Supplemental spectra

Discovery of O-GlcNAc-modified proteins in published large-scale proteome data

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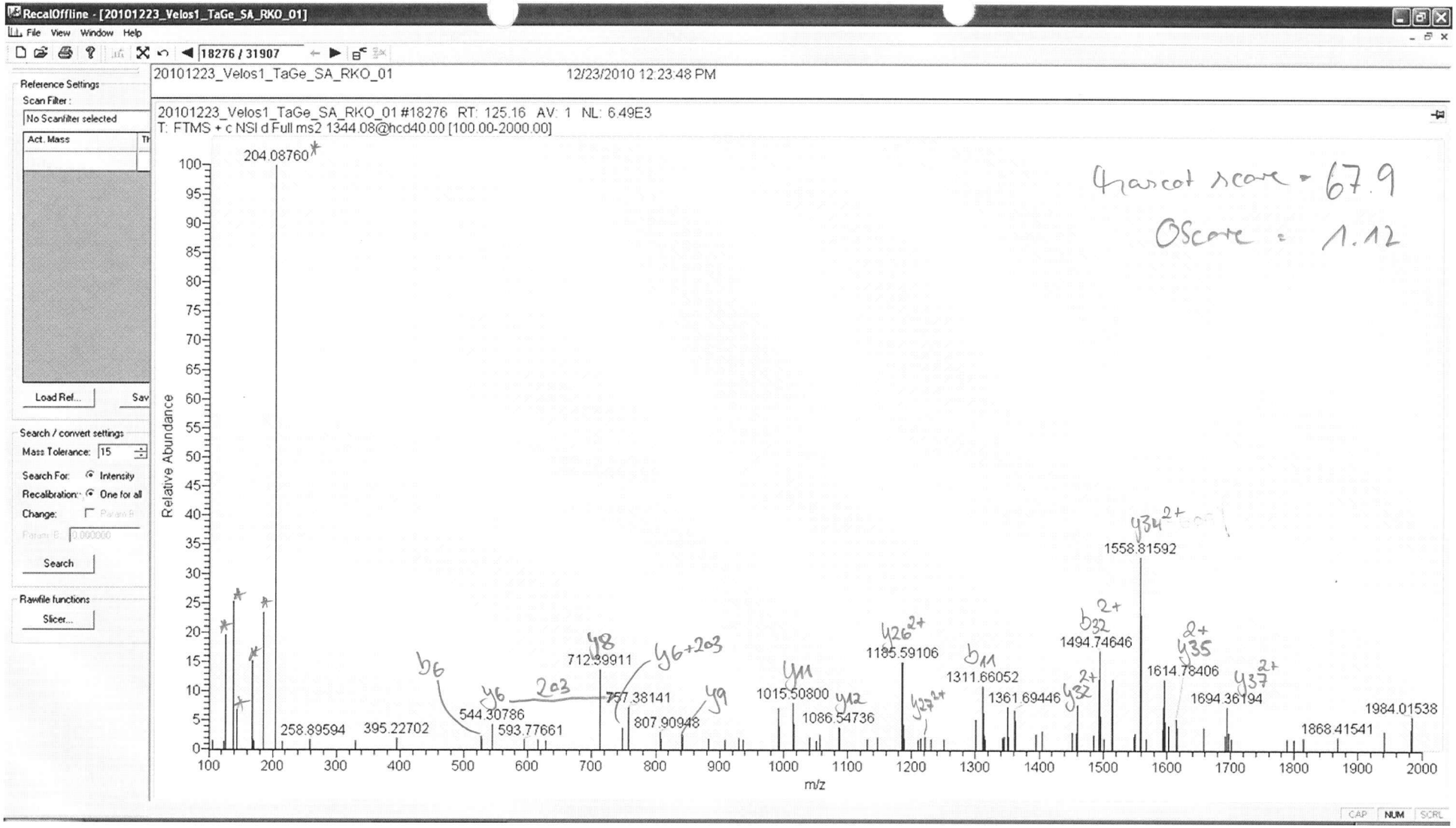
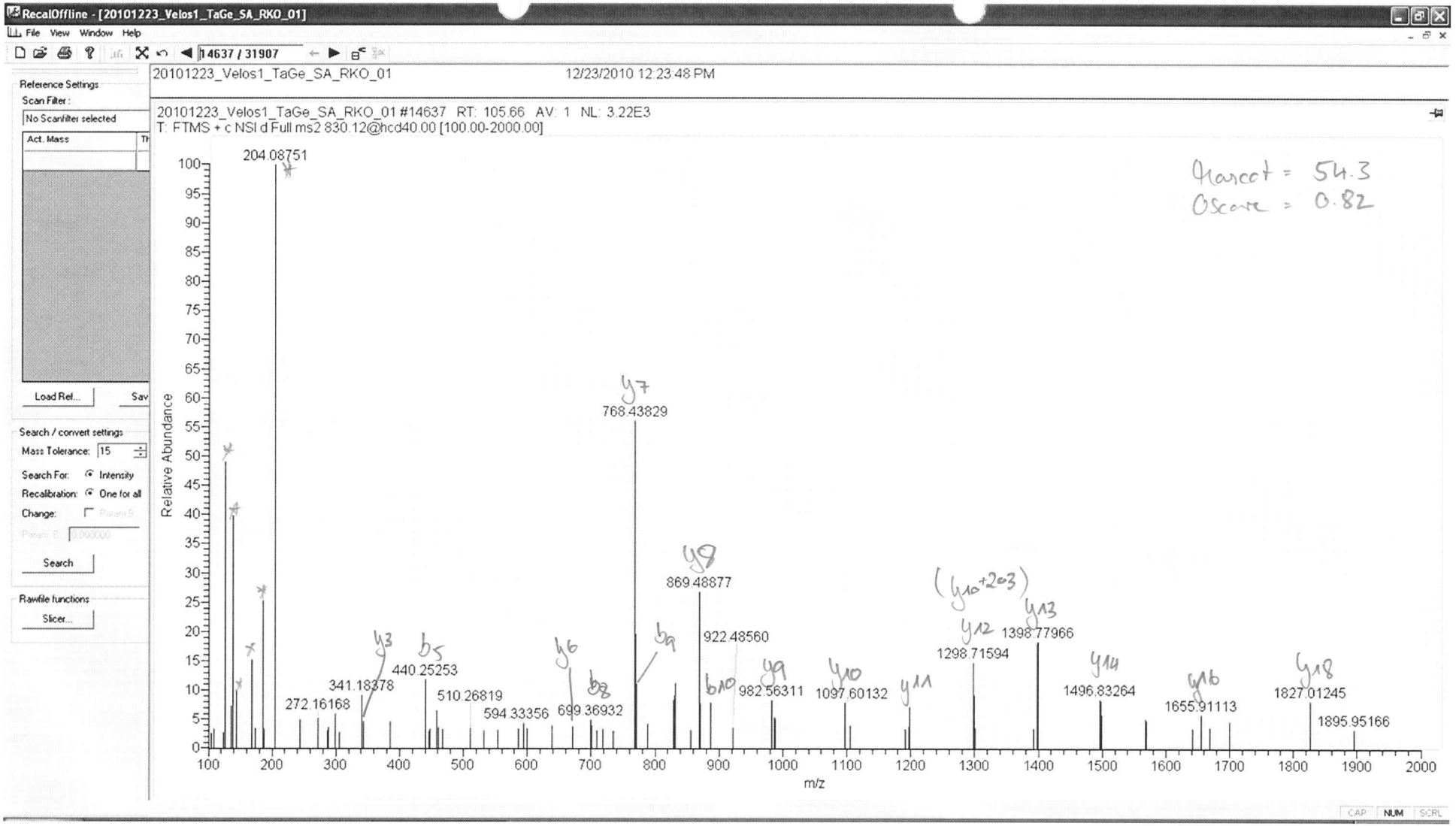
Legend

This Supplemental File contains the manually validated tandem mass spectra of O-GlcNAc peptides described in the main manuscript. The spectrum number corresponds to the spectrum number given in Supplemental Table S4 and S7. Owing to the high lability of the O-glycosidic bond, usually fragments do not retain the modification during HCD fragmentation. Consequently, it is often impossible to localize the O-GlcNAc site and to identify the fragments which have undergone a neutral HexNAc loss. Therefore, we modified the standard nomenclature and annotated modified fragments with the delta mass to the unmodified fragment. For example, fragments which retain the GlcNAc group would be denoted e.g. as "y_5+203", whereas the fragment with a GlcNAc neutral loss (which leaves the fragment unmodified) would be simply "y_5". Accordingly, the neutral loss of phosphoric acid (H_3PO_4) from an y_5 ion is according to common nomenclature denoted as "y_5-98", but according to our nomenclature as "y_5-18" in the annotated spectra.



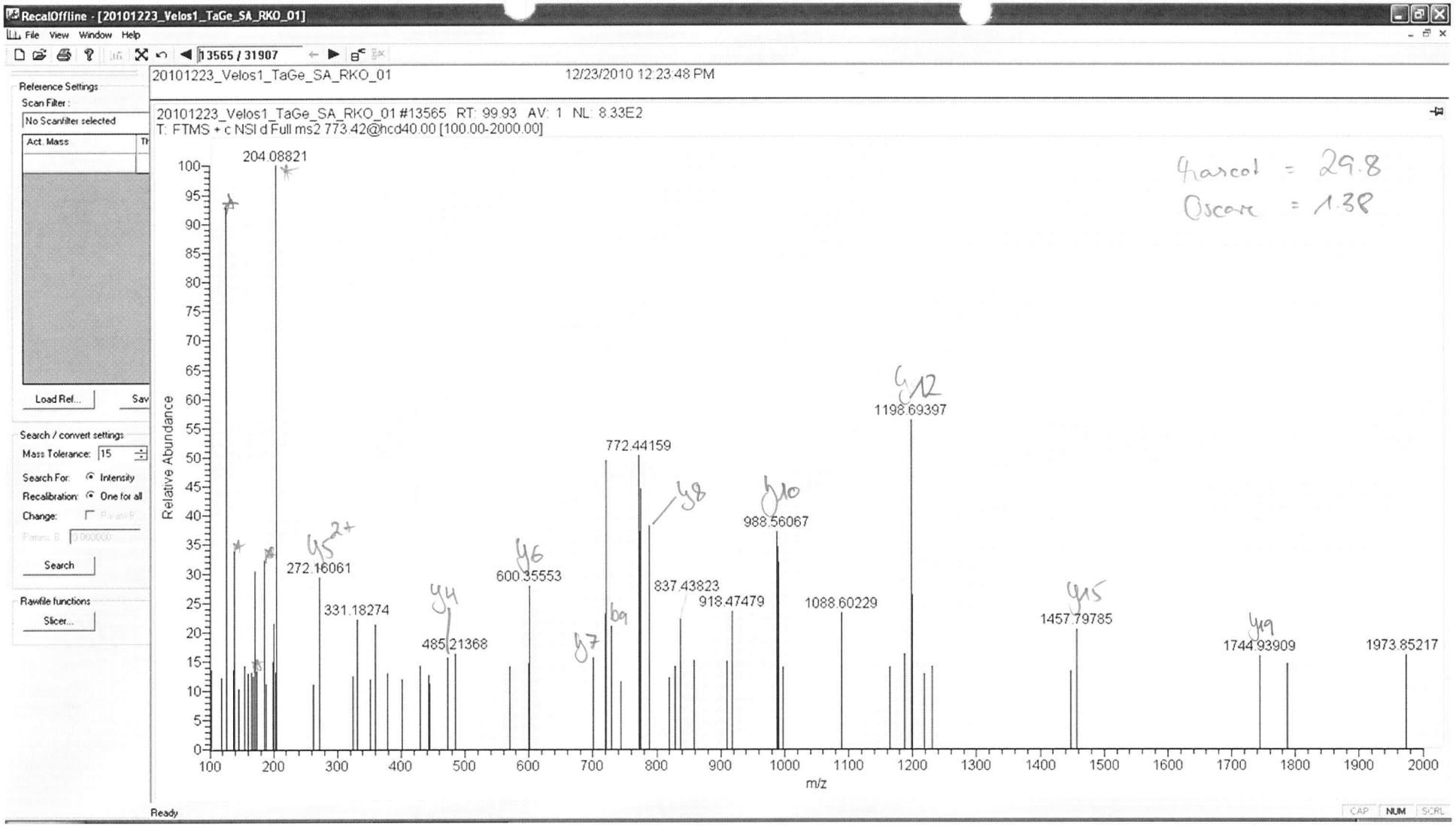
AVSTPAPATTQQSAPASTTAVTSSTTTTVAQAPTPVPALAPTSTPASITPASATAssEPAPAsAAK

