Supplementary Data

for

Hyper-truncated Asn355- and Asn391-glycans modulate the activity of neutrophil granule myeloperoxidase

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Annotation and Fragmentation Key

🟢 **Mannose (162.0528 Da)**

🟡 **Galactose (162.0528 Da)**

🟦 ***N*-Acetylglucosamine (203.0794 Da)**

🟨 ***N*-Acetylgalactosamine (203.0794 Da)**

◆ ***N*-Acetylneuraminic acid (291.0954 Da)**

🔺 **Fucose (146.0579 Da)**

⬡ **Cross-ring fragment (unspecified)**

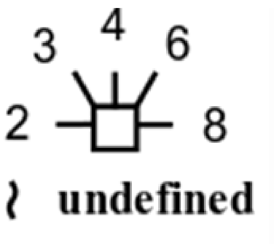
Ac **Acetyl group (42.0106 Da)**

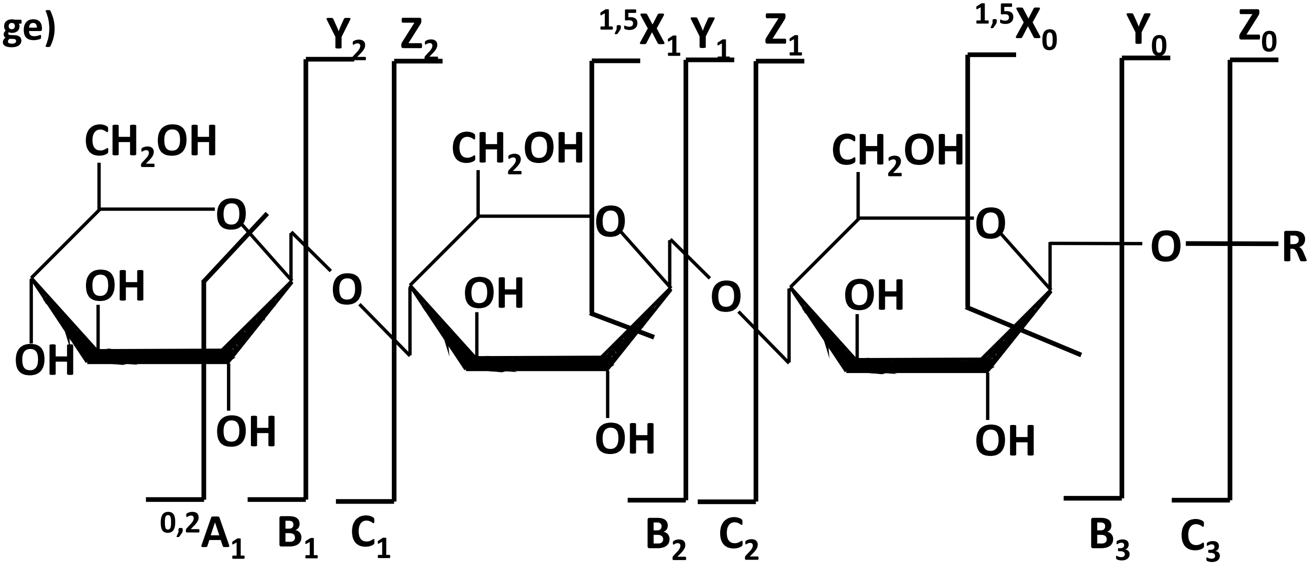
┰ **Indicates mostly Y ions (includes oxygen of glyosidic linkage)**

┬ **Indicates mostly Z ions (excludes oxygen of glyosidic linkage)**

∽ **Reduced reducing end**

P **Phosphate (79.9700 Da)**





Han, L. & Costello, C.E. Mass spectrometry of glycans. *Biochemistry (Moscow)* 78, 710-720 (2013).

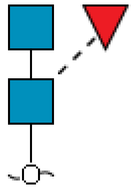
Supplementary Data S1

Manually annotated PGC-LC-ESI-CID-MS/MS (-) spectra of reduced *N*-glycans (alditols) released from nMPO

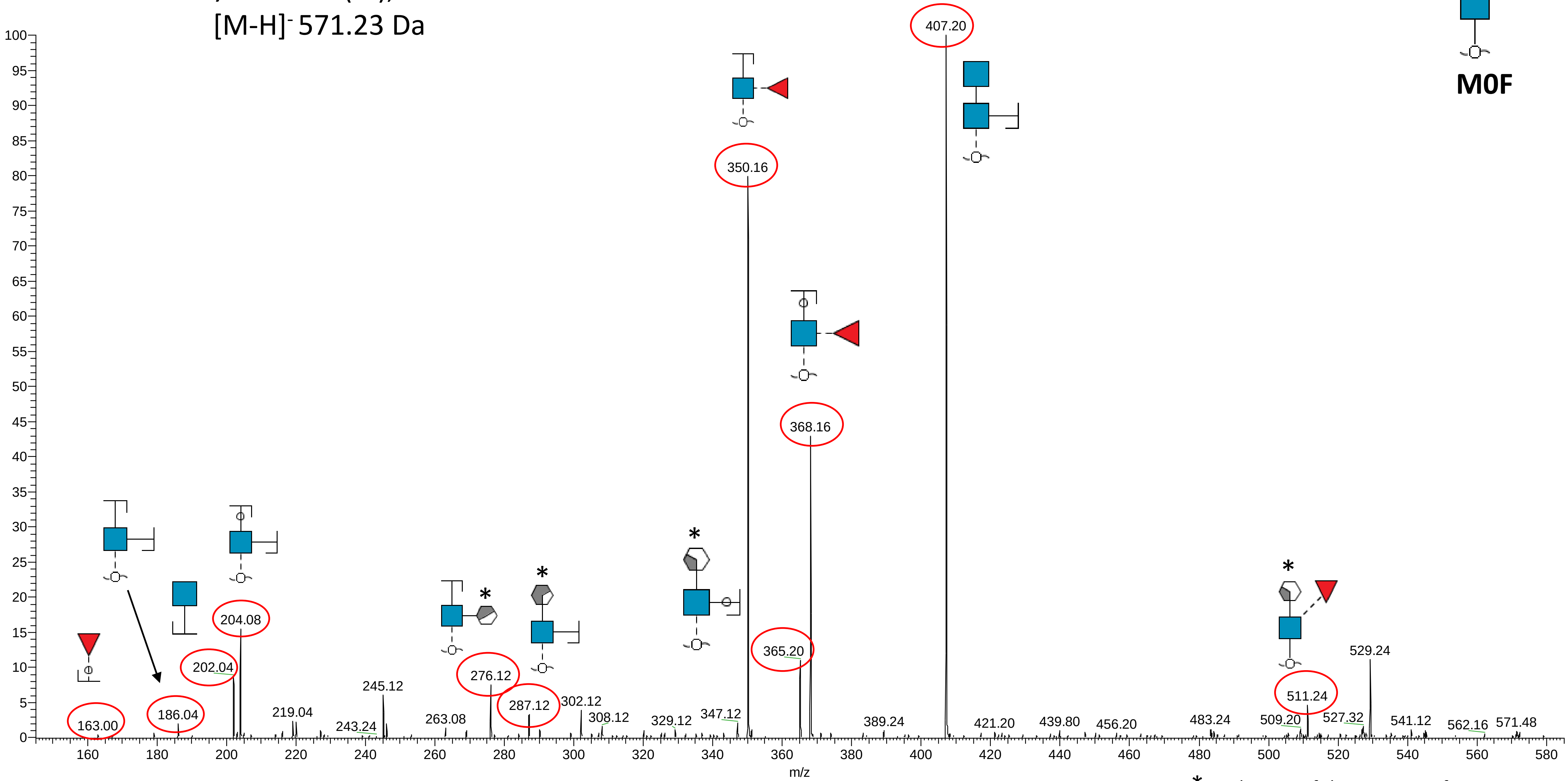
Glycan #1

Observed *m/z* 571.24 (1-), RT: ~17.8 min

$[M\text{-}H]^-$ 571.23 Da



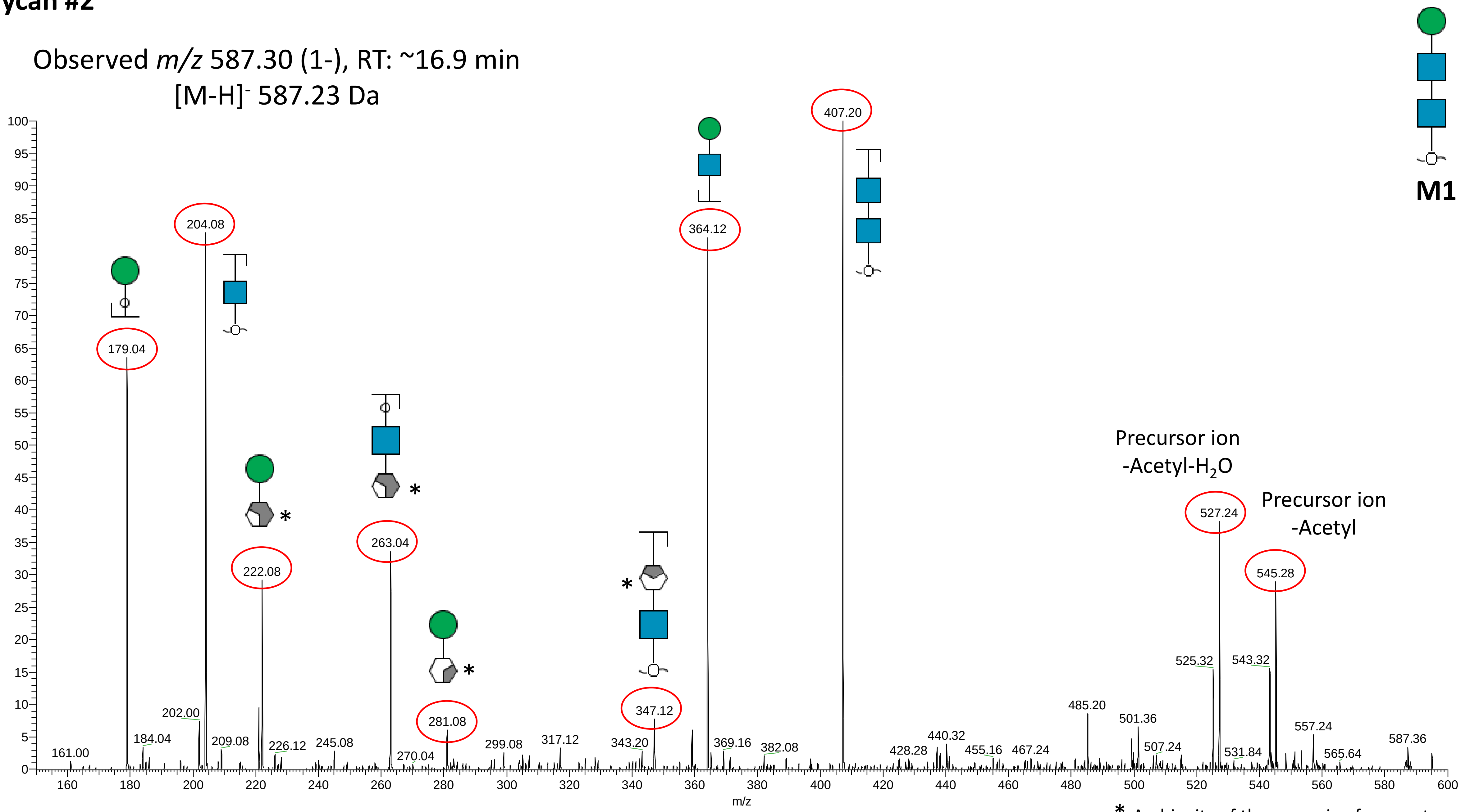
M0F



* Ambiguity of the cross-ring fragments

Glycan #2

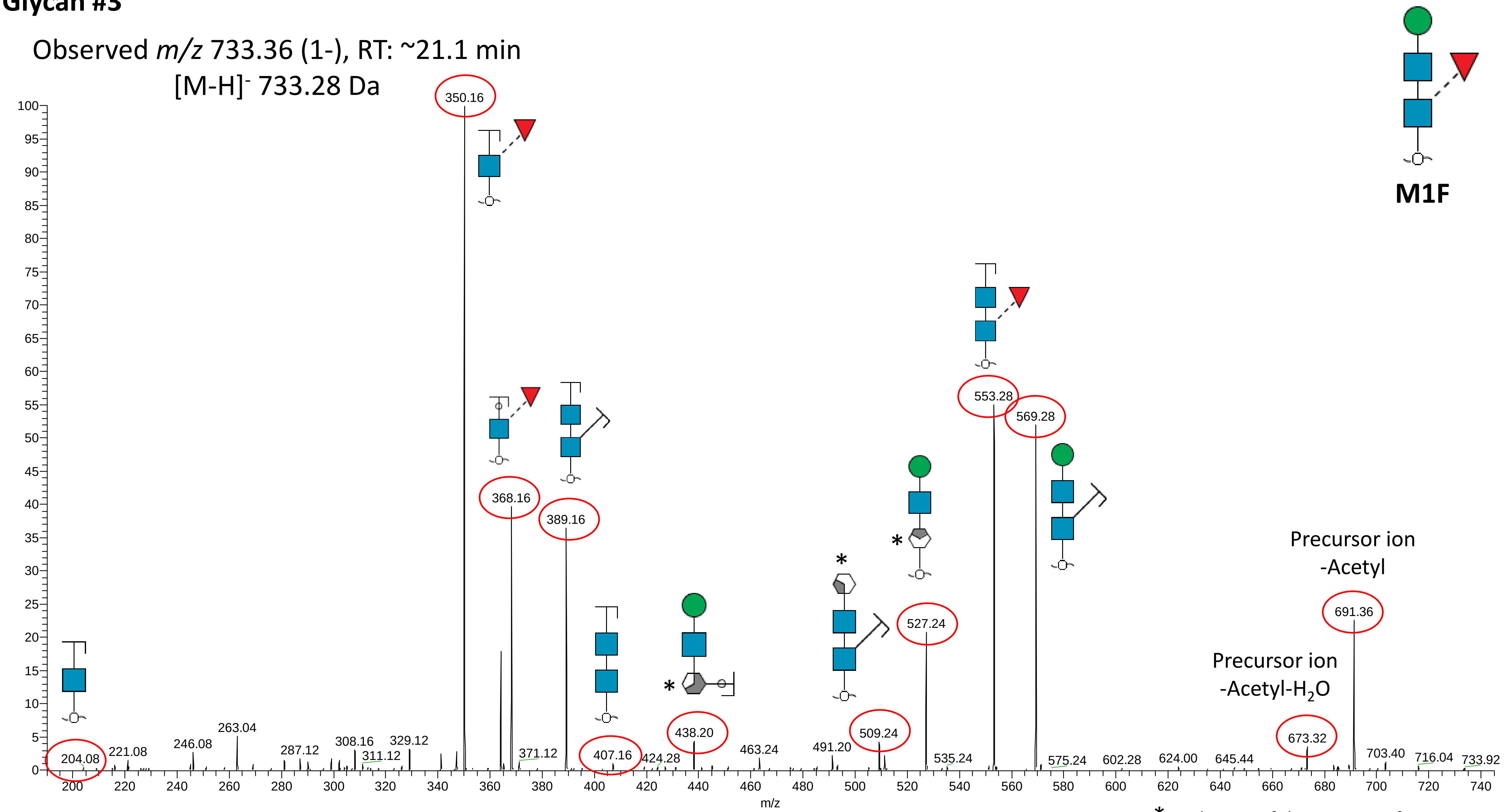
Observed *m/z* 587.30 (1-), RT: ~16.9 min
$[M\text{-}H]^-$ 587.23 Da



* Ambiguity of the cross-ring fragments

Glycan #3

Observed *m/z* 733.36 (1-), RT: ~21.1 min
$[M\text{-}H]^-$ 733.28 Da



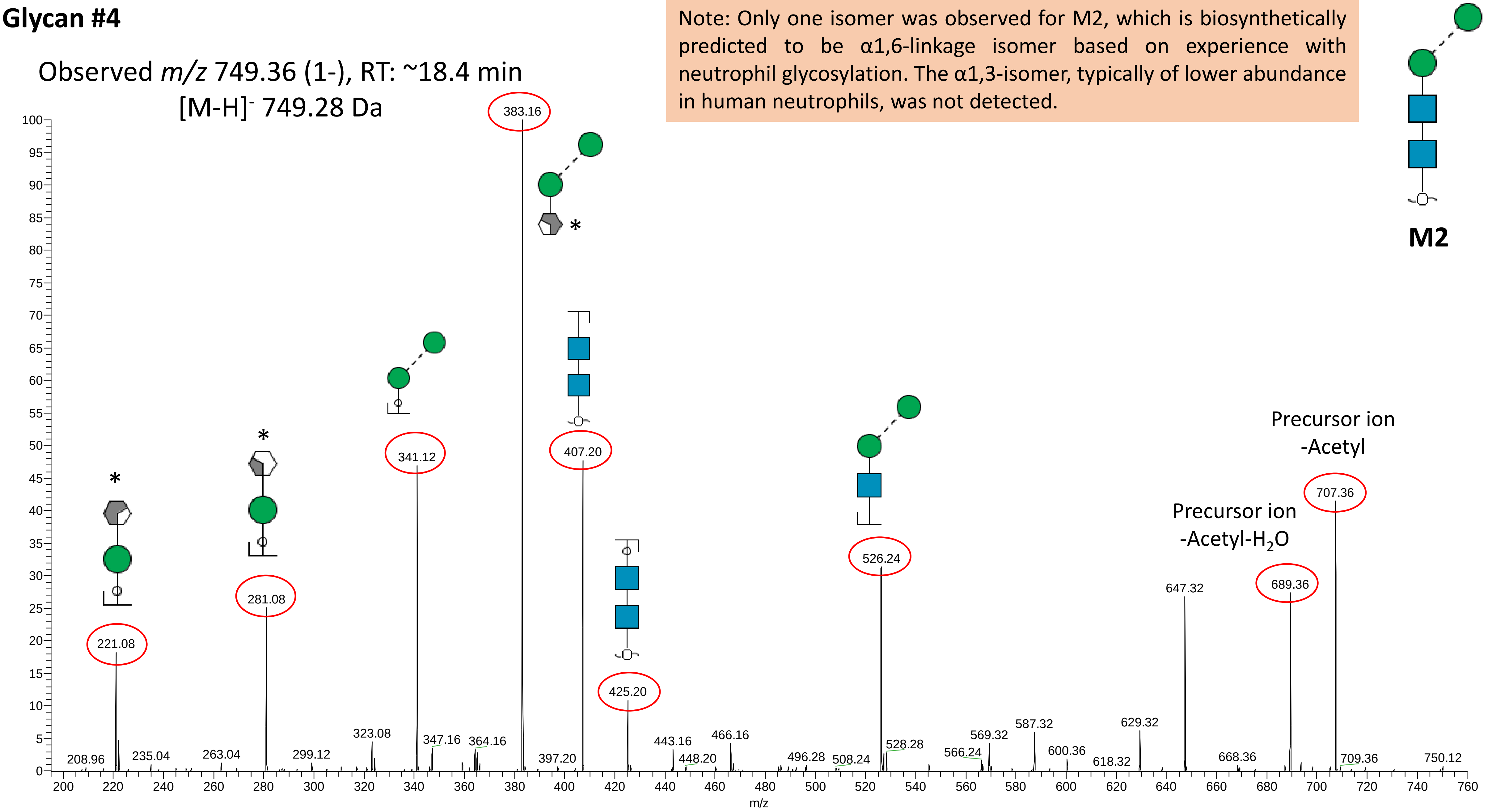
* Ambiguity of the cross-ring fragments

Glycan #4

Observed *m/z* 749.36 (1-), RT: ~18.4 min
$[M\text{-}H]^-$ 749.28 Da

Note: Only one isomer was observed for M2, which is biosynthetically predicted to be α1,6-linkage isomer based on experience with neutrophil glycosylation. The α1,3-isomer, typically of lower abundance in human neutrophils, was not detected.

M2



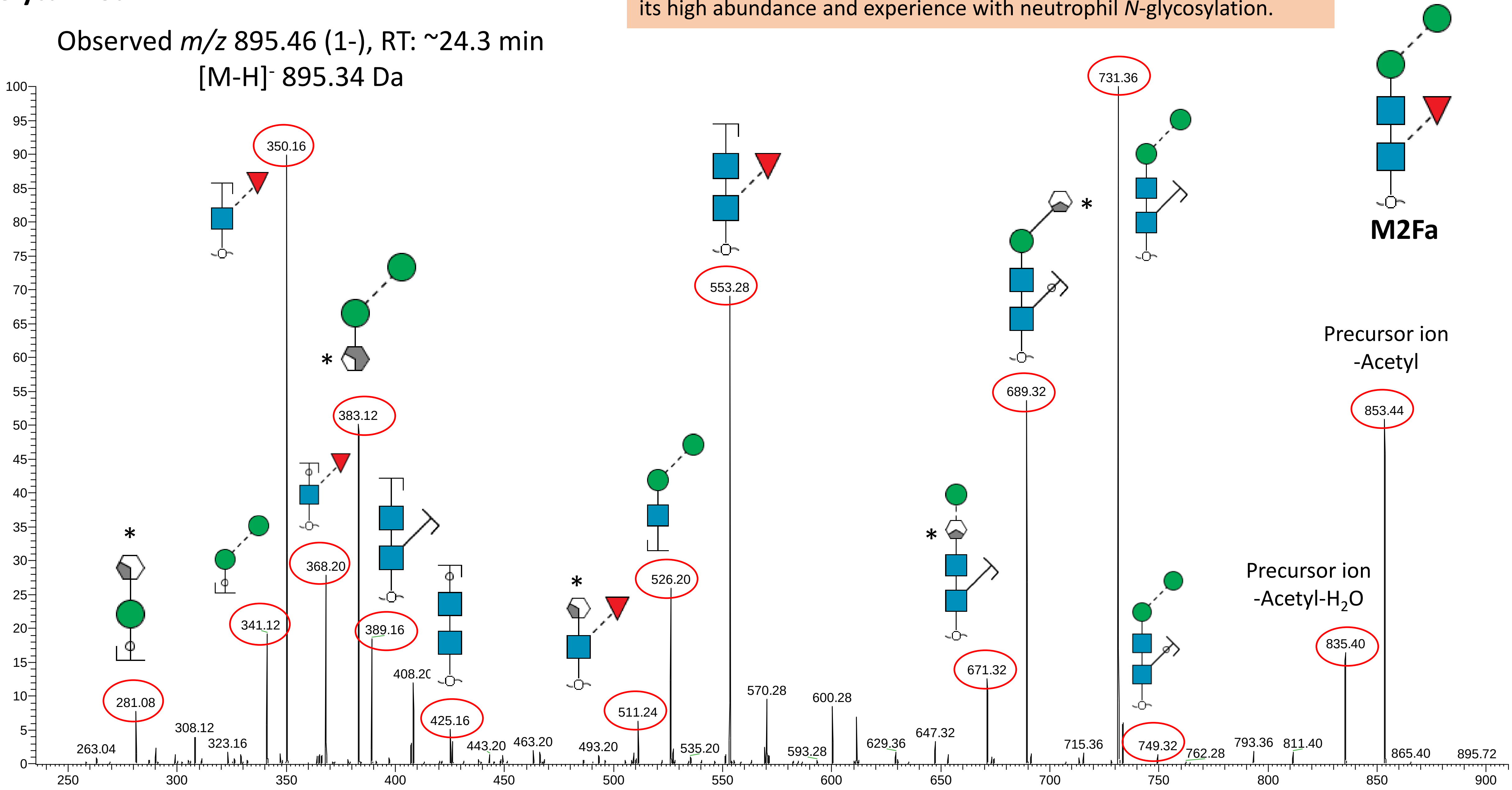
* Ambiguity of the cross-ring fragments

Glycan #5a

Note: Identified as the α1,6-Man isomer based on PGC LC elution time, its high abundance and experience with neutrophil *N*-glycosylation.

Observed *m/z* 895.46 (1-), RT: ~24.3 min

$[M-H]^-$ 895.34 Da



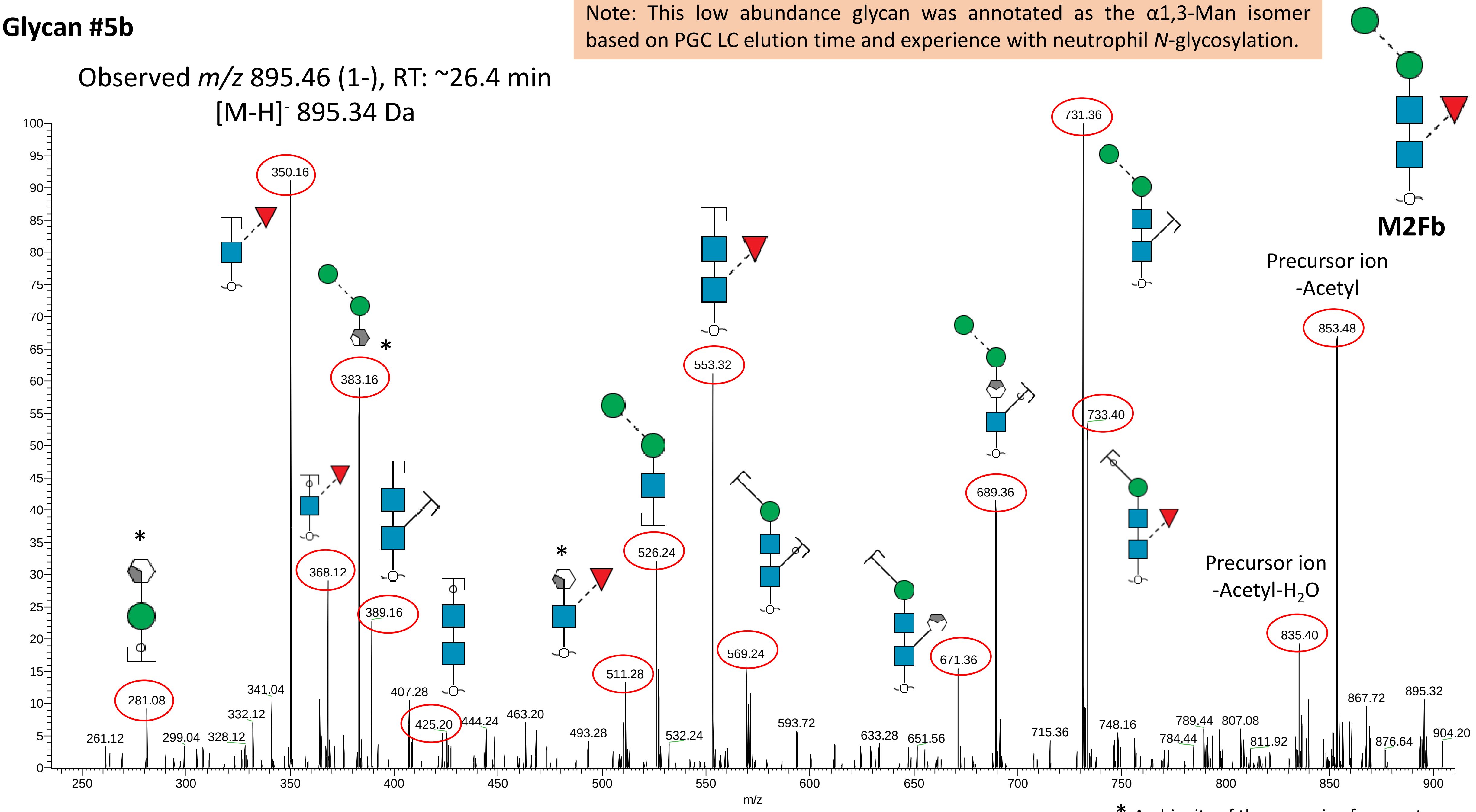
* Ambiguity of the cross-ring fragments

Glycan #5b

Note: This low abundance glycan was annotated as the α1,3-Man isomer based on PGC LC elution time and experience with neutrophil *N*-glycosylation.

Observed *m/z* 895.46 (1-), RT: ~26.4 min

$[M\text{-}H]^-$ 895.34 Da

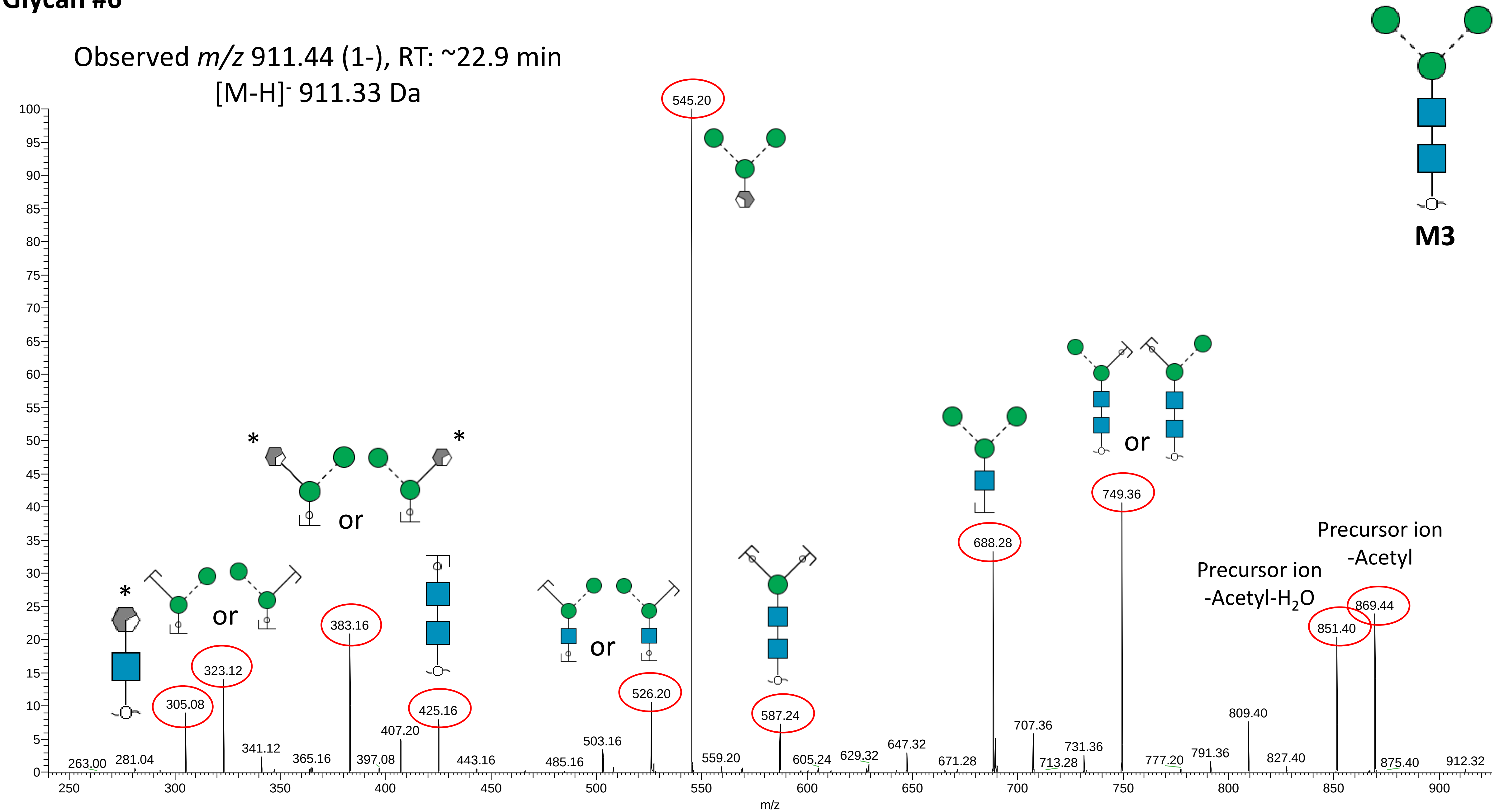


* Ambiguity of the cross-ring fragments

Glycan #6

Observed *m/z* 911.44 (1-), RT: ~22.9 min

[M-H]$^-$ 911.33 Da

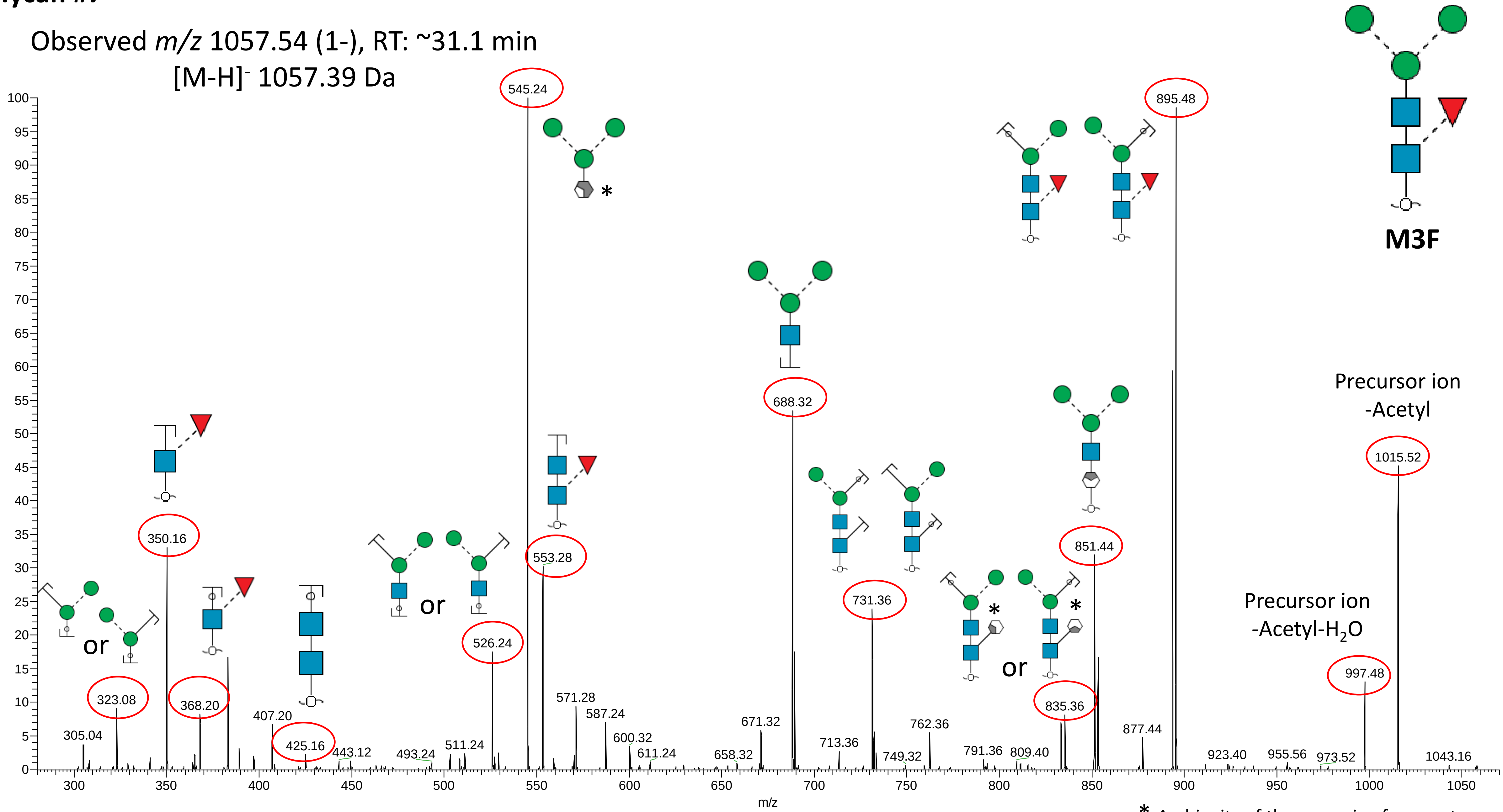


* Ambiguity of the cross-ring fragments

Glycan #7

Observed *m/z* 1057.54 (1-), RT: ~31.1 min

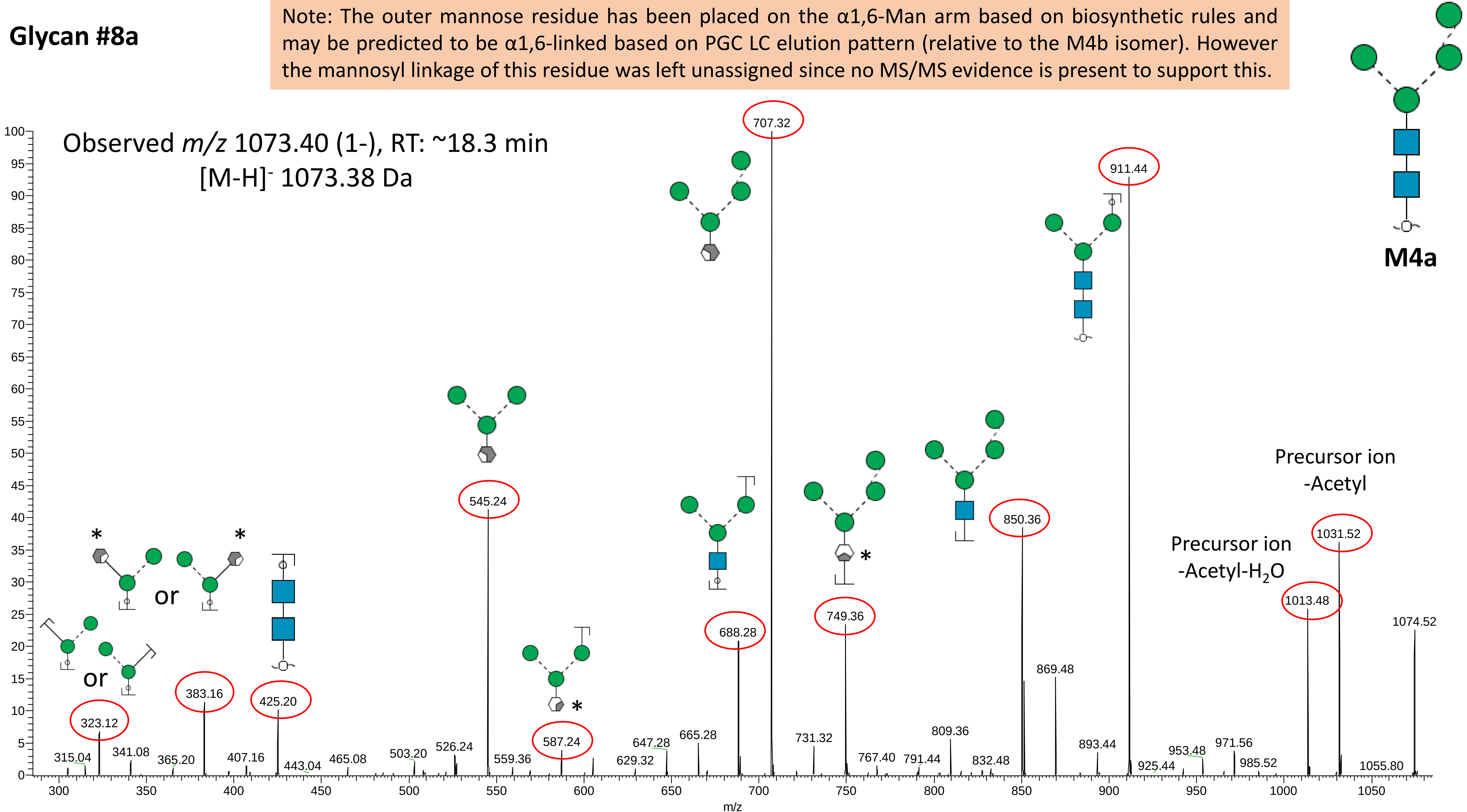
$[M-H]^-$ 1057.39 Da



* Ambiguity of the cross-ring fragments

Glycan #8a

Note: The outer mannose residue has been placed on the α1,6-Man arm based on biosynthetic rules and may be predicted to be α1,6-linked based on PGC LC elution pattern (relative to the M4b isomer). However the mannosyl linkage of this residue was left unassigned since no MS/MS evidence is present to support this.



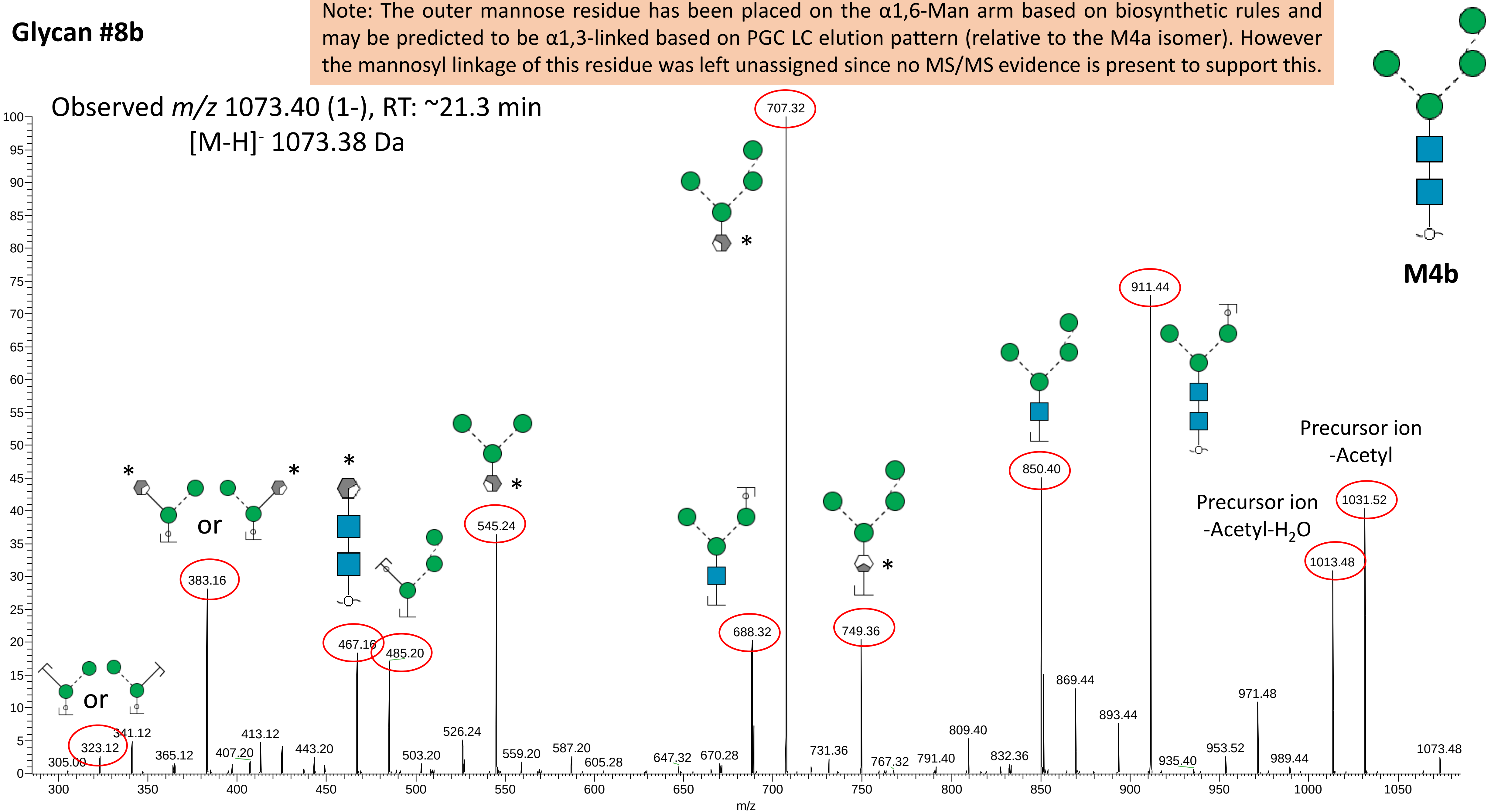
Observed *m/z* 1073.40 (1-), RT: ~18.3 min
$[M-H]^-$ 1073.38 Da

M4a

* Ambiguity of the cross-ring fragments

Glycan #8b

Note: The outer mannose residue has been placed on the α1,6-Man arm based on biosynthetic rules and may be predicted to be α1,3-linked based on PGC LC elution pattern (relative to the M4a isomer). However the mannosyl linkage of this residue was left unassigned since no MS/MS evidence is present to support this.



Observed *m/z* 1073.40 (1-), RT: ~21.3 min

[M-H]$^-$ 1073.38 Da

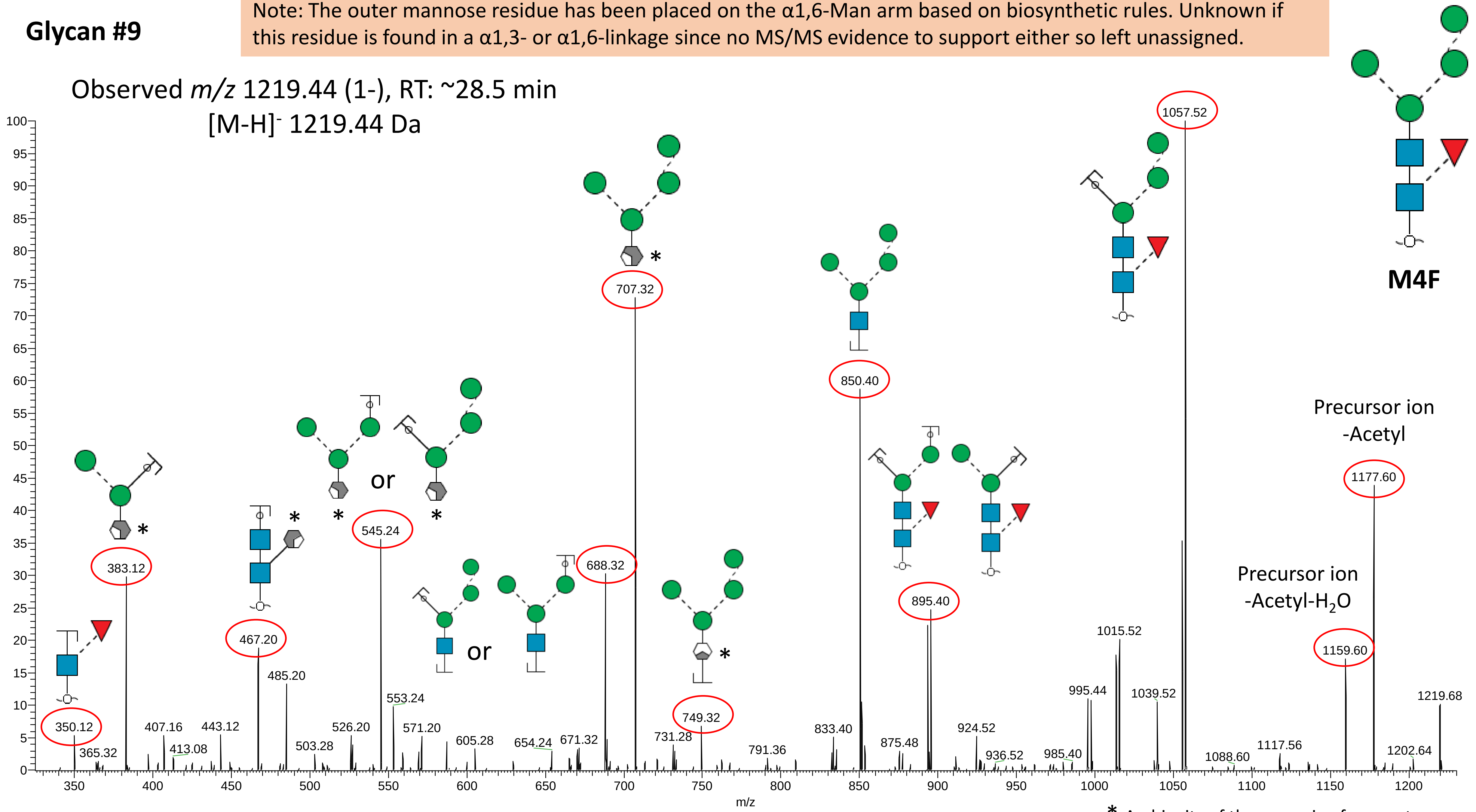
* Ambiguity of the cross-ring fragments

Glycan #9

Note: The outer mannose residue has been placed on the α1,6-Man arm based on biosynthetic rules. Unknown if this residue is found in a α1,3- or α1,6-linkage since no MS/MS evidence to support either so left unassigned.

Observed *m/z* 1219.44 (1-), RT: ~28.5 min

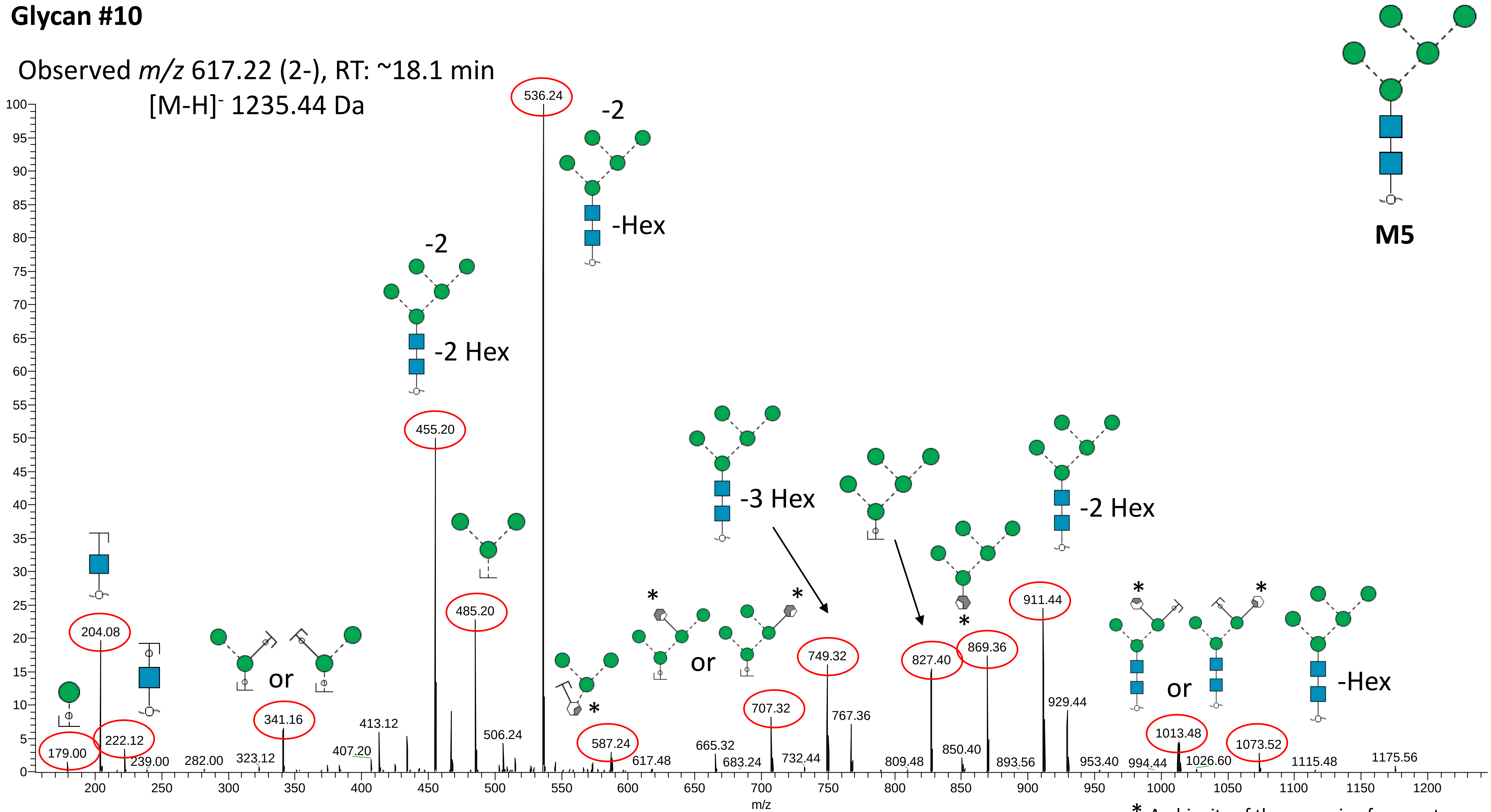
$[M-H]^-$ 1219.44 Da



* Ambiguity of the cross-ring fragments

Glycan #10

Observed *m/z* 617.22 (2-), RT: ~18.1 min
[M-H]$^-$ 1235.44 Da



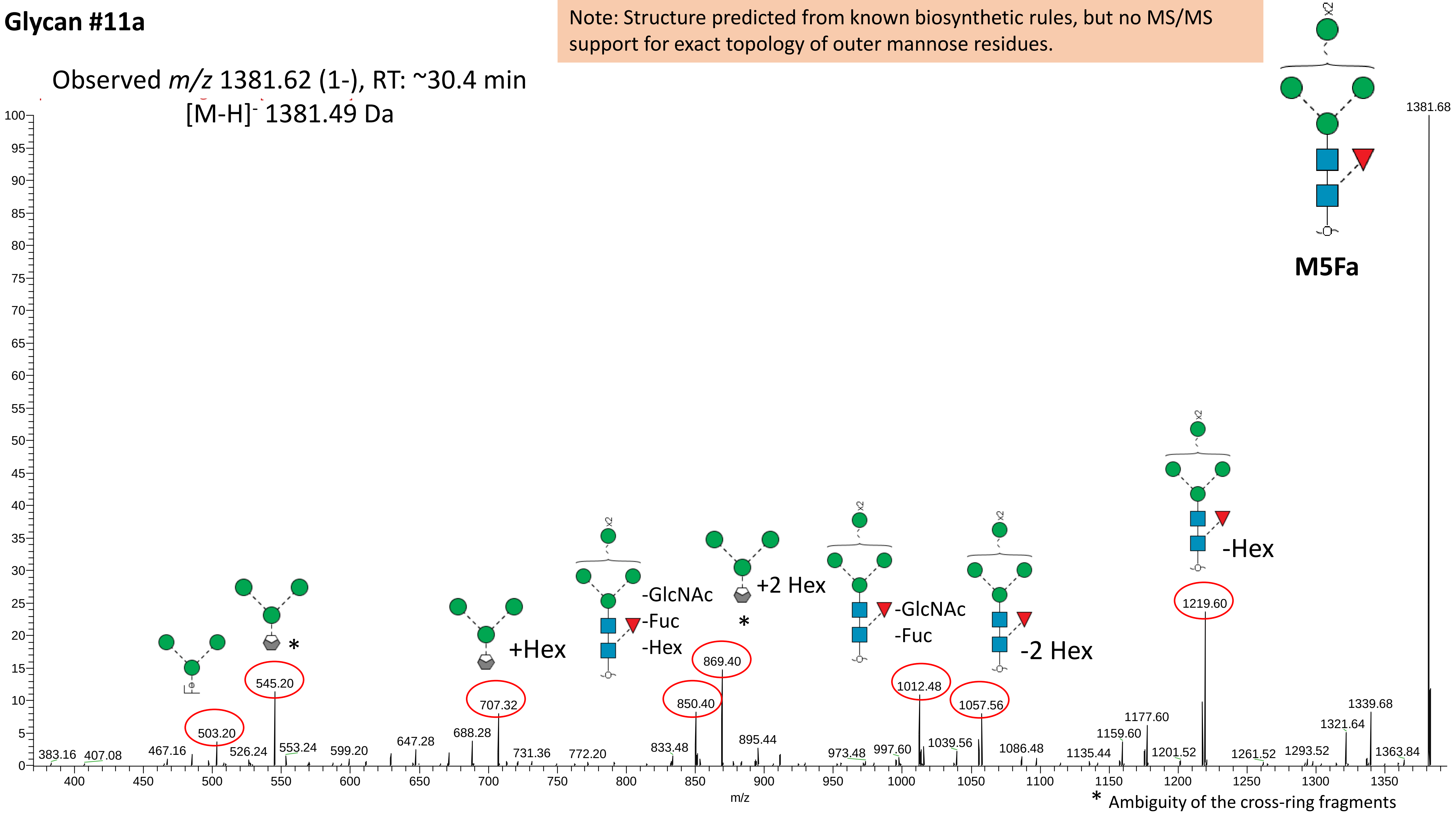
* Ambiguity of the cross-ring fragments

Glycan #11a

Note: Structure predicted from known biosynthetic rules, but no MS/MS support for exact topology of outer mannose residues.

Observed *m/z* 1381.62 (1-), RT: ~30.4 min

[M-H]$^-$ 1381.49 Da



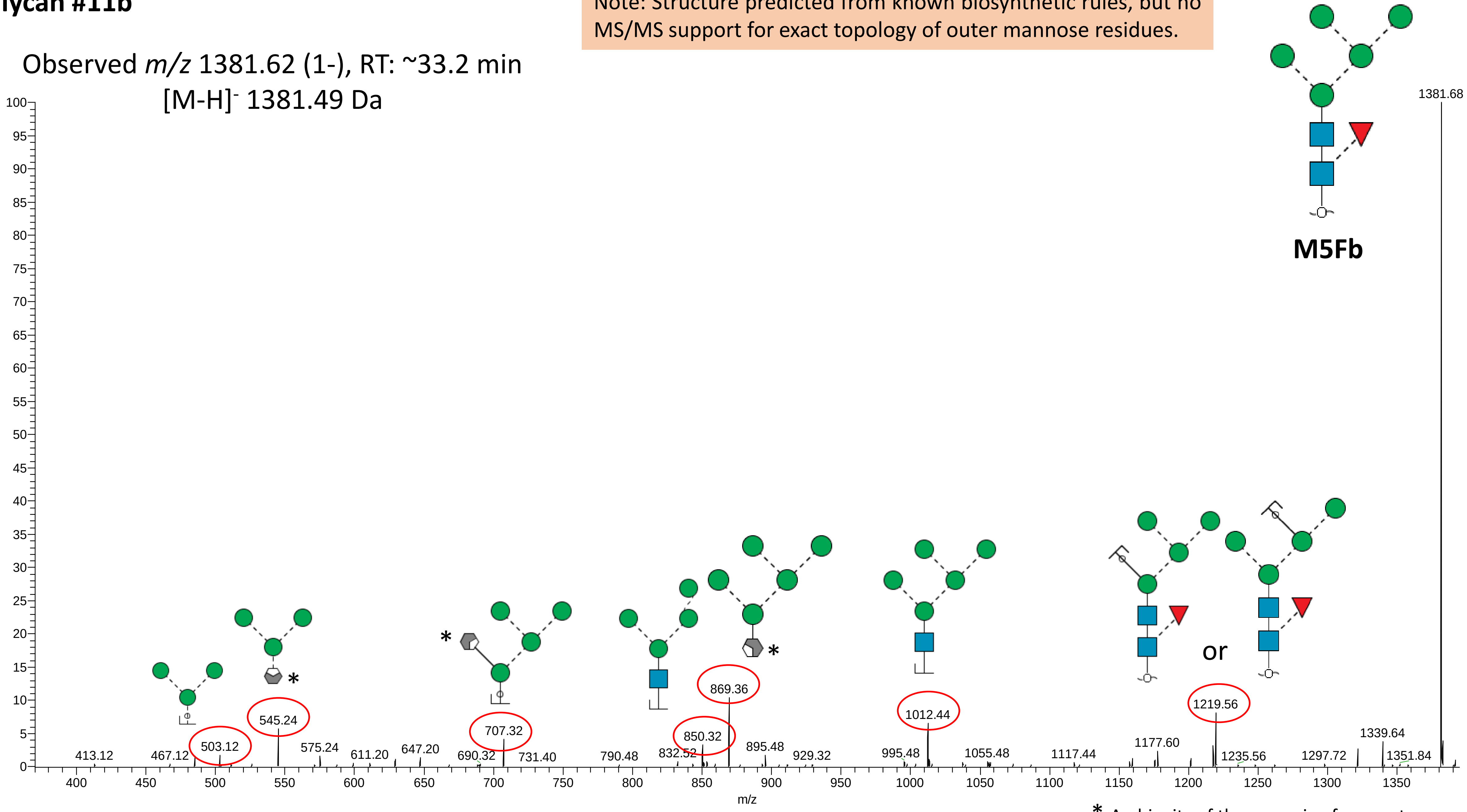
* Ambiguity of the cross-ring fragments

Glycan #11b

Note: Structure predicted from known biosynthetic rules, but no MS/MS support for exact topology of outer mannose residues.

