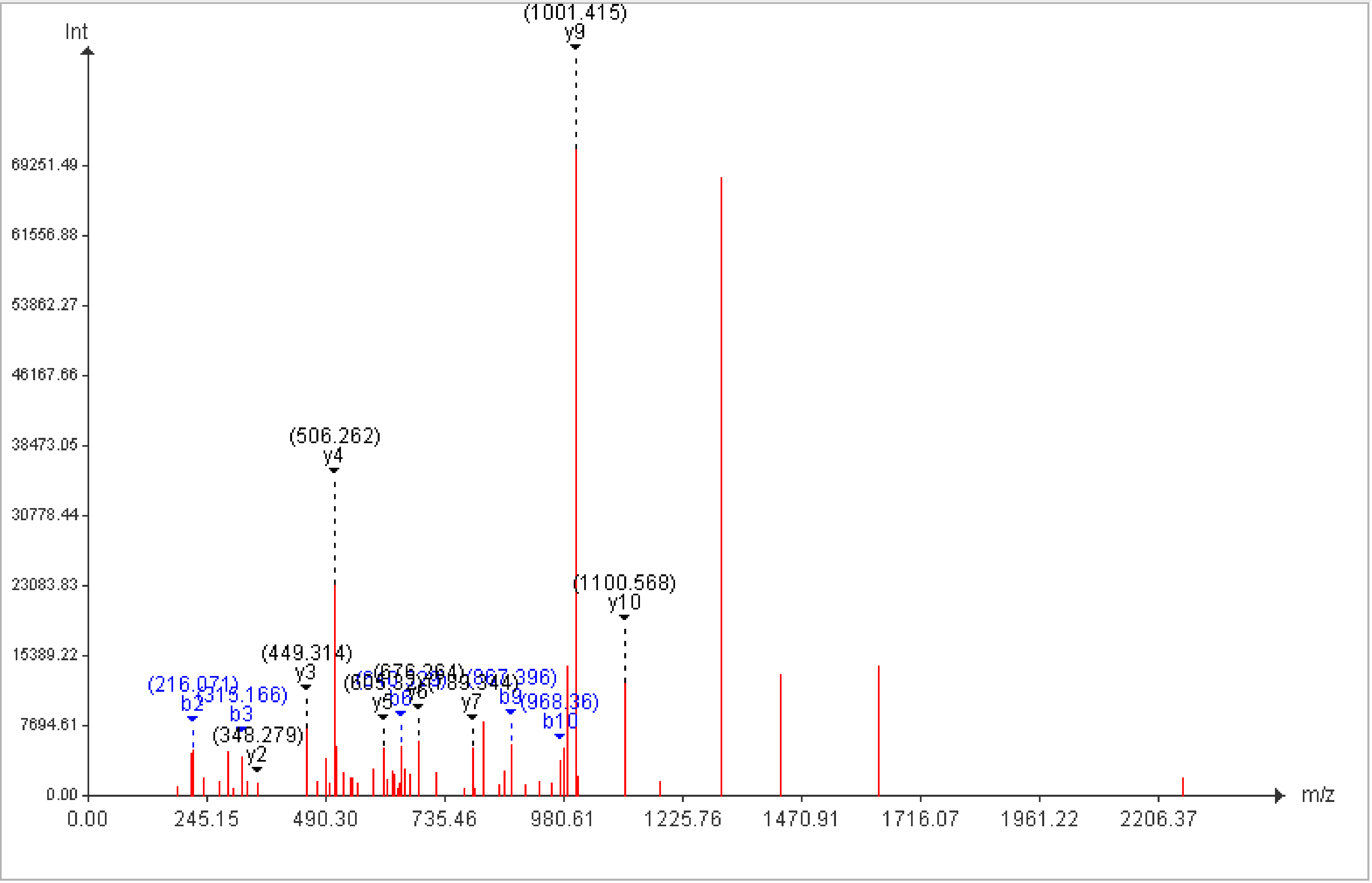


AcD3-GIVPDIAVGTK(AcD3K)R-COOH*

precursor mass: 658.3580 Da (charge: +2) protein: P17225 (3-14)

score (threshold): 51.0 (31.0)

instrument: Bruker Esquire HCT

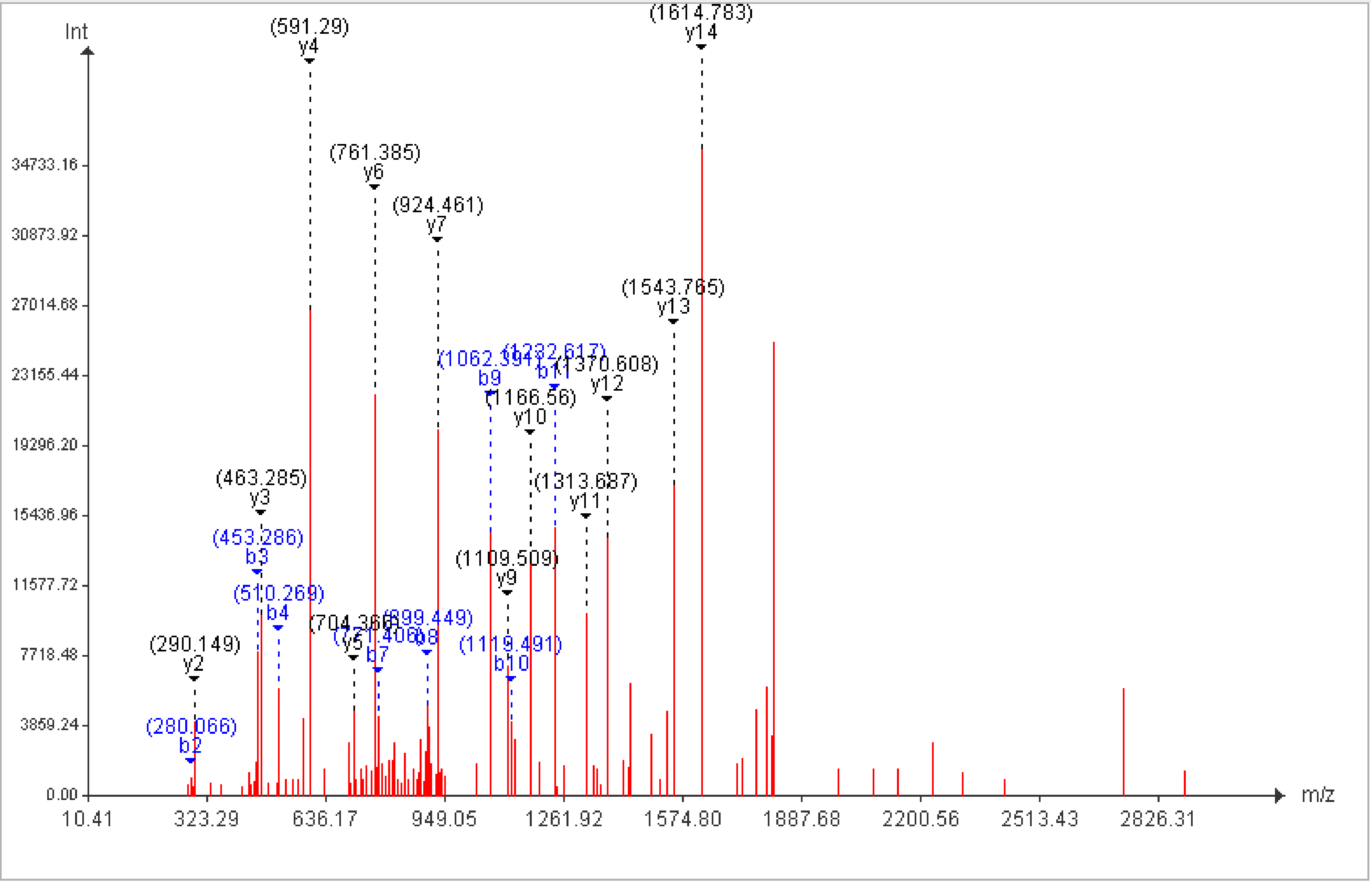


AcD3-YAK(AcD3K)GFGGQYGIQK(AcD3K*)DR-COOH*

precursor mass: 911.9110 Da (charge: +2) protein: P49710 (190-204)

score (threshold): 85.0 (31.0)

instrument: Bruker Esquire HCT

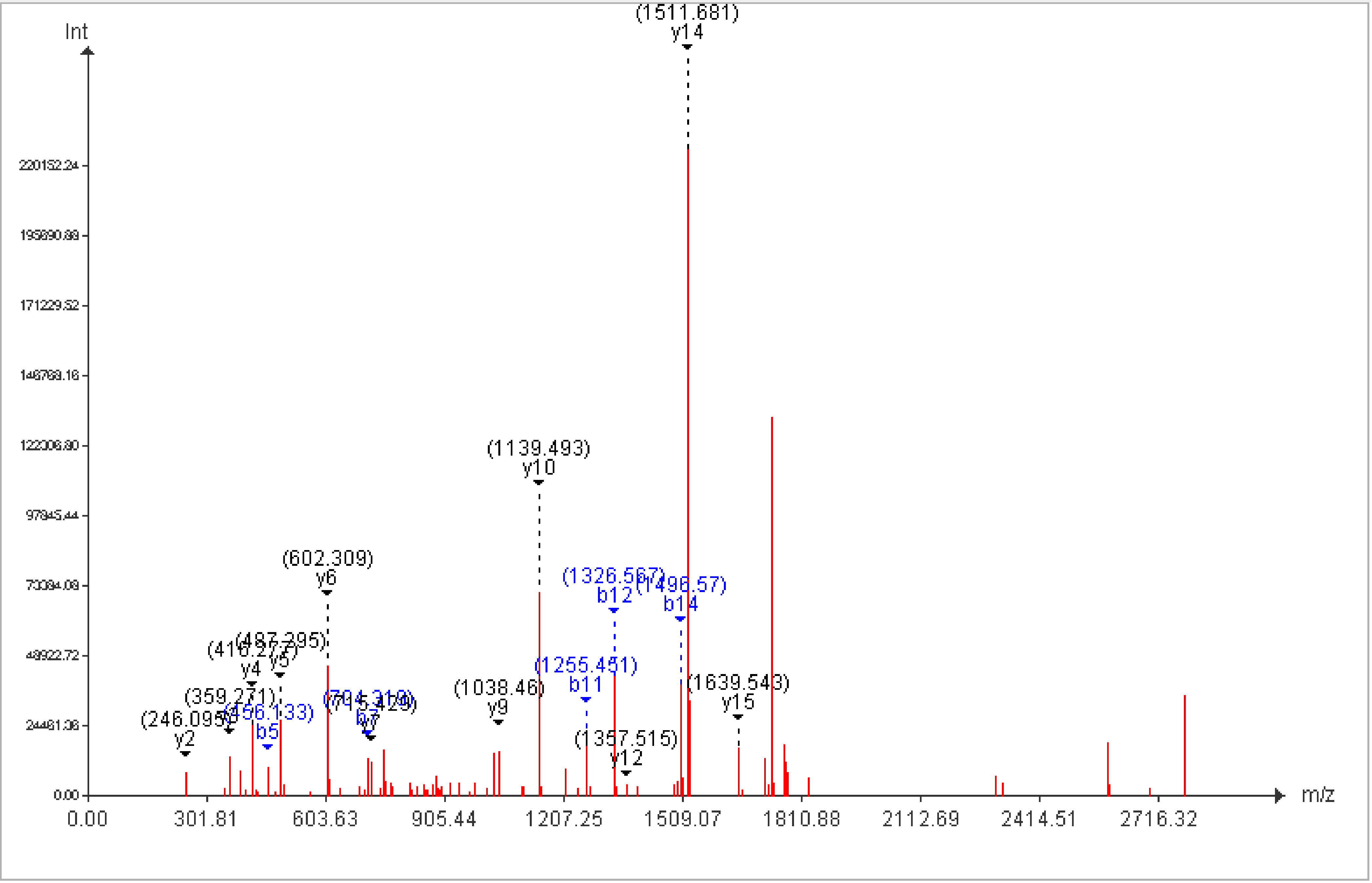


AcD3-GQPGAFTC(Cmm)YLDAGLAR-COOH*

precursor mass: 871.4260 Da (charge: +2) protein: P47962 (136-151)

score (threshold): 93.0 (31.0)

instrument: Bruker Esquire HCT

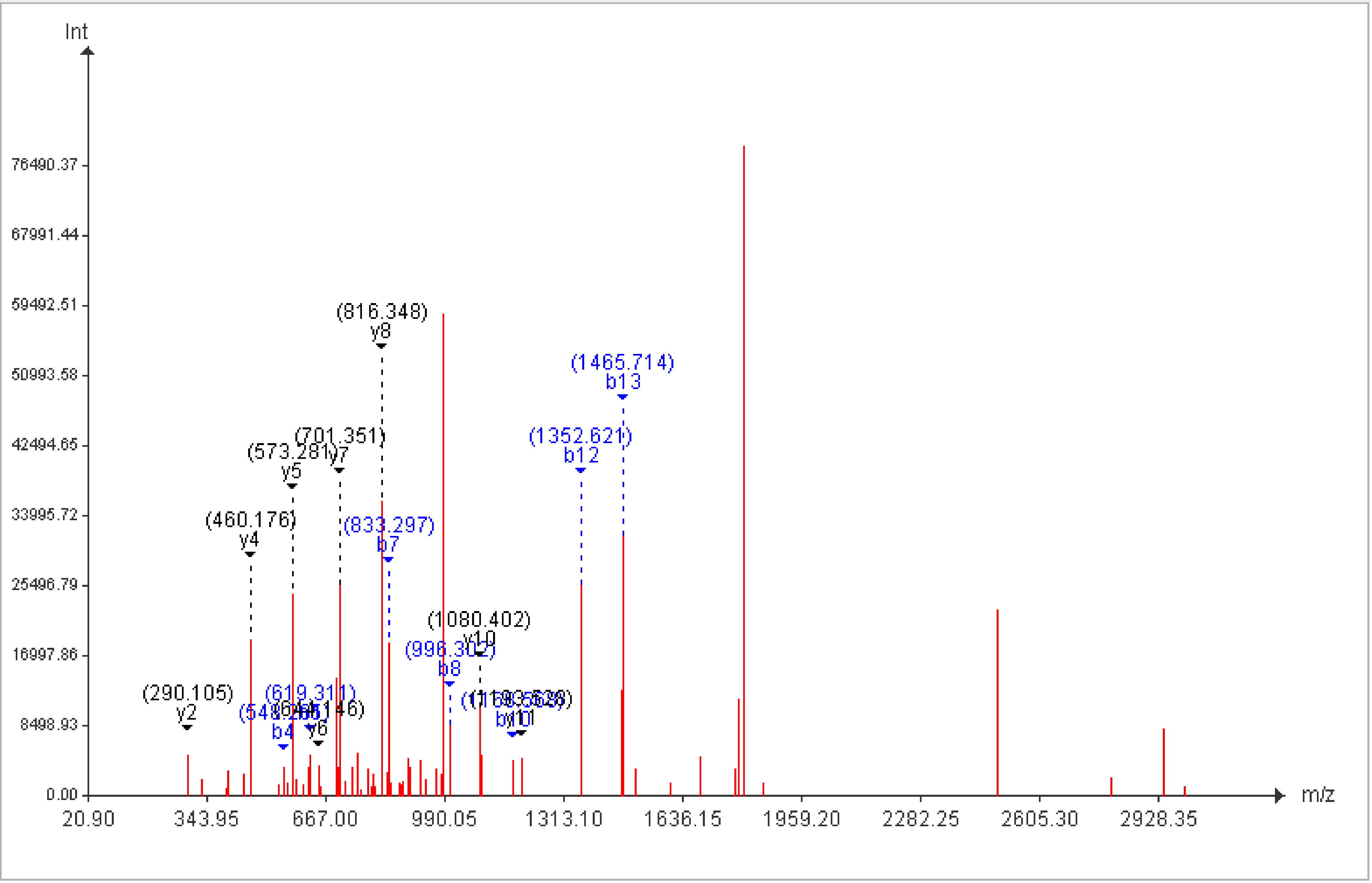


AcD3-SLK(AcD3K)EALTYDGALLGDR-COOH*

precursor mass: 906.4180 Da (charge: +2) protein: Q9WUK2 (93-108)

score (threshold): 67.0 (36.0)

instrument: Bruker Esquire HCT

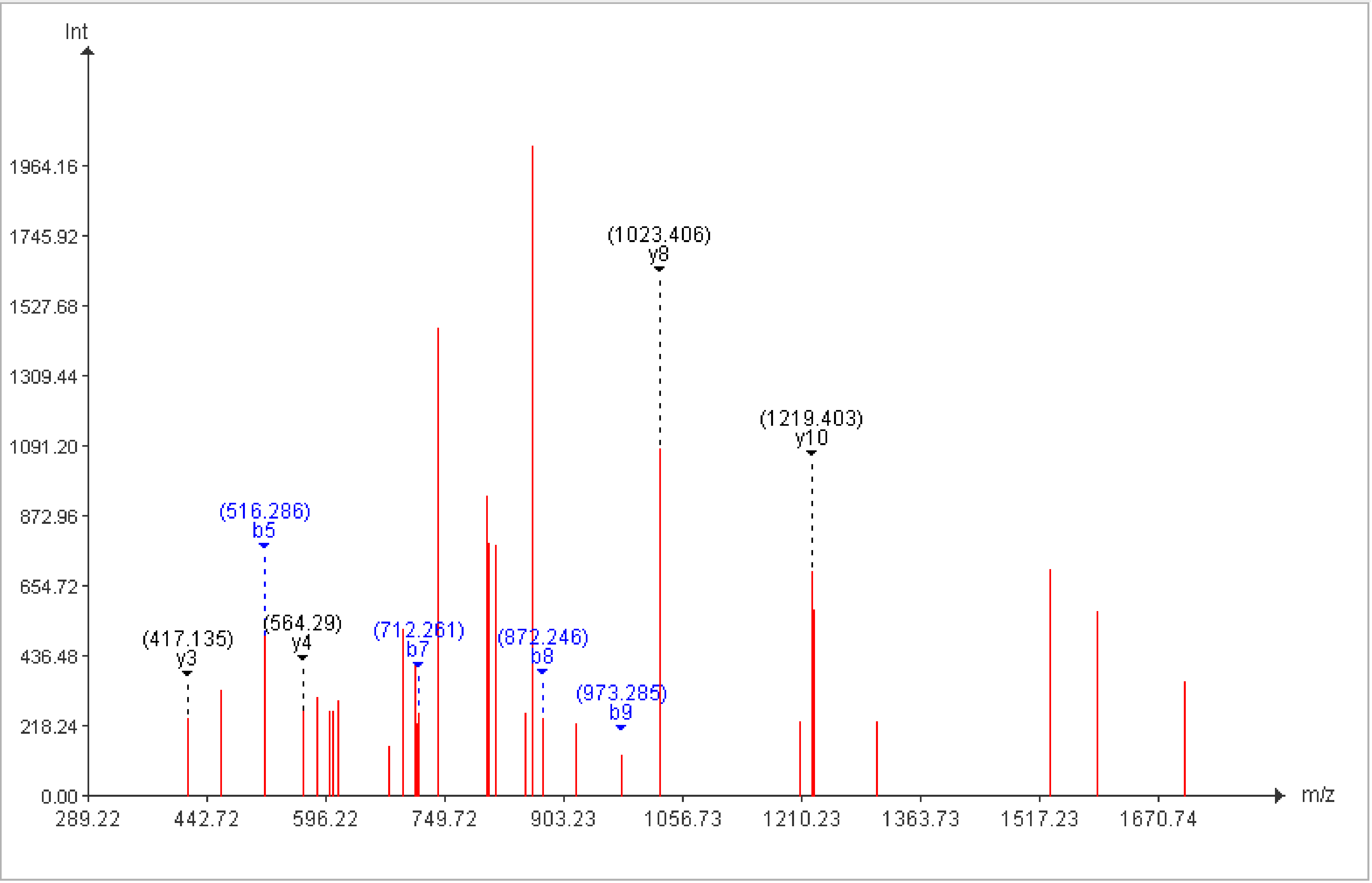


AcD3-SQGPTPVC(Cmm)TPTFLER-COOH*

precursor mass: 867.9450 Da (charge: +2) protein: Q91VE6 (253-267)

score (threshold): 32.0 (31.0)

instrument: Bruker Esquire HCT

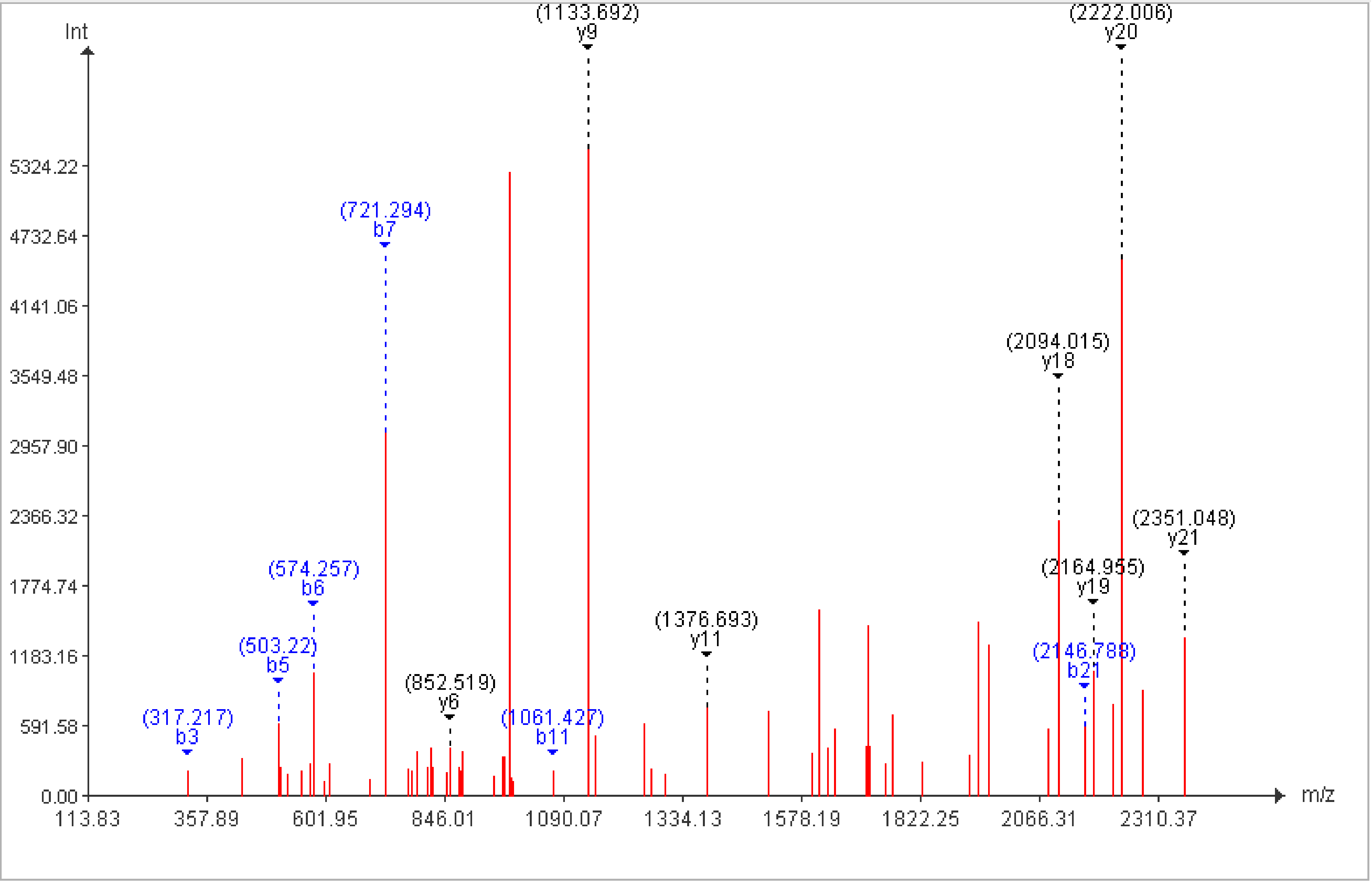


AcD3-AVTEGAM(Mox)PAATGK(AcD3K)DQPPSTGK(AcD3K*)K(AcD3K*)K(AcD3K*)R-COOH*

precursor mass: 889.9320 Da (charge: +3) protein: Q7TPV4 (1202-1225)

score (threshold): 41.0 (36.0)

instrument: Bruker Esquire HCT

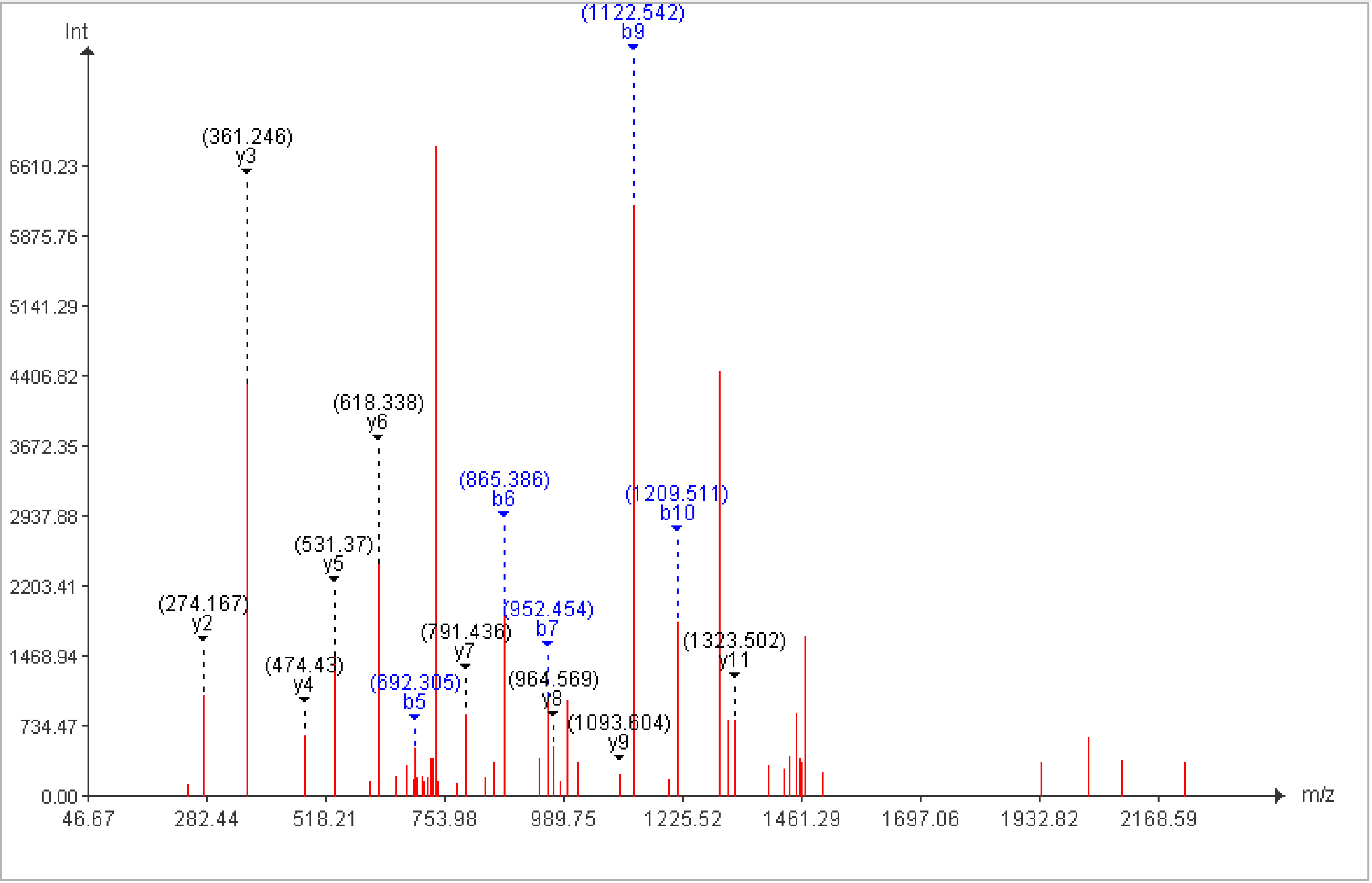


AcD3-NTEEK(AcD3K*)K(AcD3K*)SGLSVR-COOH

precursor mass: 741.8880 Da (charge: +2) protein: Q923D5 (298-309)

score (threshold): 67.0 (31.0)

instrument: Bruker Esquire HCT

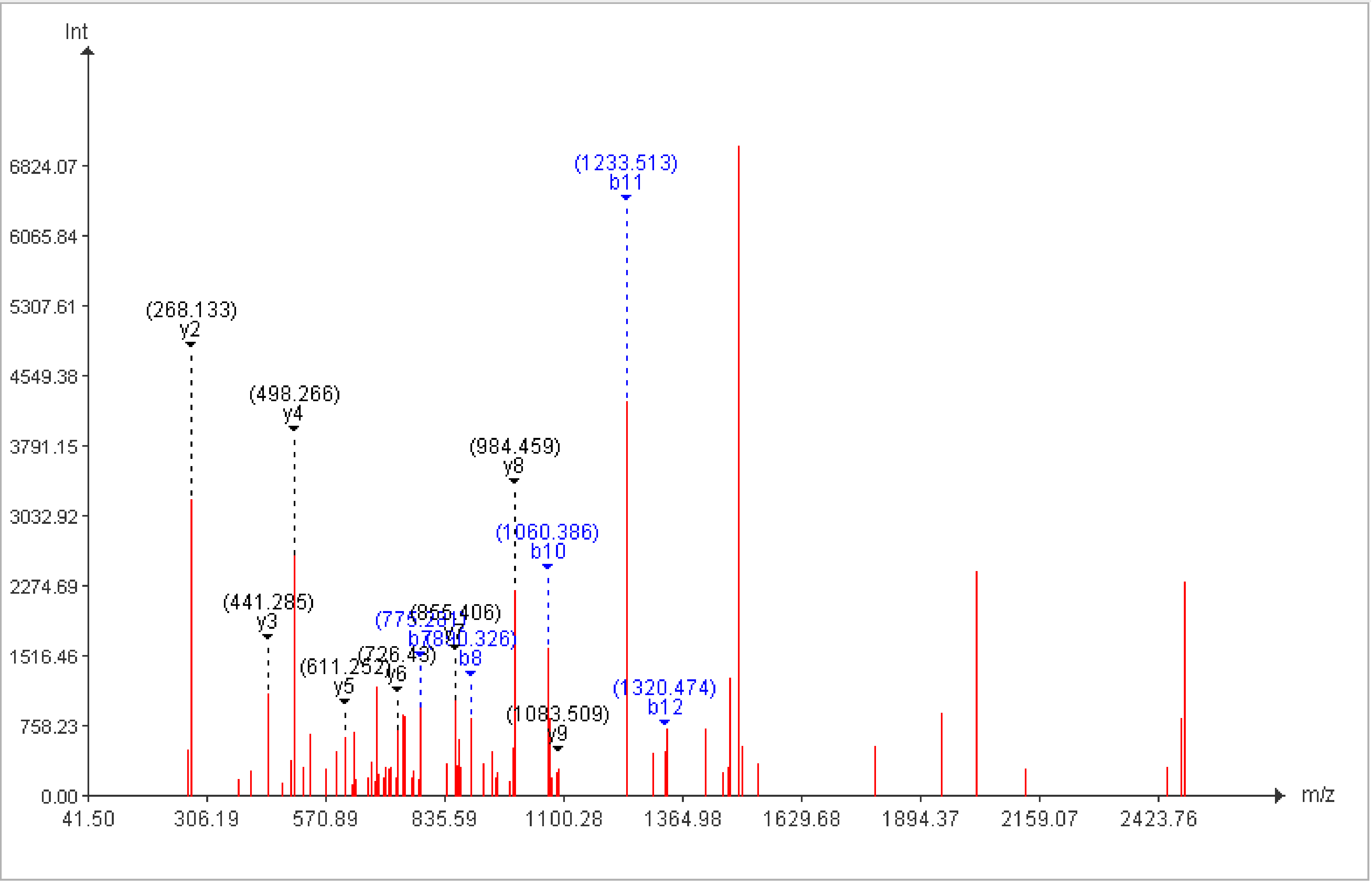


AcD3-VDGTVEEDLGK(AcD3K)SR(C13*)-COOH*

precursor mass: 750.7710 Da (charge: +2) protein: P08113 (27-39)

score (threshold): 45.0 (36.0)

instrument: Bruker Esquire HCT

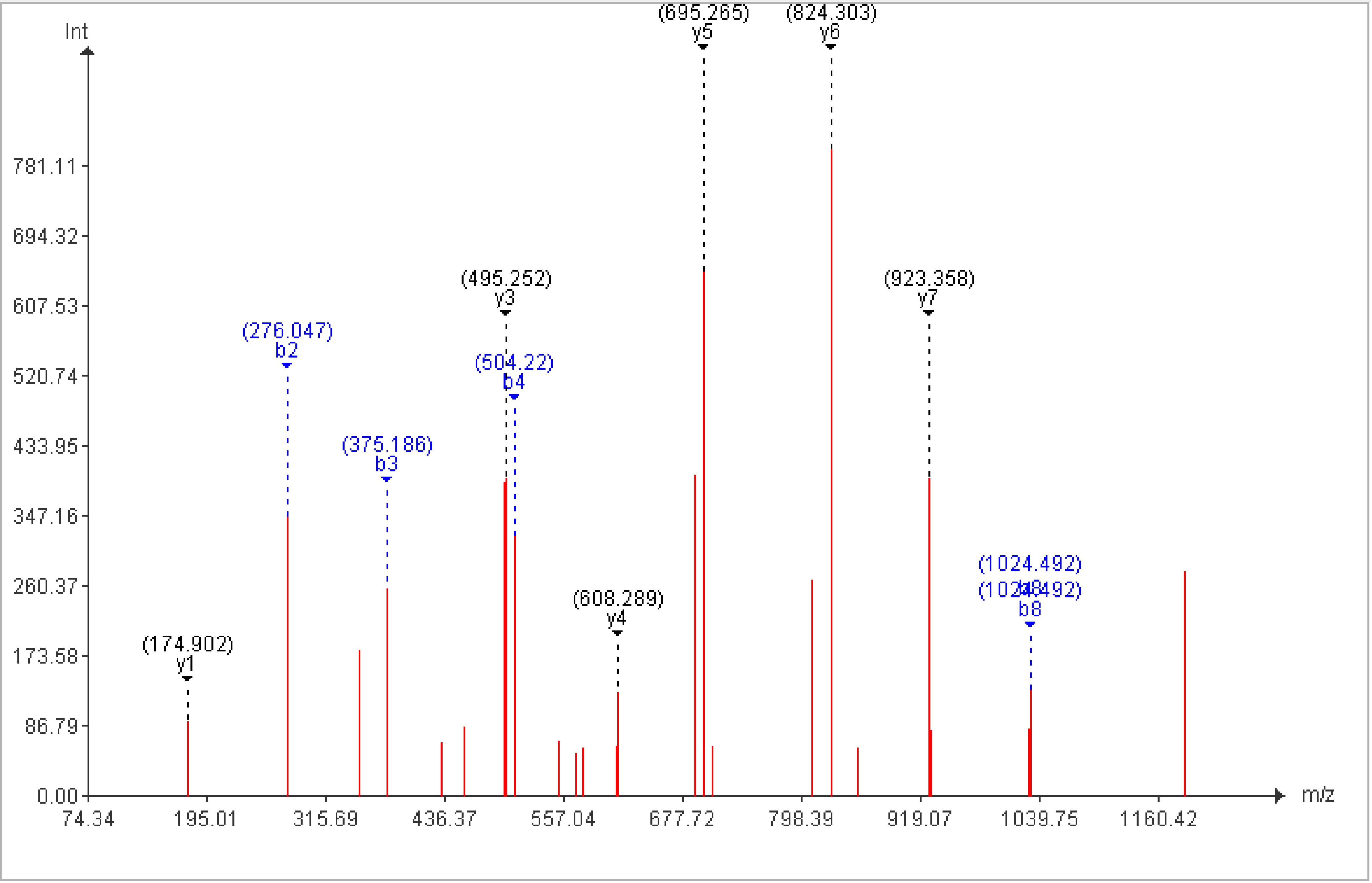


AcD3-GK(AcD3K)VESIM(Mox)K(AcD3K*)R-COOH*

precursor mass: 599.8750 Da (charge: +2) protein: IPI00007682.2 (300-308)

score (threshold): 63.0 (34.0)

instrument: Bruker Esquire HCT

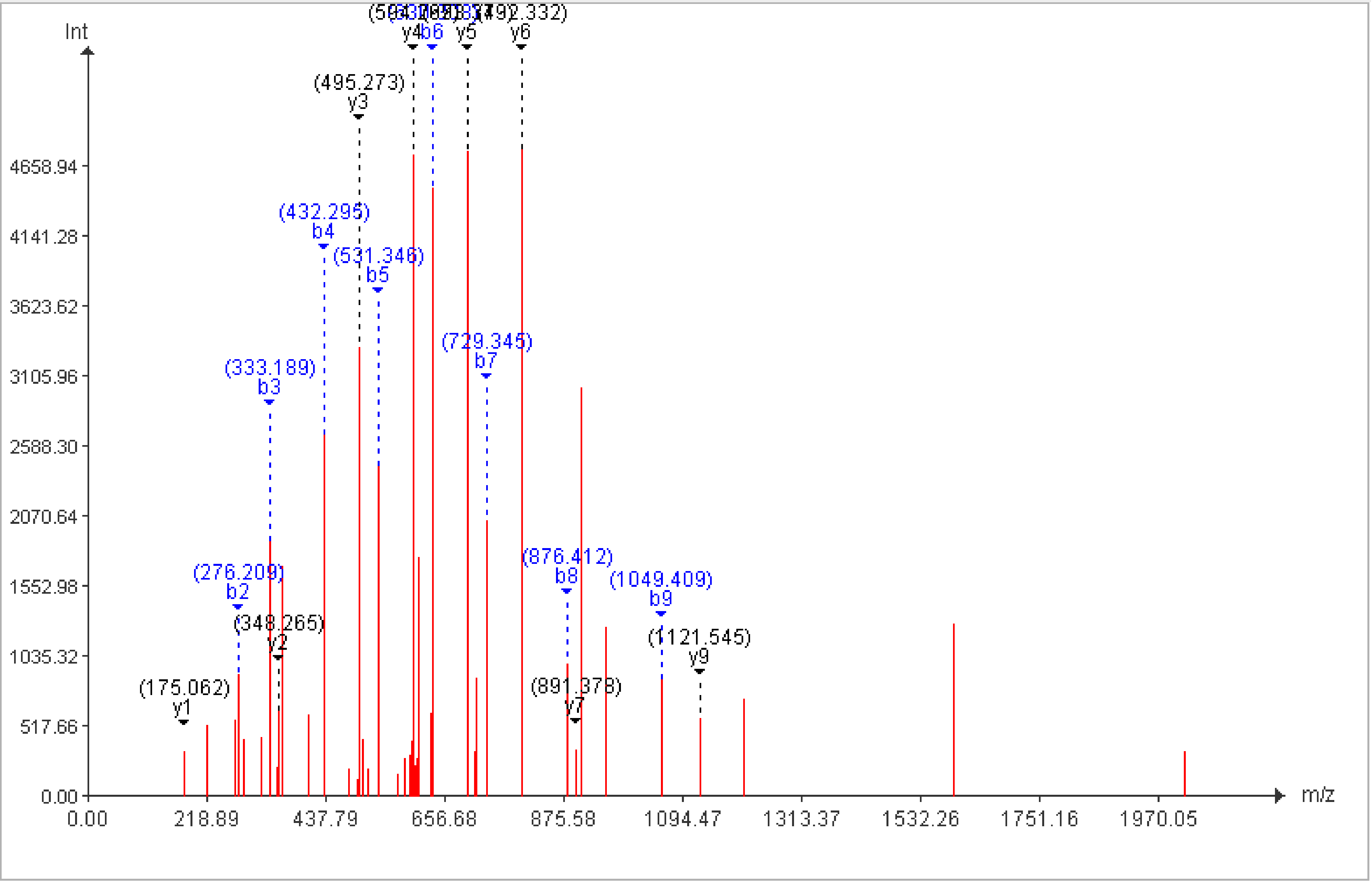


AcD3-GK(AcD3K)GVVVVM(Mox)K(AcD3K*)R-COOH*

precursor mass: 612.3510 Da (charge: +2) protein: P41105 (56-65)

score (threshold): 55.0 (31.0)

instrument: Bruker Esquire HCT

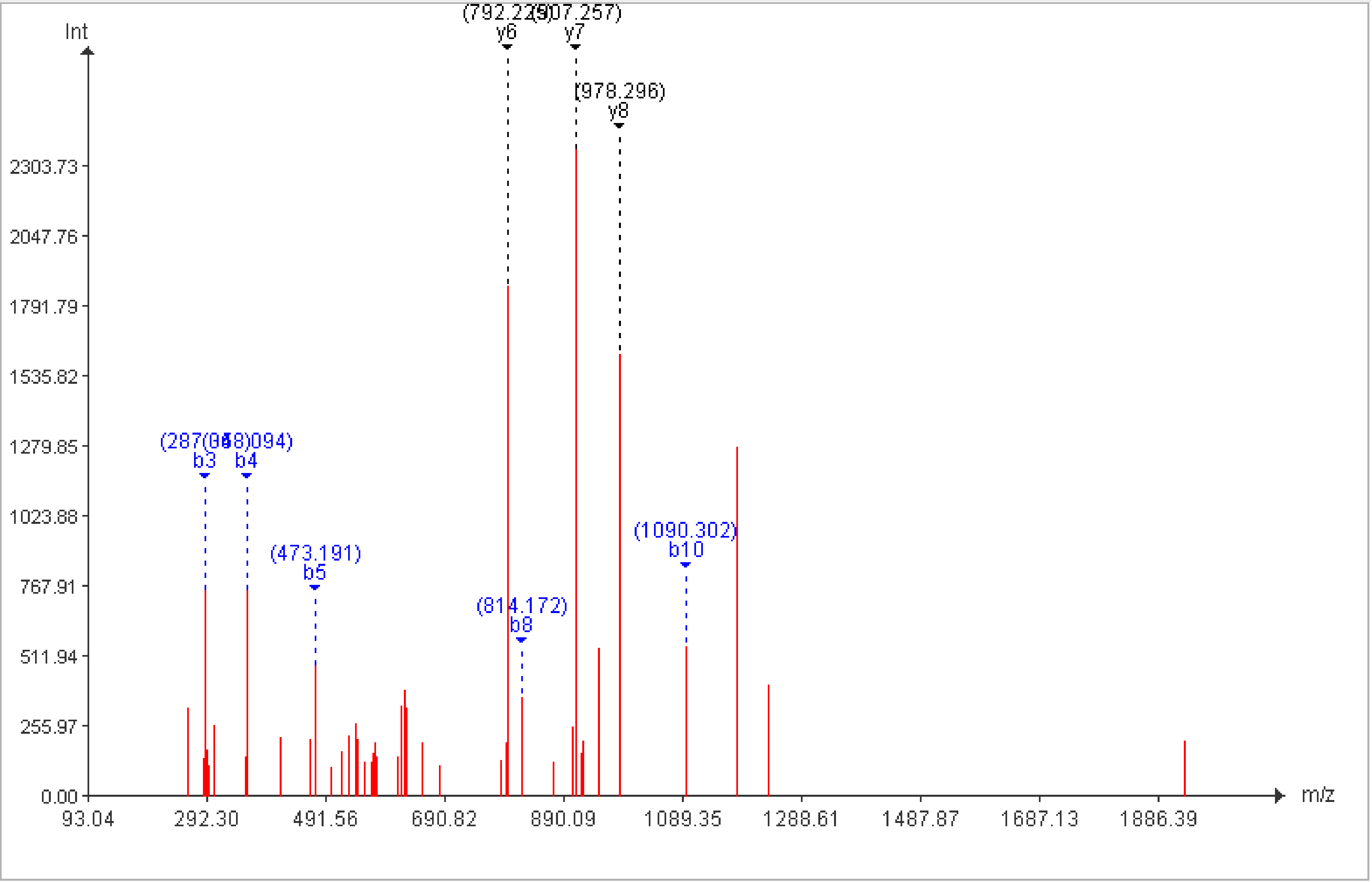


AcD3-AAVADPDEFER-COOH

precursor mass: 632.7740 Da (charge: +2) protein: P47713 (522-532)

score (threshold): 32.0 (31.0)

instrument: Bruker Esquire HCT

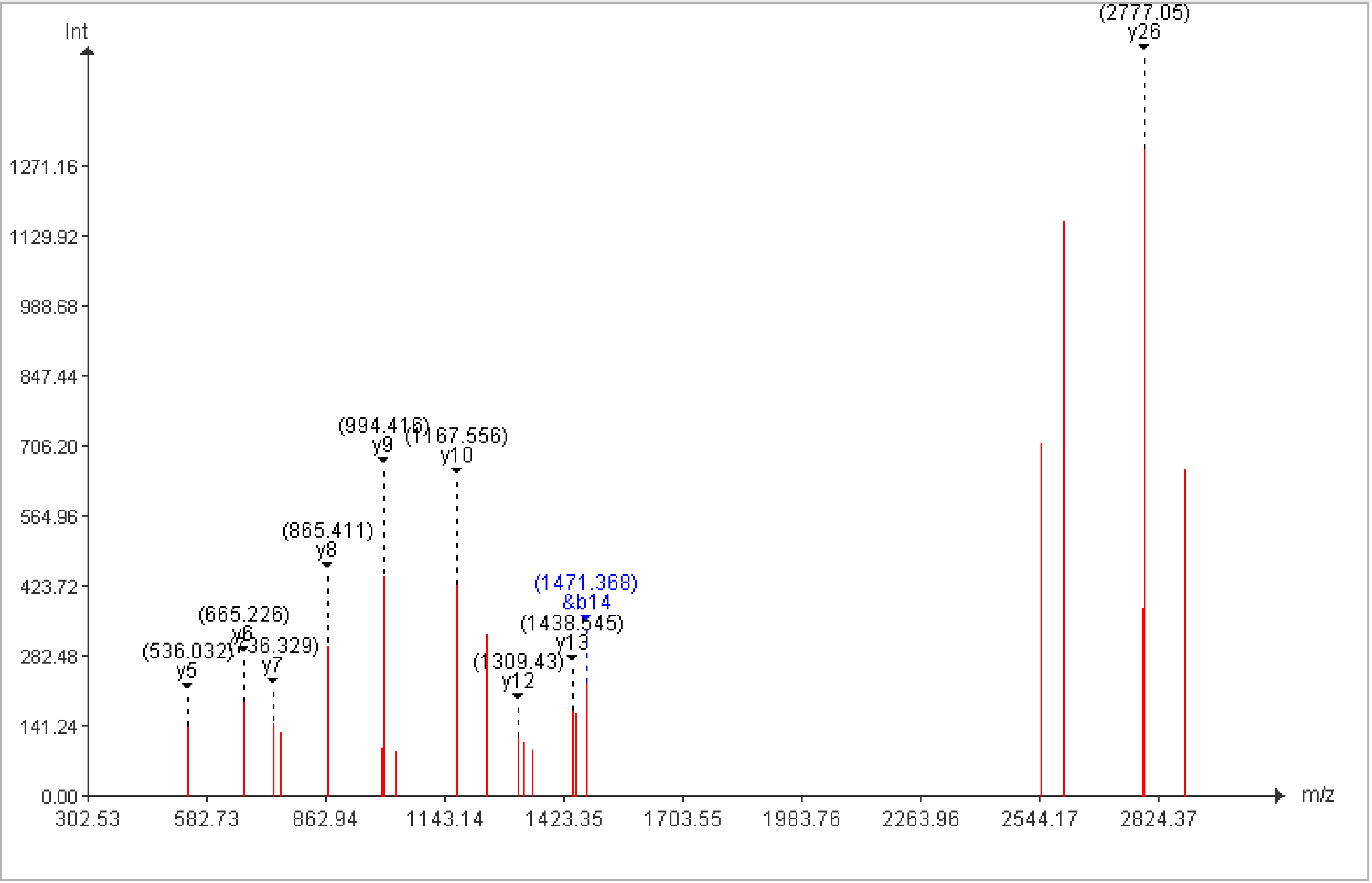


AcD3-SGQGPPAEEEEGEEEAAK(AcD3K)EEAEAQGVR(C13*)-COOH*

precursor mass: 1455.0120 Da (charge: +2) protein: P51859 (206-232)

score (threshold): 43.0 (31.0)

instrument: Bruker Esquire HCT

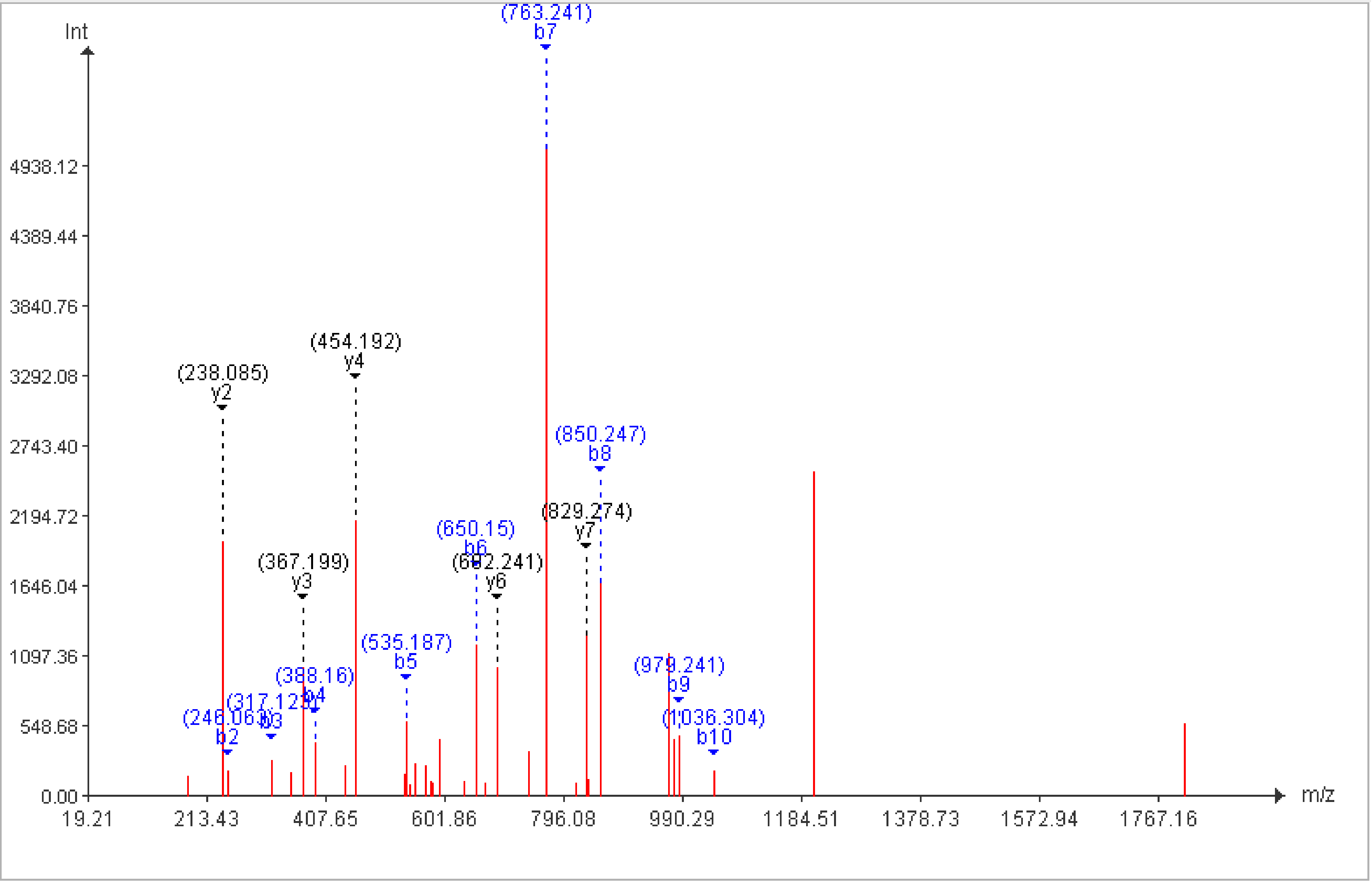


AcD3-AEAAM(Mox)DISEGR(C13*)-COOH

precursor mass: 608.8150 Da (charge: +2) protein: P56399 (768-778)

score (threshold): 107.0 (31.0)

instrument: Bruker Esquire HCT

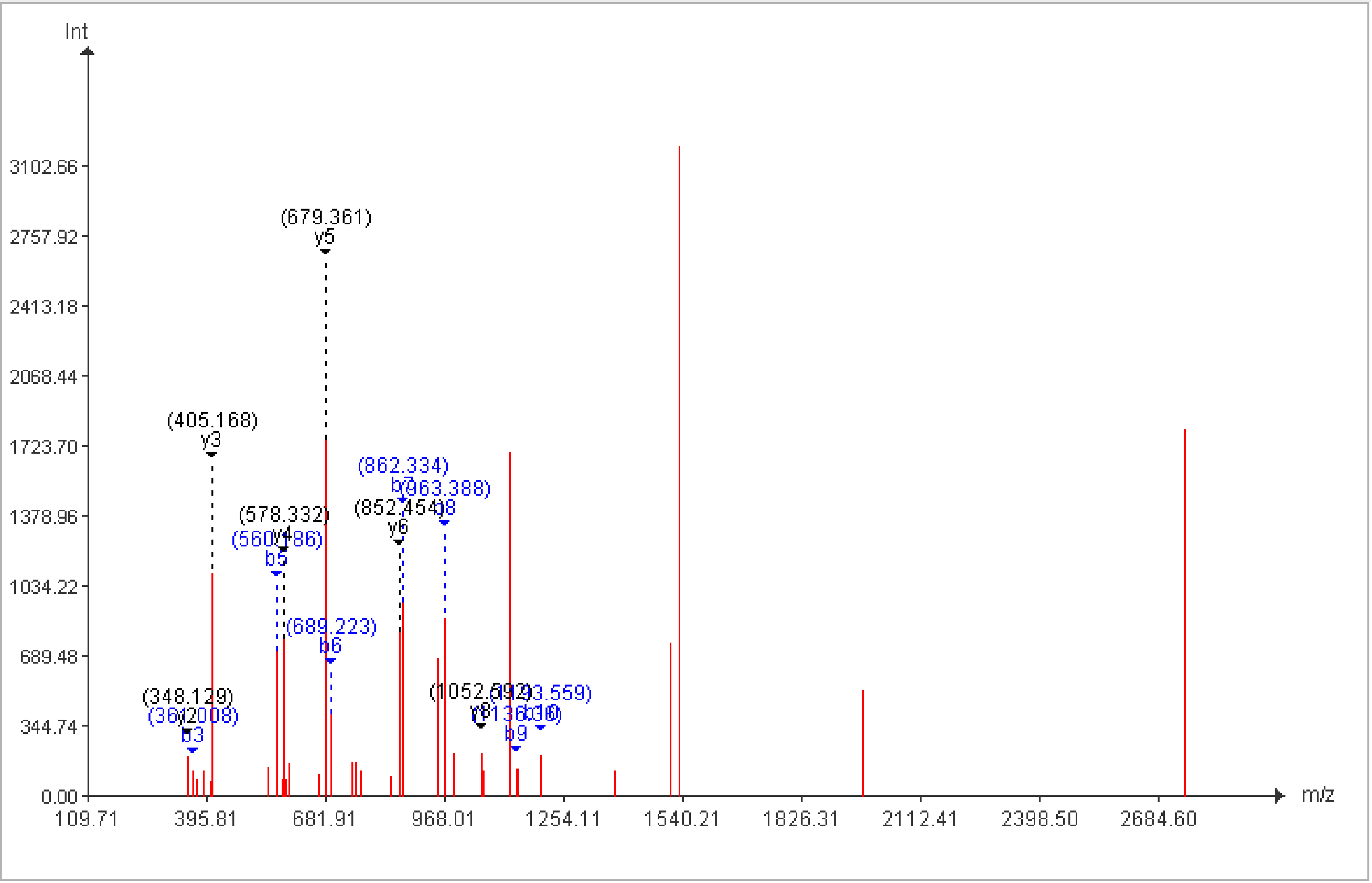


AcD3-GEEQAEK(AcD3K)TK(AcD3K*)GK(AcD3K*)R-COOH*

precursor mass: 770.8810 Da (charge: +2) protein: O88271 (41-52)

score (threshold): 52.0 (31.0)