S63 ; 2 sites unknown



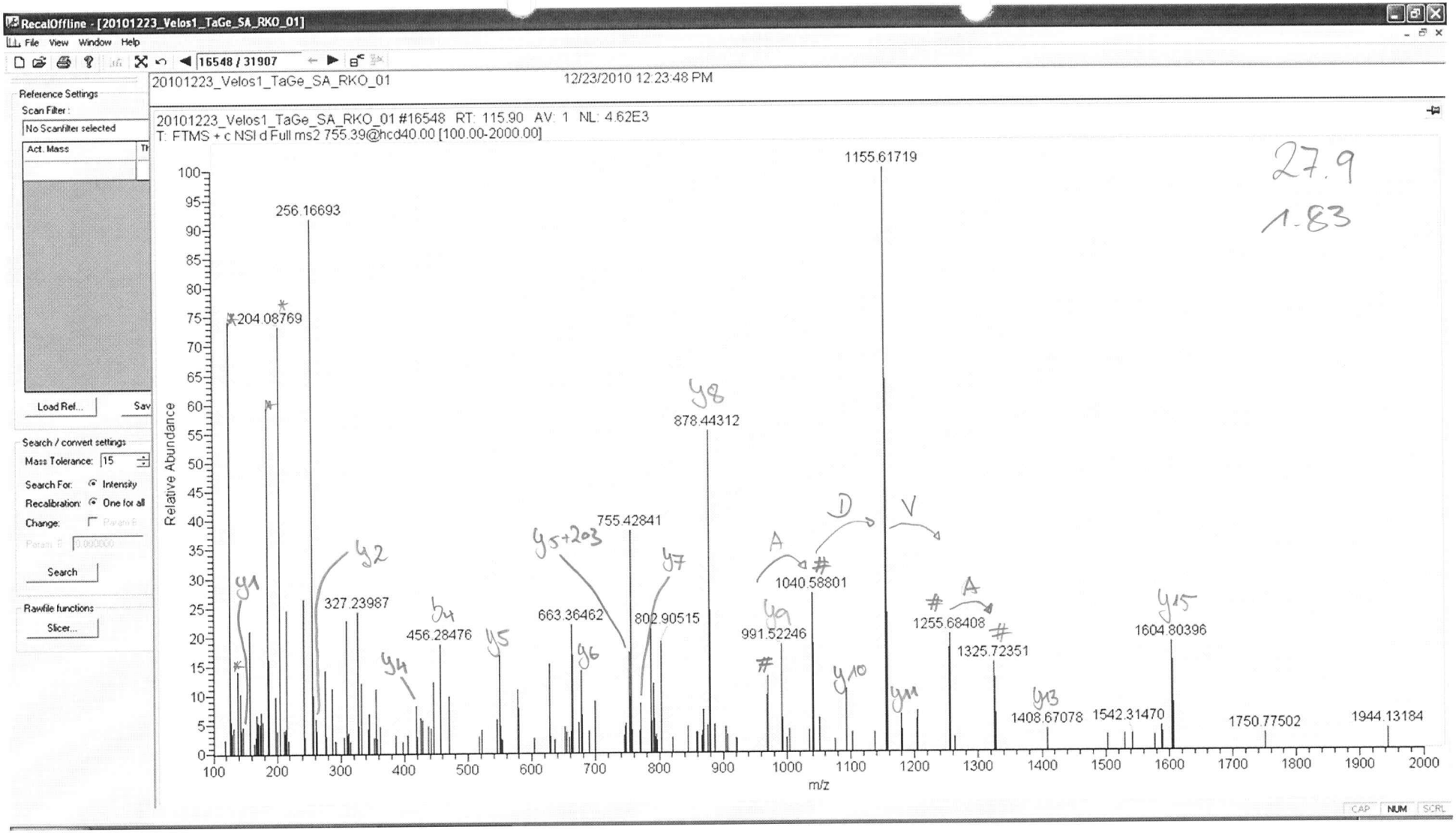
AVTsVTASAVVTTNLTPVQTPAR

No site evidence



TVAVASGAASTPISISTGAPtVR

no site evidence



27.9

1.83

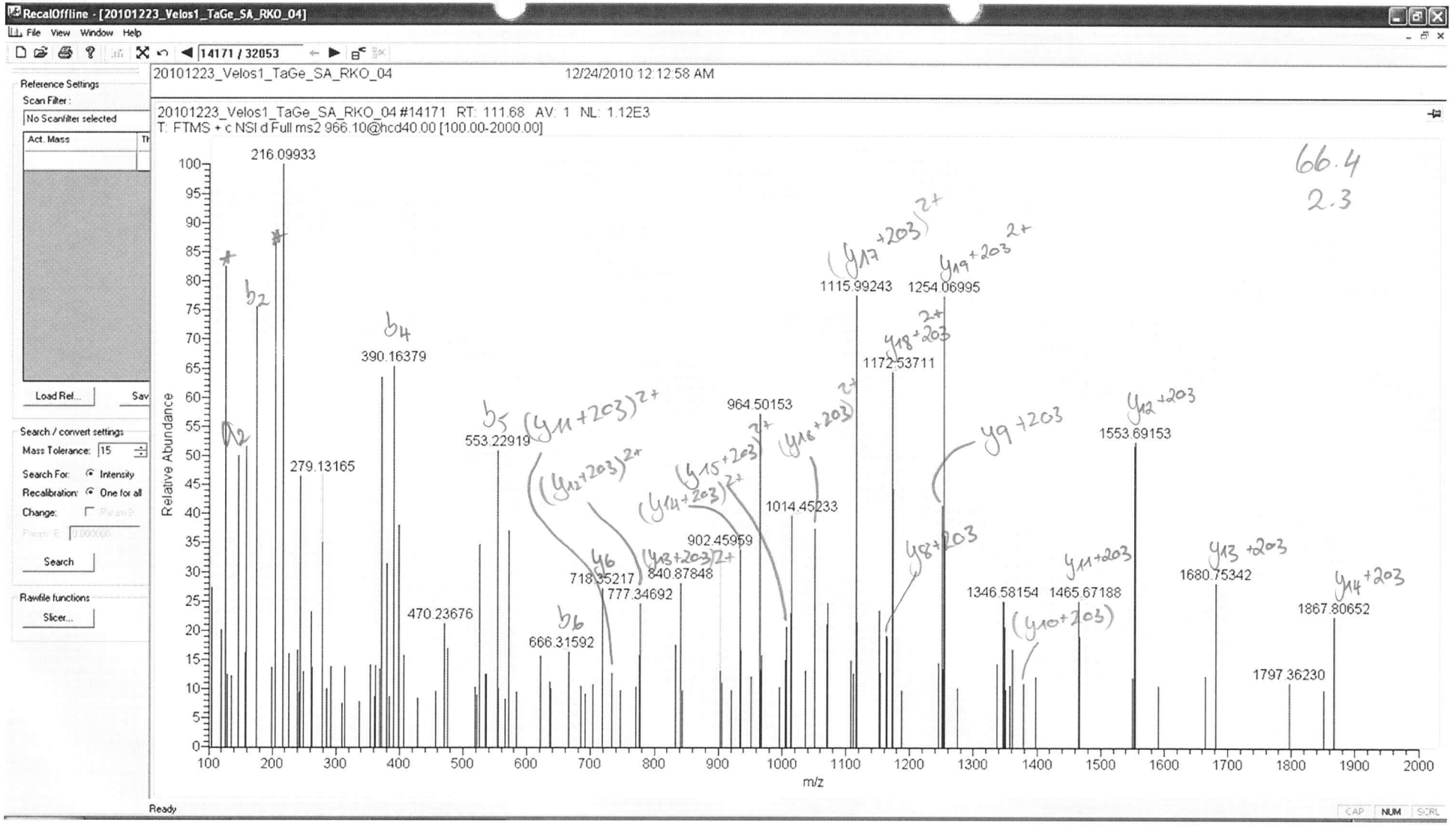
LTLQPVDNSTISLQMGTnK

y13 y5

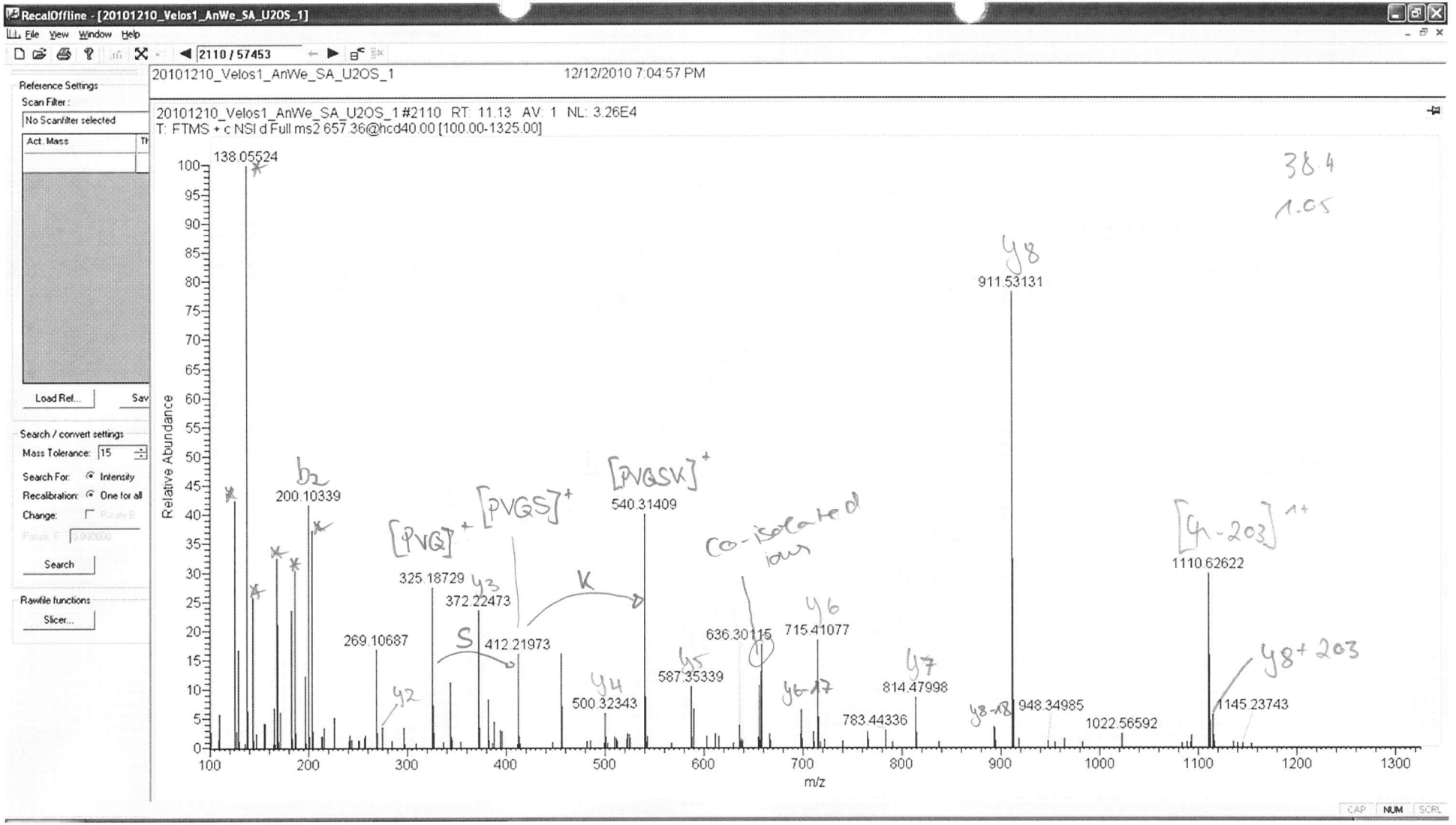
T17

Chimeric Spectrum; Series from 2nd precursor

