

Figure S1. Reproducible peak area and retention times and good correlation between peak area and concentration are observed for peptides from casein.

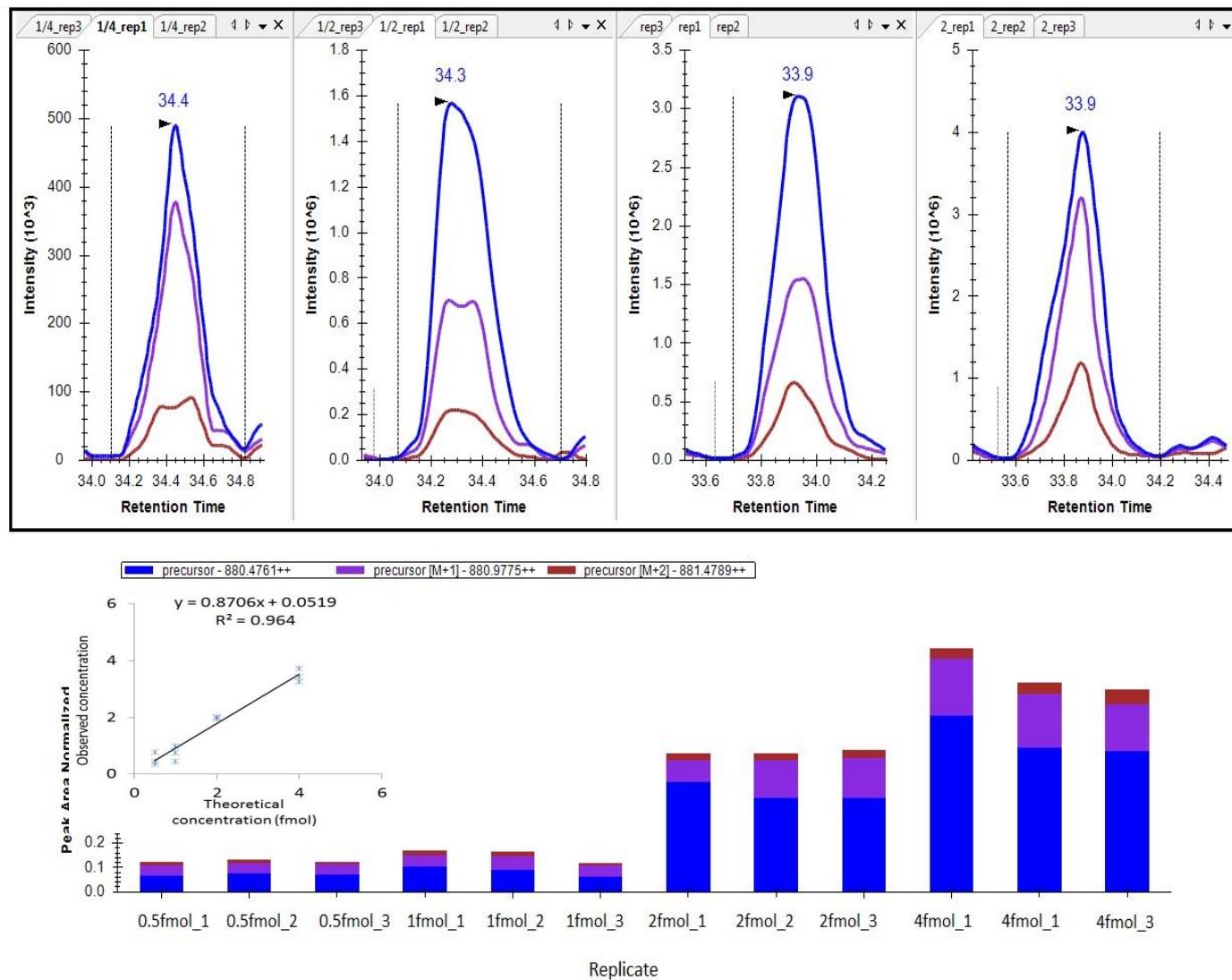
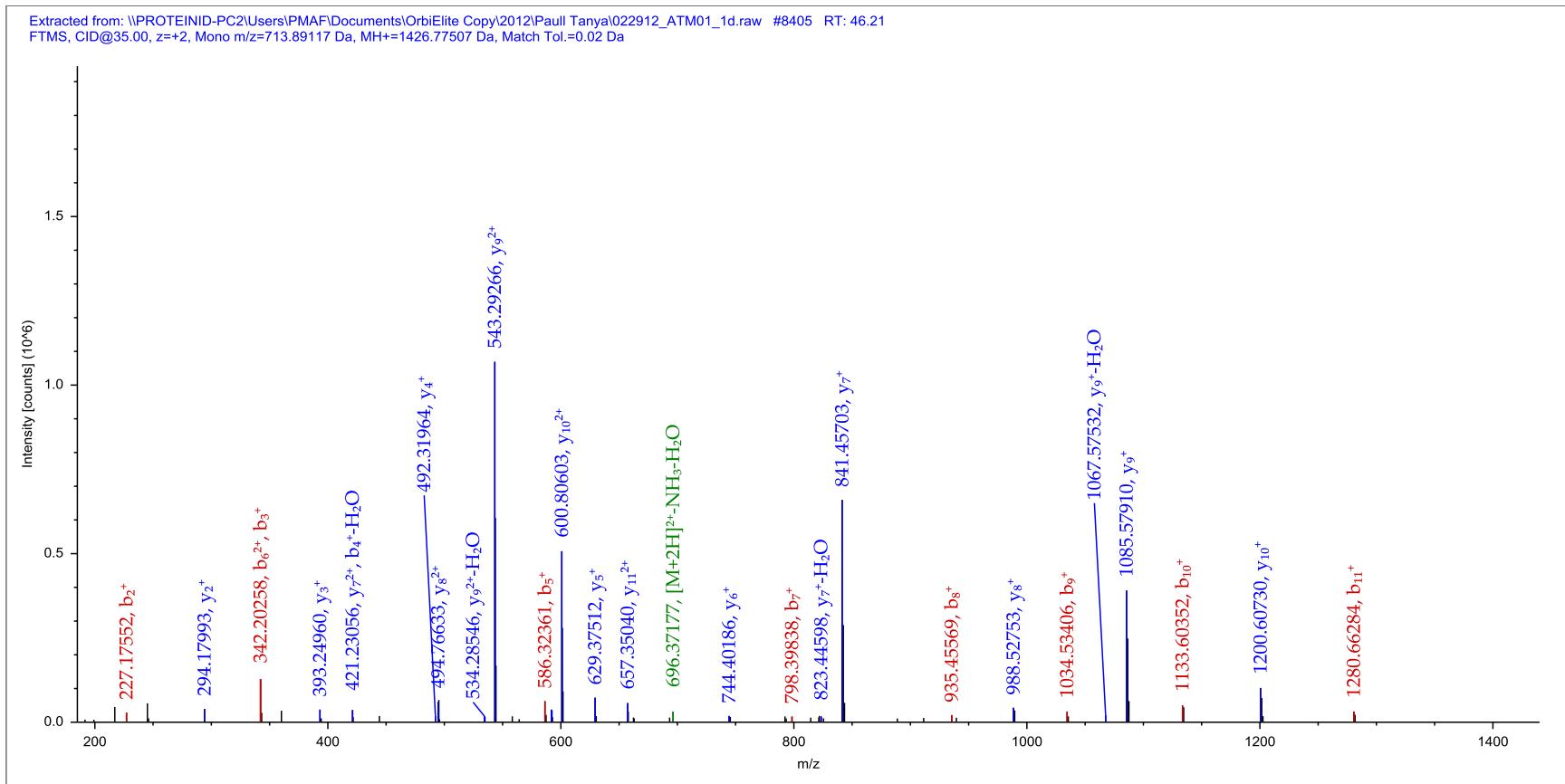


Figure S2. MS/MS from ATM and PRMT5 internal reference, sulfinic and sulfonic acid peptides. A, internal reference and modified peptides used for MS1 quantitation B, all other modified peptides with Cys number from peptide sequence

A, internal reference and
modified peptides used for MS1
quantitation

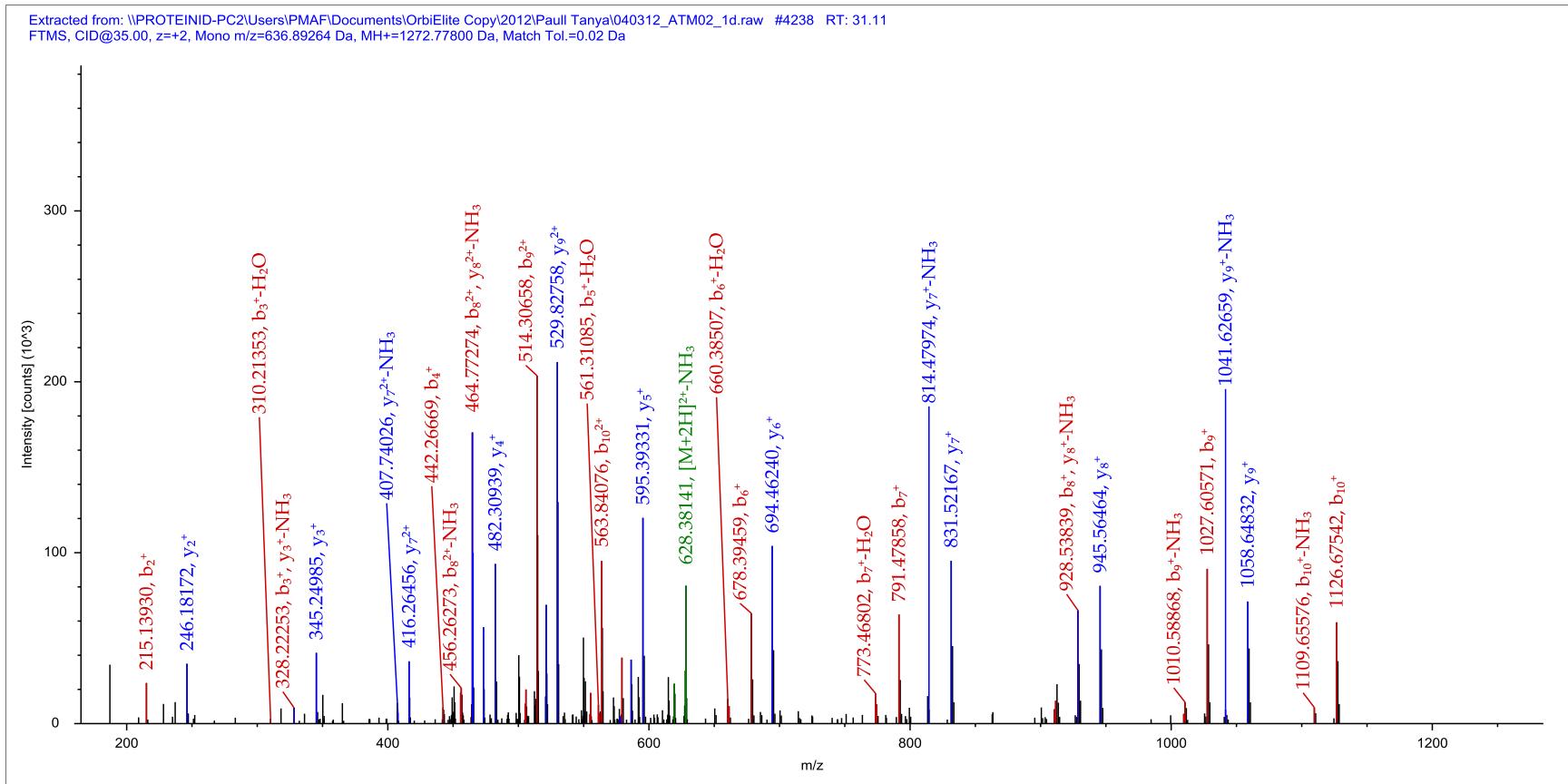
ATM LLDPFPDHVVFK

internal reference peptide



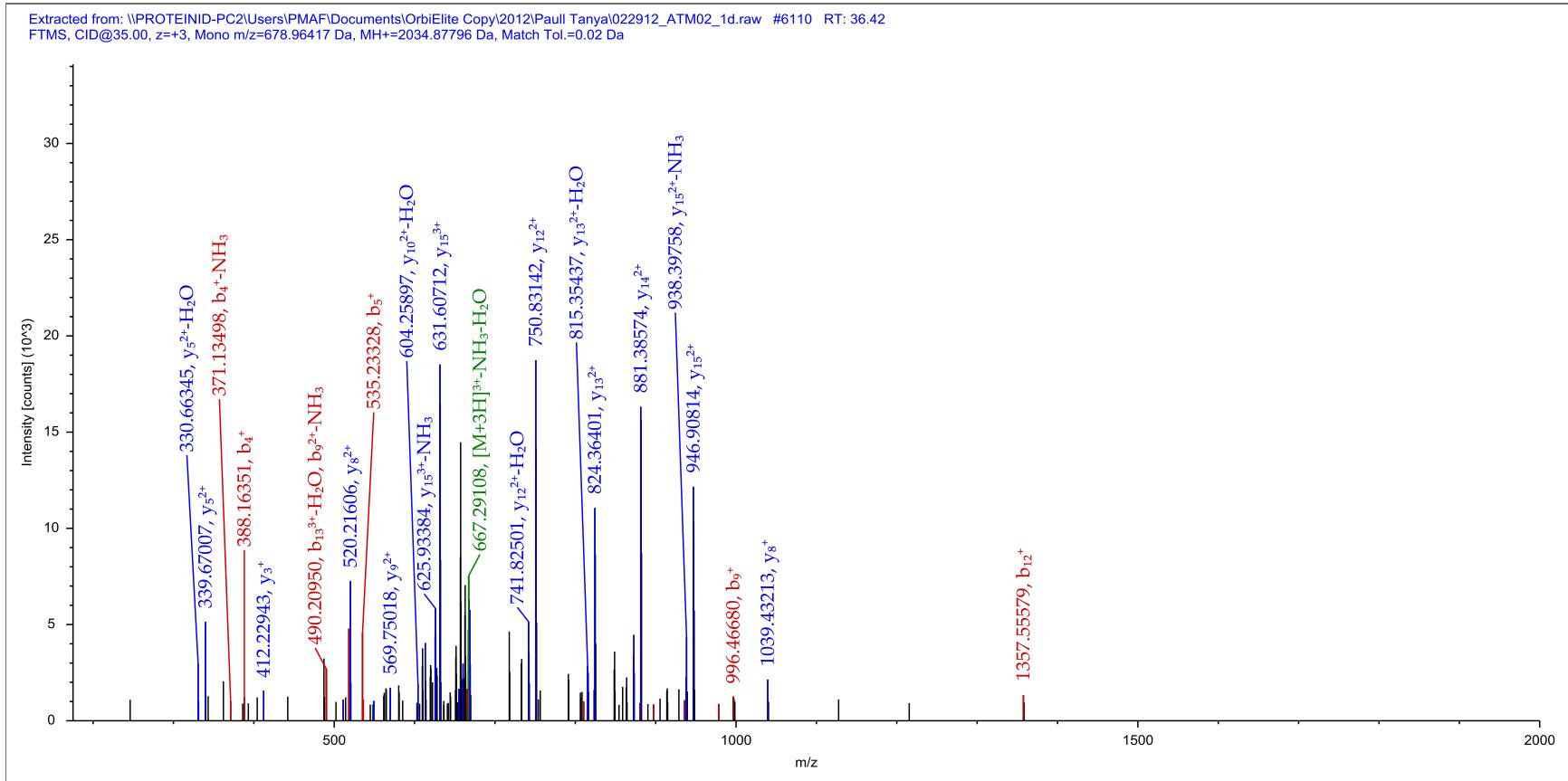
ATM TILNHVLHVVK

internal reference peptide



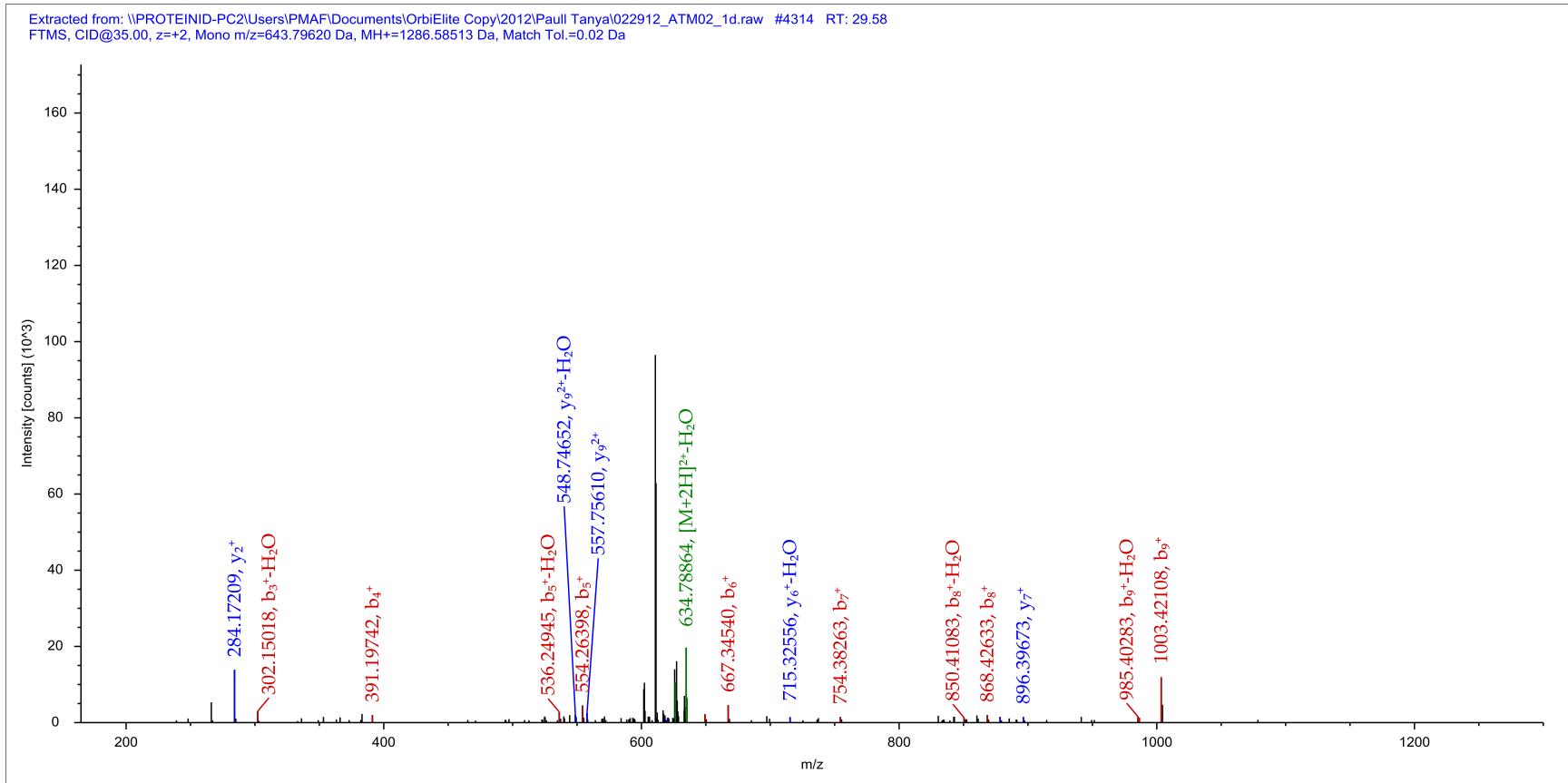
ATM AAMNFFQS**V**P**E**CEHHQK

Cys633 sulfinic acid



ATM ATFAYISNCHK

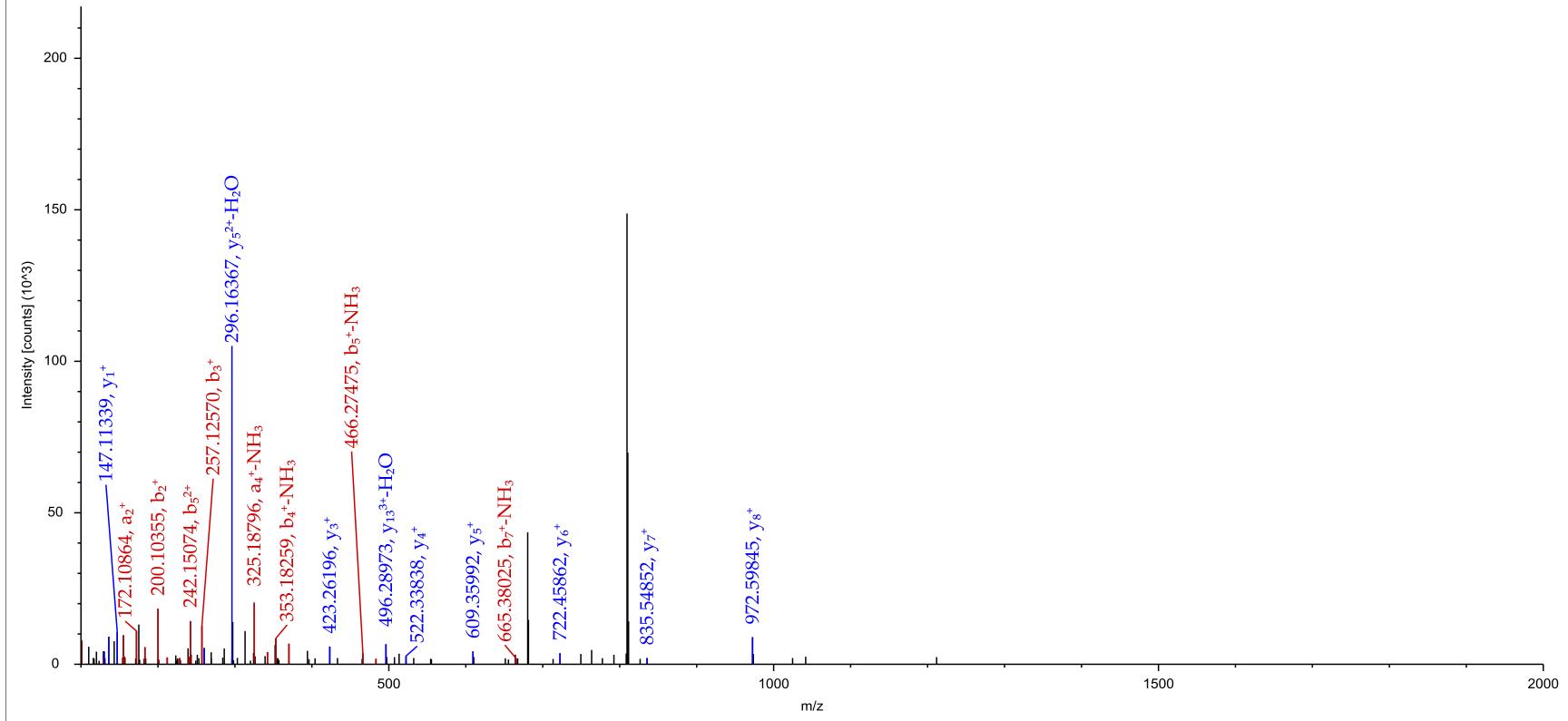
Cys1396 sulfinic acid



ATM QAGIIQALQNLGLCHILSVYLK

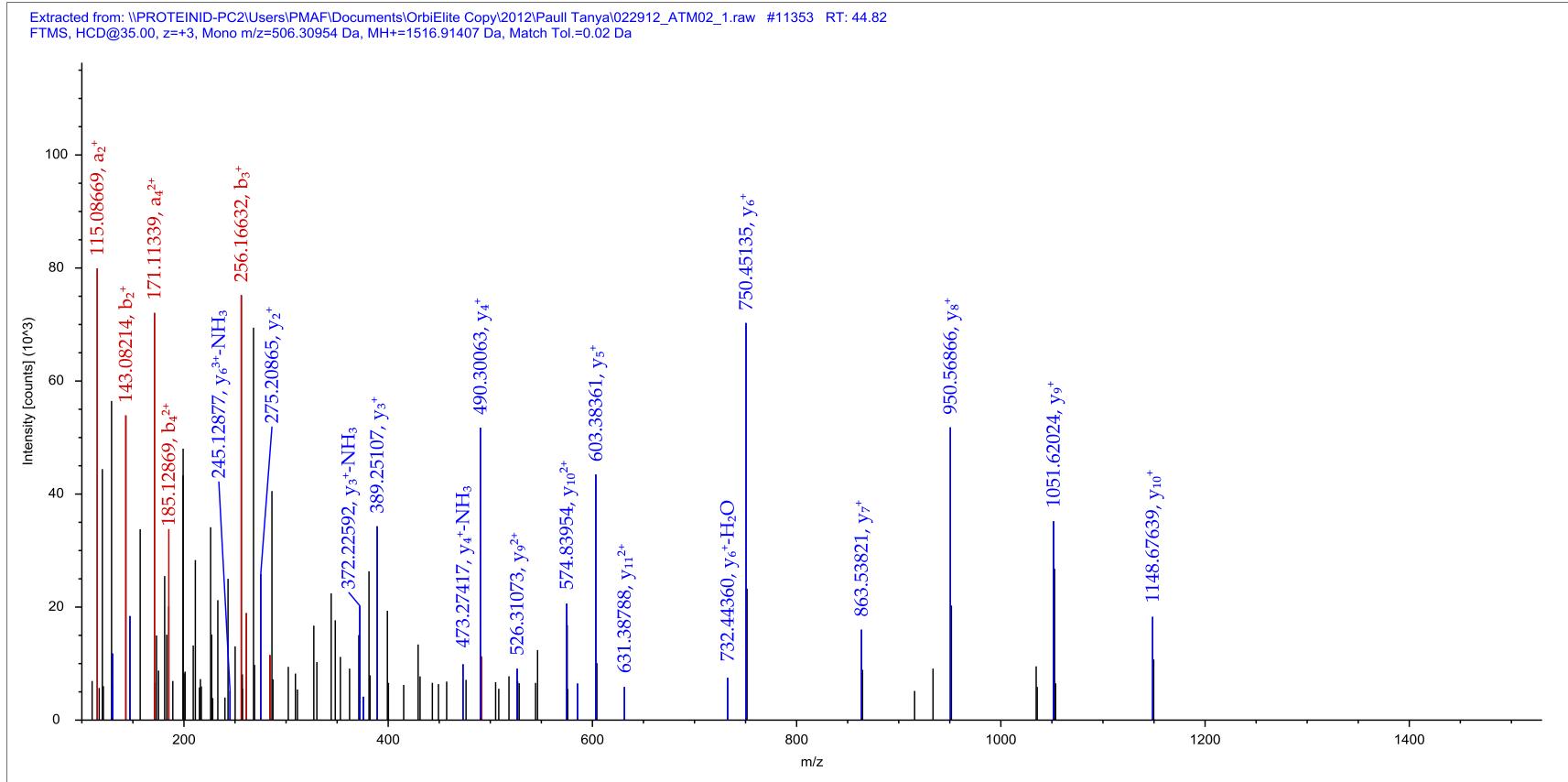
Cys2074 sulfinic acid

Extracted from: \\PROTEINID-PC2\\Users\\PMAF\\Documents\\OrbiElite Copy\\2012\\Pauli Tanya\\022912_ATM02_2.raw #16720 RT: 62.56
FTMS, HCD@35.00, z=+3, Mono m/z=809.78888 Da, MH+=2427.35208 Da, Match Tol.=0.02 Da



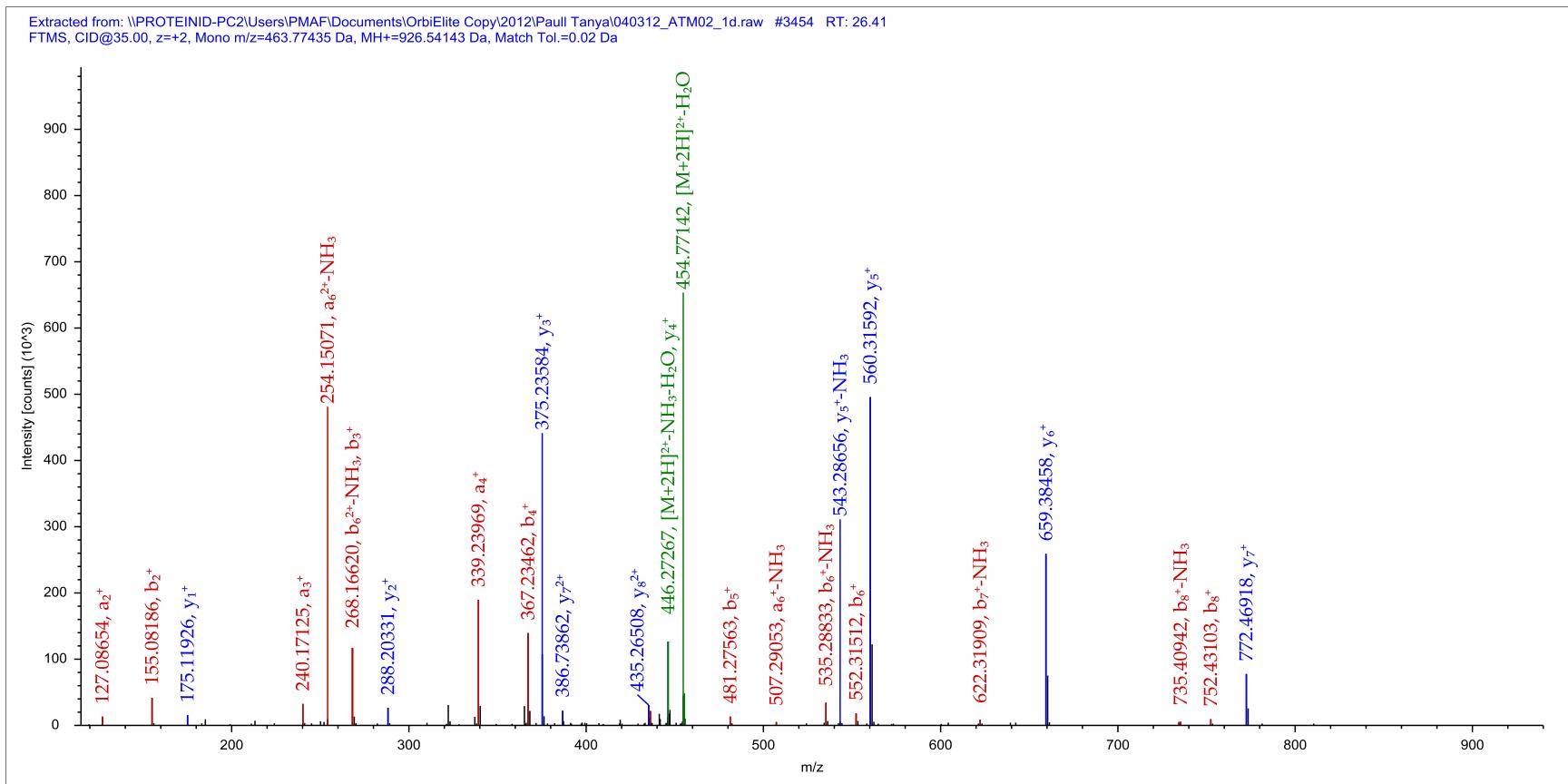
PRMT5 AAILPTSIFLTNKK

internal reference peptide



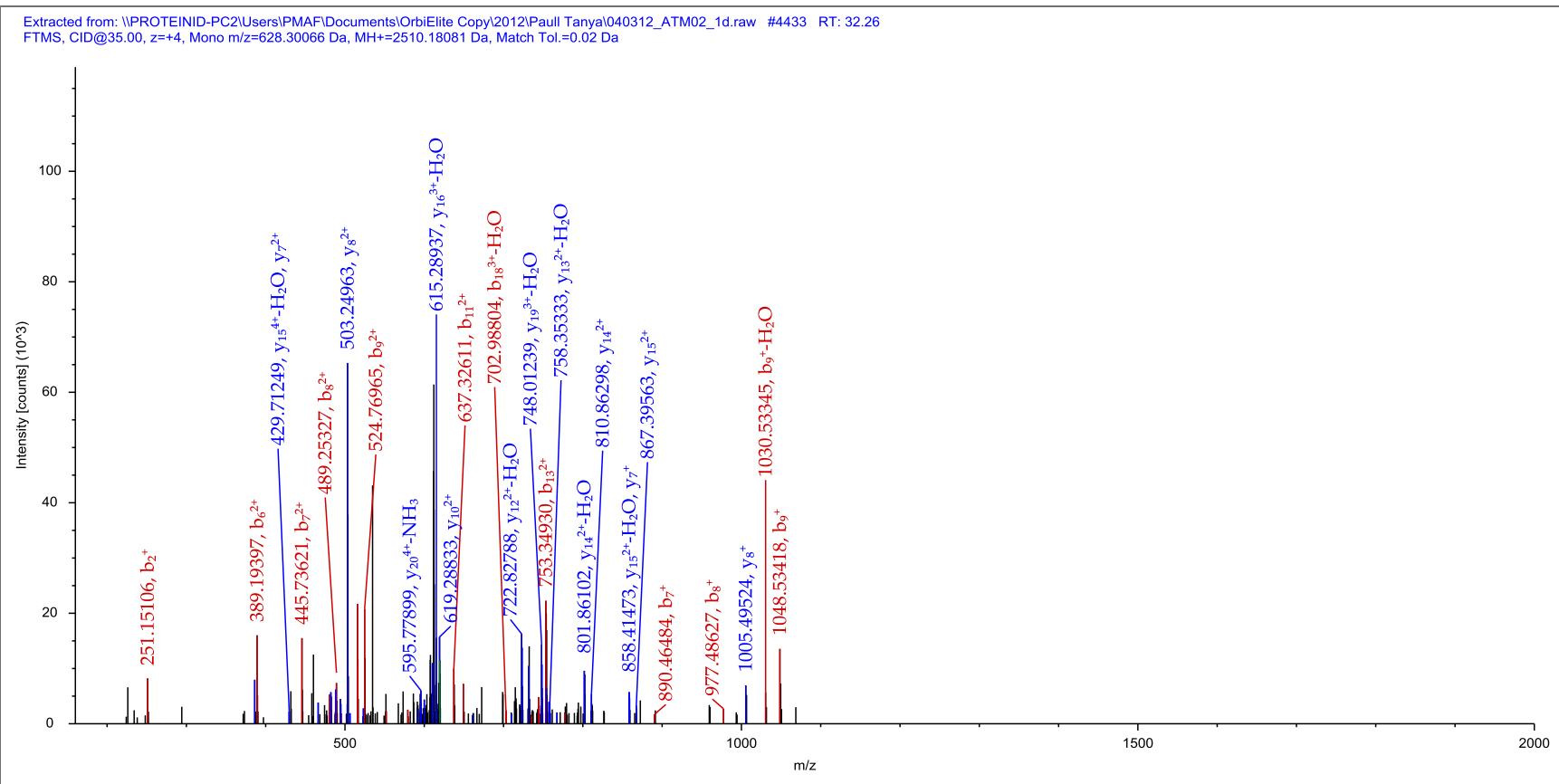
PRMT5 GPLVNASLR

internal reference peptide



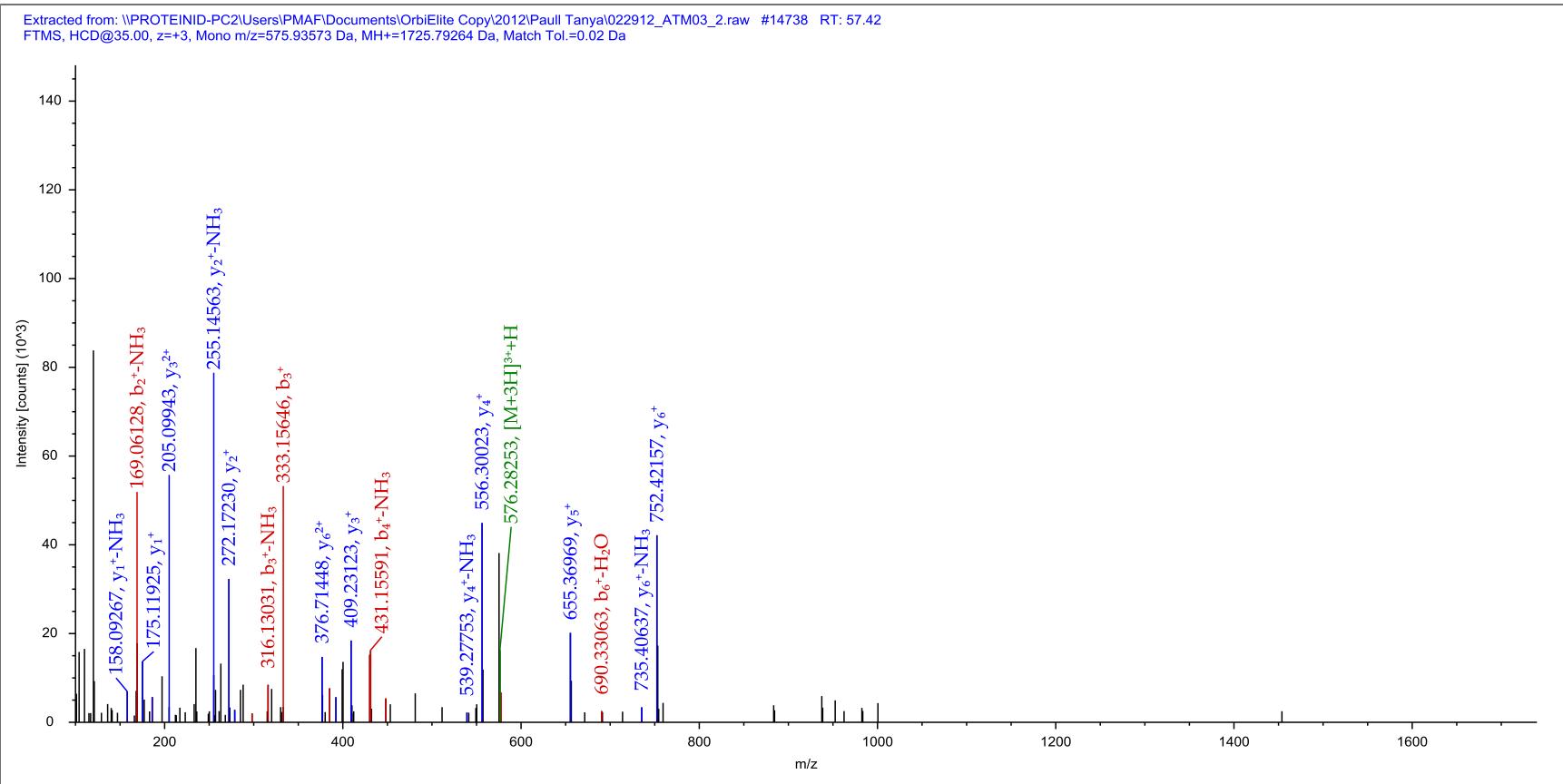
PRMT5 LHNFHQLSAPQPCFTFSHPNR

Cys518 sulfinic acid



PRMT5 QGFDFLCMPVFHPR

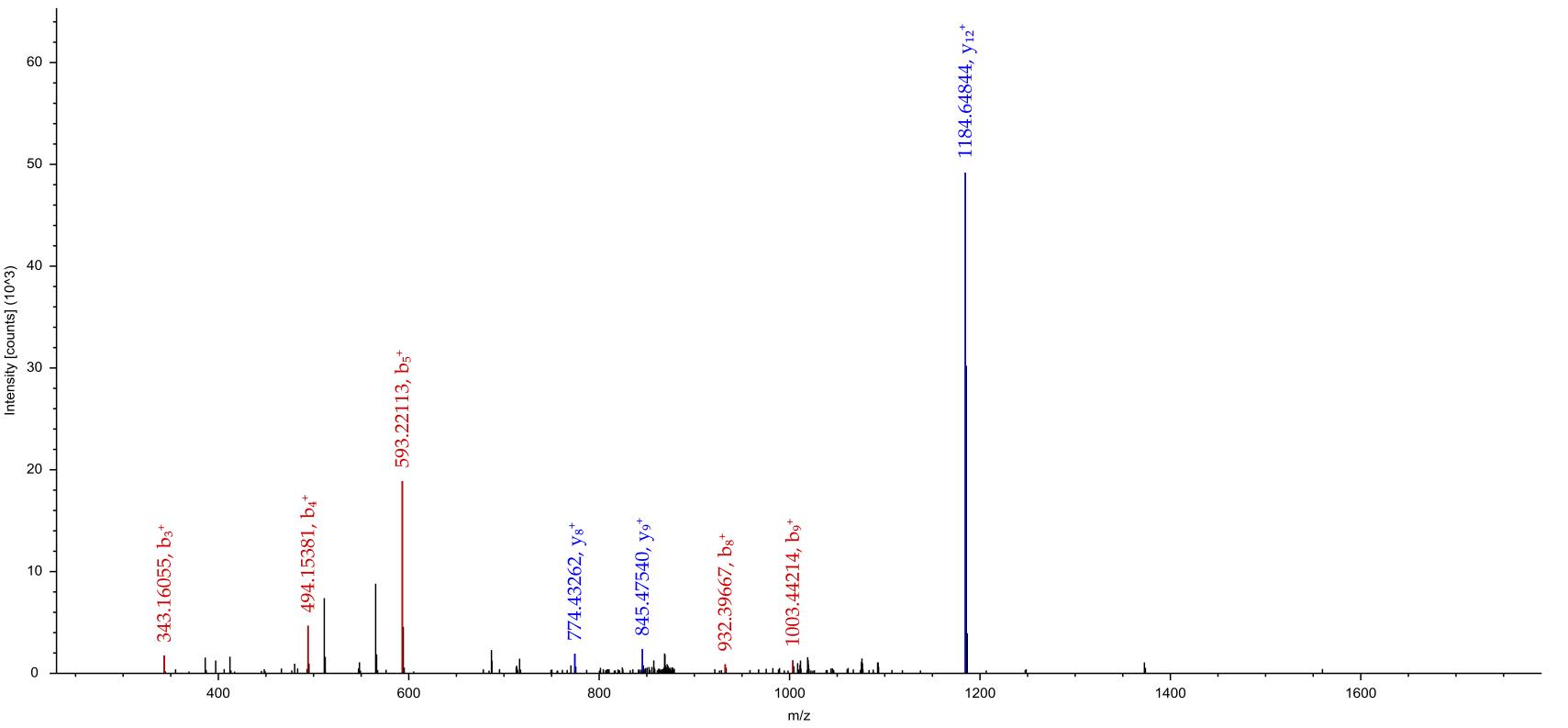
Cys42 sulfenic acid



PRMT5 DLNCCVPEIADTLGAVAK

Cys22 sulfonic acid

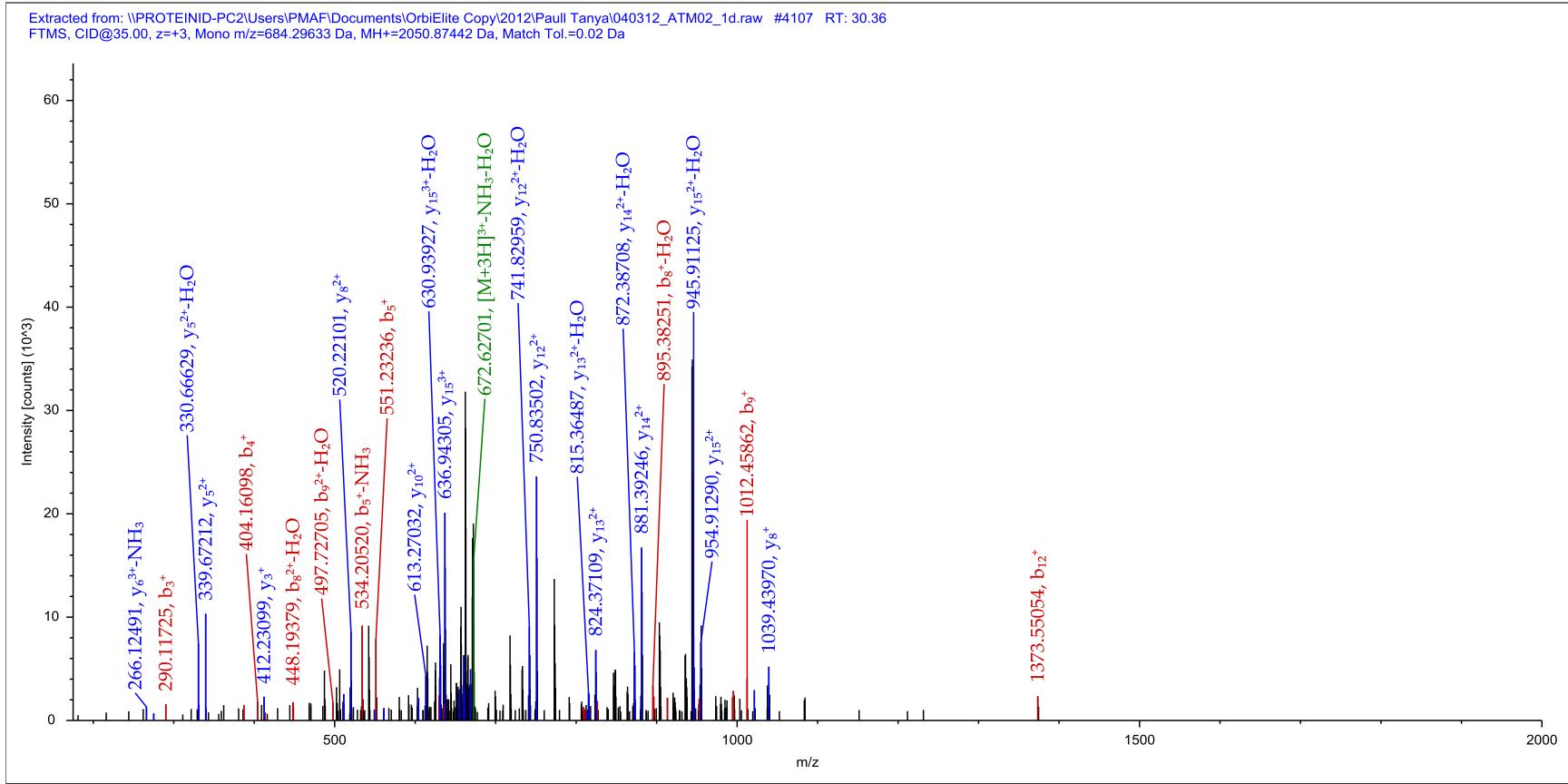
Extracted from: \\PROTEINID-PC2\\Users\\PMAF\\Documents\\OrbiElite Copy\\2012\\Pauli Tanya\\040312_ATM02_1d.raw #7240 RT: 49.20
FTMS, CID@35.00, z=+2, Mono m/z=888.93927 Da, MH+=1776.87126 Da, Match Tol.=0.02 Da



B, all other modified peptides
with Cys number from peptide
sequence

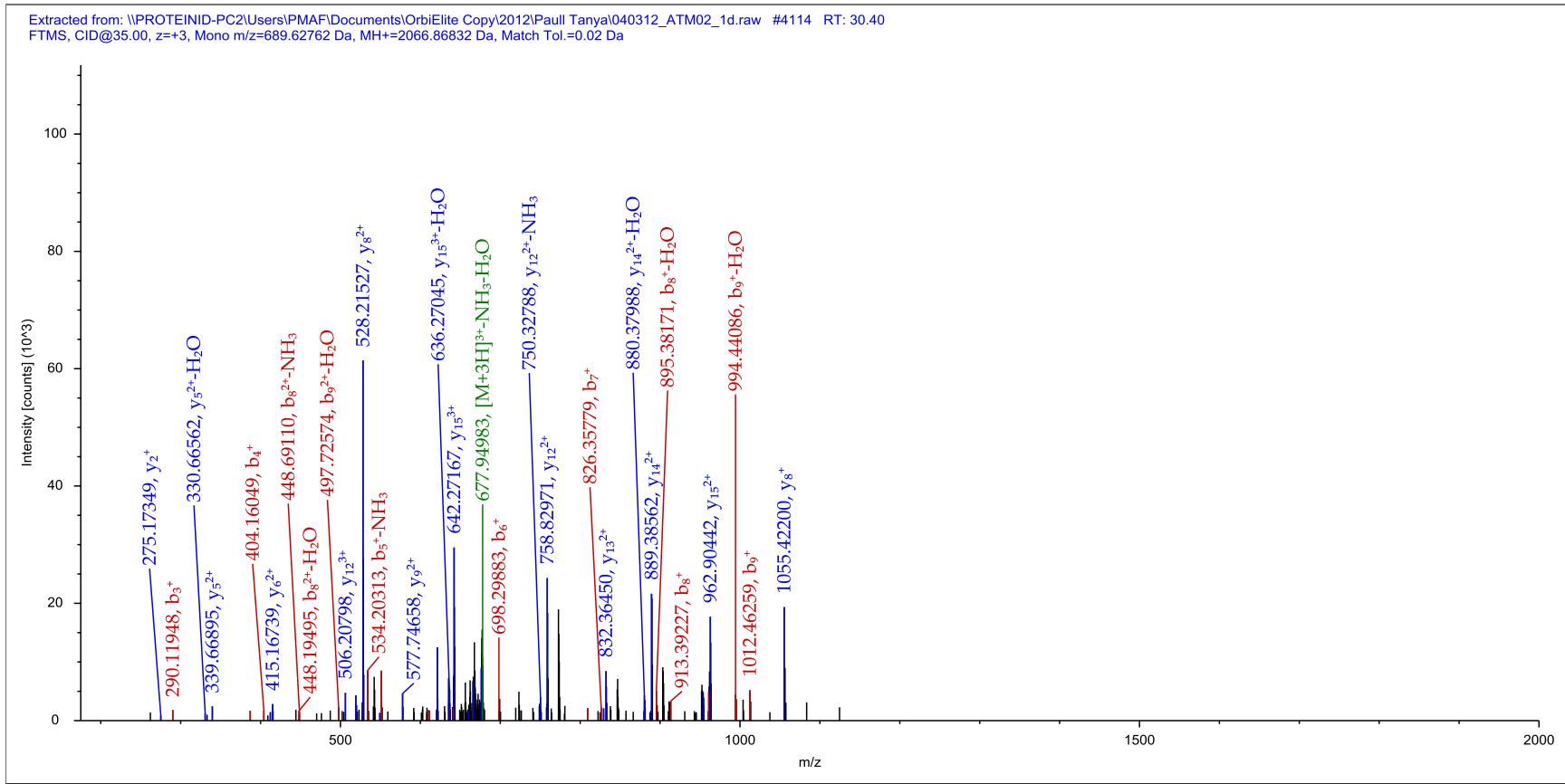
ATM AAMNFFQS**V**P**E**CEHHQK

C12 sulfinic acid M3 oxidation



ATM AAMNFFQS**V**P**E**CEHHHQK

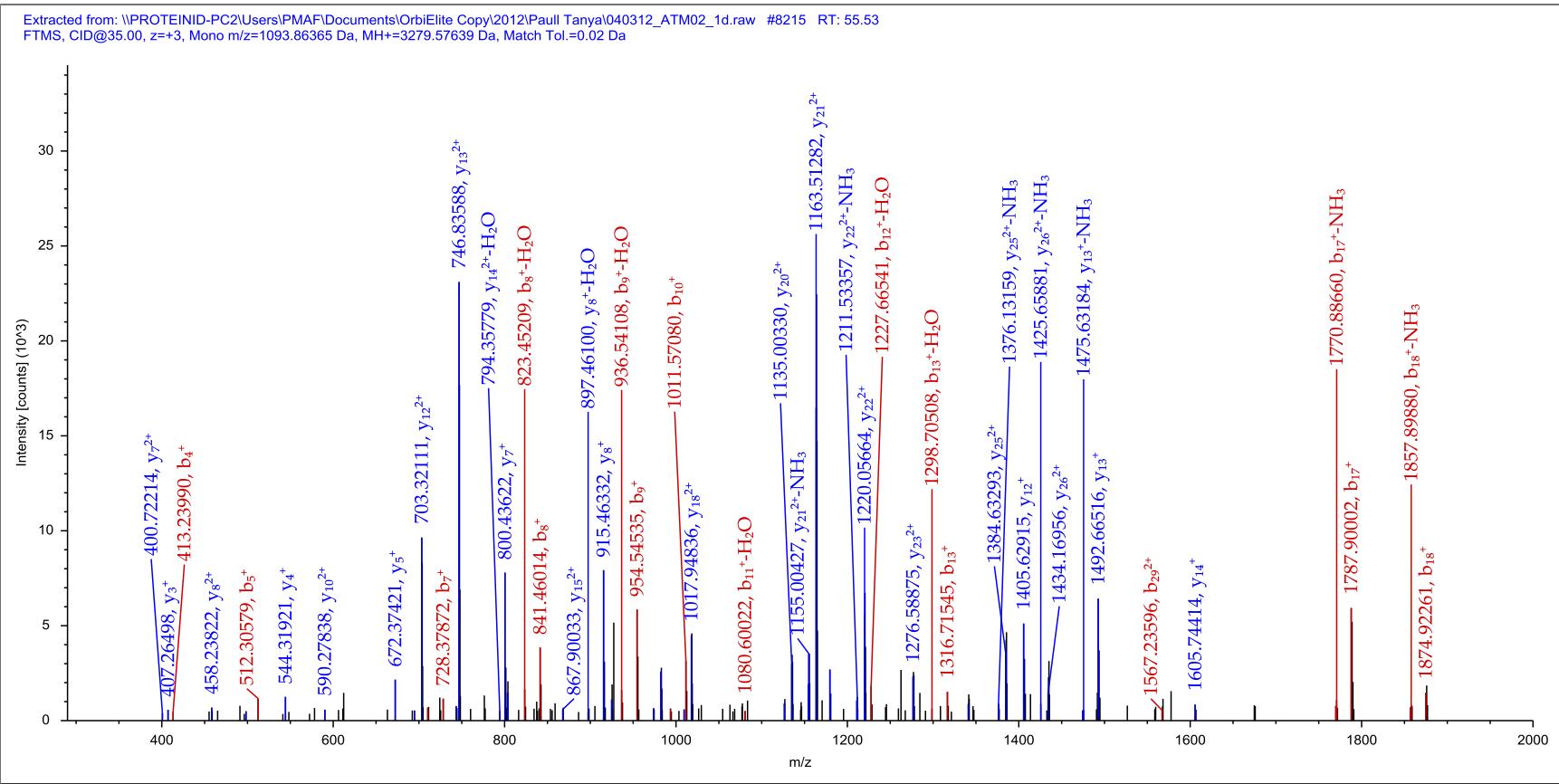
C12 sulfonic acid M3 oxidation



PRMT5

ADIIIVSELLGSFADNELSPECLDGAQHFLK

C21 sulfonic acid

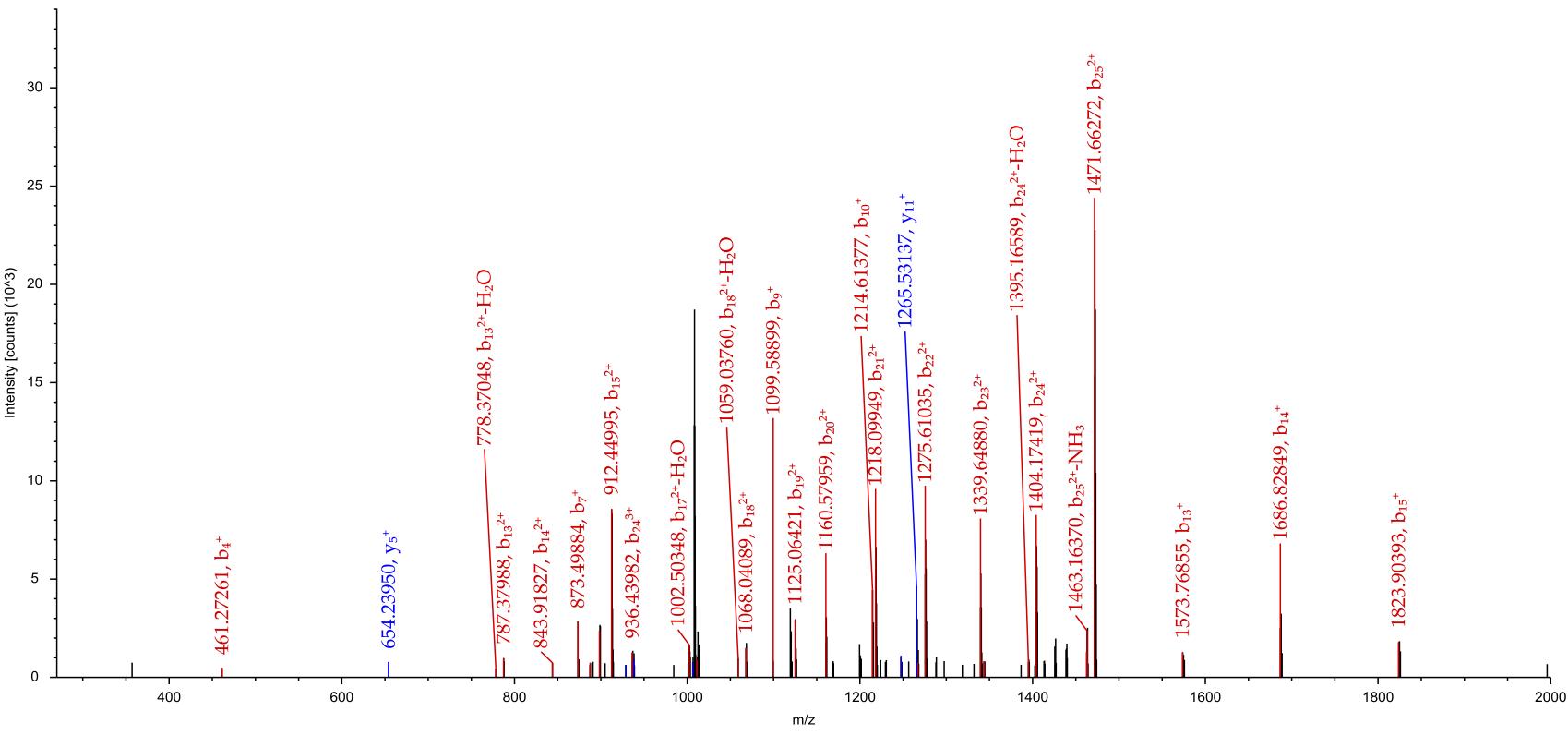


ATM

ALYLQQRPEDETELHPTLNADDQECK

C25 sulfinic acid

Extracted from: \\PROTEINID-PC2\\Users\\PMAF\\Documents\\OrbiElite Copy\\2012\\Pauli Tanya\\030112_ATM03_1d.raw #5461 RT: 35.05
FTMS, CID@35.00, z=+3, Mono m/z=1030.14417 Da, MH+=3088.41794 Da, Match Tol.=0.02 Da

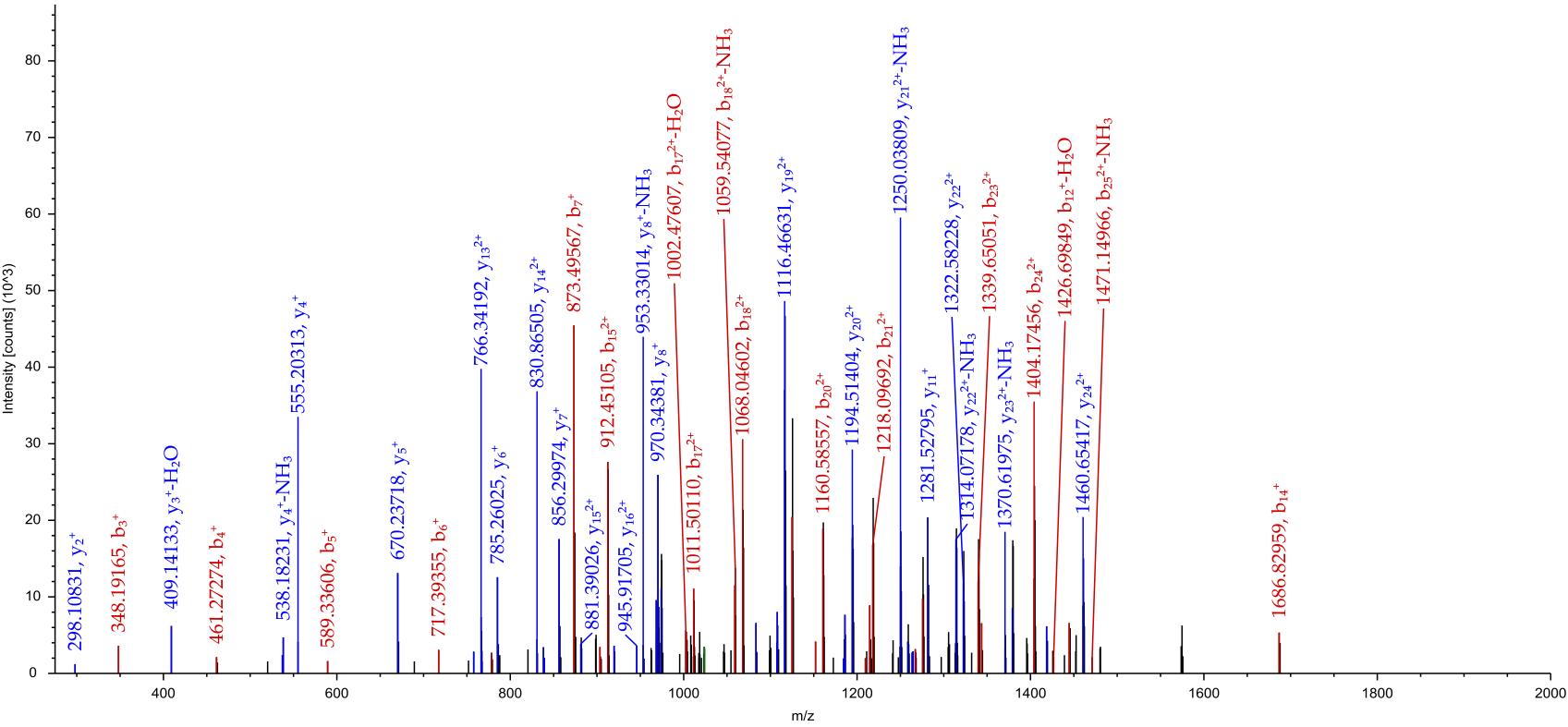


ATM

ALYLQQRPEDETELHPTLNADDQECK

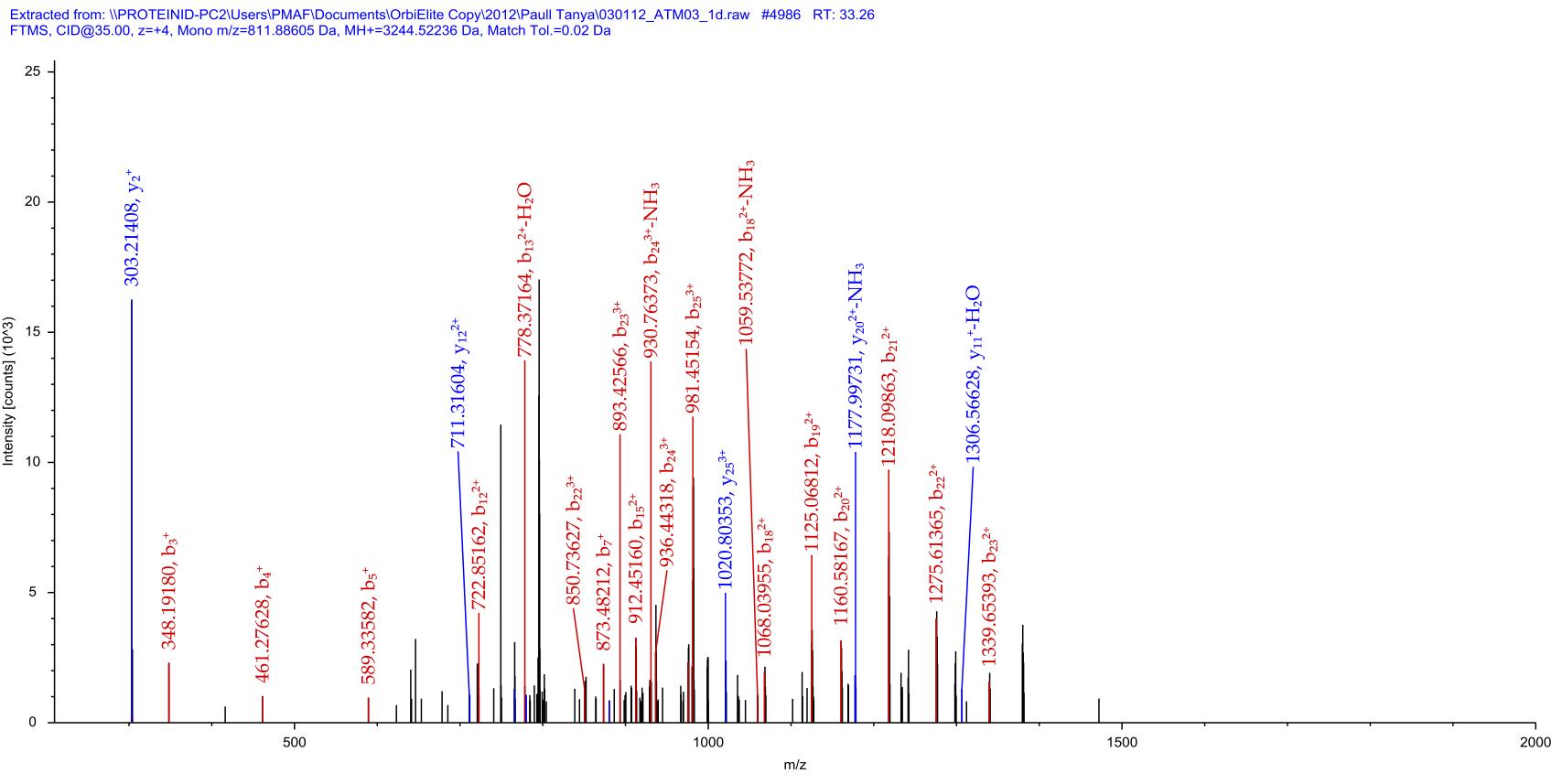
C25 sulfonic acid

Extracted from: \PROTEINID-PC2\Users\PMARF\Documents\OrbiElite Copy\2012\Pauli Tanya\040312_ATM02_1d.raw #4317 RT: 31.56
FTMS, CID@35.00, z=+3, Mono m/z=1035.47583 Da, MH+=3104.41294 Da, Match Tol.=0.02 Da



ATM

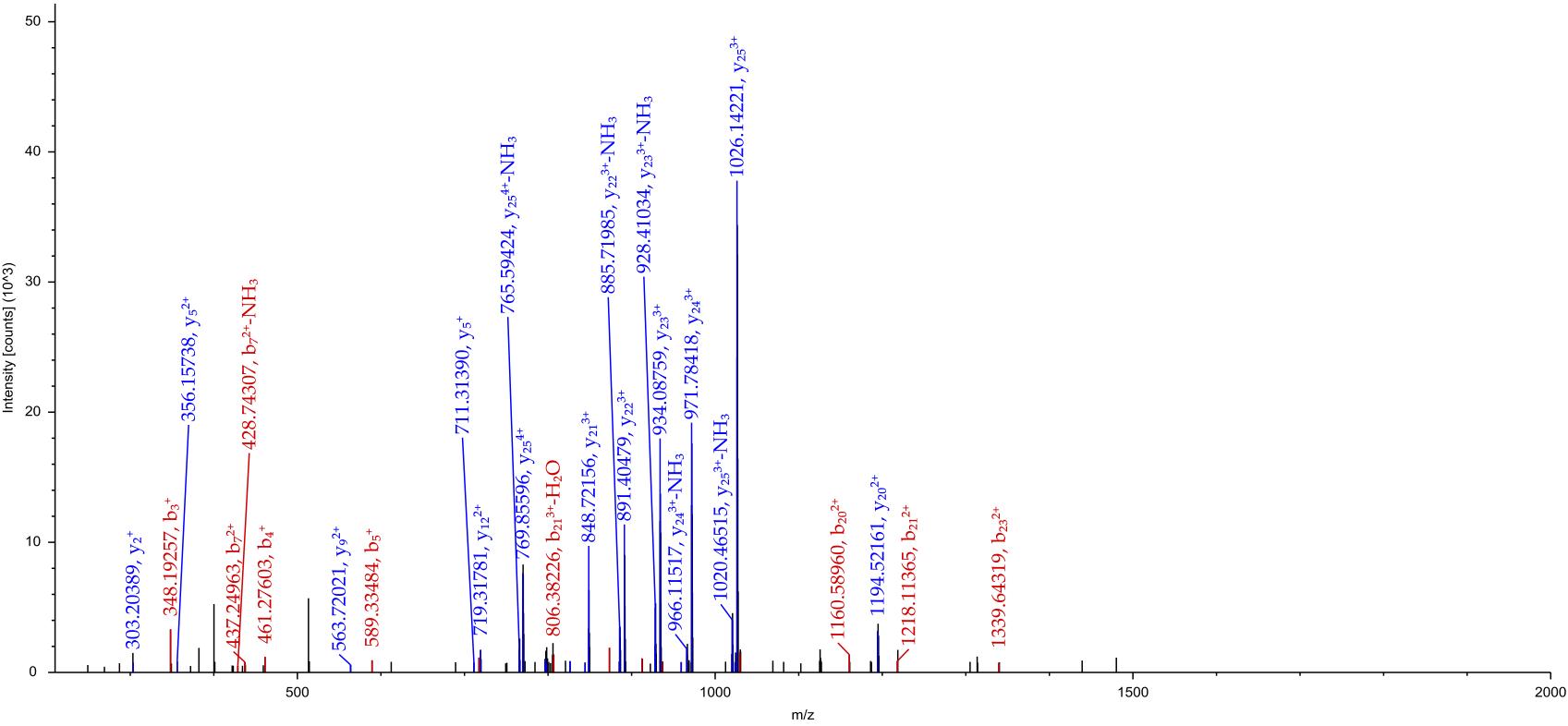
ALYLQQRPEDETELHPTLNADDQECKR C25 sulfinic acid



ATM

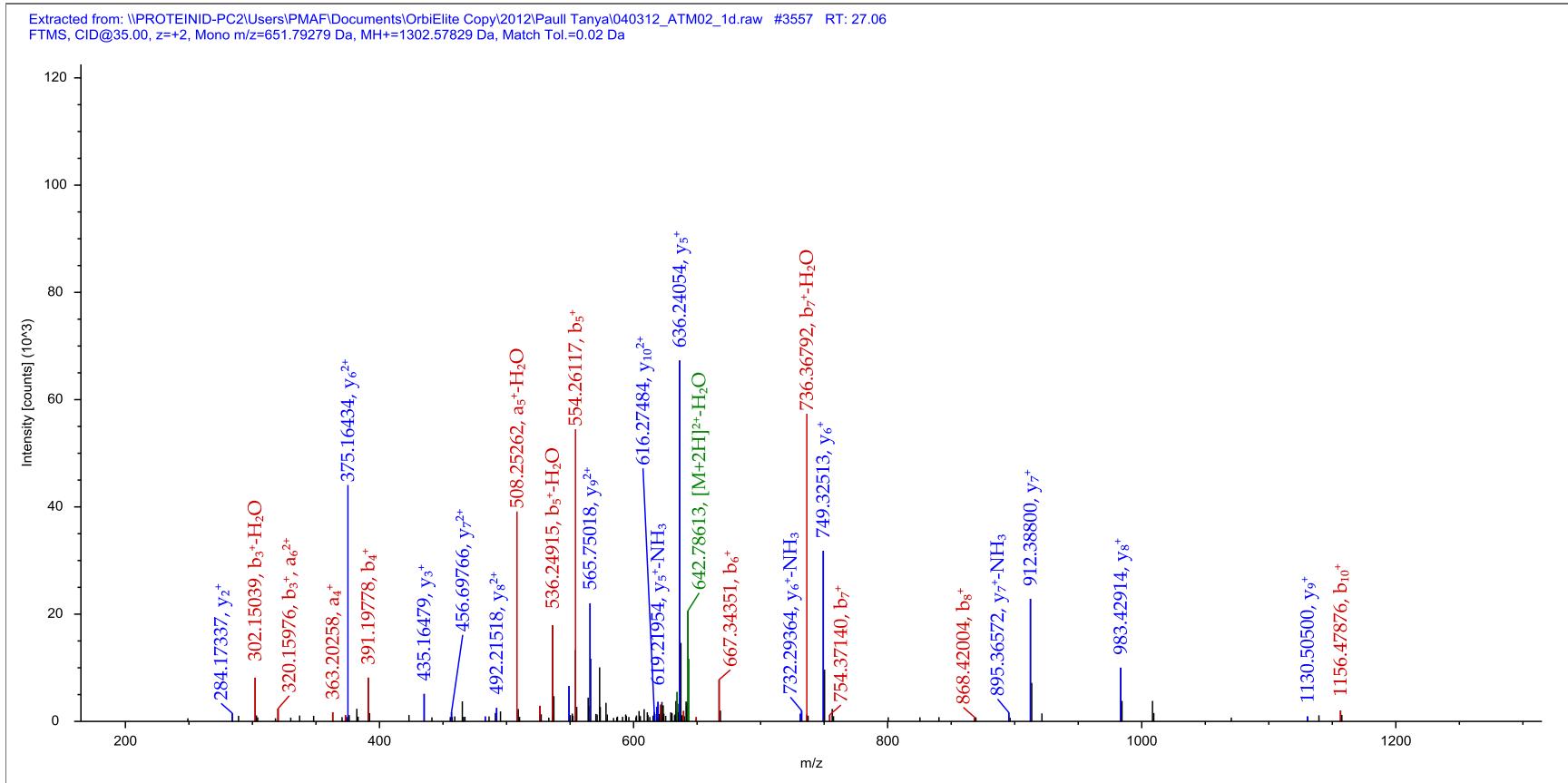
ALYLQQRPEDETELHPTLNADDQECKR C25 sulfonic acid

Extracted from: \\PROTEINID-PC2\\Users\\PMAF\\Documents\\OrbiElite Copy\\2012\\Pauli Tanya\\040312_ATM02_1d.raw #4013 RT: 29.80
FTMS, CID@35.00, z=+4, Mono m/z=815.88232 Da, MH+=3260.50747 Da, Match Tol.=0.02 Da



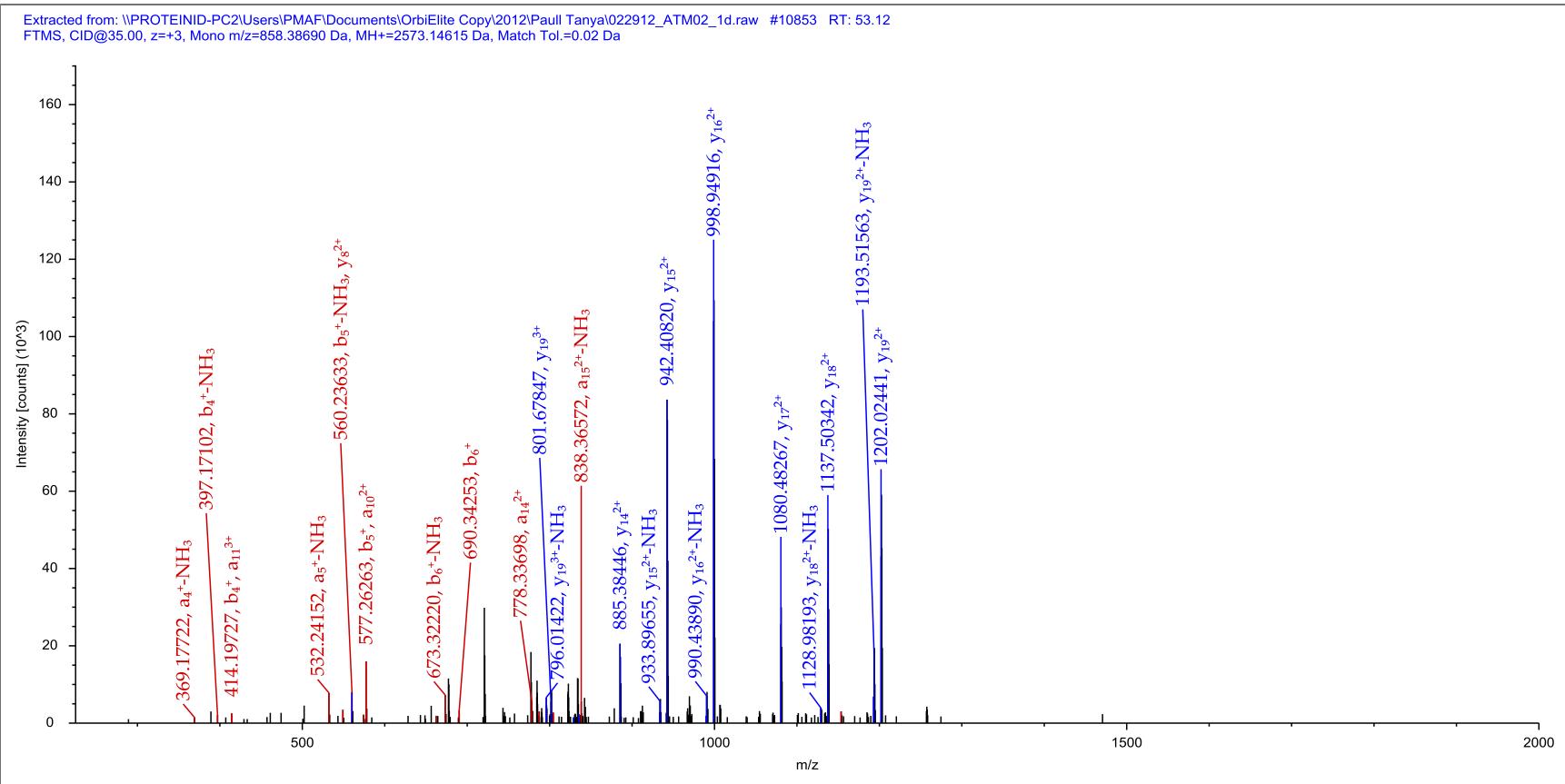
ATM ATFAYISNCHK

C9 sulfonic acid



ATM AVENYINCLLSGEEHDMWVFR

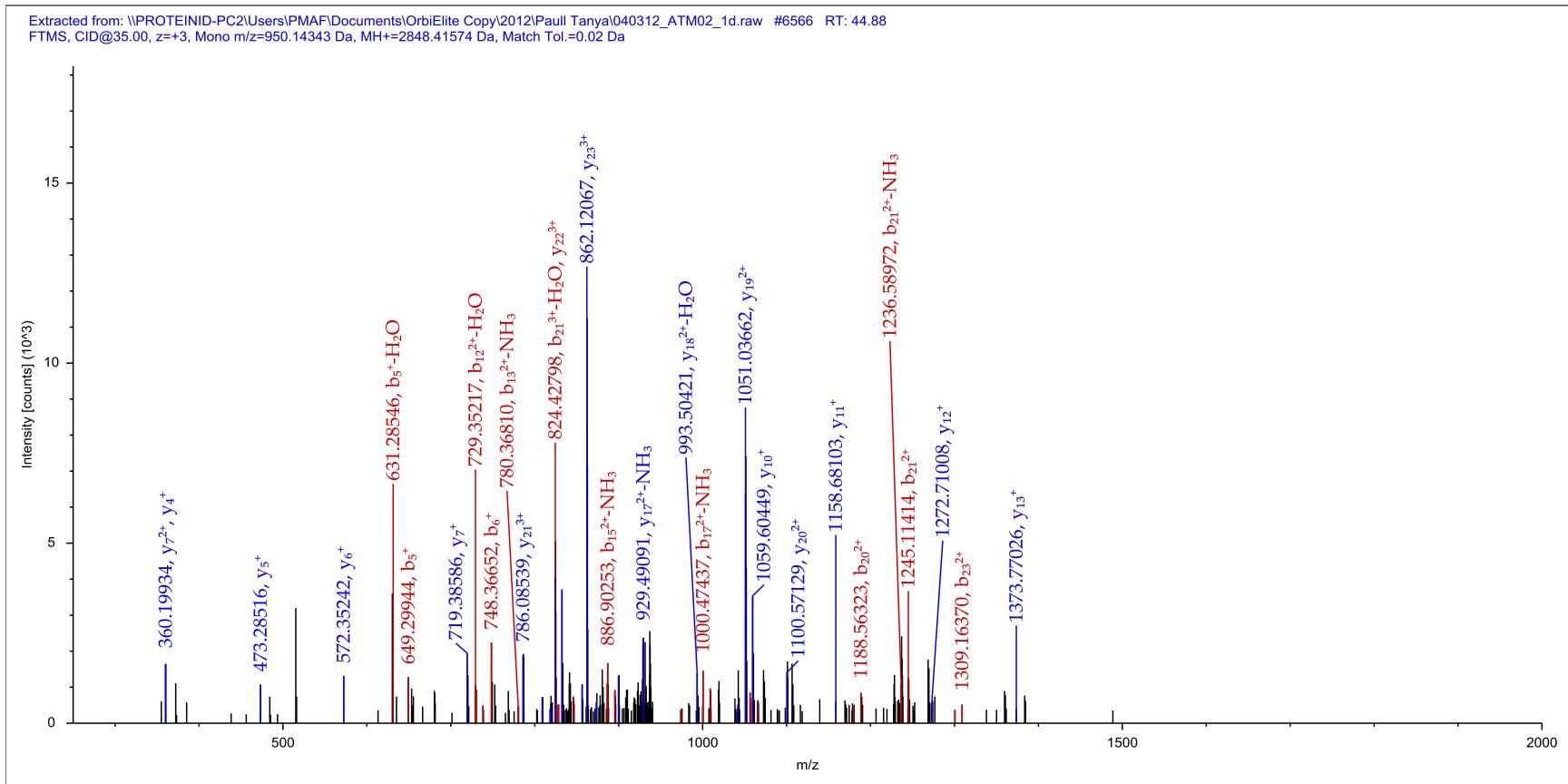
C8 sulfonic acid



PRMT5

CLLDRVPEEEKDTNVQVLMVLGAGR

C1 sulfonic acid M19 oxidation

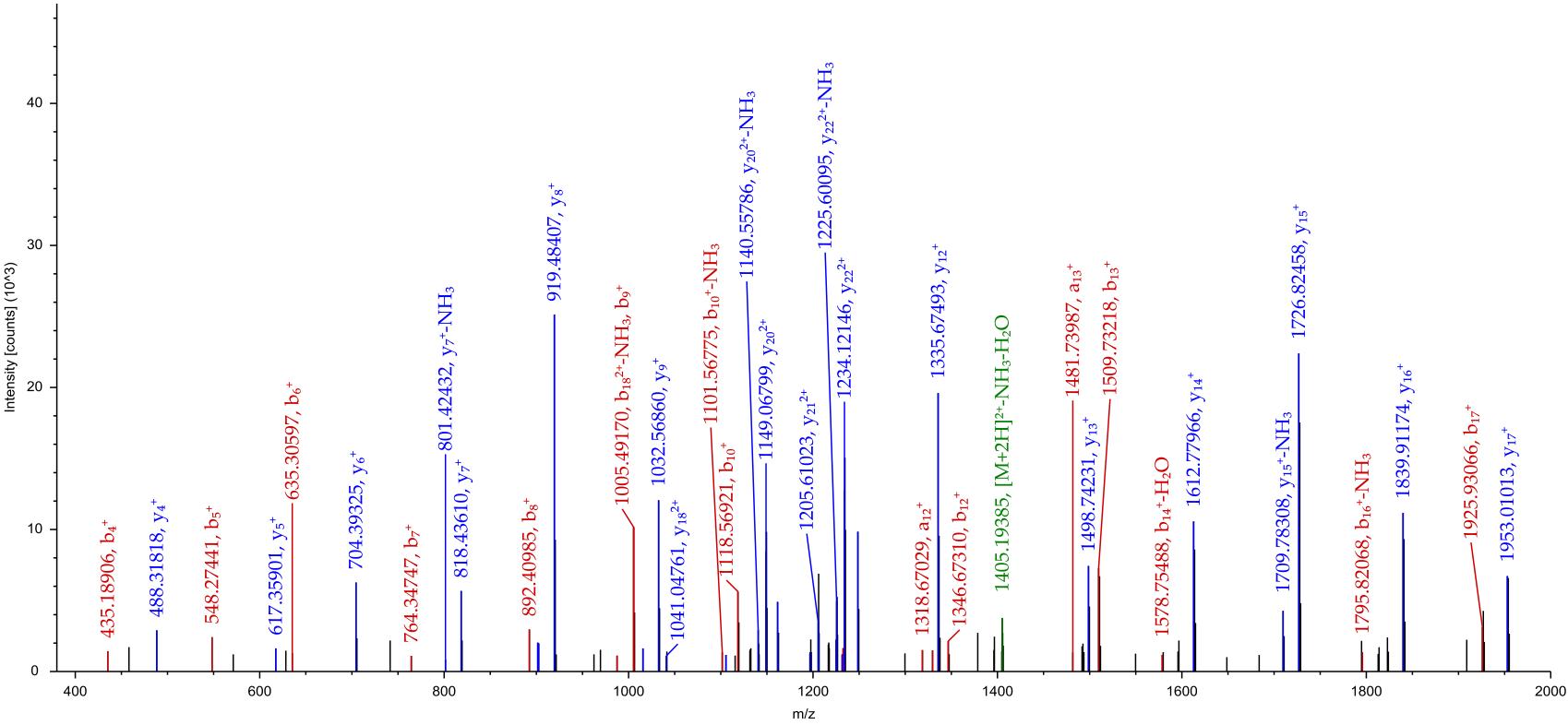


ATM

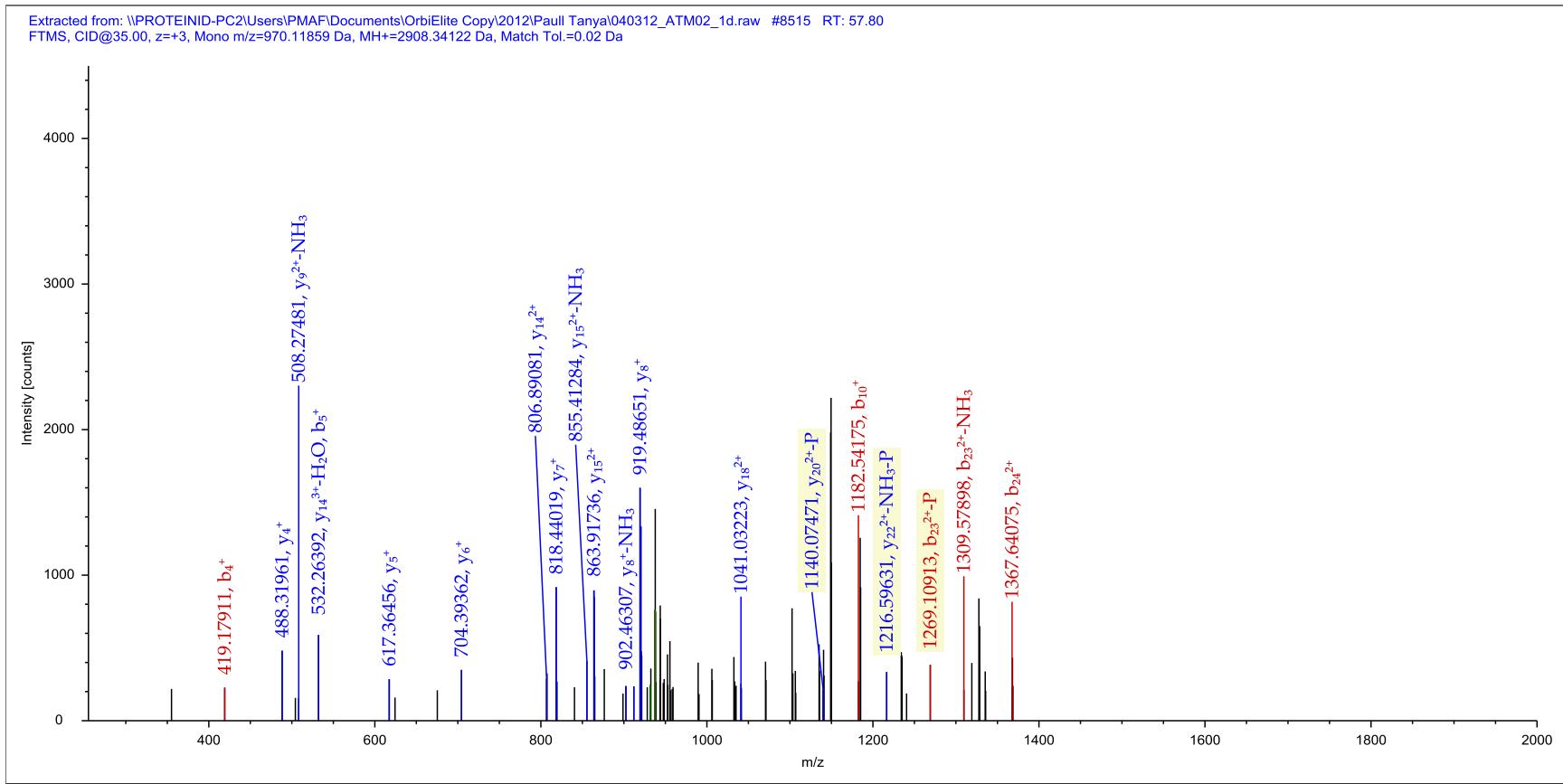
CLLGLSEQLLNNYSSEITNSETLVR

C1 sulfonic acid

Extracted from: \\PROTEINID-PC2\\Users\\PMAR\\Documents\\OrbiElite Copy\\2012\\Pauli Tanya\\040312_ATM02_1d.raw #8727 RT: 59.92
FTMS, CID@35.00, z=+2, Mono m/z=1422.70105 Da, MH+=2844.39482 Da, Match Tol.=0.02 Da