Observed *m/z* 1381.62 (1-), RT: ~33.2 min

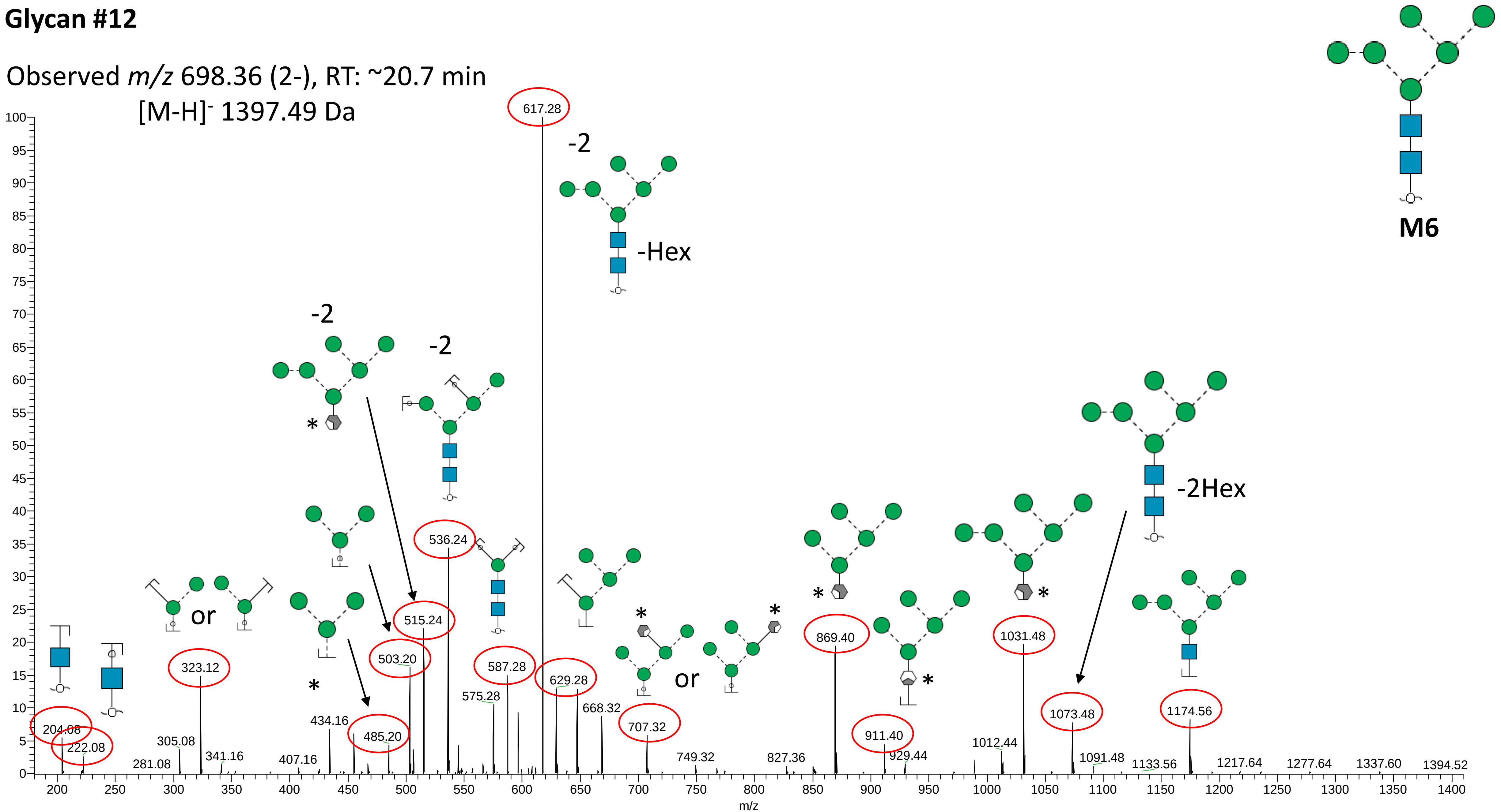
$[M-H]^-$ 1381.49 Da



* Ambiguity of the cross-ring fragments

Glycan #12

Observed *m/z* 698.36 (2-), RT: ~20.7 min
[M-H]$^-$ 1397.49 Da

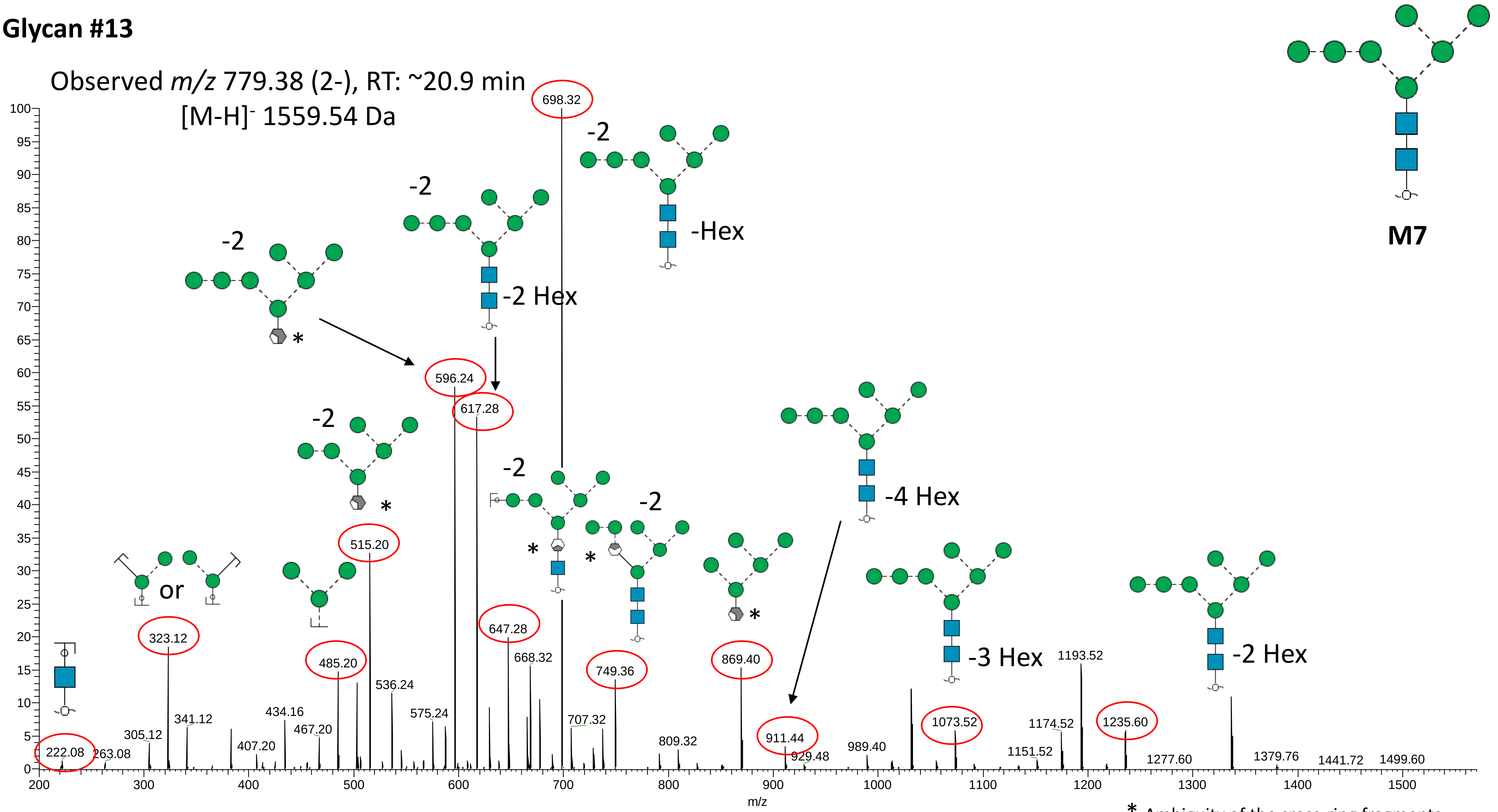


* Ambiguity of the cross-ring fragments

Glycan #13

Observed *m/z* 779.38 (2-), RT: ~20.9 min

[M-H]$^-$ 1559.54 Da



* Ambiguity of the cross-ring fragments

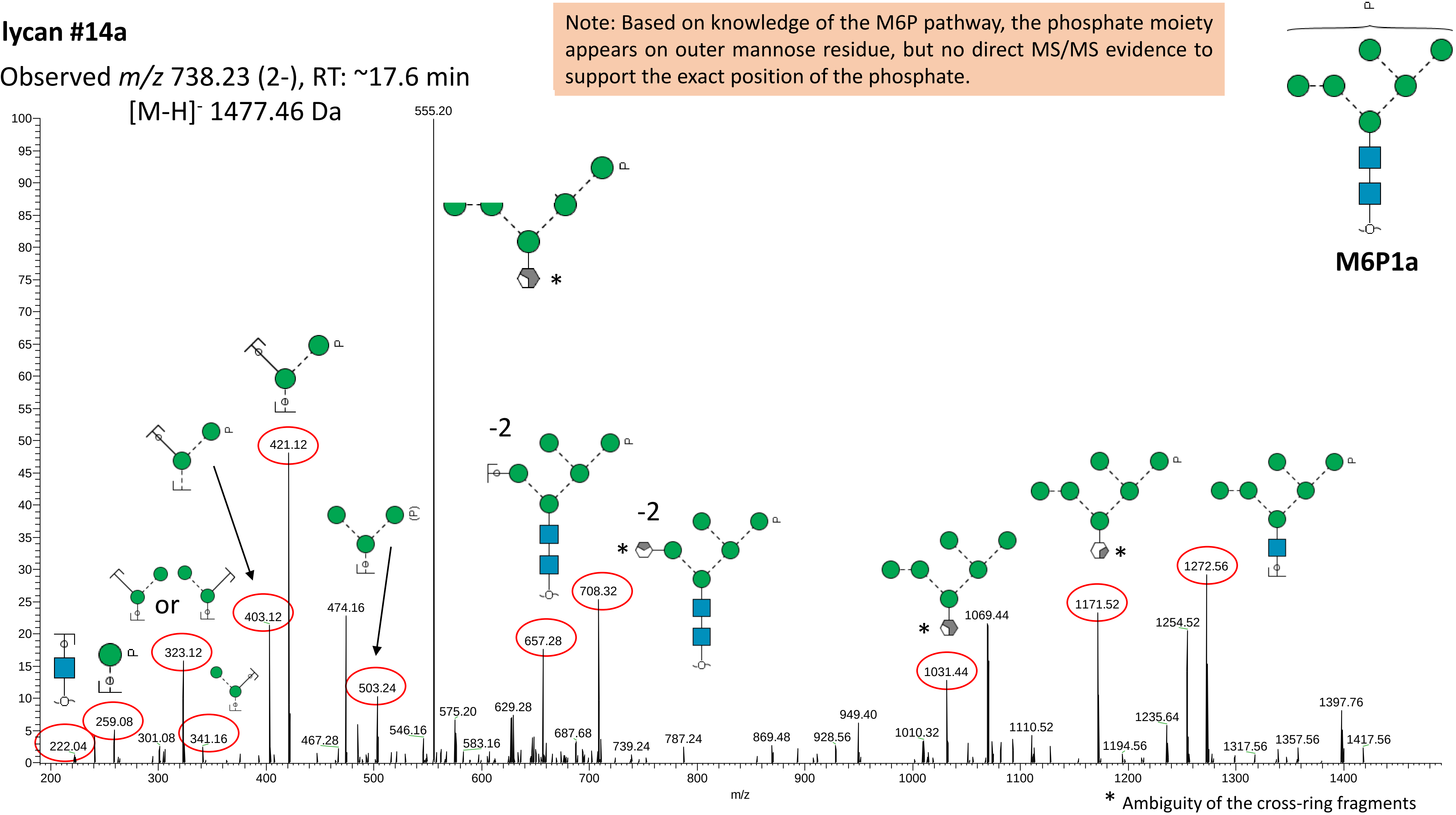
Glycan #14a

Observed *m/z* 738.23 (2-), RT: ~17.6 min

$[M-H]^-$ 1477.46 Da

Note: Based on knowledge of the M6P pathway, the phosphate moiety appears on outer mannose residue, but no direct MS/MS evidence to support the exact position of the phosphate.

M6P1a

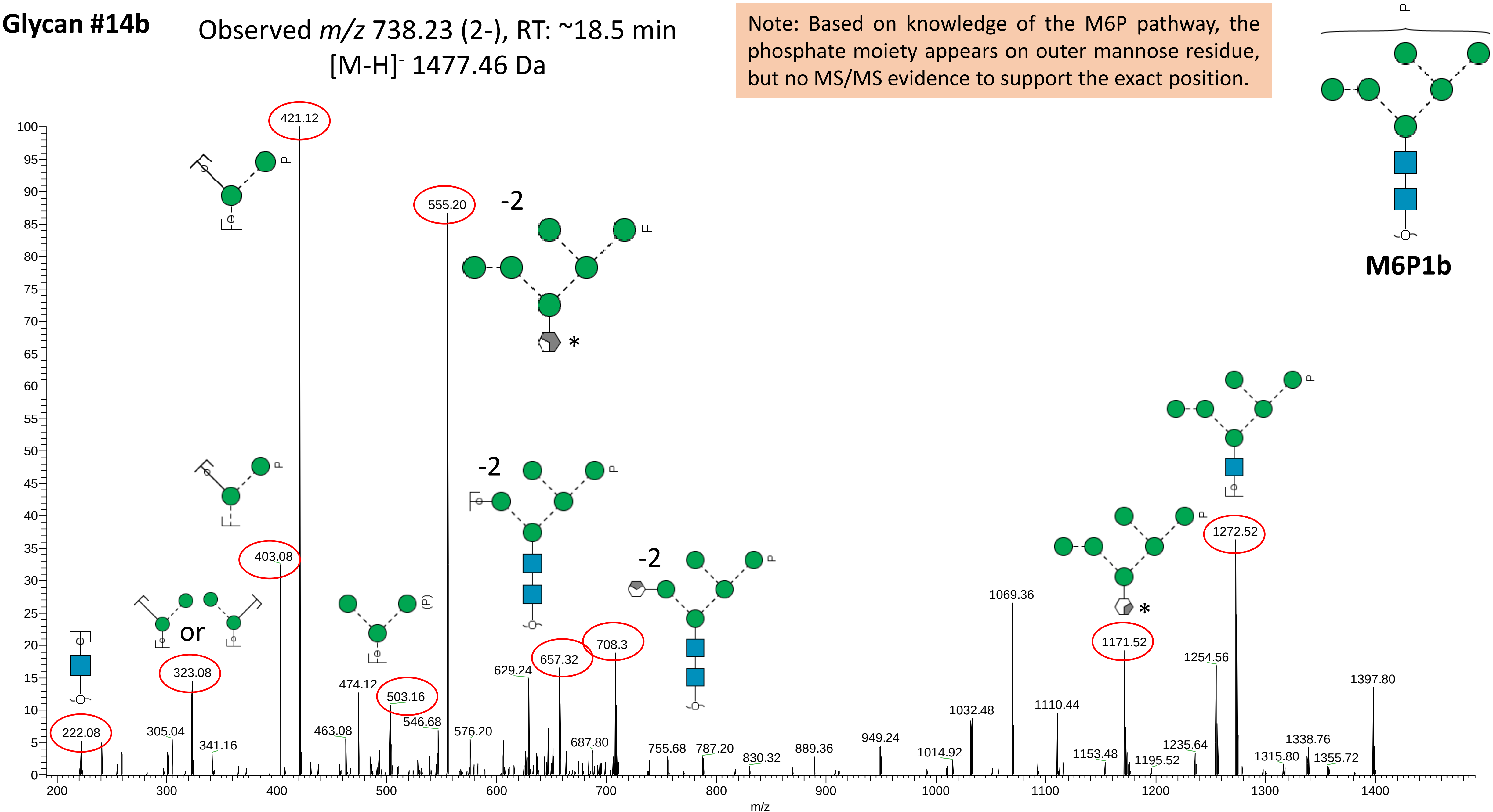


* Ambiguity of the cross-ring fragments

Glycan #14b

Observed *m/z* 738.23 (2-), RT: ~18.5 min
$[M-H]^-$ 1477.46 Da

Note: Based on knowledge of the M6P pathway, the phosphate moiety appears on outer mannose residue, but no MS/MS evidence to support the exact position.



* Ambiguity of the cross-ring fragments

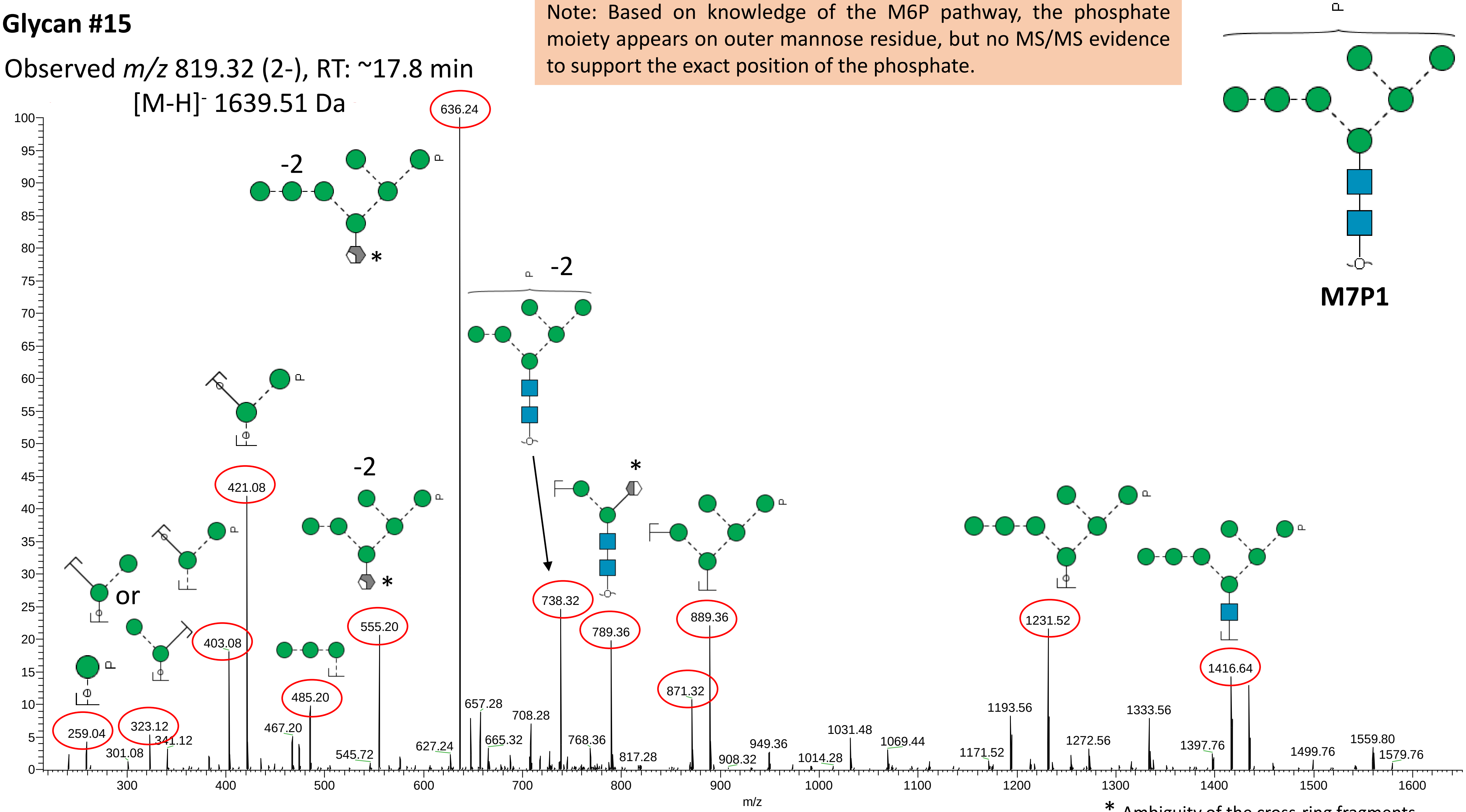
Glycan #15

Observed *m/z* 819.32 (2-), RT: ~17.8 min

[M-H]$^-$ 1639.51 Da

Note: Based on knowledge of the M6P pathway, the phosphate moiety appears on outer mannose residue, but no MS/MS evidence to support the exact position of the phosphate.

M7P1

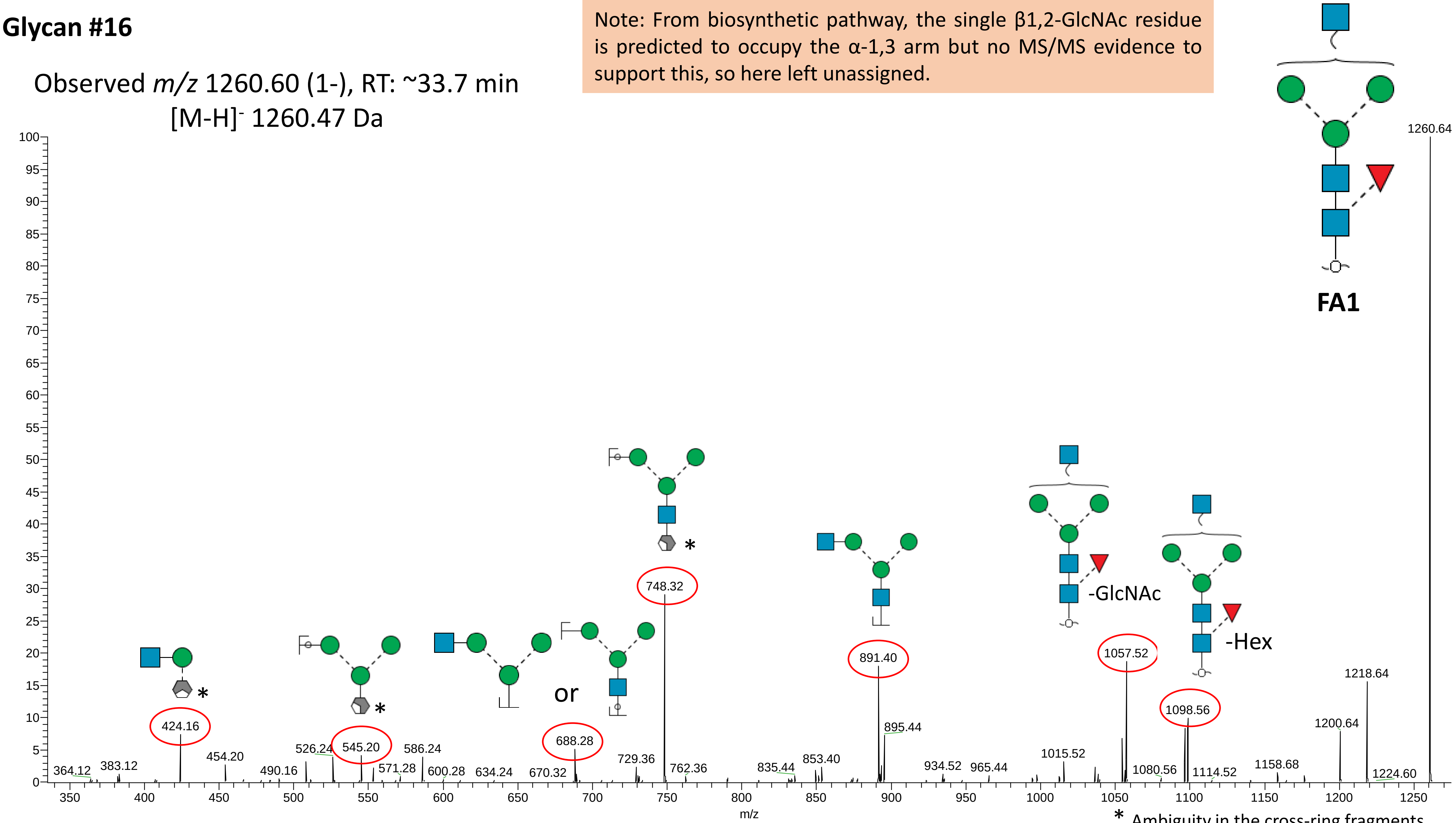


* Ambiguity of the cross-ring fragments

Glycan #16

Observed *m/z* 1260.60 (1-), RT: ~33.7 min
$[M-H]^-$ 1260.47 Da

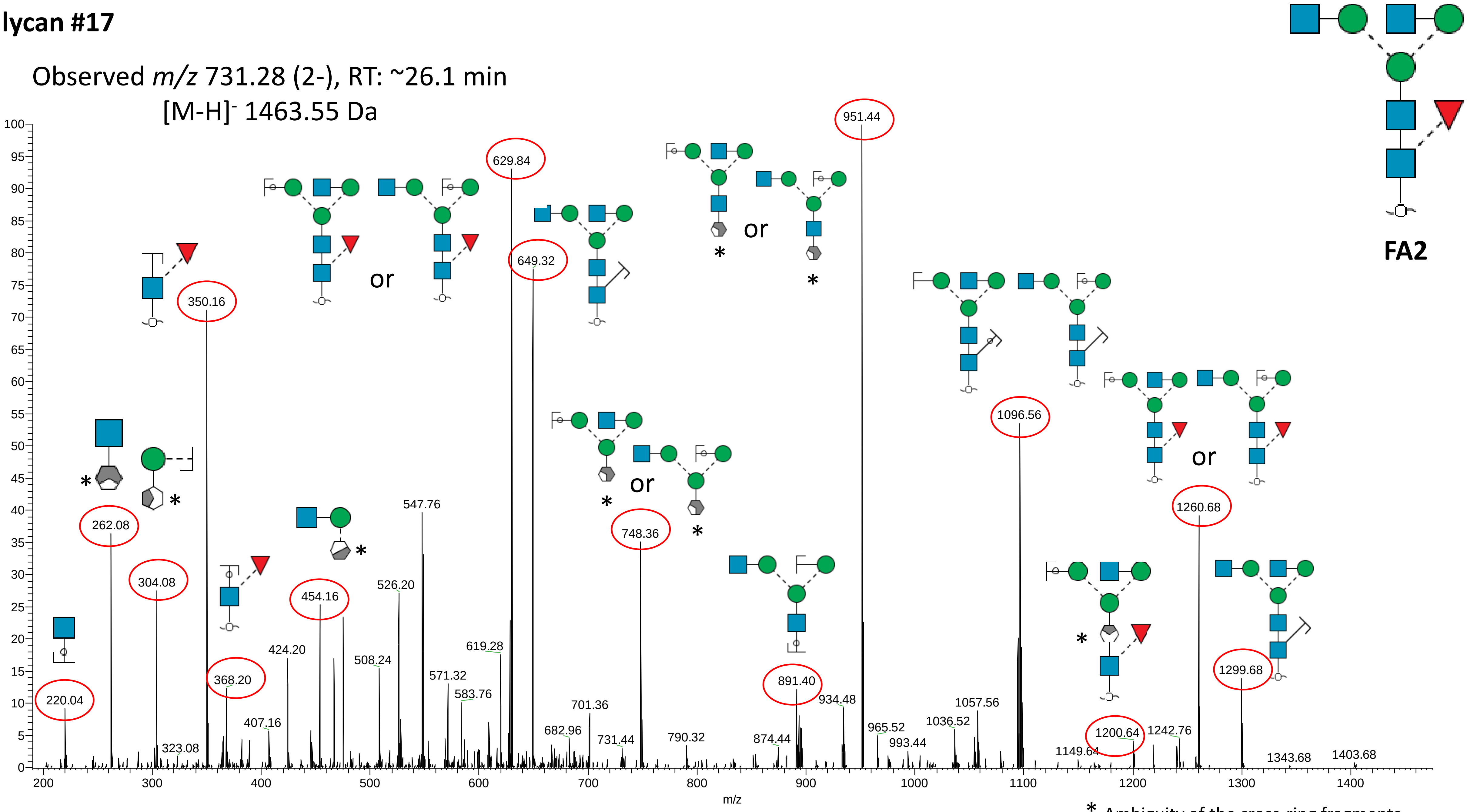
Note: From biosynthetic pathway, the single β1,2-GlcNAc residue is predicted to occupy the α-1,3 arm but no MS/MS evidence to support this, so here left unassigned.



* Ambiguity in the cross-ring fragments

Glycan #17

Observed *m/z* 731.28 (2-), RT: ~26.1 min
$[M-H]^-$ 1463.55 Da



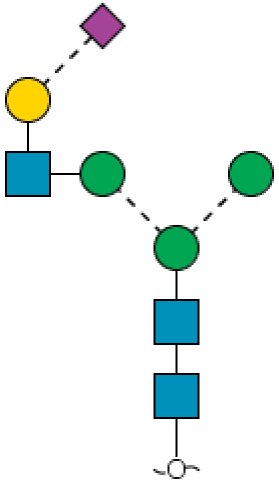
* Ambiguity of the cross-ring fragments

Glycan #18

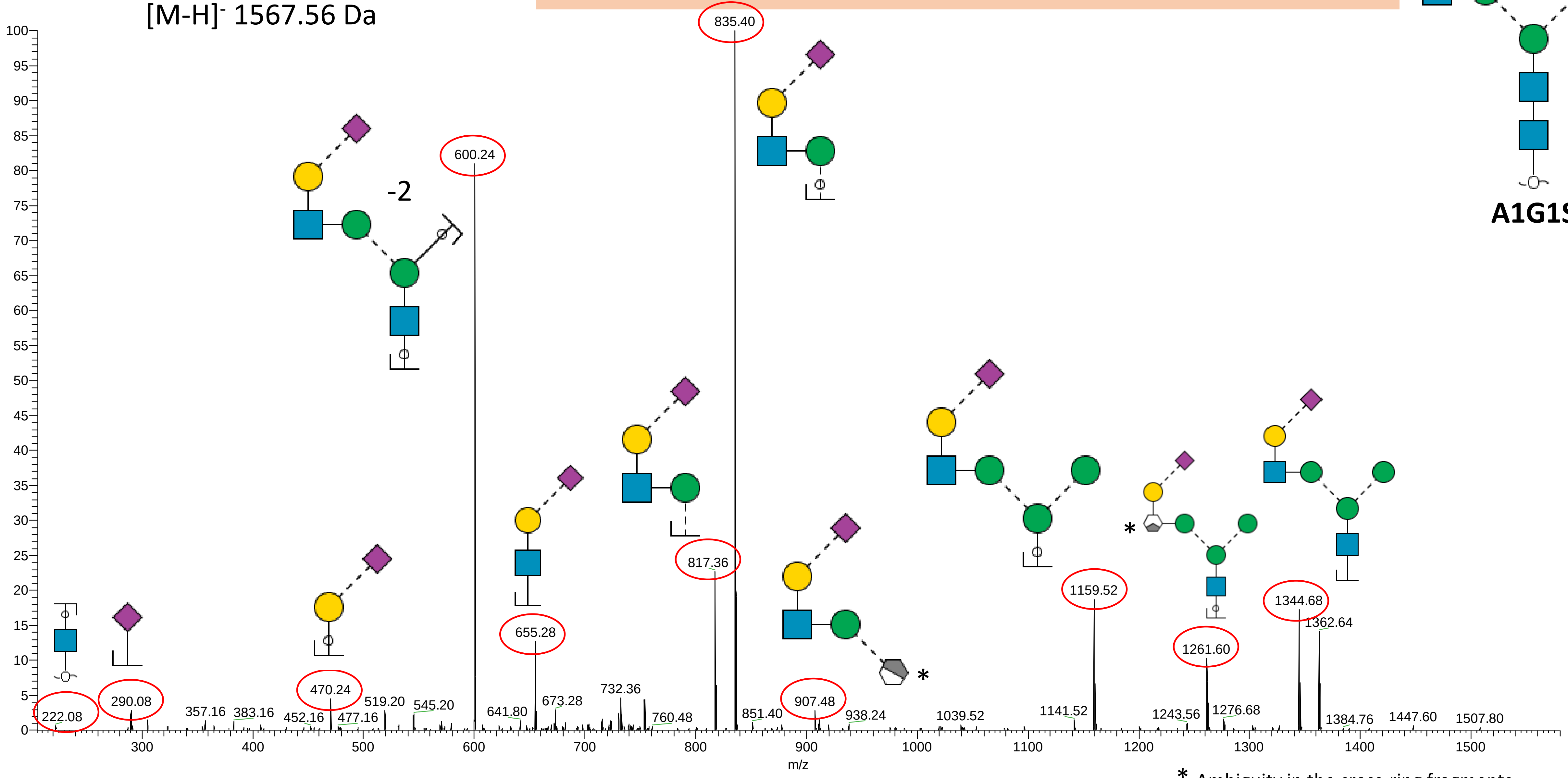
Observed *m/z* 783.28 (2-), RT: ~22.3 min

$[M-H]^-$ 1567.56 Da

Note: This glycan is annotated as the α2,6-sialyl linkage isomer based on the early PGC-LC elution and experience with neutrophil N-glycan profiling. The elongated antenna is known to frequently occupy the α1,3-arm rather than the α1,6-arm of neutrophil *N*-glycans and have thus been assigned as such.



A1G1S1



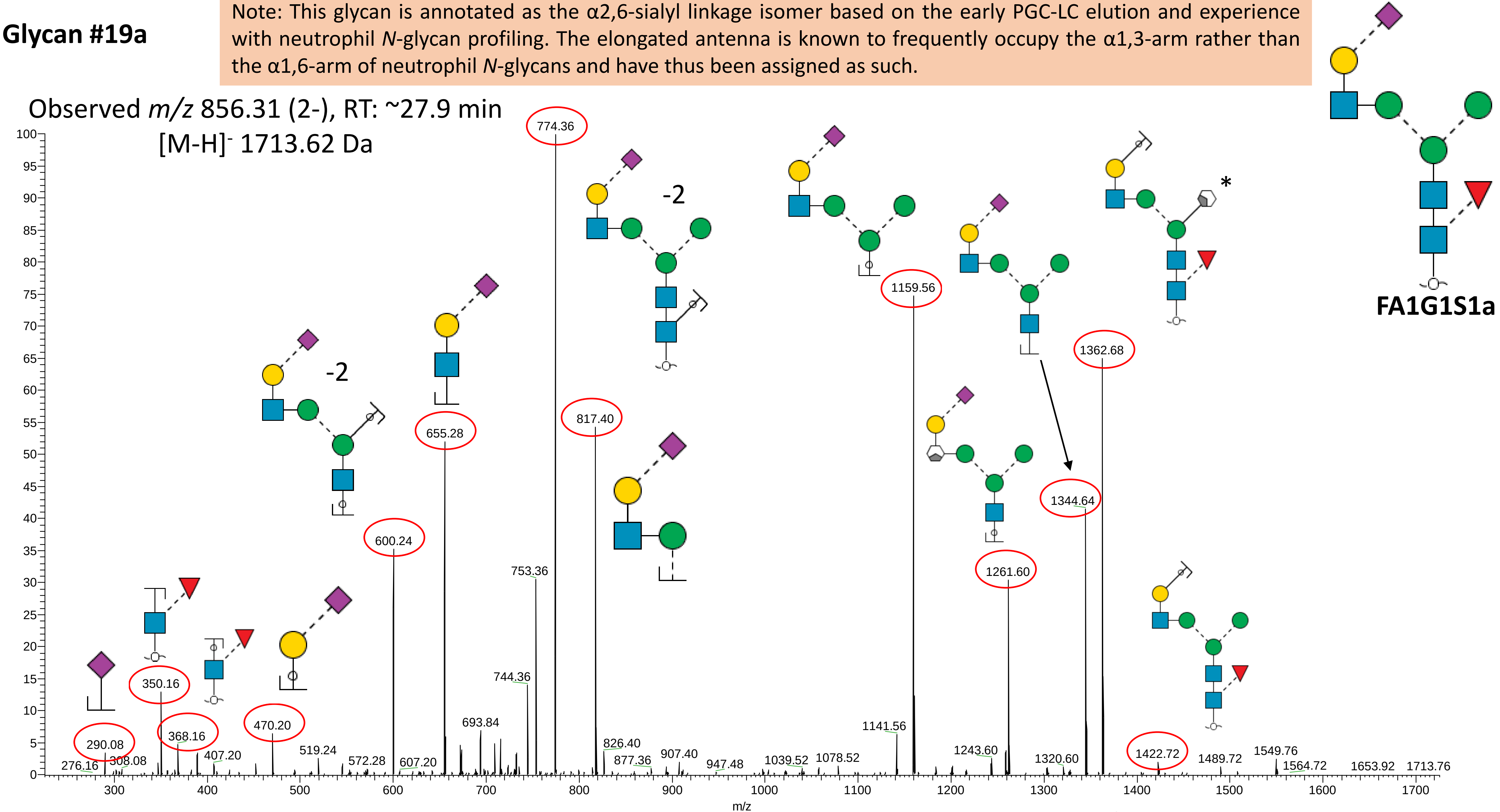
* Ambiguity in the cross-ring fragments

Glycan #19a

Note: This glycan is annotated as the α2,6-sialyl linkage isomer based on the early PGC-LC elution and experience with neutrophil *N*-glycan profiling. The elongated antenna is known to frequently occupy the α1,3-arm rather than the α1,6-arm of neutrophil *N*-glycans and have thus been assigned as such.

Observed *m/z* 856.31 (2-), RT: ~27.9 min

[M-H]$^-$ 1713.62 Da



FA1G1S1a

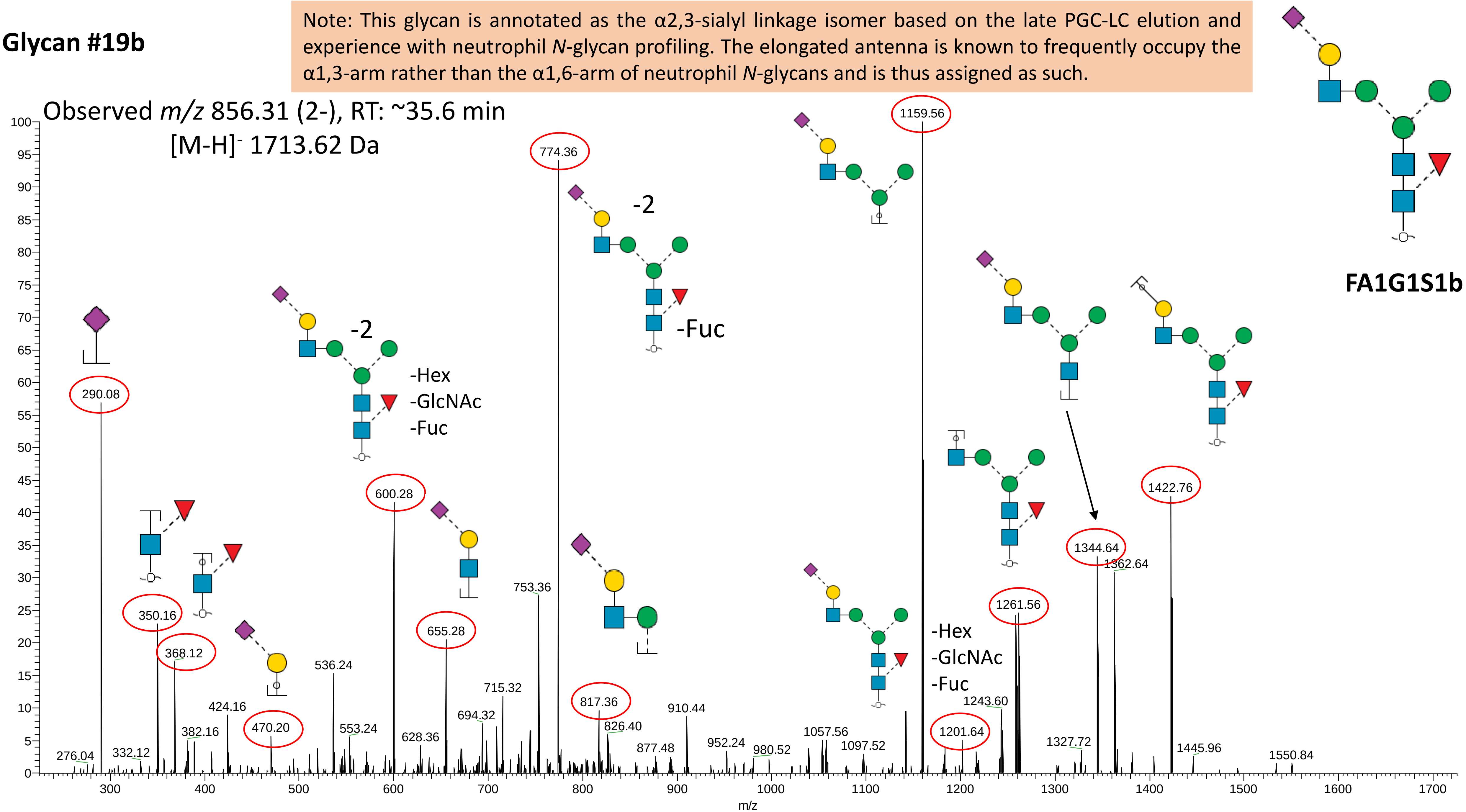
* Ambiguity of the cross-ring fragments

Glycan #19b

Note: This glycan is annotated as the α2,3-sialyl linkage isomer based on the late PGC-LC elution and experience with neutrophil *N*-glycan profiling. The elongated antenna is known to frequently occupy the α1,3-arm rather than the α1,6-arm of neutrophil *N*-glycans and is thus assigned as such.

Observed *m/z* 856.31 (2-), RT: ~35.6 min

[M-H]$^-$ 1713.62 Da



FA1G1S1b

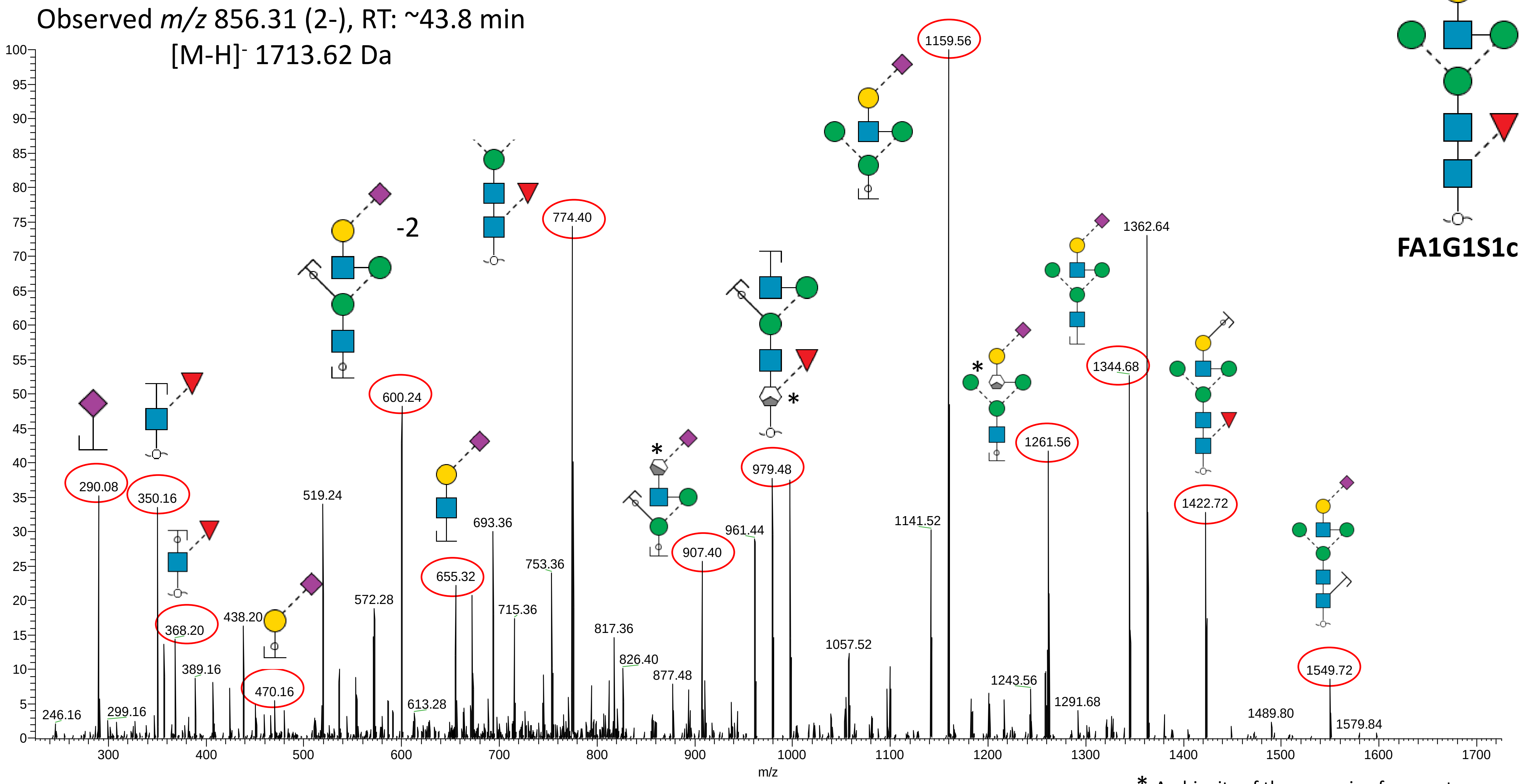
* Ambiguity of the cross-ring fragments

Glycan #19c

Note: This low abundance glycan is possibly the isomer where the Sia-Gal-GlcNAc antenna occupy the α1,6-arm rather than the α1,3-arm common for neutrophil *N*-glycans but no direct MS/MS evidence to support this

Observed *m/z* 856.31 (2-), RT: ~43.8 min

[M-H]$^-$ 1713.62 Da



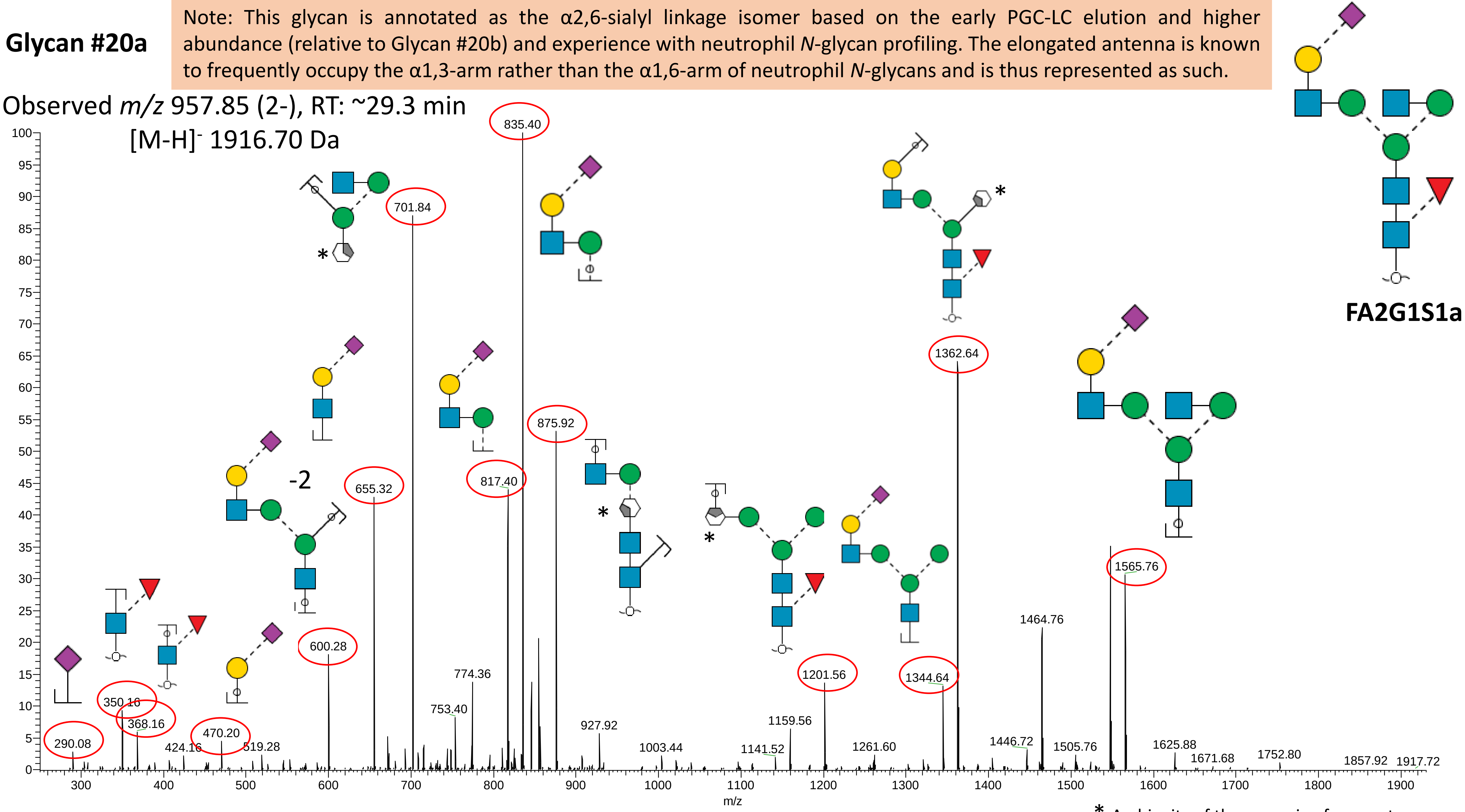
* Ambiguity of the cross-ring fragments

Glycan #20a

Note: This glycan is annotated as the α2,6-sialyl linkage isomer based on the early PGC-LC elution and higher abundance (relative to Glycan #20b) and experience with neutrophil *N*-glycan profiling. The elongated antenna is known to frequently occupy the α1,3-arm rather than the α1,6-arm of neutrophil *N*-glycans and is thus represented as such.

Observed *m/z* 957.85 (2-), RT: ~29.3 min

$[M\text{-}H]^-$ 1916.70 Da



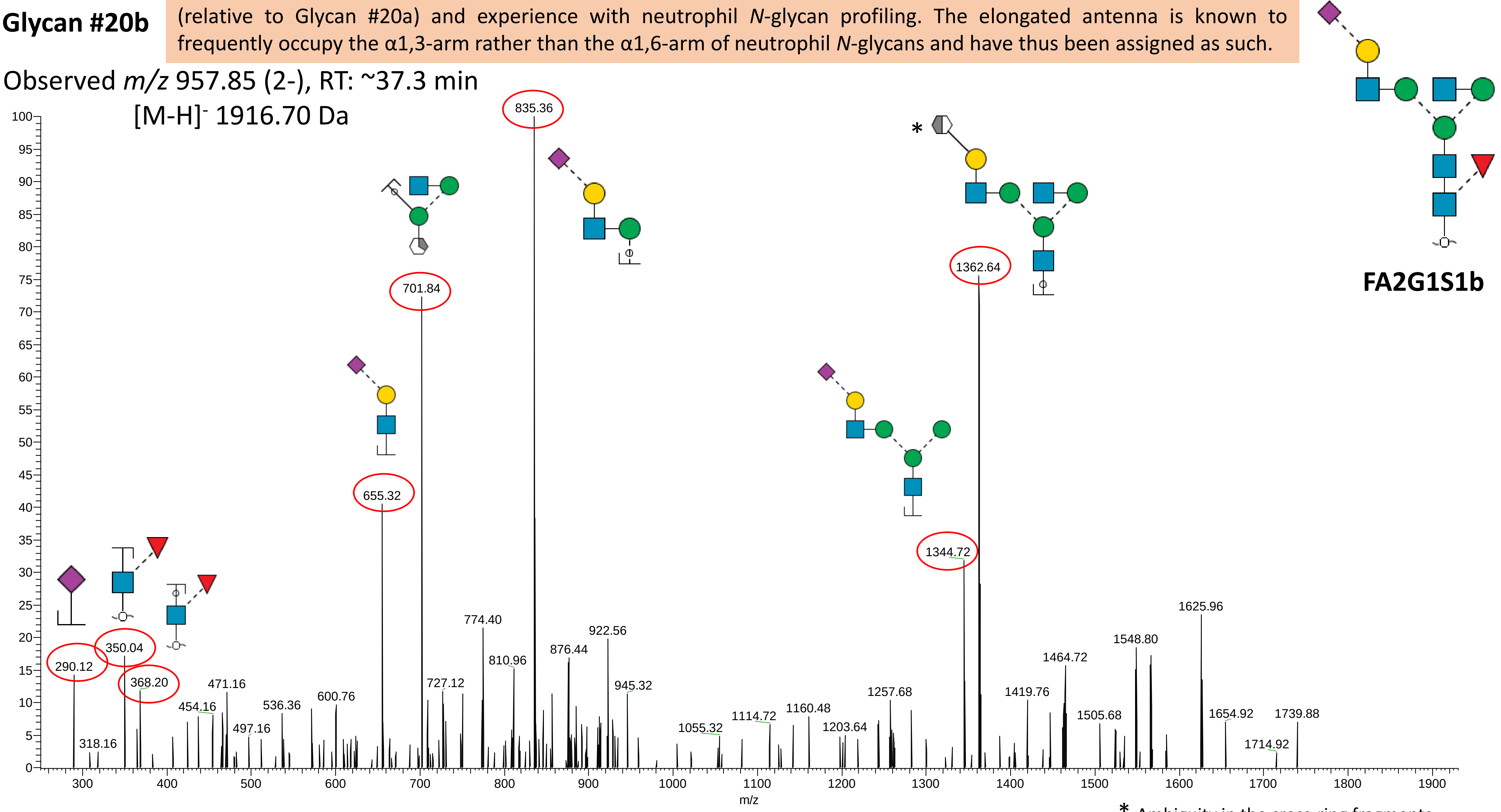
* Ambiguity of the cross-ring fragments

Glycan #20b

Note: This glycan is annotated as the α2,3-sialyl linkage isomer based on the later PGC-LC elution and lower abundance (relative to Glycan #20a) and experience with neutrophil *N*-glycan profiling. The elongated antenna is known to frequently occupy the α1,3-arm rather than the α1,6-arm of neutrophil *N*-glycans and have thus been assigned as such.

Observed *m/z* 957.85 (2-), RT: ~37.3 min

$[M-H]^-$ 1916.70 Da



FA2G1S1b

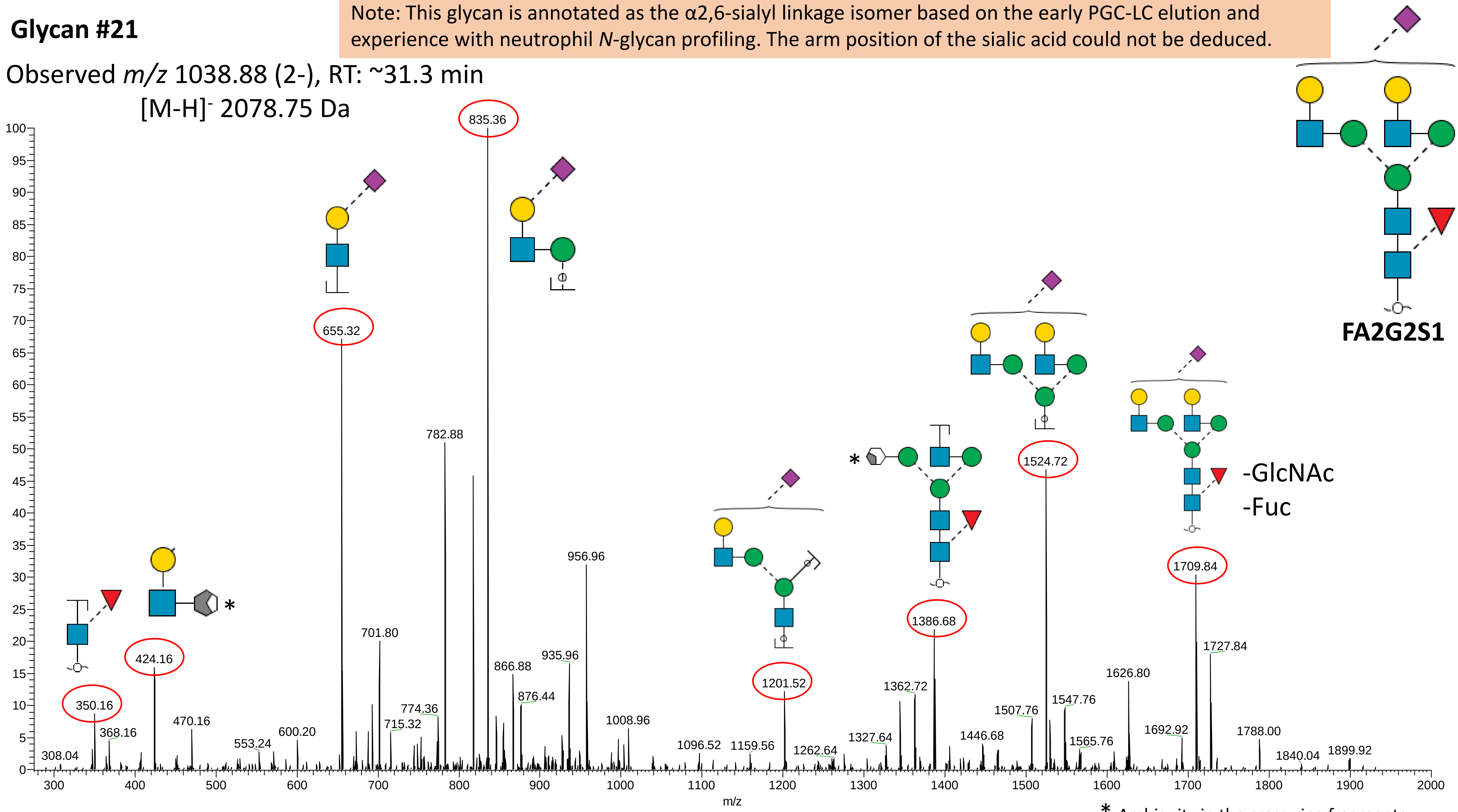
* Ambiguity in the cross-ring fragments

Glycan #21

Note: This glycan is annotated as the α2,6-sialyl linkage isomer based on the early PGC-LC elution and experience with neutrophil *N*-glycan profiling. The arm position of the sialic acid could not be deduced.

Observed *m/z* 1038.88 (2-), RT: ~31.3 min

$[M\text{-}H]^-$ 2078.75 Da



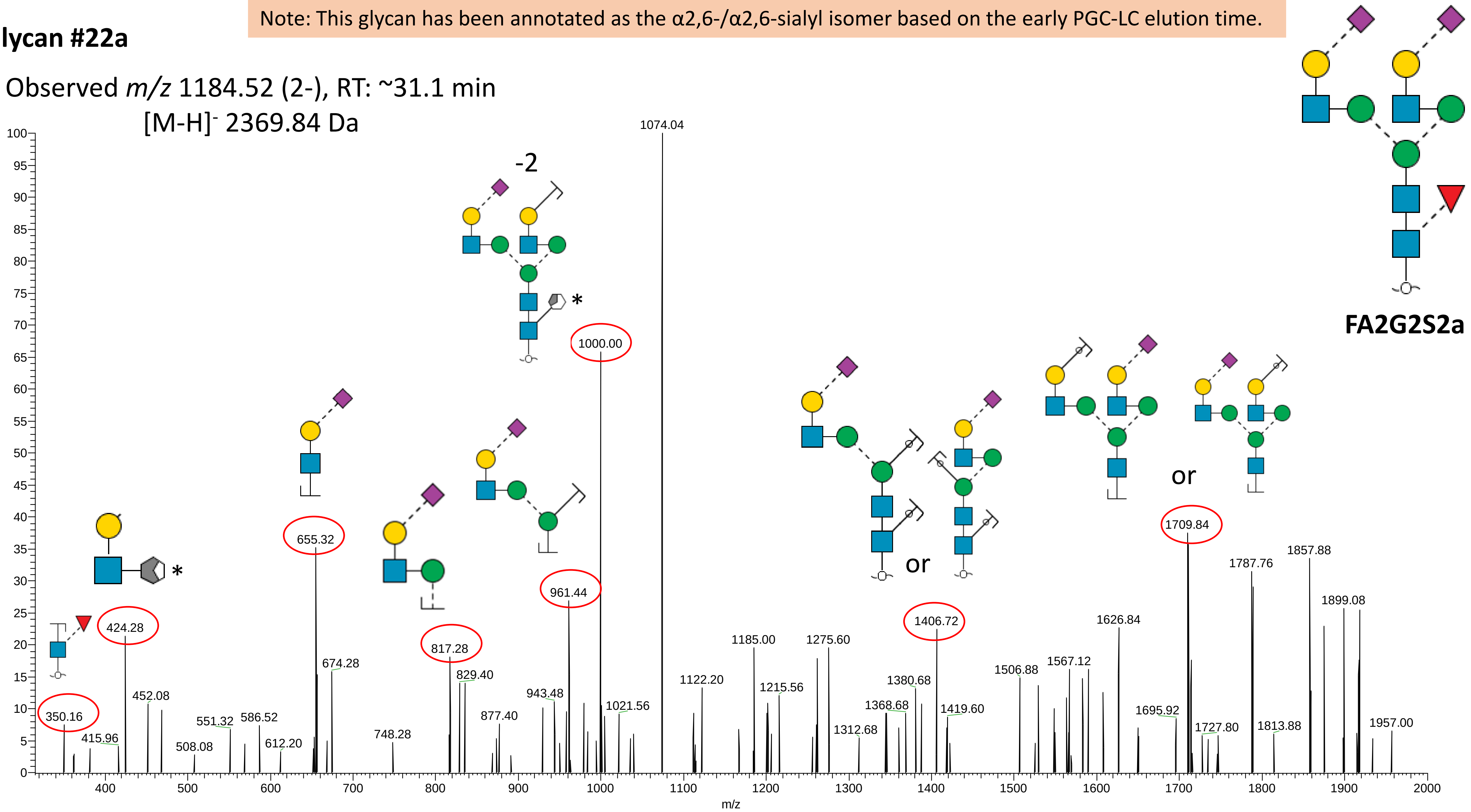
* Ambiguity in the cross-ring fragments

Glycan #22a

Note: This glycan has been annotated as the α2,6-/α2,6-sialyl isomer based on the early PGC-LC elution time.

Observed *m/z* 1184.52 (2-), RT: ~31.1 min

[M-H]$^-$ 2369.84 Da



FA2G2S2a

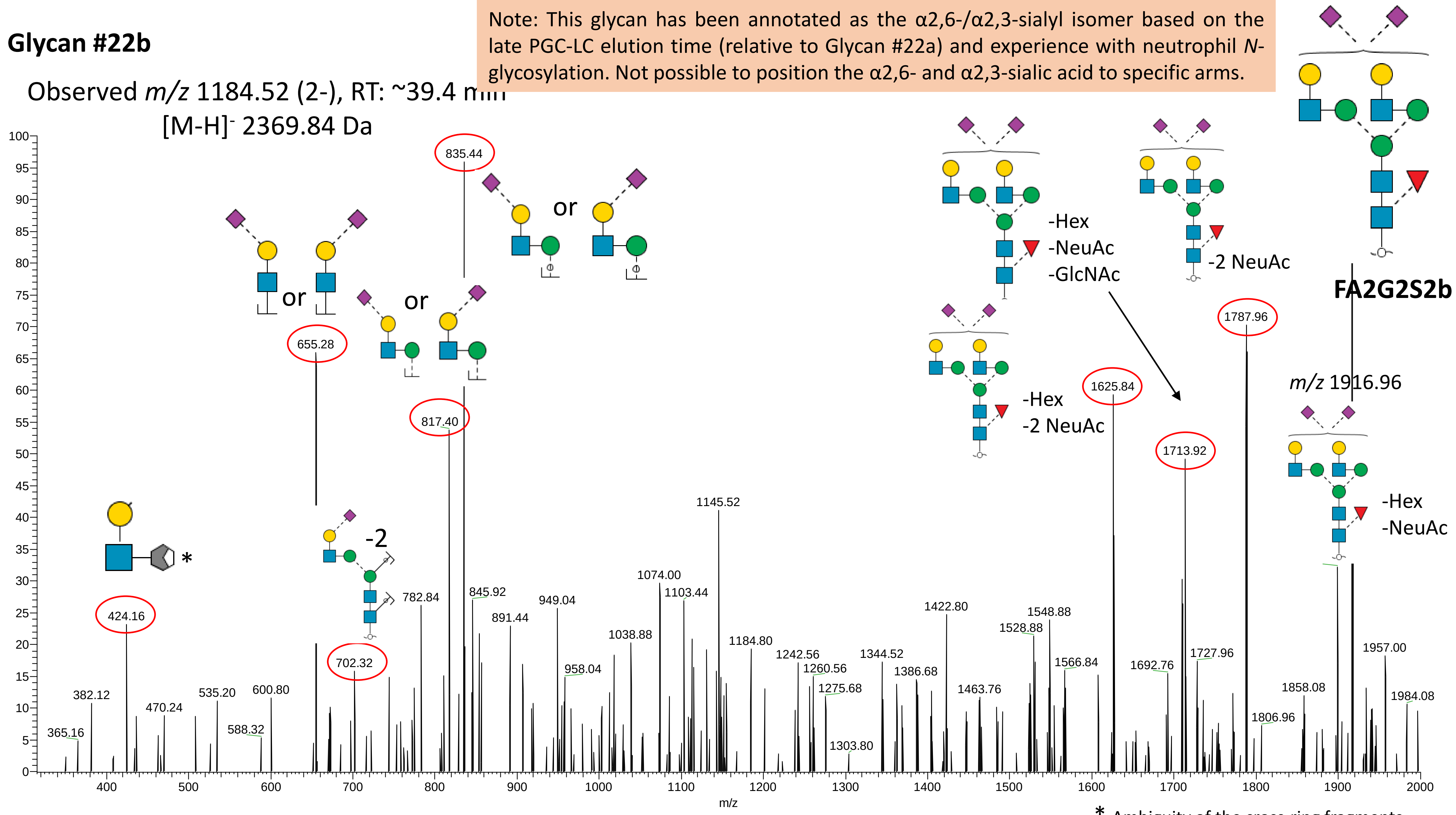
* Ambiguity of the cross-ring fragments

Glycan #22b

Note: This glycan has been annotated as the α2,6-/α2,3-sialyl isomer based on the late PGC-LC elution time (relative to Glycan #22a) and experience with neutrophil *N*-glycosylation. Not possible to position the α2,6- and α2,3-sialic acid to specific arms.