5

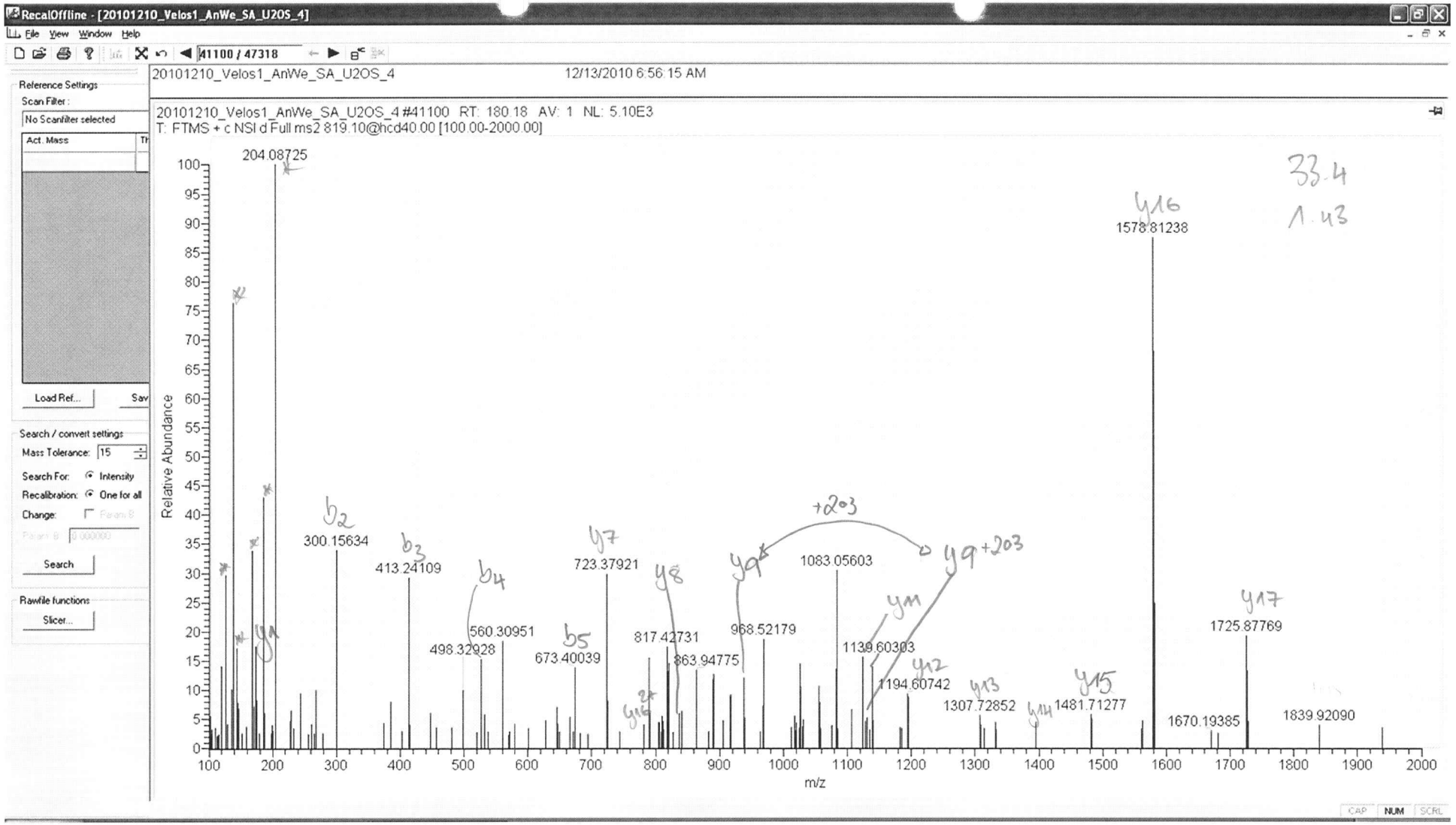


SSSQYIESFWQSSQSQnFTAHDK



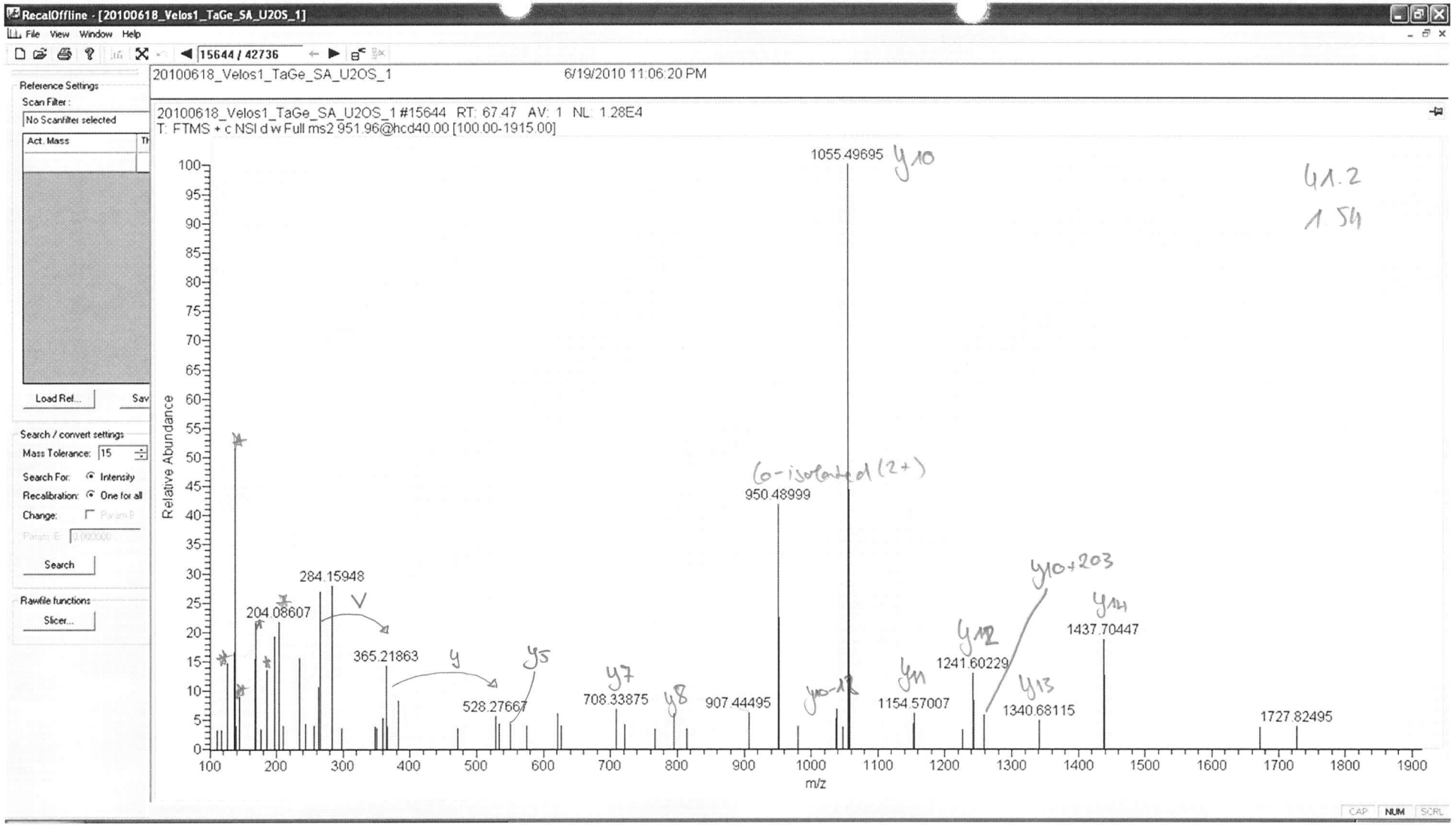
S6

AQPVQsKPQK



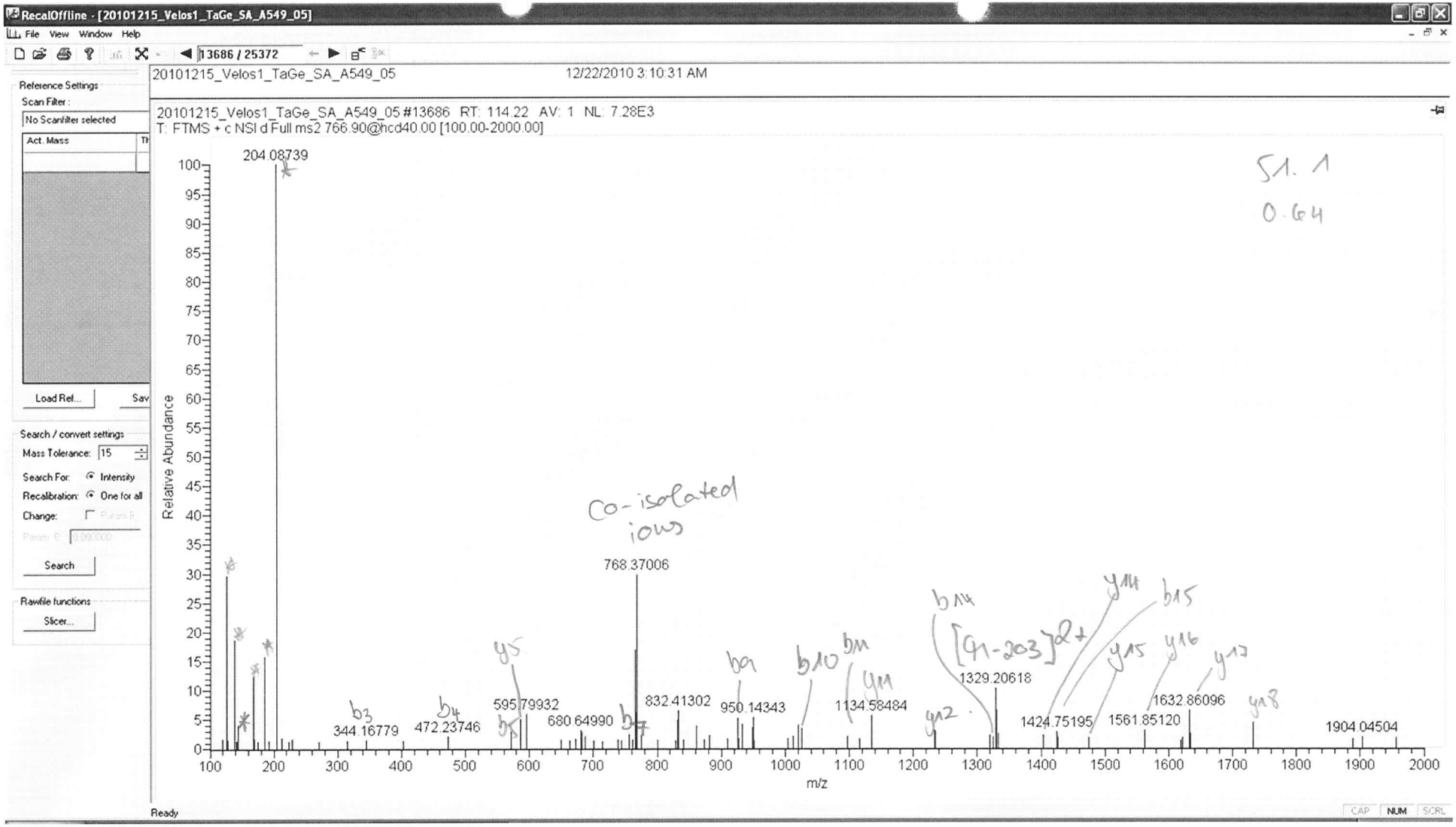
LGELLFPSSLAGEtLGSFSGLR

T14



VYPVSVPYSSAQSTsK

not S5;
S9, S10, S13, T14 or S15



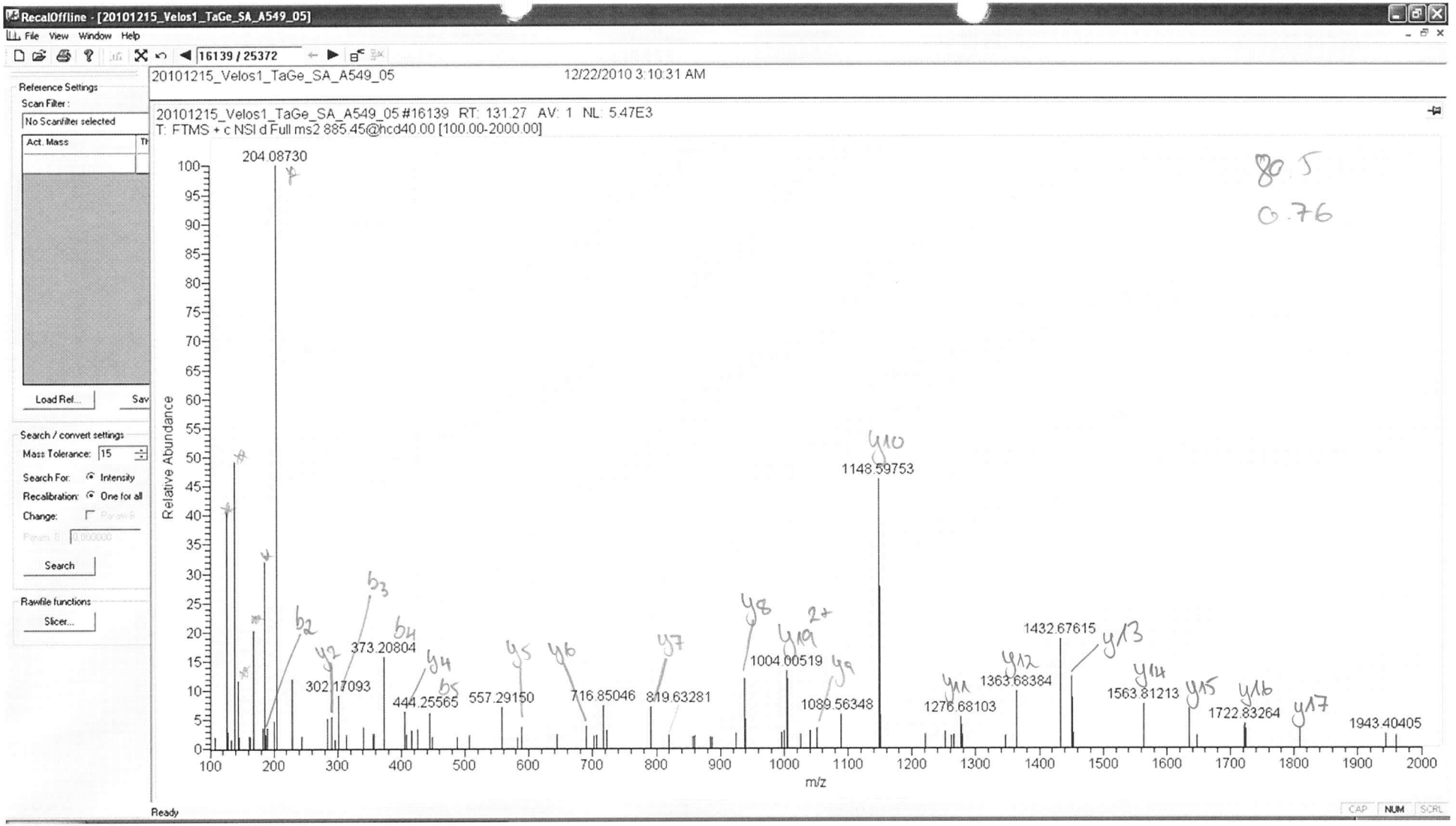