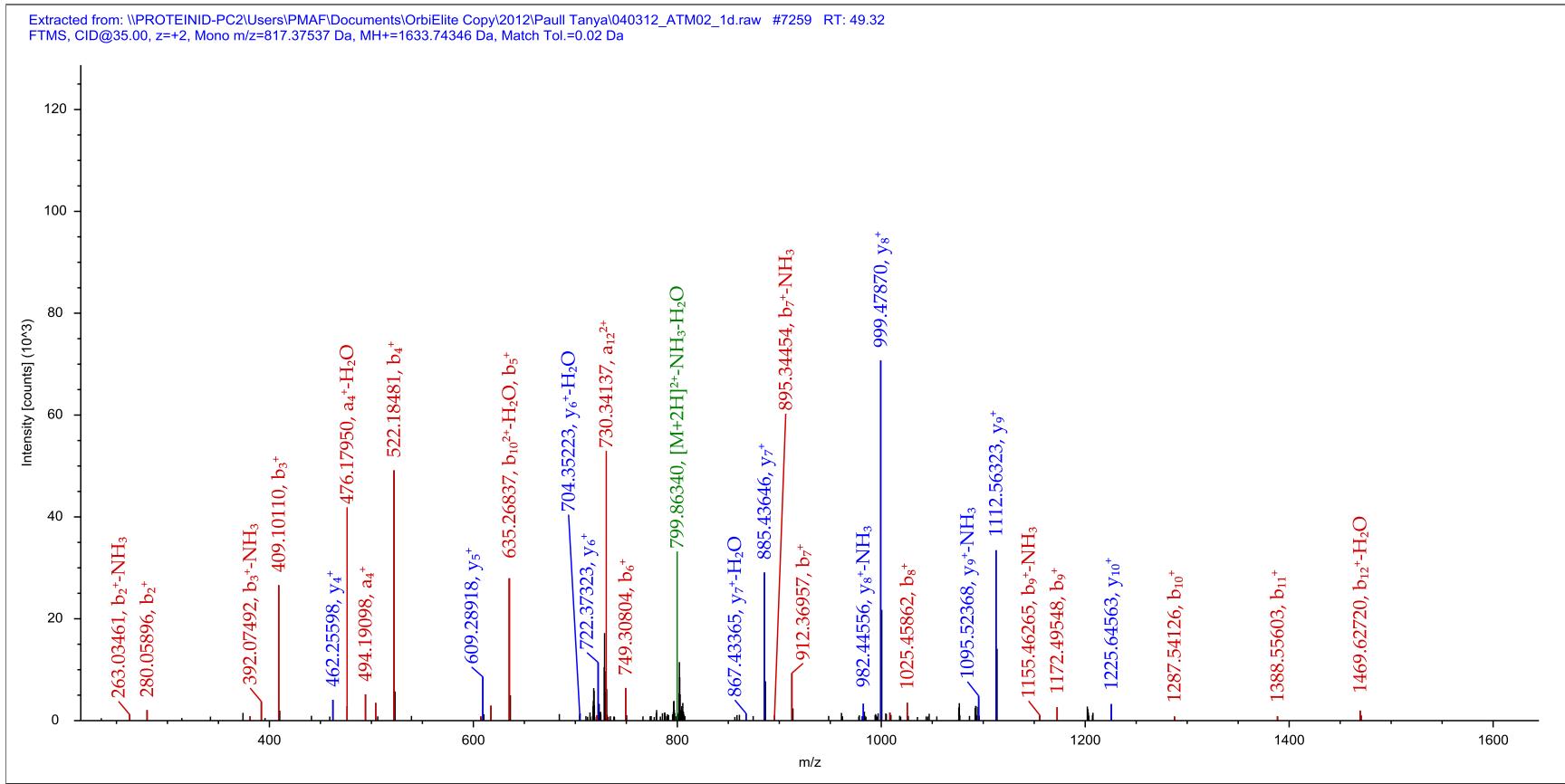


CLLGLSEQLLNNYSSEITNSETLVR C1 sulfinic acid S6 phosphorylation

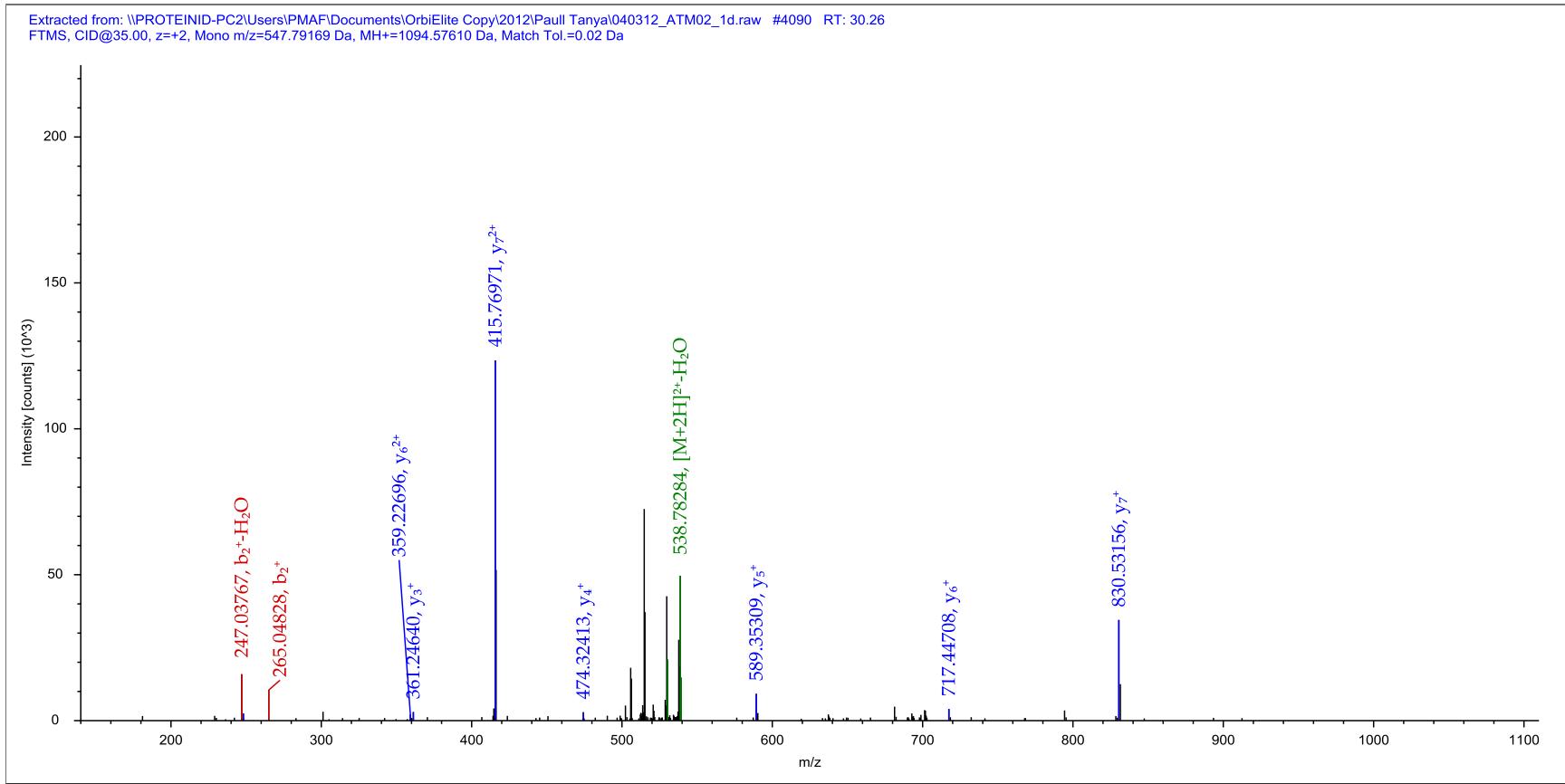


ATM CQELLNYIMDTVK

C1 sulfonic acid M9 oxidation

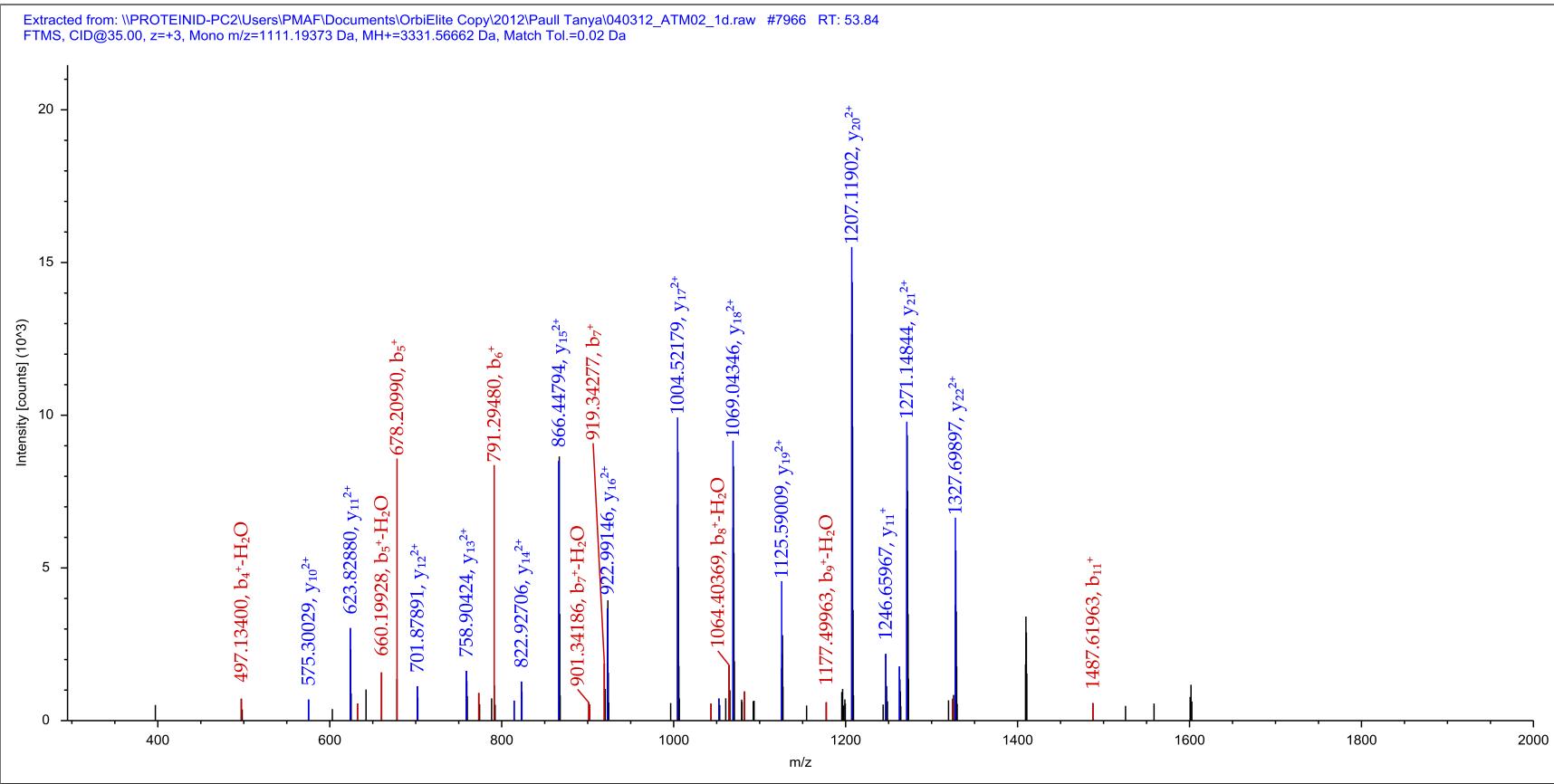


ATM ECIKDILTK C2 sulfinic acid



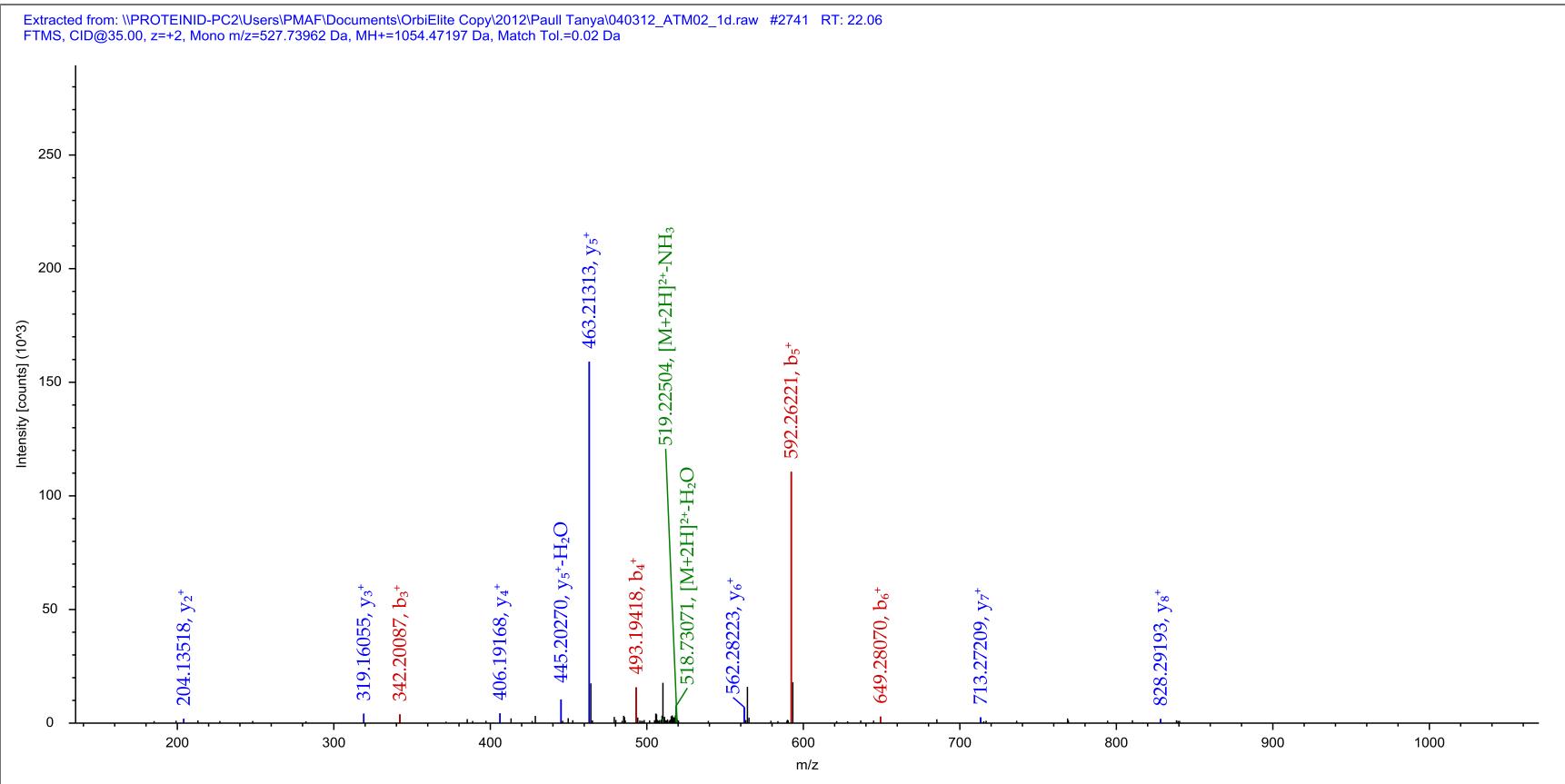
PRMT5

EFCSYLYQYLEYLSQNRPPPNAYELFAK C4 sulfonic acid



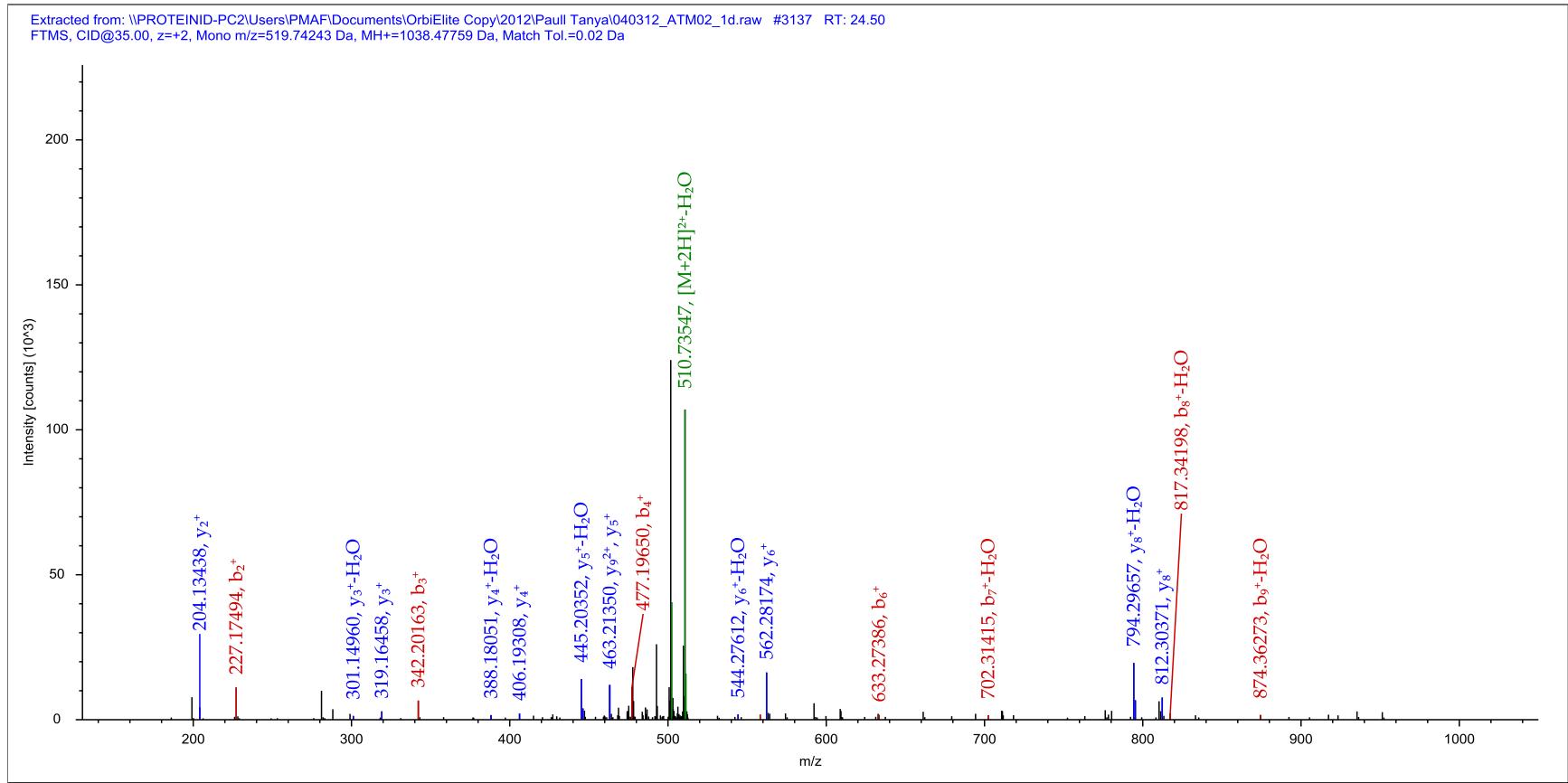
ATM I IDCVGSDGK

C4 sulfonic acid



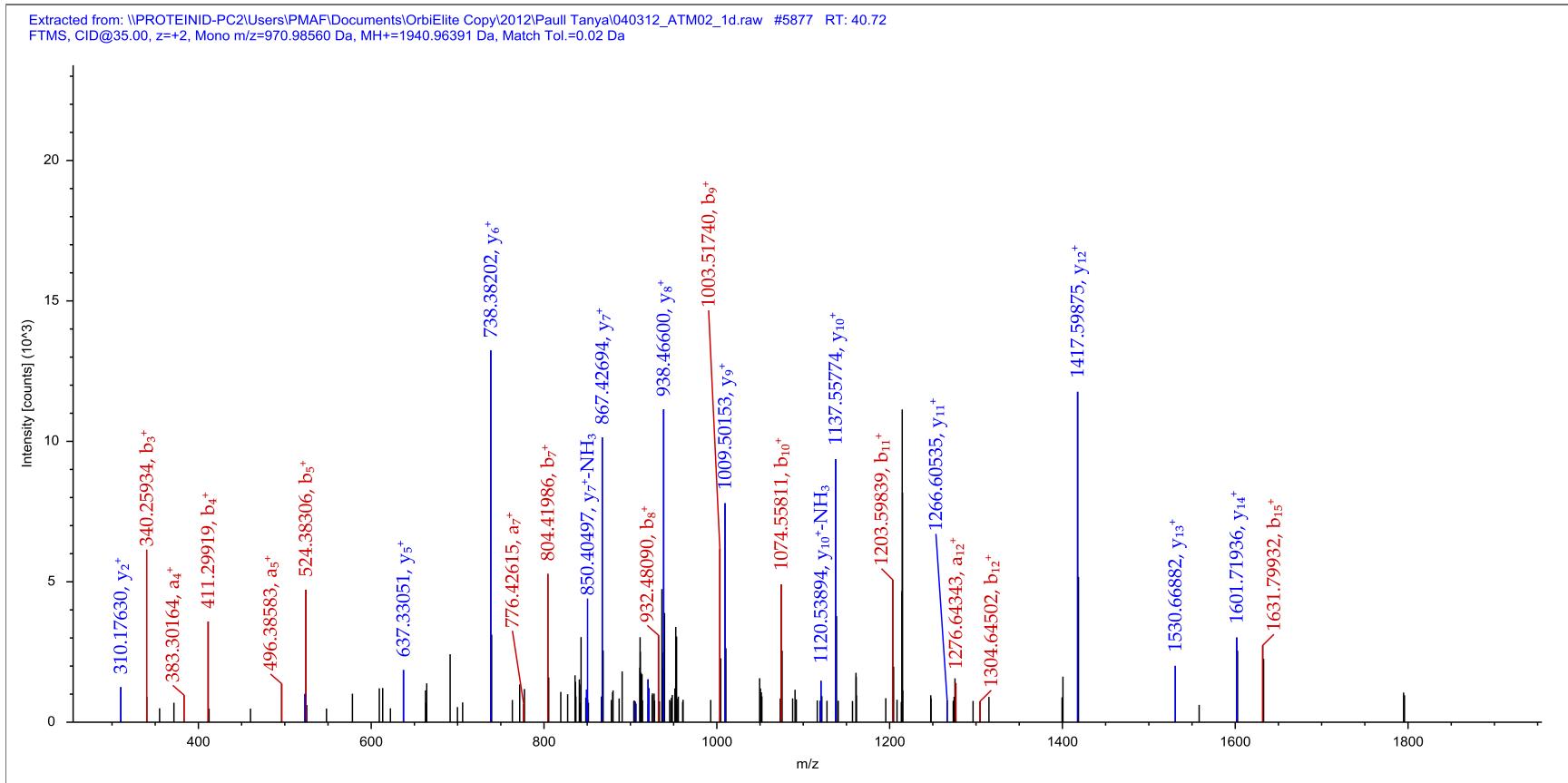
ATM IIDCVGSDGK

C4 sulfinic acid



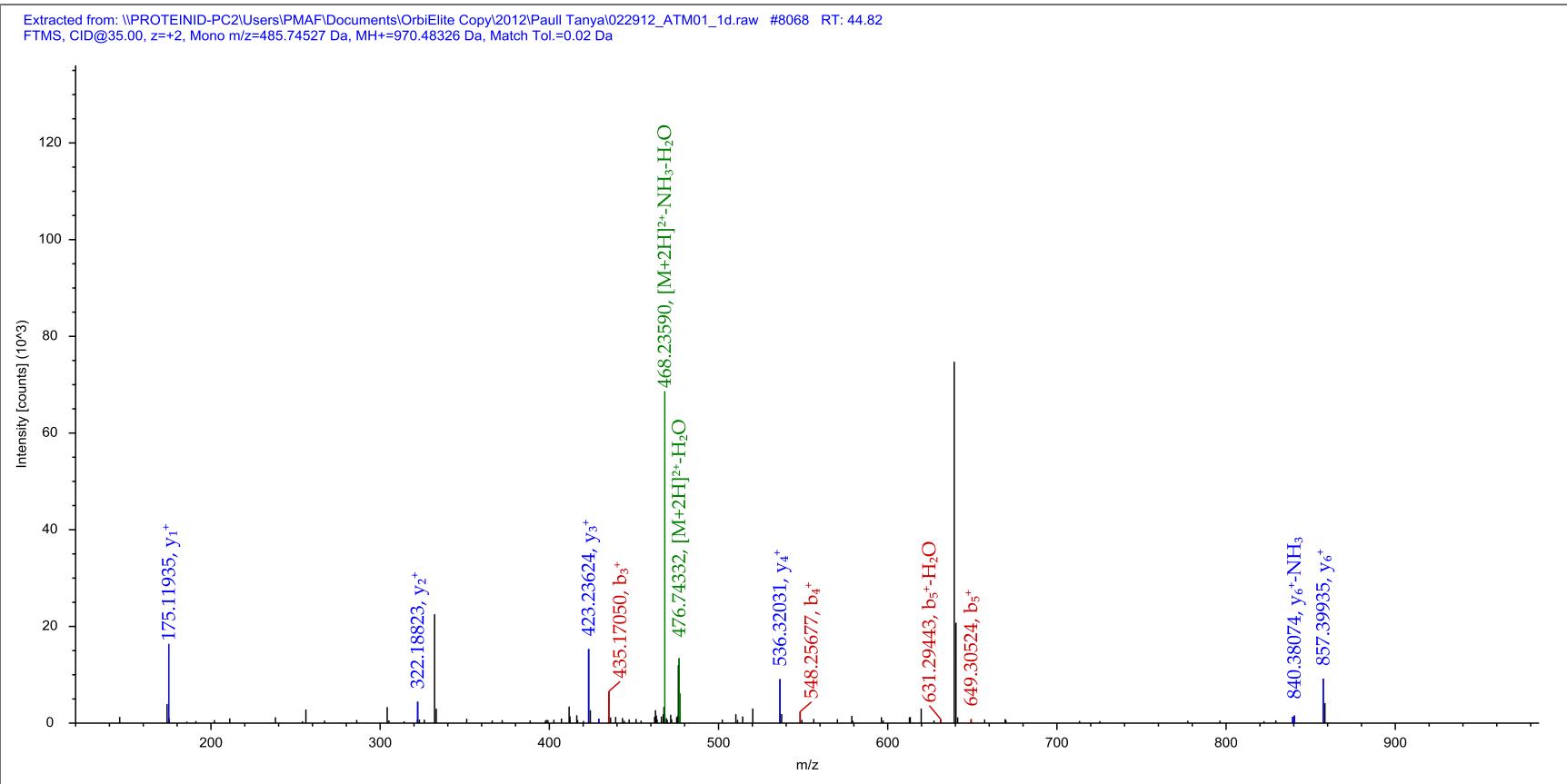
ATM ILLAICEQAAETNNVYK

C6 sulfonic acid



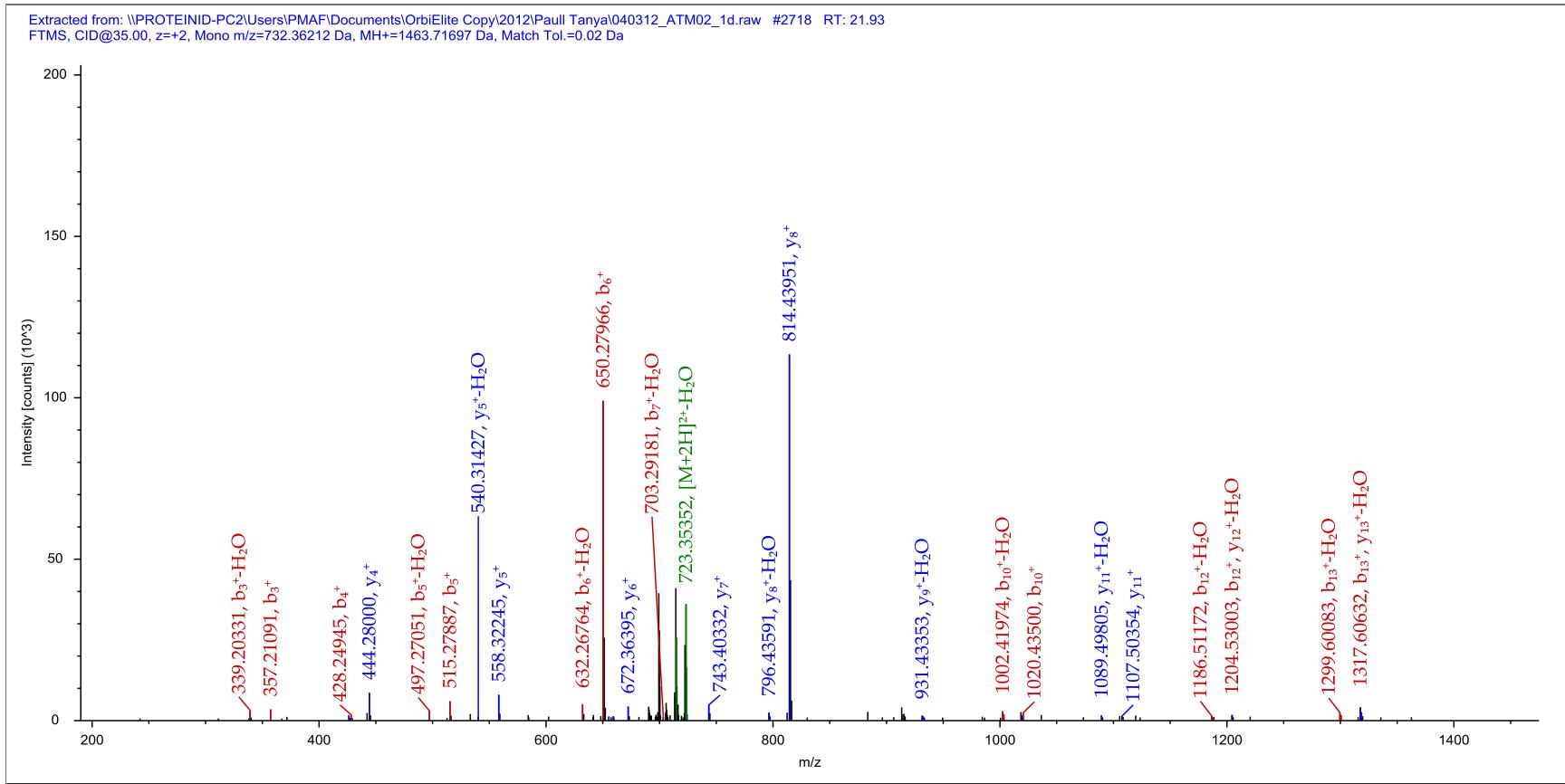
ATM IWCITFR

C3 sulfinic acid



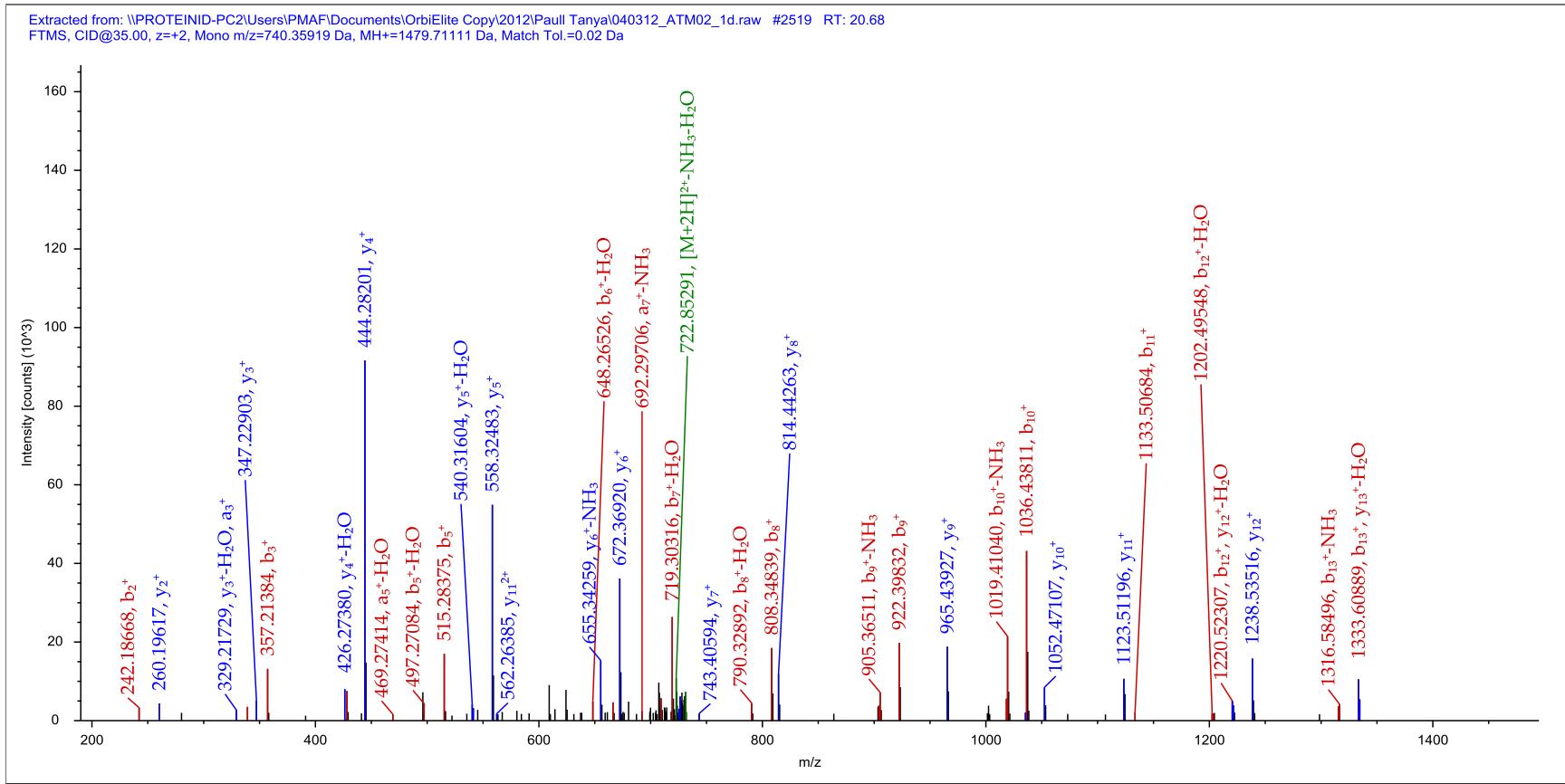
ATM KLDASCAANNPSLK

C6 sulfinic acid



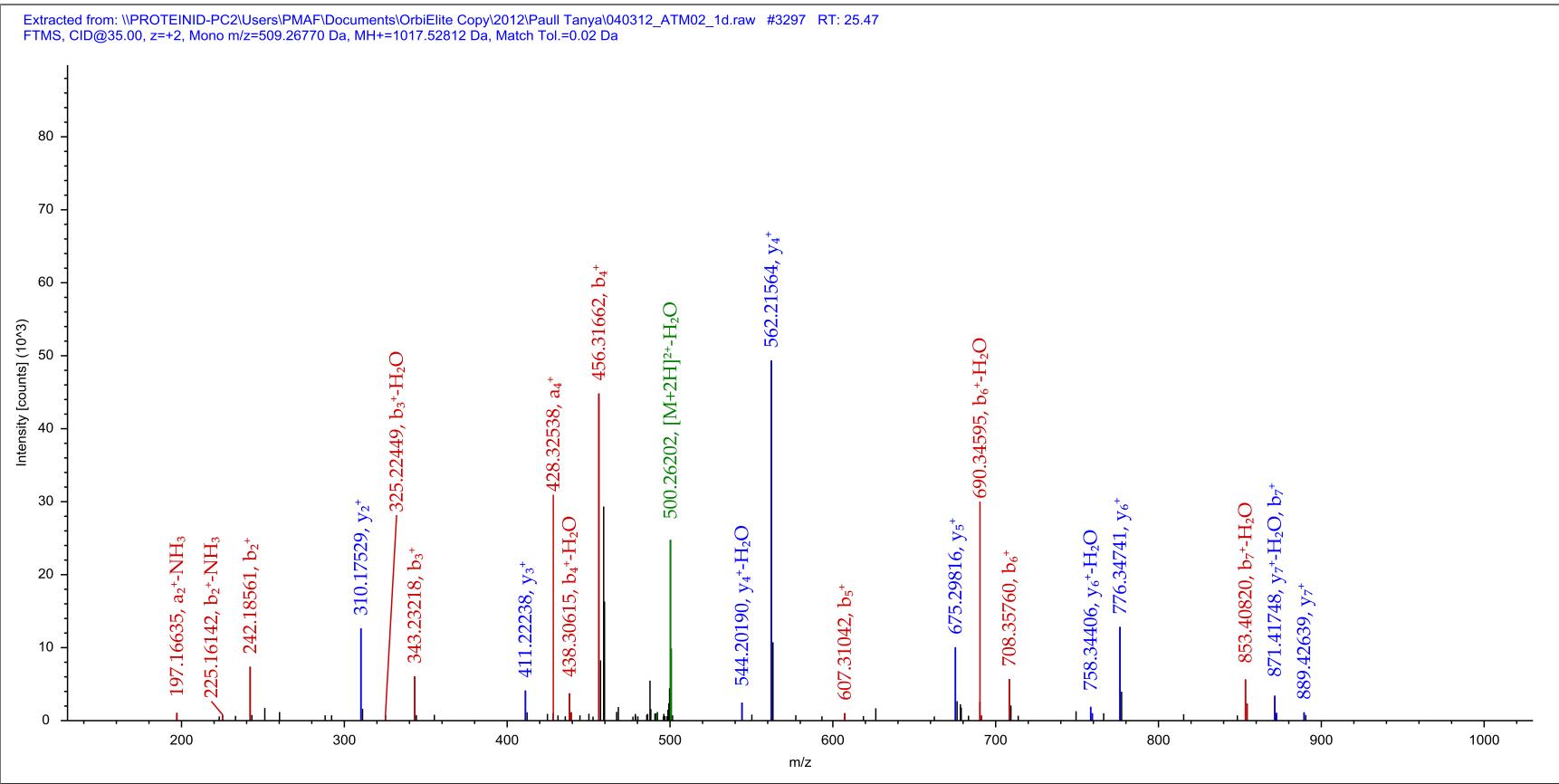
ATM KLDASCAANNPSLK

C6 sulfonic acid



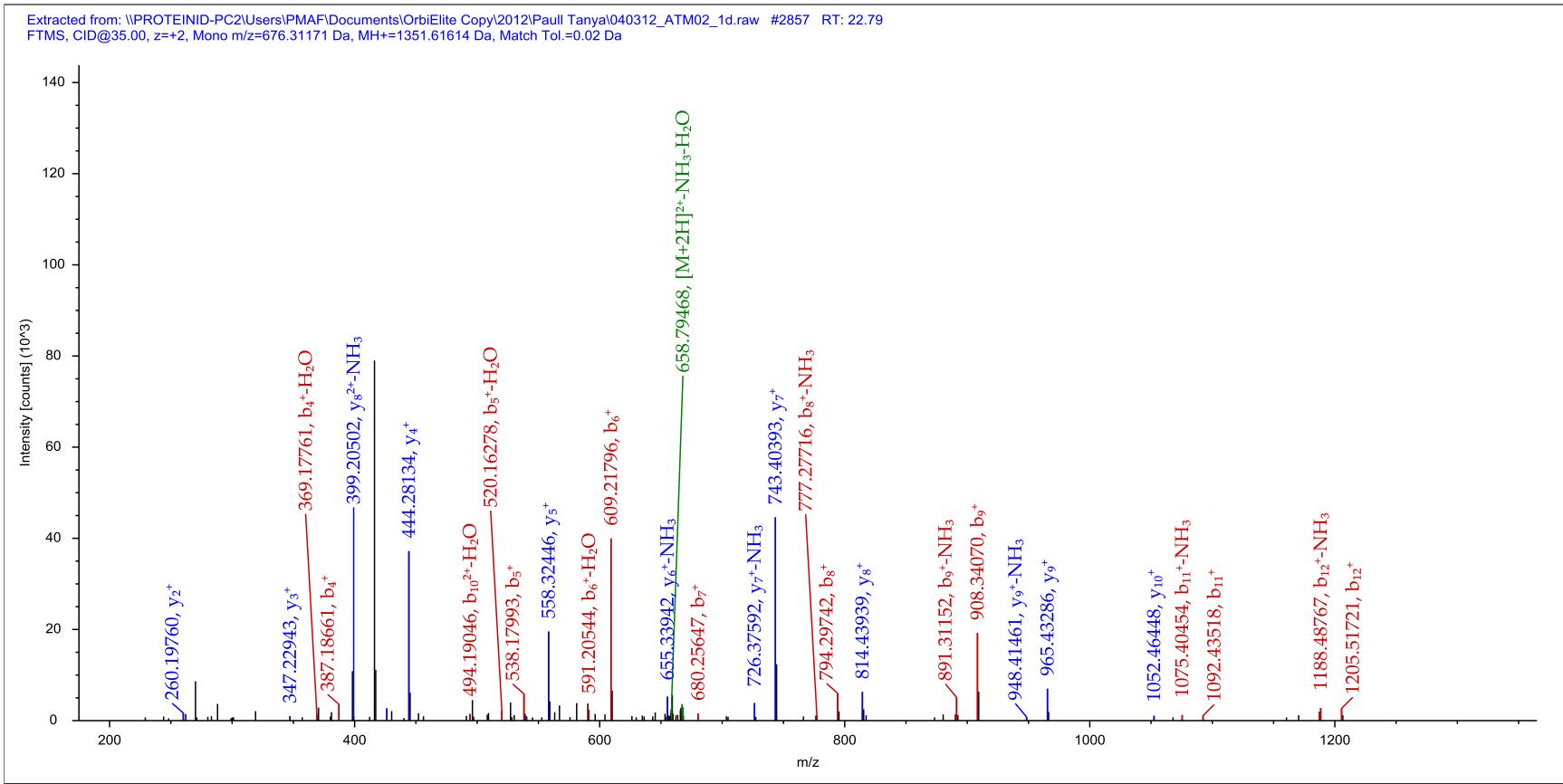
ATM KLTICTYK

C5 sulfonic acid



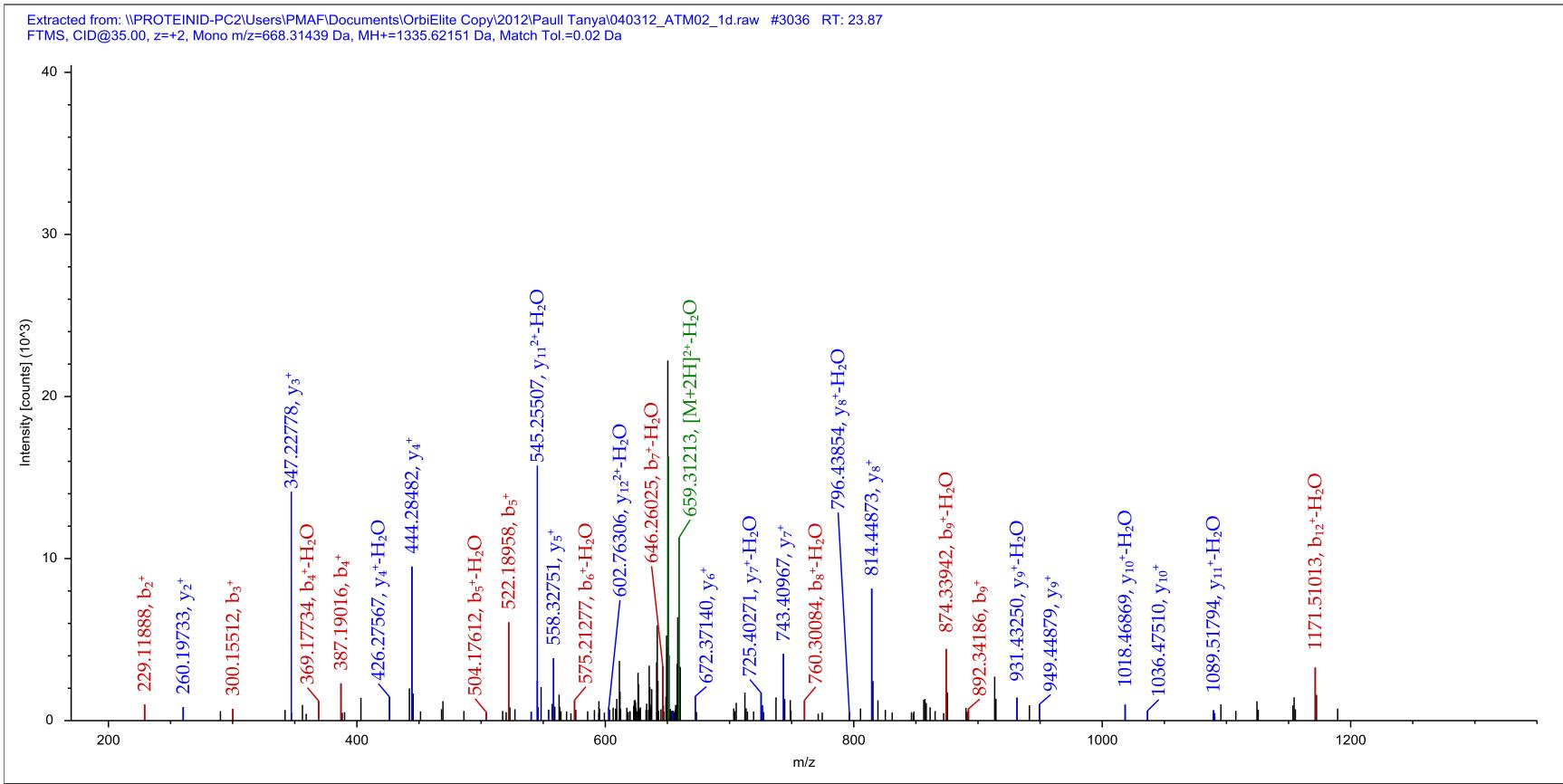
ATM LDASCAANNPSLK

C5 sulfonic acid



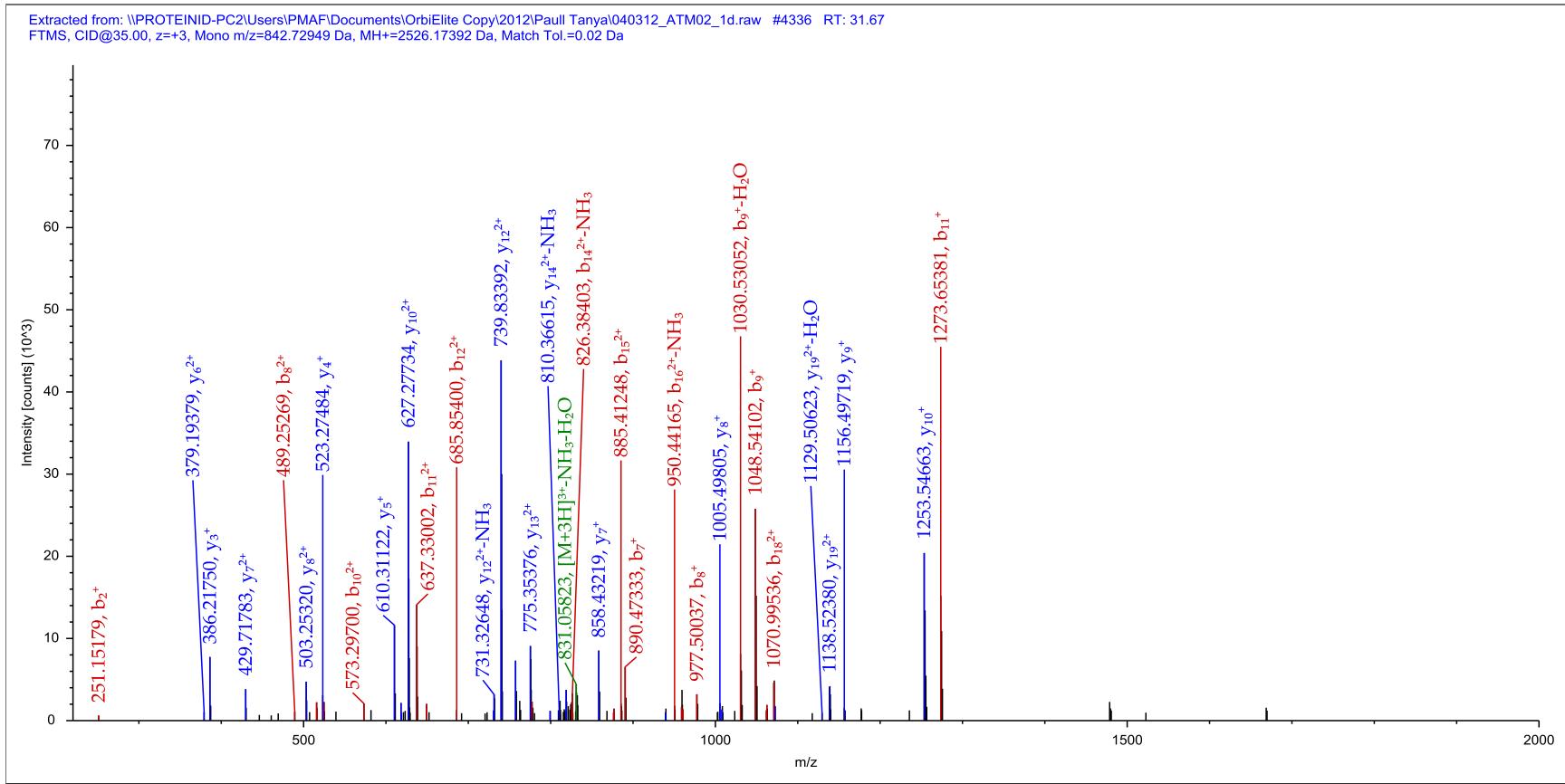
ATM LDASCAANNPSLK

C5 sulfonic acid



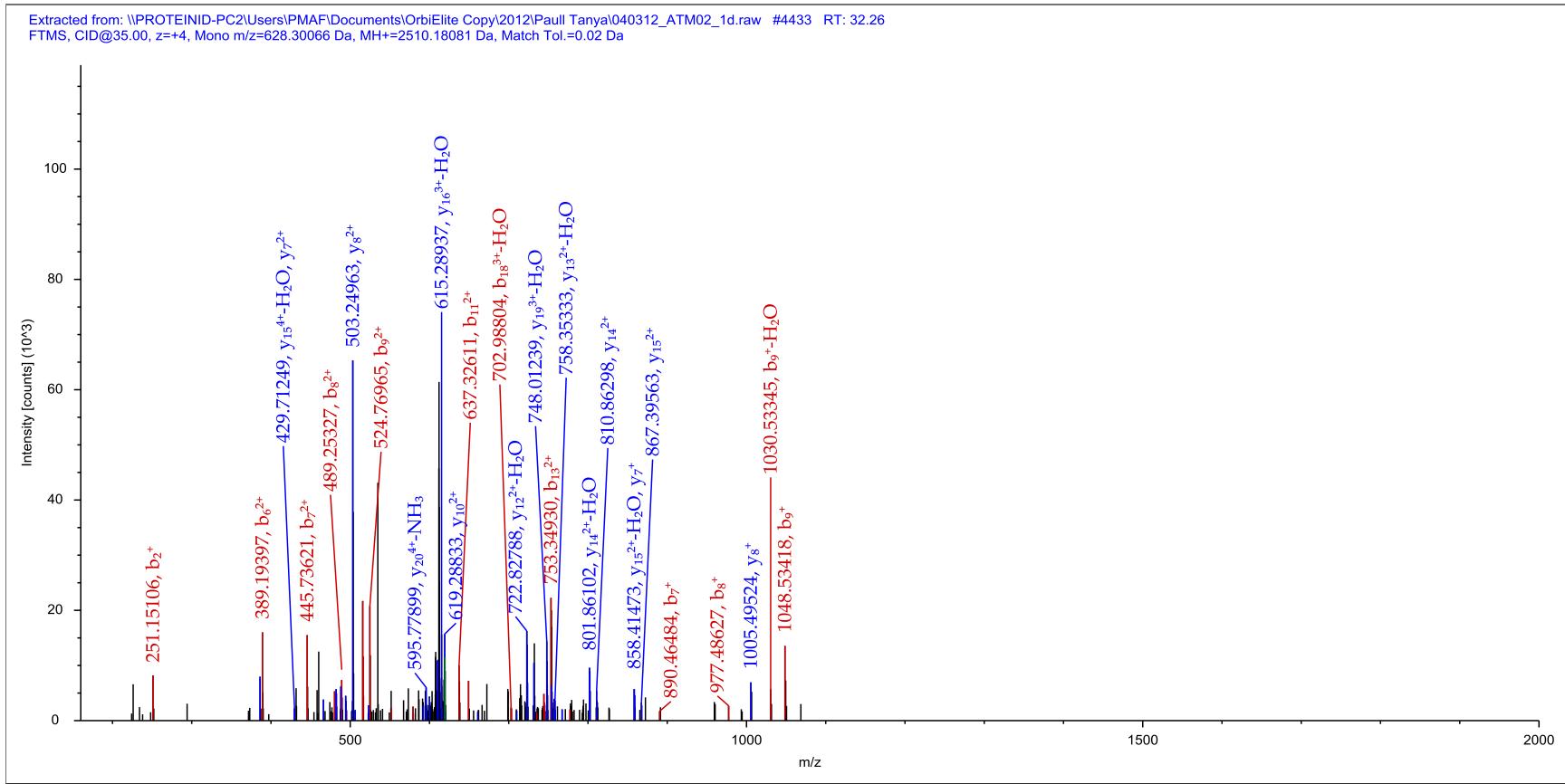
PRMT5 LHNFHQLSAPQPCFTFSHPNR

C13 sulfonic acid



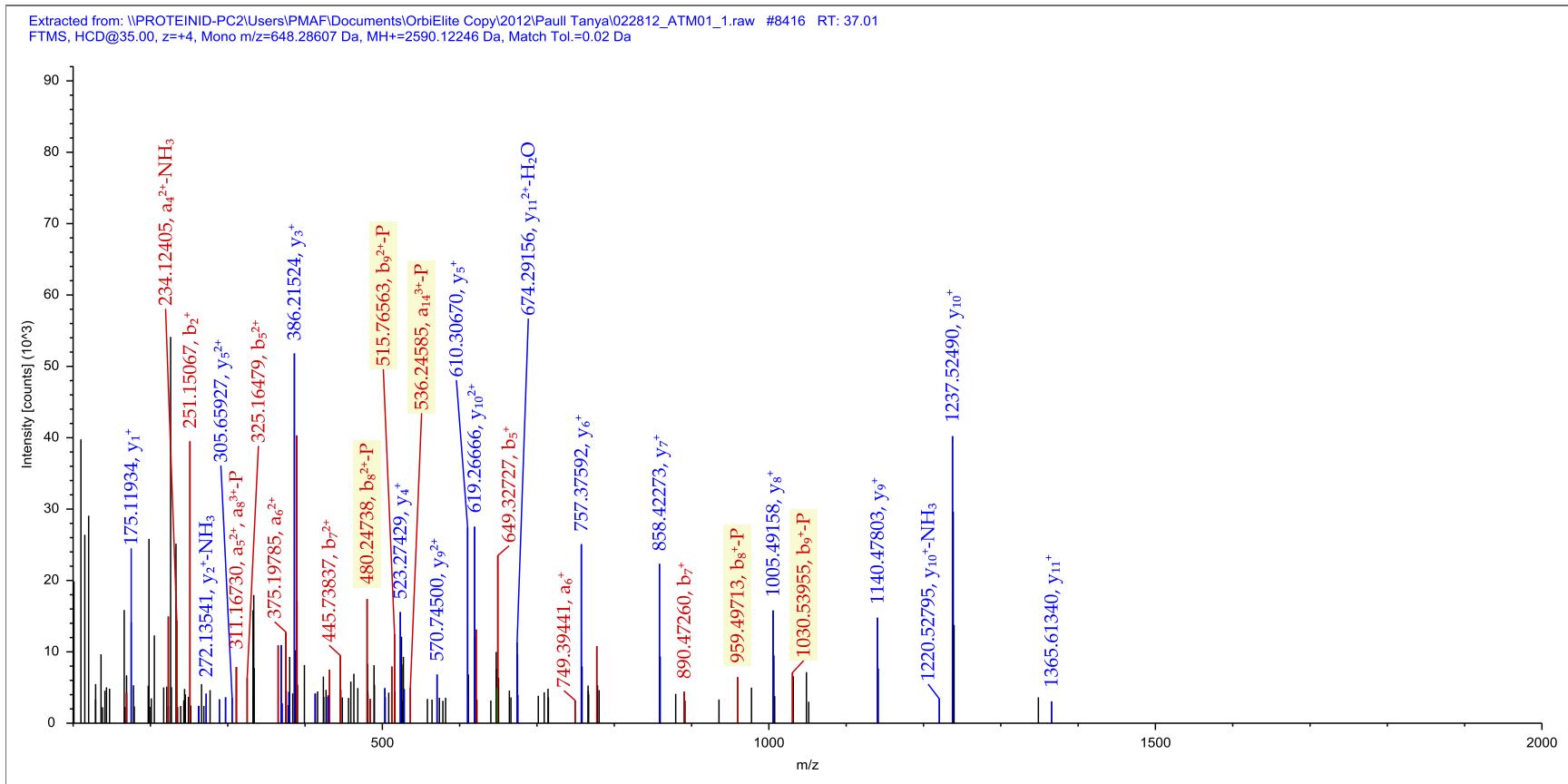
PRMT5 LHNFHQLSAPQPCFTFSHPNR

C13 sulfinic acid



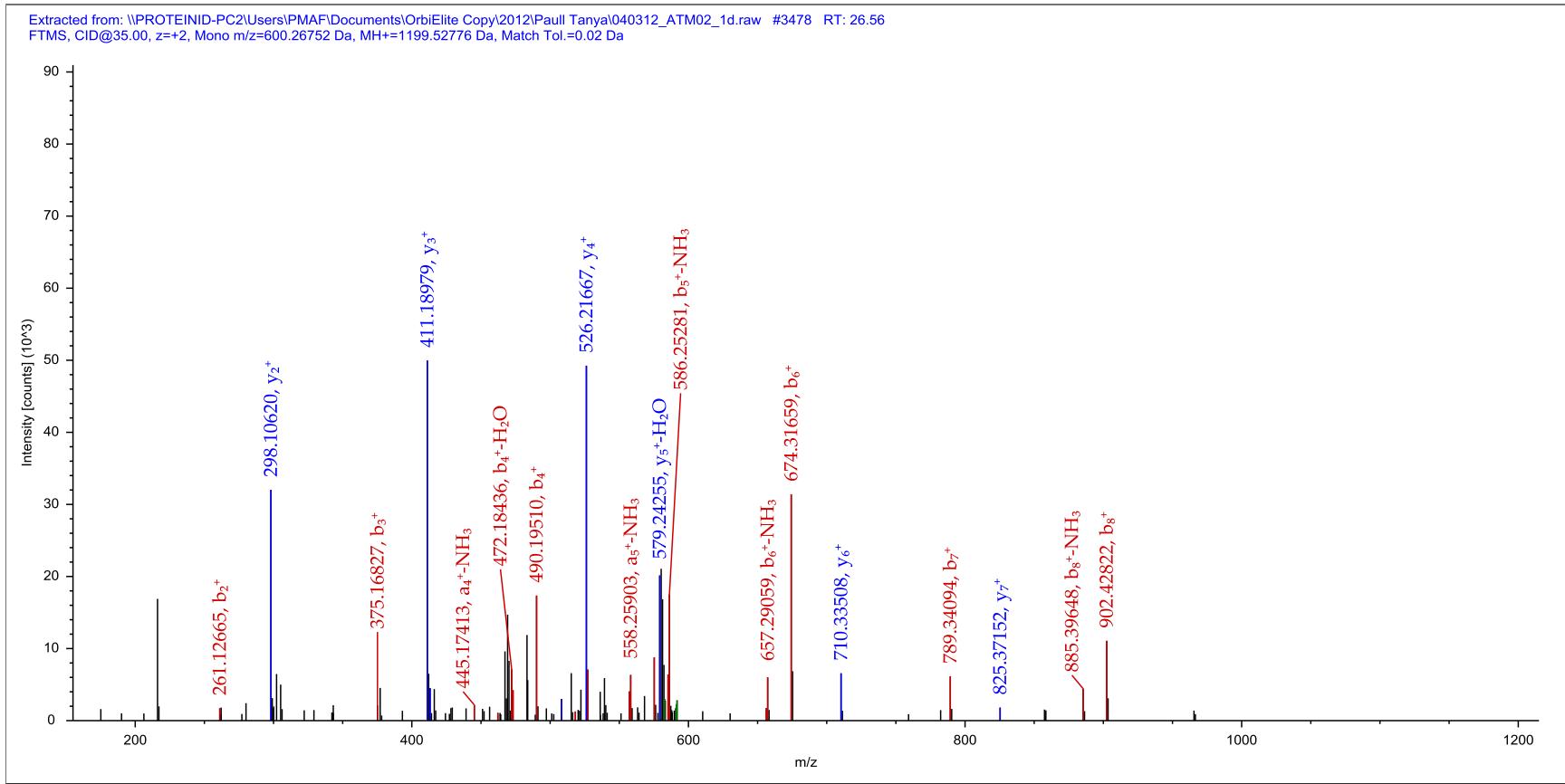
PRMT5 LHNFHQLSAPQPCFTFSHPNR

C13 sulfinic acid S8 phosphorylation



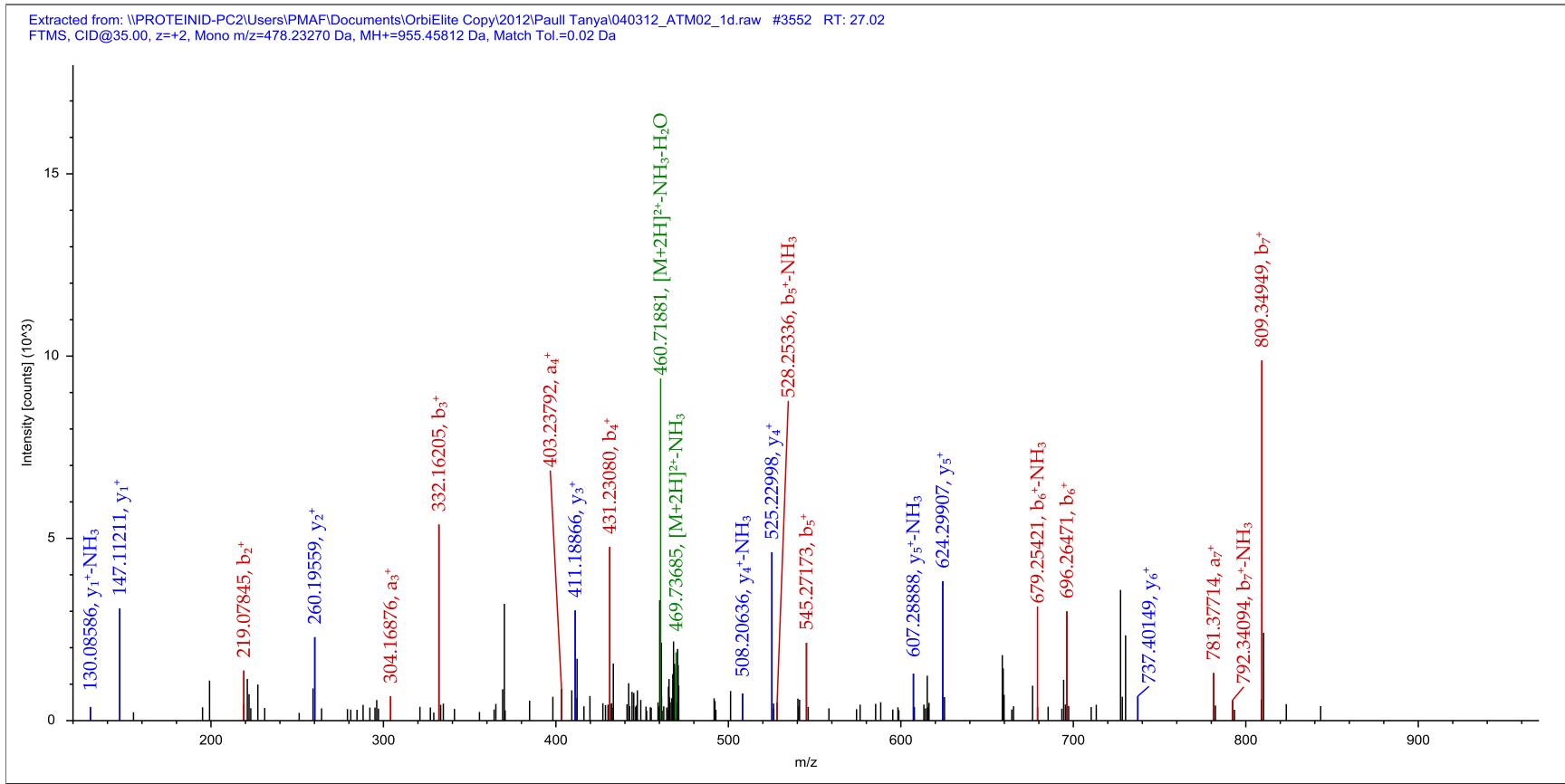
LMNDIADICK

C9 sulfonic acid M2 oxidation



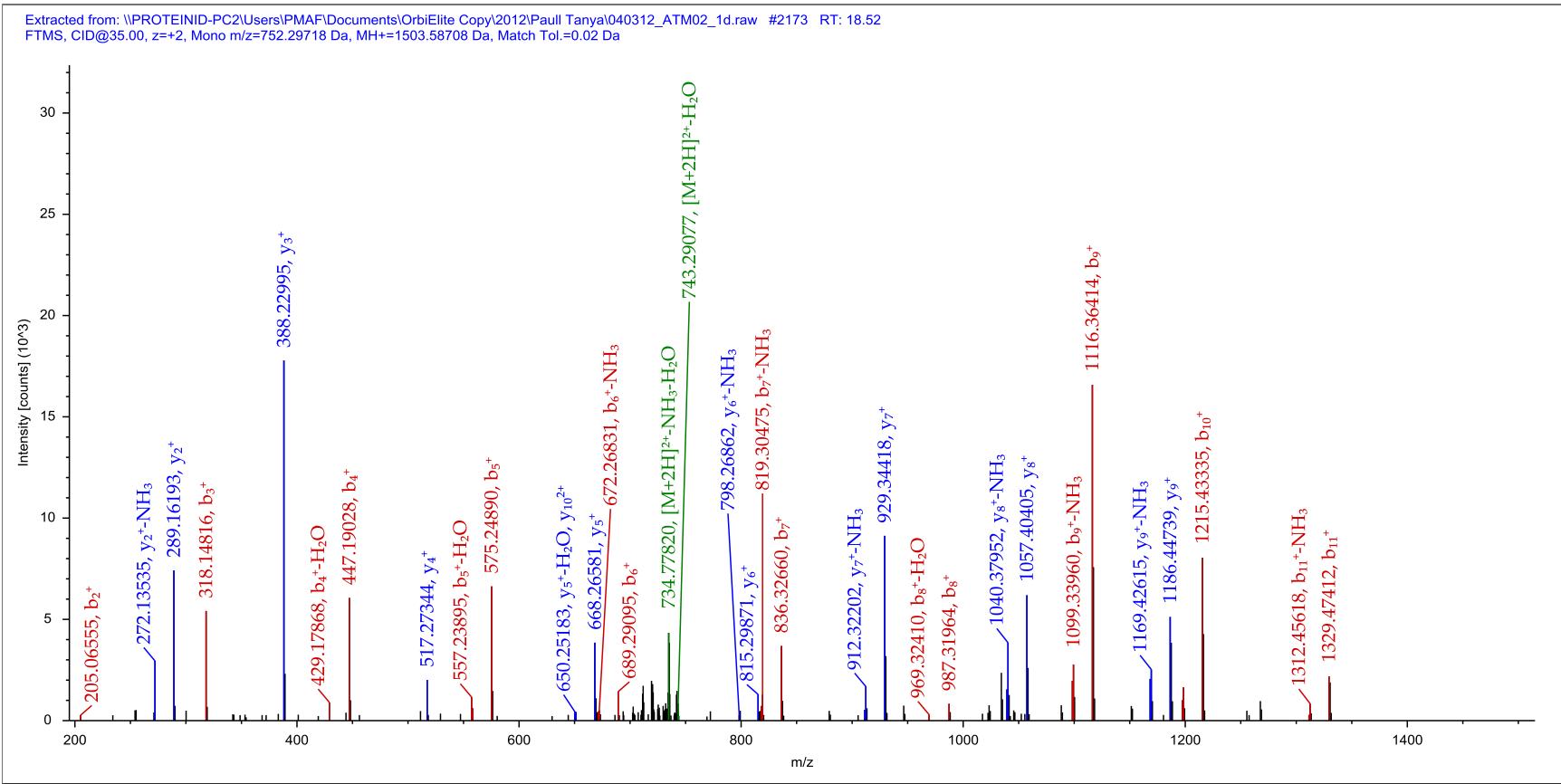
ATM MALVNCLK

C6 sulfonic acid M1 oxidation



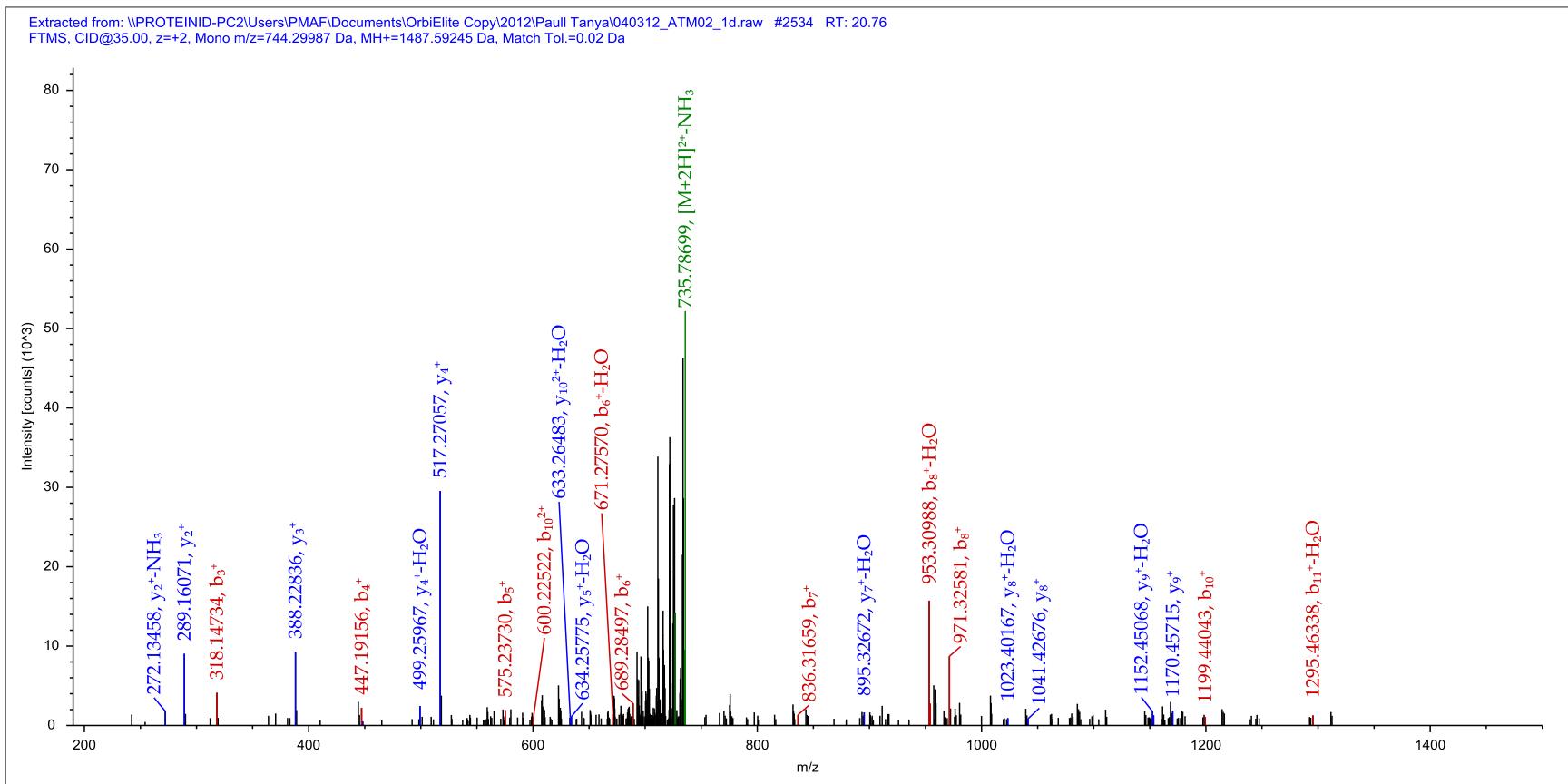
ATM MGIEQNMCEVNR

C8 sulfonic acid M1,M7 oxidation



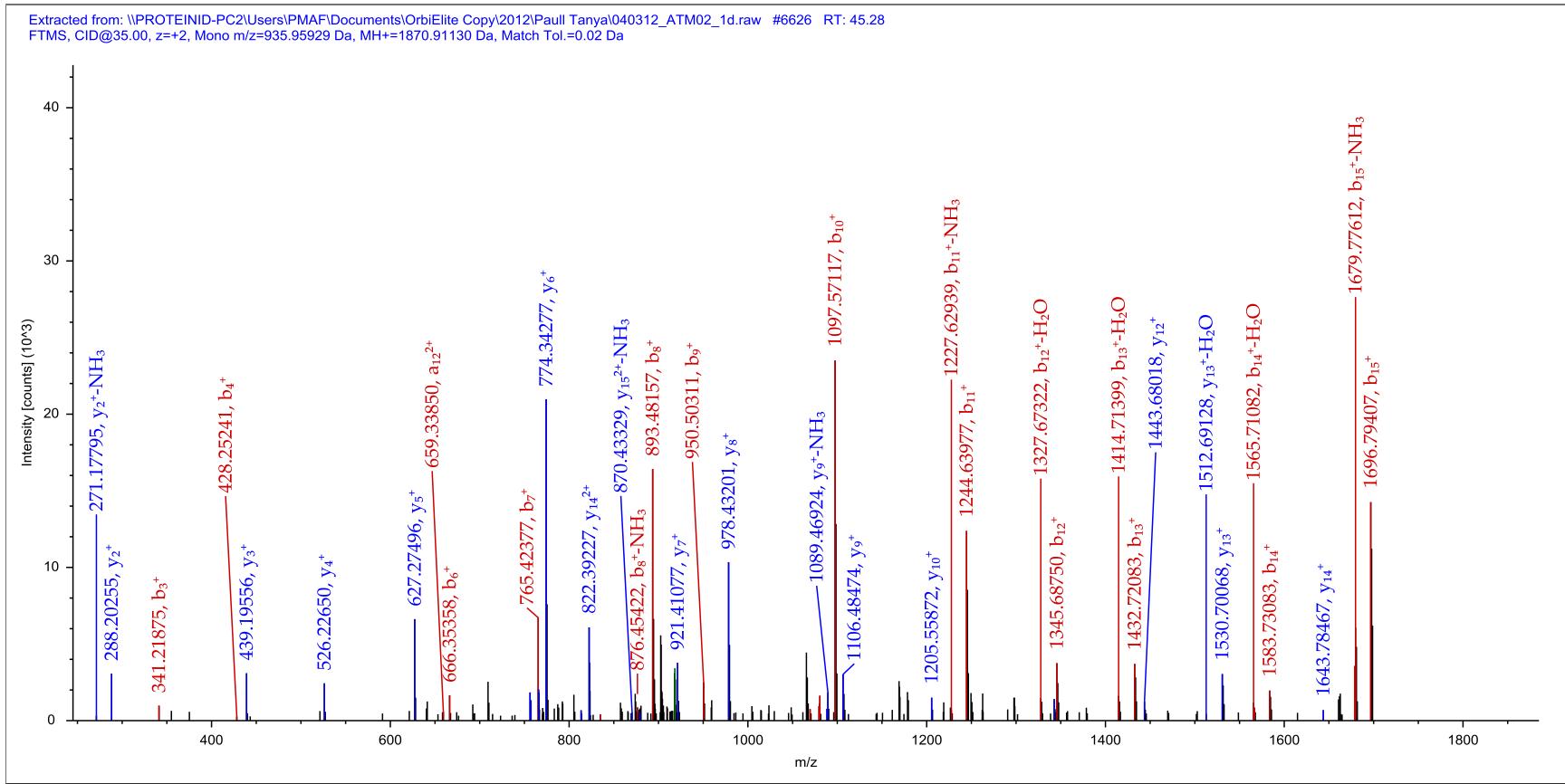
ATM MGIEQNMCEVNR

C8 sulfinic acid M1,M7 oxidation



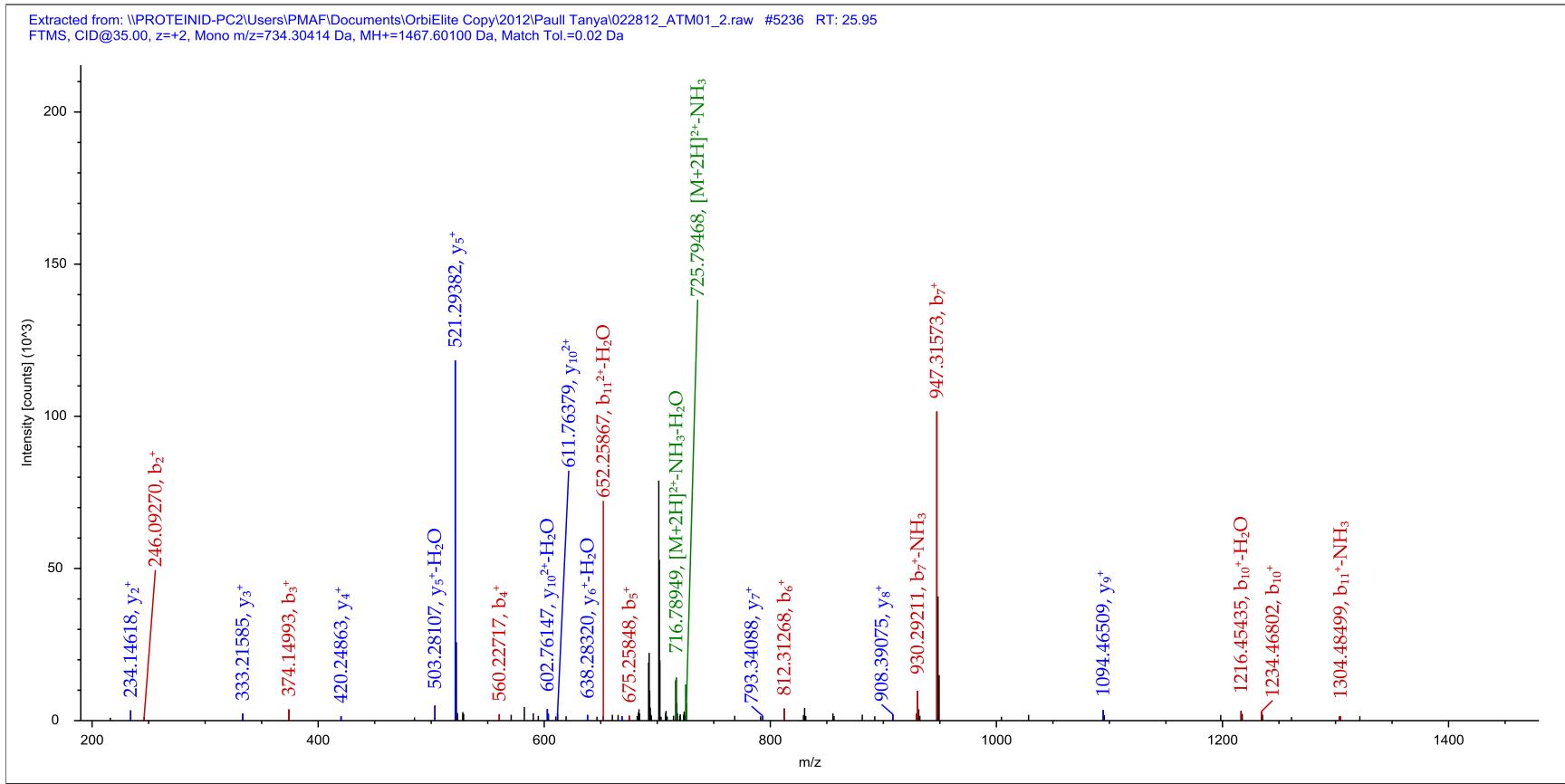
ATM NLLSTHVQGFFTSCLR

C14 sulfonic acid



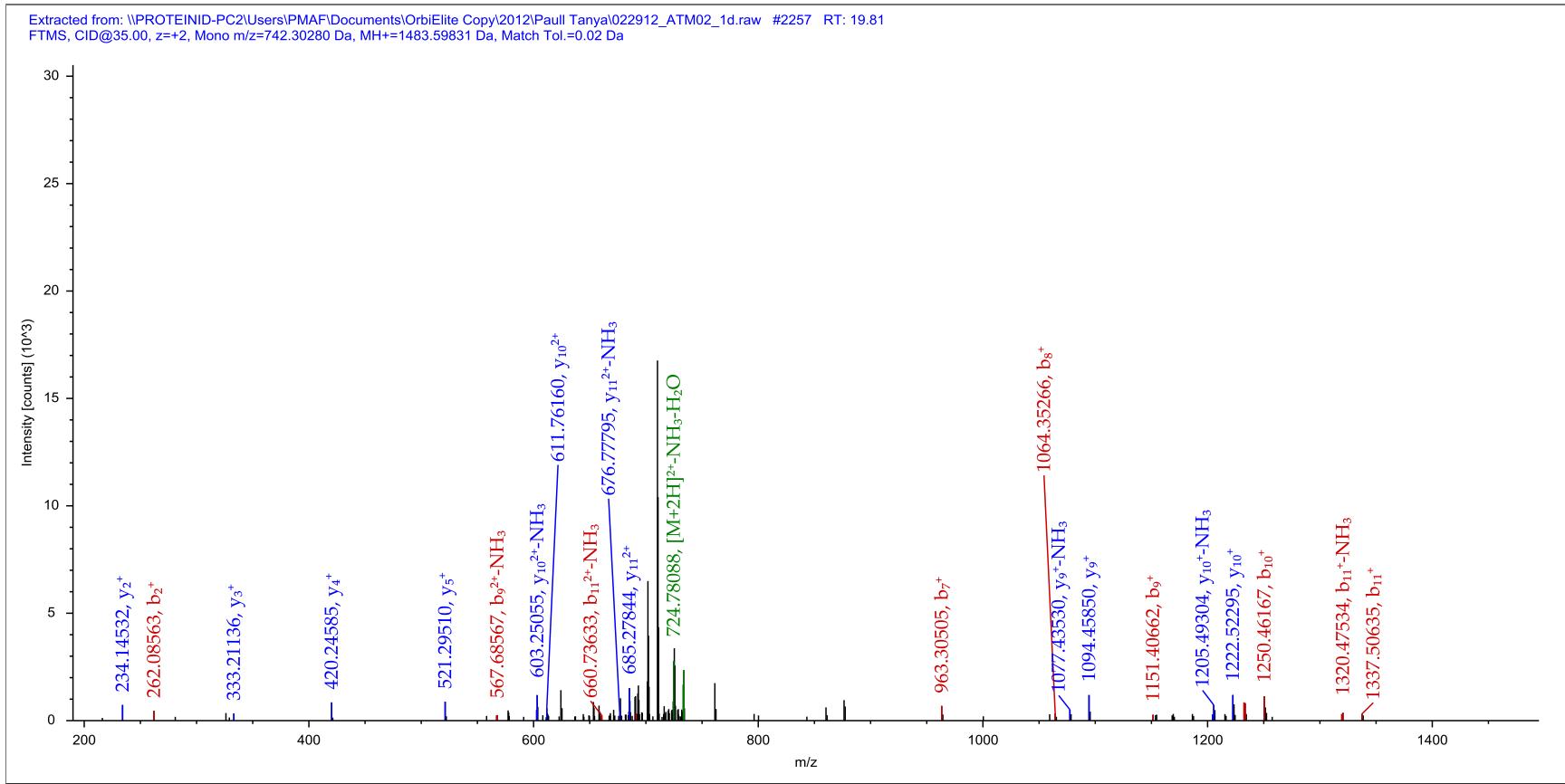
ATM NMQWDHCTSVSK

C7 sulfinic acid



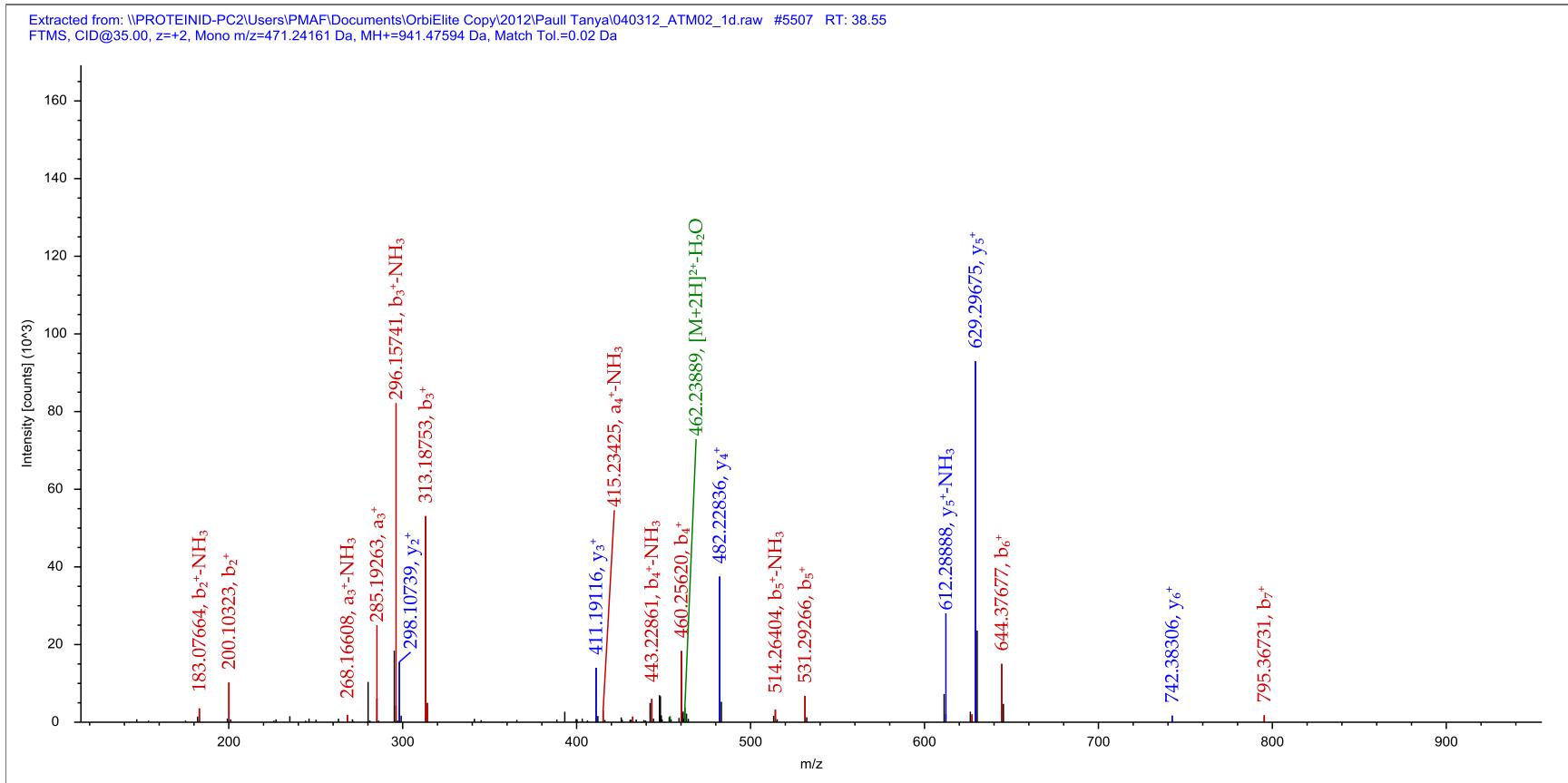
ATM NMQWDHCTSVSK

C7 sulfinic acid M2 oxidation



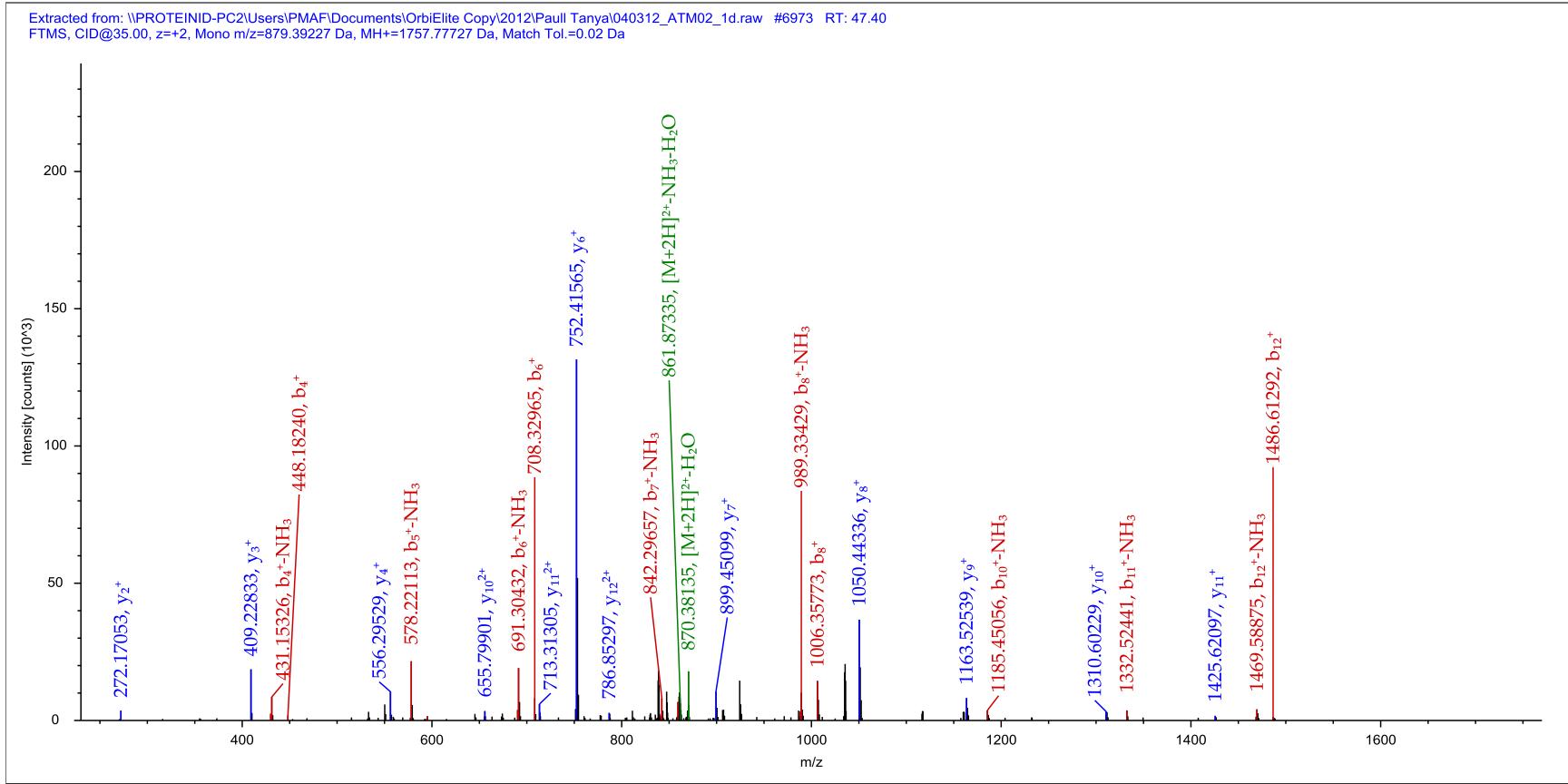