Observed *m/z* 1184.52 (2-), RT: ~39.4 min

$[M-H]^-$ 2369.84 Da



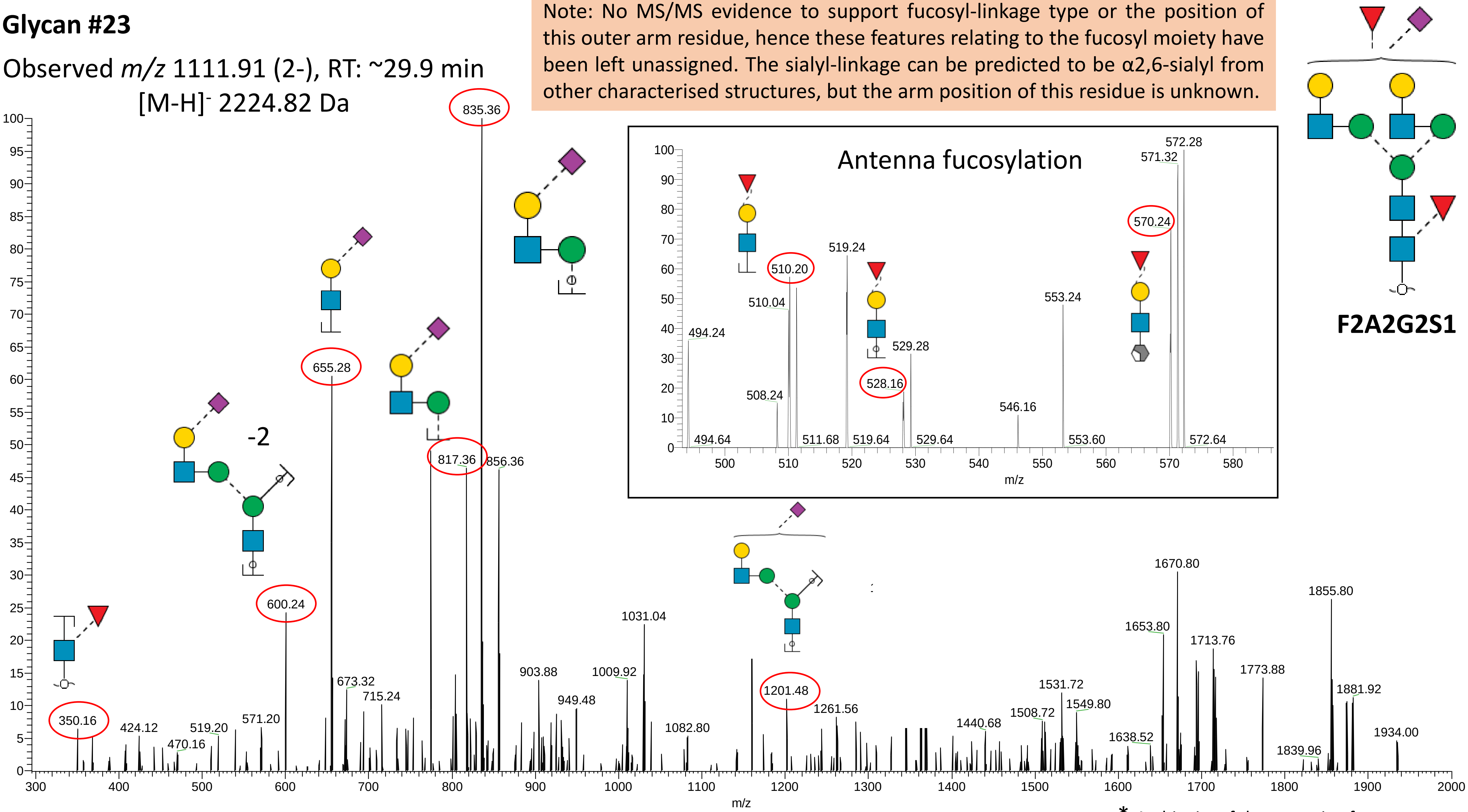
* Ambiguity of the cross-ring fragments

Glycan #23

Observed *m/z* 1111.91 (2-), RT: ~29.9 min

$[M-H]^-$ 2224.82 Da

Note: No MS/MS evidence to support fucosyl-linkage type or the position of this outer arm residue, hence these features relating to the fucosyl moiety have been left unassigned. The sialyl-linkage can be predicted to be α2,6-sialyl from other characterised structures, but the arm position of this residue is unknown.



* Ambiguity of the cross-ring fragments

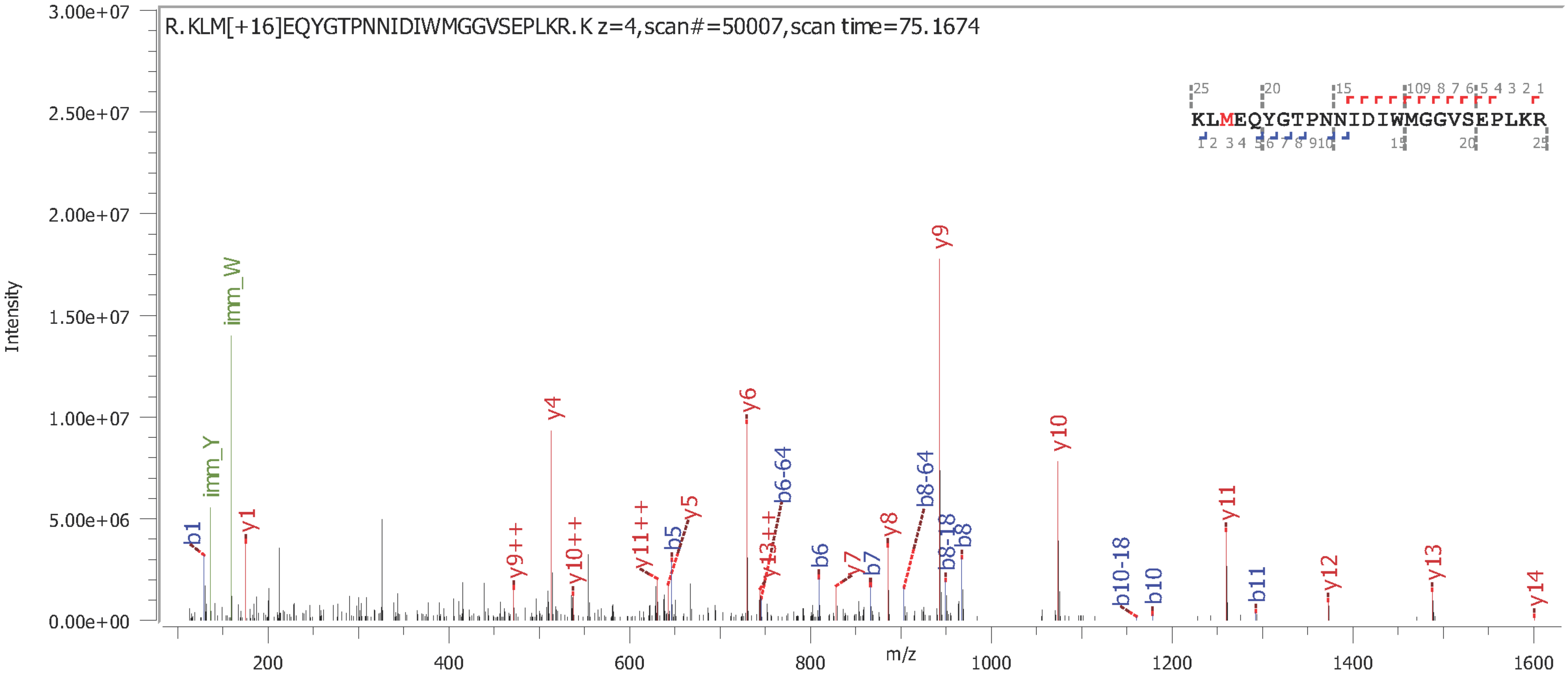
Supplementary Data S2A

Examples of Byonic-annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of peptides identified with non-glyco PTMs (i.e. Met and Trp mono- and di-oxidation and Tyr mono-chlorination) from the analysis of unenriched peptide mixtures of nMPO

Human myeloperoxidase (P05164)

Mono-oxidised methionine-containing peptide

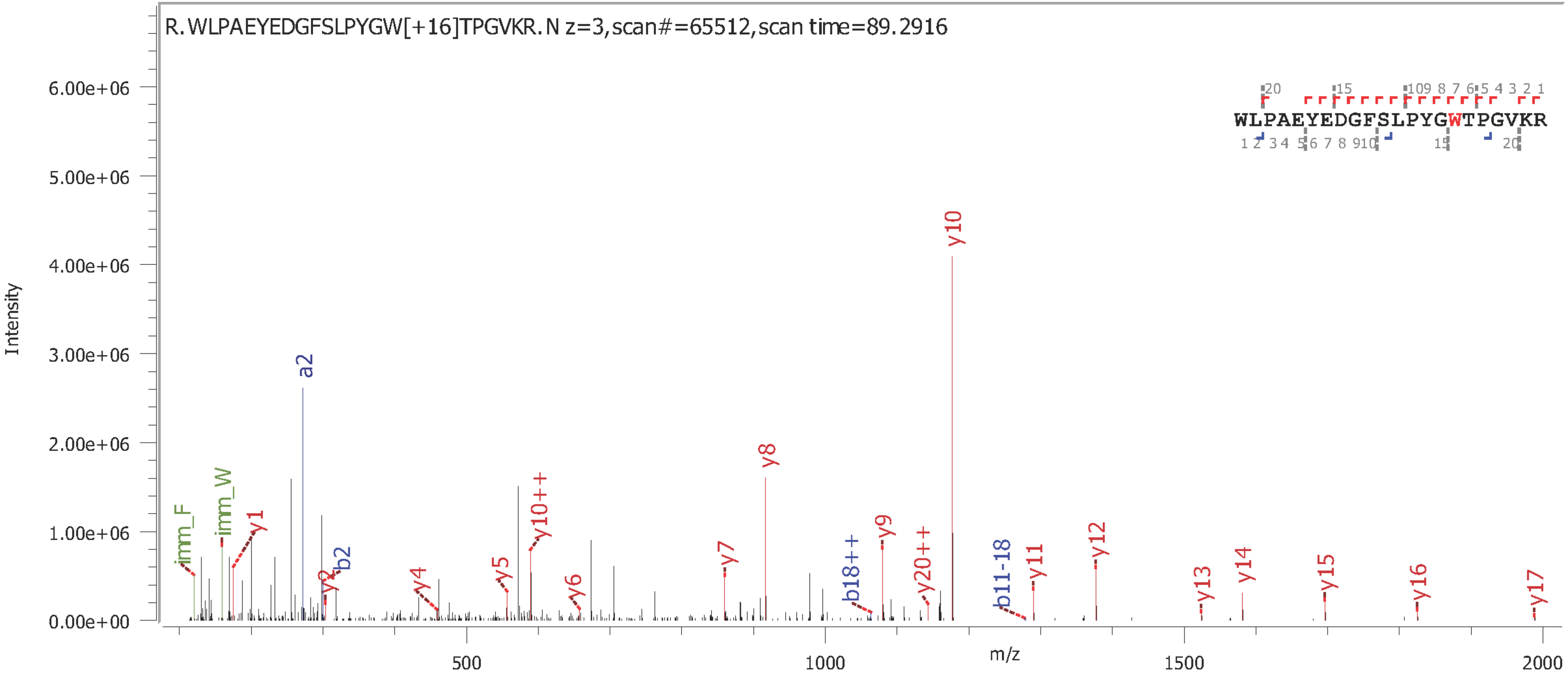
^{629}KL**M**EQYGTPNNIDIWMGGVSEPLKR^{641} (identification confidence level, PEP 2D: 2.4x10^{-20})



Human myeloperoxidase (P05164)

Mono-oxidised tryptophan-containing peptide

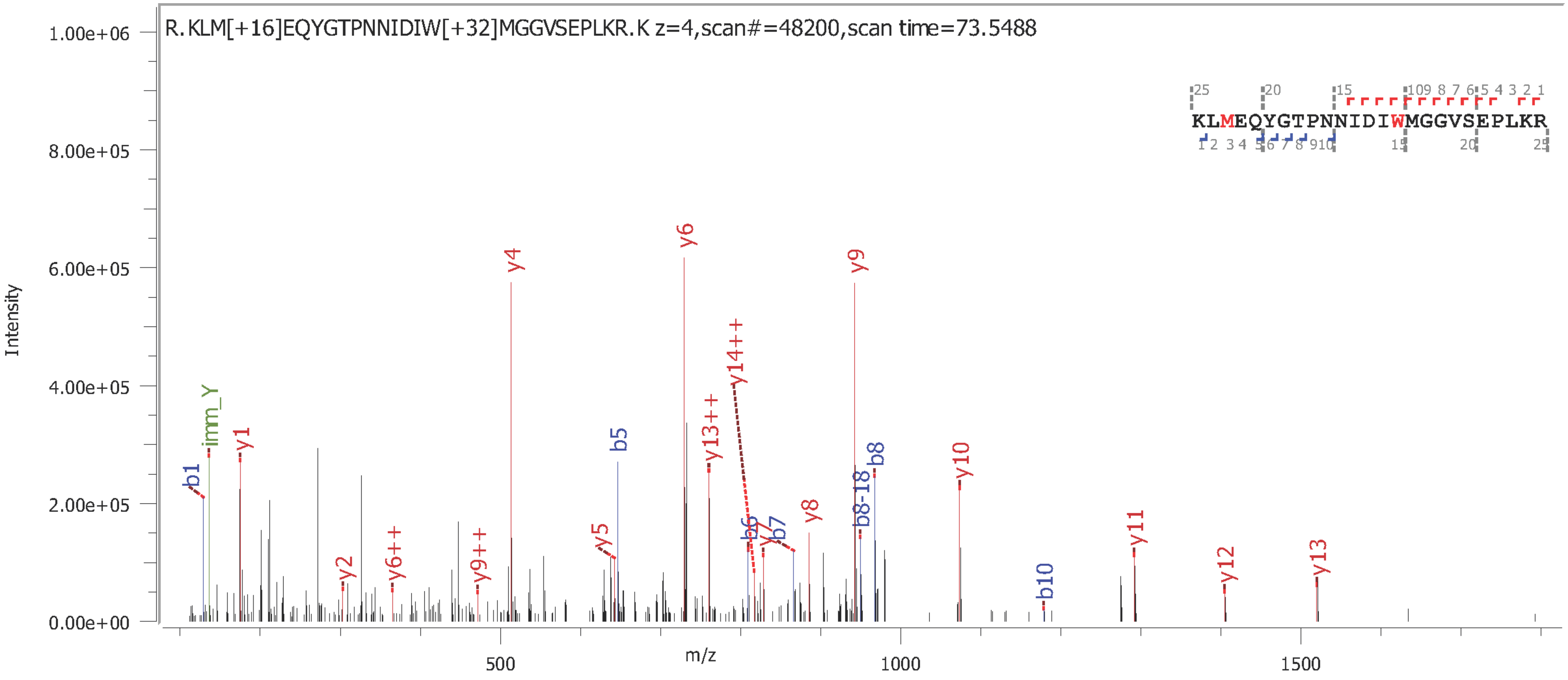
^{198}WLPAEYEDGFSLPYGWTPGVKR^{219} (identification confidence level, PEP 2D: 1.9x10^{-15})



Human myeloperoxidase (P05164)

Di-oxidised tryptophan-containing peptide

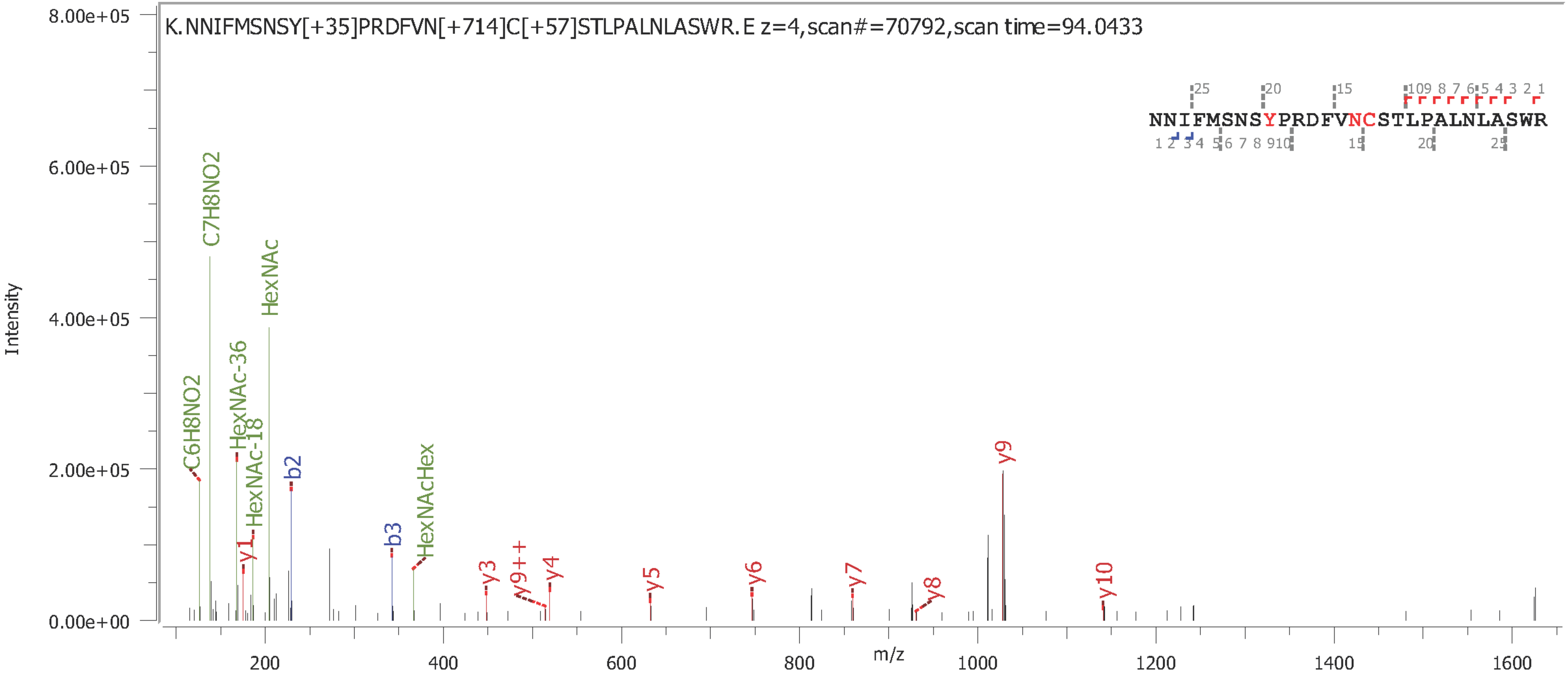
^{629}KLMEQYGTPNNIDIWMGGVSEPLKR^{641} (identification confidence level, PEP 2D: 1.9x10^{-18})



Human myeloperoxidase (P05164)

Mono-chlorinated tyrosine-containing peptide

^{715}NNIFMSNS**Y**PRDFVNCSTLPALNLASWR^{742} (identification confidence level, PEP 2D: 3.3x10^{-8})



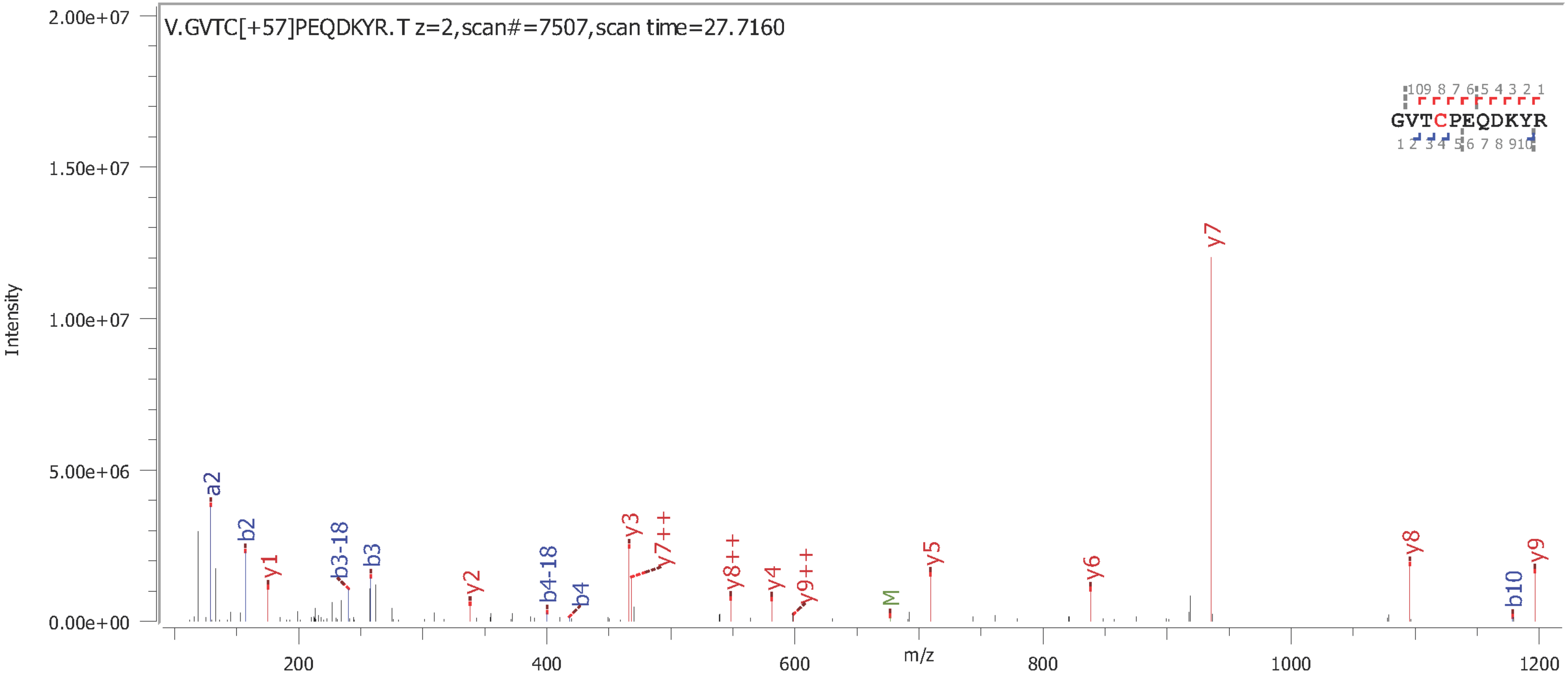
Supplementary Data S2B

Byonic-annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of N- and C-terminal truncation variants of the MPO α- and β-chain identified from the analysis of unenriched peptide mixtures of nMPO

Human myeloperoxidase (P05164)

α-chain N-terminal (truncation variant)

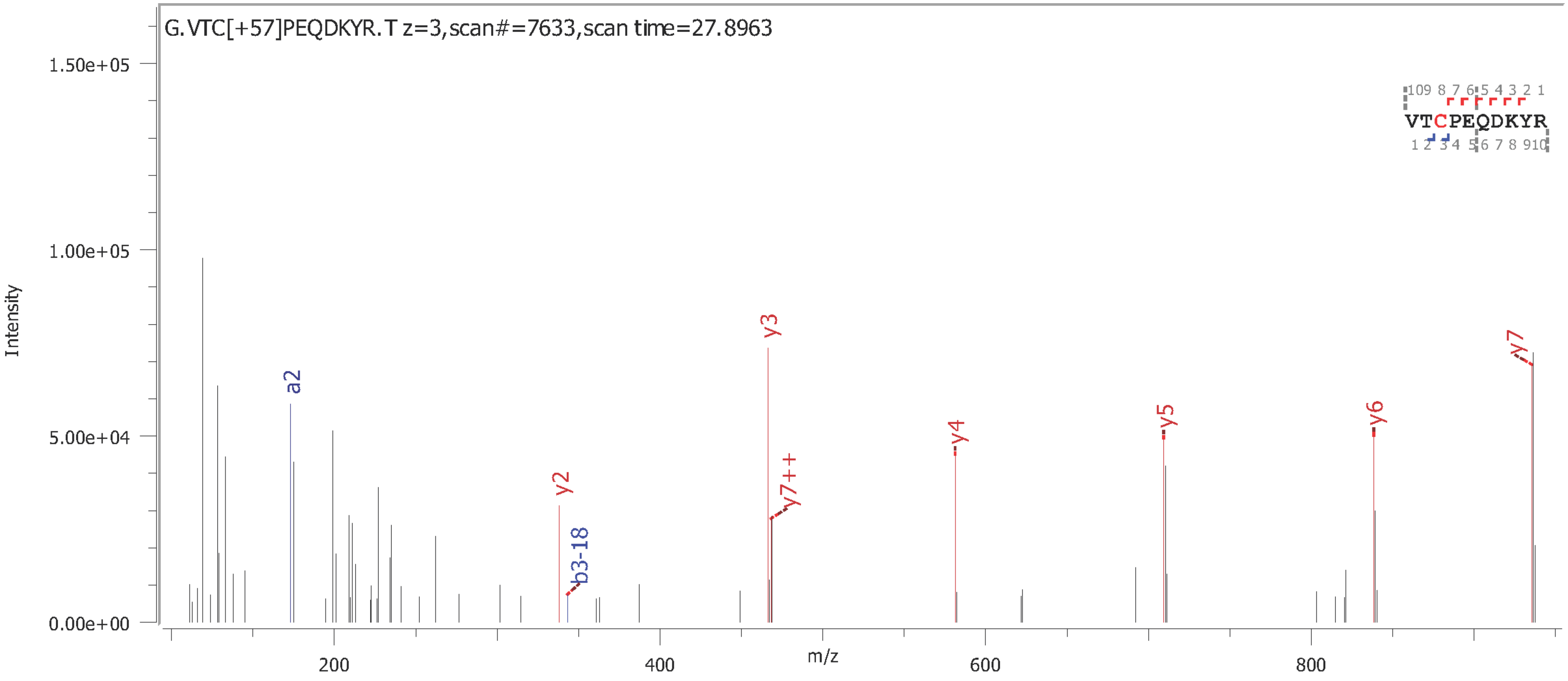
^{164}**G**VTCPEQDKYR (identification confidence level, PEP 2D: 4.0x10^{-11})



Human myeloperoxidase (P05164)

α-chain N-terminal (truncation variant)

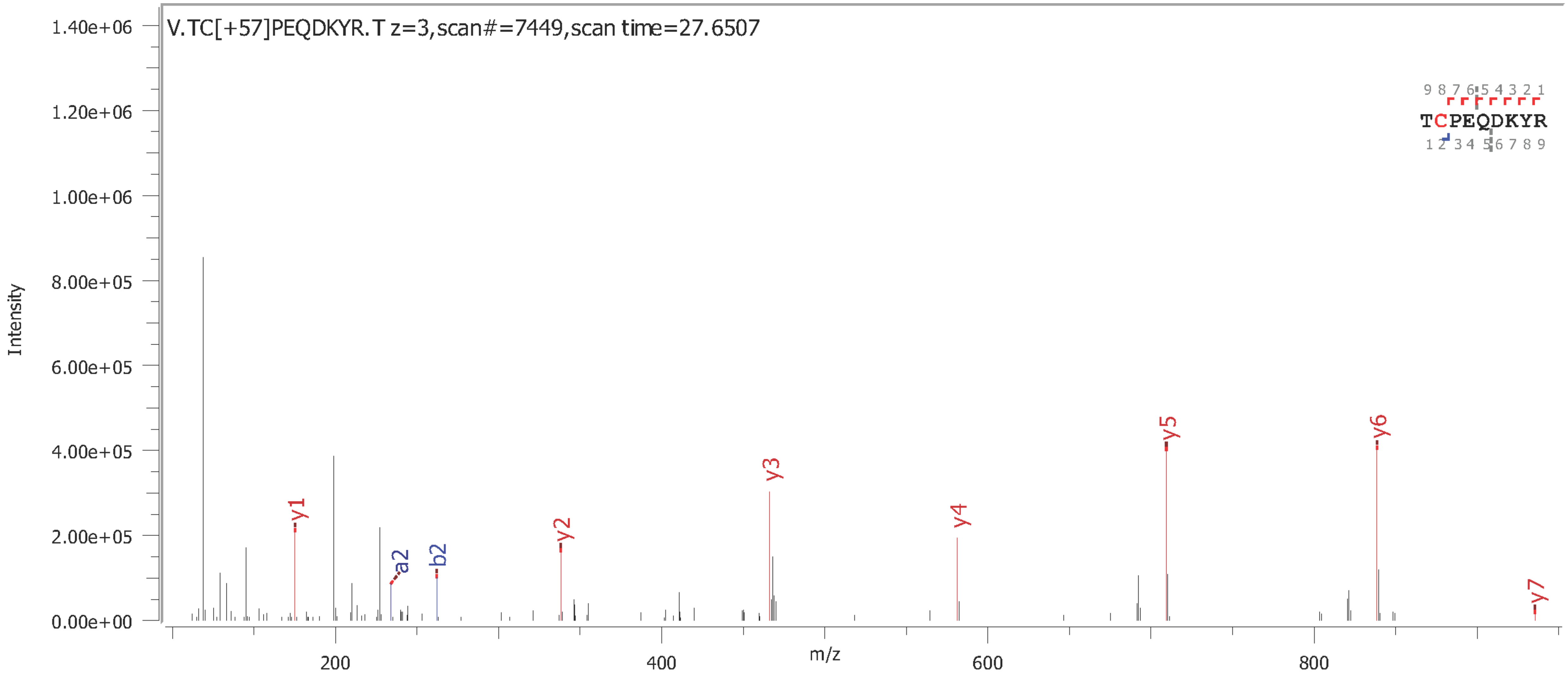
^{165}VTCPEQDKYR (identification confidence level, PEP 2D: 5.7 x 10^{-7})



Human myeloperoxidase (P05164)

α-chain N-terminal (truncation variant)

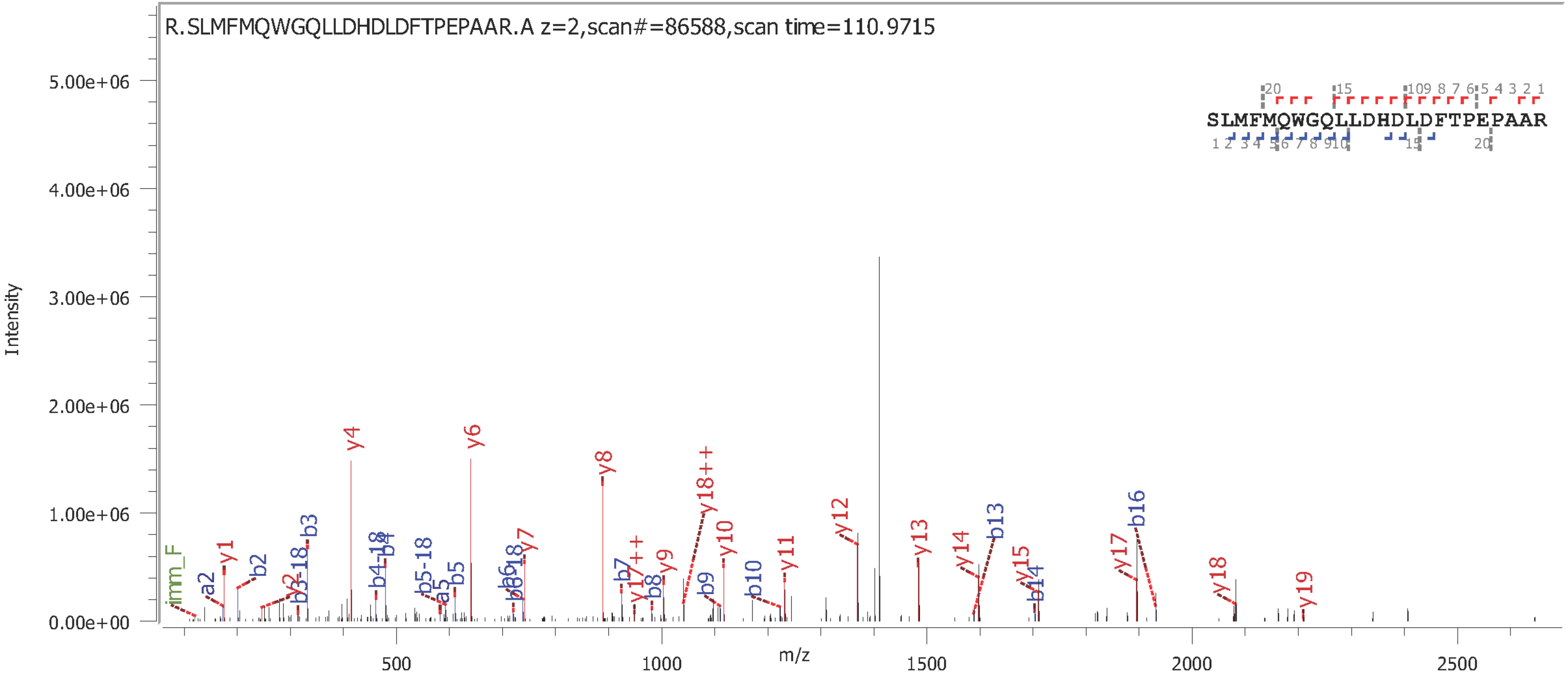
^{166}TCPEQDKYR (identification confidence level, PEP 2D: $3.3x10^{-8}$)



Human myeloperoxidase (P05164)

α-chain N-terminal (truncation variant)

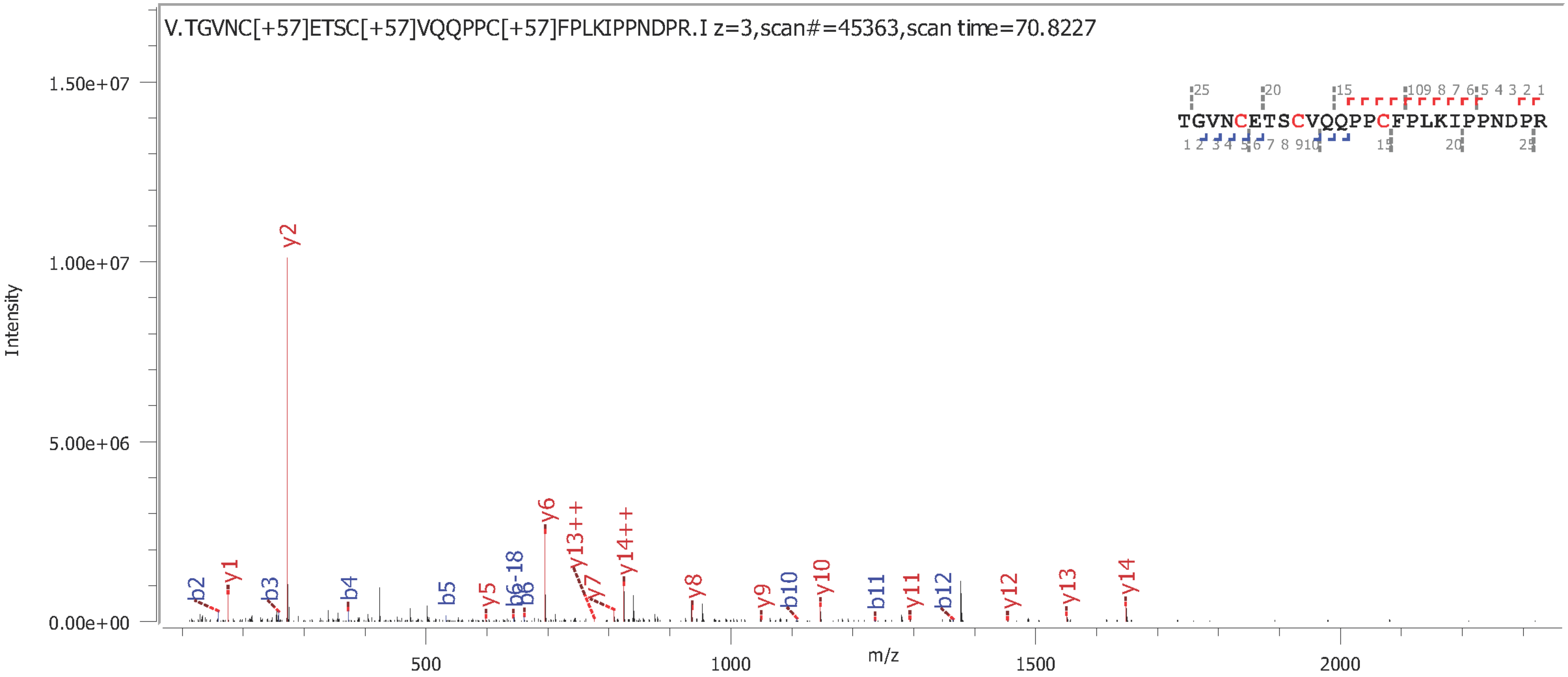
SLMFMQWGQLLDHDLDFTPEPAA**R**^{272} (identification confidence level, PEP 2D: 1.9×10^{-23})



Human myeloperoxidase (P05164)

β-chain N-terminal (truncation variant)

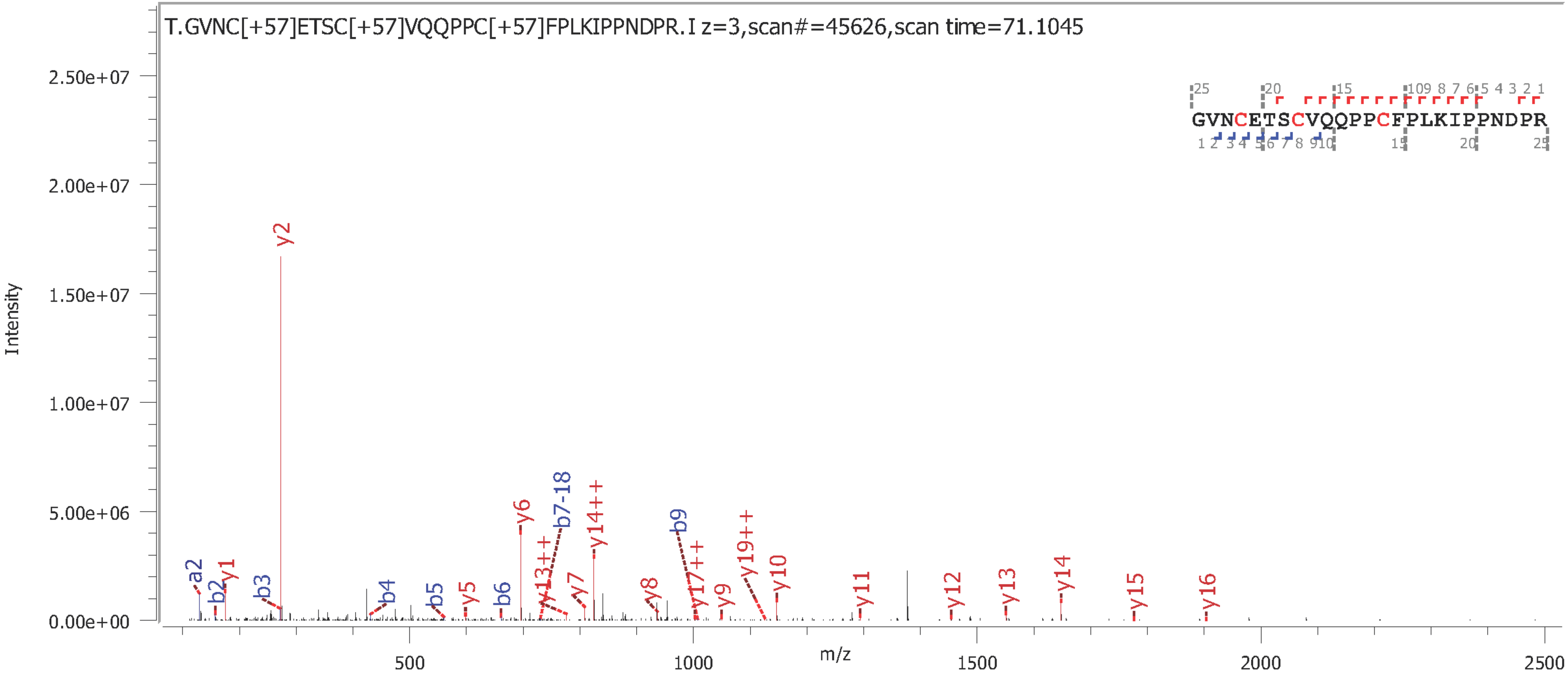
^{277}TGVNCETSCVQQPPCFPLKIPPNDPR (identification confidence level, PEP 2D: 8.7x10^{-14})



Human myeloperoxidase (P05164)

β-chain N-termini (truncation variant)

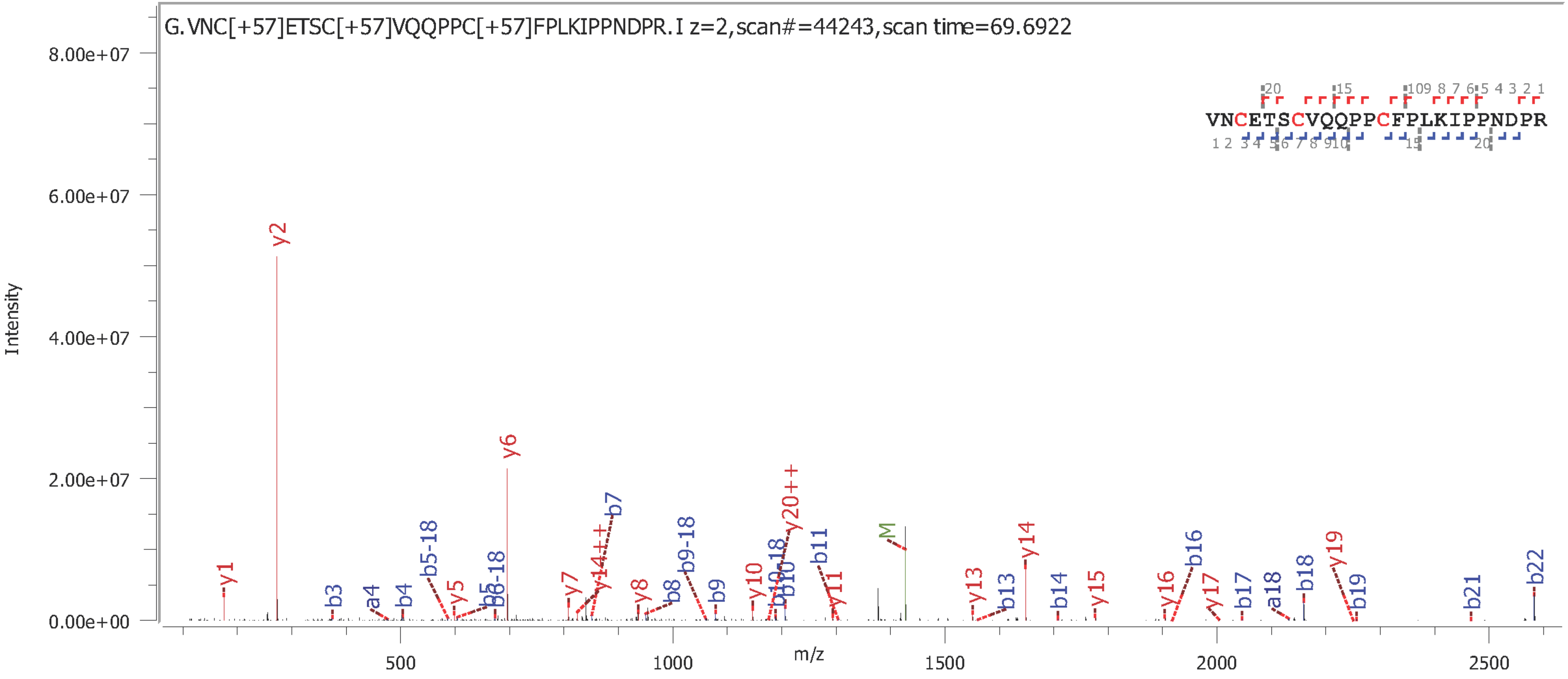
^{278}GVNCETSCVQQPPCFPLKIPPNDPR (identification confidence level, PEP 2D: 1.1x10^{-15})



Human myeloperoxidase (P05164)

β-chain N-terminal (truncation variant)

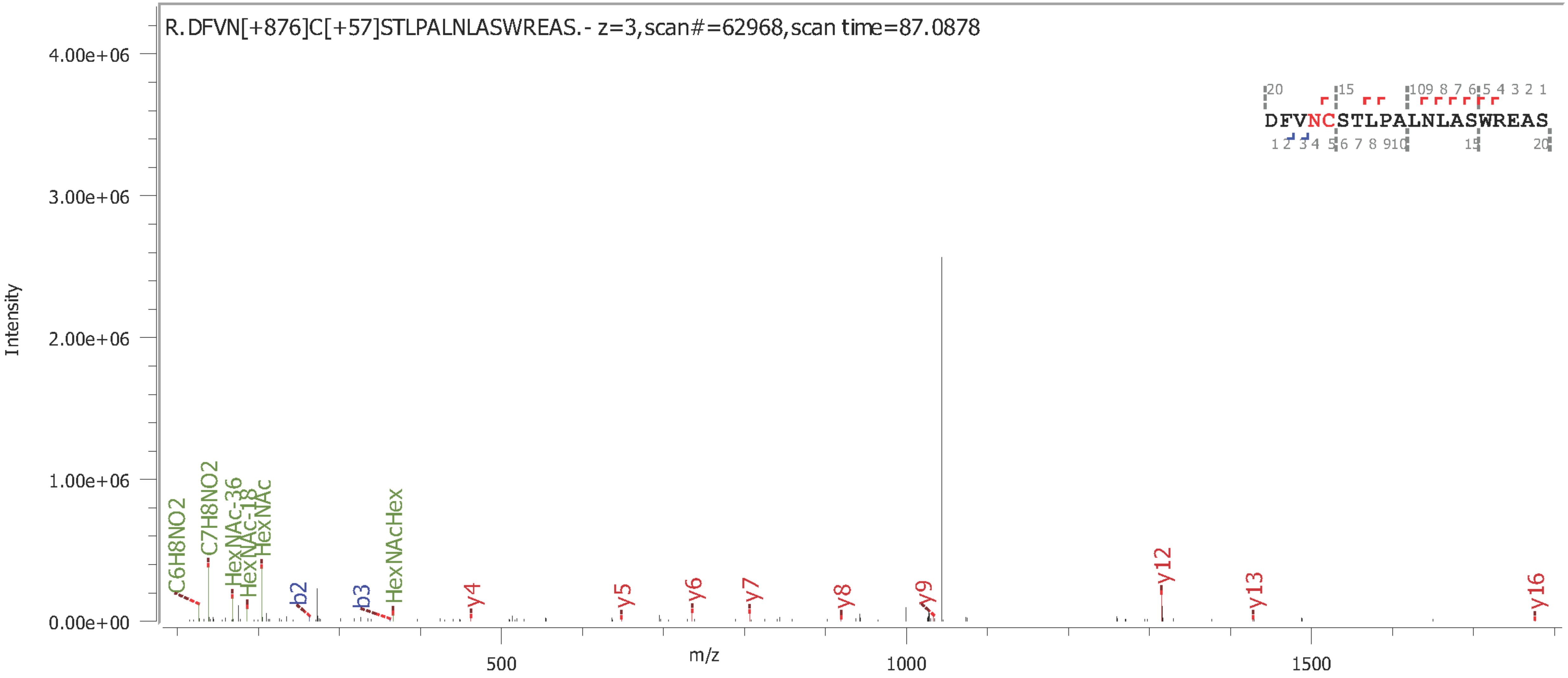
^{279}VNCETSCVQQPPCFPLKIPPNDPR (identification confidence level, PEP 2D: 1.5x10^{-17})



Human myeloperoxidase (P05164)

β-chain C-terminal

DFVNCSTLPALNLASWREA**S**^{745} (identification confidence level, PEP 2D: 1.4x10^{-8})

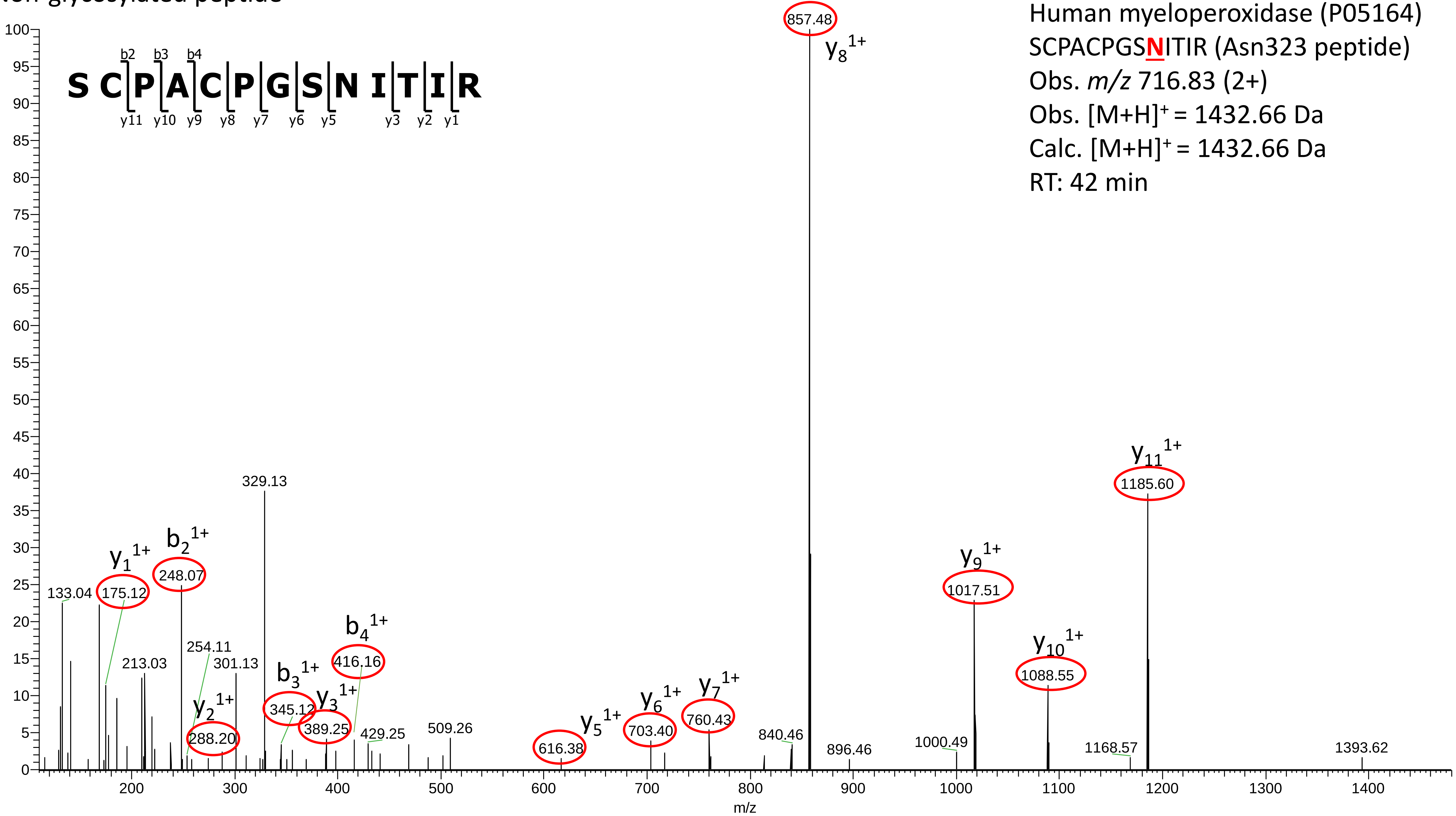


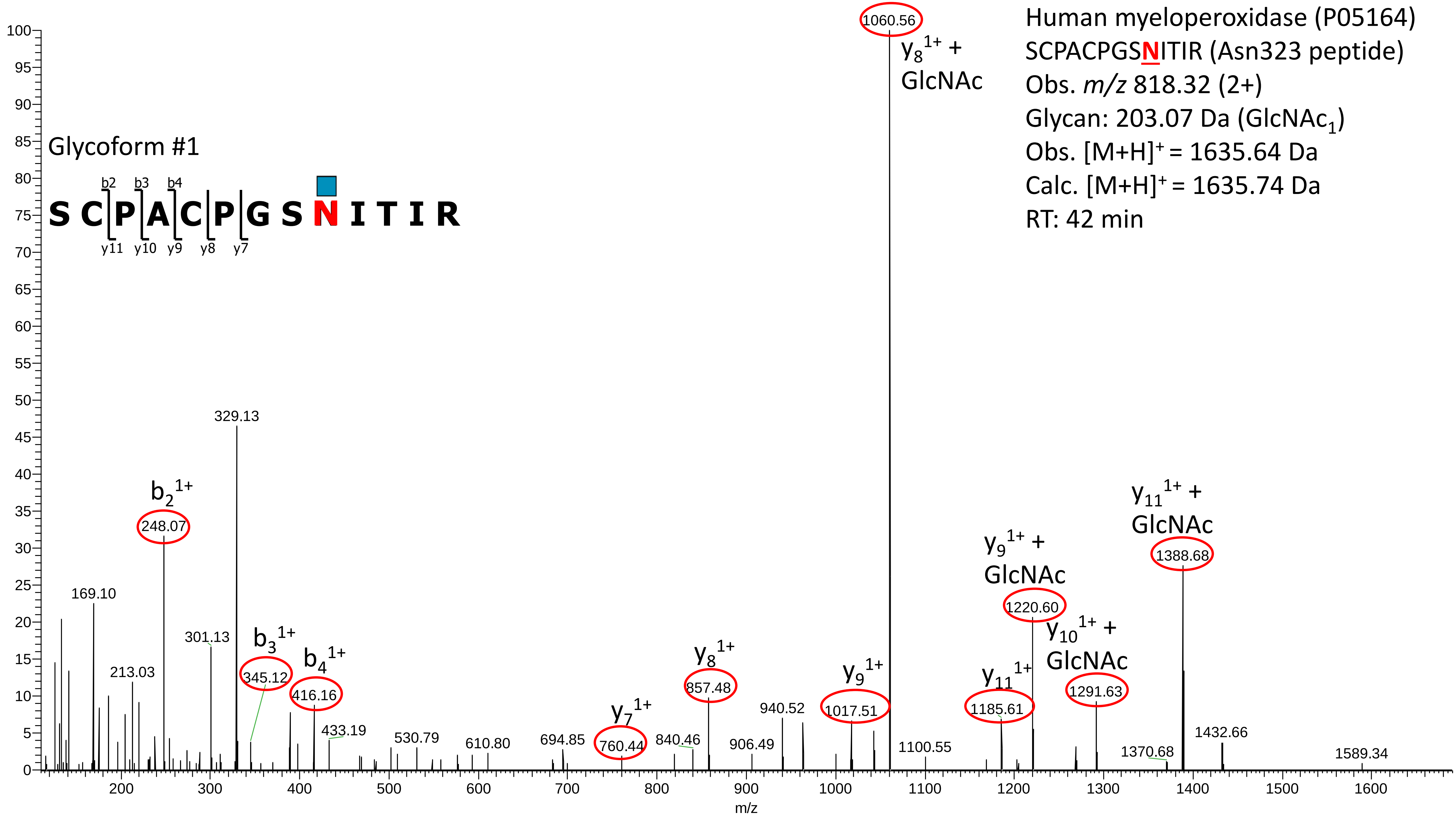
Supplementary Data S3A

Manually annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of all glycosylated and non-glycosylated peptides containing Asn323 identified from the analysis of the unenriched peptide mixtures of nMPO.