instrument: Bruker Esquire HCT

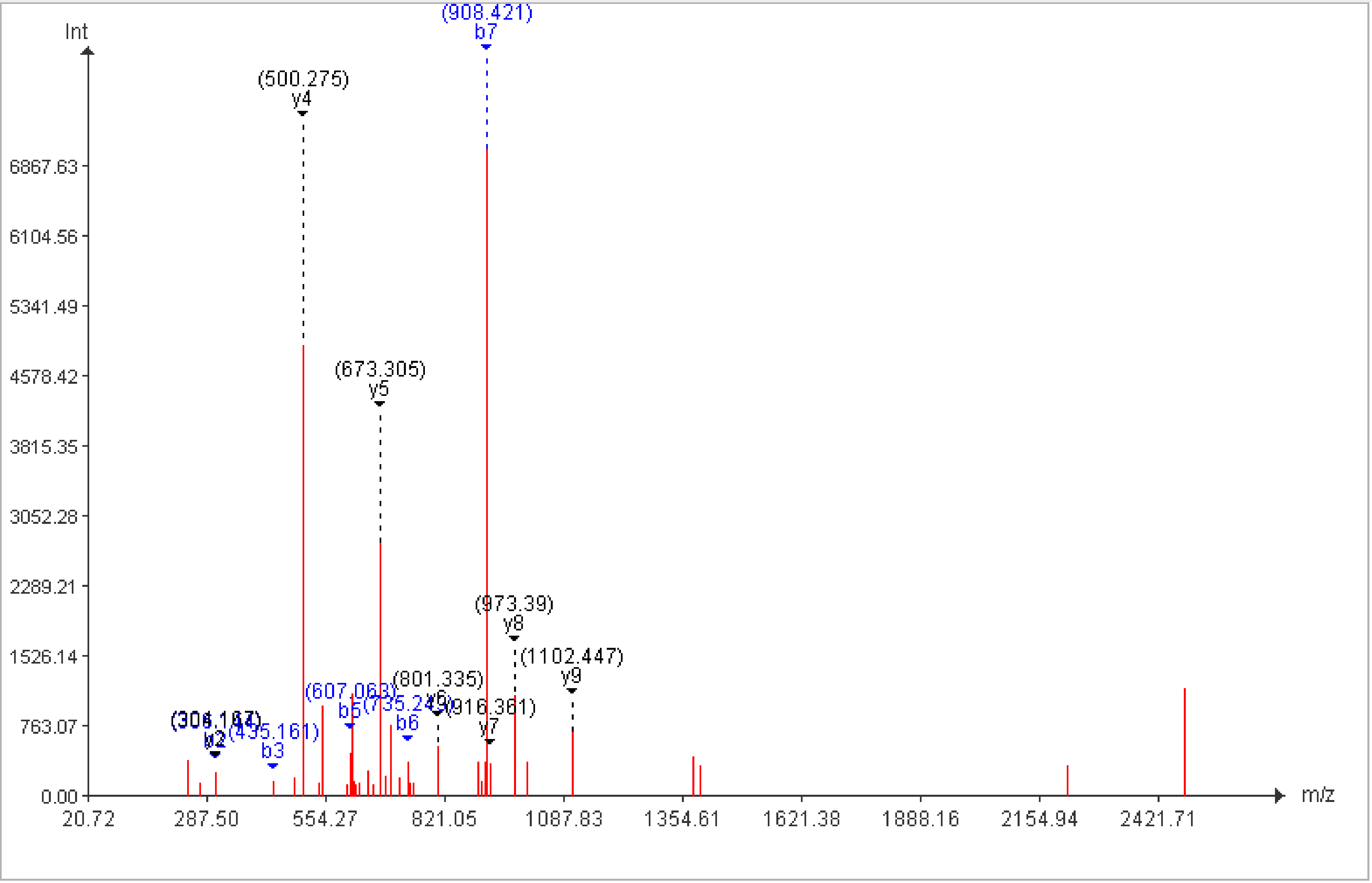


AcD3-FLEGDQK(AcD3K)PVER-COOH*

precursor mass: 704.4440 Da (charge: +2) protein: Q9D903 (212-222)

score (threshold): 49.0 (31.0)

instrument: Bruker Esquire HCT

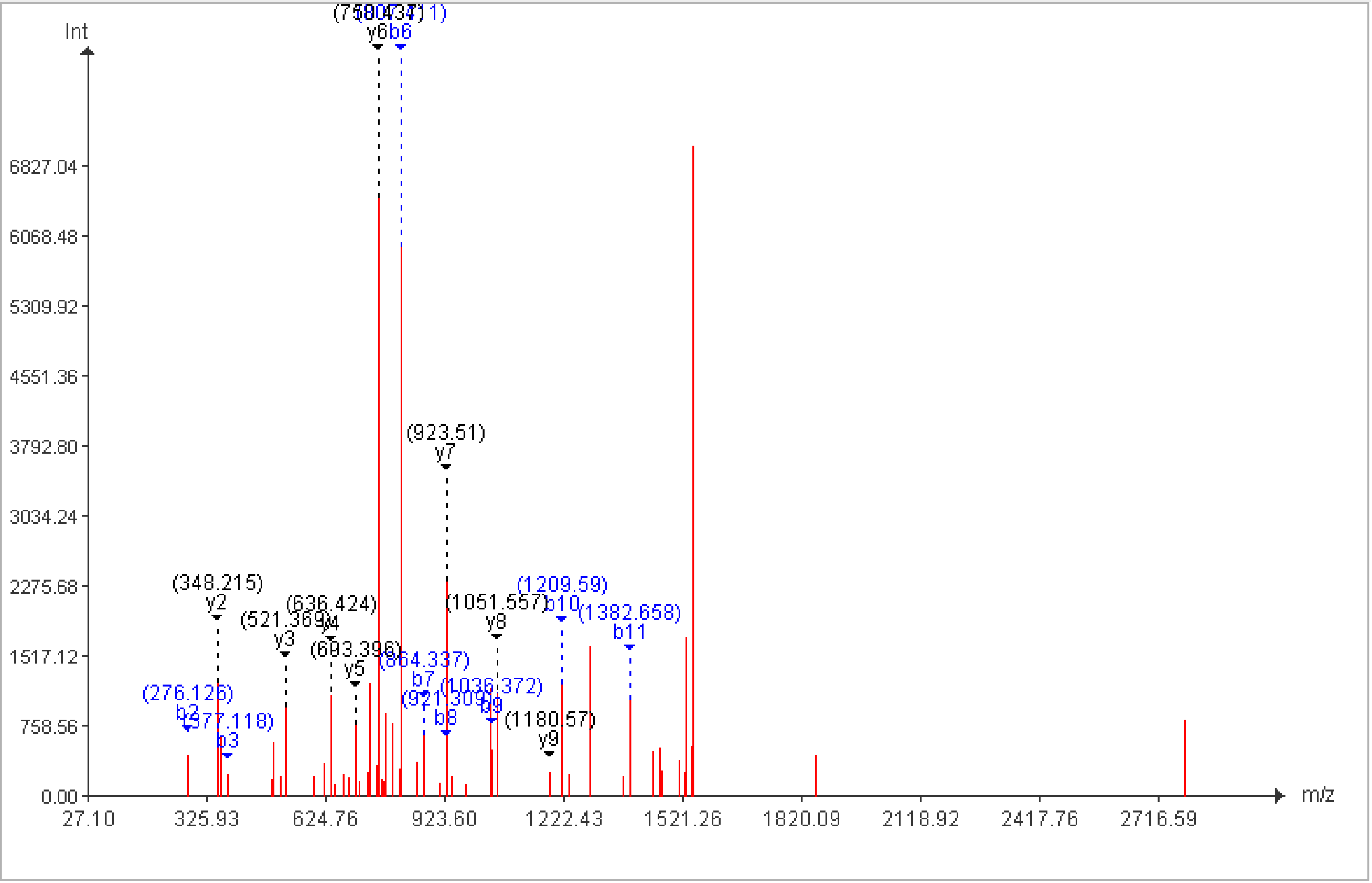


AcD3-GK(AcD3K)TEQK(AcD3K*)GGDK(AcD3K*)K(AcD3K*)R-COOH*

precursor mass: 778.9680 Da (charge: +2) protein: IPI00479217.1 (214-225)

score (threshold): 69.0 (34.0)

instrument: Bruker Esquire HCT

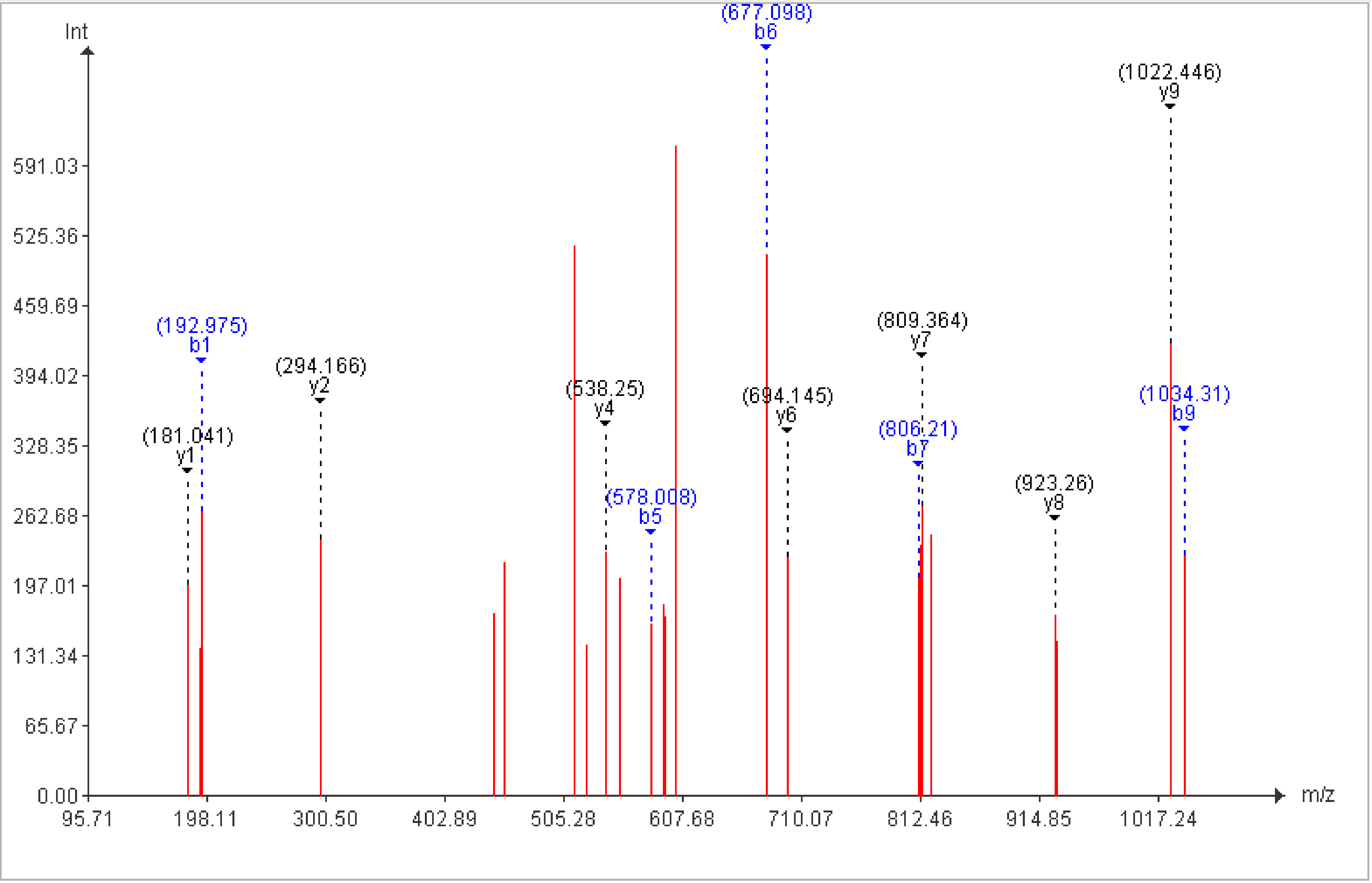


AcD3-M(Mox)VNDGVEDLR(C13)-COOH*

precursor mass: 607.8840 Da (charge: +2) protein: P19157 (91-100)

score (threshold): 54.0 (31.0)

instrument: Bruker Esquire HCT

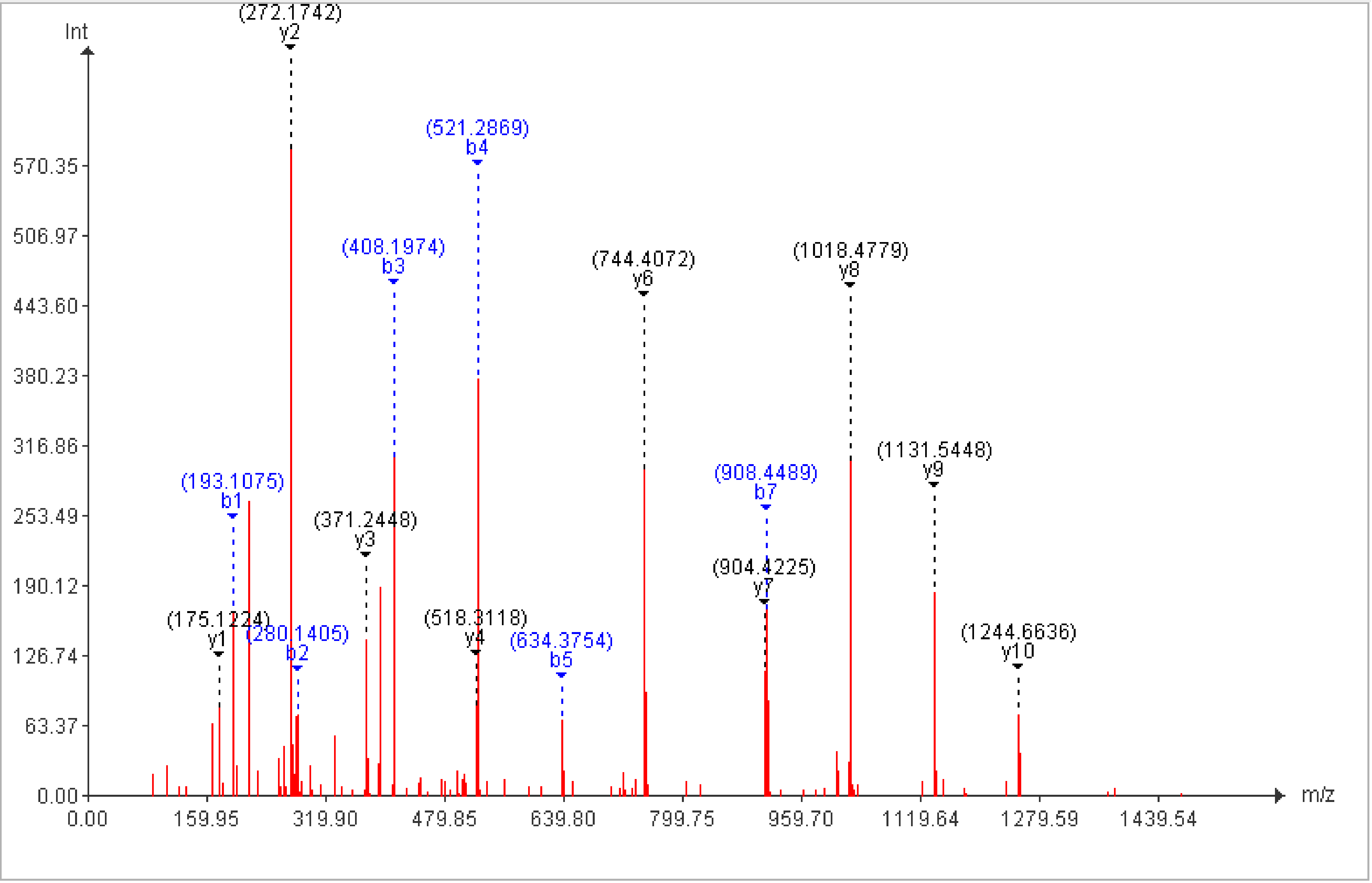


AcD3-FSQLLNC(Cmm)PEFVPR-COOH*

precursor mass: 826.4189 Da (charge: +2) protein: Q3UU34 (298-310)

score (threshold): 68.0 (32.0)

instrument: Waters Q-TOF Premier

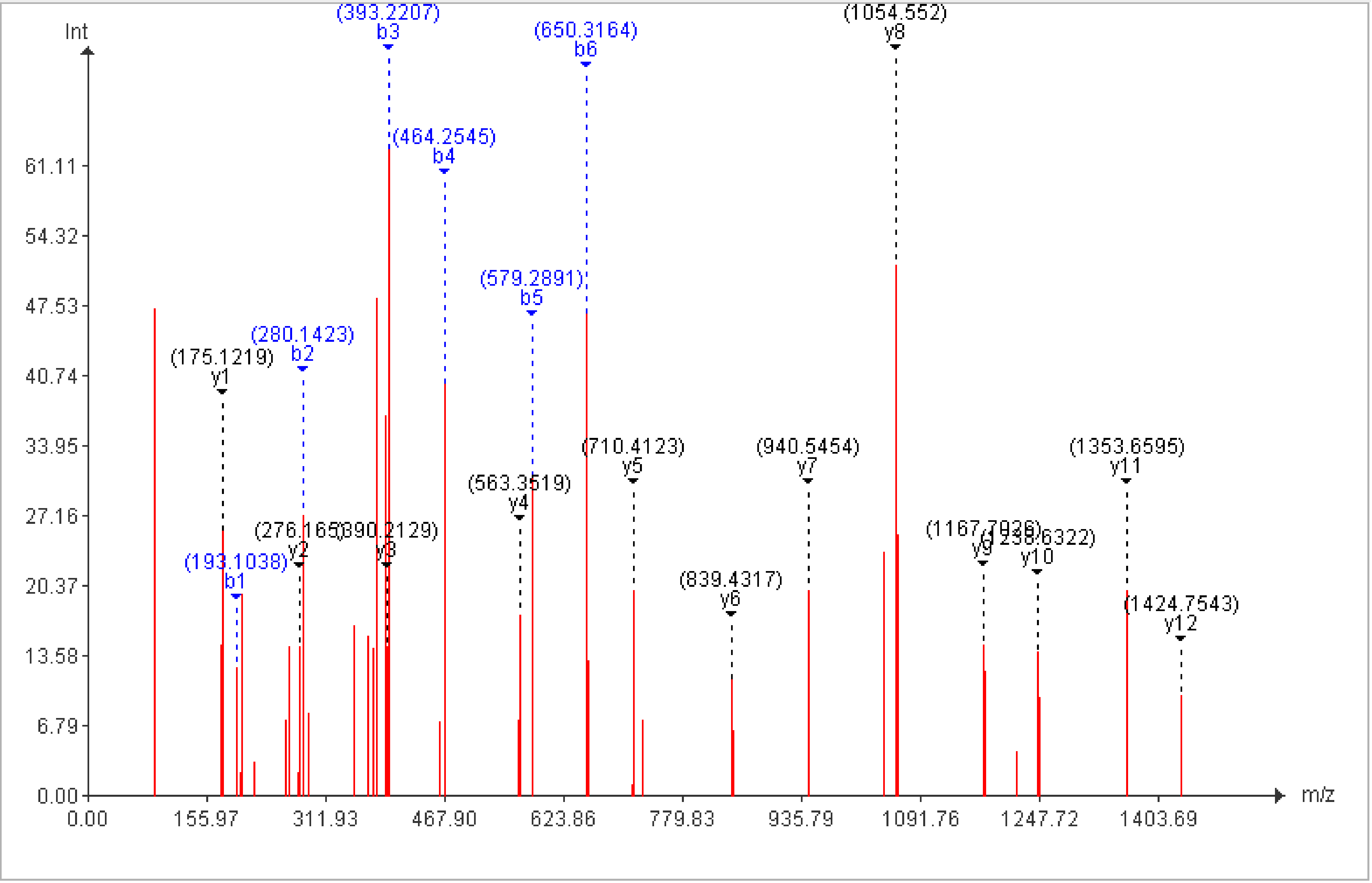


AcD3-FSLADAINTEFK(AcD3K)NTR-COOH*

precursor mass: 908.9656 Da (charge: +2) protein: P20152 (86-100)

score (threshold): 89.0 (31.0)

instrument: Waters Q-TOF Premier

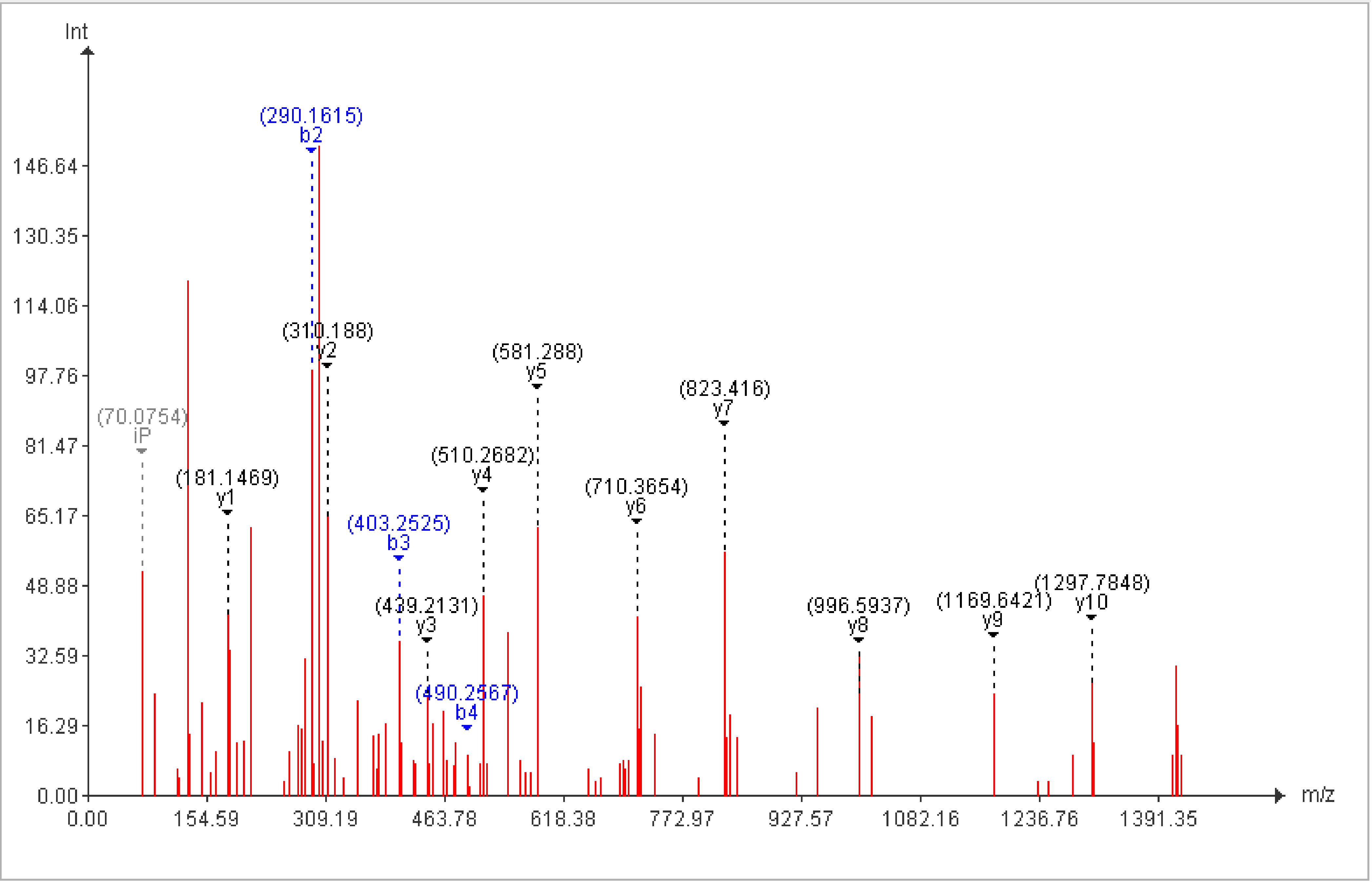


AcD3-FPLSPPK(AcD3K)K(AcD3K*)K(AcD3K*)DLSLEEIQK(AcD3K*)K(AcD3K*)LEAAEER(C13*)-COOH*

precursor mass: 1100.6226 Da (charge: +3) protein: P54227 (35-60)

score (threshold): 39.0 (29.0)

instrument: Waters Q-TOF Premier

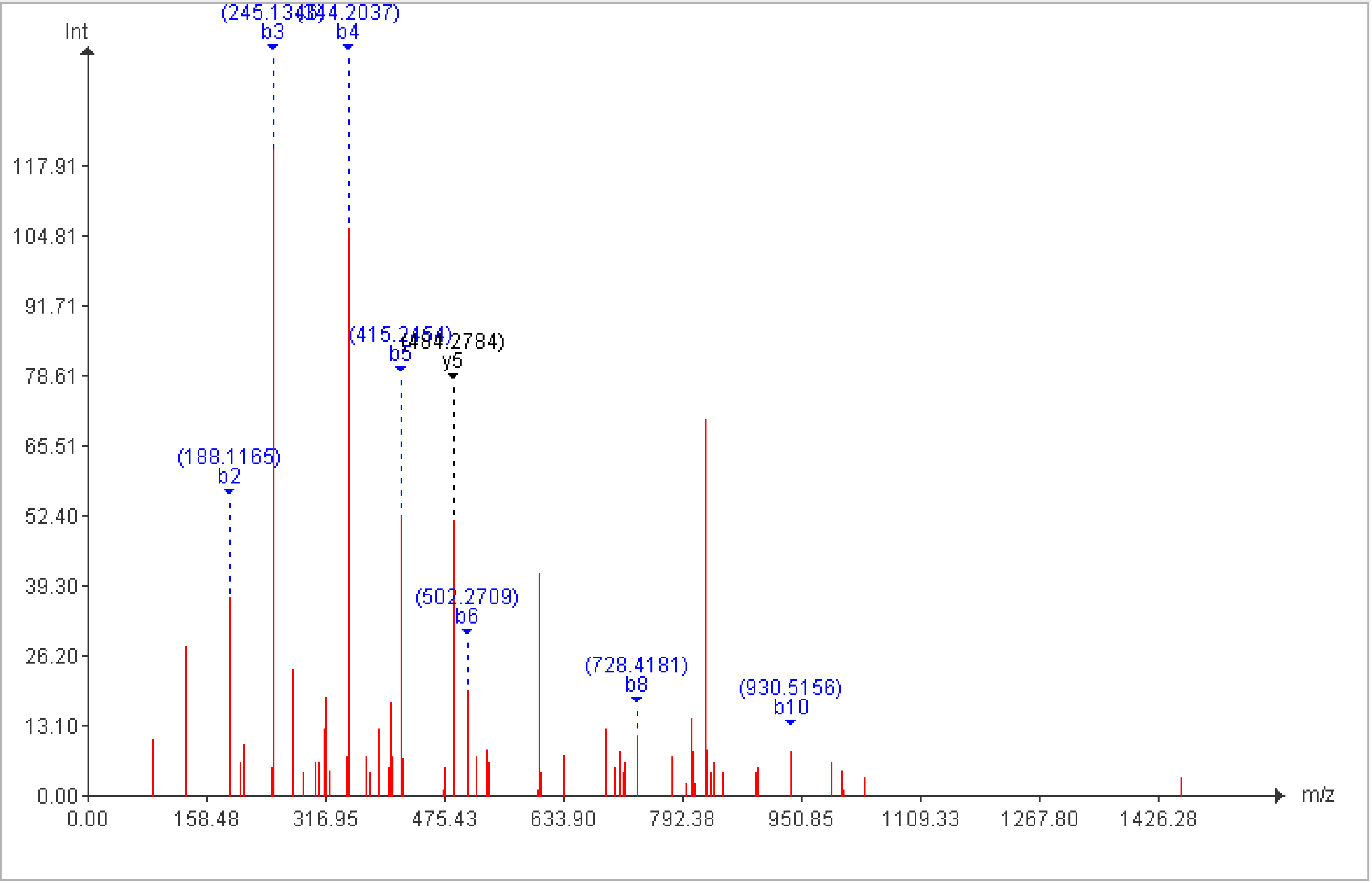


AcD3-AAGVASLLTTAEAVVTEIPK(AcD3K)EEK(AcD3K*)DPGM(Mox*)GAM(Mox*)GGM(Mox*)GGGM(Mox*)GGGM(Mox*)F-COOH*

precursor mass: 1050.2289 Da (charge: +4) protein: P63038 (532-573)

score (threshold): 26.0 (20.0)

instrument: Waters Q-TOF Premier

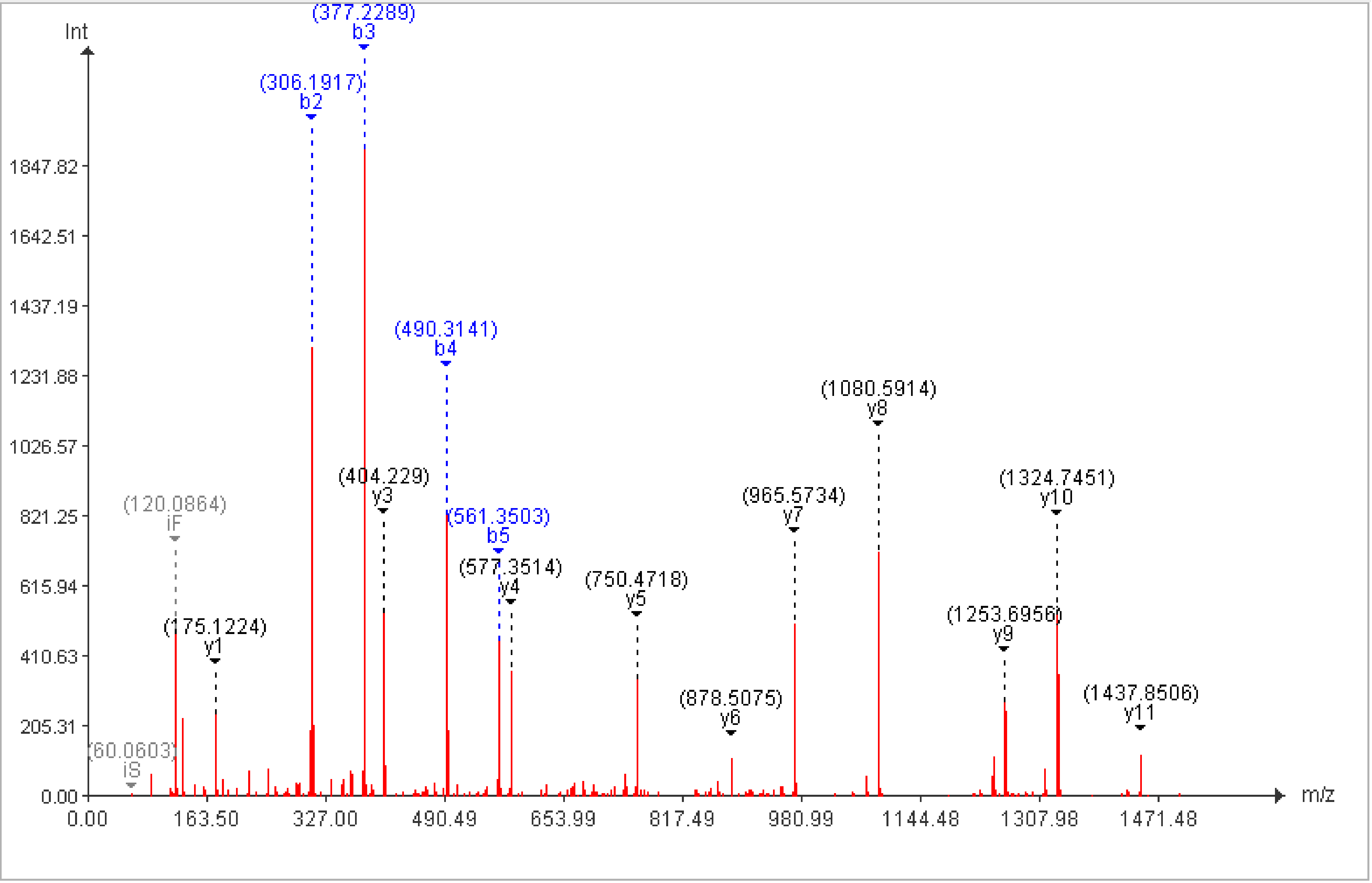


AcD3-LFAIAK(AcD3K*)DSQK(AcD3K*)K(AcD3K*)TQR-COOH

precursor mass: 907.5250 Da (charge: +2) protein: Q6PGL7 (669-682)

score (threshold): 70.0 (31.0)

instrument: Waters Q-TOF Premier

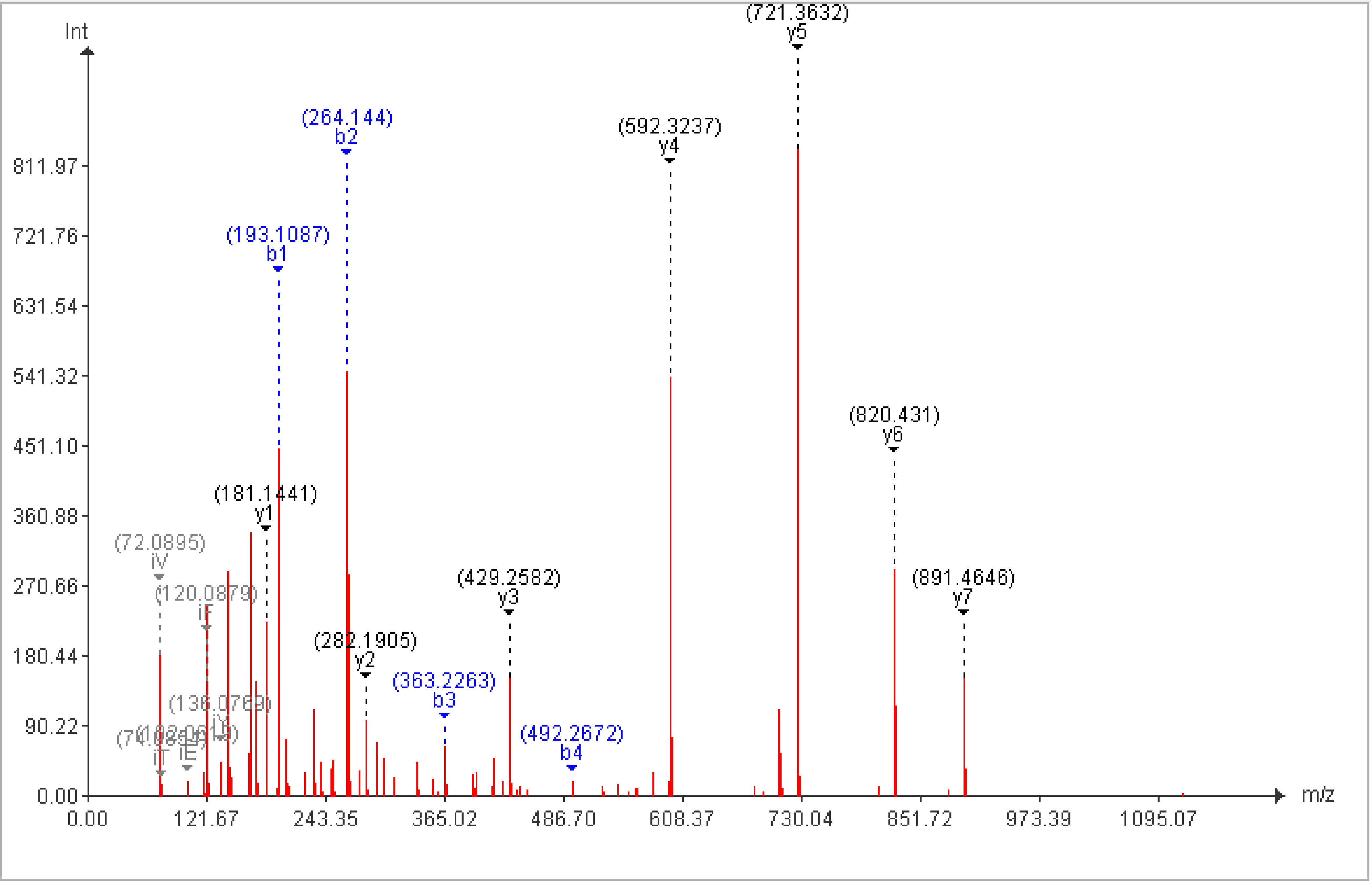


AcD3-FAVEYFTR(C13)-COOH*

precursor mass: 542.2842 Da (charge: +2) protein: P12367 (31-38)

score (threshold): 57.0 (30.0)

instrument: Waters Q-TOF Premier

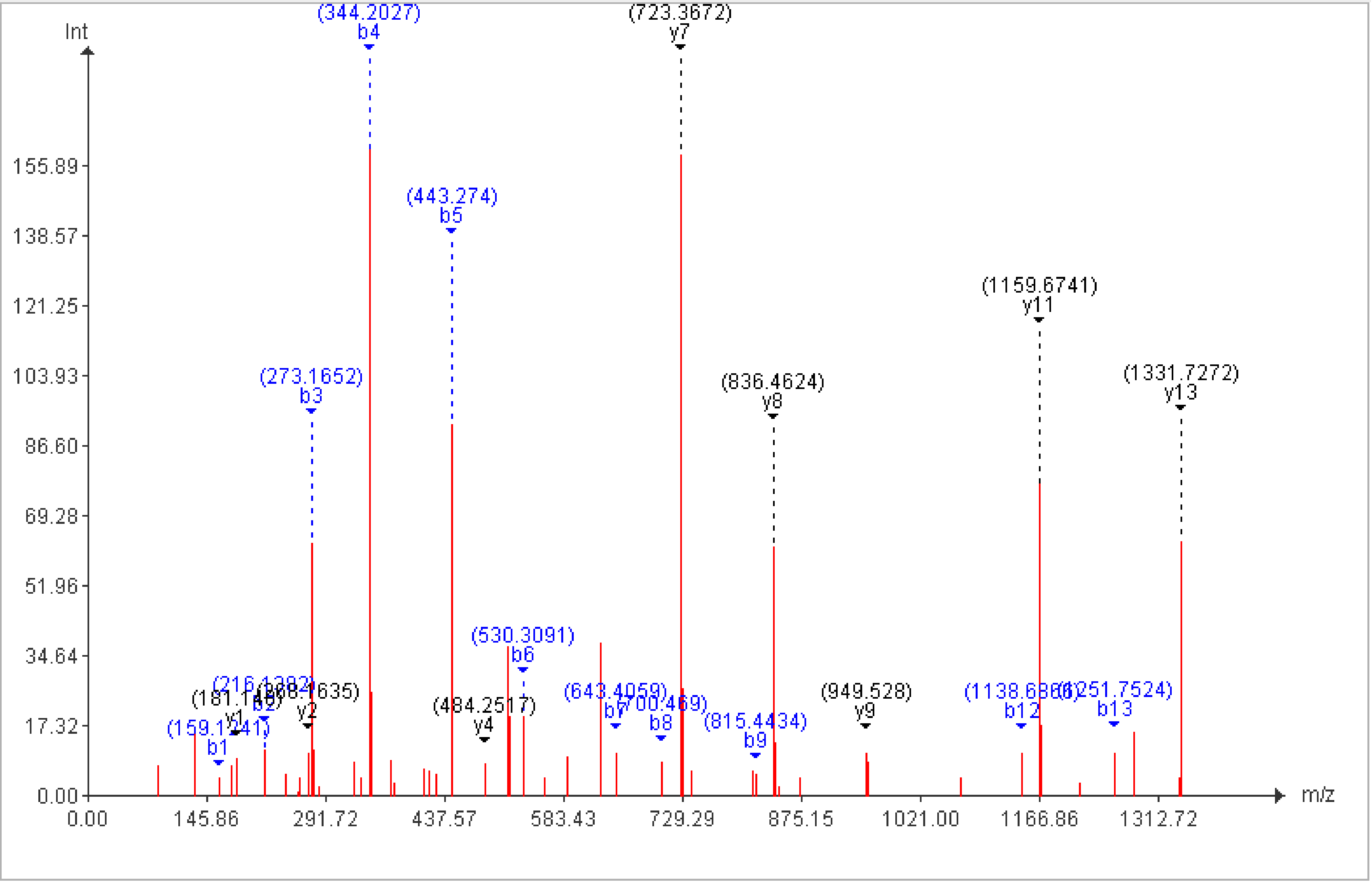


AcD3-LGGAVSLGDPLLLPAASESR(C13)-COOH*

precursor mass: 987.5508 Da (charge: +2) protein: Q8C910 (36-55)

score (threshold): 59.0 (31.0)

instrument: Waters Q-TOF Premier

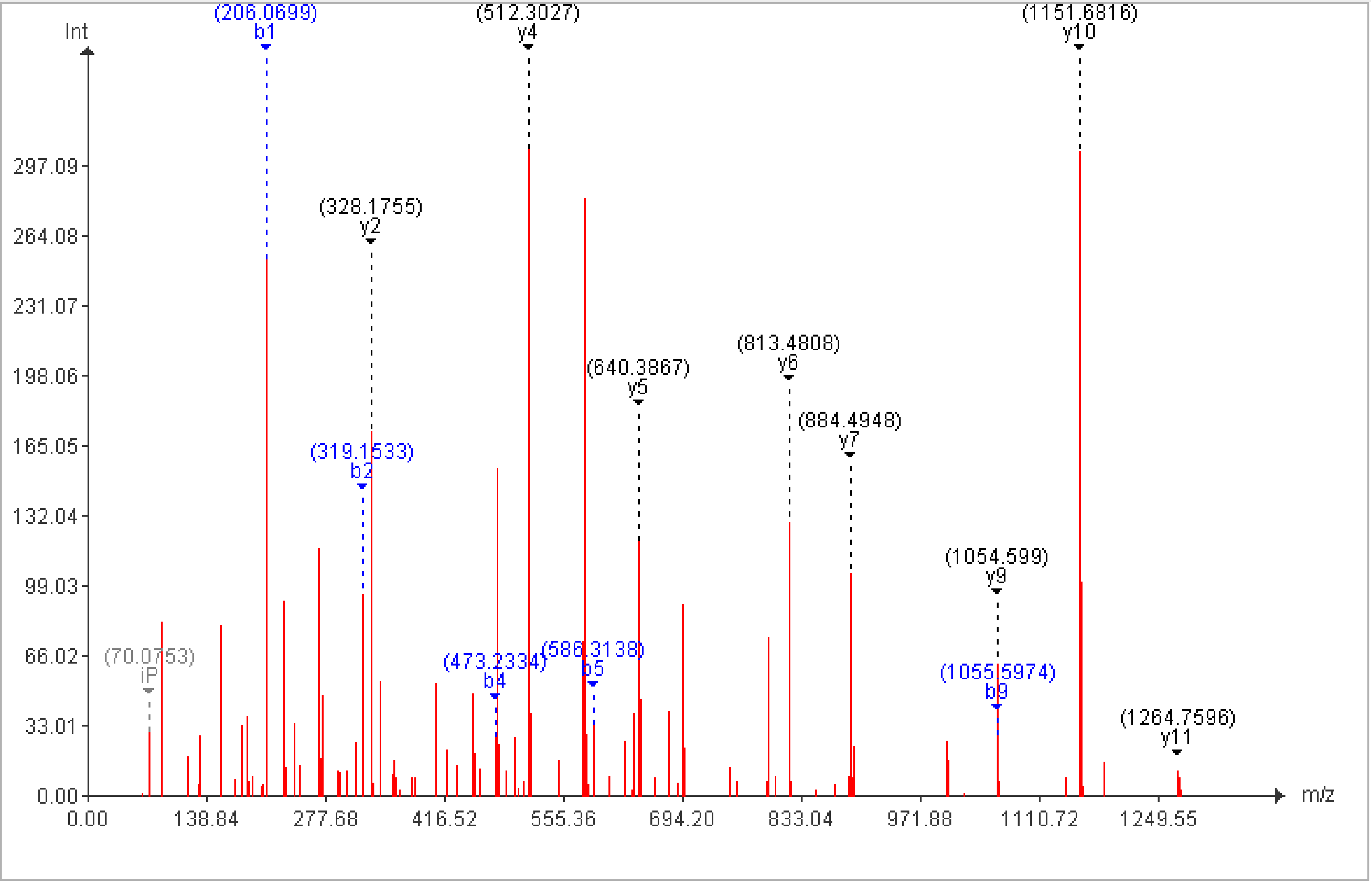


AcD3-C(Cmm)LPGLAK(AcD3K*)QPSFR(C13*)-COOH*

precursor mass: 735.4077 Da (charge: +2) protein: P16675 (32-43)

score (threshold): 52.0 (30.0)

instrument: Waters Q-TOF Premier

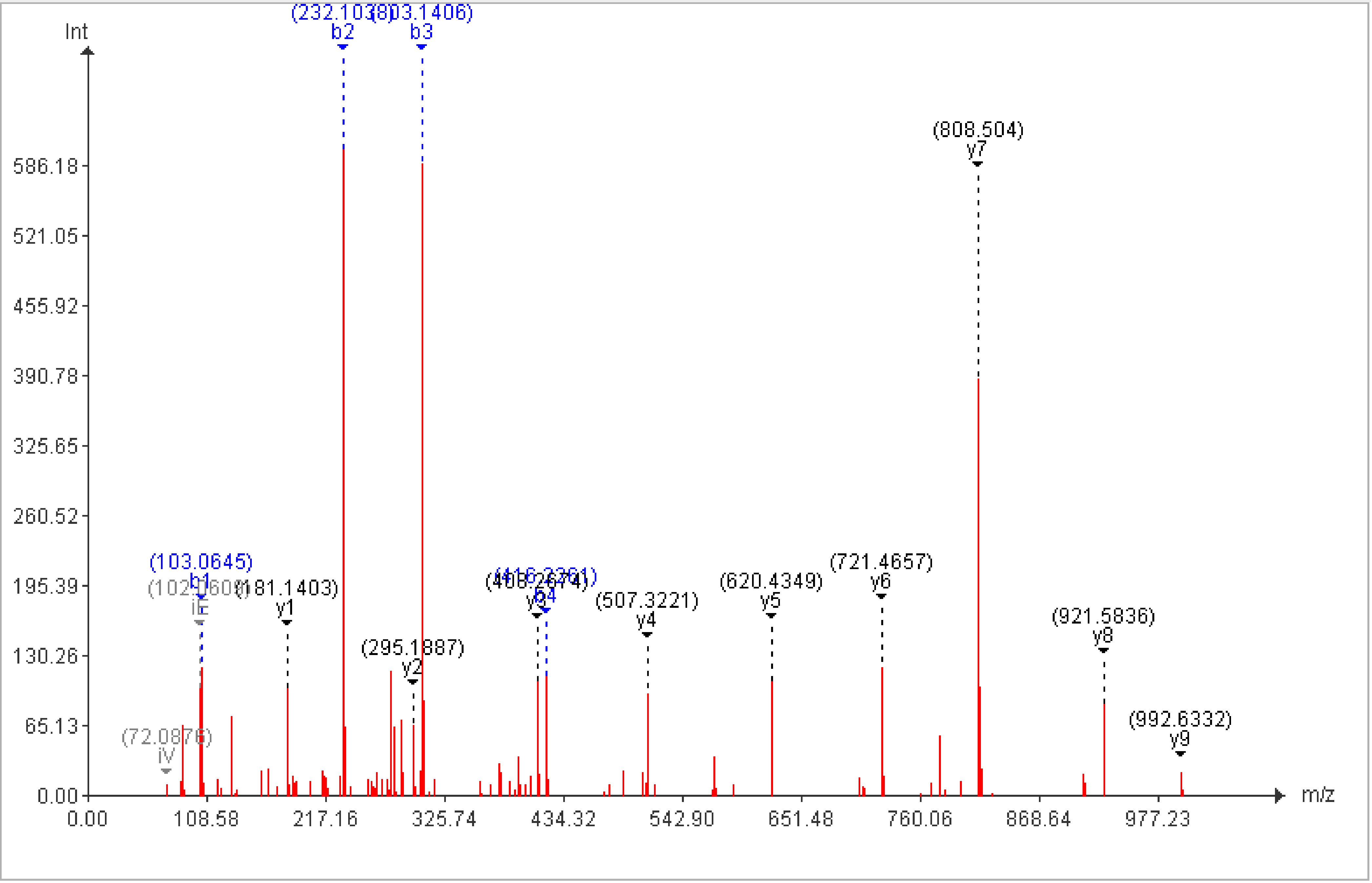


AcD3-GEALSTLVLNR(C13)-COOH*

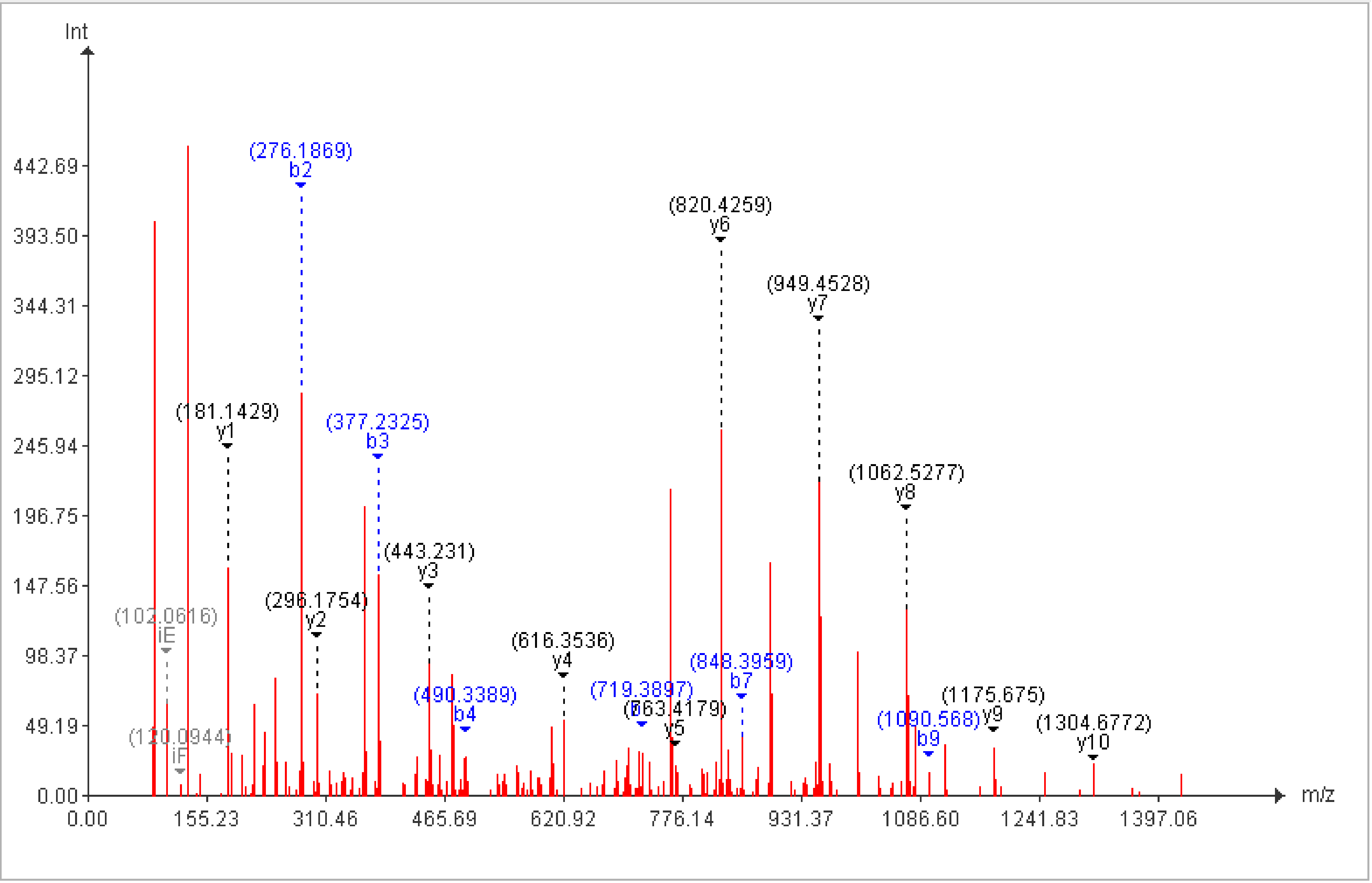
precursor mass: 612.3579 Da (charge: +2) protein: P63038 (280-290)

score (threshold): 62.0 (30.0)

instrument: Waters Q-TOF Premier



AcD3-GK(AcD3K*)TLNDELEIIEGM(Mox*)K(AcD3K*)FDR(C13*)-COOH
precursor mass: 755.7221 Da (charge: +3) protein: P63038 (204-221)
score (threshold): 50.0 (30.0)
instrument: Waters Q-TOF Premier