ATM QALFALLCK

C7 sulfonic acid



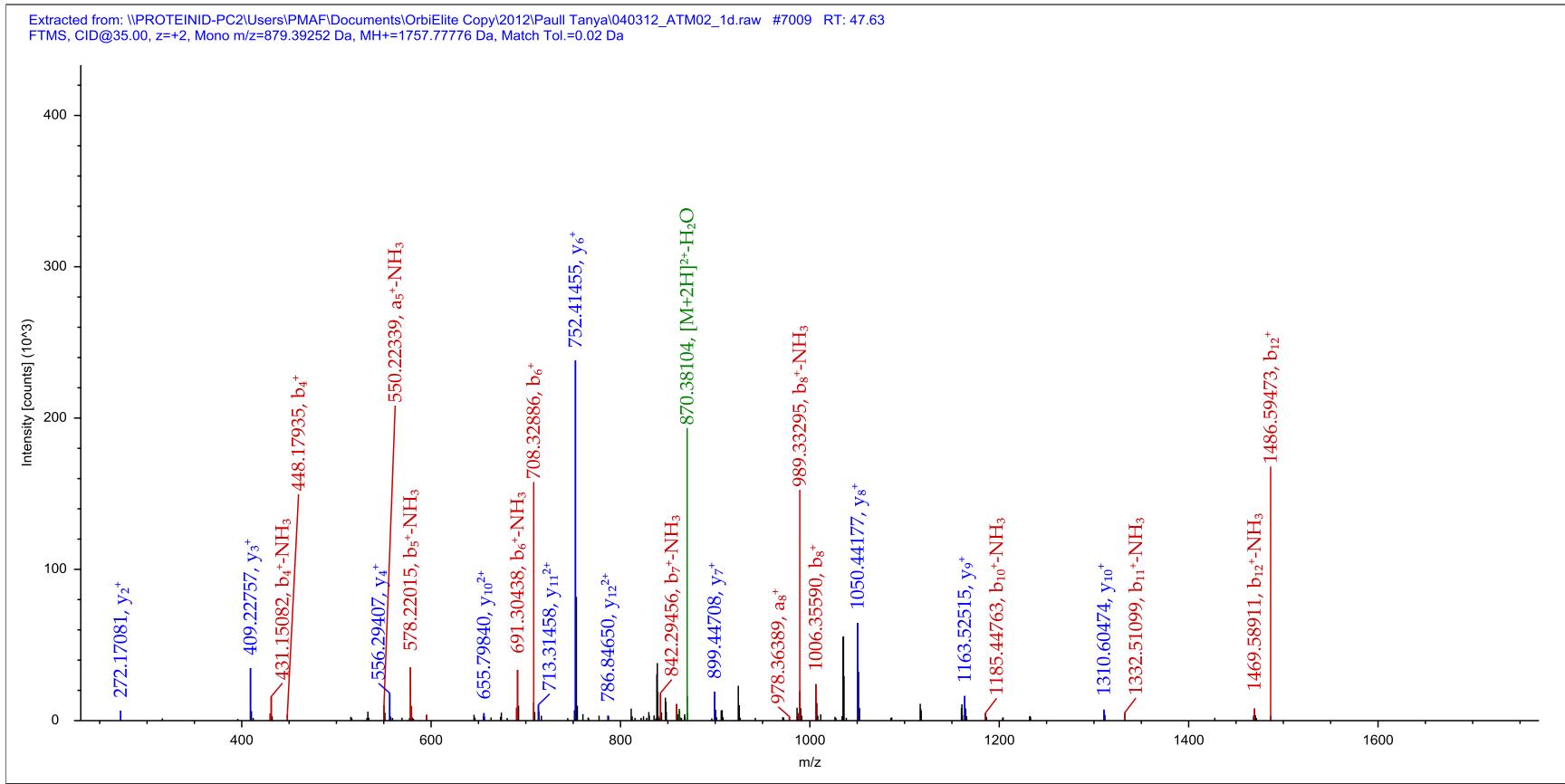
PRMT5 QGFDFLCMPVFHPR

C7 sulfonic acid M8 oxidation



PRMT5 QGFDFLCMPVFHPR

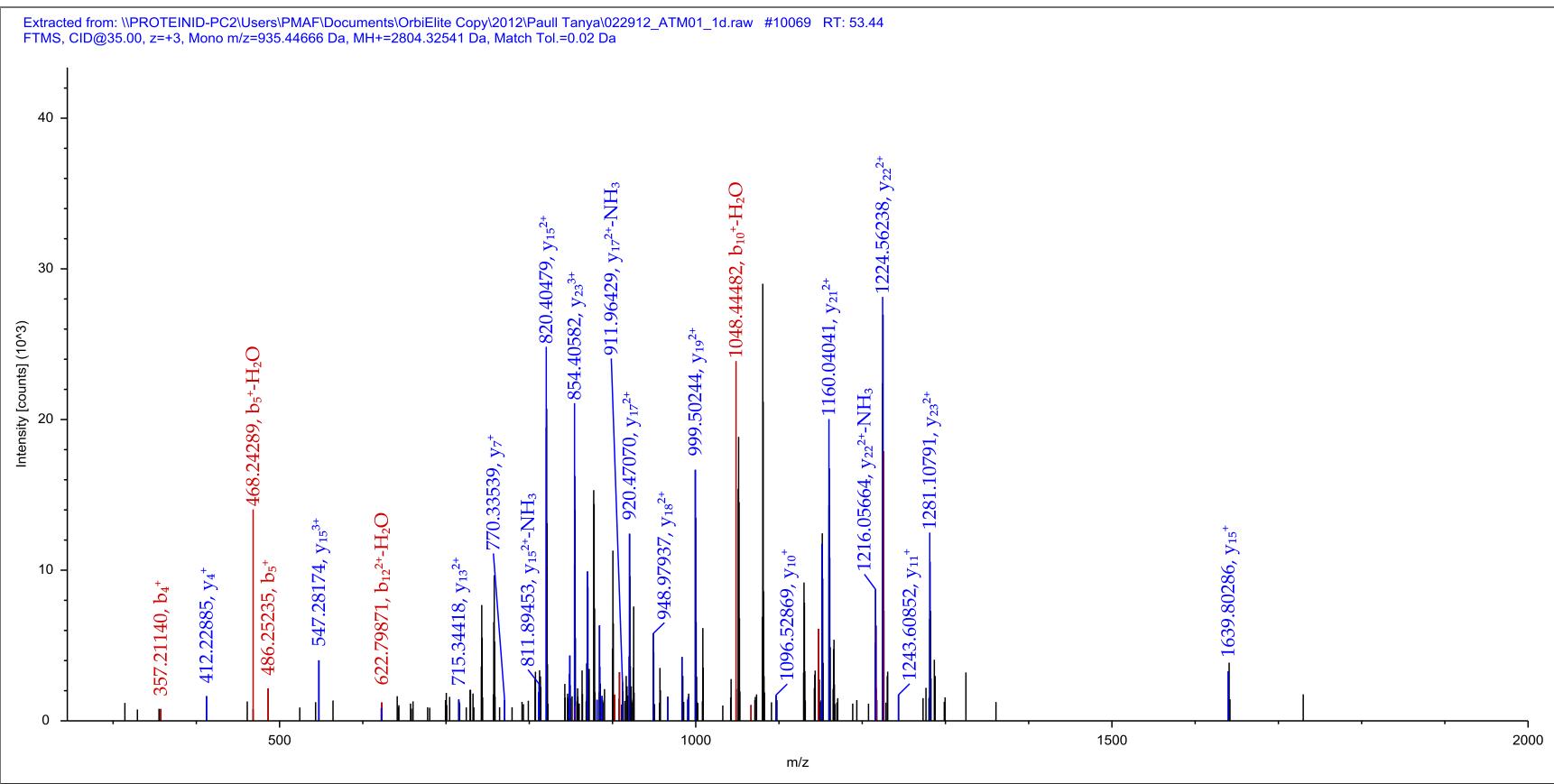
C7 sulfonic acid M8 oxidation



ATM

SGVLEWCTGTVPIGEFLVNNEDGAHK

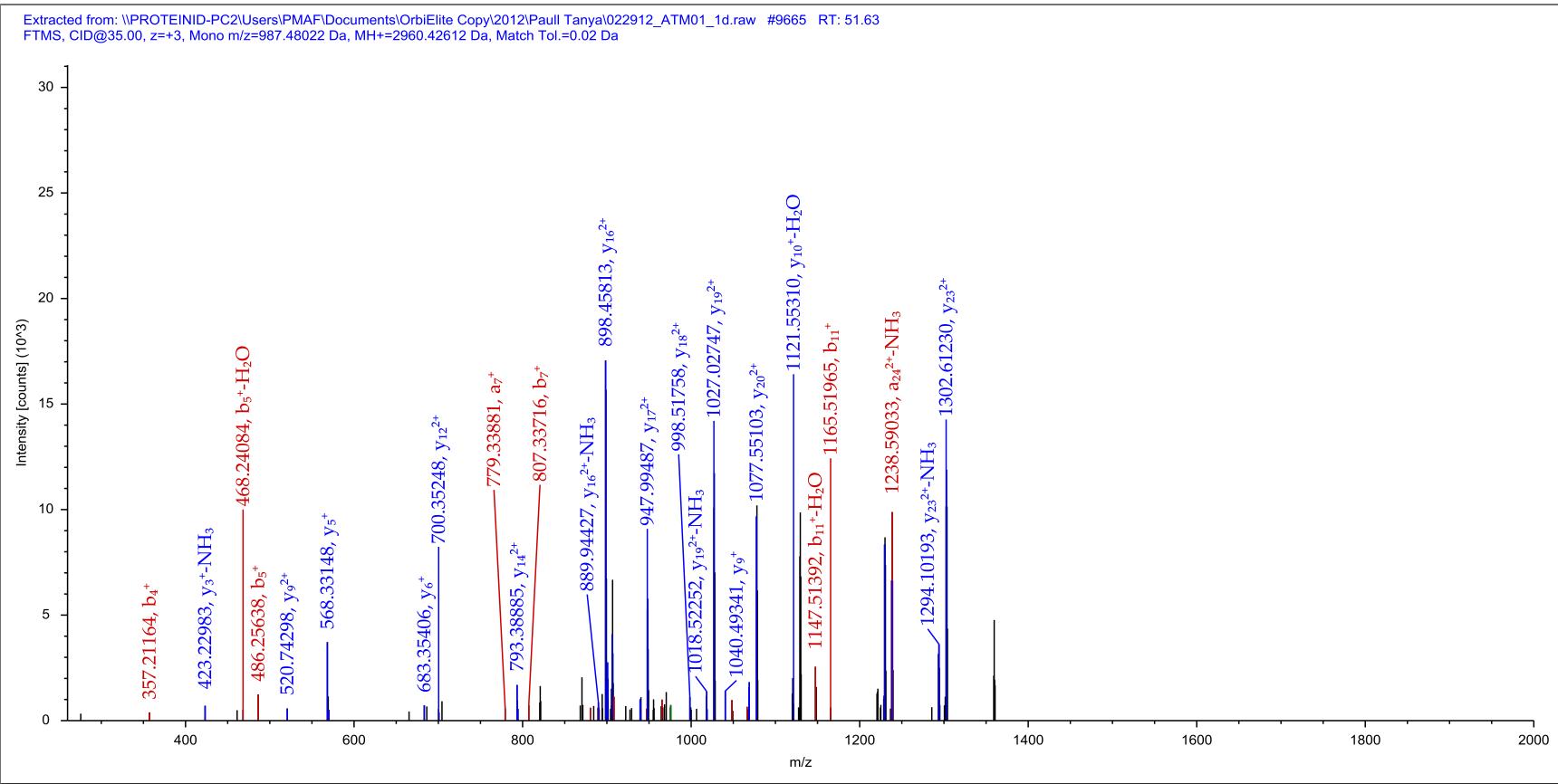
C7 sulfinic acid



ATM

SGVLEWCTGTVPIGEFLVNNEDGAHKR

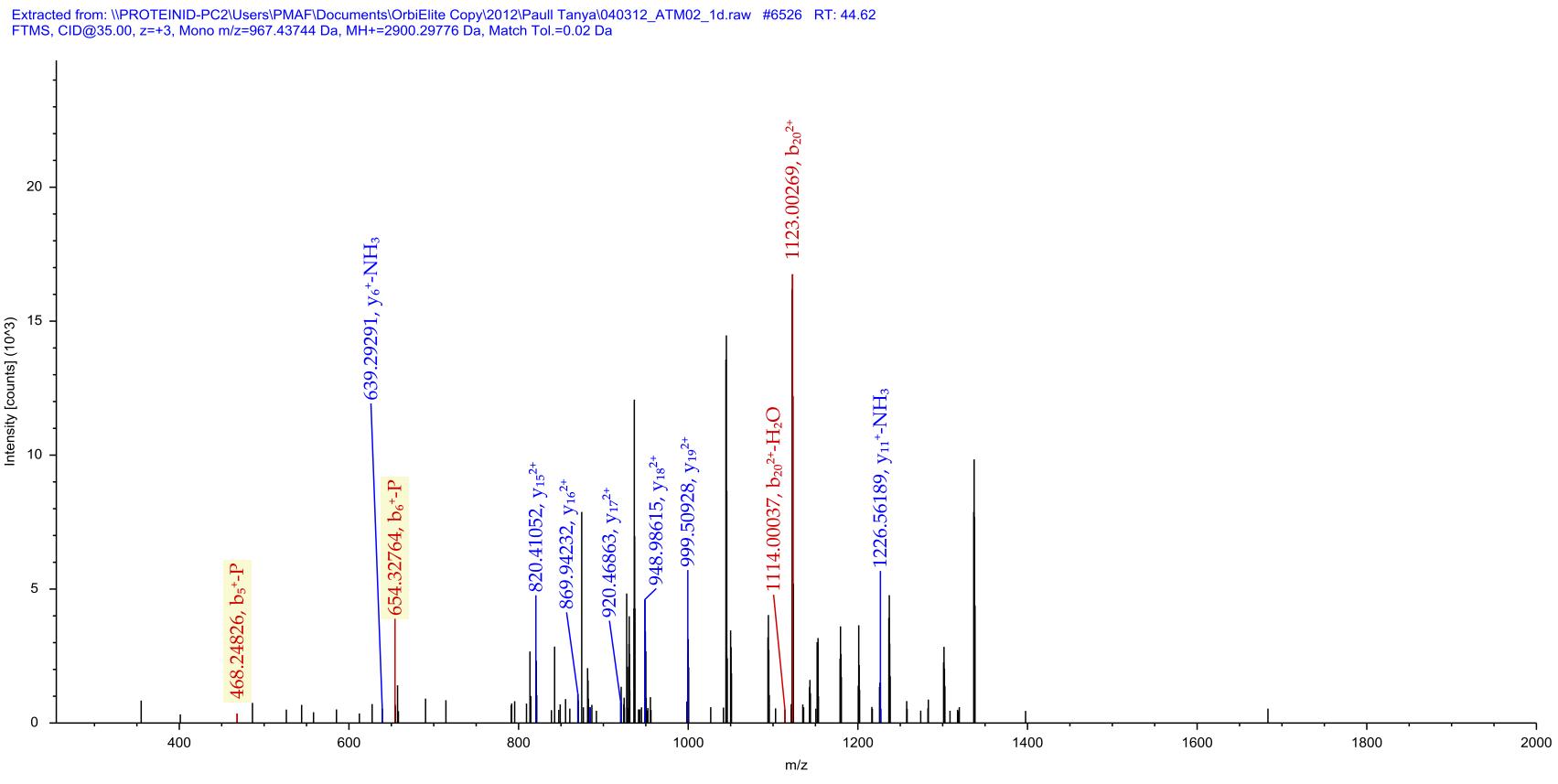
C7 sulfonic acid



ATM

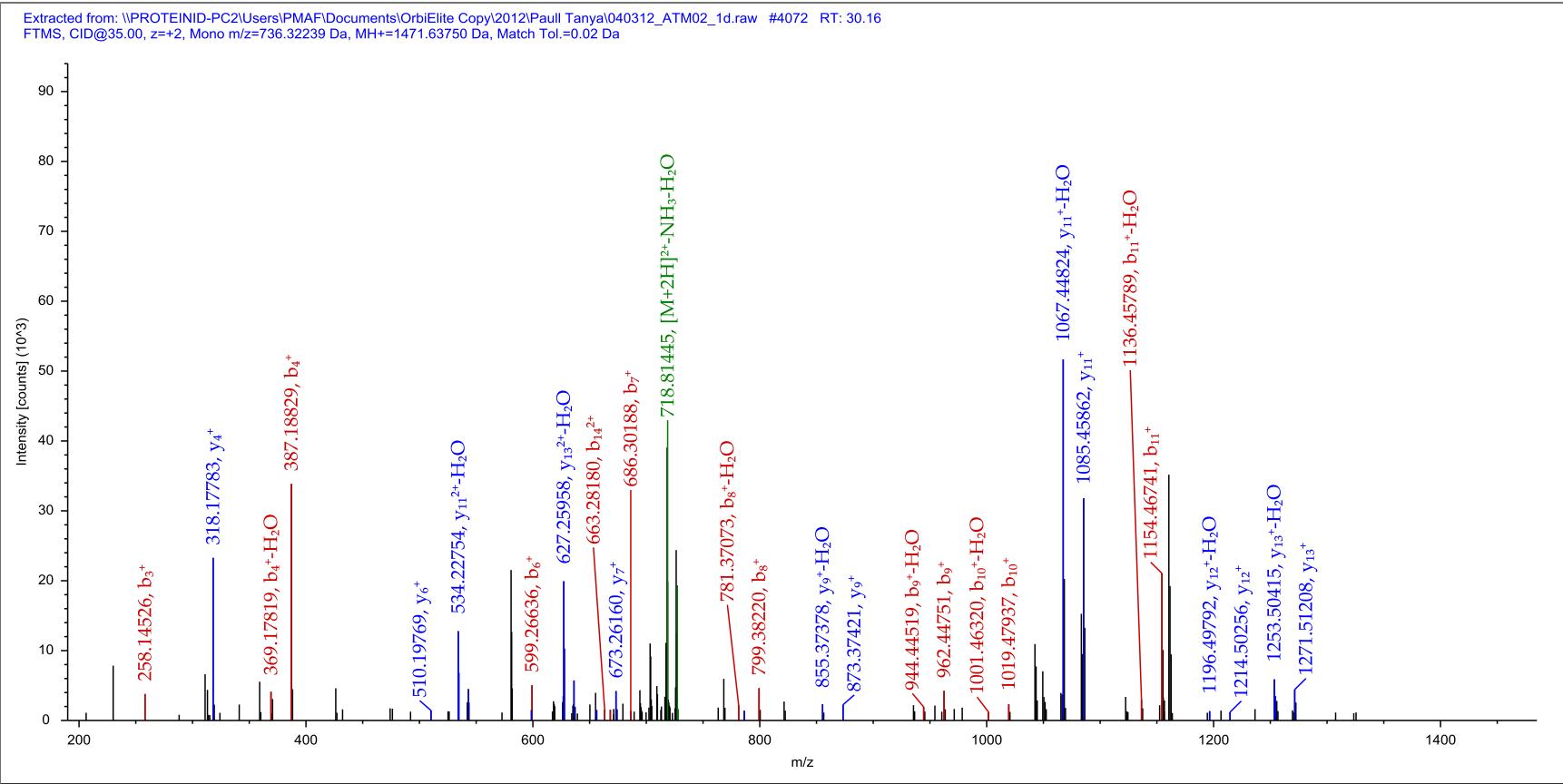
SGVLEWCTGTVPIGEFLVNNEDGAHKR

C7 sulfonic acid S1 phosphorylation



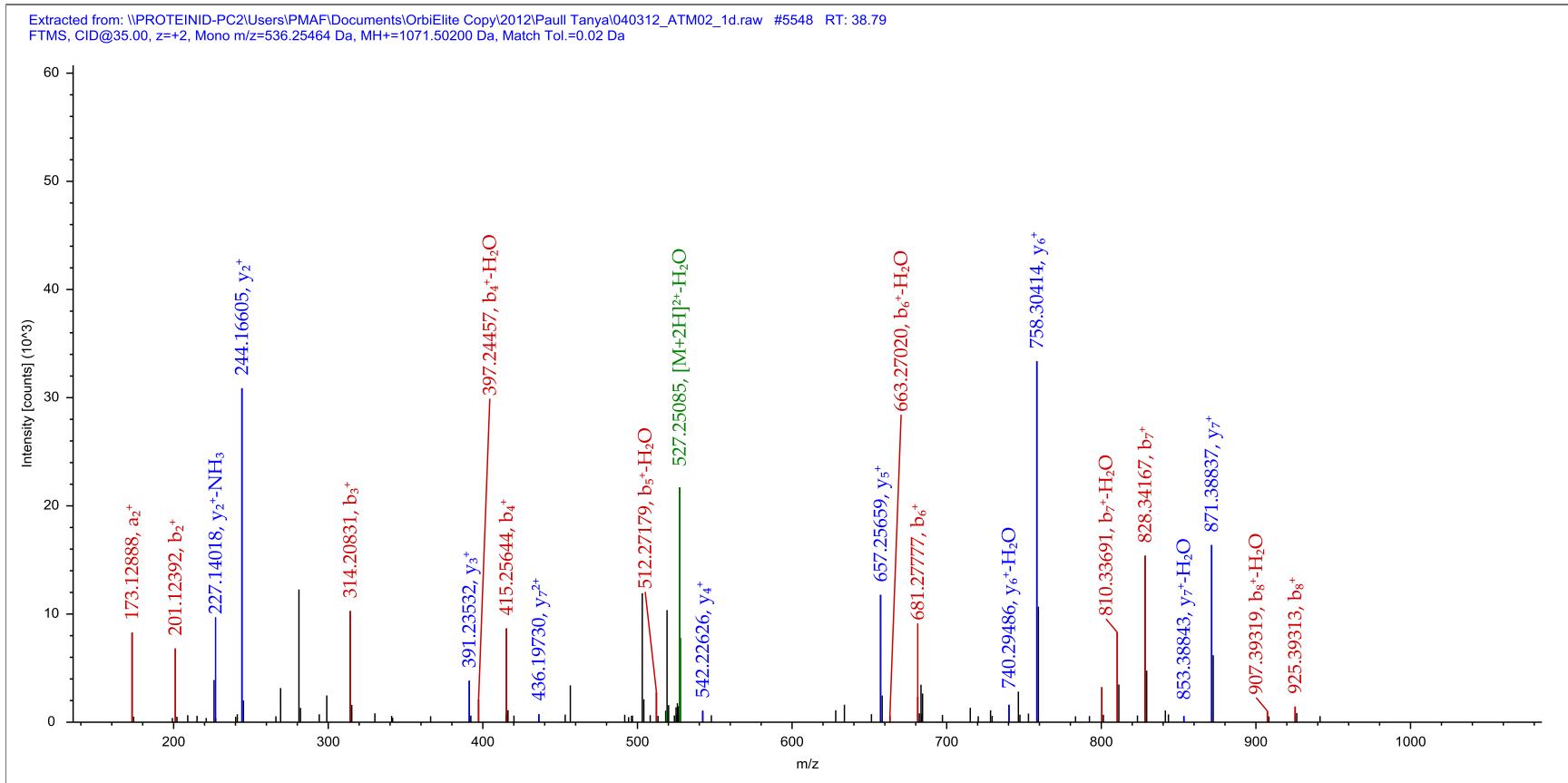
ATM SIGEPDSL~~Y~~GCGGGK

C11 sulfinic acid



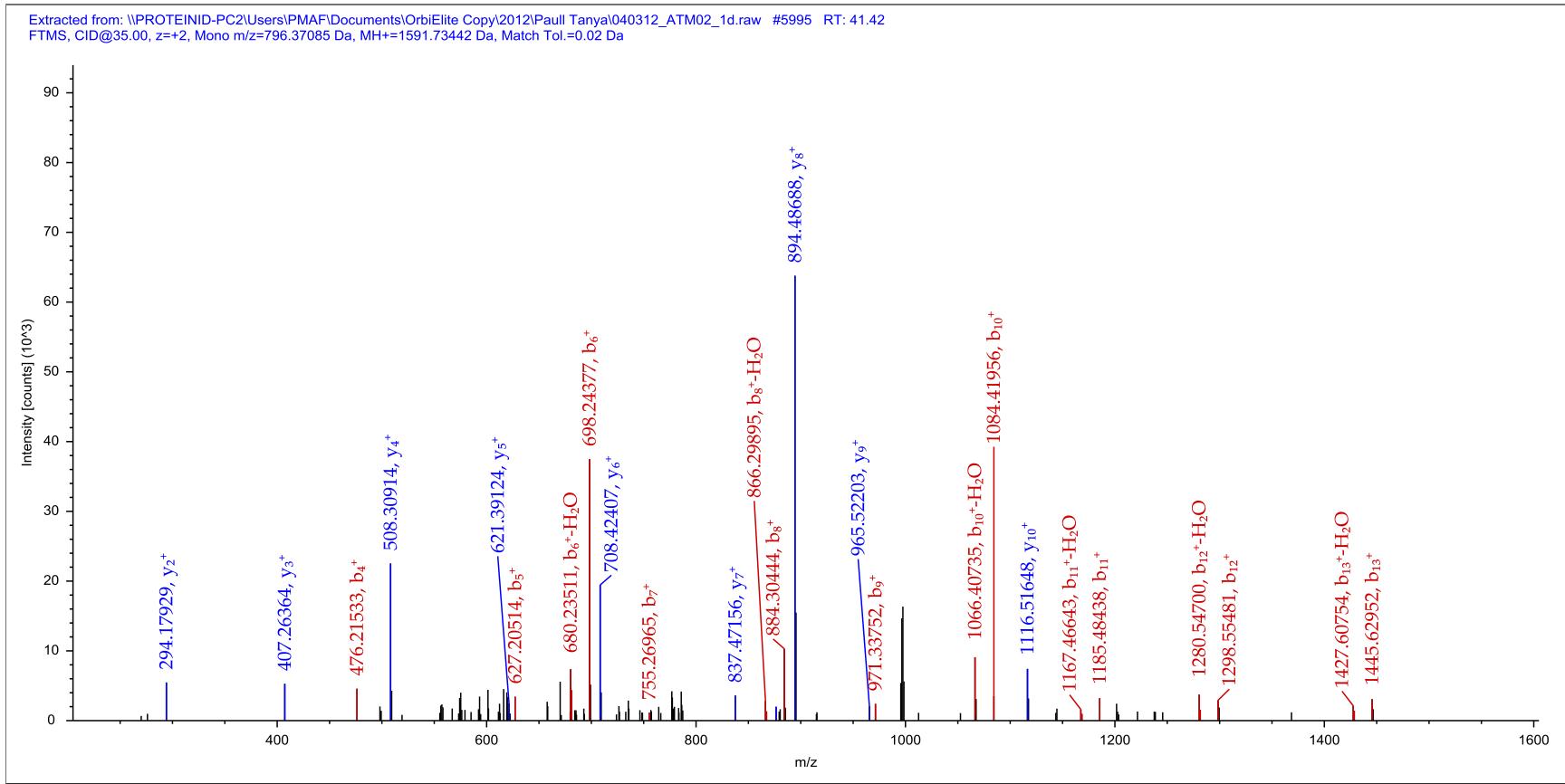
ATM SLLTDCCFPK

C6 sulfonic acid



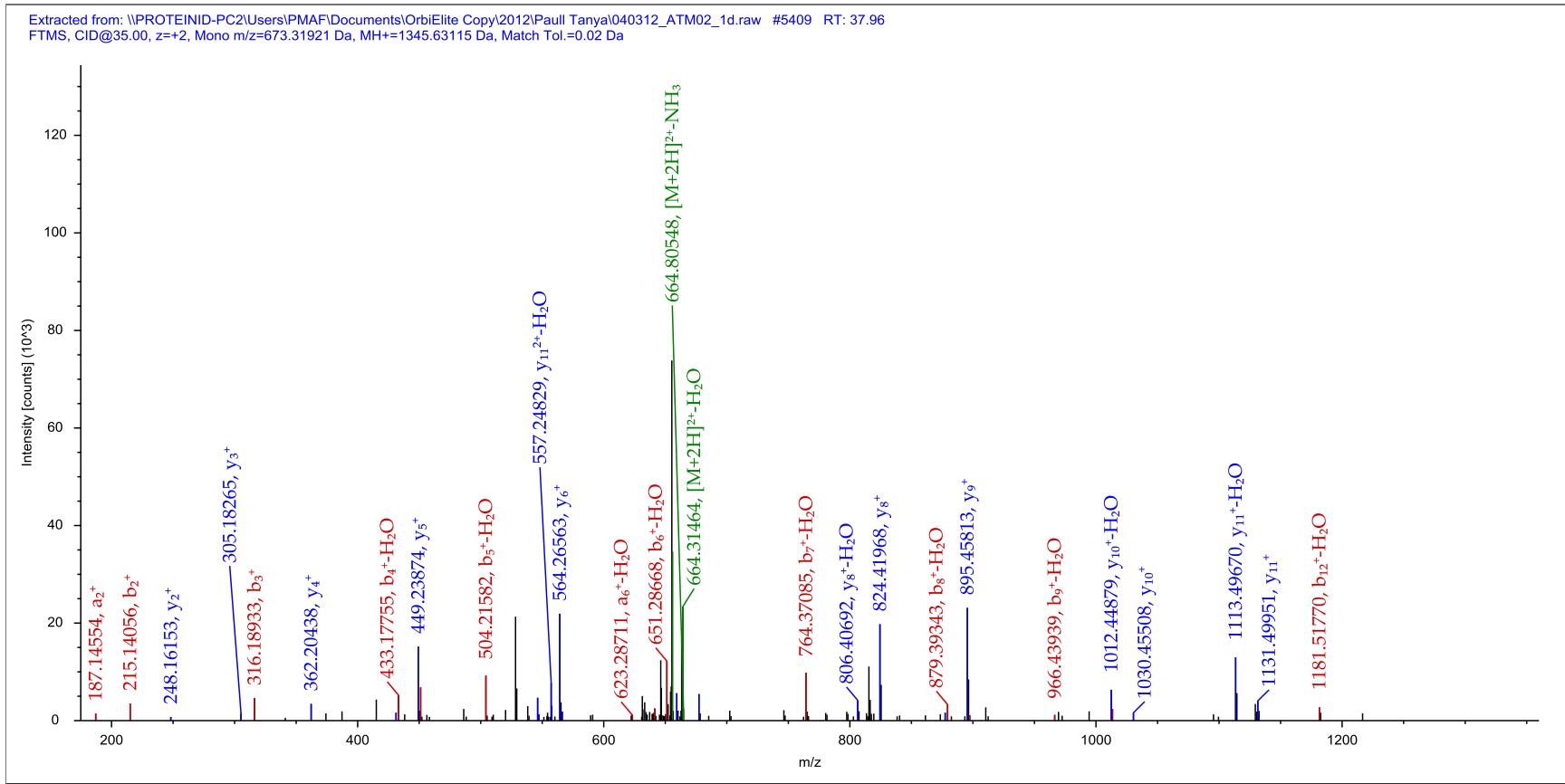
ATM SLMQCGAGESITLFK

C5 sulfonic acid M3 oxidation



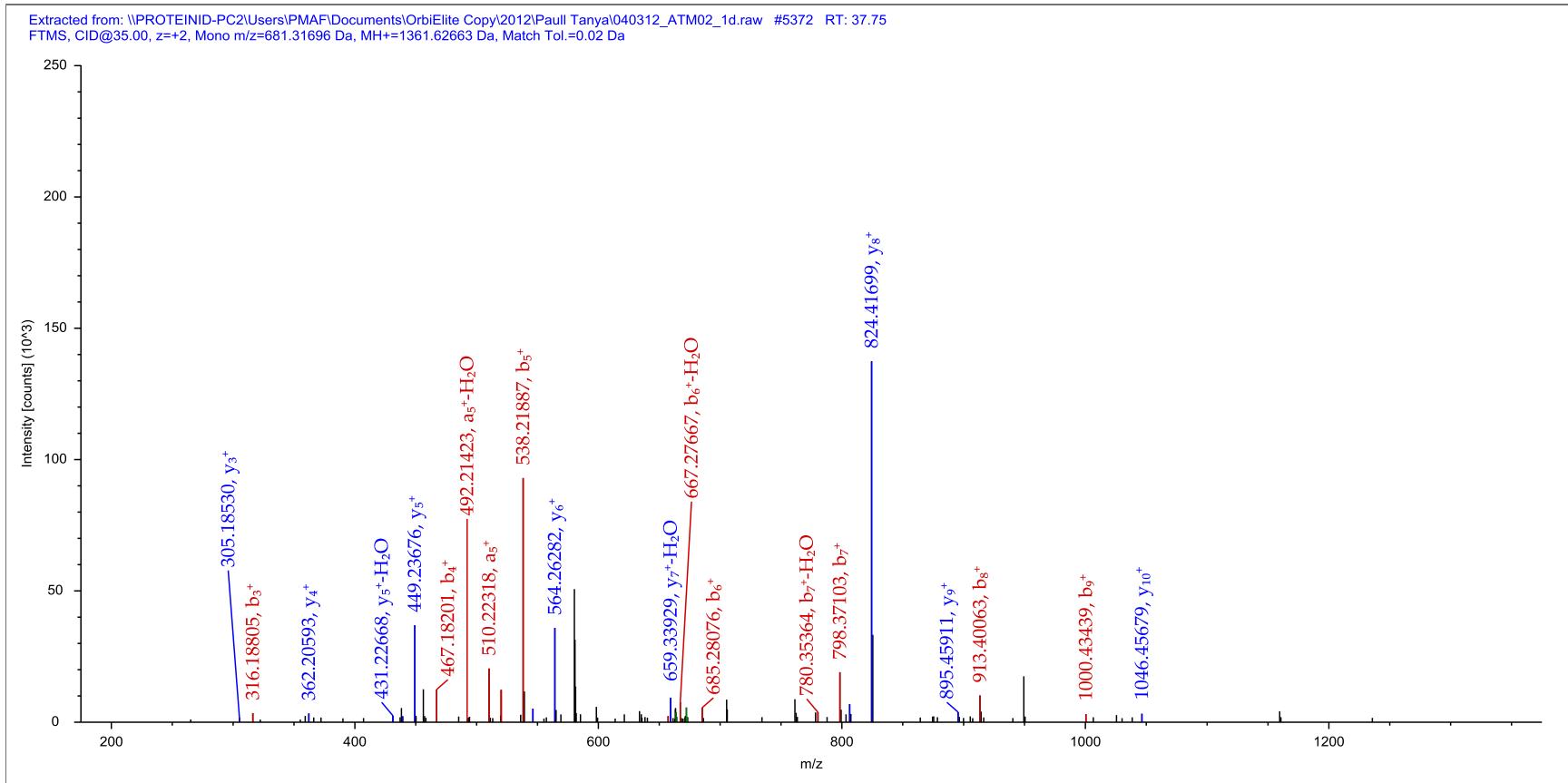
ATM TLTCAFLDSGGTK

C4 sulfinic acid



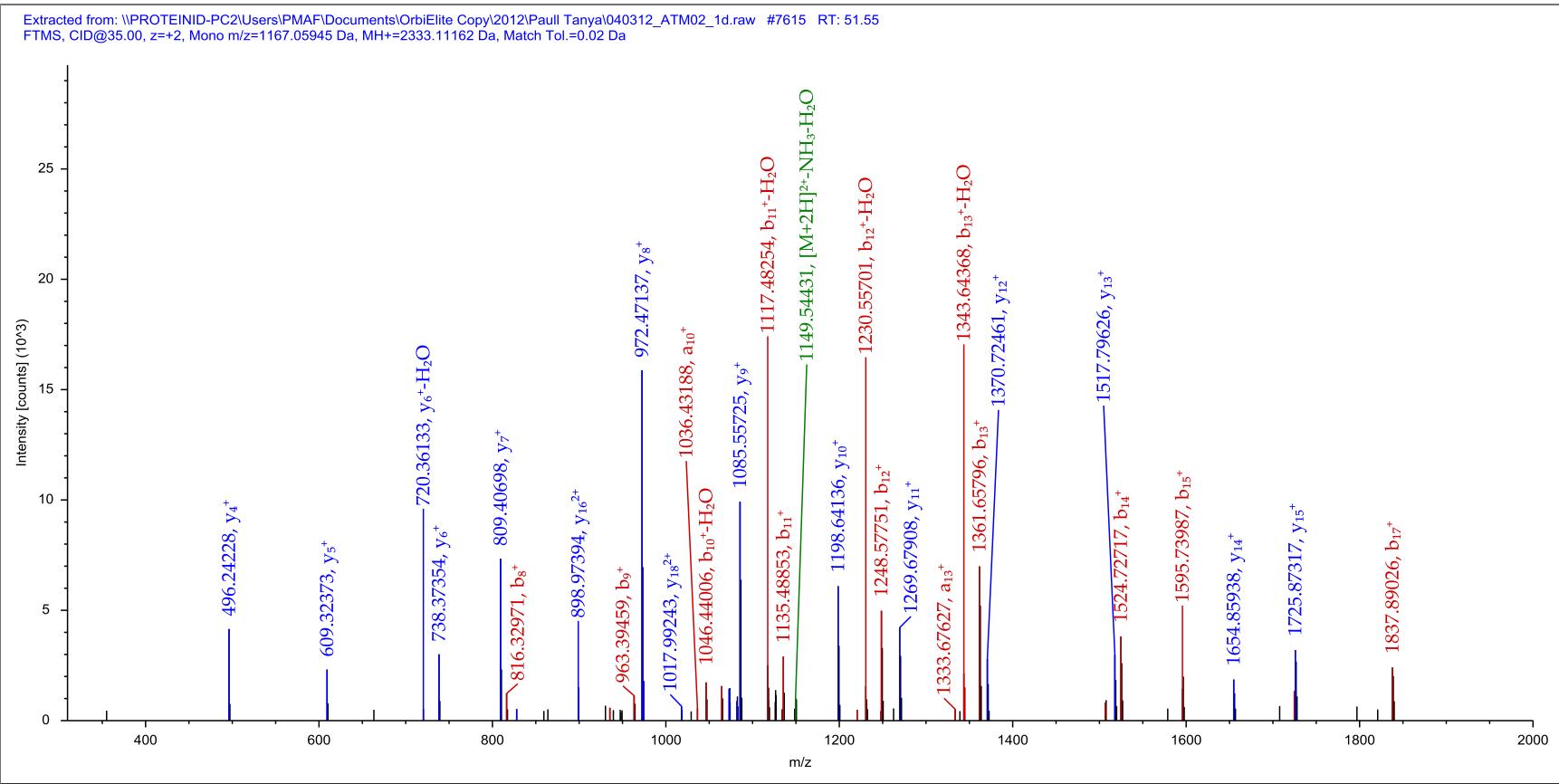
ATM TLTCAFLDSGGTK

C4 sulfonic acid



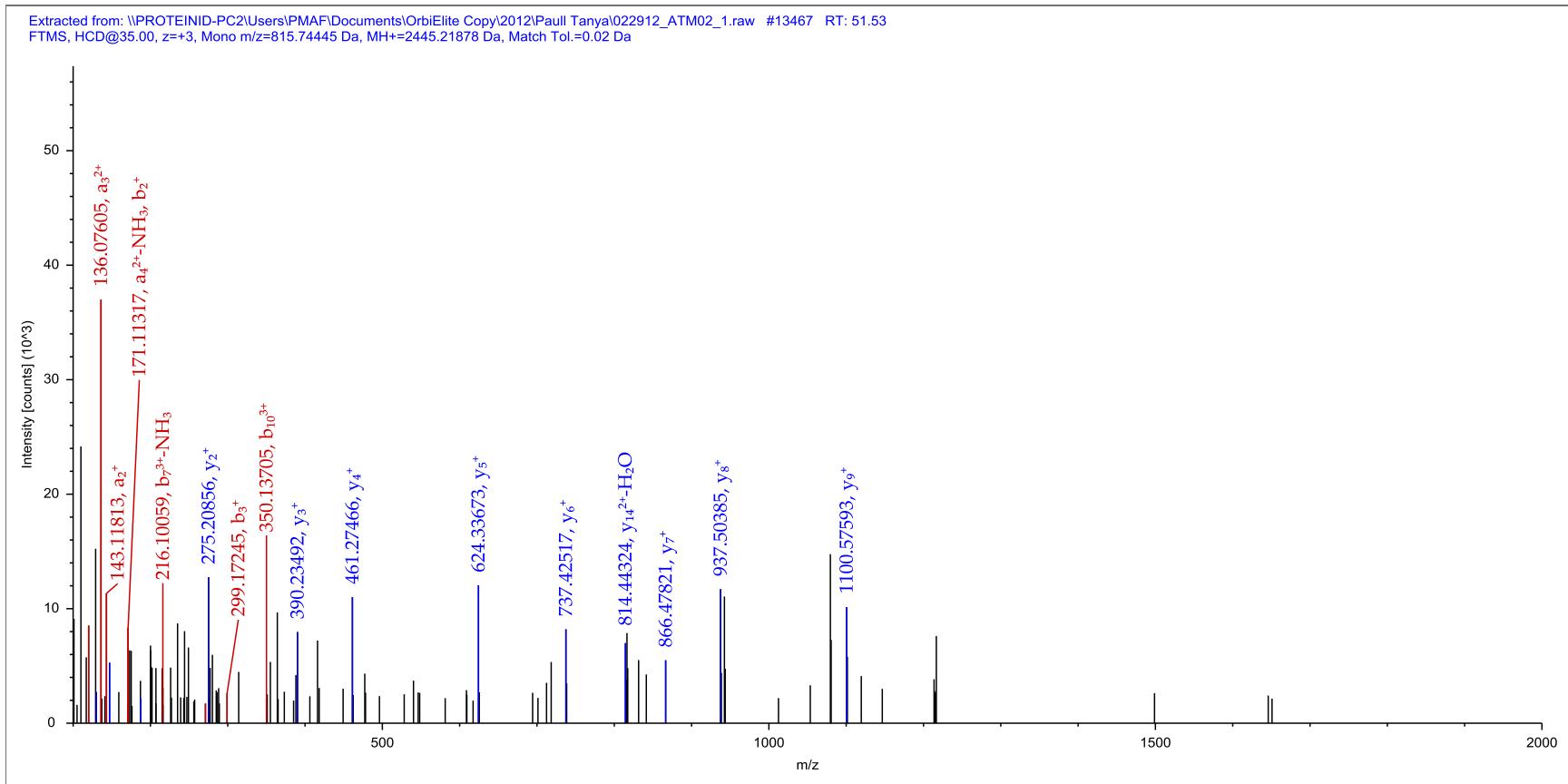
ATM VAQSCAHFTALLYAEIYADK

C5 sulfonic acid



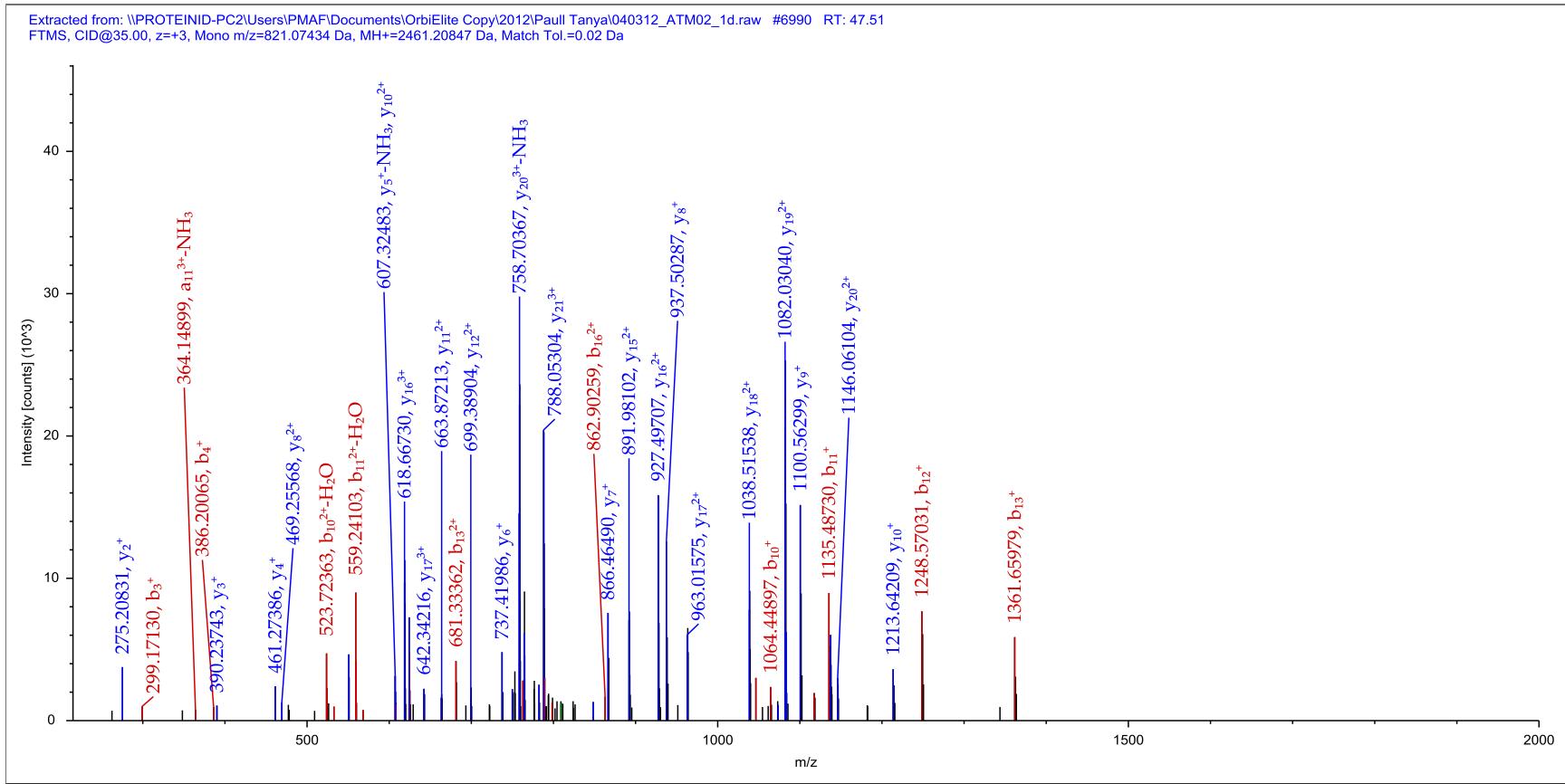
ATM VAQSCAAHFTALLYAEIYADKK

C5 sulfinic acid



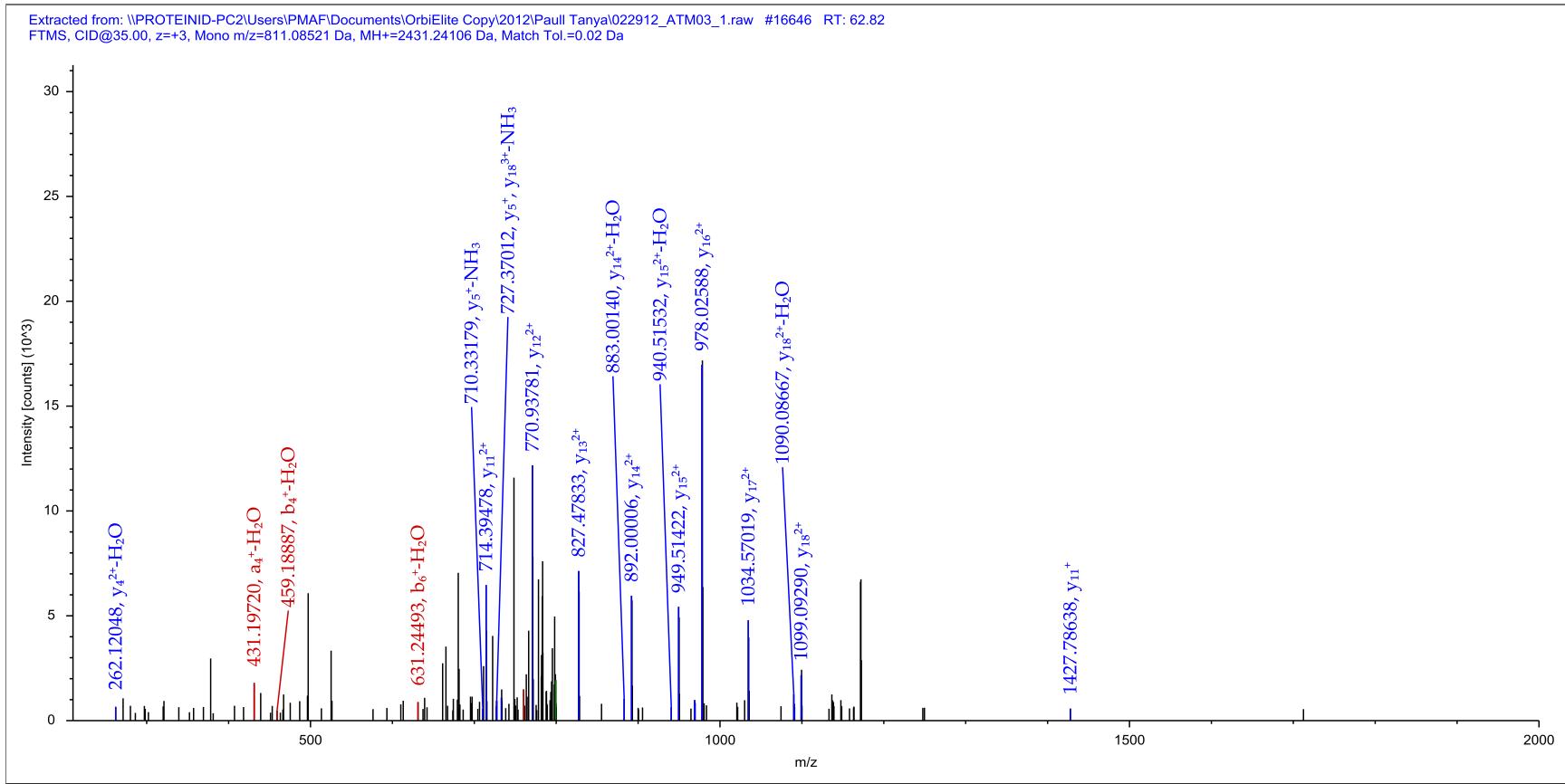
ATM VAQSCAAHFTALLYAEIYADKK

C5 sulfonic acid

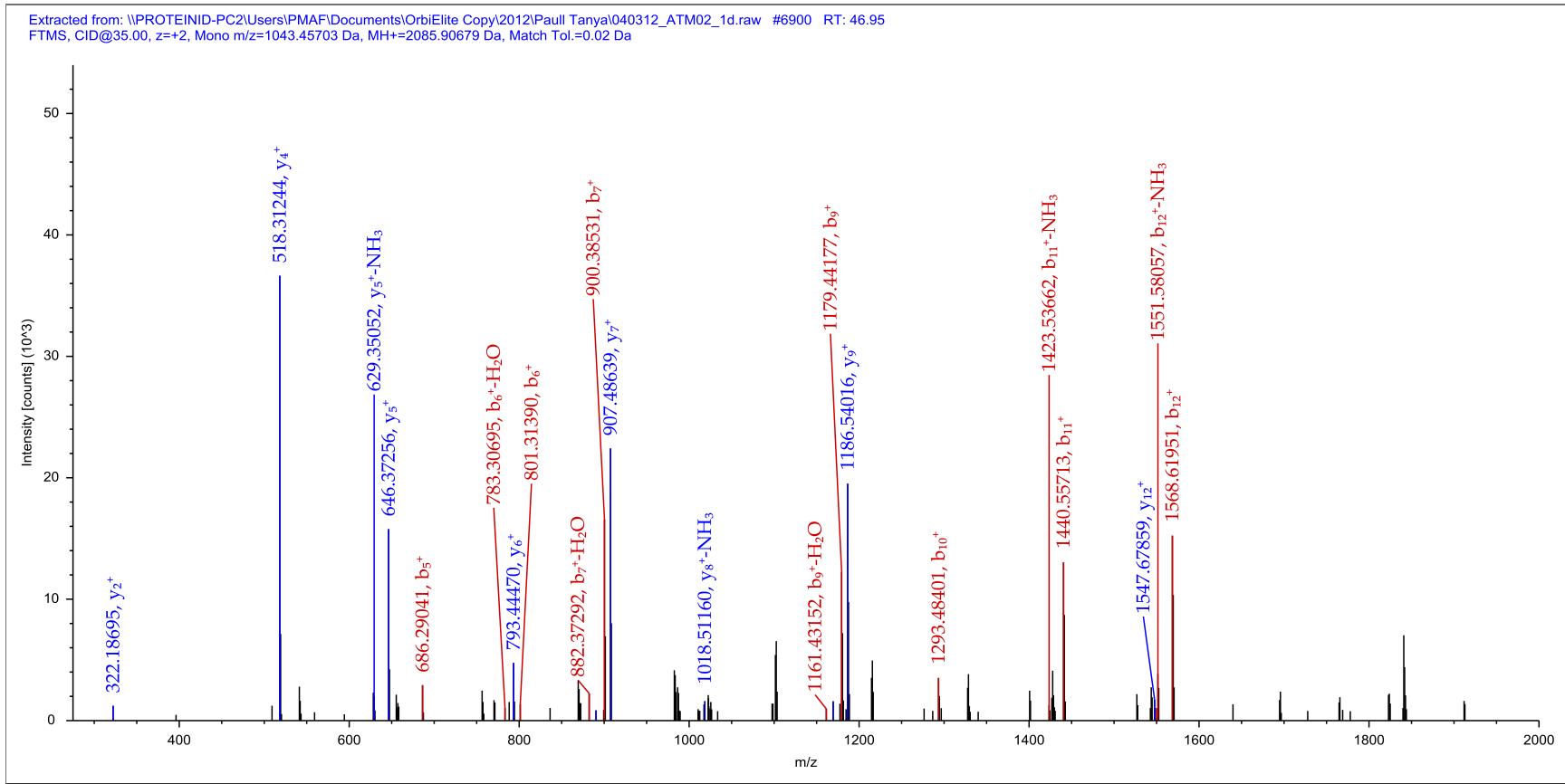


ATM VCELGDEILPTLLYIWTQHR

C2 sulfinic acid

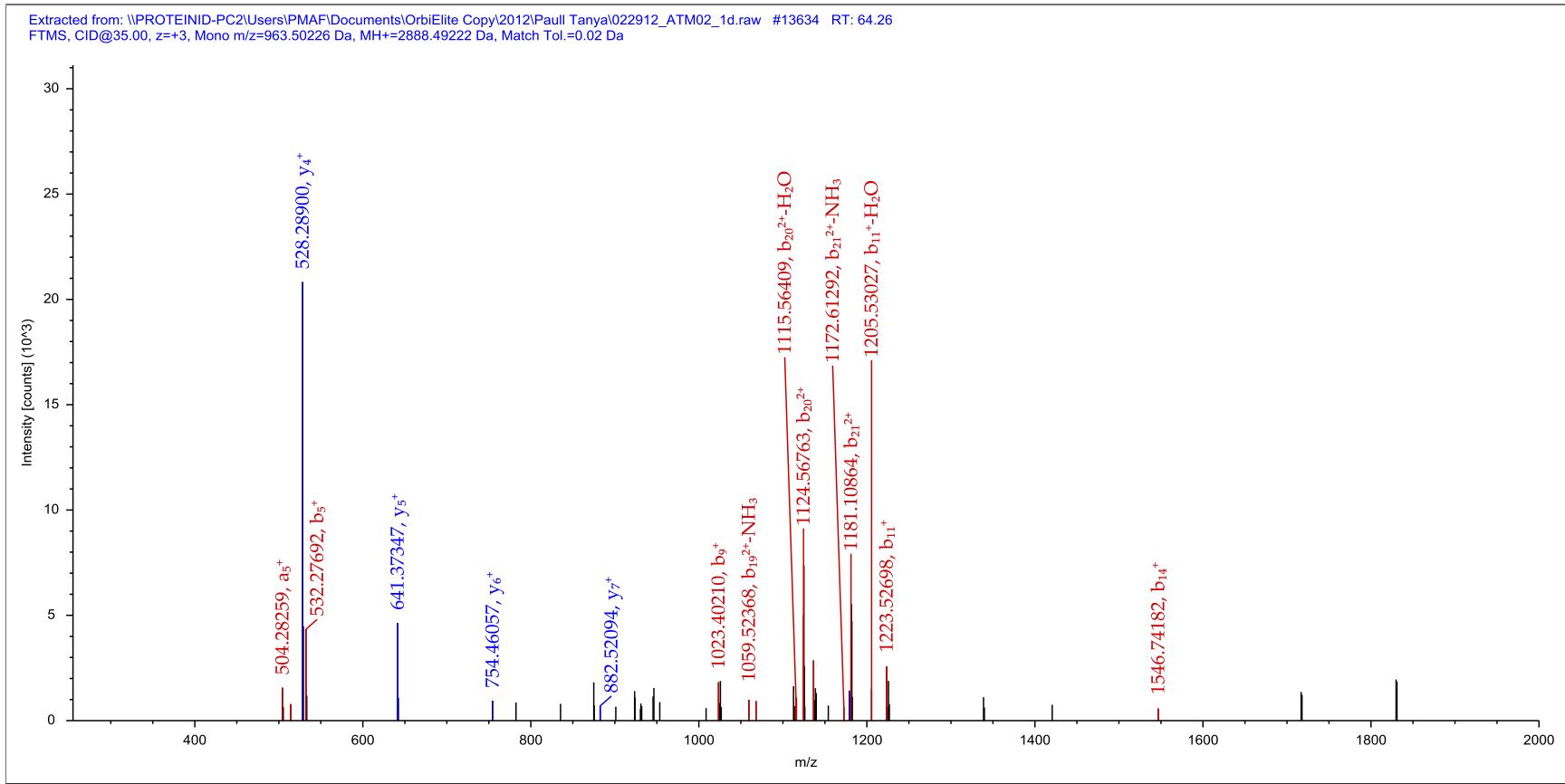


ATM YEVFMDVCQNFQPVFR C8 sulfonic acid M5 oxidation



ATM YPASLPNCELSPLLMILSQLLPQQR

C8 sulfonic acid M15 oxidation



ATM YRPNDFSAFQCQK

C11 sulfonic acid

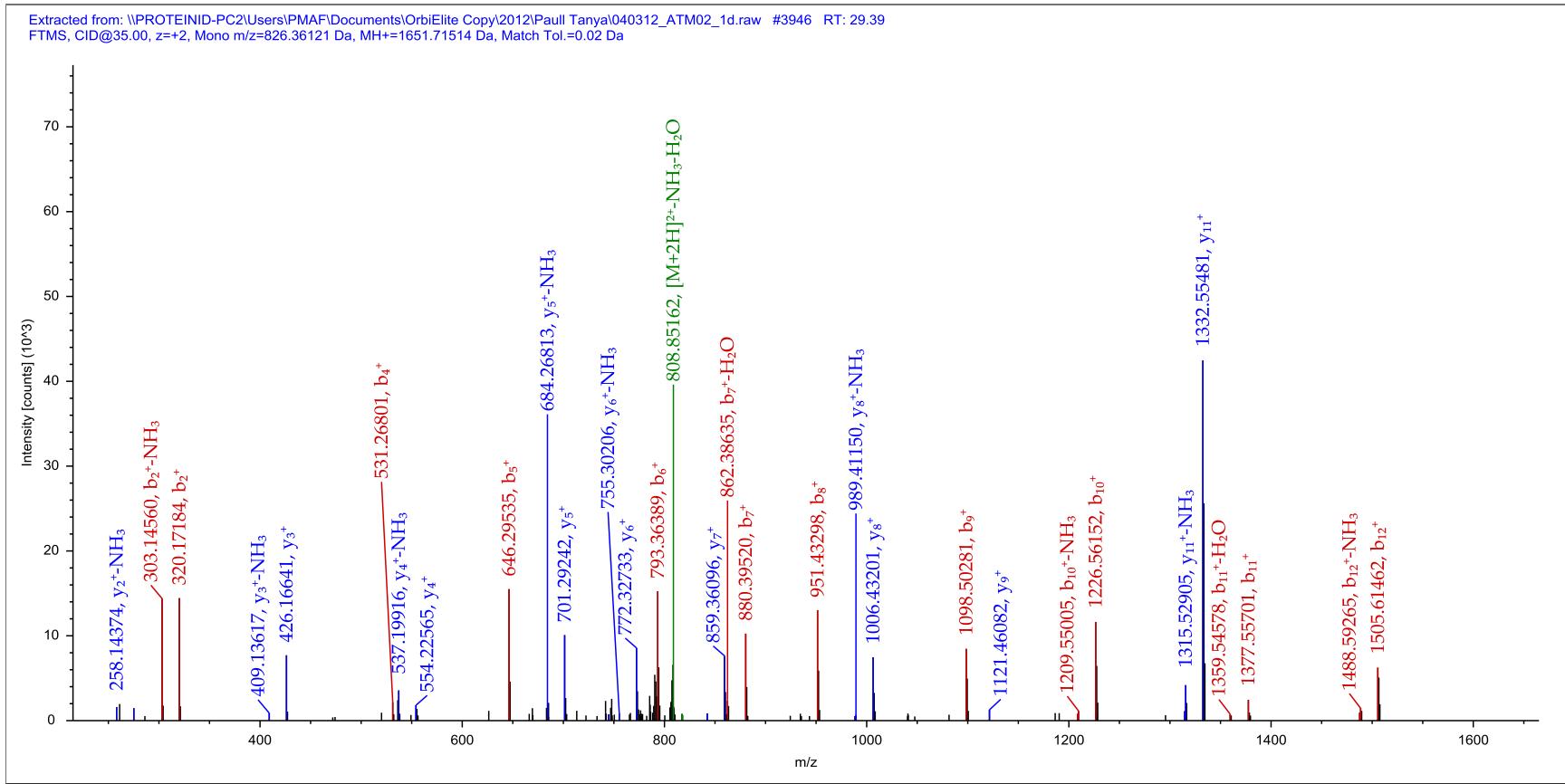
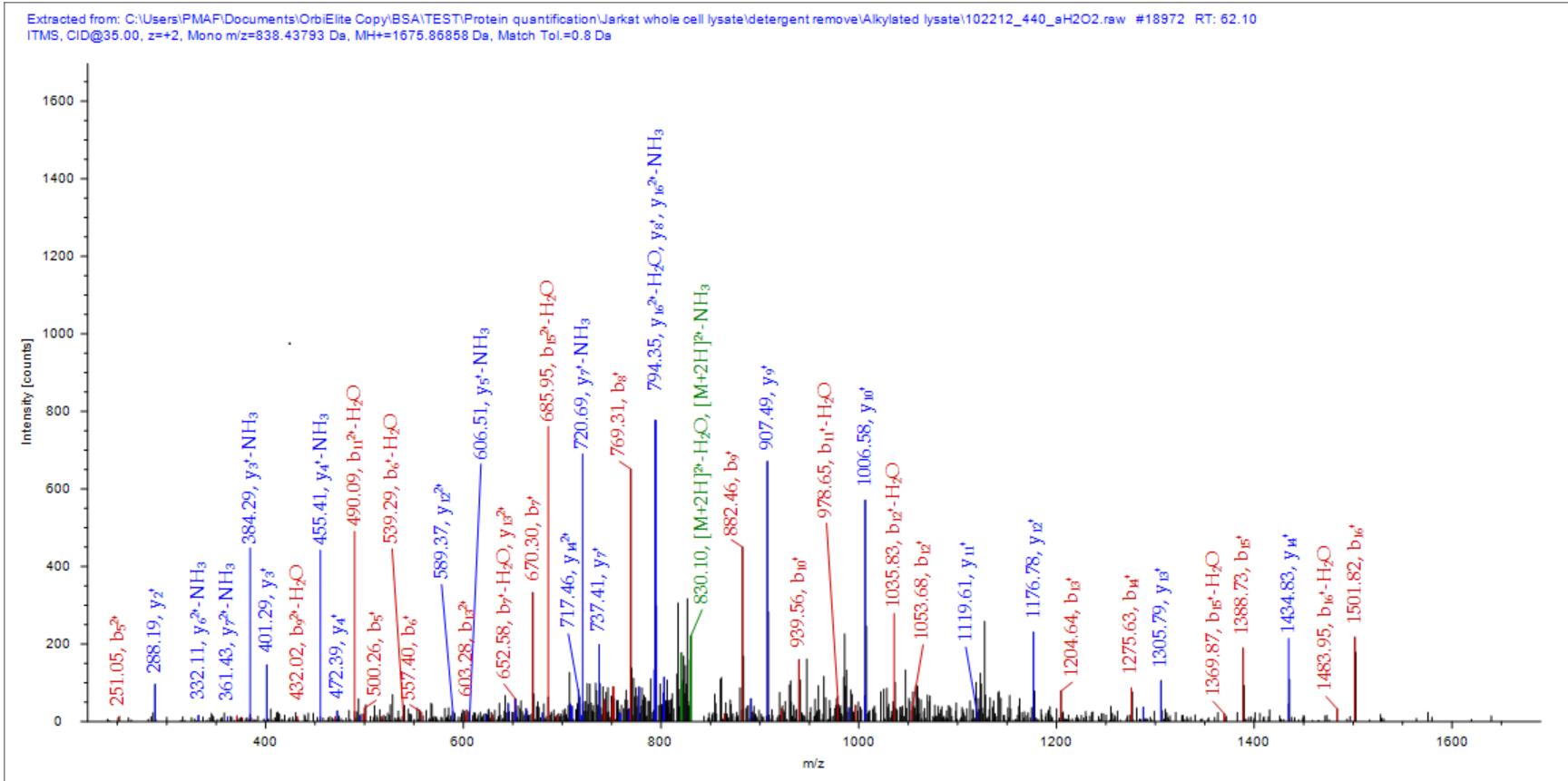
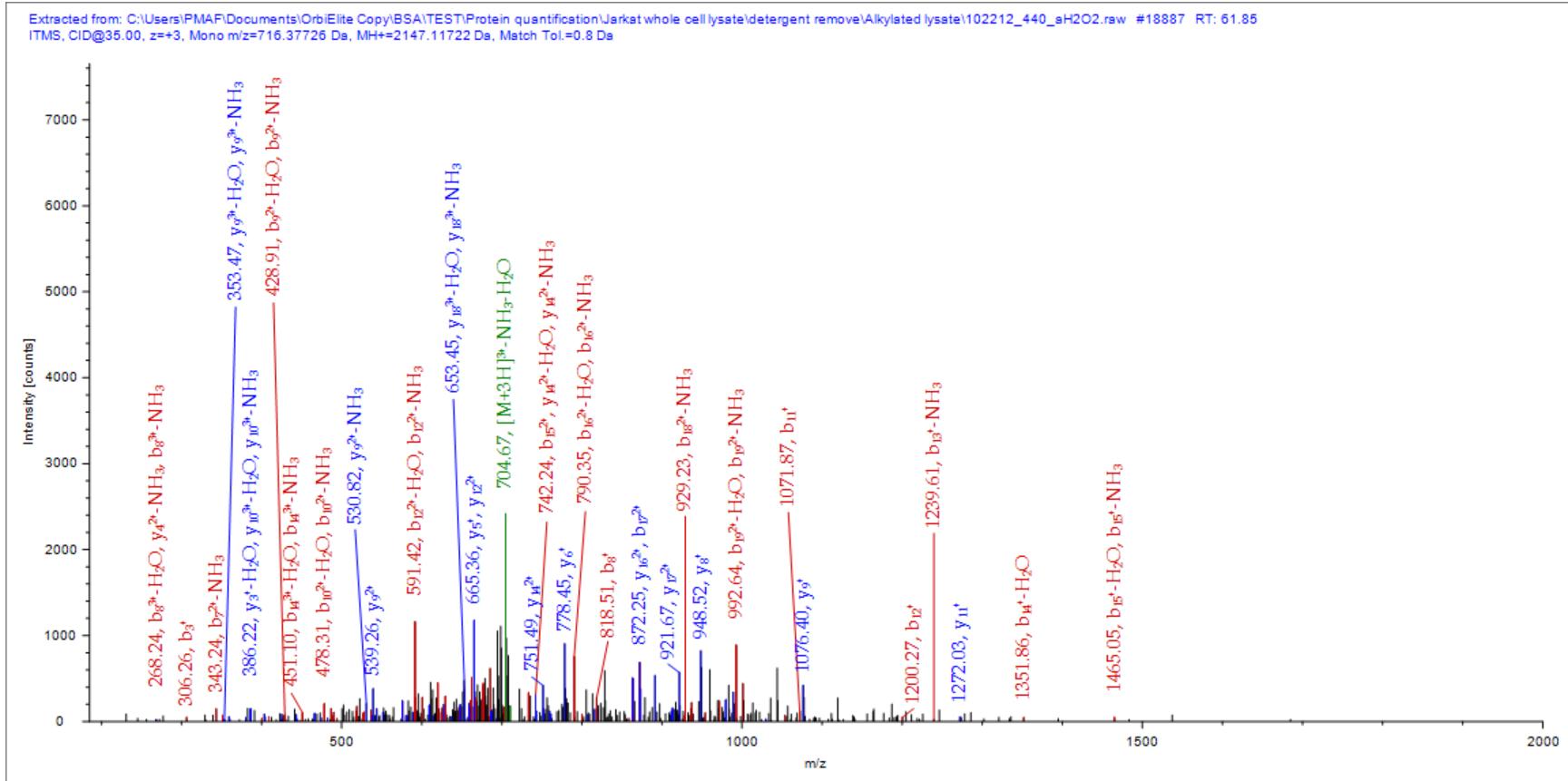


Figure S3. MS/MS of sulfinic and sulfonic acid peptides identified from H₂O₂ treated lysate

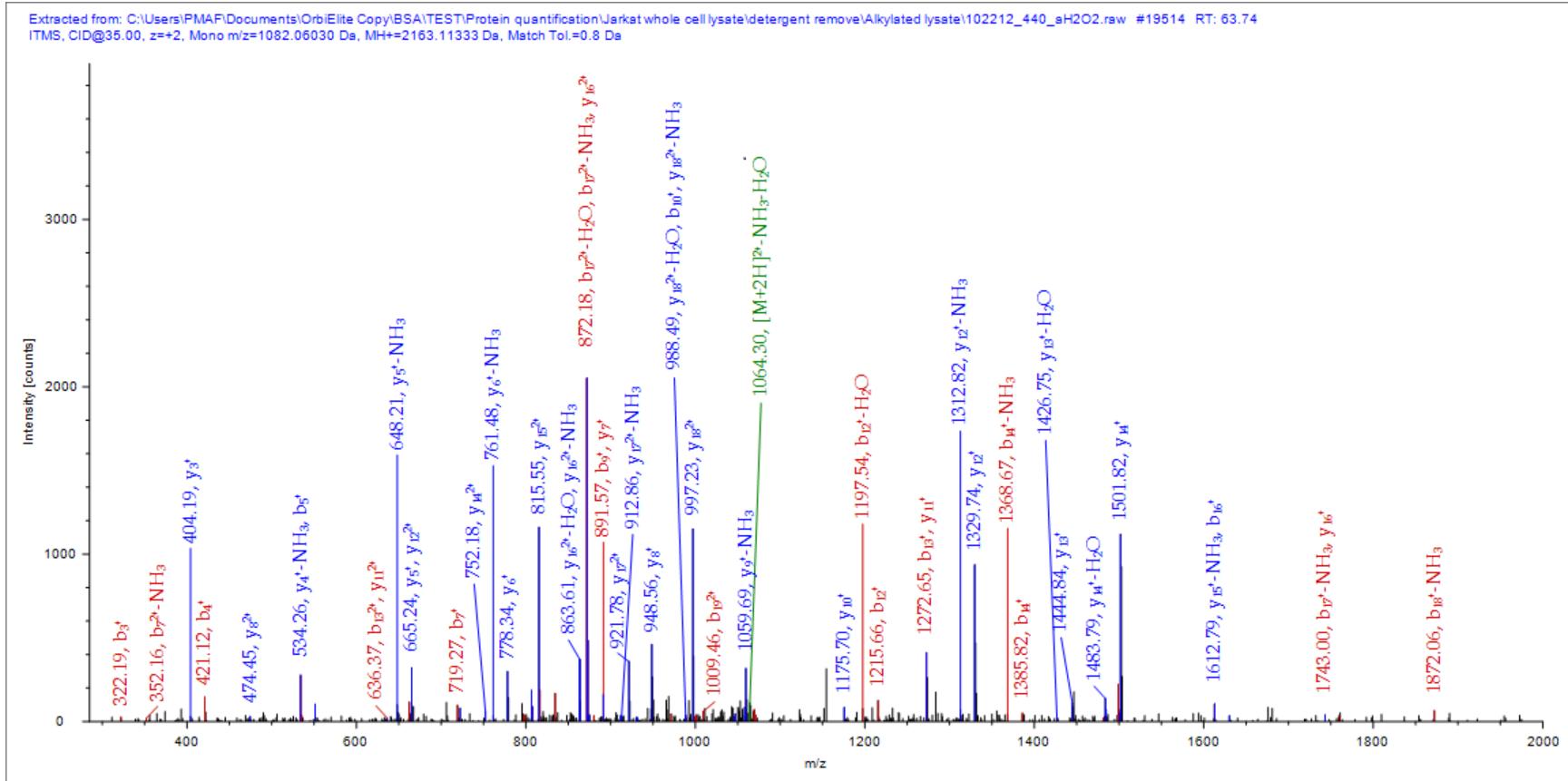
AAVEEGIVLGGGCALLR C13 SO3H



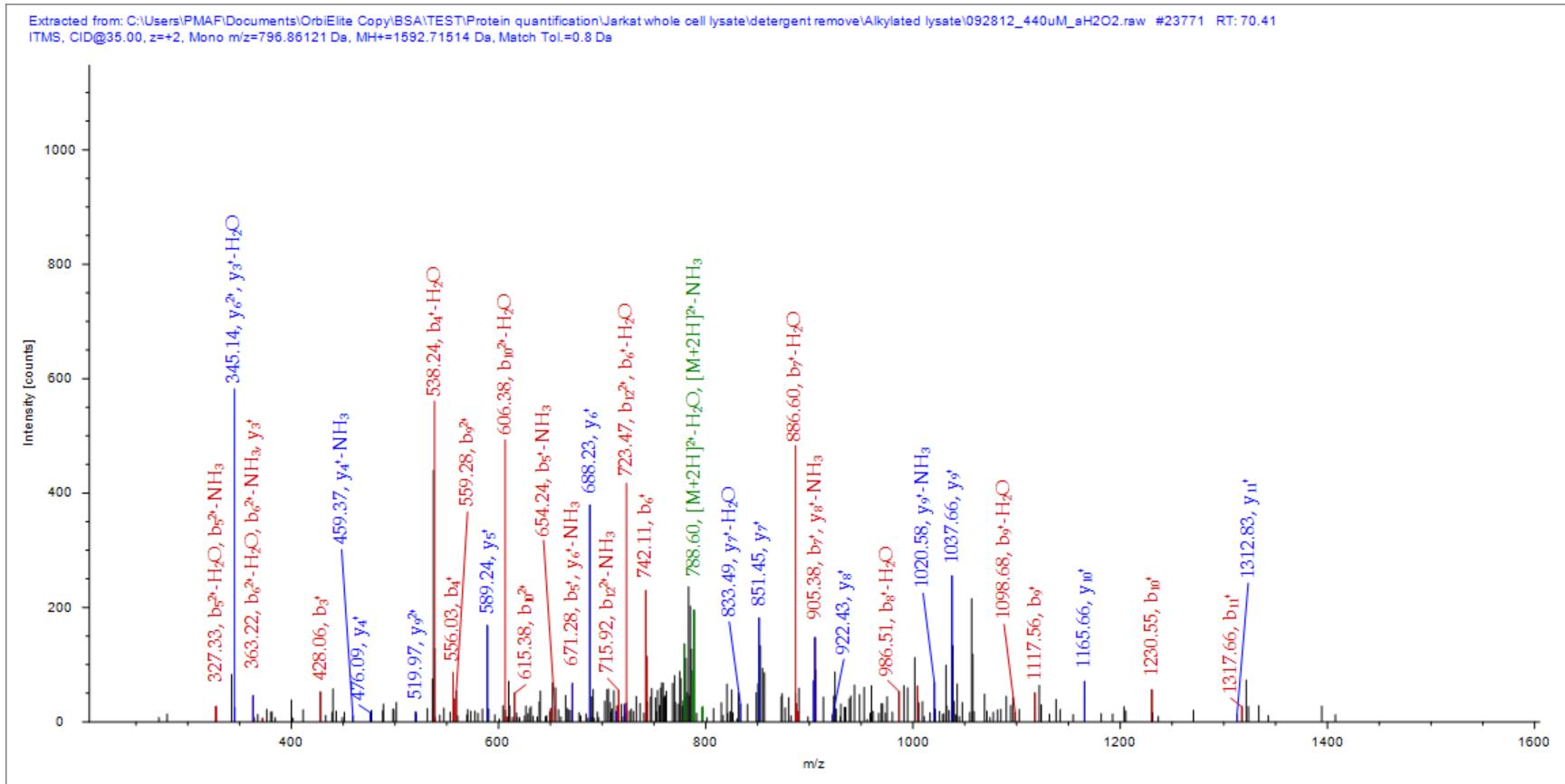
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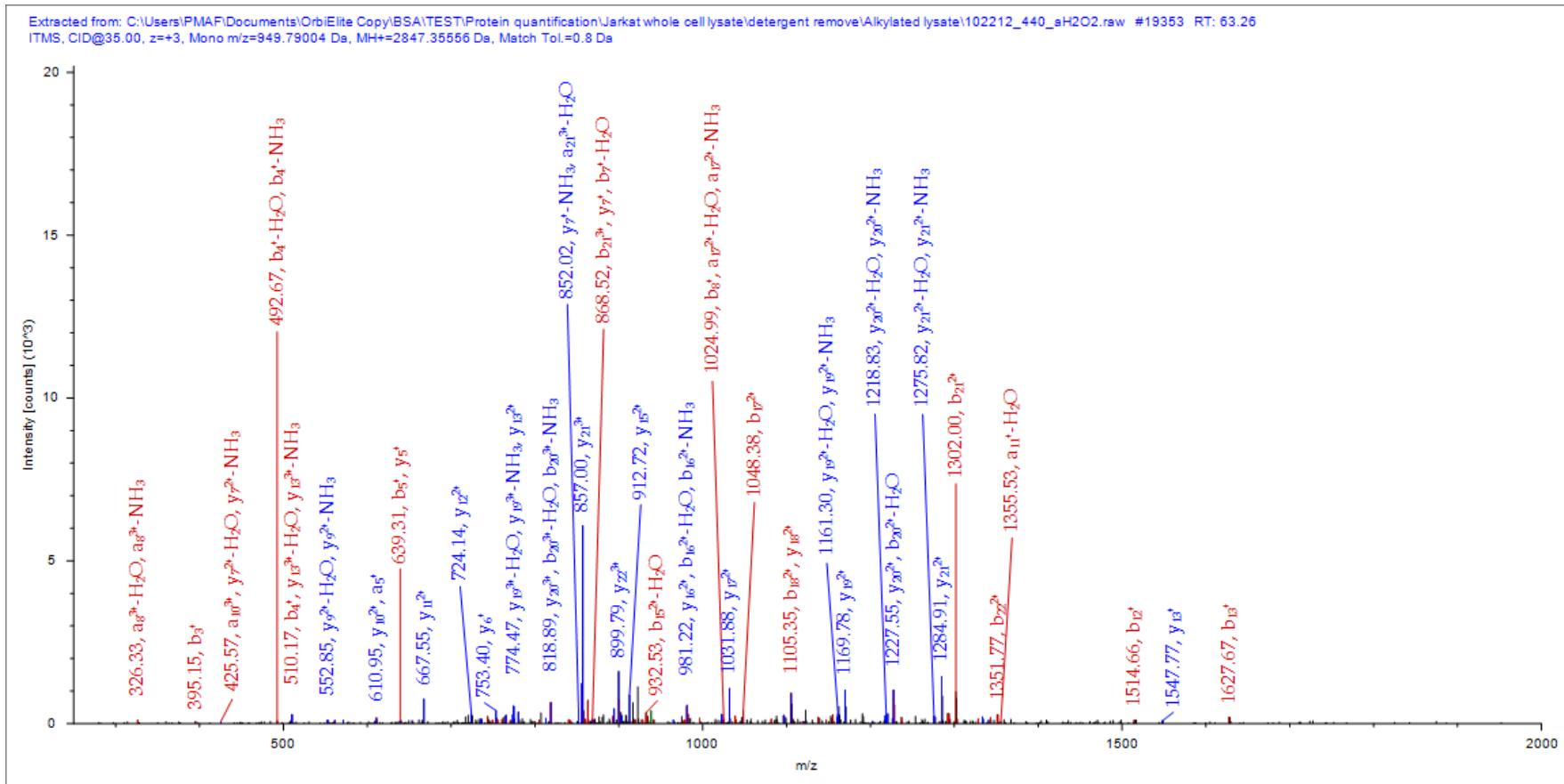
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CEFQDAYVLLSEK_C1_SO3H