51.1

0.64

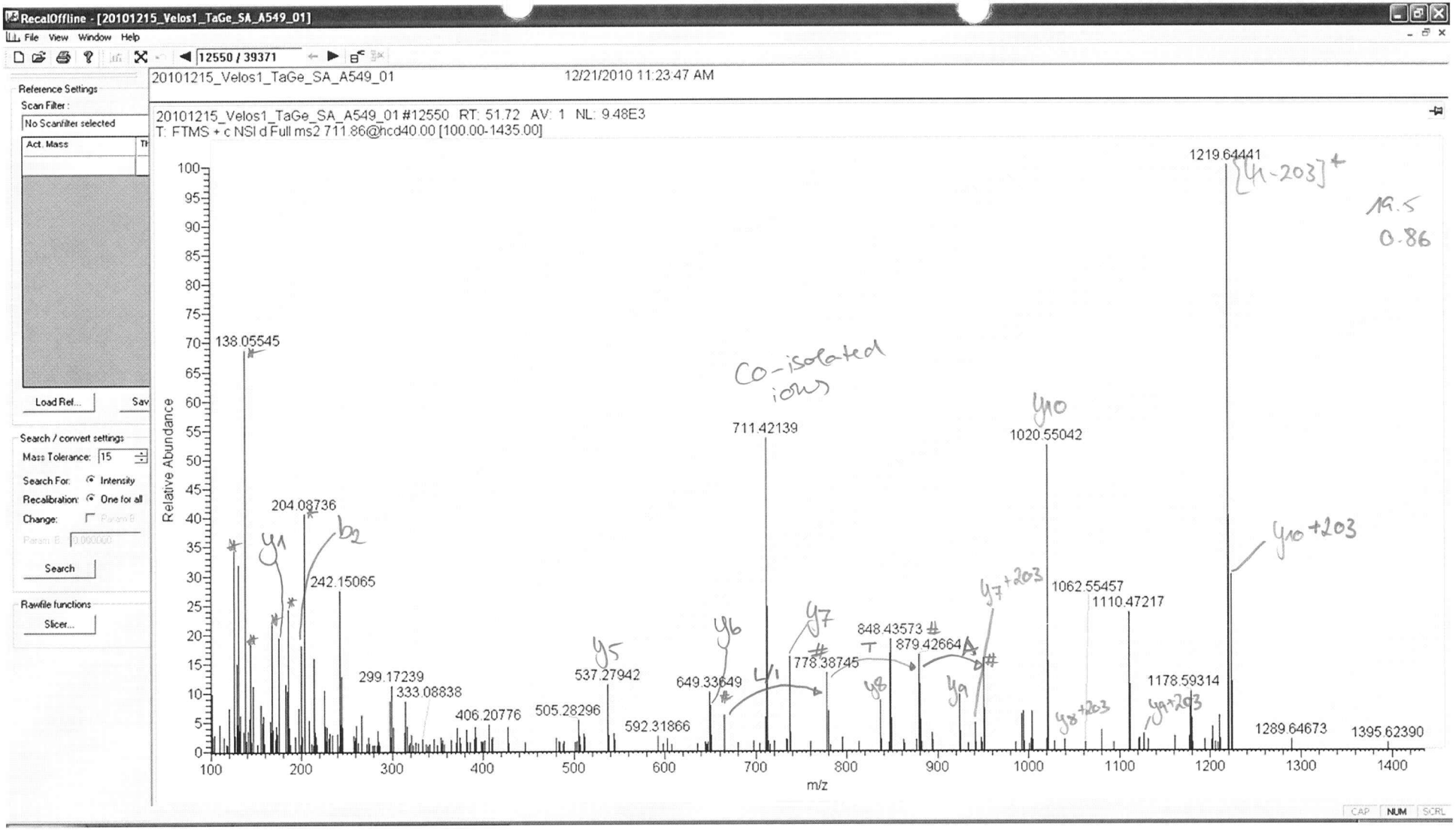
Co-isolated ions

TLEQVGQGIVASAAVVTTASSTPntVR

no site evidence



STIAAPTSSALSSQPIFTtAIDDR

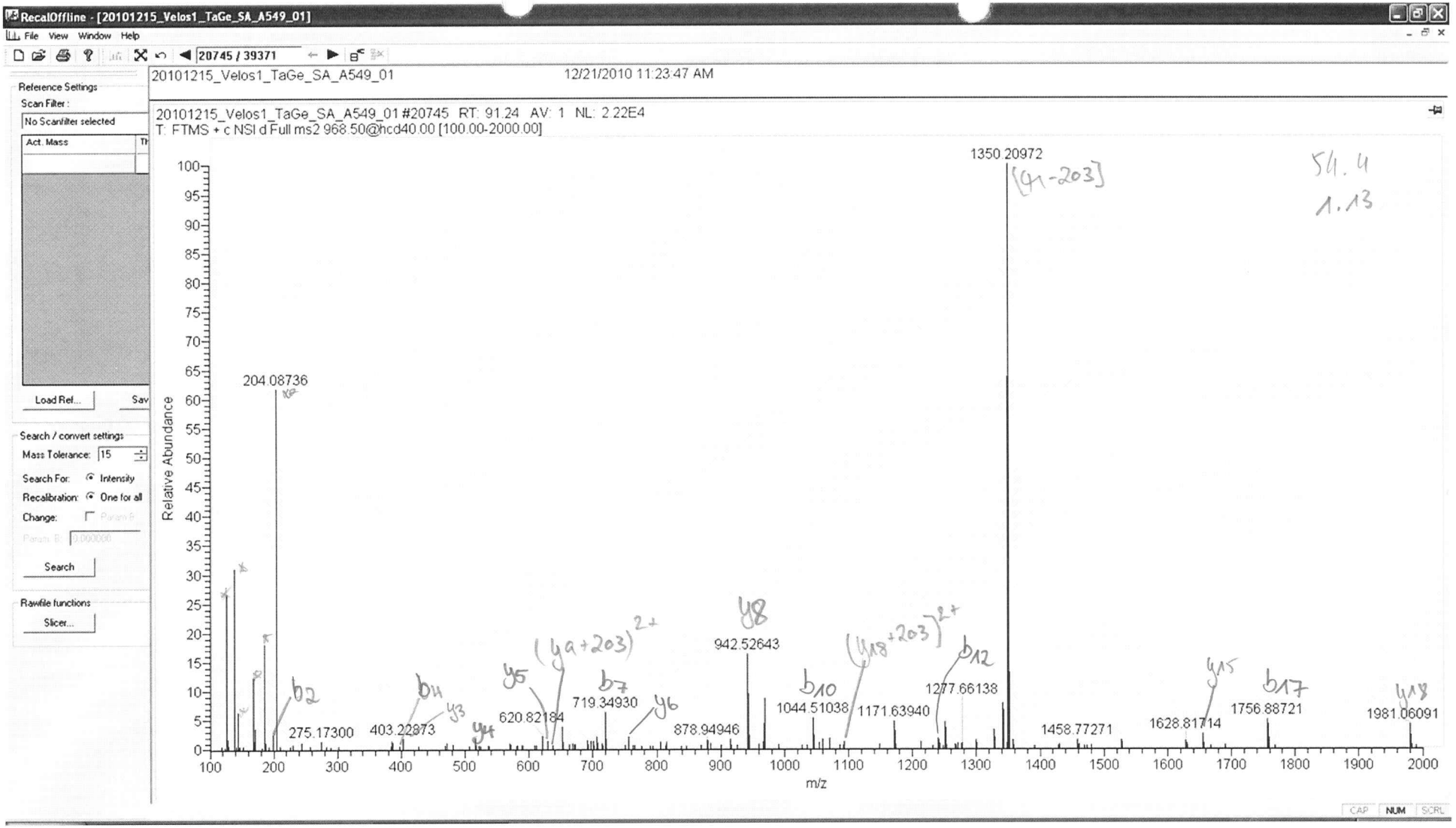


y7

AQPSVsLGAAYR

S6

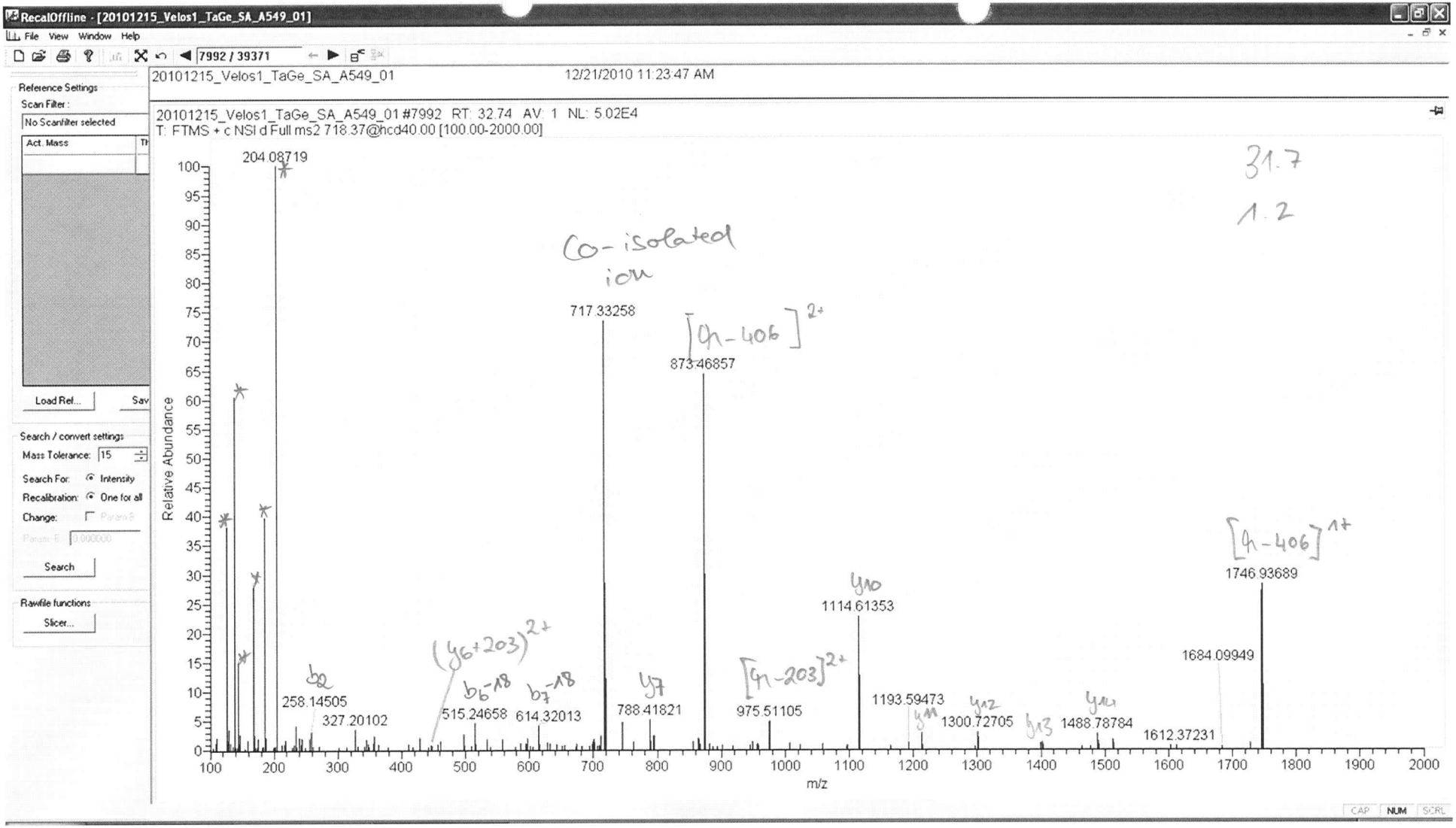
chimeric spectrum; series from second precursor