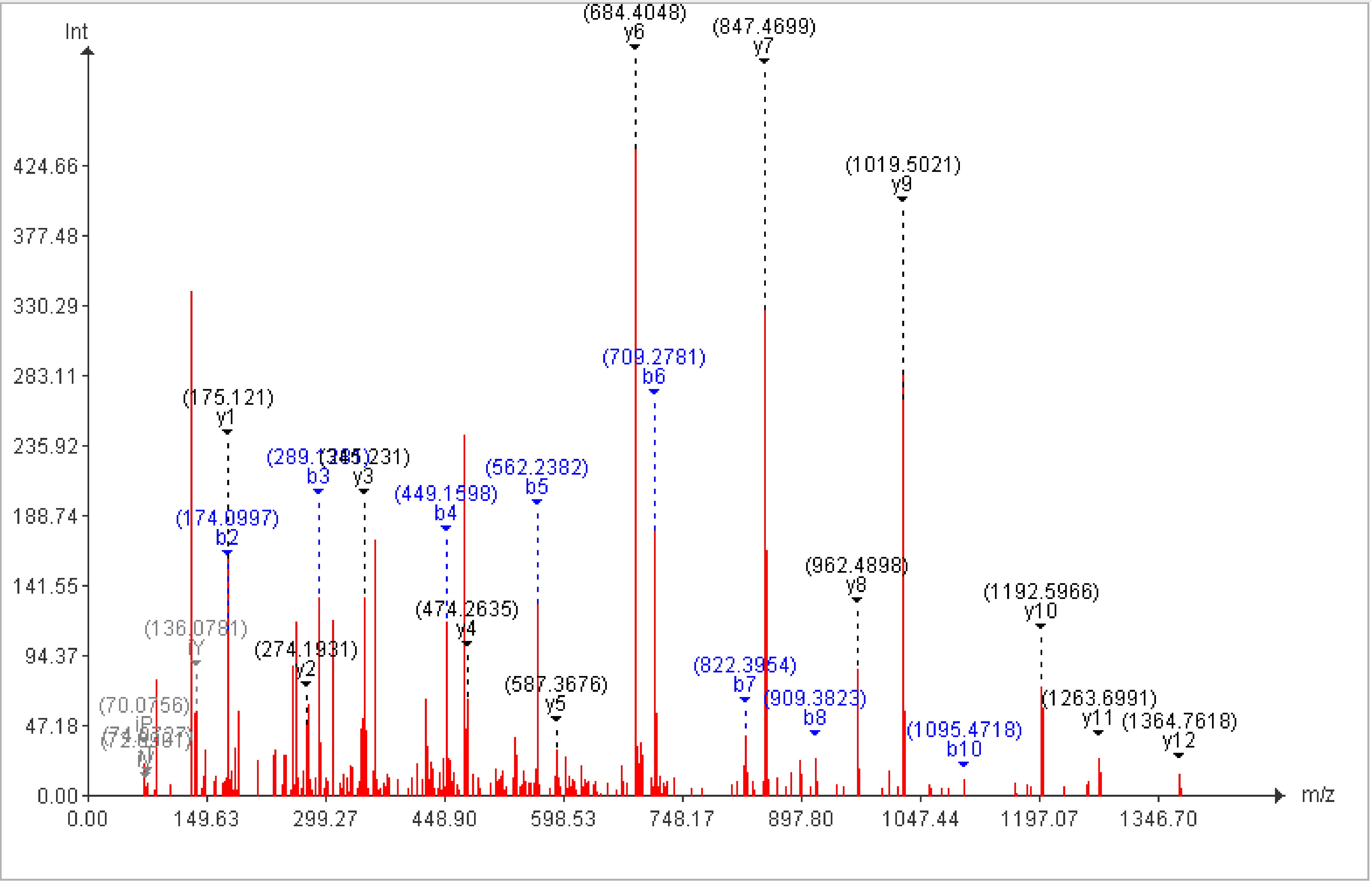


AcD3-GADC(Cmm*)IM(Mox*)LSGETAK(AcD3K*)GDYPLEAVR-COOH

precursor mass: 820.3886 Da (charge: +3) protein: P52480 (355-376)

score (threshold): 71.0 (30.0)

instrument: Waters Q-TOF Premier

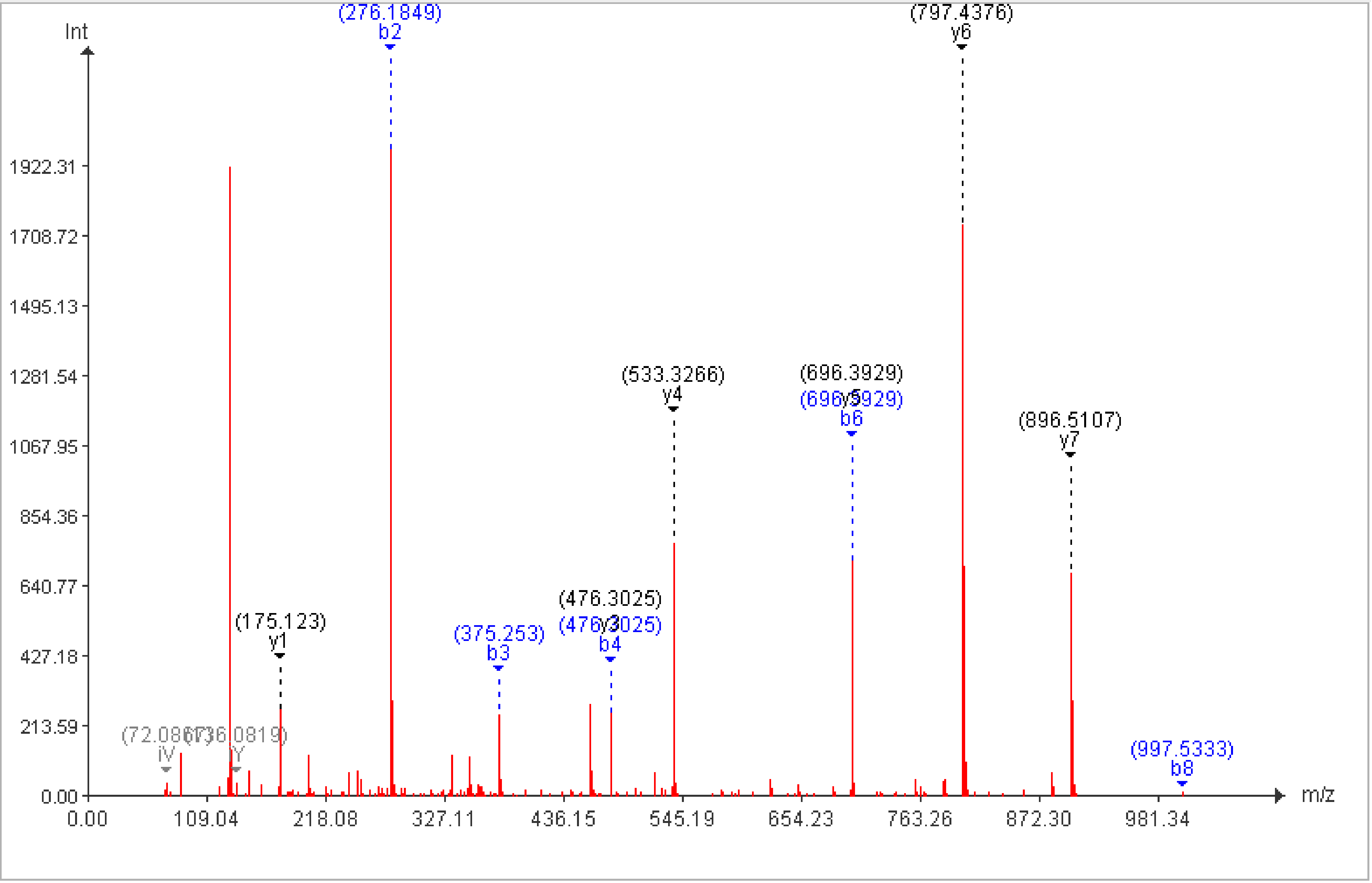


AcD3-GK(AcD3K)VTYGQK(AcD3K*)R-COOH*

precursor mass: 586.3380 Da (charge: +2) protein: Q91VR5 (686-694)

score (threshold): 44.0 (30.0)

instrument: Waters Q-TOF Premier

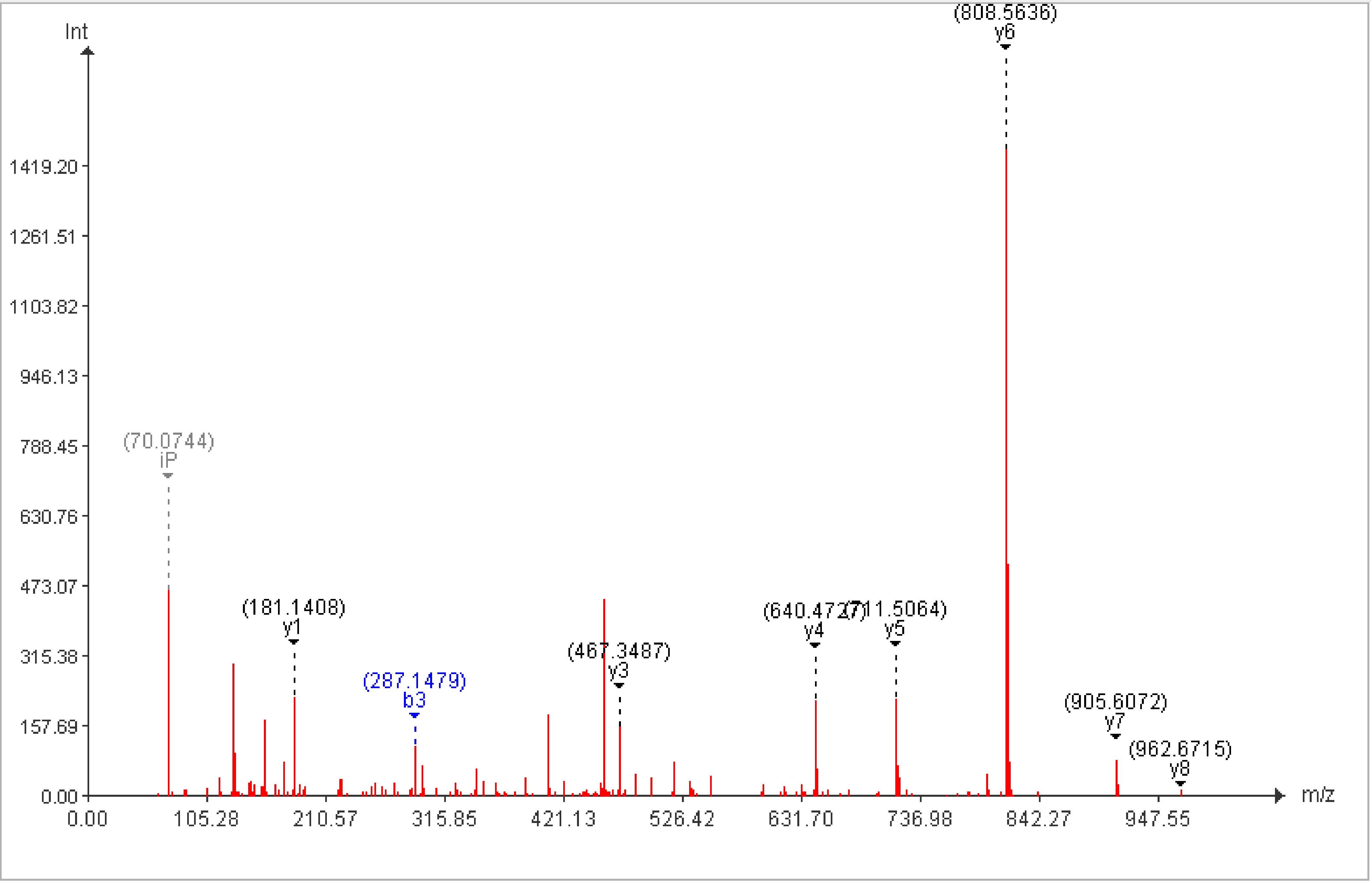


AcD3-SGPPAK(AcD3K*)K(AcD3K*)IR(C13*)-COOH

precursor mass: 547.8477 Da (charge: +2) protein: Q80XU3 (30-38)

score (threshold): 71.0 (30.0)

instrument: Waters Q-TOF Premier

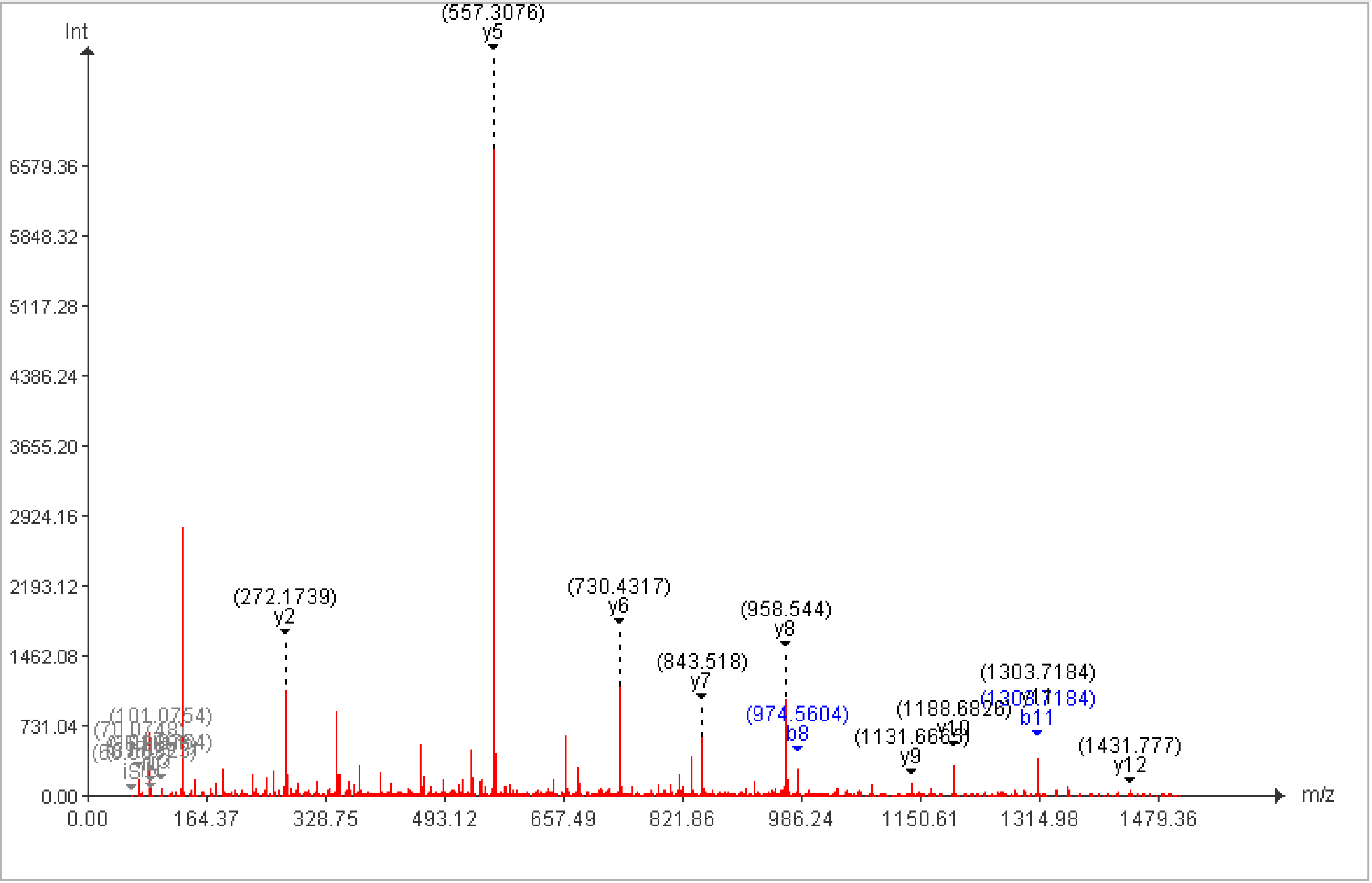


AcD3-TPAK(AcD3K)NAQK(AcD3K*)SNQN(Dam)GK(AcD3K*)DLK(AcD3K*)PSTPR-COOH*

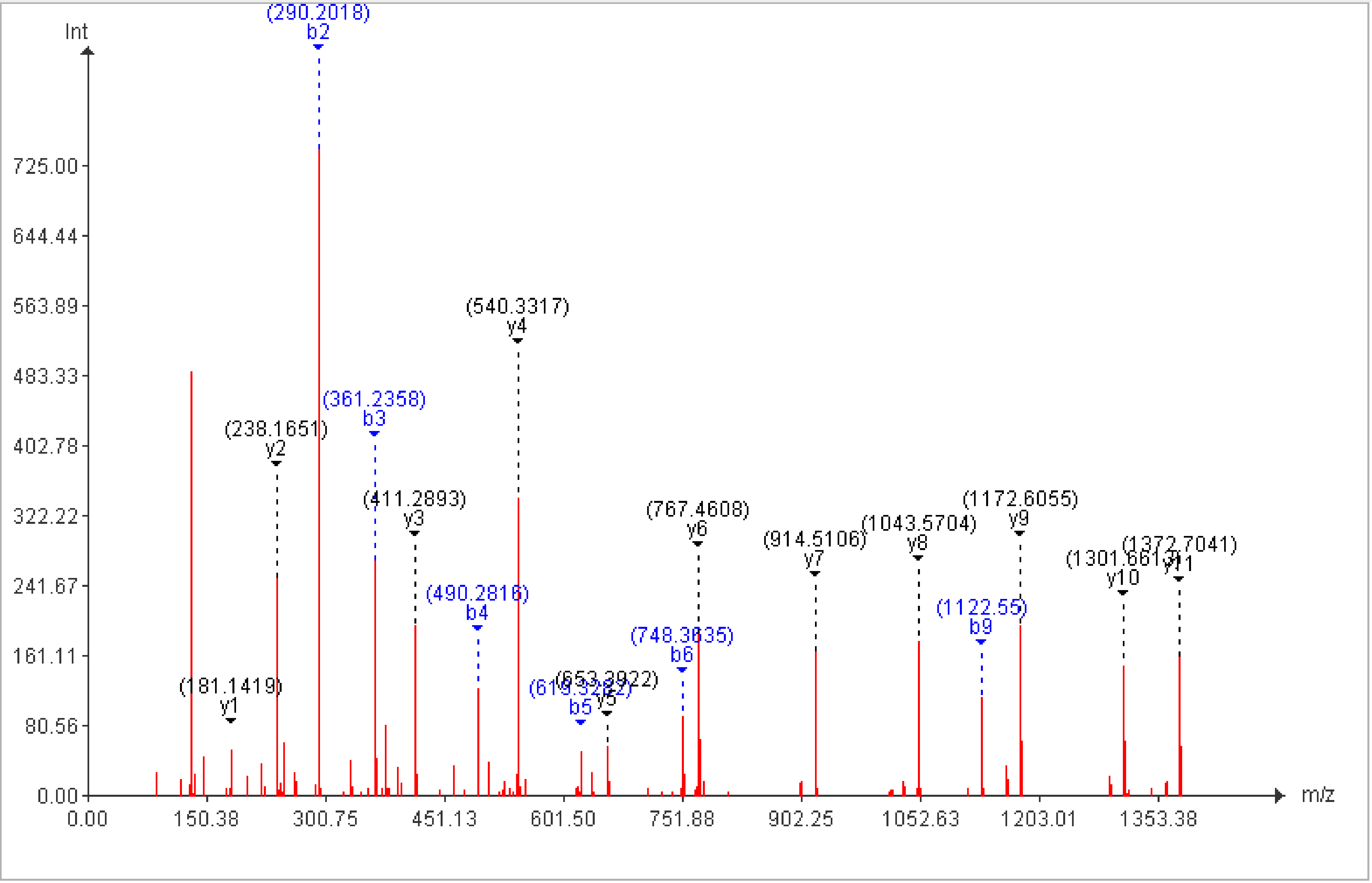
precursor mass: 869.4599 Da (charge: +3) protein: Q61937 (198-219)

score (threshold): 69.0 (30.0)

instrument: Waters Q-TOF Premier



AcD3-AK(AcD3K*)AEEEFNIEK(AcD3K*)GR(C13*)-COOH
precursor mass: 831.4399 Da (charge: +2) protein: P50518 (32-44)
score (threshold): 99.0 (30.0)
instrument: Waters Q-TOF Premier

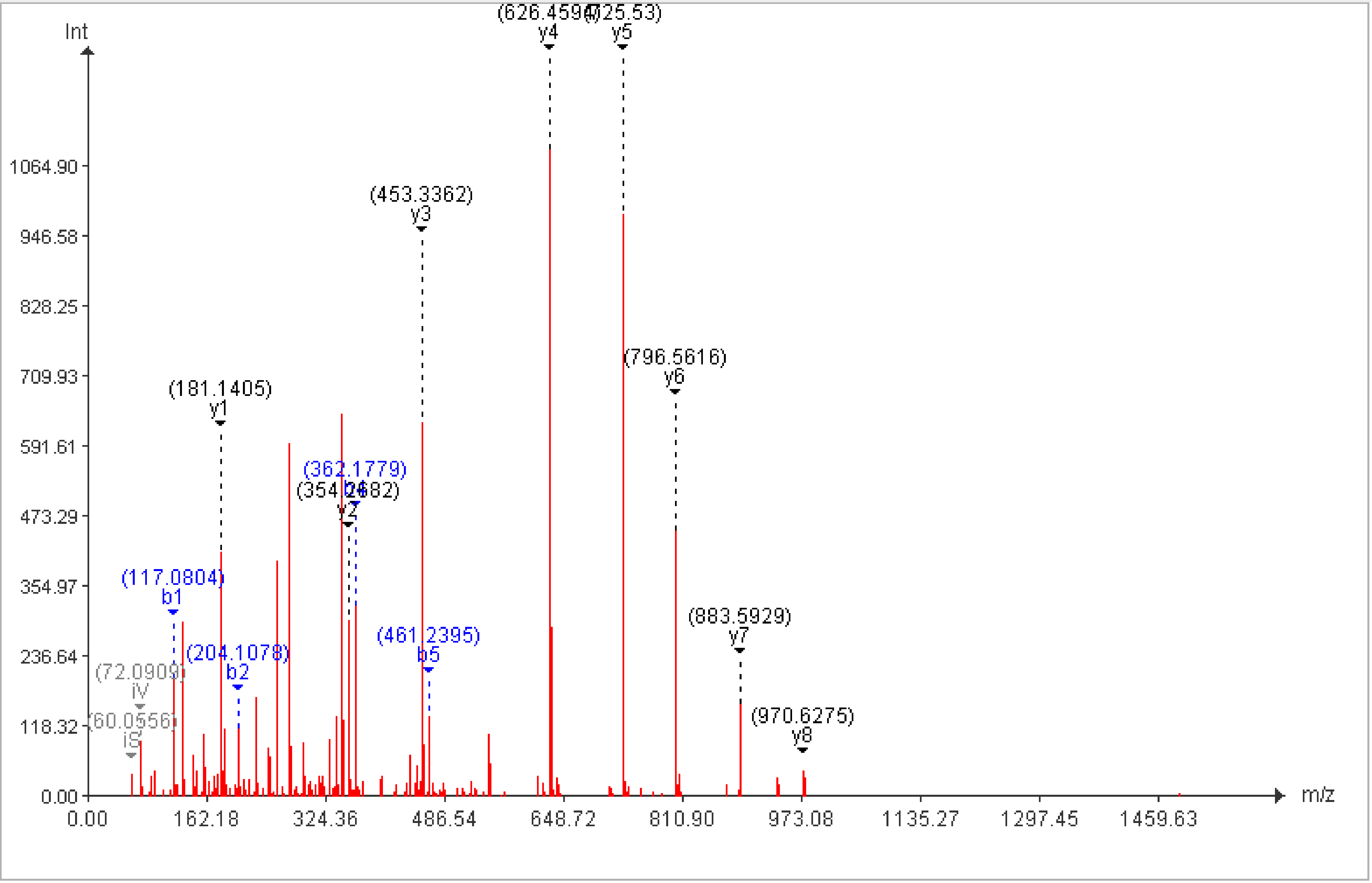


AcD3-ASSAVK(AcD3K*)VK(AcD3K*)R(C13*)-COOH

precursor mass: 543.8462 Da (charge: +2) protein: Q921F2 (90-98)

score (threshold): 71.0 (30.0)

instrument: Waters Q-TOF Premier

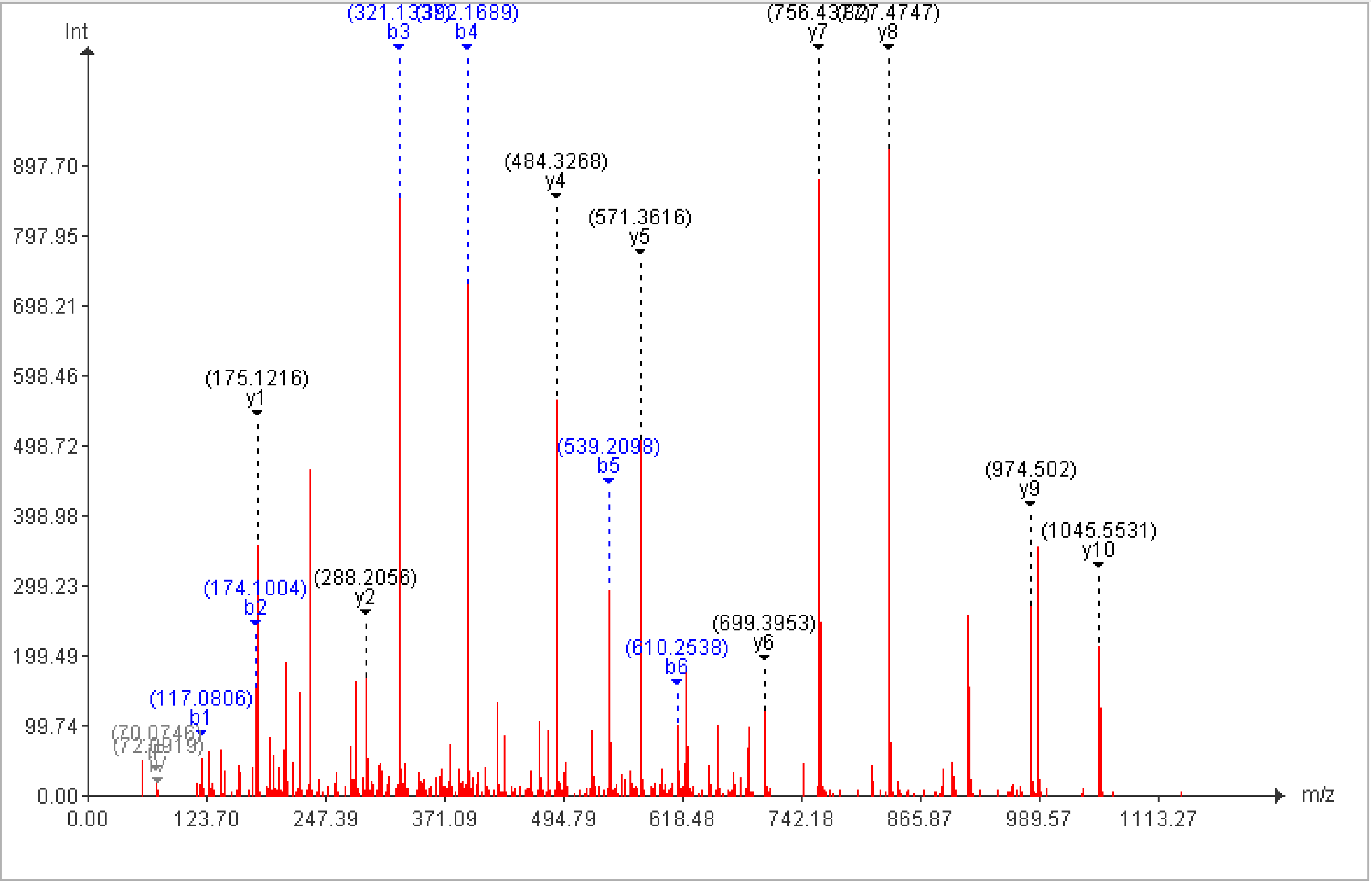


AcD3-AGM(Mox)AM(Mox*)AGQSPVLR-COOH*

precursor mass: 683.3322 Da (charge: +2) protein: P17225 (172-184)

score (threshold): 57.0 (31.0)

instrument: Waters Q-TOF Premier

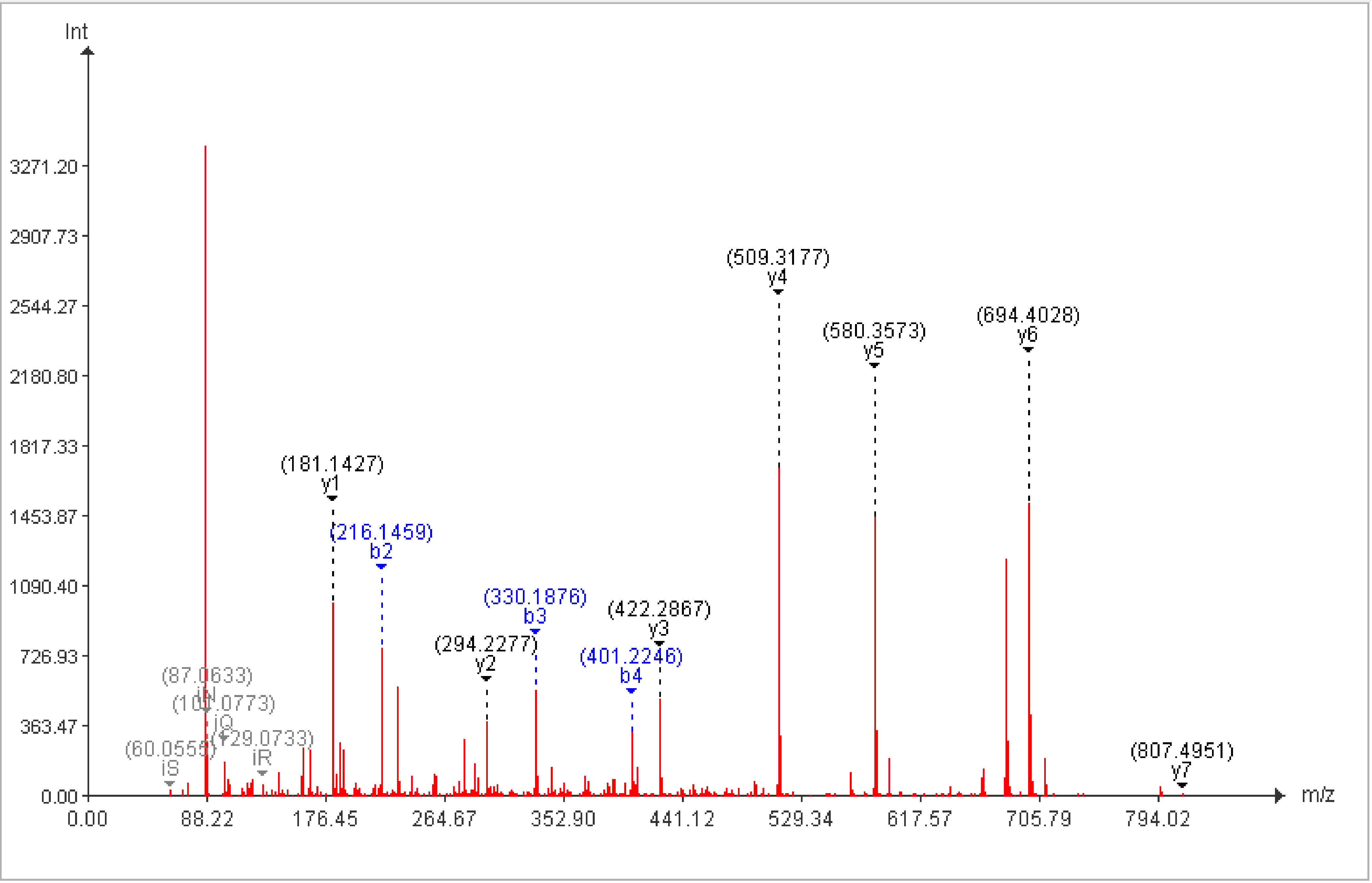


AcD3-GLNASQIR(C13)-COOH*

precursor mass: 455.2632 Da (charge: +2) protein: P08113 (60-67)

score (threshold): 54.0 (31.0)

instrument: Waters Q-TOF Premier

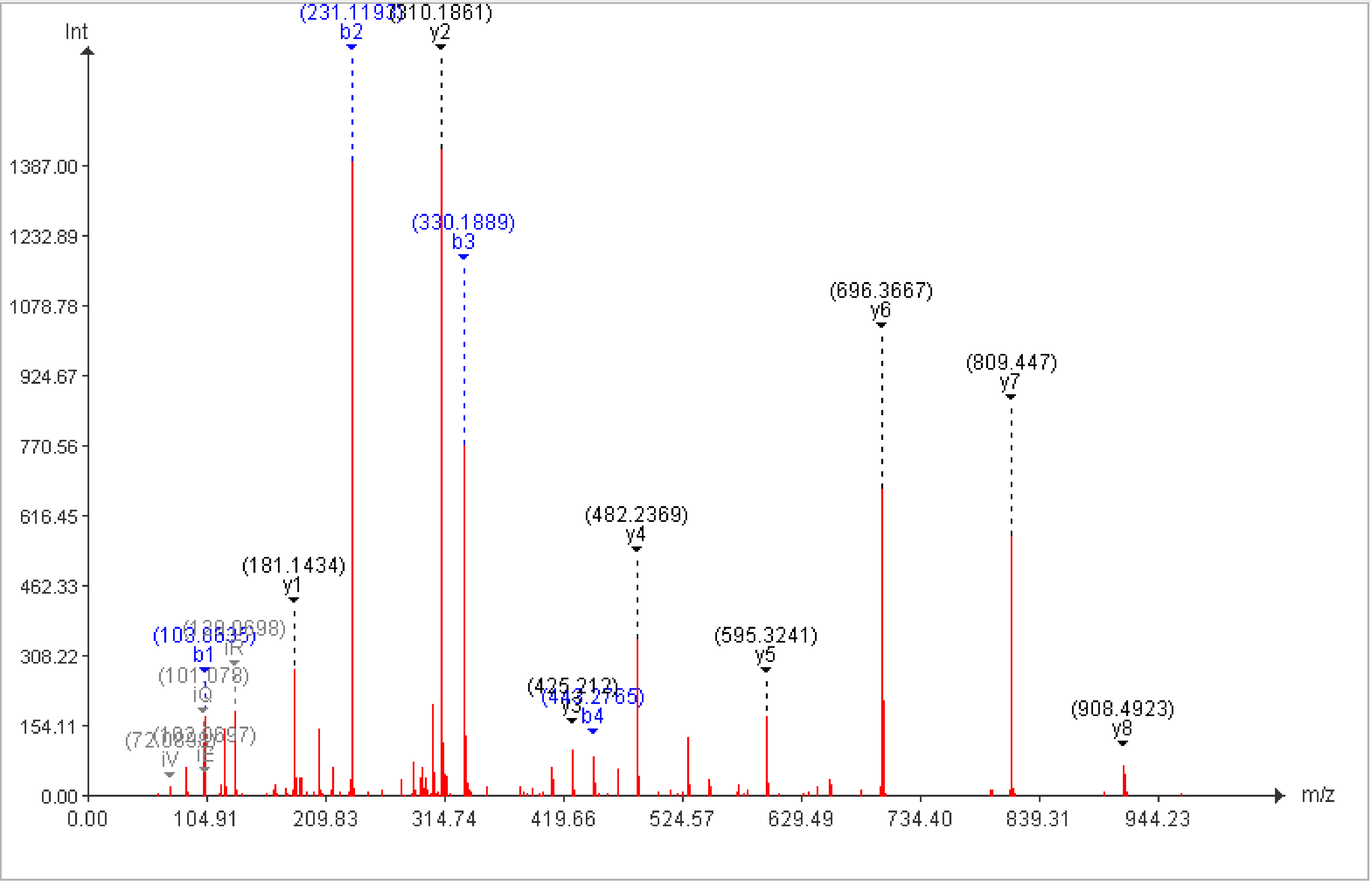


AcD3-GQVITIGN(Dam)ER(C13)-COOH*

precursor mass: 569.8129 Da (charge: +2) protein: P62737 (247-256)

score (threshold): 74.0 (31.0)

instrument: Waters Q-TOF Premier

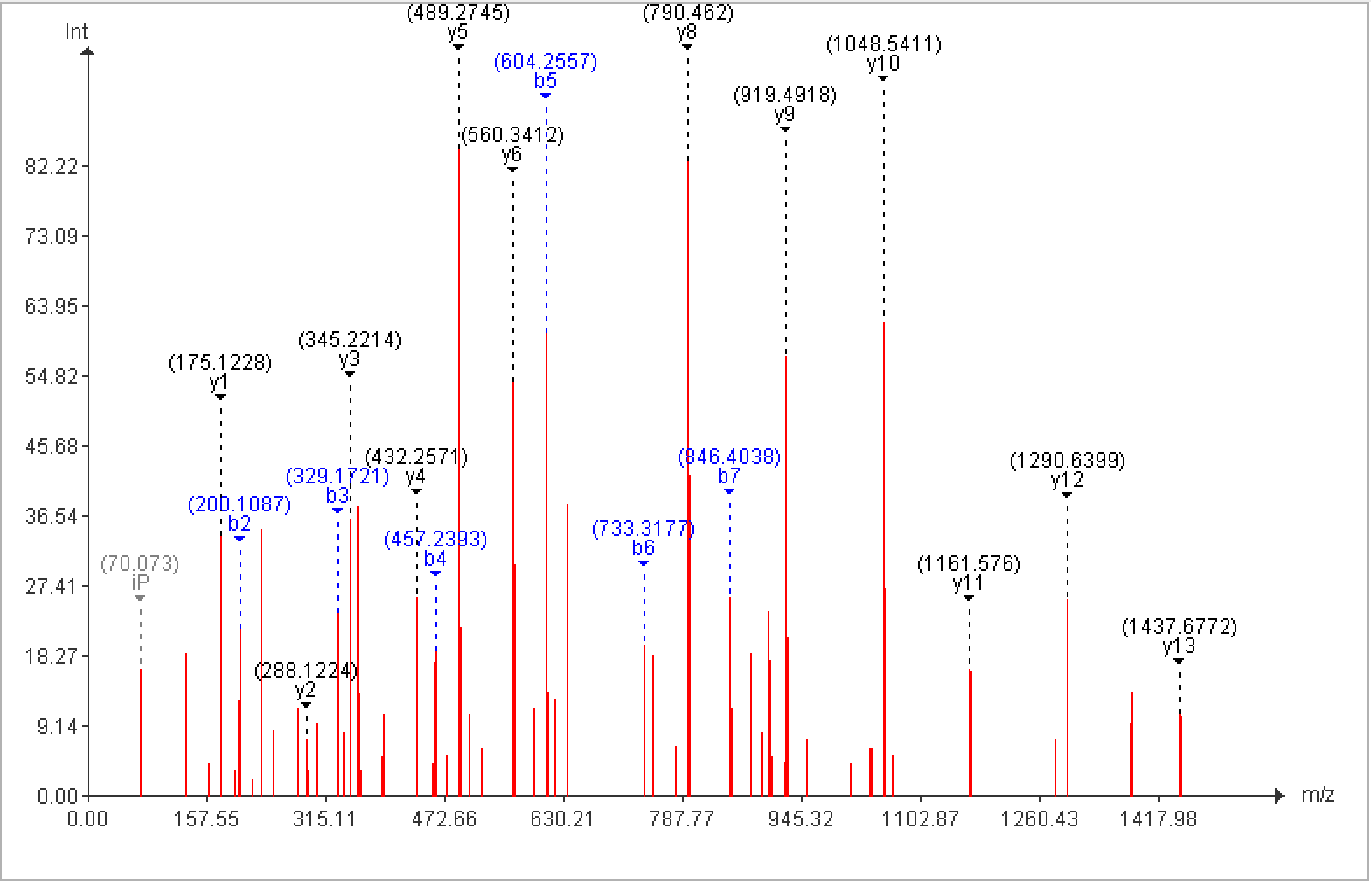


AcD3-GPEQM(Mox)ELEEGK(AcD3K*)AGSGLR-COOH*

precursor mass: 947.4578 Da (charge: +2) protein: P62196 (5-21)

score (threshold): 77.0 (31.0)

instrument: Waters Q-TOF Premier

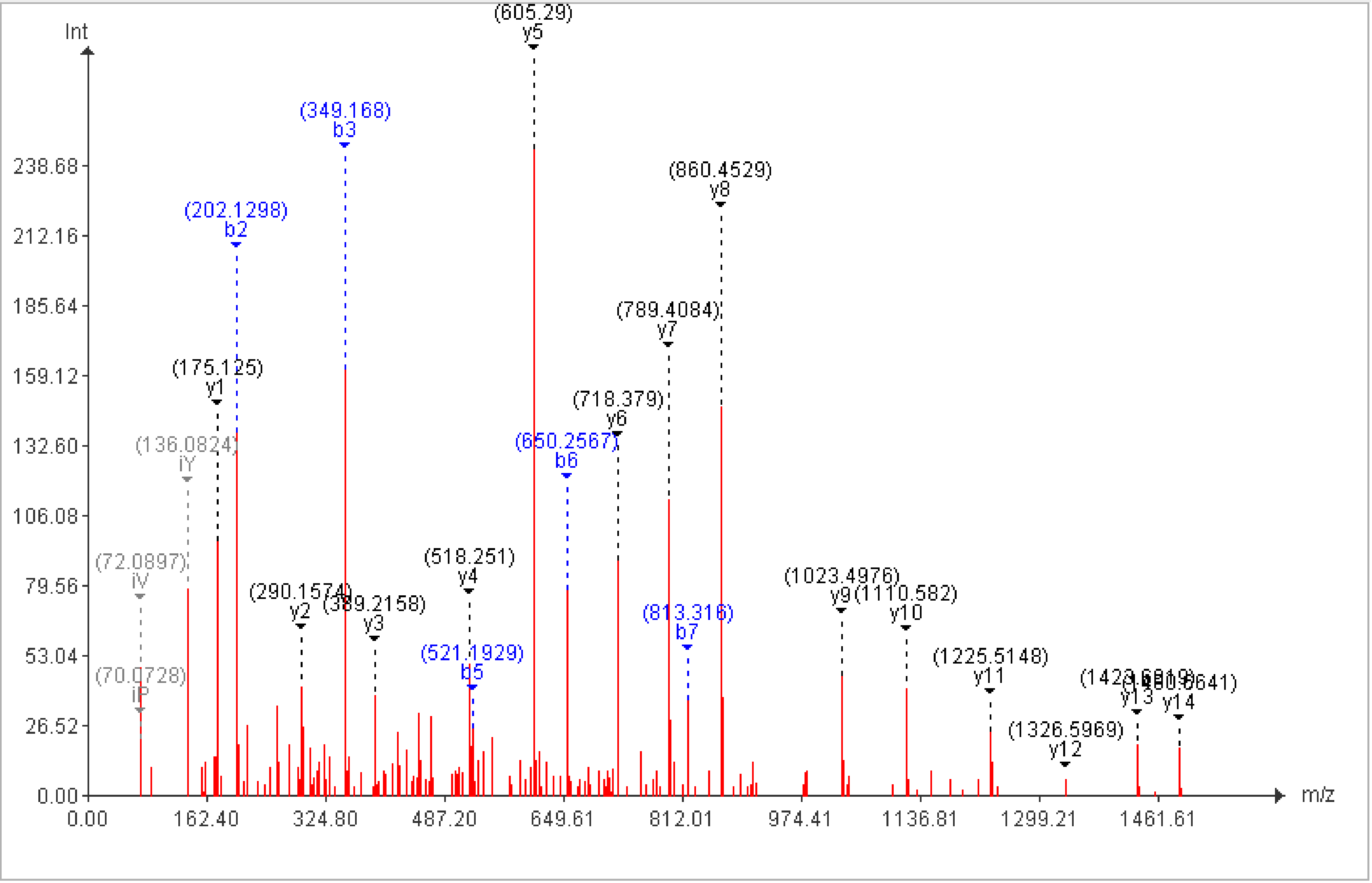


AcD3-GVM(Mox)N(Dam)GEYYQESNGPTDSYAAISEVDR-COOH*

precursor mass: 972.0705 Da (charge: +3) protein: O08585 (76-101)

score (threshold): 98.0 (26.0)

instrument: Waters Q-TOF Premier

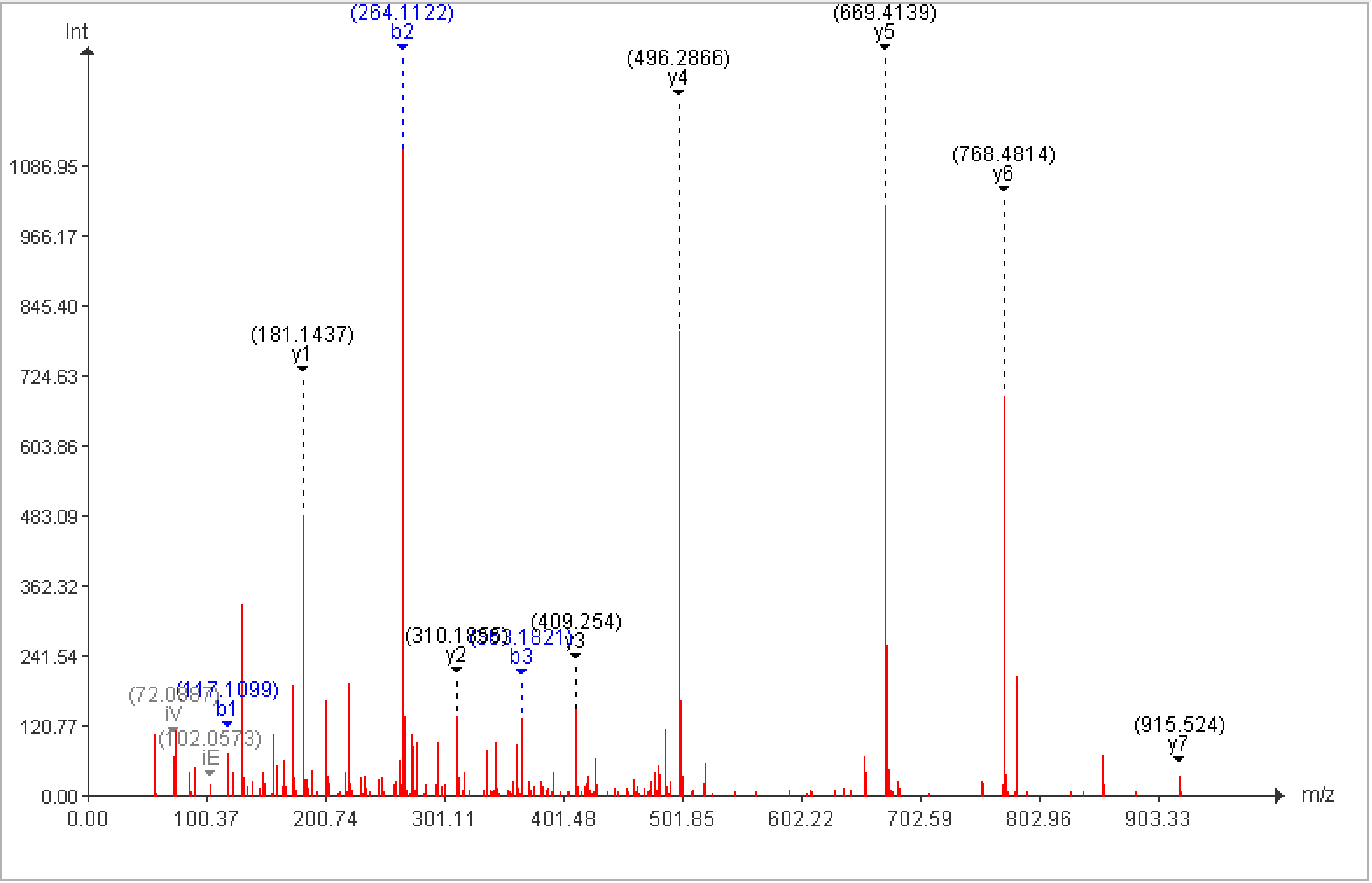


AcD3-AM(Mox*)VK(AcD3K*)SVER(C13*)-COOH

precursor mass: 516.2888 Da (charge: +2) protein: Q9CR98 (15-22)

score (threshold): 58.0 (32.0)

instrument: Waters Q-TOF Premier

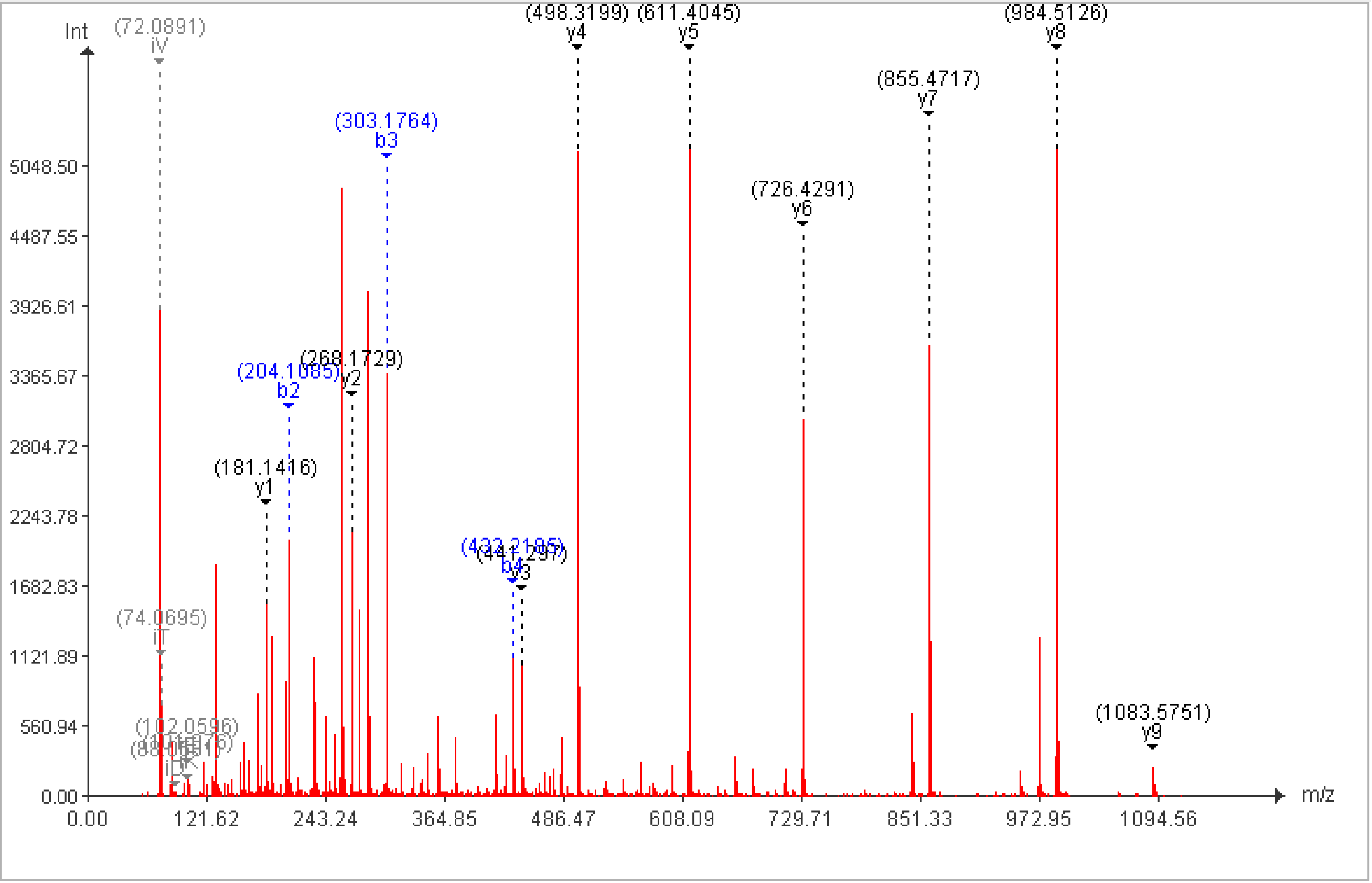


AcD3-GTVEEDLGK(AcD3K)SR(C13*)-COOH*

precursor mass: 643.8311 Da (charge: +2) protein: P08113 (29-39)

score (threshold): 62.0 (30.0)

instrument: Waters Q-TOF Premier

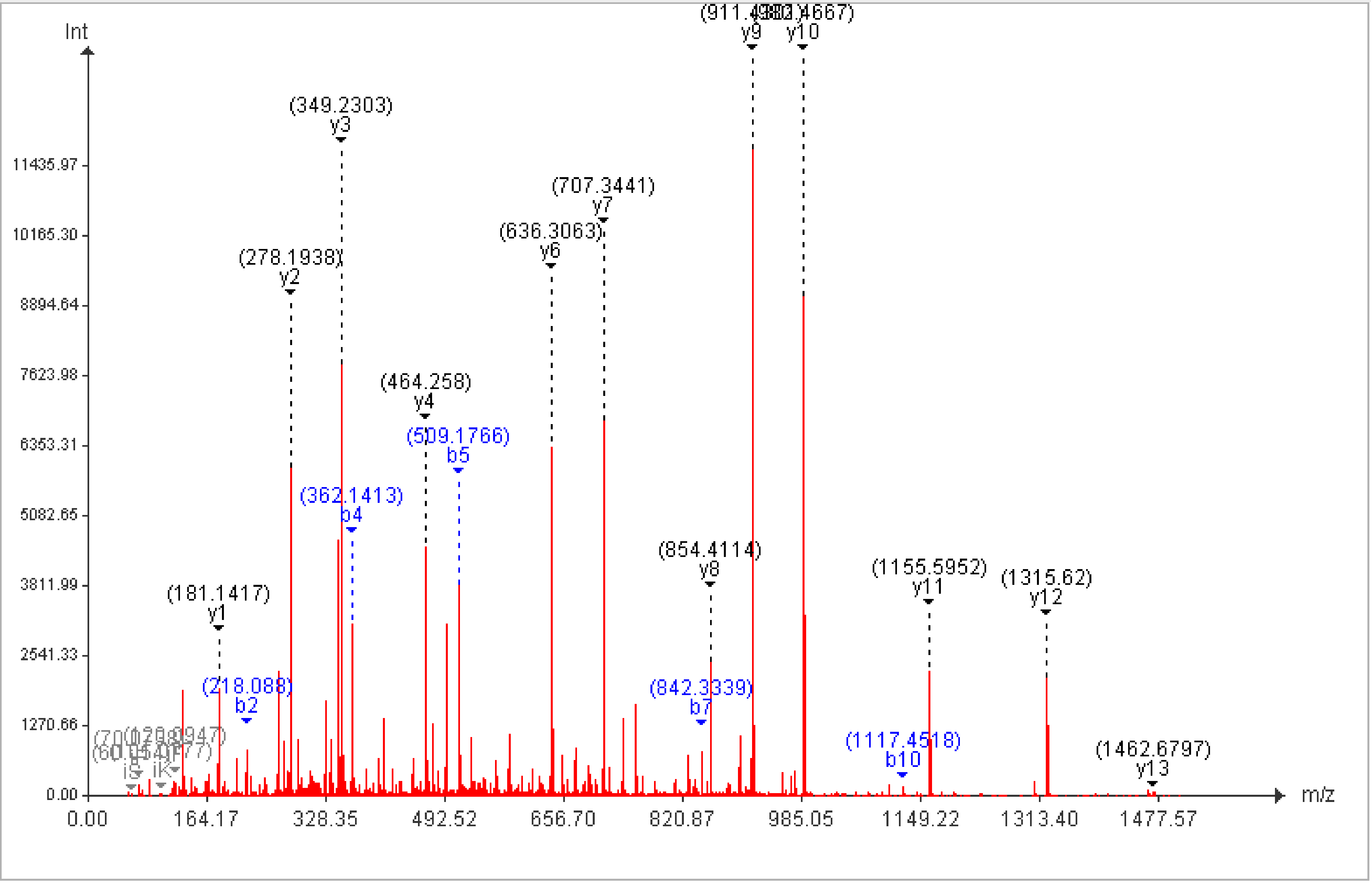


AcD3-N(Dam)GSGM(Mox)C(Cmm*)K(AcD3K*)AGFAGDDAPR(C13*)-COOH*

precursor mass: 912.3651 Da (charge: +2) protein: P60710 (12-28)

score (threshold): 91.0 (25.0)

instrument: Waters Q-TOF Premier

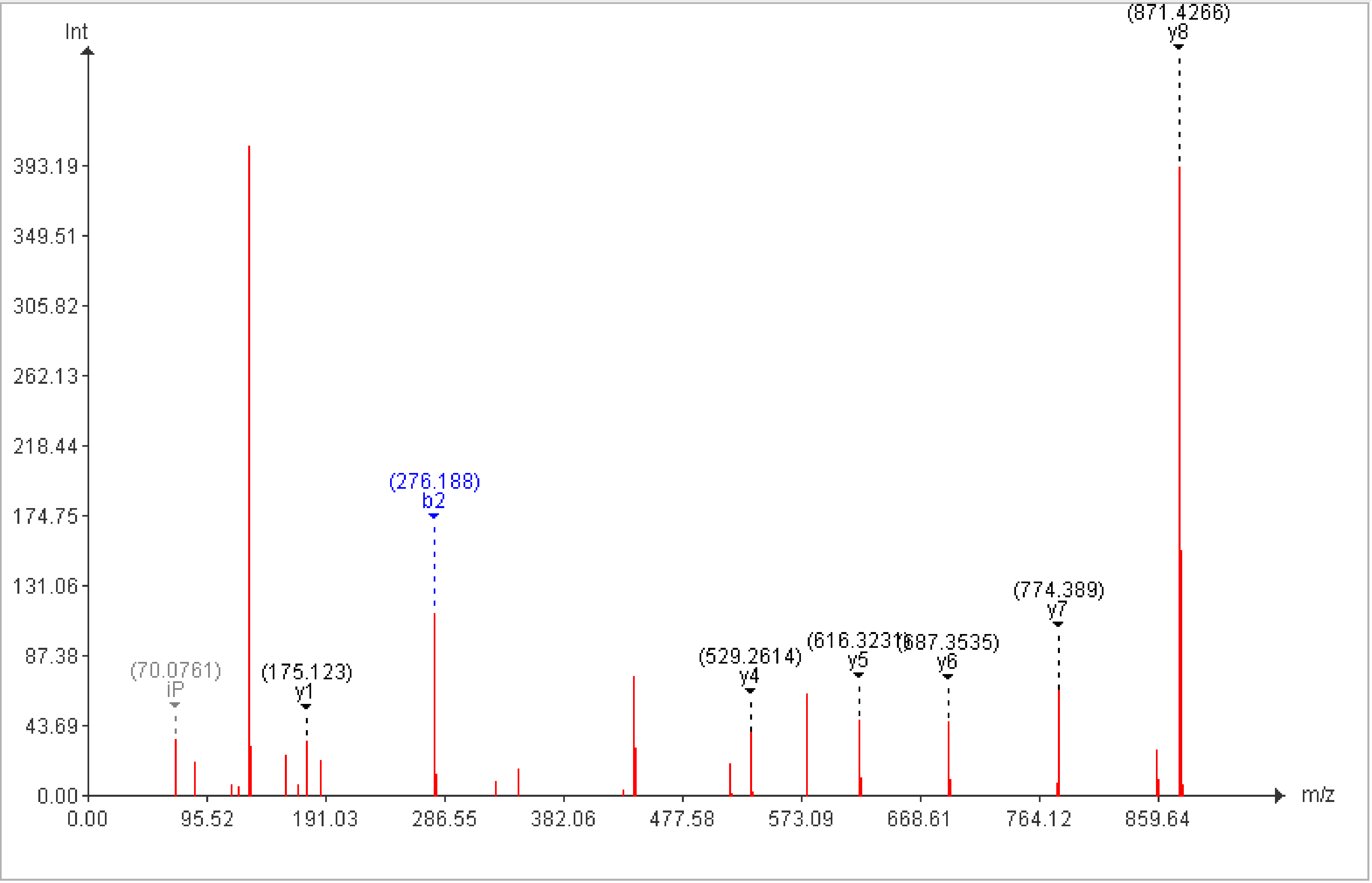


AcD3-GK(AcD3K)PSASPQER-COOH*

precursor mass: 573.8047 Da (charge: +2) protein: Q8BTI8 (1503-1512)