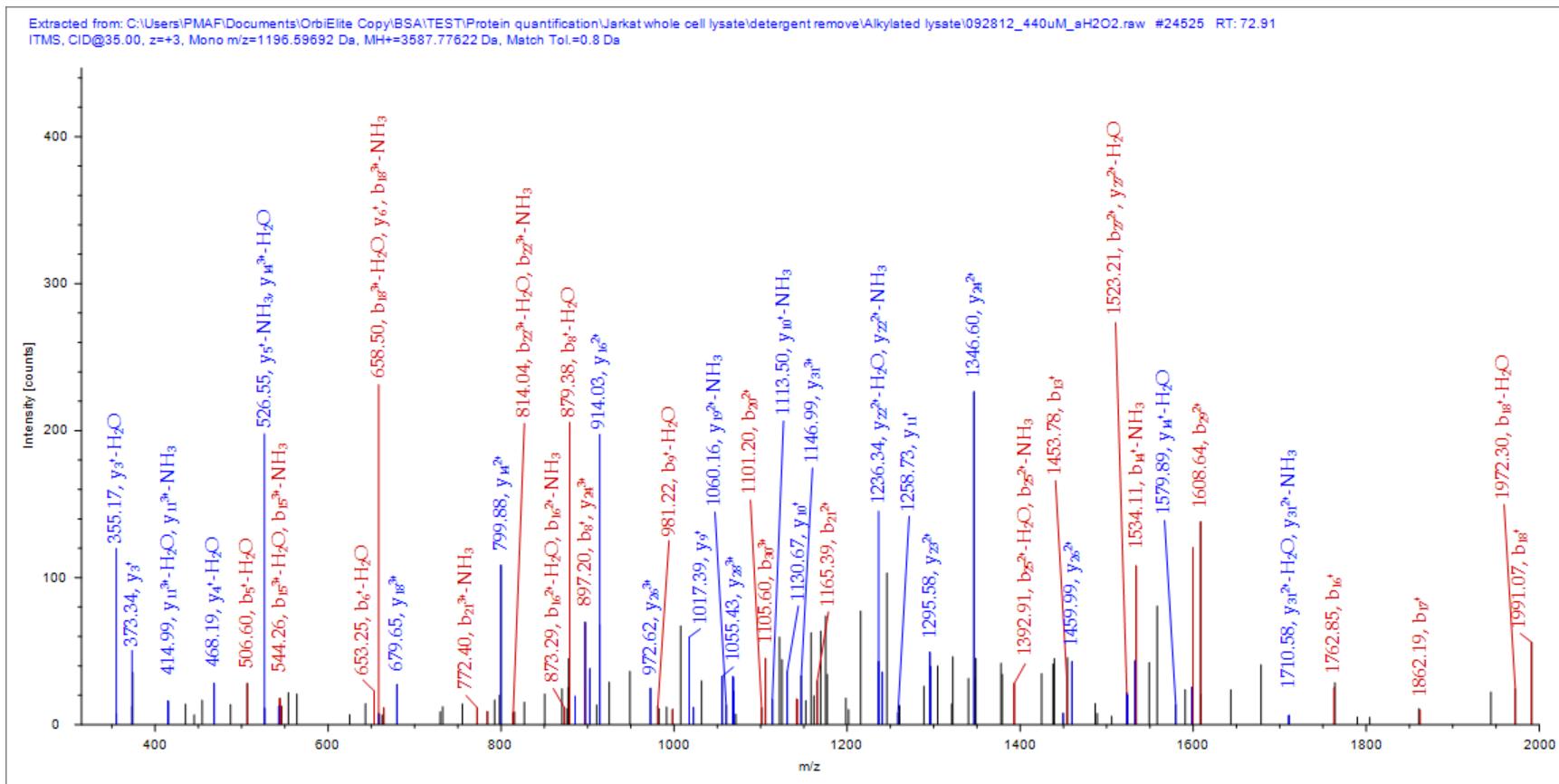


CKDDEFTHLYTLIVRPDNTYEVK_C1_SO3H



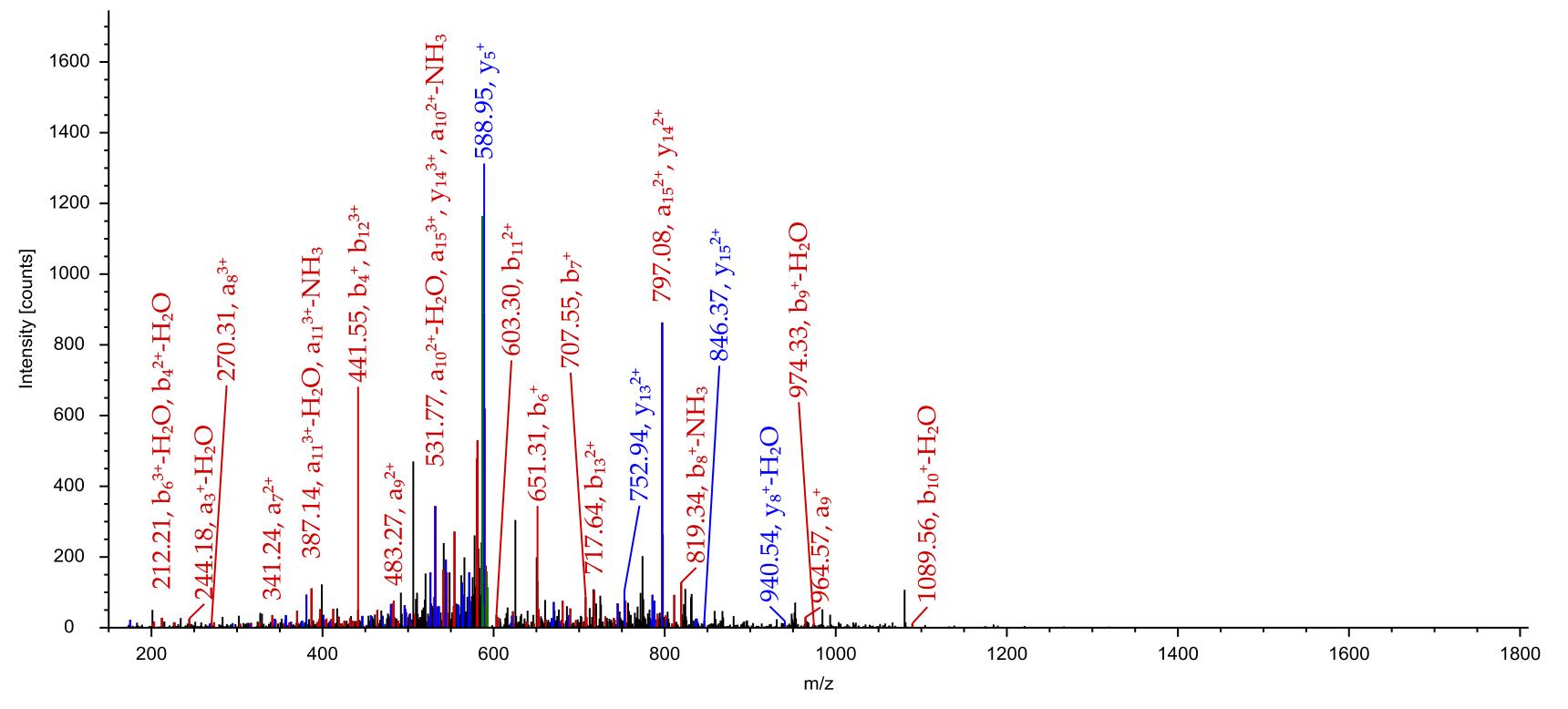
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_C1_SO3H

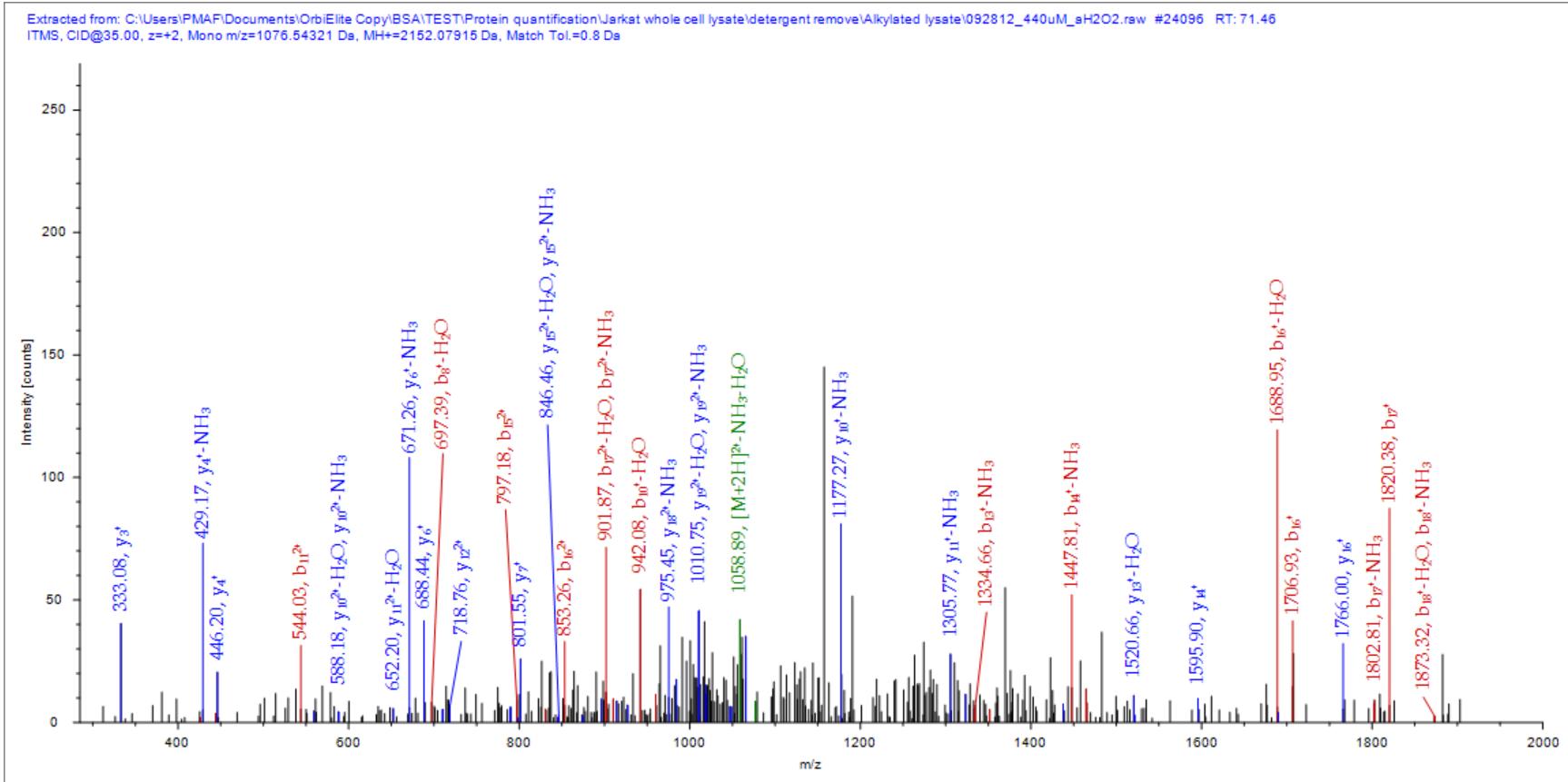


CVSCLPGQRDVDNALR_C4_SO3H

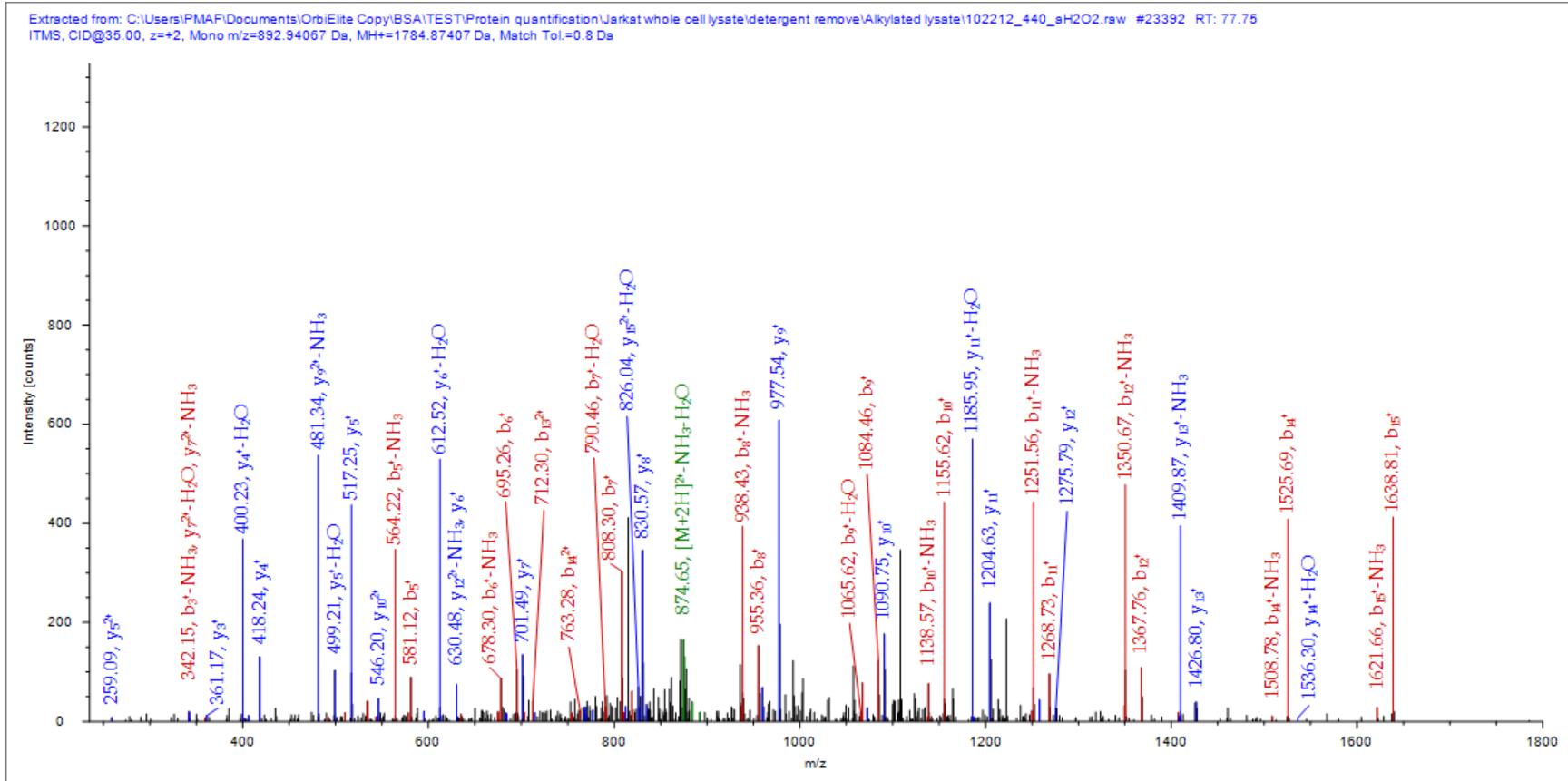
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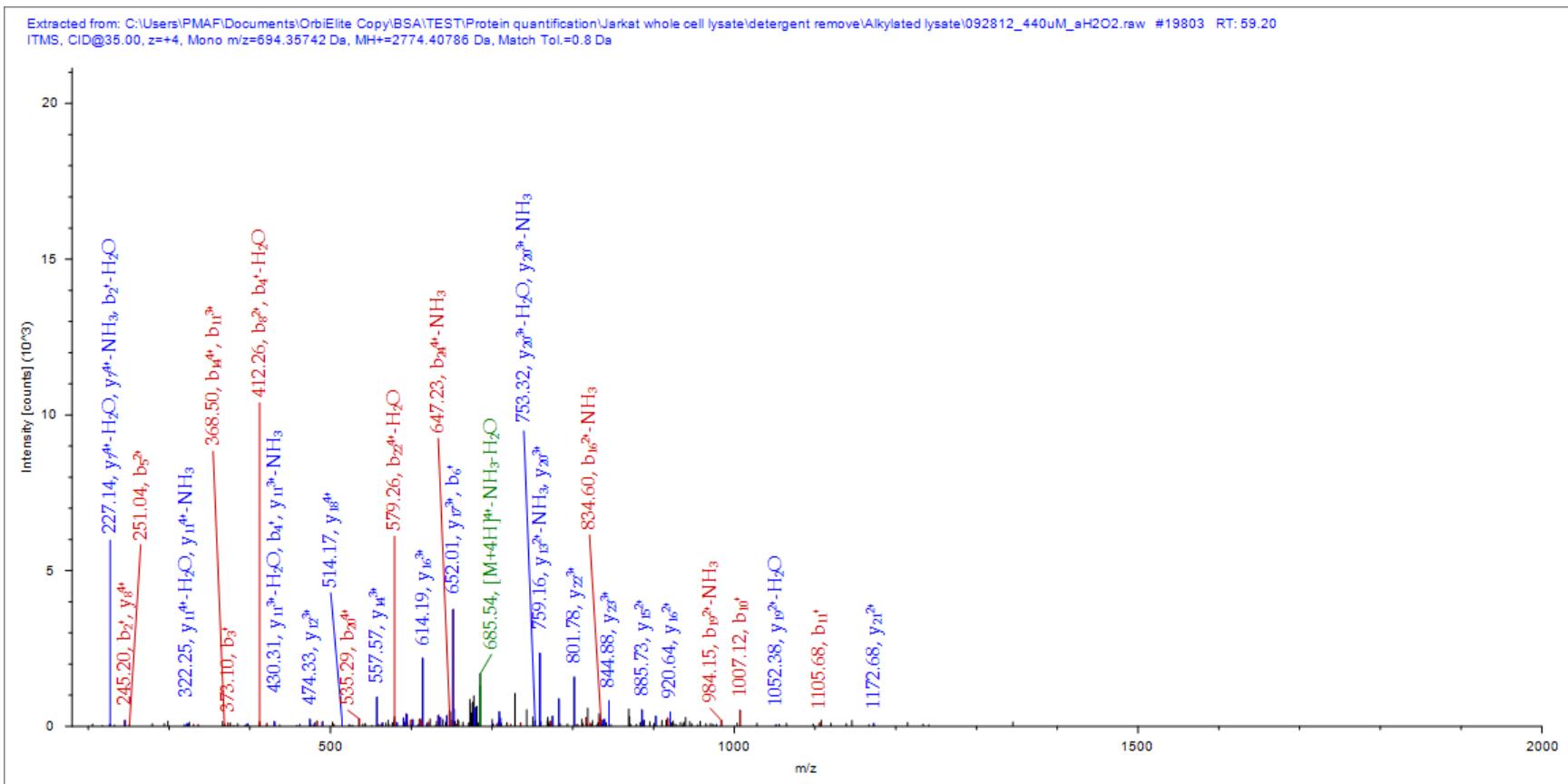
DAISGIGTDEKCLIEILASR_C12_SO3H



DDKCANLFEALVGTLK_-C4_SO3H

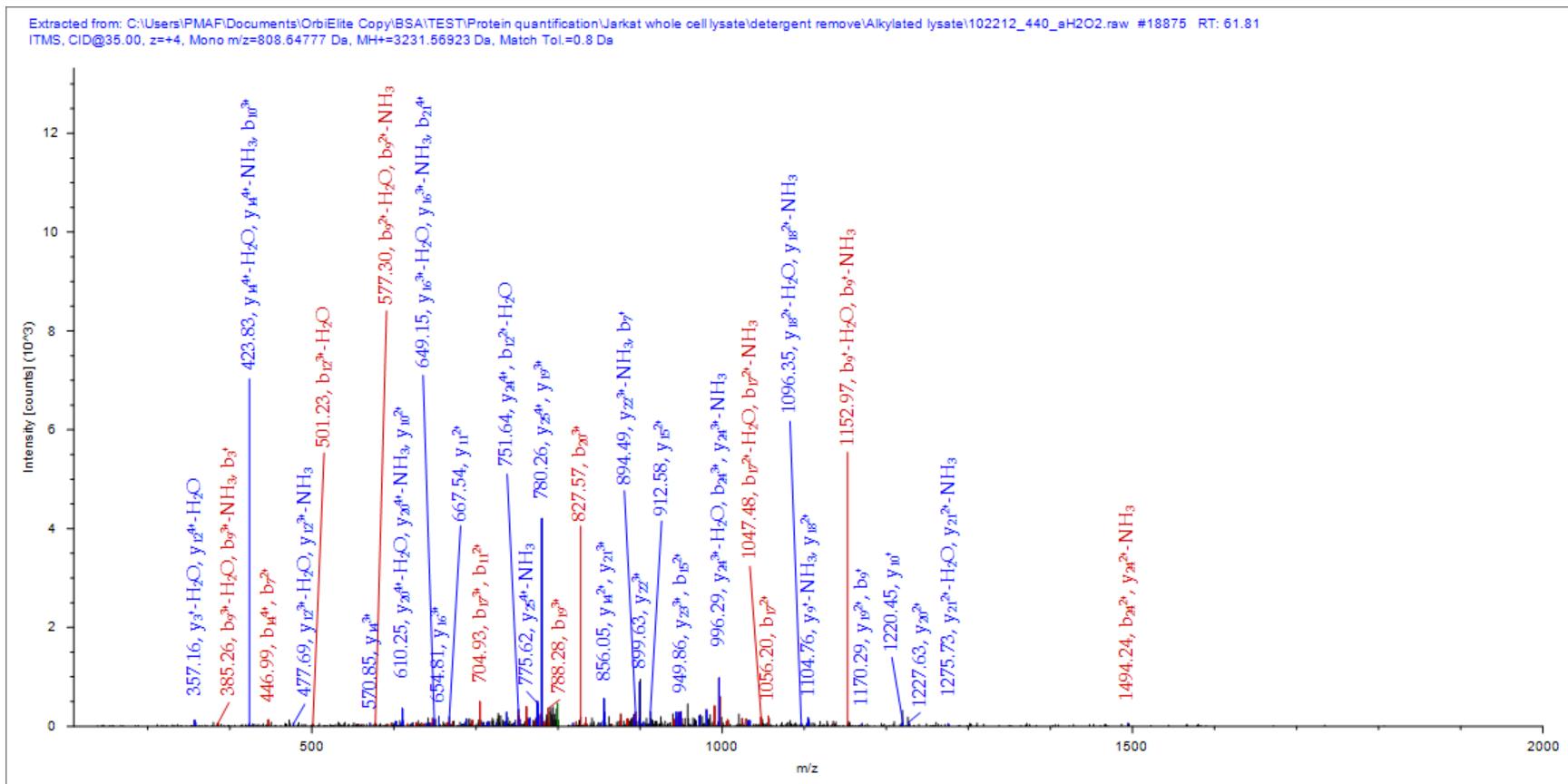


DEQGACAVLAVHLNTLLGERPVQHR
C6 SO3H

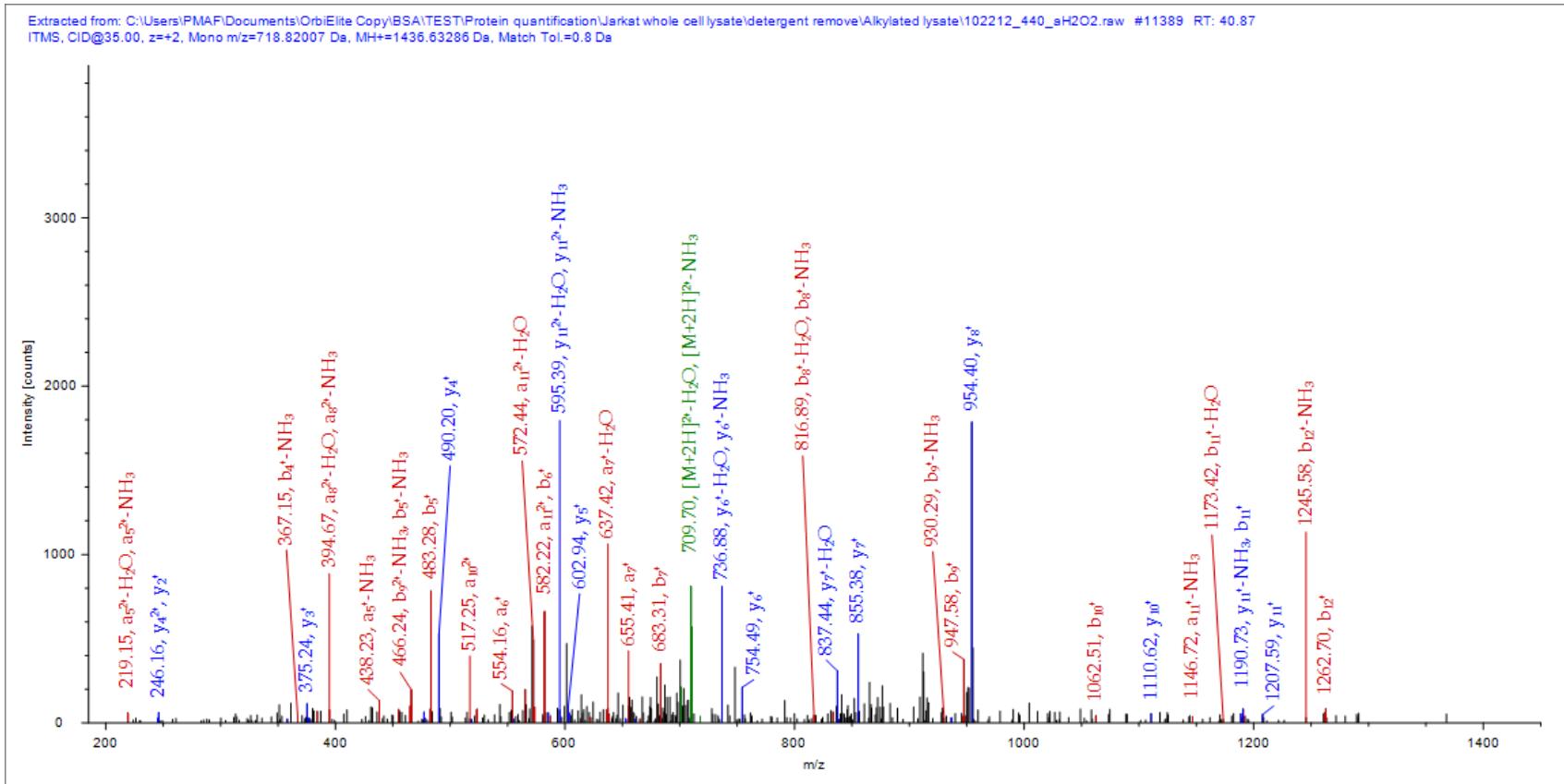


DIRCKDDEFTHLYTLVRPDNTYEVK

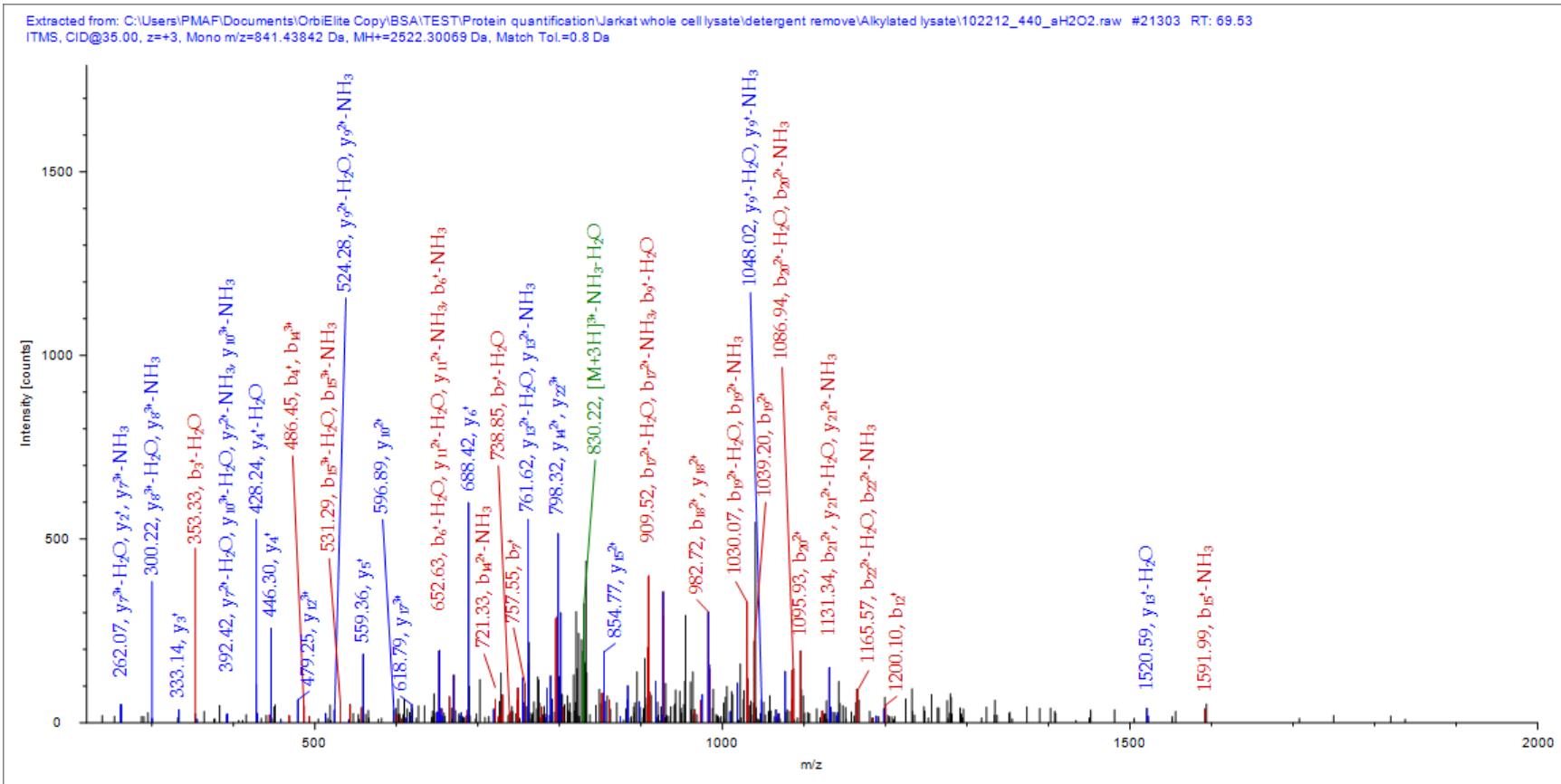
_C4_SO3H



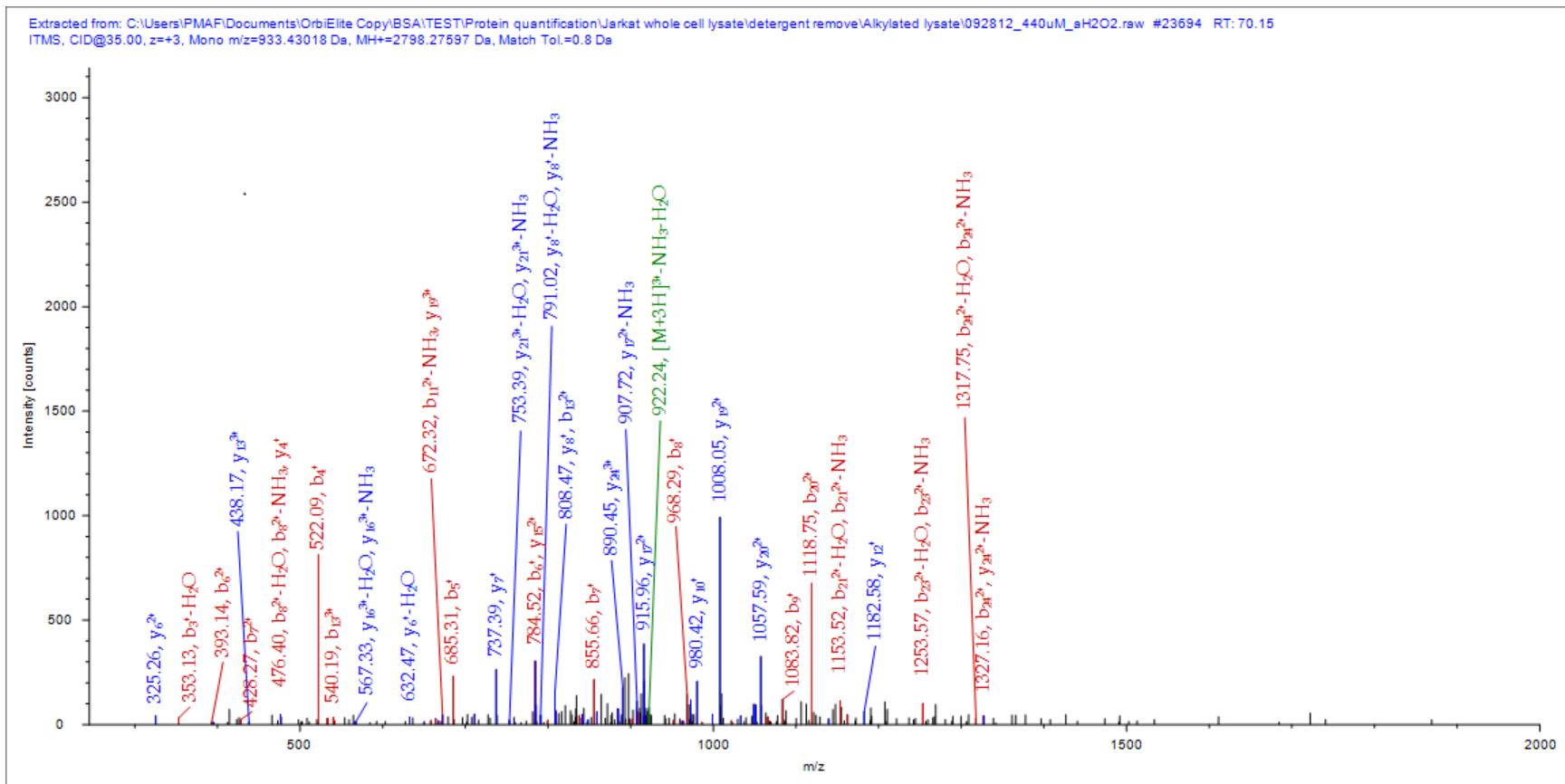
DNPGVVTCLEAR_C8_SO3H



EIKDAISGIGTDEKCLIEILASR_C15_SO3H

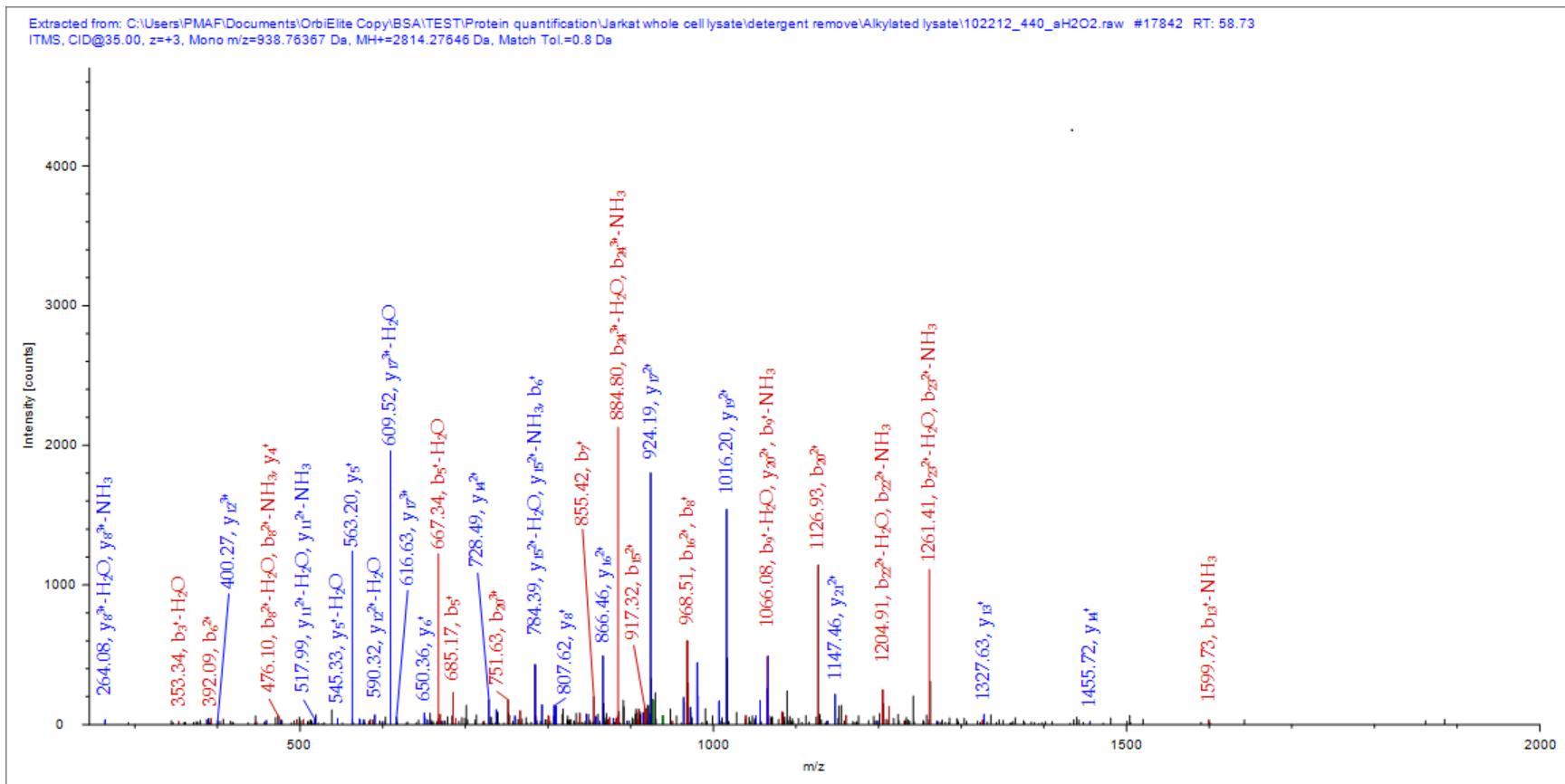


EKLCYVALDFEQEMATAASSSSLEK _C4_SO3H

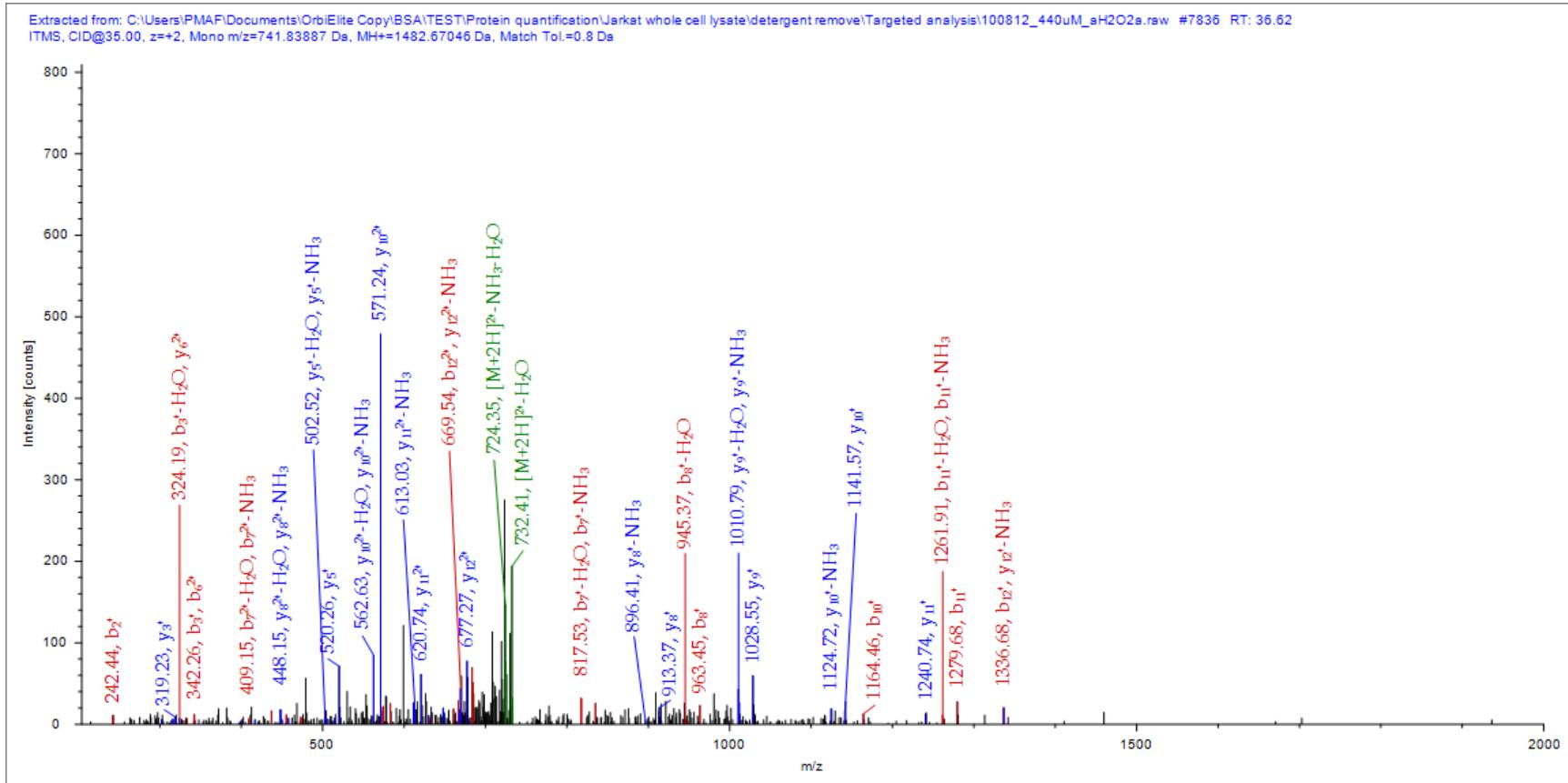


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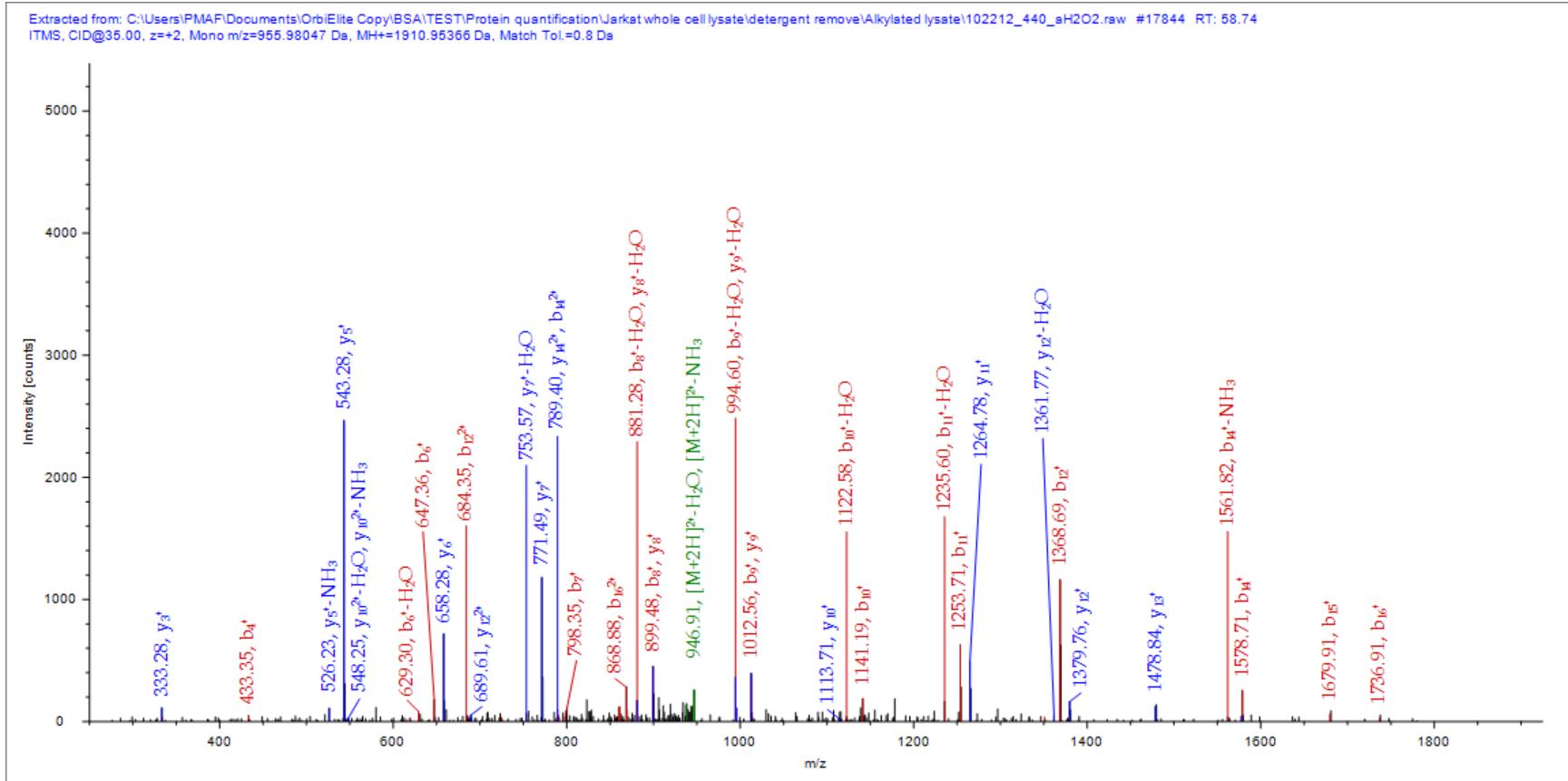
_C4_SO3H_Mox



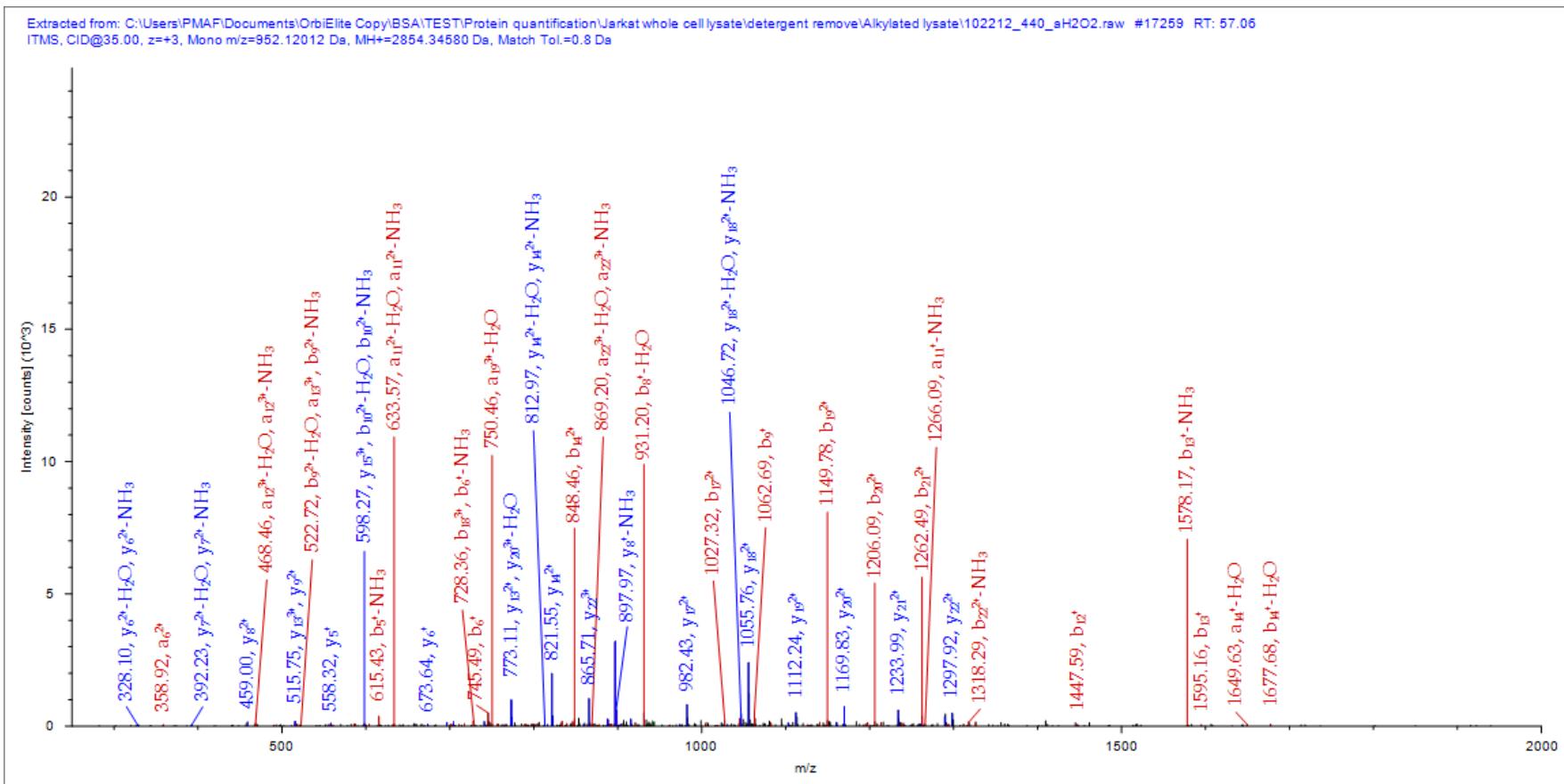
ELVLDNCKSNDGK_C7_SO3H



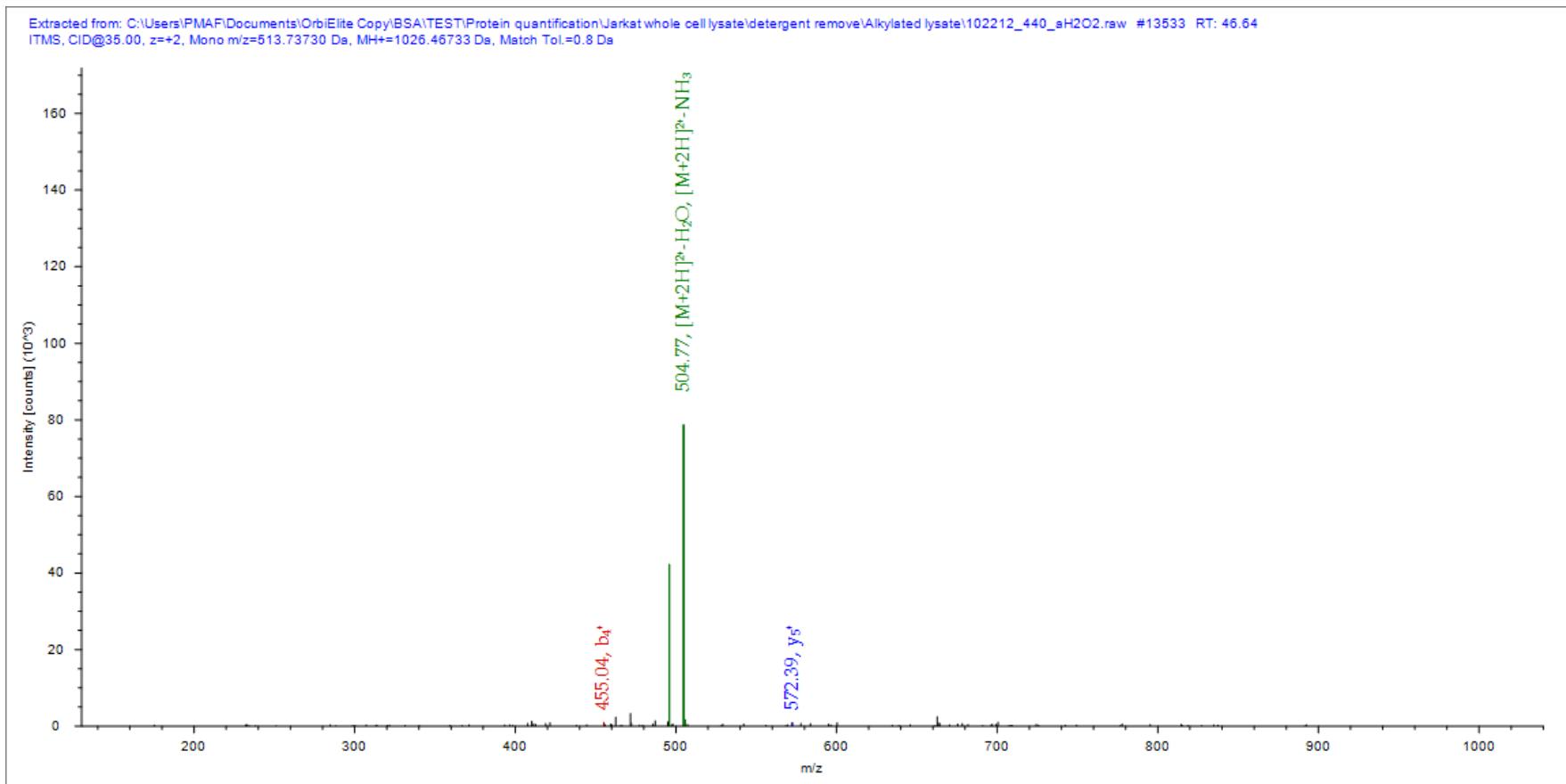
FGEVVCTLKLDPITGR_C7_SO3H



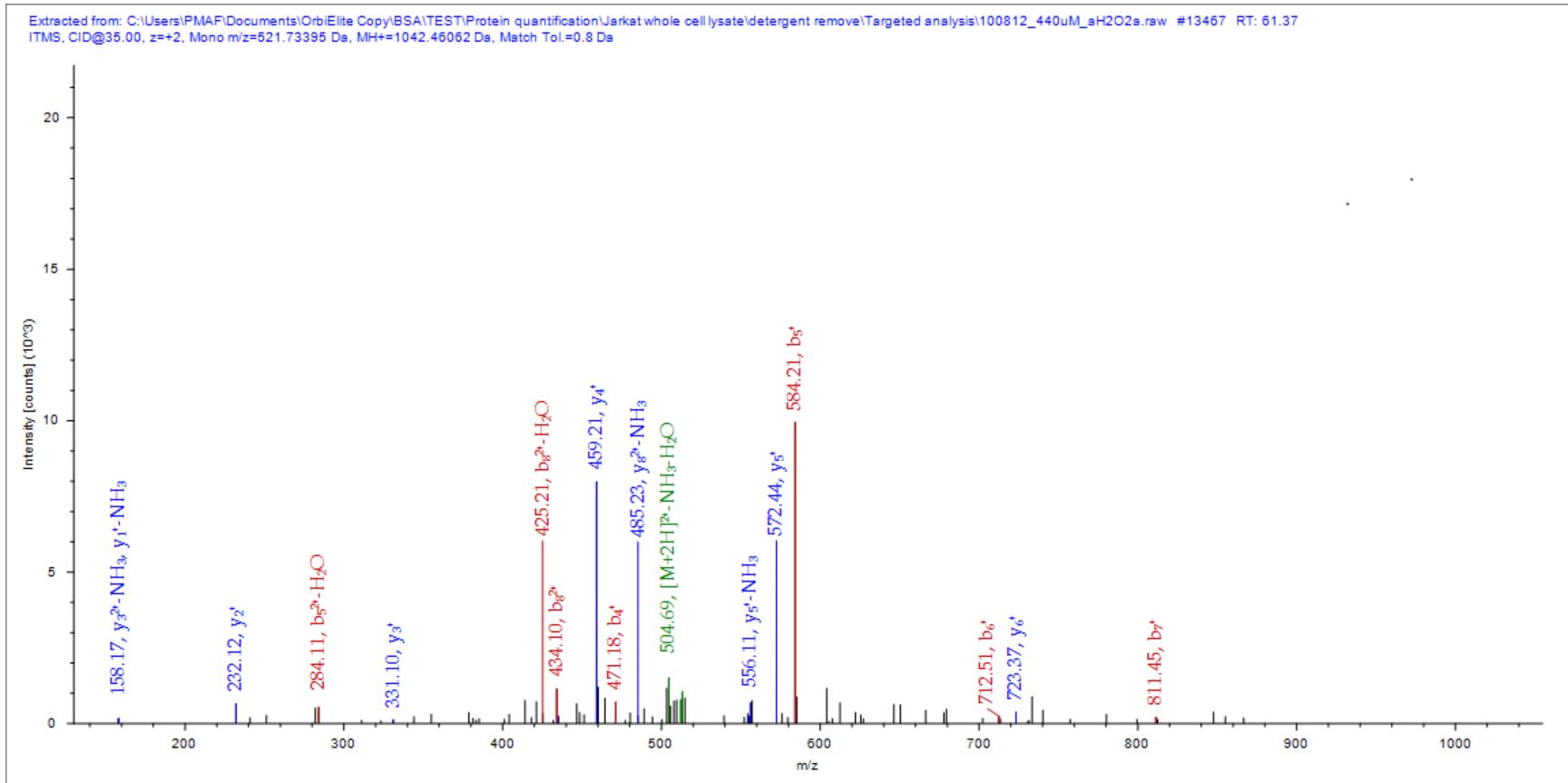
FIQENIFGICPHMTEDNKDLIQGK _C10_SO3H



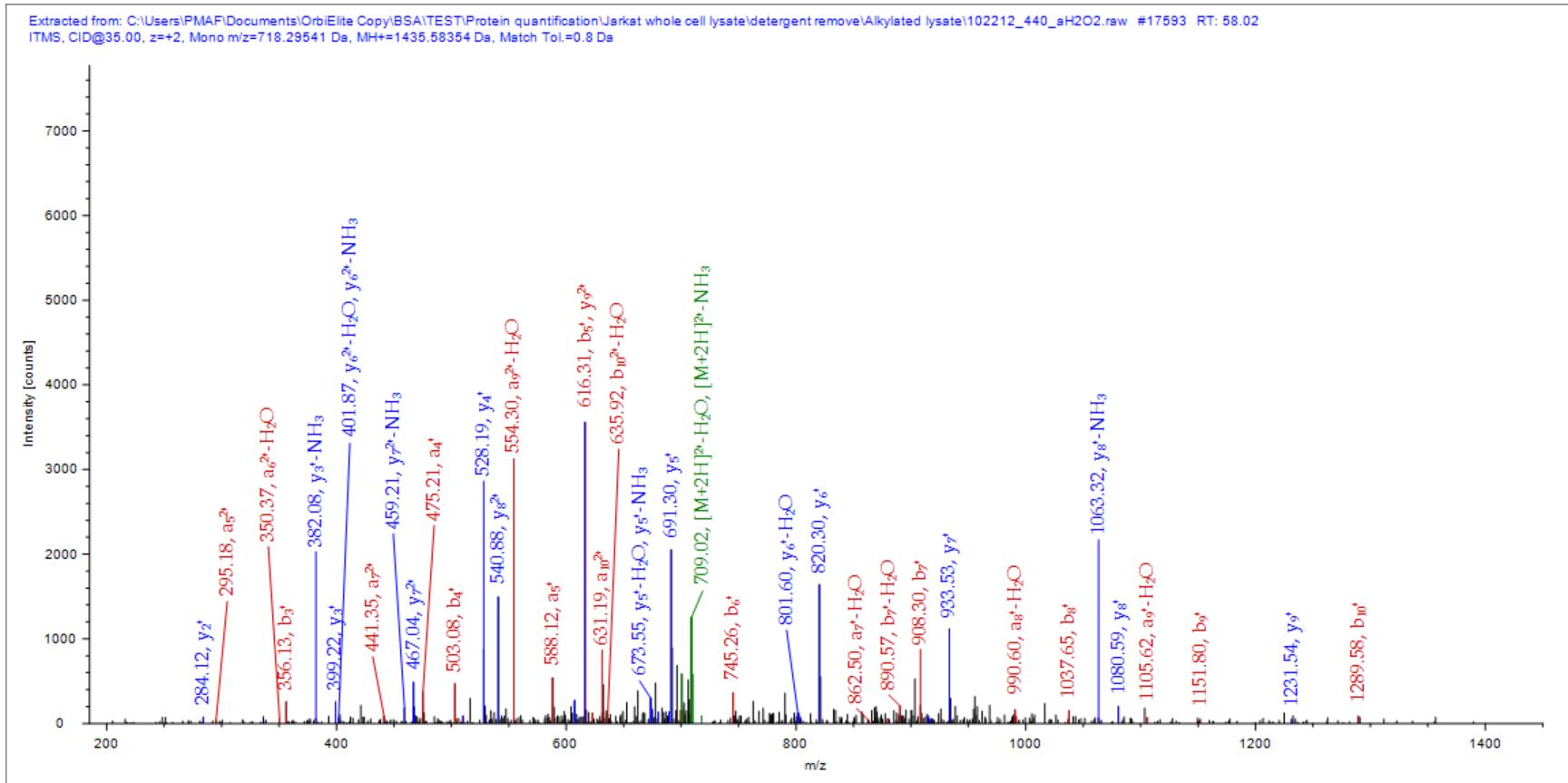
GDFCIQVGR_C4_SO2H



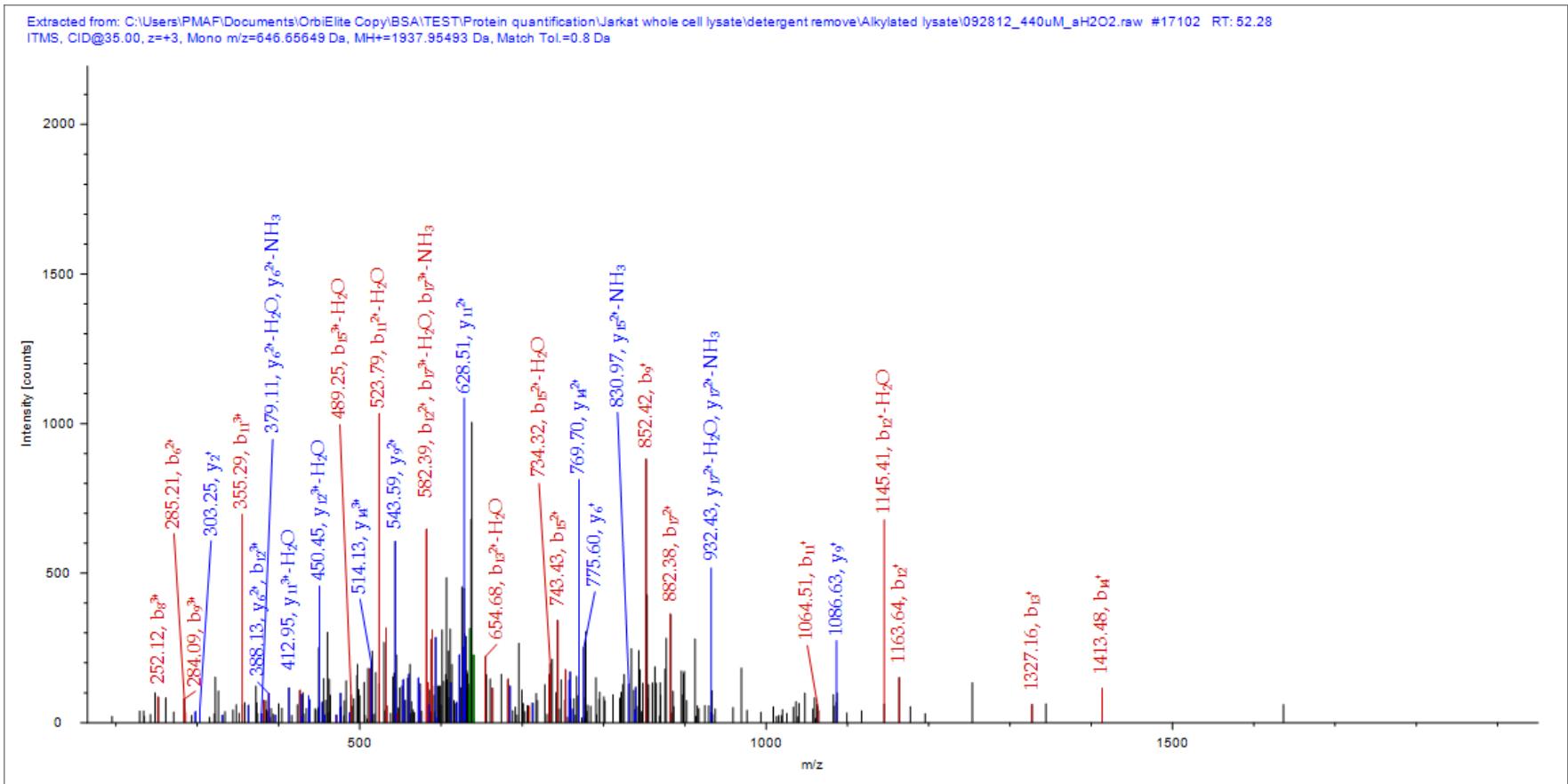
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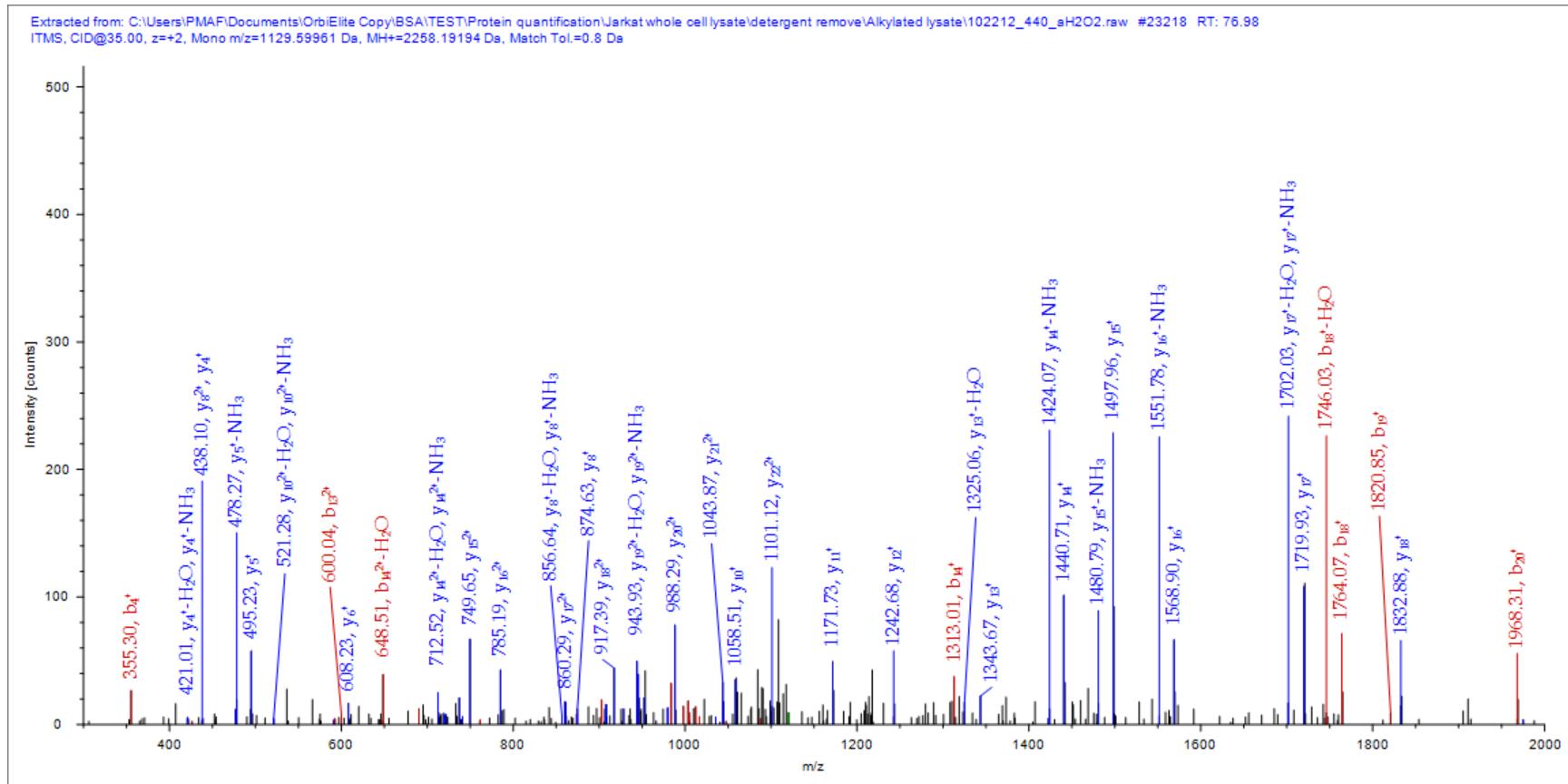
GFCFLEYEDHK_C3_SO3H



GFGHIGIAVPDVYSACKR_C16_SO3H

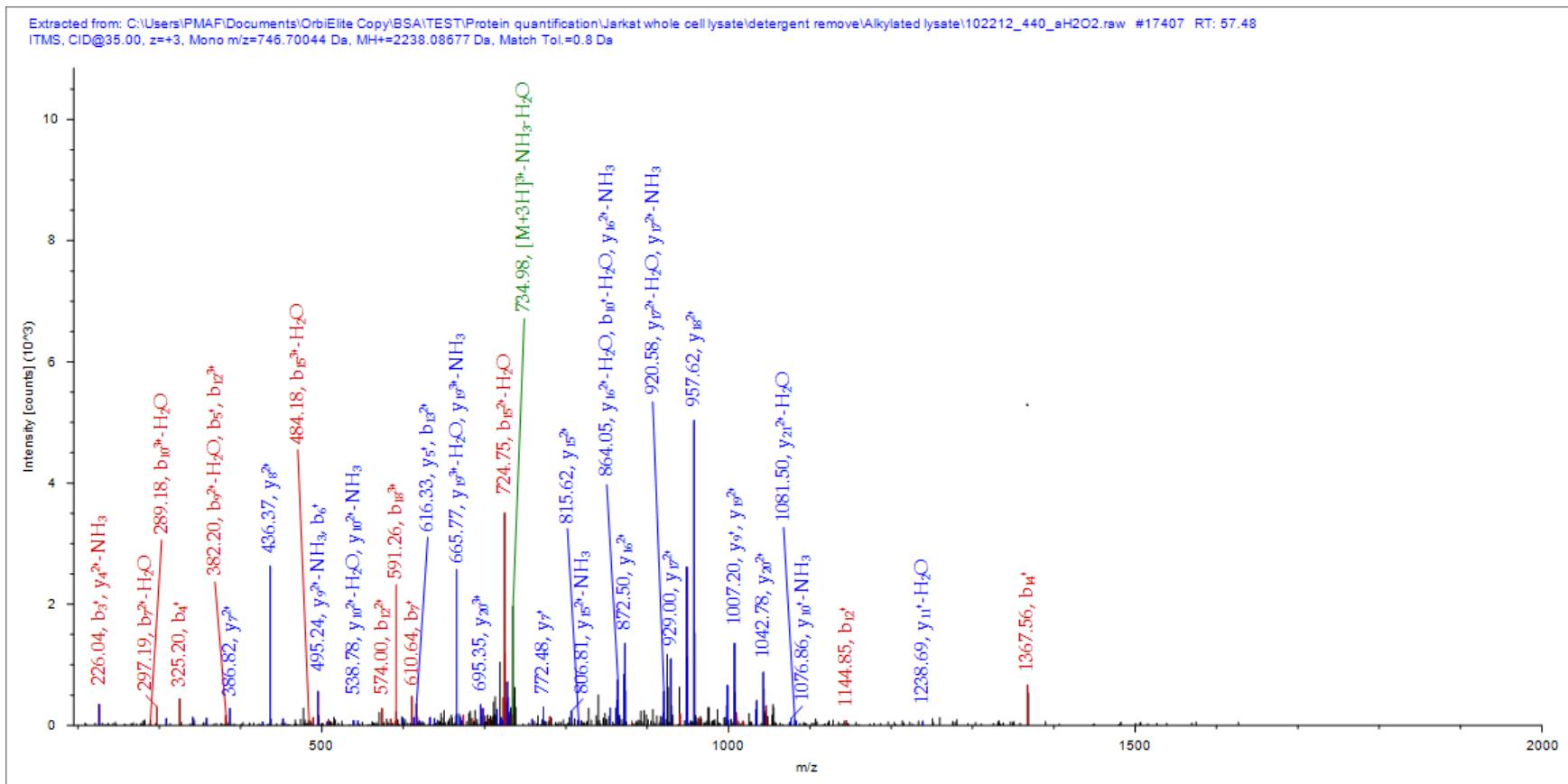


GLIAAICAGPTALLAHEIGFGSK_C7_SO3H



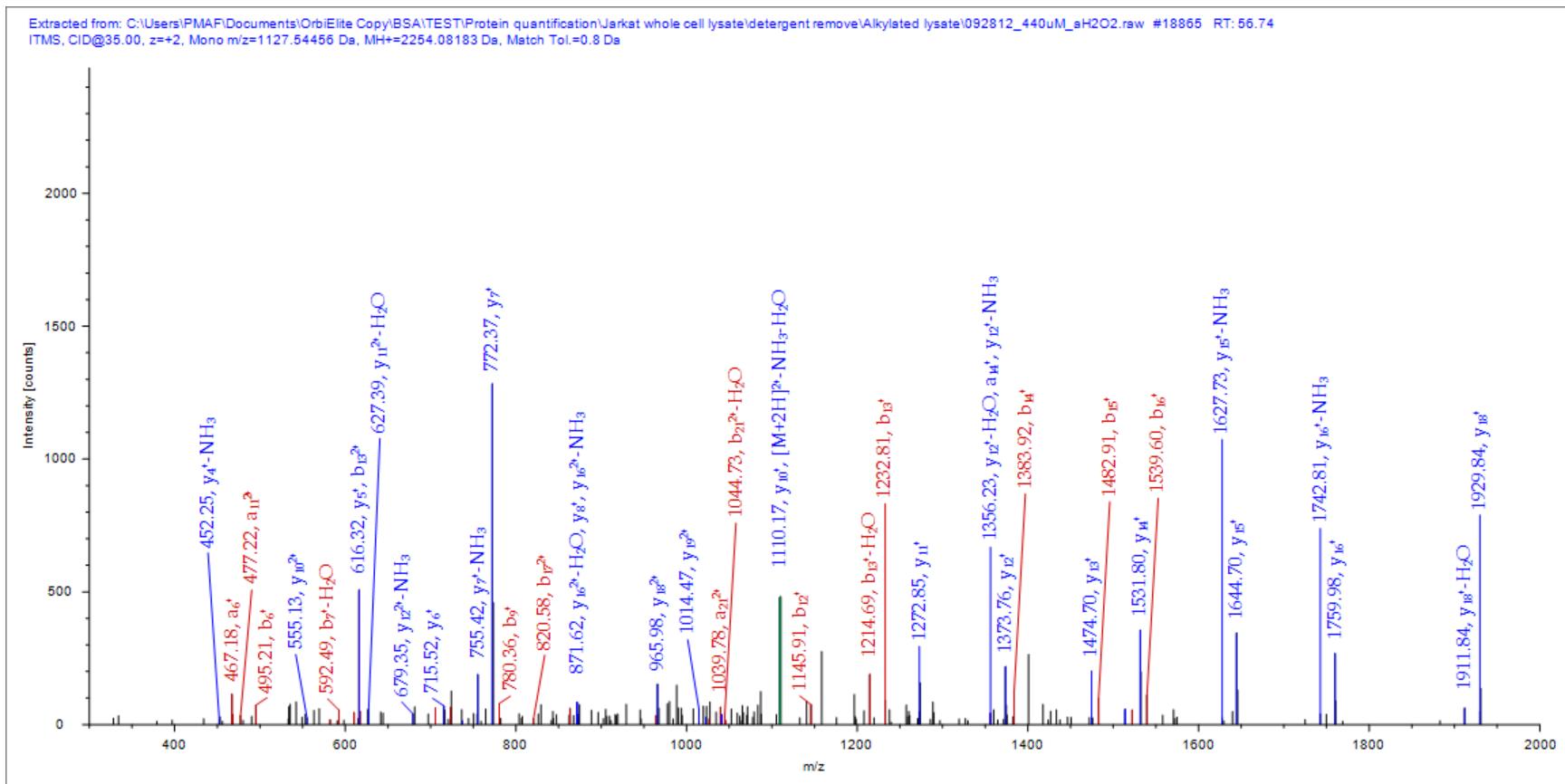
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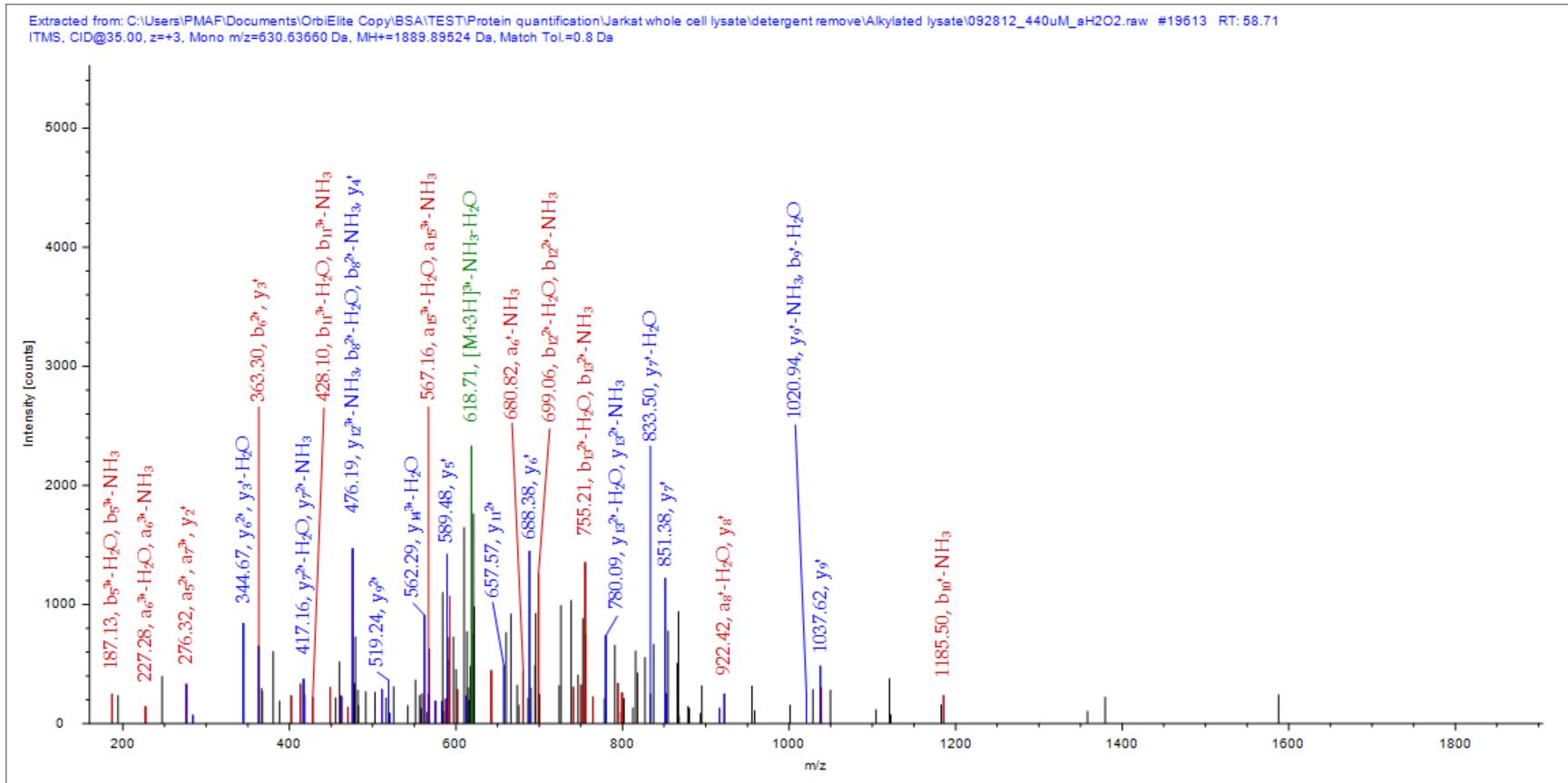


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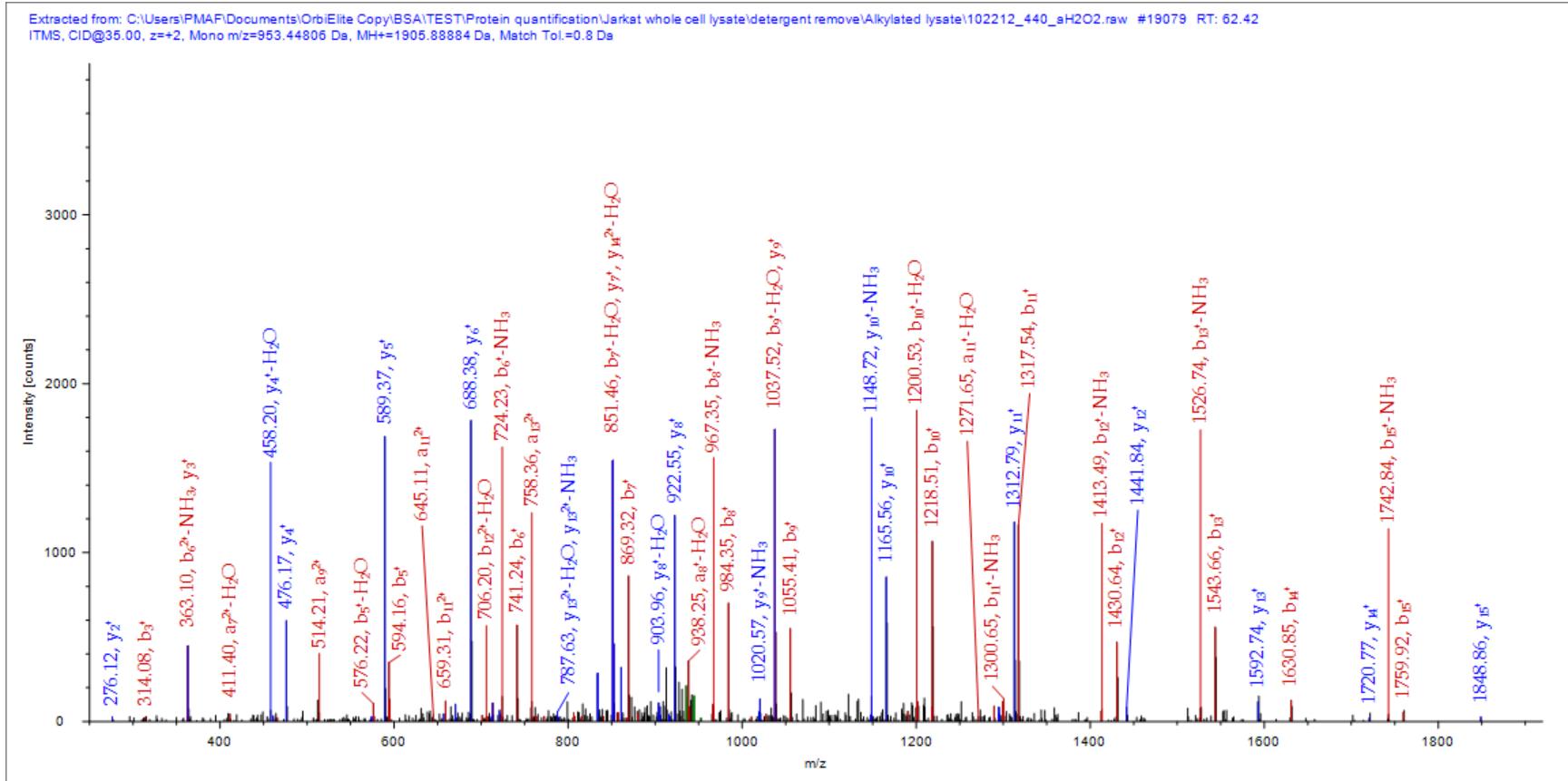
_C14_SO3H