S19

TPPTANHPVEPVTSVTQPsELLQQK

15



31.7

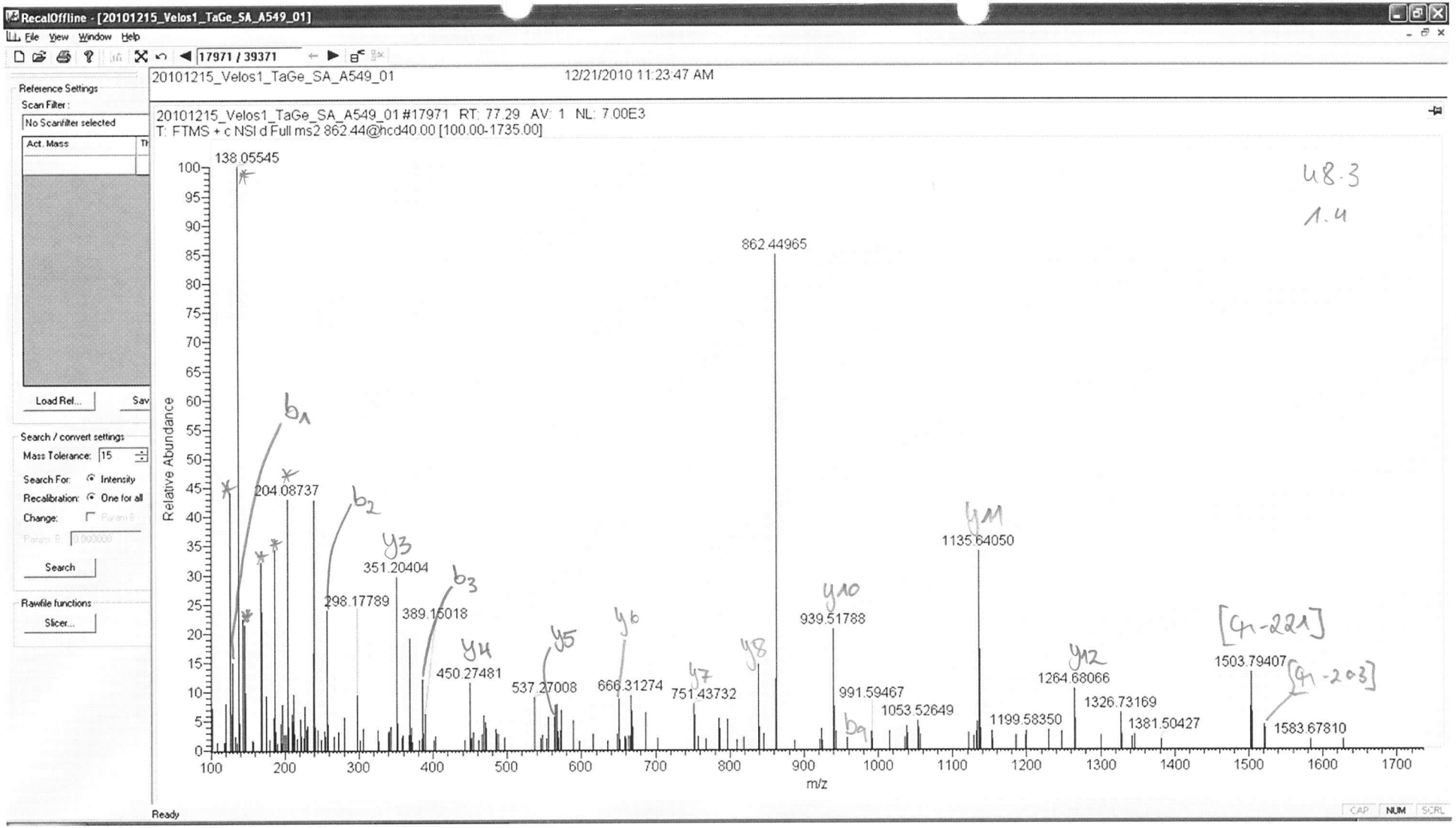
1.2

Co-isolated ion

SAVSTSVPTKPTEnIsK

1 site @ T12, N14 or S16

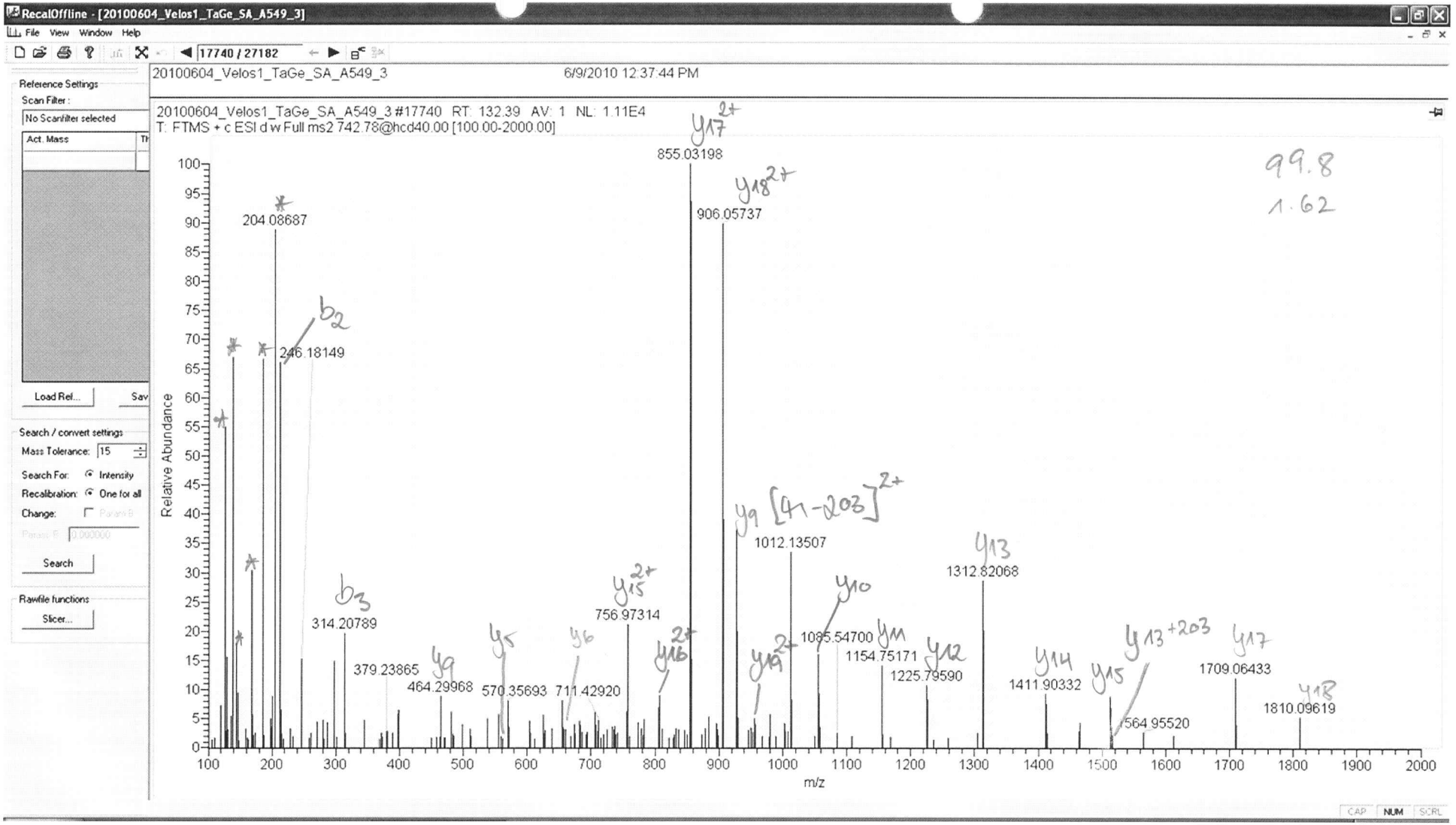
2nd site unknown



48.3
1.4

QQEPVTSTsLVFGK

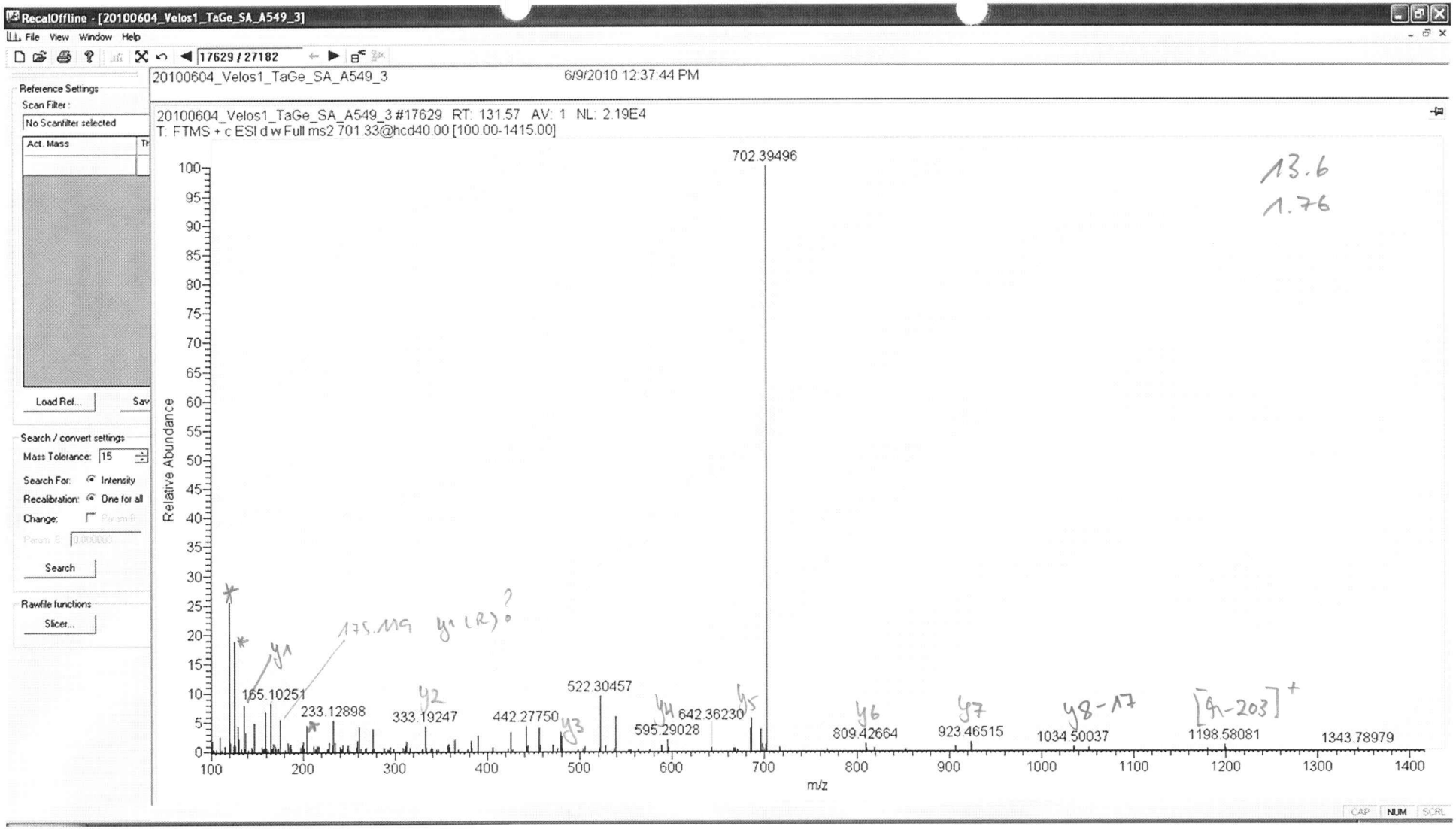
No site evidence