Non-glycosylated peptide

Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 716.83 (2+)
Obs. $[M+H]^+$ = 1432.66 Da
Calc. $[M+H]^+$ = 1432.66 Da
RT: 42 min

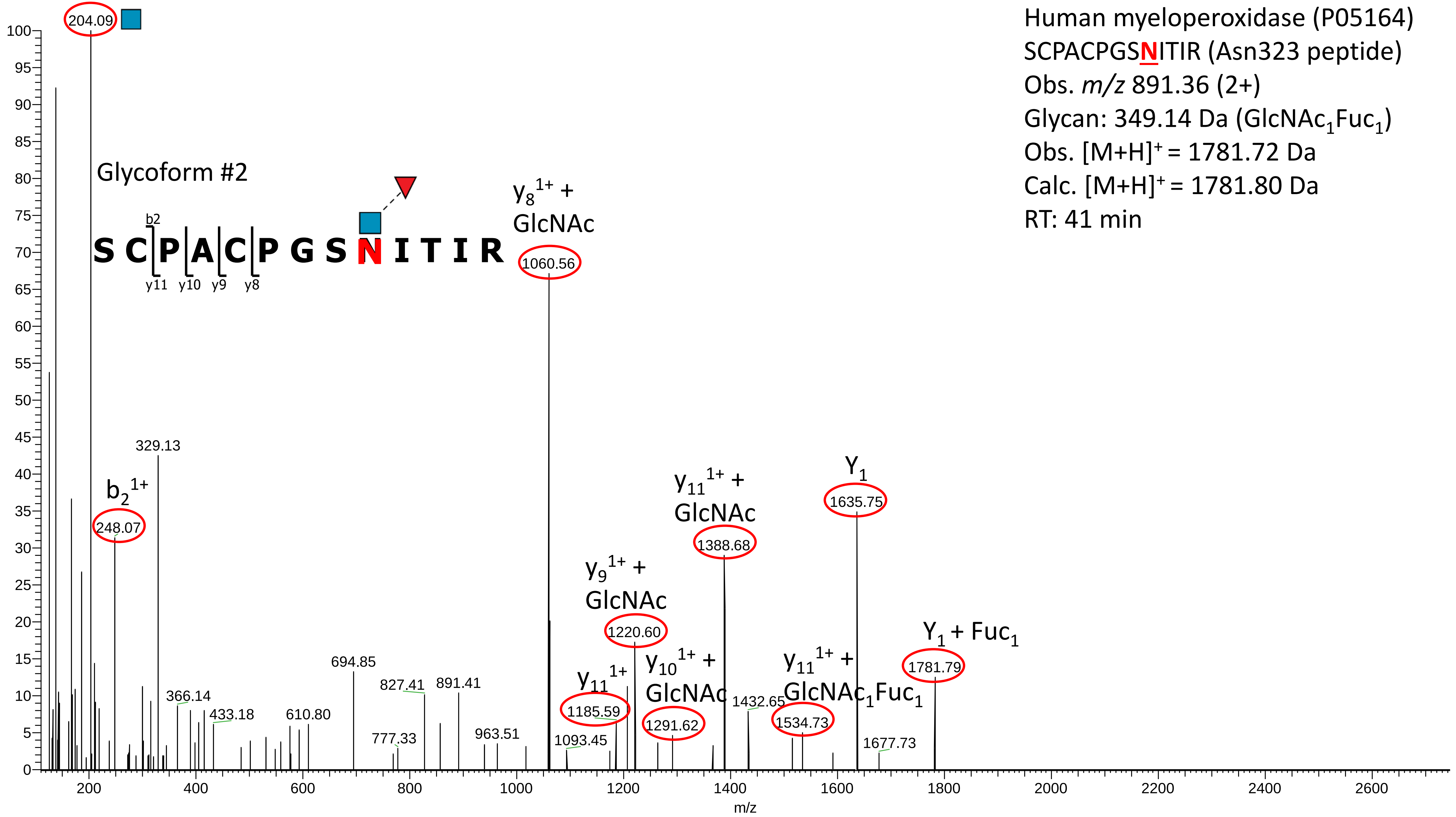




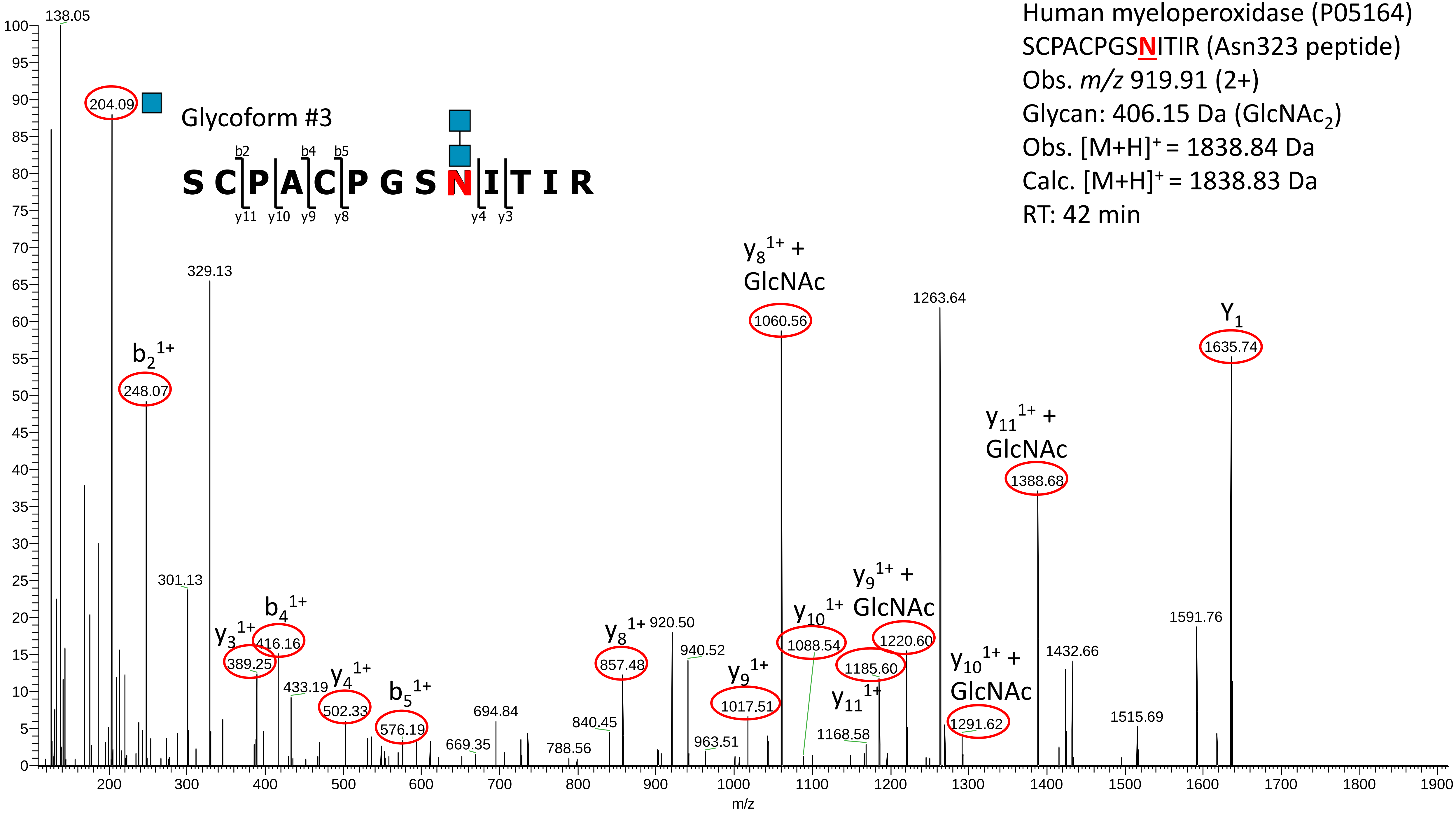
Glycoform #1

Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 818.32 (2+)
Glycan: 203.07 Da ($GlcNAc_1$)
Obs. $[M+H]^+$ = 1635.64 Da
Calc. $[M+H]^+$ = 1635.74 Da
RT: 42 min

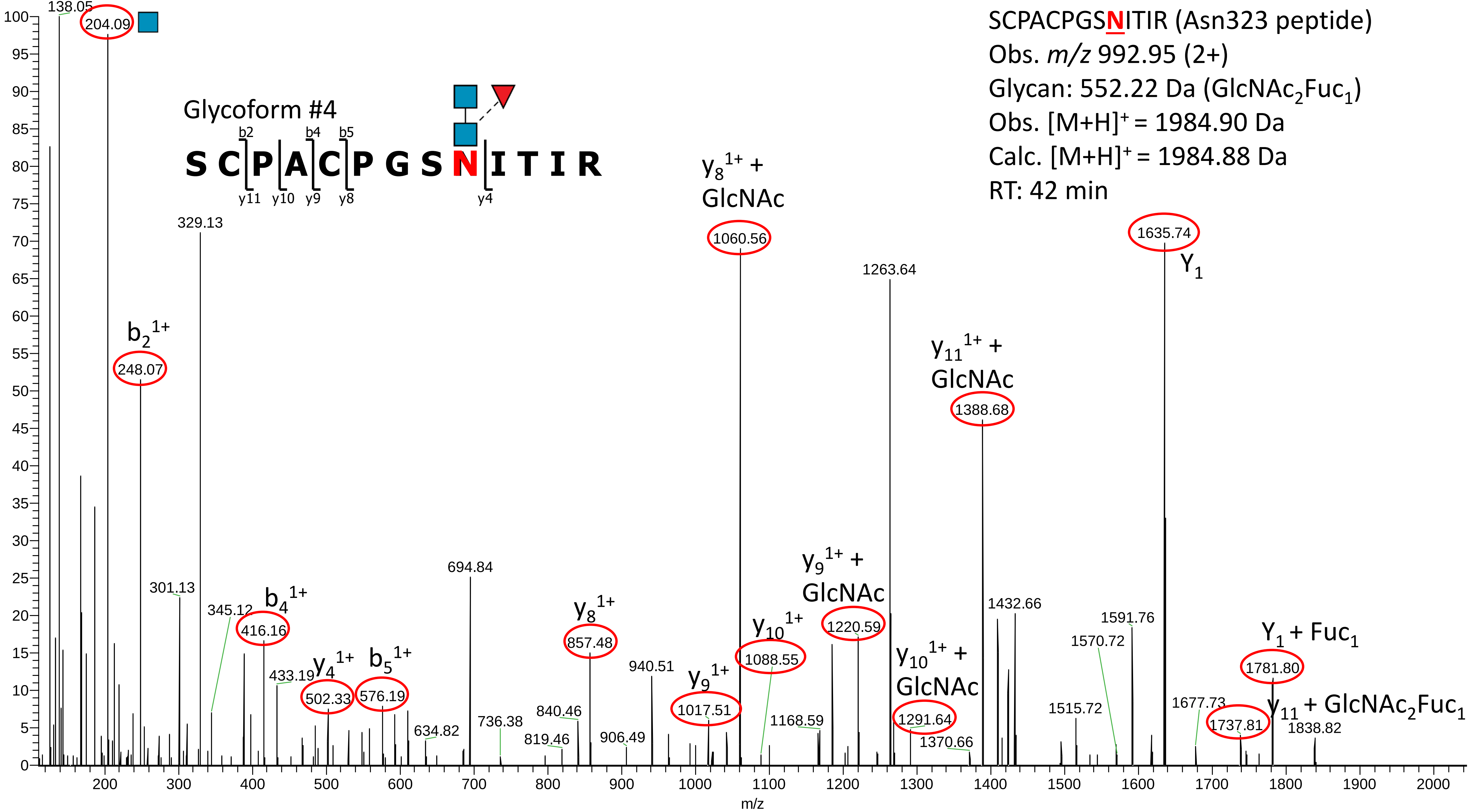
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 891.36 (2+)
Glycan: 349.14 Da ($GlcNAc_1Fuc_1$)
Obs. $[M+H]^+$ = 1781.72 Da
Calc. $[M+H]^+$ = 1781.80 Da
RT: 41 min



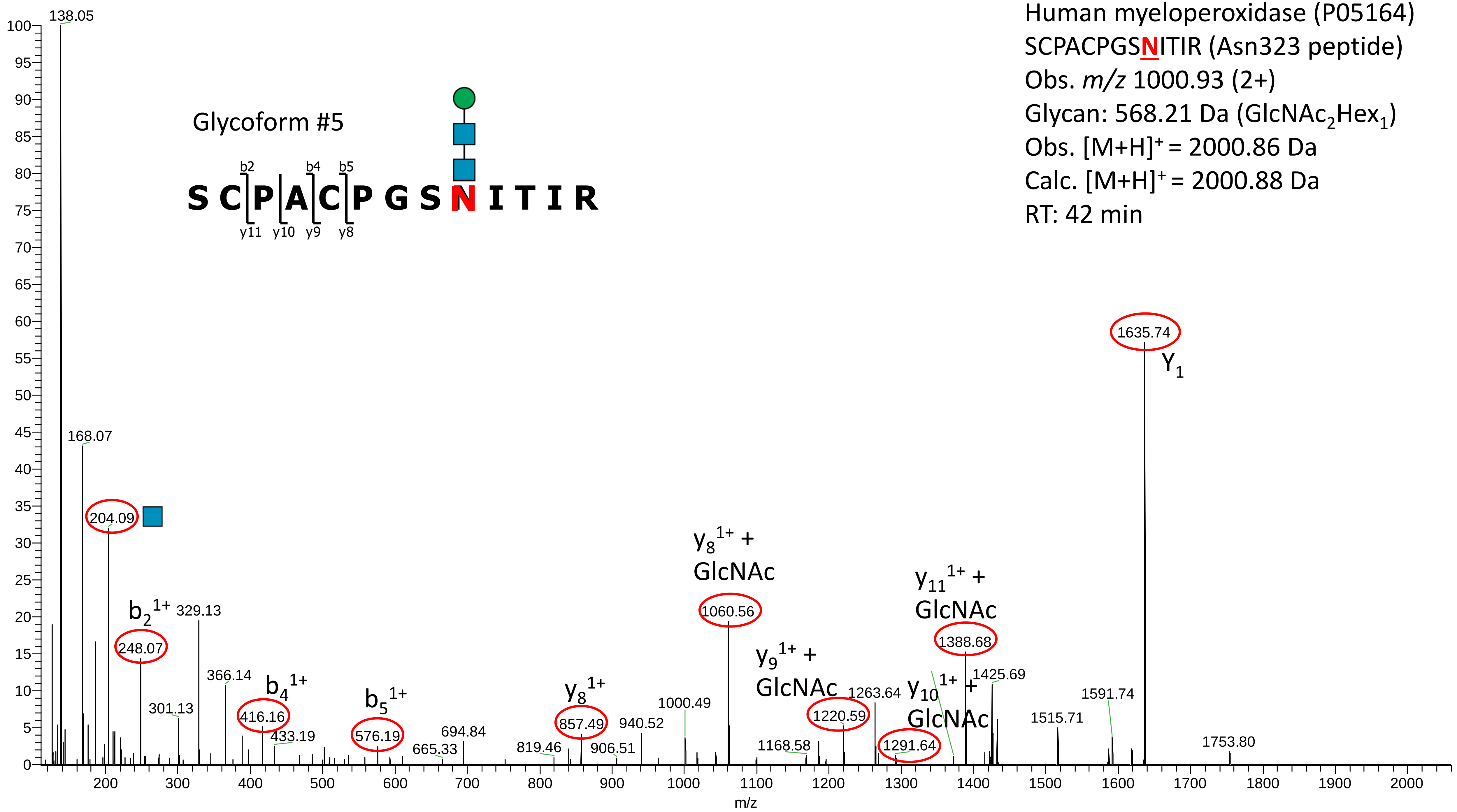
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 919.91 (2+)
Glycan: 406.15 Da (GlcNAc$_2$)
Obs. $[M+H]^+$ = 1838.84 Da
Calc. $[M+H]^+$ = 1838.83 Da
RT: 42 min



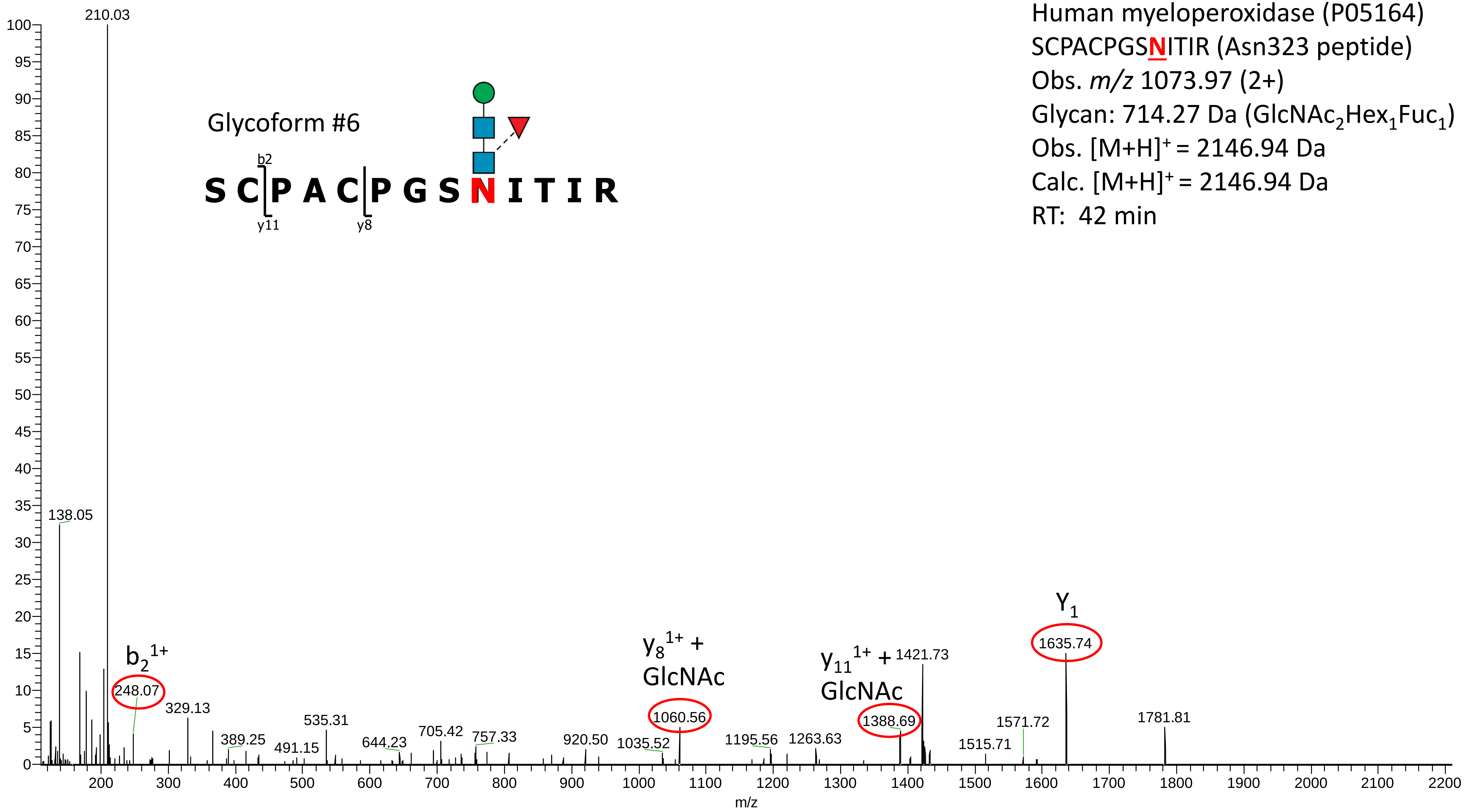
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 992.95 (2+)
Glycan: 552.22 Da ($\mathrm{GlcNAc_2Fuc_1}$)
Obs. $[\mathrm{M+H}]^+$ = 1984.90 Da
Calc. $[\mathrm{M+H}]^+$ = 1984.88 Da
RT: 42 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1000.93 (2+)
Glycan: 568.21 Da ($GlcNAc_2Hex_1$)
Obs. $[M+H]^+$ = 2000.86 Da
Calc. $[M+H]^+$ = 2000.88 Da
RT: 42 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1073.97 (2+)
Glycan: 714.27 Da ($GlcNAc_2Hex_1Fuc_1$)
Obs. $[M+H]^+$ = 2146.94 Da
Calc. $[M+H]^+$ = 2146.94 Da
RT: 42 min



Human myeloperoxidase (P05164)

SCPACPGS**N**ITIR (Asn323 peptide)

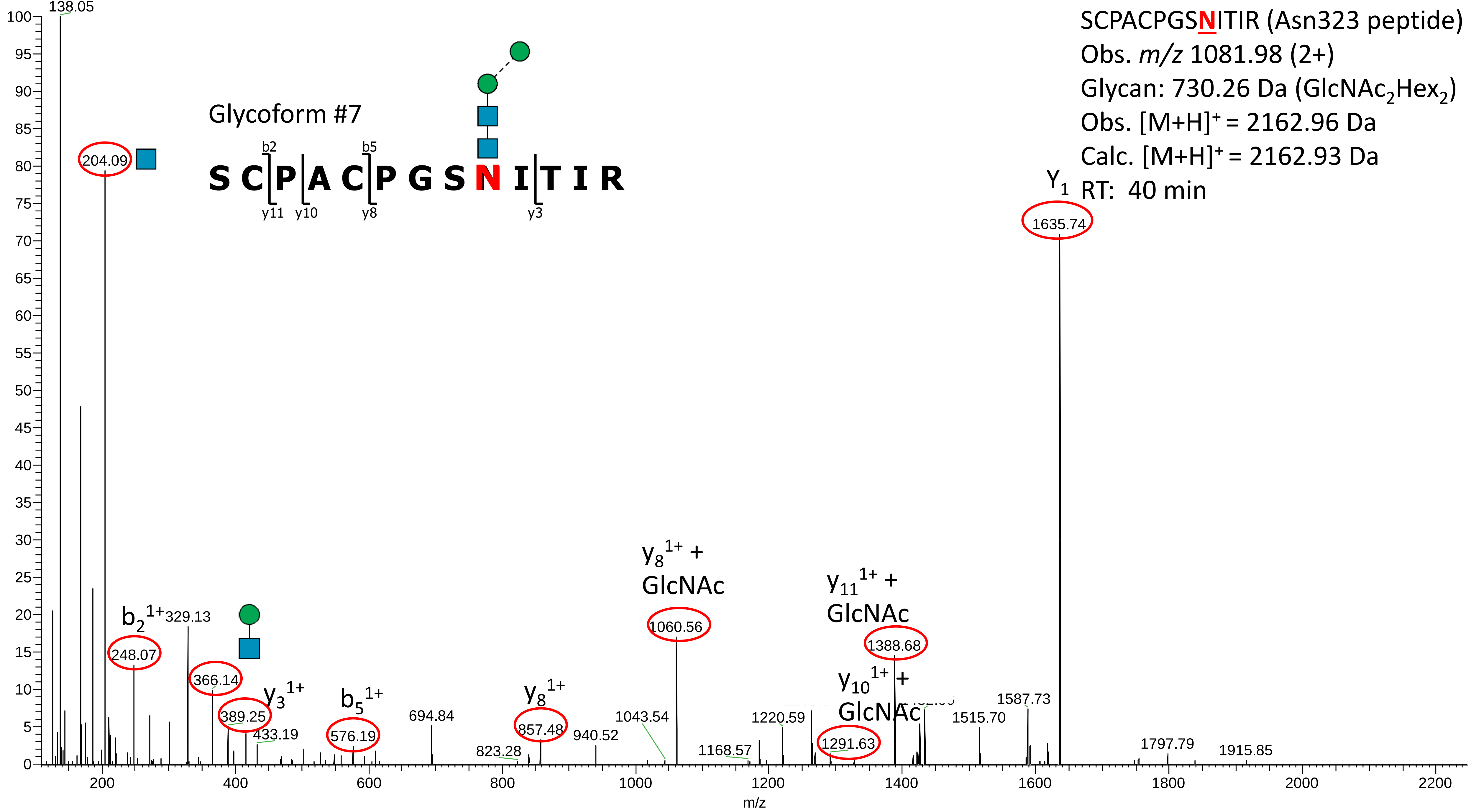
Obs. *m/z* 1081.98 (2+)

Glycan: 730.26 Da ($GlcNAc_2Hex_2$)

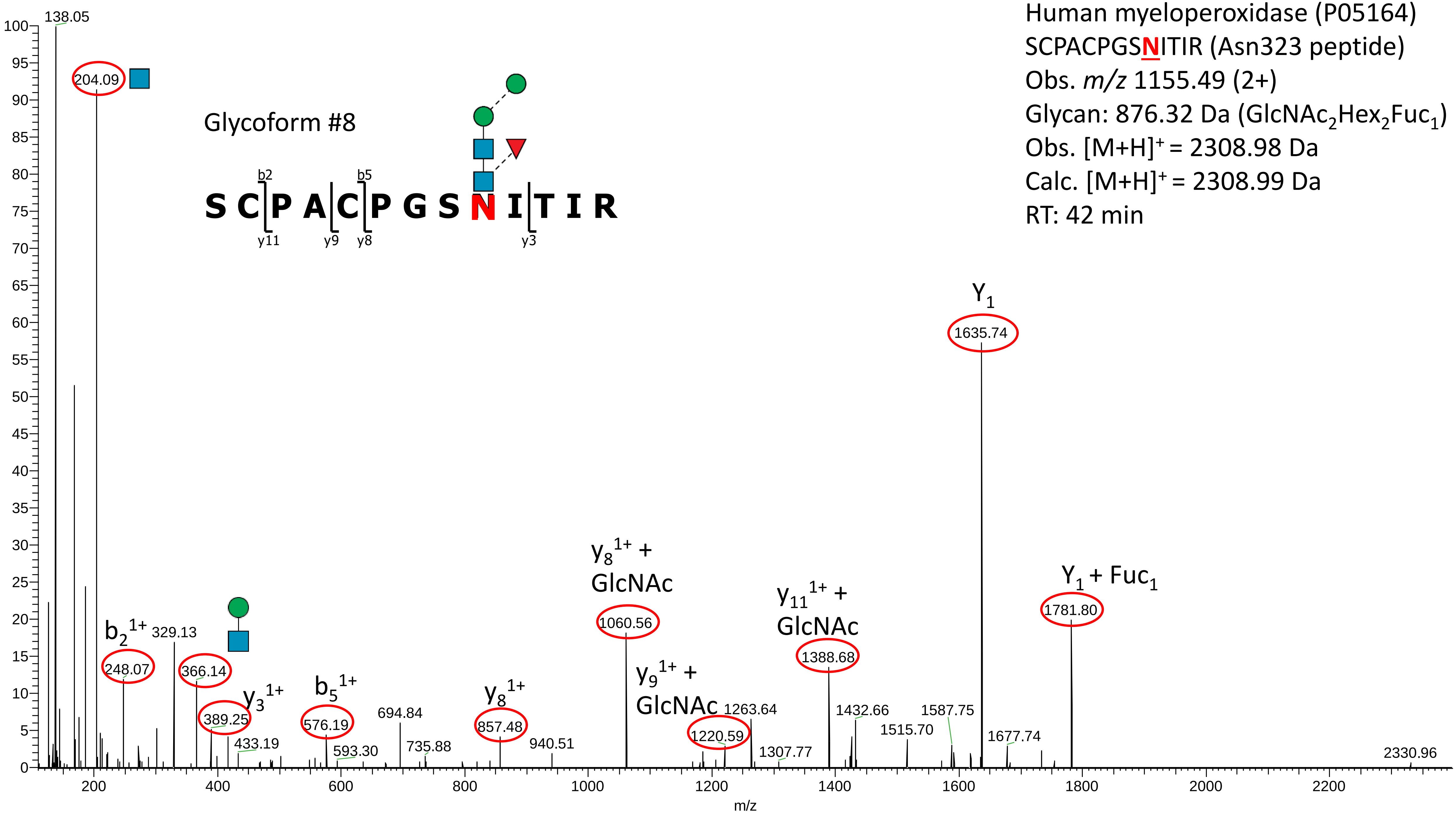
Obs. $[M+H]^+$ = 2162.96 Da

Calc. $[M+H]^+$ = 2162.93 Da

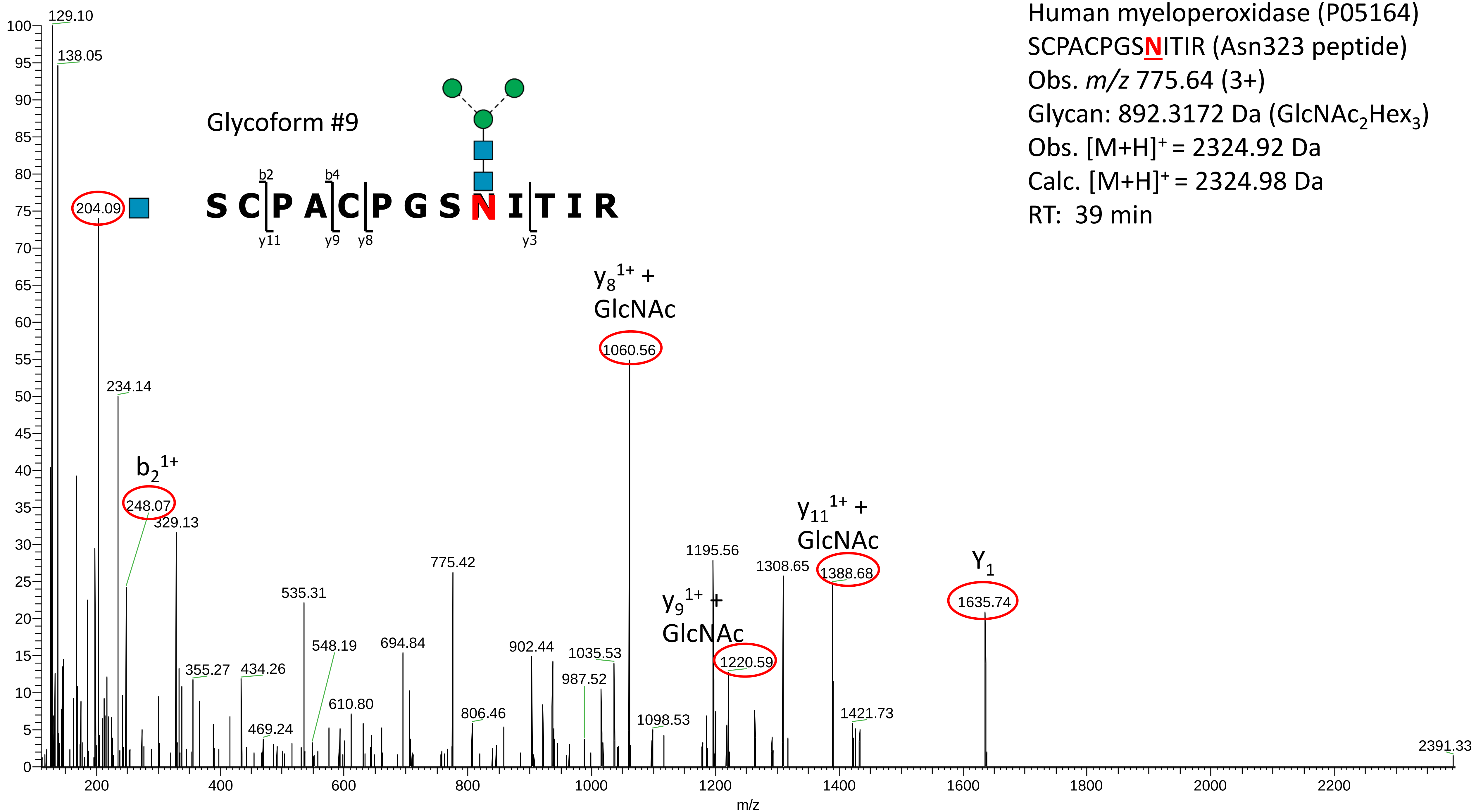
RT: 40 min



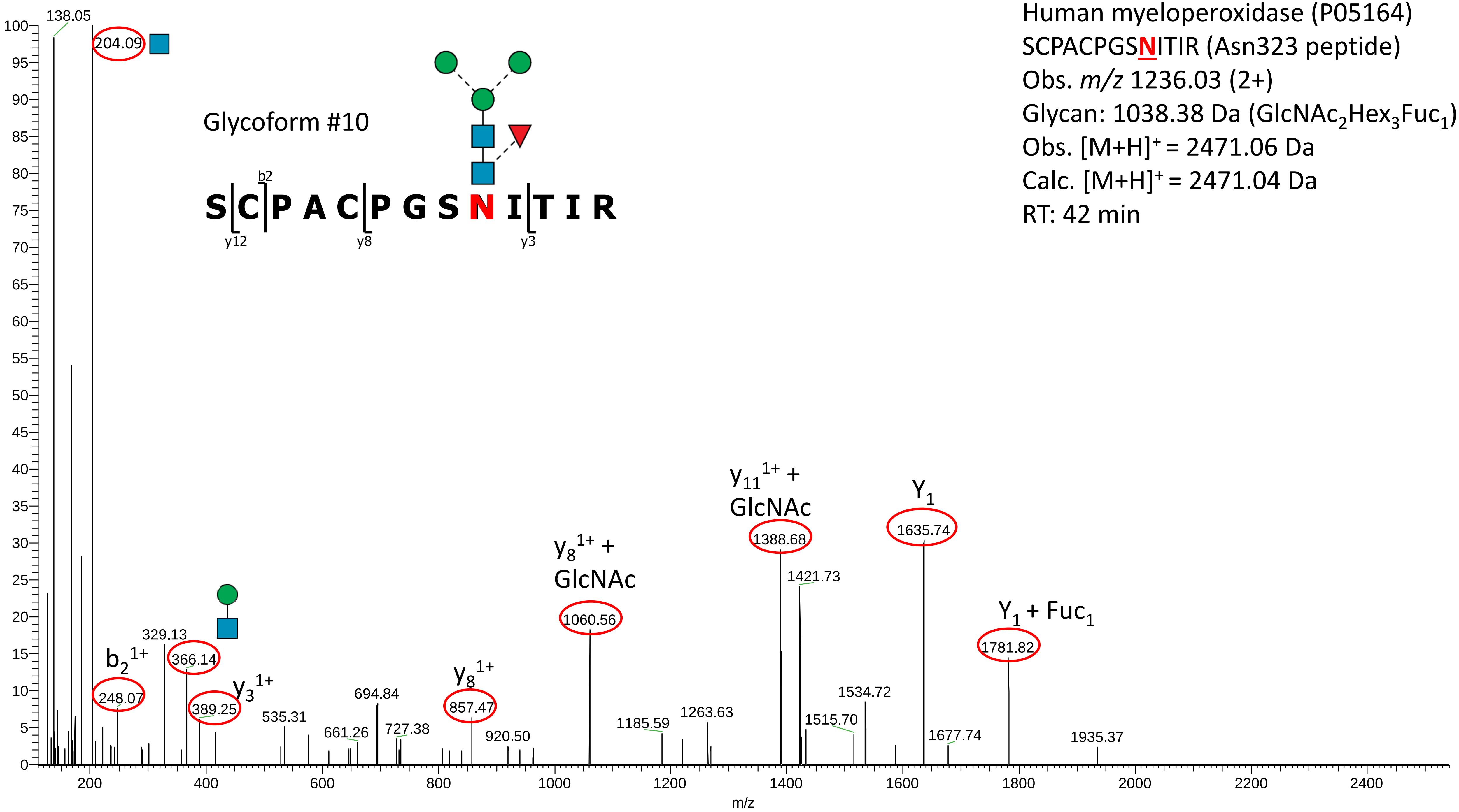
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1155.49 (2+)
Glycan: 876.32 Da (GlcNAc$_2$Hex$_2$Fuc$_1$)
Obs. $[M+H]^+$ = 2308.98 Da
Calc. $[M+H]^+$ = 2308.99 Da
RT: 42 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 775.64 (3+)
Glycan: 892.3172 Da ($GlcNAc_2Hex_3$)
Obs. $[M+H]^+$ = 2324.92 Da
Calc. $[M+H]^+$ = 2324.98 Da
RT: 39 min

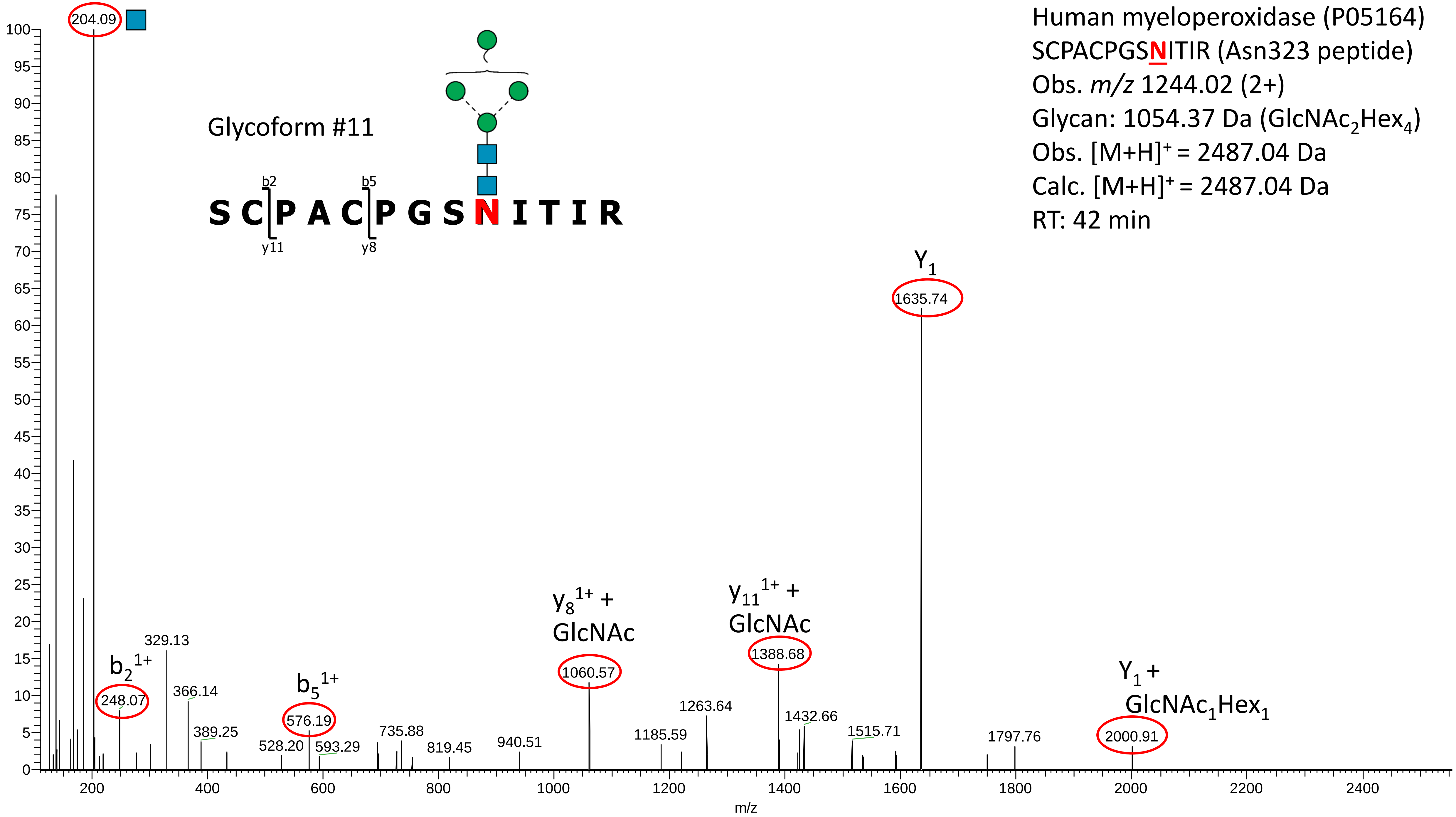


Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1236.03 (2+)
Glycan: 1038.38 Da (GlcNAc$_2$Hex$_3$Fuc$_1$)
Obs. [M+H]$^+$ = 2471.06 Da
Calc. [M+H]$^+$ = 2471.04 Da
RT: 42 min

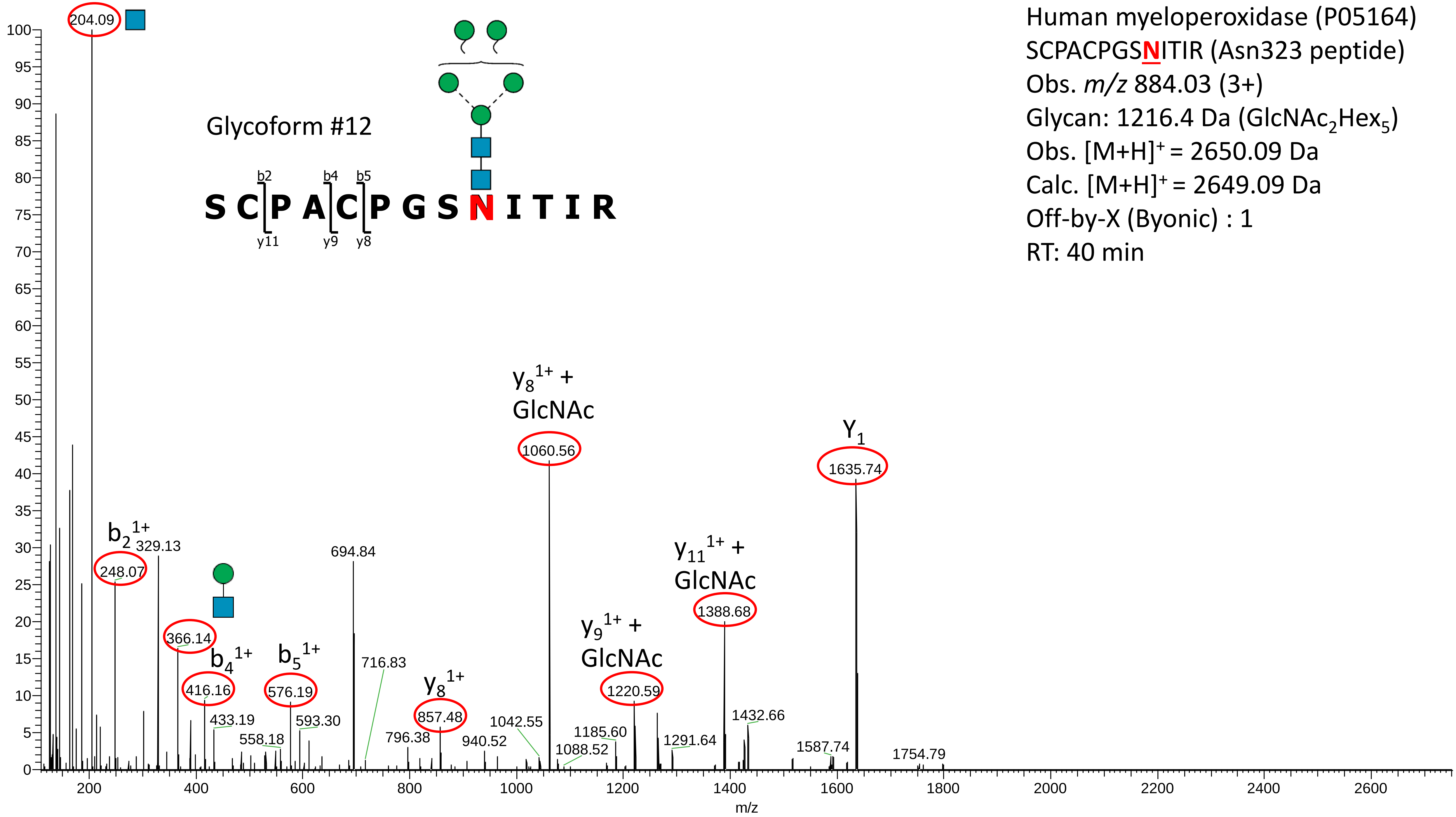


Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1244.02 (2+)
Glycan: 1054.37 Da (GlcNAc$_2$Hex$_4$)
Obs. [M+H]$^+$ = 2487.04 Da
Calc. [M+H]$^+$ = 2487.04 Da
RT: 42 min

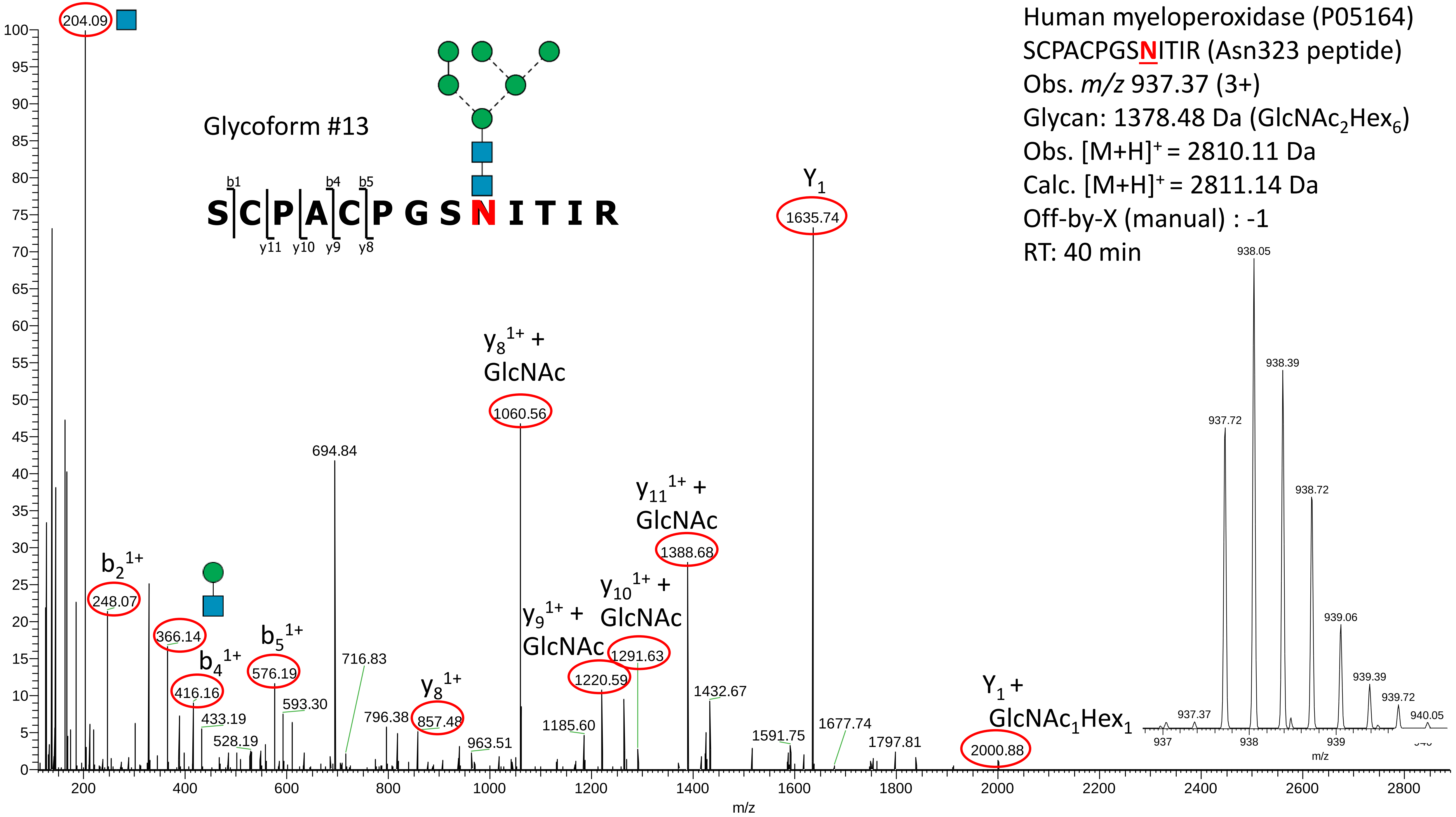
Glycoform #11



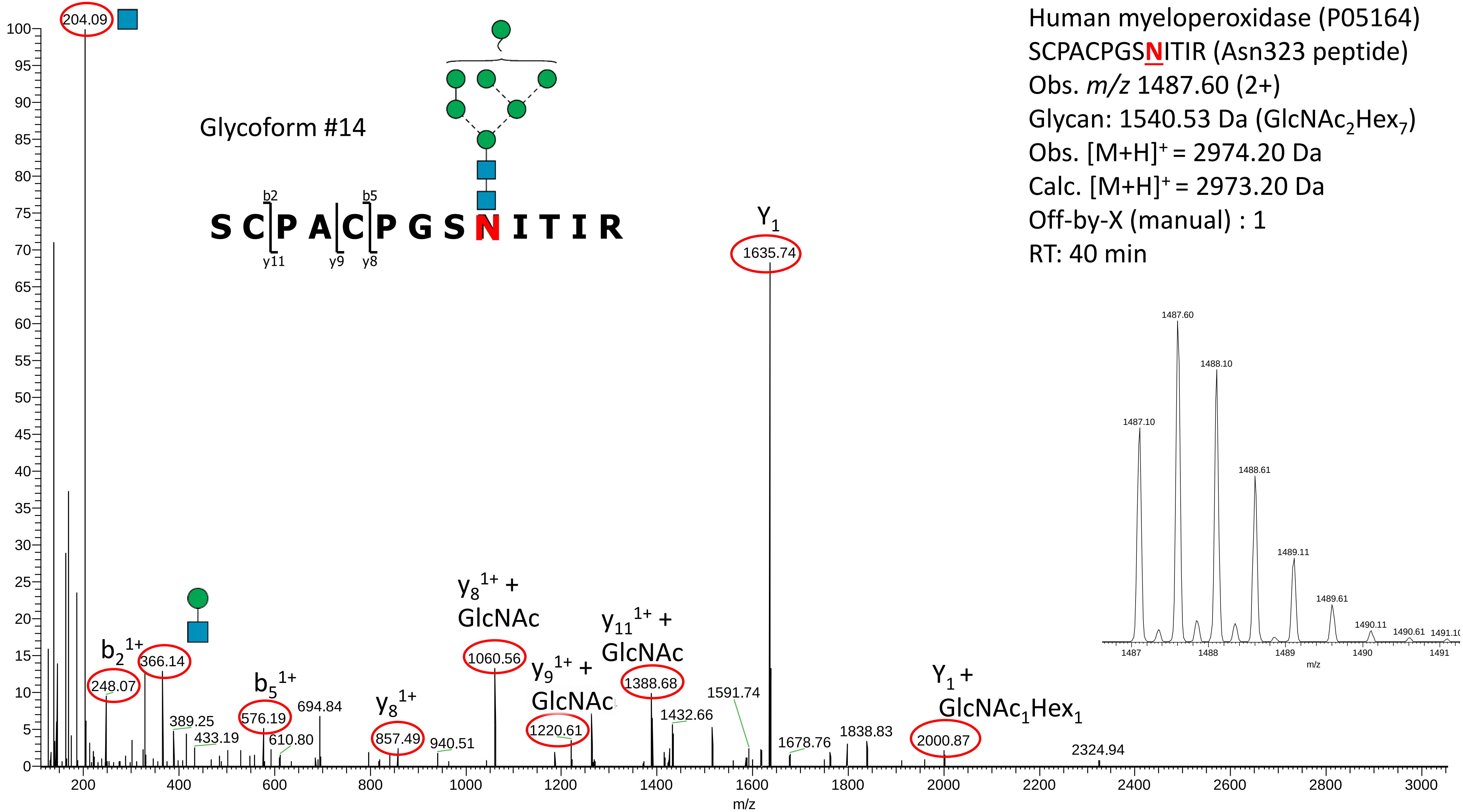
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 884.03 (3+)
Glycan: 1216.4 Da (GlcNAc$_2$Hex$_5$)
Obs. [M+H]$^+$ = 2650.09 Da
Calc. [M+H]$^+$ = 2649.09 Da
Off-by-X (Byonic) : 1
RT: 40 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 937.37 (3+)
Glycan: 1378.48 Da (GlcNAc$_2$Hex$_6$)
Obs. [M+H]$^+$ = 2810.11 Da
Calc. [M+H]$^+$ = 2811.14 Da
Off-by-X (manual) : -1
RT: 40 min

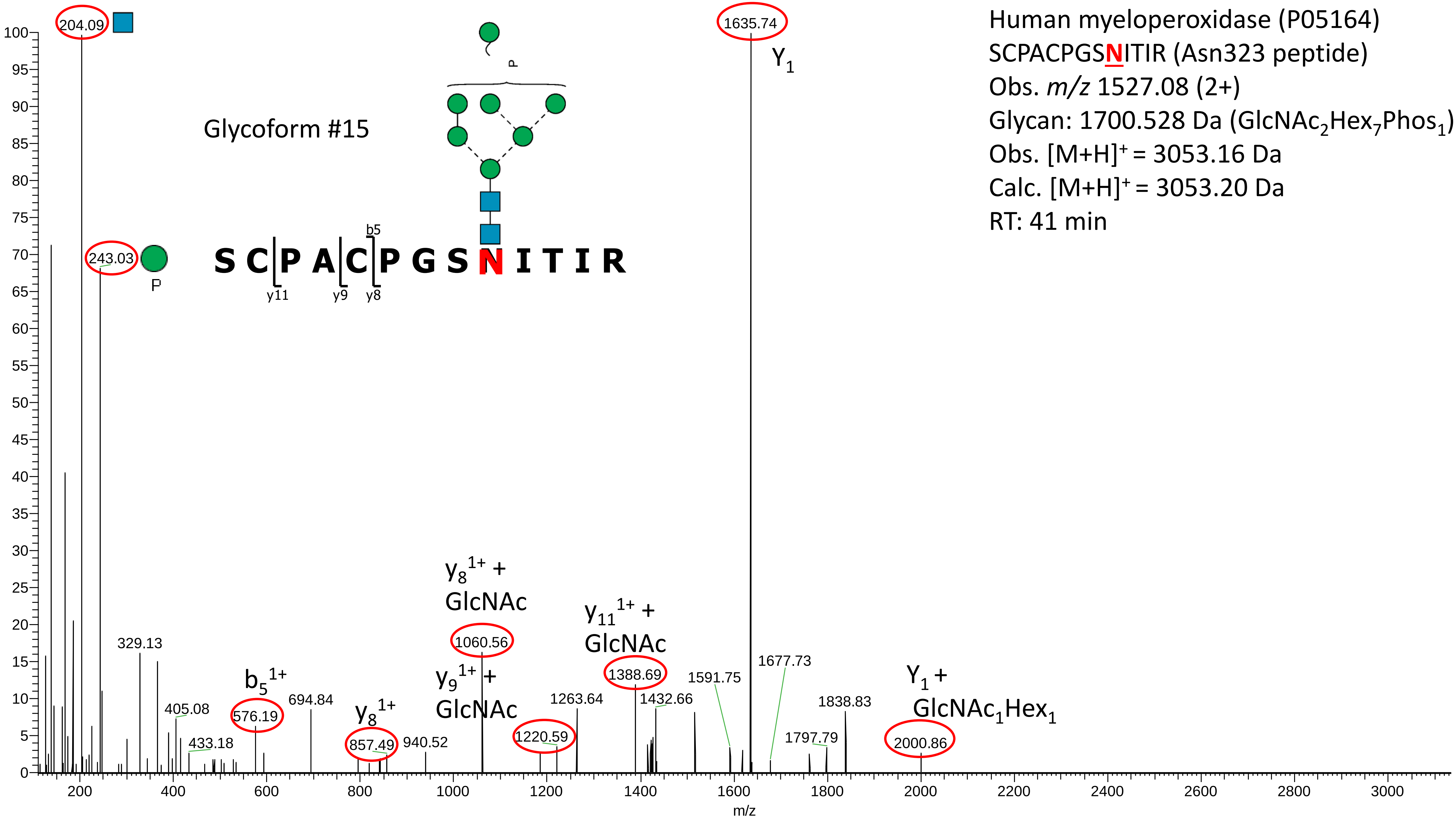


Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1487.60 (2+)
Glycan: 1540.53 Da ($GlcNAc_2Hex_7$)
Obs. $[M+H]^+$ = 2974.20 Da
Calc. $[M+H]^+$ = 2973.20 Da
Off-by-X (manual) : 1
RT: 40 min



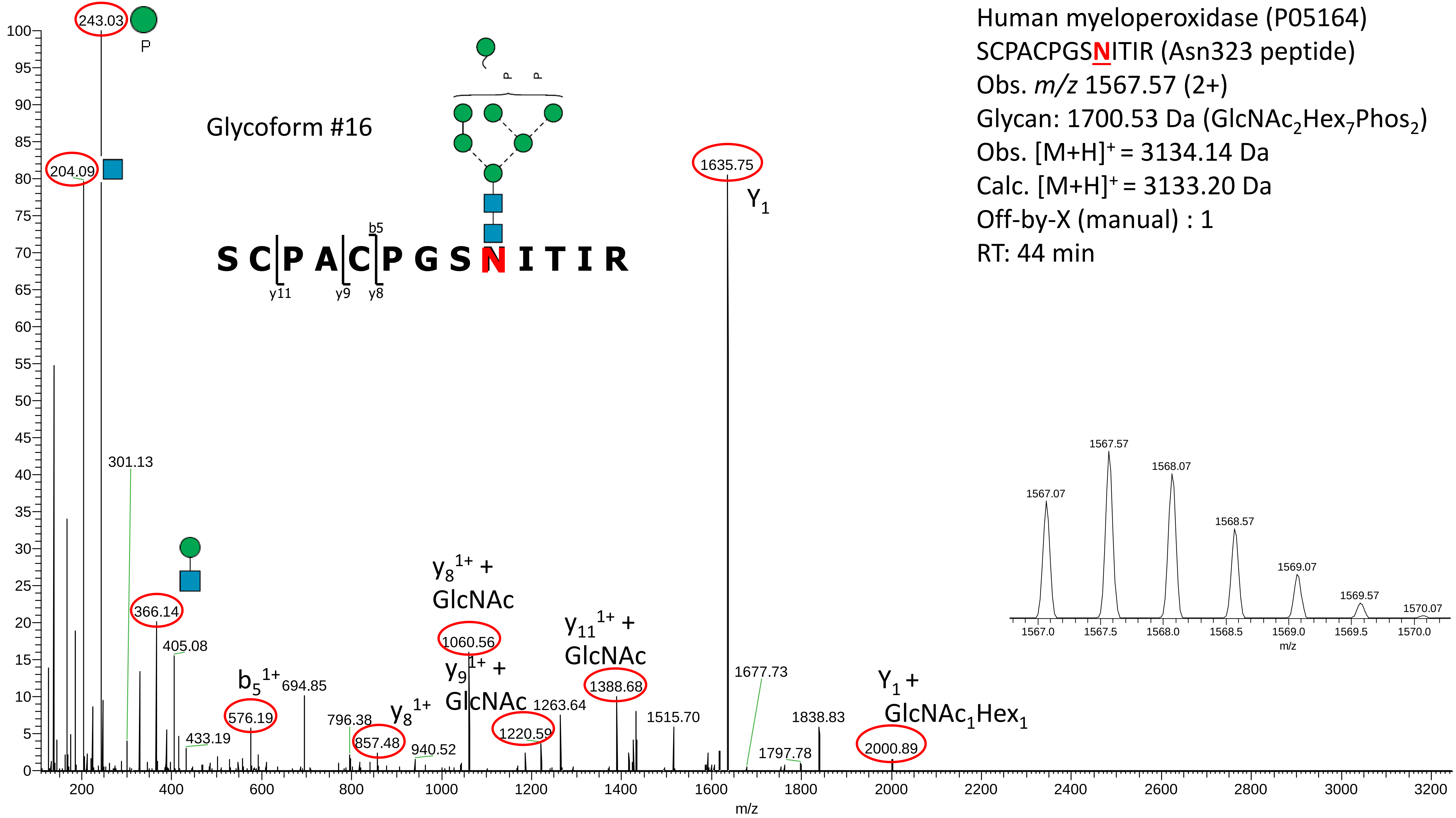
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1527.08 (2+)
Glycan: 1700.528 Da ($GlcNAc_2Hex_7Phos_1$)
Obs. $[M+H]^+$ = 3053.16 Da
Calc. $[M+H]^+$ = 3053.20 Da
RT: 41 min

Glycoform #15

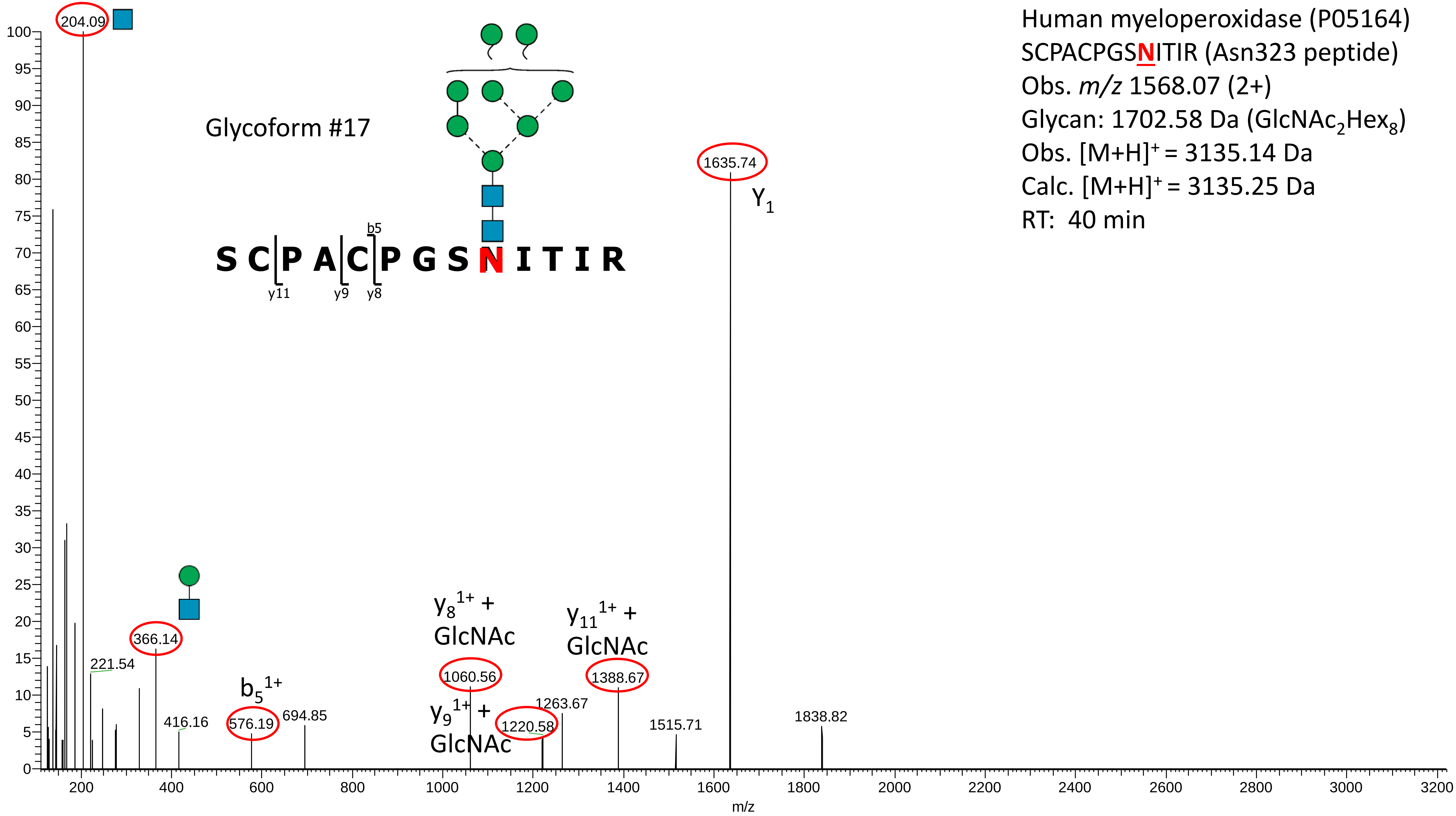


Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1567.57 (2+)
Glycan: 1700.53 Da ($GlcNAc_2Hex_7Phos_2$)
Obs. $[M+H]^+$ = 3134.14 Da
Calc. $[M+H]^+$ = 3133.20 Da
Off-by-X (manual) : 1
RT: 44 min

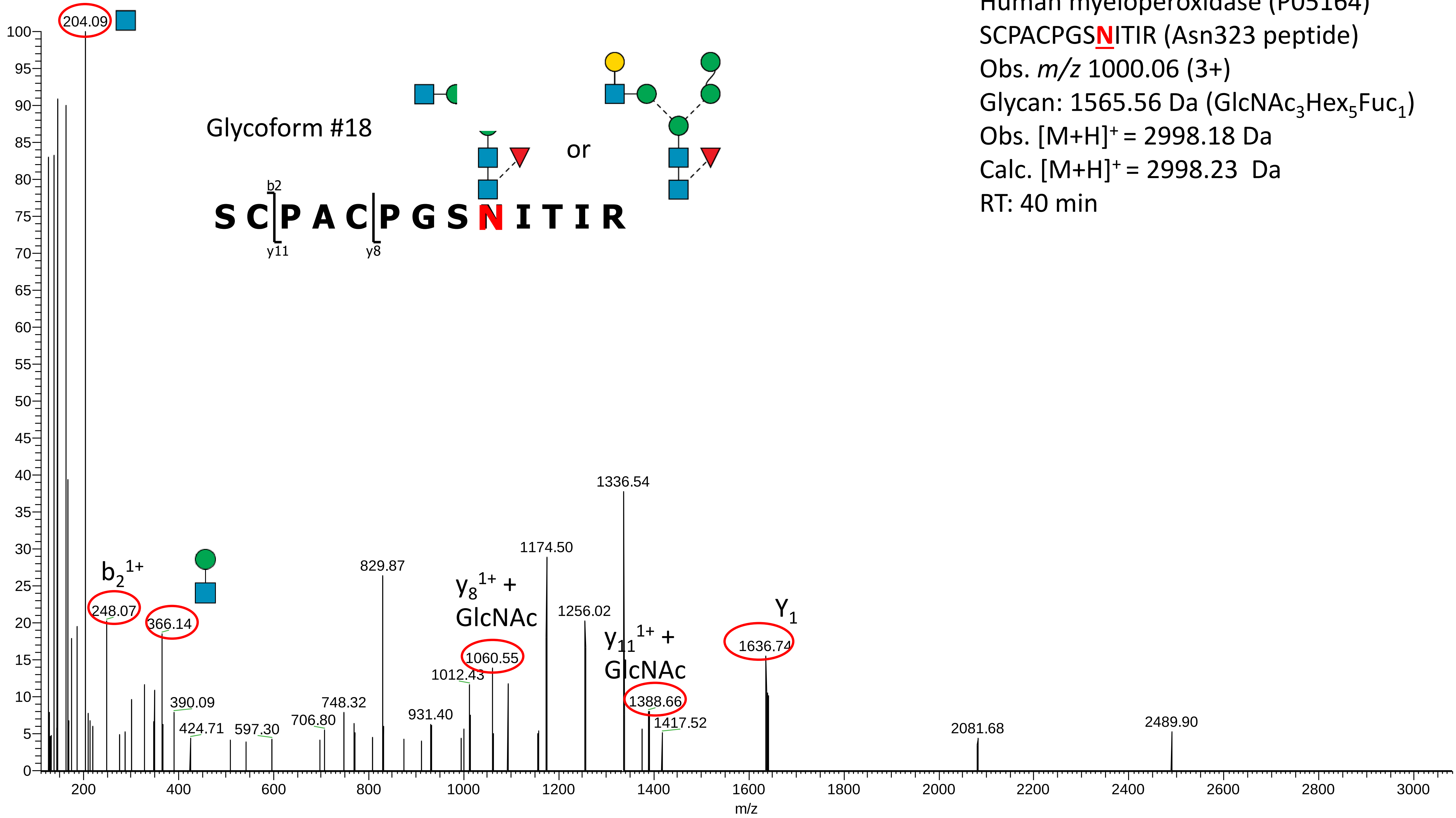
Glycoform #16



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1568.07 (2+)
Glycan: 1702.58 Da ($GlcNAc_2Hex_8$)
Obs. $[M+H]^+$ = 3135.14 Da
Calc. $[M+H]^+$ = 3135.25 Da
RT: 40 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1000.06 (3+)
Glycan: 1565.56 Da ($GlcNAc_3Hex_5Fuc_1$)
Obs. $[M+H]^+$ = 2998.18 Da
Calc. $[M+H]^+$ = 2998.23 Da
RT: 40 min



Human myeloperoxidase (P05164)

SCPACPGS**N**ITIR (Asn323 peptide)