score (threshold): 40.0 (31.0)

instrument: Waters Q-TOF Premier

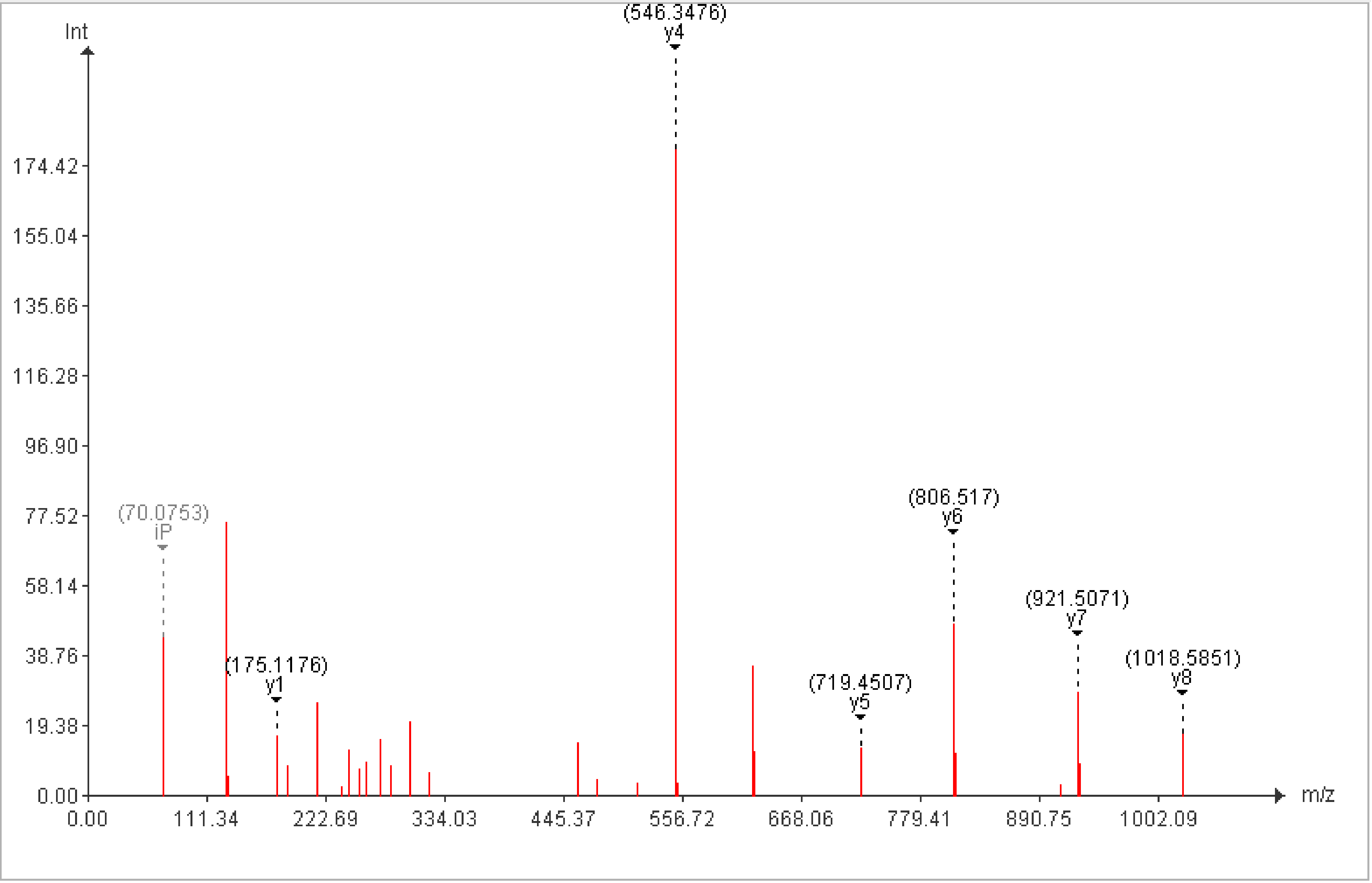


AcD3-SSPDSK(AcD3K*)PK(AcD3K*)TR-COOH

precursor mass: 619.3387 Da (charge: +2) protein: Q8BTI8 (1517-1526)

score (threshold): 32.0 (31.0)

instrument: Waters Q-TOF Premier

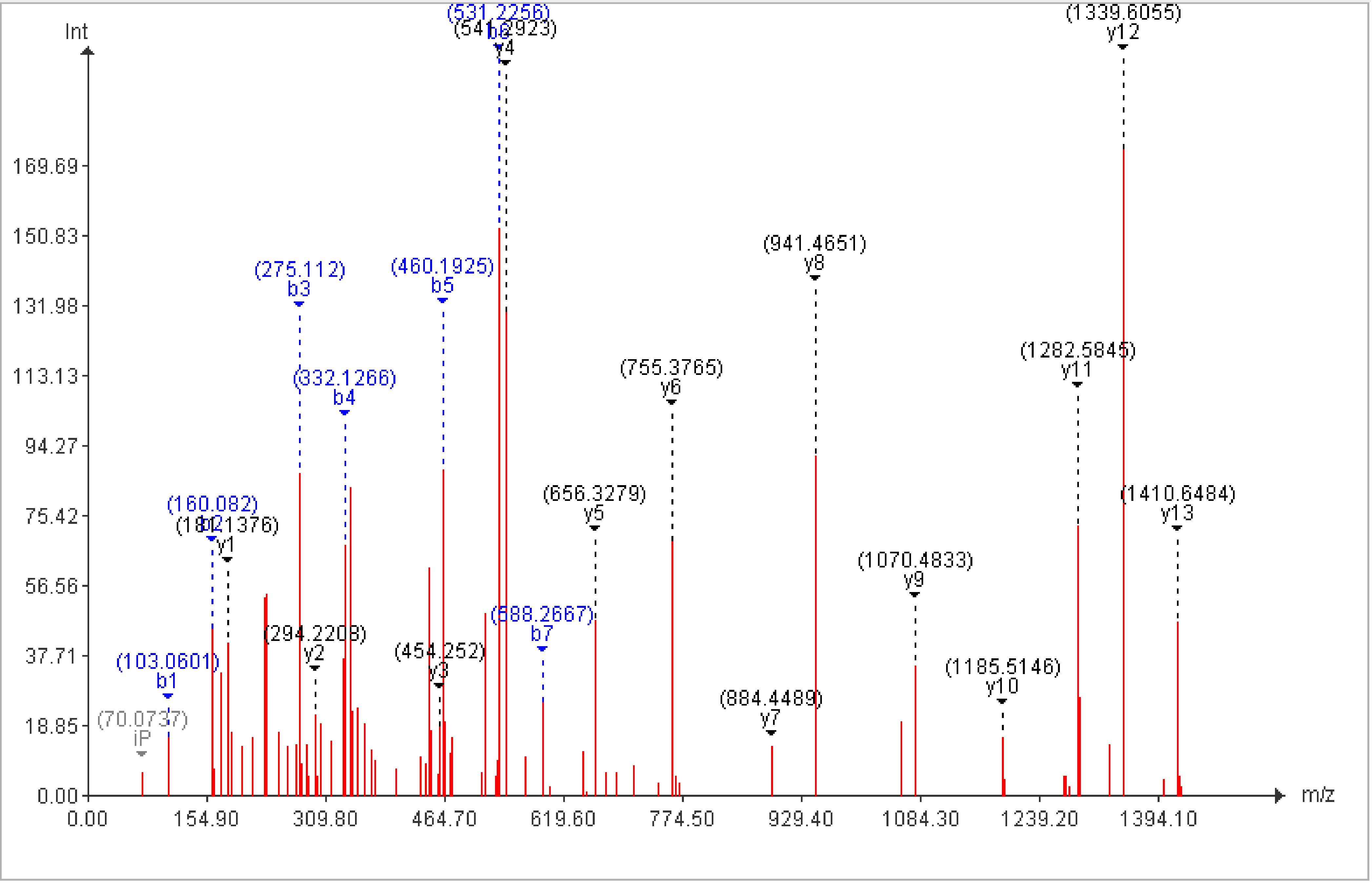


AcD3-GGDGQAGPDEGEVDSC(Cmm)LR(C13*)-COOH*

precursor mass: 935.4052 Da (charge: +2) protein: Q9CPW4 (30-47)

score (threshold): 97.0 (27.0)

instrument: Waters Q-TOF Premier

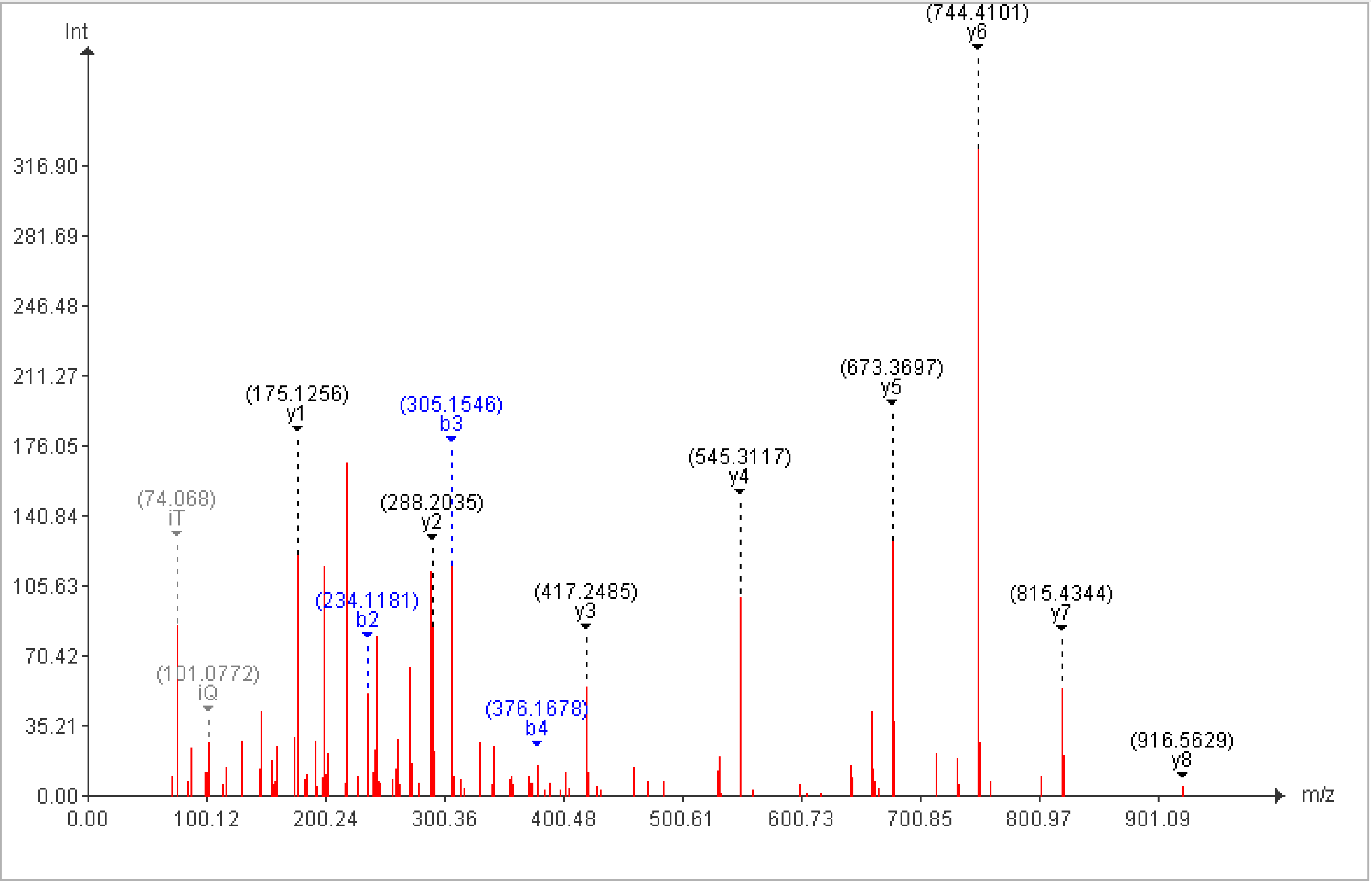


AcD3-STAAQQELR-COOH

precursor mass: 524.7723 Da (charge: +2) protein: Q8VDD5 (1154-1162)

score (threshold): 65.0 (31.0)

instrument: Waters Q-TOF Premier

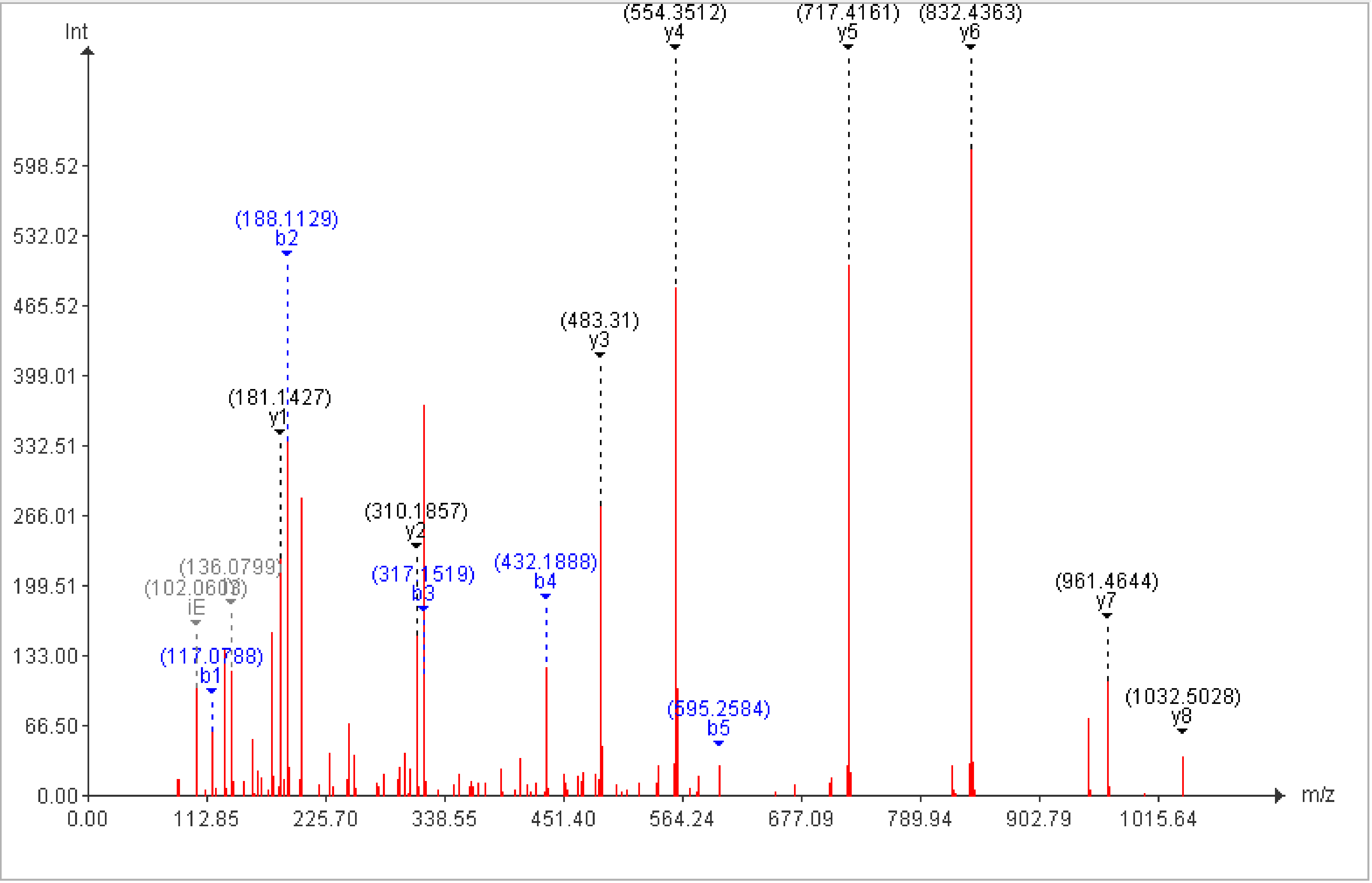


AcD3-AAEDYAK(AcD3K)ER(C13*)-COOH*

precursor mass: 574.7883 Da (charge: +2) protein: Q922B2 (20-28)

score (threshold): 69.0 (30.0)

instrument: Waters Q-TOF Premier

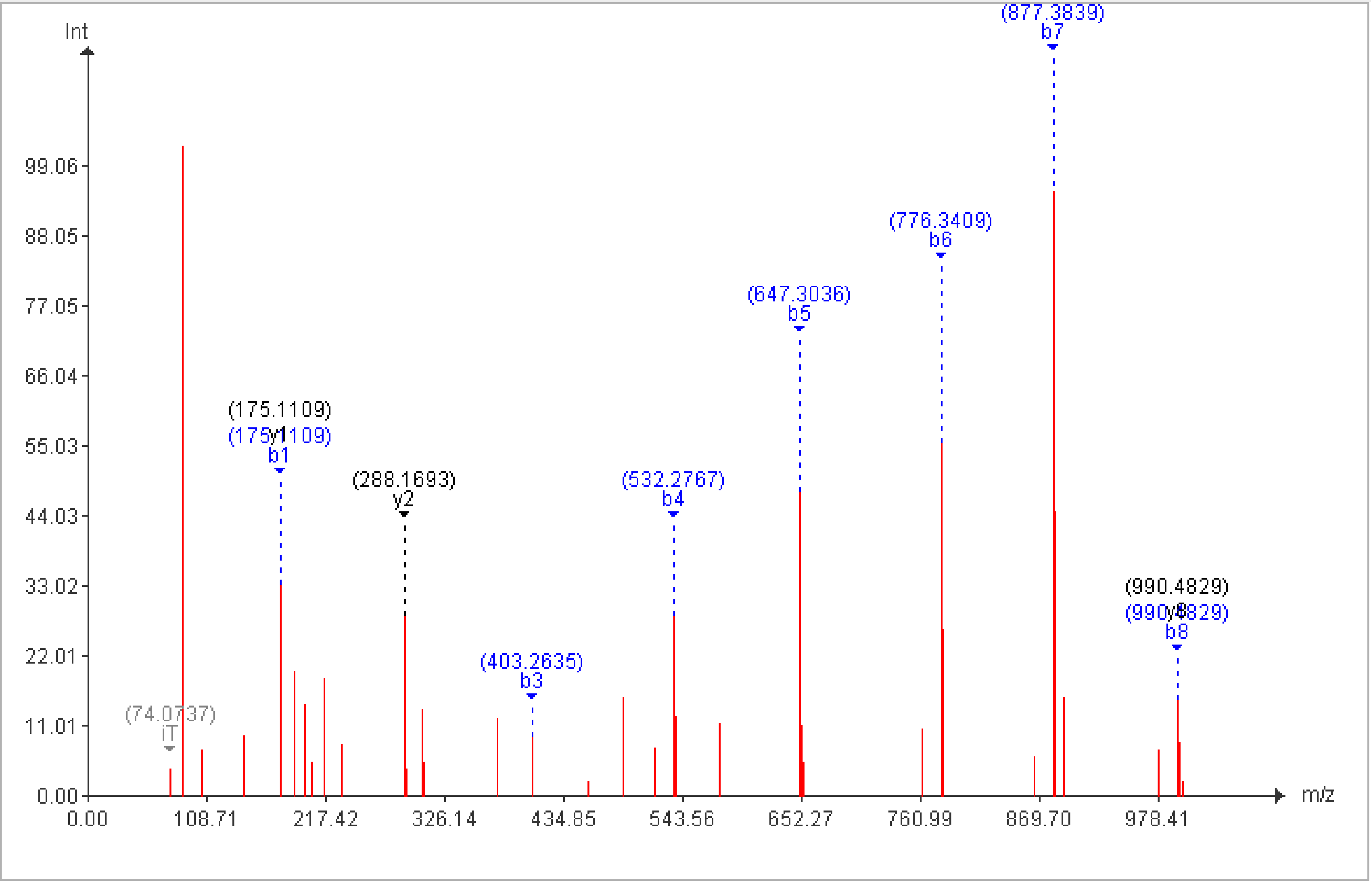


AcD3-EDLEN(Dam)Q(Dam)TLR-COOH

precursor mass: 582.7749 Da (charge: +2) protein: P70188 (250-258)

score (threshold): 70.0 (31.0)

instrument: Waters Q-TOF Premier



Supplemental Figure 2

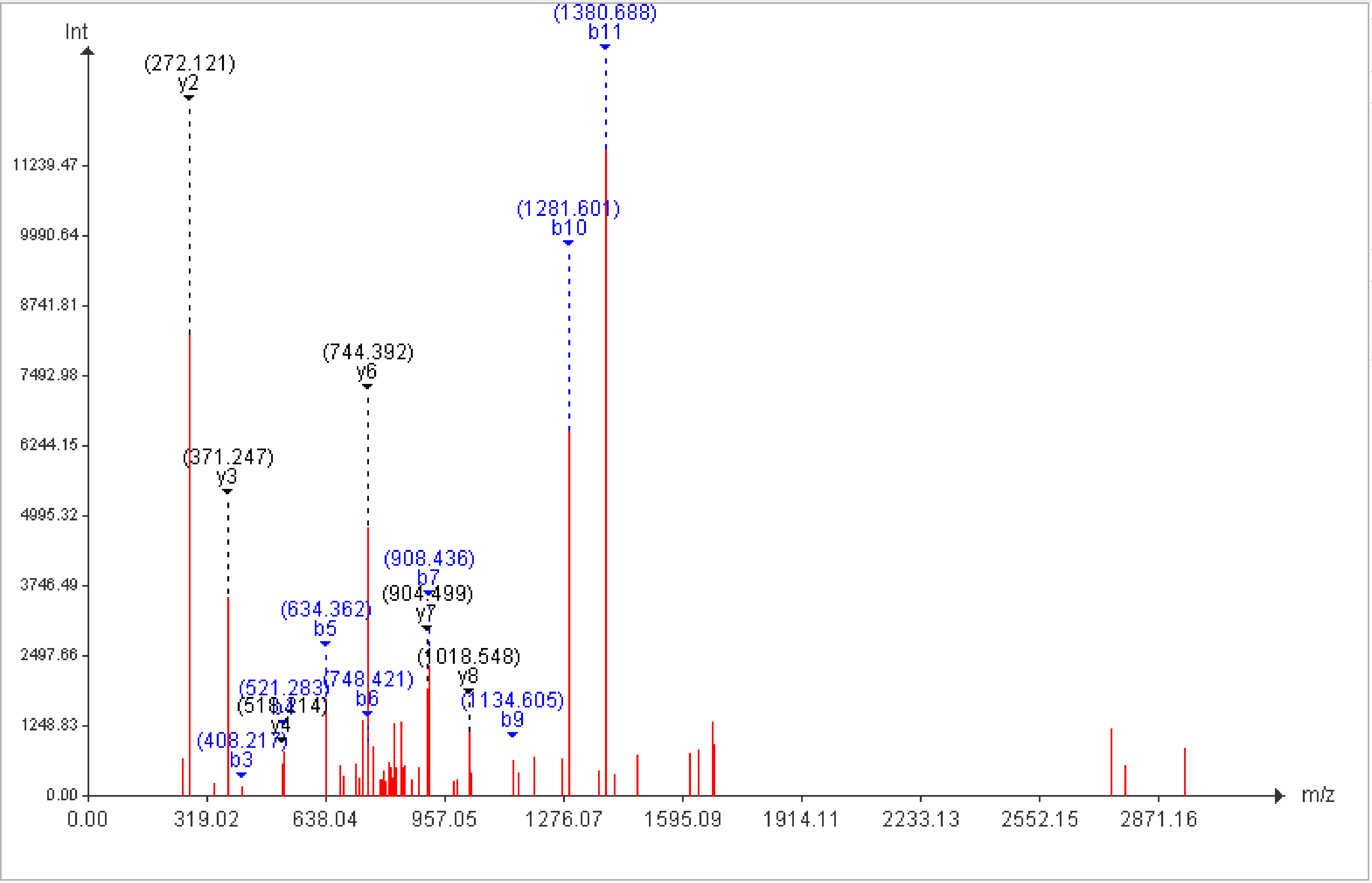
List of identified low scoring MS/MS spectra (n=65)

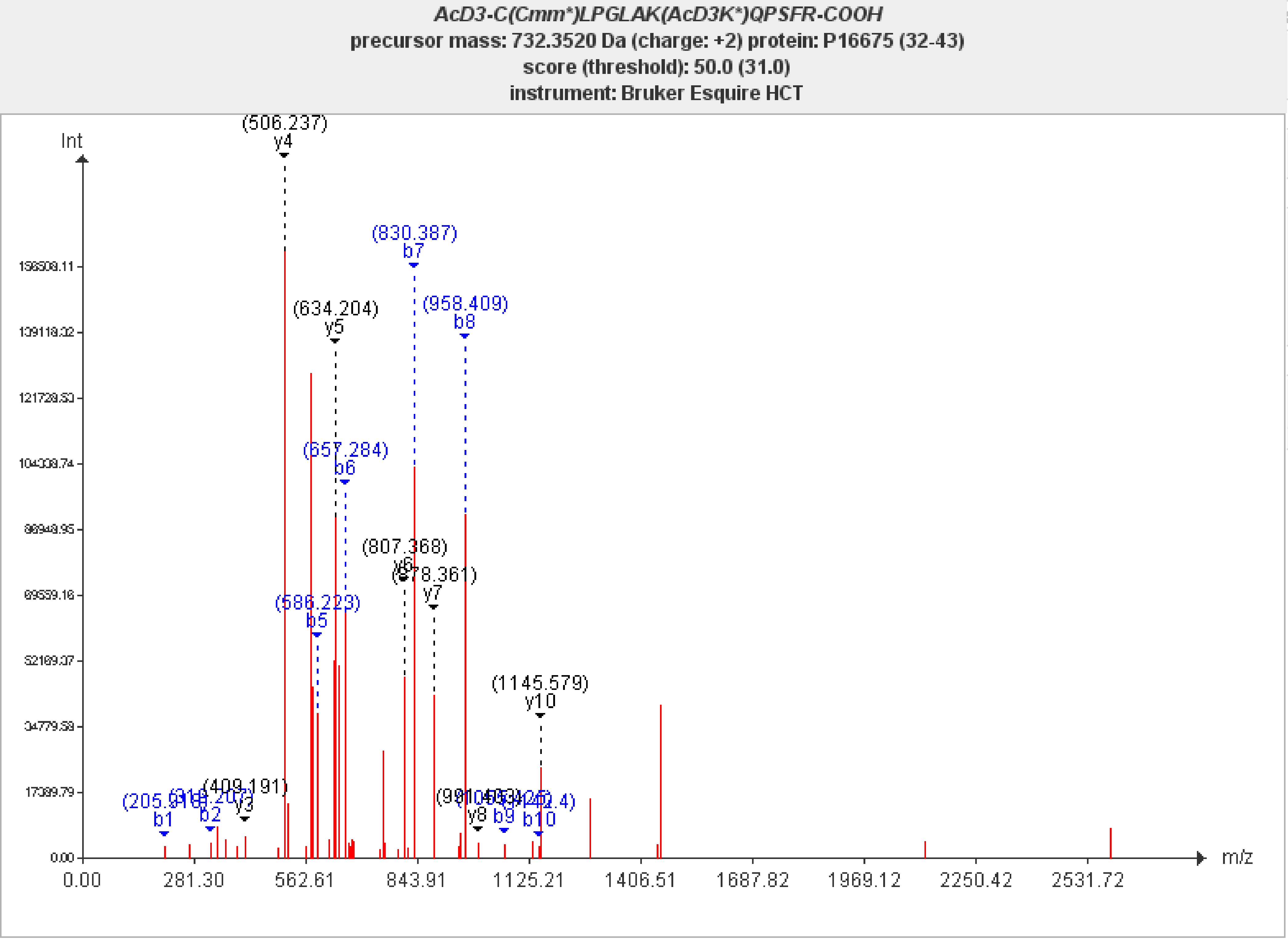
AcD3-FSQLLNC(Cmm)PEFVPR-COOH*

precursor mass: 826.2790 Da (charge: +2) protein: IPI00185919.3 (496-508)

score (threshold): 48.0 (35.0)

instrument: Bruker Esquire HCT





AcD3-C(Cmm)LPGLAK(AcD3K*)QPSFR-COOH*

precursor mass: 732.3520 Da (charge: +2) protein: P16675 (32-43)

score (threshold): 50.0 (31.0)

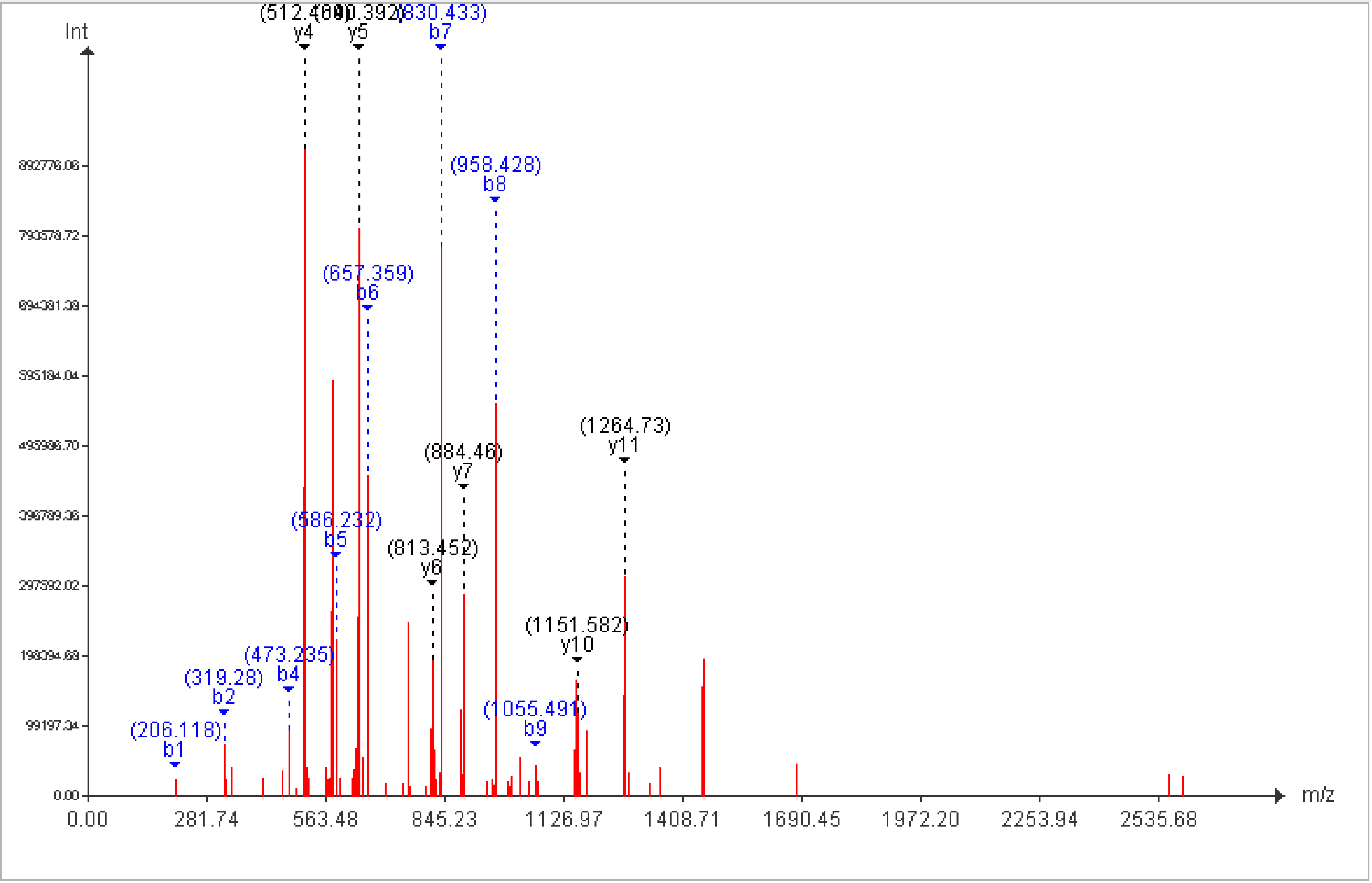
instrument: Bruker Esquire HCT

AcD3-C(Cmm*)LPGLAK(AcD3K*)QPSFR(C13*)-COOH

precursor mass: 735.3890 Da (charge: +2) protein: P16675 (32-43)

score (threshold): 40.0 (31.0)

instrument: Bruker Esquire HCT

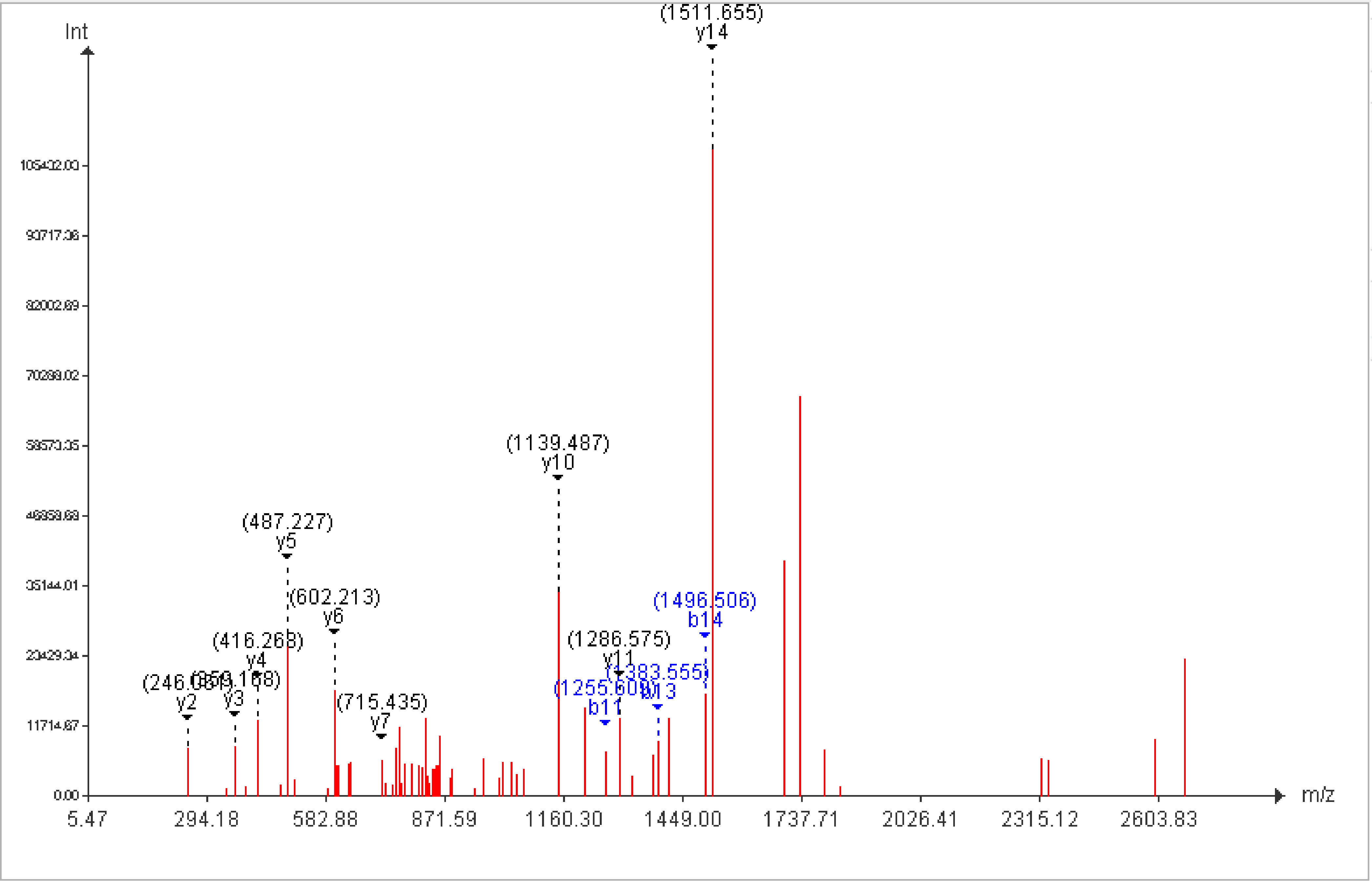


AcD3-GQPGAFTC(Cmm*)YLDAGLAR-COOH

precursor mass: 871.4720 Da (charge: +2) protein: P47962 (136-151)

score (threshold): 56.0 (31.0)

instrument: Bruker Esquire HCT

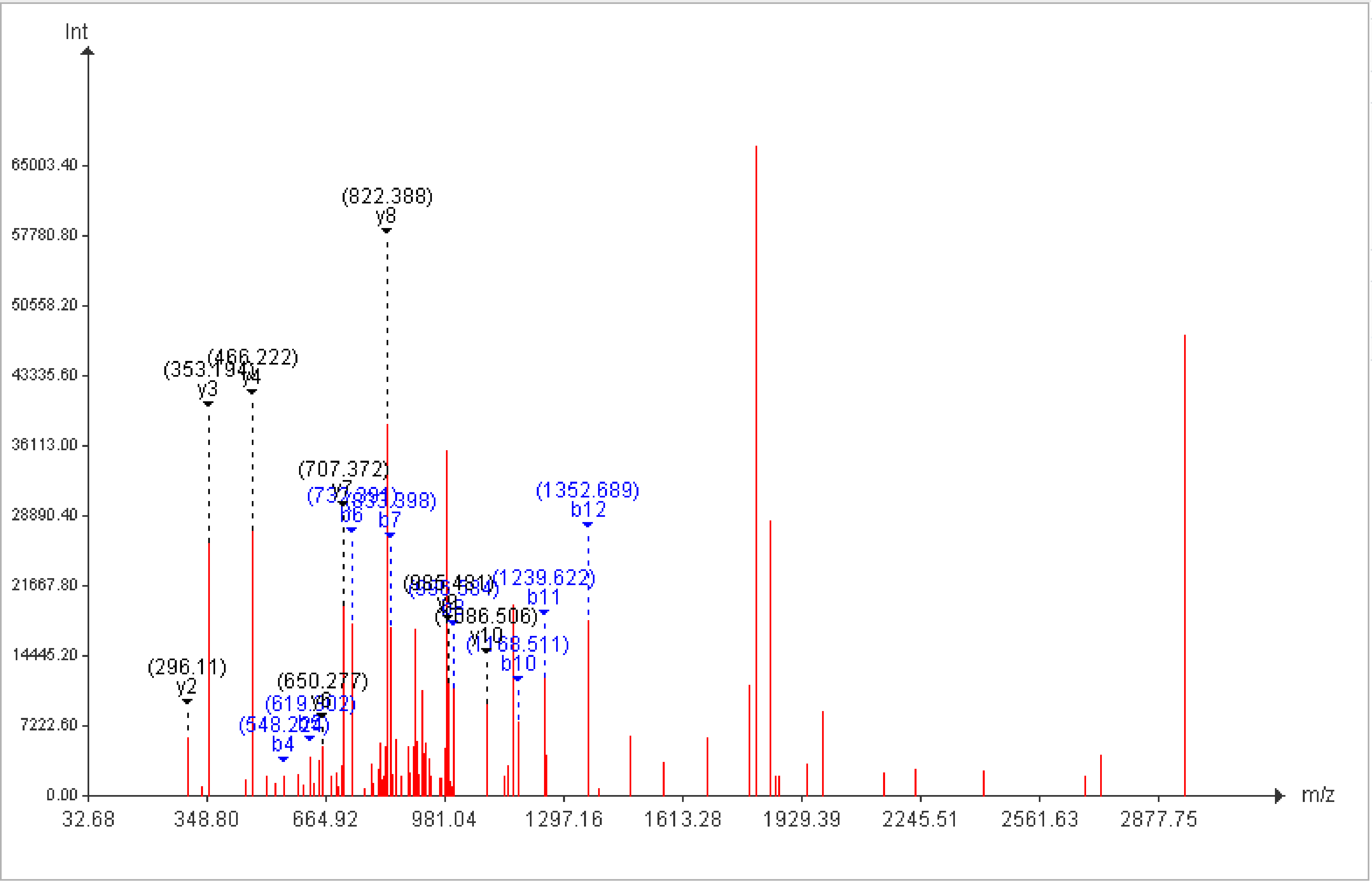


AcD3-SLK(AcD3K)EALTYDGALLGDR(C13*)-COOH*

precursor mass: 909.5150 Da (charge: +2) protein: Q9WUK2 (93-108)

score (threshold): 46.0 (31.0)

instrument: Bruker Esquire HCT

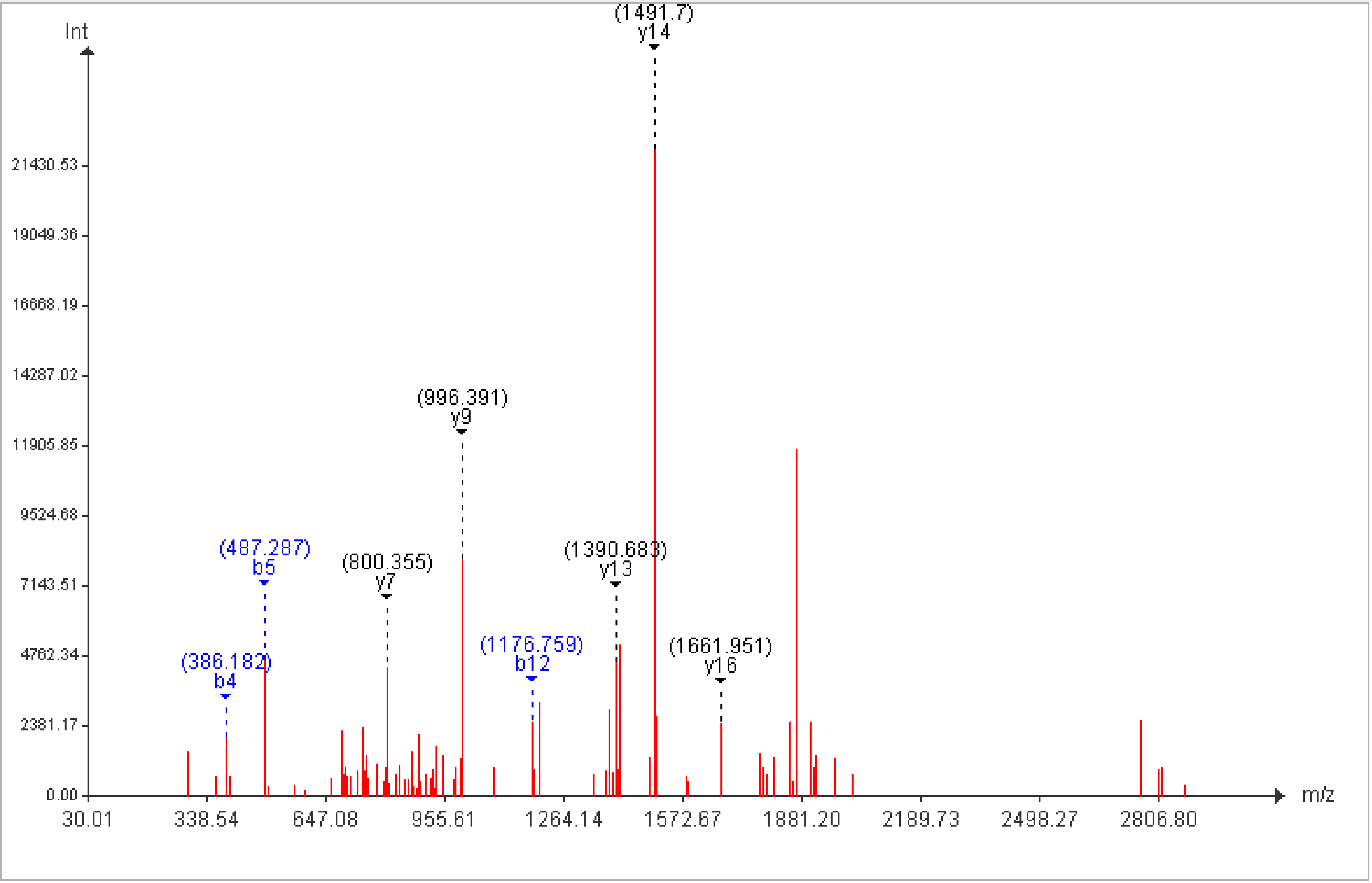


AcD3-GLAVTPTPVPVVGSQM(Mox)TR(C13)-COOH*

precursor mass: 939.0150 Da (charge: +2) protein: P26369 (129-146)

score (threshold): 31.0 (31.0)

instrument: Bruker Esquire HCT

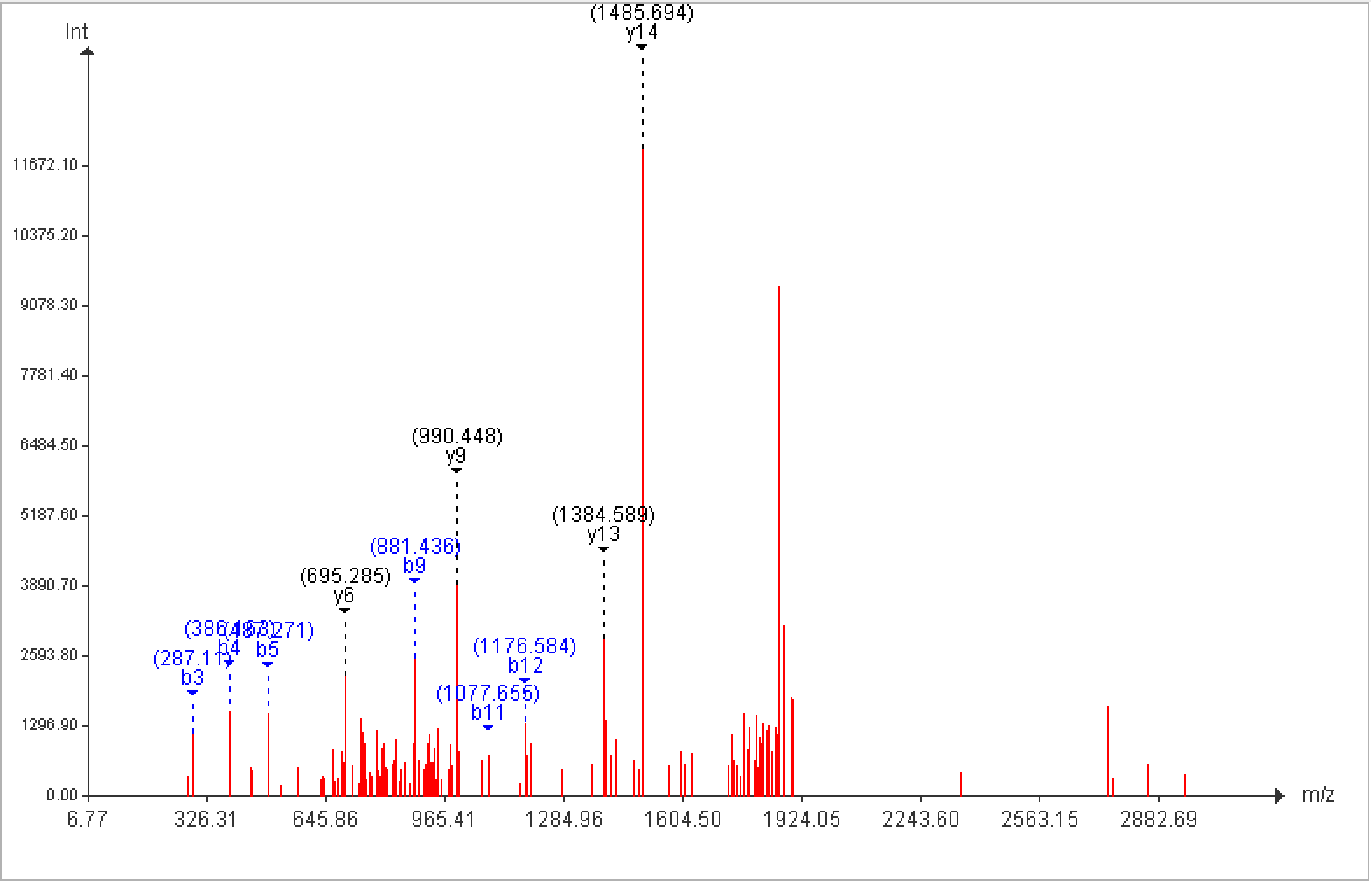


AcD3-GLAVTPTPVPVVGSQM(Mox)TR-COOH

precursor mass: 935.9680 Da (charge: +2) protein: P26369 (129-146)

score (threshold): 37.0 (31.0)

instrument: Bruker Esquire HCT

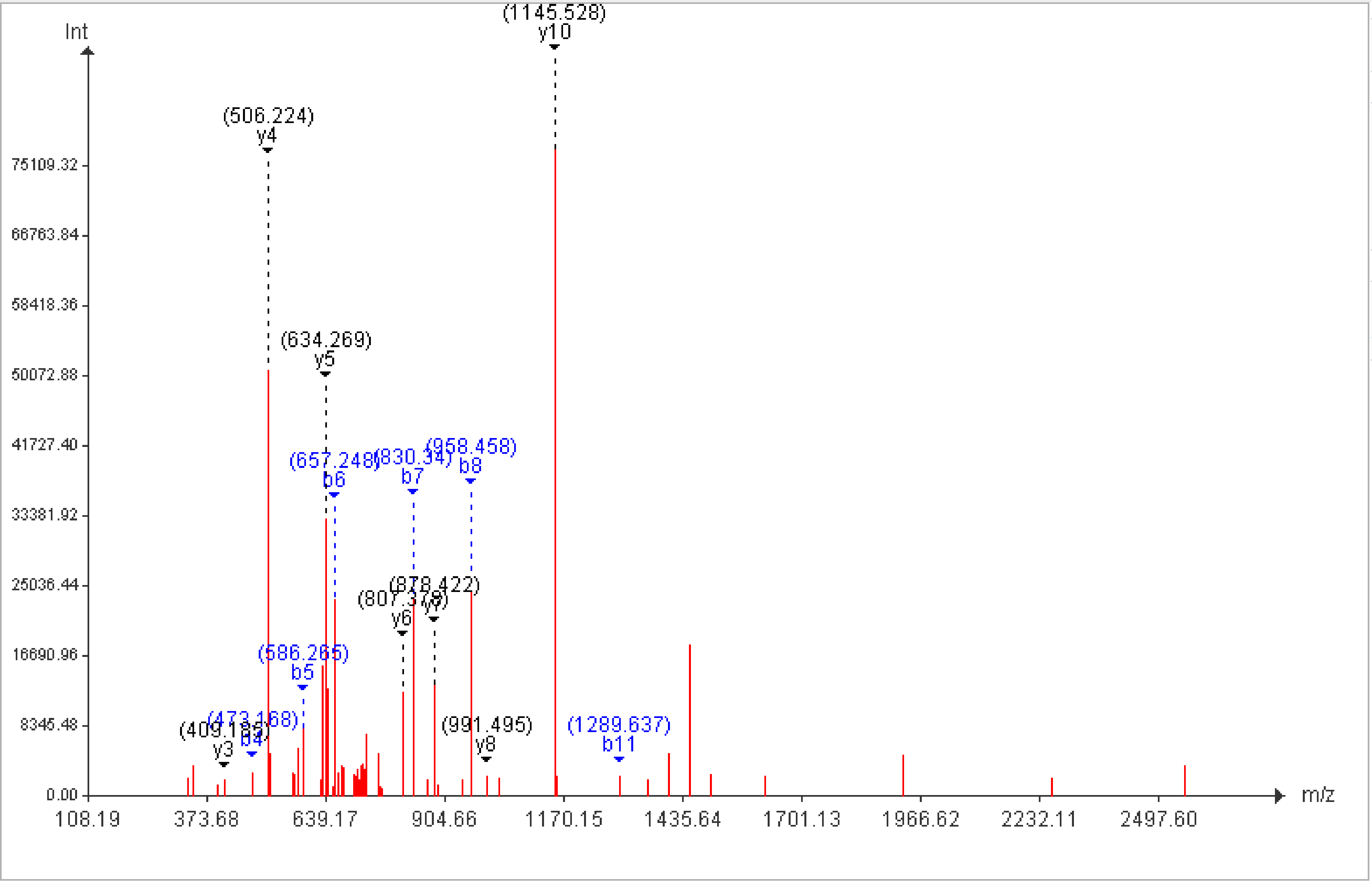


AcD3-C(Cmm)LPGLAK(AcD3K*)QPSFR-COOH*

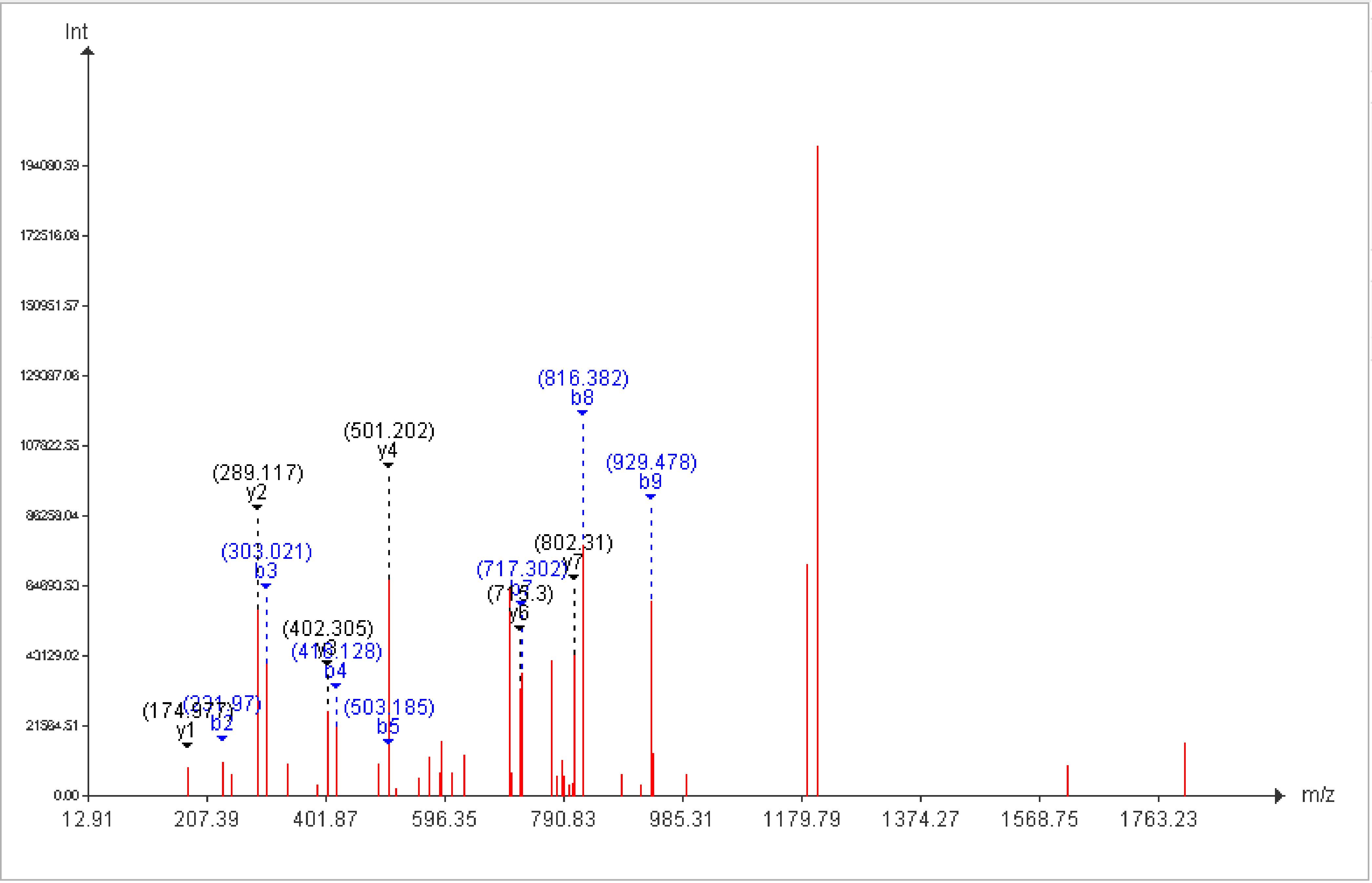
precursor mass: 732.4140 Da (charge: +2) protein: P16675 (32-43)

score (threshold): 42.0 (31.0)

instrument: Bruker Esquire HCT



AcD3-GEALSTLVLNR-COOH
precursor mass: 609.2780 Da (charge: +2) protein: P63038 (280-290)
score (threshold): 47.0 (31.0)
instrument: Bruker Esquire HCT