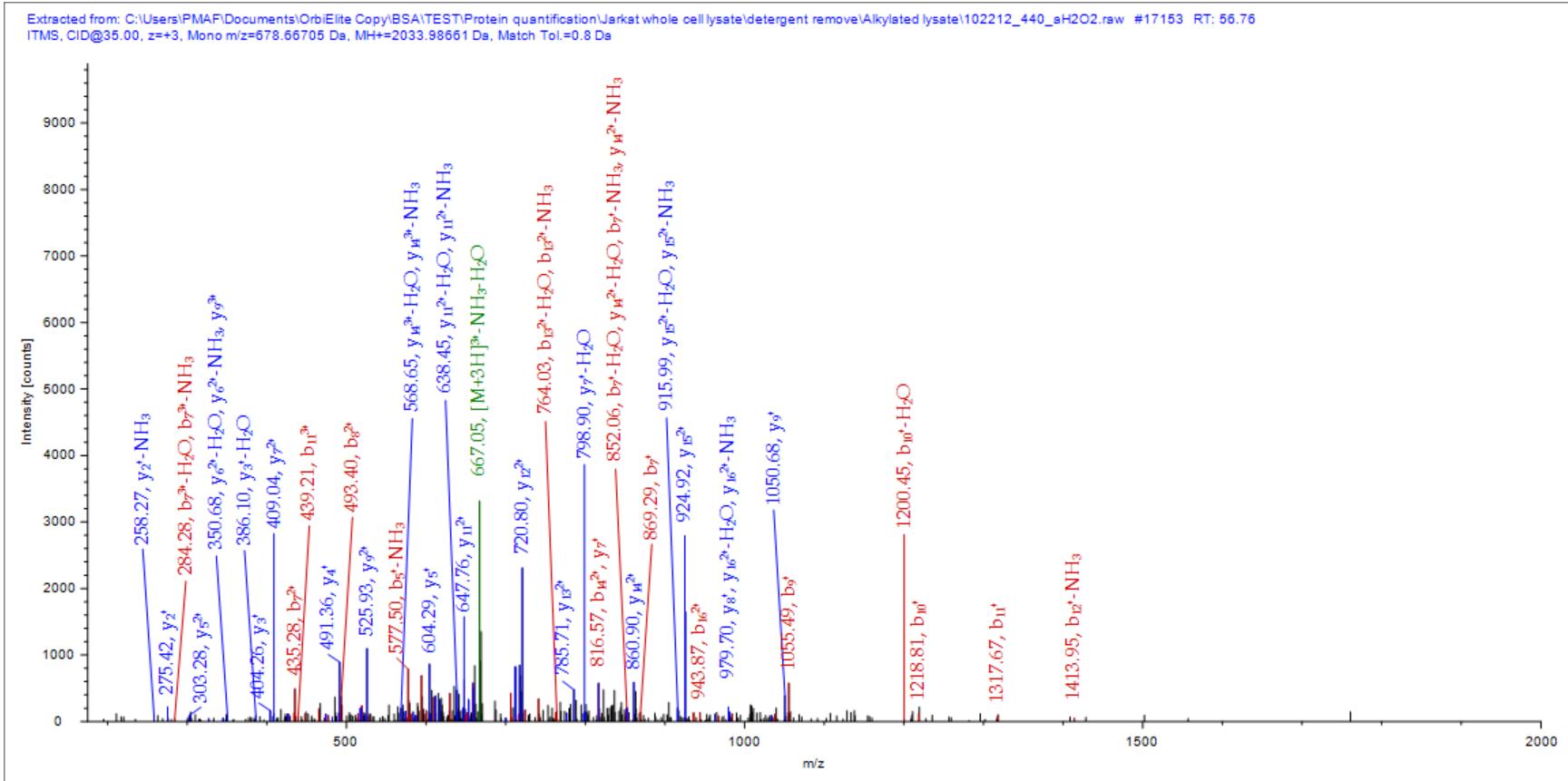
GQKCEFQDAYVLLSEK_C4_SO2H



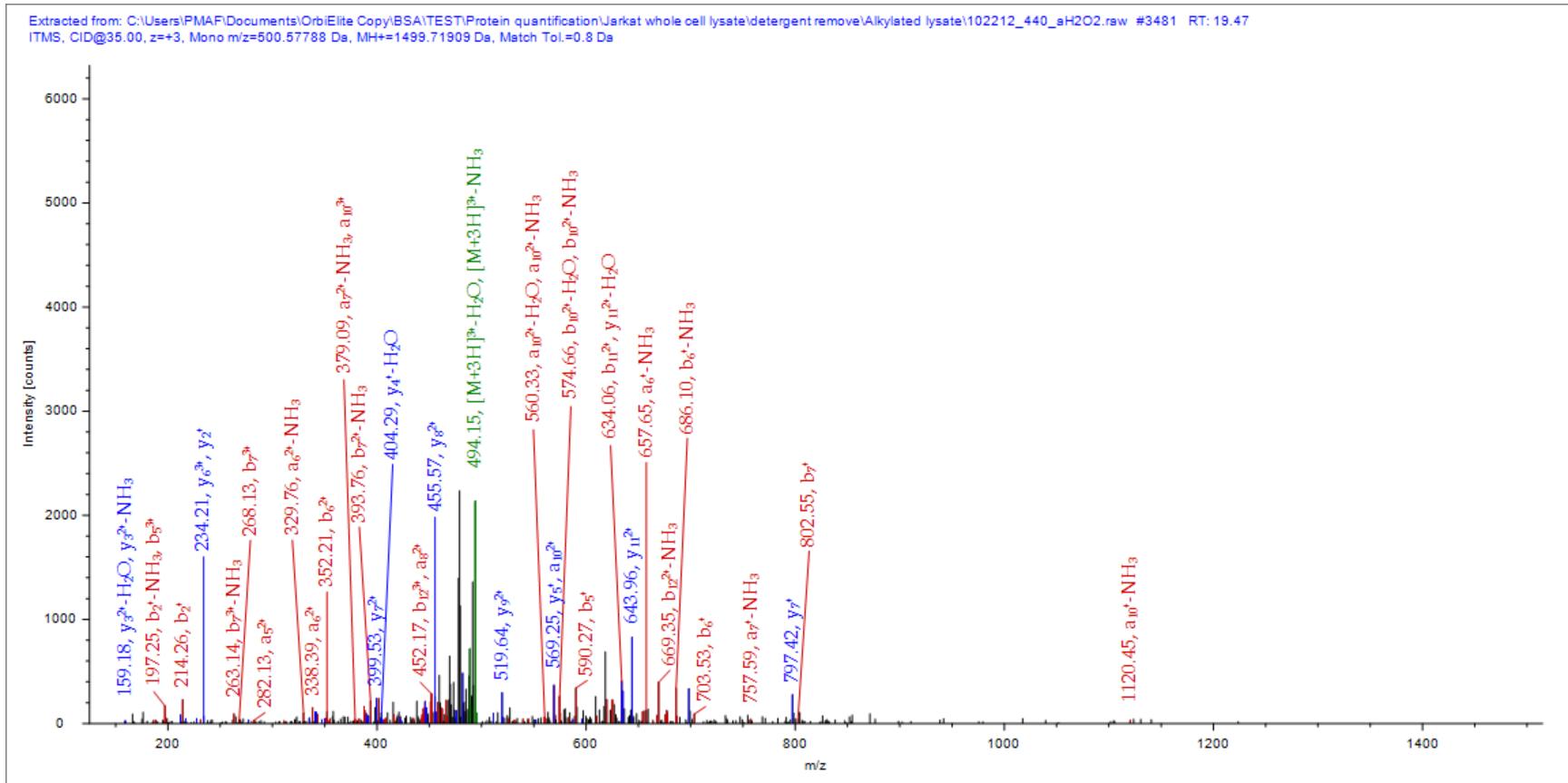
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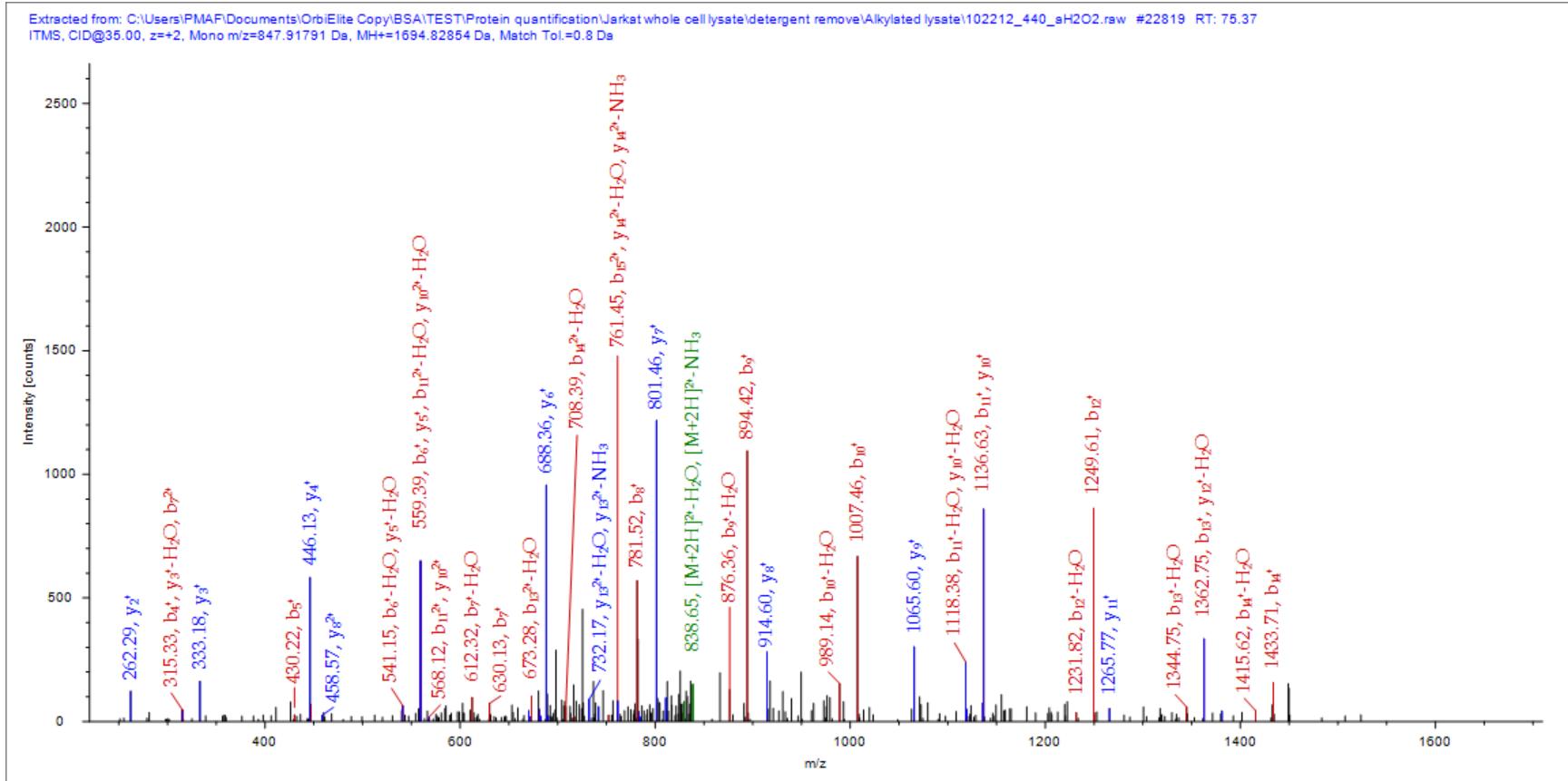
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GRPCKIVEMSTSK_C4_SO3H

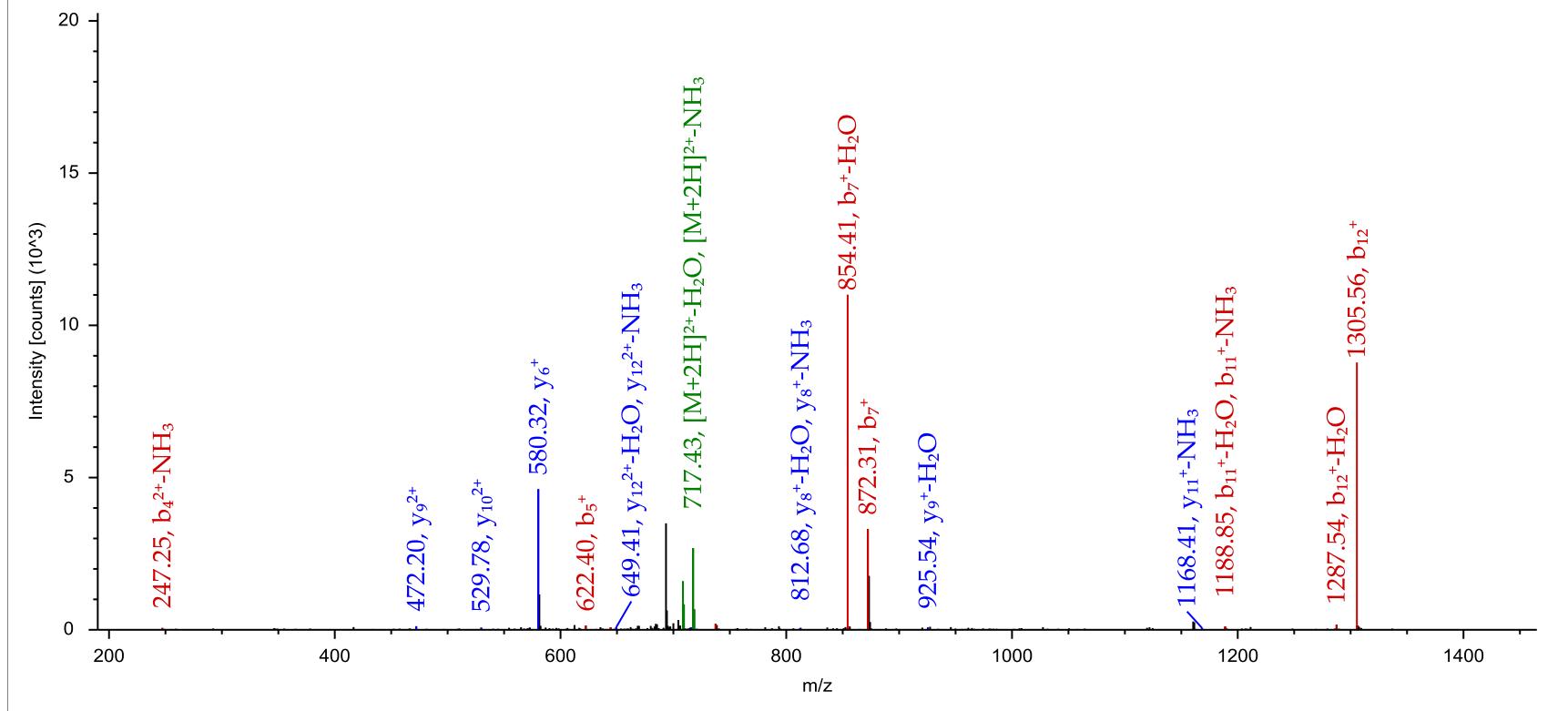


GVGTDEACLIEILASR_C8_SO3H

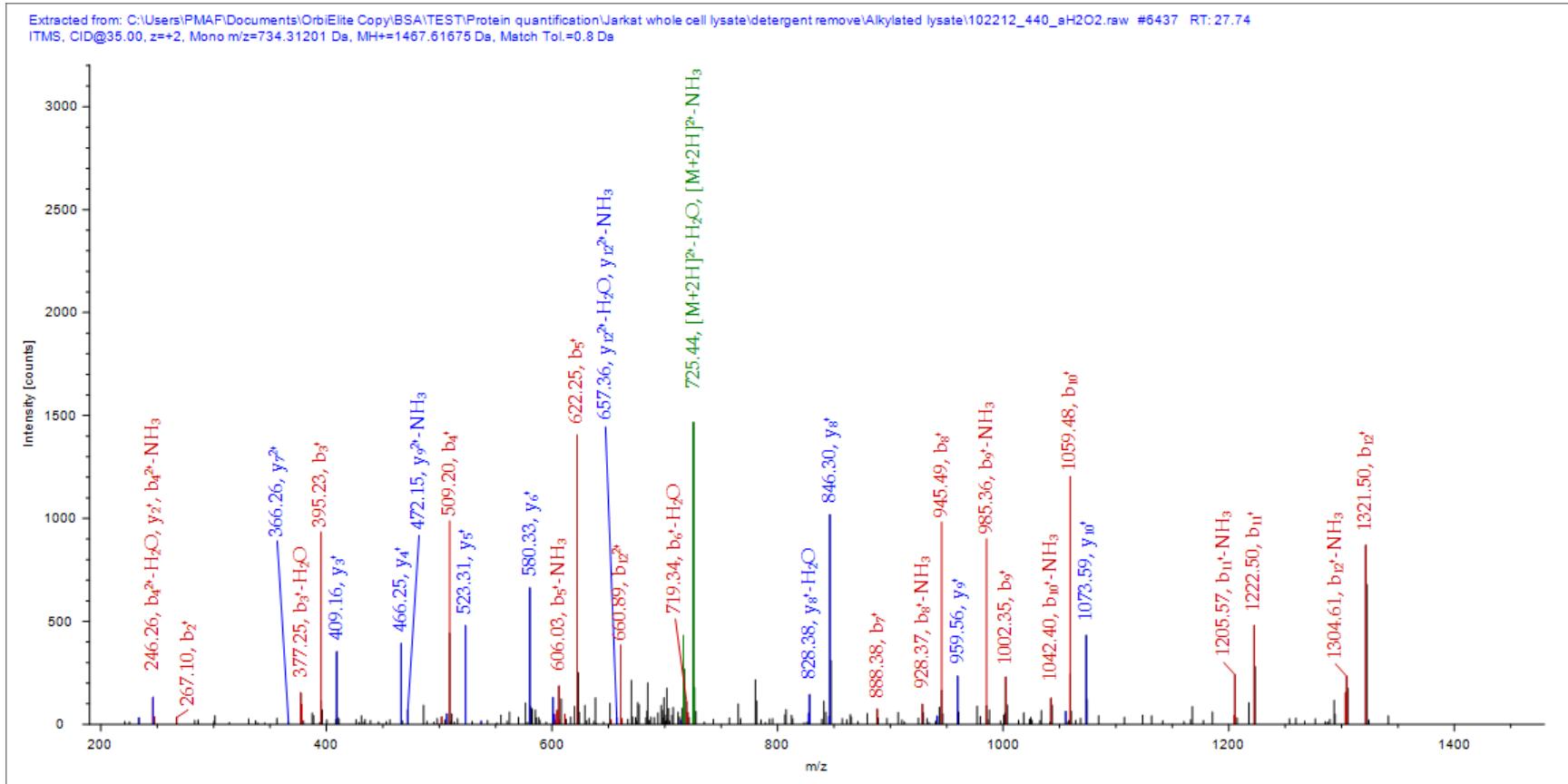


HEQNIDCGGGYVK_C7_SO2H

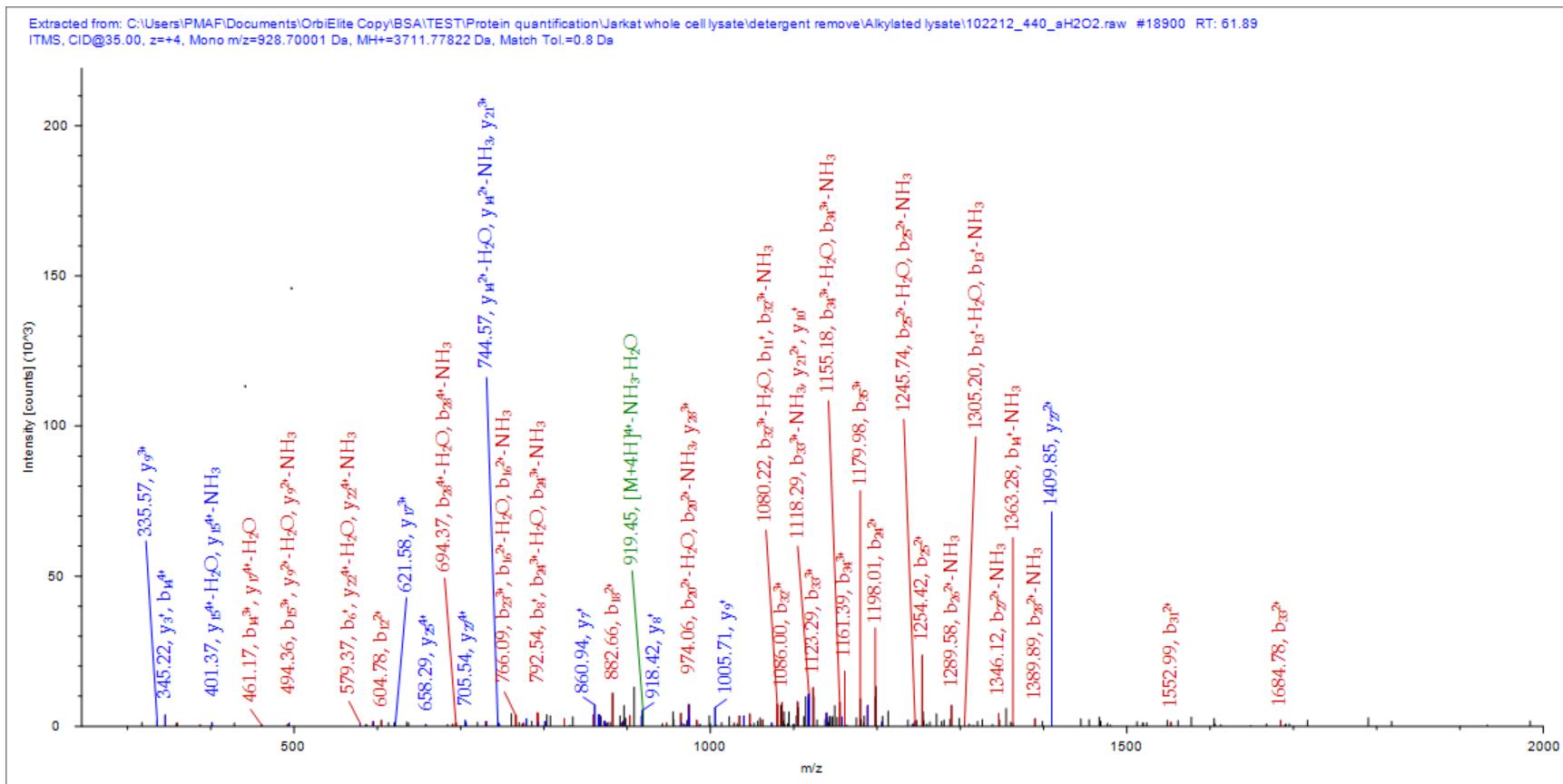
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ITMS, CID@35.00, z=+2, Mono m/z=726.31567 Da, MH+=1451.62407 Da, Match Tol.=0.8 Da



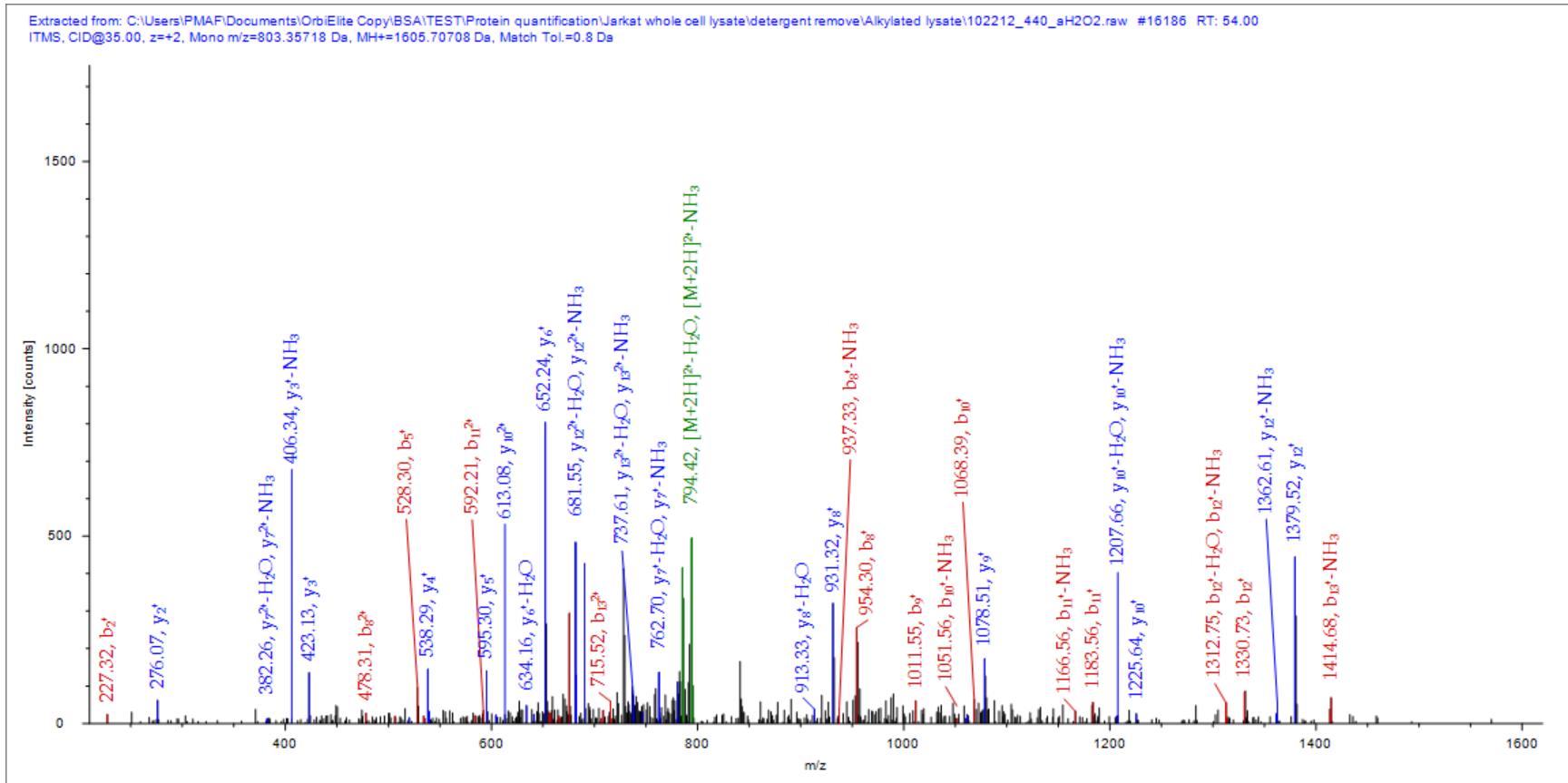
HEQNIDCGGGYVK_C7_SO3H



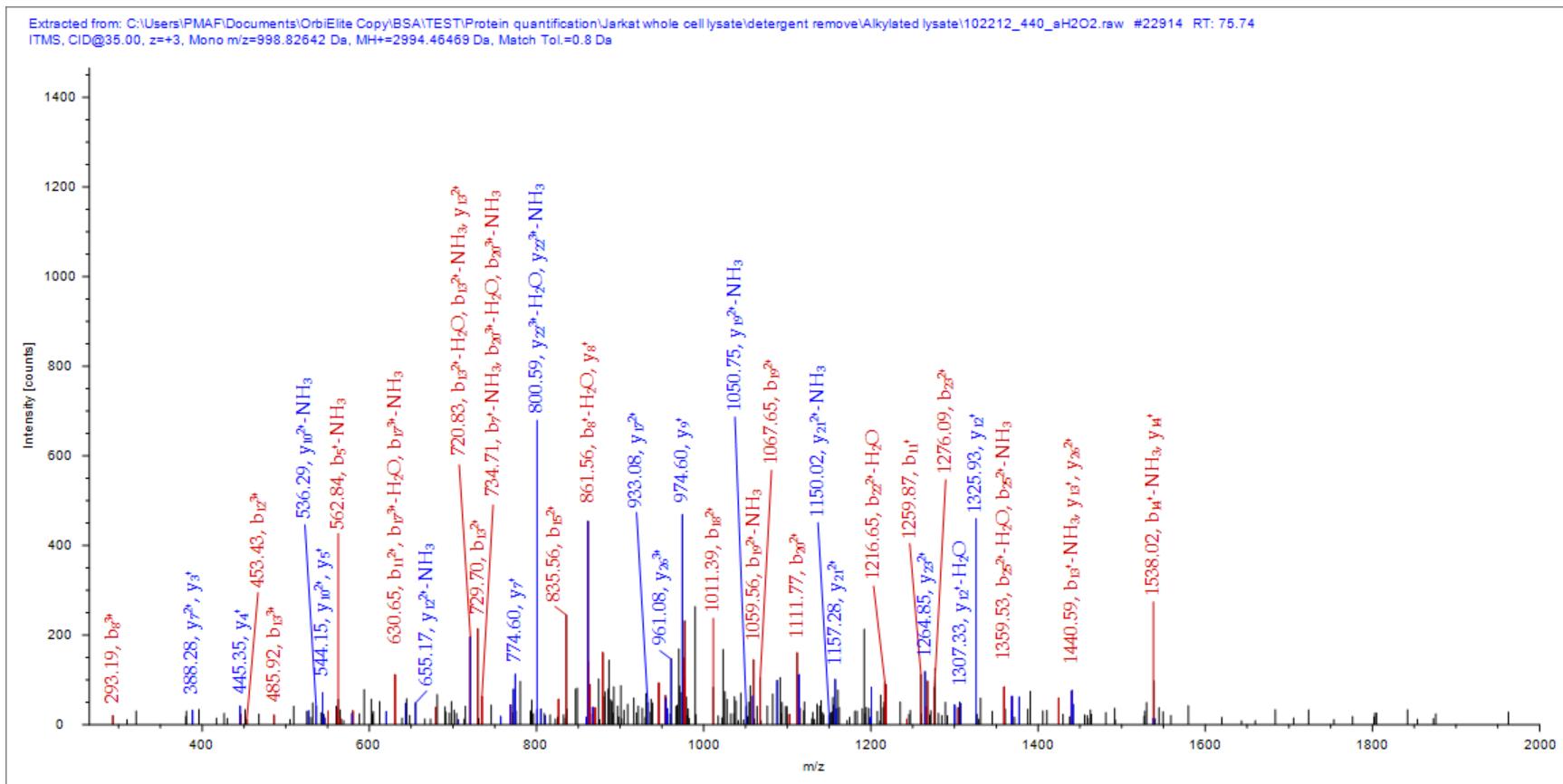
HVGDLGNVTADKDGVADVSIEDSVISLSG DHCIIGR_C32_SO3H



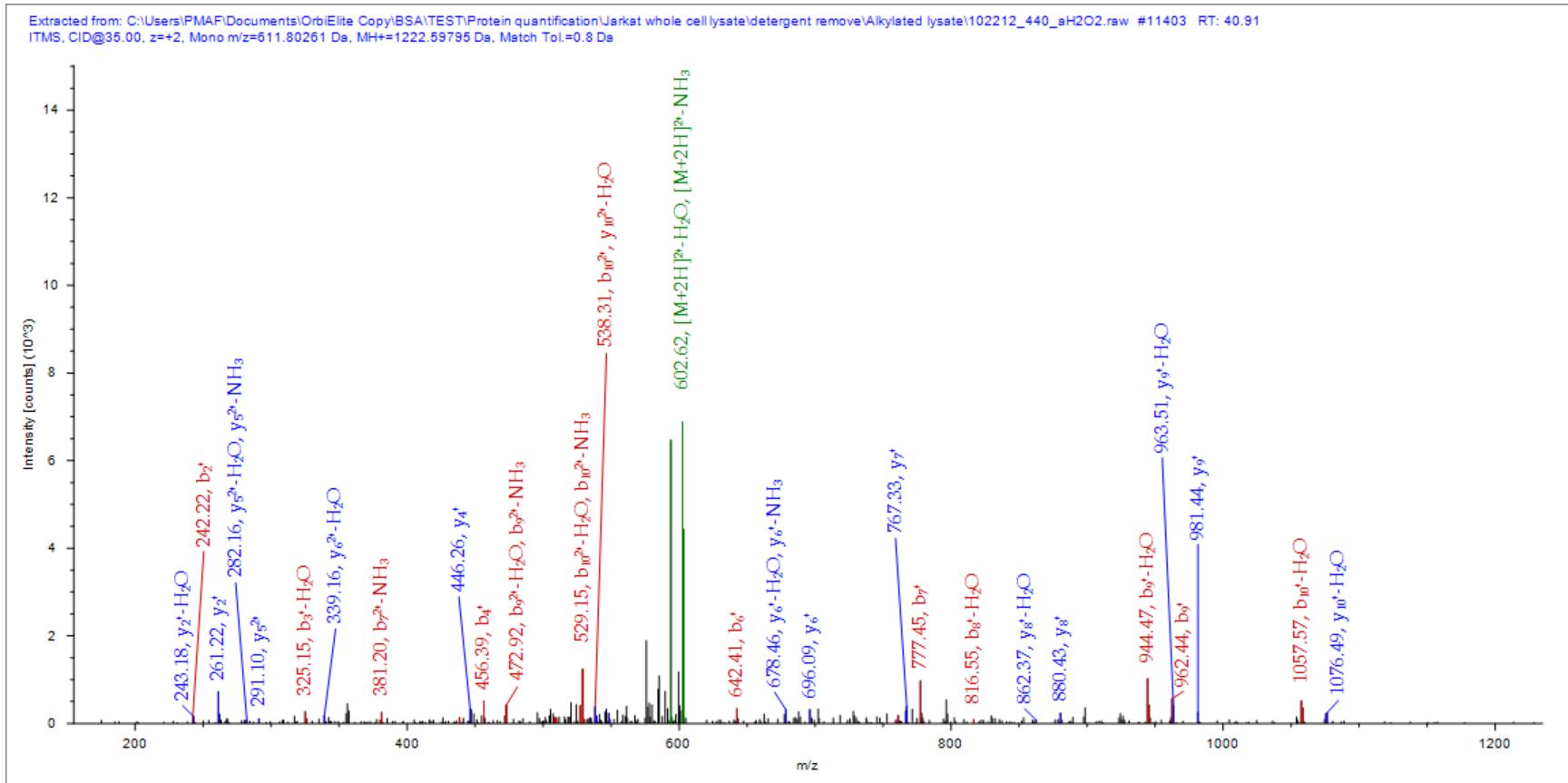
IIPGFMCQGGDFTR_C7_SO3H



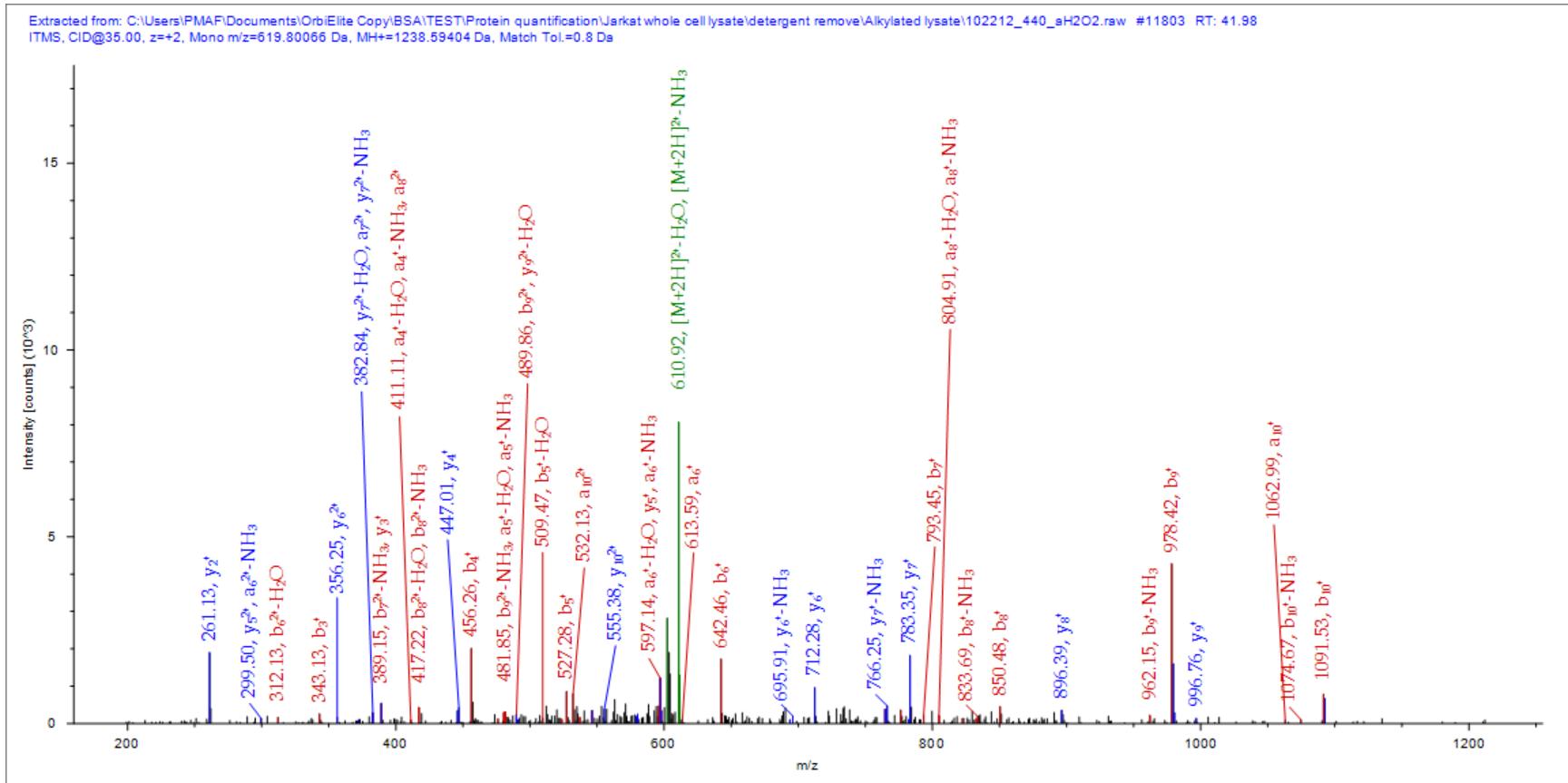
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KITIADCGQLE_C7_SO2H

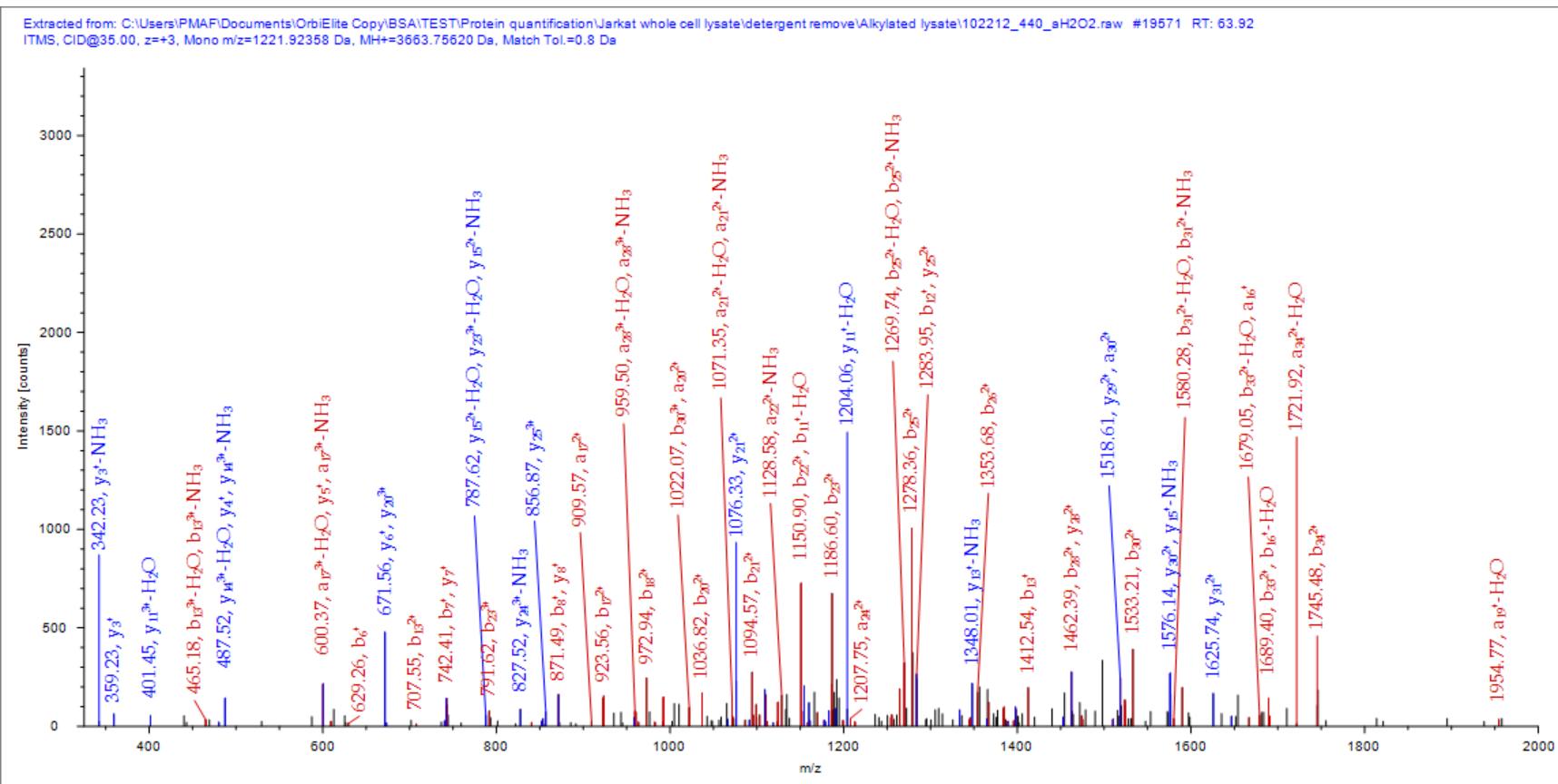


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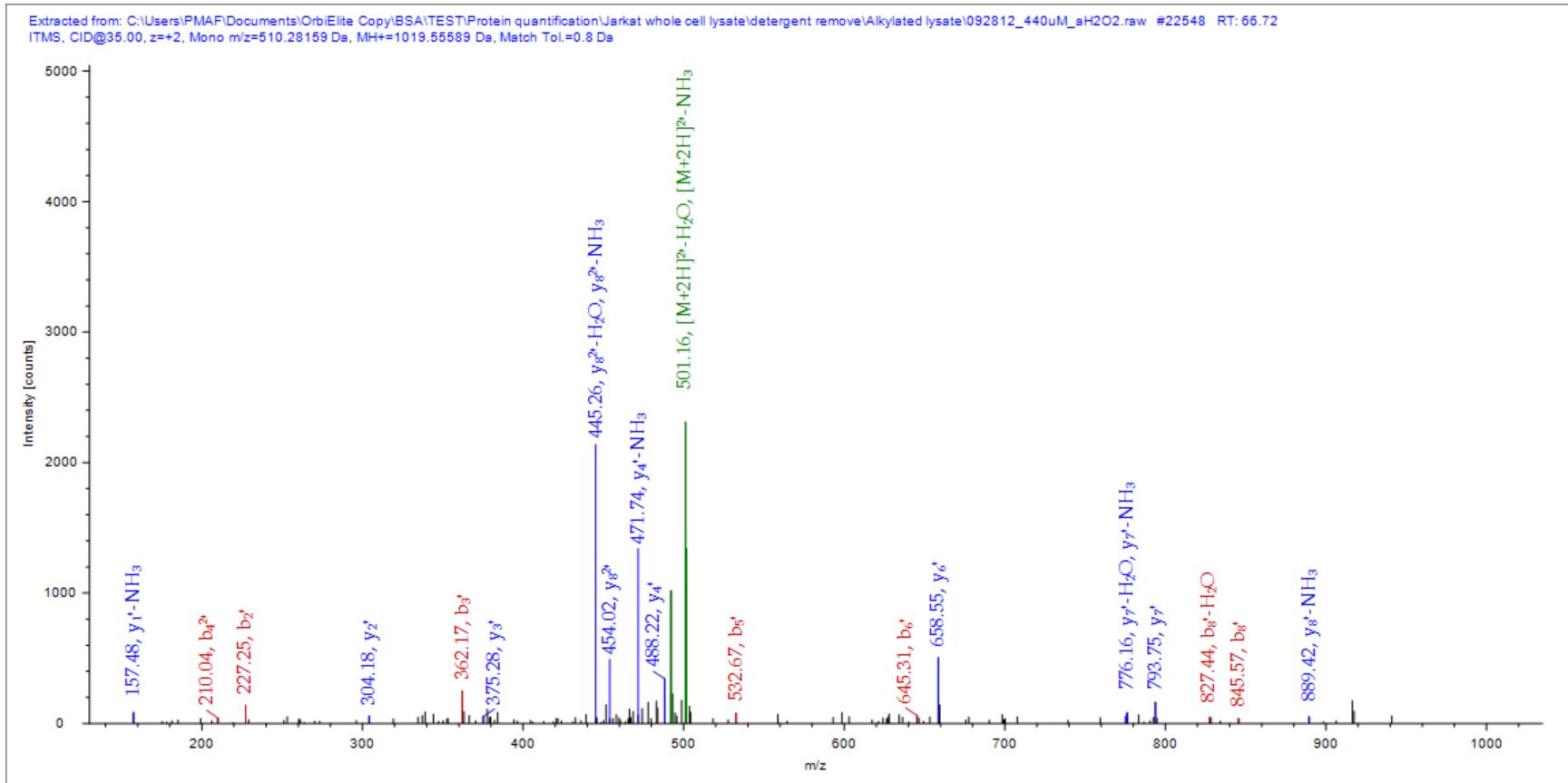


LADDVDLEQVANETHGHVGADLAALCSE

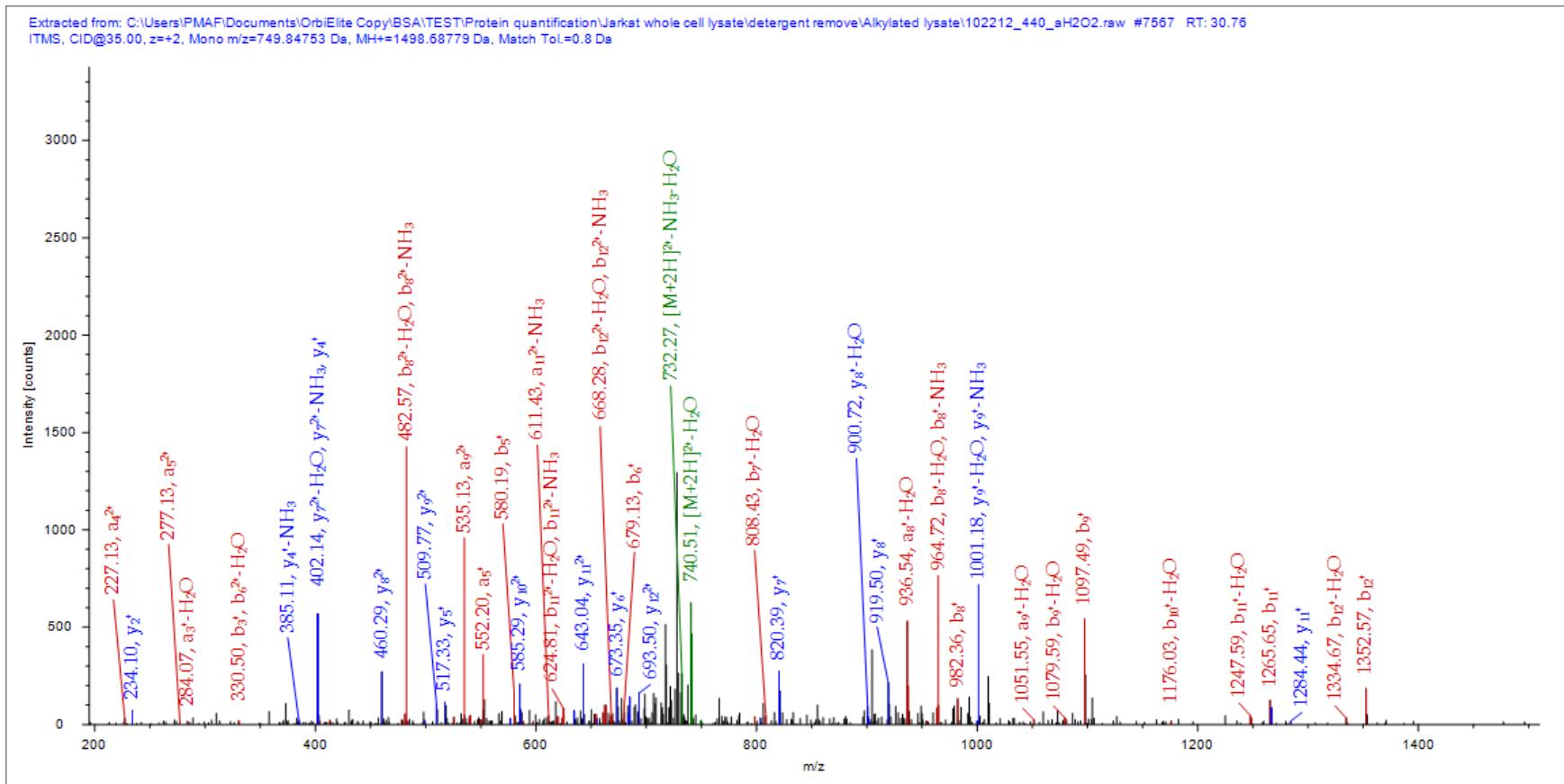
AALQAIR_C26_SO3H



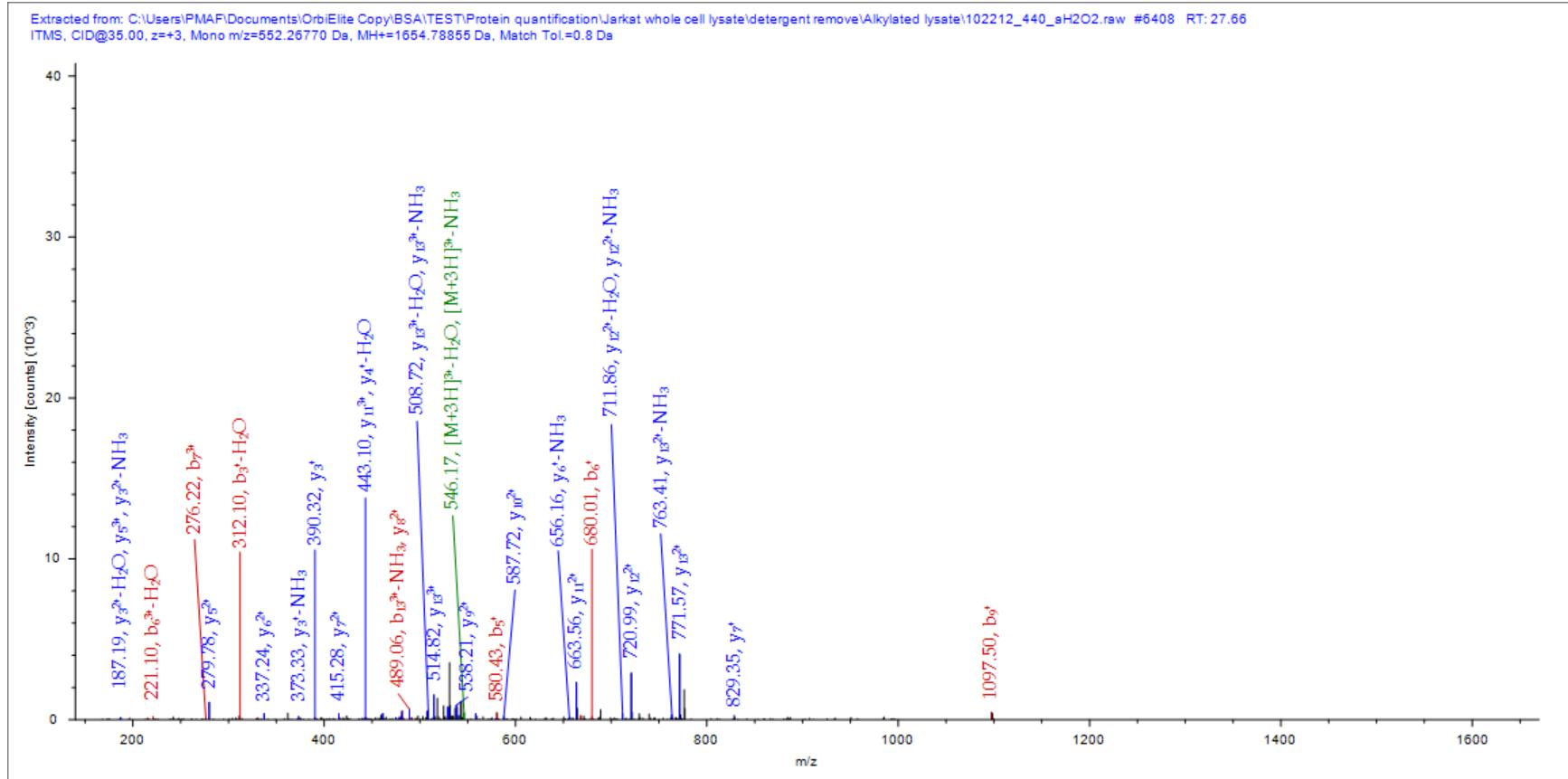
LLCGLLAER_C3_SO2H



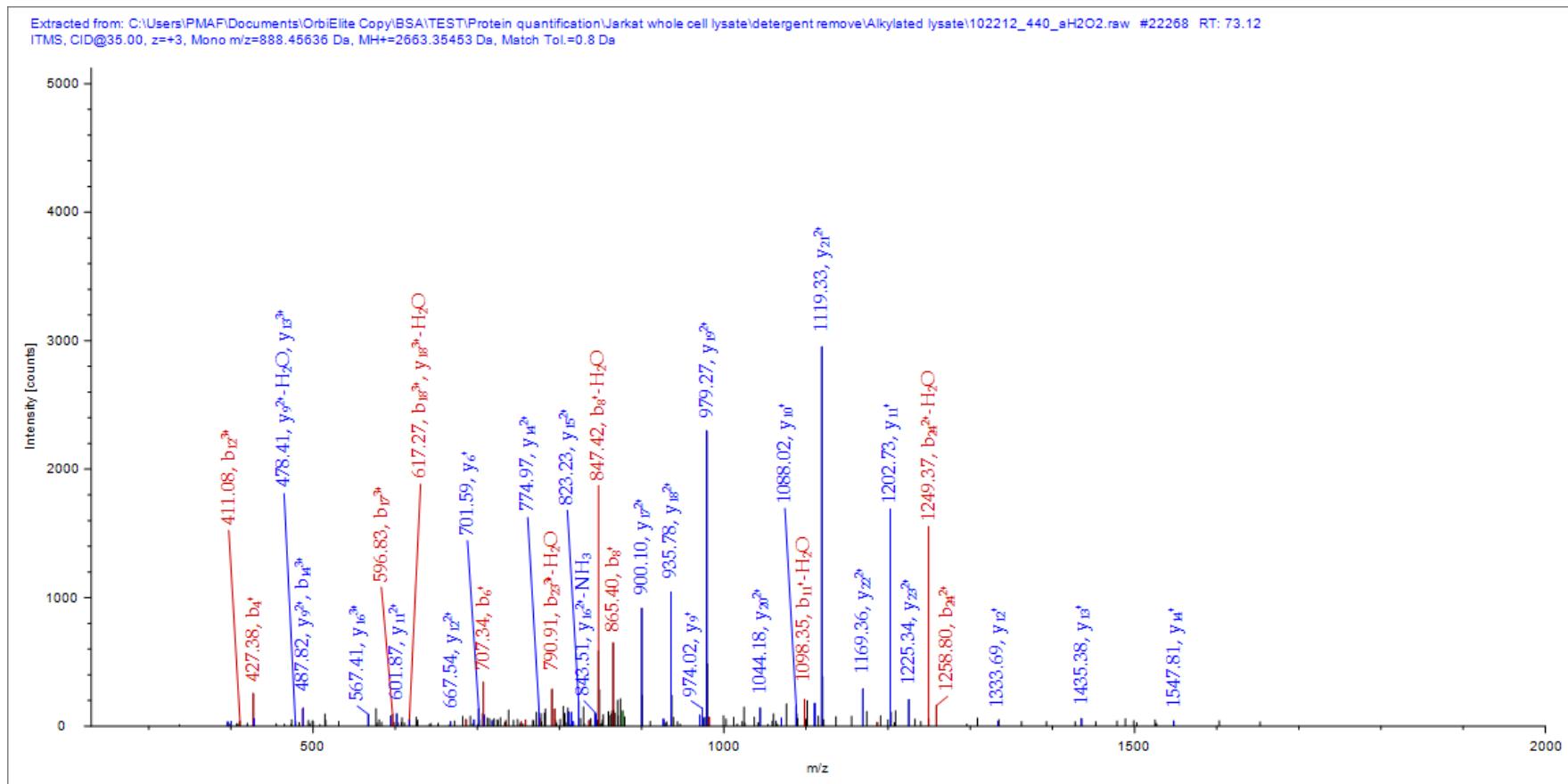
LTDCVVMRDPASK_C4_SO3H



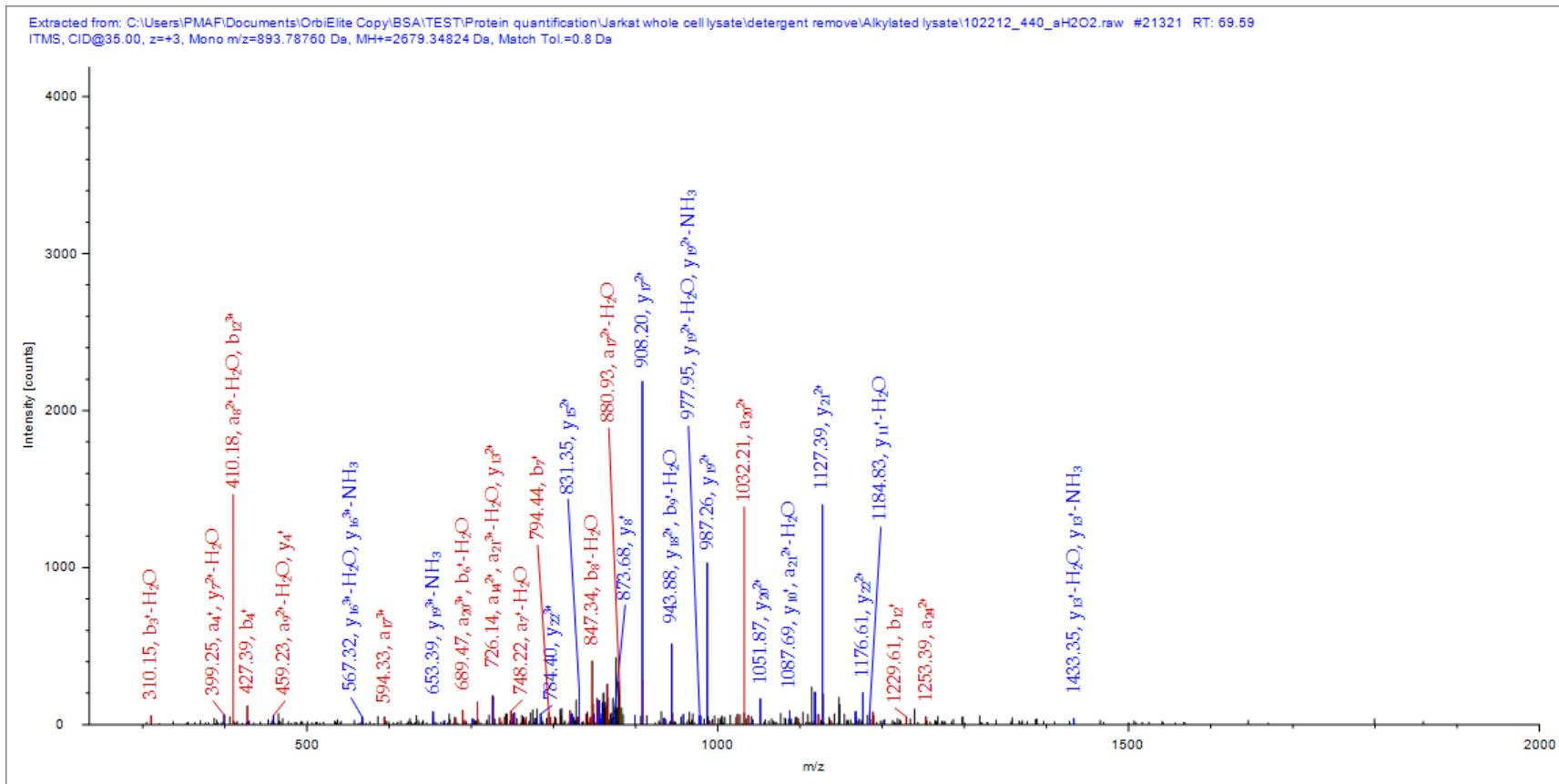
LTDCVVMRDPASKR**_C4_SO3H**



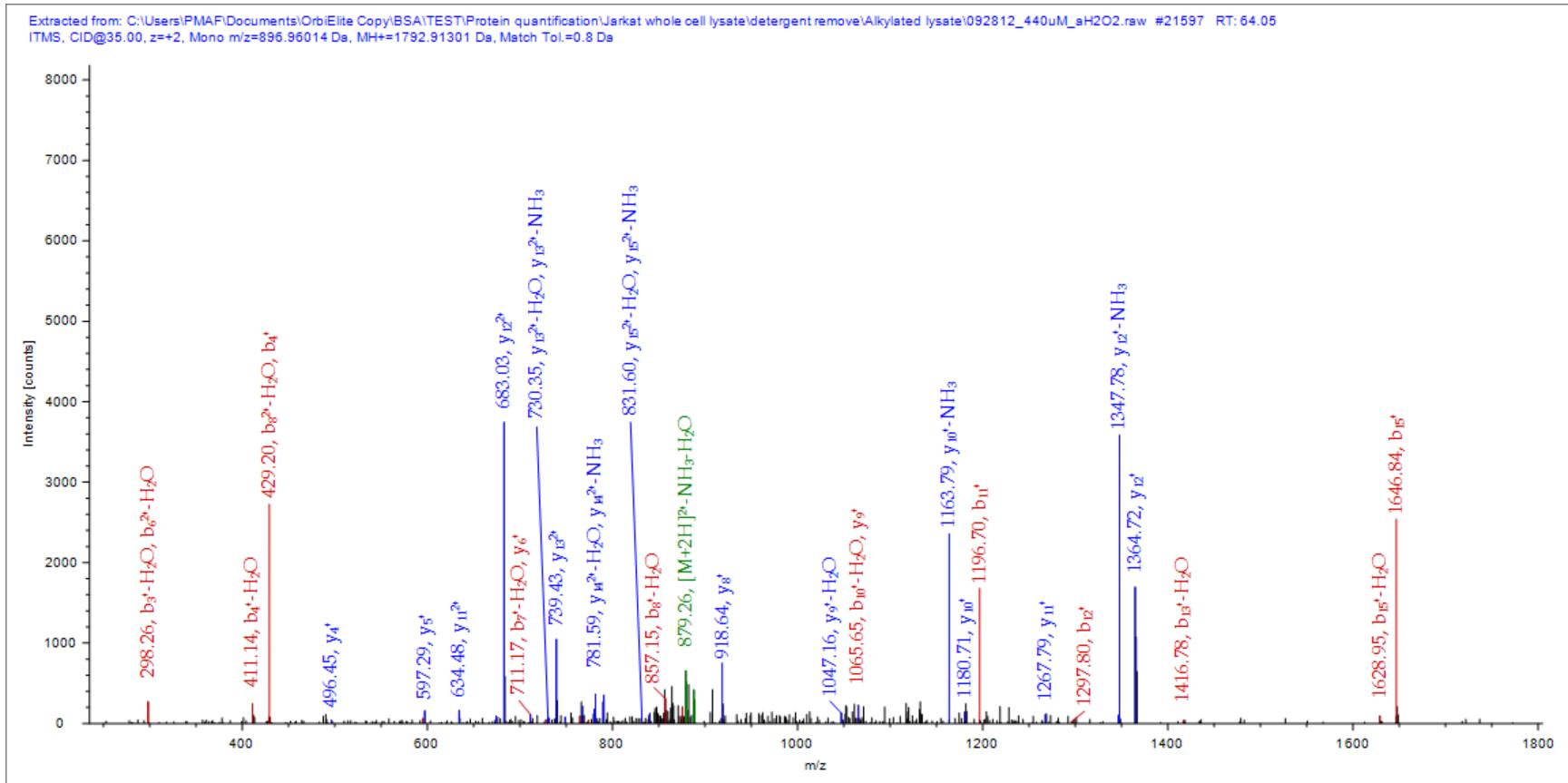
LTVCESAPGPITMDLTGDLEALKK
C5SO3H



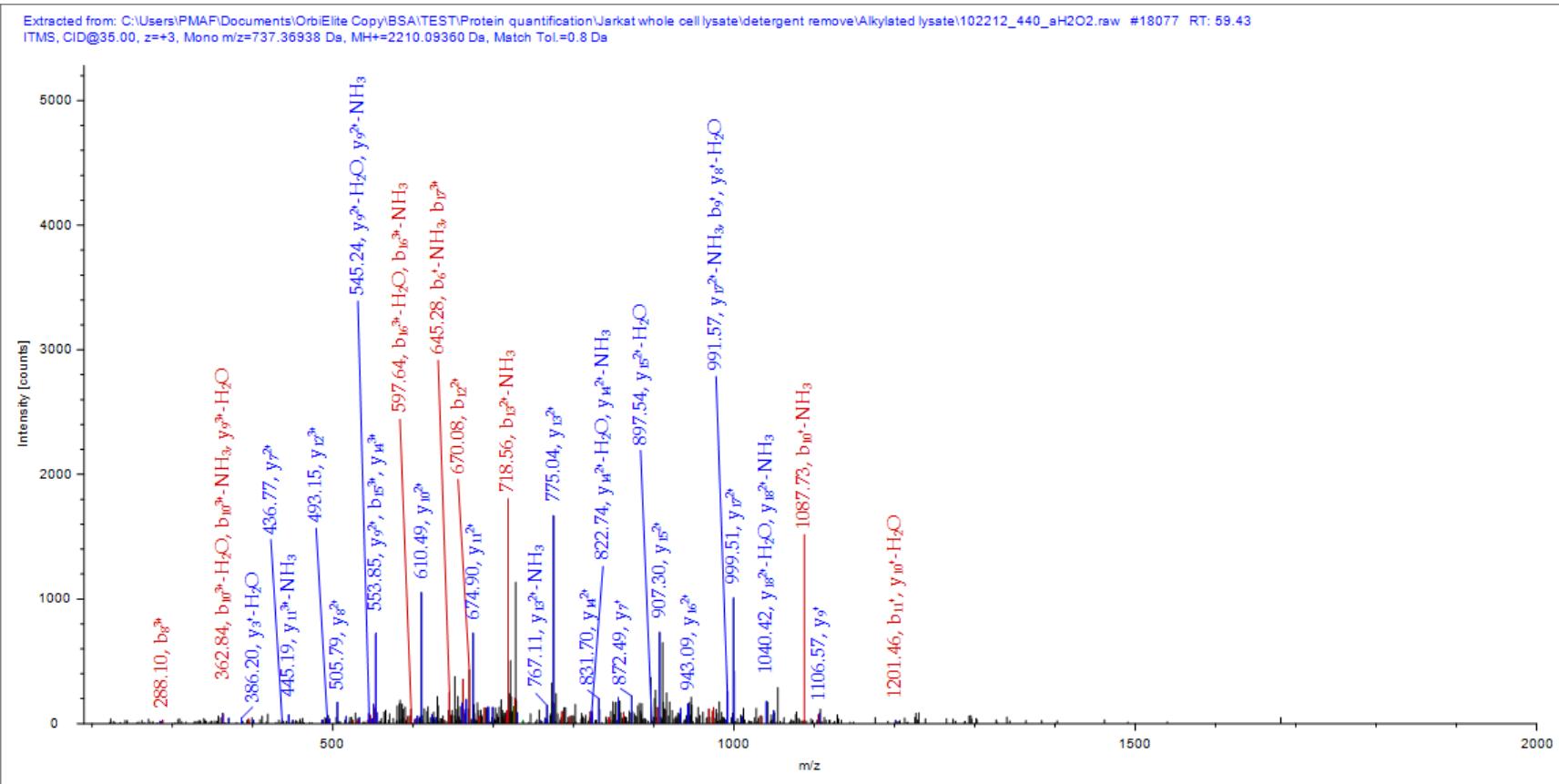
LTLVCESAPGPITMDLTGDLEALKK _C5_SO3H_Mox



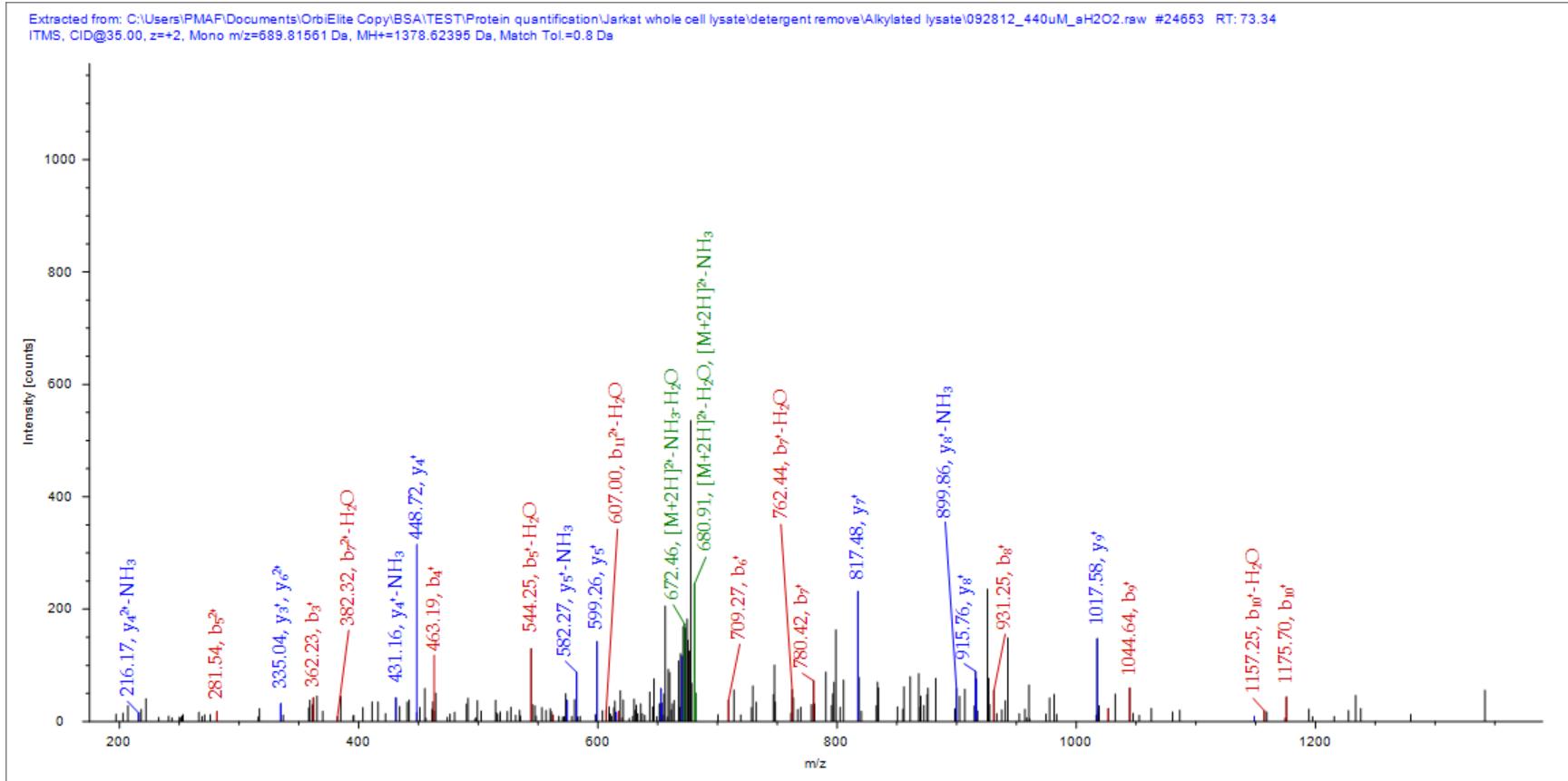
LTTLPSDFCGLTHLVK_C9_SO3H



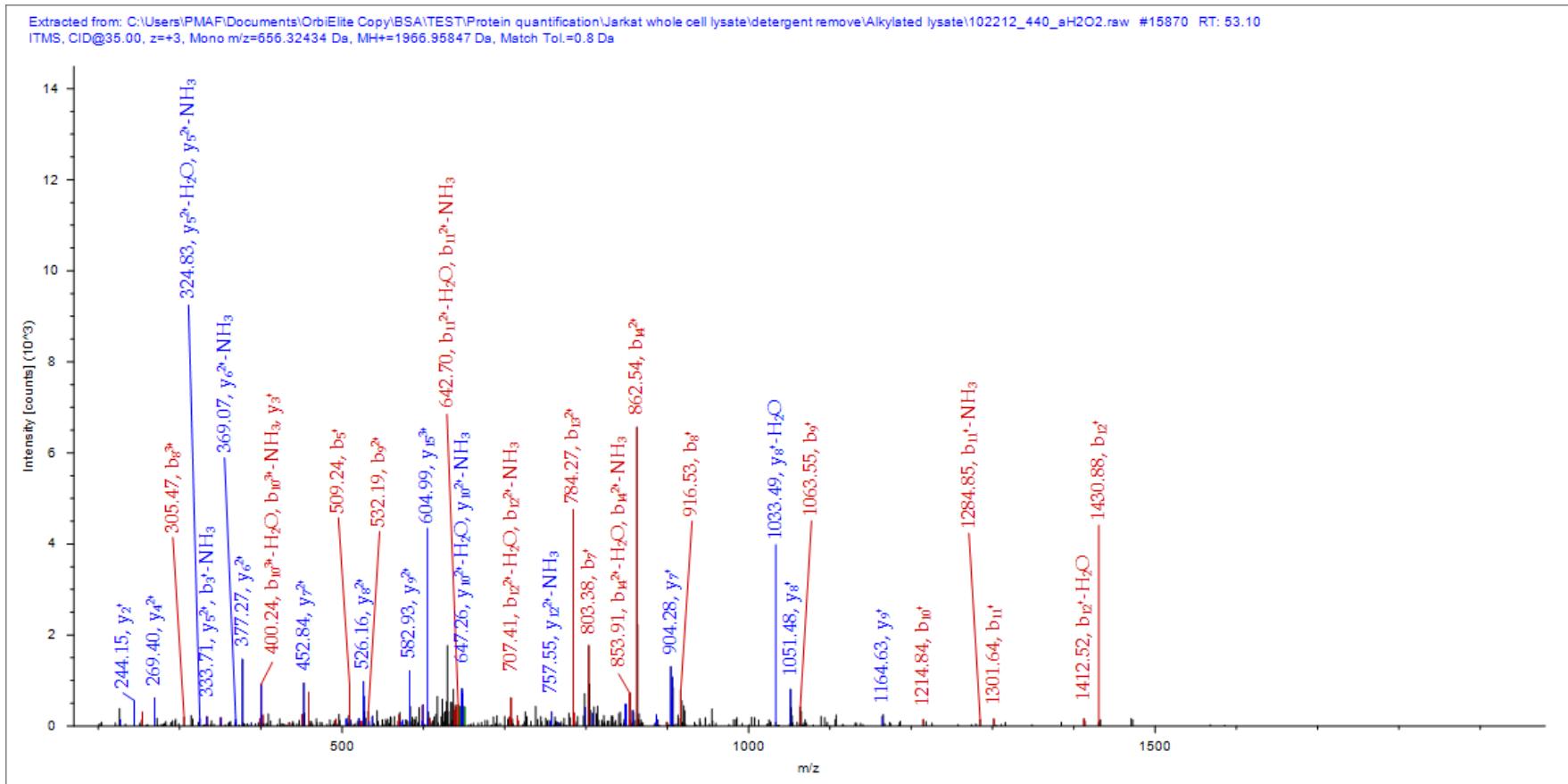
LVNACLAELPHIHAFEQK_C5_SO3H



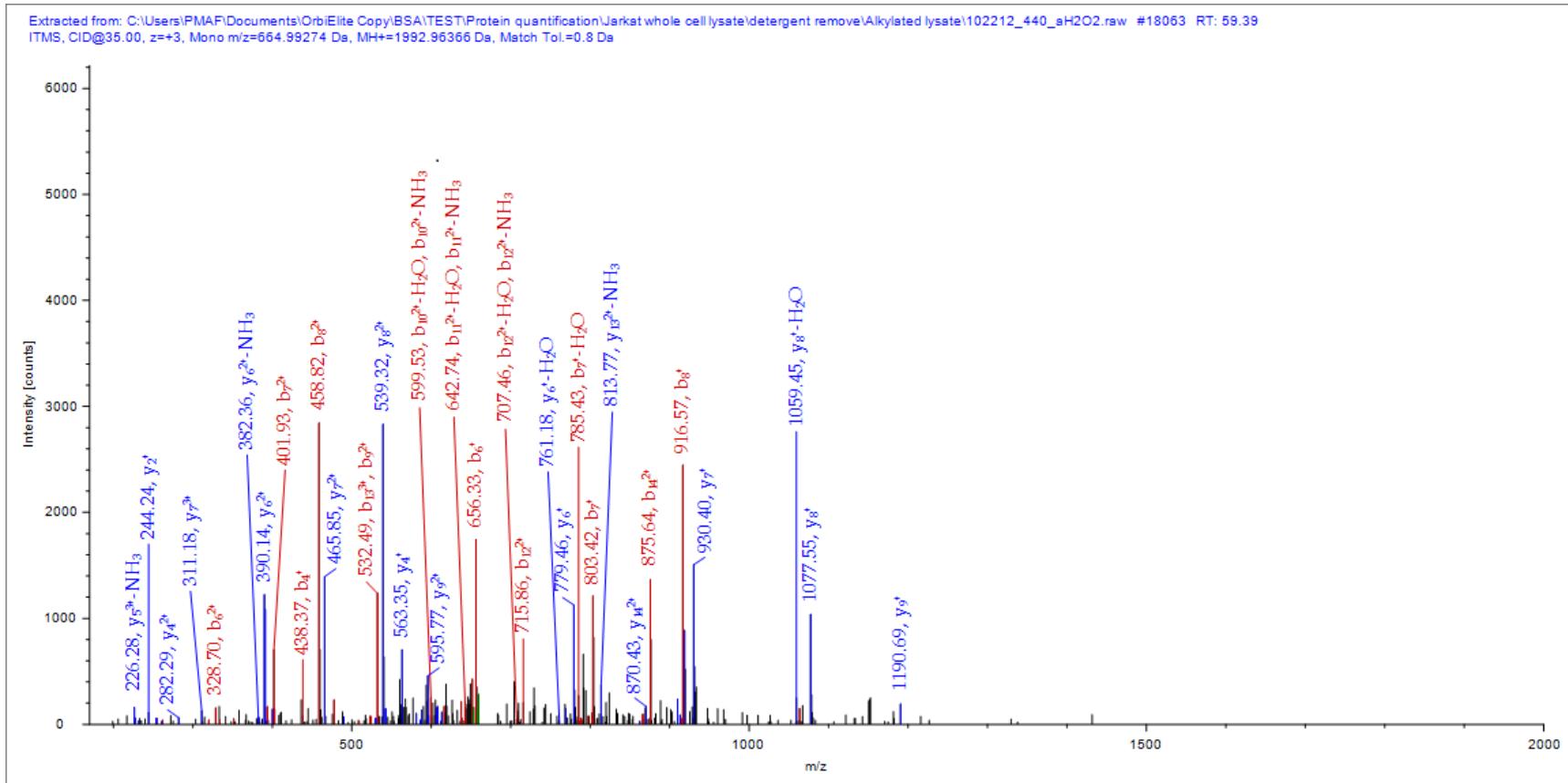
MVMTVFACLMGK_C8_SO3H



RPPSAFFLFCSEHRPK_C10_SO3H

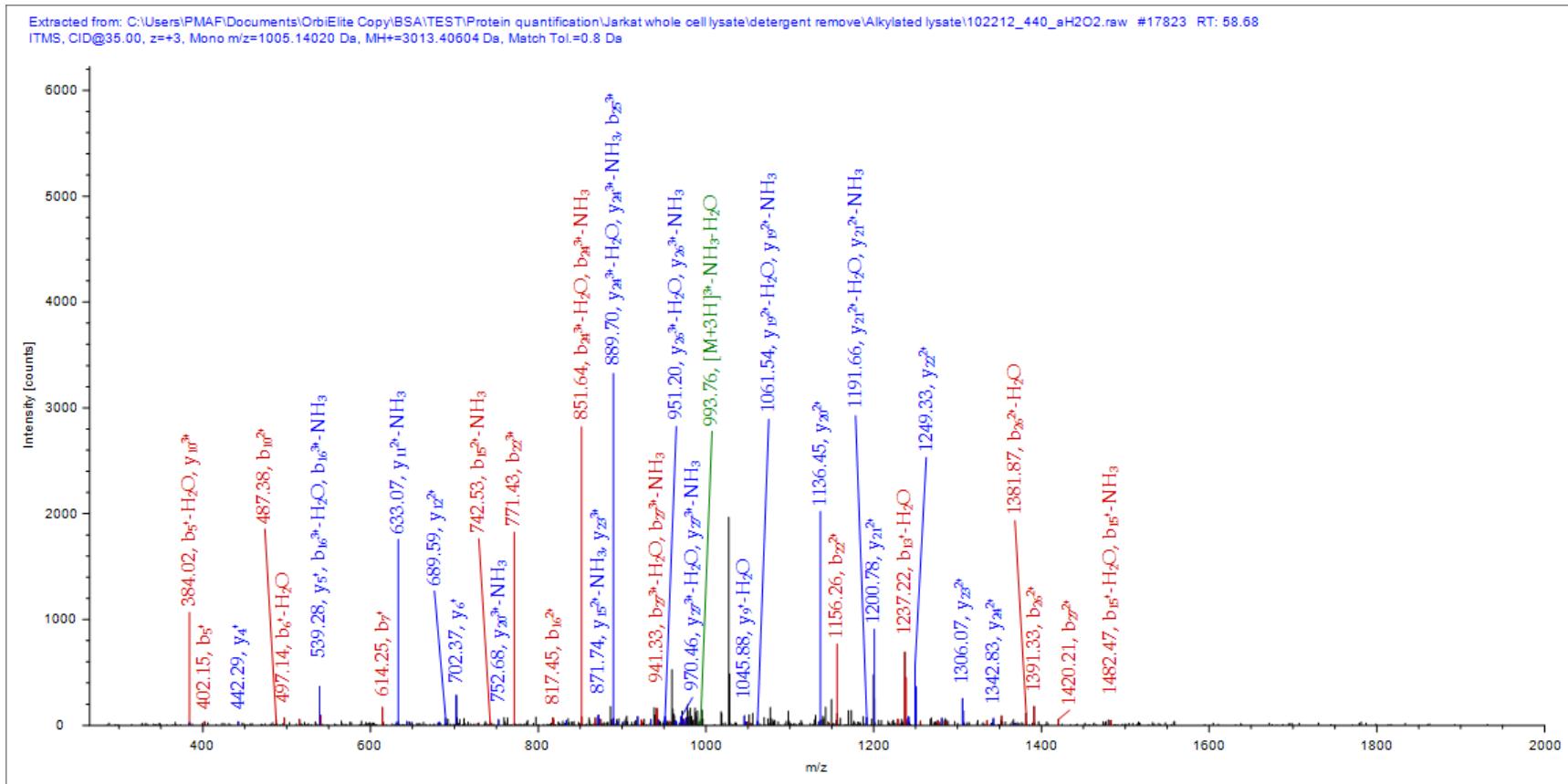


RPPSAFFLFCSEYRPK_C10_SO3H

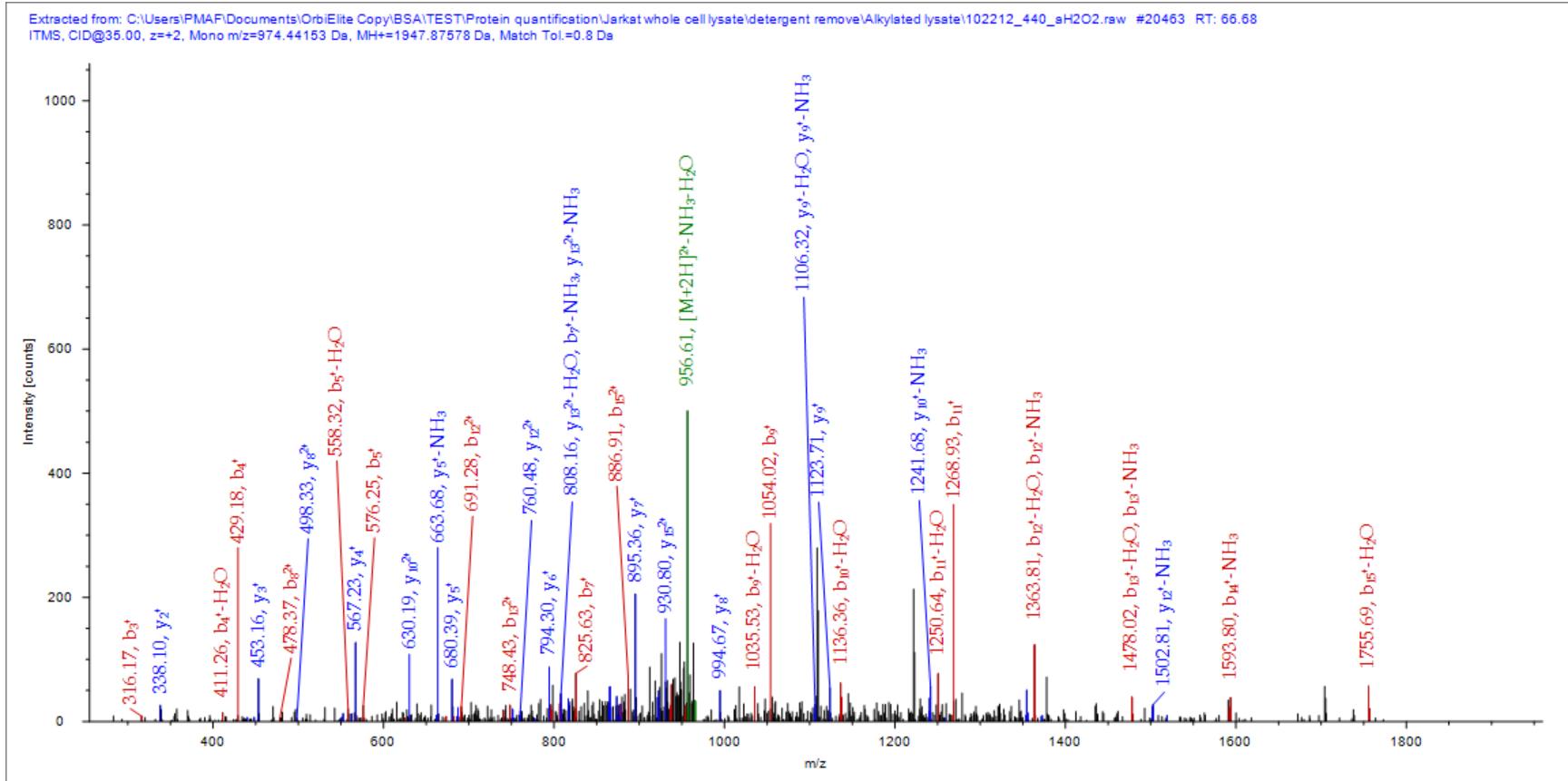


SGDAAIVEMVPGKPMCVESFSQYPPLGR_

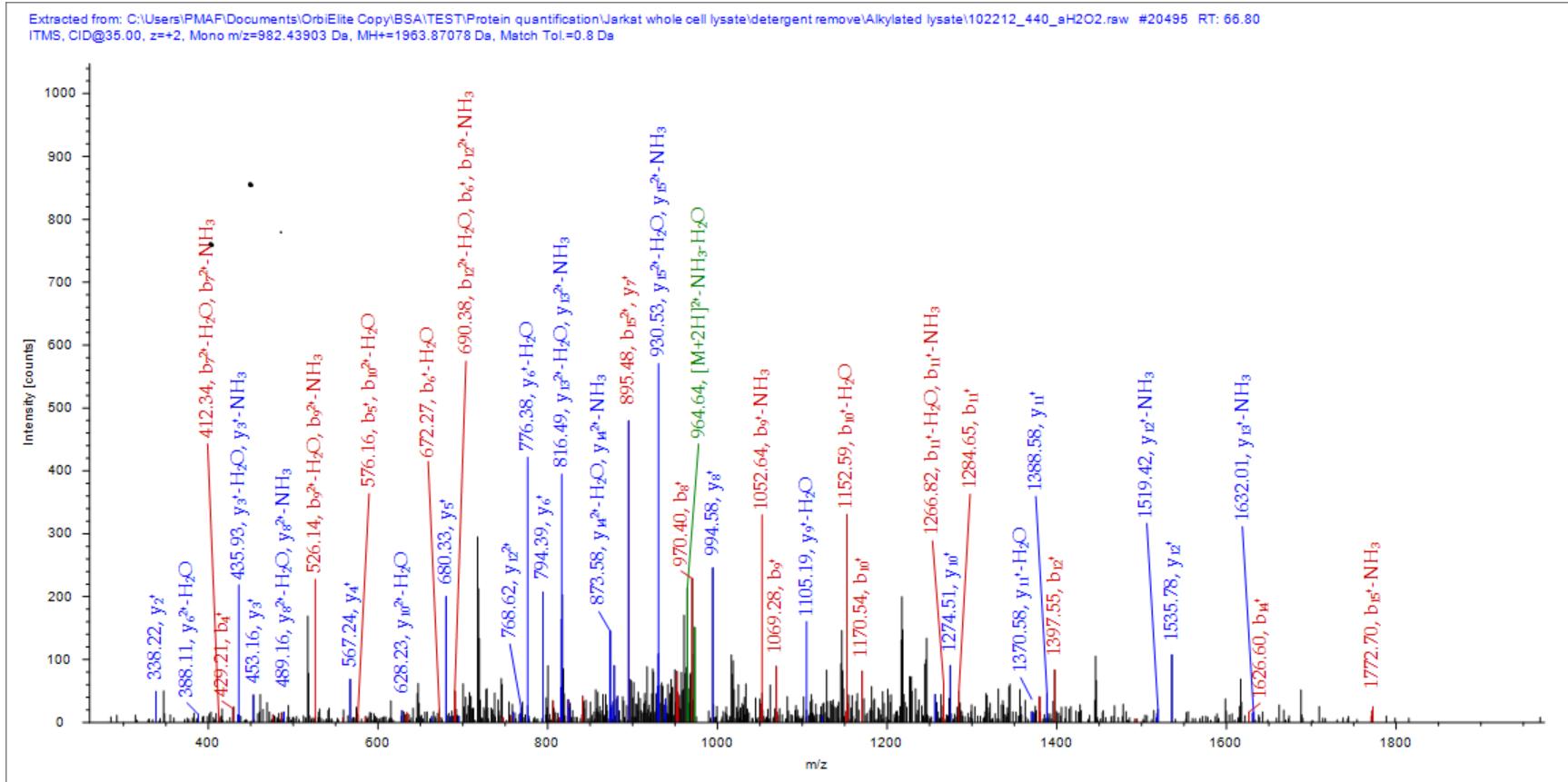
C16_SO3H



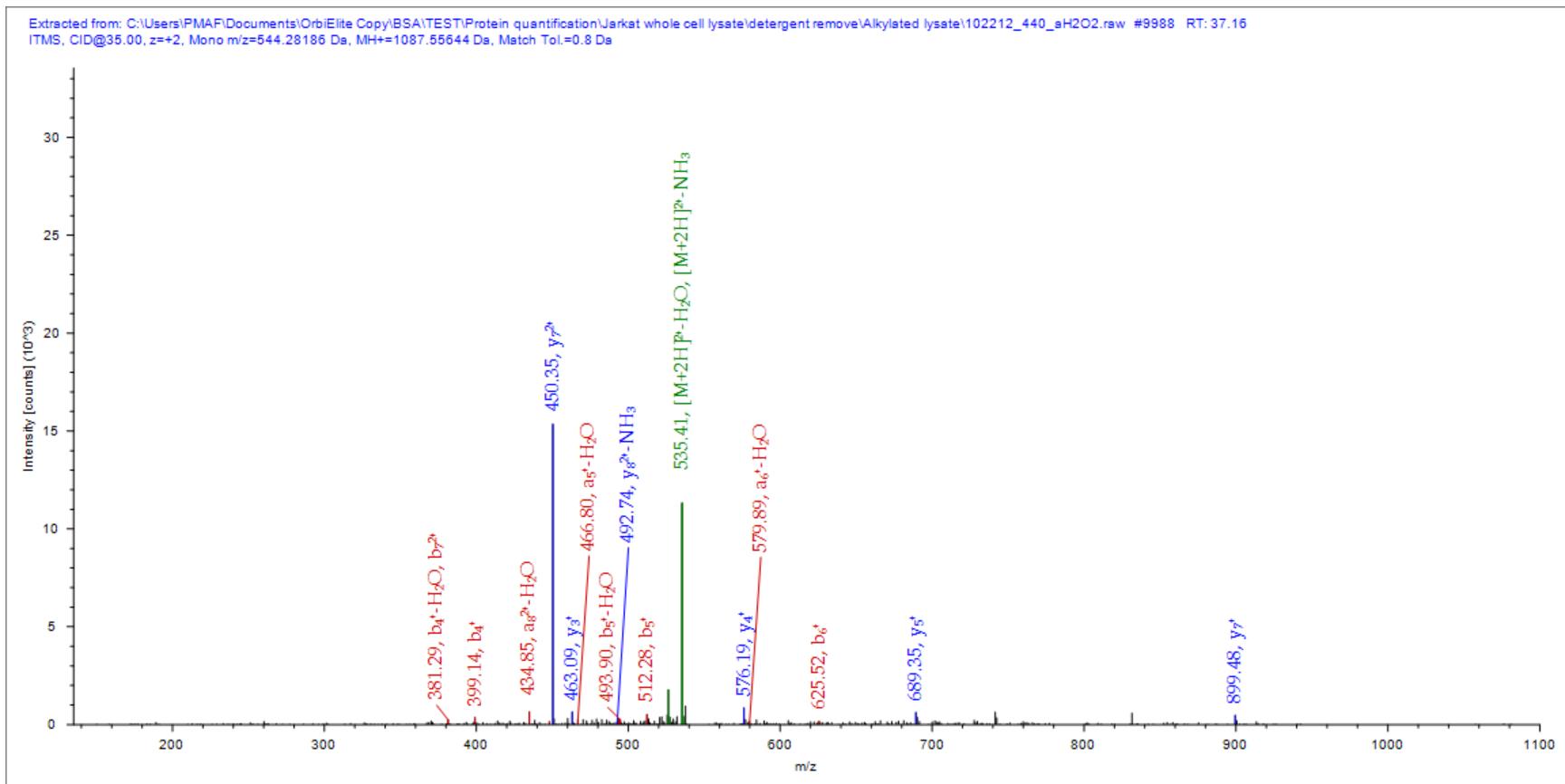
SLDLFNCEVTNLNDYR_C7_SO2H



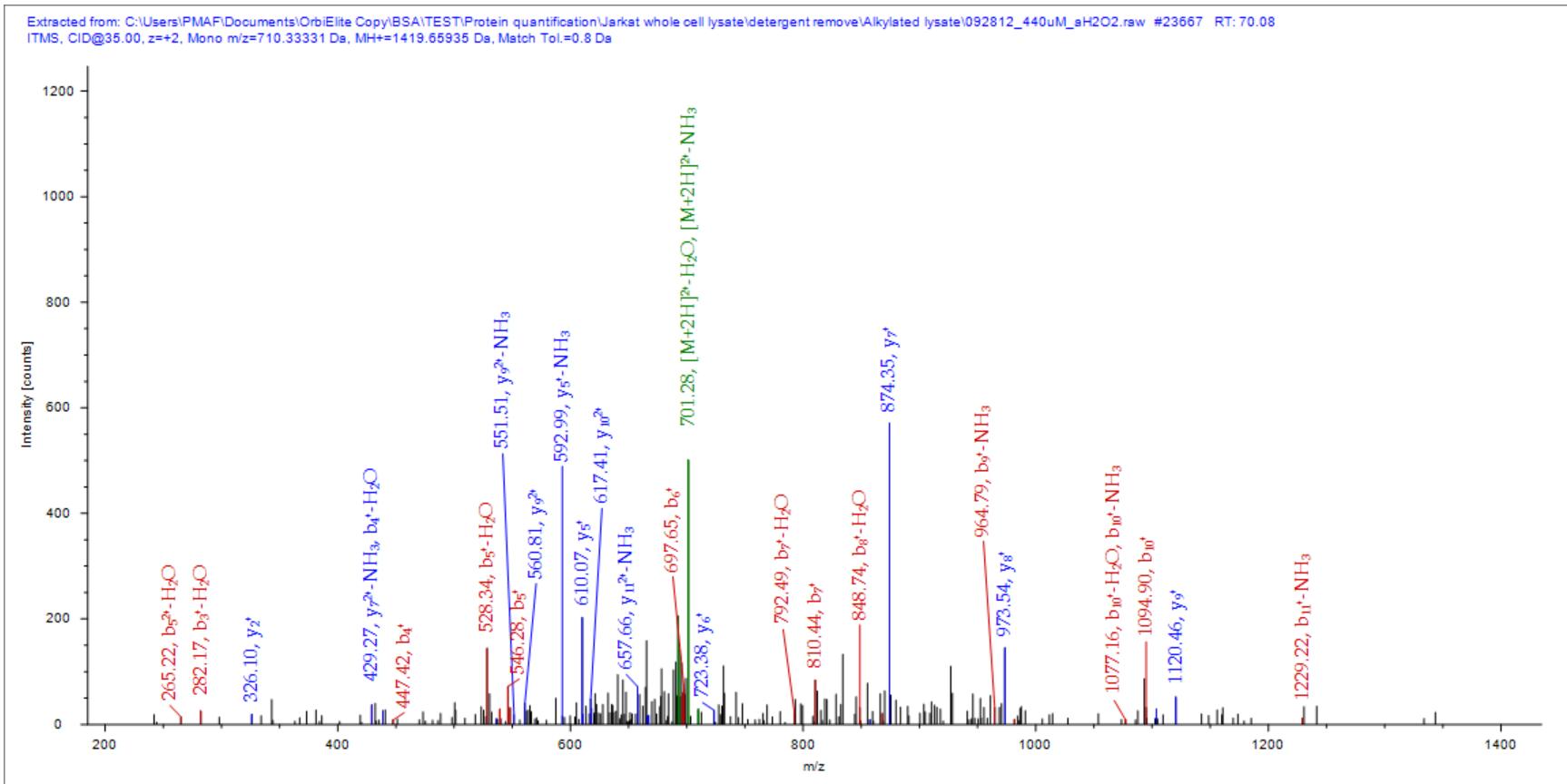
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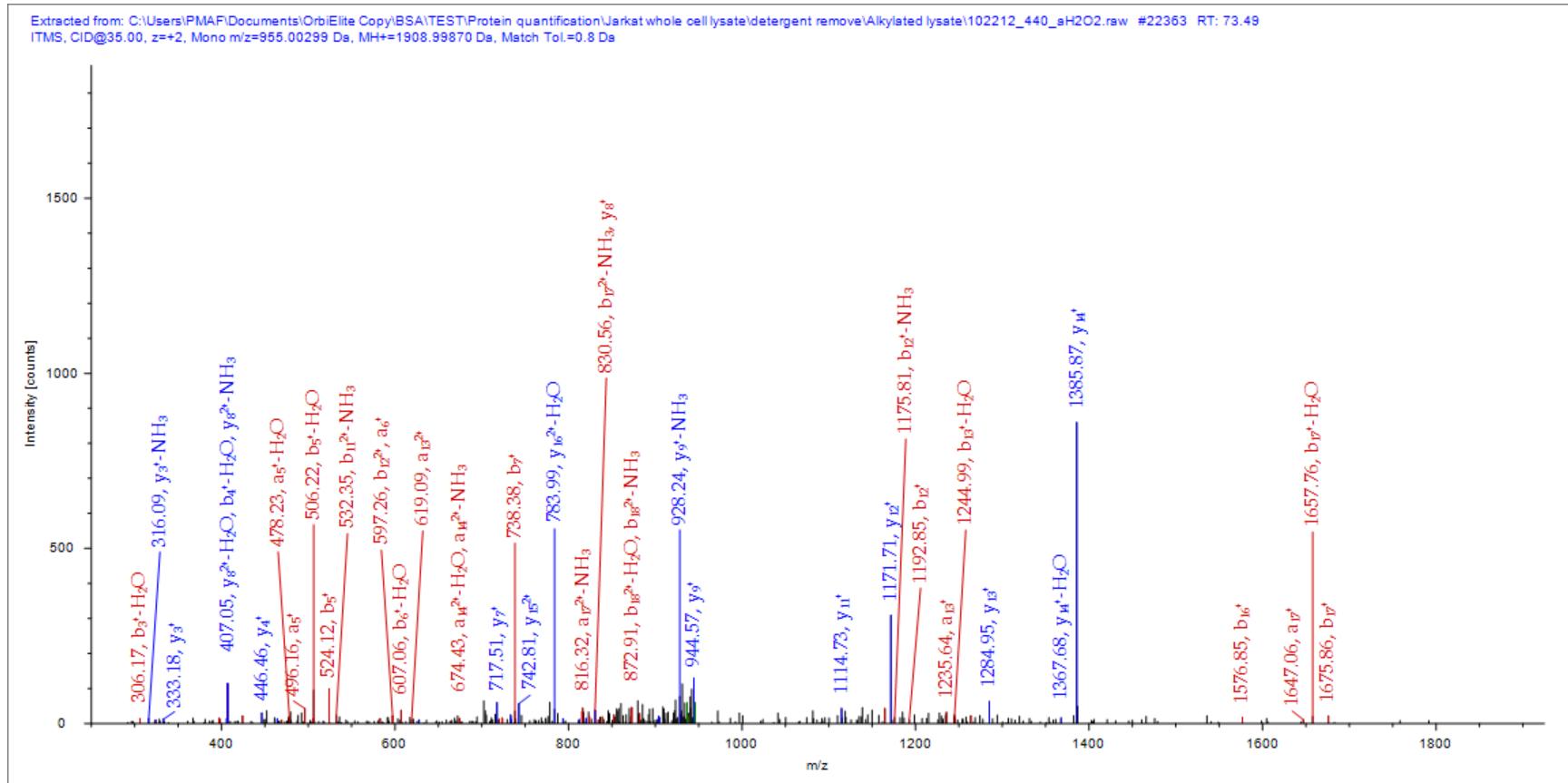
STPLLIHCR_C8_SO3H