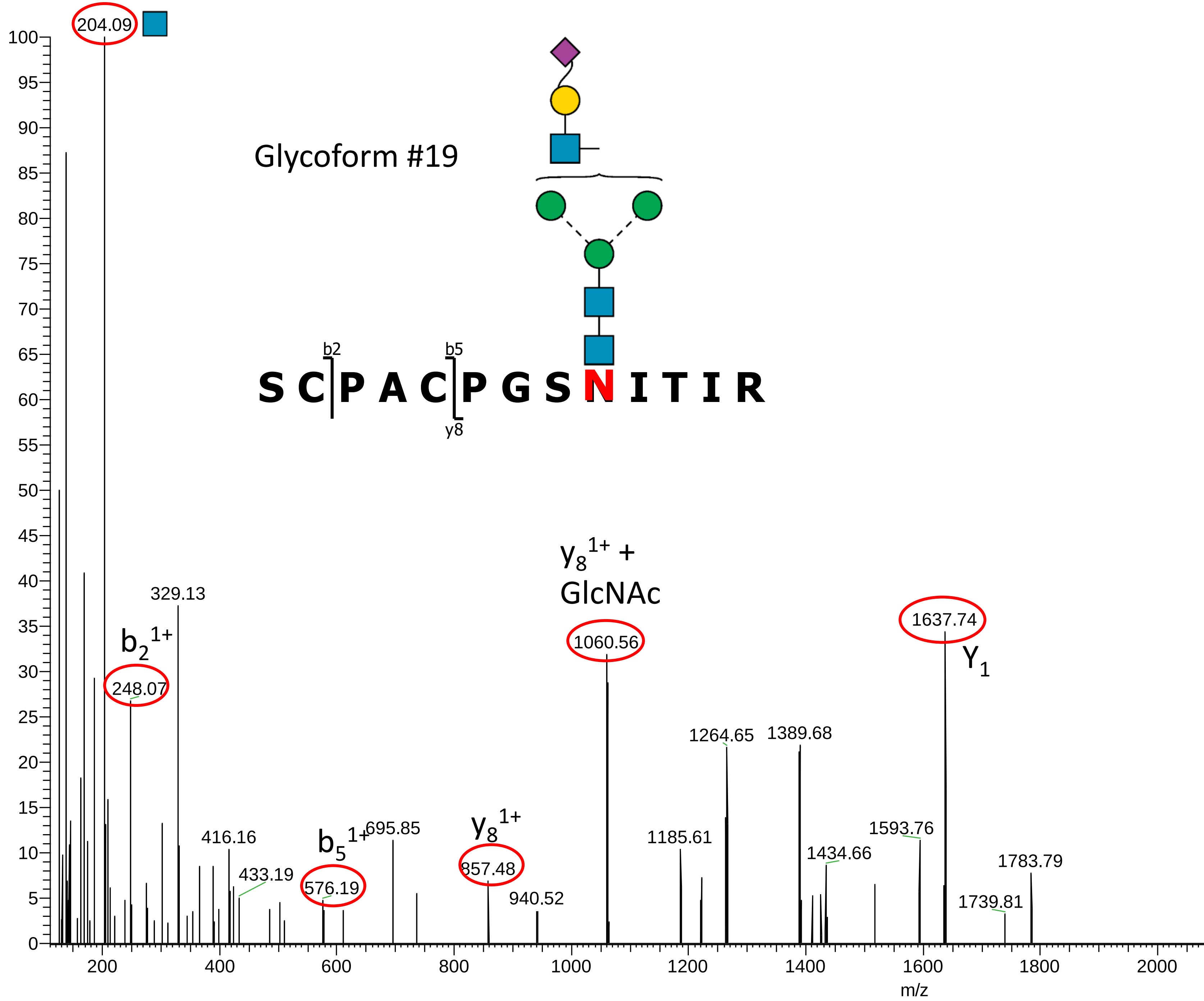
Obs. *m/z* 994.39 (3+)

Glycan: 1548.55 Da ($GlcNAc_3Hex_4NeuAc_1$)

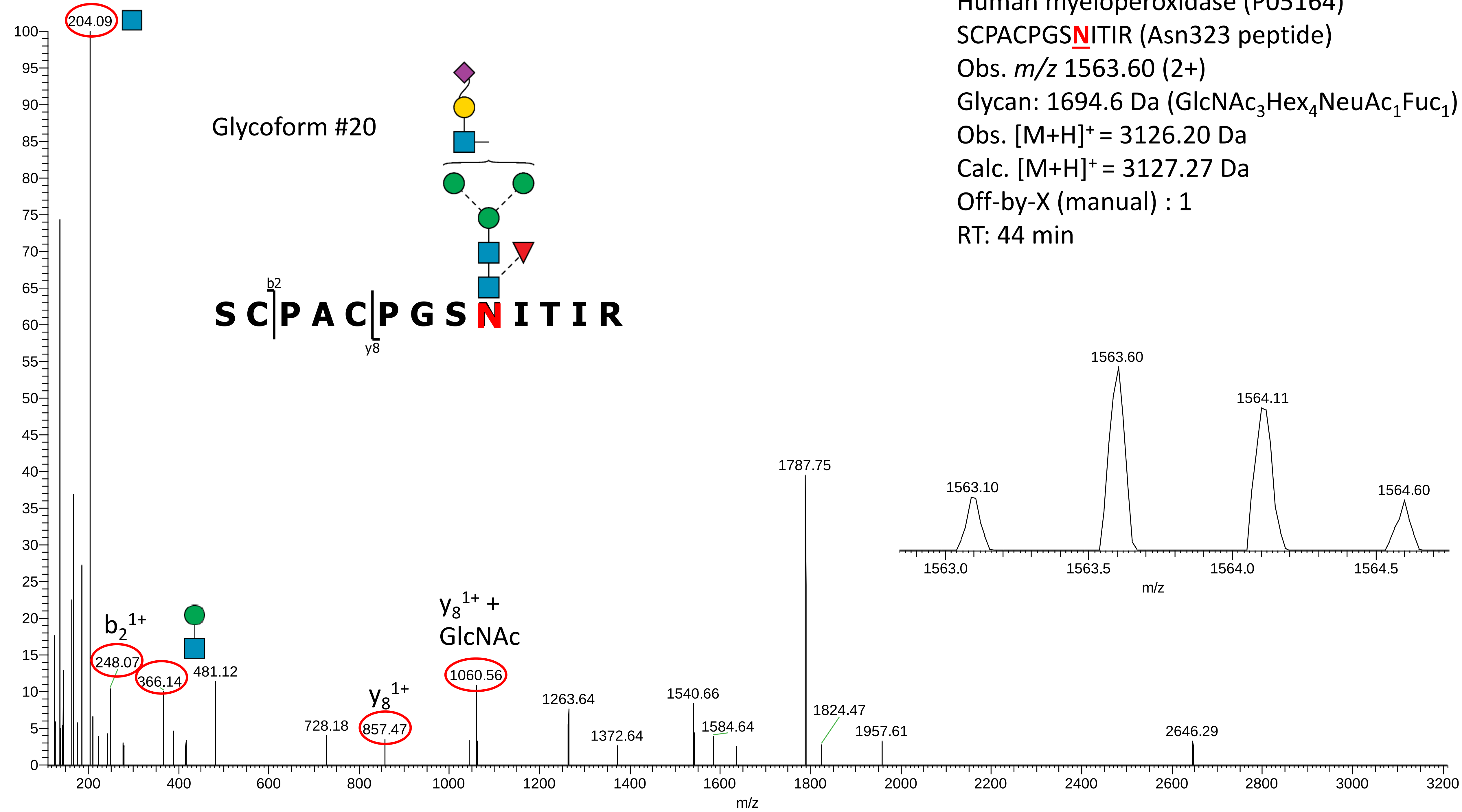
Obs. $[M+H]^+$ = 2981.17 Da

Calc. $[M+H]^+$ = 2981.21 Da

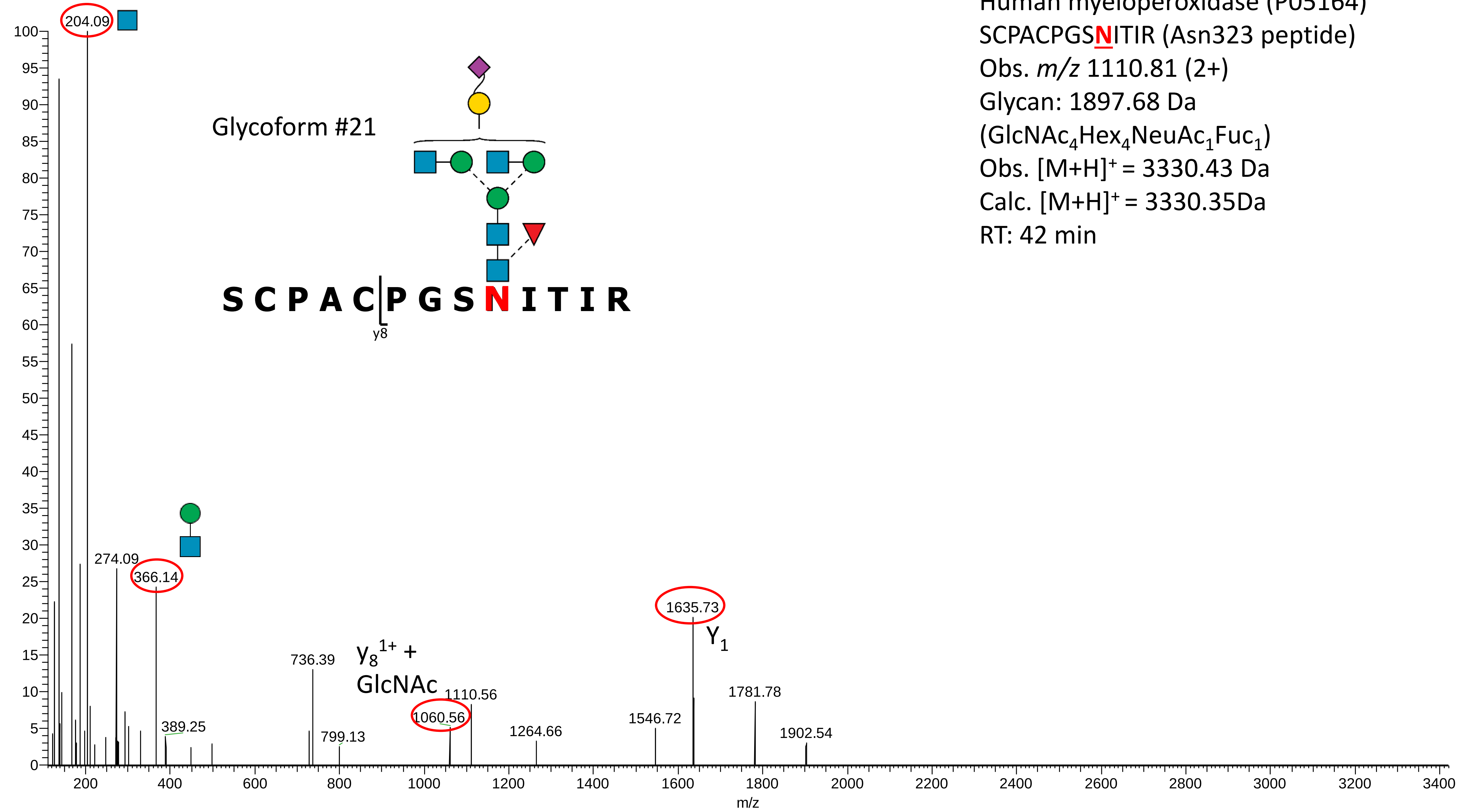
RT: 43 min



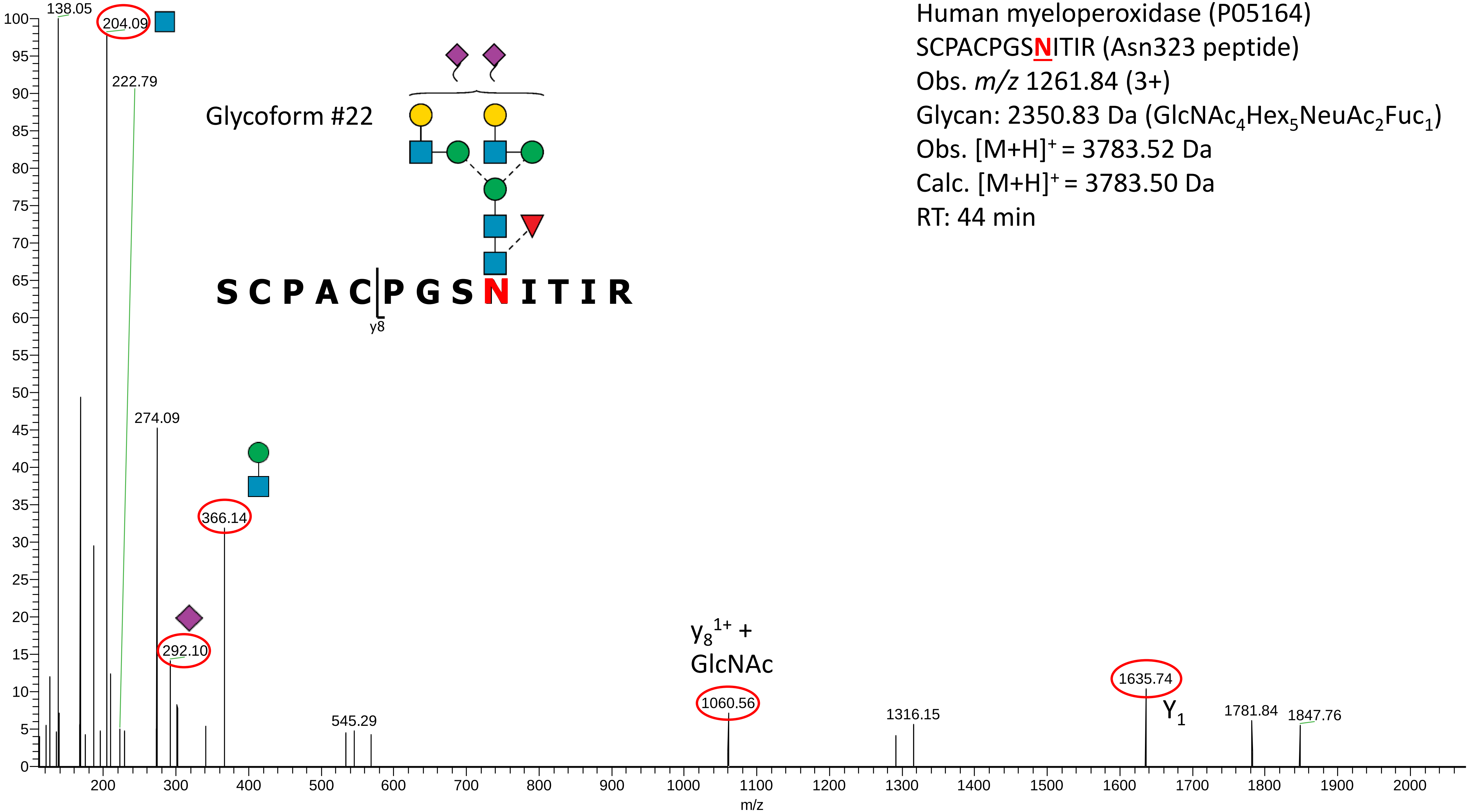
Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1563.60 (2+)
Glycan: 1694.6 Da ($GlcNAc_3Hex_4NeuAc_1Fuc_1$)
Obs. $[M+H]^+$ = 3126.20 Da
Calc. $[M+H]^+$ = 3127.27 Da
Off-by-X (manual) : 1
RT: 44 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1110.81 (2+)
Glycan: 1897.68 Da
($GlcNAc_4Hex_4NeuAc_1Fuc_1$)
Obs. $[M+H]^+ = 3330.43$ Da
Calc. $[M+H]^+ = 3330.35$Da
RT: 42 min



Human myeloperoxidase (P05164)
SCPACPGS**N**ITIR (Asn323 peptide)
Obs. *m/z* 1261.84 (3+)
Glycan: 2350.83 Da ($GlcNAc_4Hex_5NeuAc_2Fuc_1$)
Obs. $[M+H]^+$ = 3783.52 Da
Calc. $[M+H]^+$ = 3783.50 Da
RT: 44 min

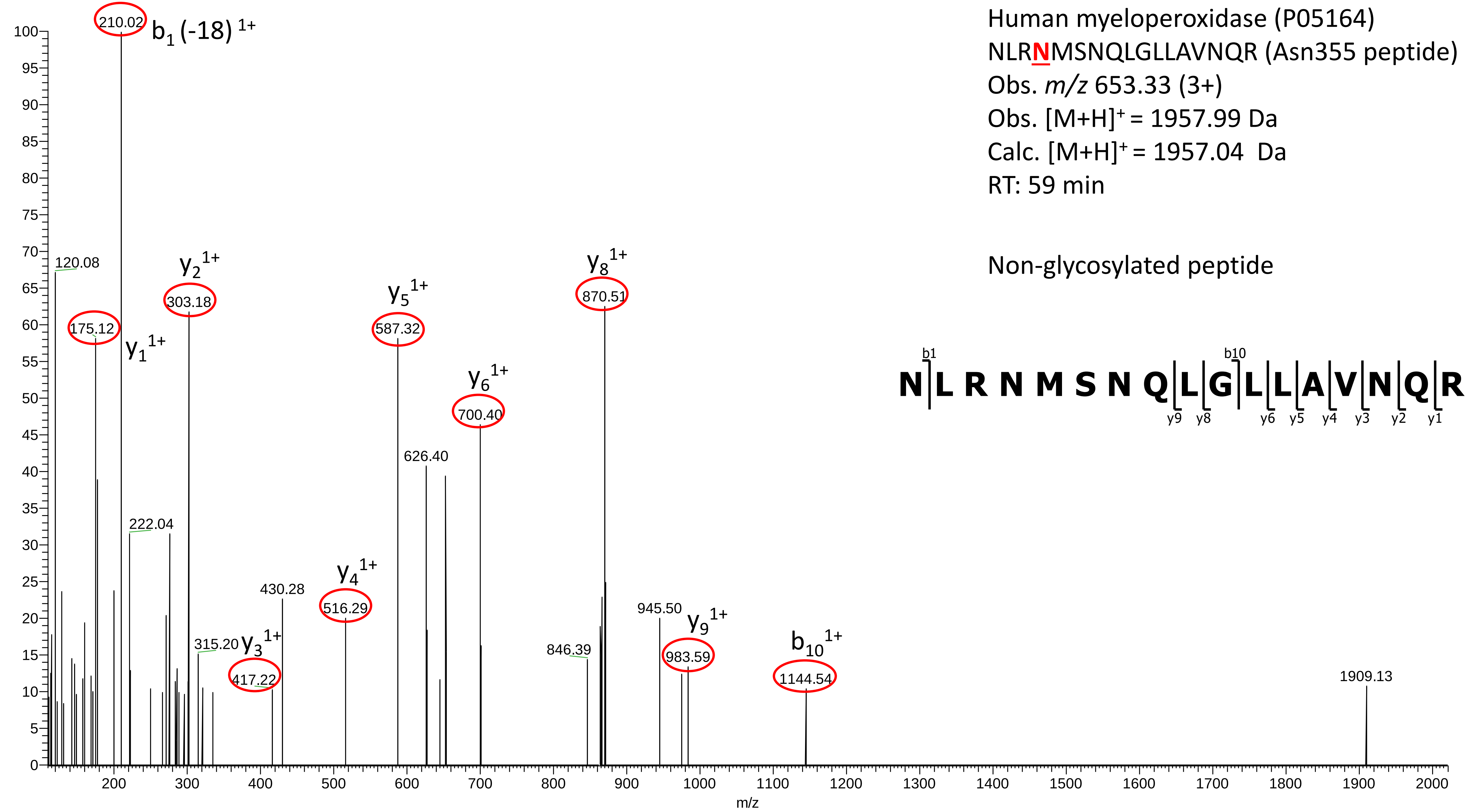


Supplementary Data S3B

Manually annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of all glycosylated and non-glycosylated peptides containing Asn355 identified from the analysis of the unenriched peptide mixtures of nMPO.

Human myeloperoxidase (P05164)
NLR**N**MSNQLGLLAVNQR (Asn355 peptide)
Obs. *m/z* 653.33 (3+)
Obs. $[M+H]^+$ = 1957.99 Da
Calc. $[M+H]^+$ = 1957.04 Da
RT: 59 min

Non-glycosylated peptide



Human myeloperoxidase (P05164)

NLR**N**MSNQLGLLAVNQR (Asn355 peptide)

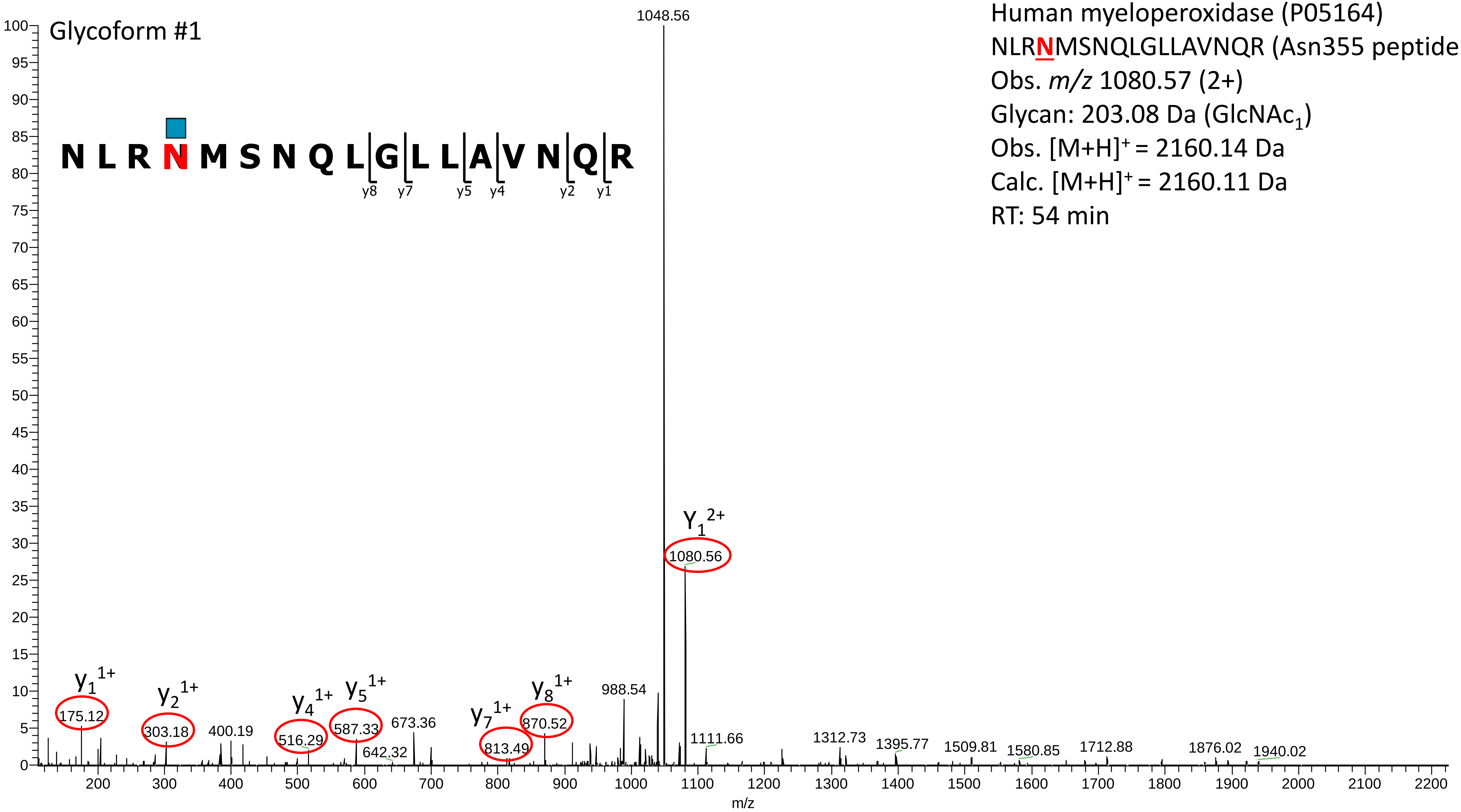
Obs. *m/z* 1080.57 (2+)

Glycan: 203.08 Da ($GlcNAc_1$)

Obs. $[M+H]^+$ = 2160.14 Da

Calc. $[M+H]^+$ = 2160.11 Da

RT: 54 min



Glycoform #2

Human myeloperoxidase (P05164)

NLRNMSNQLGLLAVNQR (Asn355 peptide)

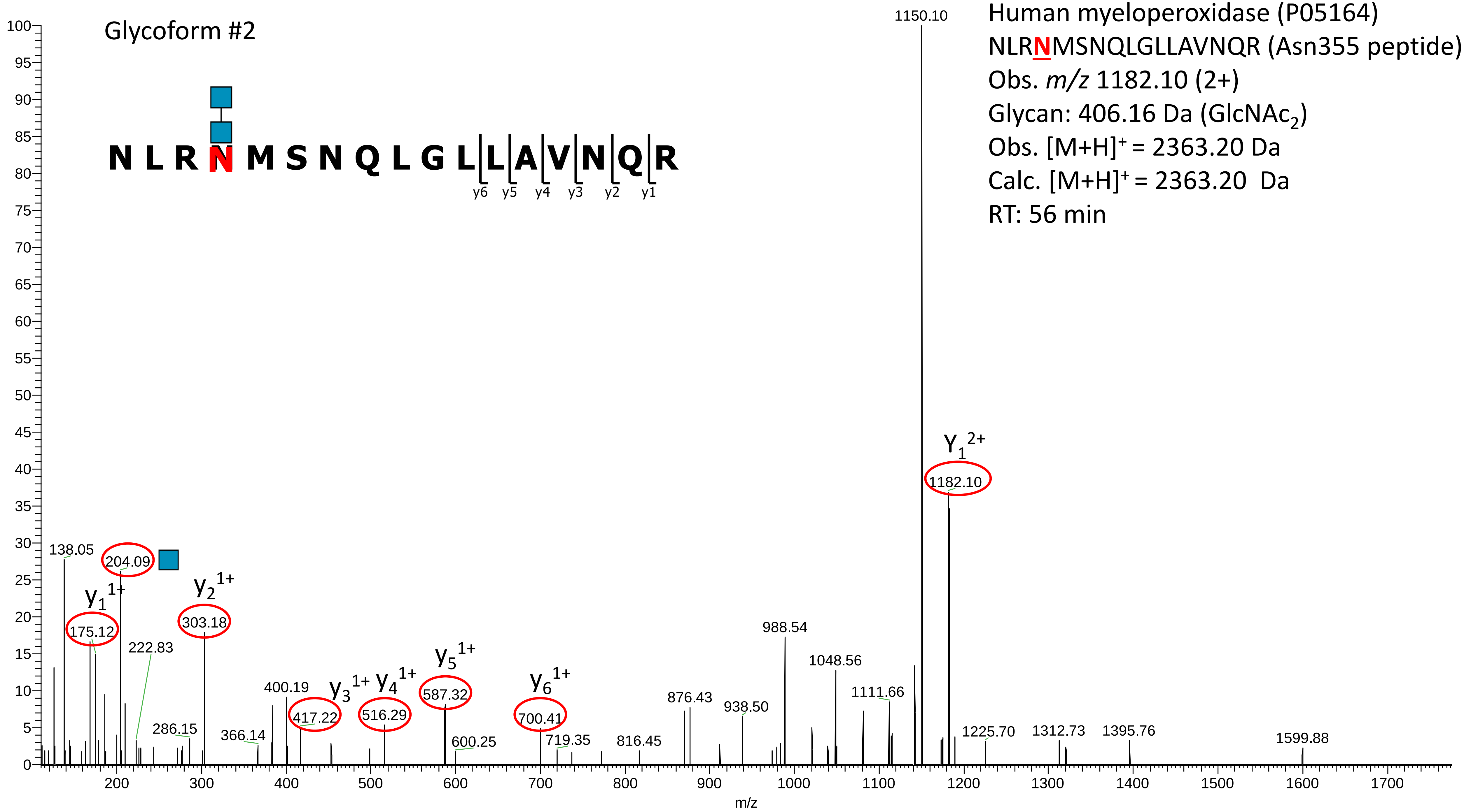
Obs. *m/z* 1182.10 (2+)

Glycan: 406.16 Da (GlcNAc$_2$)

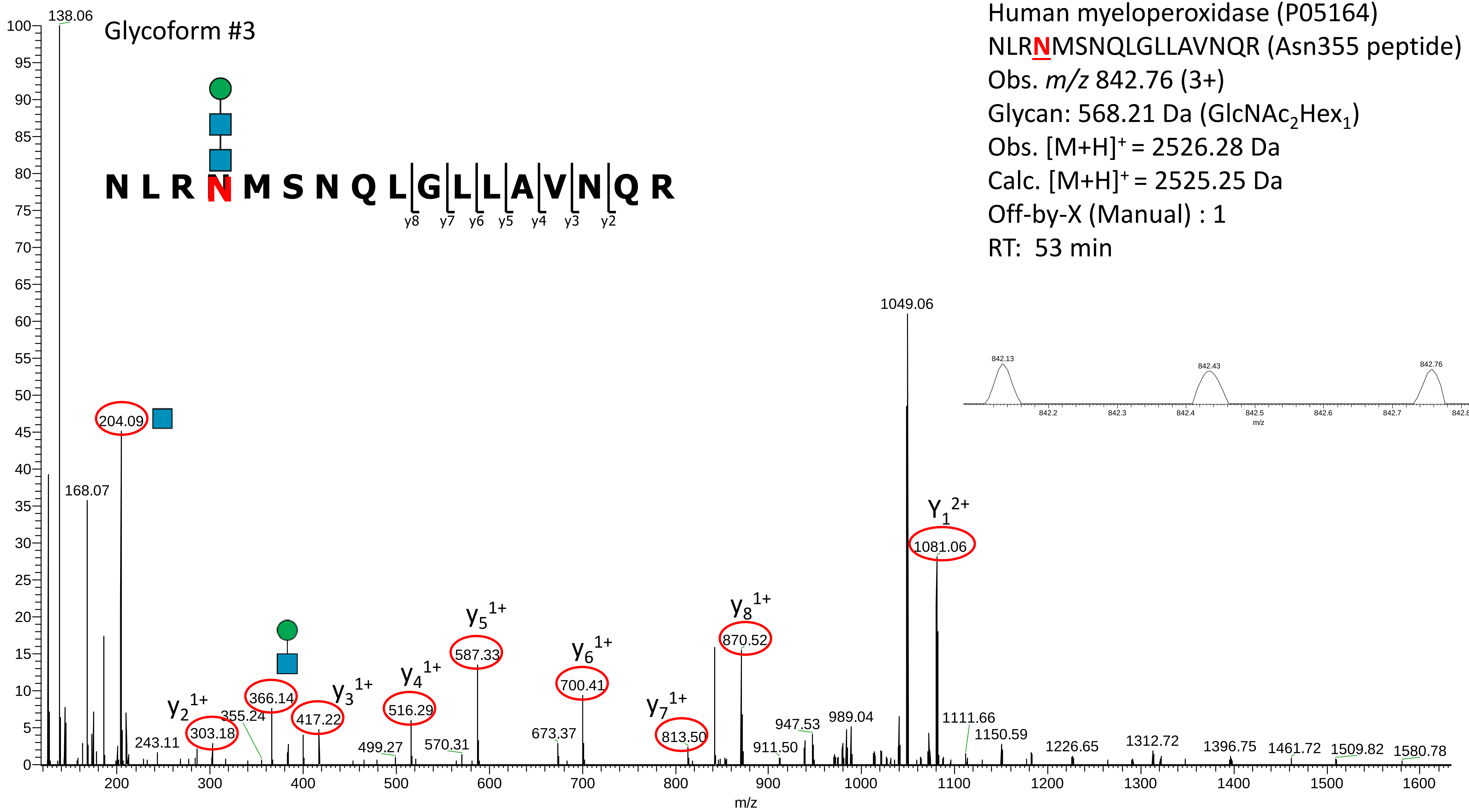
Obs. [M+H]$^+$ = 2363.20 Da

Calc. [M+H]$^+$ = 2363.20 Da

RT: 56 min

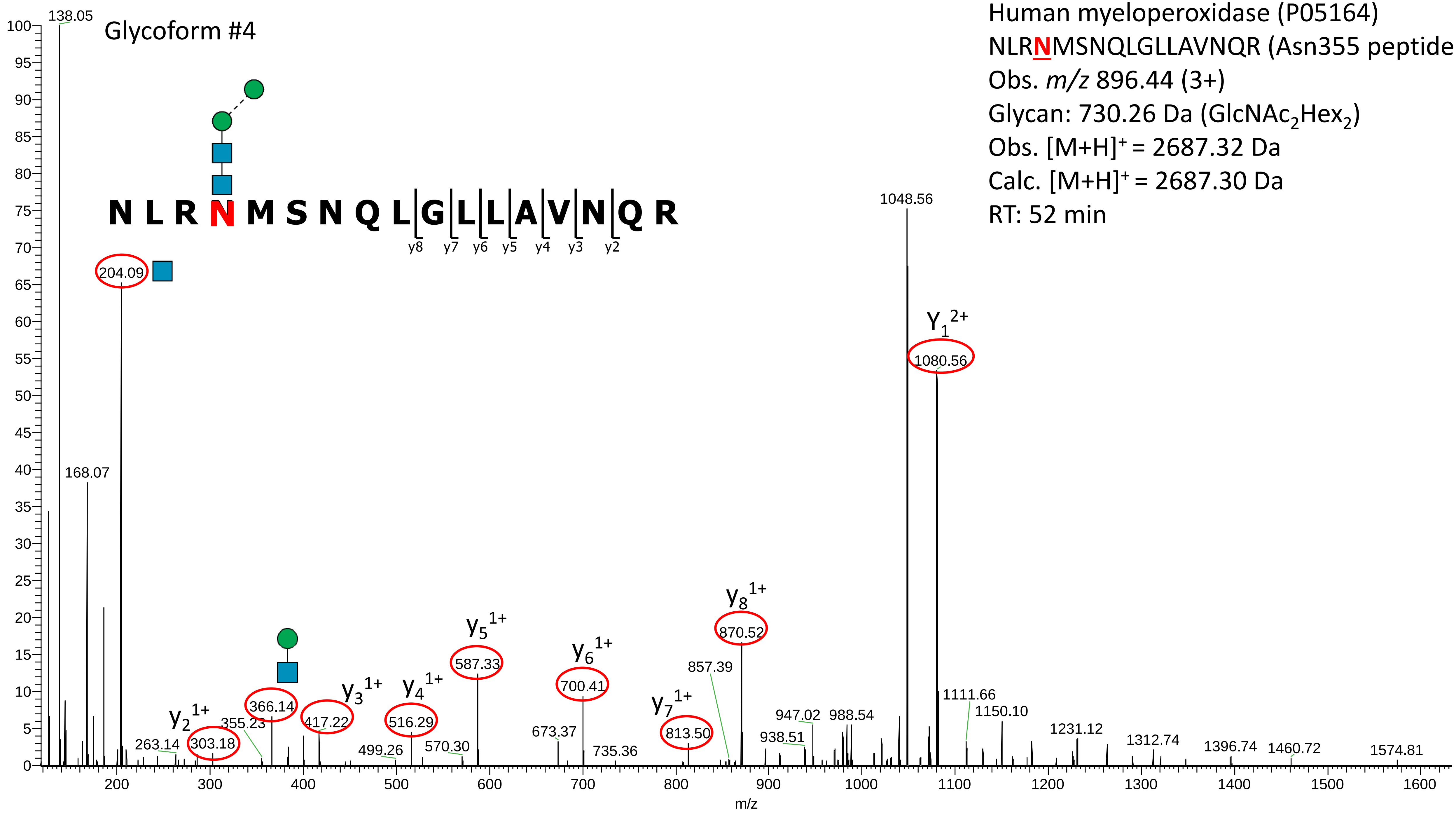


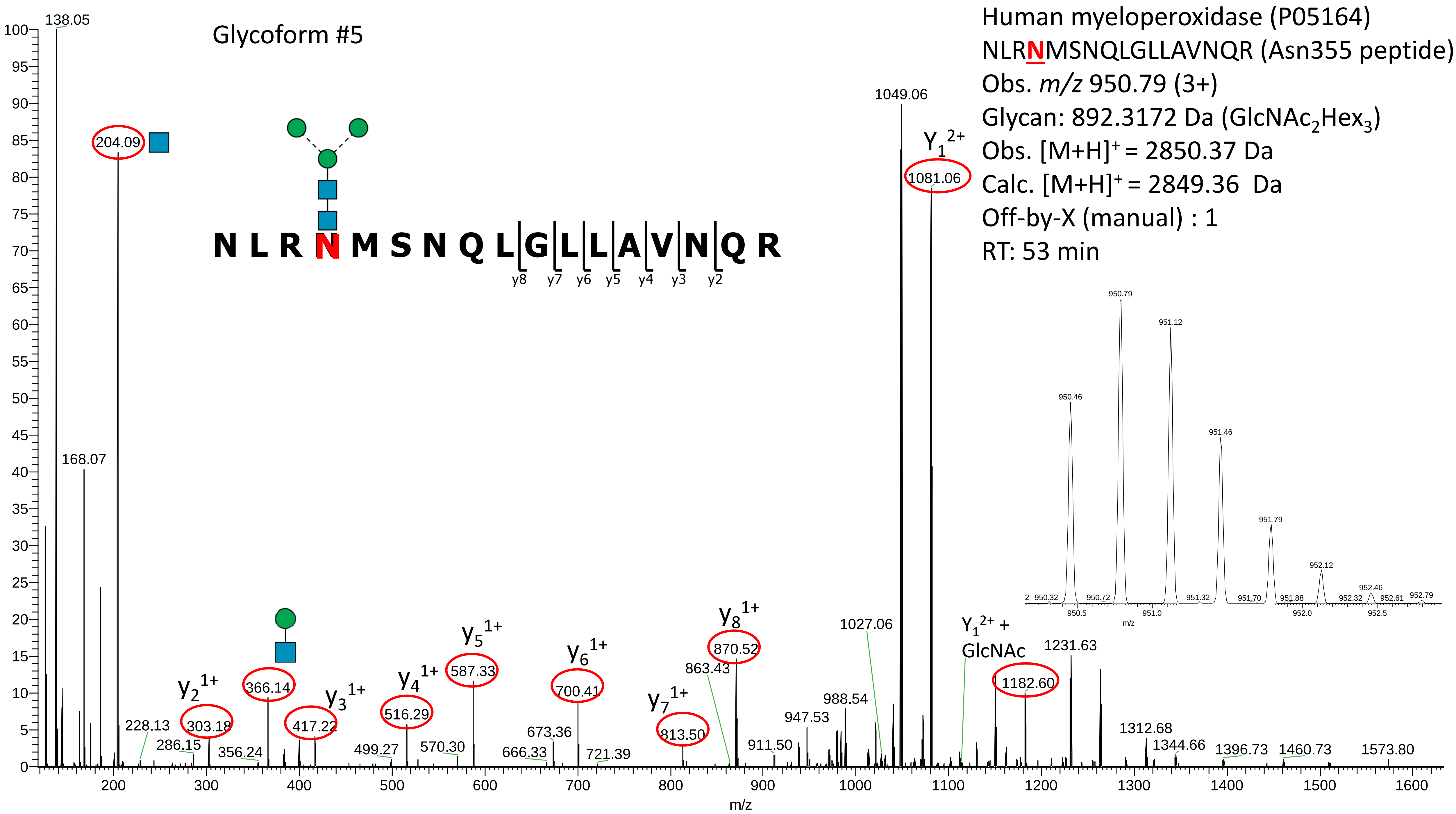
Human myeloperoxidase (P05164)
NLR**N**MSNQLGLLAVNQR (Asn355 peptide)
Obs. *m/z* 842.76 (3+)
Glycan: 568.21 Da ($GlcNAc_2Hex_1$)
Obs. $[M+H]^+$ = 2526.28 Da
Calc. $[M+H]^+$ = 2525.25 Da
Off-by-X (Manual) : 1
RT: 53 min



Glycoform #4

Human myeloperoxidase (P05164)
NLR**N**MSNQLGLLAVNQR (Asn355 peptide)
Obs. *m/z* 896.44 (3+)
Glycan: 730.26 Da ($GlcNAc_2Hex_2$)
Obs. $[M+H]^+$ = 2687.32 Da
Calc. $[M+H]^+$ = 2687.30 Da
RT: 52 min





Human myeloperoxidase (P05164)

NLR**N**MSNQLGLLAVNQR (Asn355 peptide)

Obs. *m/z* 950.79 (3+)

Glycan: 892.3172 Da ($GlcNAc_2Hex_3$)

Obs. $[M+H]^+$ = 2850.37 Da

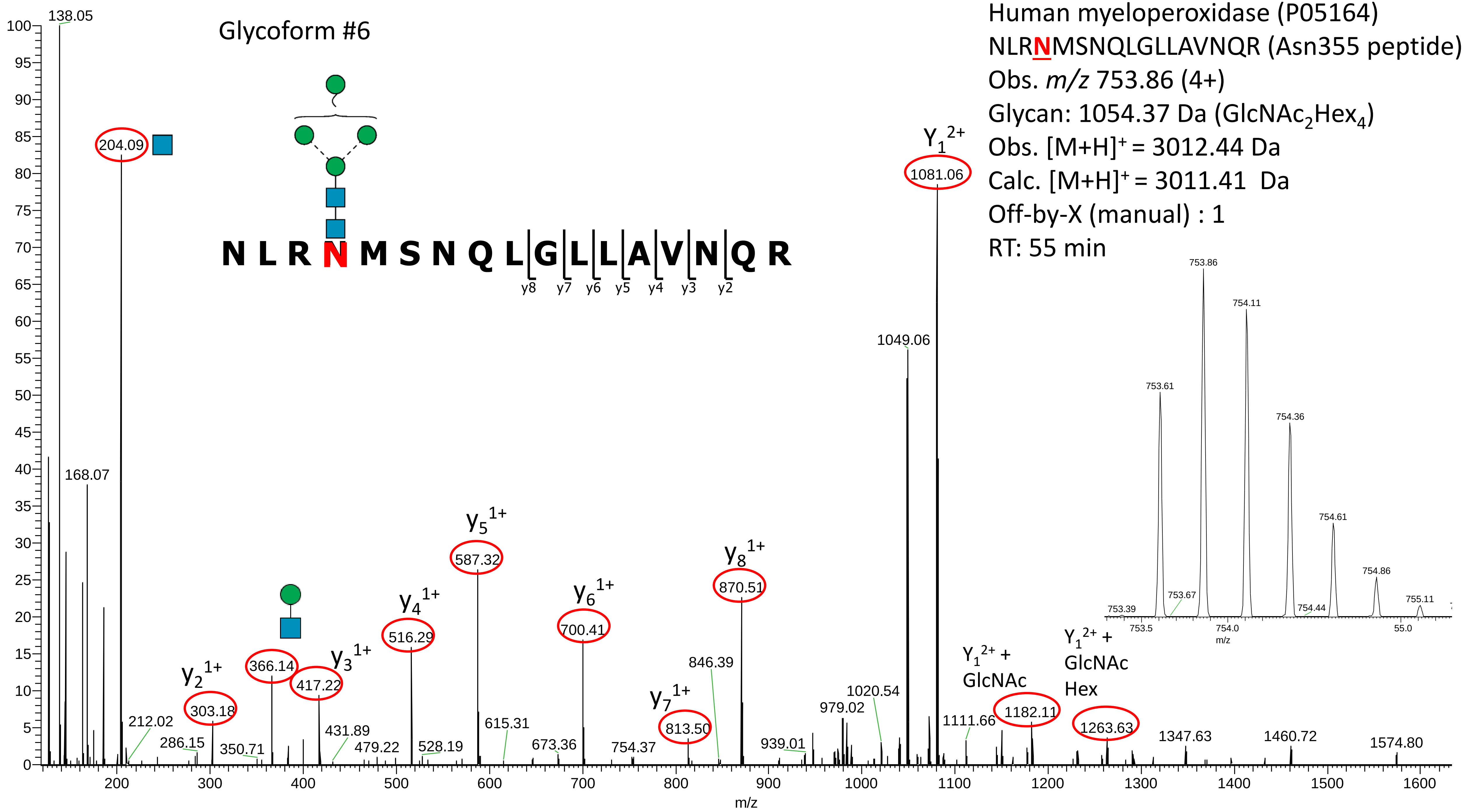
Calc. $[M+H]^+$ = 2849.36 Da

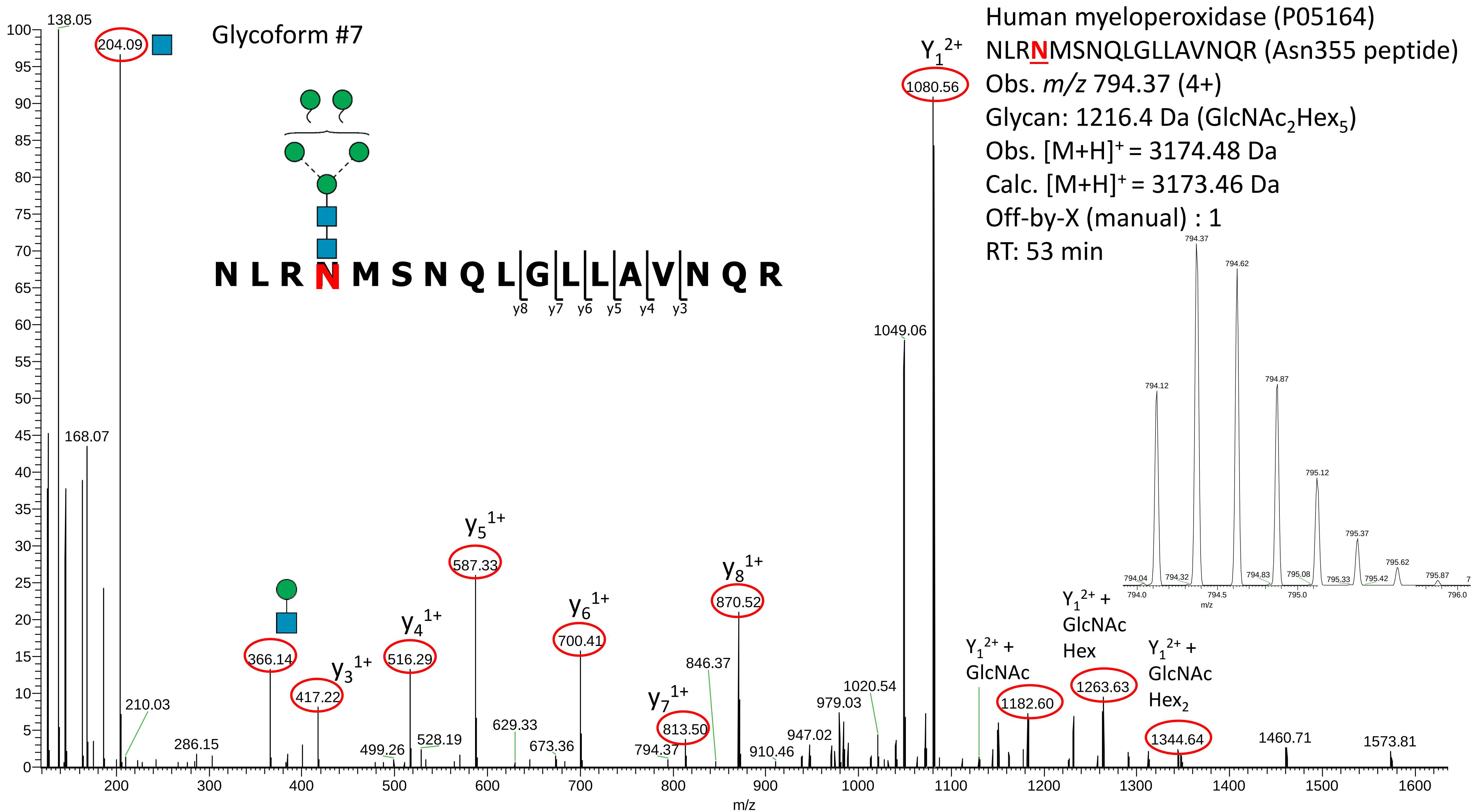
Off-by-X (manual) : 1

RT: 53 min

Glycoform #6

Human myeloperoxidase (P05164)
NLR**N**MSNQLGLLAVNQR (Asn355 peptide)
Obs. *m/z* 753.86 (4+)
Glycan: 1054.37 Da ($GlcNAc_2Hex_4$)
Obs. $[M+H]^+$ = 3012.44 Da
Calc. $[M+H]^+$ = 3011.41 Da
Off-by-X (manual) : 1
RT: 55 min





Human myeloperoxidase (P05164)

NLR**N**MSNQLGLLAVNQR (Asn355 peptide)

Obs. *m/z* 794.37 (4+)

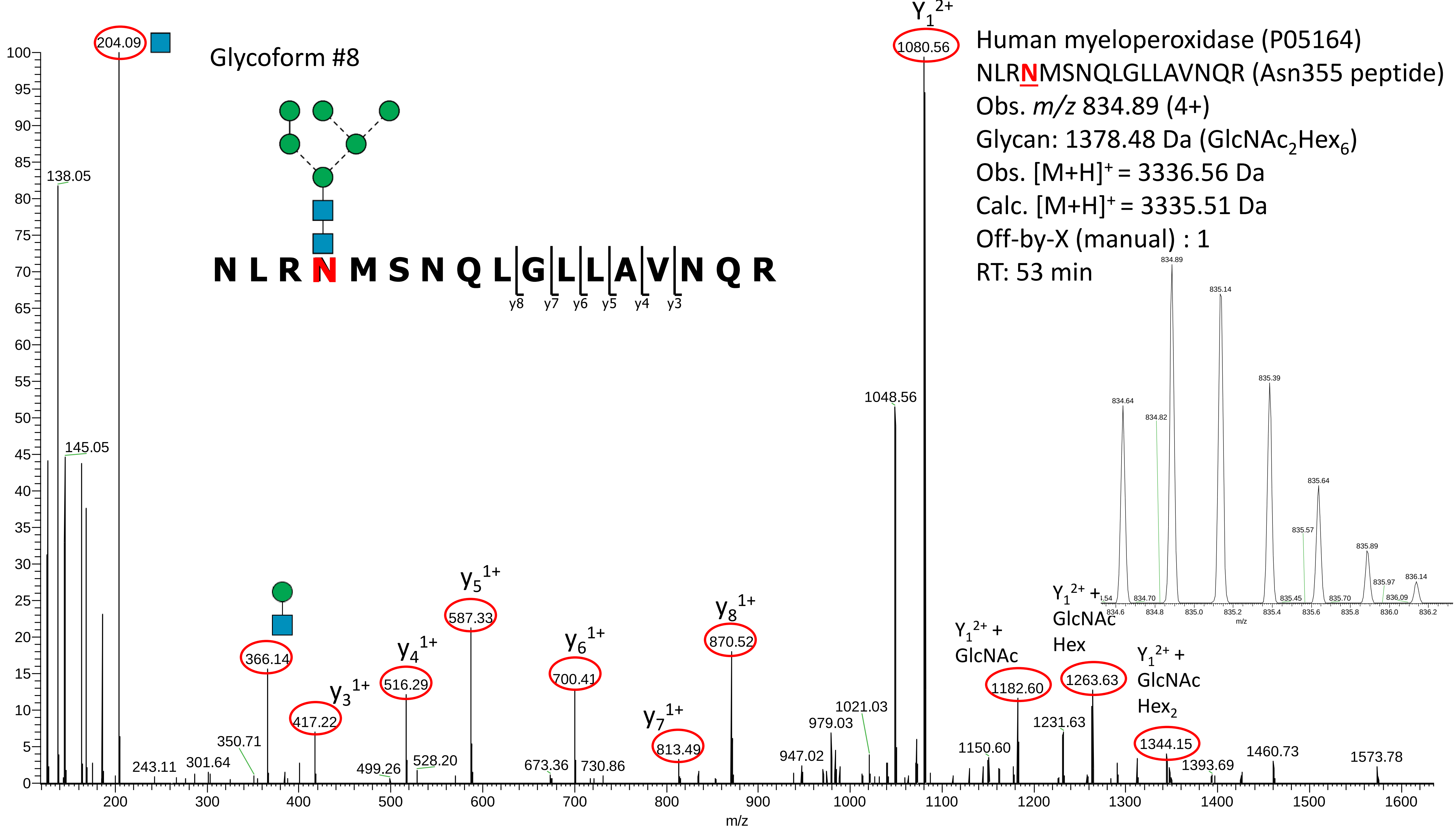
Glycan: 1216.4 Da ($GlcNAc_2Hex_5$)

Obs. $[M+H]^+$ = 3174.48 Da

Calc. $[M+H]^+$ = 3173.46 Da

Off-by-X (manual) : 1

RT: 53 min



Human myeloperoxidase (P05164)

NLR**N**MSNQLGLLAVNQR (Asn355 peptide)

Obs. *m/z* 834.89 (4+)

Glycan: 1378.48 Da ($GlcNAc_2Hex_6$)

Obs. $[M+H]^+$ = 3336.56 Da

Calc. $[M+H]^+$ = 3335.51 Da

Off-by-X (manual) : 1

RT: 53 min

Glycoform #9

Human myeloperoxidase (P05164)

NLR**N**MSNQLGLLAVNQR (Asn355 peptide)

Obs. *m/z* 875.65 (+4)

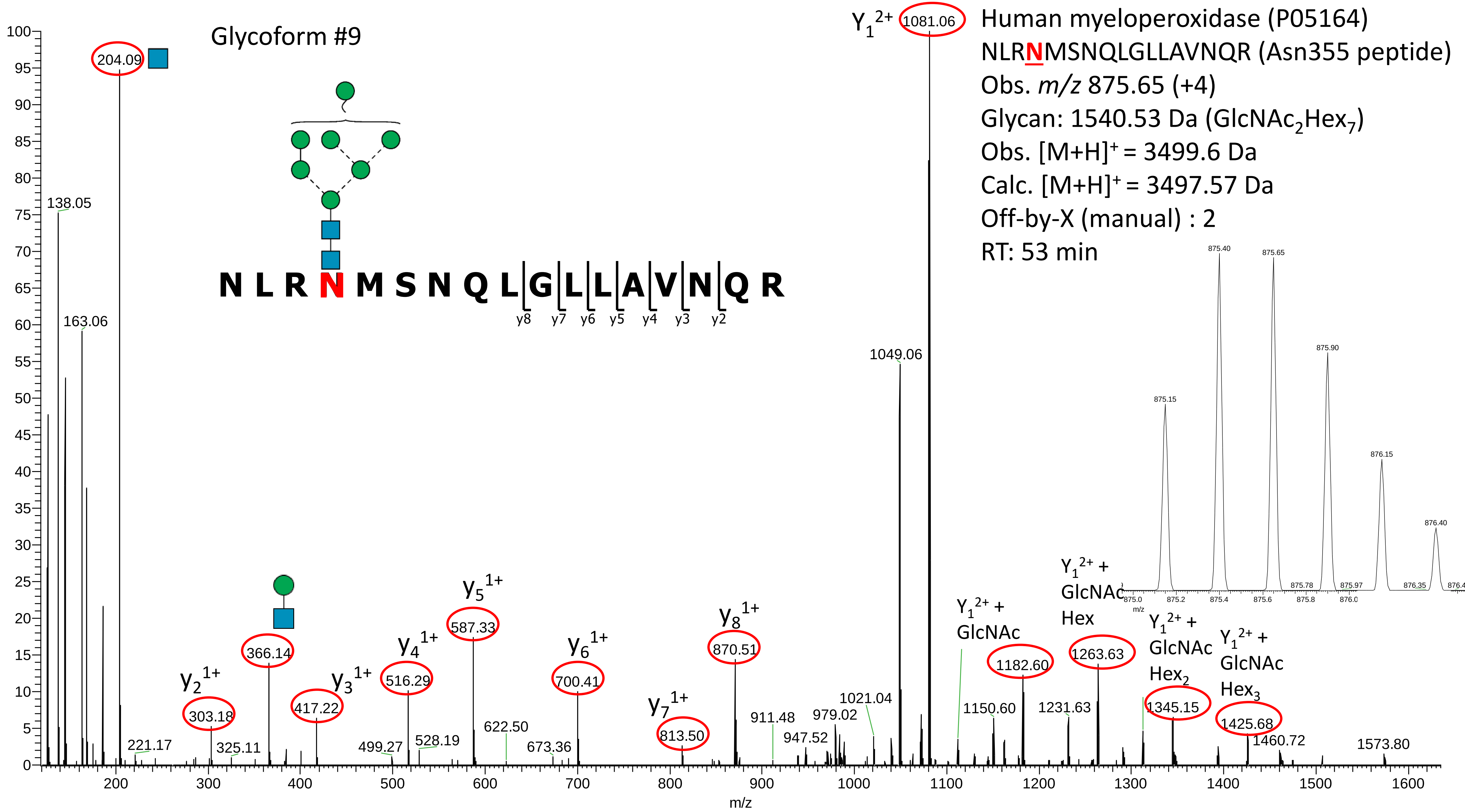
Glycan: 1540.53 Da ($GlcNAc_2Hex_7$)

Obs. $[M+H]^+$ = 3499.6 Da

Calc. $[M+H]^+$ = 3497.57 Da

Off-by-X (manual) : 2

RT: 53 min



Glycoform #10

Human myeloperoxidase (P05164)

NLR**N**MSNQLGLLAVNQR (Asn355 peptide)

Obs. *m/z* 1221.21 (3+)

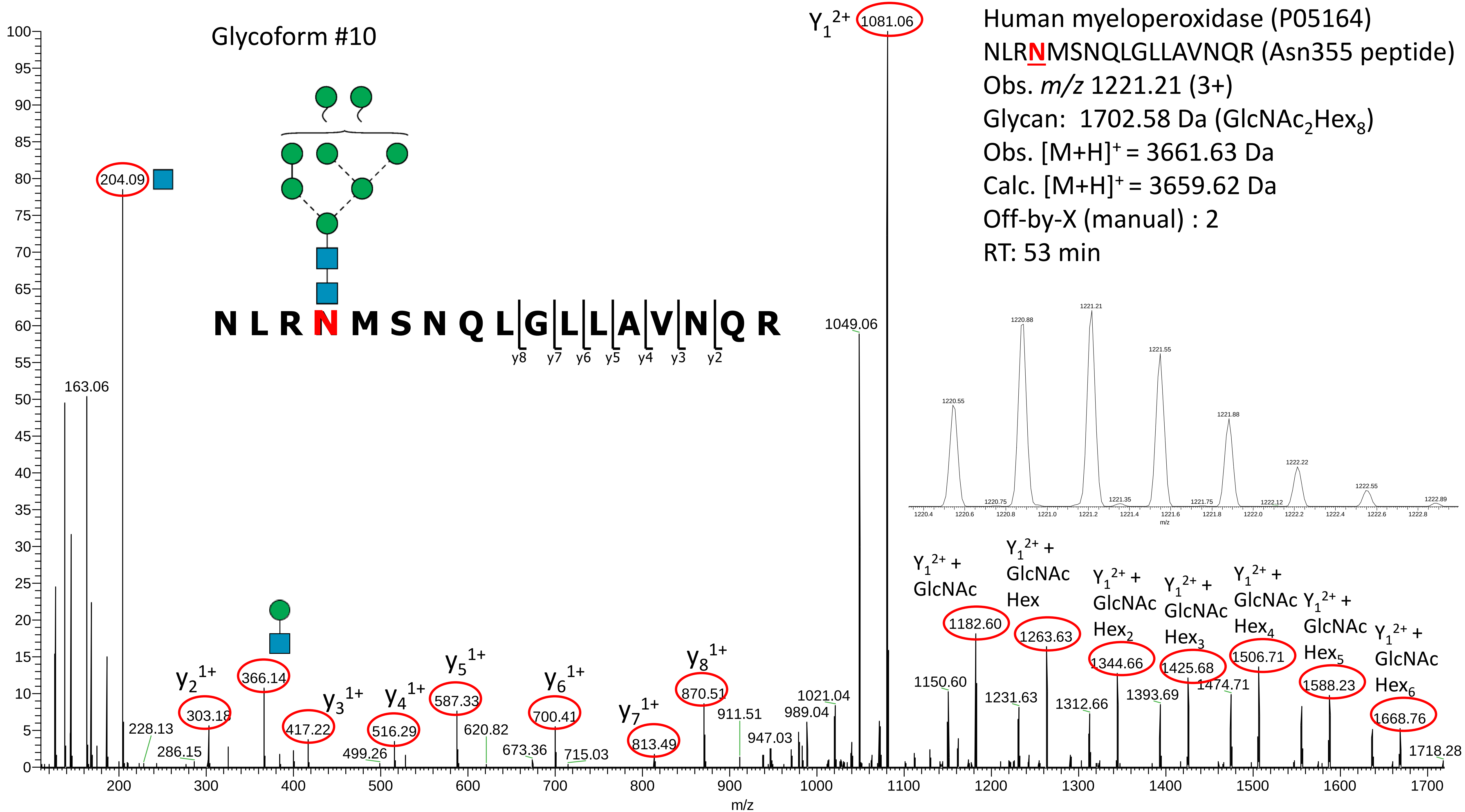
Glycan: 1702.58 Da ($GlcNAc_2Hex_8$)

Obs. $[M+H]^+$ = 3661.63 Da

Calc. $[M+H]^+$ = 3659.62 Da

Off-by-X (manual) : 2

RT: 53 min

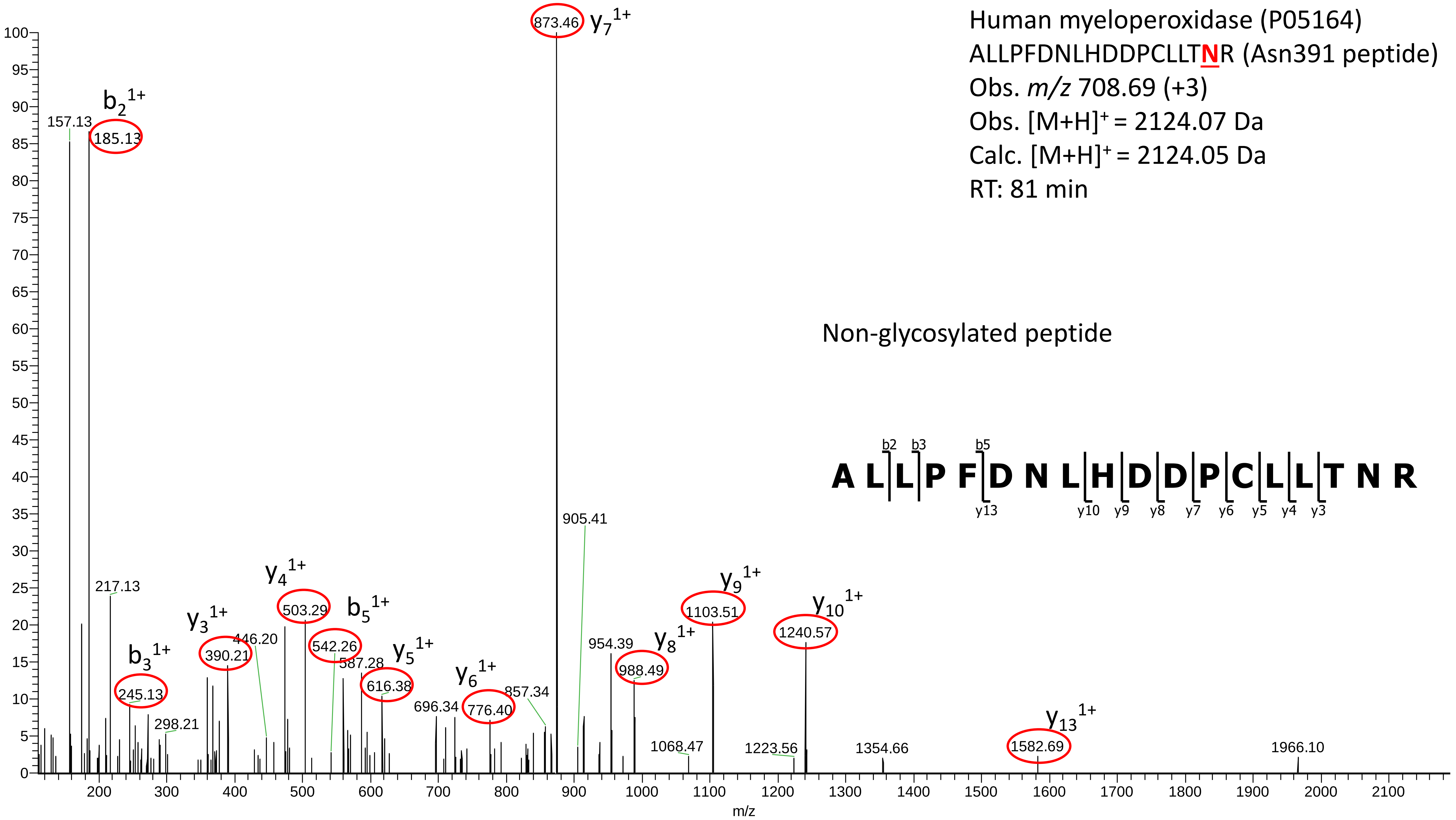


Supplementary Data S3C

Manually annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of all glycosylated and non-glycosylated peptides containing Asn391 identified from the analysis of unenriched peptide mixtures of nMPO.