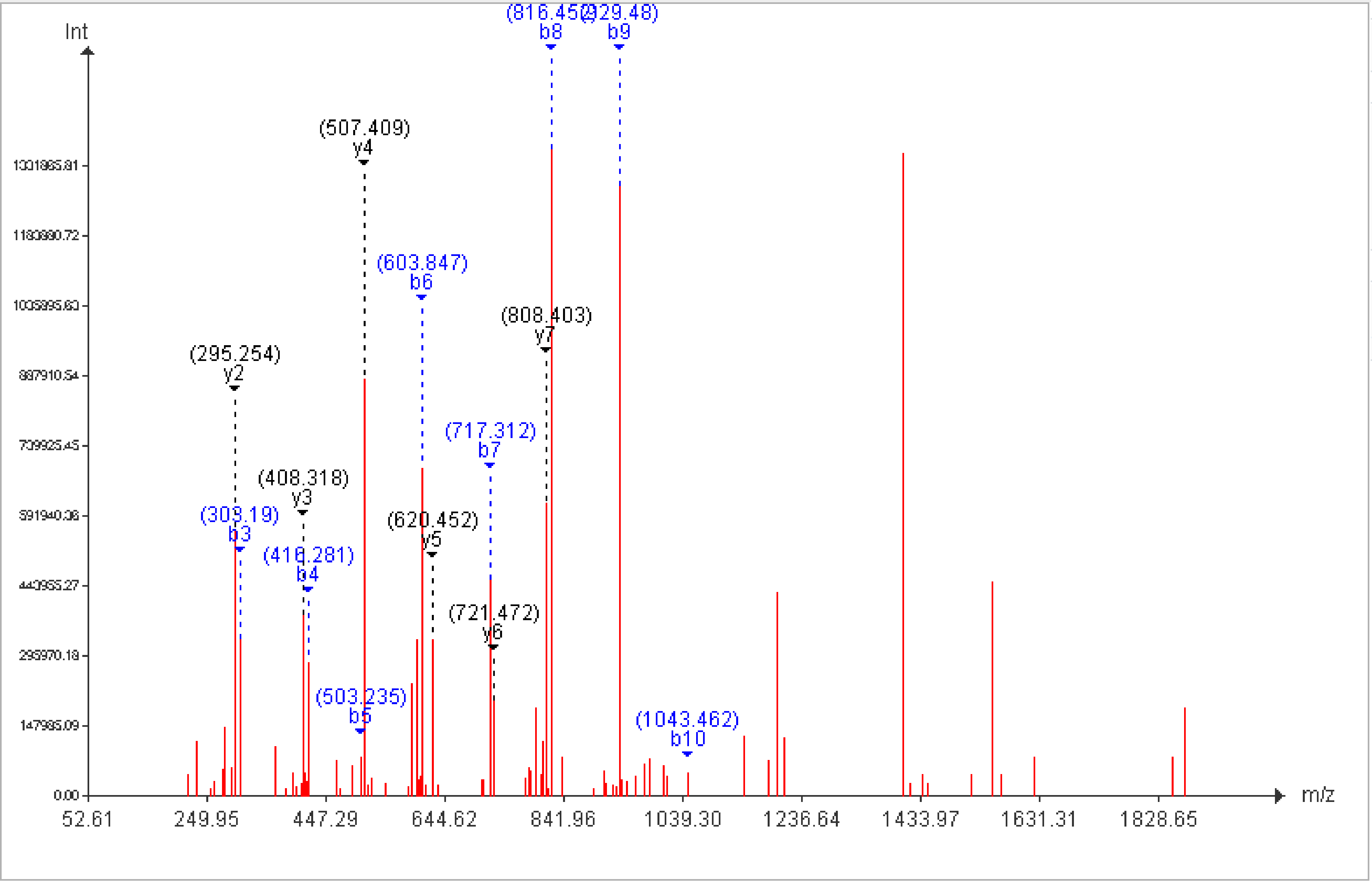


AcD3-GEALSTLVLNR(C13)-COOH*

precursor mass: 612.3460 Da (charge: +2) protein: P63038 (280-290)

score (threshold): 62.0 (31.0)

instrument: Bruker Esquire HCT

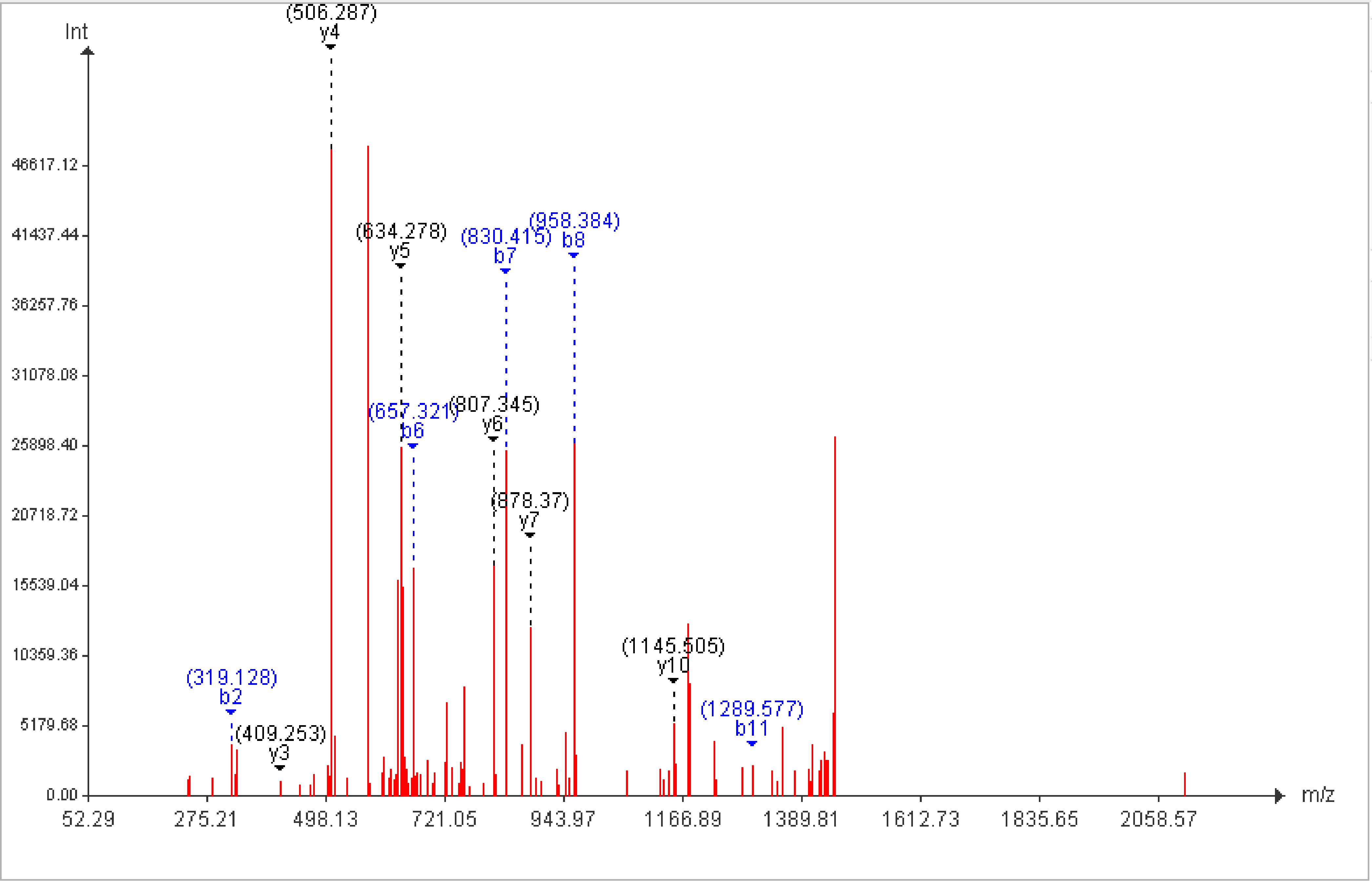


AcD3-C(Cmm)LPGLAK(AcD3K*)QPSFR-COOH*

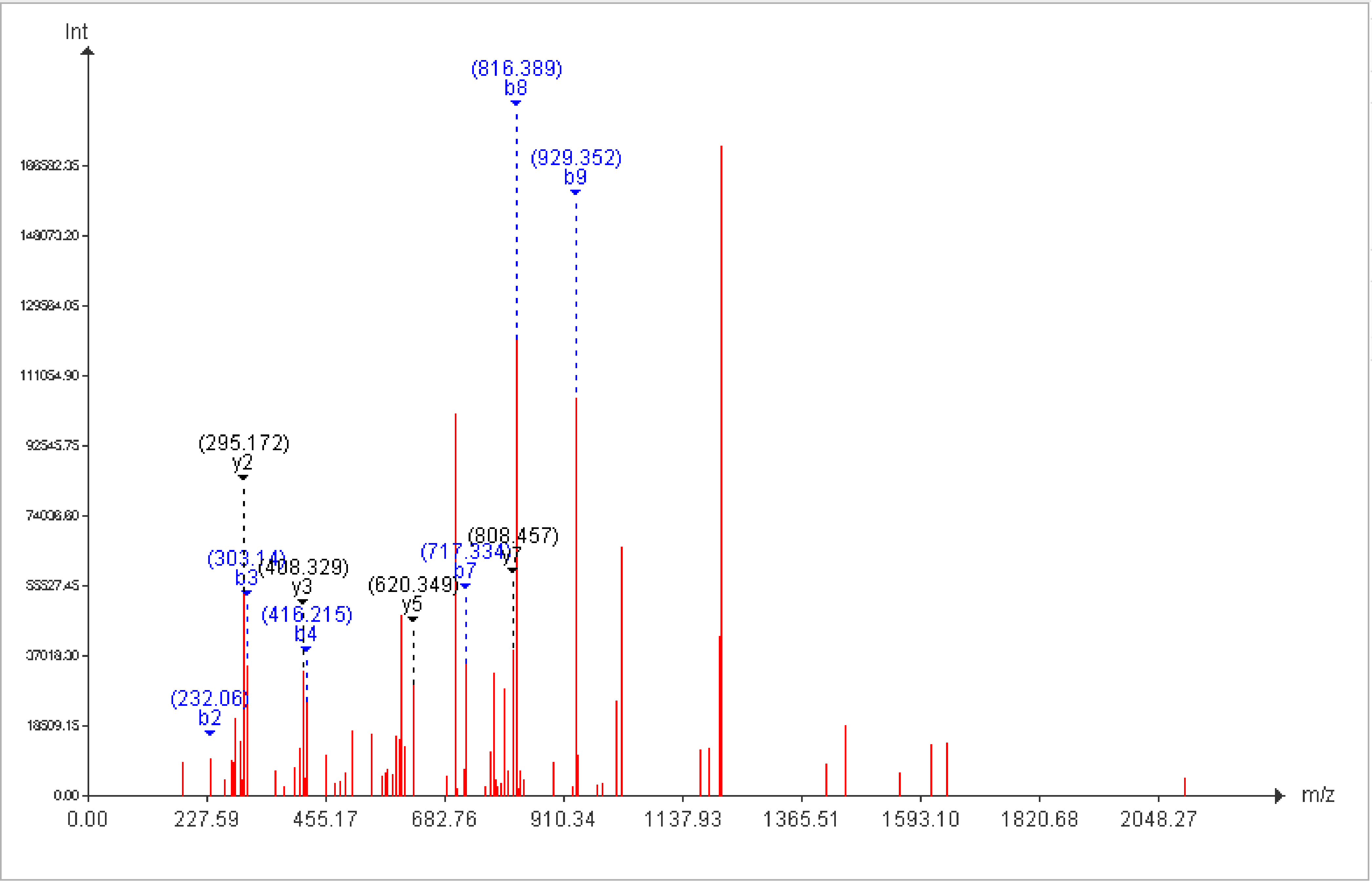
precursor mass: 732.3780 Da (charge: +2) protein: P16675 (32-43)

score (threshold): 32.0 (31.0)

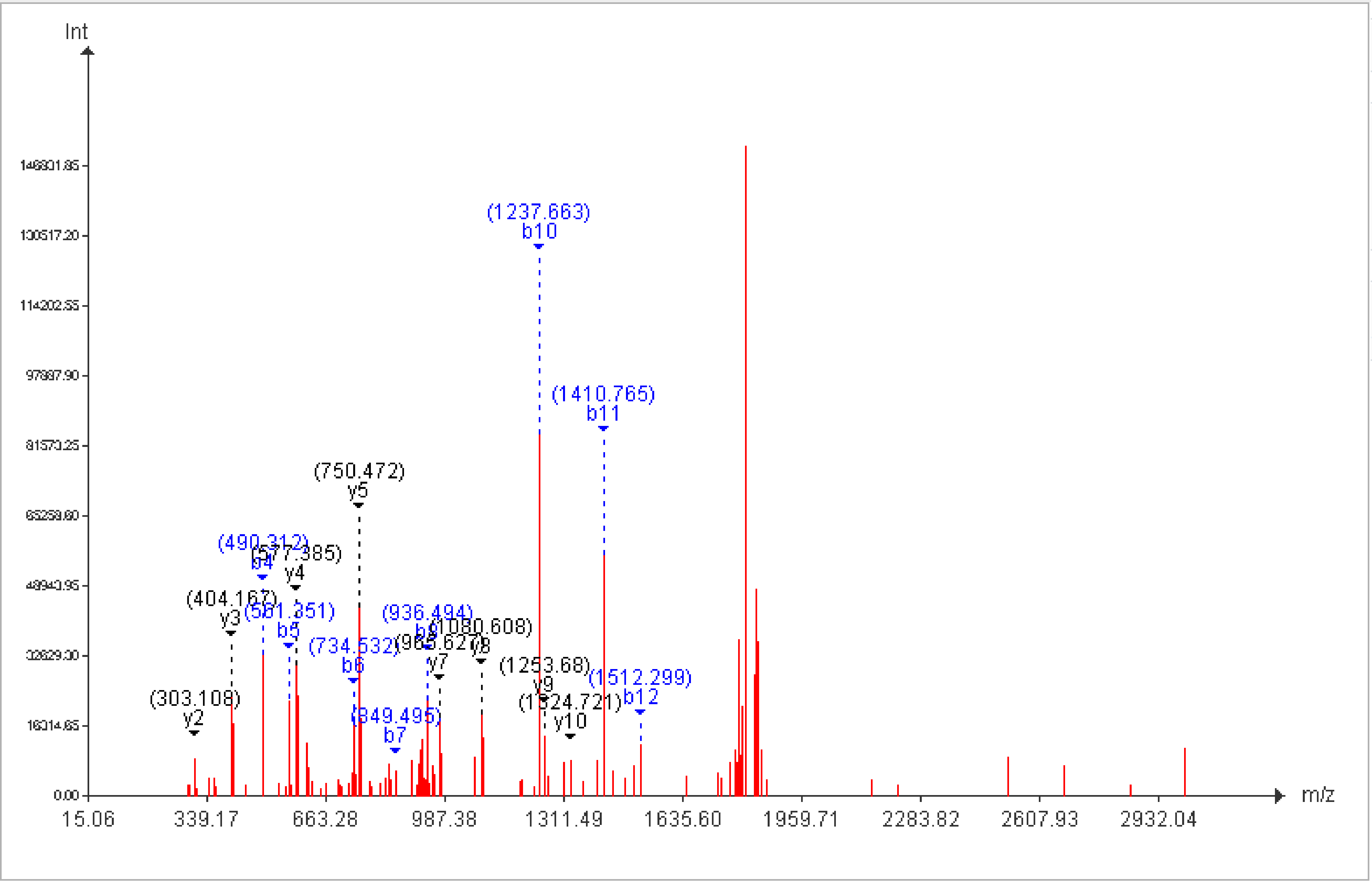
instrument: Bruker Esquire HCT



AcD3-GEALSTLVLNR(C13)-COOH*
precursor mass: 612.2870 Da (charge: +2) protein: P63038 (280-290)
score (threshold): 41.0 (31.0)
instrument: Bruker Esquire HCT



AcD3-LFAIAK(AcD3K)DSQK(AcD3K*)K(AcD3K*)TQR-COOH*
precursor mass: 907.5300 Da (charge: +2) protein: IPI00456853.3 (665-678)
score (threshold): 42.0 (35.0)
instrument: Bruker Esquire HCT

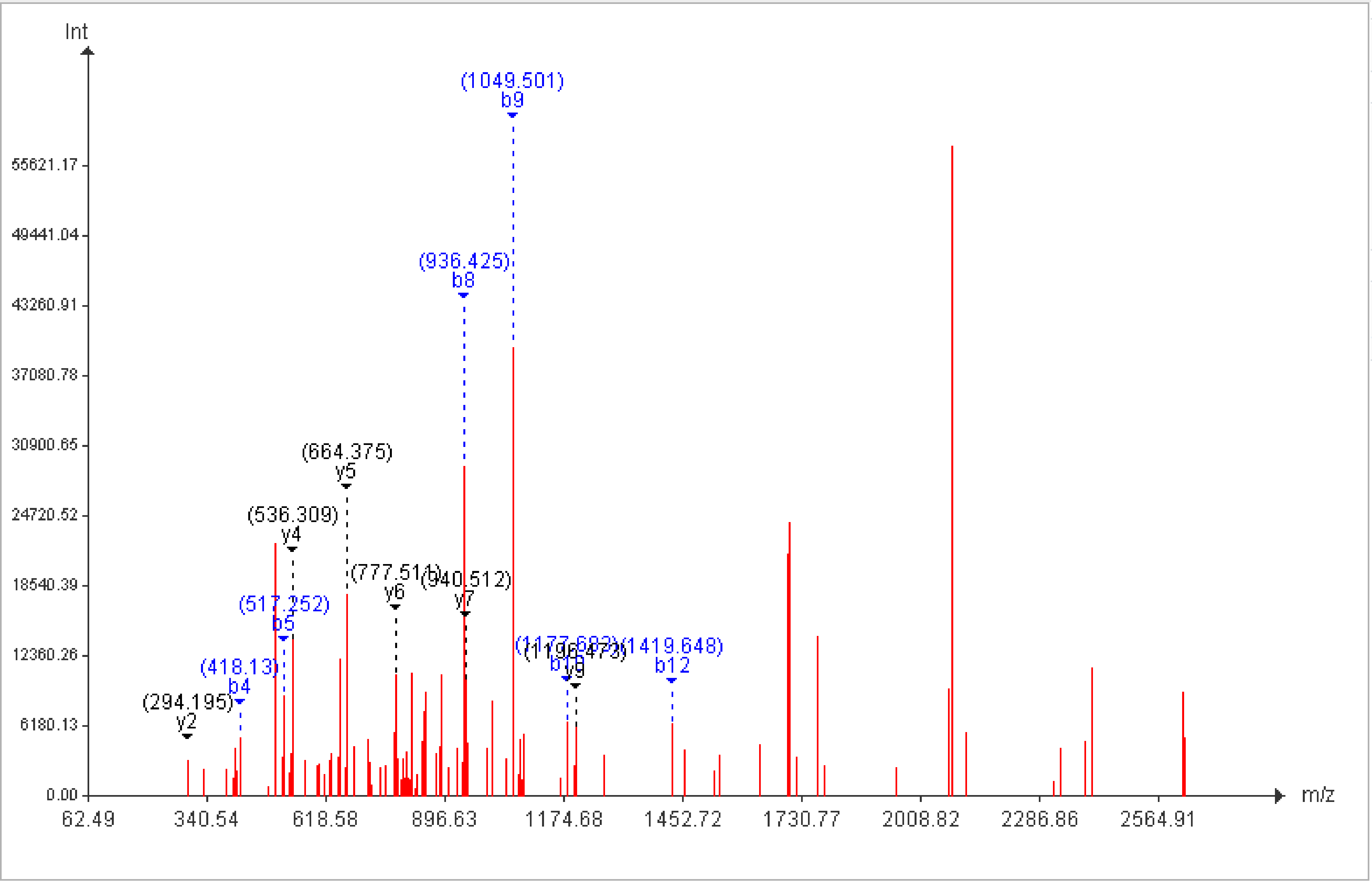


AcD3-STLAVQQYIQQNIR(C13)-COOH*

precursor mass: 856.9080 Da (charge: +2) protein: Q6PEB6 (35-48)

score (threshold): 36.0 (31.0)

instrument: Bruker Esquire HCT

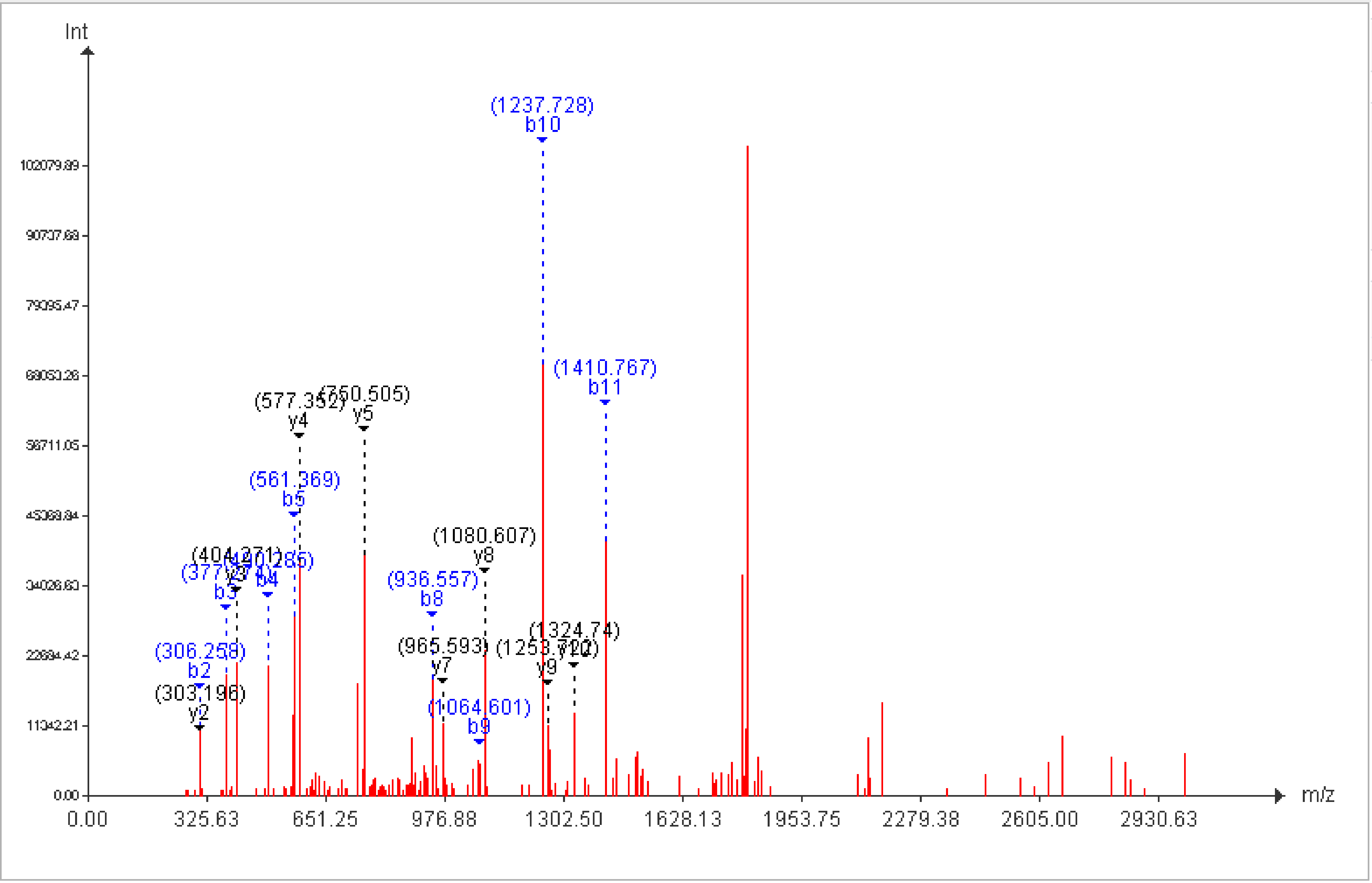


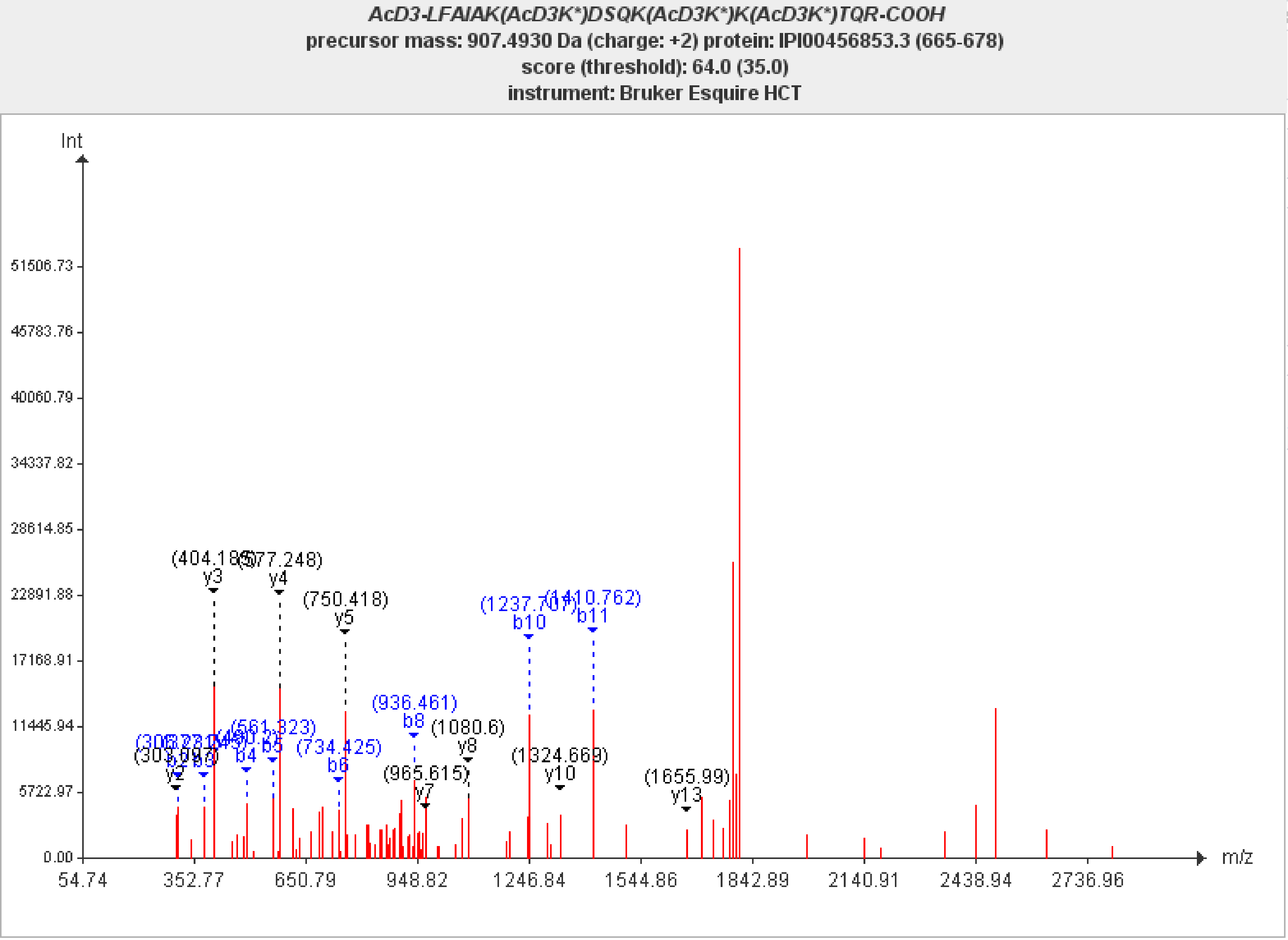
AcD3-LFAIAK(AcD3K)DSQK(AcD3K*)K(AcD3K*)TQR-COOH*

precursor mass: 907.4660 Da (charge: +2) protein: IPI00456853.3 (665-678)

score (threshold): 69.0 (35.0)

instrument: Bruker Esquire HCT



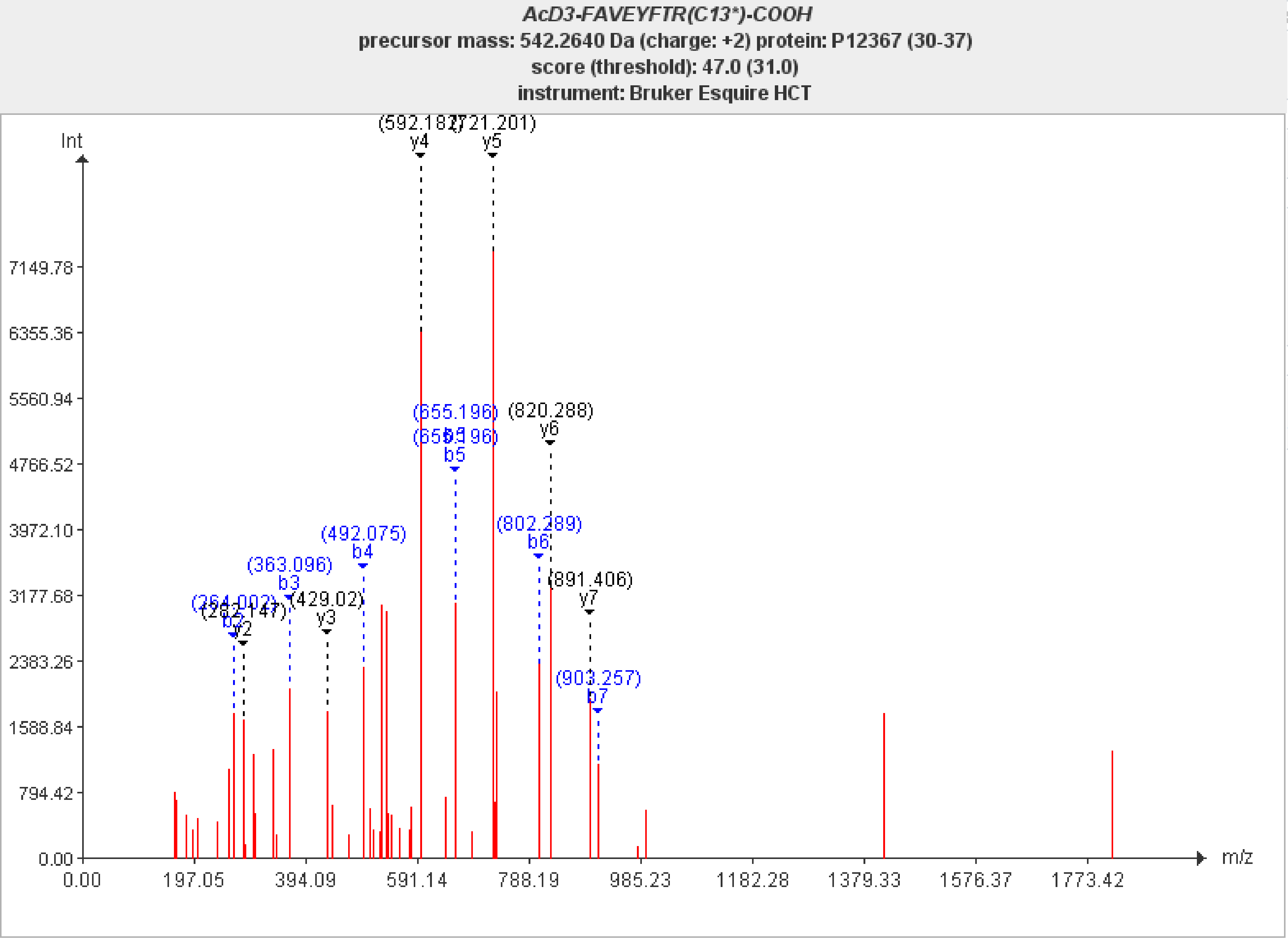


AcD3-LFAIAK(AcD3K)DSQK(AcD3K*)K(AcD3K*)TQR-COOH*

precursor mass: 907.4930 Da (charge: +2) protein: IPI00456853.3 (665-678)

score (threshold): 64.0 (35.0)

instrument: Bruker Esquire HCT



AcD3-FAVEYFTR(C13)-COOH*

precursor mass: 542.2640 Da (charge: +2) protein: P12367 (30-37)

score (threshold): 47.0 (31.0)

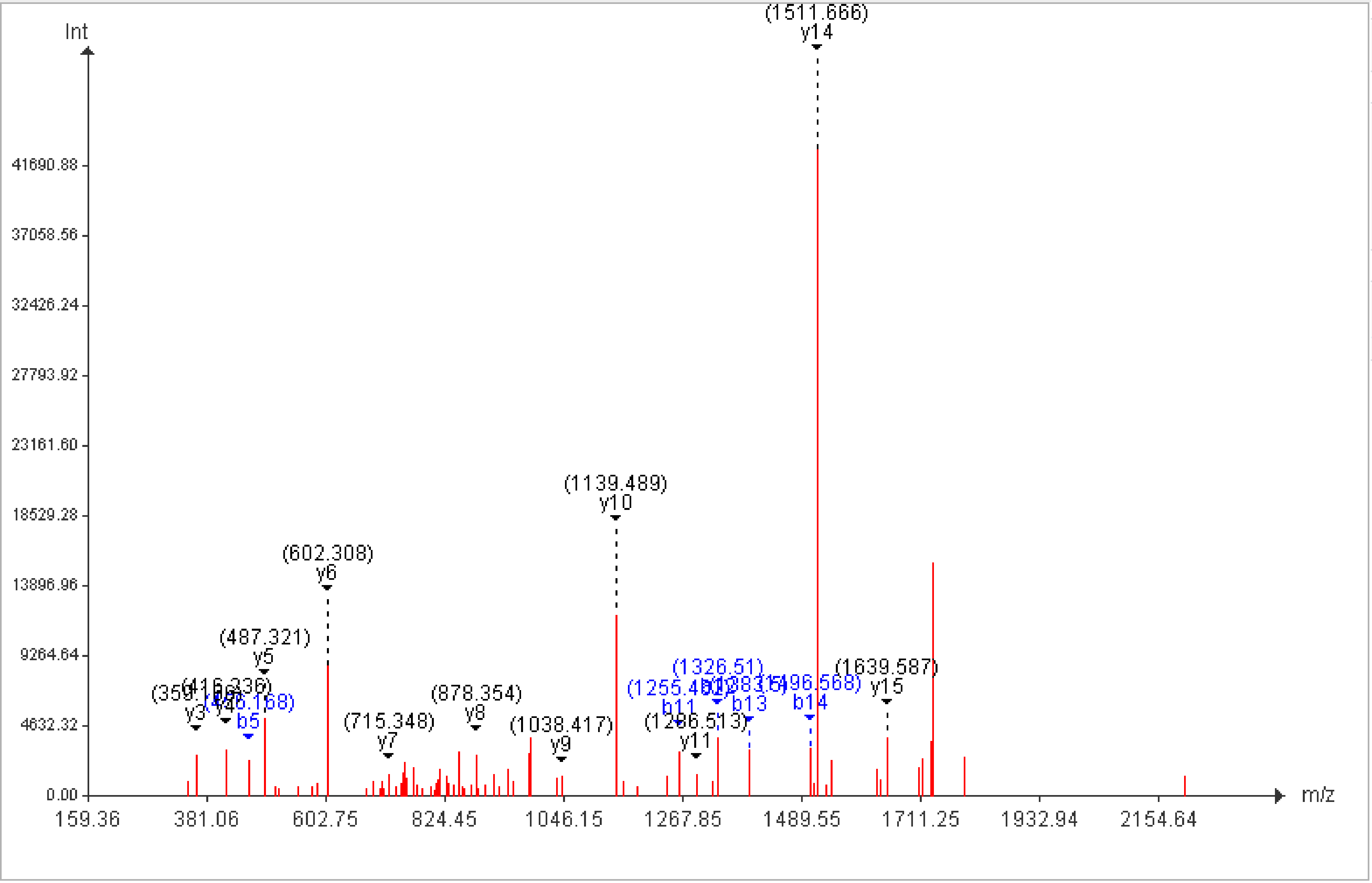
instrument: Bruker Esquire HCT

AcD3-GQPGAFTC(Cmm)YLDAGLAR-COOH*

precursor mass: 871.3510 Da (charge: +2) protein: P47962 (136-151)

score (threshold): 71.0 (31.0)

instrument: Bruker Esquire HCT

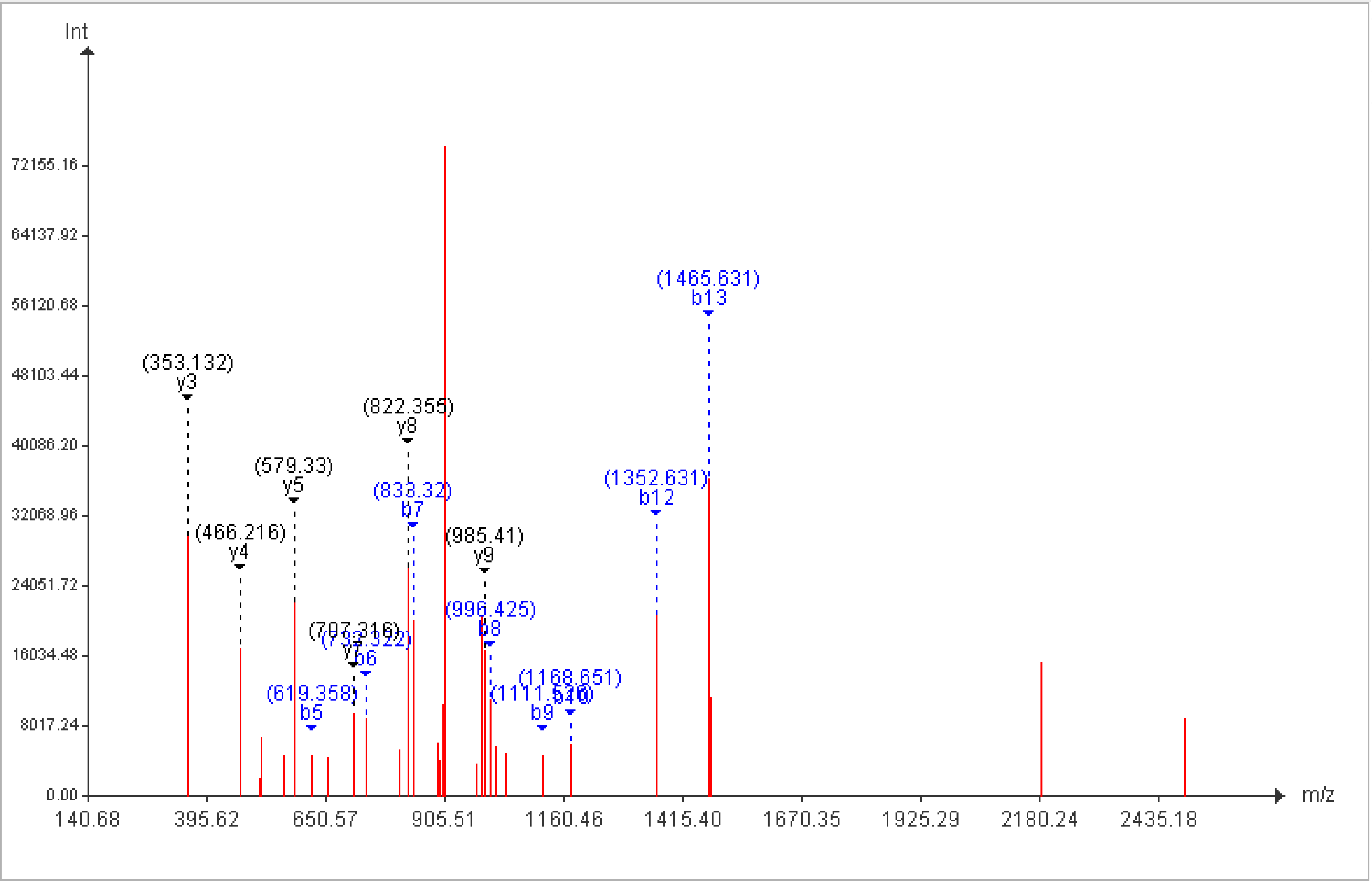


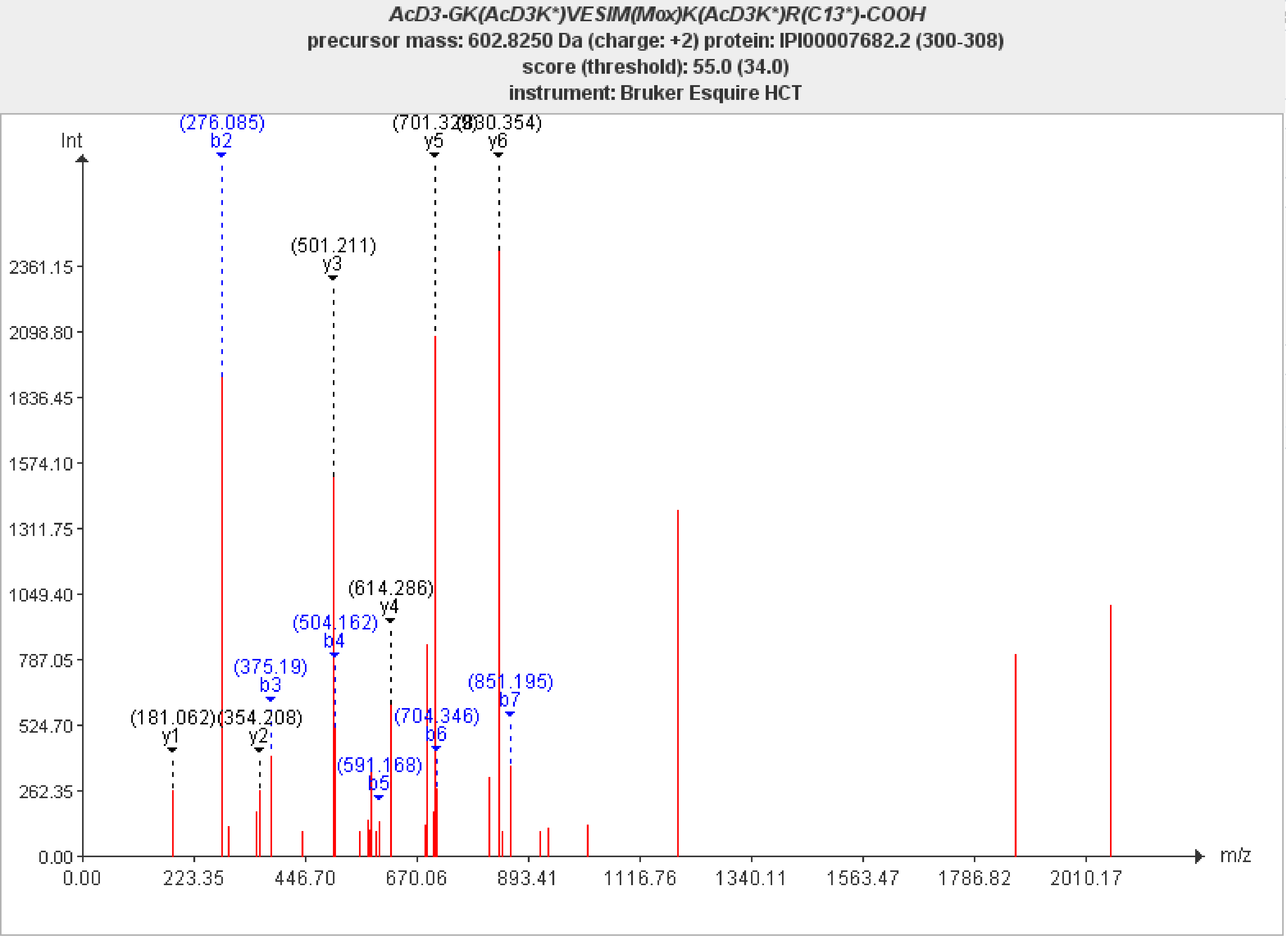
AcD3-SLK(AcD3K)EALTYDGALLGDR(C13*)-COOH*

precursor mass: 909.4680 Da (charge: +2) protein: Q9WUK2 (93-108)

score (threshold): 58.0 (31.0)

instrument: Bruker Esquire HCT





AcD3-GK(AcD3K)VESIM(Mox)K(AcD3K*)R(C13*)-COOH*

precursor mass: 602.8250 Da (charge: +2) protein: IPI00007682.2 (300-308)

score (threshold): 55.0 (34.0)

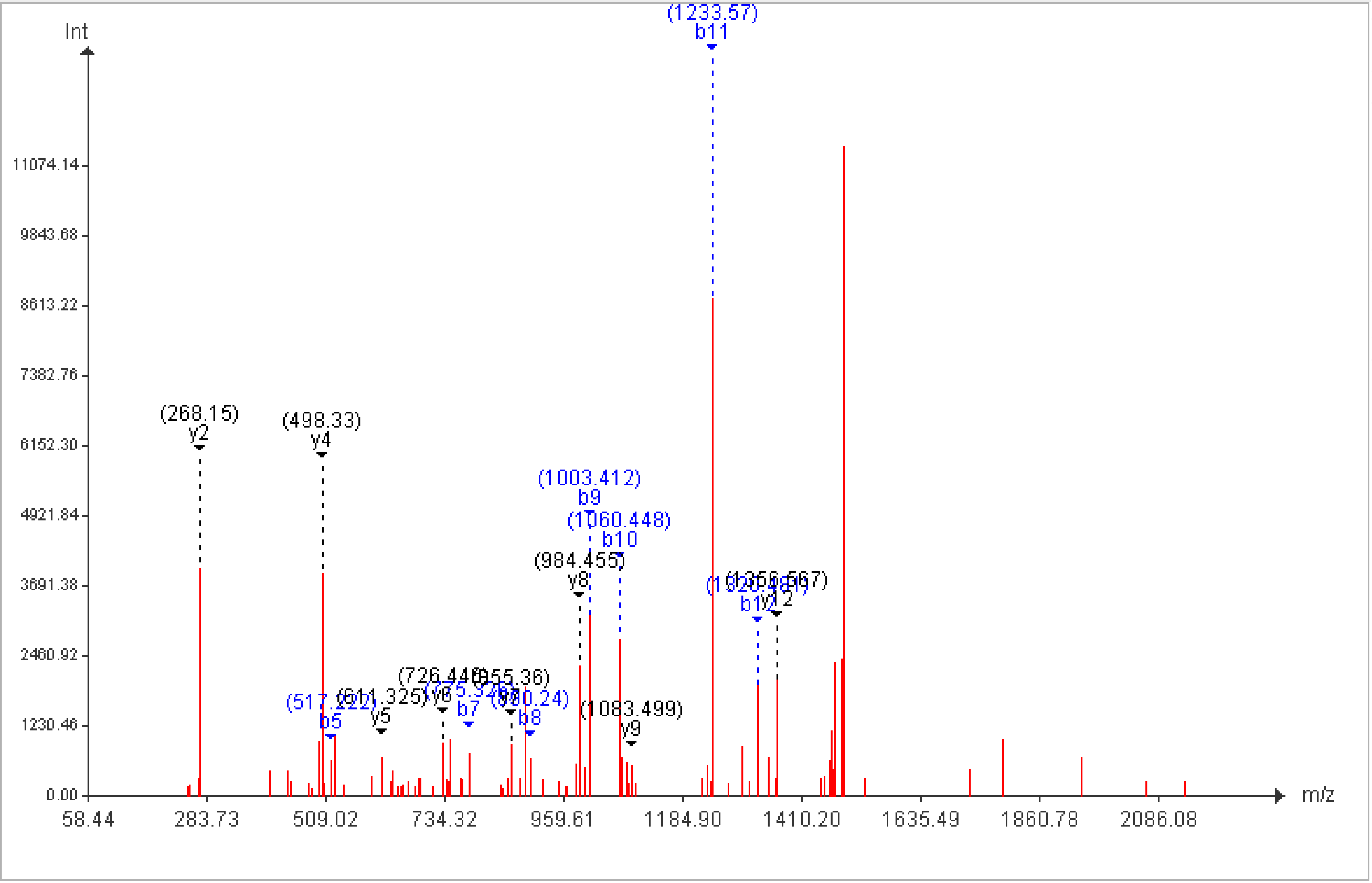
instrument: Bruker Esquire HCT

AcD3-VDGTVEEDLGK(AcD3K)SR(C13*)-COOH*

precursor mass: 750.9060 Da (charge: +2) protein: P08113 (27-39)

score (threshold): 41.0 (31.0)

instrument: Bruker Esquire HCT

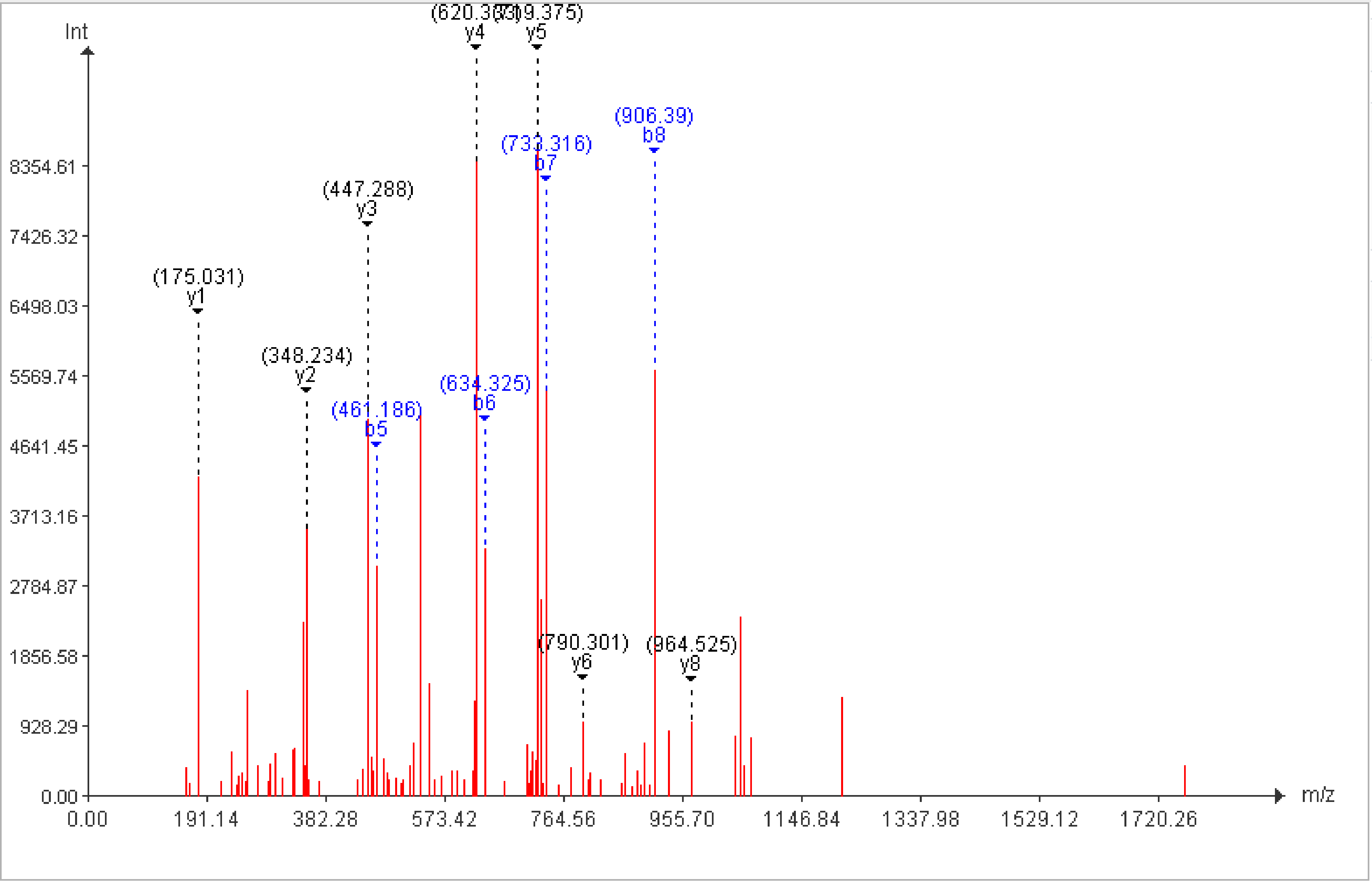


AcD3-ASSAVK(AcD3K*)VK(AcD3K*)R-COOH

precursor mass: 540.7580 Da (charge: +2) protein: Q921F2 (90-98)

score (threshold): 55.0 (31.0)

instrument: Bruker Esquire HCT

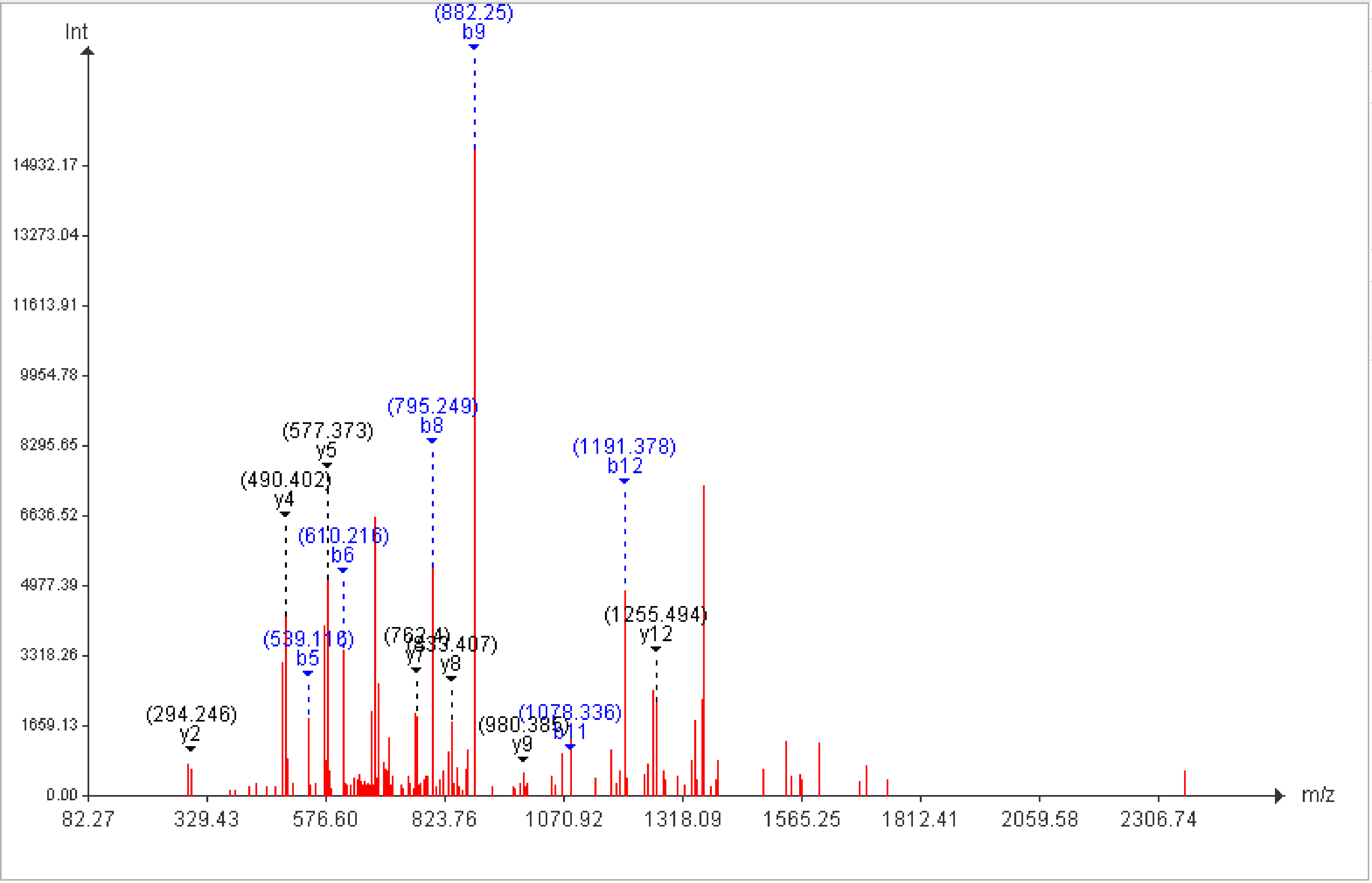


AcD3-AGM(Mox)AM(Mox)AGQSPVLR(C13)-COOH*

precursor mass: 686.2960 Da (charge: +2) protein: P17225 (172-184)