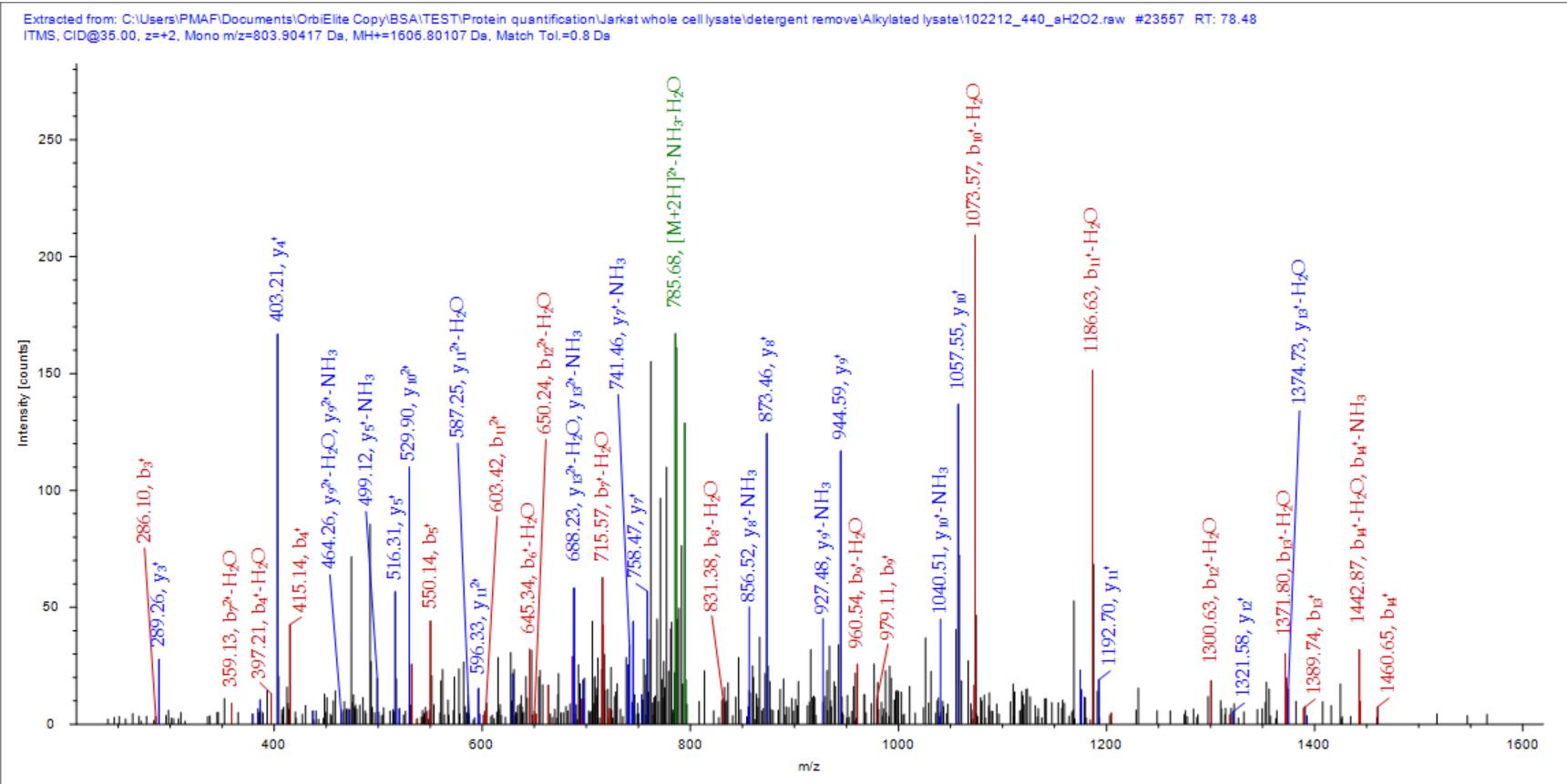
SVLFVCLGNICR_C6_SO3H_C11_SO3H



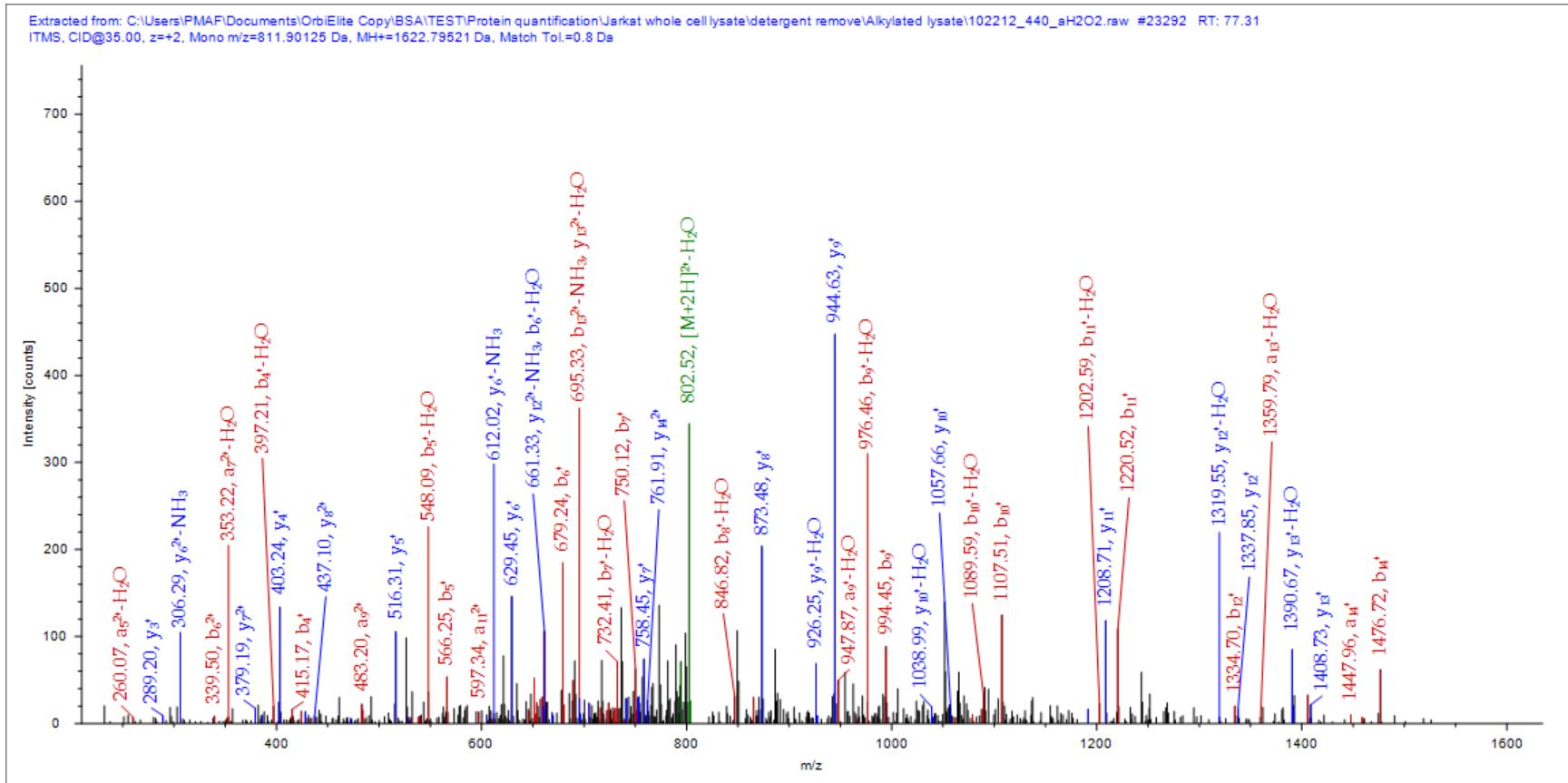
TCATVTIGGINIAEALVSK_C2_SO3H



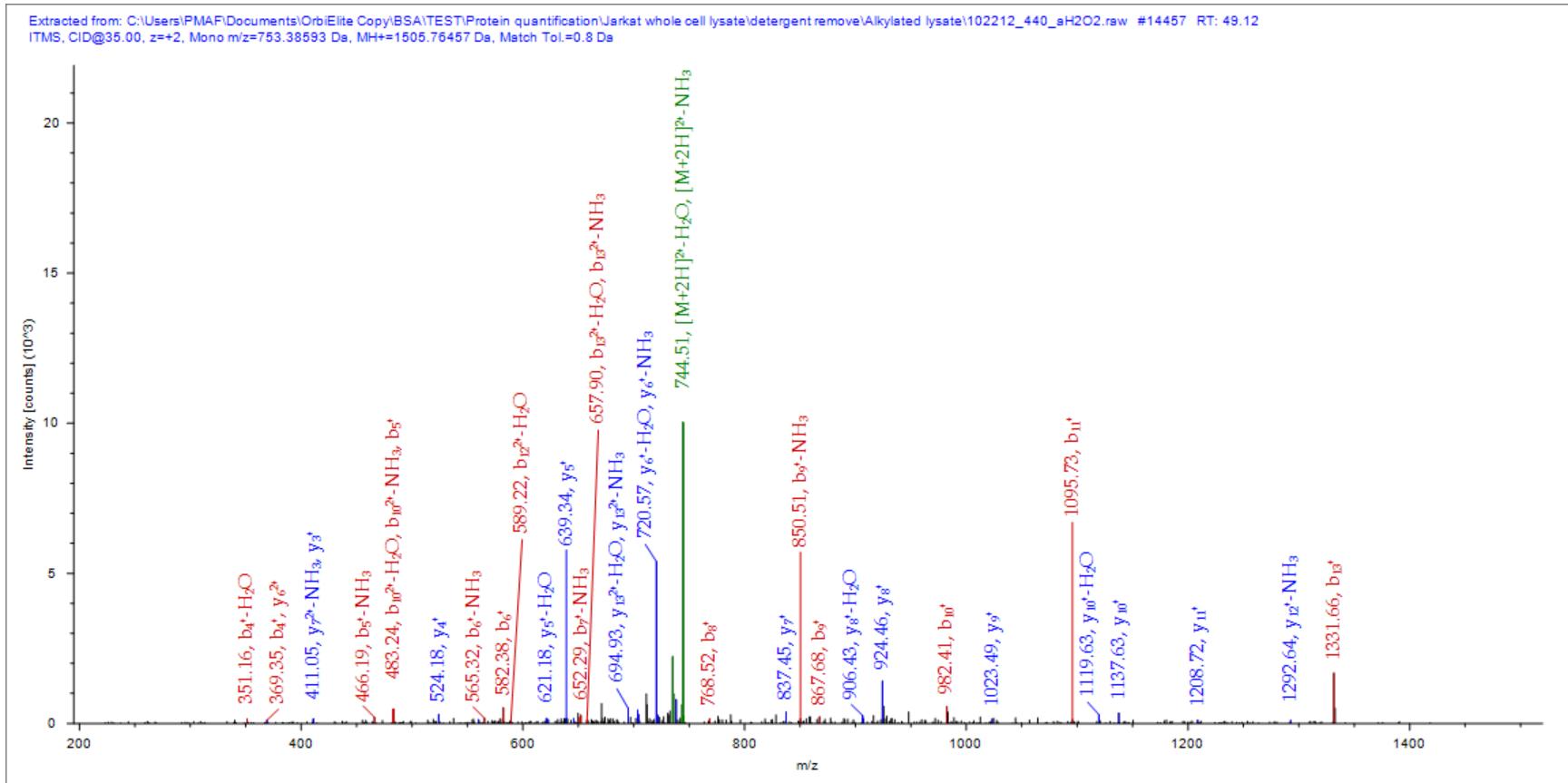
TIAECLADELINA AK_C5_SO2H



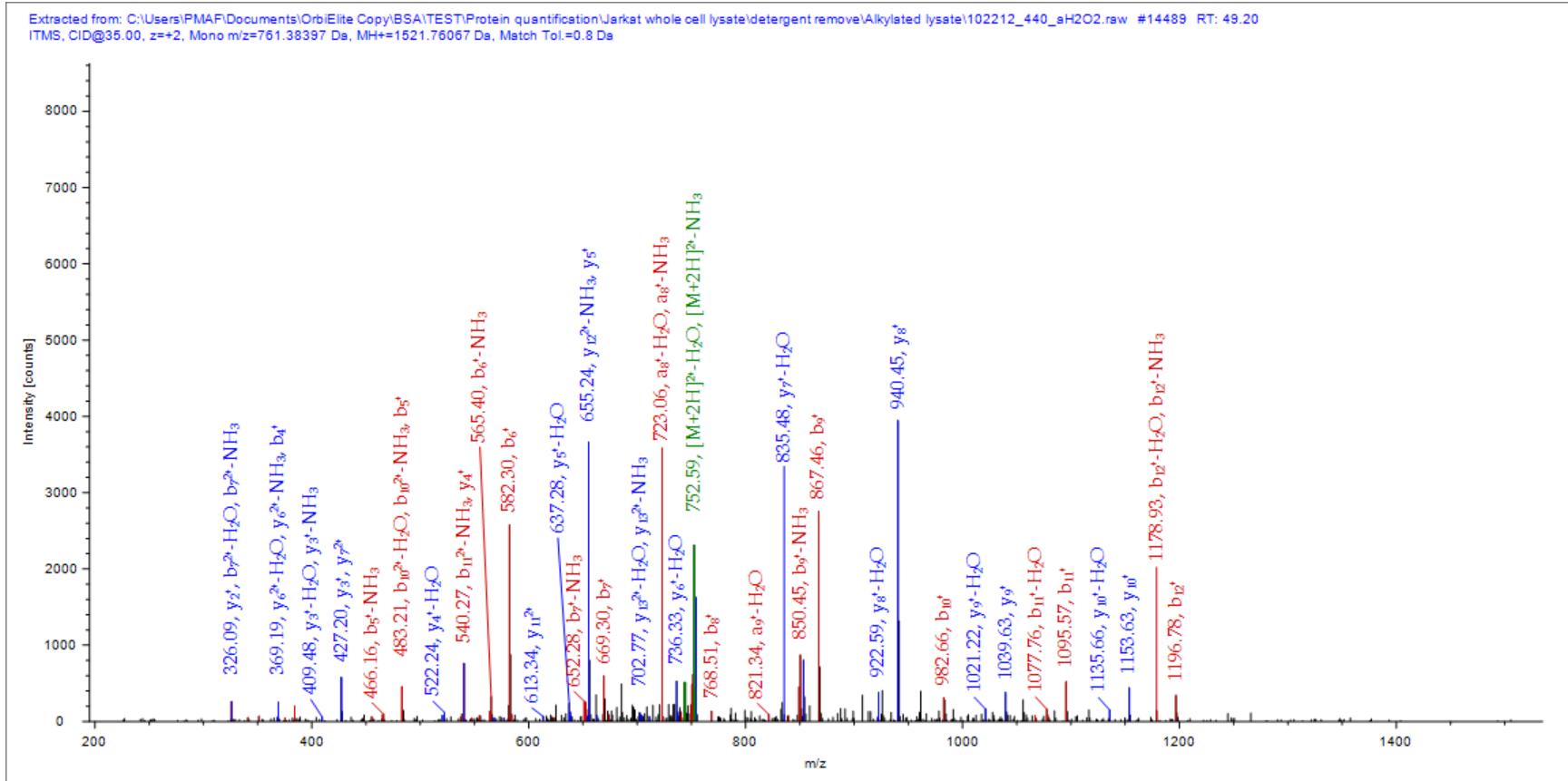
TIAECLADELINA AK_C5_SO3H



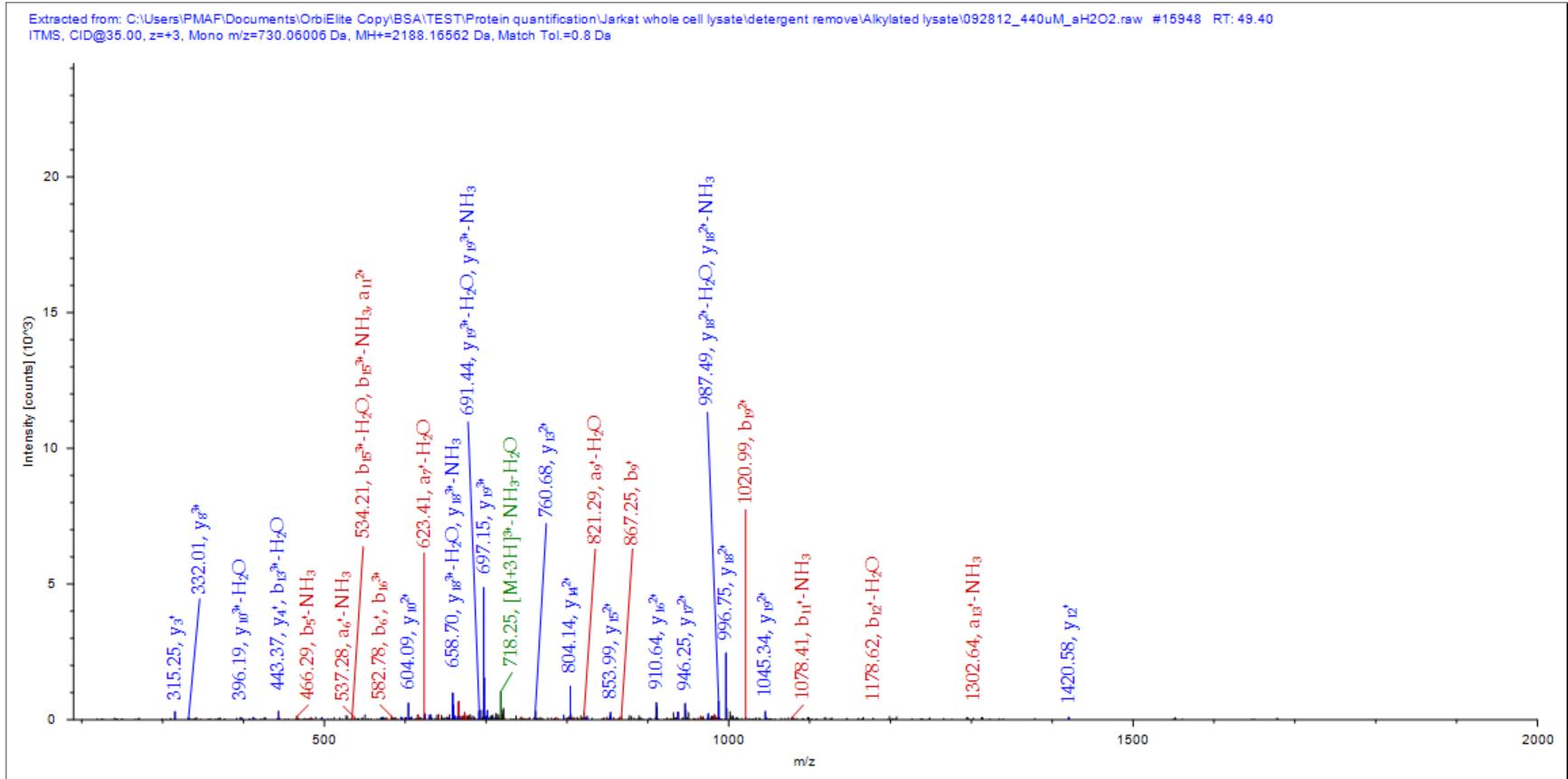
VPTANVSVVDLTCR_C13_SO2H



VPTANVSVVDLTCR_C13_SO3H

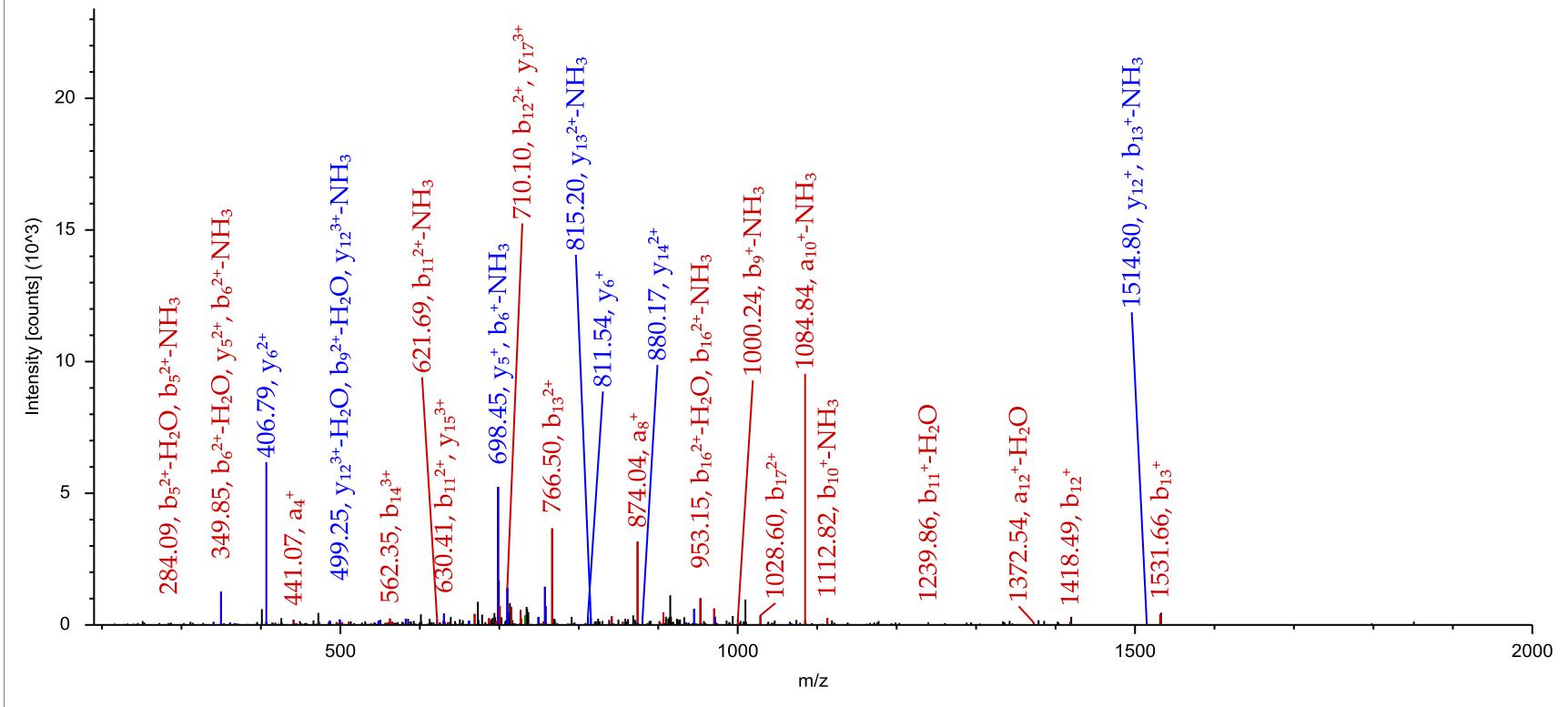


VPTANVSVDLTCRLEKPAK_C13_SO3H



VQLKDMGEDLECLCQIMR_C14_SO3H

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YHTINGHNCEVKK_C9_SO3H

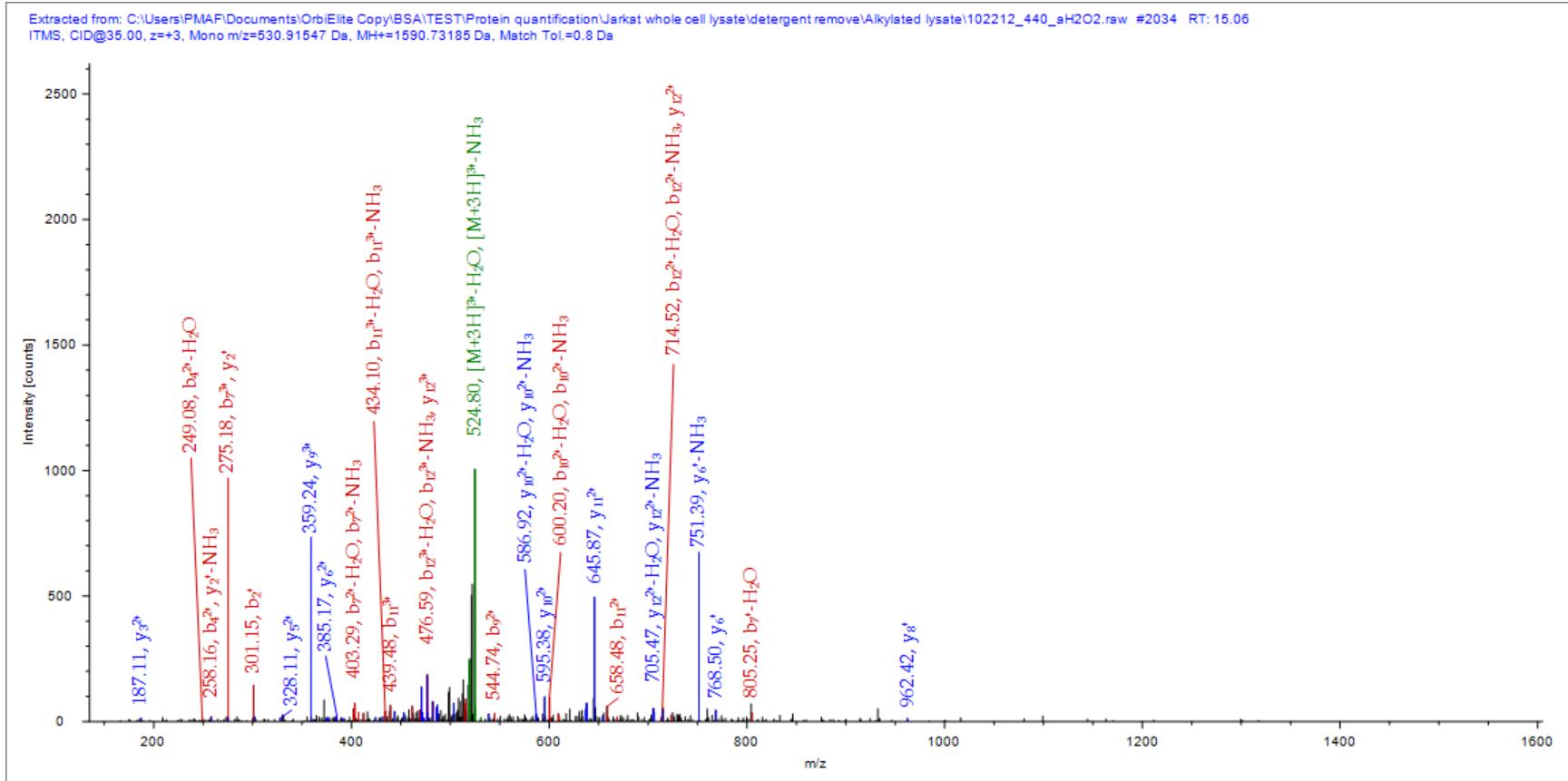
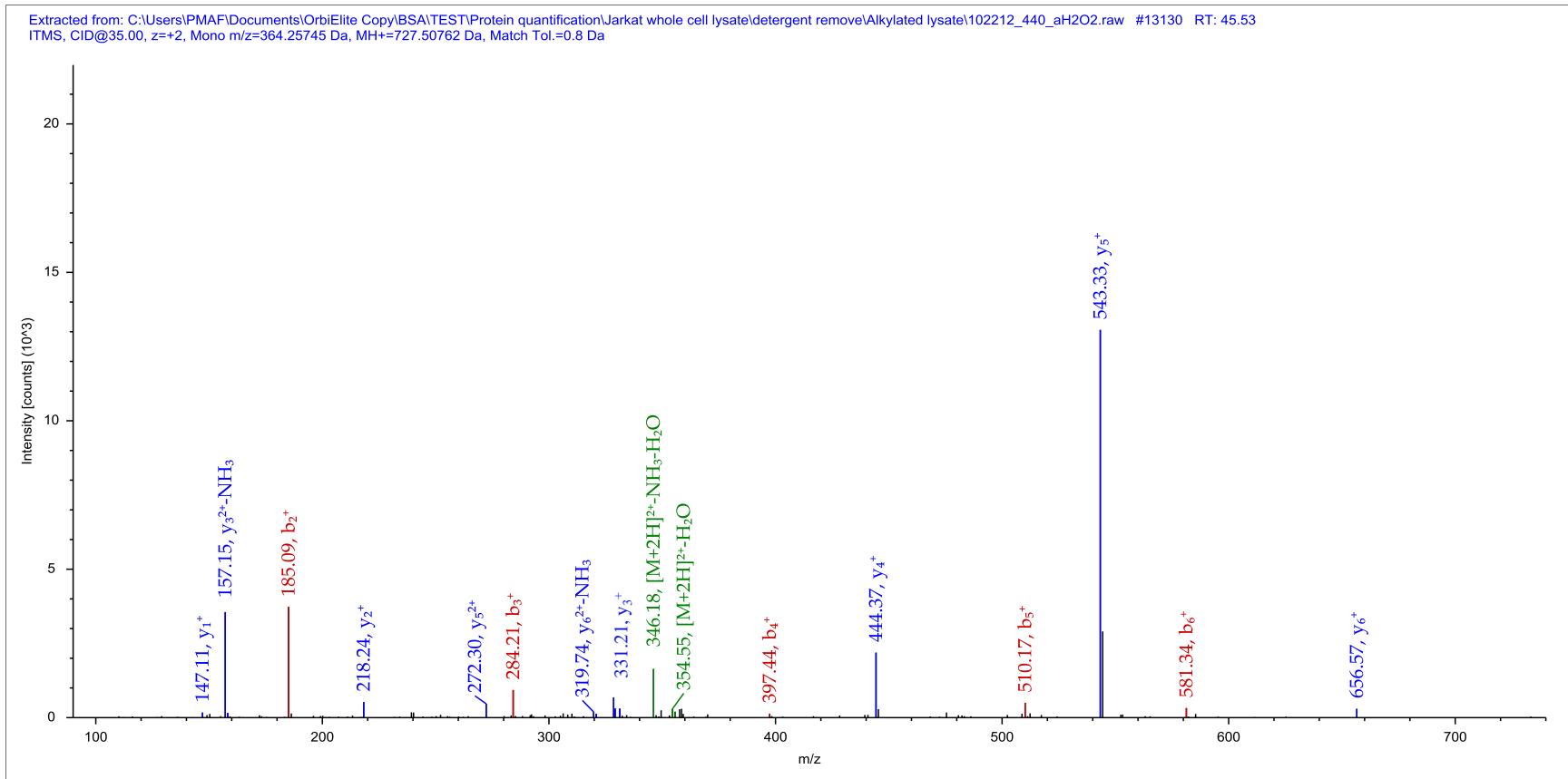


Figure S4. MS/MS from DJ-1, NM23-H1, and Hsc70 and MS2 ion intensity from Skyline. A, MS/MS from H₂O₂ treated lysate pSRM peptides. B, Skyline pSRM ion intensities for Hsc70 and DJ-1A, MS/MS from H₂O₂ treated lysate pSRM peptides. B, Skyline pSRM peak areas for Hsc70 and DJ-1

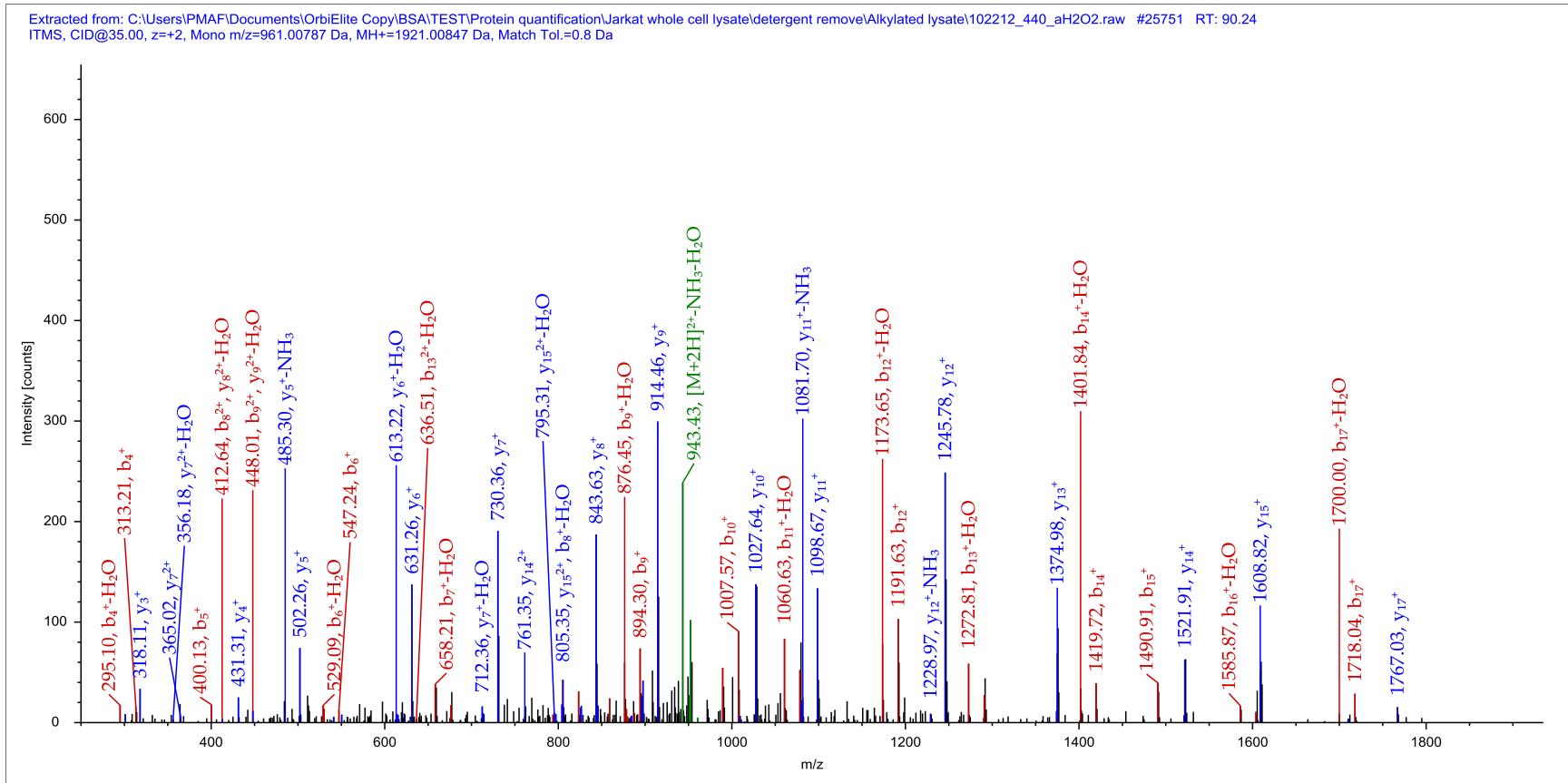
DJ-1 Internal Reference Peptide

ALVILAK



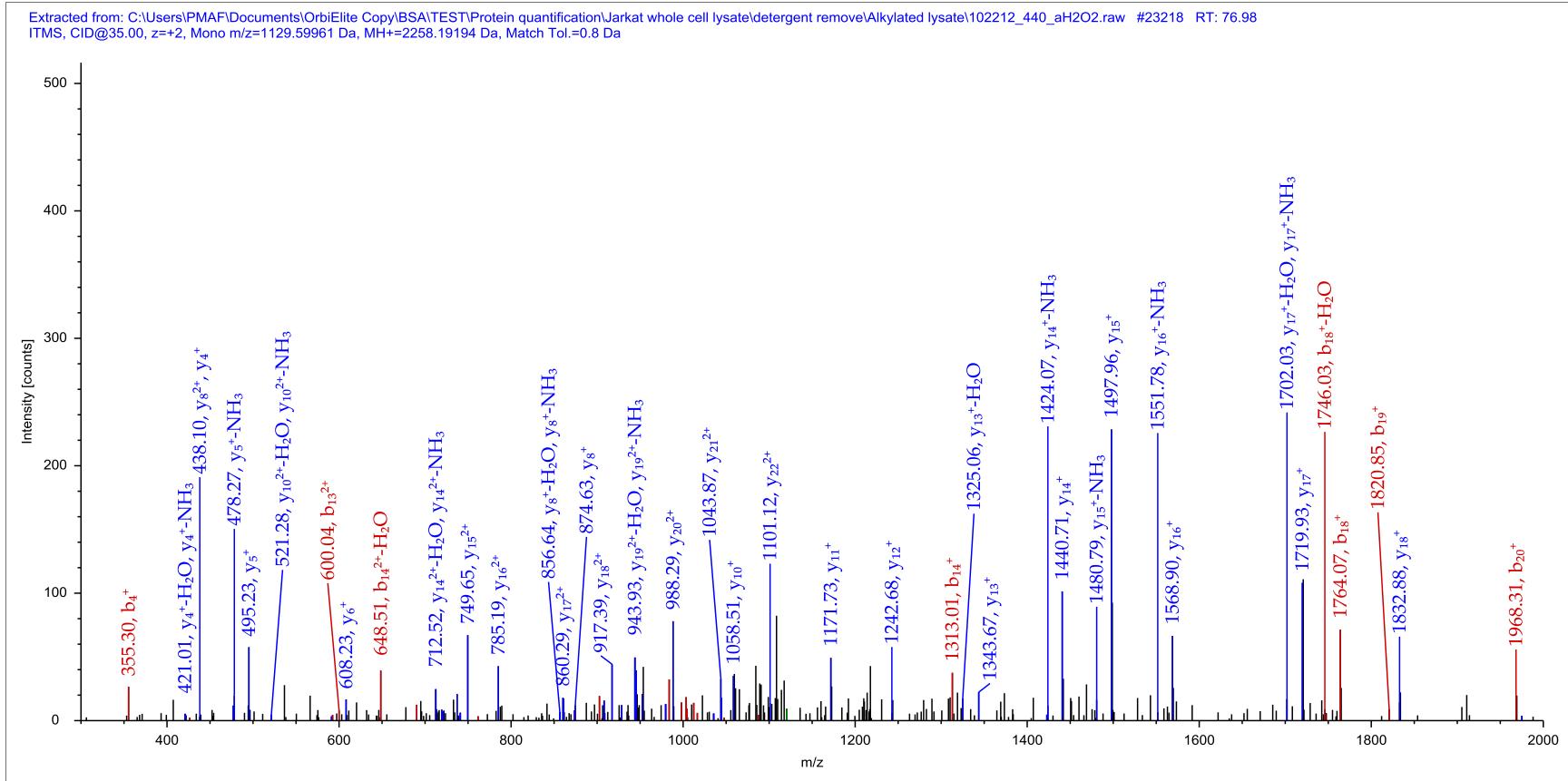
DJ-1 Internal Reference Peptide

GPGTSFEFALAI^VEALNGK



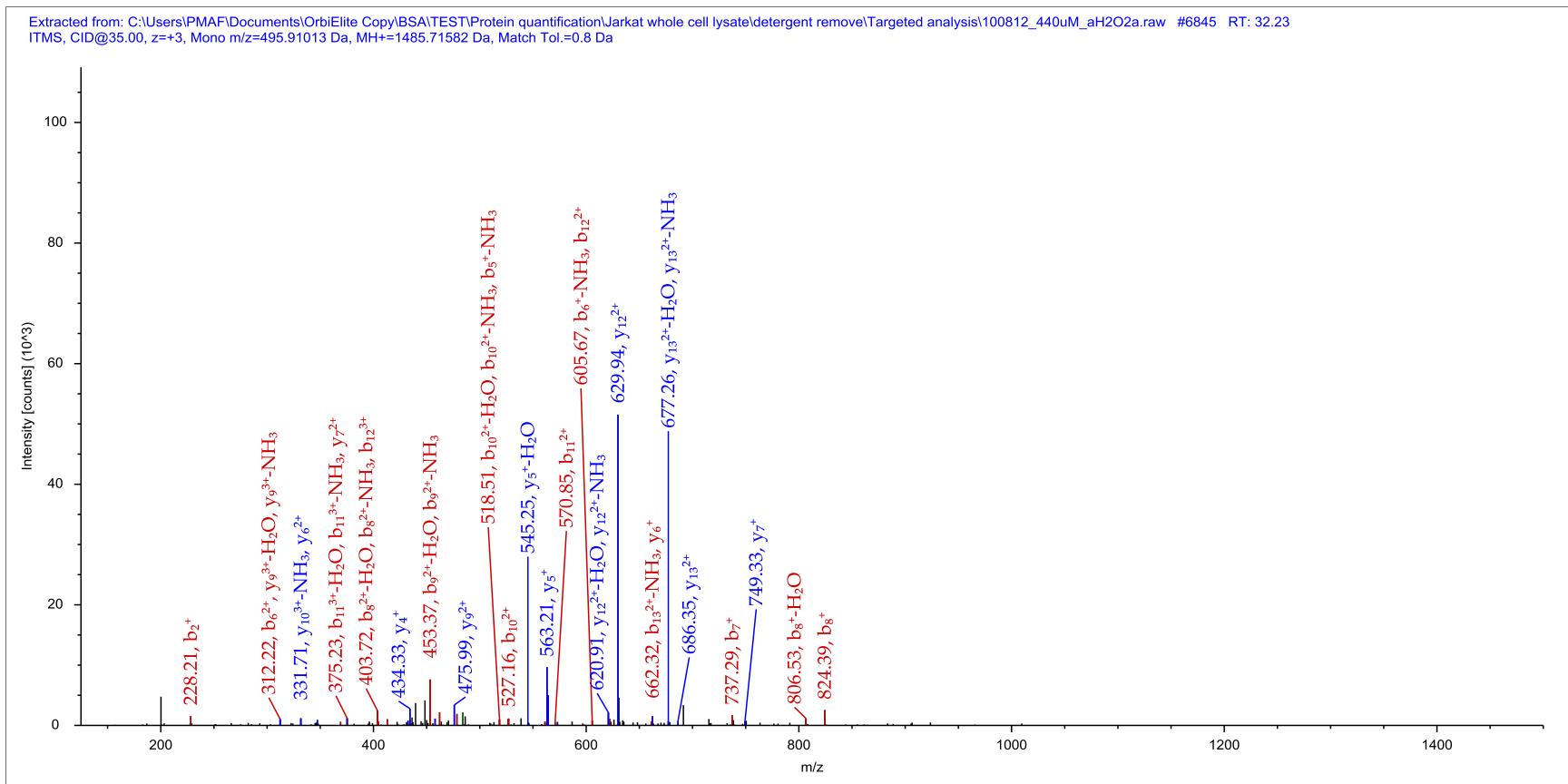
DJ-1 Cys106 sulfonic acid

GLIAAICAGPTALLAHEIGFGSK



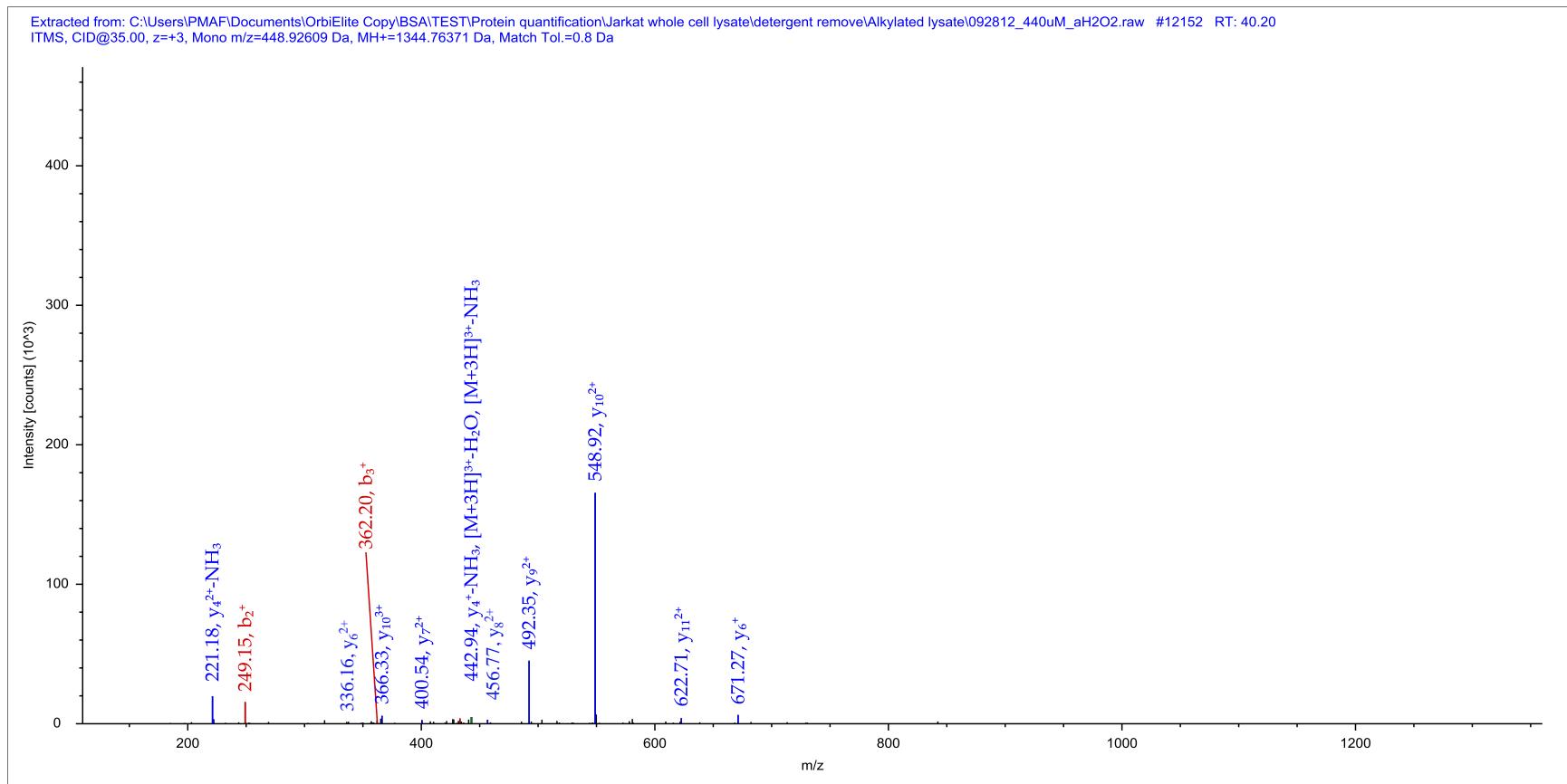
Nm23-H1 Internal Reference Peptide

NIIHGSDSVESEA**K**



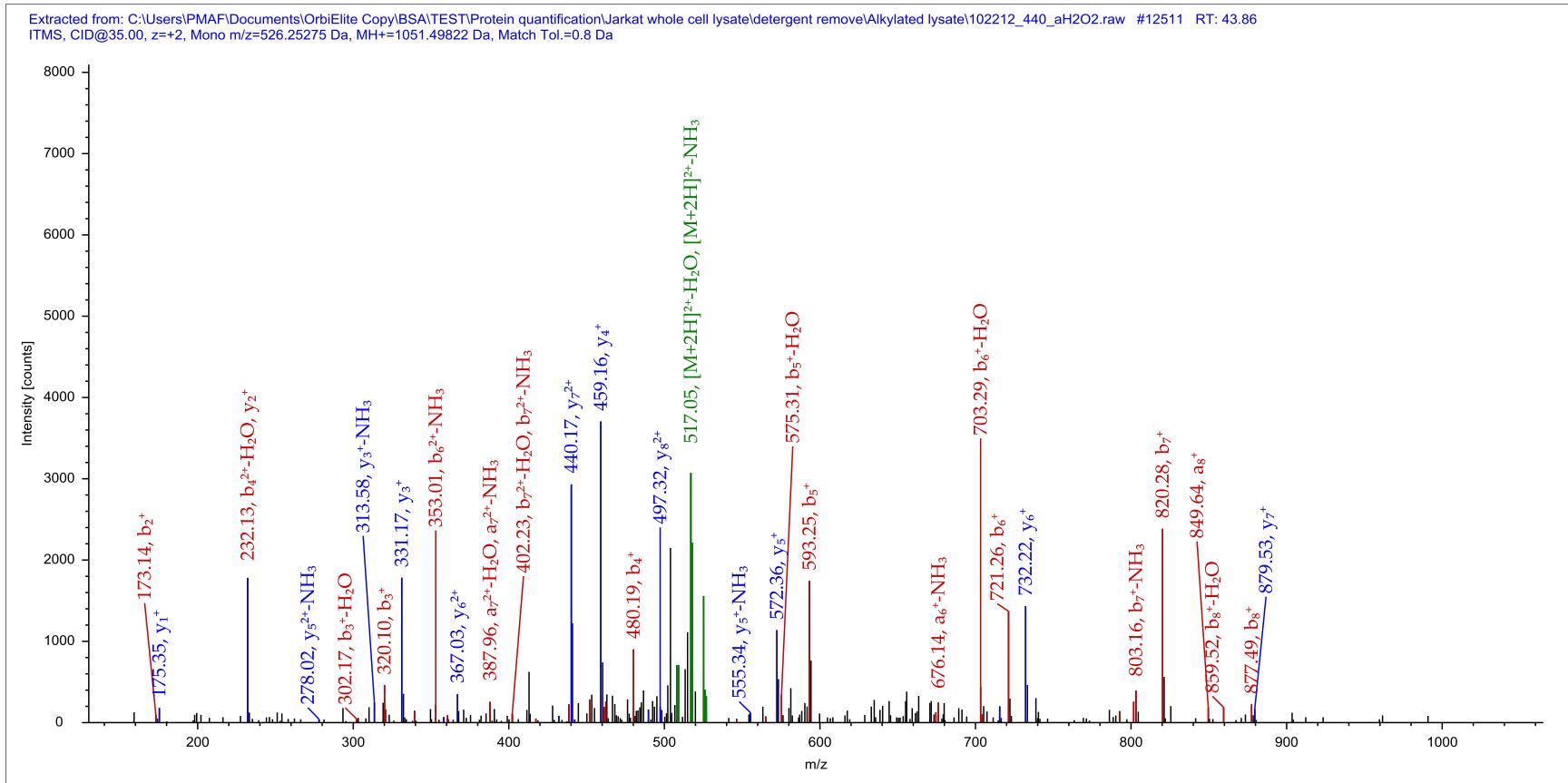
Nm23-H1 Internal Reference Peptide

TFIAIKPDGVQR



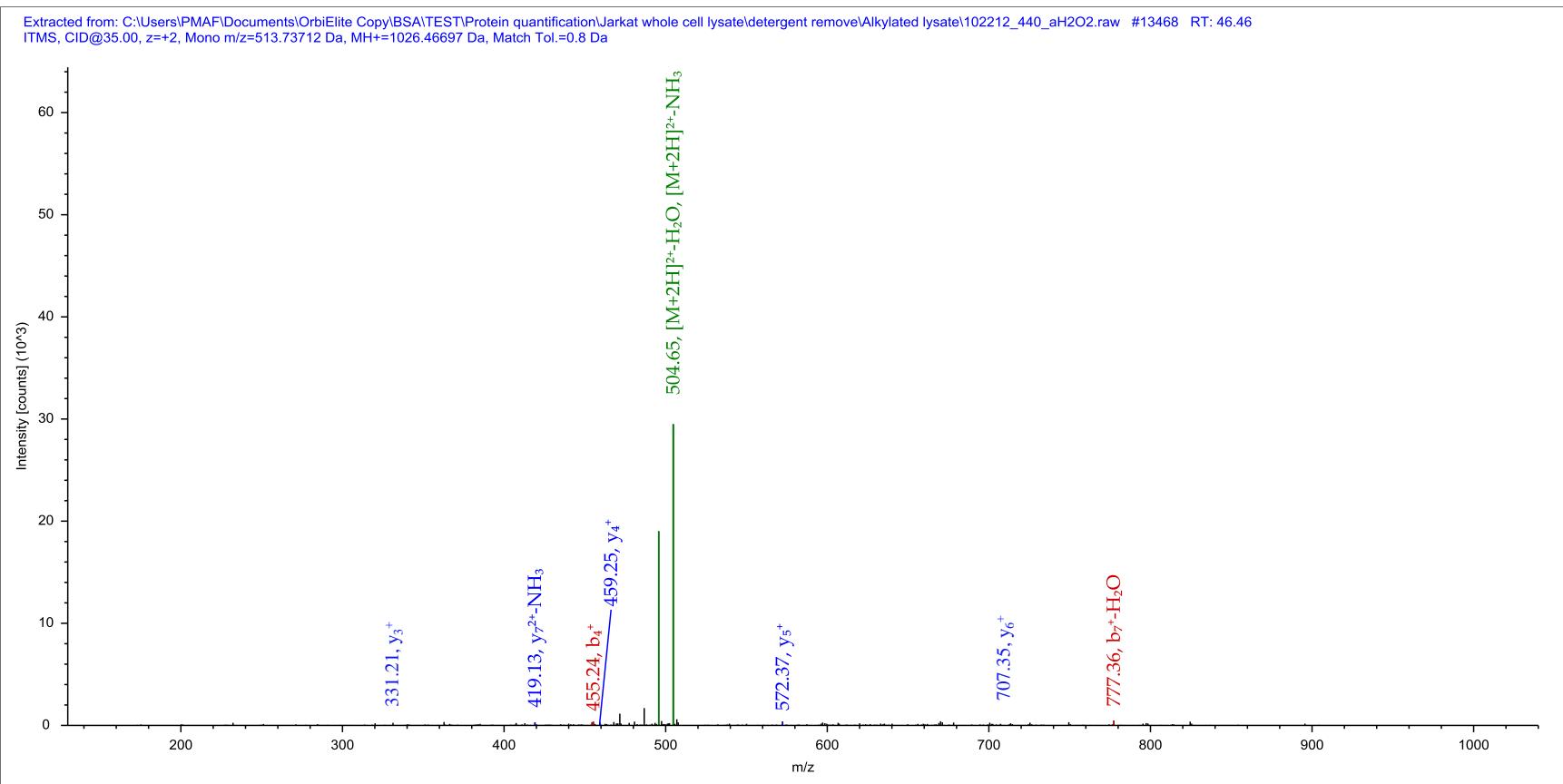
Nm23-H1 Cys109 carbamidomethyl

GDFCIQVGR



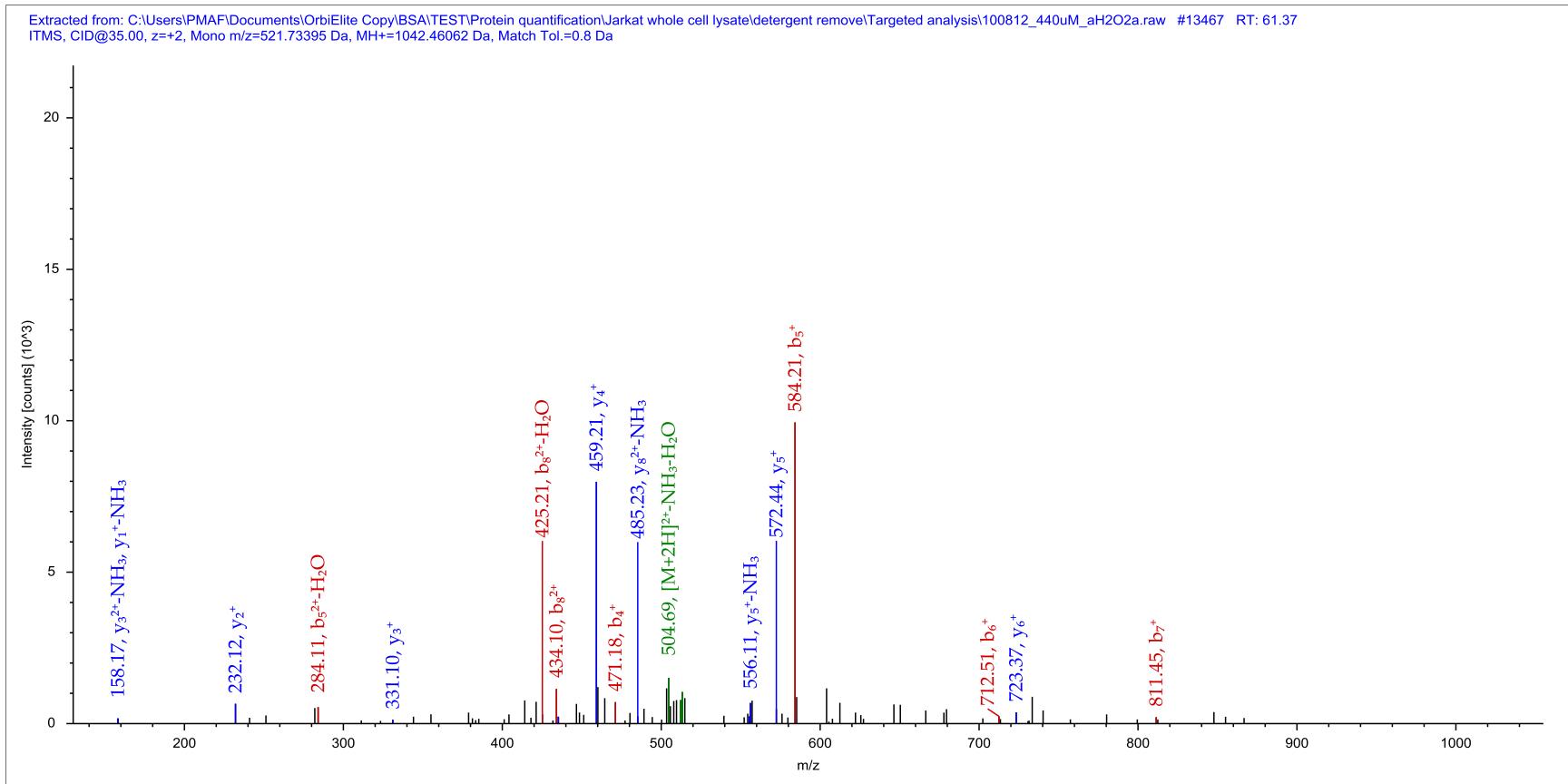
Nm23-H1 Cys109 sulfinic acid

GDFCIQVGR



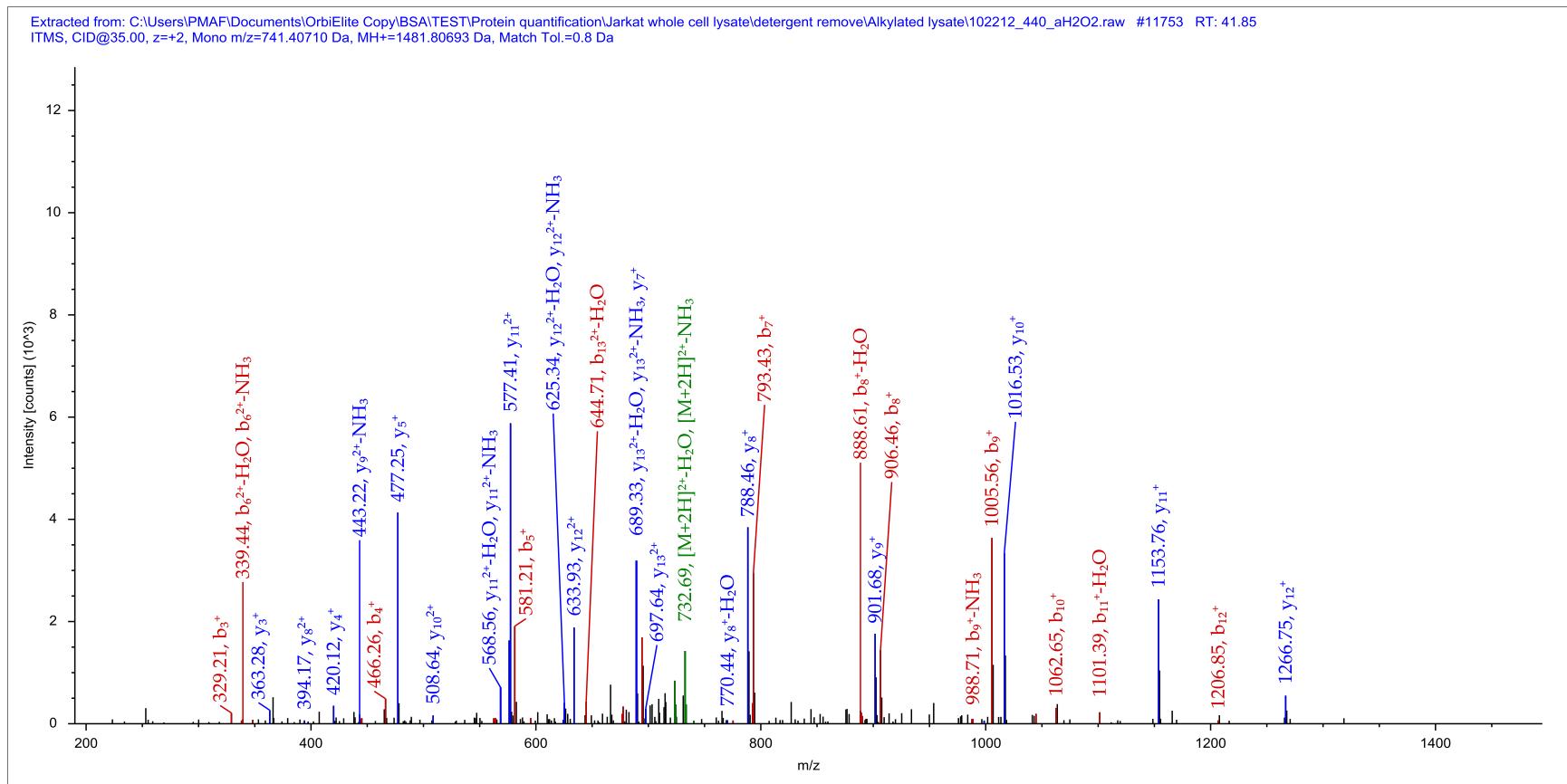
Nm23-H1 Cys109 sulfonic acid

GDFCIQVGR



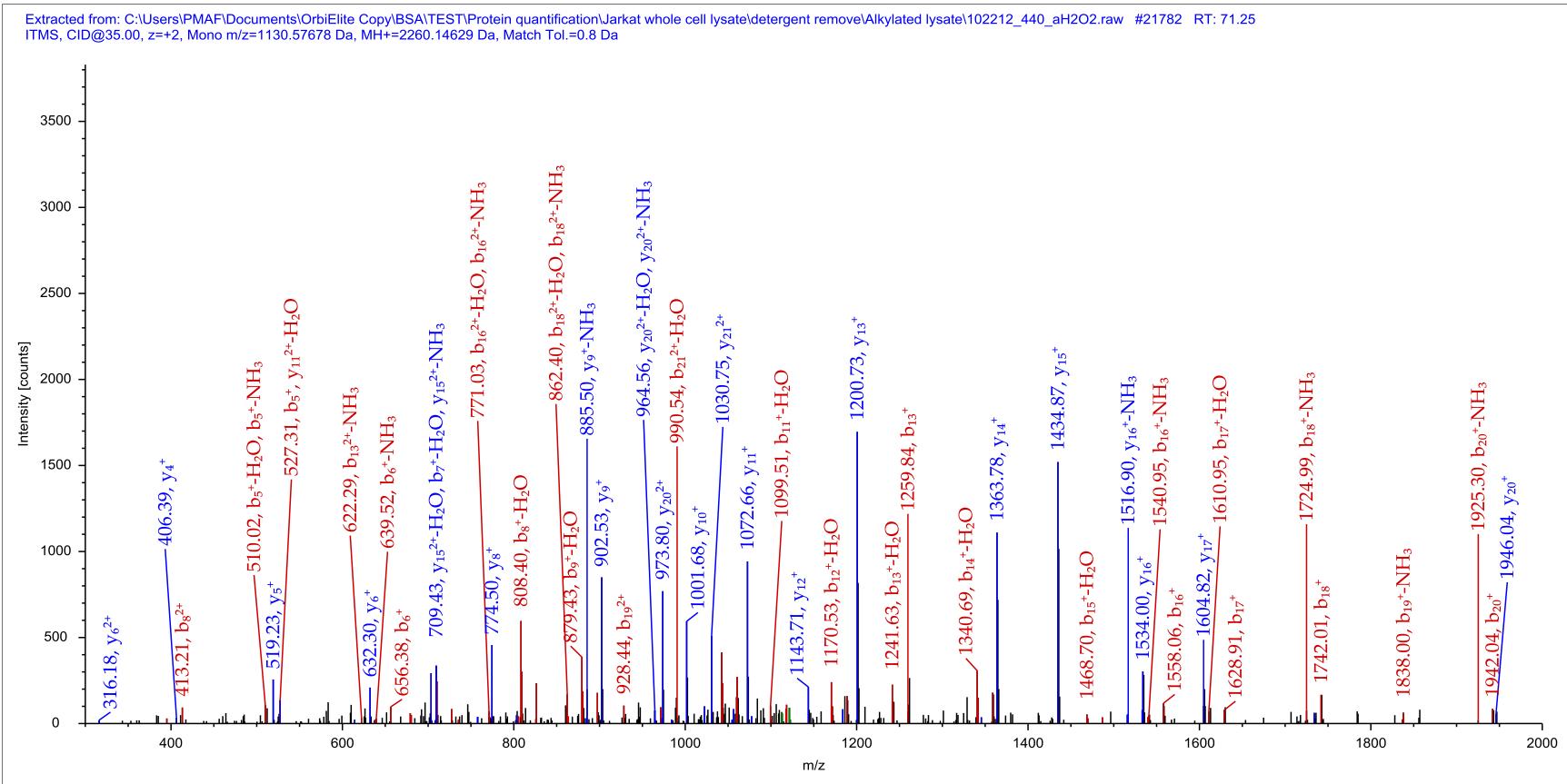
Hsc70 Internal Reference Peptide

SQIHDIVLVGGSTR



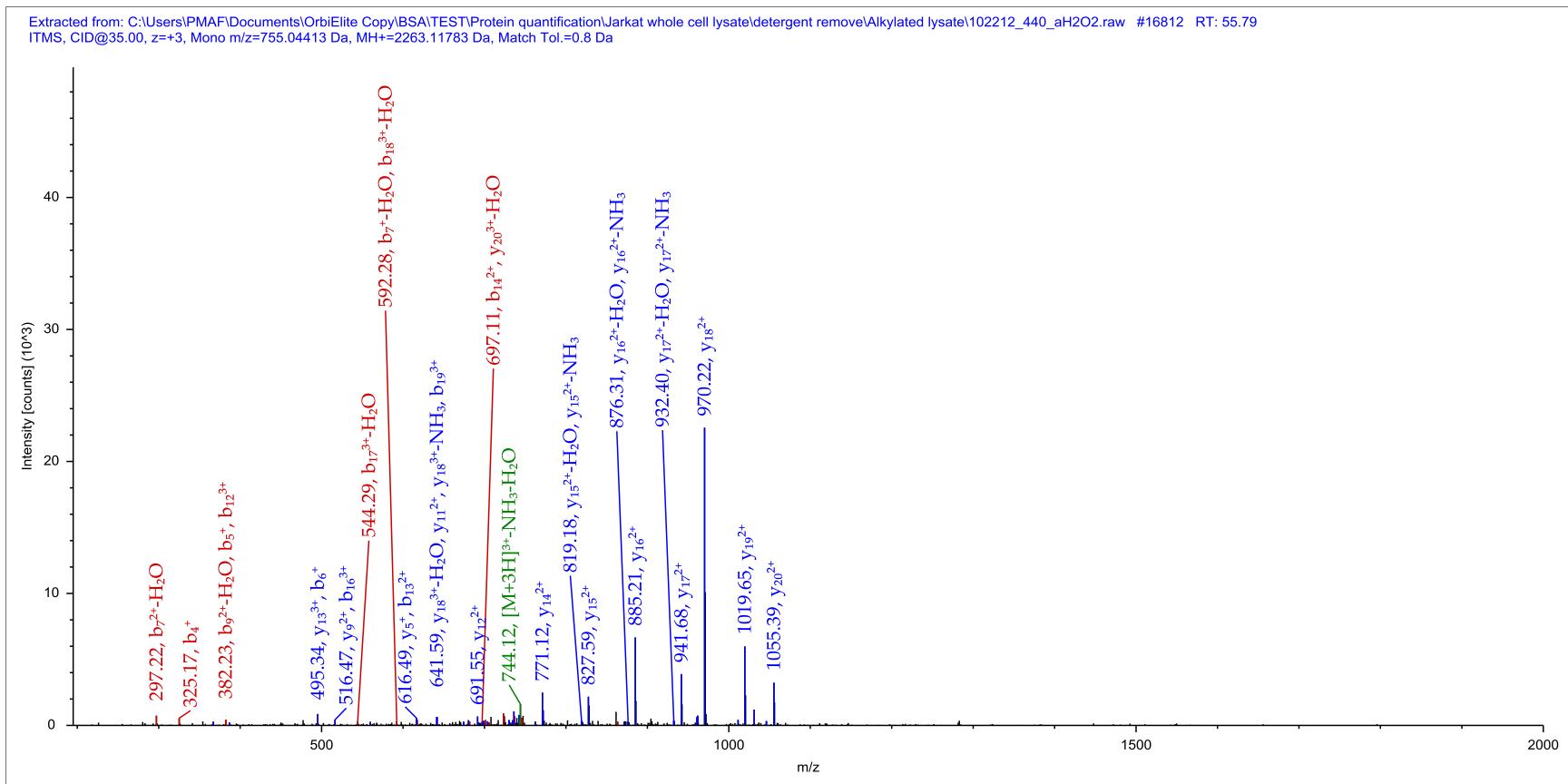
Hsc70 Internal Reference Peptide

SINPDEAVAYGAAVQAAILSGDK



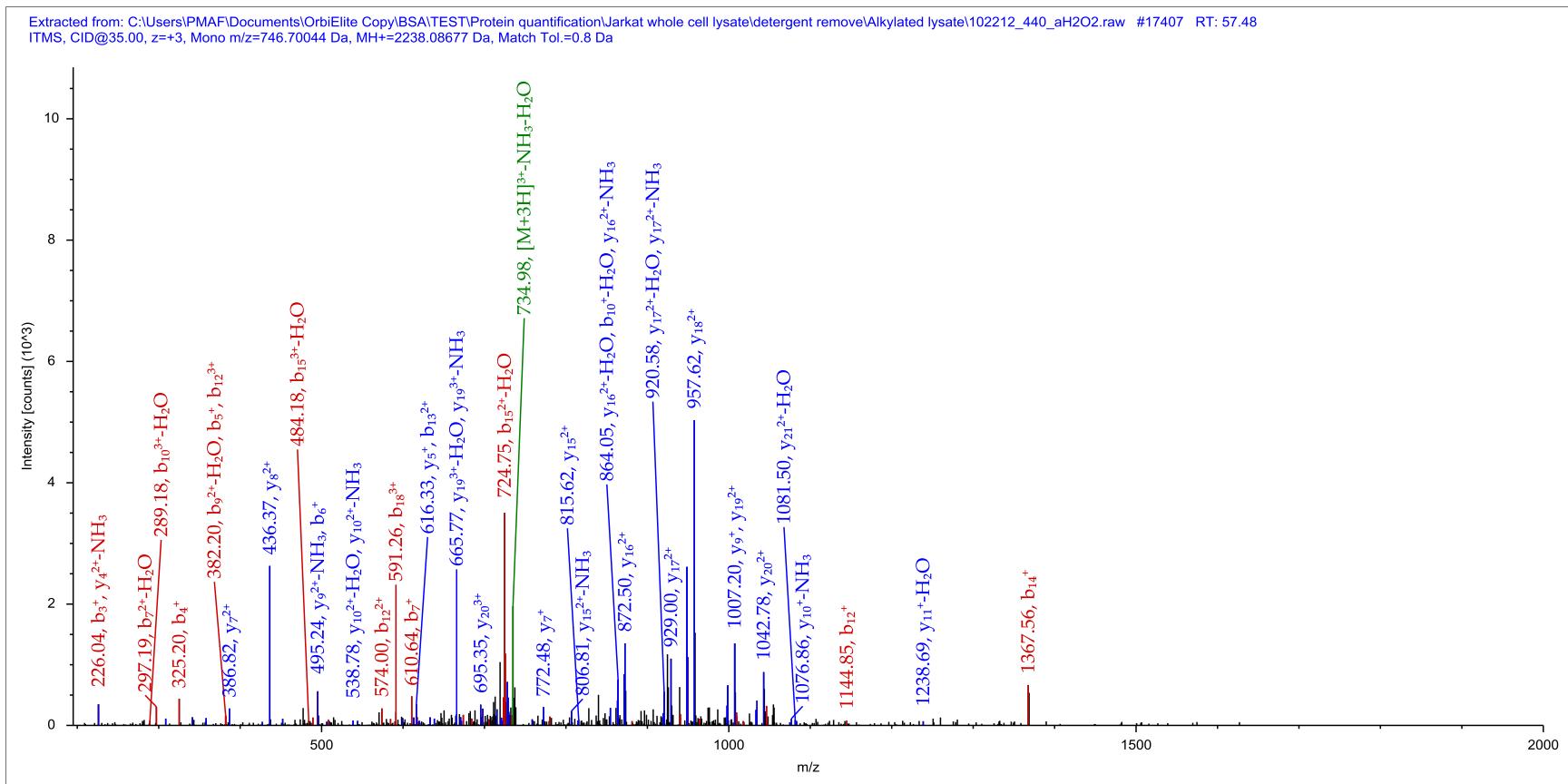
Hsc70 Cys17 carbomidomethyl

GPAVGIDLGTTYSCVGVFQHGK



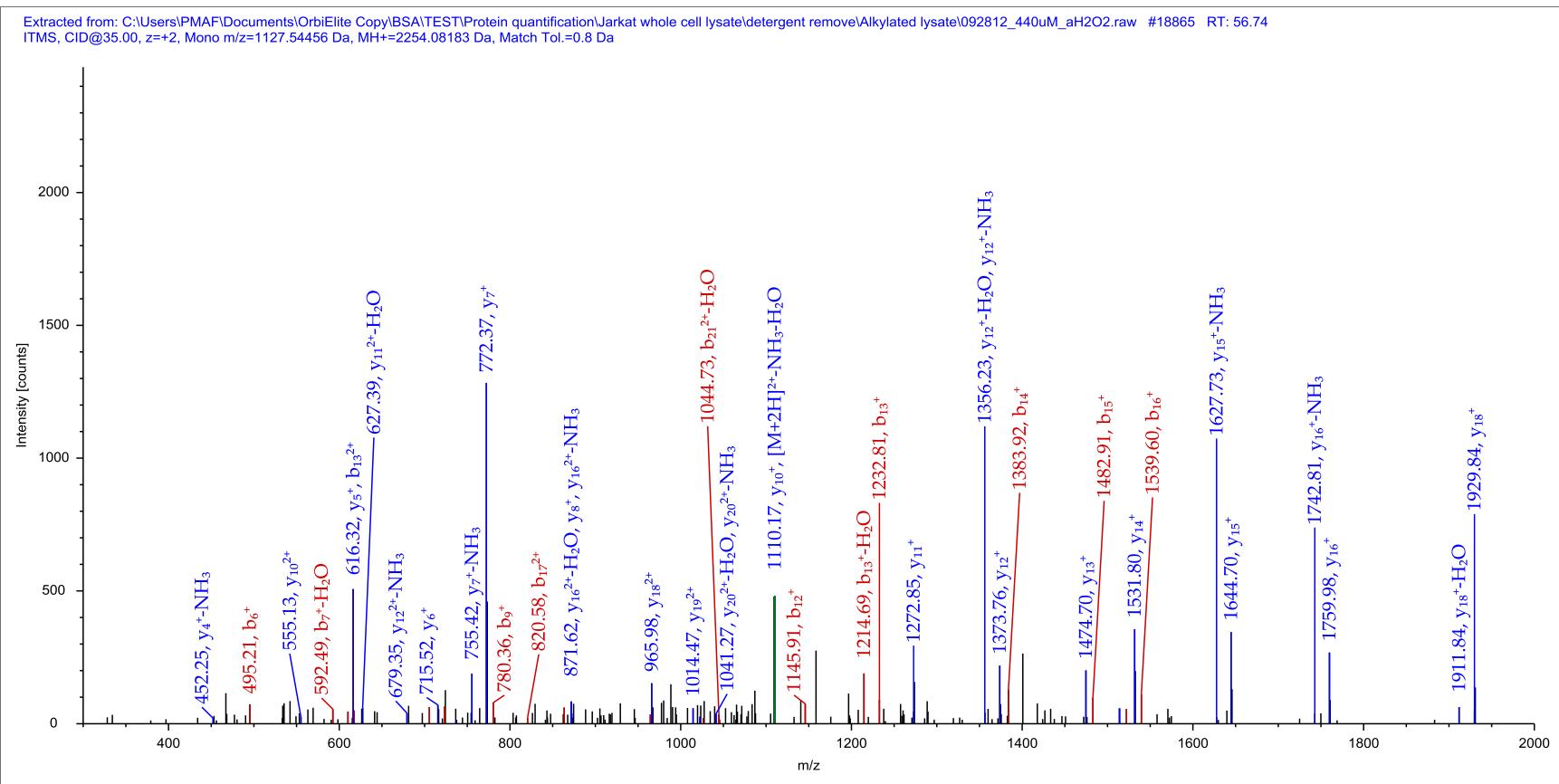
Hsc70 Cys17 sulfenic acid

GPAVGIDLGTTYSCVGVFQHGK



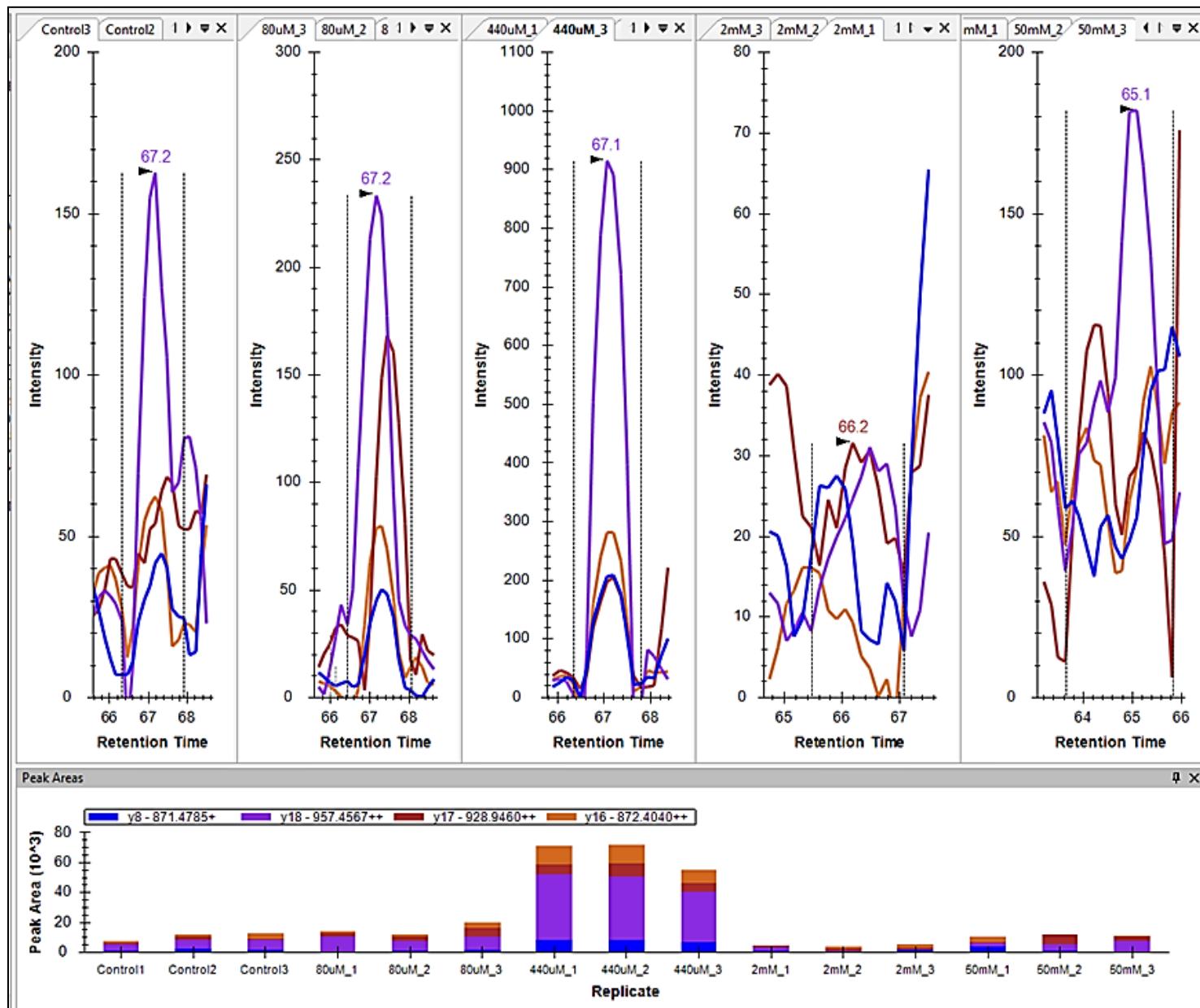
Hsc70 Cys17 sulfonic acid

GPAVGIDLGTTYSCVGVFQHGK

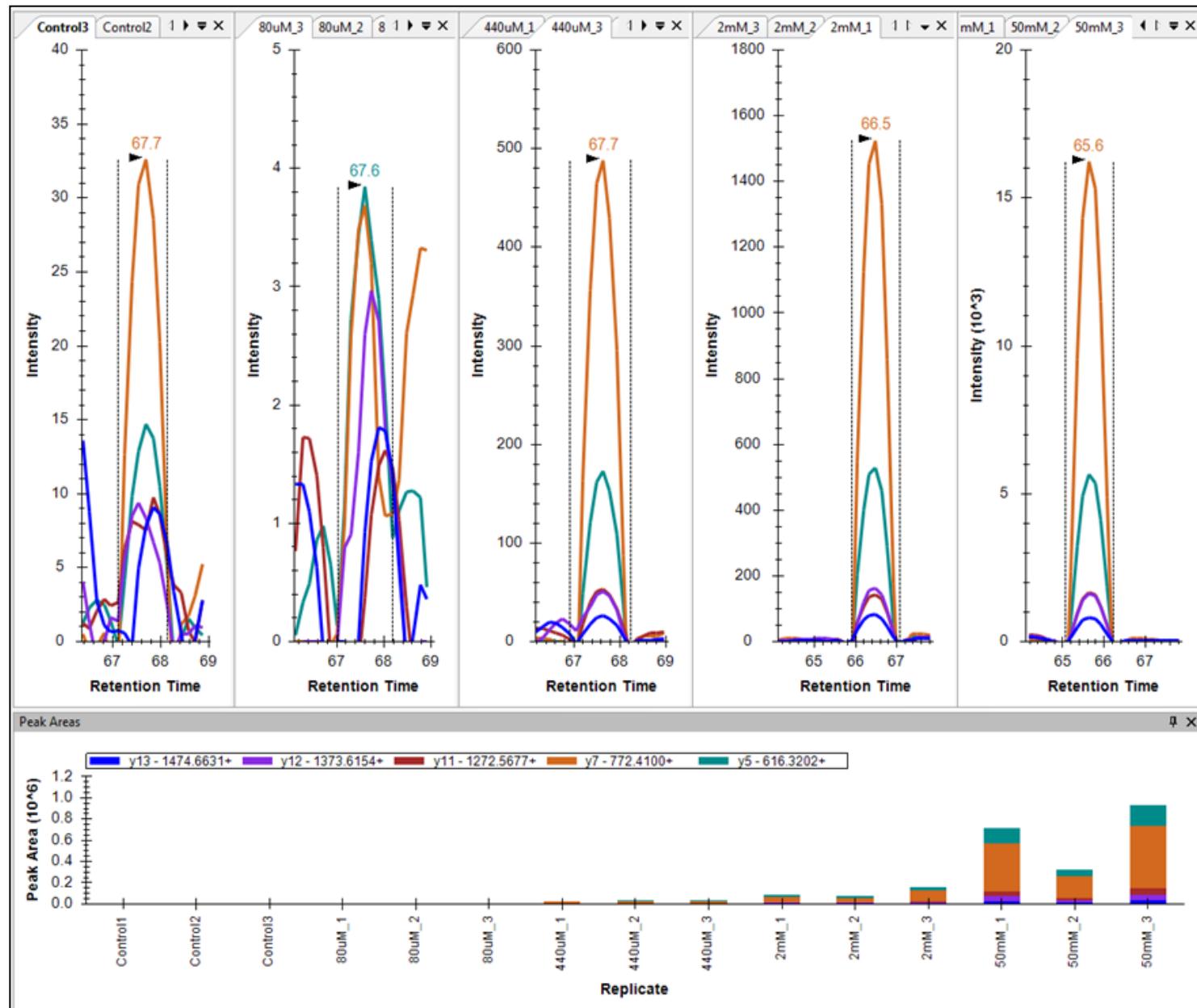


B. Skyline pSRM peak areas for Hsc70 and DJ-1

Hsc70 Cys17 (Sulfinic acid)