99.8
1.62

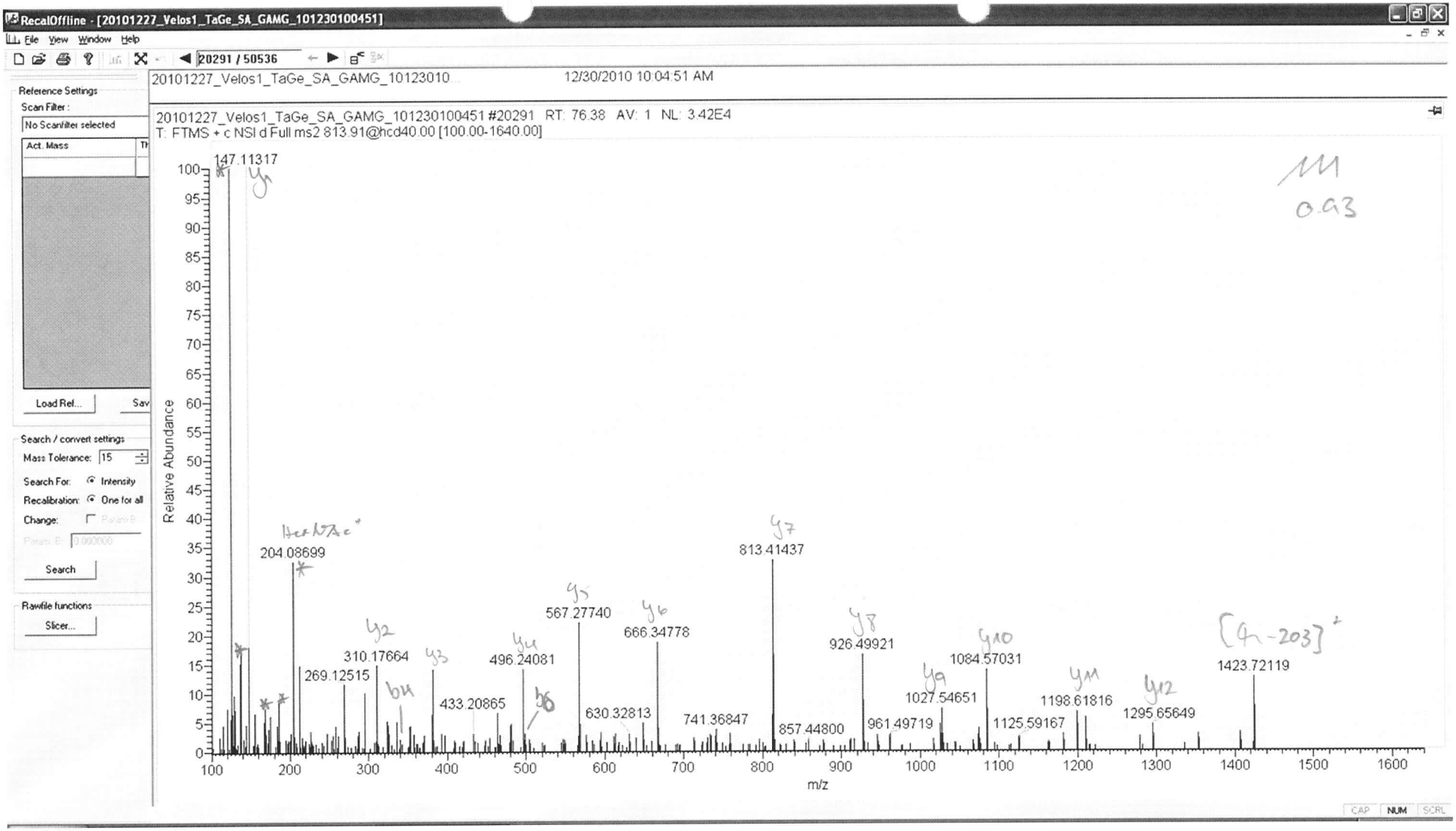
S8, T15 or T16

LVTPVTVSAVKPAVTtLVVK



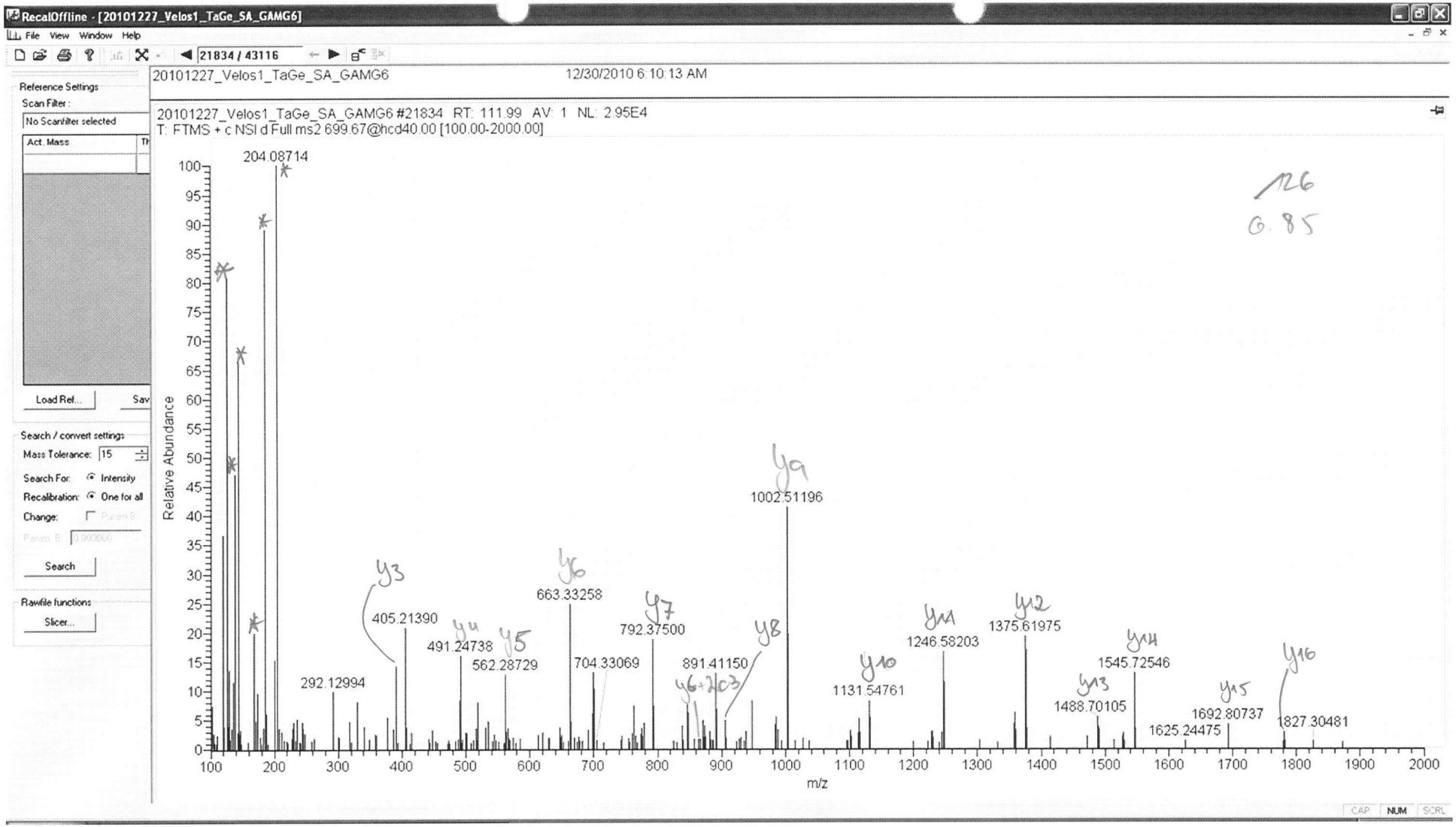
FQNItDFWK

no site evidence;
spectrum weak, but only one seq tag hit in fraction

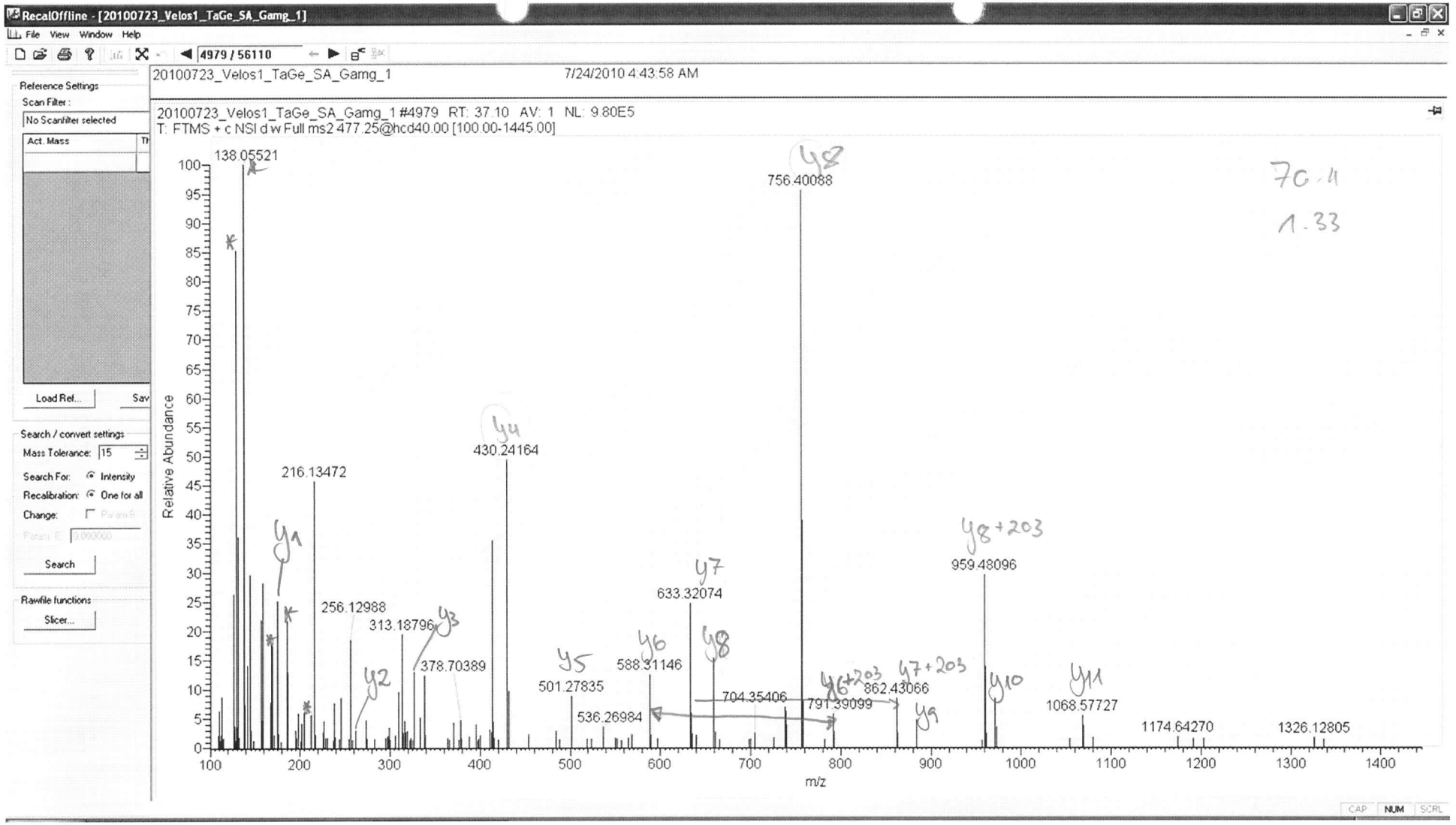


AGPNGtLFVADAYK

No site evidence