score (threshold): 34.0 (31.0)

instrument: Bruker Esquire HCT

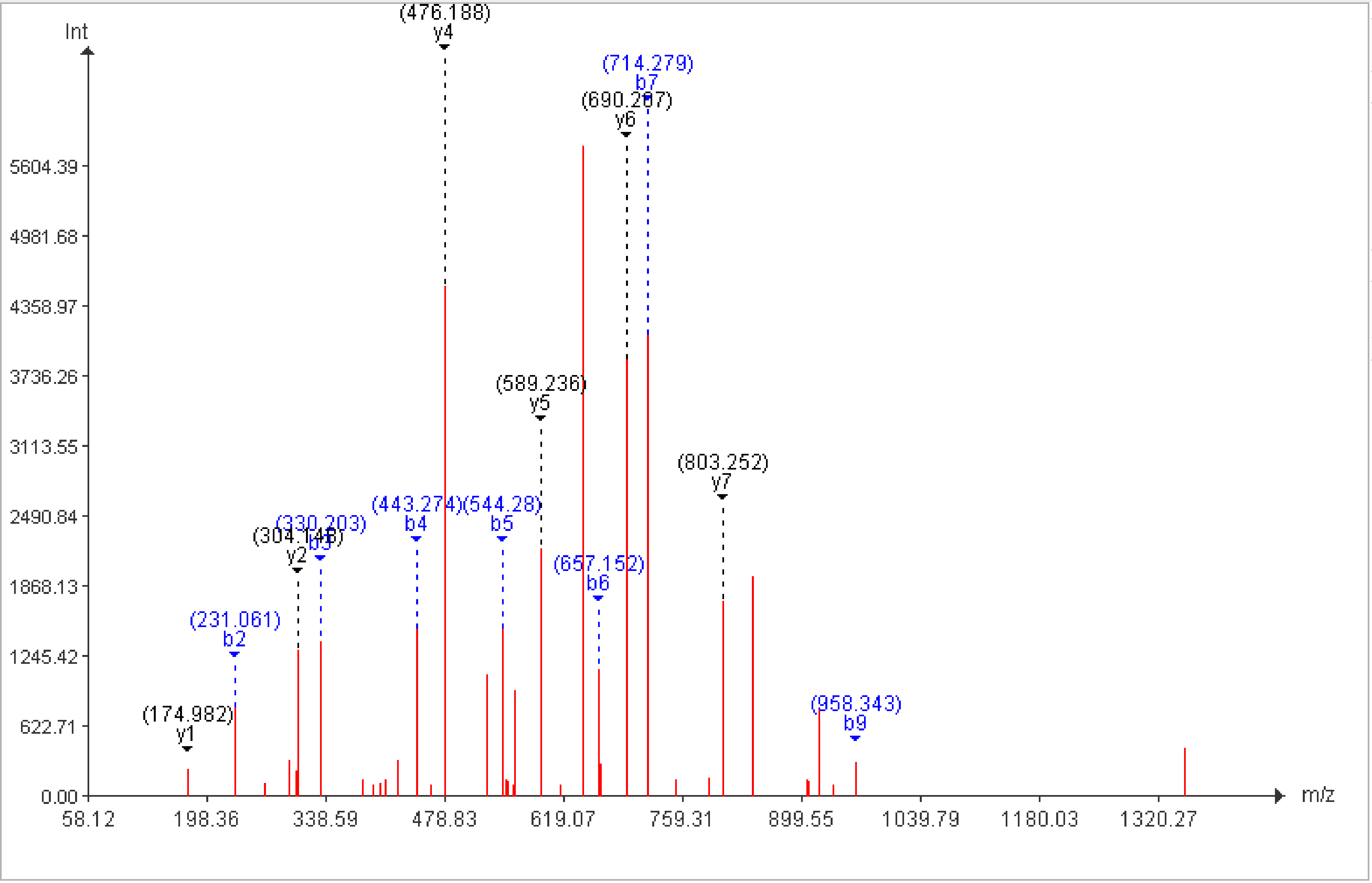


AcD3-GQVITIGN(Dam)ER-COOH

precursor mass: 566.8560 Da (charge: +2) protein: P62737 (247-256)

score (threshold): 63.0 (34.0)

instrument: Bruker Esquire HCT

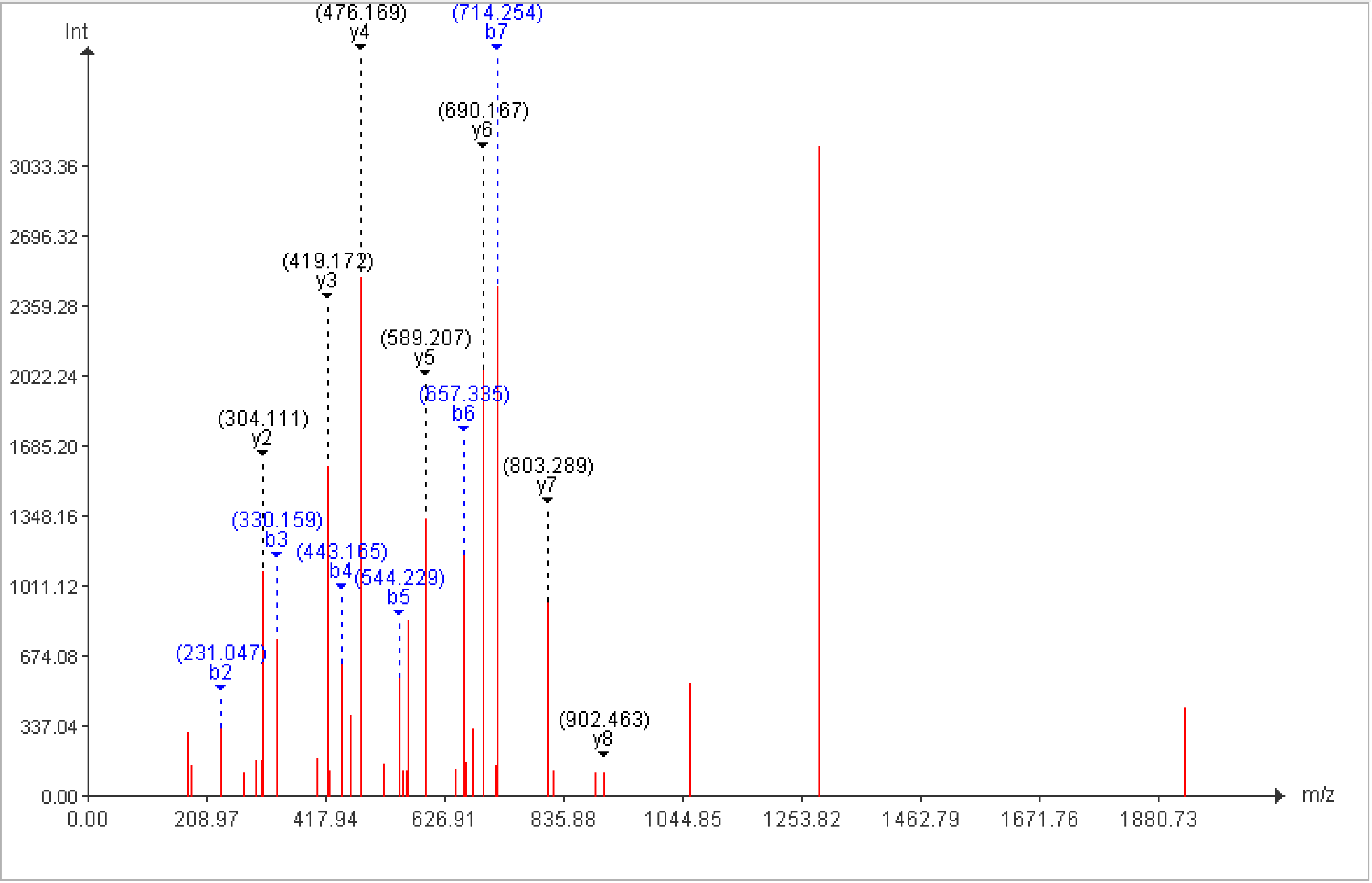


AcD3-GQVITIGN(Dam)ER-COOH

precursor mass: 566.6960 Da (charge: +2) protein: P62737 (247-256)

score (threshold): 64.0 (31.0)

instrument: Bruker Esquire HCT

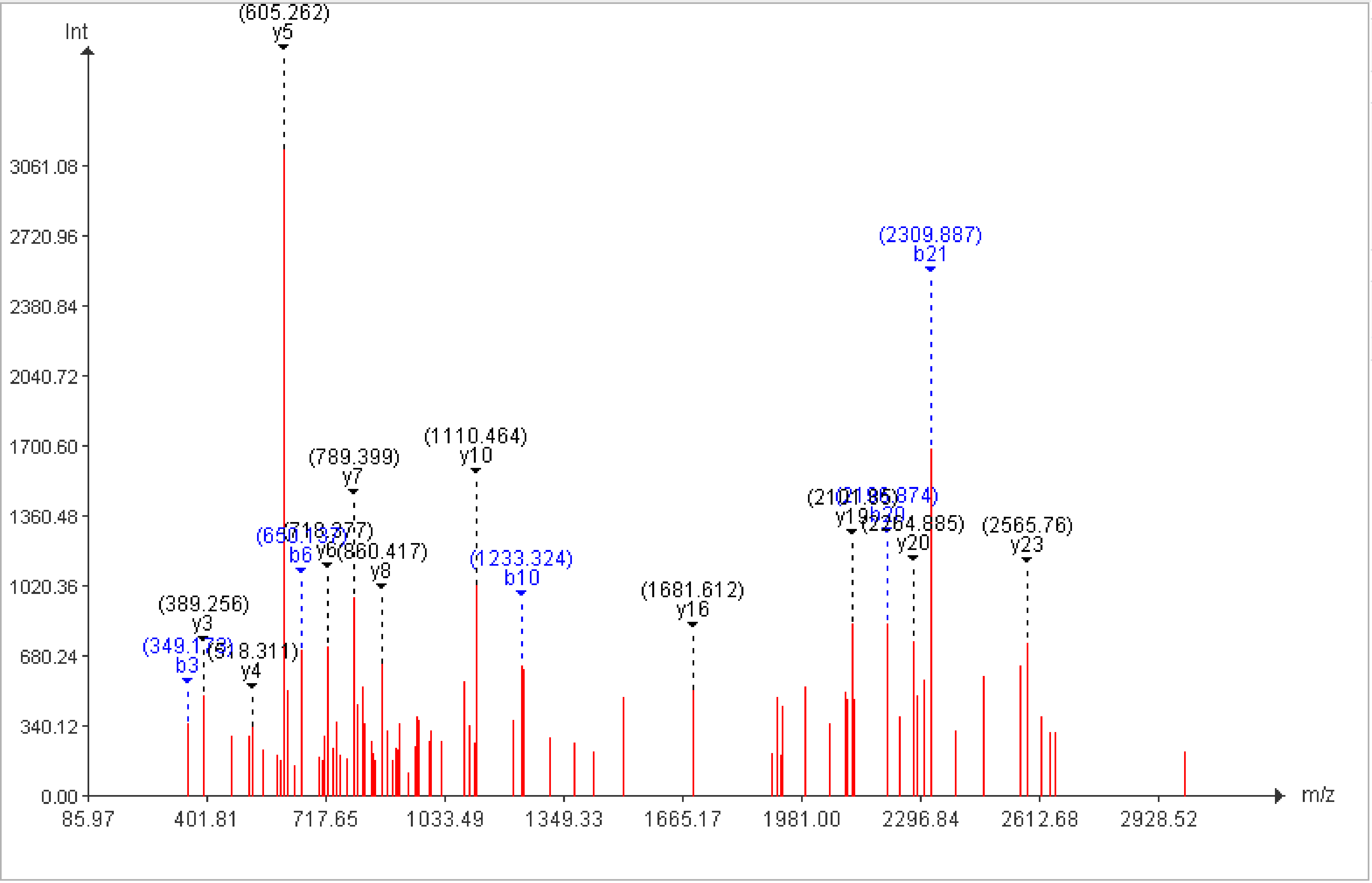


AcD3-GVM(Mox)N(Dam)GEYYQESNGPTDSYAAISEVDR-COOH

precursor mass: 972.1120 Da (charge: +3) protein: O08585 (76-101)

score (threshold): 71.0 (36.0)

instrument: Bruker Esquire HCT

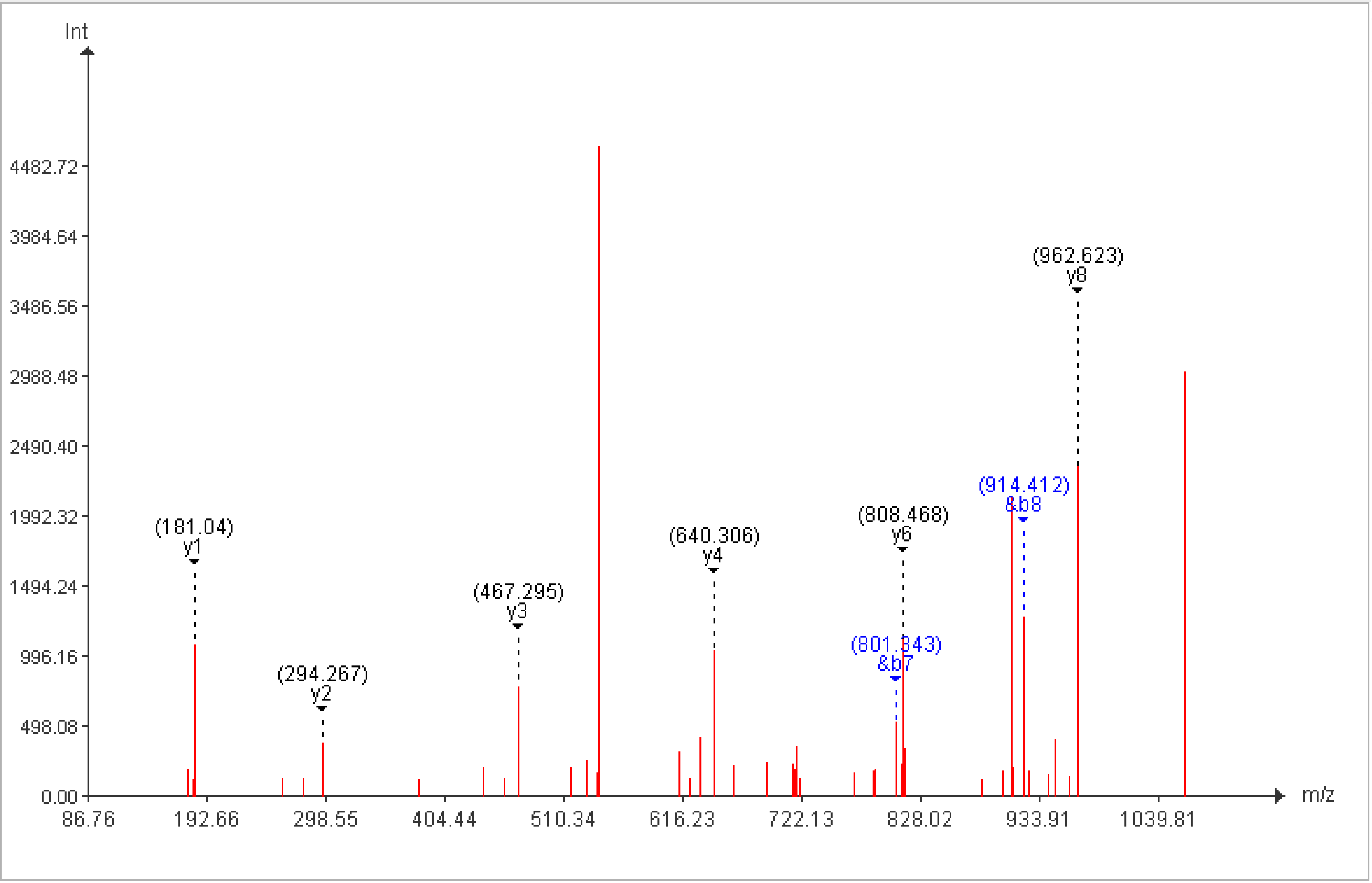


AcD3-SGPPAK(AcD3K)K(AcD3K*)IR(C13*)-COOH*

precursor mass: 547.7510 Da (charge: +2) protein: Q80XU3 (30-38)

score (threshold): 48.0 (31.0)

instrument: Bruker Esquire HCT

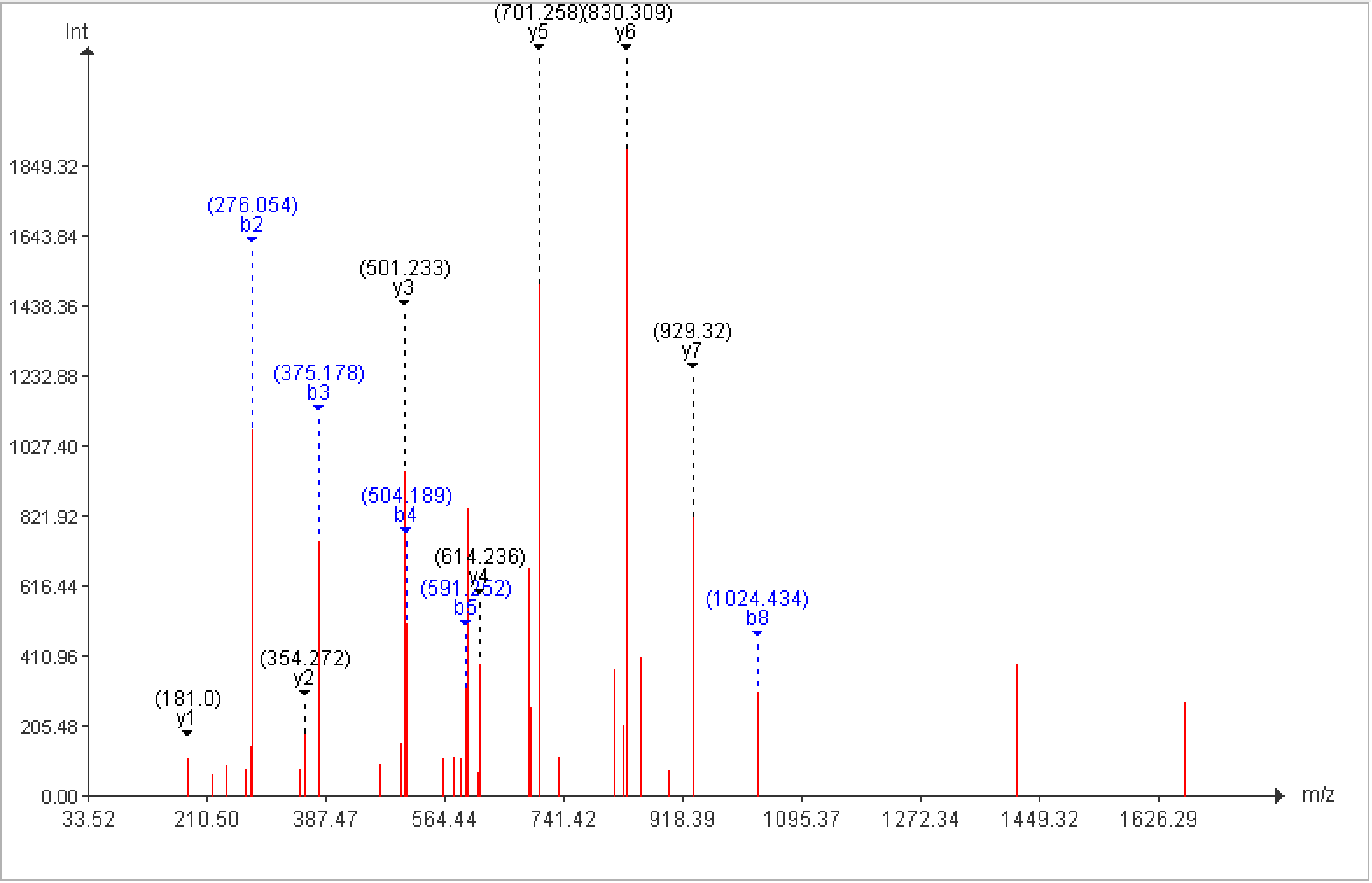


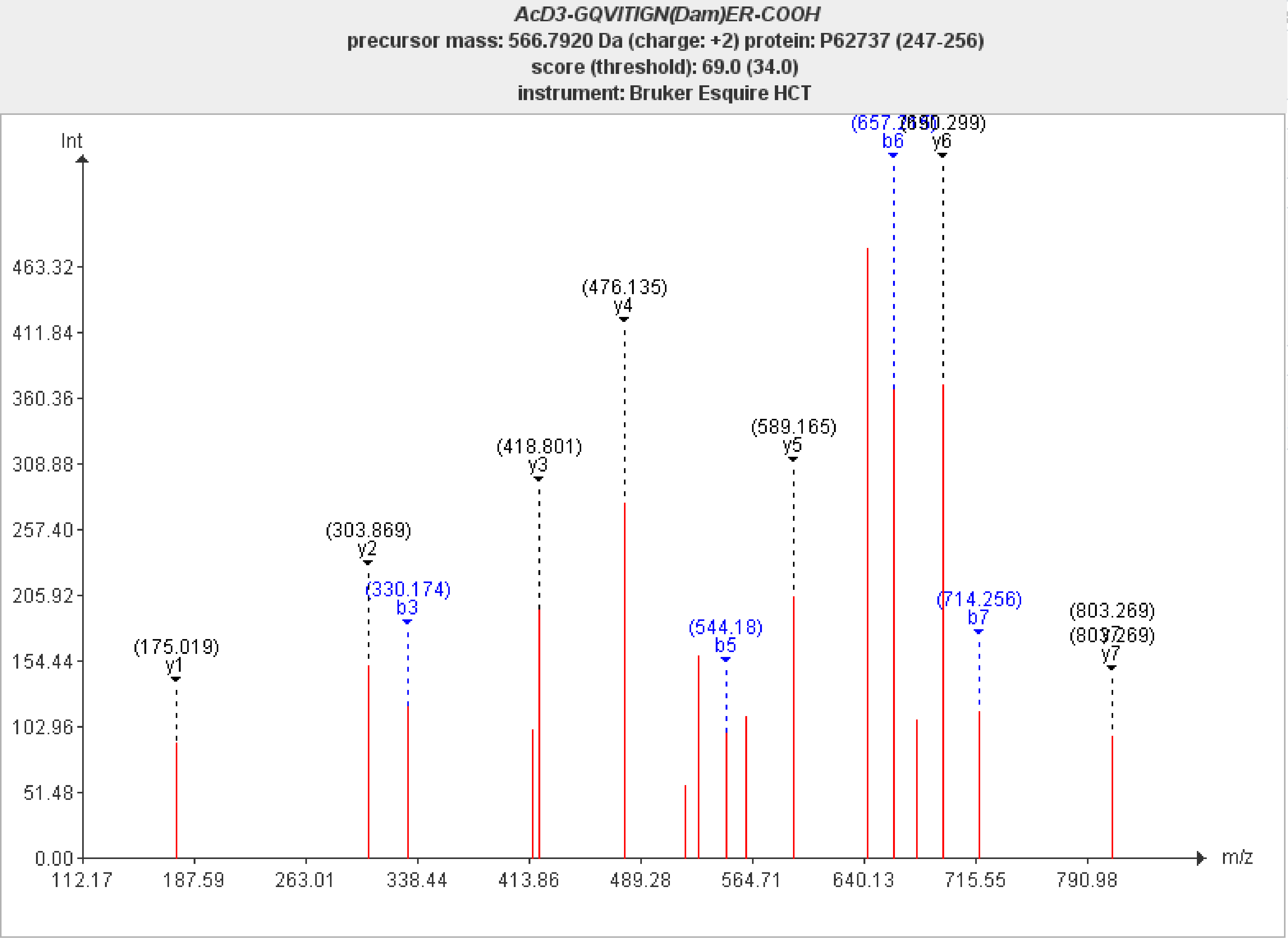
AcD3-GK(AcD3K)VESIM(Mox)K(AcD3K*)R(C13*)-COOH*

precursor mass: 602.9130 Da (charge: +2) protein: IPI00007682.2 (300-308)

score (threshold): 51.0 (34.0)

instrument: Bruker Esquire HCT





AcD3-GQVITIGN(Dam)ER-COOH

precursor mass: 566.7920 Da (charge: +2) protein: P62737 (247-256)

score (threshold): 69.0 (34.0)

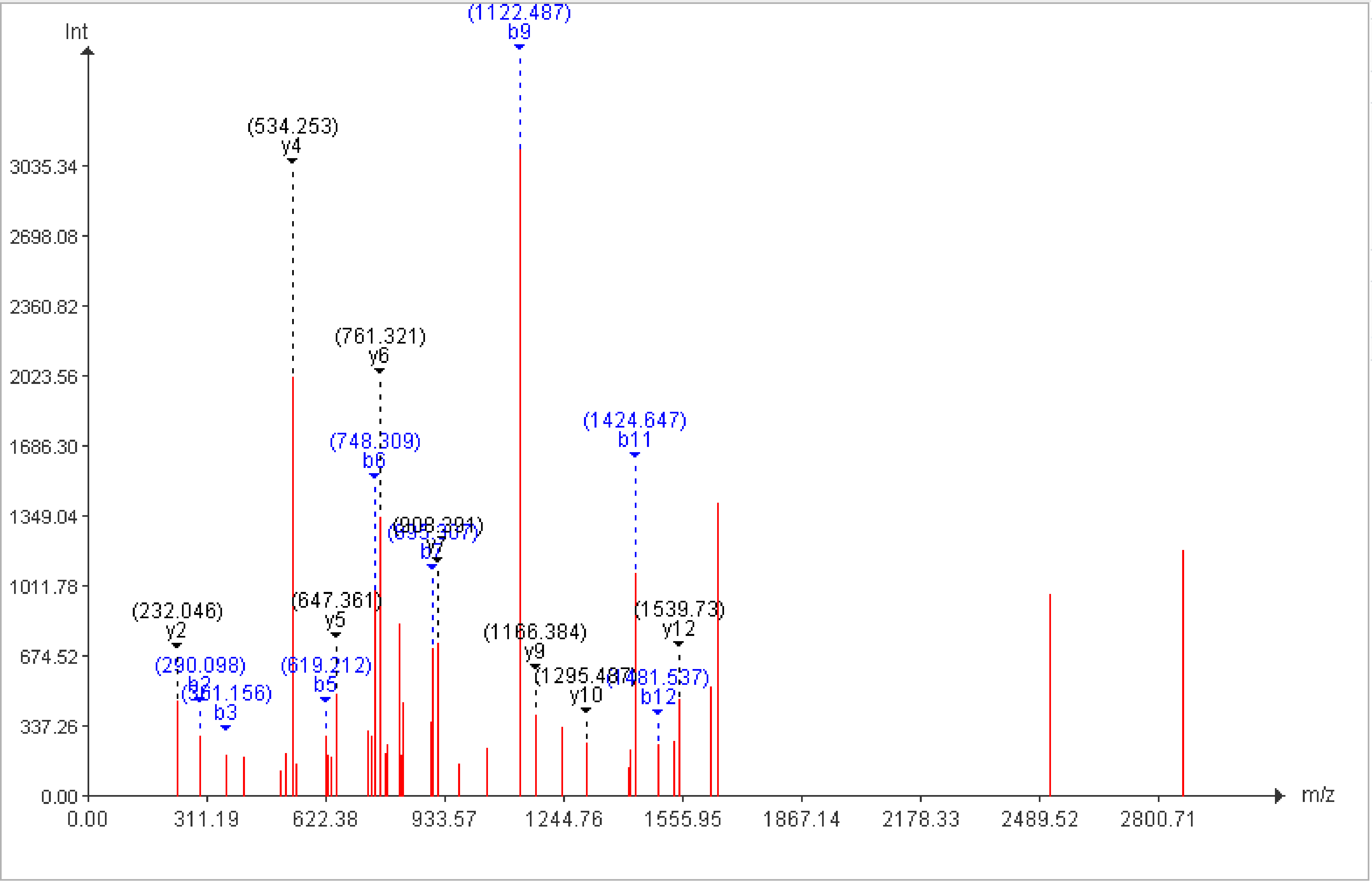
instrument: Bruker Esquire HCT

AcD3-AK(AcD3K)AEEEFNIEK(AcD3K*)GR-COOH*

precursor mass: 828.3610 Da (charge: +2) protein: P50518 (33-45)

score (threshold): 82.0 (31.0)

instrument: Bruker Esquire HCT

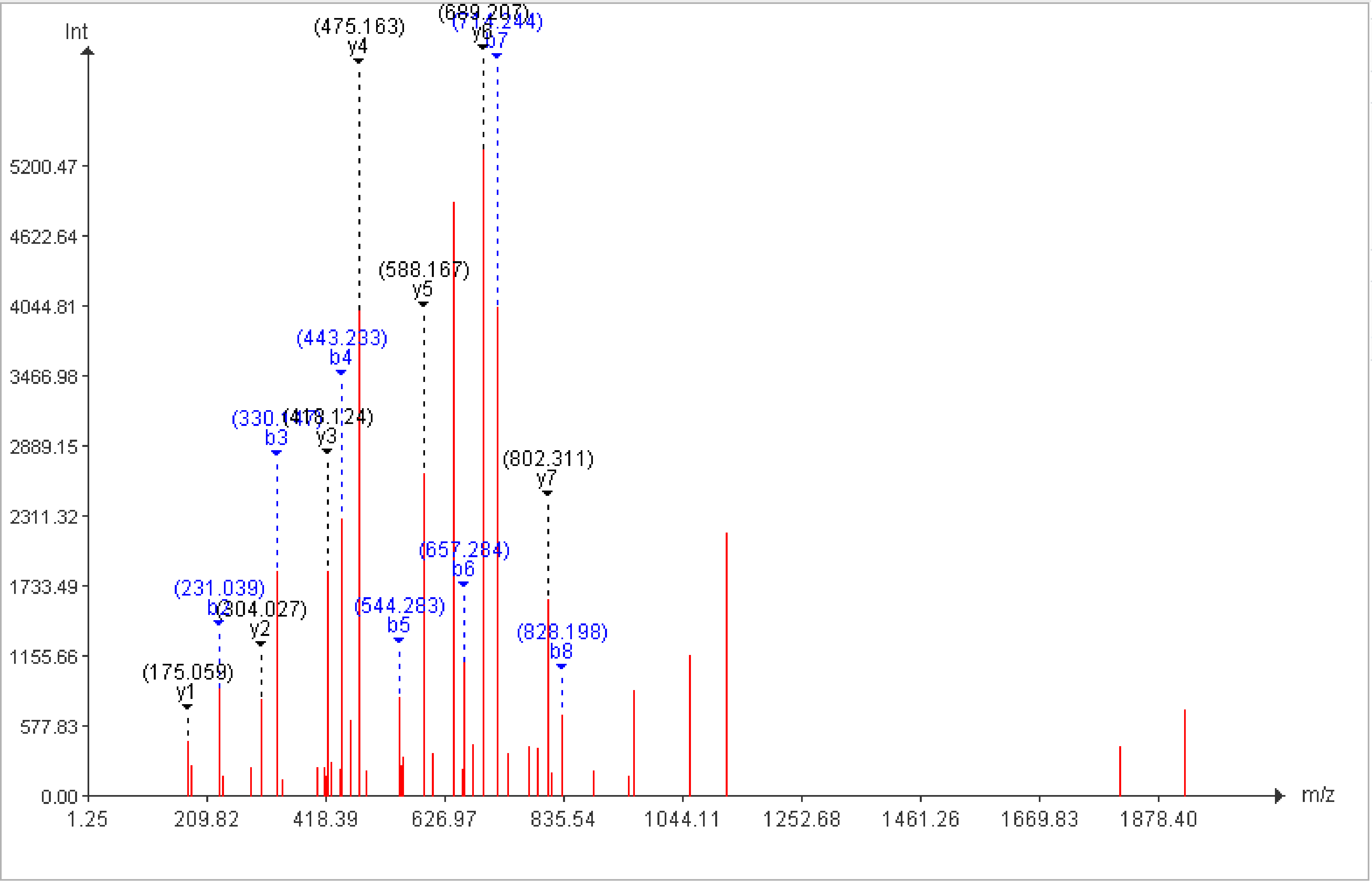


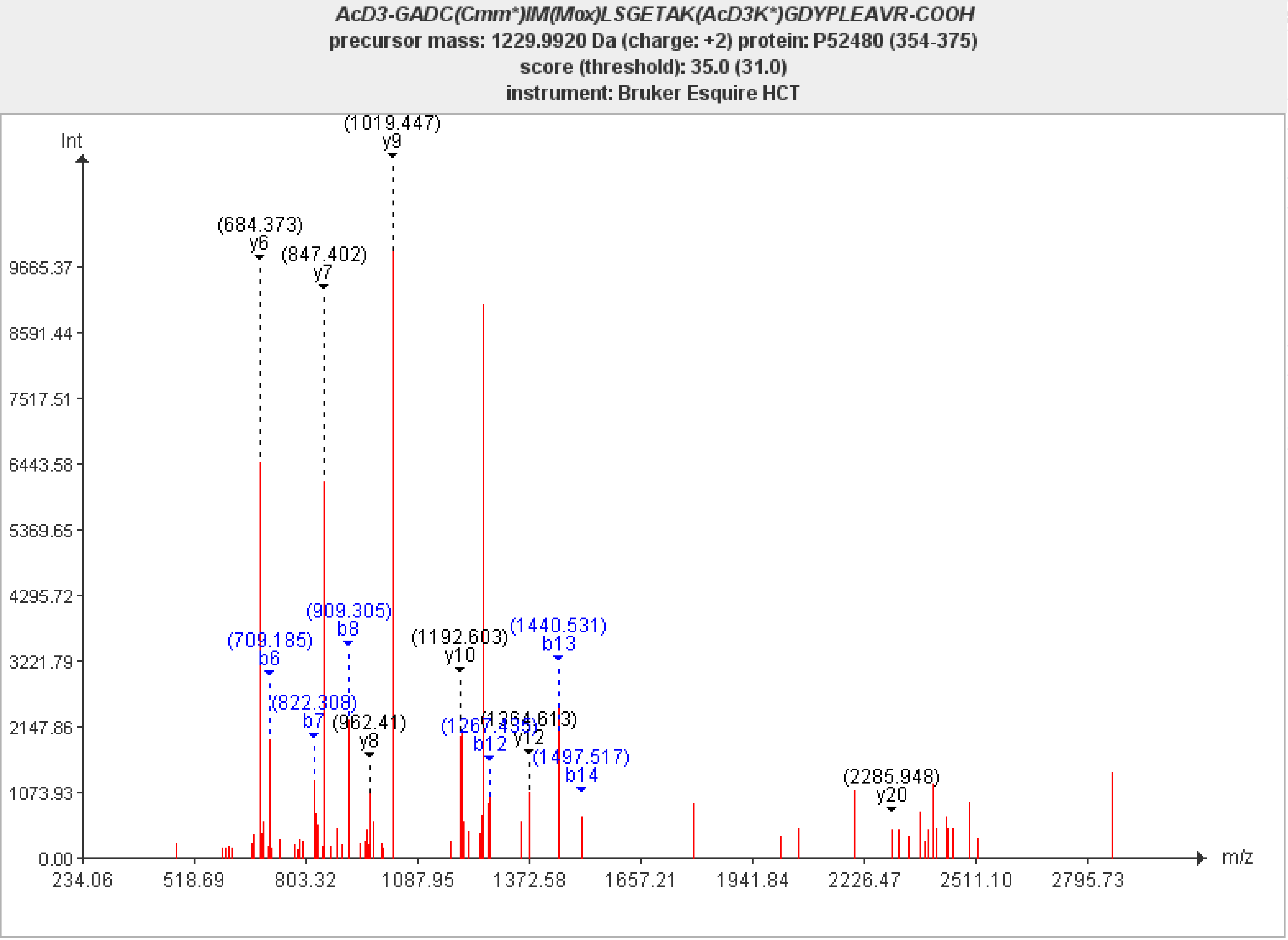
AcD3-GQVITIGNER-COOH

precursor mass: 566.4000 Da (charge: +2) protein: P62737 (247-256)

score (threshold): 71.0 (31.0)

instrument: Bruker Esquire HCT





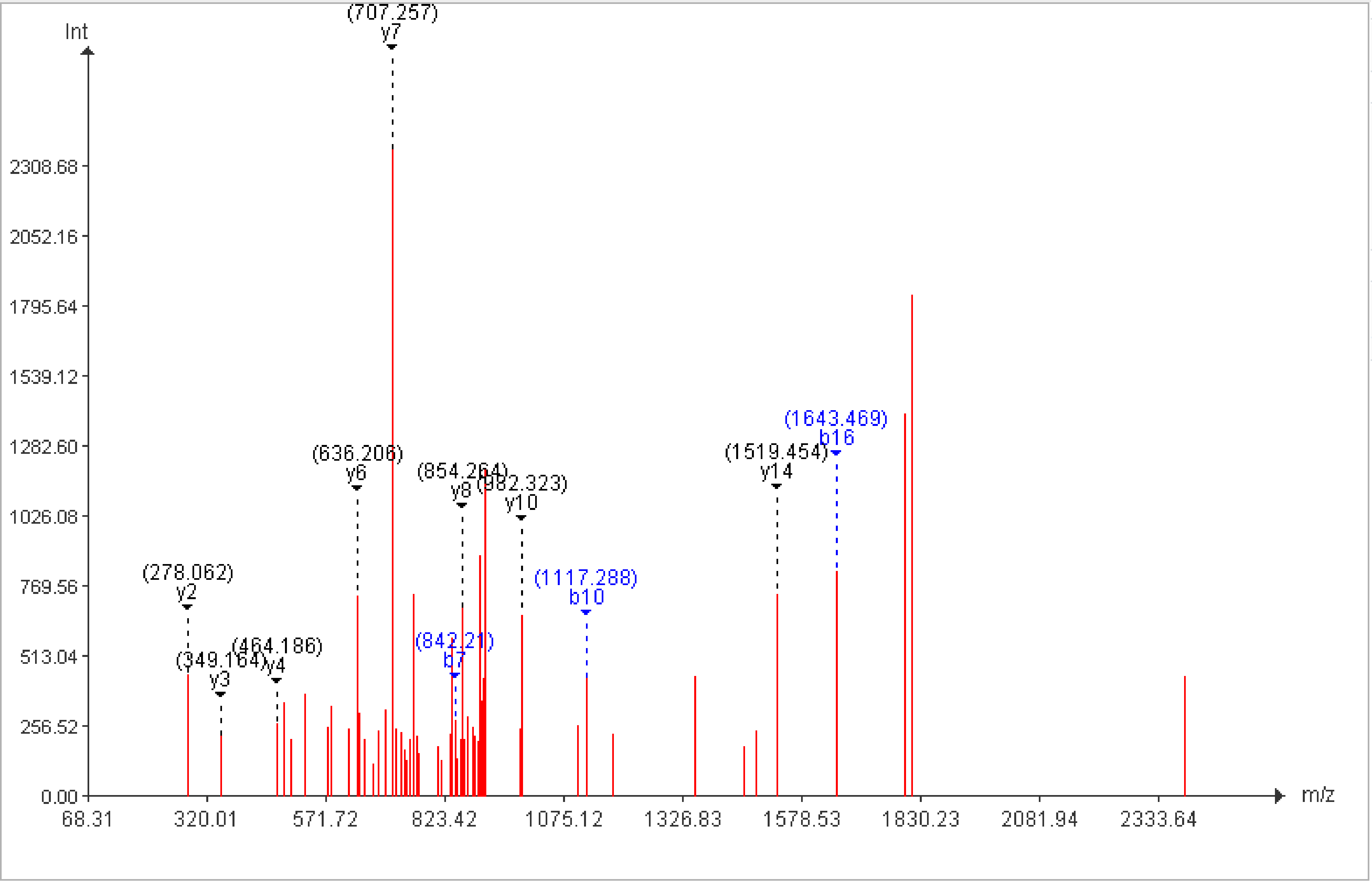
AcD3-GADC(Cmm*)IM(Mox)LSGETAK(AcD3K*)GDYPLEAVR-COOH

precursor mass: 1229.9920 Da (charge: +2) protein: P52480 (354-375)

score (threshold): 35.0 (31.0)

instrument: Bruker Esquire HCT

AcD3-N(Dam)GSGM(Mox)C(Cmm*)K(AcD3K*)AGFAGDDAPR(C13*)-COOH
precursor mass: 912.3840 Da (charge: +2) protein: P60710 (12-28)
score (threshold): 49.0 (31.0)
instrument: Bruker Esquire HCT

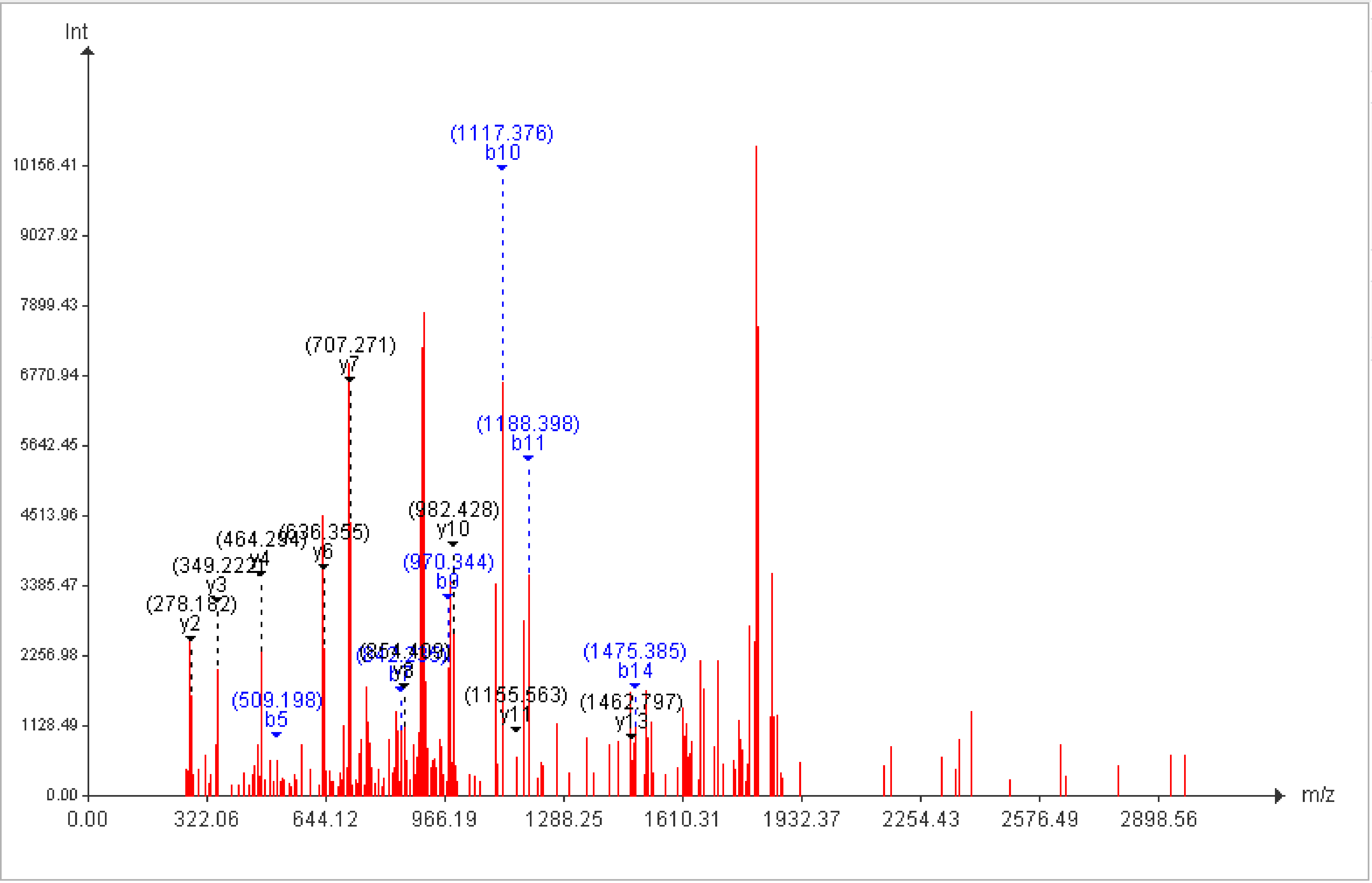


AcD3-N(Dam)GSGM(Mox)C(Cmm)K(AcD3K*)AGFAGDDAPR(C13*)-COOH*

precursor mass: 912.3630 Da (charge: +2) protein: P60710 (12-28)

score (threshold): 31.0 (31.0)

instrument: Bruker Esquire HCT

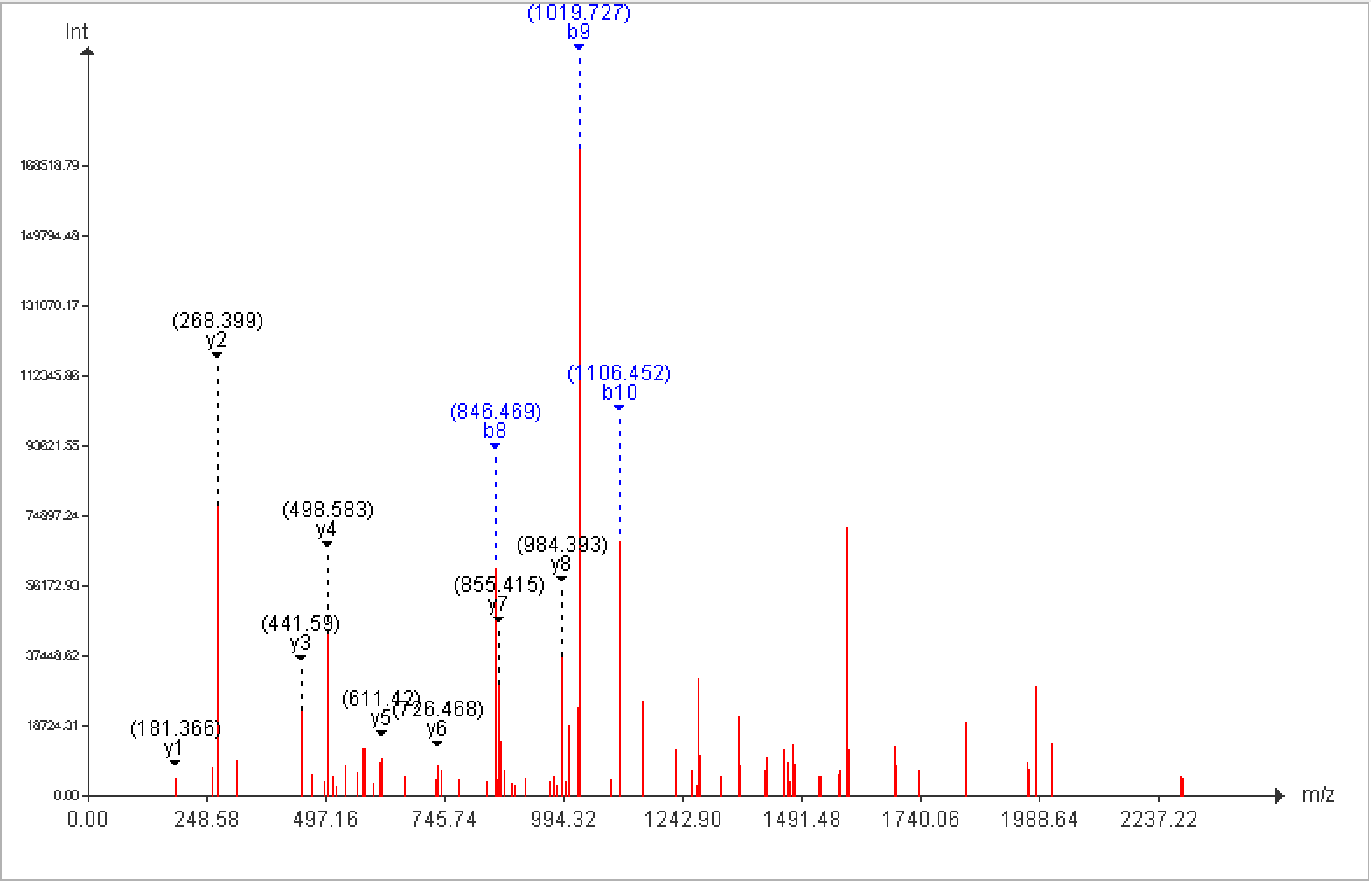


AcD3-GTVEEDLGK(AcD3K)SR(C13*)-COOH*

precursor mass: 643.8590 Da (charge: +2) protein: P08113 (29-39)

score (threshold): 52.0 (31.0)

instrument: Bruker Esquire HCT

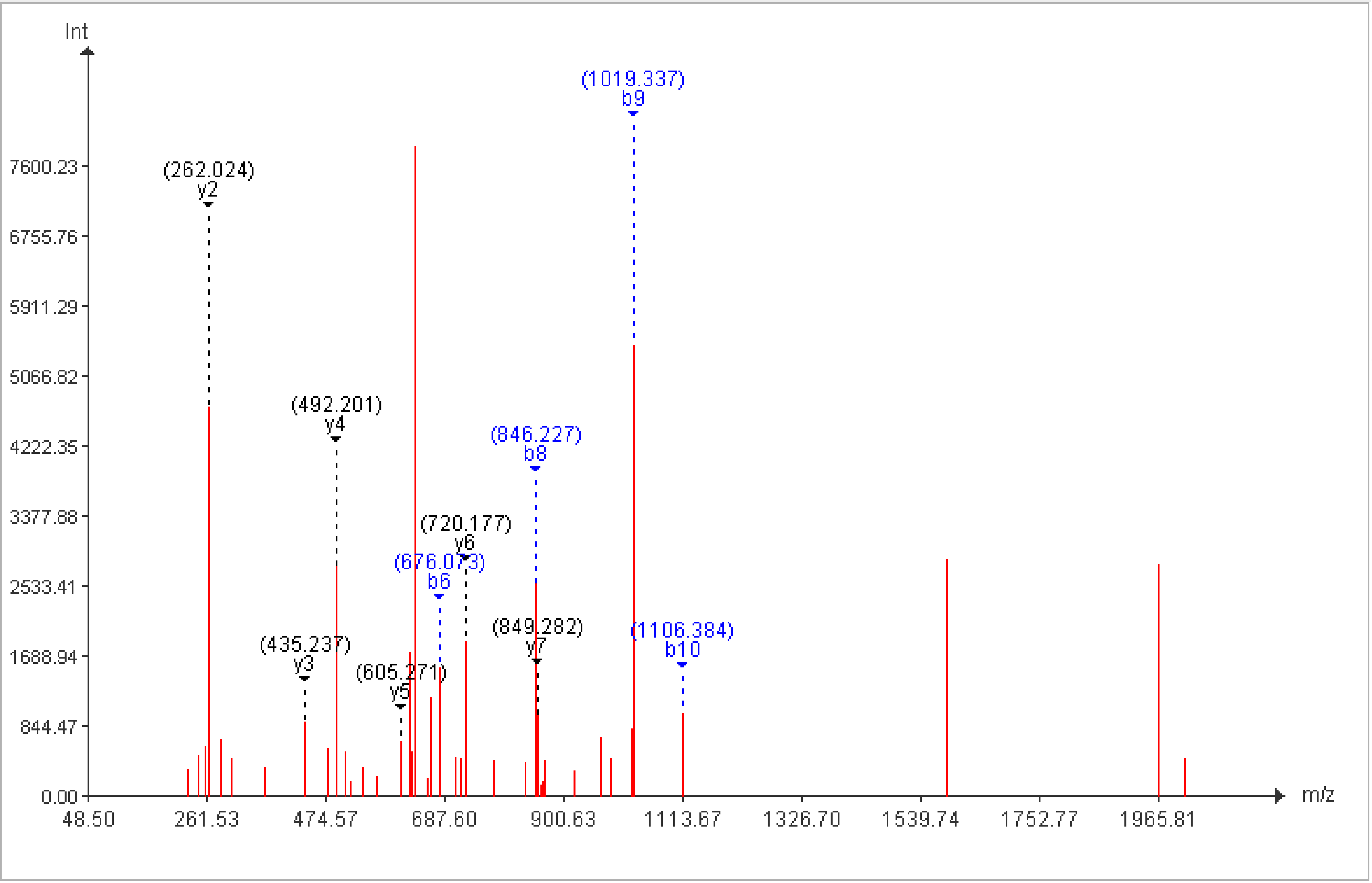


AcD3-GTVEEDLGK(AcD3K)SR-COOH*

precursor mass: 640.7600 Da (charge: +2) protein: P08113 (29-39)

score (threshold): 50.0 (31.0)

instrument: Bruker Esquire HCT

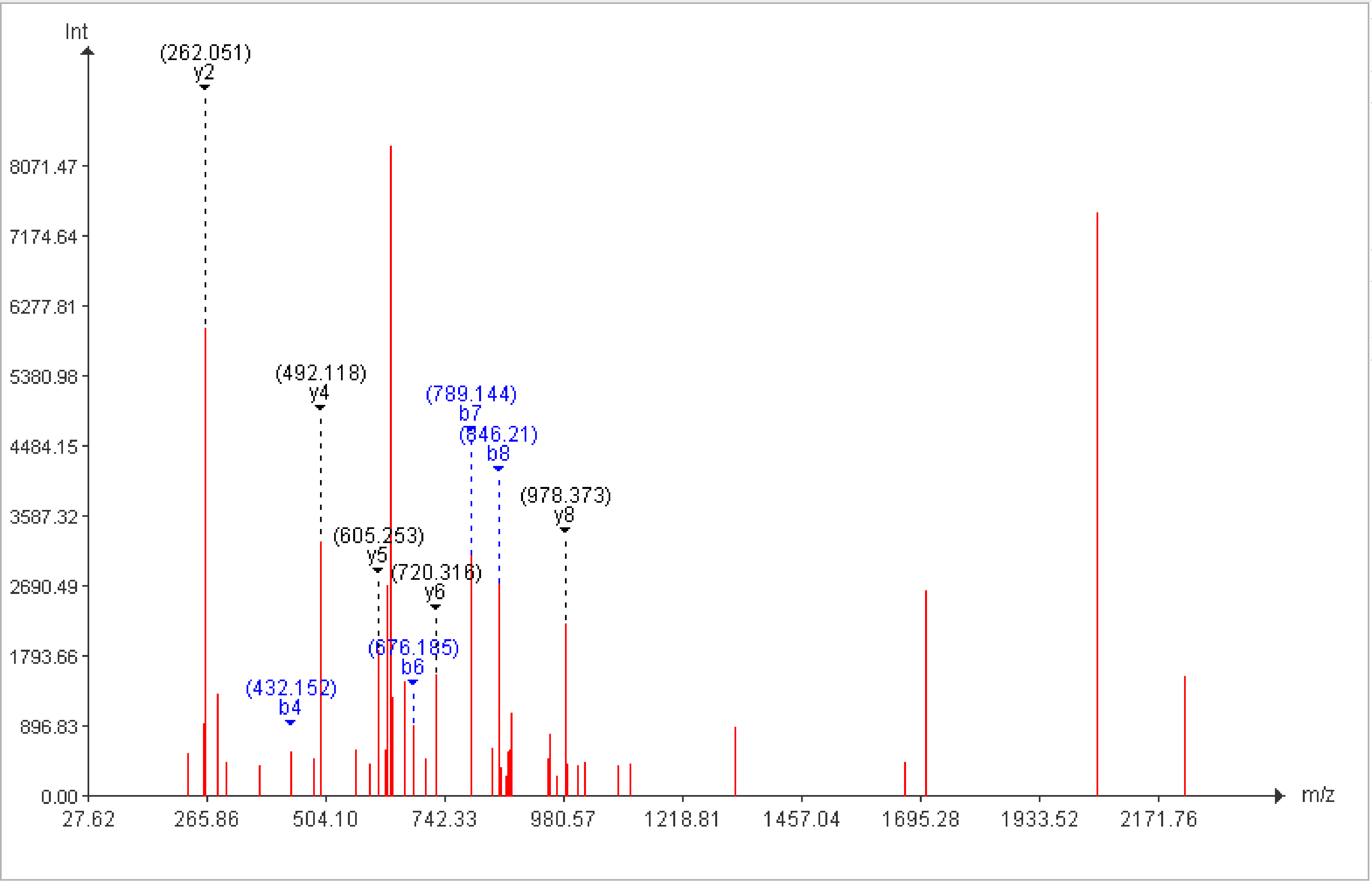


AcD3-GTVEEDLGK(AcD3K)SR-COOH*

precursor mass: 640.7970 Da (charge: +2) protein: P08113 (29-39)

score (threshold): 36.0 (31.0)