Hsc70 Cys17 (Sulfonic acid)



DJ-1 Cys106 (Sulfonic acid)

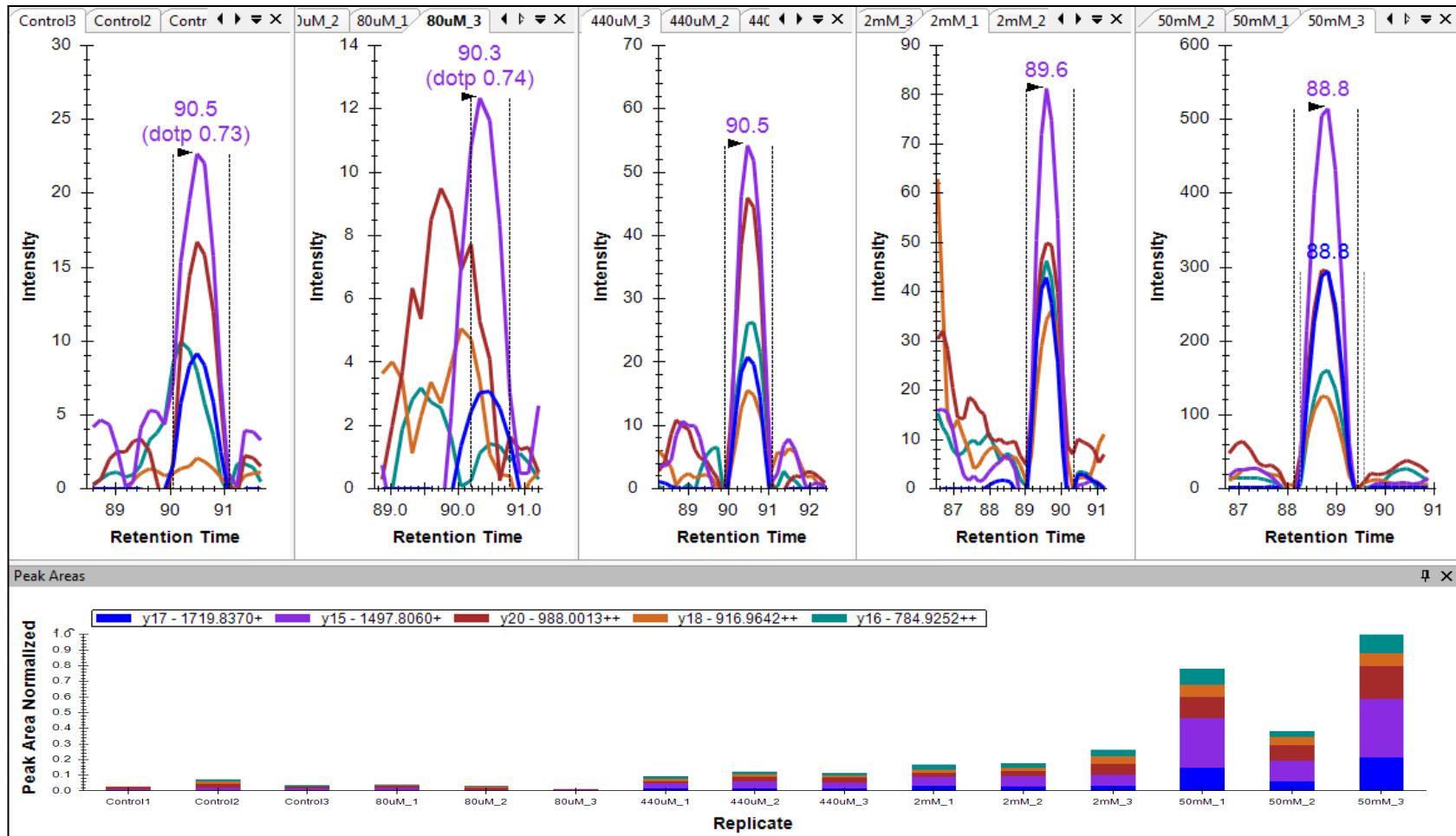
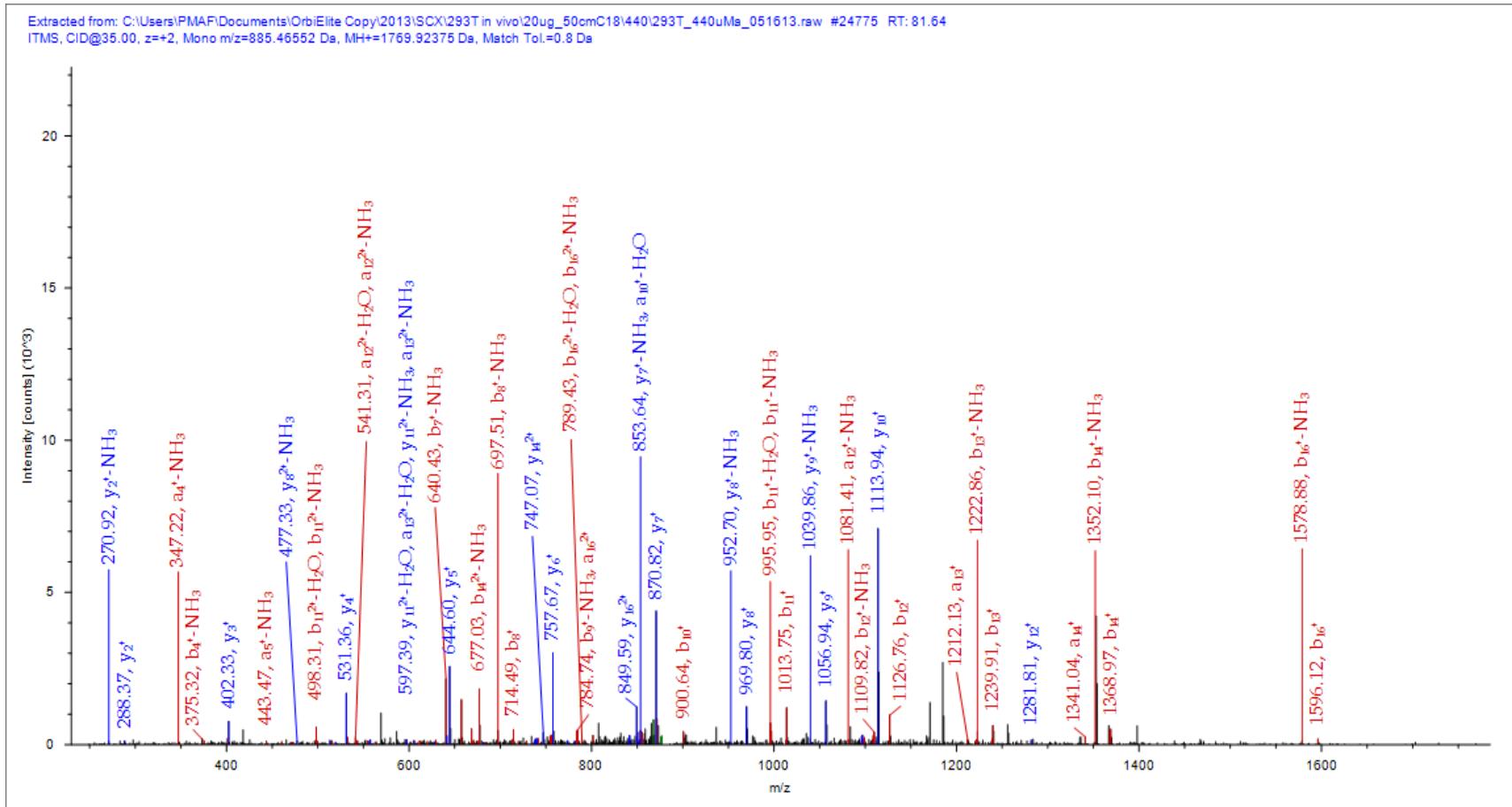
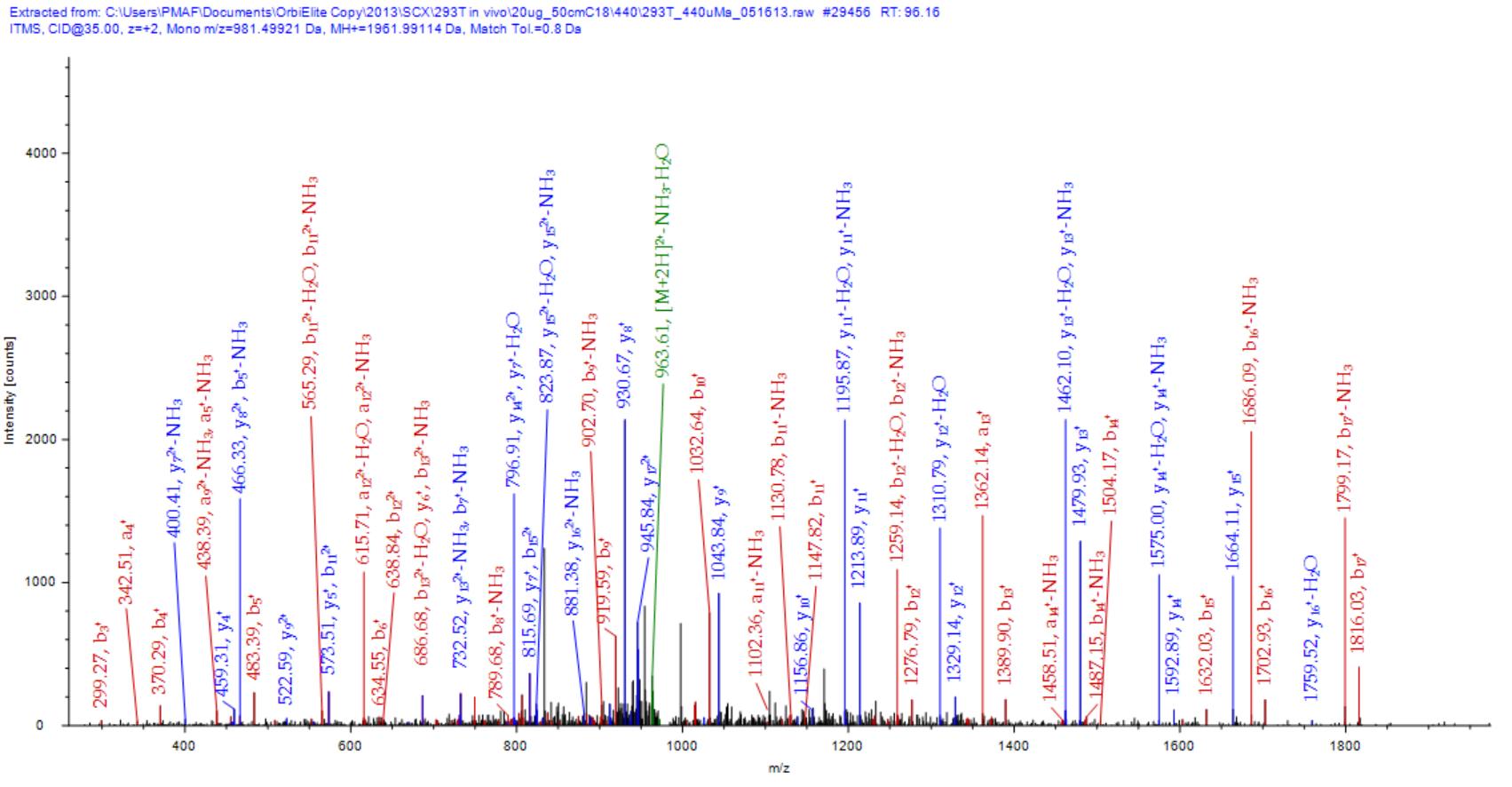


Figure S5. MS/MS of sulfinic and sulfonic acid peptides identified from H₂O₂ treated cell

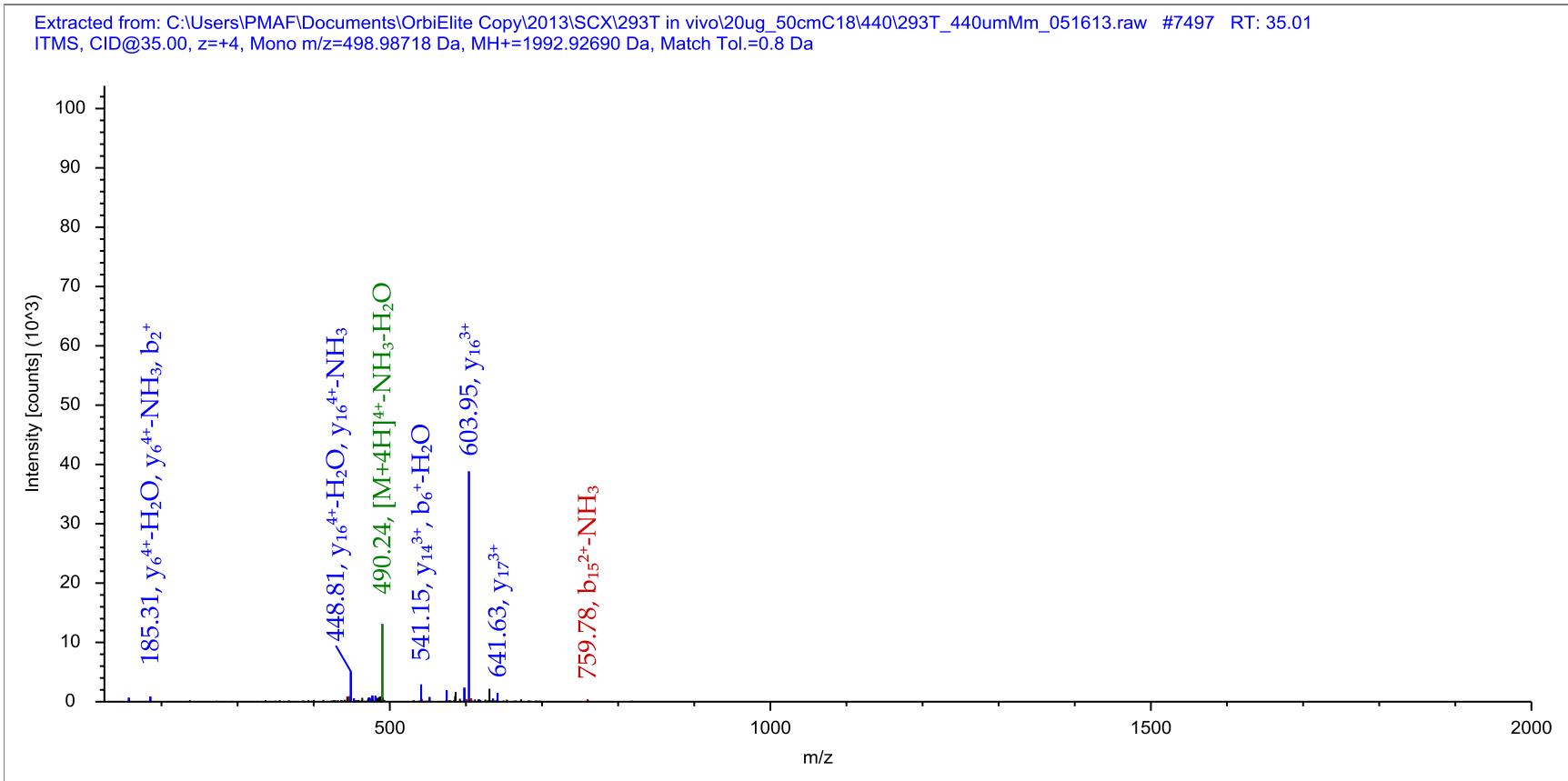
ACANPAPGSVILLENLR_C2_SO2



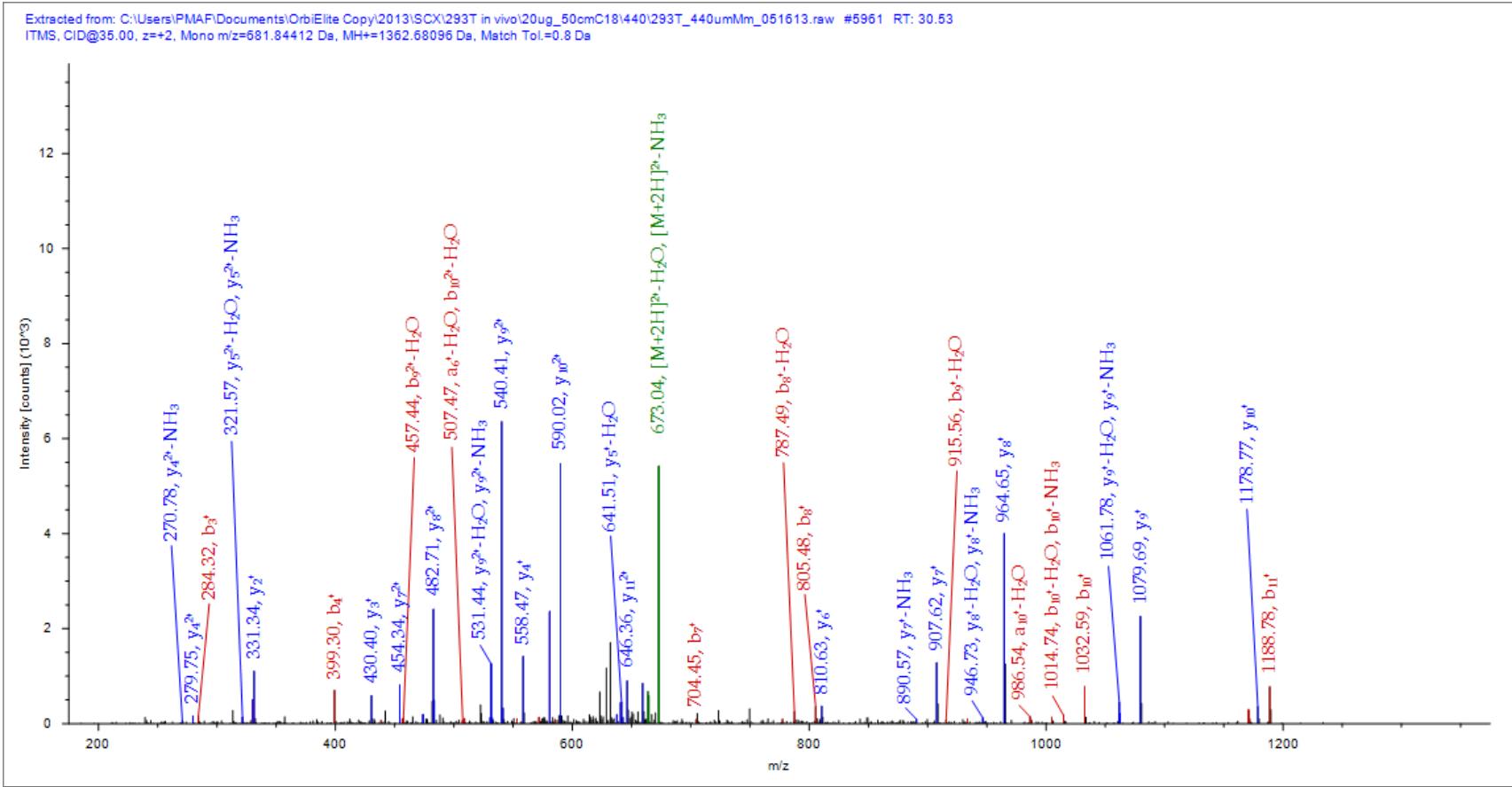
ALNALCDGLIDE^NQALK_C6_SO3H



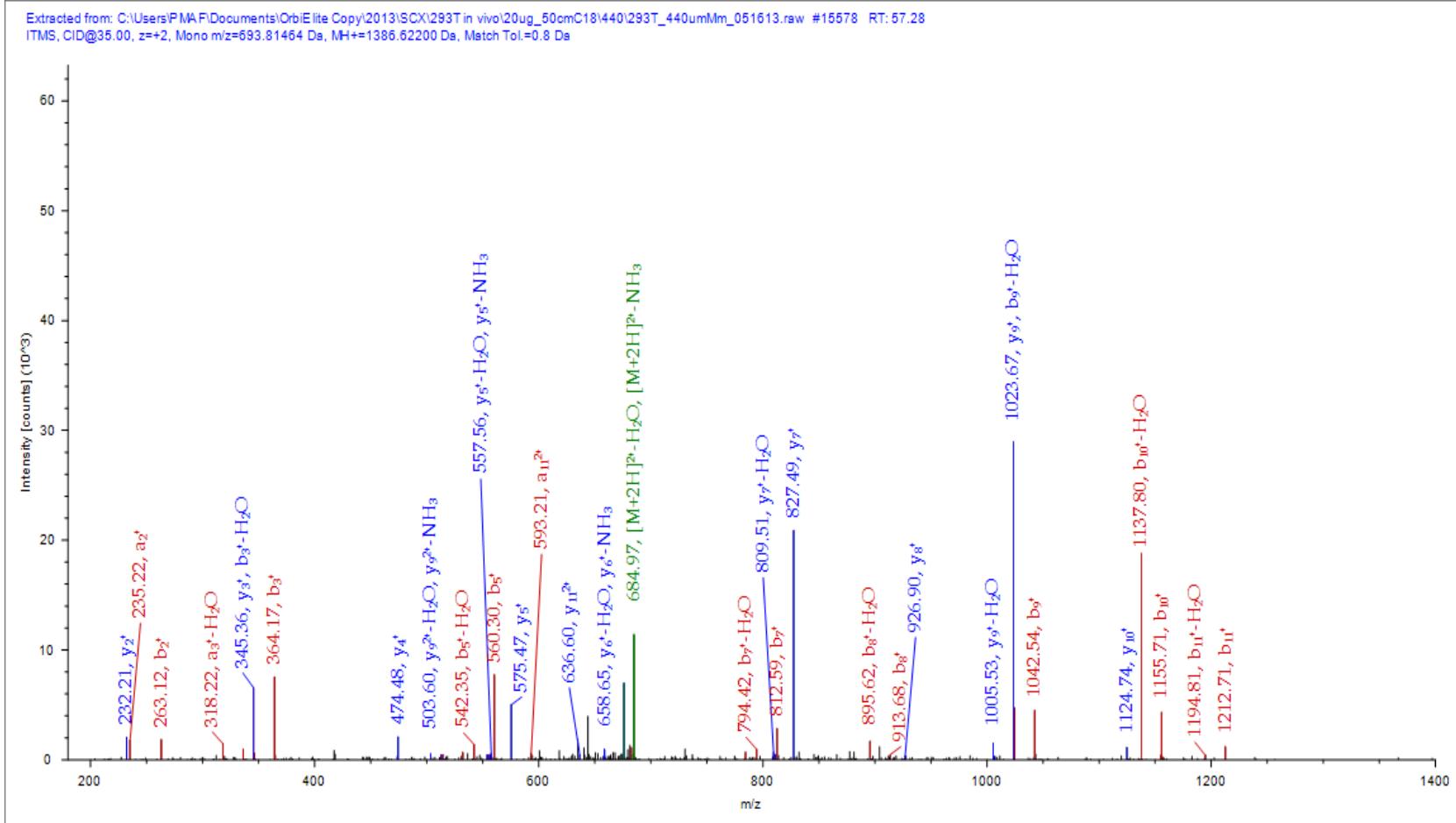
ALSTGEKGFGYKGSCFHR C15 SO3H



ALVDGPCTQVRR_C7_SO3H

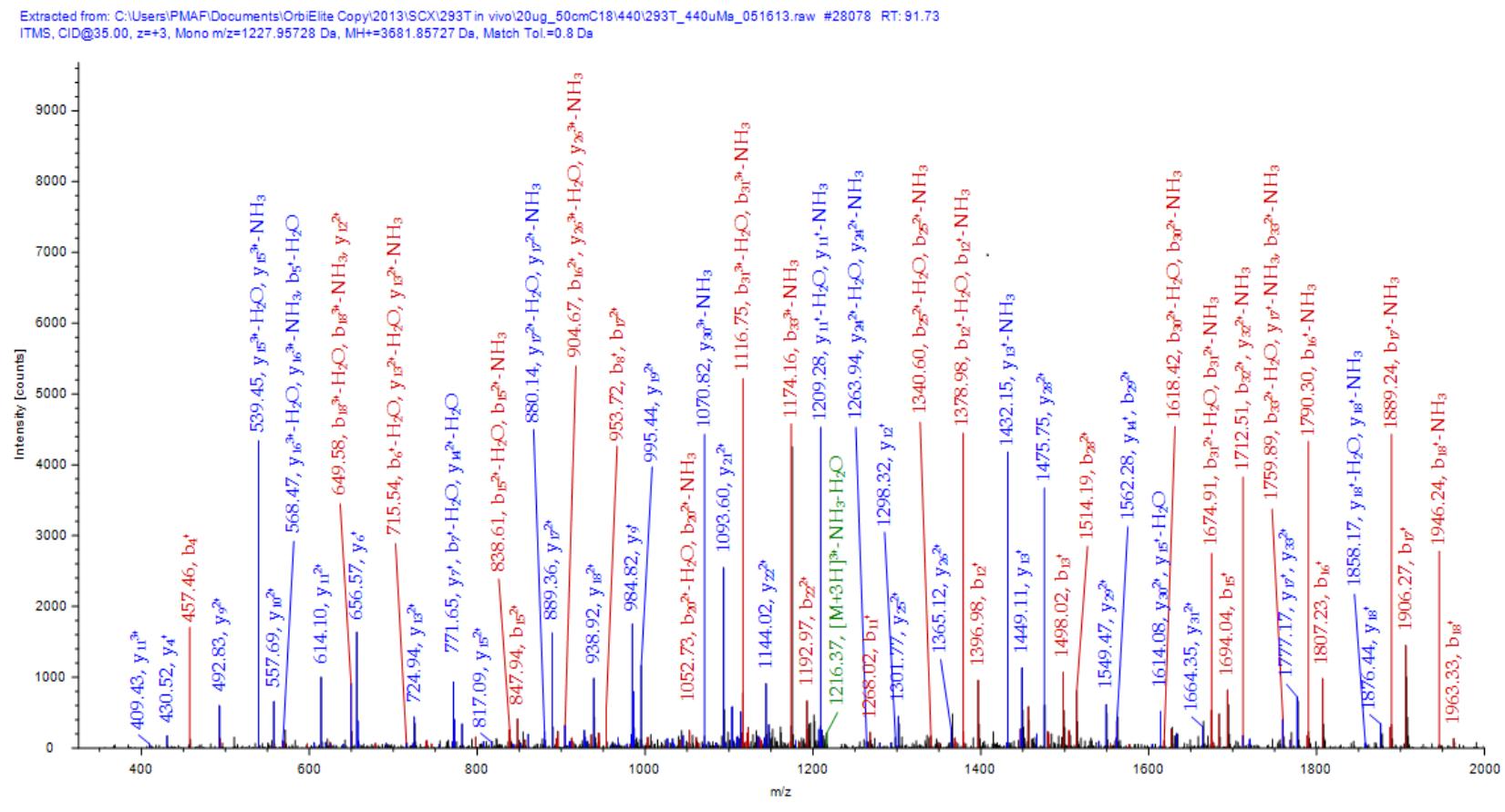


DFTPVCTTELGR_C6_SO3H

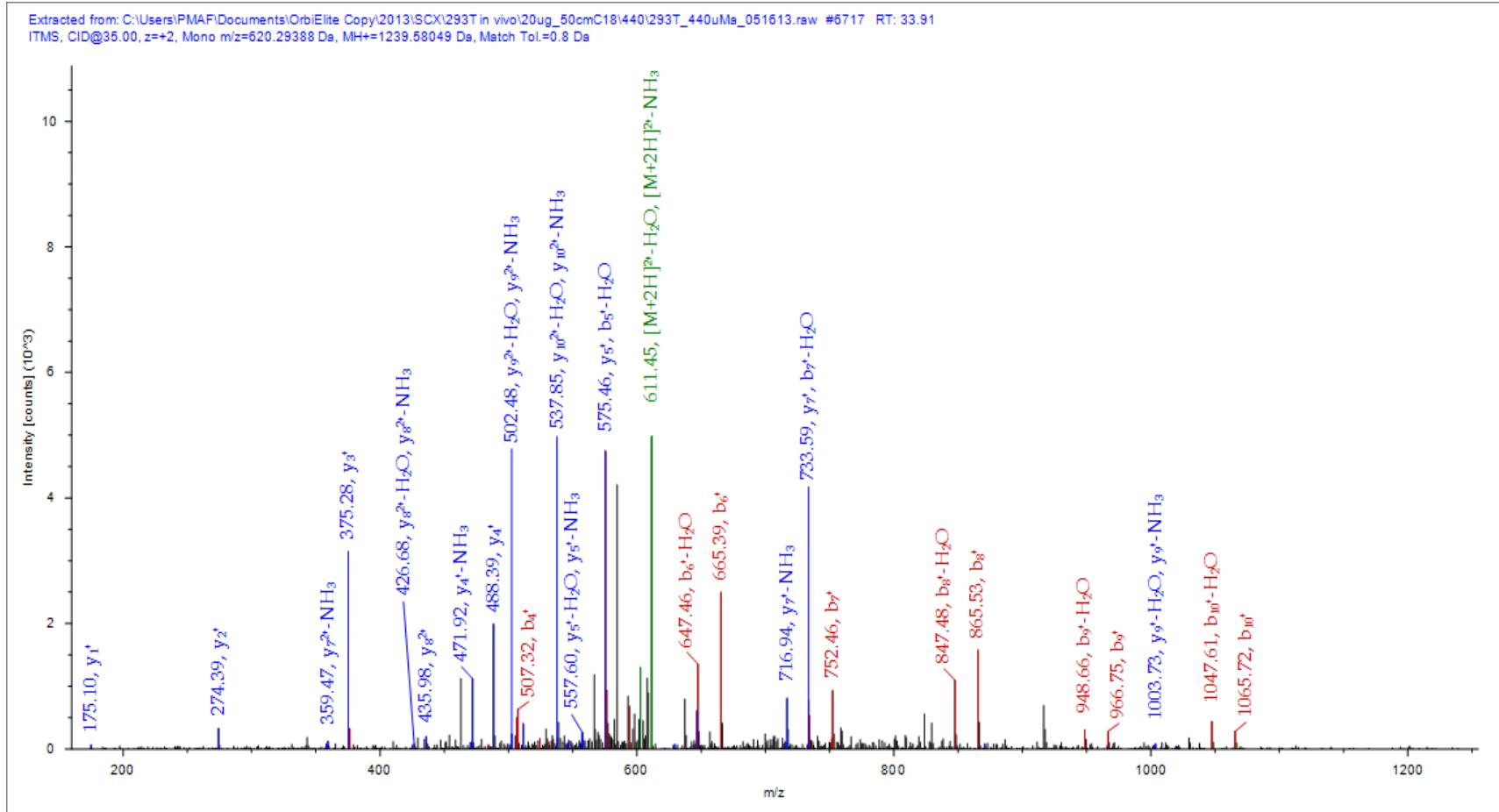


ELLTEFGYKGEETPVIVGSALCALEGRDPEL

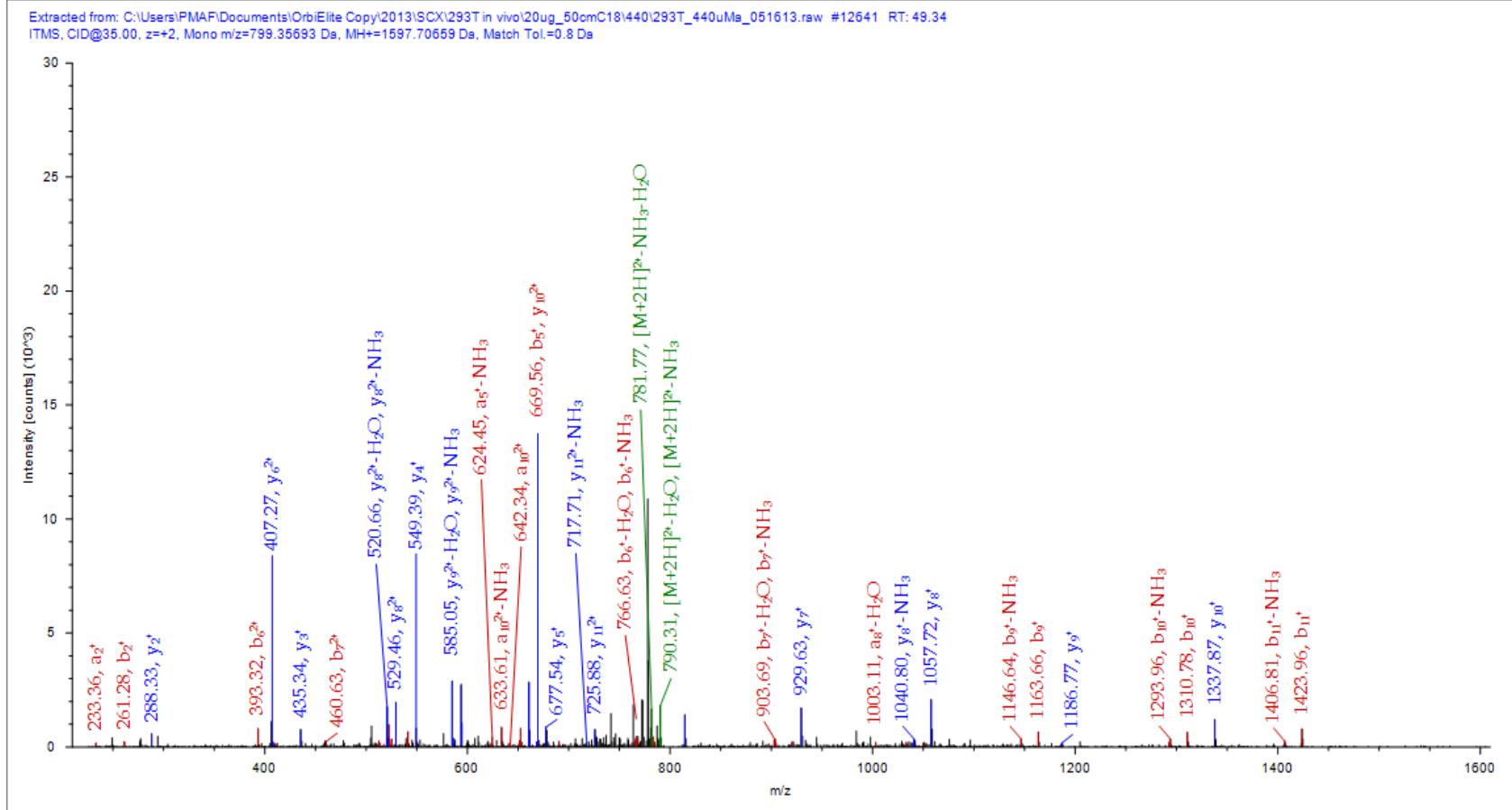
GLK_C22_SO3H



FACHSASLTVR_C3_SO3H

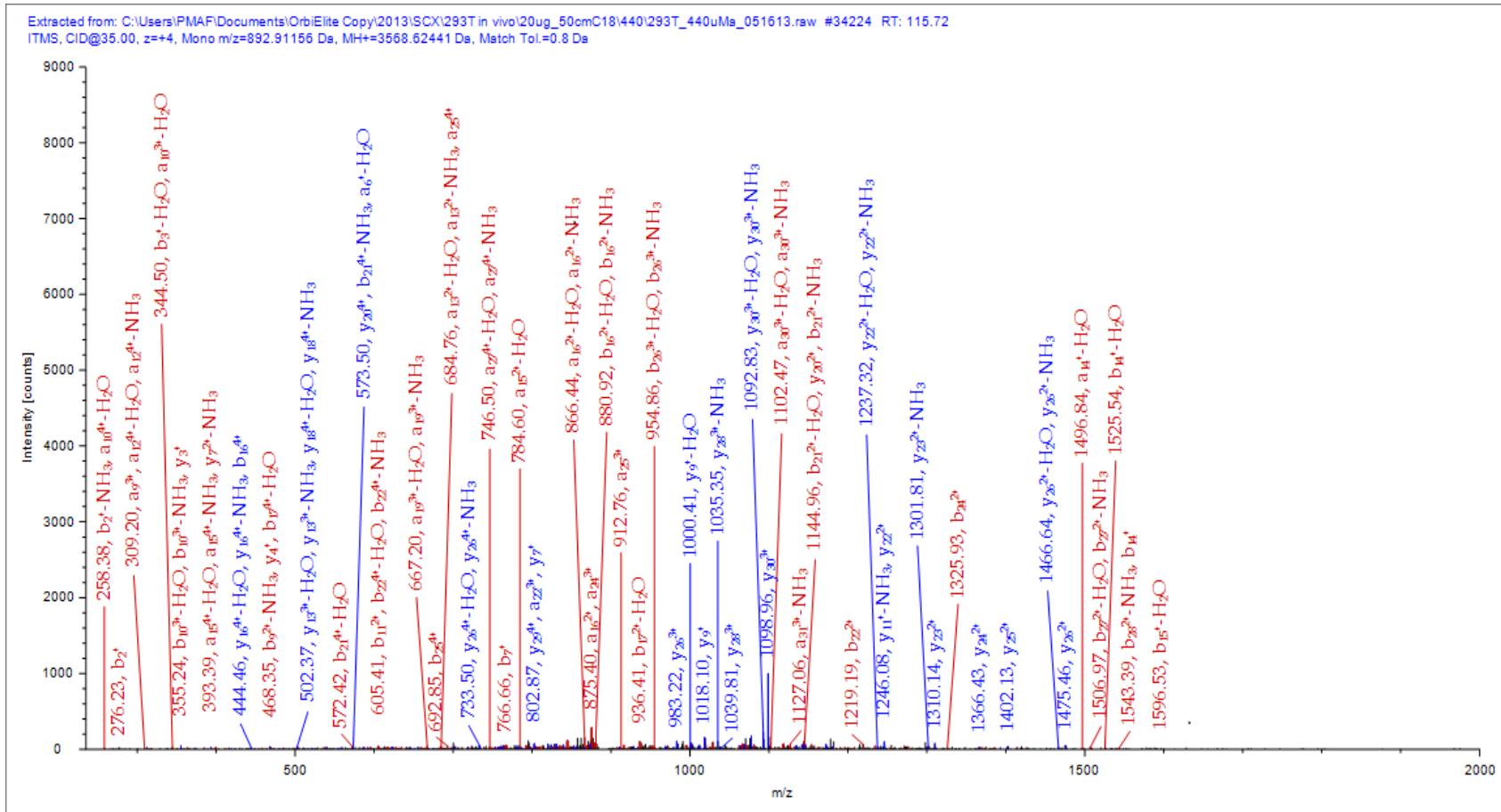


FICEQDHQNFLR_C3_SO3H



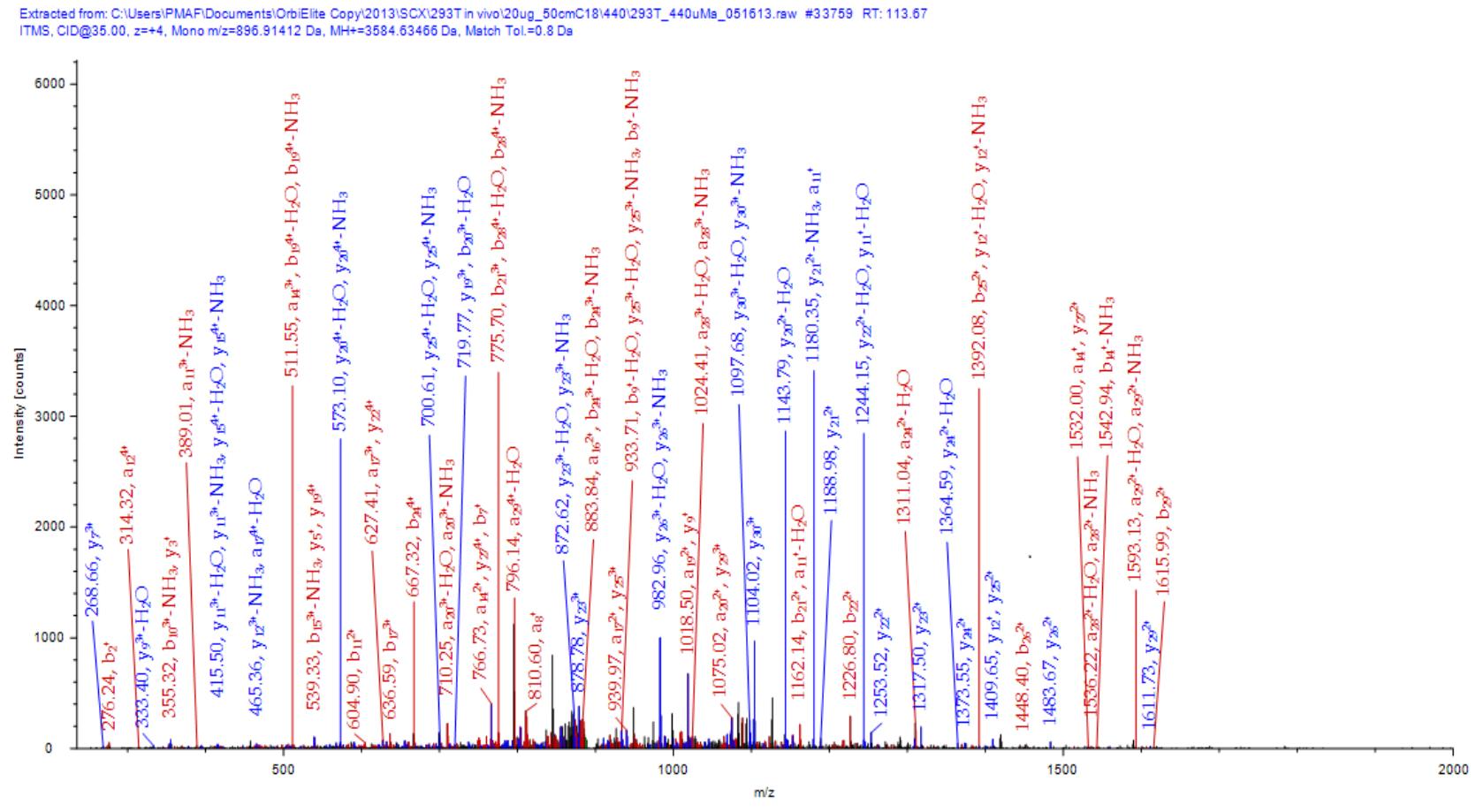
FQSSAVMALQEACEAYLVGLFEDTNLCAIH

AK_C13_SO2H_C27_SO3H



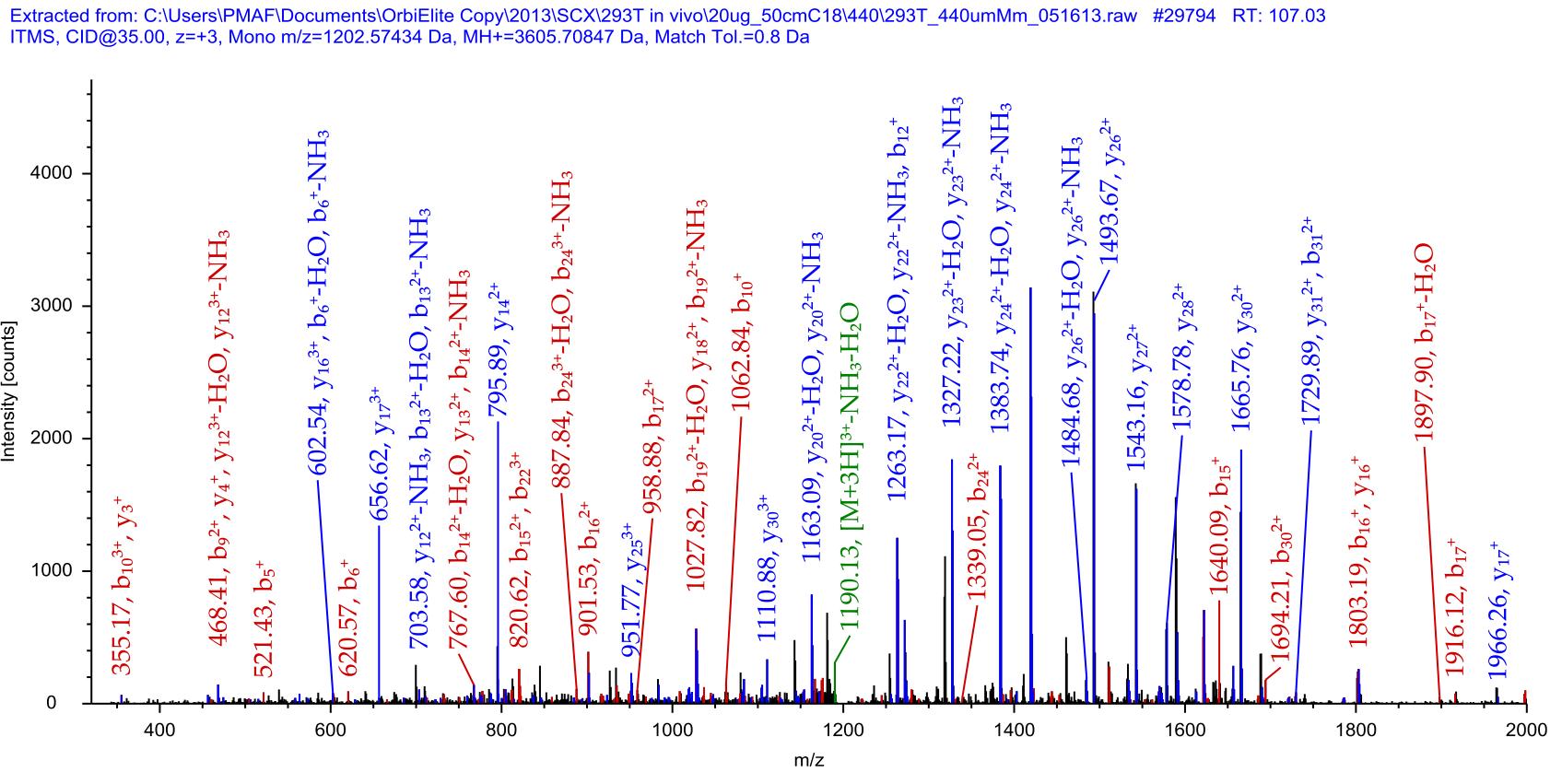
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AK_C13_SO3H_C27_SO3H



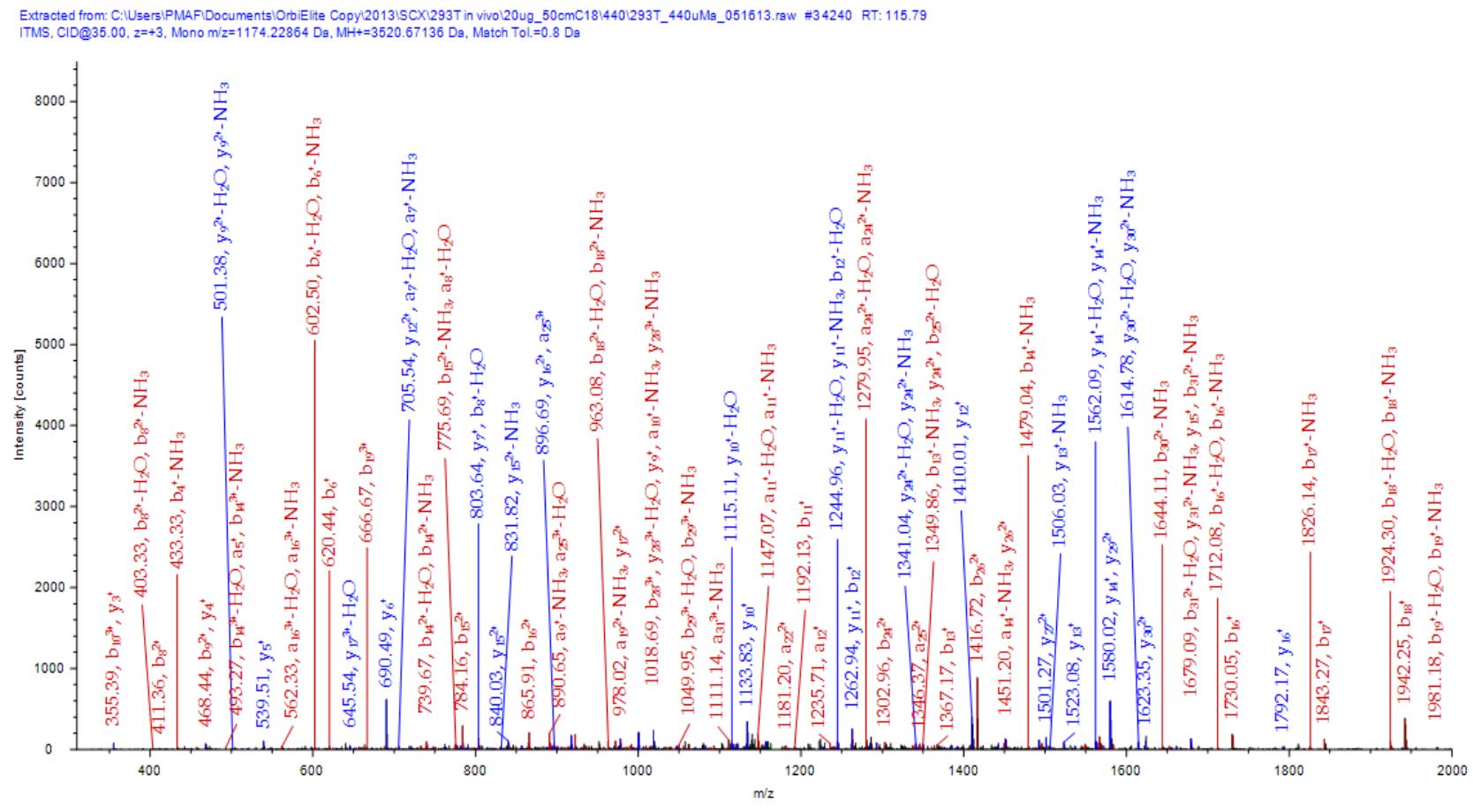
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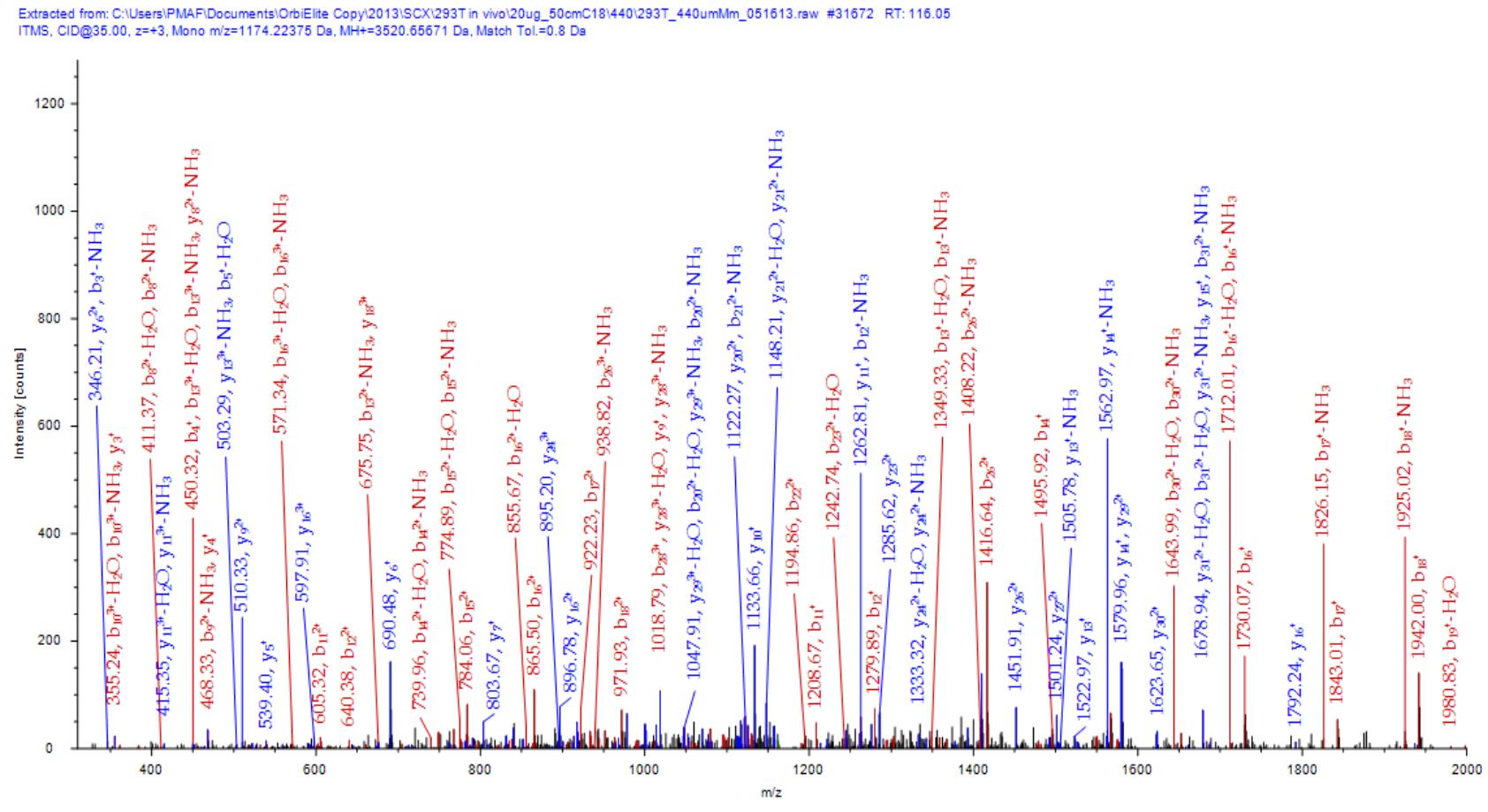
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AK_C27_SO3H