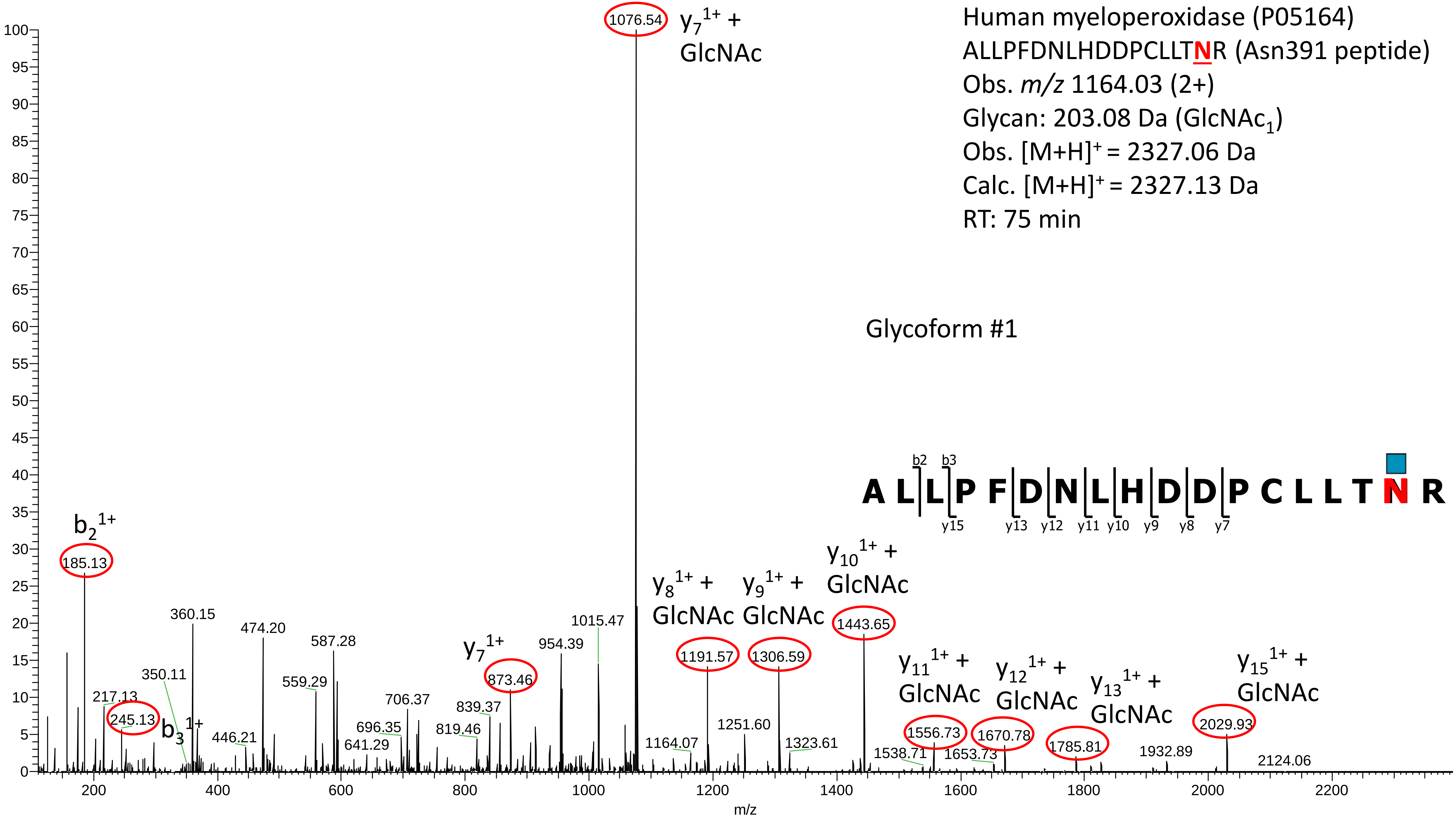
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 708.69 (+3)
Obs. [M+H]$^+$ = 2124.07 Da
Calc. [M+H]$^+$ = 2124.05 Da
RT: 81 min

Non-glycosylated peptide



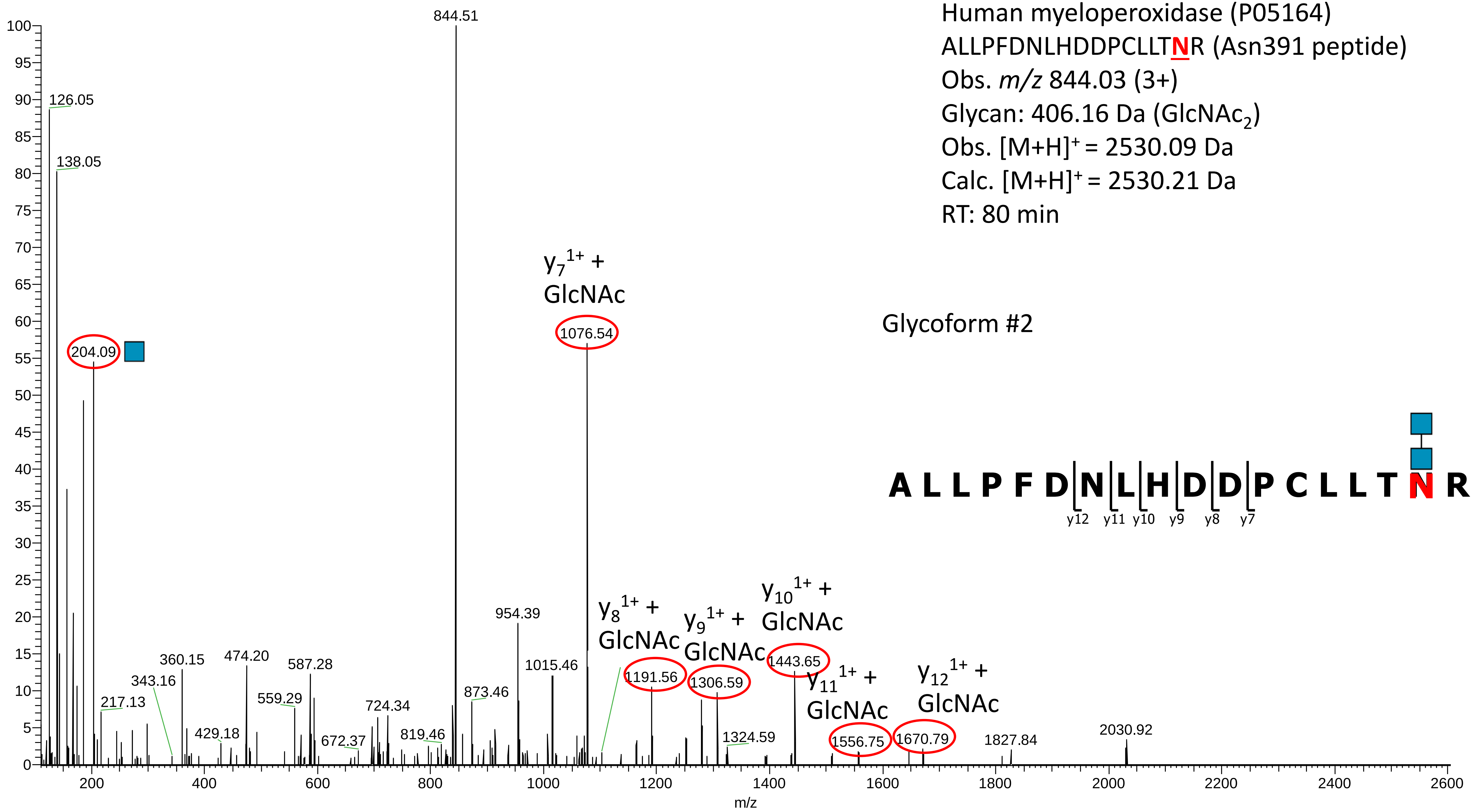
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1164.03 (2+)
Glycan: 203.08 Da ($GlcNAc_1$)
Obs. $[M+H]^+$ = 2327.06 Da
Calc. $[M+H]^+$ = 2327.13 Da
RT: 75 min

Glycoform #1



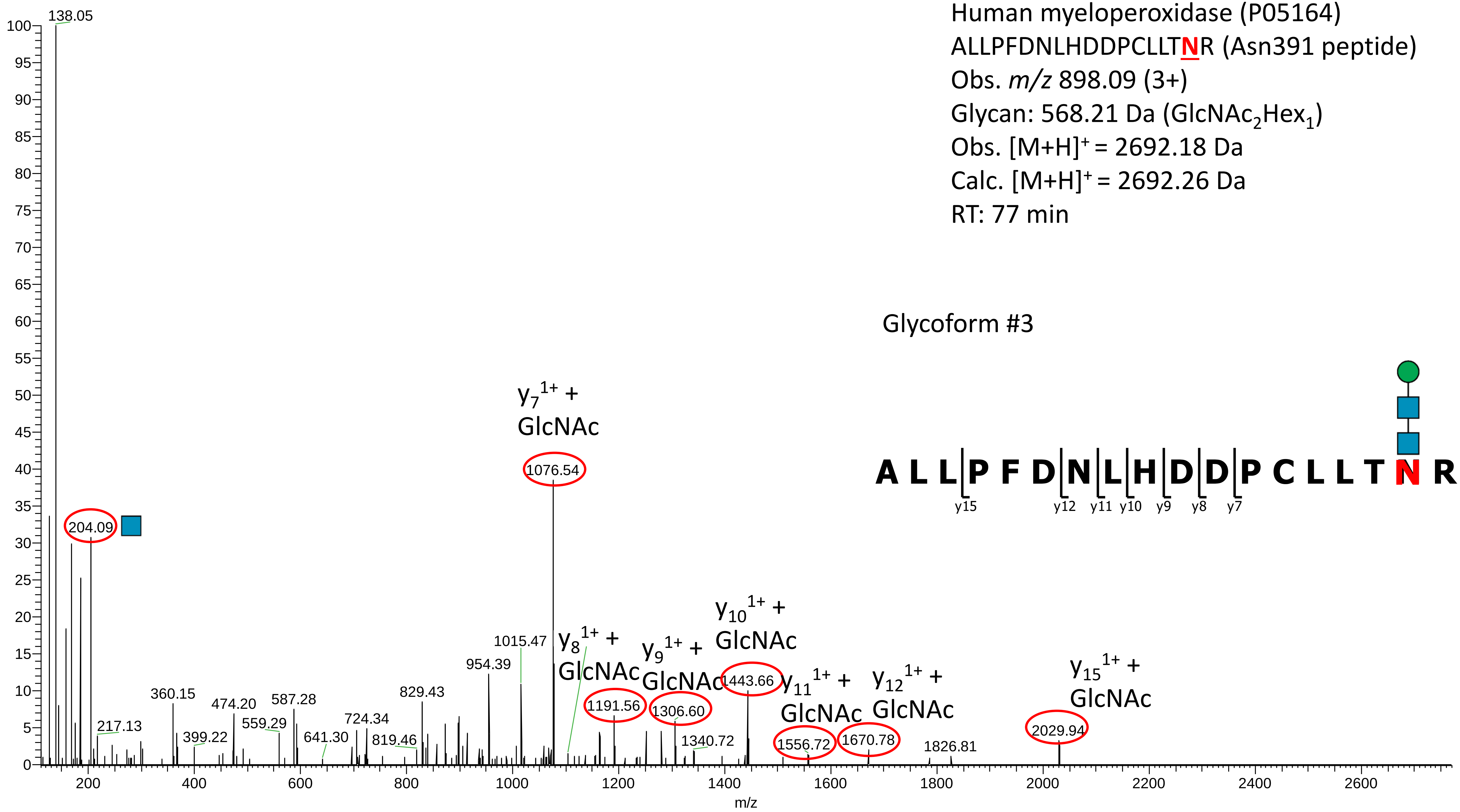
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 844.03 (3+)
Glycan: 406.16 Da (GlcNAc$_2$)
Obs. $[M+H]^+$ = 2530.09 Da
Calc. $[M+H]^+$ = 2530.21 Da
RT: 80 min

Glycoform #2



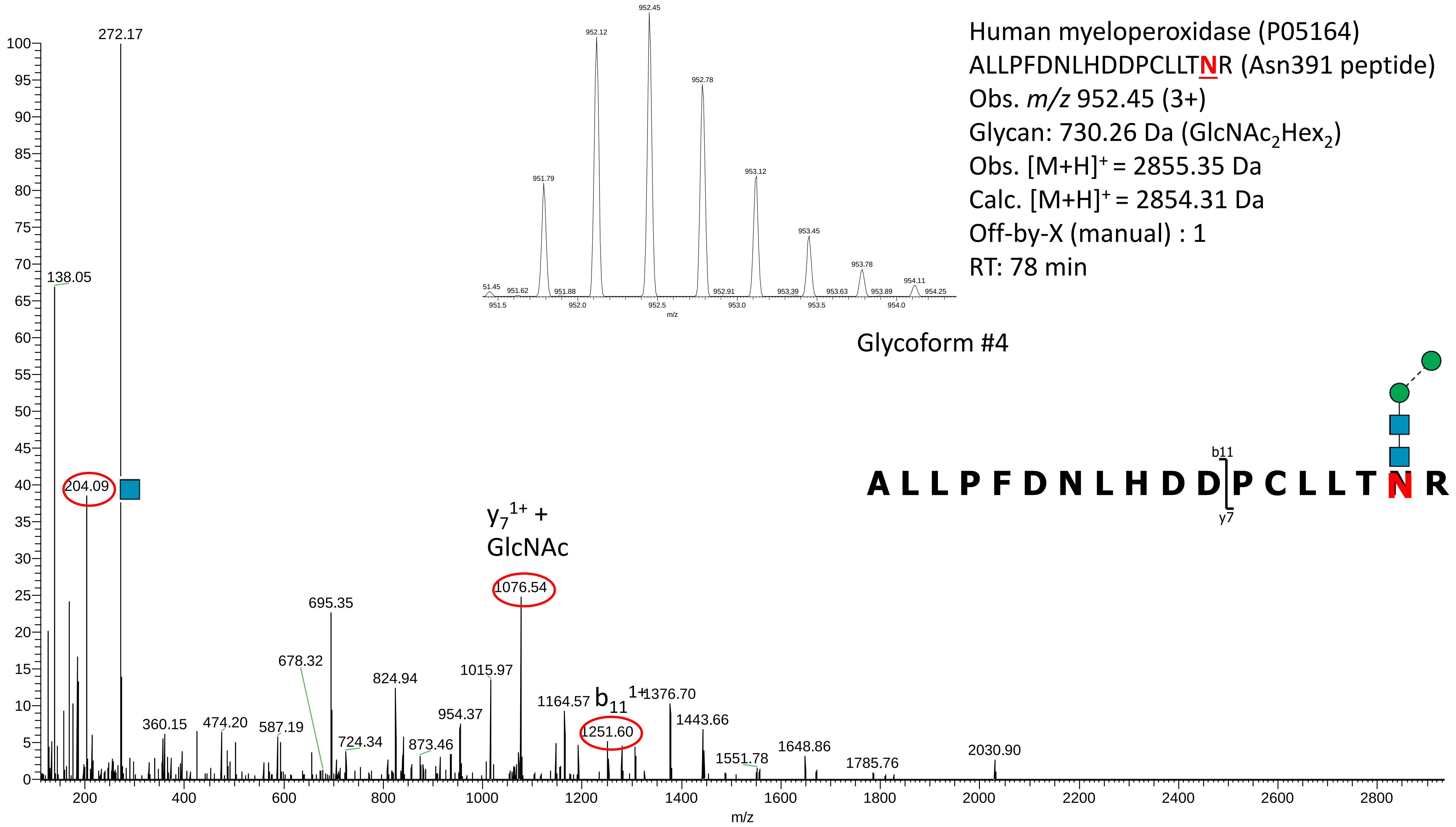
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 898.09 (3+)
Glycan: 568.21 Da ($GlcNAc_2Hex_1$)
Obs. $[M+H]^+$ = 2692.18 Da
Calc. $[M+H]^+$ = 2692.26 Da
RT: 77 min

Glycoform #3



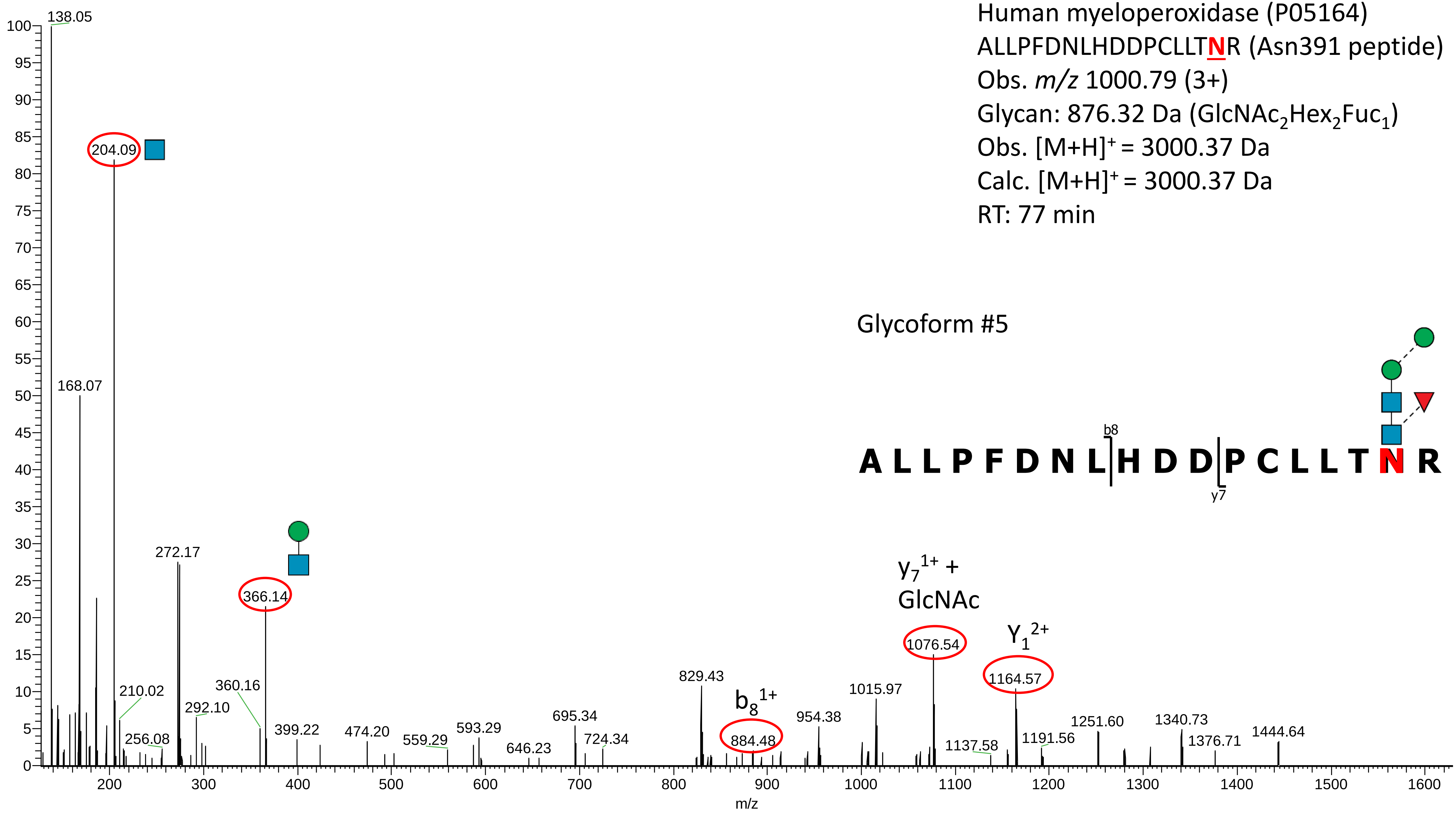
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 952.45 (3+)
Glycan: 730.26 Da ($GlcNAc_2Hex_2$)
Obs. $[M+H]^+$ = 2855.35 Da
Calc. $[M+H]^+$ = 2854.31 Da
Off-by-X (manual) : 1
RT: 78 min

Glycoform #4



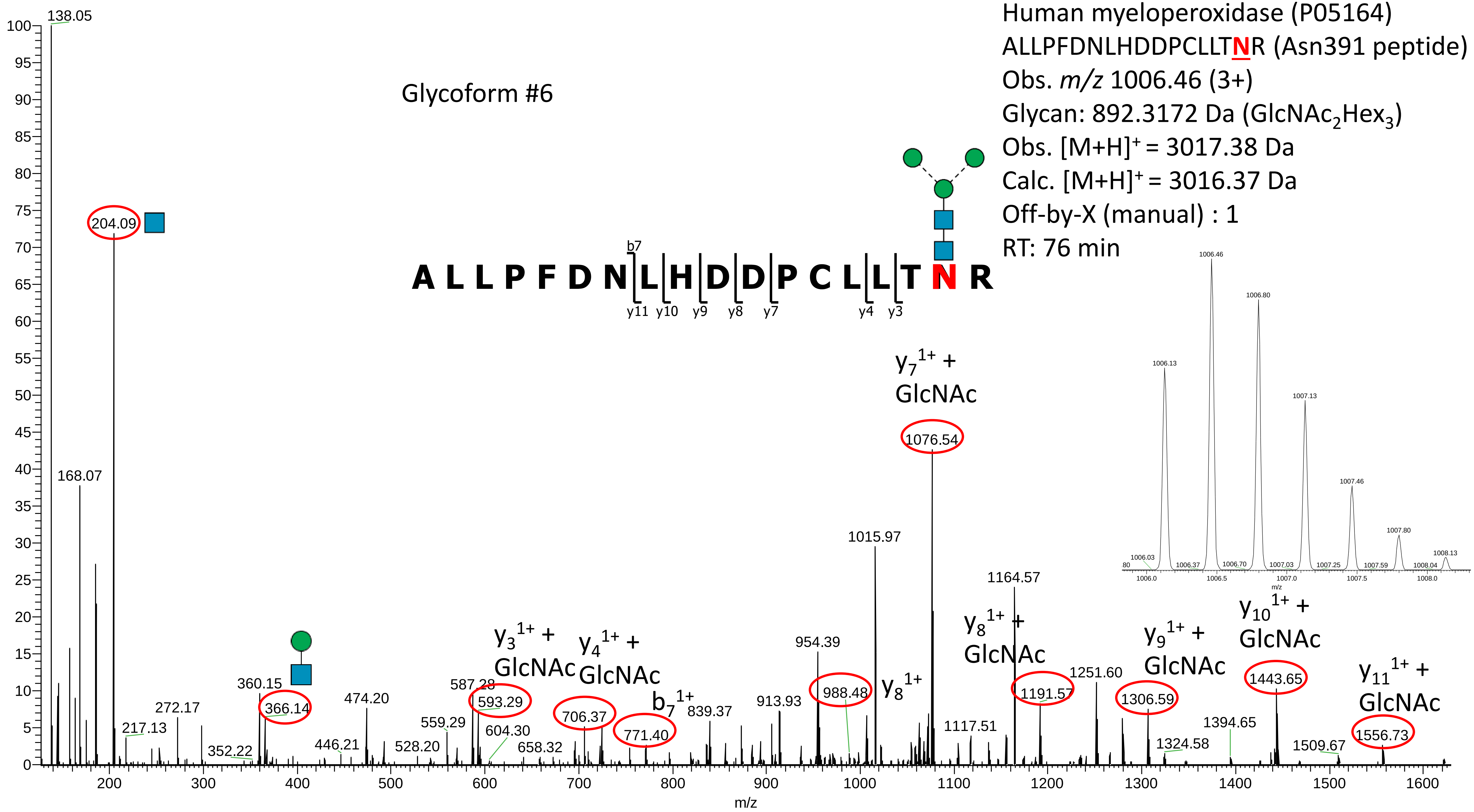
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1000.79 (3+)
Glycan: 876.32 Da ($GlcNAc_2Hex_2Fuc_1$)
Obs. $[M+H]^+$ = 3000.37 Da
Calc. $[M+H]^+$ = 3000.37 Da
RT: 77 min

Glycoform #5



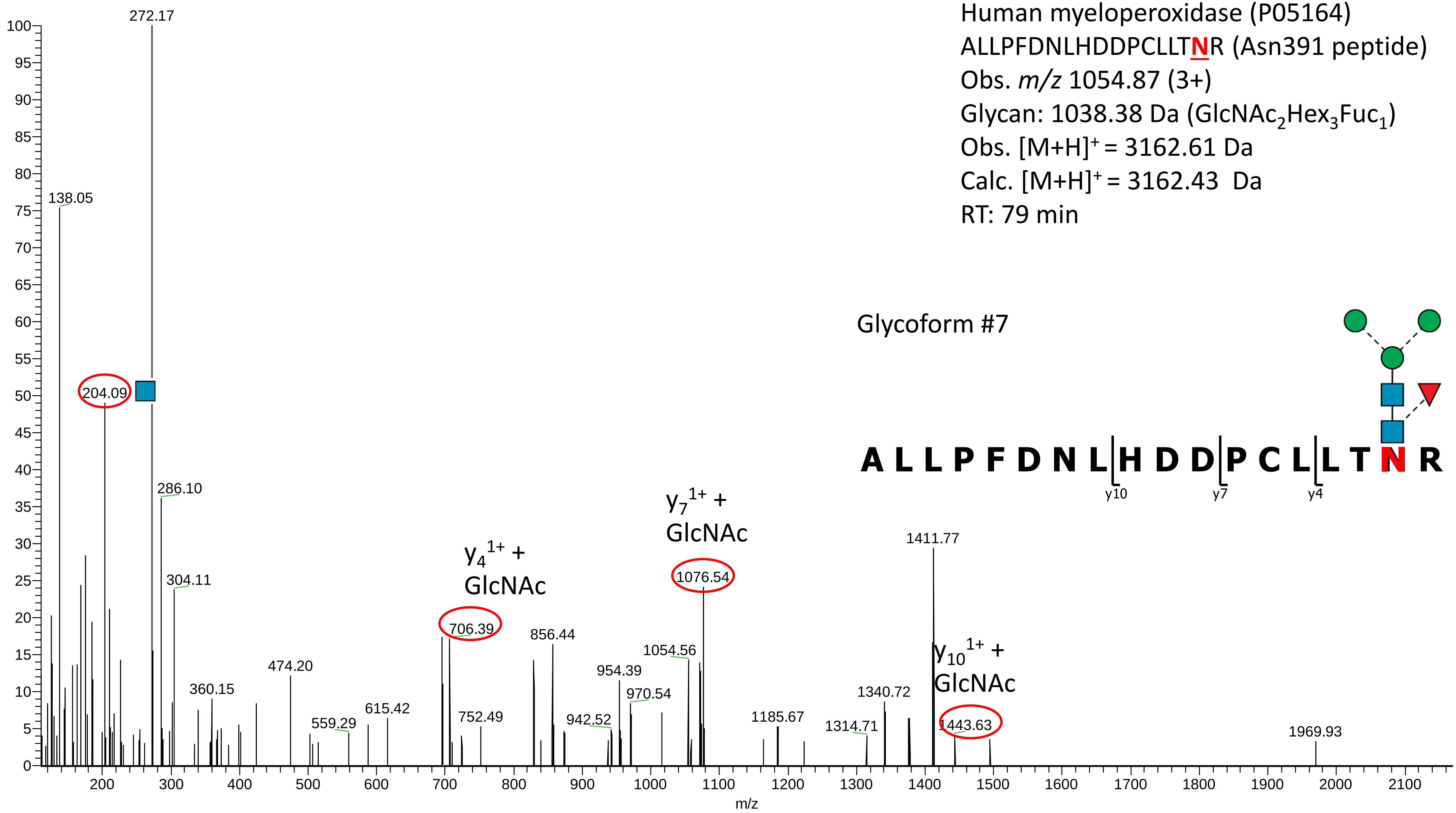
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1006.46 (3+)
Glycan: 892.3172 Da ($GlcNAc_2Hex_3$)
Obs. $[M+H]^+$ = 3017.38 Da
Calc. $[M+H]^+$ = 3016.37 Da
Off-by-X (manual) : 1
RT: 76 min

Glycoform #6



Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1054.87 (3+)
Glycan: 1038.38 Da ($GlcNAc_2Hex_3Fuc_1$)
Obs. $[M+H]^+$ = 3162.61 Da
Calc. $[M+H]^+$ = 3162.43 Da
RT: 79 min

Glycoform #7



Human myeloperoxidase (P05164)

ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)

Obs. *m/z* 1589.72 (2+)

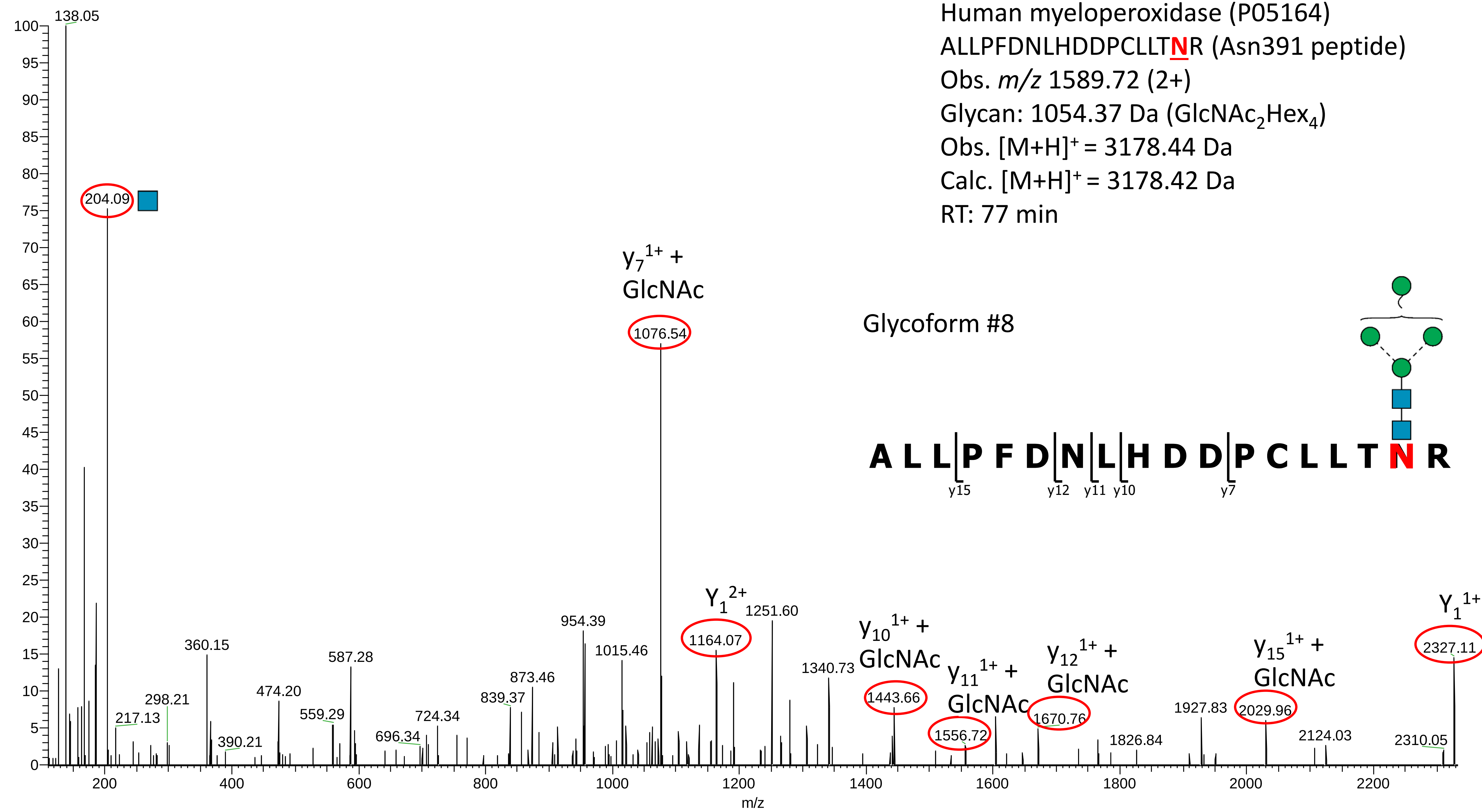
Glycan: 1054.37 Da ($GlcNAc_2Hex_4$)

Obs. $[M+H]^+$ = 3178.44 Da

Calc. $[M+H]^+$ = 3178.42 Da

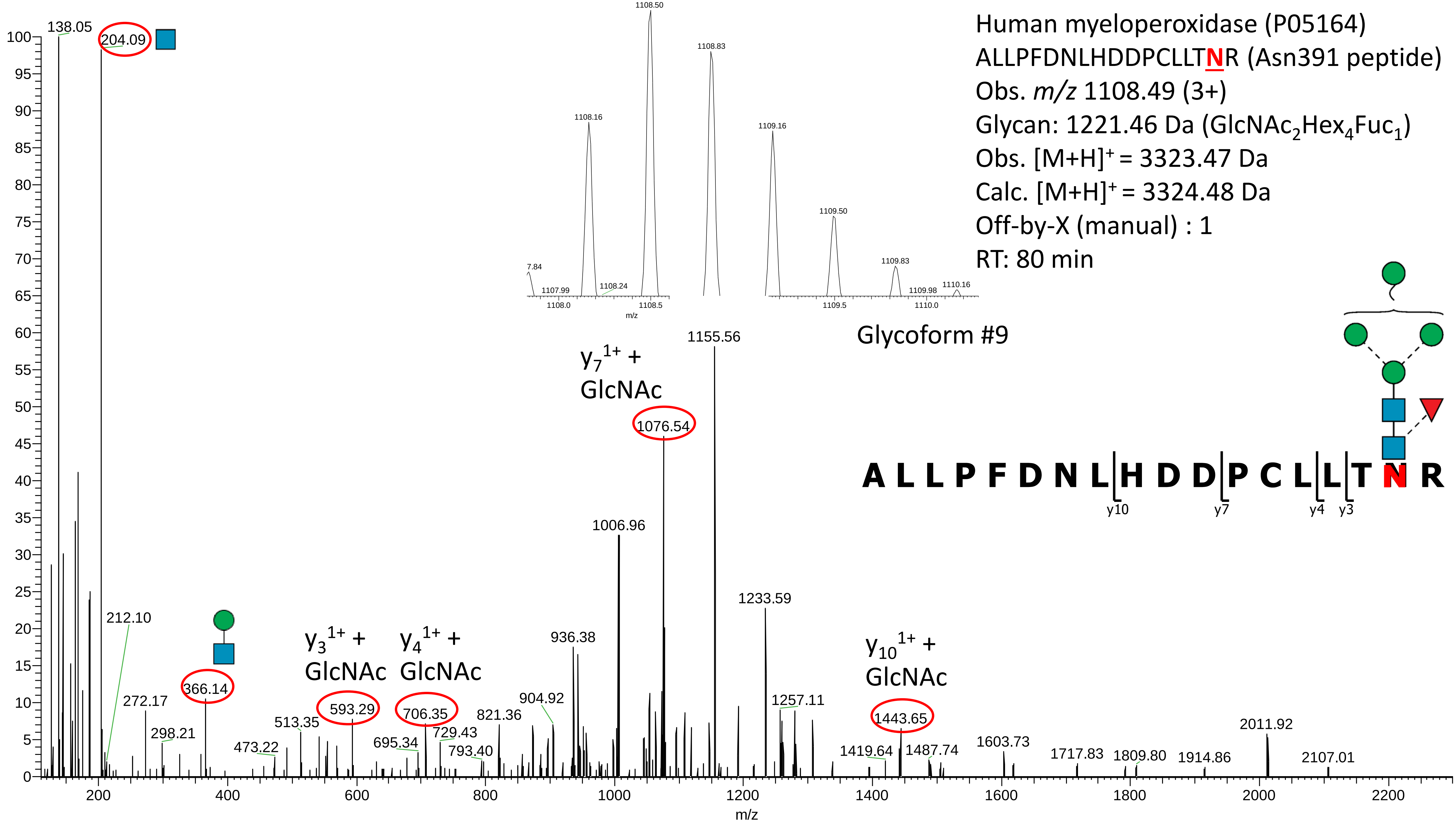
RT: 77 min

Glycoform #8



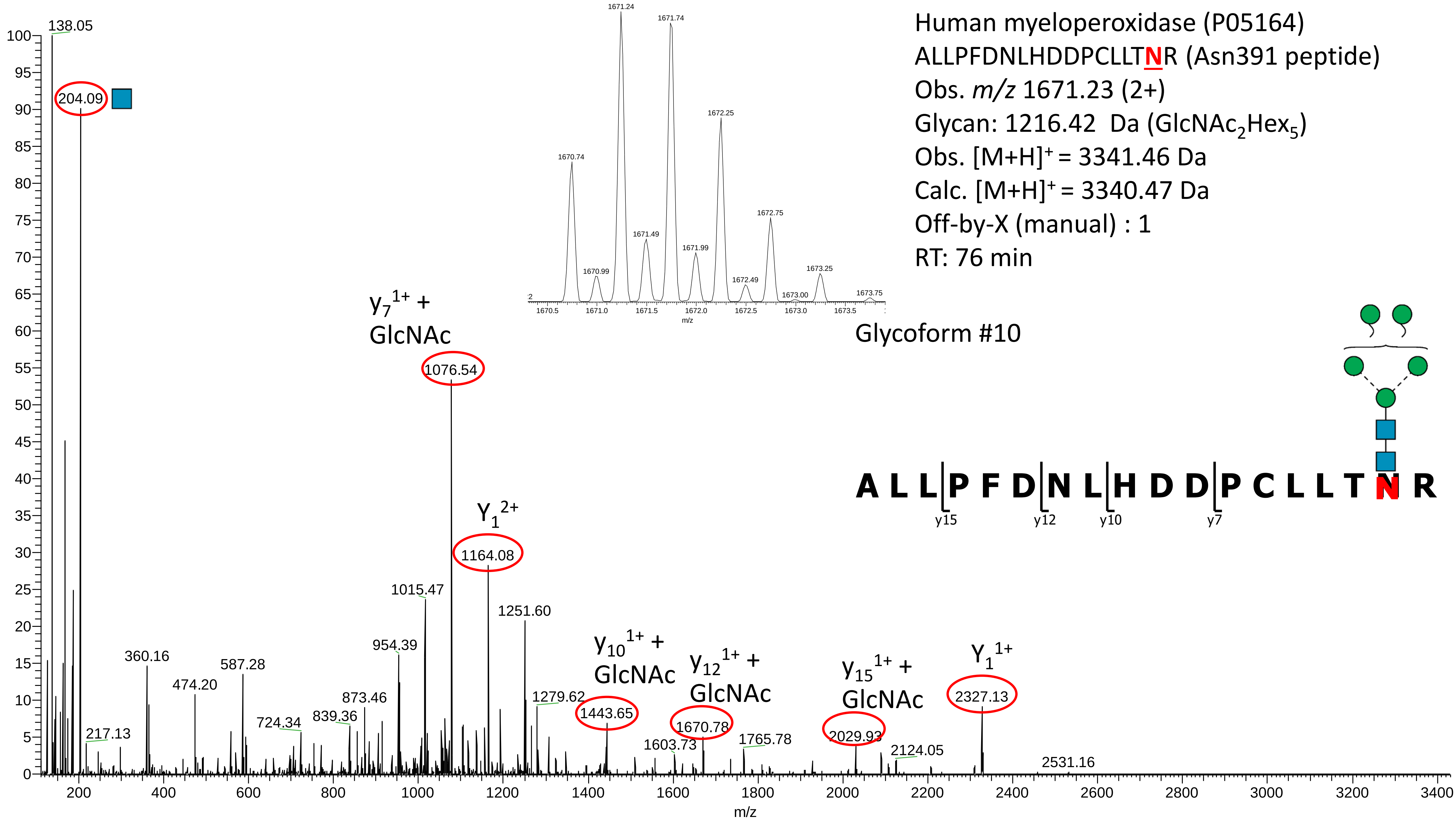
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1108.49 (3+)
Glycan: 1221.46 Da (GlcNAc$_2$Hex$_4$Fuc$_1$)
Obs. [M+H]$^+$ = 3323.47 Da
Calc. [M+H]$^+$ = 3324.48 Da
Off-by-X (manual) : 1
RT: 80 min

Glycoform #9



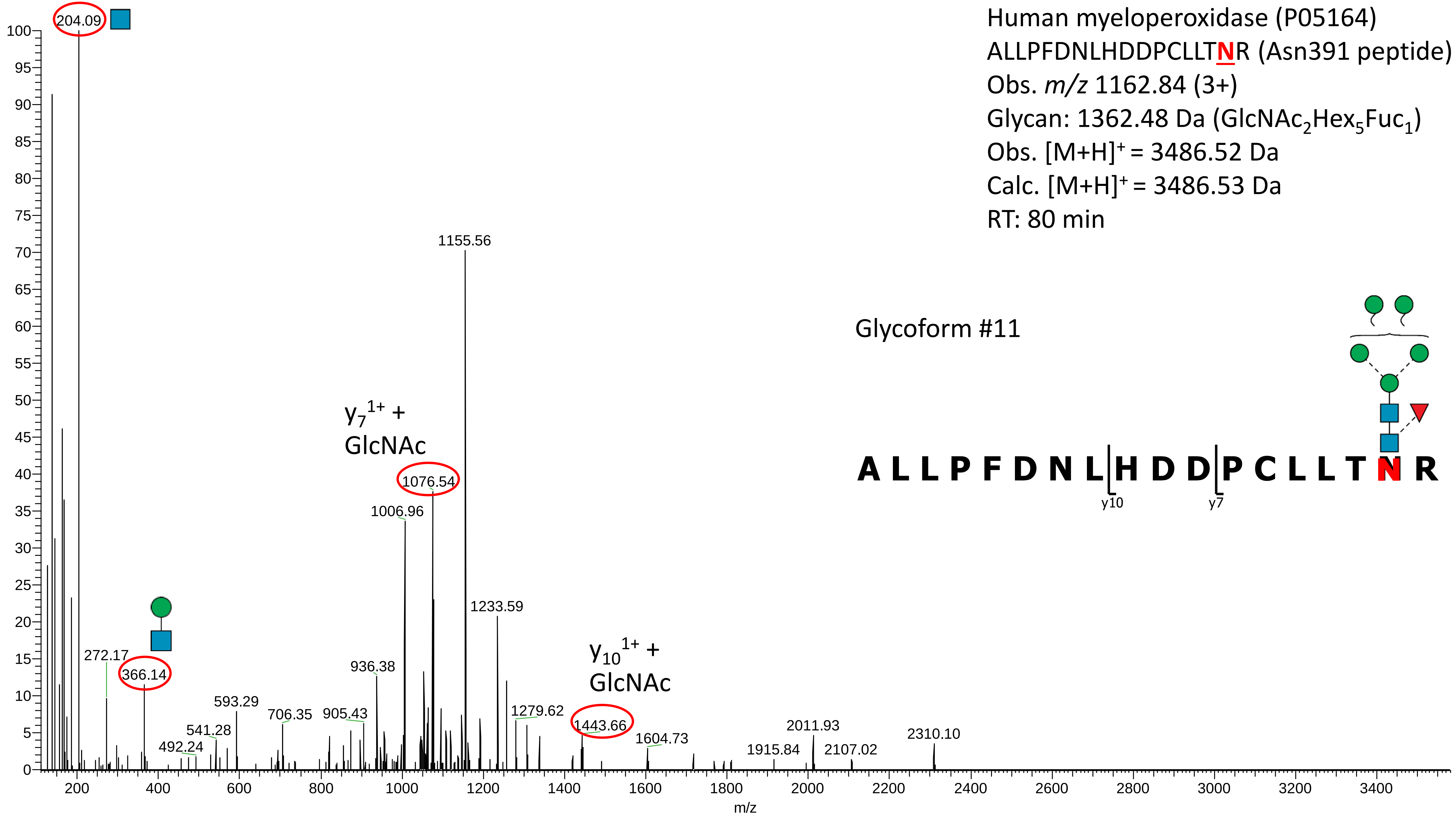
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1671.23 (2+)
Glycan: 1216.42 Da ($GlcNAc_2Hex_5$)
Obs. $[M+H]^+$ = 3341.46 Da
Calc. $[M+H]^+$ = 3340.47 Da
Off-by-X (manual) : 1
RT: 76 min

Glycoform #10



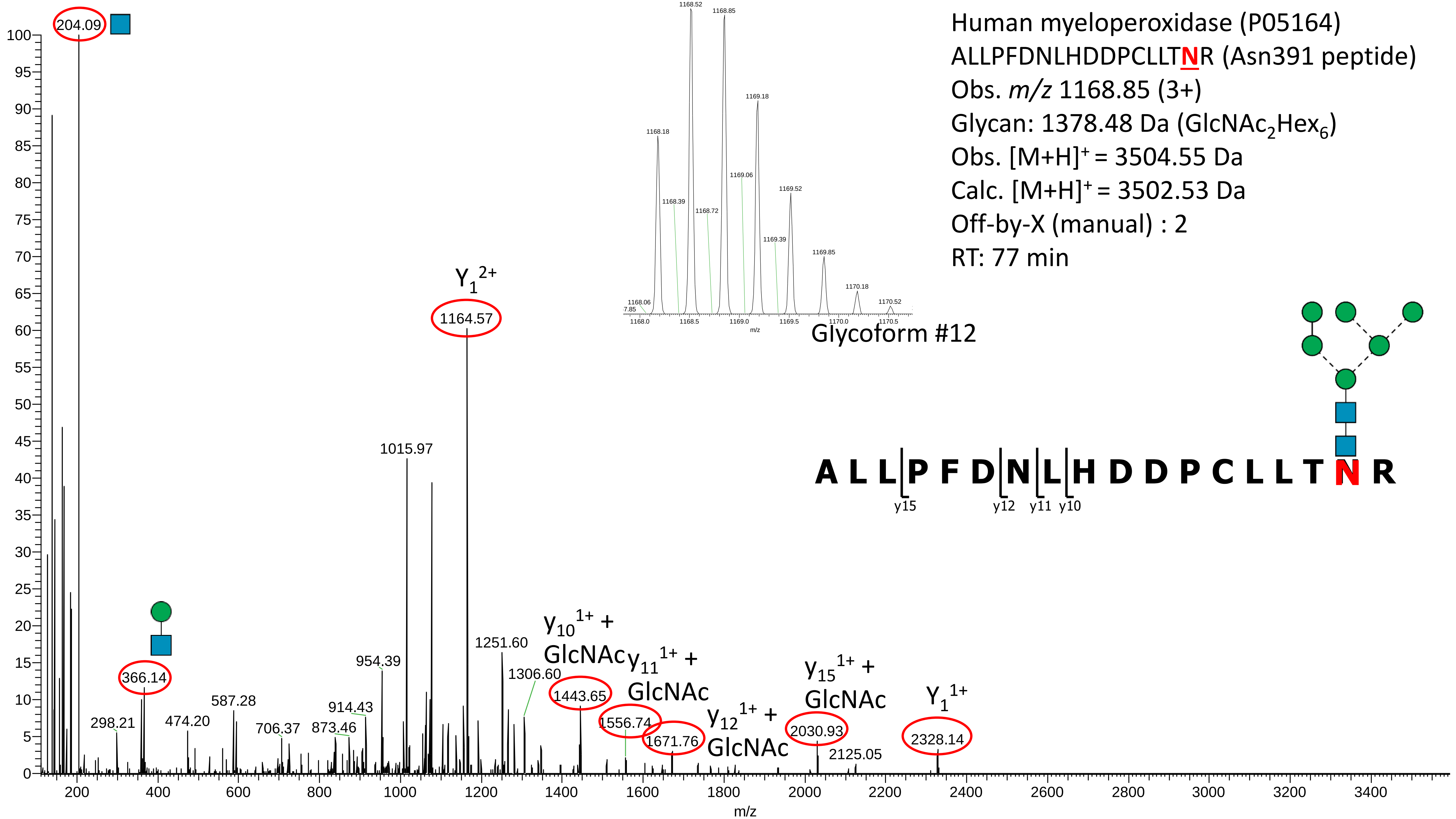
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1162.84 (3+)
Glycan: 1362.48 Da ($GlcNAc_2Hex_5Fuc_1$)
Obs. $[M+H]^+$ = 3486.52 Da
Calc. $[M+H]^+$ = 3486.53 Da
RT: 80 min

Glycoform #11



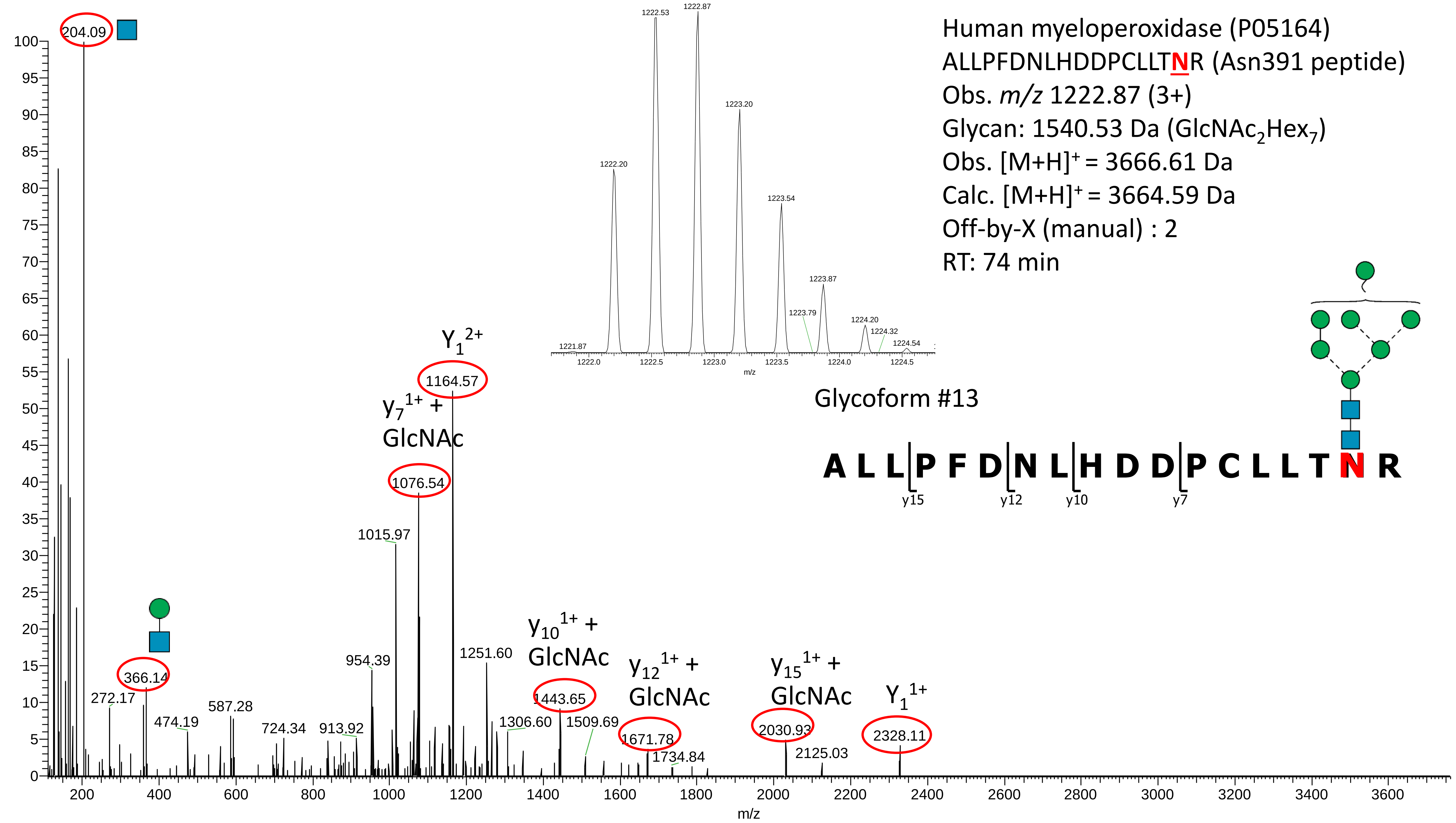
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1168.85 (3+)
Glycan: 1378.48 Da ($GlcNAc_2Hex_6$)
Obs. $[M+H]^+$ = 3504.55 Da
Calc. $[M+H]^+$ = 3502.53 Da
Off-by-X (manual) : 2
RT: 77 min

Glycoform #12



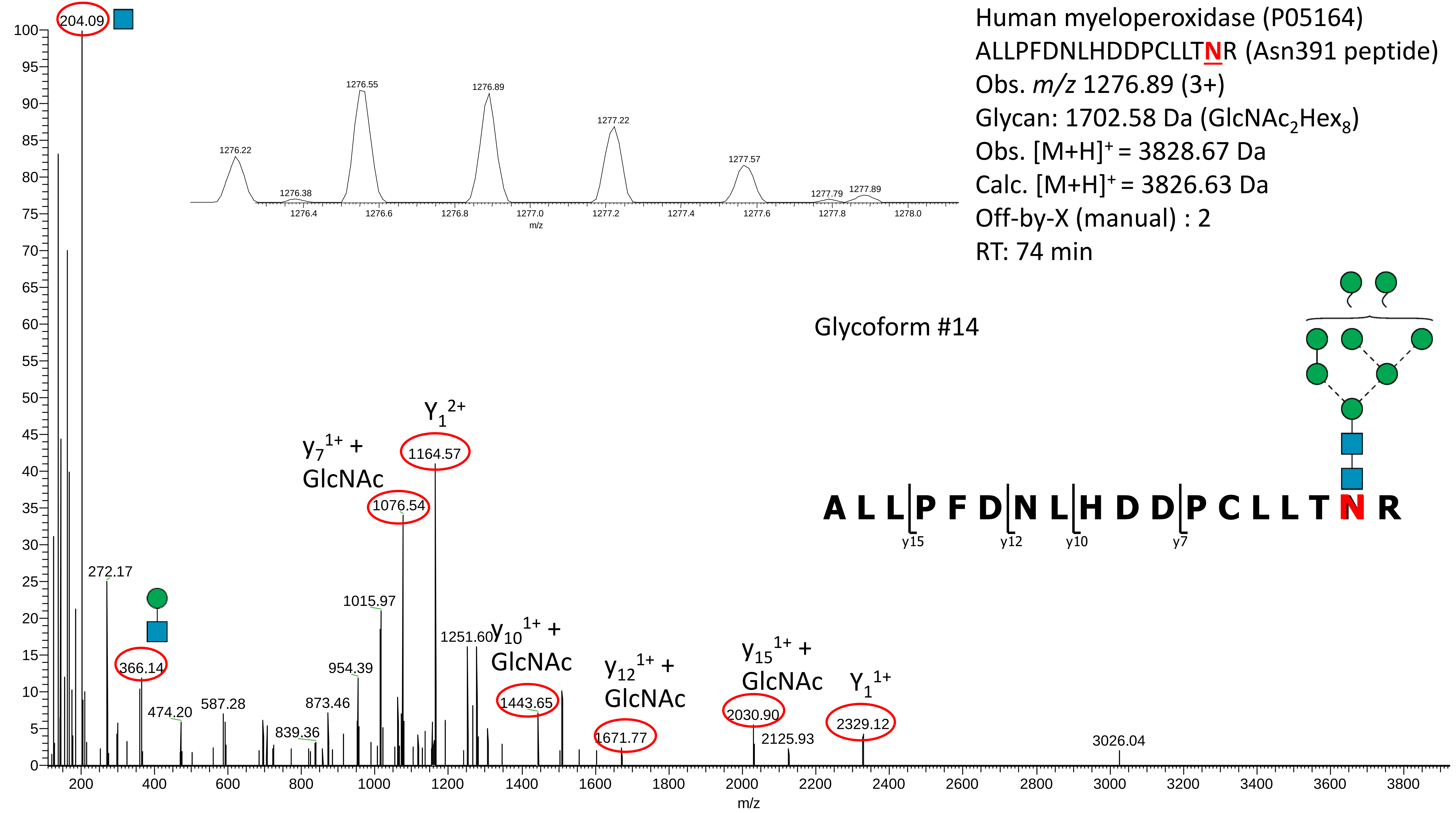
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1222.87 (3+)
Glycan: 1540.53 Da (GlcNAc$_2$Hex$_7$)
Obs. $[M+H]^+$ = 3666.61 Da
Calc. $[M+H]^+$ = 3664.59 Da
Off-by-X (manual) : 2
RT: 74 min

Glycoform #13

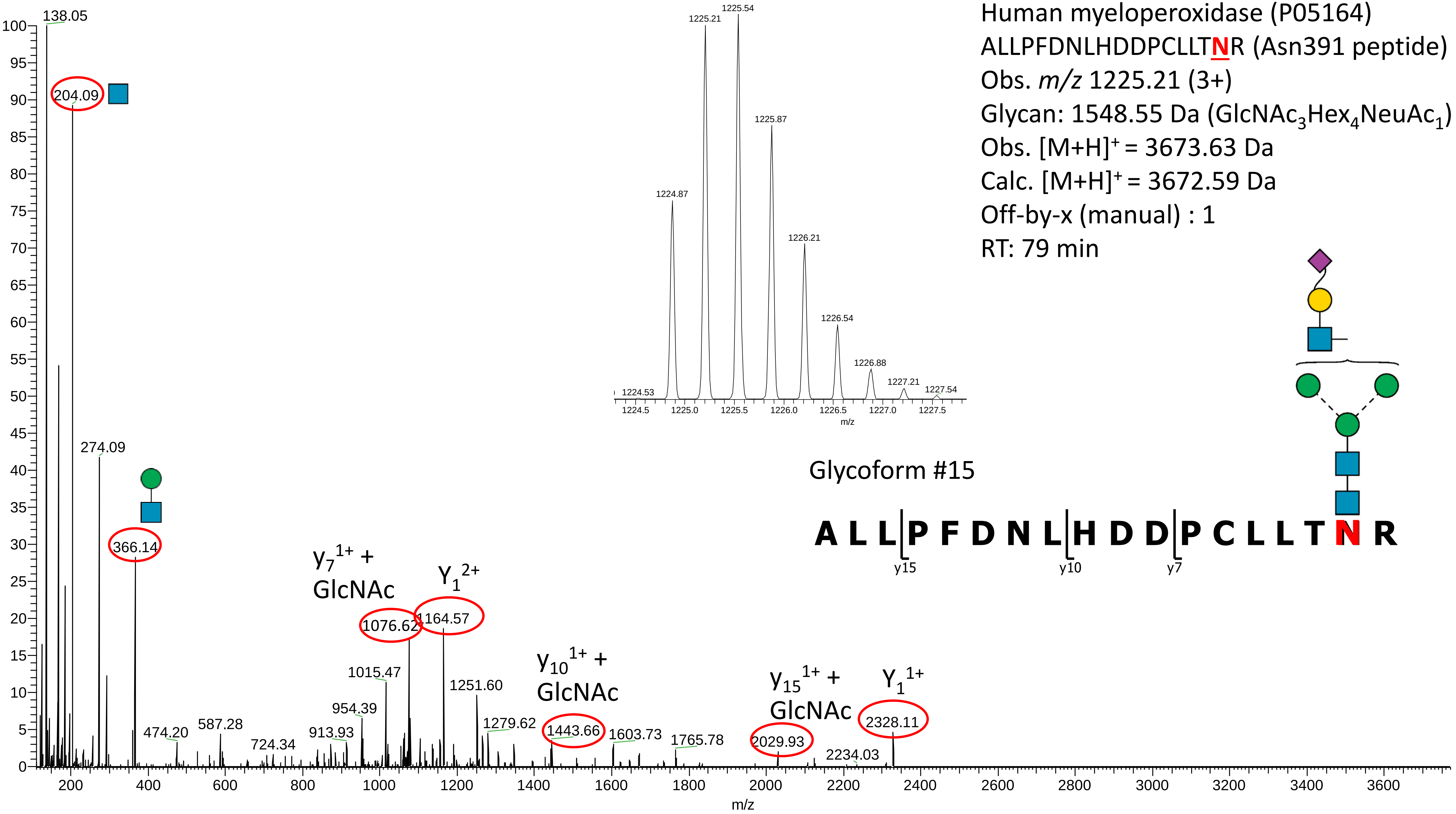


Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1276.89 (3+)
Glycan: 1702.58 Da ($GlcNAc_2Hex_8$)
Obs. $[M+H]^+$ = 3828.67 Da
Calc. $[M+H]^+$ = 3826.63 Da
Off-by-X (manual) : 2
RT: 74 min

Glycoform #14



Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1225.21 (3+)
Glycan: 1548.55 Da ($GlcNAc_3Hex_4NeuAc_1$)
Obs. $[M+H]^+$ = 3673.63 Da
Calc. $[M+H]^+$ = 3672.59 Da
Off-by-x (manual) : 1
RT: 79 min



Glycoform #15

A L L | P F D N L | H D D | P C L L T N R
y15 y10 y7

Human myeloperoxidase (P05164)

ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)

Obs. *m/z* 1279.56 (3+)

Glycan: 1710.60 Da (GlcNAc$_3$Hex$_5$NeuAc$_1$)