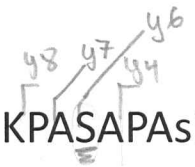


LSFGLEDEPLETATKEn



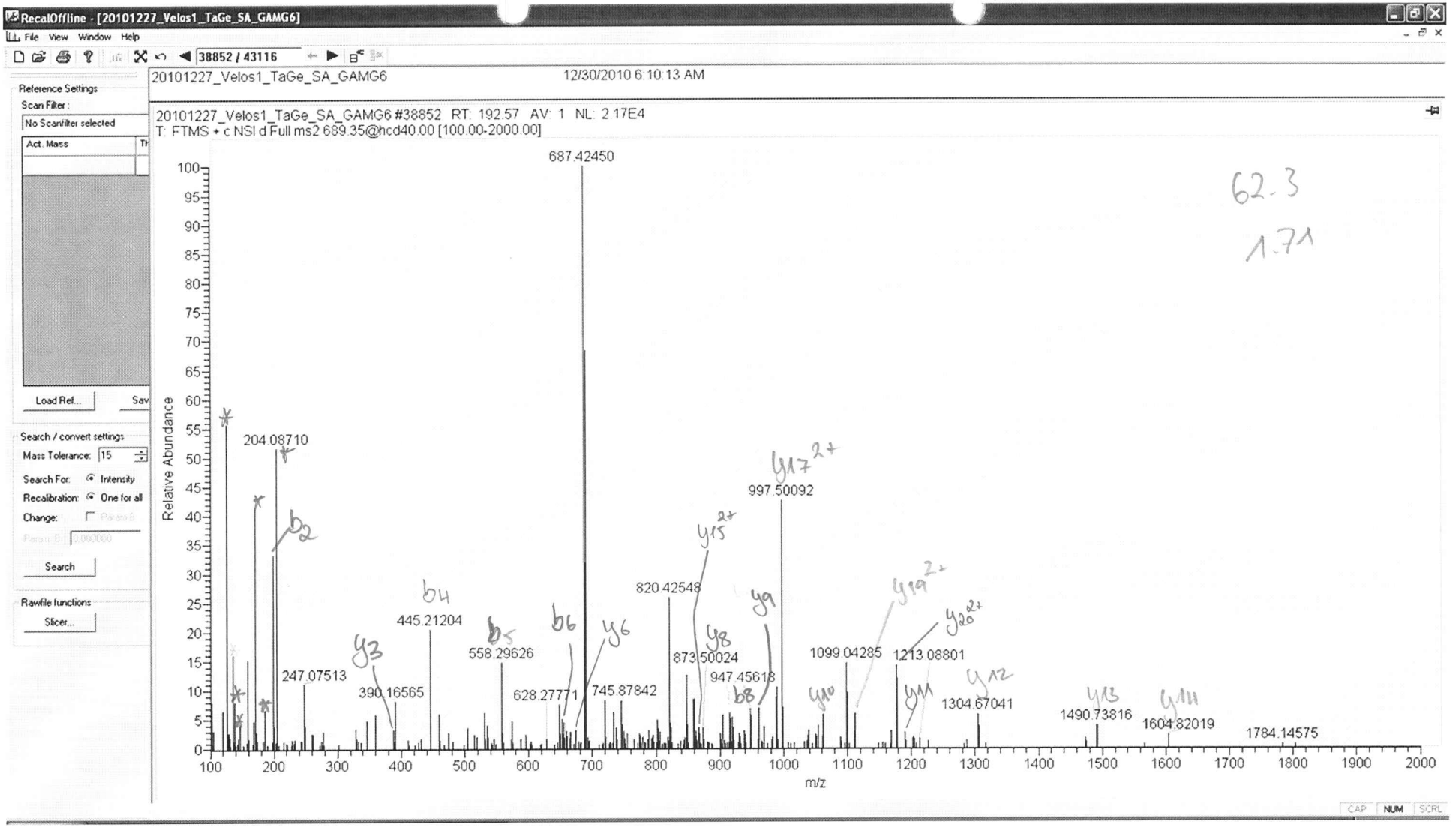
70.11

1.33



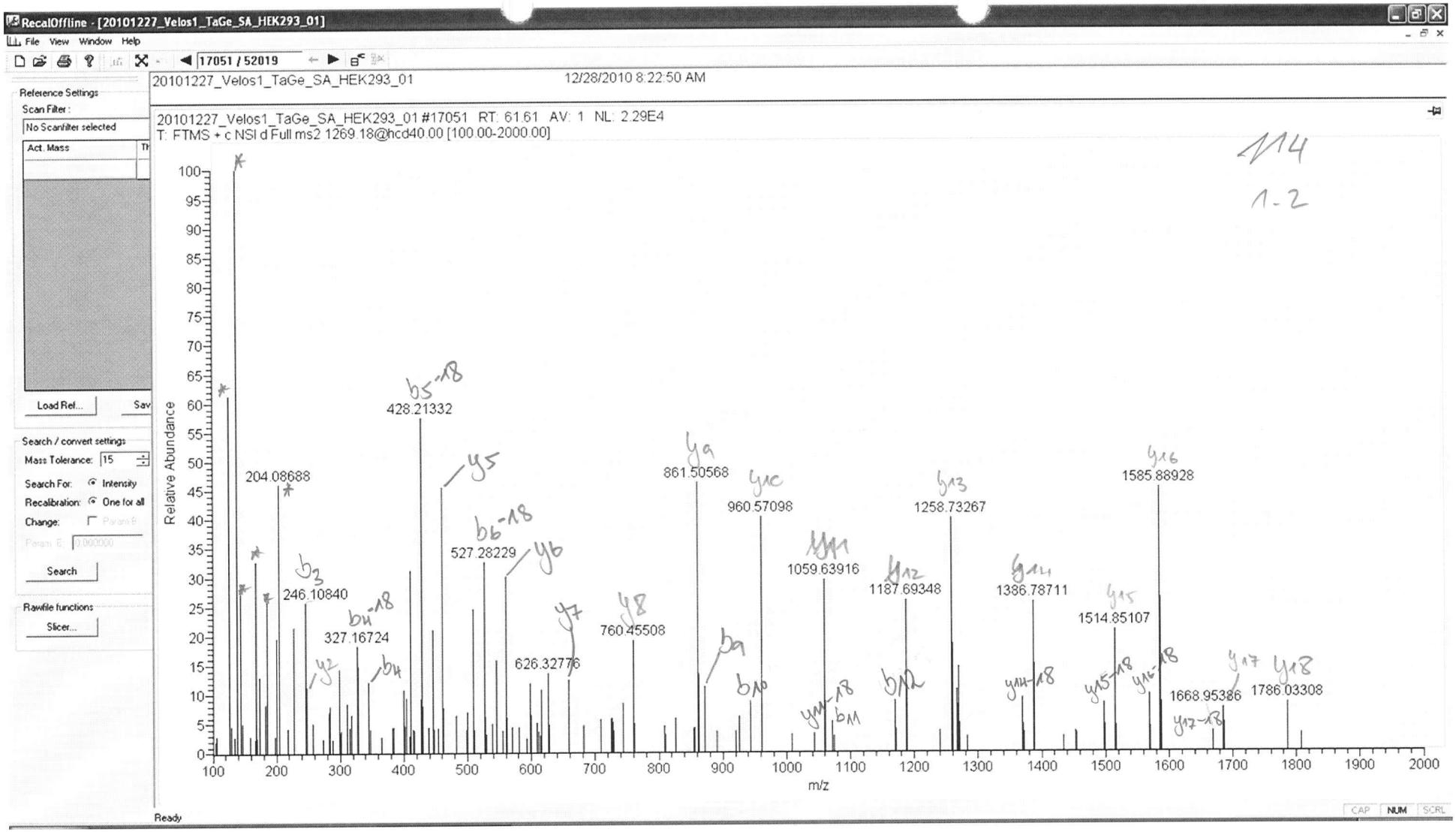
S8

ASPSKPASAPAsR



VVMDIPYELWNETsAEVADLKK

no site evidence



SGTVTVAQQAQVVTtVVGGVtK

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