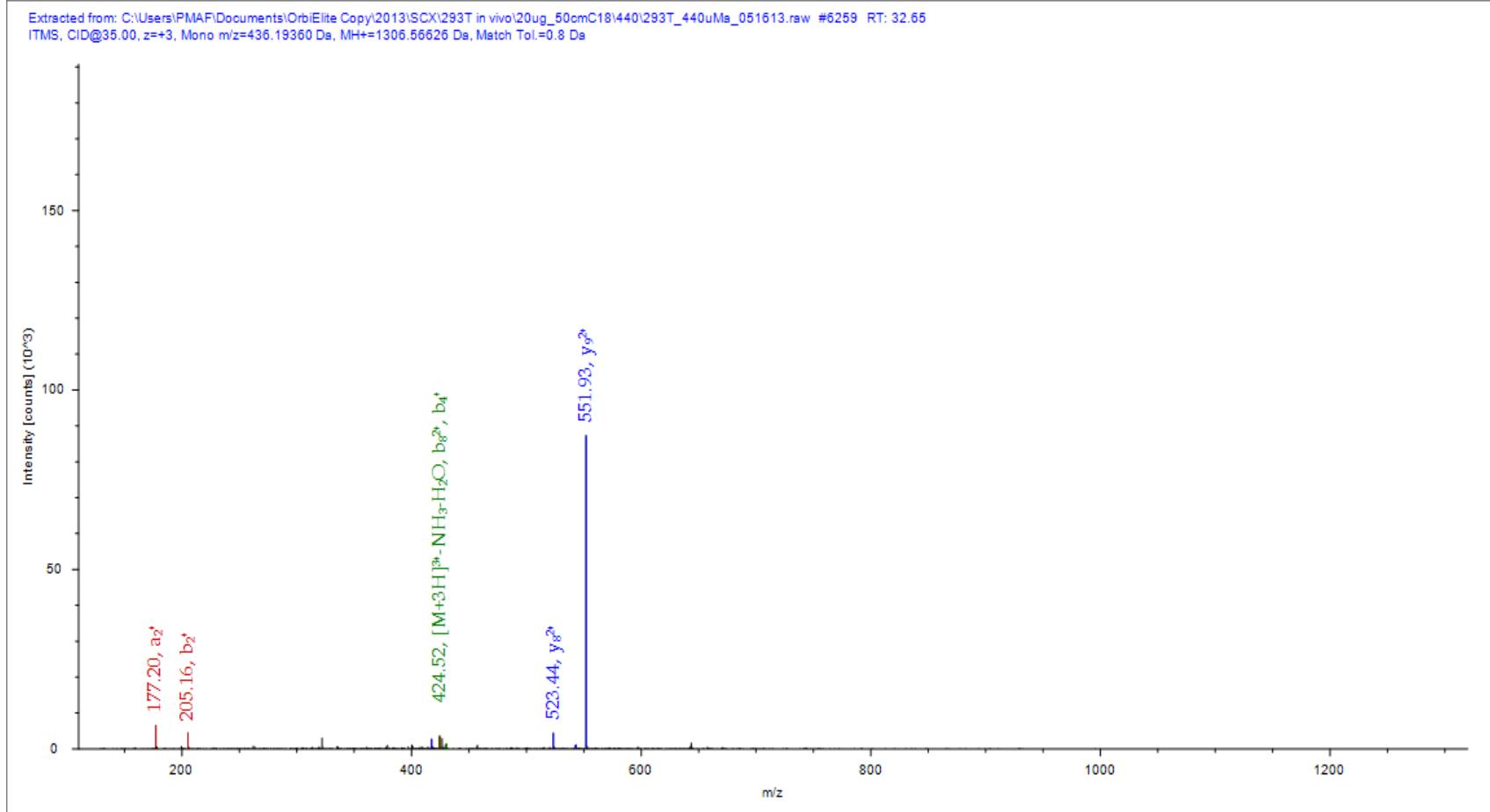


FQSSAVMALQEASEAYLVGLFEDTNLCAIH

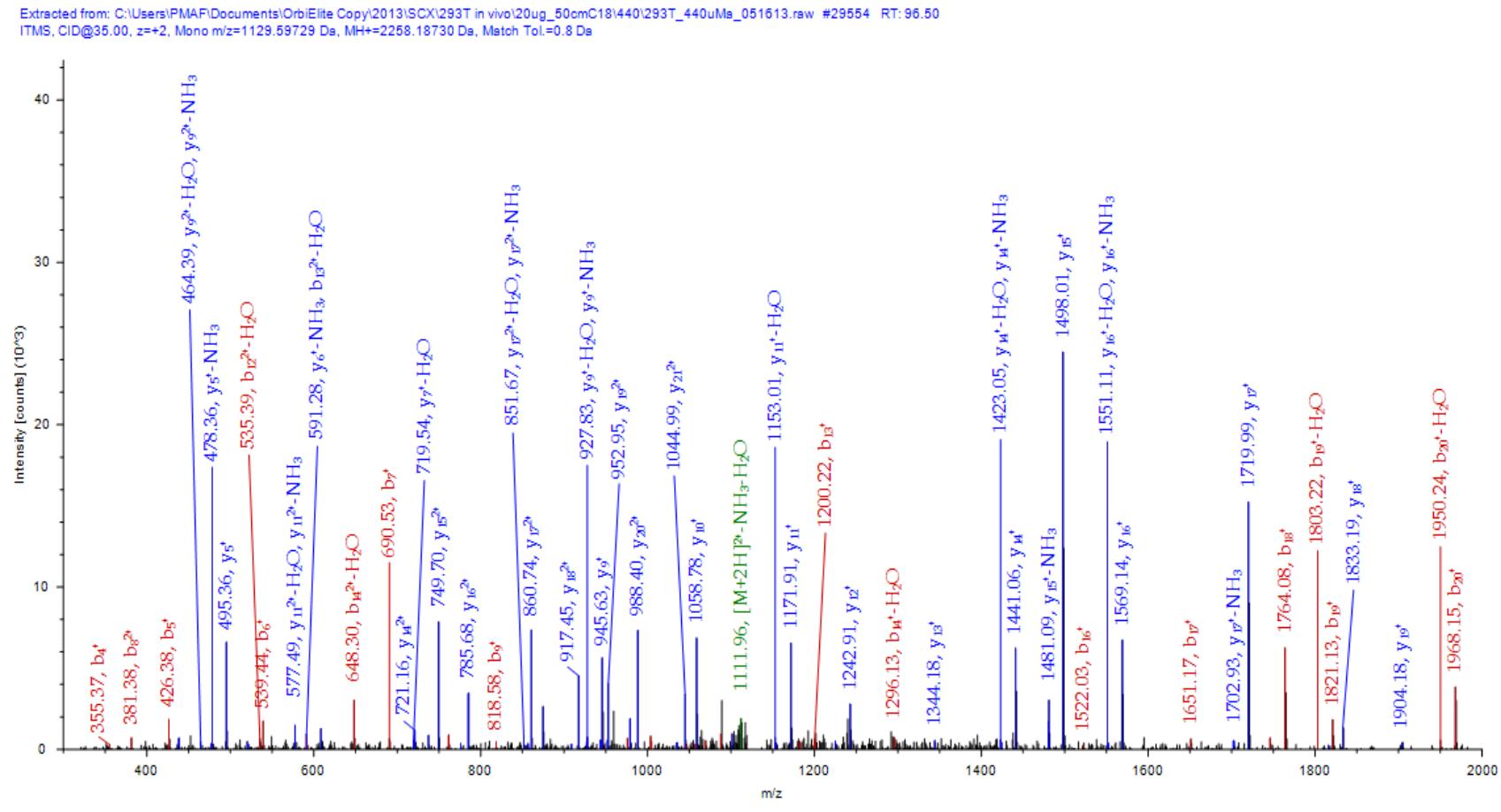
AK_C27_SO3H



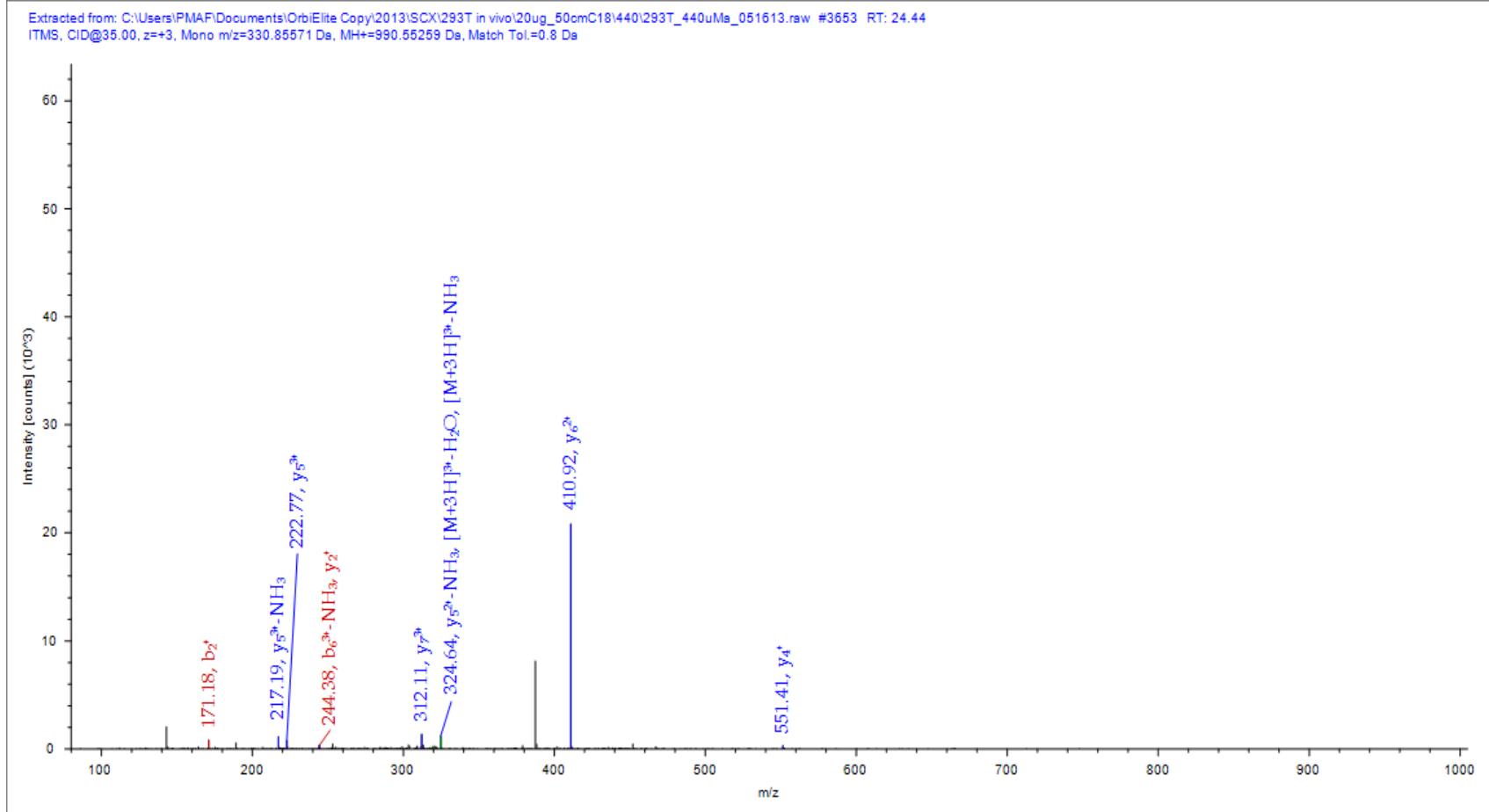
GFGYKGSCFHR_C8_SO3H



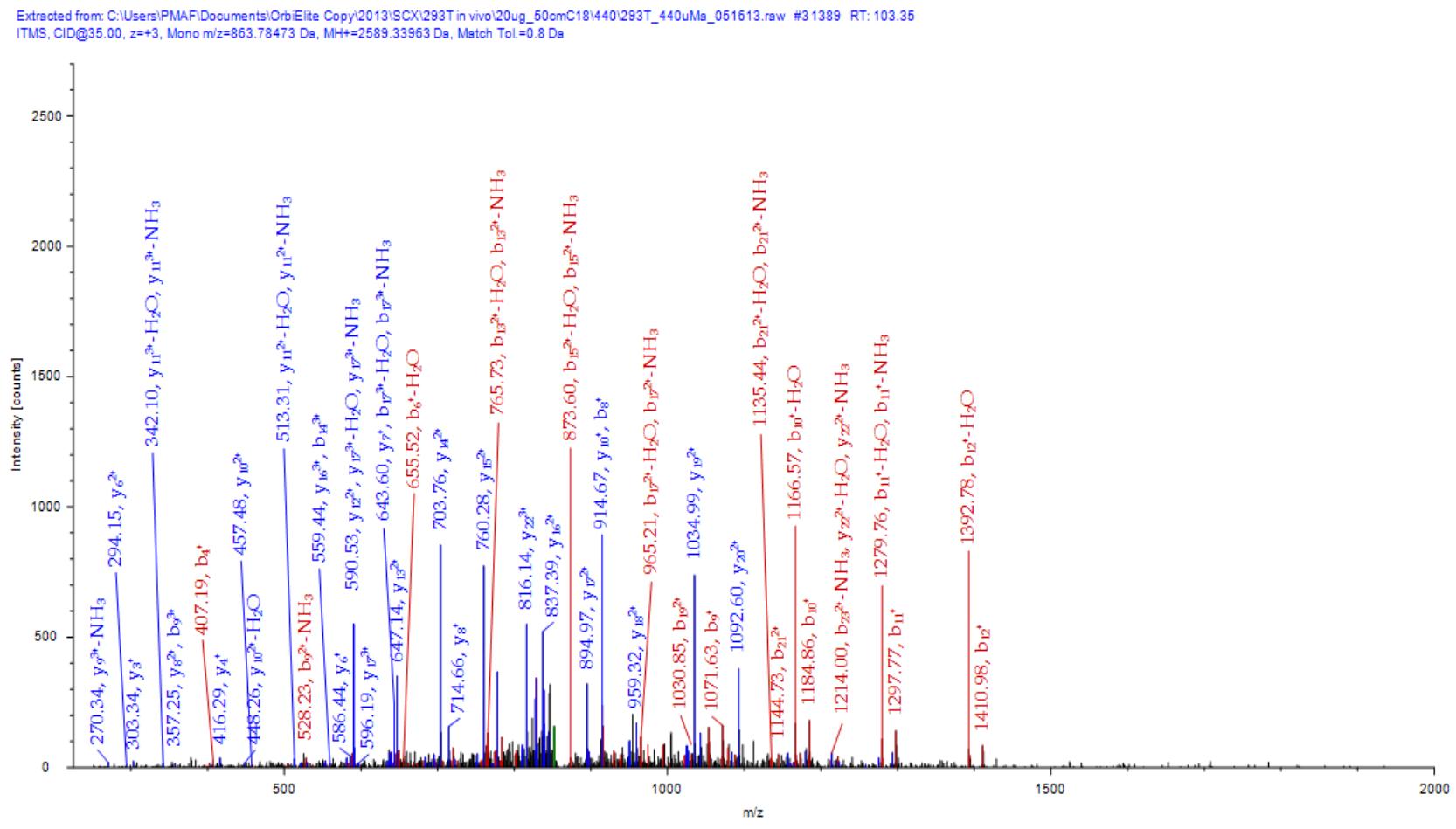
GLIAAICAGPTALLAHEIGFGSK_C7_SO3H



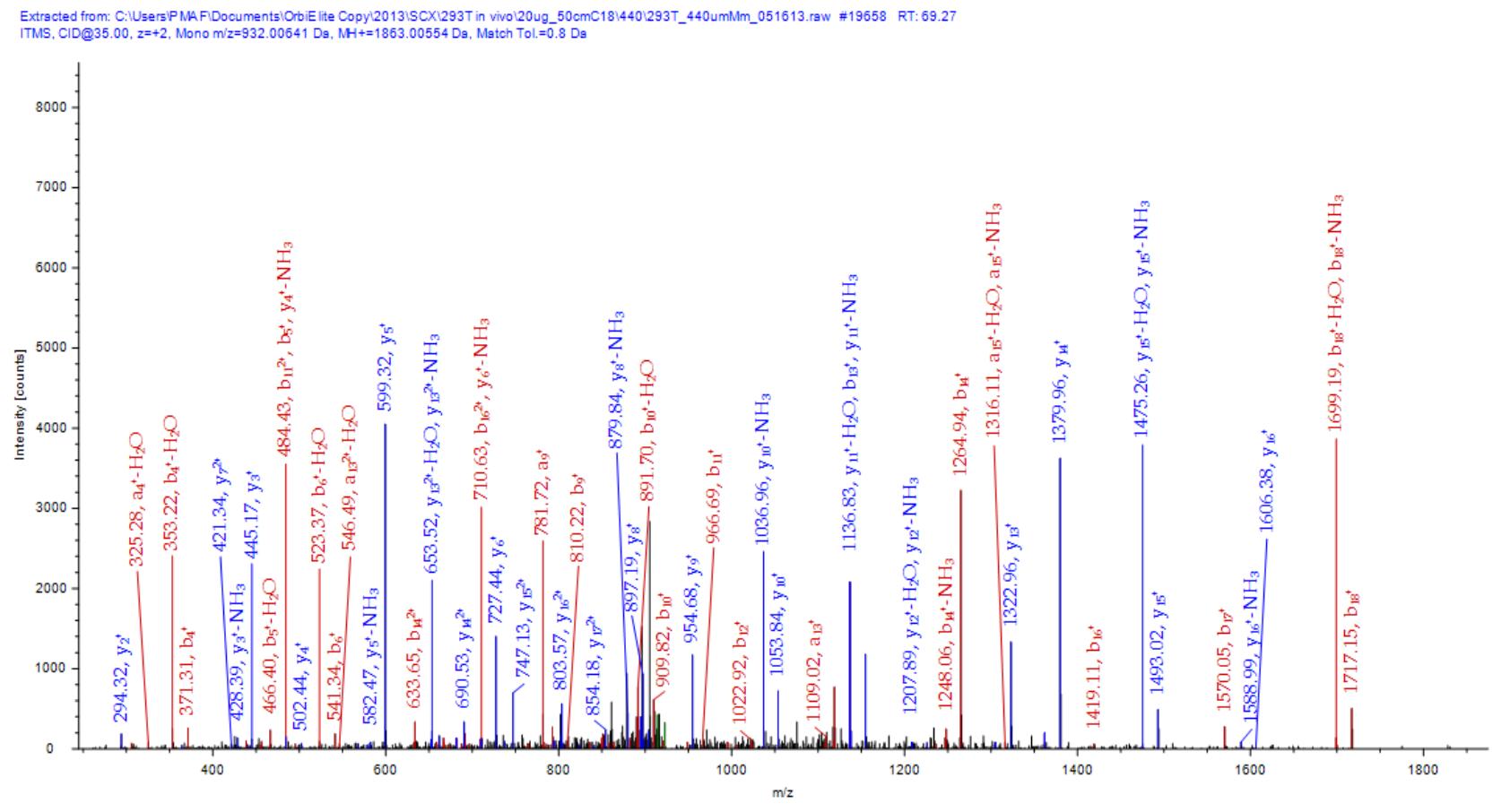
GLRLCRPK_C5_SO3H



GSDFDCELRLLIHQSLAGGIIGVK_C6_SO3H

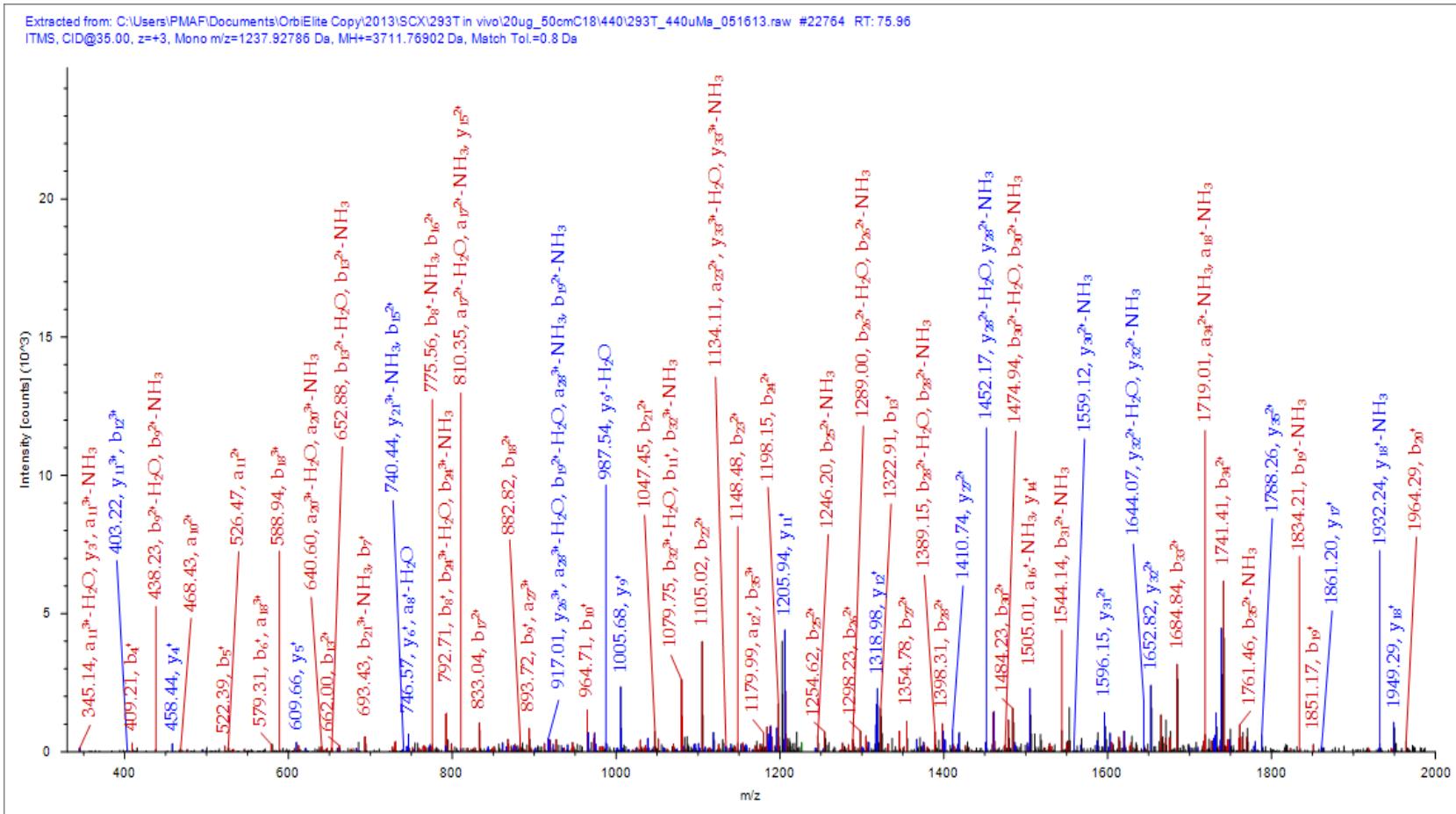


GVTIIGPATVGGIKPGCFK_C17_SO3H

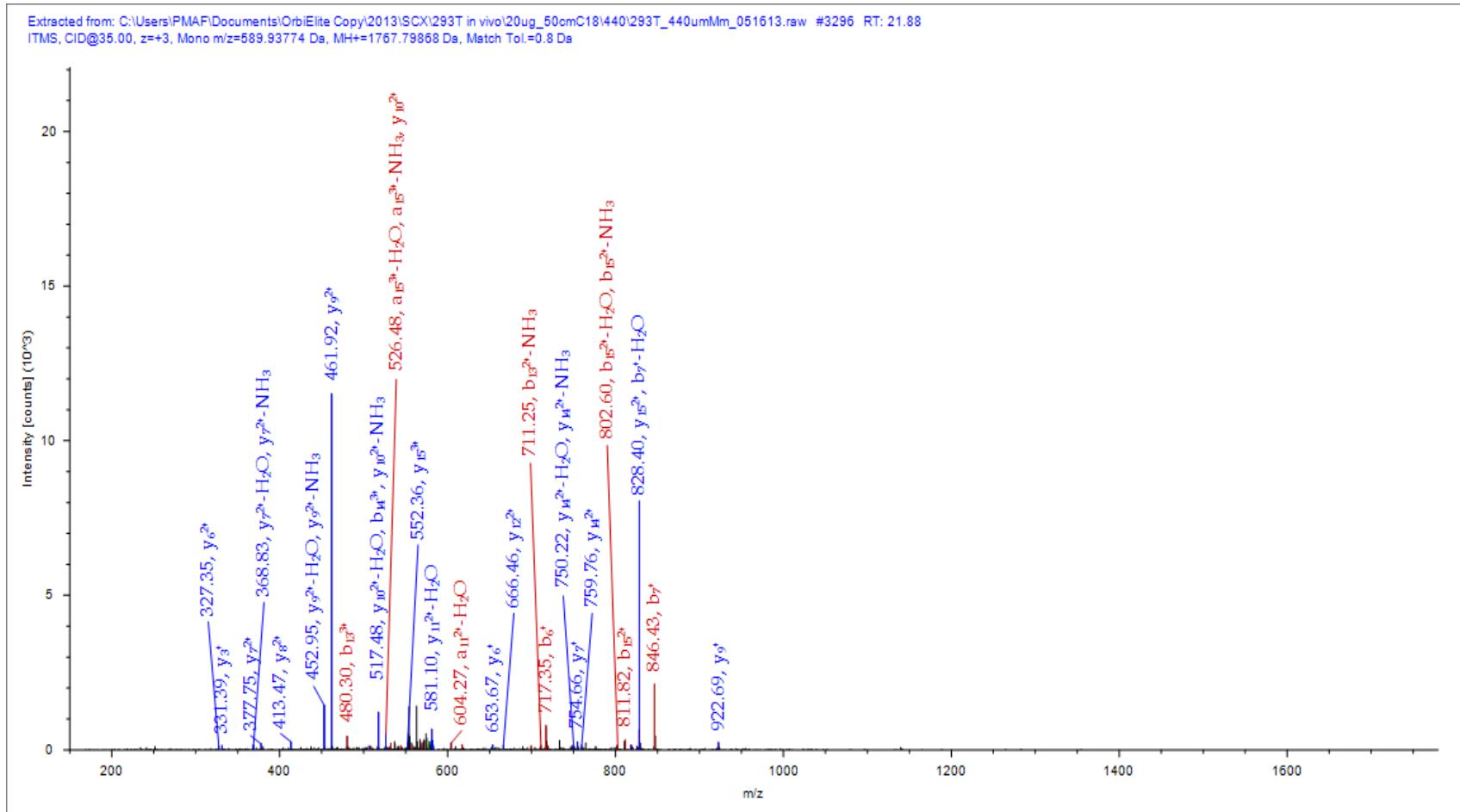


HVGDLGNVTADKDGVADVSIEDSVISLSG

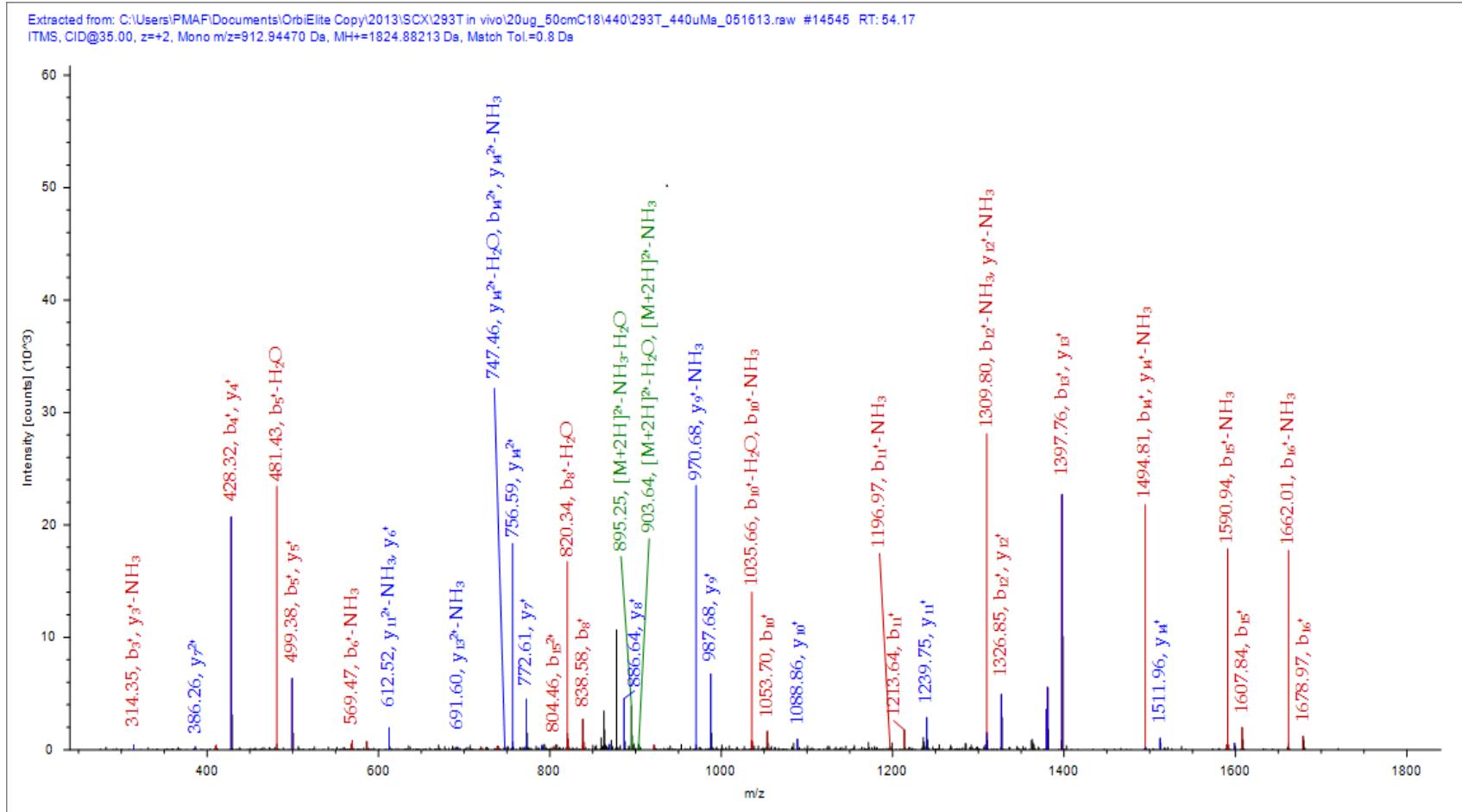
DHCIIGR_C32_SO3H



IHEGCEEPATHNALAK_C5_SO3H

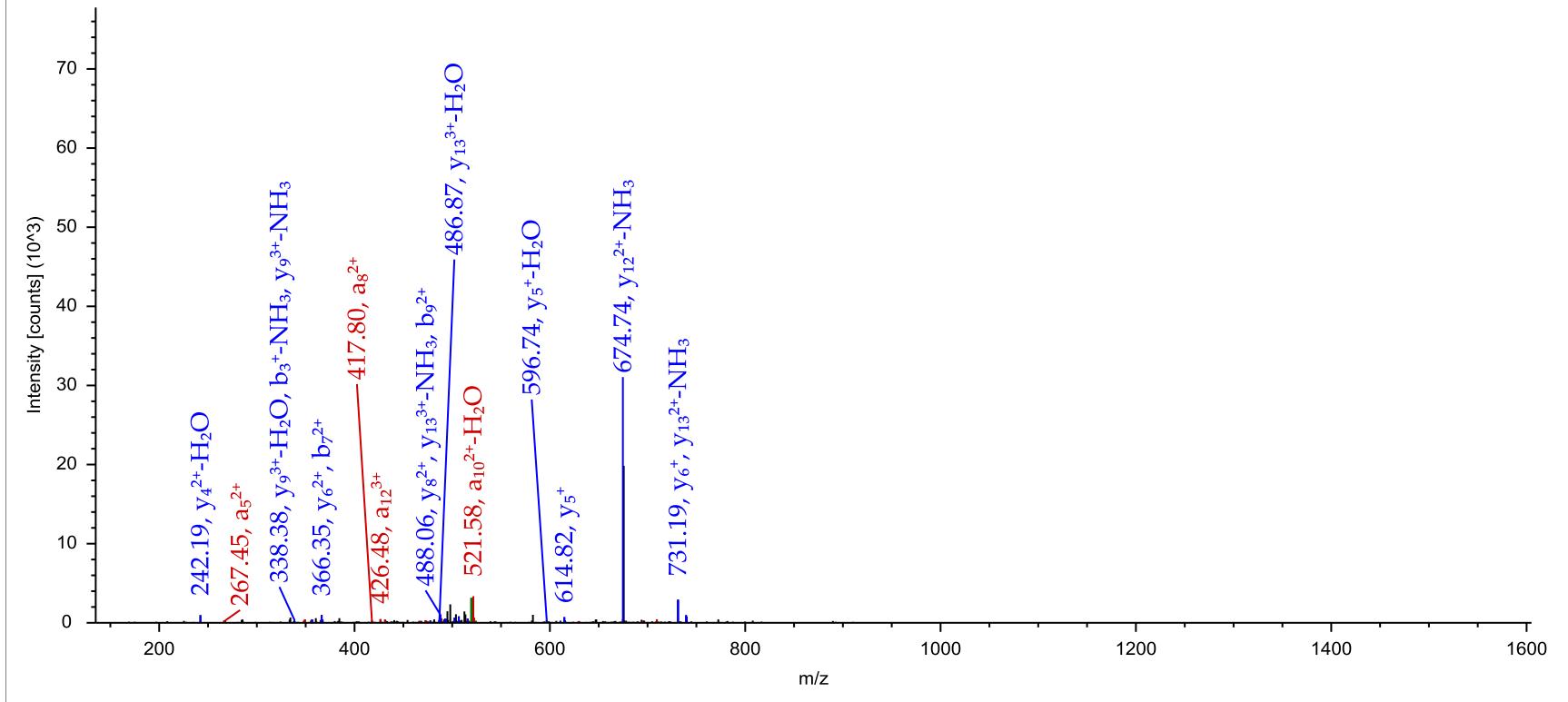


IISNASCTTNCLAPLAK_C7_SO3H

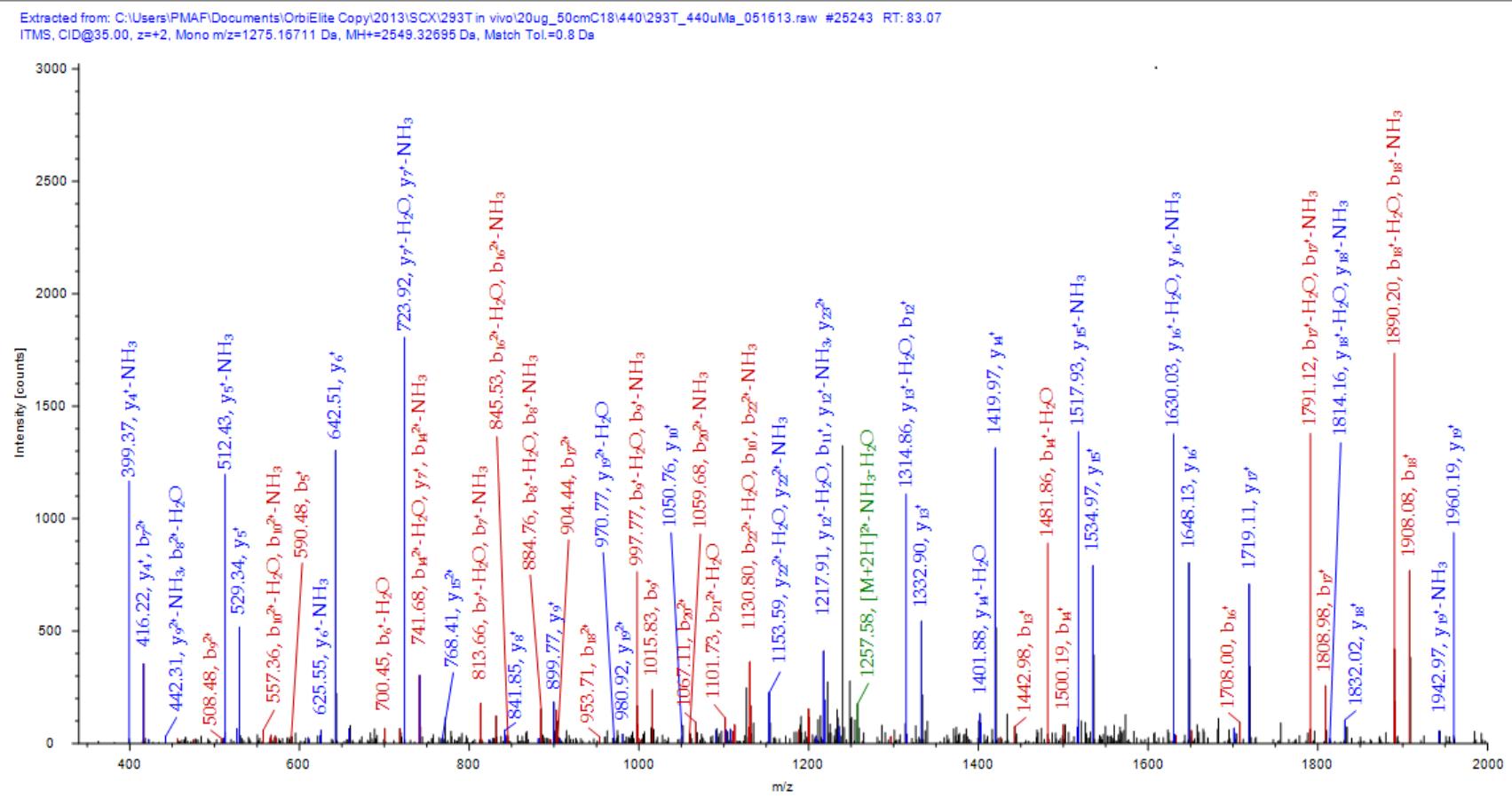


ILKCAGNEDIITLR C4 SO2H

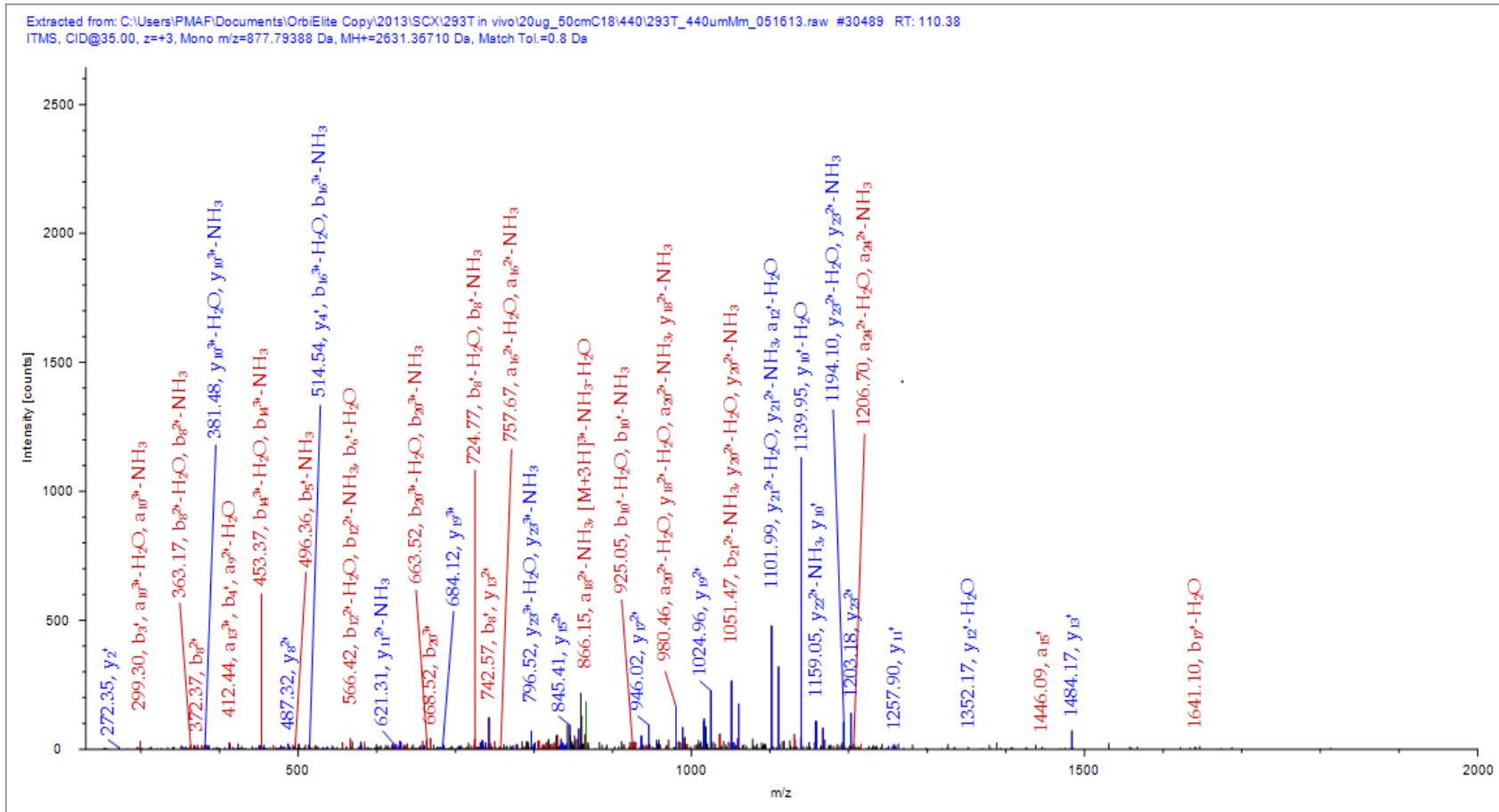
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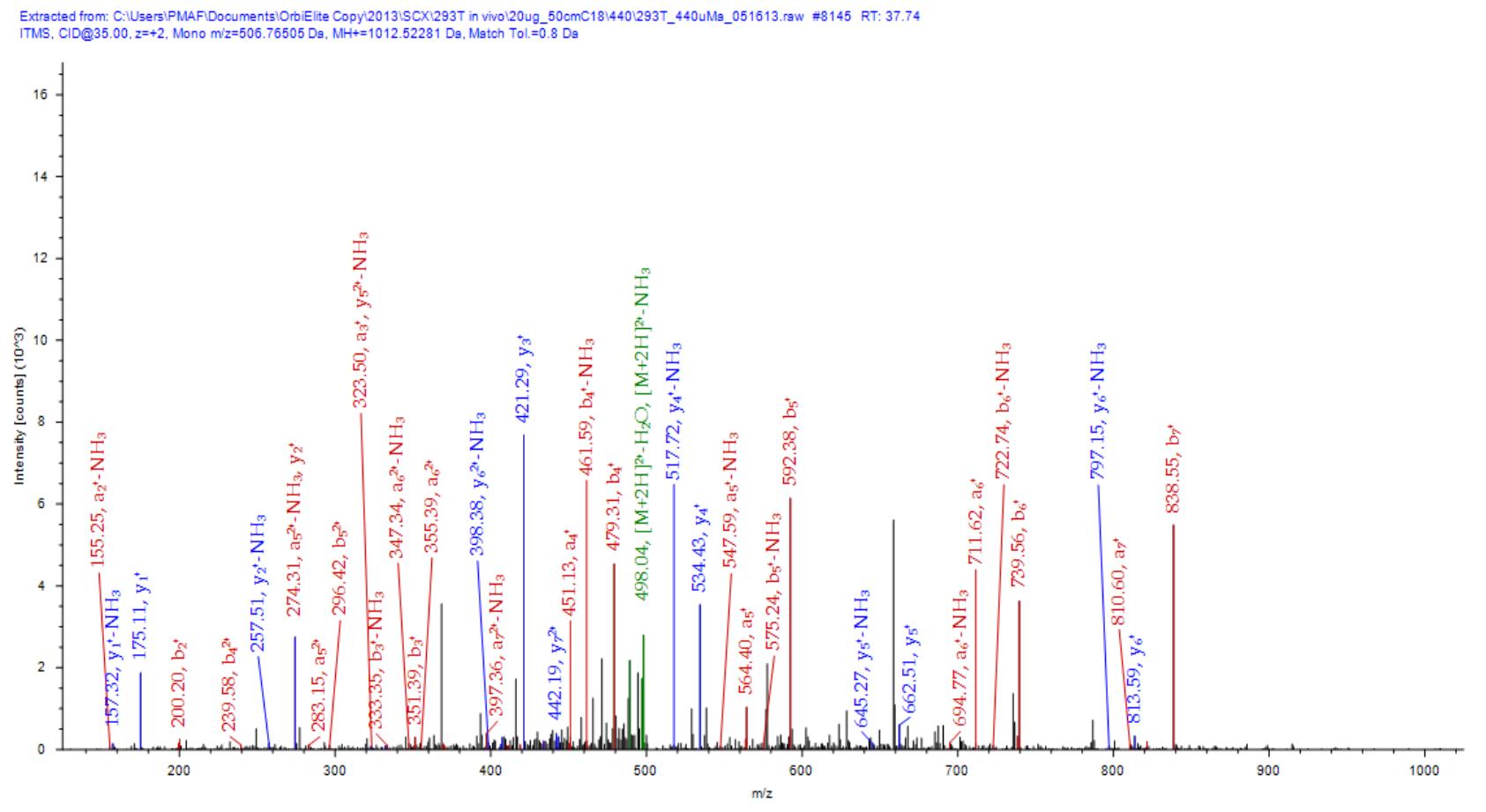
ILTFDQLALDSPKGCGTVLLSGPR_C15_SO3H



INALTAASEAACLIVSVDETIKNPR_C12_SO2H

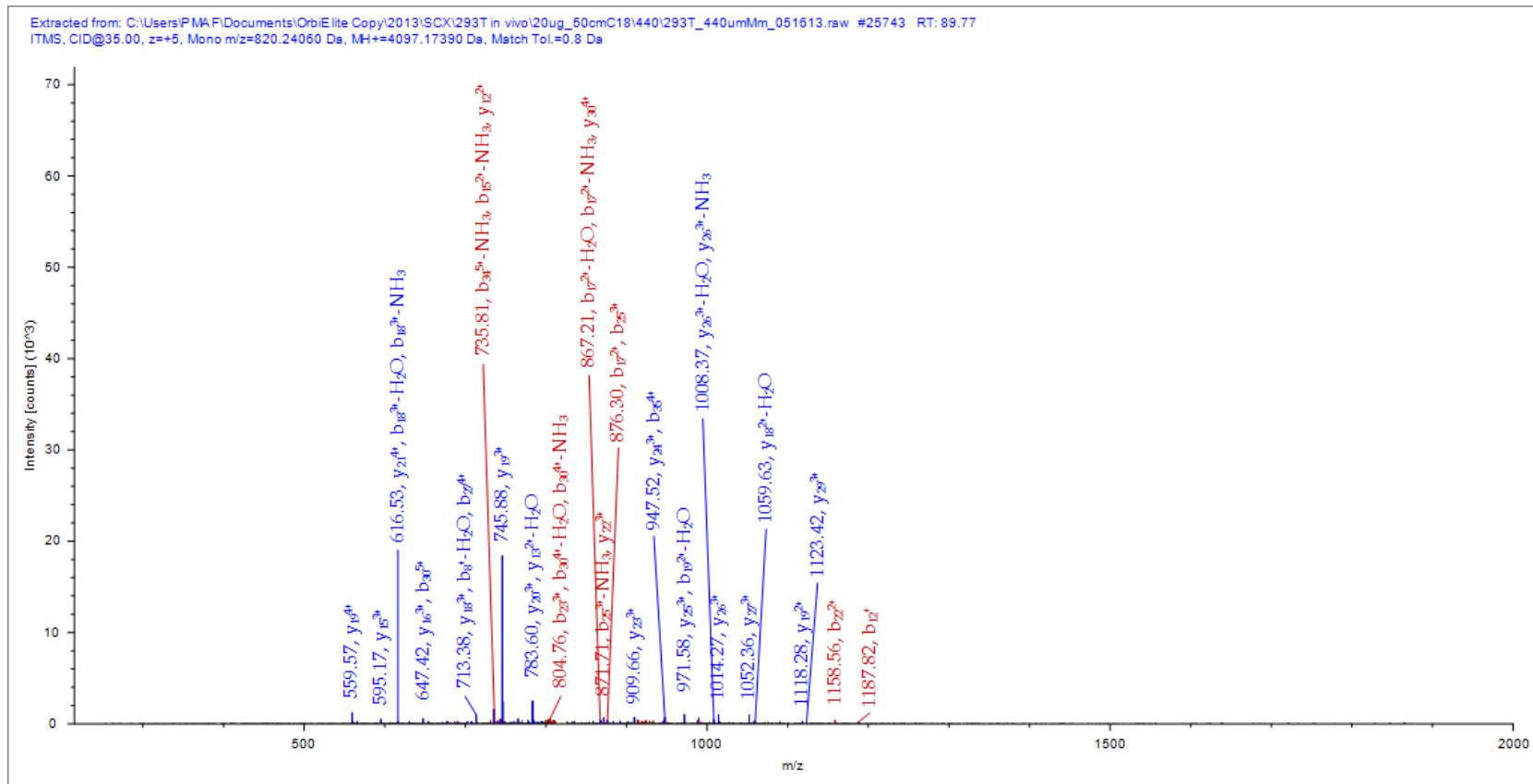


KACQIFVR_C3_SO3H

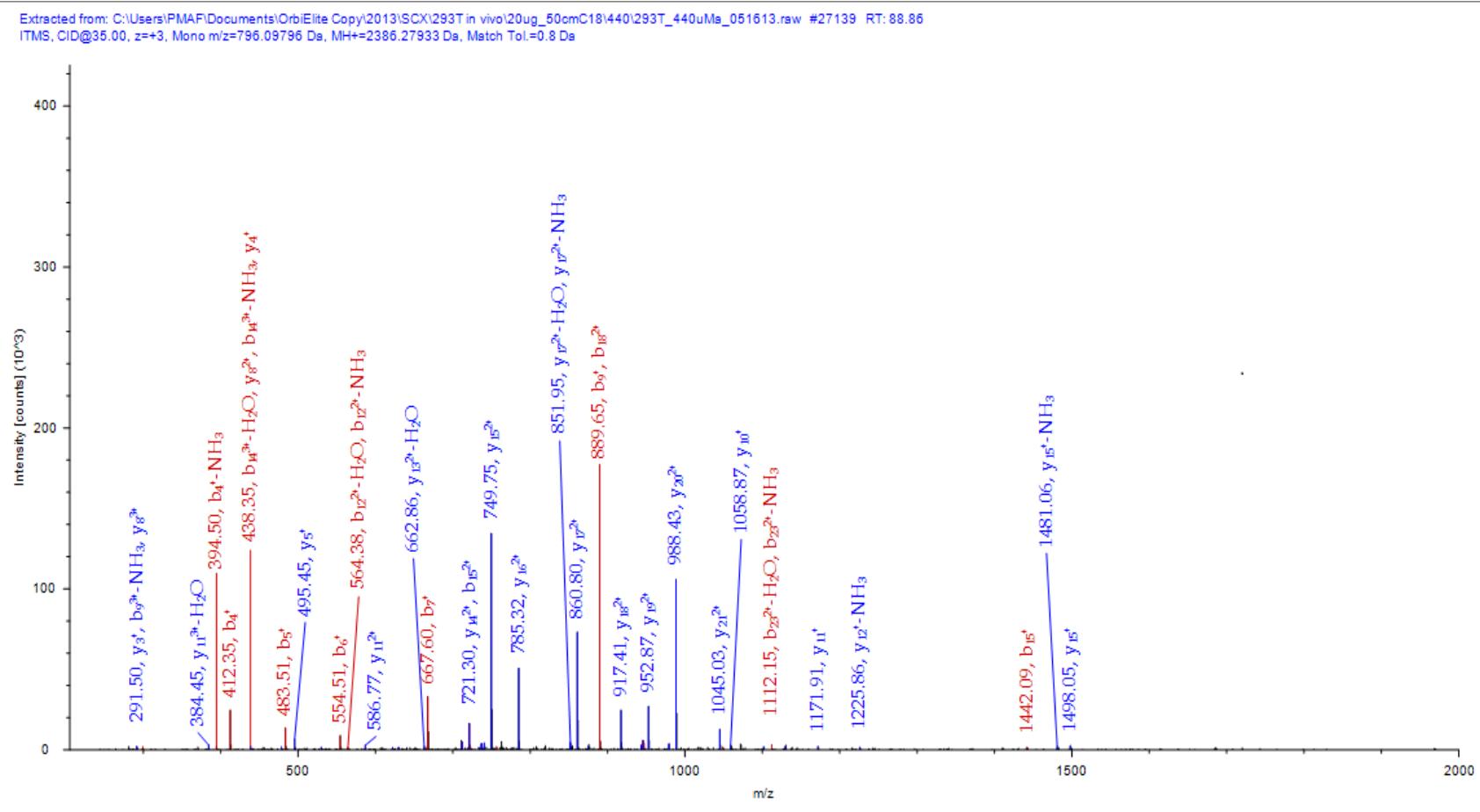


KDGNASGTTLEALDCILPPTRPTDKPLRLP

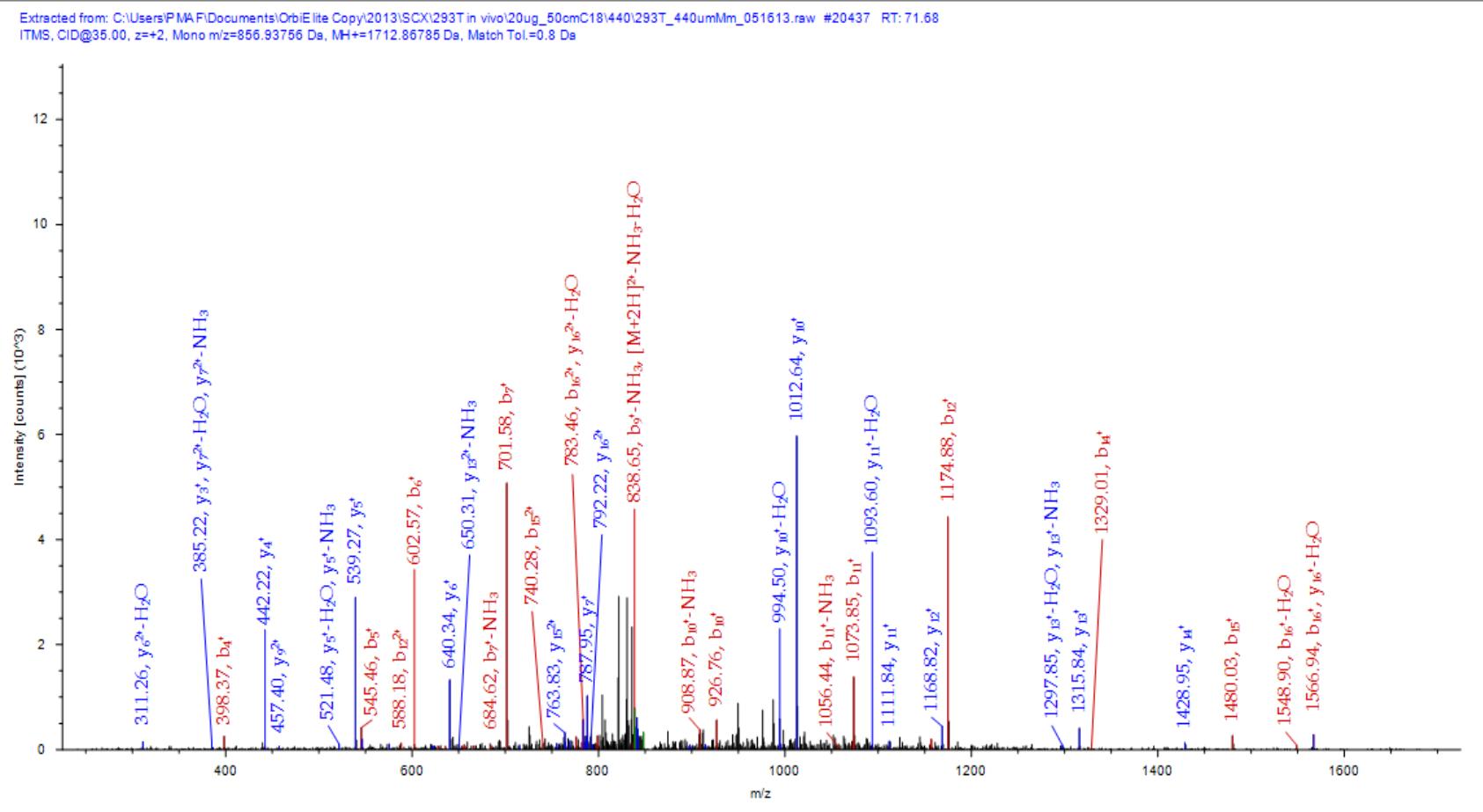
LQDVYK_C16_SO3H



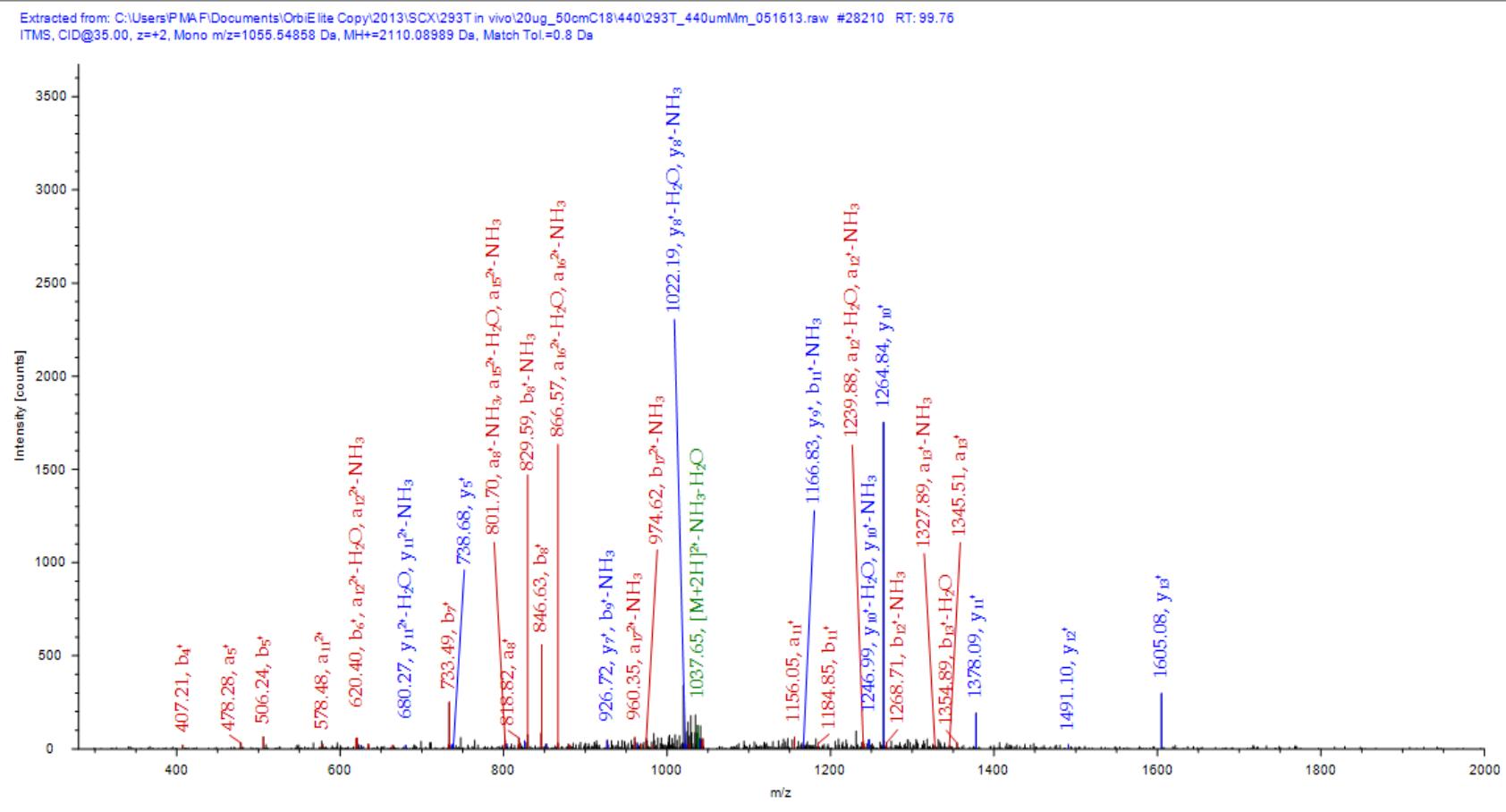
KGLIAAICAGPTALLAHEIGFGSK_C8_ SO3H



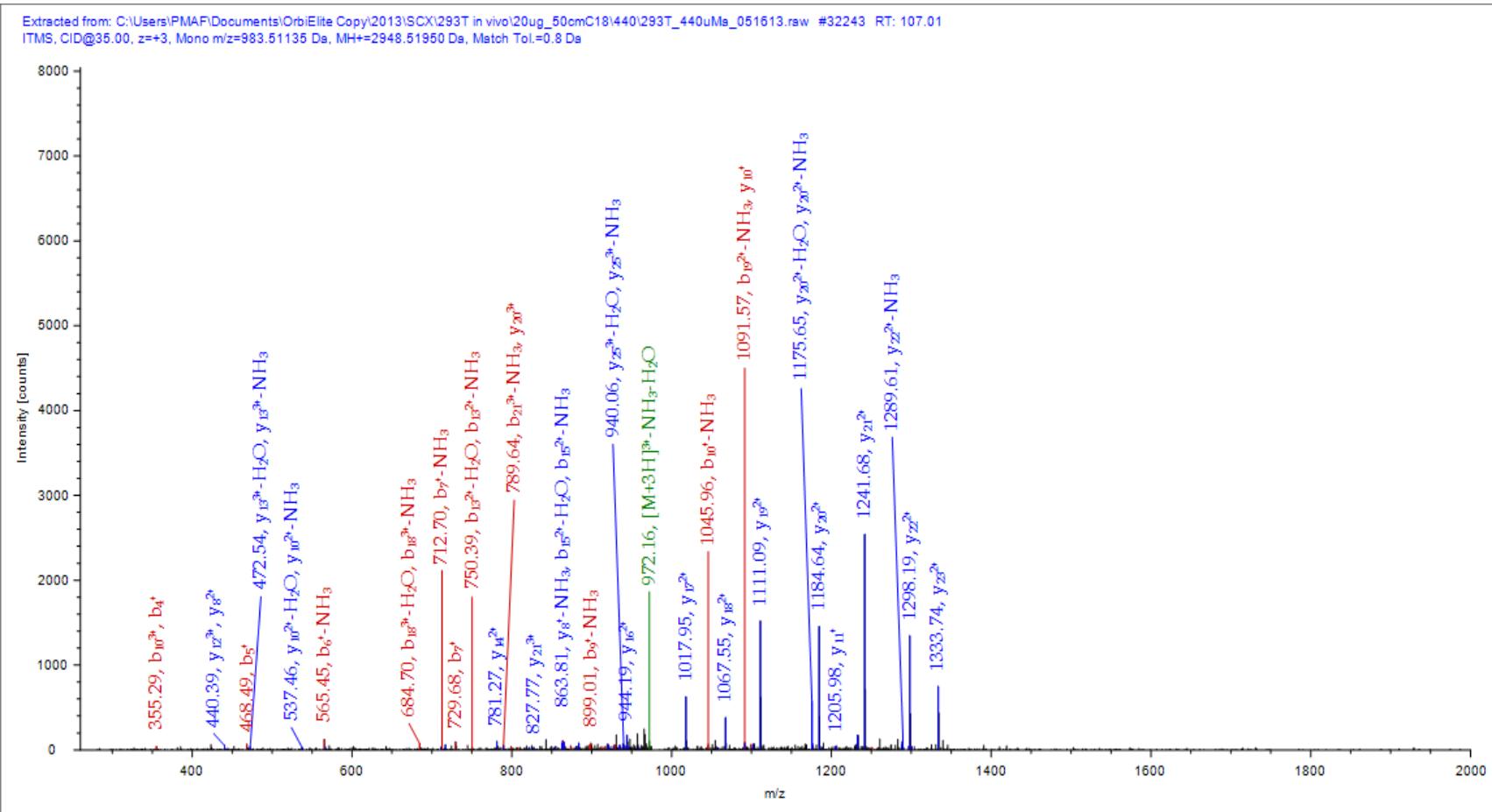
KGVLFGVPGAFTPGCSK_C15_SO3H



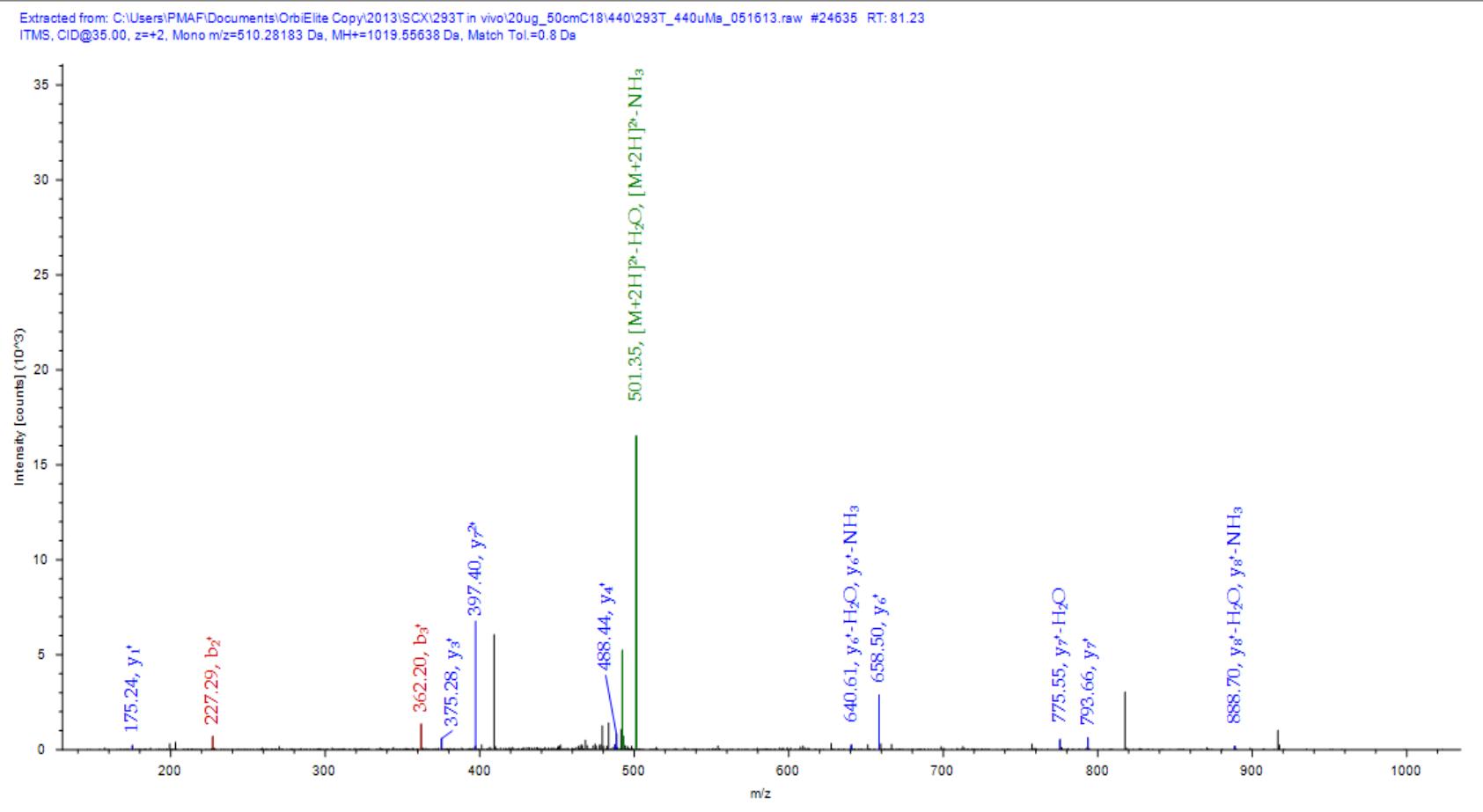
LAACVNLI^PQITSIYEWK_C3_SO3H



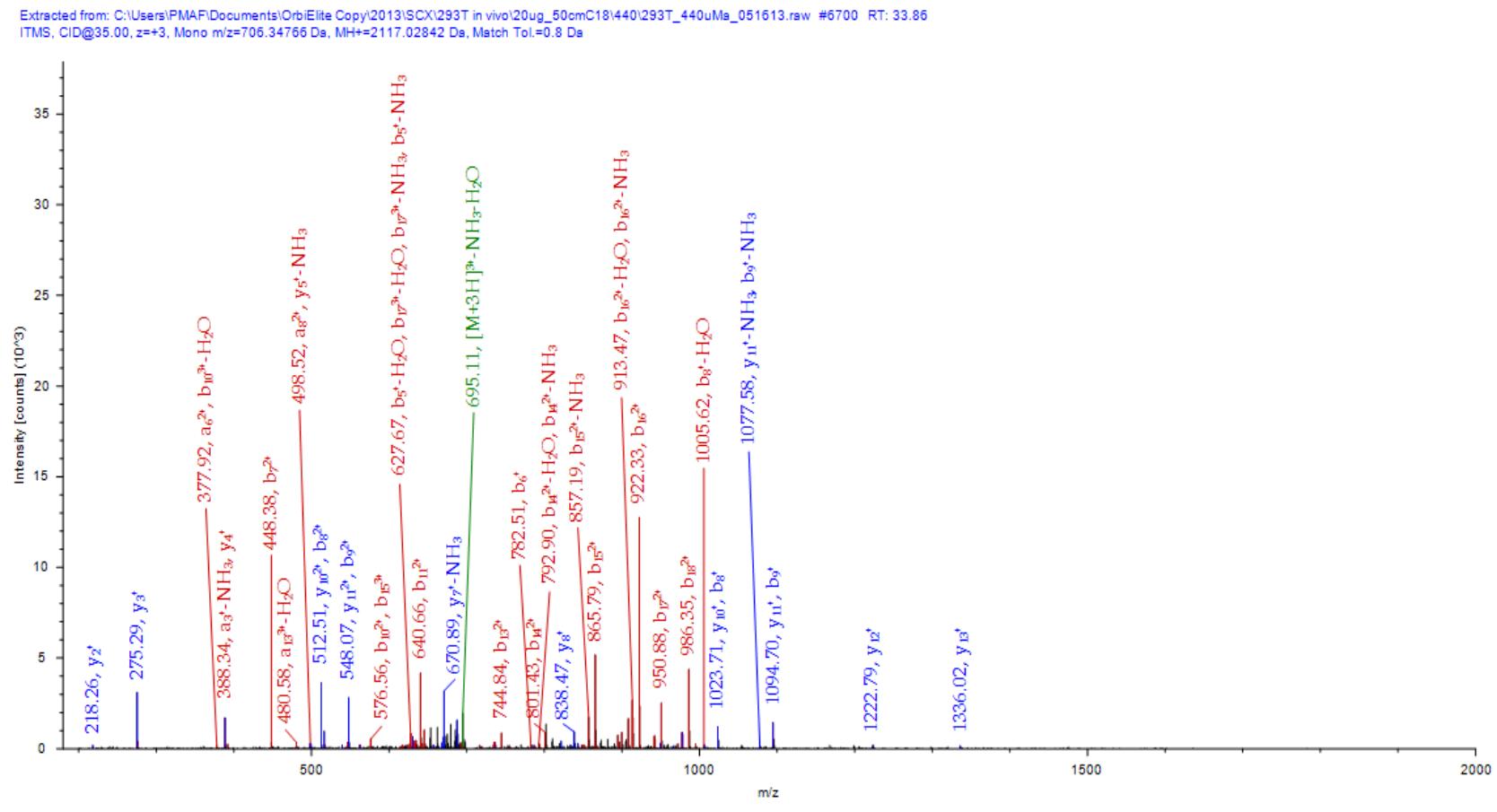
LGLALNFSVFYYEILNNPELACTLAK_C22_ SO2H



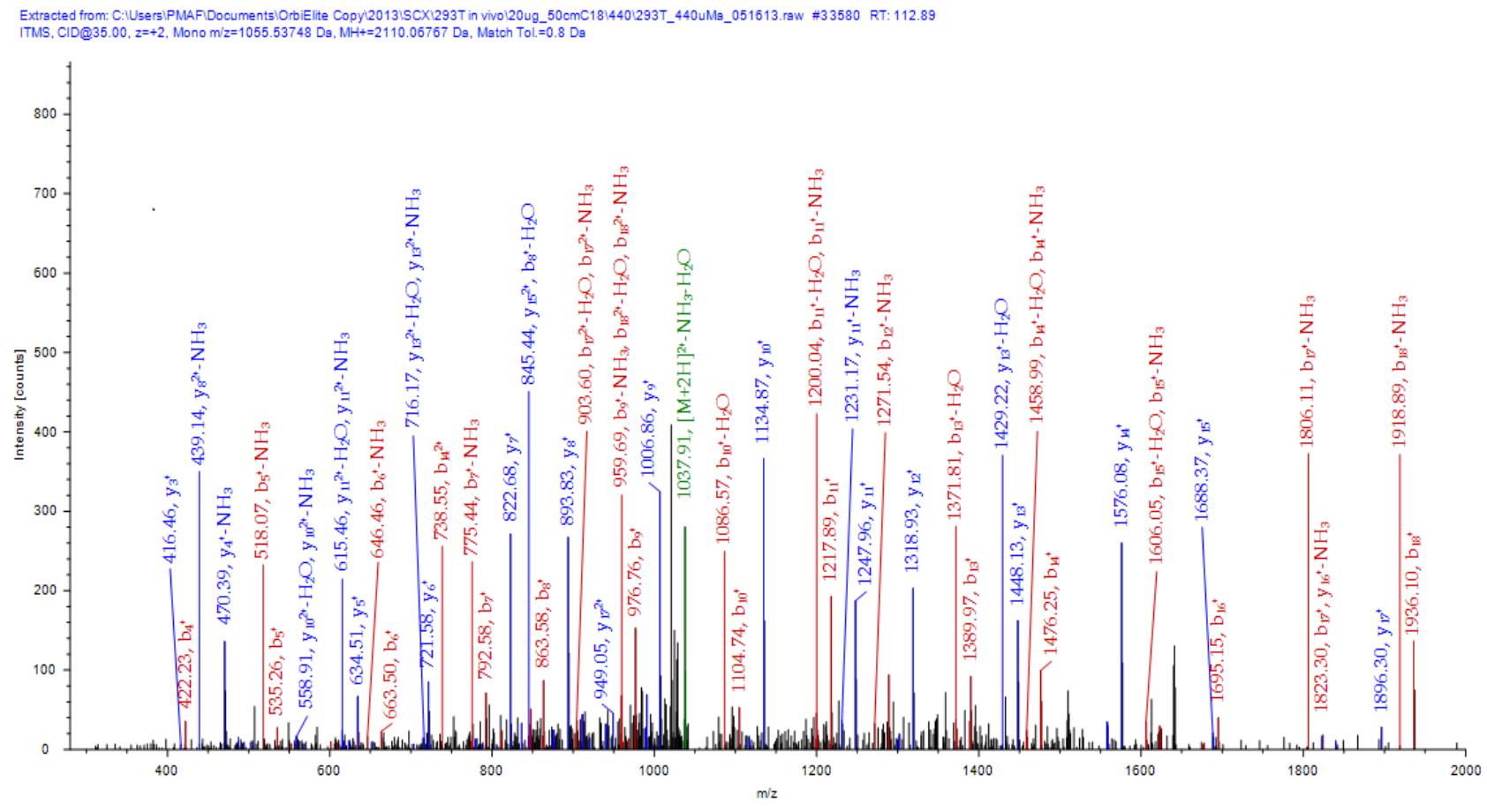
LLCGLLAER_C3_SO2H



MREIVHIQAGQCGNQIGAK_C12_SO3H

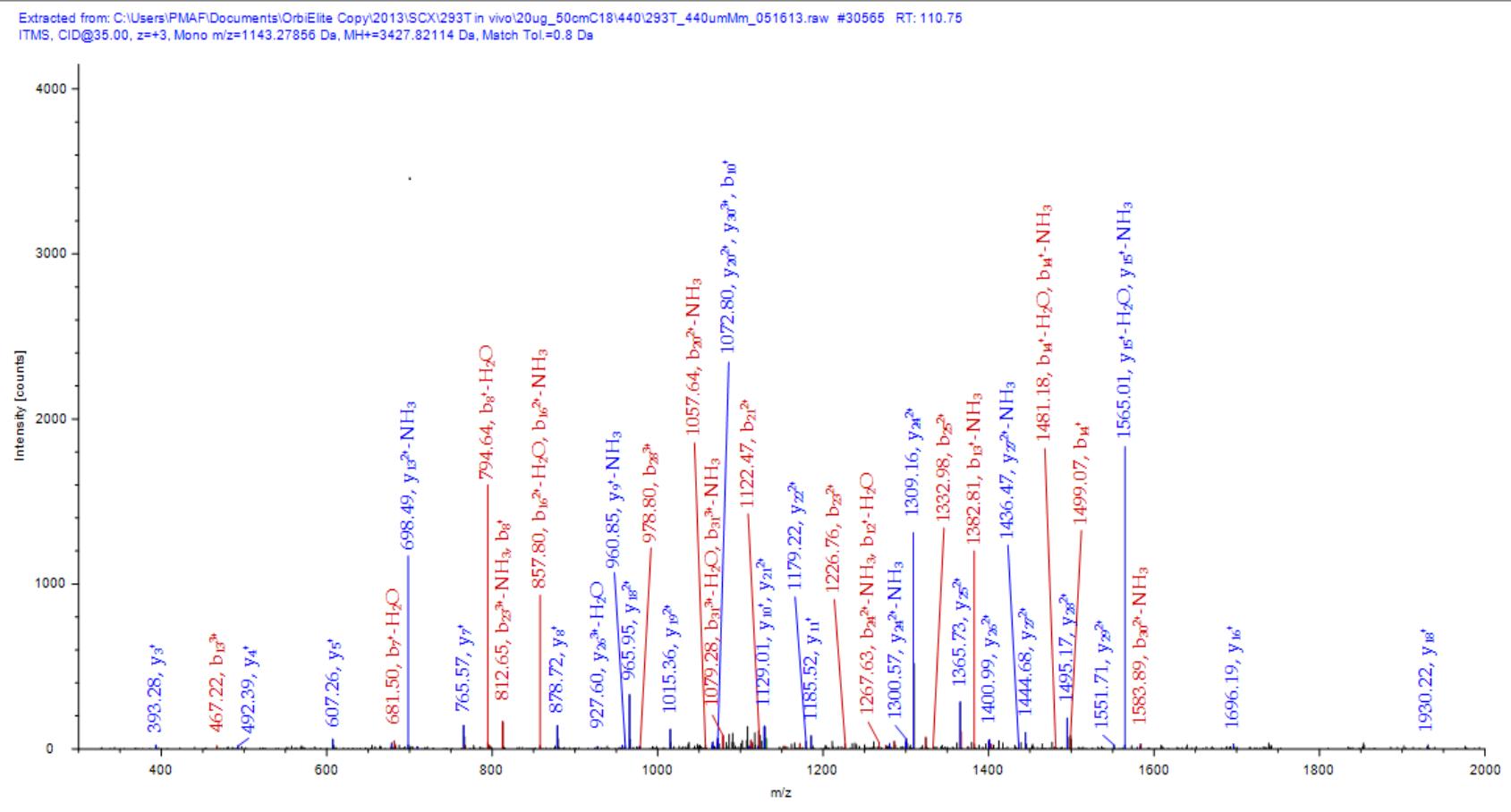


NVGCLQEALQLATSFAQLR_C4_SO3H

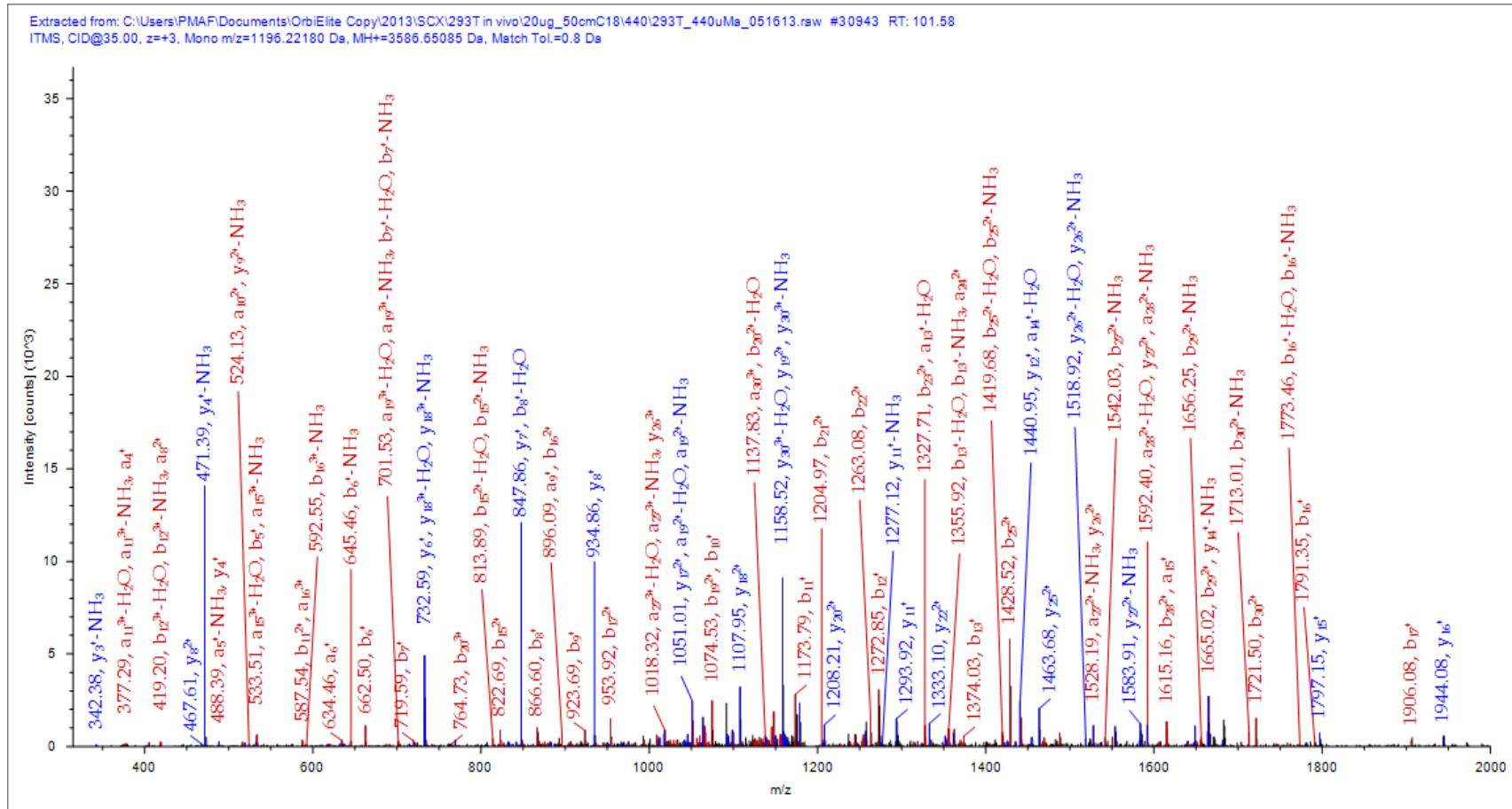


NVLITSALPYVNNVPHLGNIIGCVLSADVF

AR_C23_SO3H

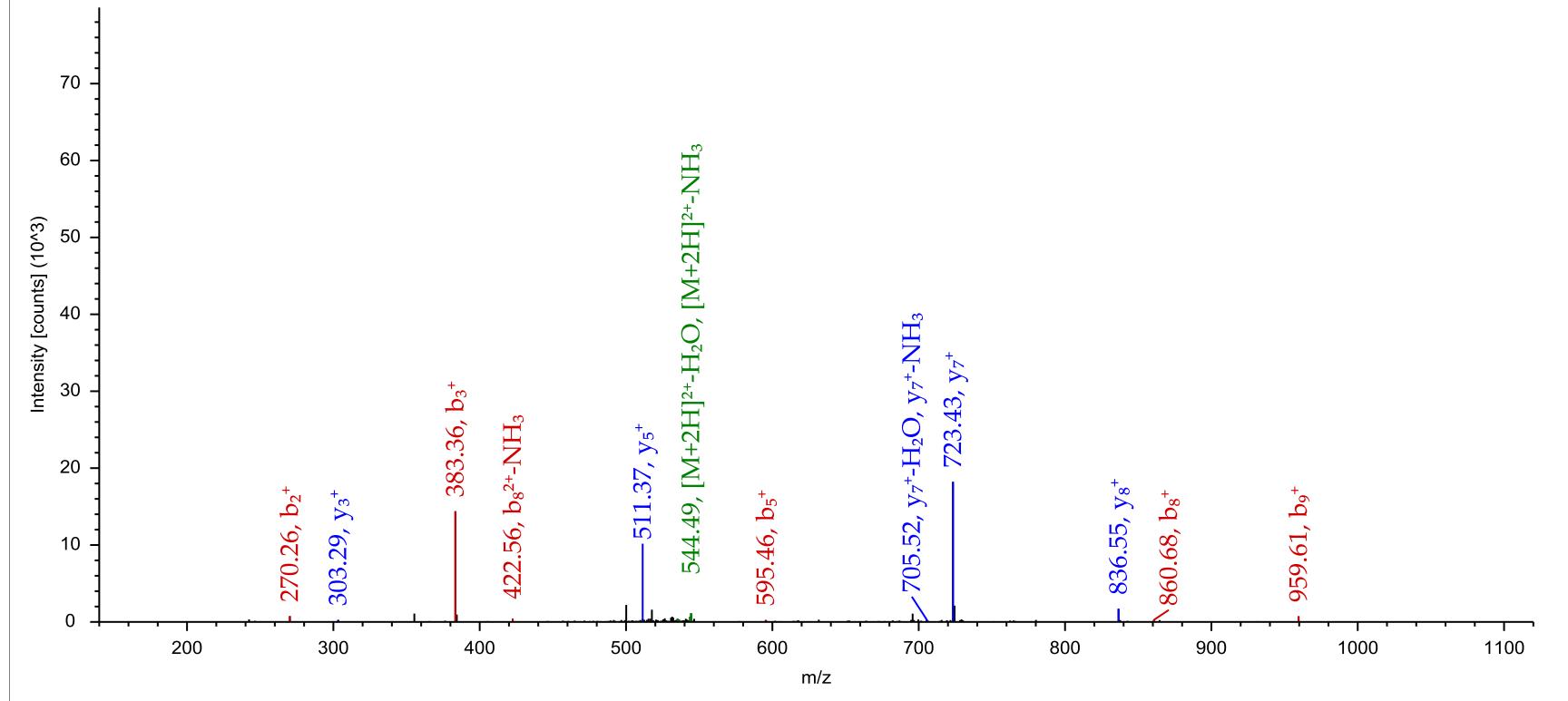


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LK_C10_SO3H

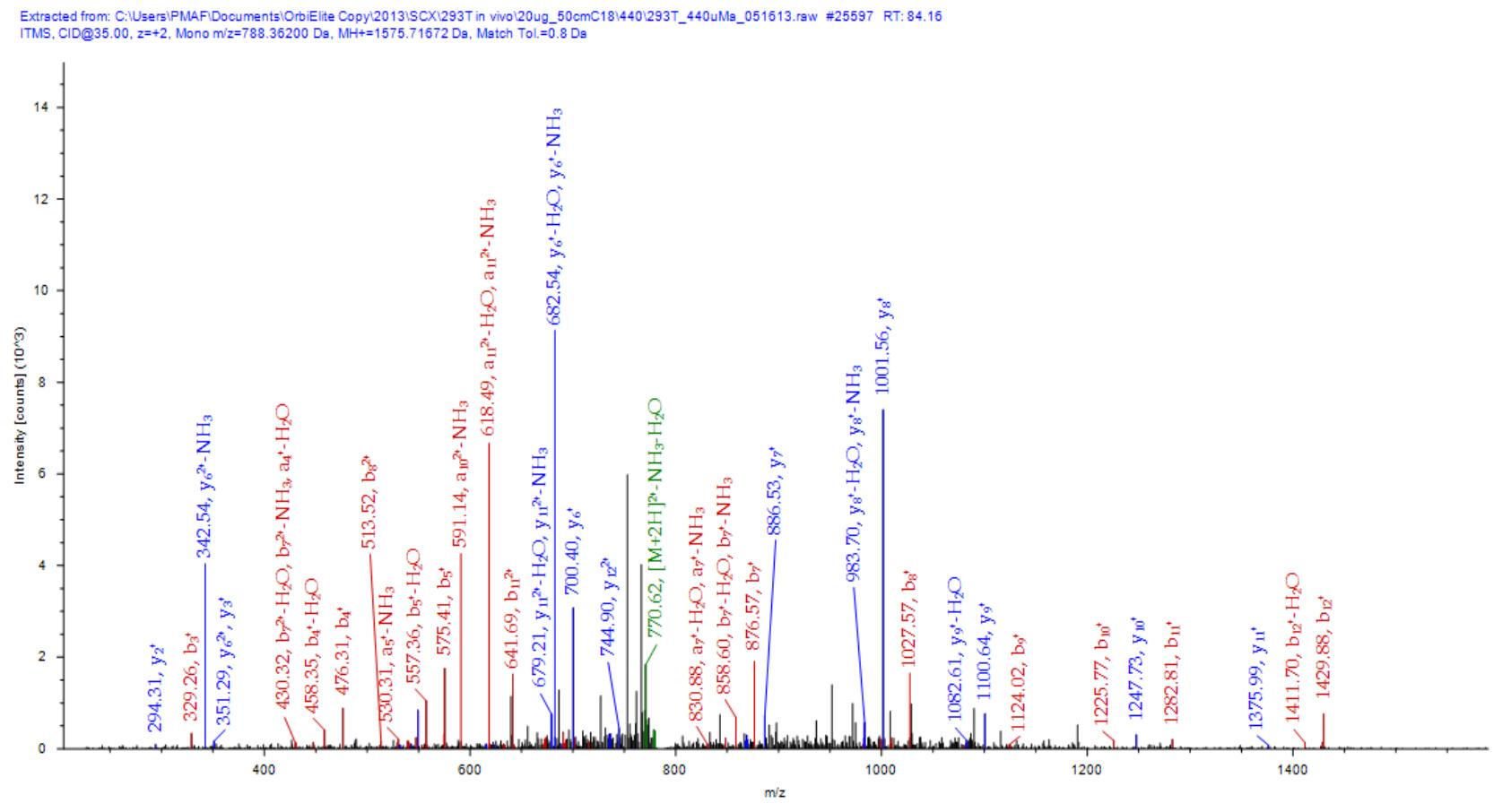


RLIPDGCGVK C7 SO3H

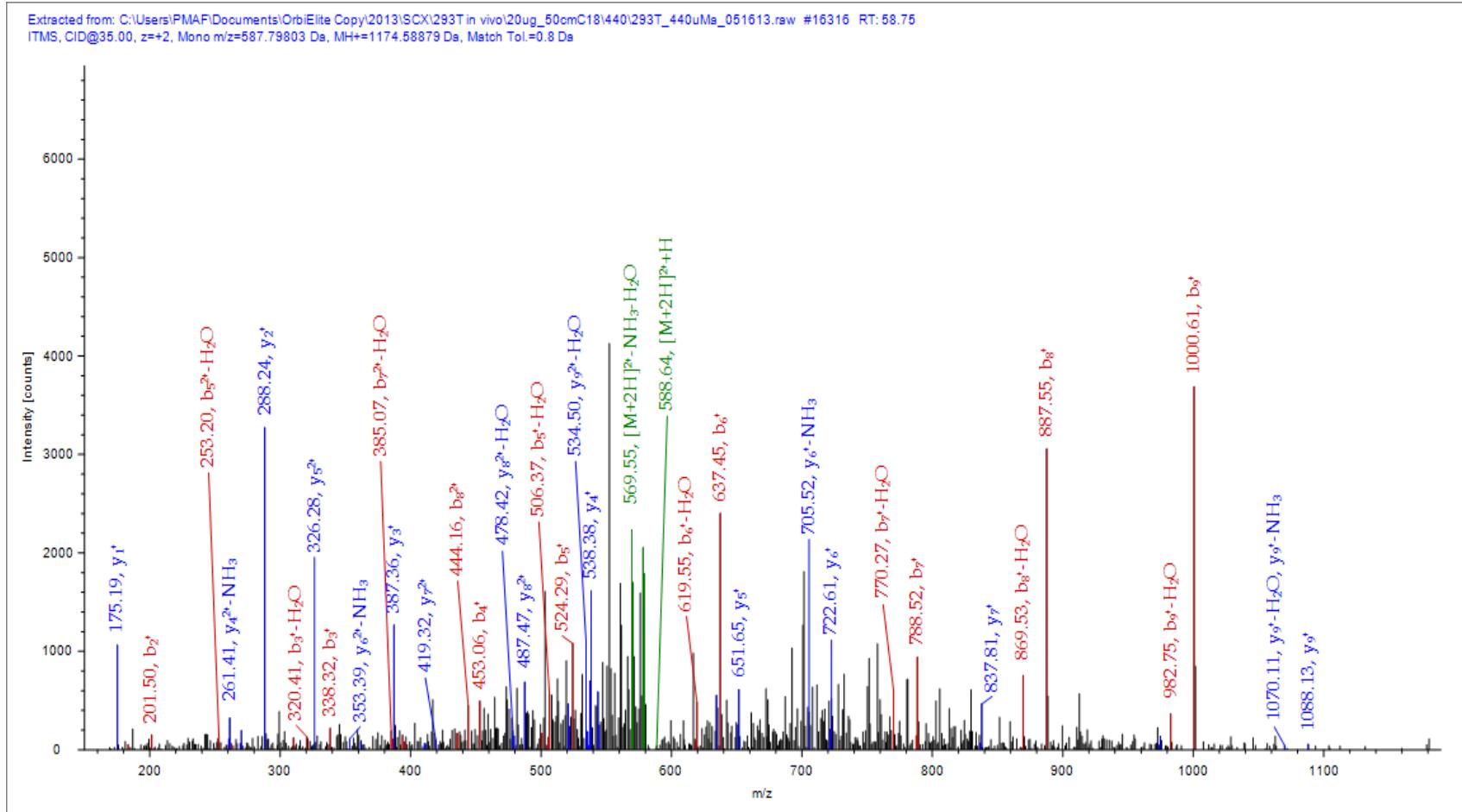
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ITMS, CID@35.00, z=+2, Mono m/z=553.28784 Da, MH+=1105.56841 Da, Match Tol.=0.8 Da



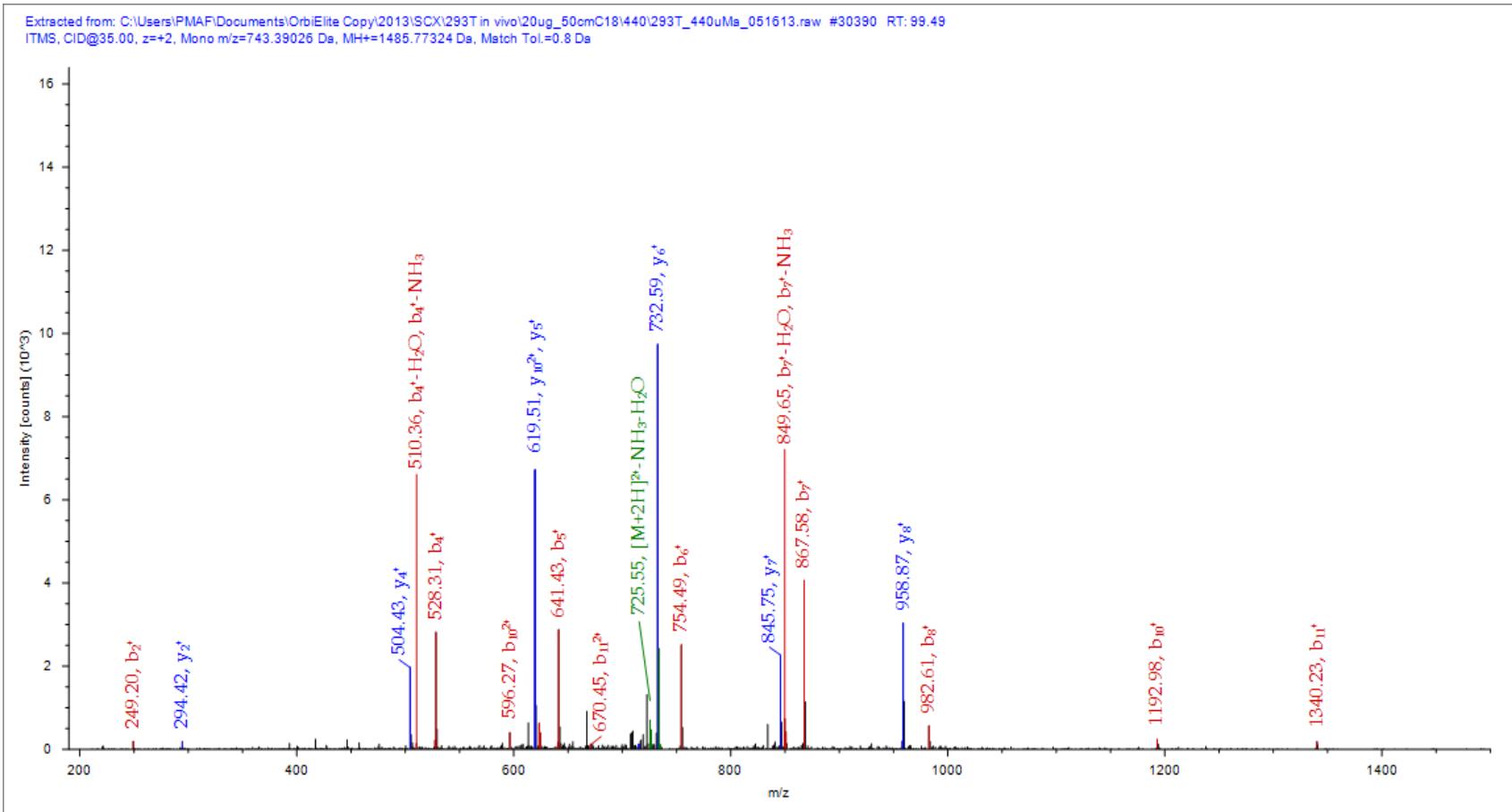
SIQFVWCPTGFK_C8_SO3H



SLHDALCVIR_C7_SO3H

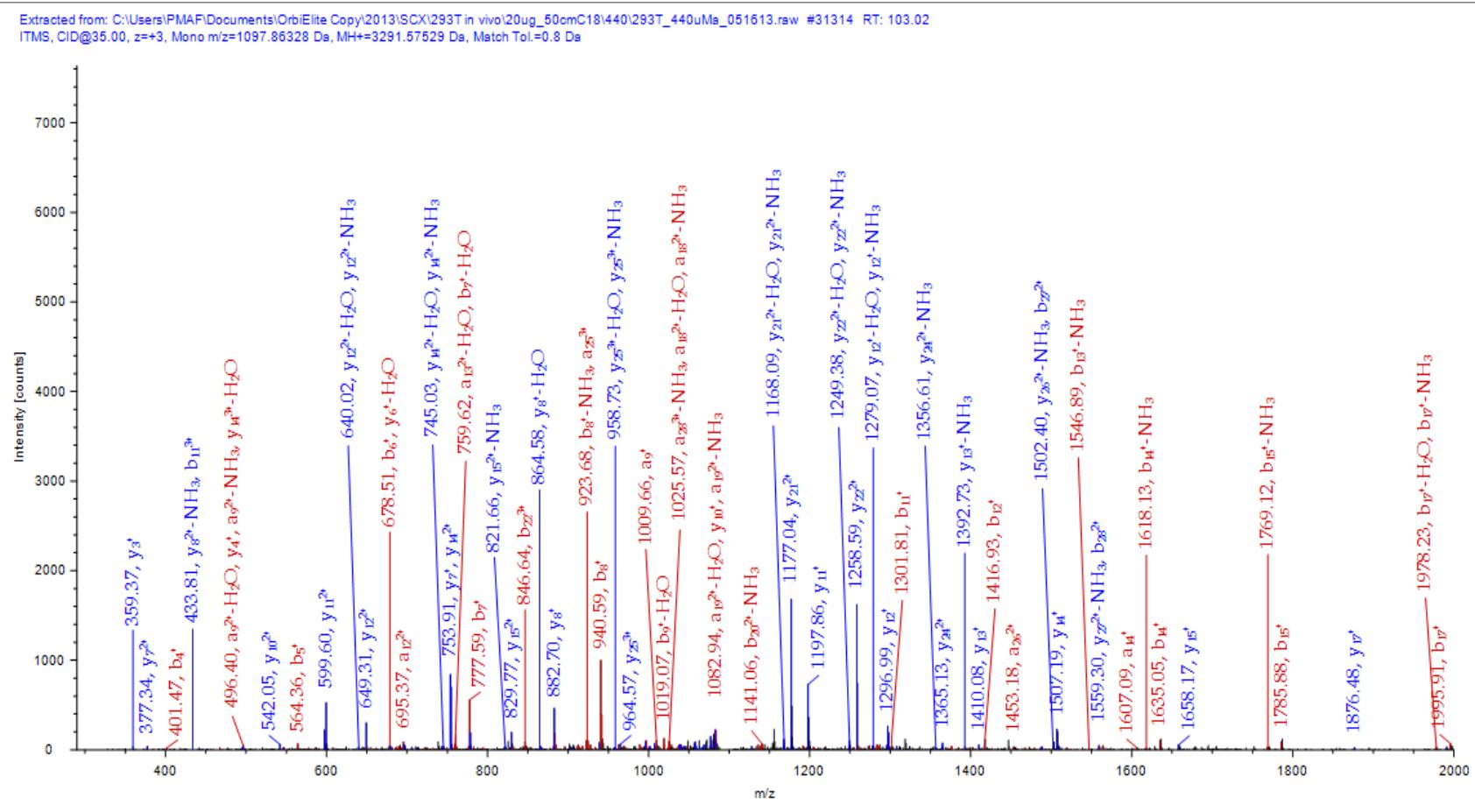


TFCQLILDPIFK_C3_SO3H

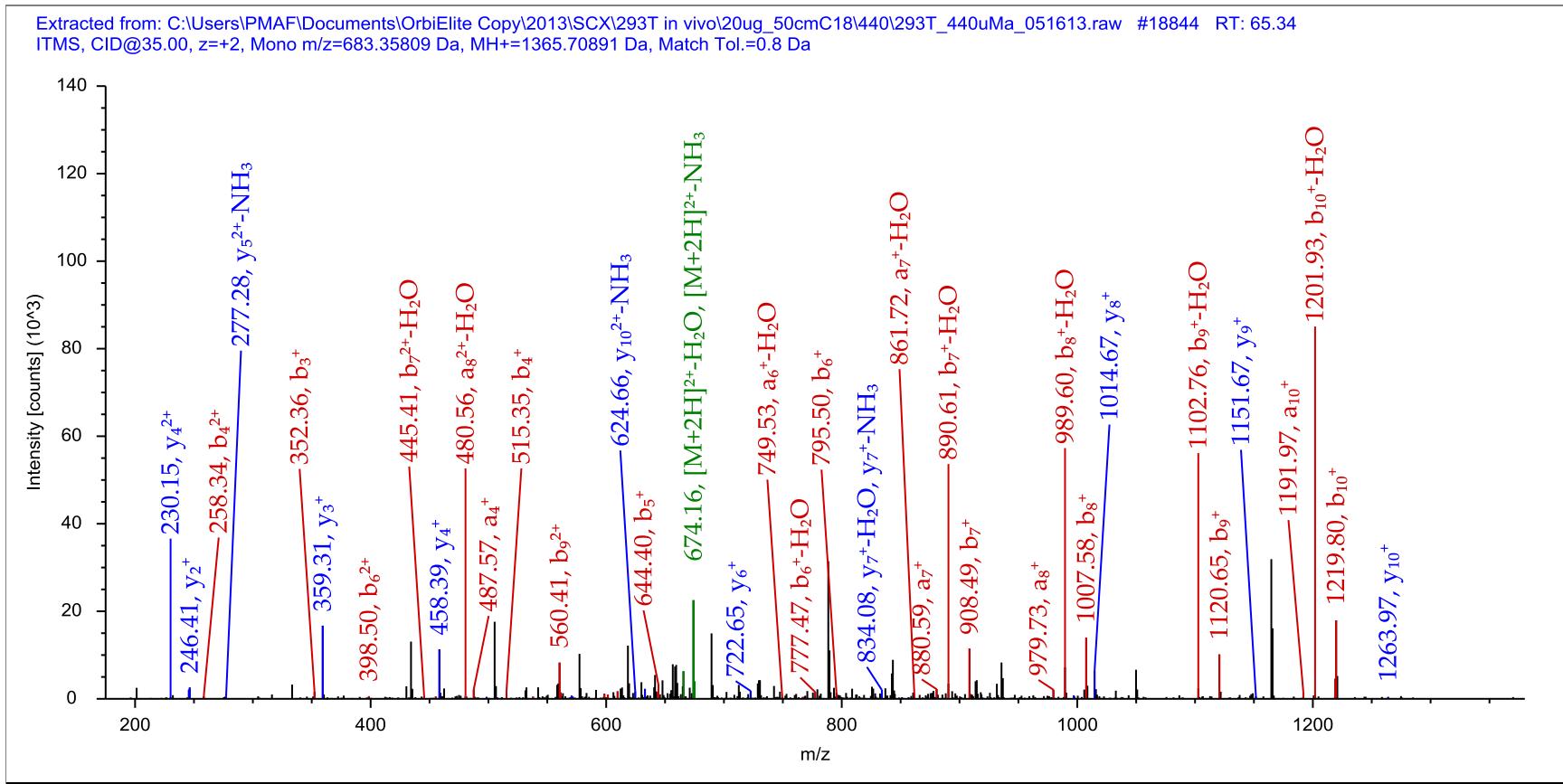


TGNKYNVYPTYDFACPIVDSIEGVTHALR_

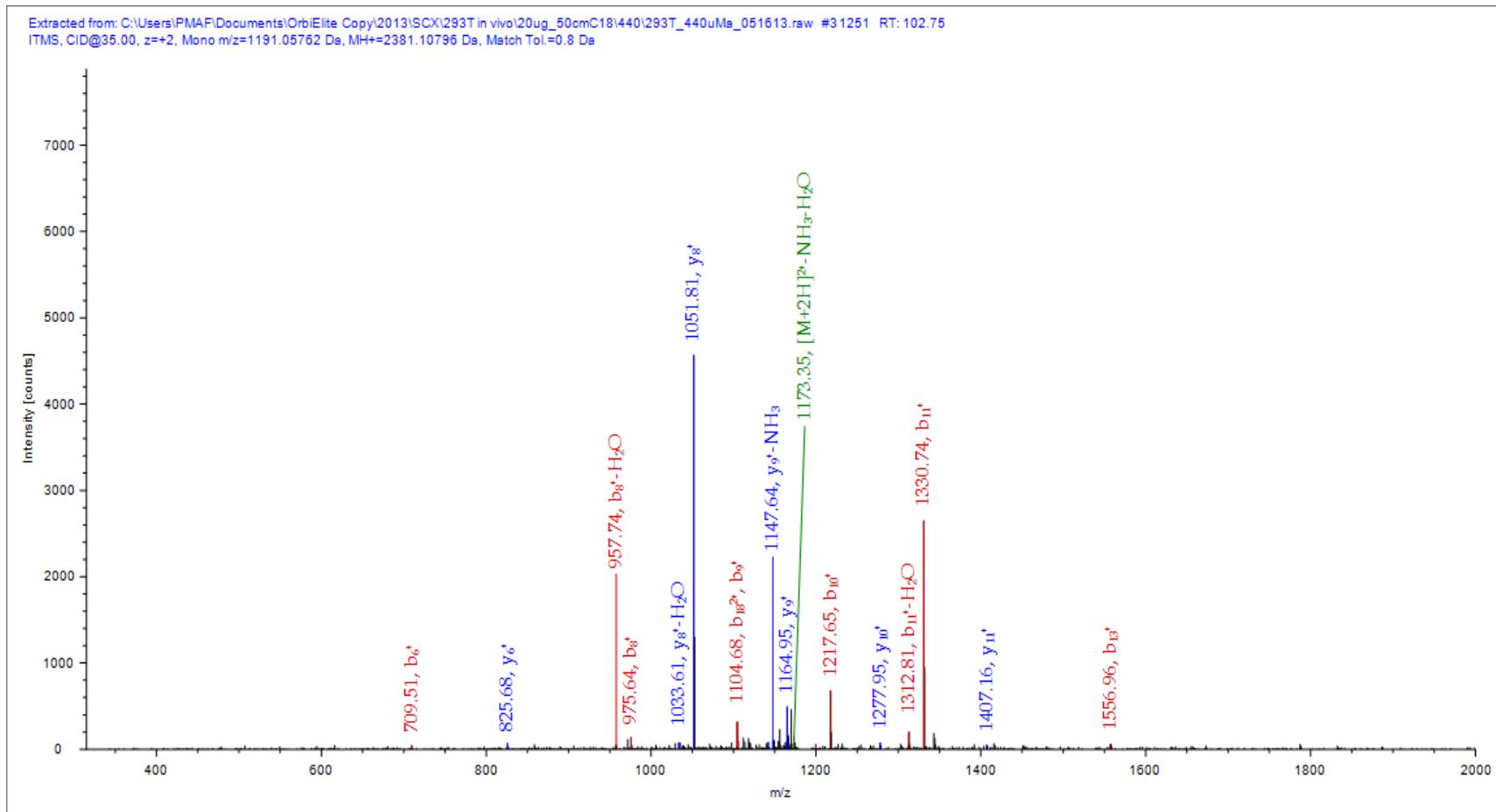
C15_SO3H



TLHYECIVLVK C6 SO3H

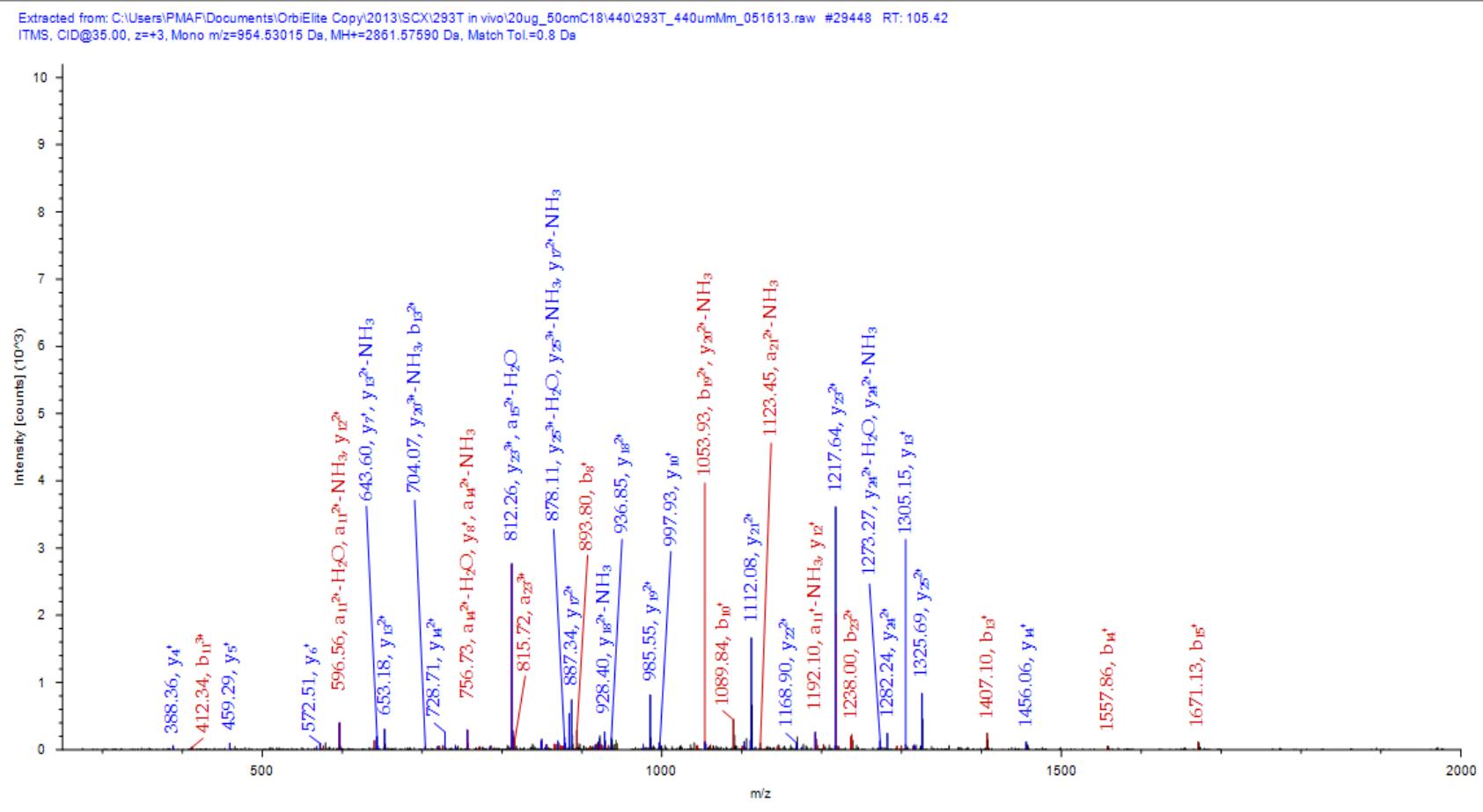


VFIMDSCDELIPEYLNFIR_C7_SO3H



VLSEPNPRPVFGICLGHQLLALAIGAK_C1

4_SO3H



WYHPGCFVK_C6_SO3H