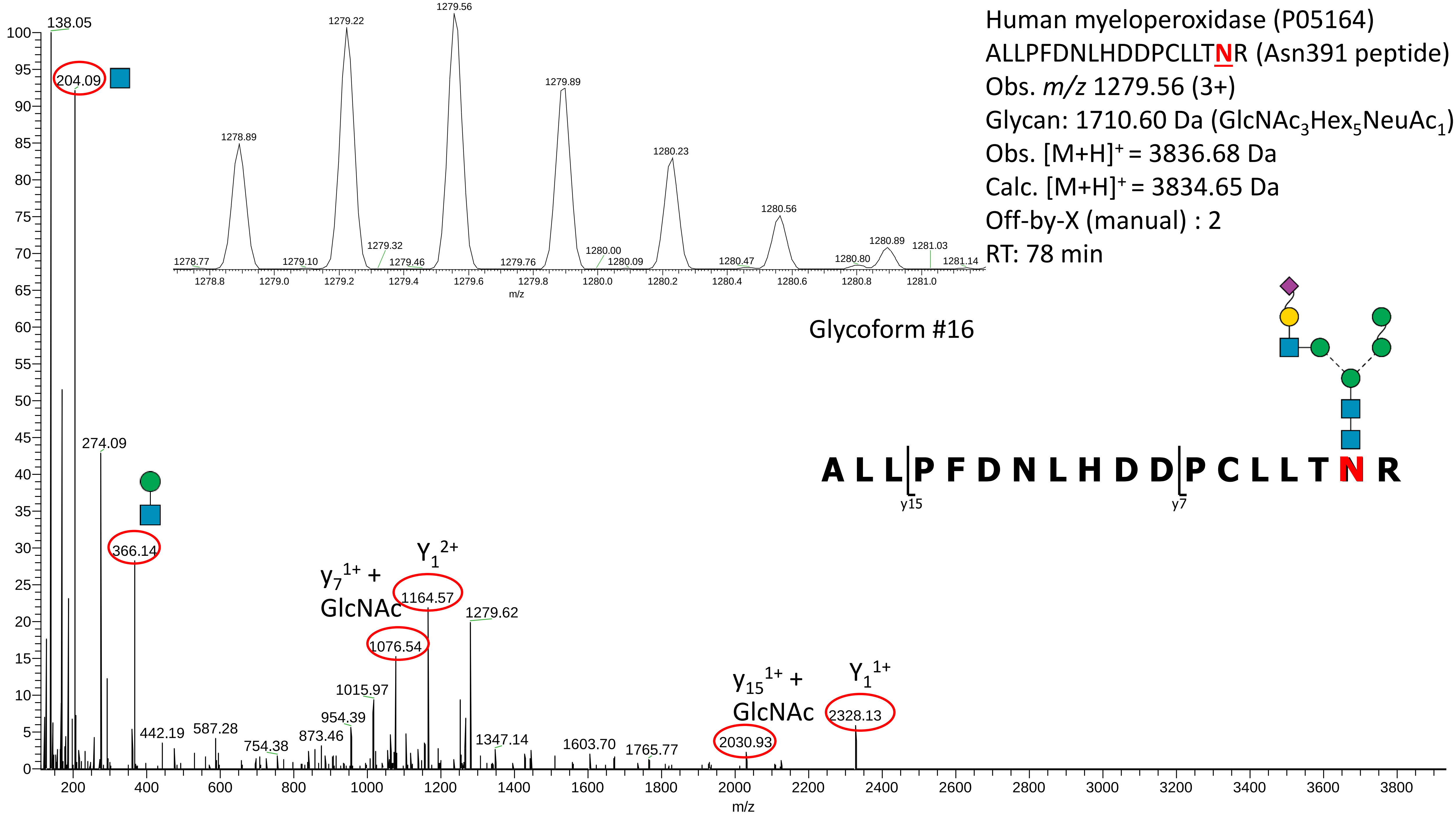
Obs. [M+H]$^+$ = 3836.68 Da

Calc. [M+H]$^+$ = 3834.65 Da

Off-by-X (manual) : 2

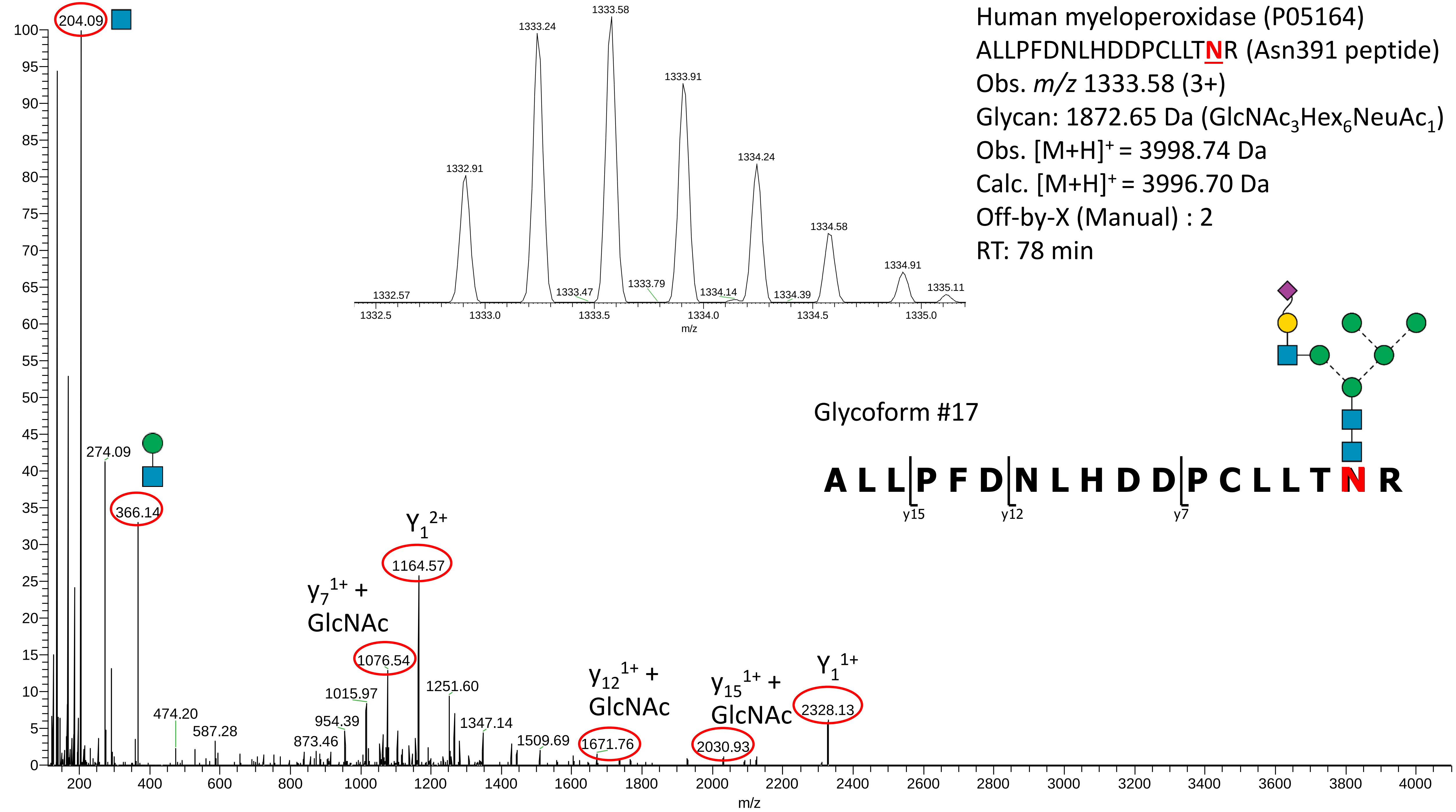
RT: 78 min

Glycoform #16



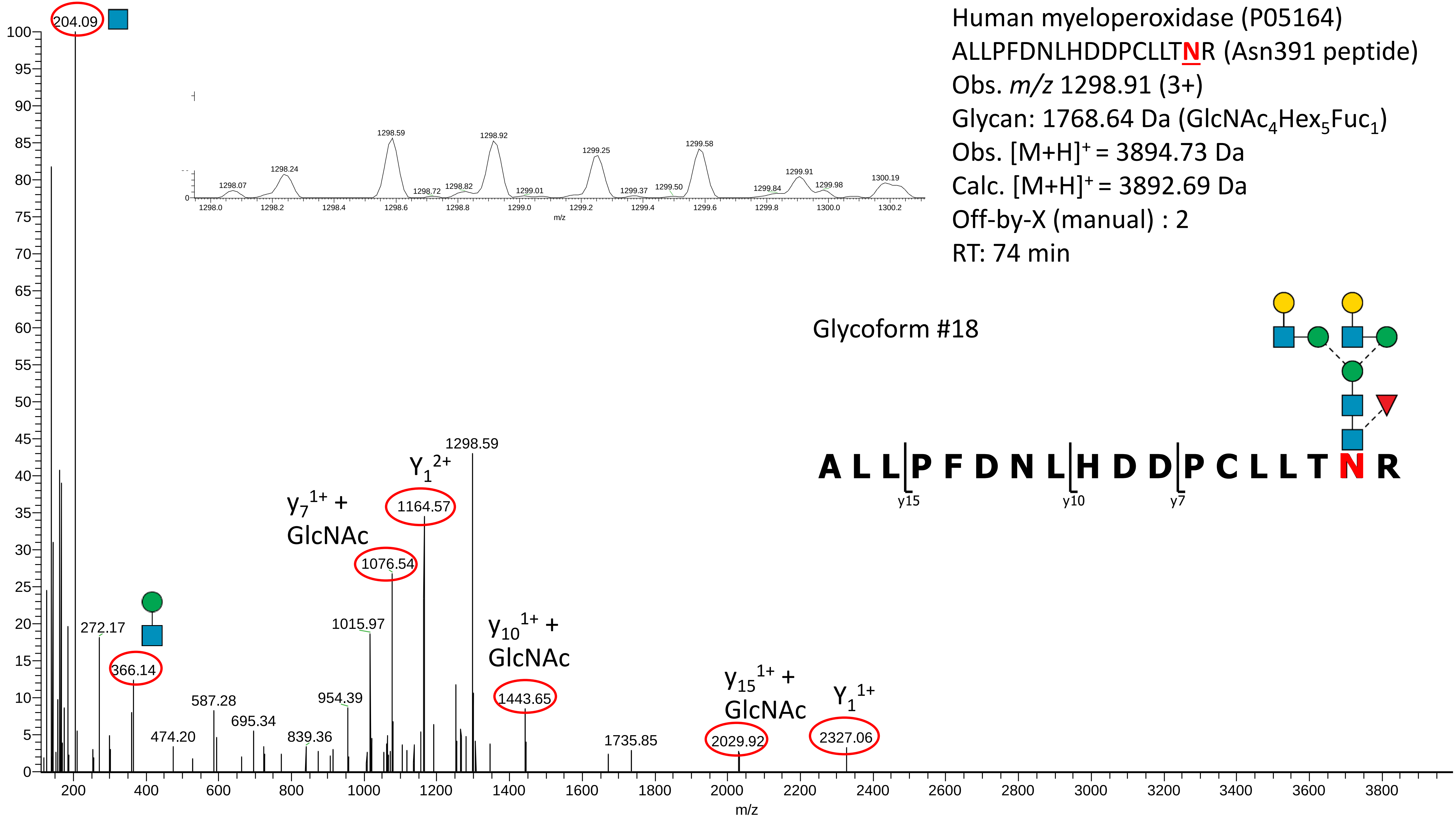
Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLT**N**R (Asn391 peptide)
Obs. *m/z* 1333.58 (3+)
Glycan: 1872.65 Da ($GlcNAc_3Hex_6NeuAc_1$)
Obs. $[M+H]^+$ = 3998.74 Da
Calc. $[M+H]^+$ = 3996.70 Da
Off-by-X (Manual) : 2
RT: 78 min

Glycoform #17



Human myeloperoxidase (P05164)
ALLPFDNLHDDPCLLTNR (Asn391 peptide)
Obs. *m/z* 1298.91 (3+)
Glycan: 1768.64 Da ($GlcNAc_4Hex_5Fuc_1$)
Obs. $[M+H]^+$ = 3894.73 Da
Calc. $[M+H]^+$ = 3892.69 Da
Off-by-X (manual) : 2
RT: 74 min

Glycoform #18



Supplementary Data S3D

Manually annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of all glycosylated and non-glycosylated peptides containing Asn483 identified from the analysis of the unenriched peptide mixtures of nMPO.

Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

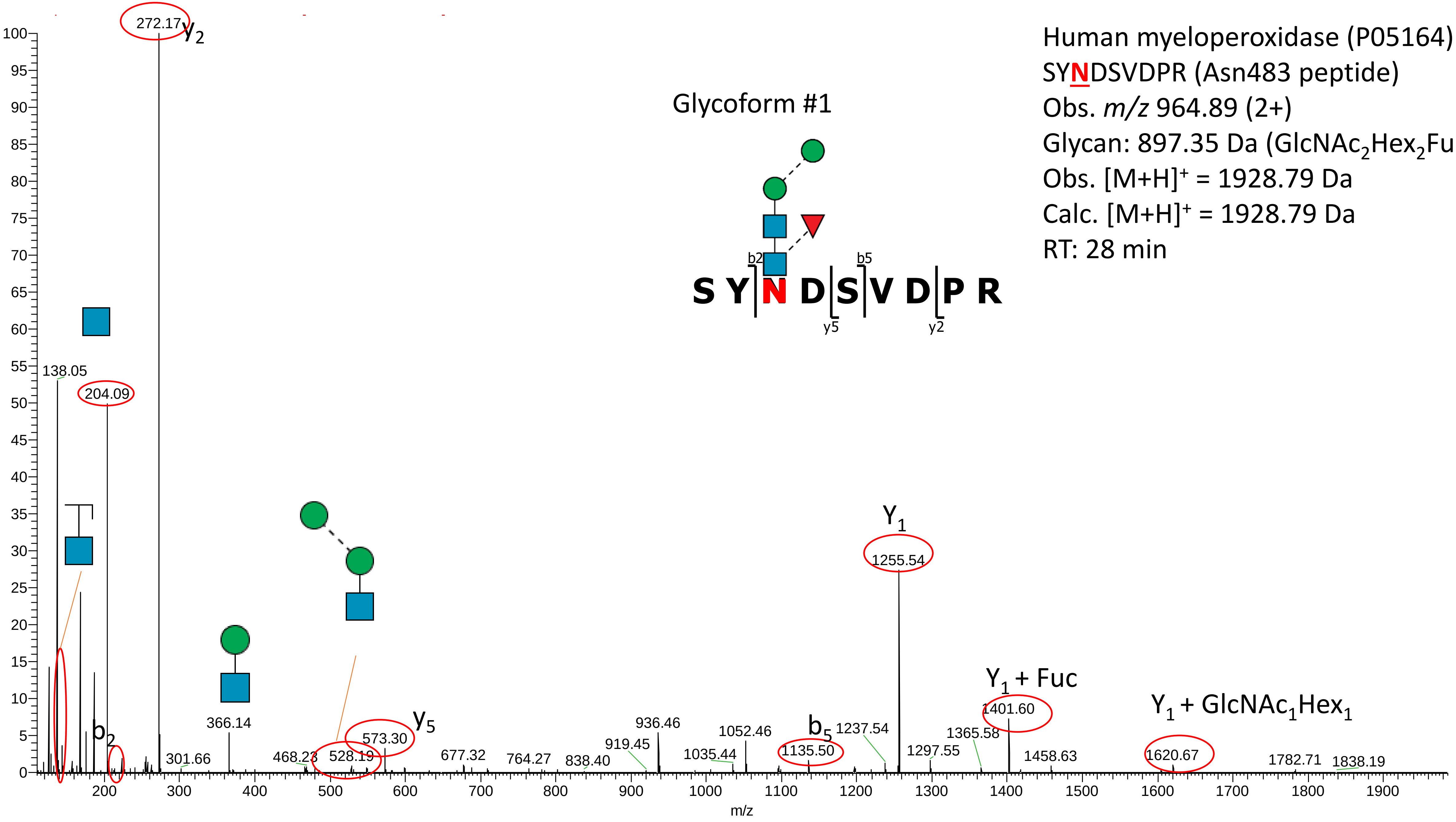
Obs. *m/z* 964.89 (2+)

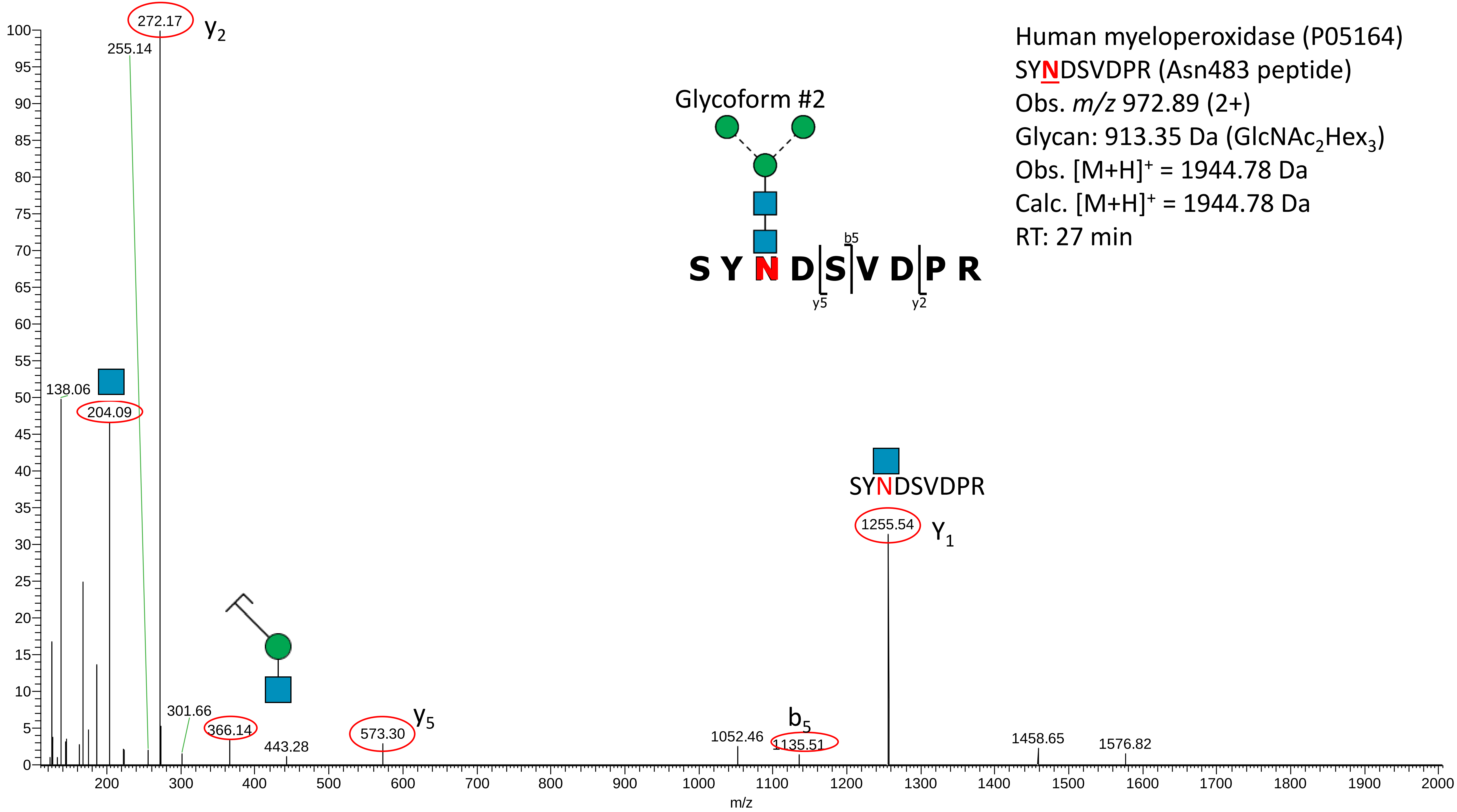
Glycan: 897.35 Da ($GlcNAc_2Hex_2Fuc_1$)

Obs. $[M+H]^+$ = 1928.79 Da

Calc. $[M+H]^+$ = 1928.79 Da

RT: 28 min





Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

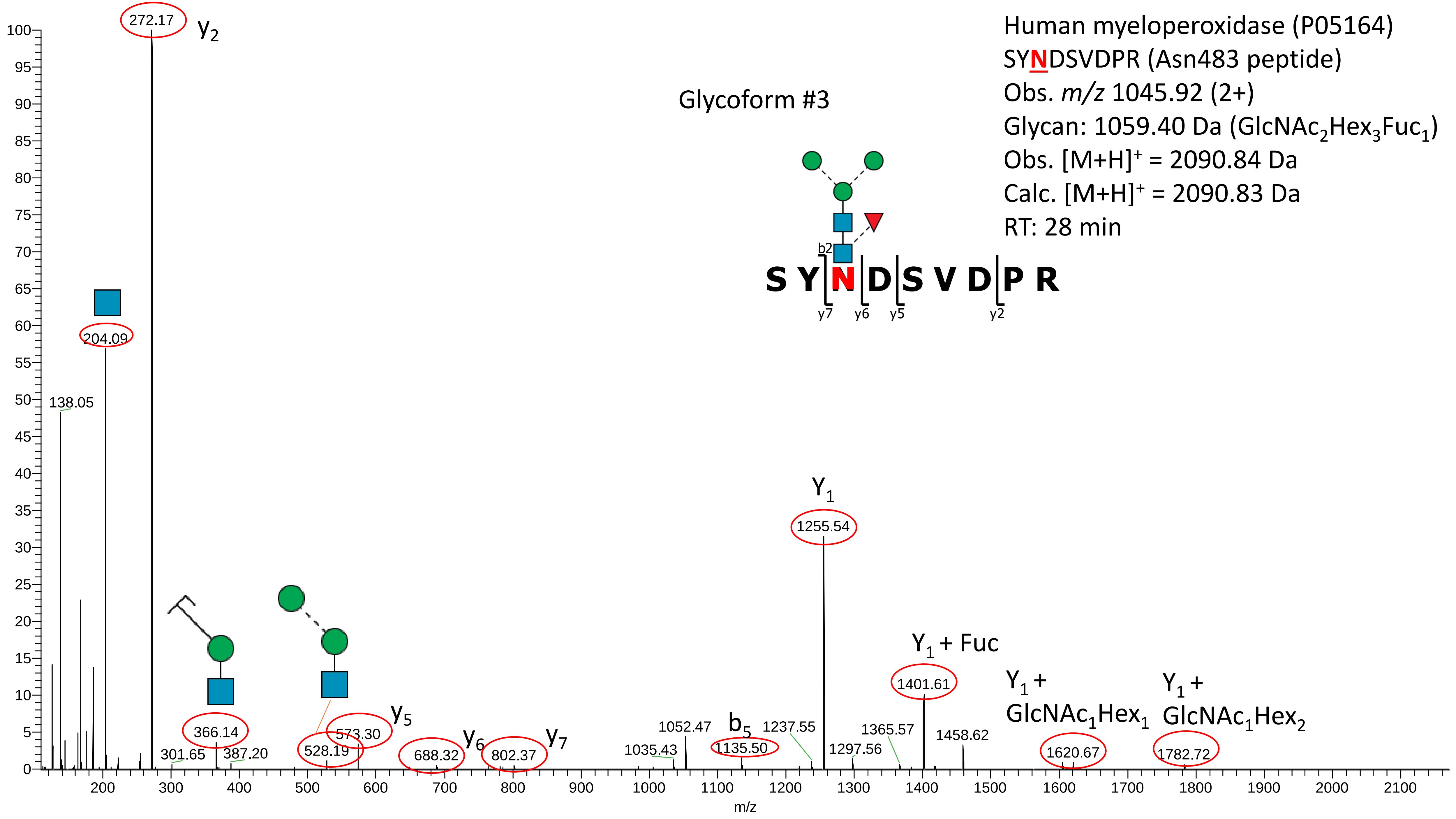
Obs. *m/z* 972.89 (2+)

Glycan: 913.35 Da (GlcNAc$_2$Hex$_3$)

Obs. [M+H]$^+$ = 1944.78 Da

Calc. [M+H]$^+$ = 1944.78 Da

RT: 27 min



Glycoform #3

Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

Obs. *m/z* 1045.92 (2+)

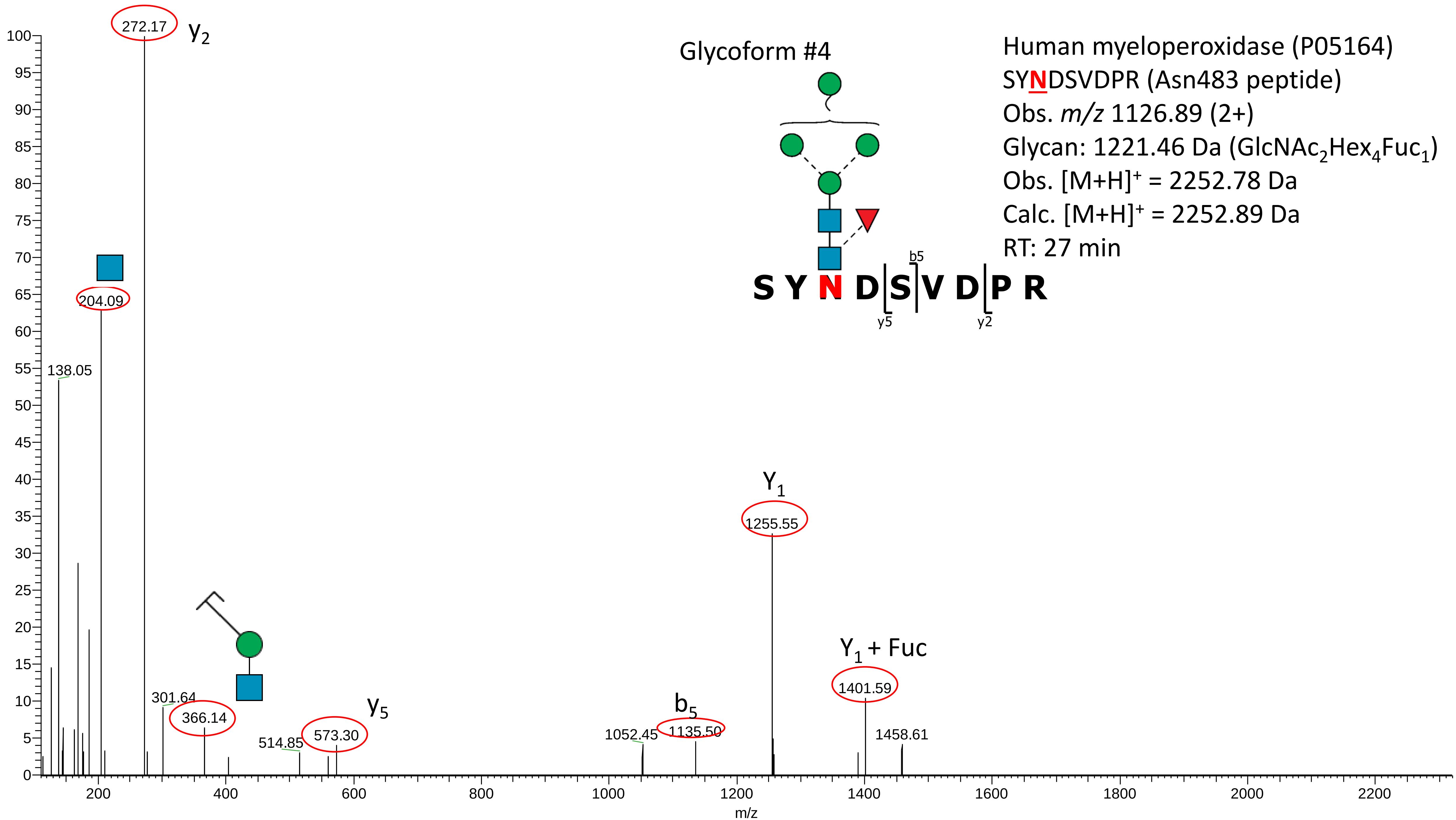
Glycan: 1059.40 Da ($GlcNAc_2Hex_3Fuc_1$)

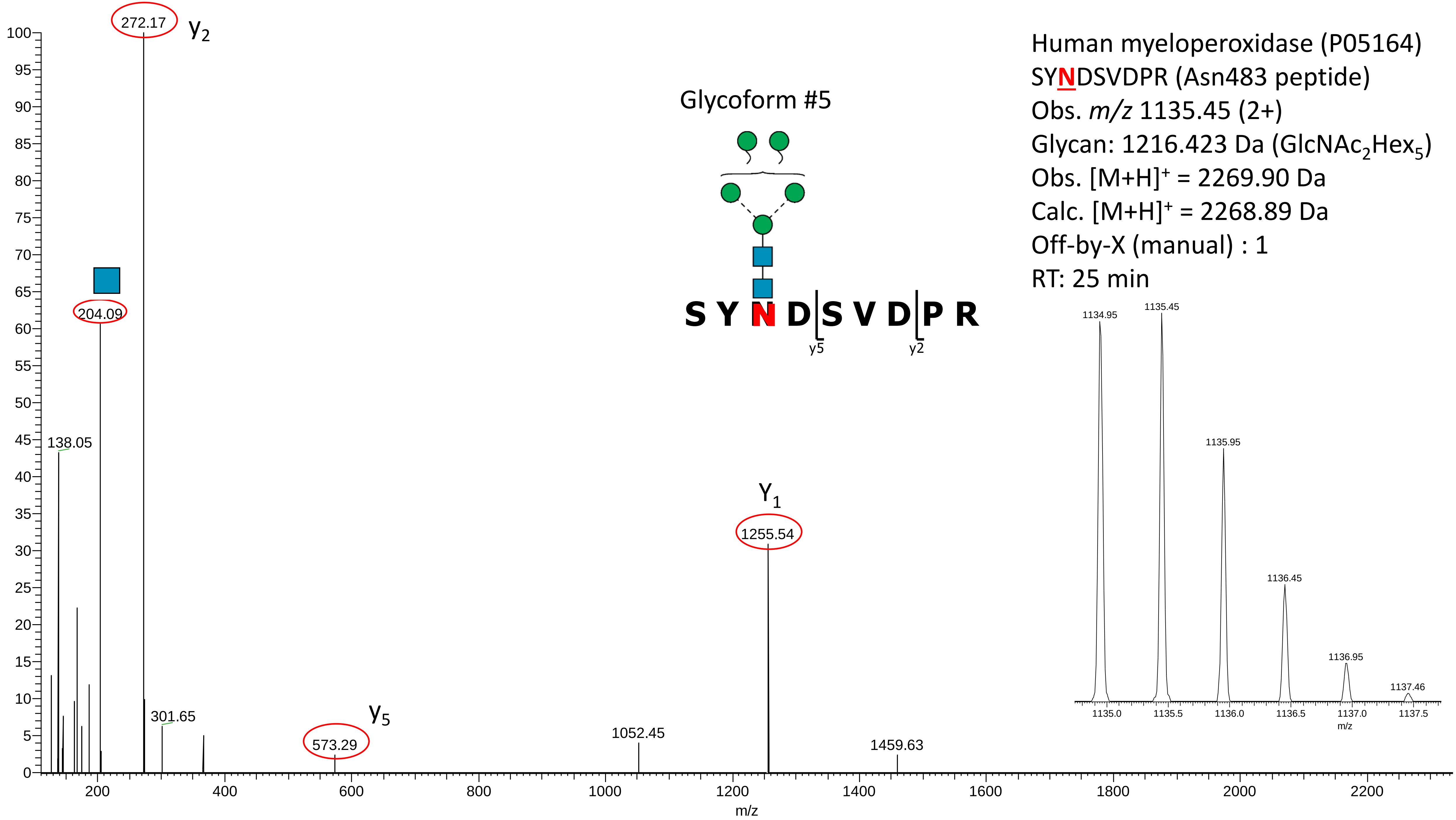
Obs. $[M+H]^+$ = 2090.84 Da

Calc. $[M+H]^+$ = 2090.83 Da

RT: 28 min

Human myeloperoxidase (P05164)
SY**N**DSVDPR (Asn483 peptide)
Obs. *m/z* 1126.89 (2+)
Glycan: 1221.46 Da ($GlcNAc_2Hex_4Fuc_1$)
Obs. $[M+H]^+$ = 2252.78 Da
Calc. $[M+H]^+$ = 2252.89 Da
RT: 27 min





Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

Obs. *m/z* 1135.45 (2+)

Glycan: 1216.423 Da ($GlcNAc_2Hex_5$)

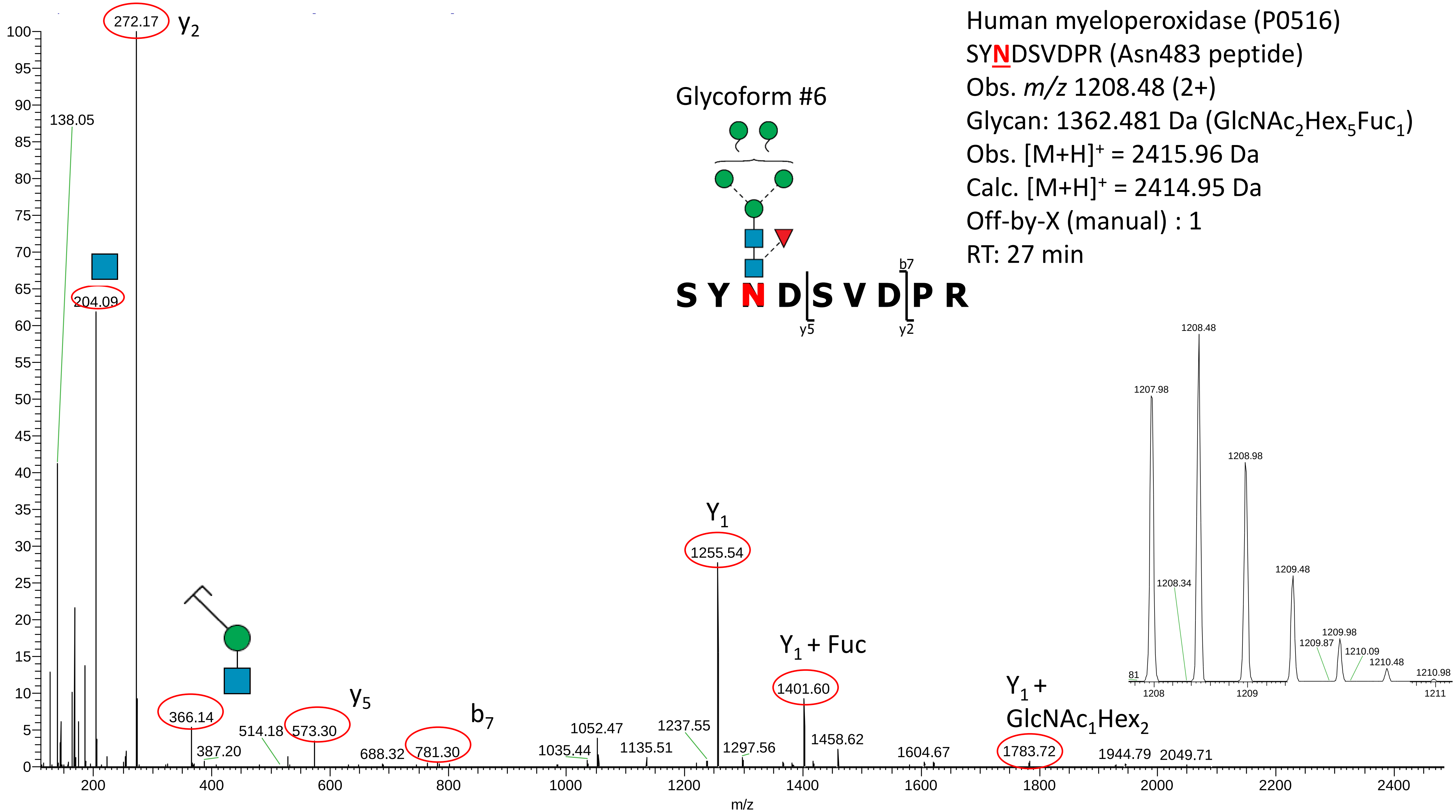
Obs. $[M+H]^+$ = 2269.90 Da

Calc. $[M+H]^+$ = 2268.89 Da

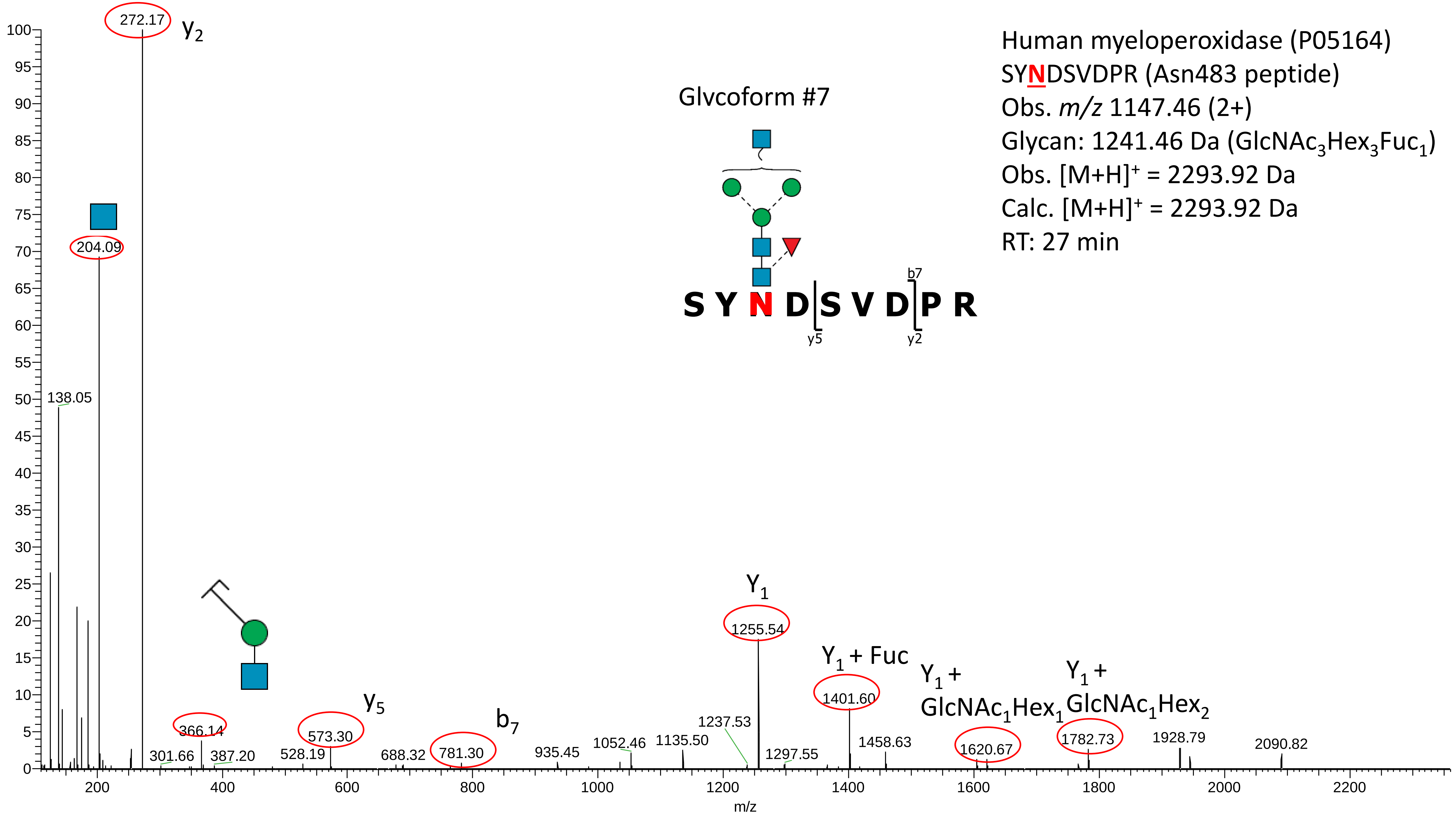
Off-by-X (manual) : 1

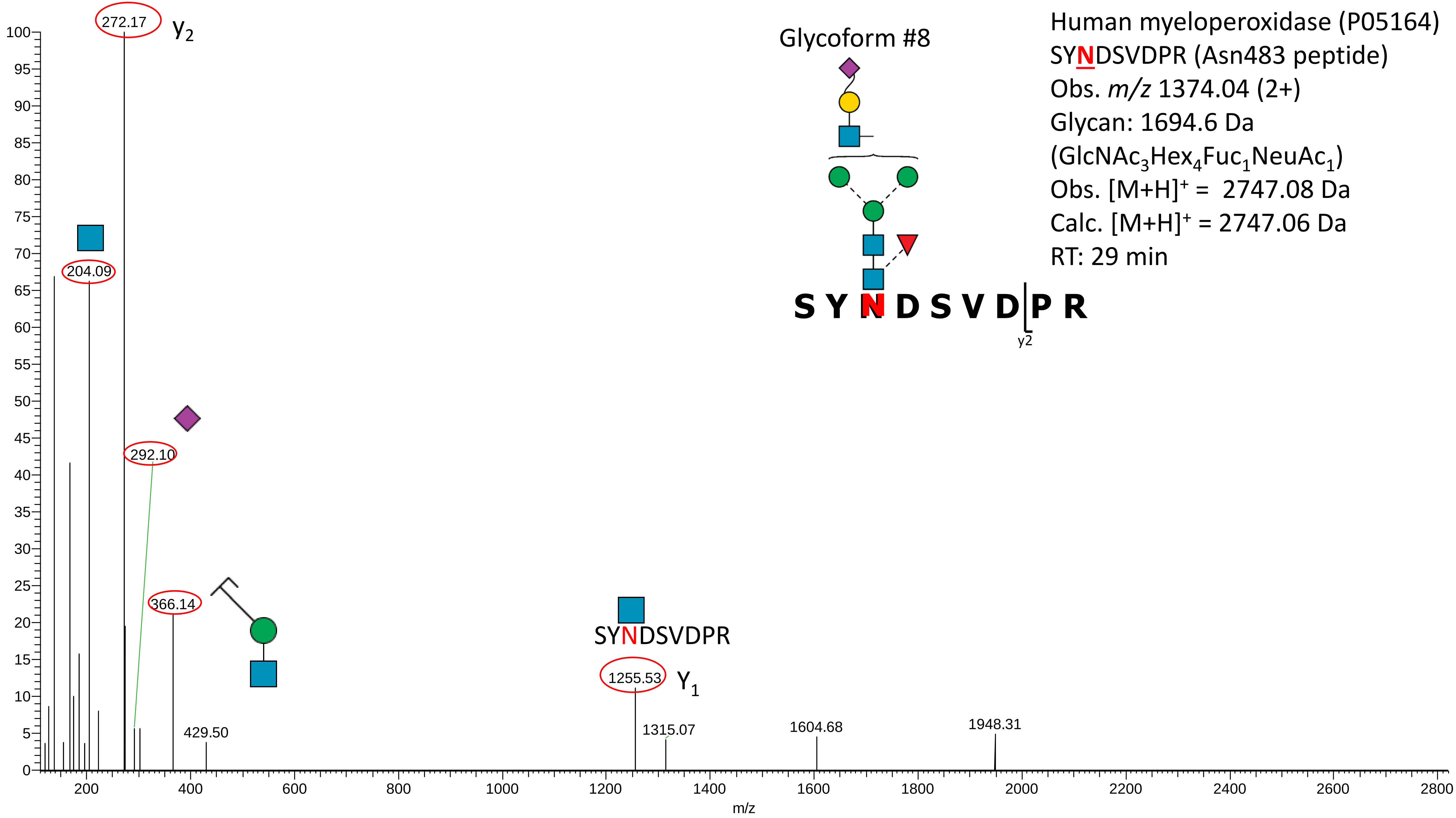
RT: 25 min

Human myeloperoxidase (P0516)
SY**N**DSVDPR (Asn483 peptide)
Obs. *m/z* 1208.48 (2+)
Glycan: 1362.481 Da ($GlcNAc_2Hex_5Fuc_1$)
Obs. $[M+H]^+$ = 2415.96 Da
Calc. $[M+H]^+$ = 2414.95 Da
Off-by-X (manual) : 1
RT: 27 min



Human myeloperoxidase (P05164)
SY**N**DSVDPR (Asn483 peptide)
Obs. *m/z* 1147.46 (2+)
Glycan: 1241.46 Da (GlcNAc$_3$Hex$_3$Fuc$_1$)
Obs. [M+H]$^+$ = 2293.92 Da
Calc. [M+H]$^+$ = 2293.92 Da
RT: 27 min





Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

Obs. *m/z* 1374.04 (2+)

Glycan: 1694.6 Da

($GlcNAc_3Hex_4Fuc_1NeuAc_1$)

Obs. $[M+H]^+$ = 2747.08 Da

Calc. $[M+H]^+$ = 2747.06 Da

RT: 29 min

Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

Obs. *m/z* 1024.39 (3+)

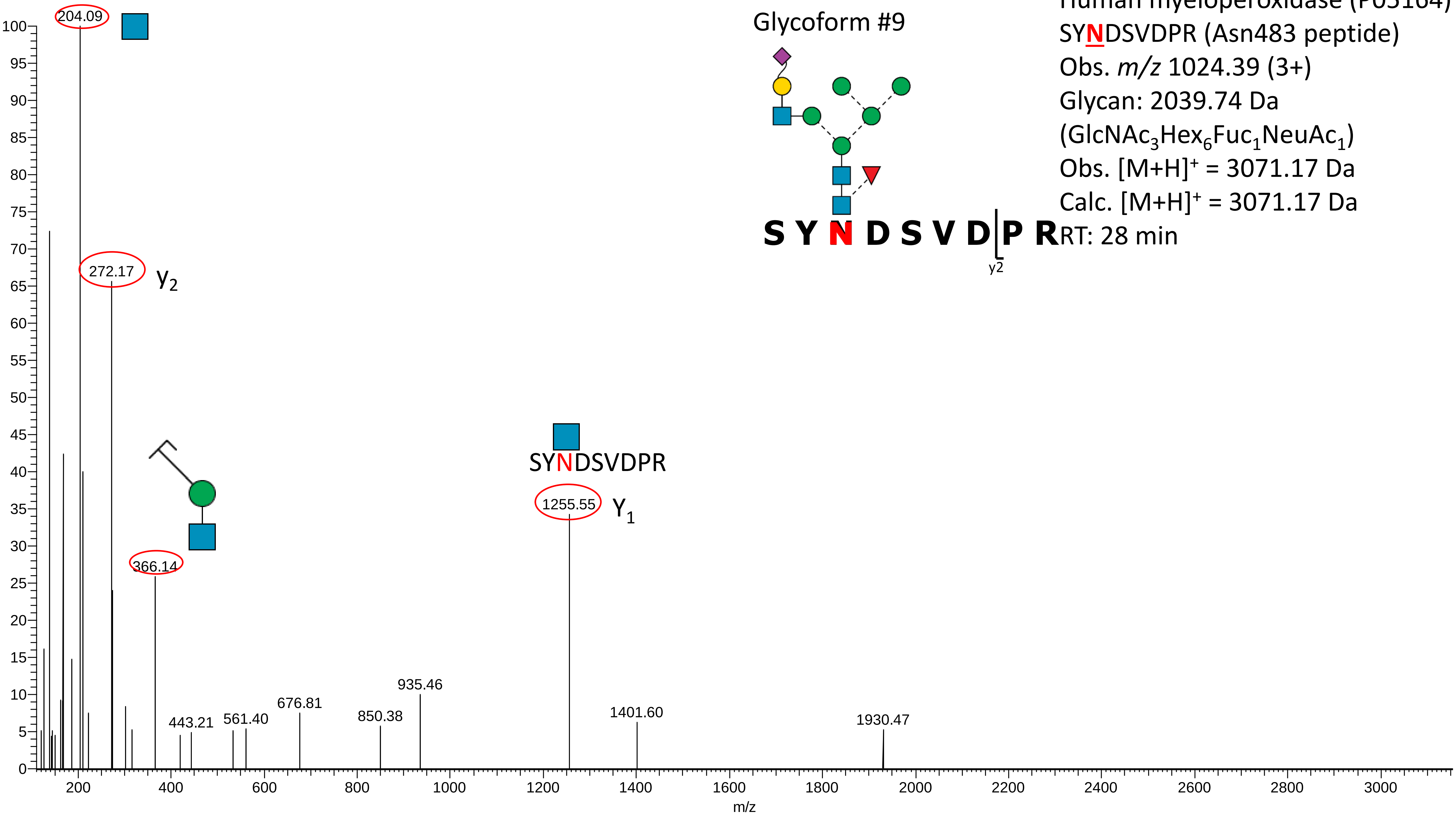
Glycan: 2039.74 Da

($GlcNAc_3Hex_6Fuc_1NeuAc_1$)

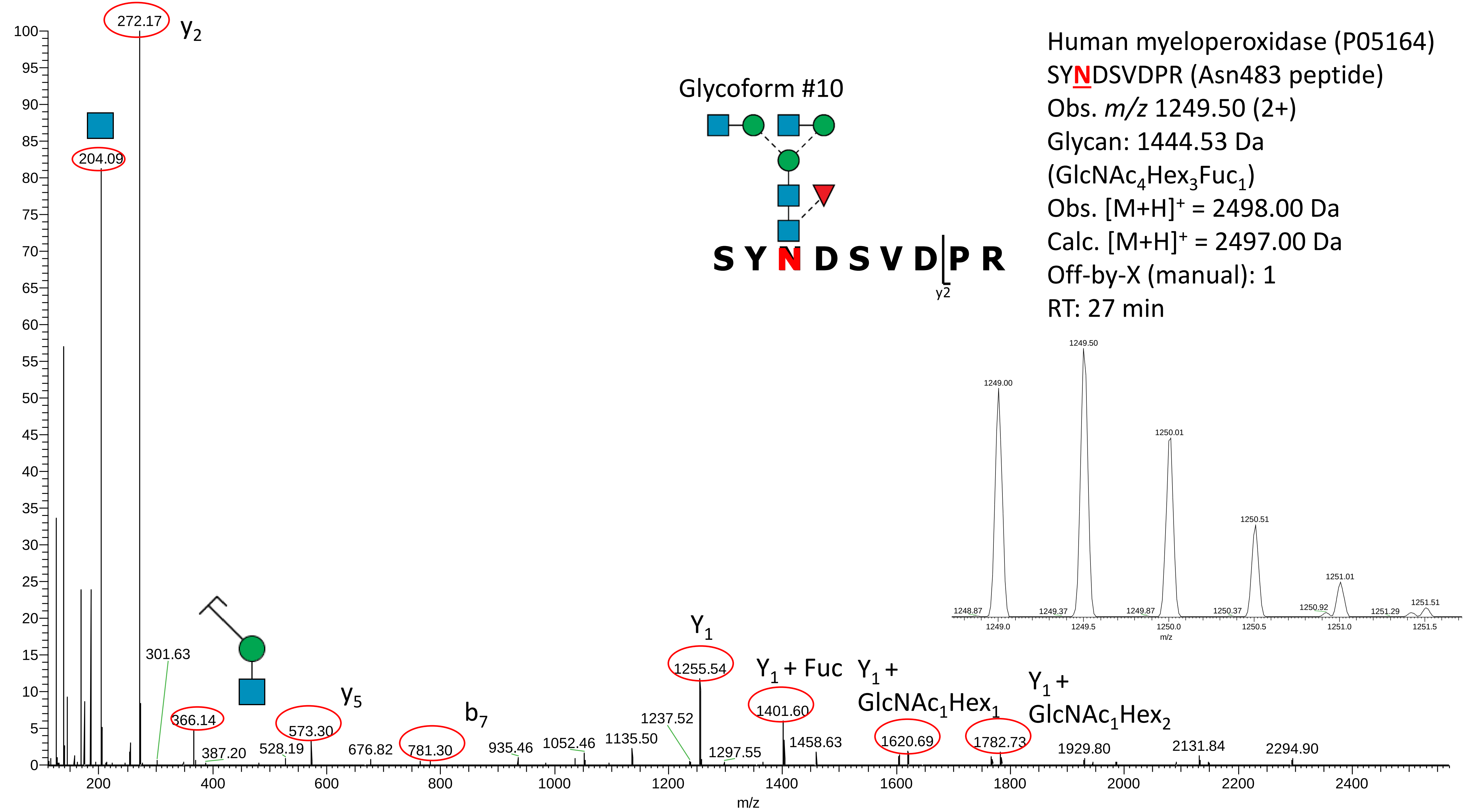
Obs. $[M+H]^+$ = 3071.17 Da

Calc. $[M+H]^+$ = 3071.17 Da

RT: 28 min



Glycoform #10



Human myeloperoxidase (P05164)

SY**N**DSVDPR (Asn483 peptide)

Obs. *m/z* 1249.50 (2+)

Glycan: 1444.53 Da

(GlcNAc$_4$Hex$_3$Fuc$_1$)

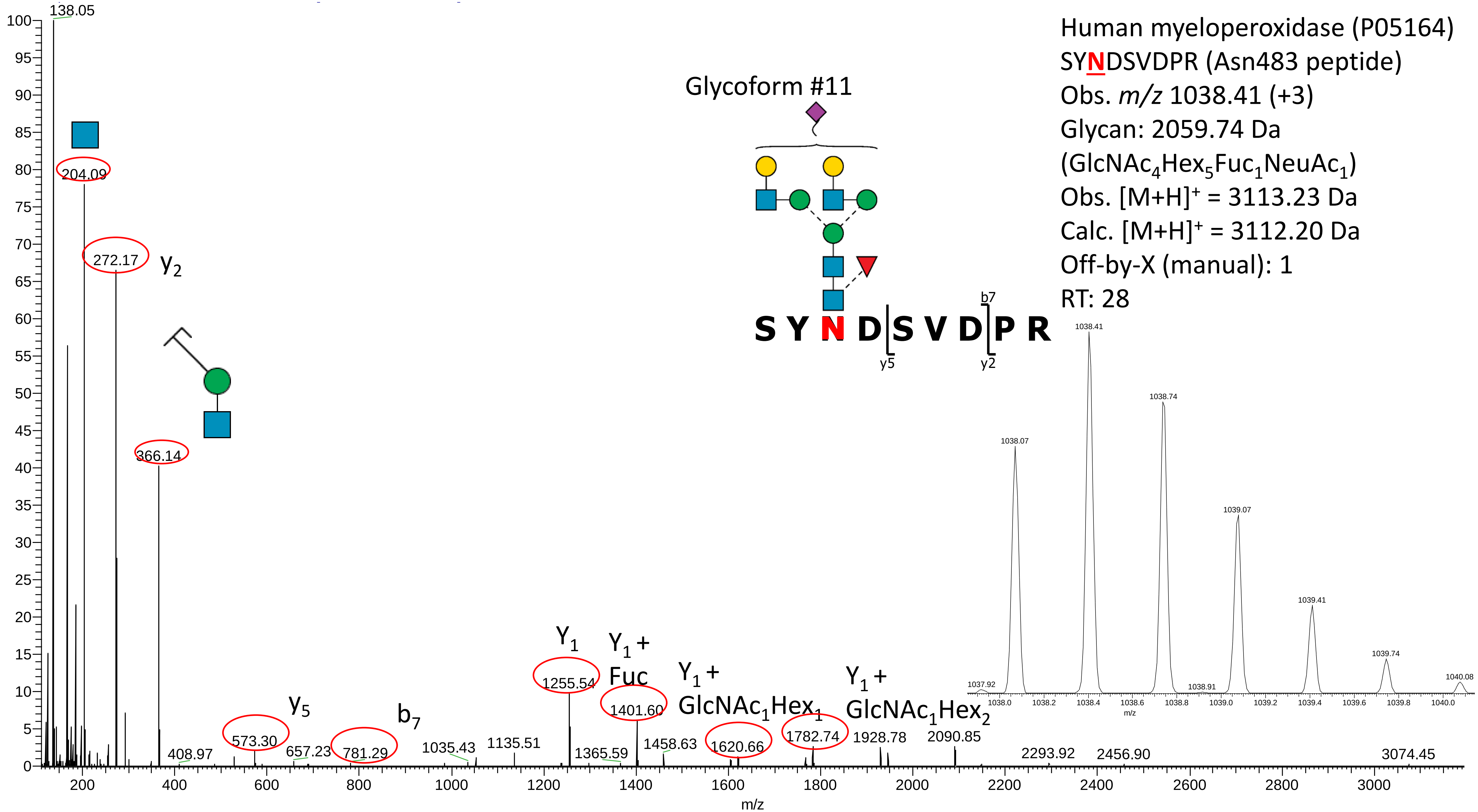
Obs. [M+H]$^+$ = 2498.00 Da

Calc. [M+H]$^+$ = 2497.00 Da

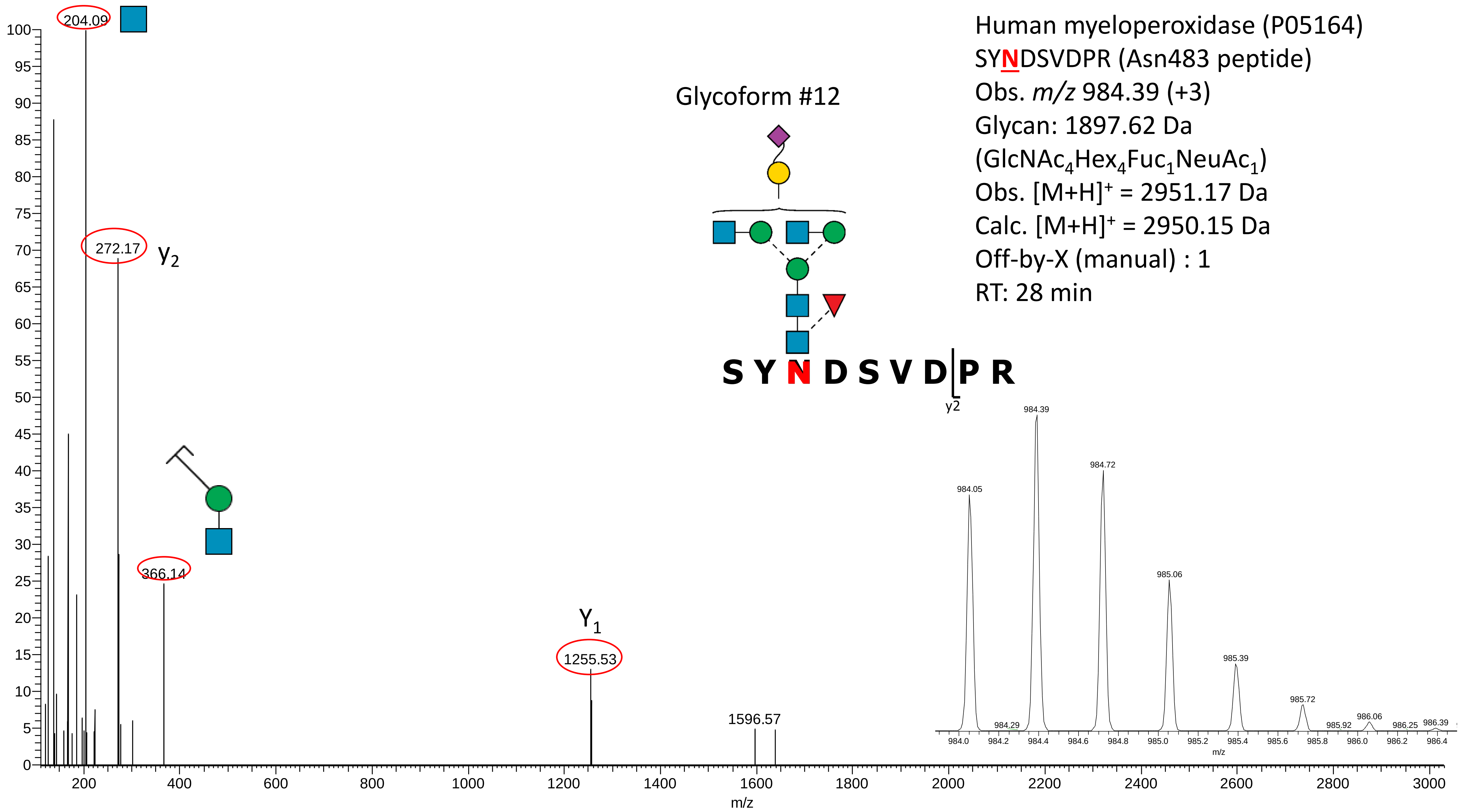
Off-by-X (manual): 1

RT: 27 min

Human myeloperoxidase (P05164)
SY**N**DSVDPR (Asn483 peptide)
Obs. *m/z* 1038.41 (+3)
Glycan: 2059.74 Da
($GlcNAc_4Hex_5Fuc_1NeuAc_1$)
Obs. $[M+H]^+$ = 3113.23 Da
Calc. $[M+H]^+$ = 3112.20 Da
Off-by-X (manual): 1
RT: 28



Human myeloperoxidase (P05164)
SY**N**DSVDPR (Asn483 peptide)
Obs. *m/z* 984.39 (+3)
Glycan: 1897.62 Da
($GlcNAc_4Hex_4Fuc_1NeuAc_1$)
Obs. $[M+H]^+$ = 2951.17 Da
Calc. $[M+H]^+$ = 2950.15 Da
Off-by-X (manual) : 1
RT: 28 min

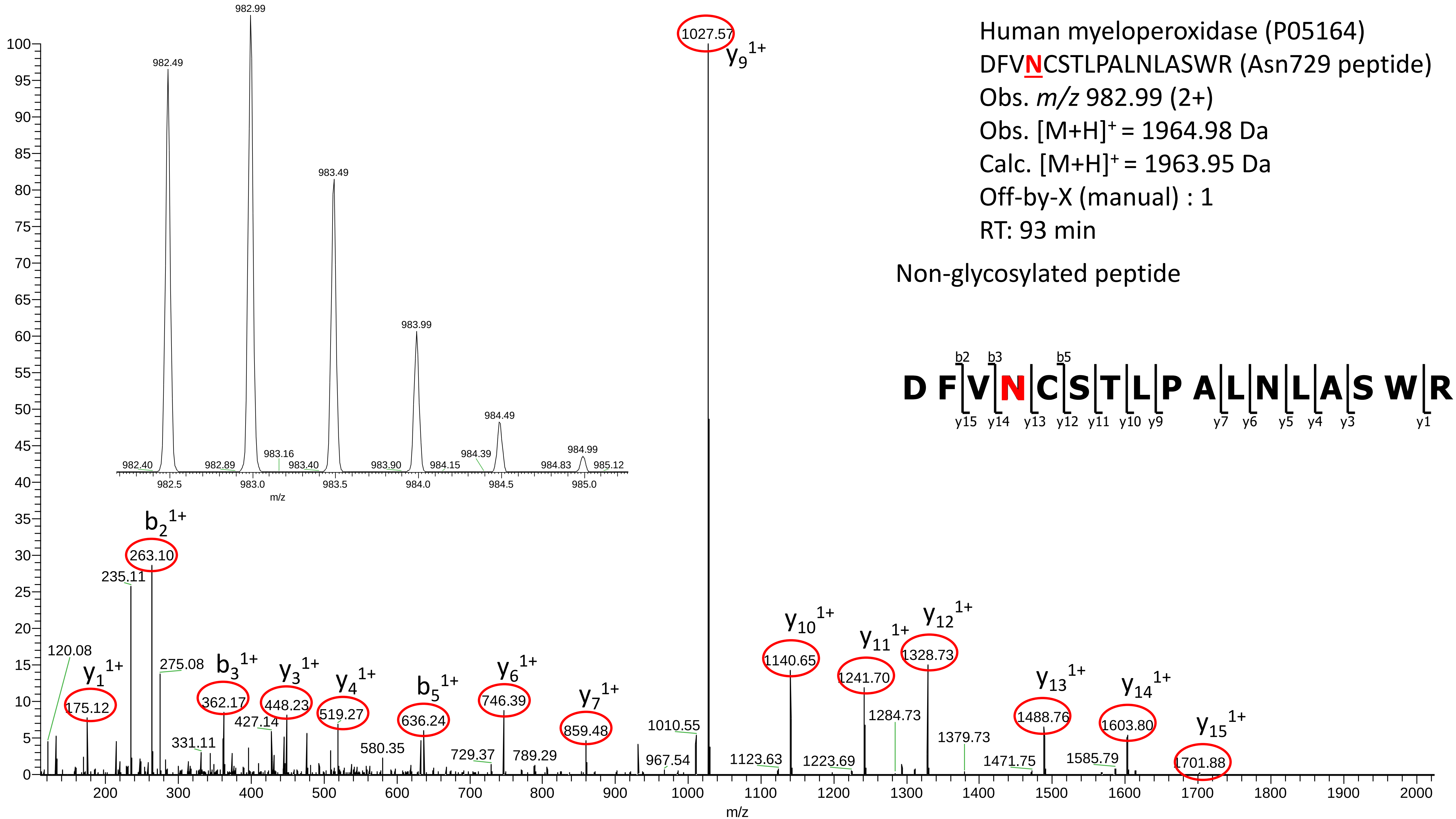


Supplementary Data S3E

Manually annotated reversed phase-LC-ESI-HCD-MS/MS (+) spectra of all glycosylated and non-glycosylated peptides containing Asn729 identified from the analysis of unenriched peptide mixtures of nMPO.