instrument: Bruker Esquire HCT

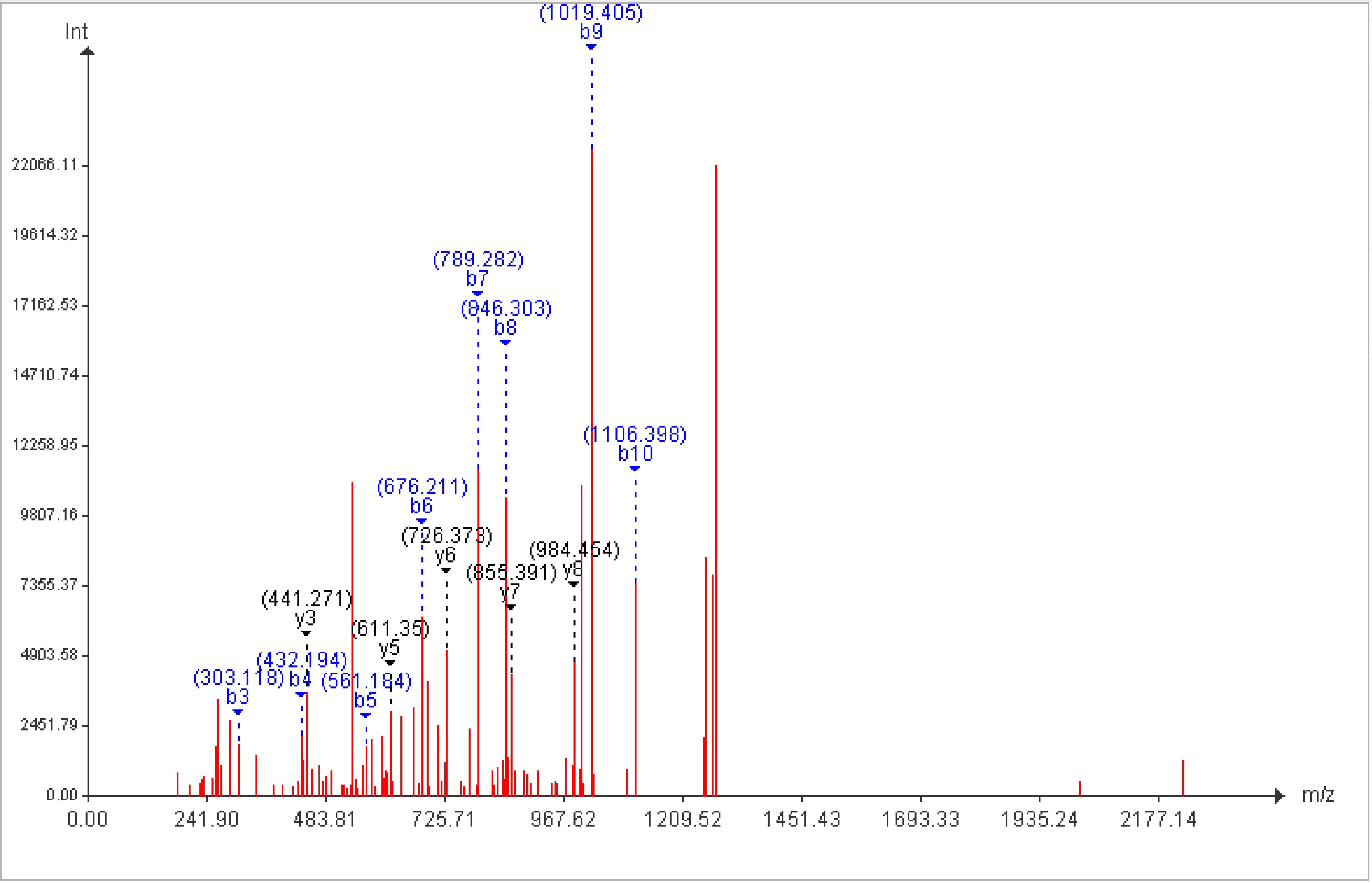


AcD3-GTVEEDLGK(AcD3K)SR(C13*)-COOH*

precursor mass: 643.7950 Da (charge: +2) protein: P08113 (29-39)

score (threshold): 54.0 (31.0)

instrument: Bruker Esquire HCT

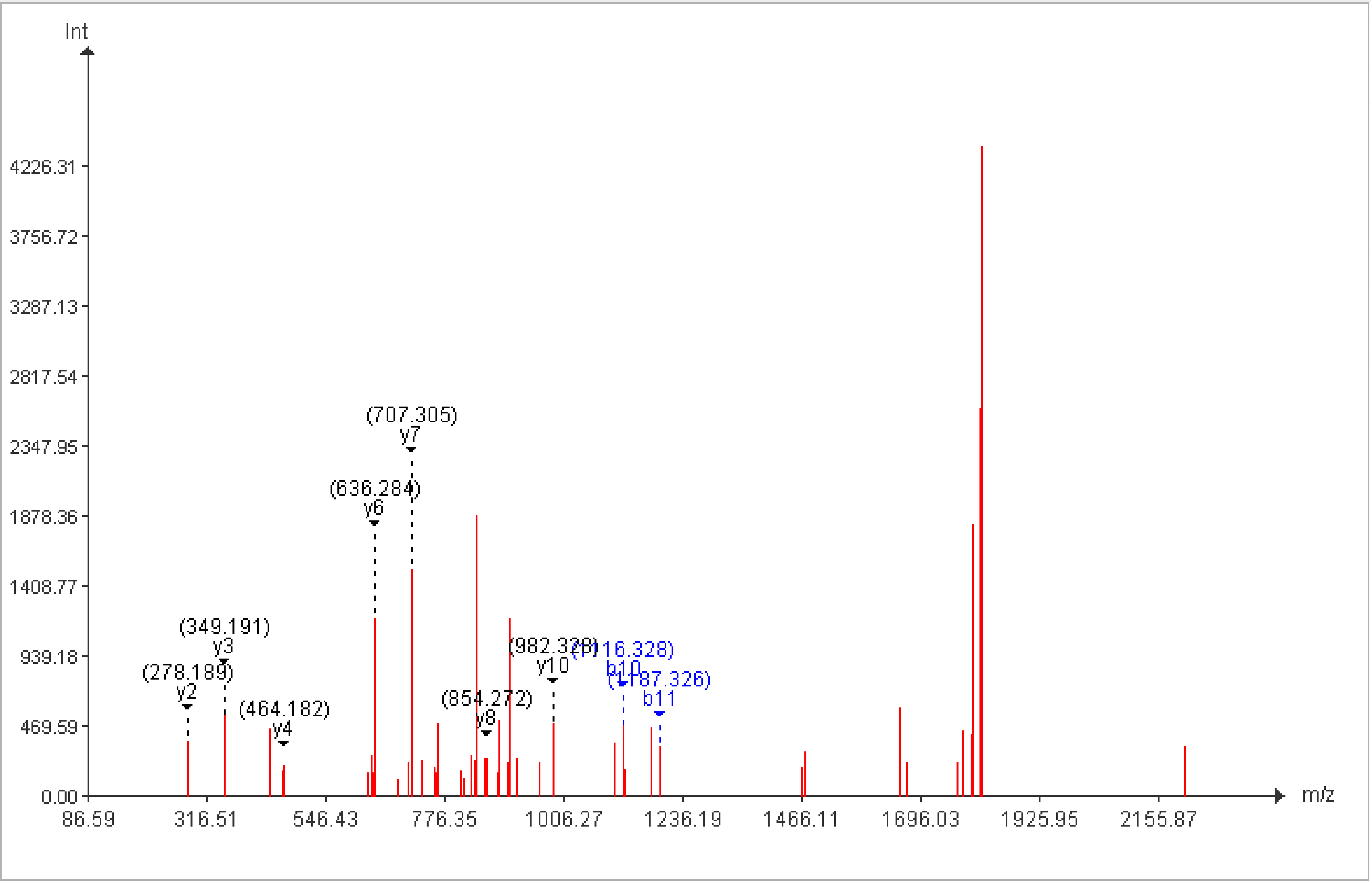


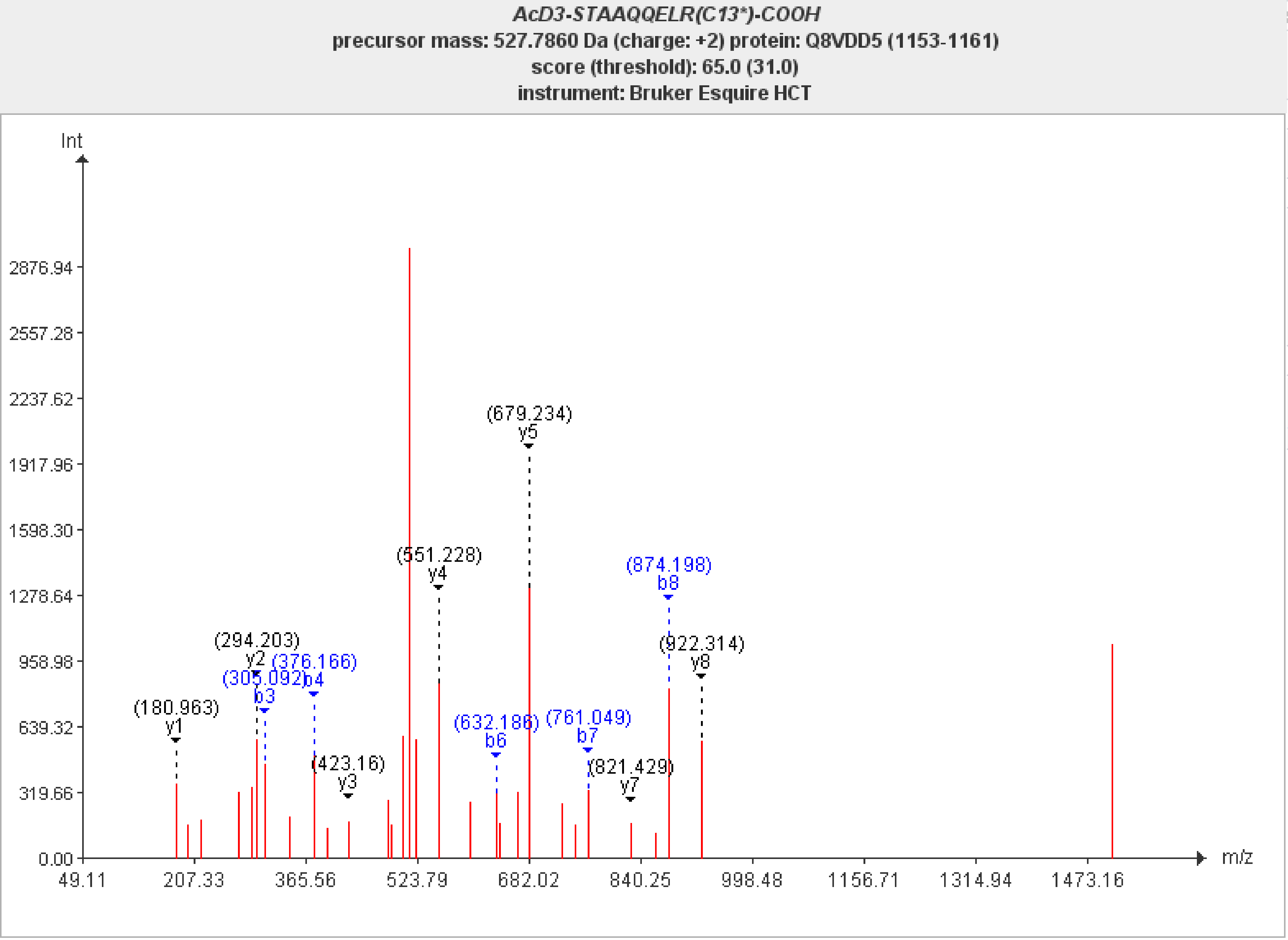
AcD3-NGSGM(Mox)C(Cmm)K(AcD3K*)AGFAGDDAPR(C13*)-COOH*

precursor mass: 911.8890 Da (charge: +2) protein: P60710 (12-28)

score (threshold): 35.0 (31.0)

instrument: Bruker Esquire HCT





AcD3-STAAQQELR(C13)-COOH*

precursor mass: 527.7860 Da (charge: +2) protein: Q8VDD5 (1153-1161)

score (threshold): 65.0 (31.0)

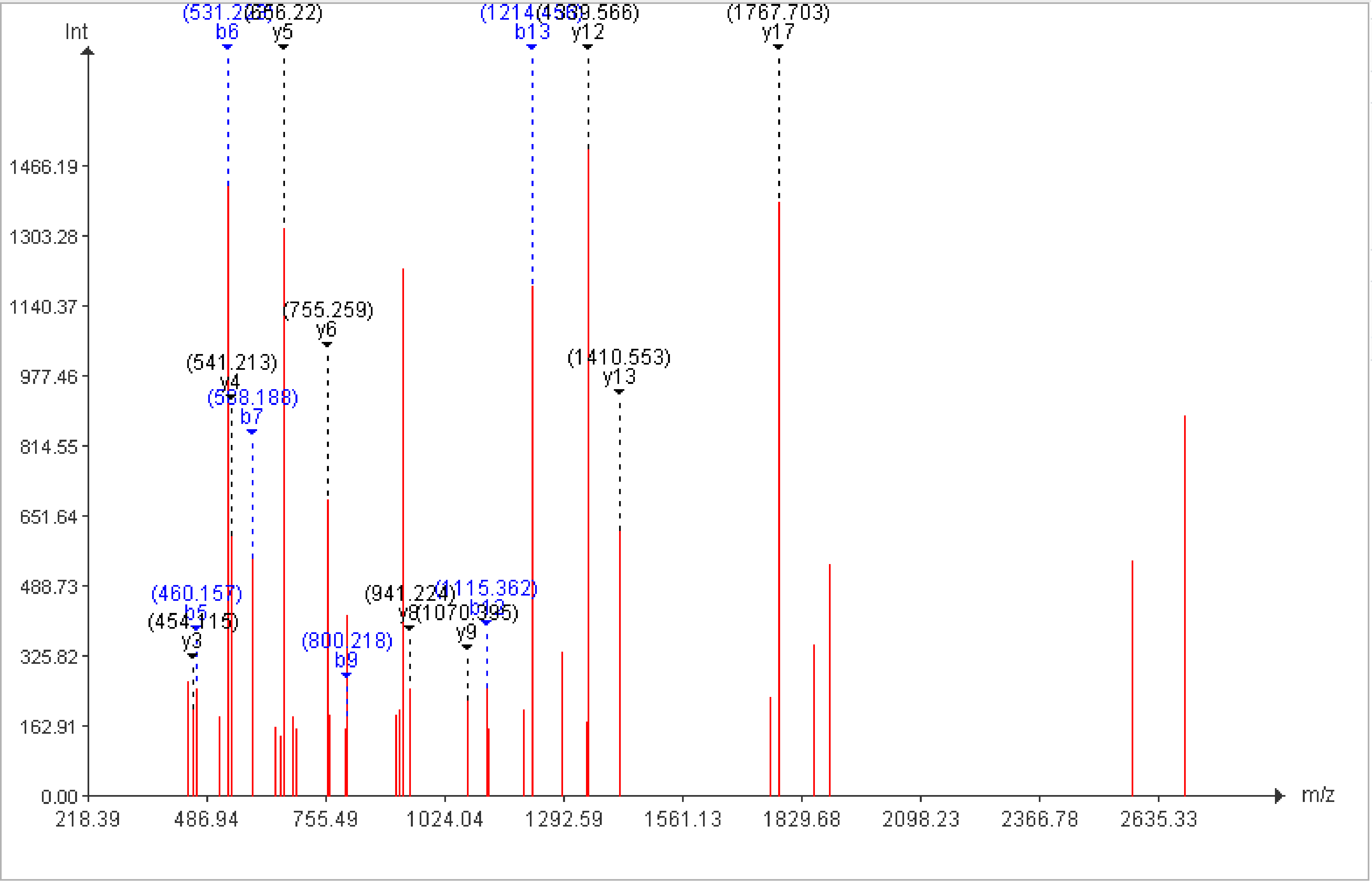
instrument: Bruker Esquire HCT

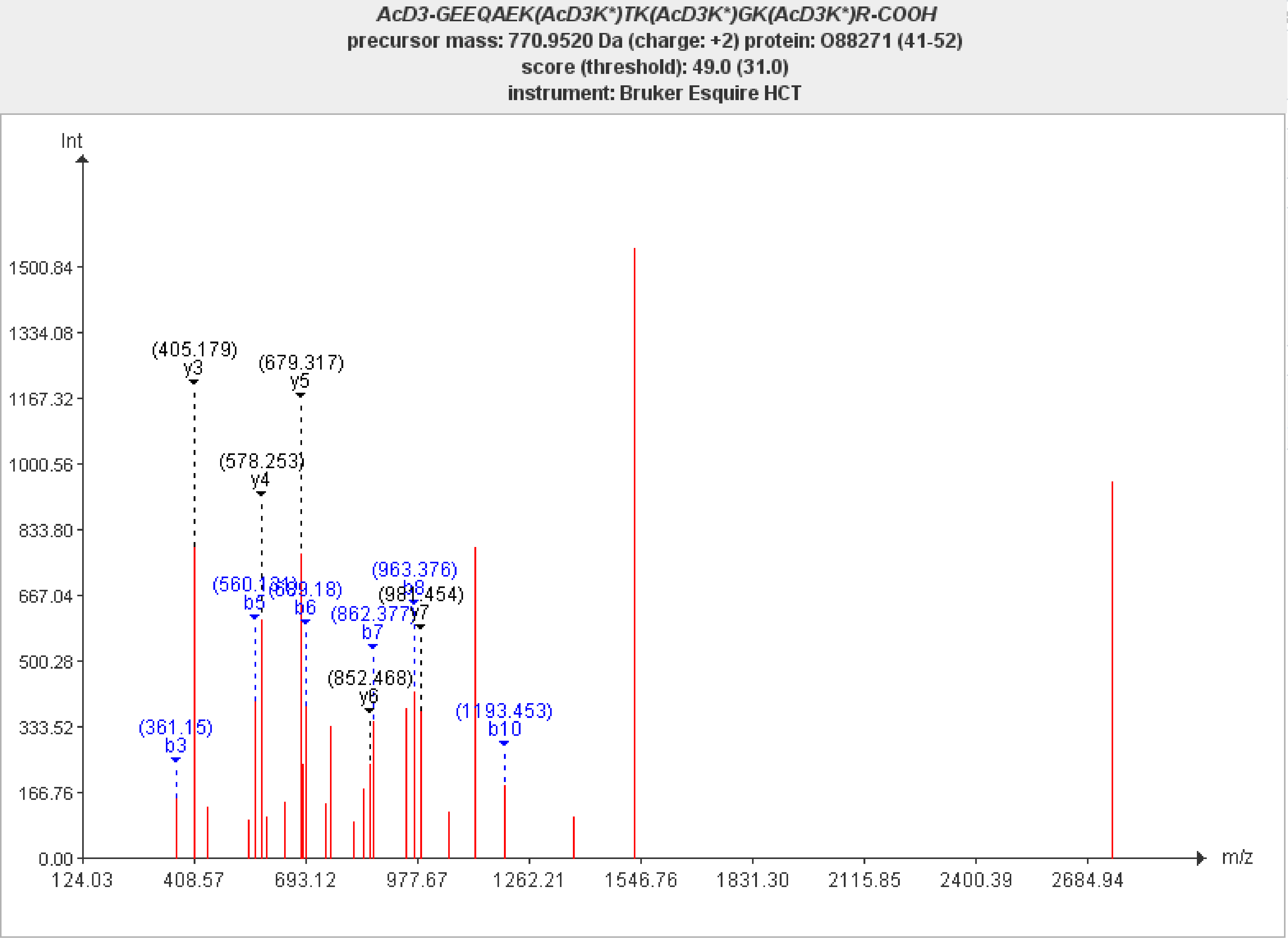
AcD3-GGDGQAGPDEGEVDSC(Cmm)LR(C13*)-COOH*

precursor mass: 935.4020 Da (charge: +2) protein: Q9CPW4 (29-46)

score (threshold): 58.0 (36.0)

instrument: Bruker Esquire HCT





AcD3-GEEQAEK(AcD3K)TK(AcD3K*)GK(AcD3K*)R-COOH*

precursor mass: 770.9520 Da (charge: +2) protein: O88271 (41-52)

score (threshold): 49.0 (31.0)

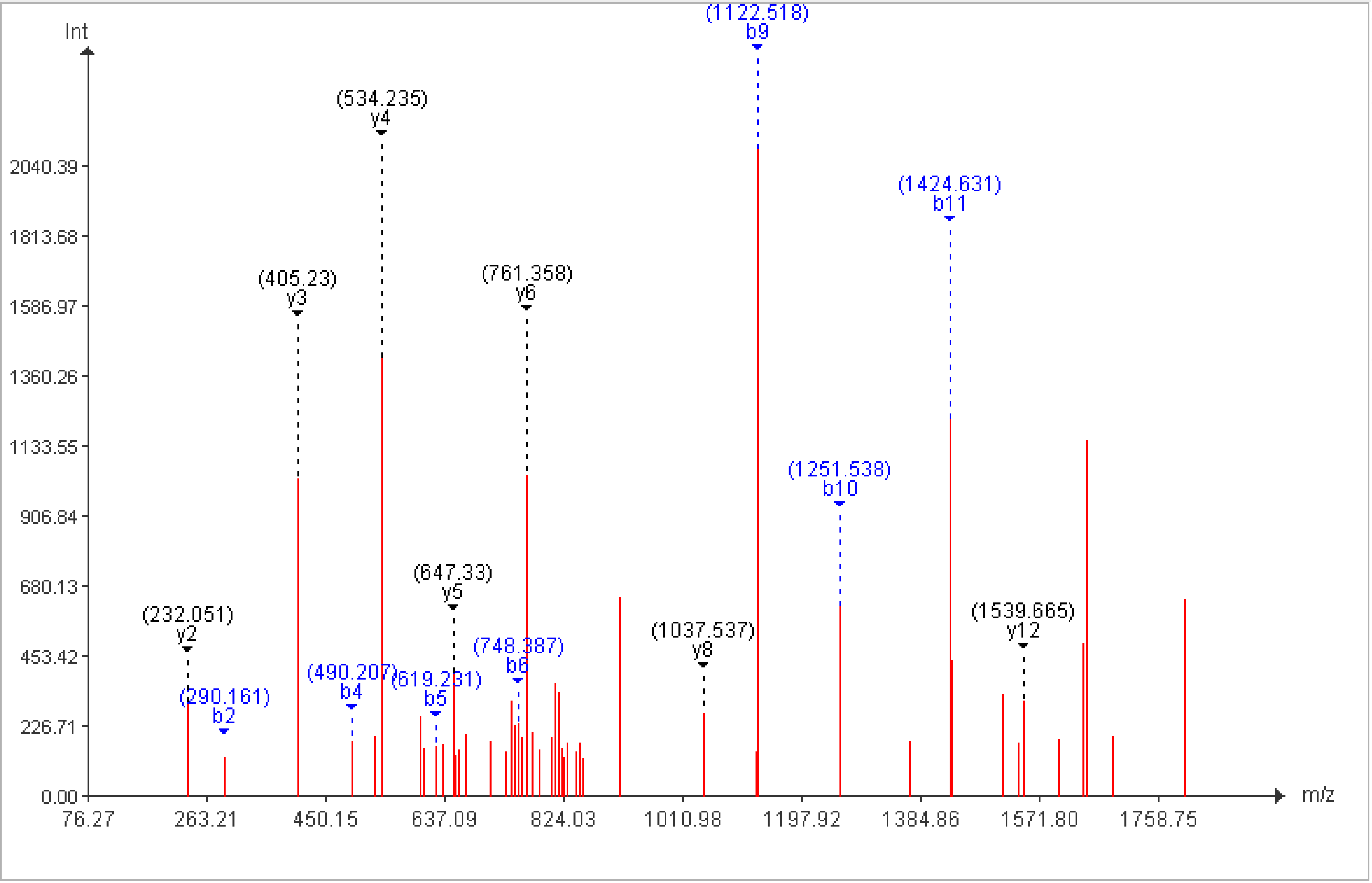
instrument: Bruker Esquire HCT

AcD3-AK(AcD3K)AEEEFNIEK(AcD3K*)GR-COOH*

precursor mass: 828.4880 Da (charge: +2) protein: P50518 (33-45)

score (threshold): 38.0 (31.0)

instrument: Bruker Esquire HCT

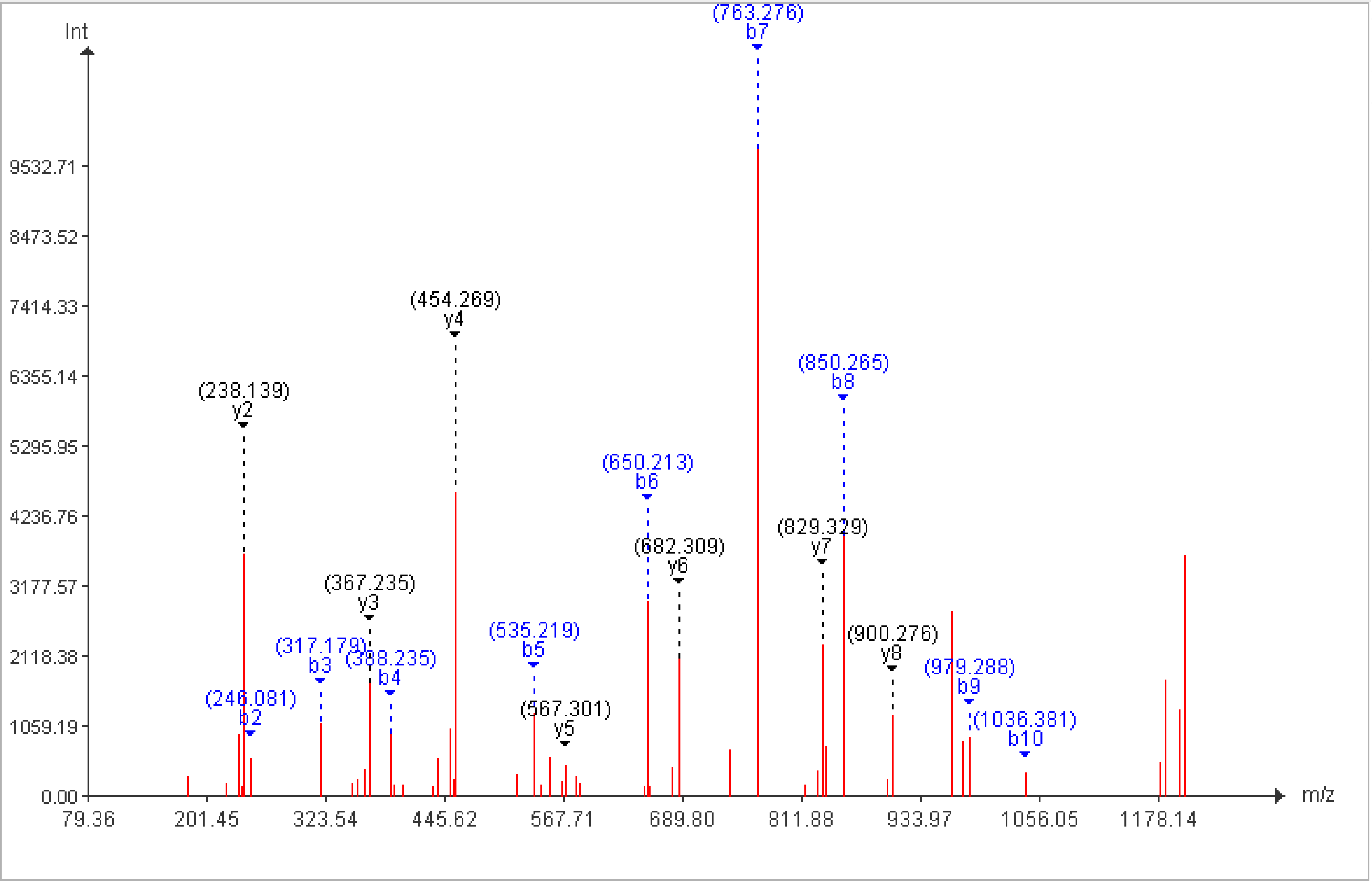


AcD3-AEAAM(Mox)DISEGR(C13)-COOH*

precursor mass: 608.7880 Da (charge: +2) protein: P56399 (768-778)

score (threshold): 78.0 (31.0)

instrument: Bruker Esquire HCT

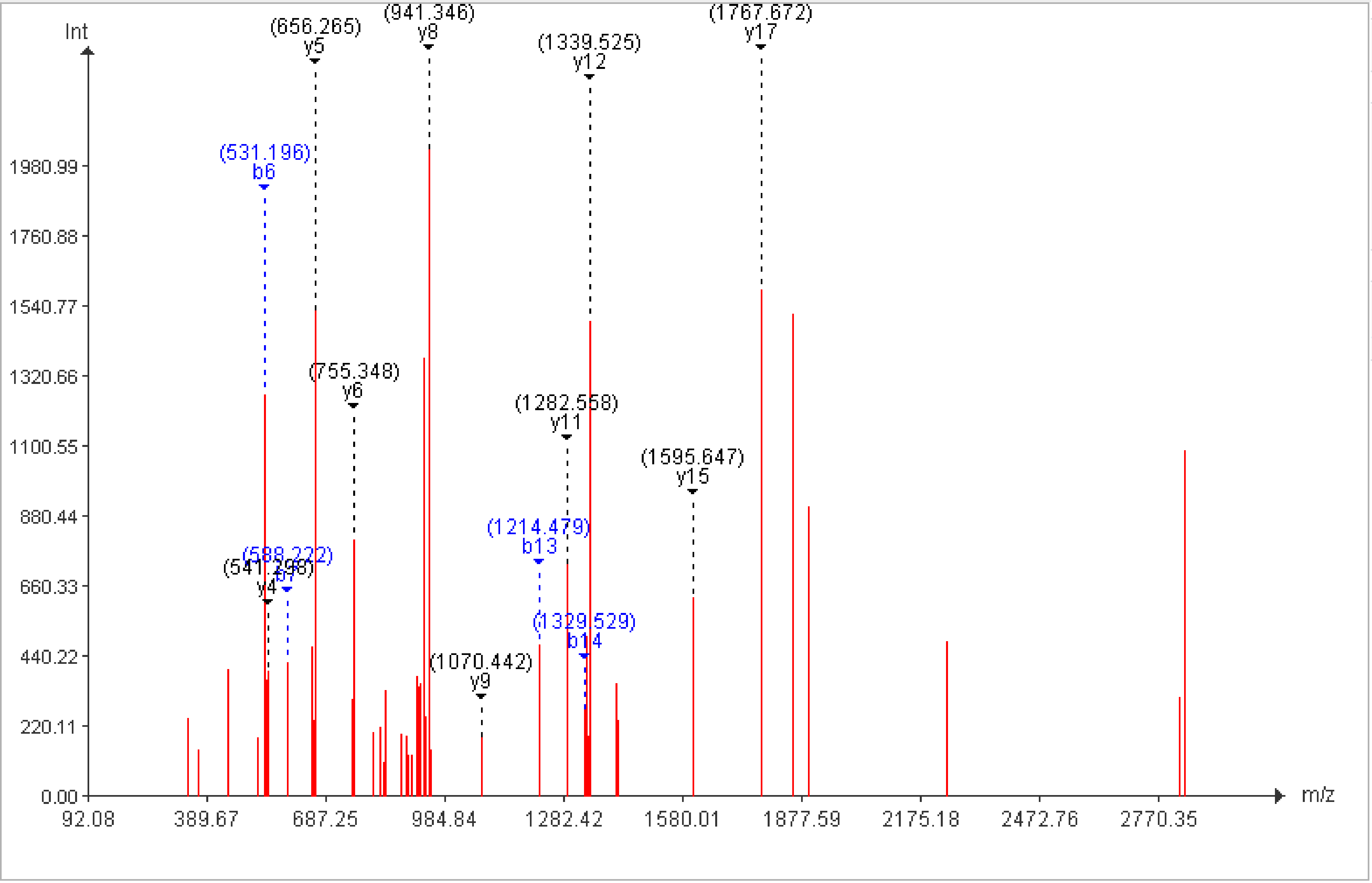


AcD3-GGDGQAGPDEGEVDSC(Cmm)LR(C13*)-COOH*

precursor mass: 935.3860 Da (charge: +2) protein: Q9CPW4 (29-46)

score (threshold): 58.0 (31.0)

instrument: Bruker Esquire HCT

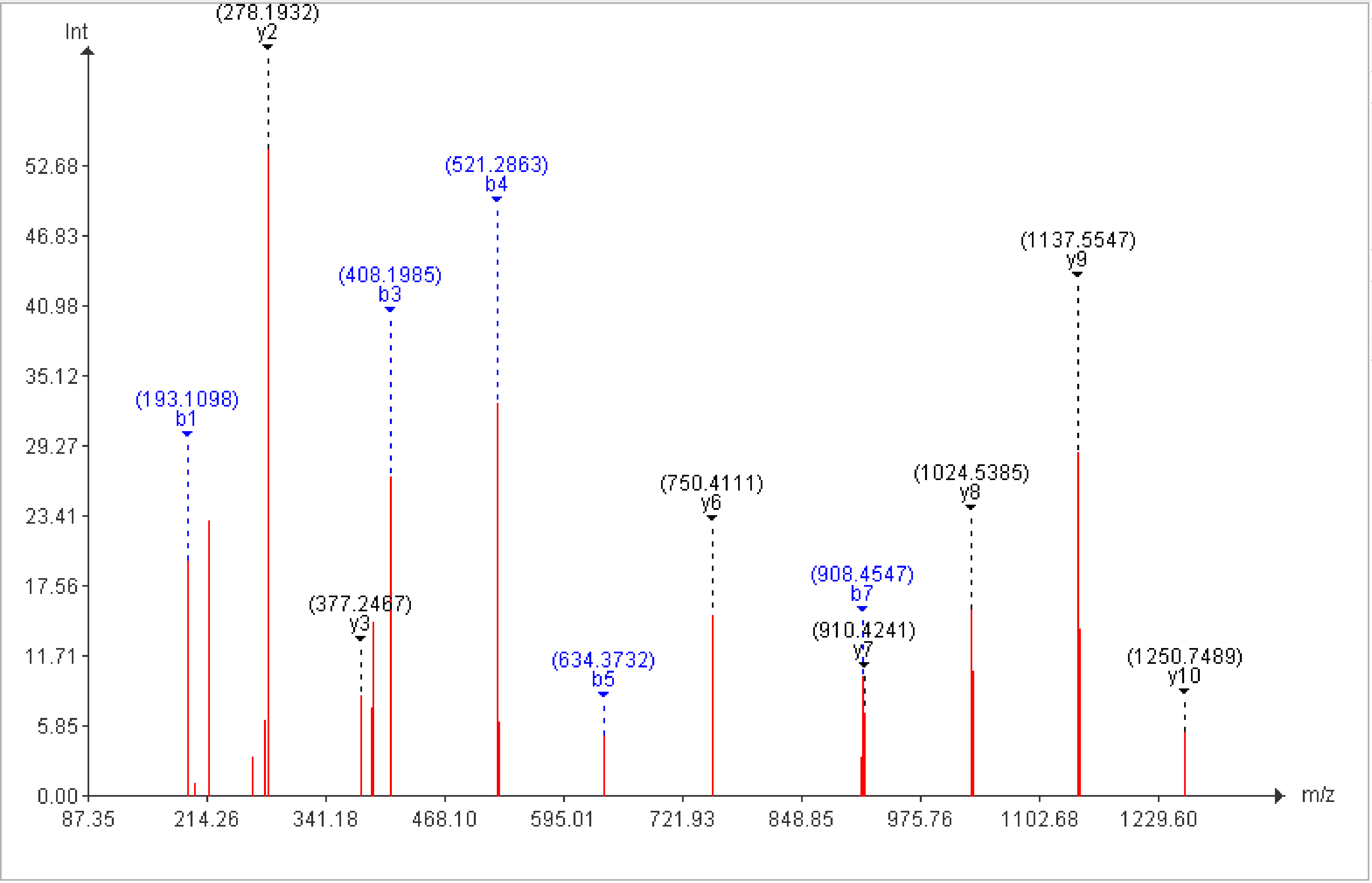


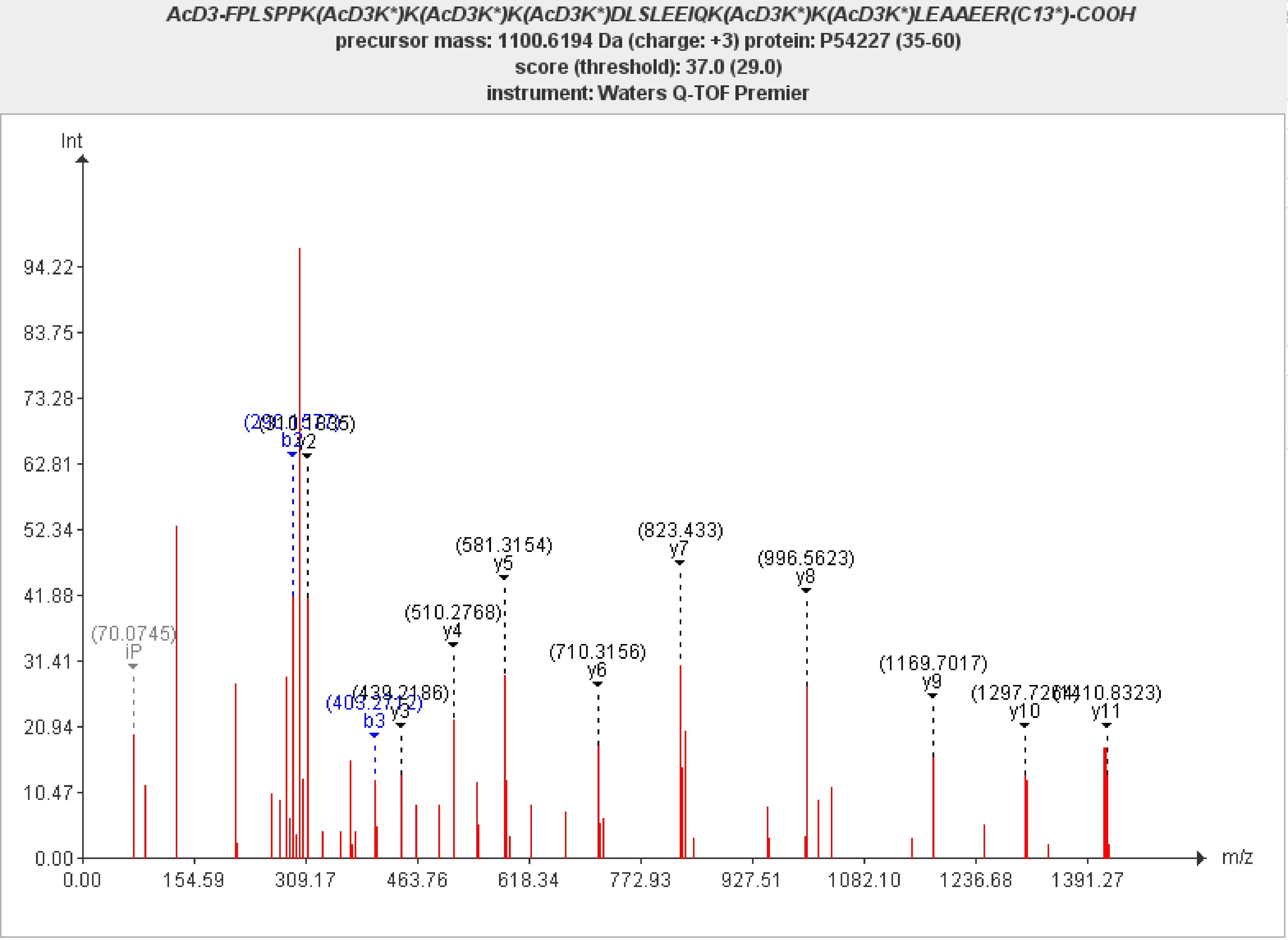
AcD3-FSQLLNC(Cmm)PEFVPR(C13*)-COOH*

precursor mass: 829.4267 Da (charge: +2) protein: Q3UU34 (298-310)

score (threshold): 59.0 (32.0)

instrument: Waters Q-TOF Premier





AcD3-FPLSPPK(AcD3K)K(AcD3K*)K(AcD3K*)DLSLEEIQK(AcD3K*)K(AcD3K*)LEAAEER(C13*)-COOH*

precursor mass: 1100.6194 Da (charge: +3) protein: P54227 (35-60)

score (threshold): 37.0 (29.0)

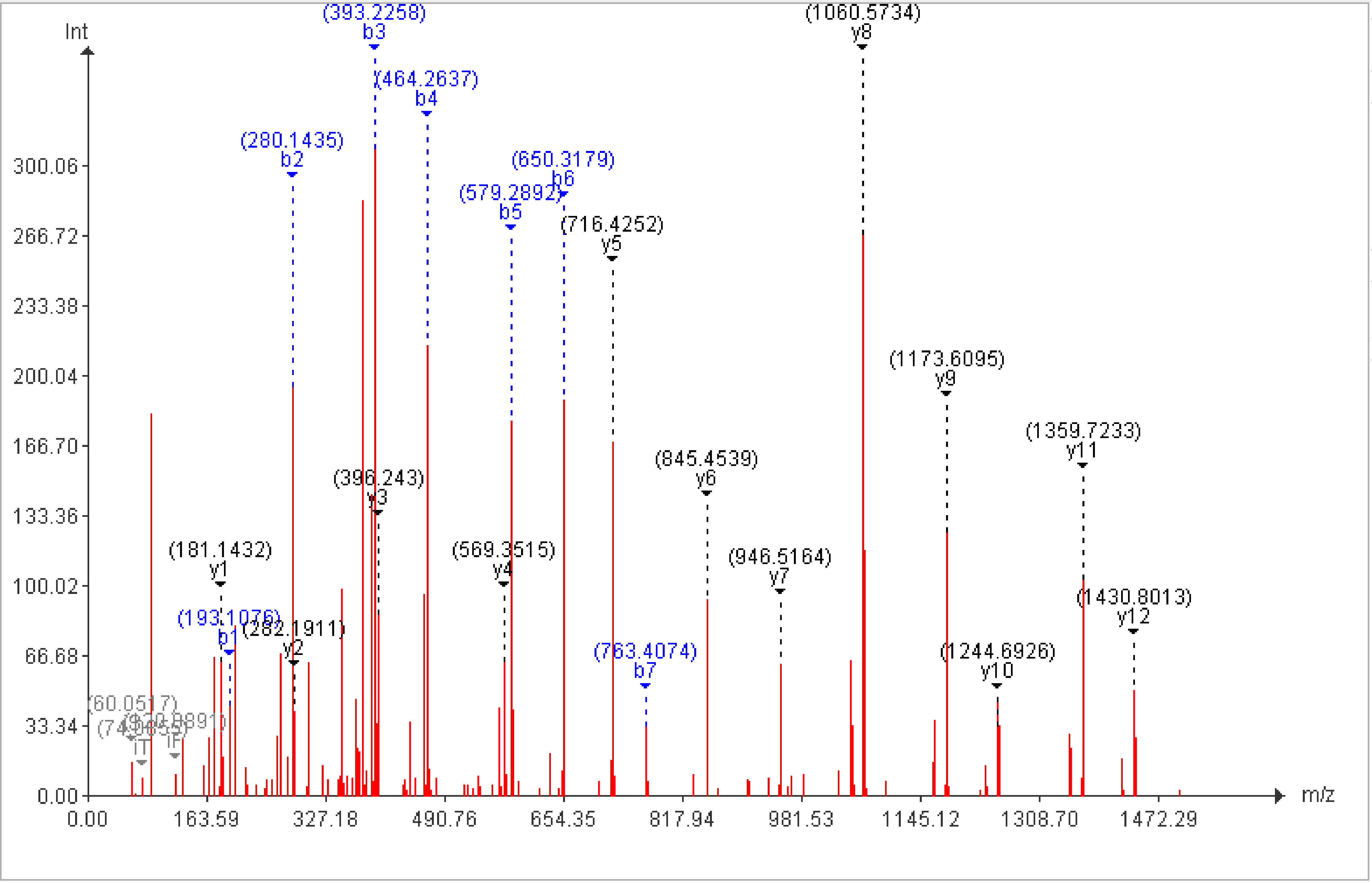
instrument: Waters Q-TOF Premier

AcD3-FSLADAINTEFK(AcD3K*)NTR(C13*)-COOH

precursor mass: 911.9753 Da (charge: +2) protein: P20152 (86-100)

score (threshold): 64.0 (30.0)

instrument: Waters Q-TOF Premier

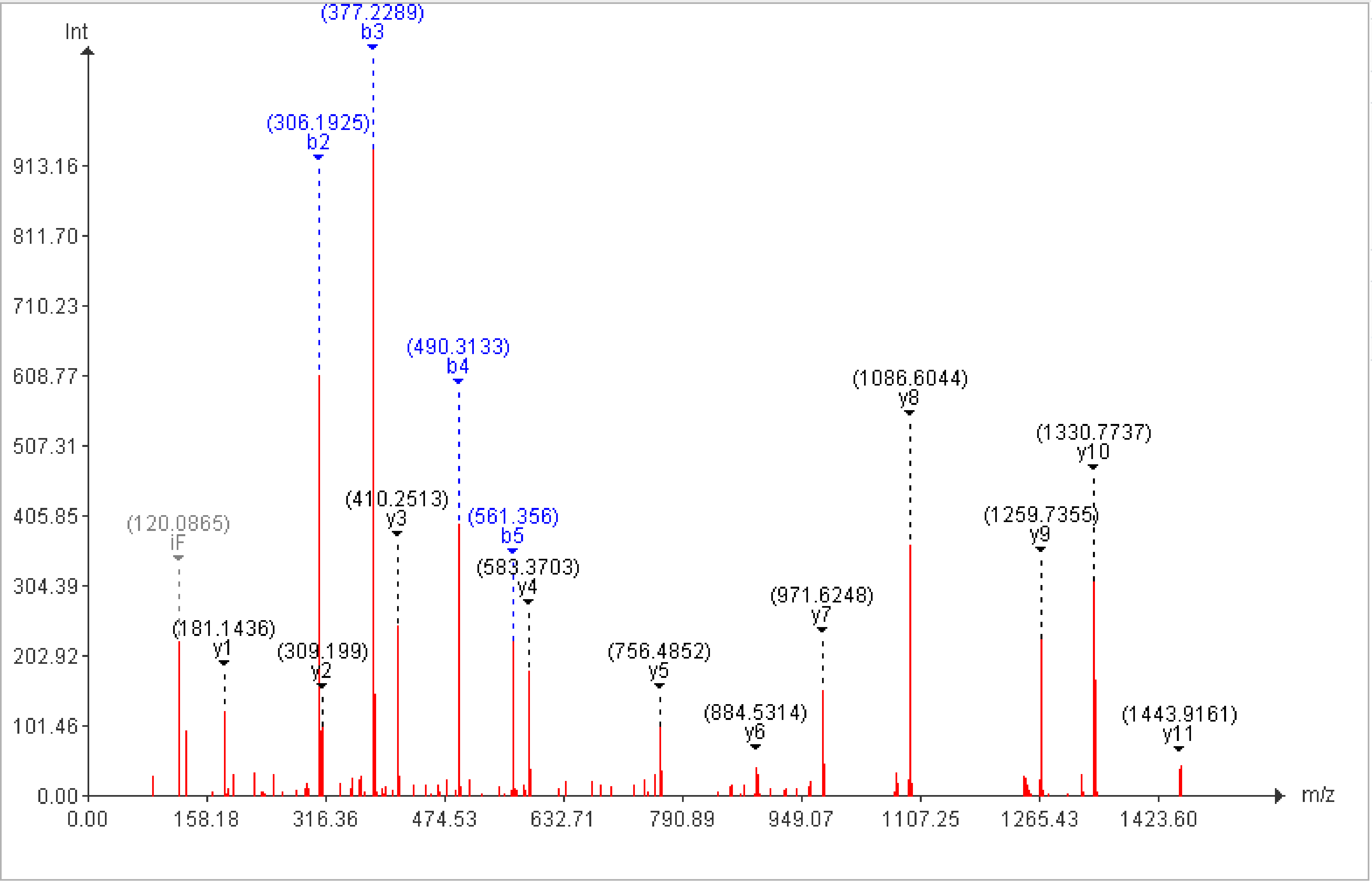


AcD3-LFAIAK(AcD3K)DSQK(AcD3K*)K(AcD3K*)TQR(C13*)-COOH*

precursor mass: 910.5367 Da (charge: +2) protein: Q6PGL7 (669-682)

score (threshold): 69.0 (31.0)

instrument: Waters Q-TOF Premier

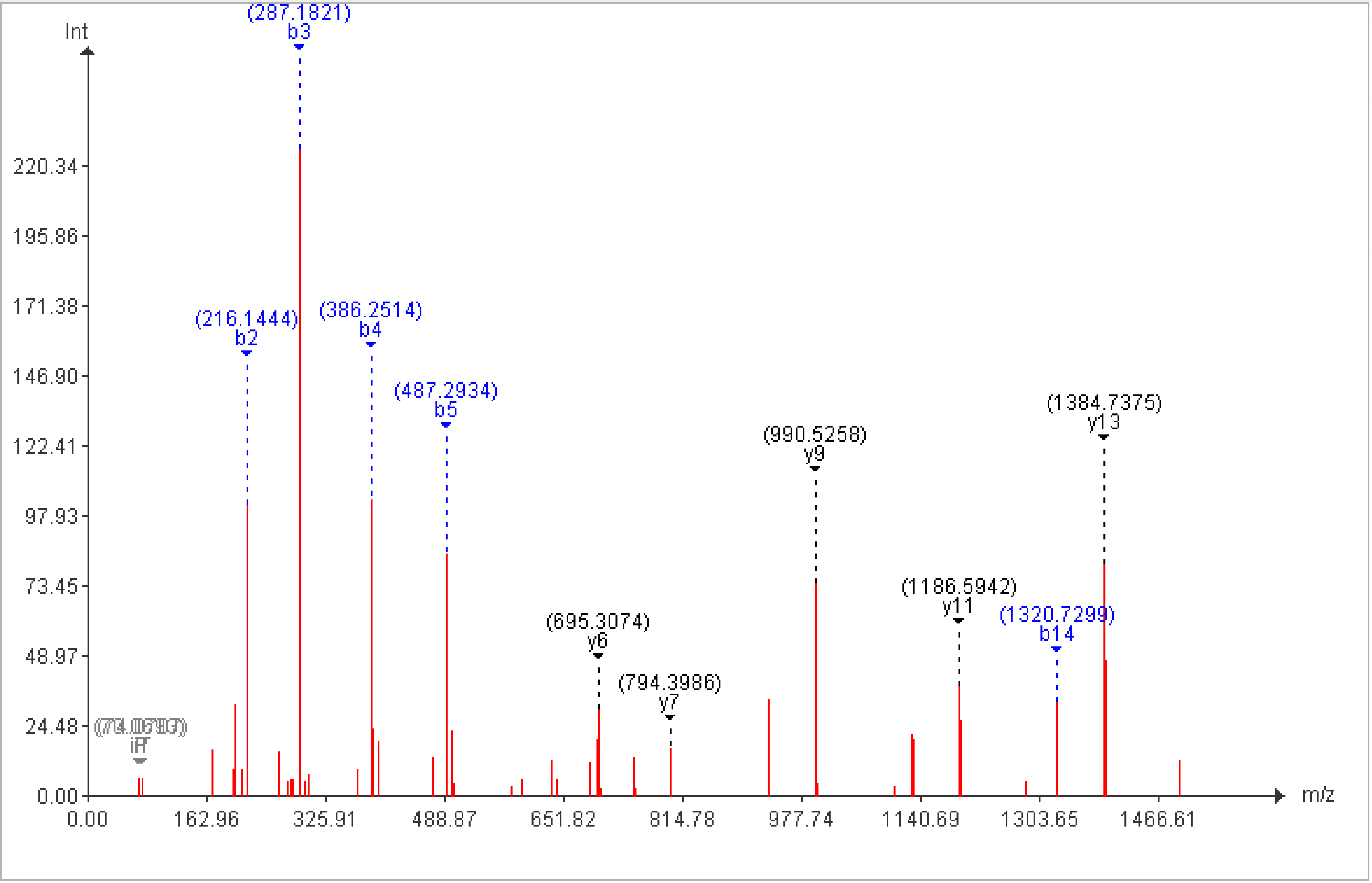


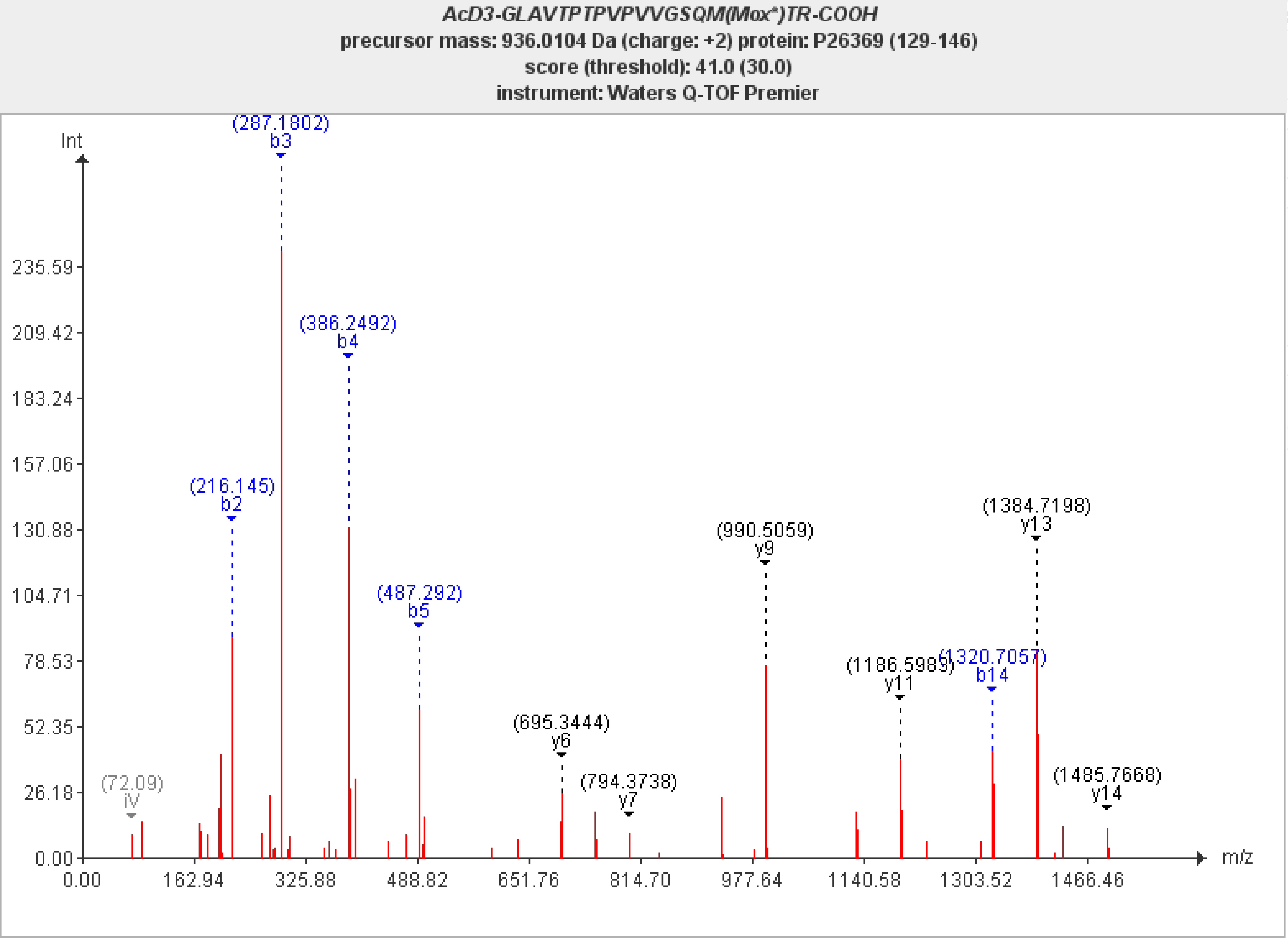
AcD3-GLAVTPTPVPVVGSQM(Mox)TR-COOH*

precursor mass: 936.0070 Da (charge: +2) protein: P26369 (129-146)

score (threshold): 44.0 (30.0)

instrument: Waters Q-TOF Premier





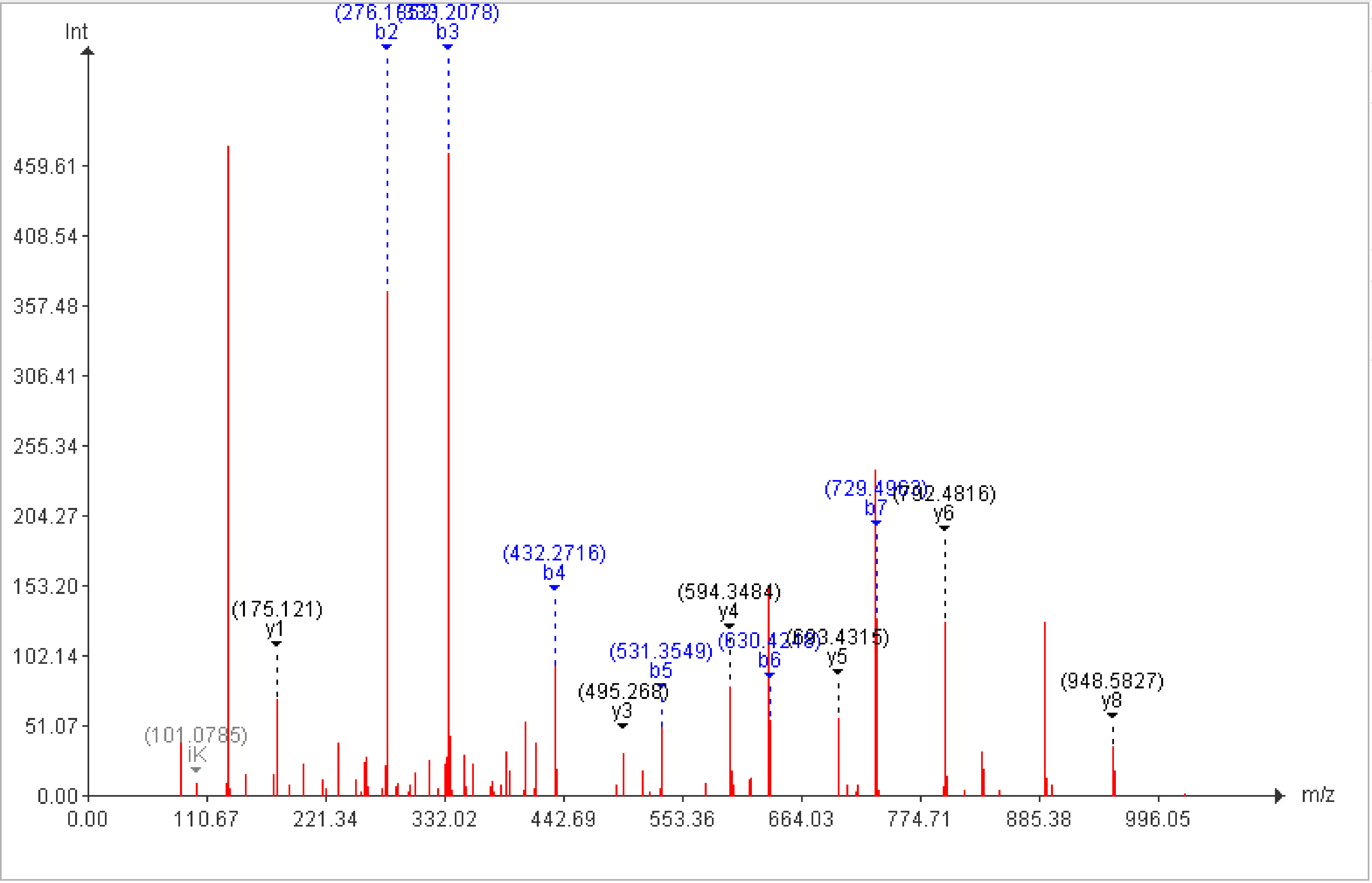
AcD3-GLAVTPTPVPVVGSQM(Mox)TR-COOH*
precursor mass: 936.0104 Da (charge: +2) protein: P26369 (129-146)
score (threshold): 41.0 (30.0)
instrument: Waters Q-TOF Premier