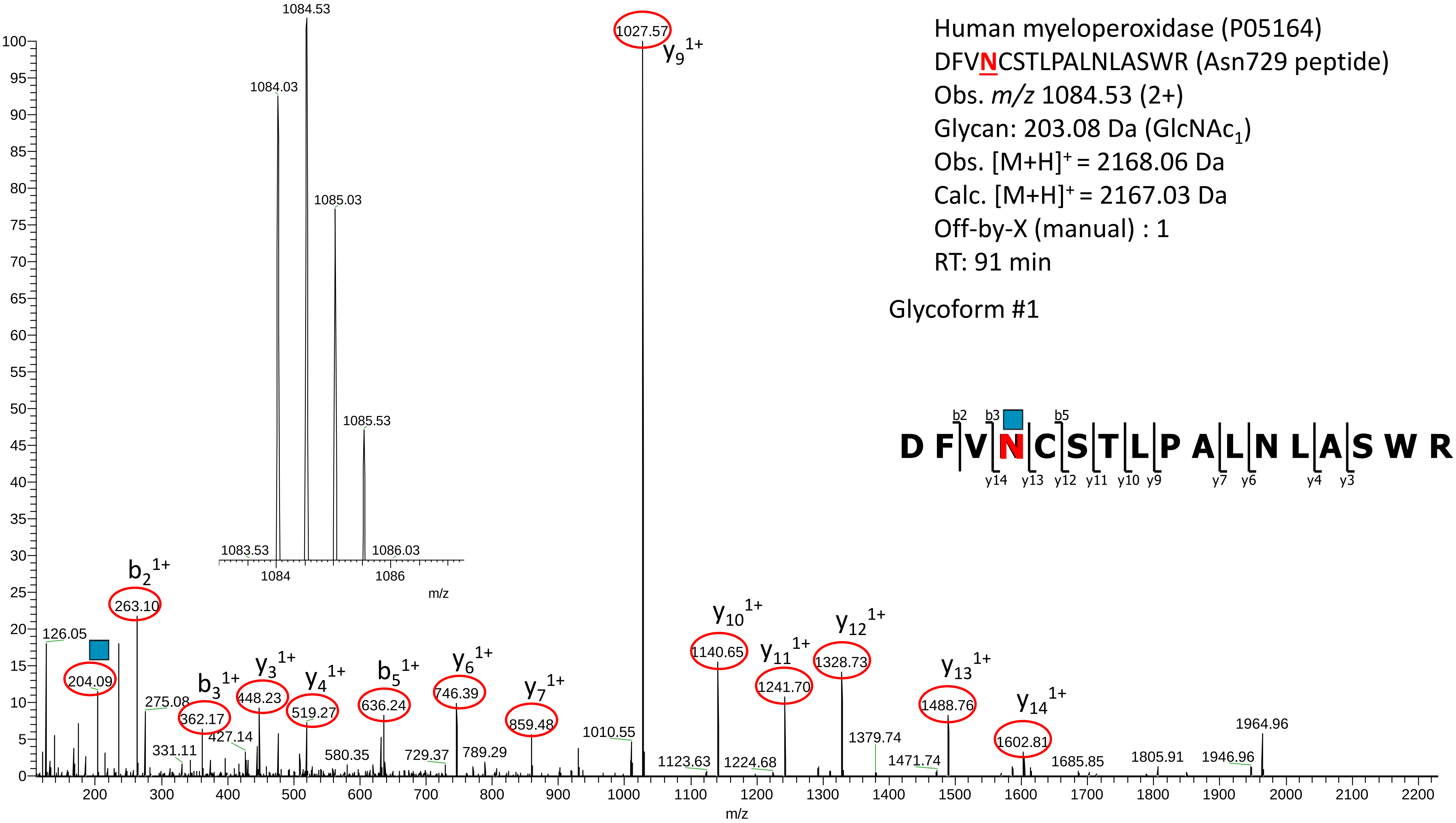
Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 982.99 (2+)
Obs. $[M+H]^+$ = 1964.98 Da
Calc. $[M+H]^+$ = 1963.95 Da
Off-by-X (manual) : 1
RT: 93 min

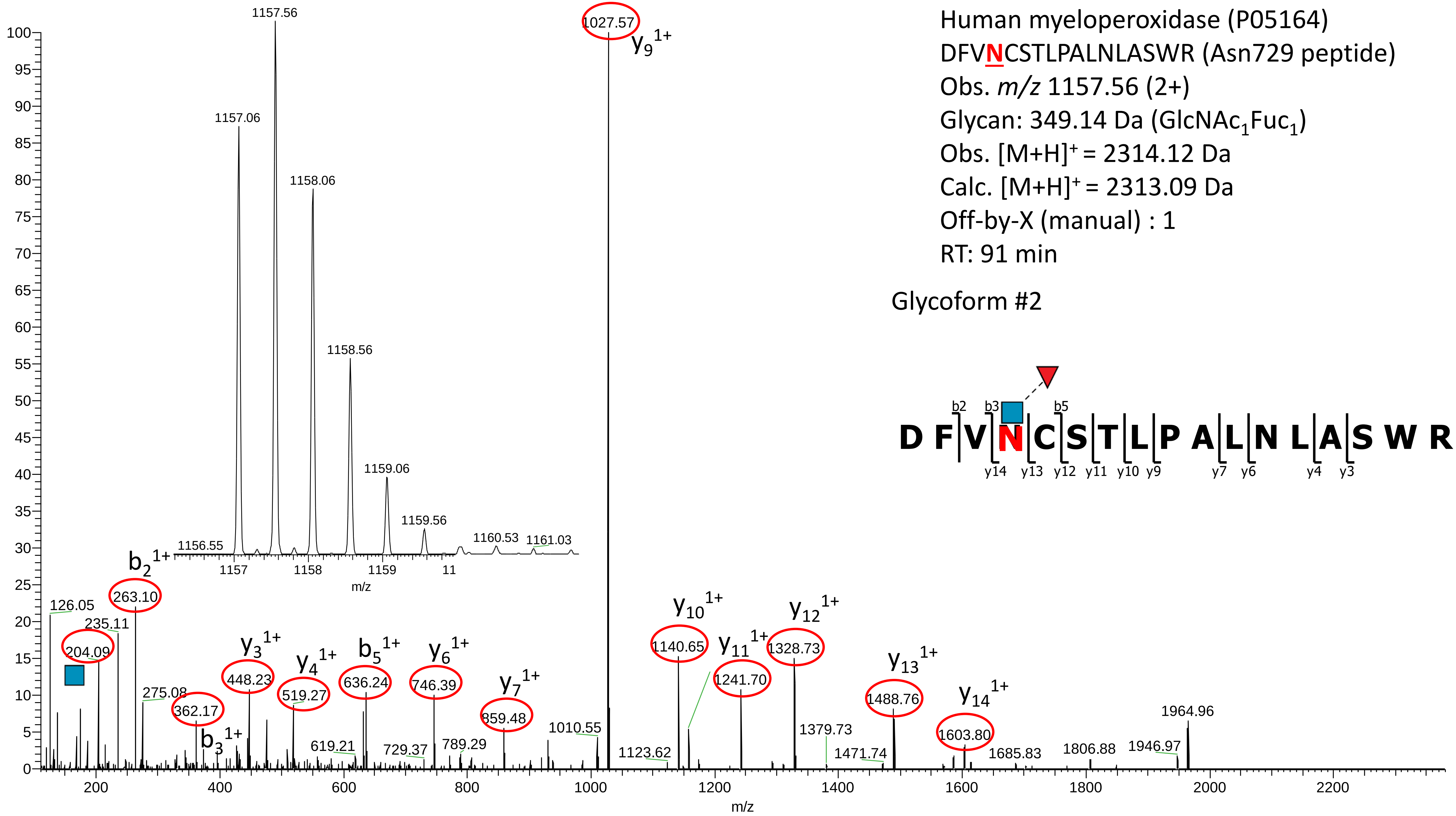
Non-glycosylated peptide



Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 1084.53 (2+)
Glycan: 203.08 Da (GlcNAc$_1$)
Obs. $[M+H]^+$ = 2168.06 Da
Calc. $[M+H]^+$ = 2167.03 Da
Off-by-X (manual) : 1
RT: 91 min

Glycoform #1





Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 1157.56 (2+)

Glycan: 349.14 Da ($GlcNAc_1Fuc_1$)

Obs. $[M+H]^+$ = 2314.12 Da

Calc. $[M+H]^+$ = 2313.09 Da

Off-by-X (manual) : 1

RT: 91 min

Glycoform #2

Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 1185.57 (2+)

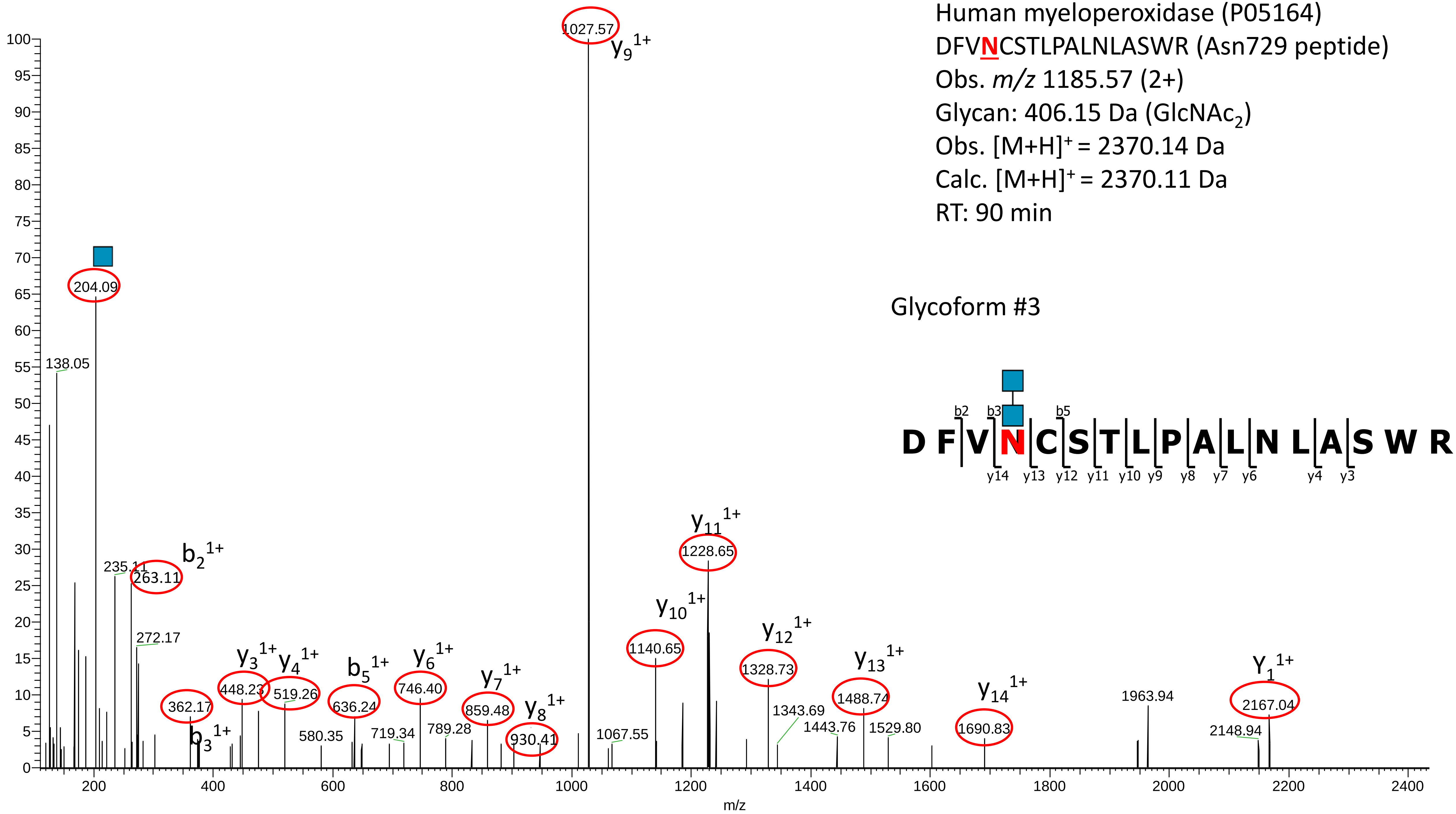
Glycan: 406.15 Da (GlcNAc$_2$)

Obs. [M+H]$^+$ = 2370.14 Da

Calc. [M+H]$^+$ = 2370.11 Da

RT: 90 min

Glycoform #3



Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. m/z 1259.10 (2+)

Glycan: 552.22 Da ($GlcNAc_2Fuc_1$)

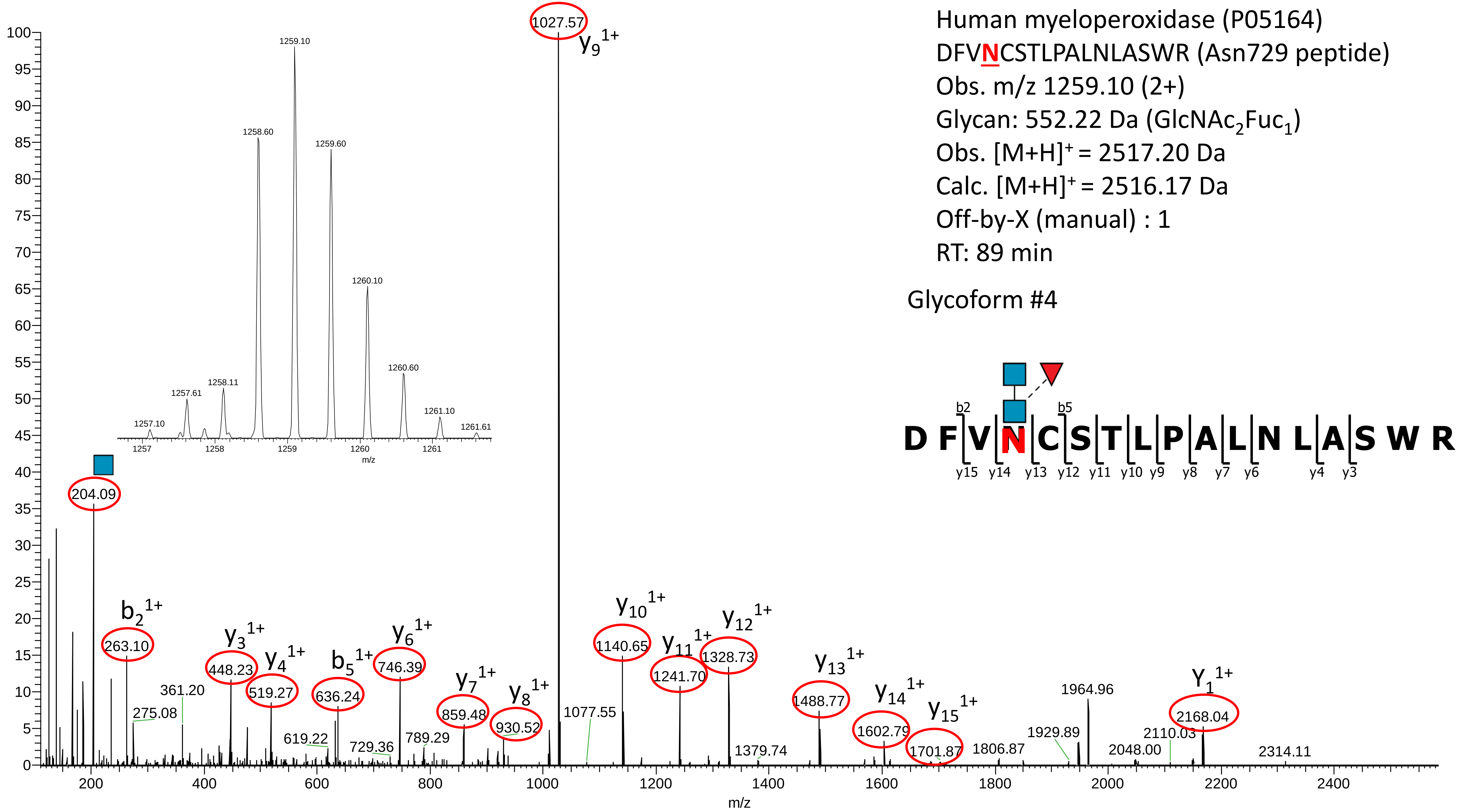
Obs. $[M+H]^+$ = 2517.20 Da

Calc. $[M+H]^+$ = 2516.17 Da

Off-by-X (manual) : 1

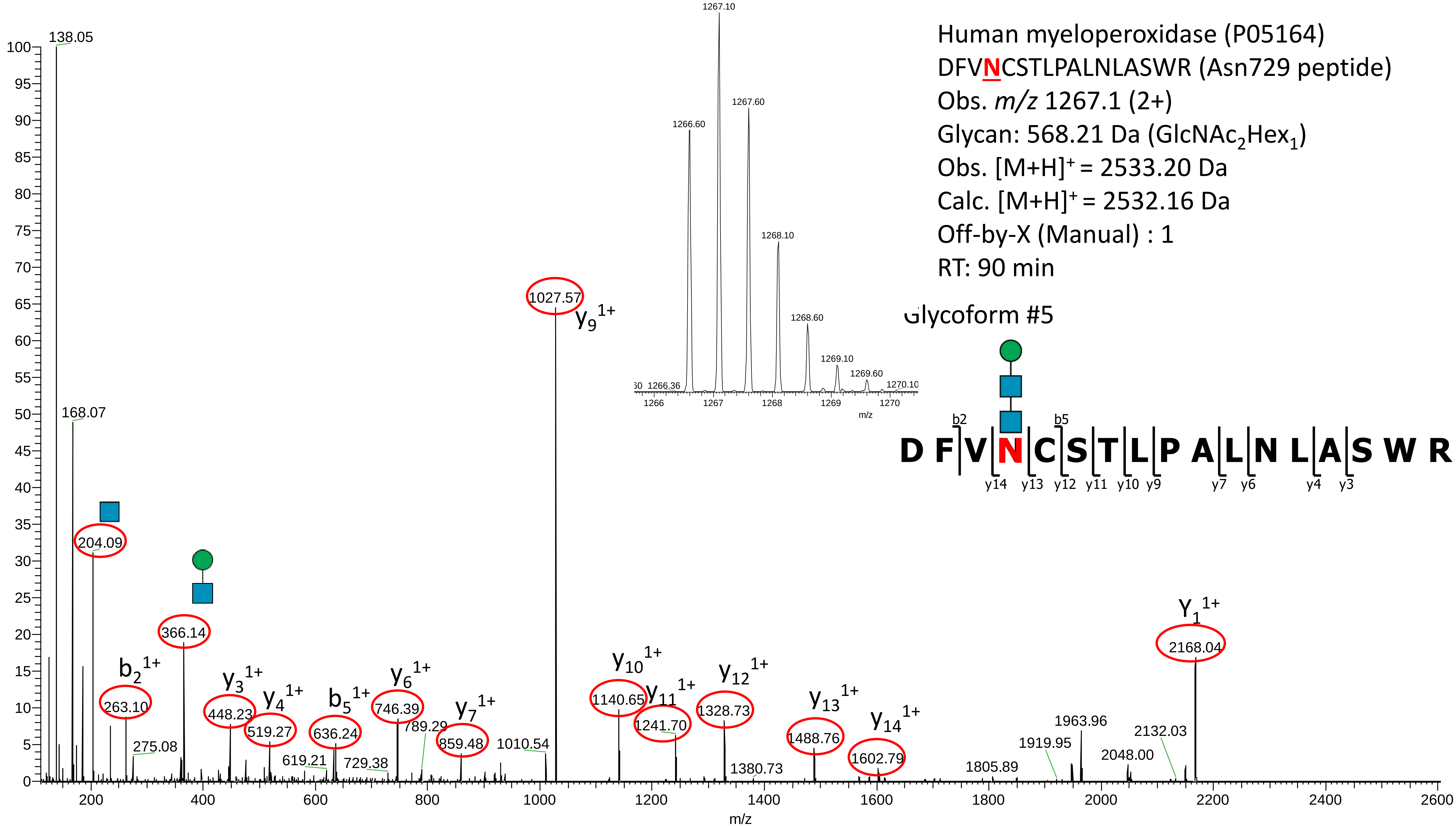
RT: 89 min

Glycoform #4



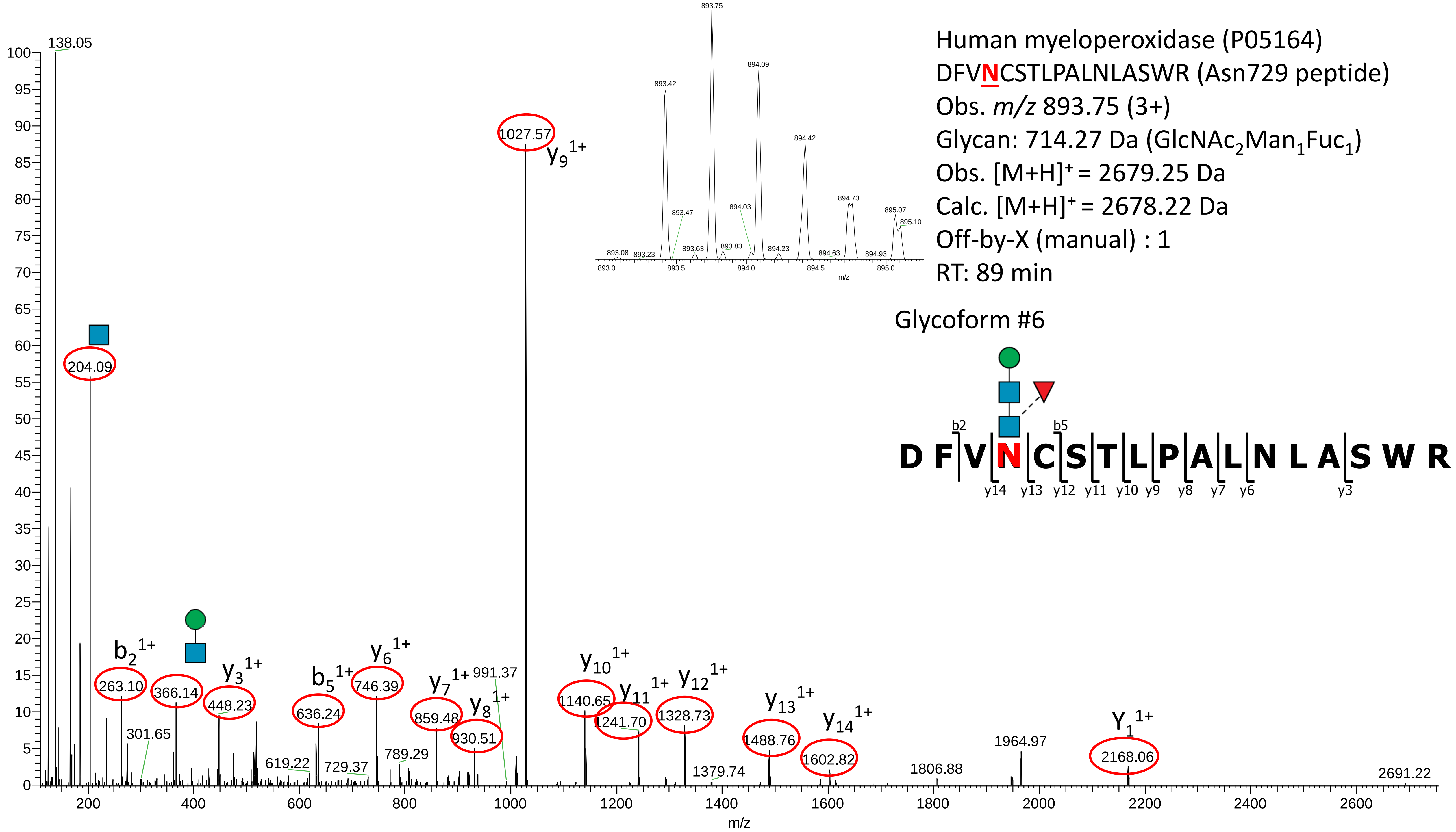
Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 1267.1 (2+)
Glycan: 568.21 Da ($GlcNAc_2Hex_1$)
Obs. $[M+H]^+$ = 2533.20 Da
Calc. $[M+H]^+$ = 2532.16 Da
Off-by-X (Manual) : 1
RT: 90 min

Glycoform #5



Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. m/z 893.75 (3+)
Glycan: 714.27 Da (GlcNAc$_2$Man$_1$Fuc$_1$)
Obs. [M+H]$^+$ = 2679.25 Da
Calc. [M+H]$^+$ = 2678.22 Da
Off-by-X (manual) : 1
RT: 89 min

Glycoform #6



Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 899.09 (3+)

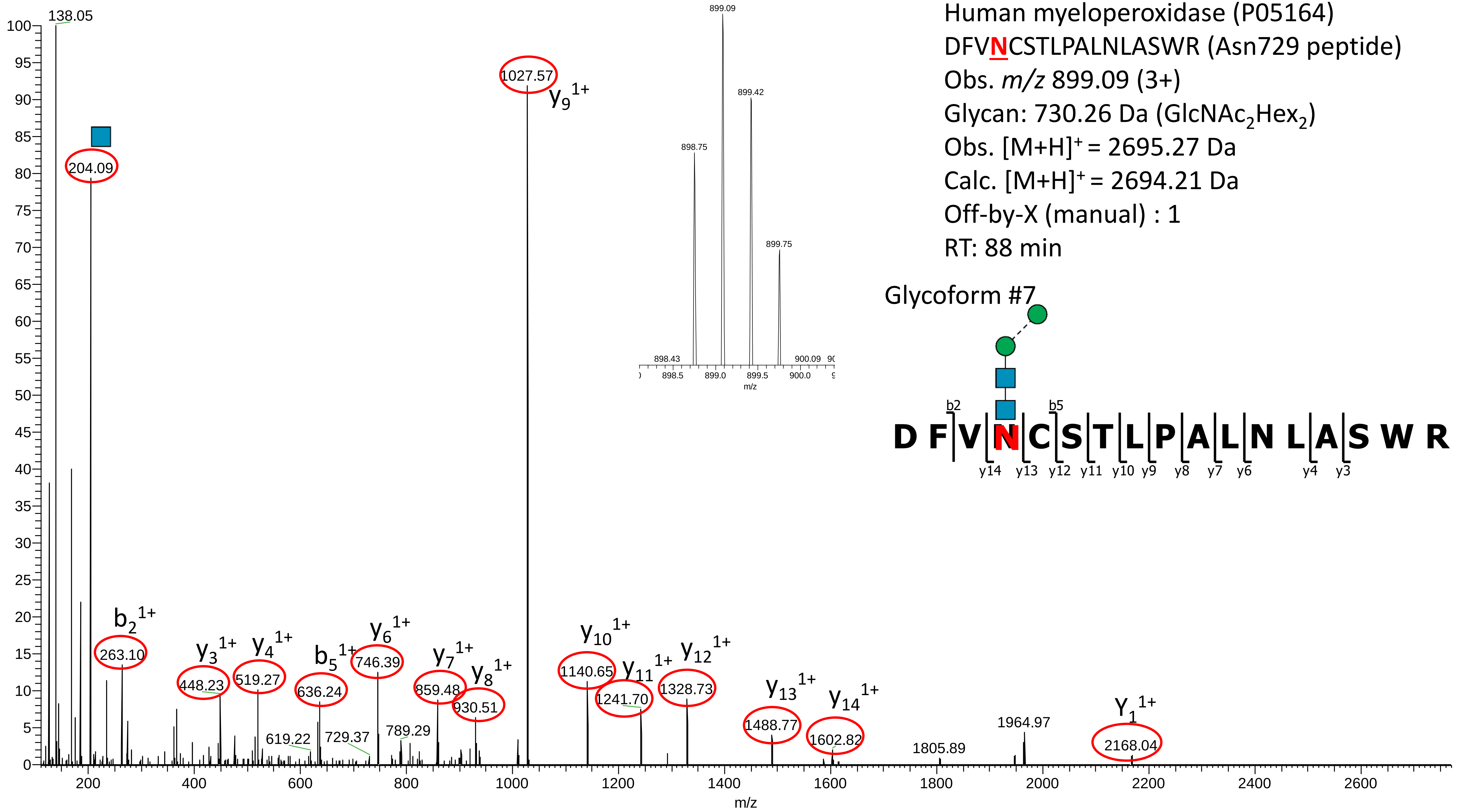
Glycan: 730.26 Da ($GlcNAc_2Hex_2$)

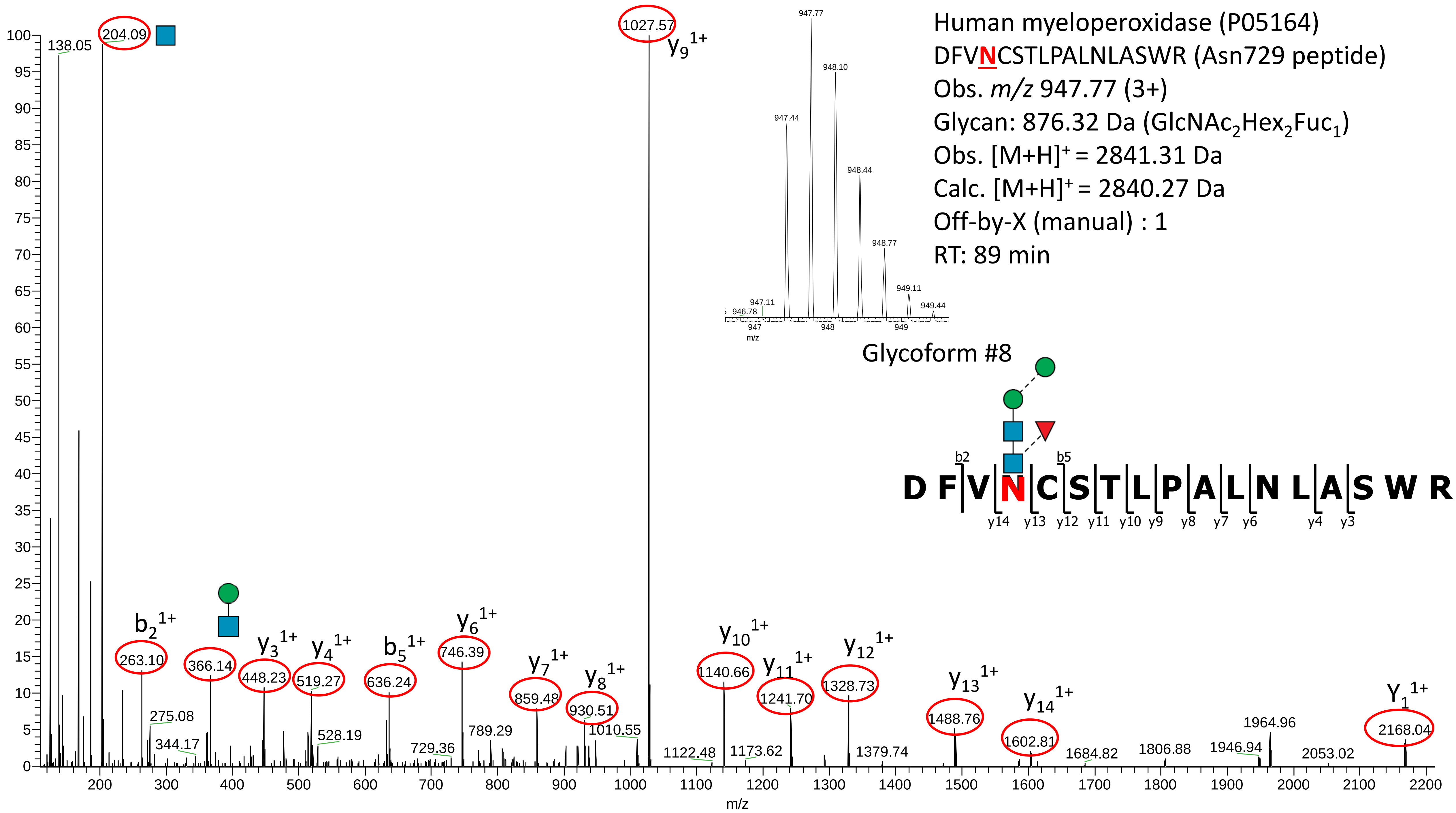
Obs. $[M+H]^+$ = 2695.27 Da

Calc. $[M+H]^+$ = 2694.21 Da

Off-by-X (manual) : 1

RT: 88 min





Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 947.77 (3+)

Glycan: 876.32 Da (GlcNAc$_2$Hex$_2$Fuc$_1$)

Obs. [M+H]$^+$ = 2841.31 Da

Calc. [M+H]$^+$ = 2840.27 Da

Off-by-X (manual) : 1

RT: 89 min

Glycoform #8

Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 953.44 (3+)

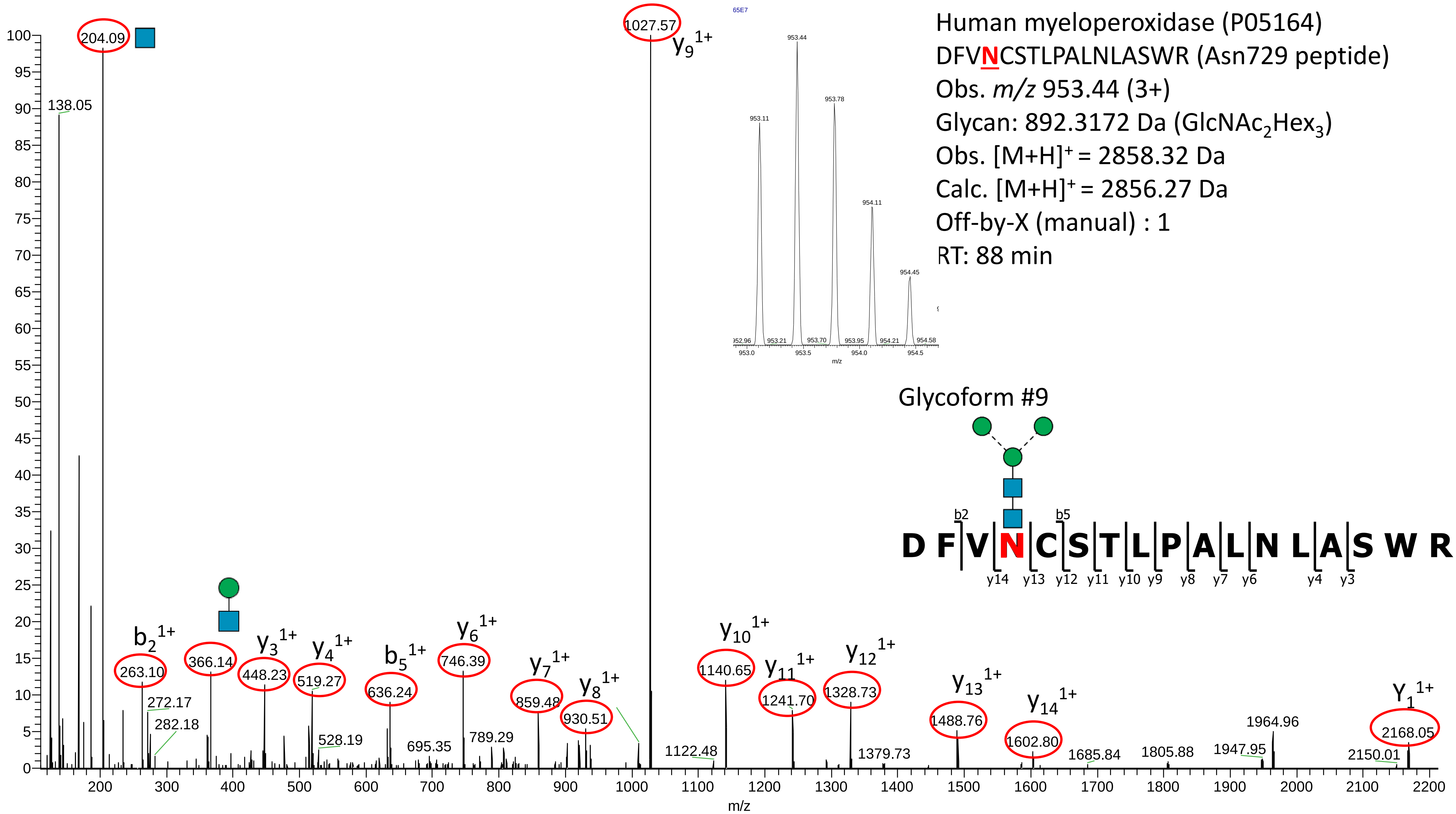
Glycan: 892.3172 Da (GlcNAc$_2$Hex$_3$)

Obs. [M+H]$^+$ = 2858.32 Da

Calc. [M+H]$^+$ = 2856.27 Da

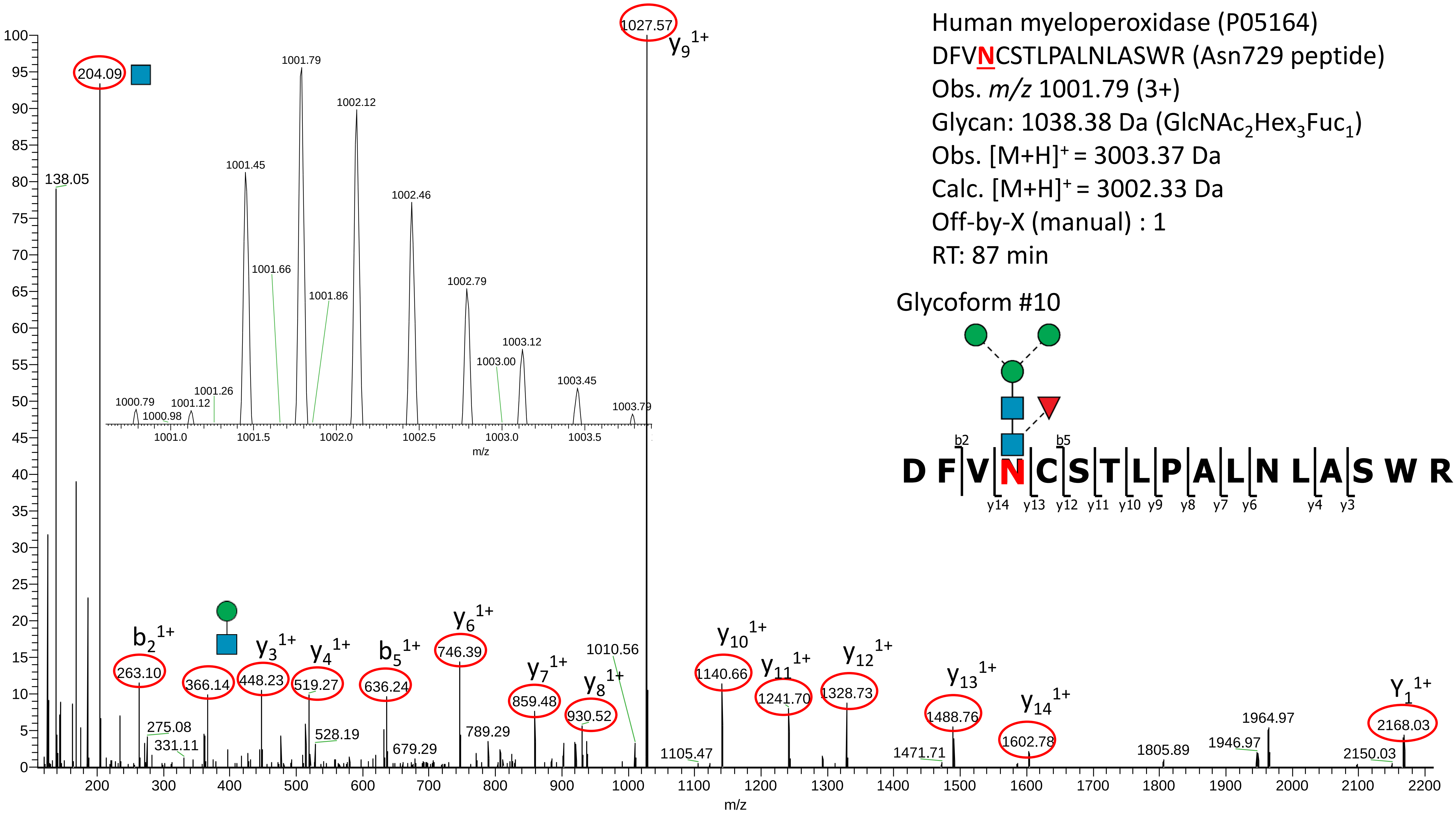
Off-by-X (manual) : 1

RT: 88 min



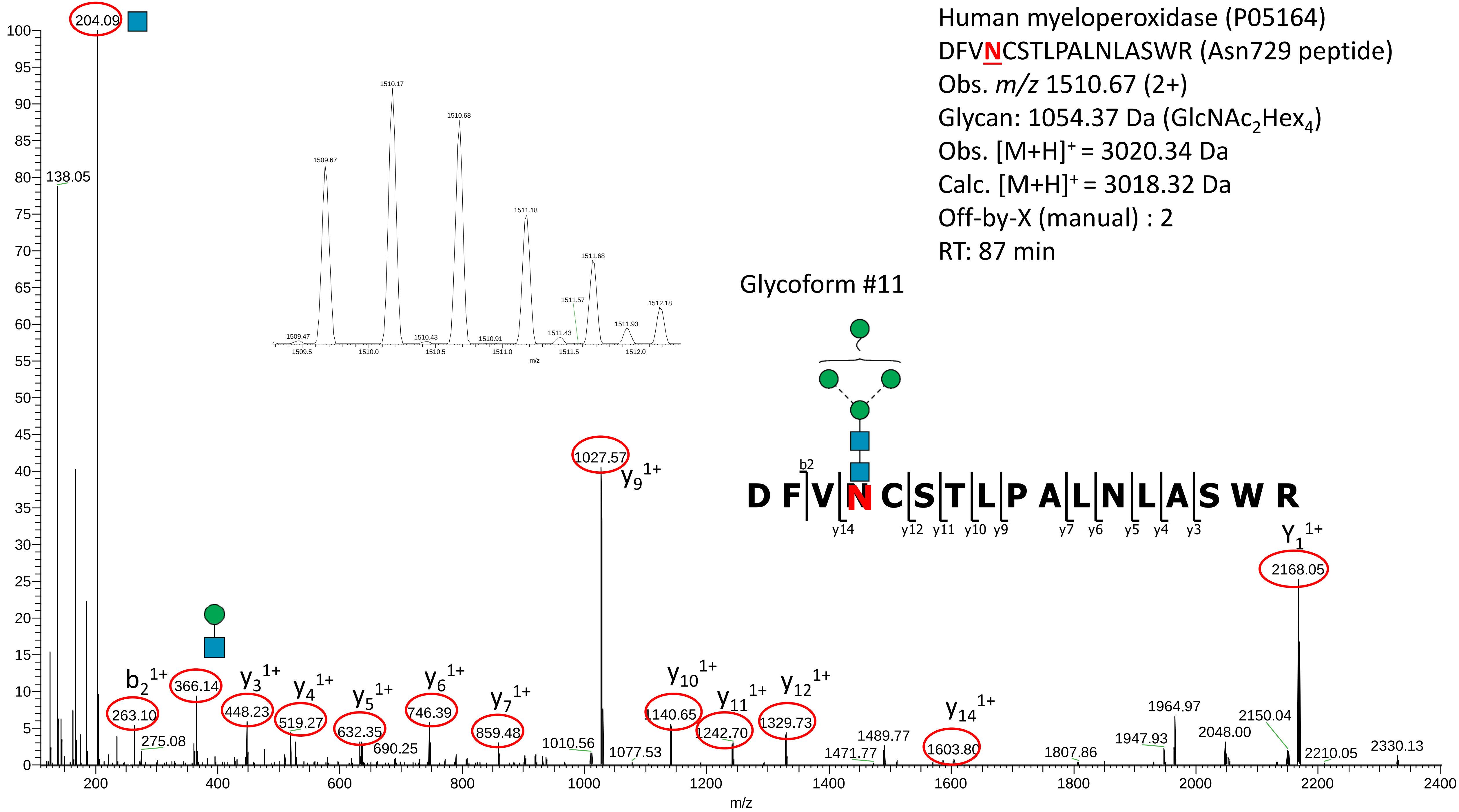
Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 1001.79 (3+)
Glycan: 1038.38 Da ($GlcNAc_2Hex_3Fuc_1$)
Obs. $[M+H]^+$ = 3003.37 Da
Calc. $[M+H]^+$ = 3002.33 Da
Off-by-X (manual) : 1
RT: 87 min

Glycoform #10



Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 1510.67 (2+)
Glycan: 1054.37 Da ($GlcNAc_2Hex_4$)
Obs. $[M+H]^+$ = 3020.34 Da
Calc. $[M+H]^+$ = 3018.32 Da
Off-by-X (manual) : 2
RT: 87 min

Glycoform #11



Human myeloperoxidase (P05164)

DF**V**<u>**N**</u>CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 1055.81 (3+)

Glycan: 1221.46 Da (GlcNAc$_2$Hex$_4$Fuc$_1$)

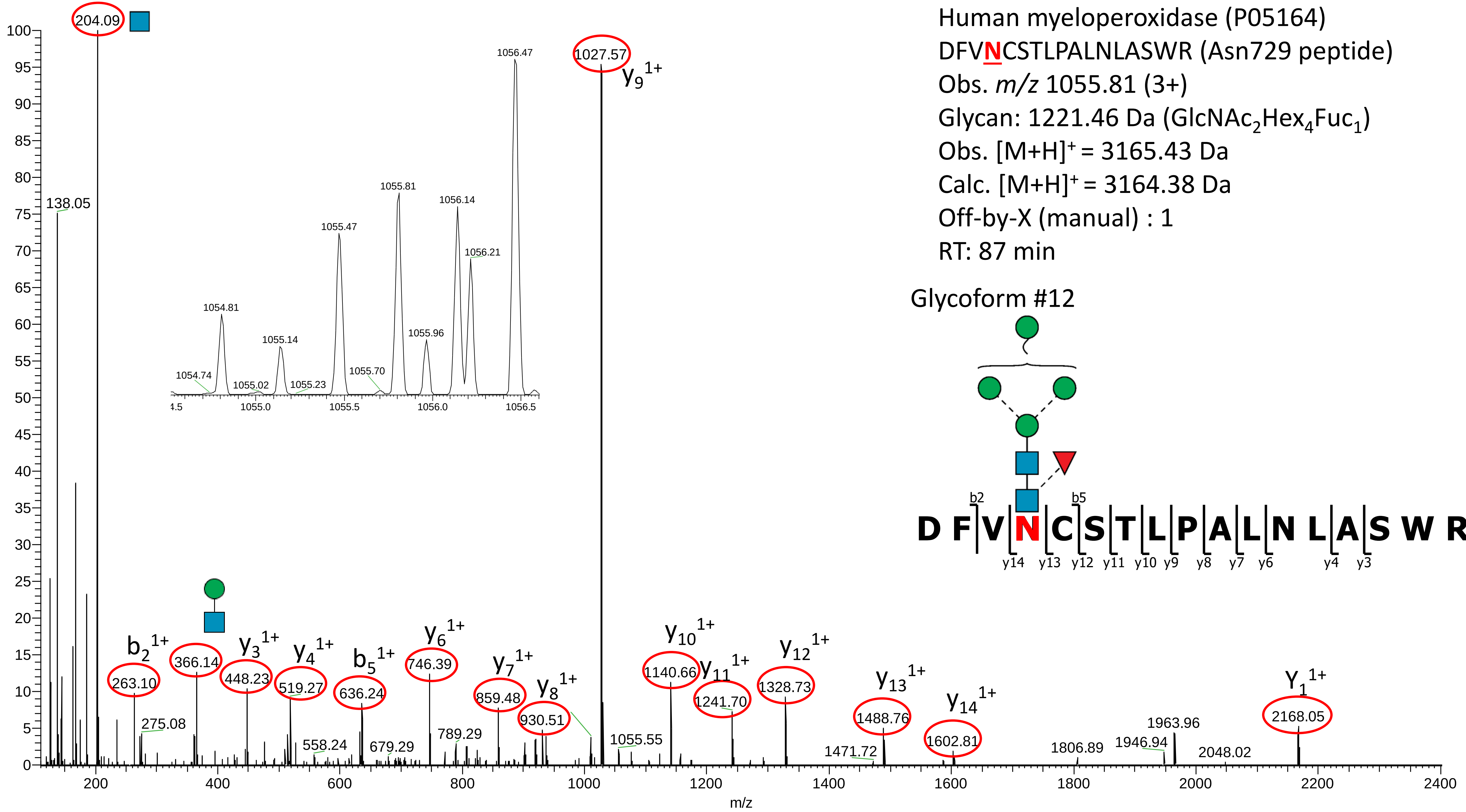
Obs. [M+H]$^+$ = 3165.43 Da

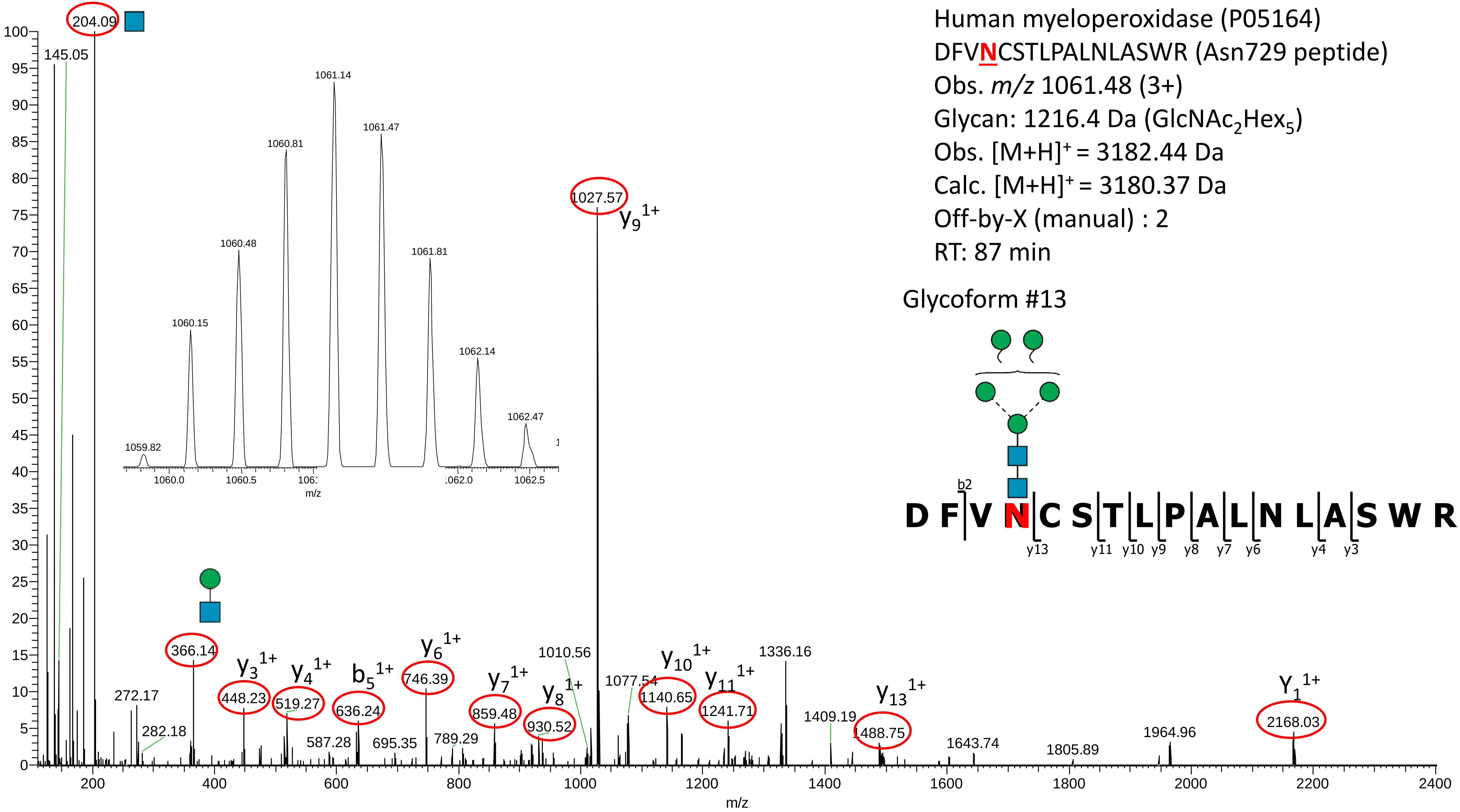
Calc. [M+H]$^+$ = 3164.38 Da

Off-by-X (manual) : 1

RT: 87 min

Glycoform #12





Human myeloperoxidase (P05164)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 1061.48 (3+)

Glycan: 1216.4 Da (GlcNAc$_2$Hex$_5$)

Obs. [M+H]$^+$ = 3182.44 Da

Calc. [M+H]$^+$ = 3180.37 Da

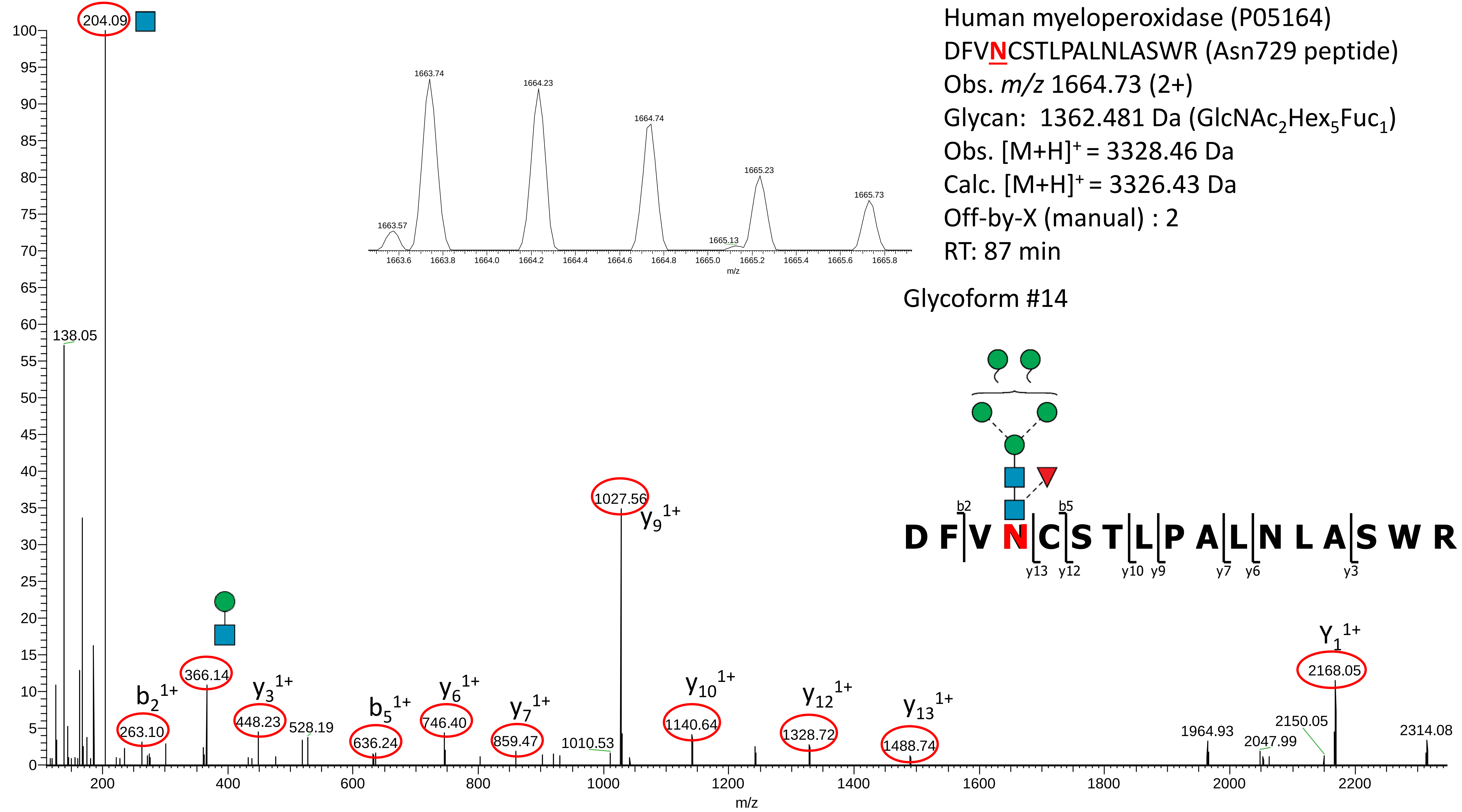
Off-by-X (manual) : 2

RT: 87 min

Glycoform #13

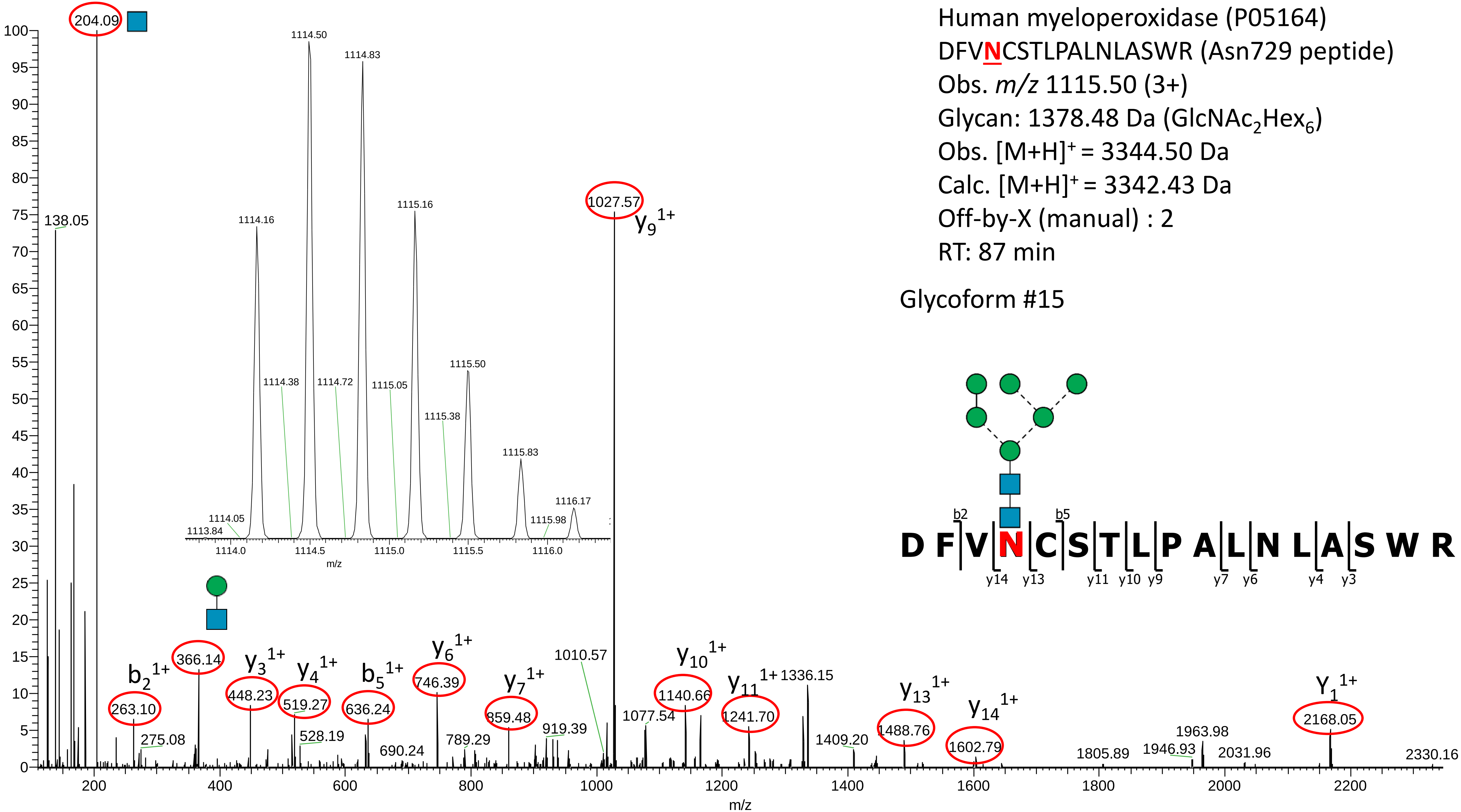
Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 1664.73 (2+)
Glycan: 1362.481 Da ($GlcNAc_2Hex_5Fuc_1$)
Obs. $[M+H]^+$ = 3328.46 Da
Calc. $[M+H]^+$ = 3326.43 Da
Off-by-X (manual) : 2
RT: 87 min

Glycoform #14



Human myeloperoxidase (P05164)
DFV**N**CSTLPALNLASWR (Asn729 peptide)
Obs. *m/z* 1115.50 (3+)
Glycan: 1378.48 Da (GlcNAc$_2$Hex$_6$)
Obs. [M+H]$^+$ = 3344.50 Da
Calc. [M+H]$^+$ = 3342.43 Da
Off-by-X (manual) : 2
RT: 87 min

Glycoform #15



Human myeloperoxidase (P51064)

DFV**N**CSTLPALNLASWR (Asn729 peptide)

Obs. *m/z* 1220.53 (3+)

Glycan: 1694.6 Da ($GlcNAc_3Hex_4NeuAc_1Fuc_1$)

Obs. $[M+H]^+$ = 3659.59 Da

Calc. $[M+H]^+$ = 3658.55 Da

Off-by-X (manual): 1

RT: 88 min

Glycoform #16