AcD3-GK(AcD3K)GVVVVM(Mox*)K(AcD3K*)R-COOH*

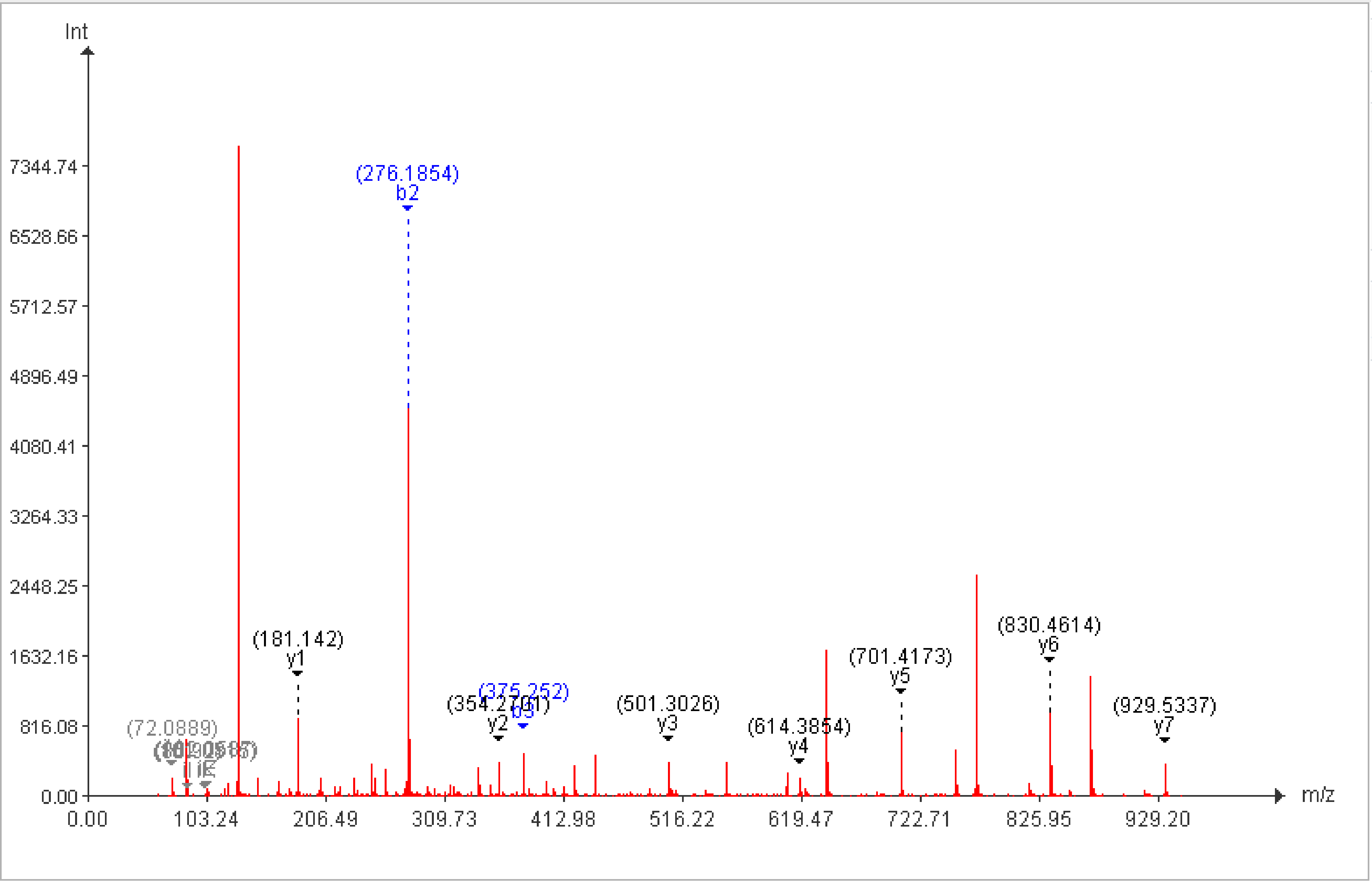
precursor mass: 612.3773 Da (charge: +2) protein: P41105 (57-66)

score (threshold): 34.0 (30.0)

instrument: Waters Q-TOF Premier



AcD3-GK(AcD3K)VESIM(Mox*)K(AcD3K*)R(C13*)-COOH*
precursor mass: 602.8497 Da (charge: +2) protein: P50516 (300-308)
score (threshold): 35.0 (30.0)
instrument: Waters Q-TOF Premier

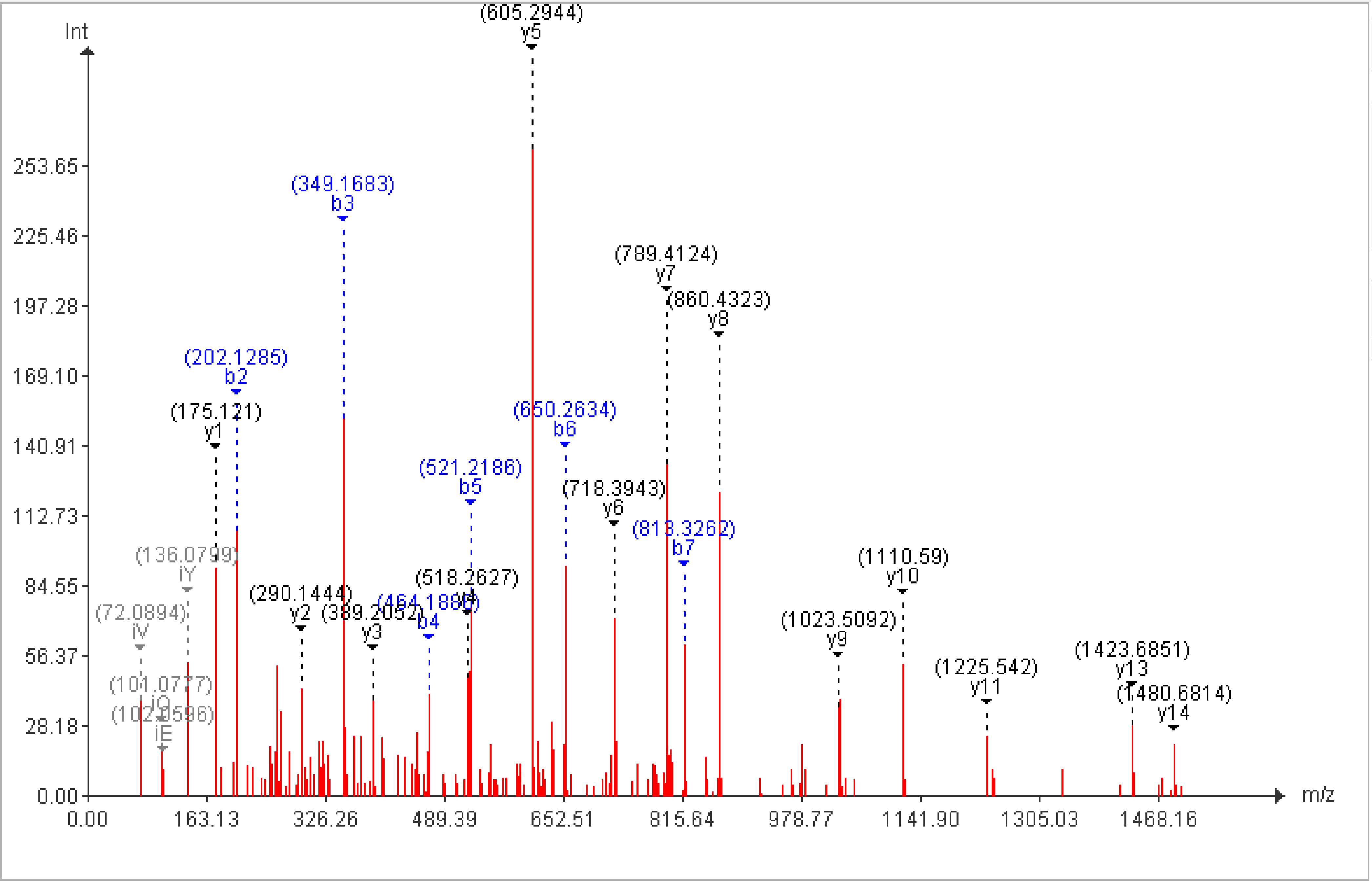


AcD3-GVM(Mox)N(Dam)GEYYQESNGPTDSYAAISEVDR-COOH*

precursor mass: 972.0778 Da (charge: +3) protein: O08585 (76-101)

score (threshold): 77.0 (27.0)

instrument: Waters Q-TOF Premier

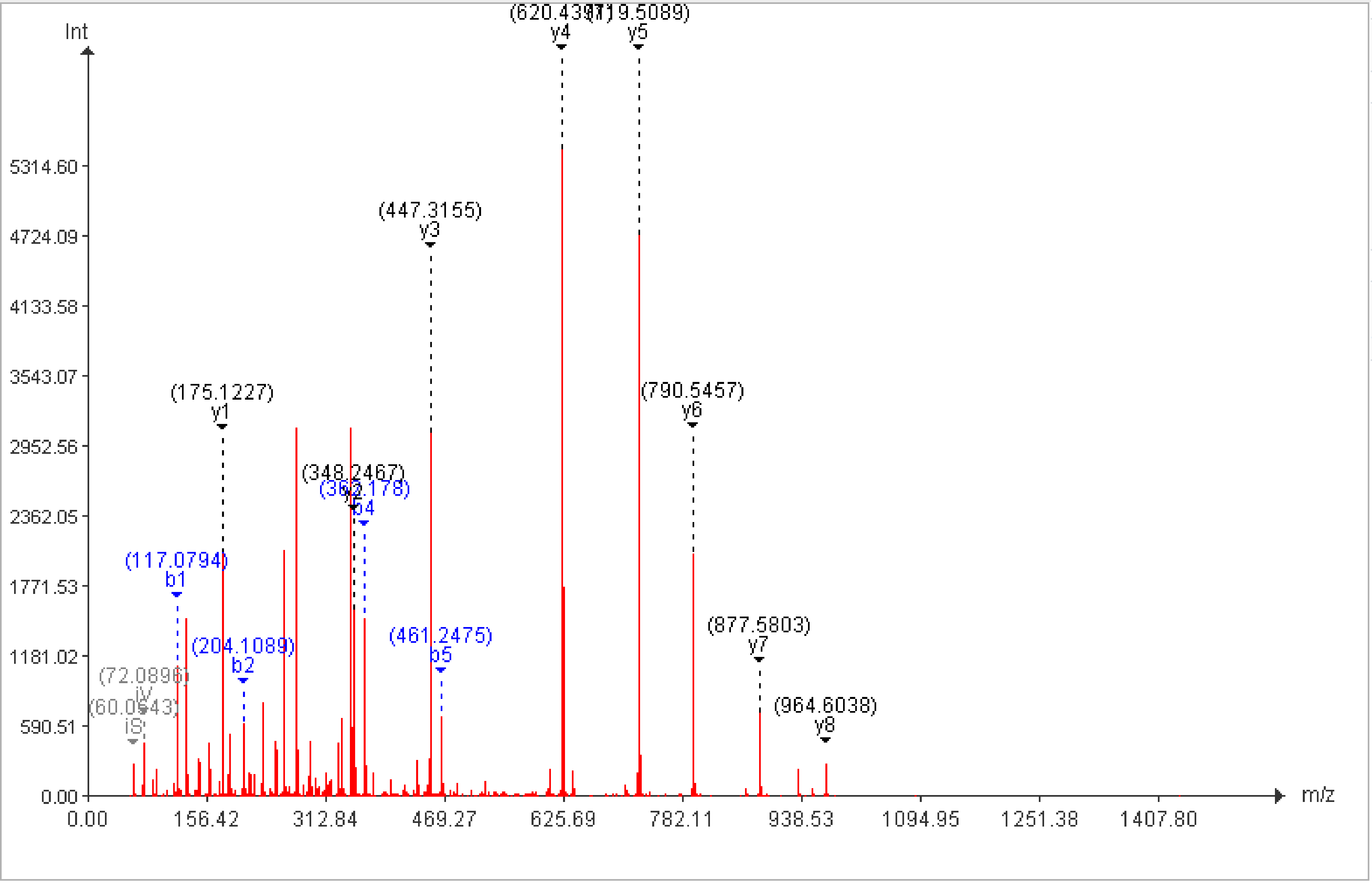


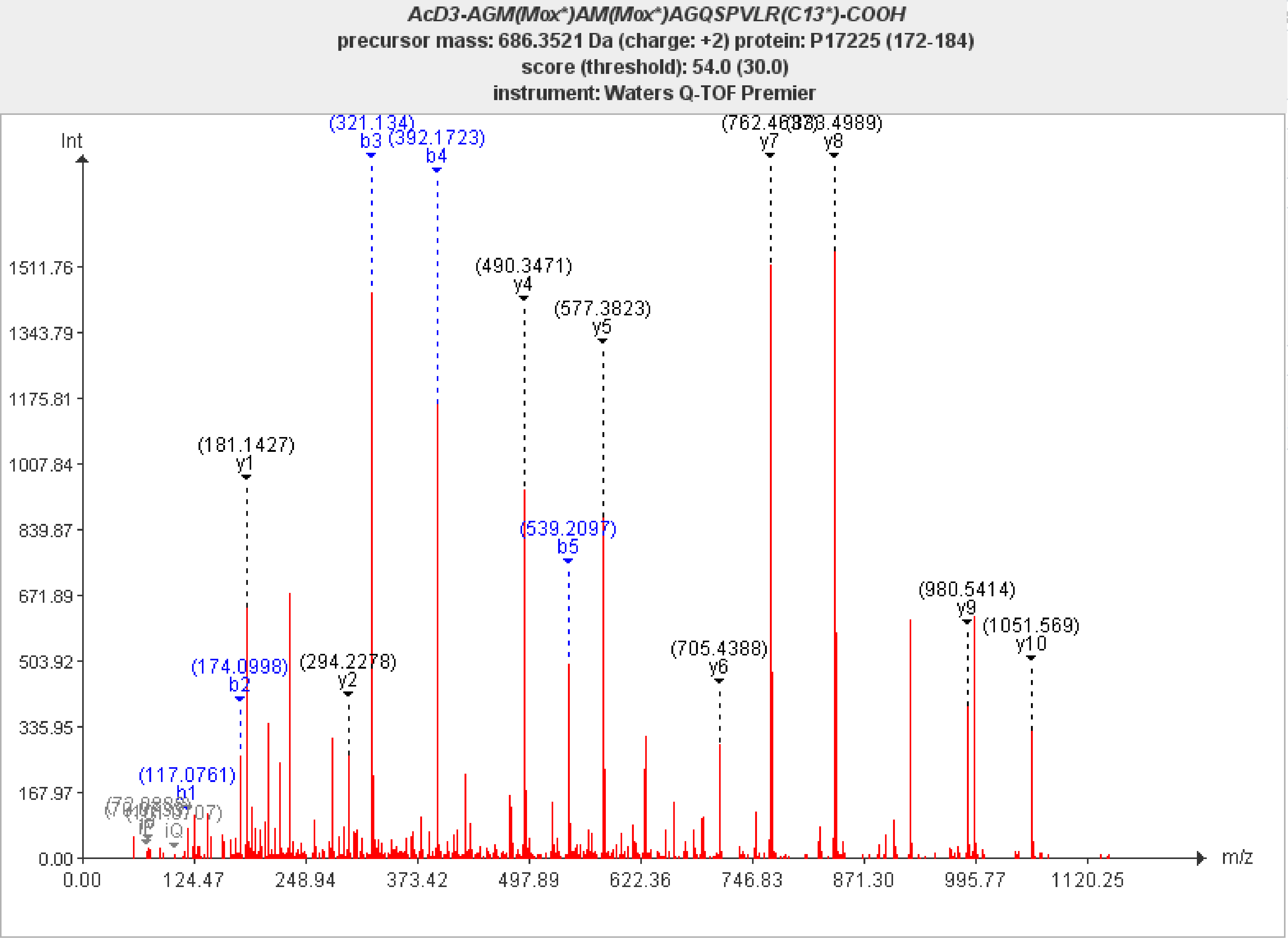
AcD3-ASSAVK(AcD3K)VK(AcD3K*)R-COOH*

precursor mass: 540.8302 Da (charge: +2) protein: Q921F2 (90-98)

score (threshold): 71.0 (30.0)

instrument: Waters Q-TOF Premier





AcD3-AGM(Mox)AM(Mox*)AGQSPVLR(C13*)-COOH*

precursor mass: 686.3521 Da (charge: +2) protein: P17225 (172-184)

score (threshold): 54.0 (30.0)

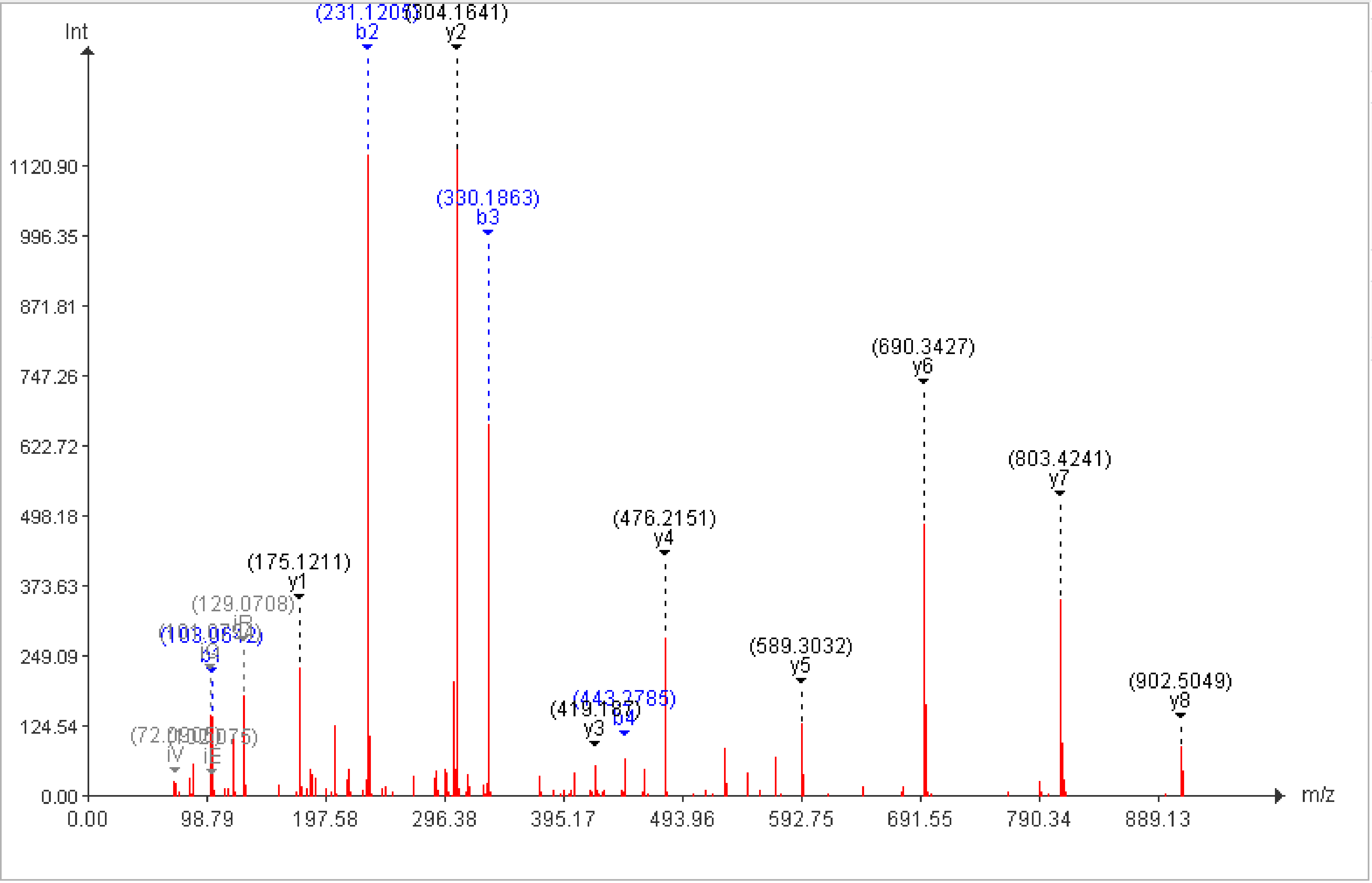
instrument: Waters Q-TOF Premier

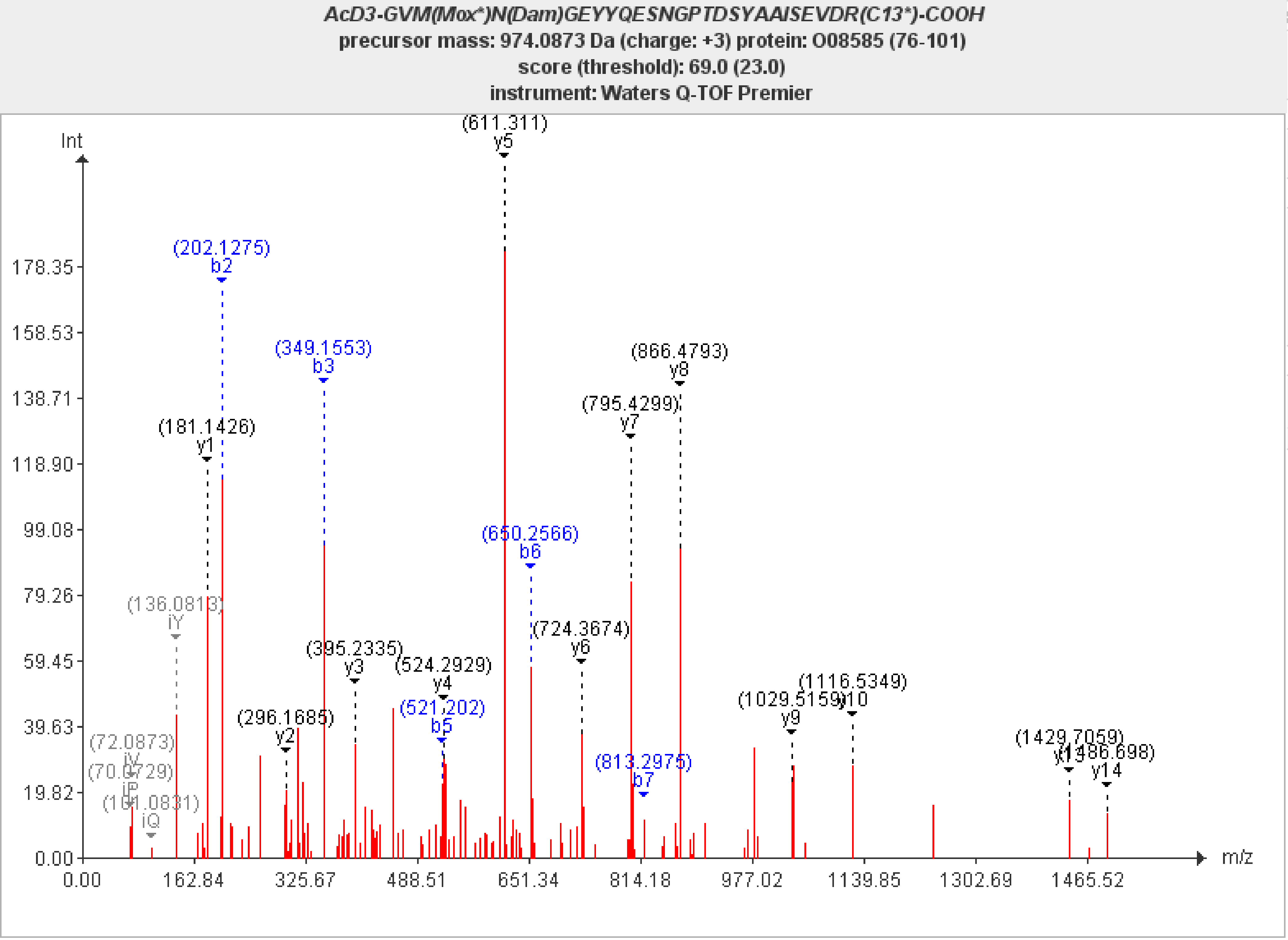
AcD3-GQVITIGN(Dam)ER-COOH

precursor mass: 566.8011 Da (charge: +2) protein: P62737 (247-256)

score (threshold): 68.0 (31.0)

instrument: Waters Q-TOF Premier





AcD3-GVM(Mox)N(Dam)GEYYQESNGPTDSYAAISEVDR(C13*)-COOH*

precursor mass: 974.0873 Da (charge: +3) protein: O08585 (76-101)

score (threshold): 69.0 (23.0)

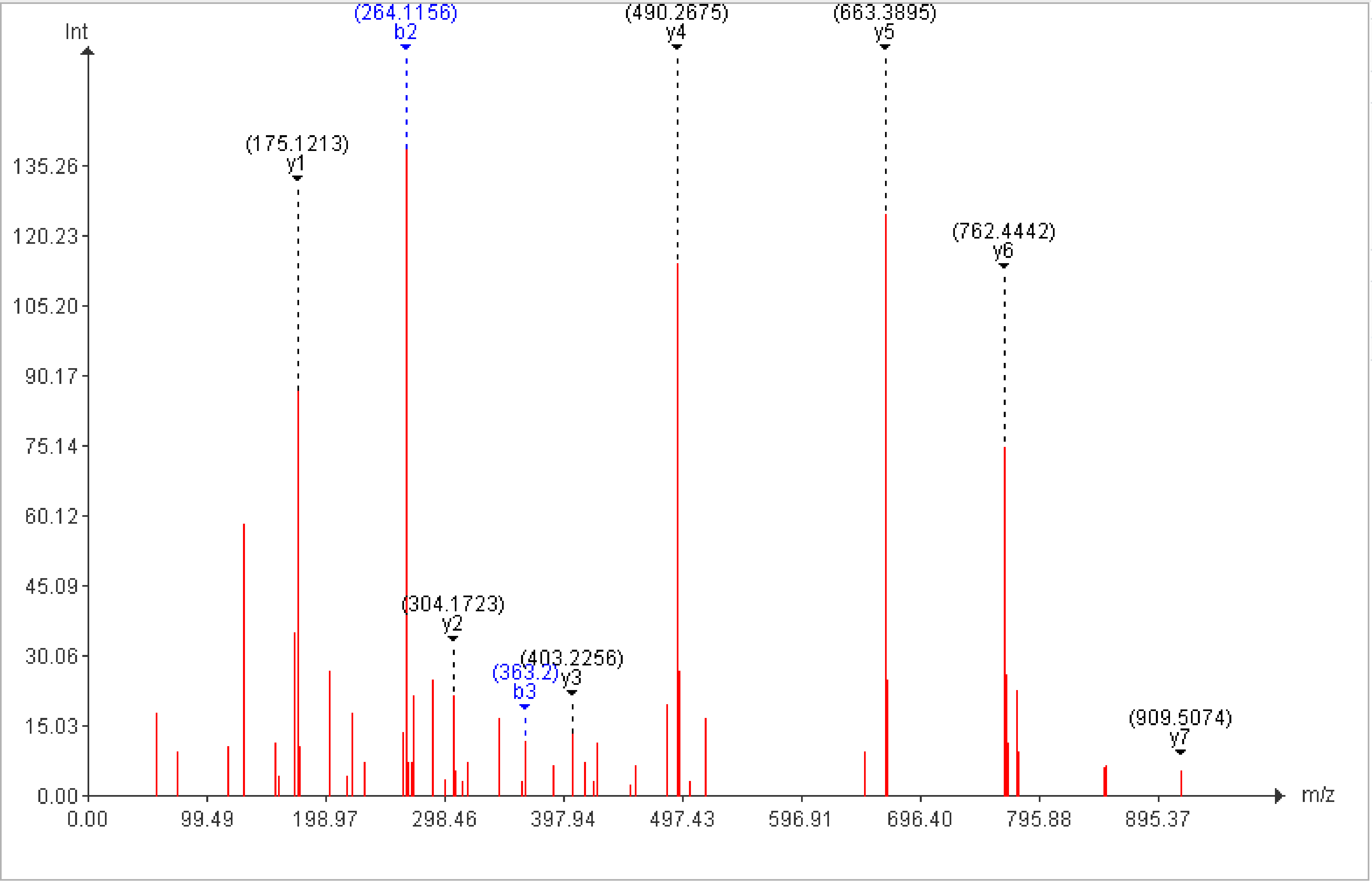
instrument: Waters Q-TOF Premier

AcD3-AM(Mox*)VK(AcD3K*)SVER-COOH

precursor mass: 513.2813 Da (charge: +2) protein: Q9CR98 (15-22)

score (threshold): 58.0 (31.0)

instrument: Waters Q-TOF Premier

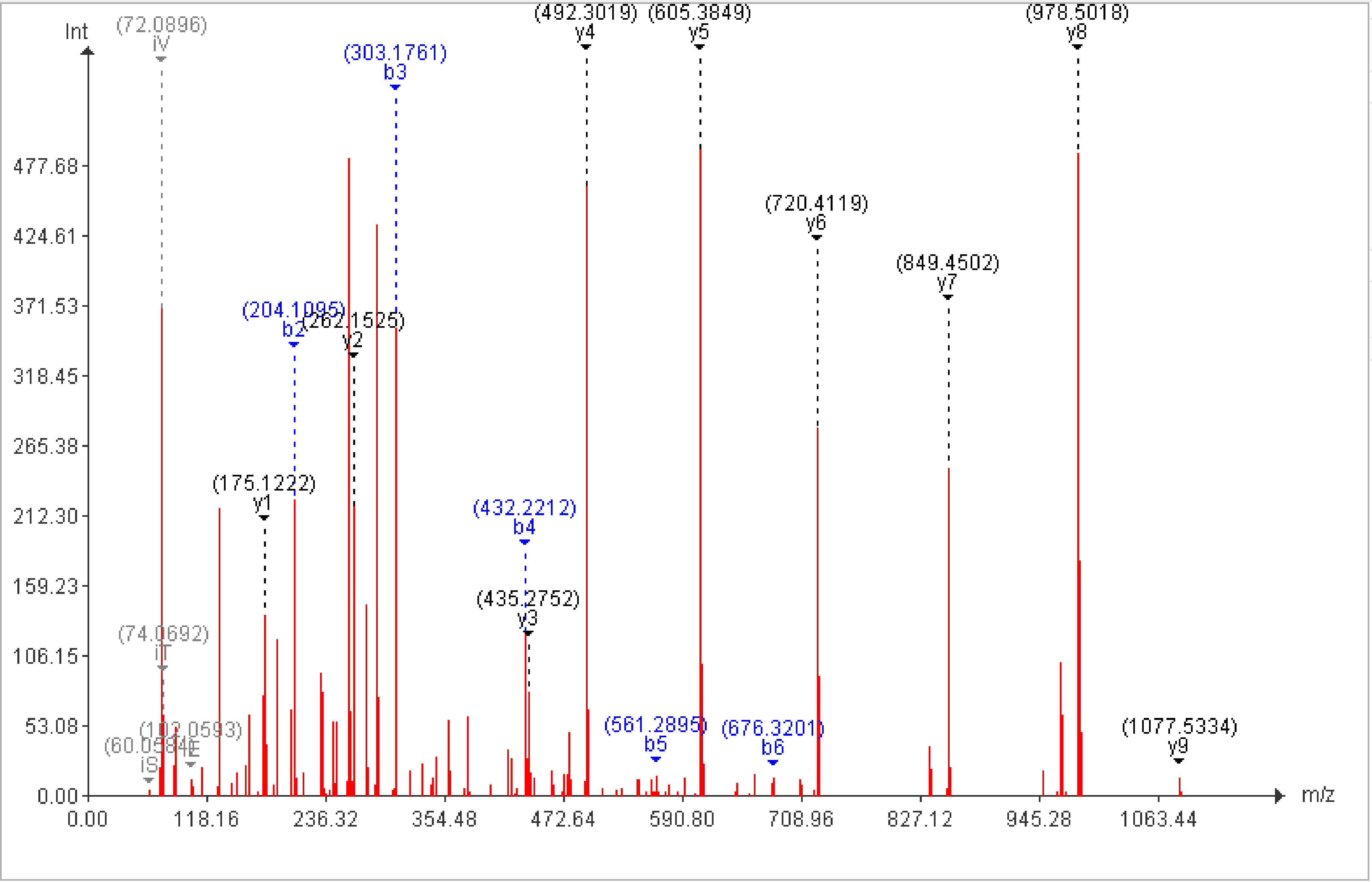


AcD3-GTVEEDLGK(AcD3K)SR-COOH*

precursor mass: 640.8316 Da (charge: +2) protein: P08113 (29-39)

score (threshold): 61.0 (31.0)

instrument: Waters Q-TOF Premier

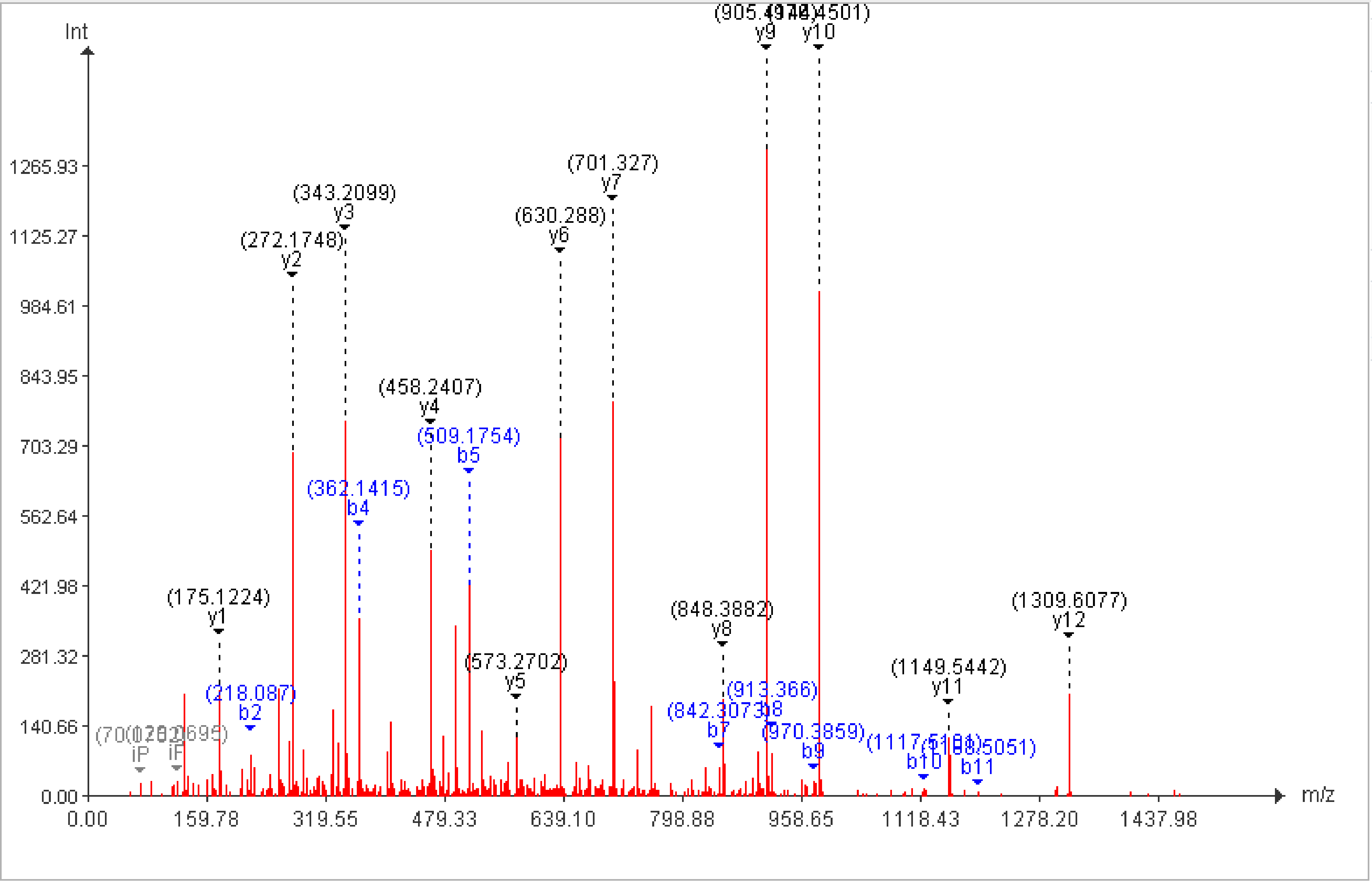


AcD3-N(Dam)GSGM(Mox)C(Cmm*)K(AcD3K*)AGFAGDDAPR-COOH*

precursor mass: 909.3747 Da (charge: +2) protein: P60710 (12-28)

score (threshold): 84.0 (29.0)

instrument: Waters Q-TOF Premier

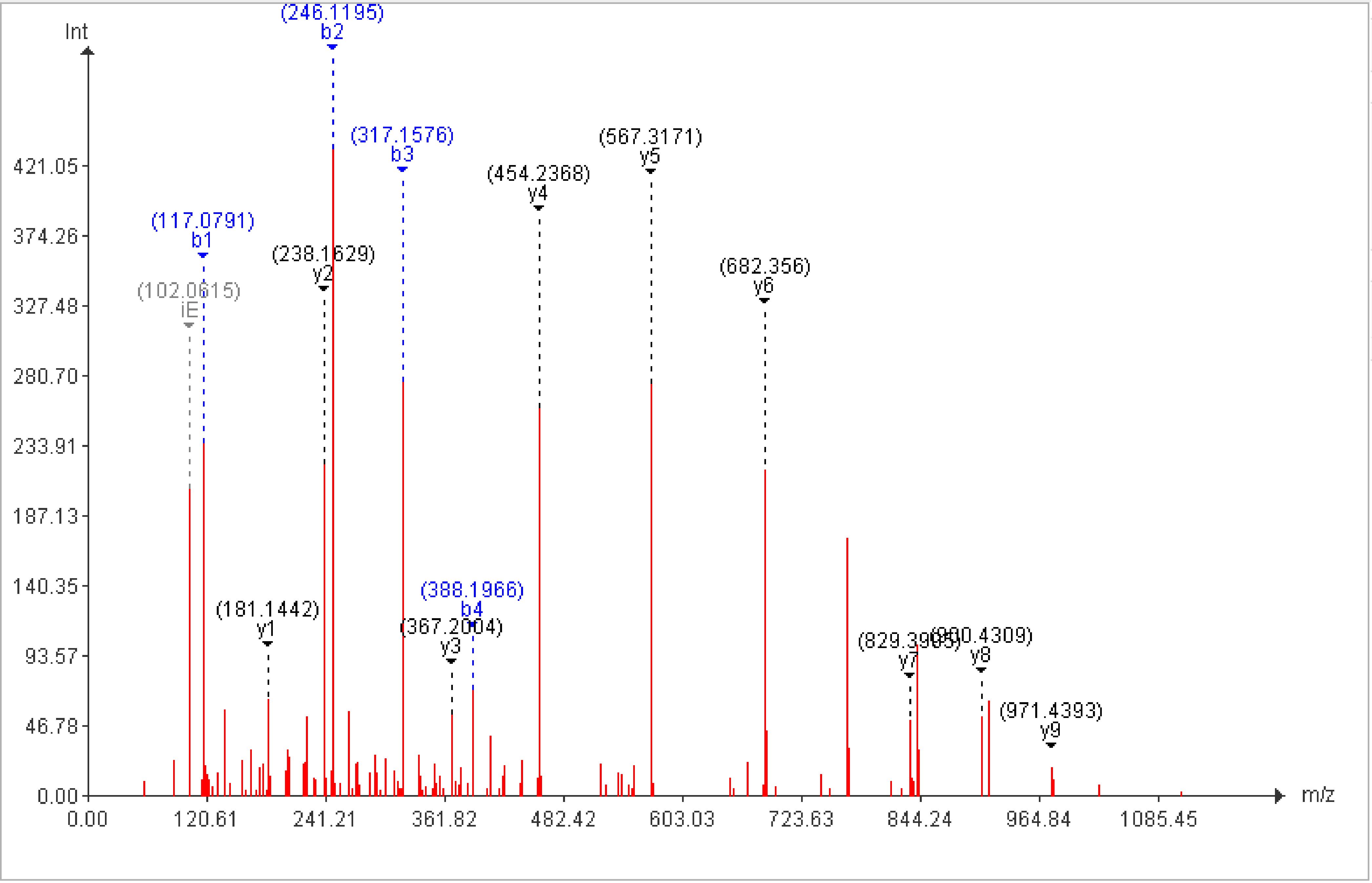


AcD3-AEAAM(Mox)DISEGR(C13*)-COOH*

precursor mass: 608.7858 Da (charge: +2) protein: P56399 (768-778)

score (threshold): 60.0 (30.0)

instrument: Waters Q-TOF Premier

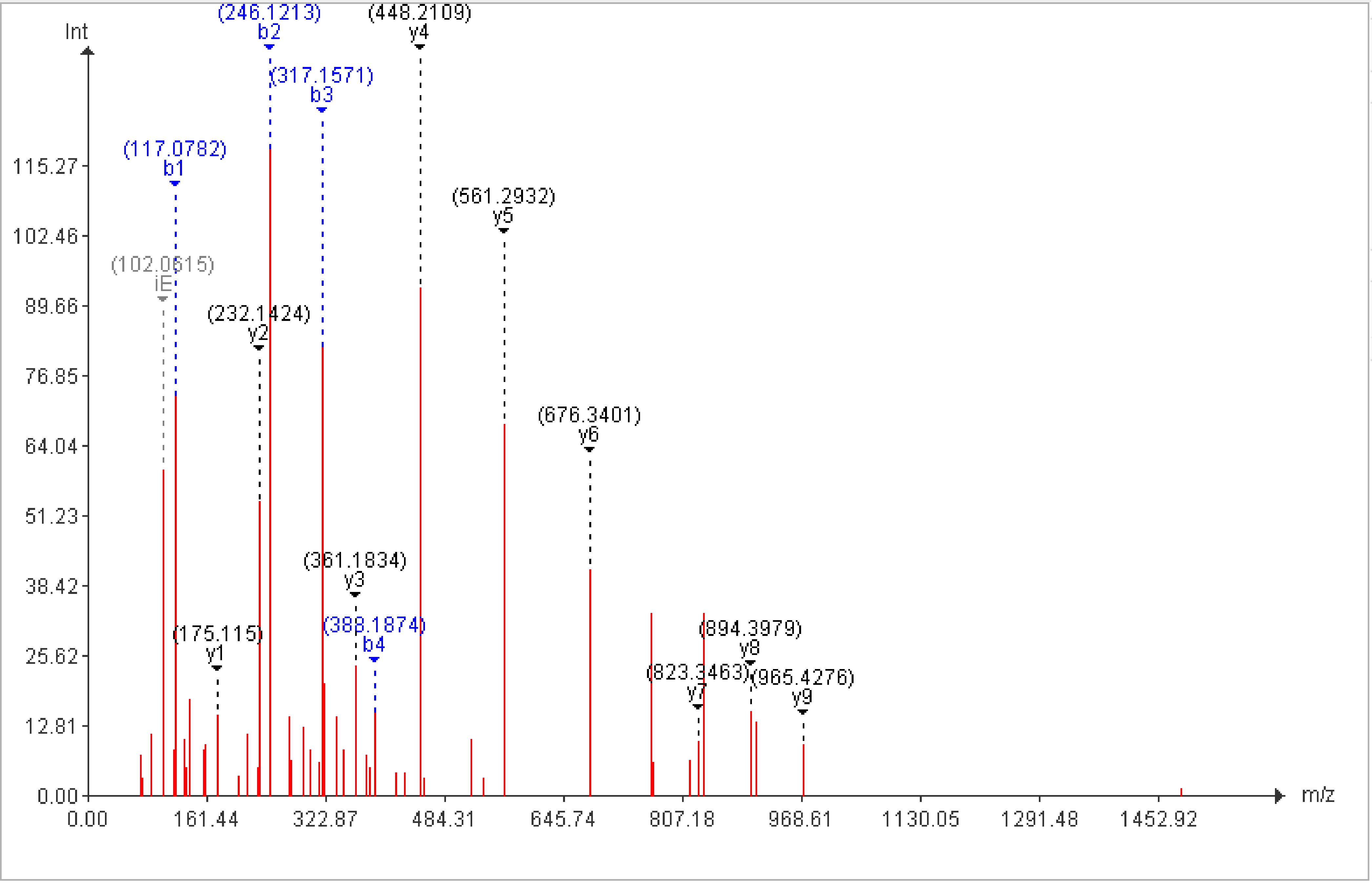


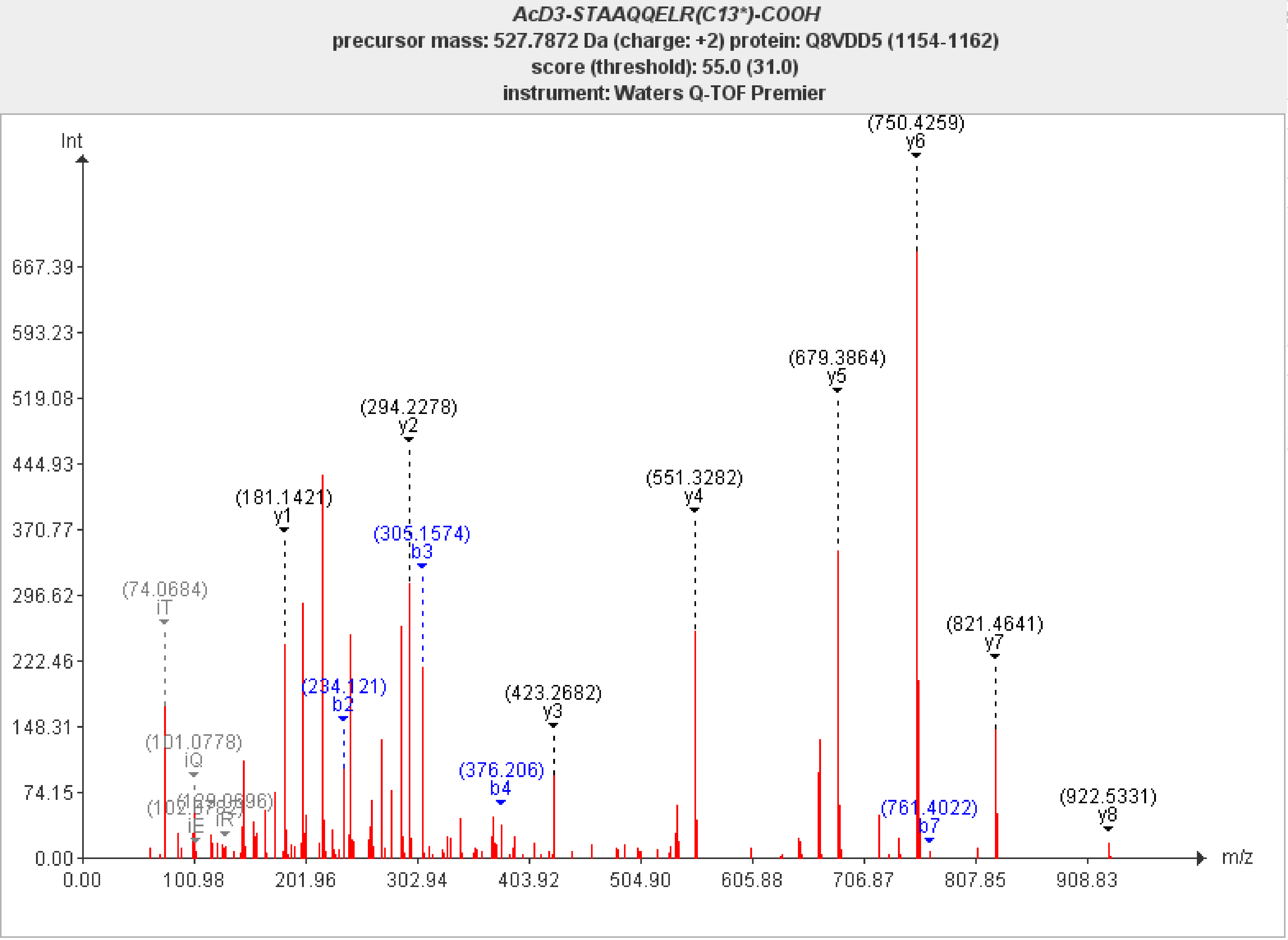
AcD3-AEAAM(Mox*)DISEGR-COOH

precursor mass: 605.7739 Da (charge: +2) protein: P56399 (768-778)

score (threshold): 60.0 (31.0)

instrument: Waters Q-TOF Premier



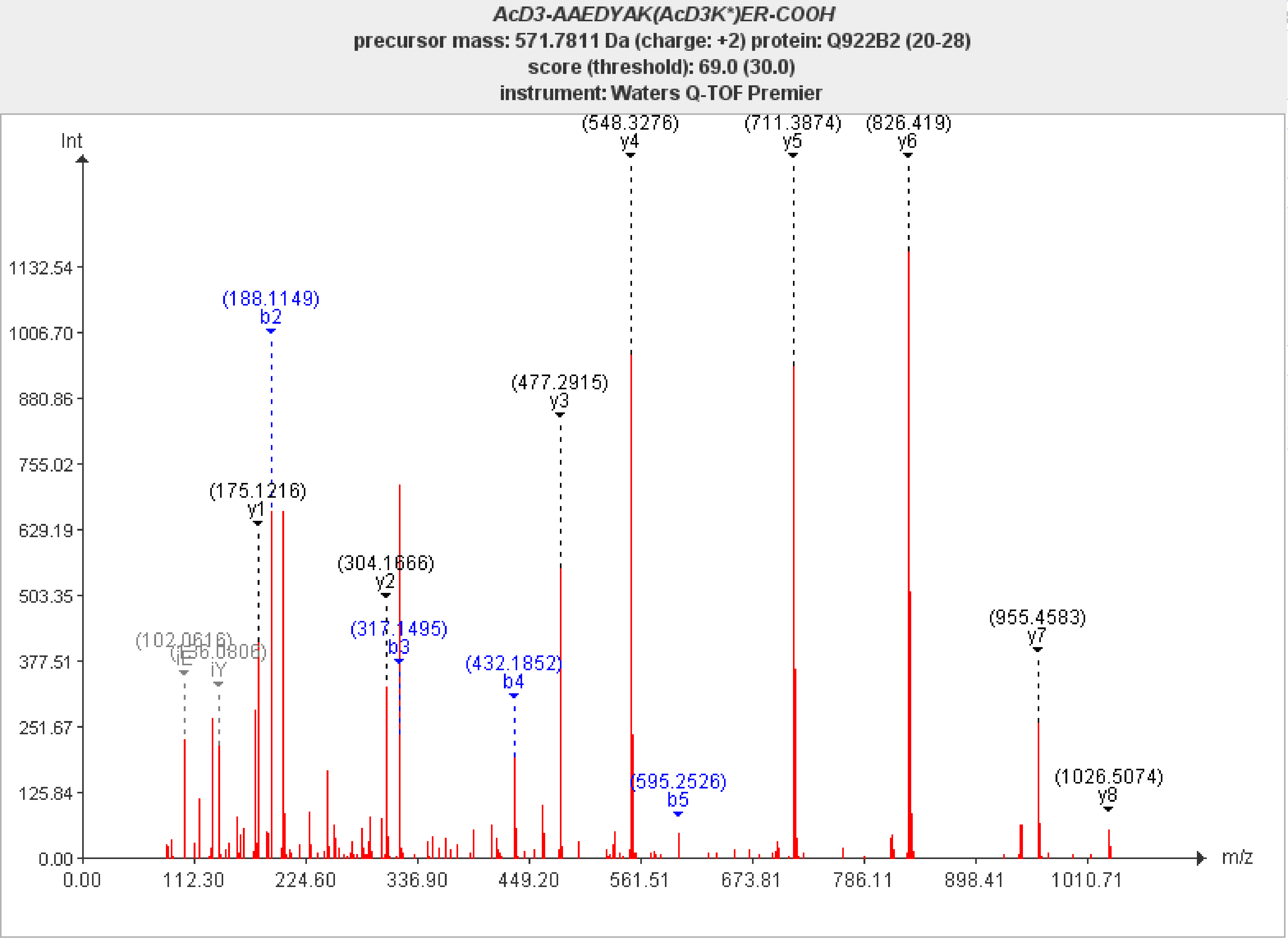


AcD3-STAAQQELR(C13)-COOH*

precursor mass: 527.7872 Da (charge: +2) protein: Q8VDD5 (1154-1162)

score (threshold): 55.0 (31.0)

instrument: Waters Q-TOF Premier



AcD3-AAEDYAK(AcD3K)ER-COOH*

precursor mass: 571.7811 Da (charge: +2) protein: Q922B2 (20-28)

score (threshold): 69.0 (30.0)

instrument: Waters Q-TOF Premier