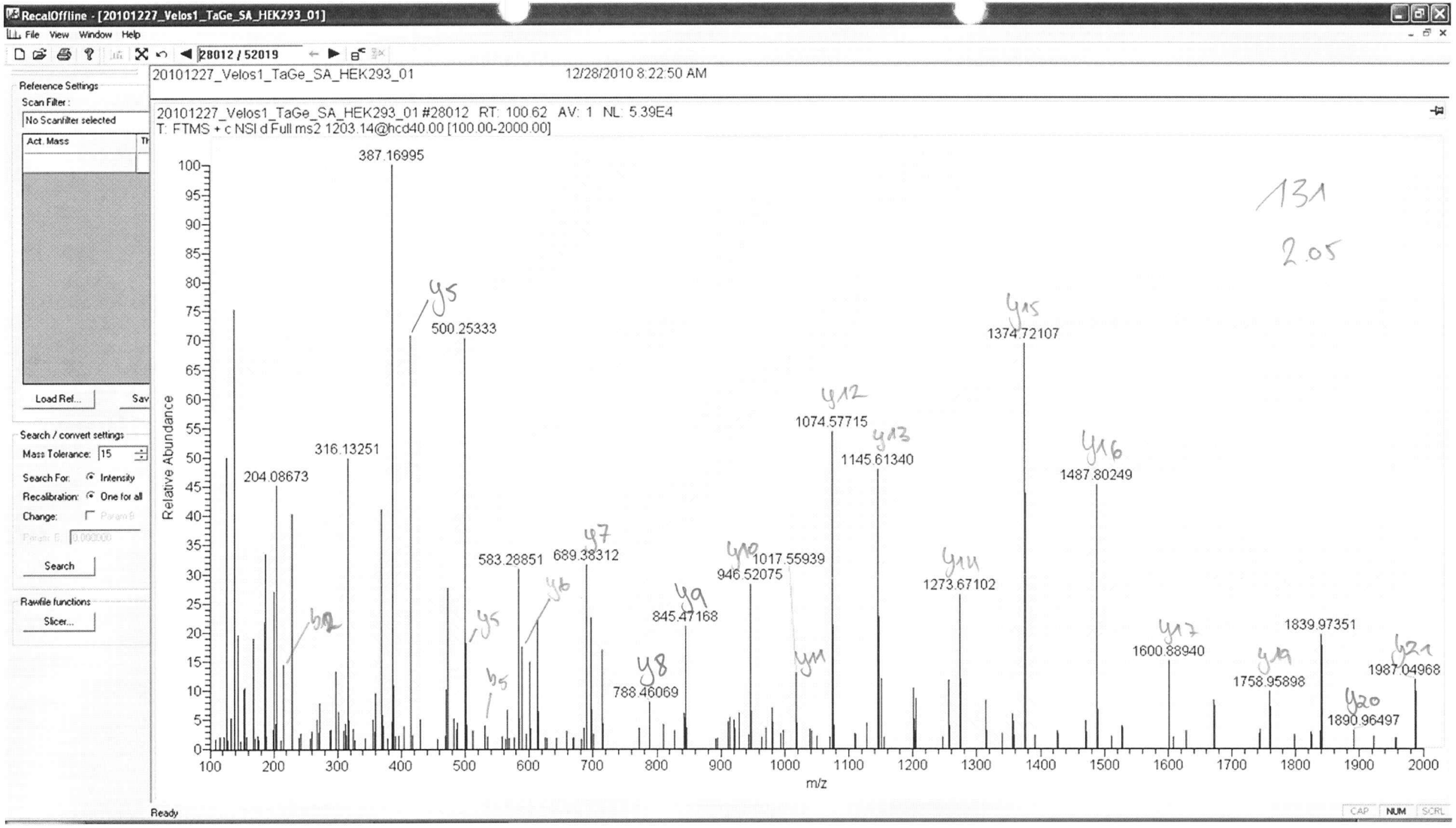
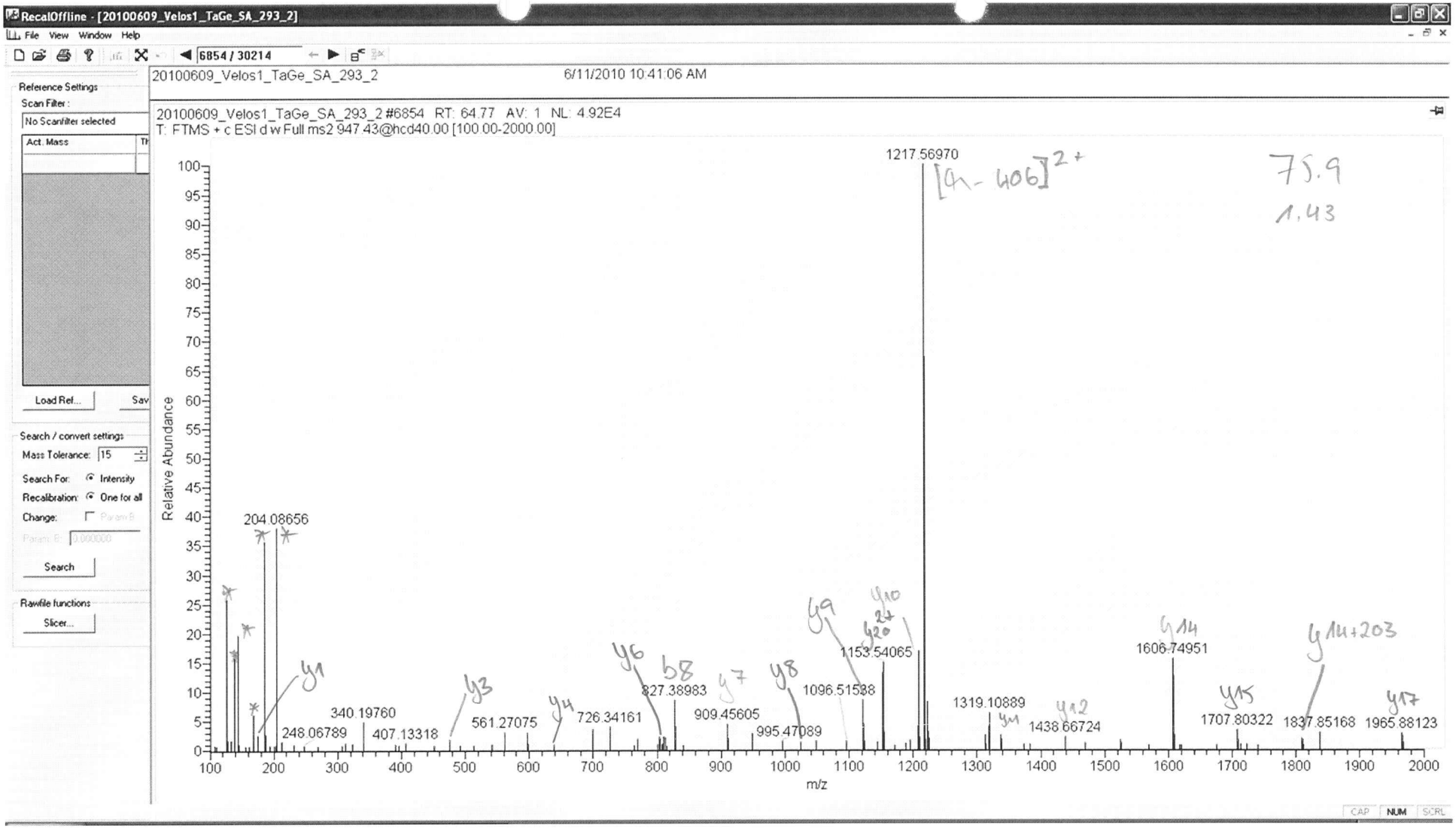


131

2.05

TIPMSAIITQAGATGVTSsPGIK

no site evidence

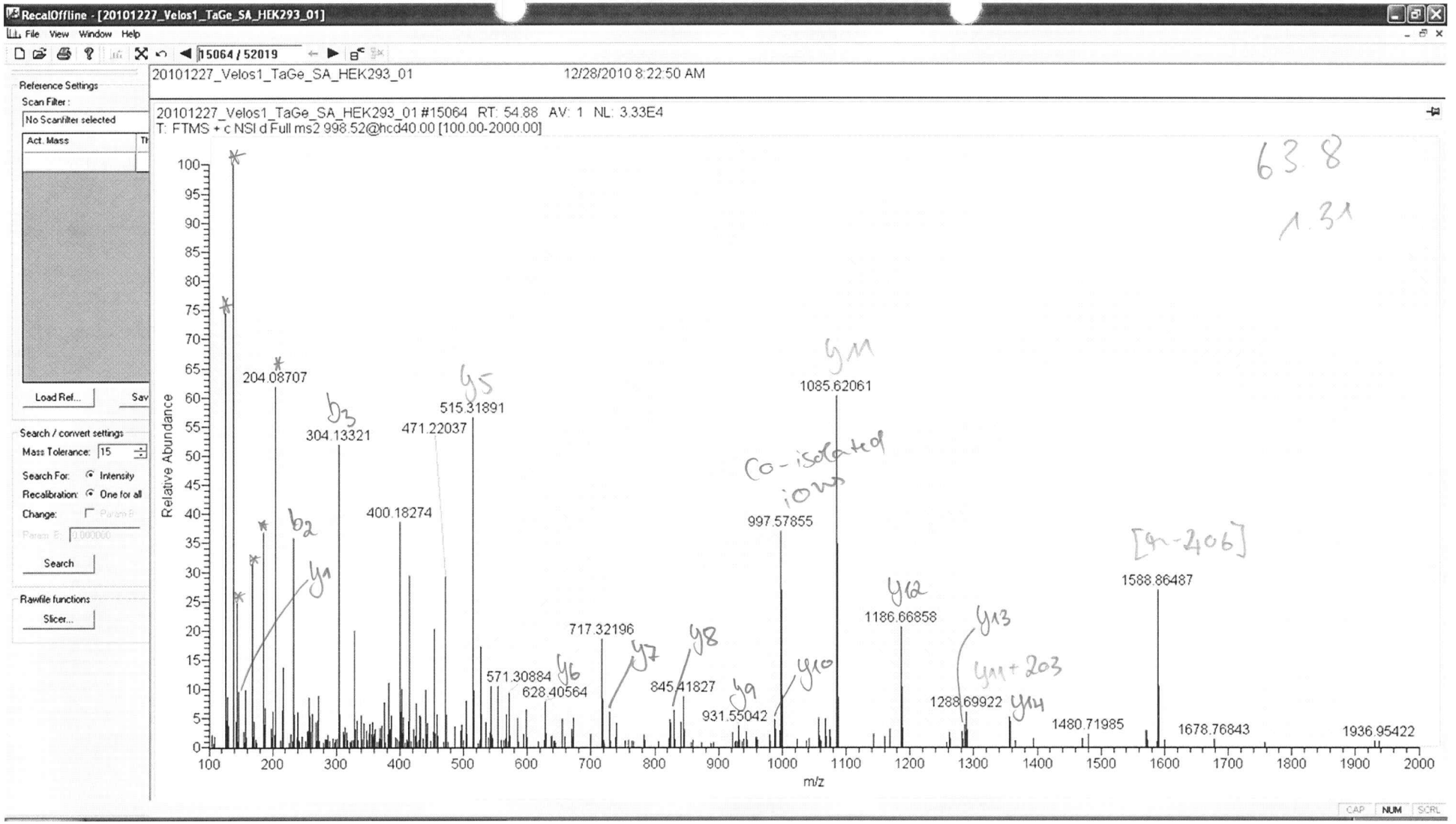


GAPNKEETPATEsPDtGLYYHR

y14 y10

b8

no site evidence



638

1.31

Co-isolated ions

y11

y11+203

[y-406]

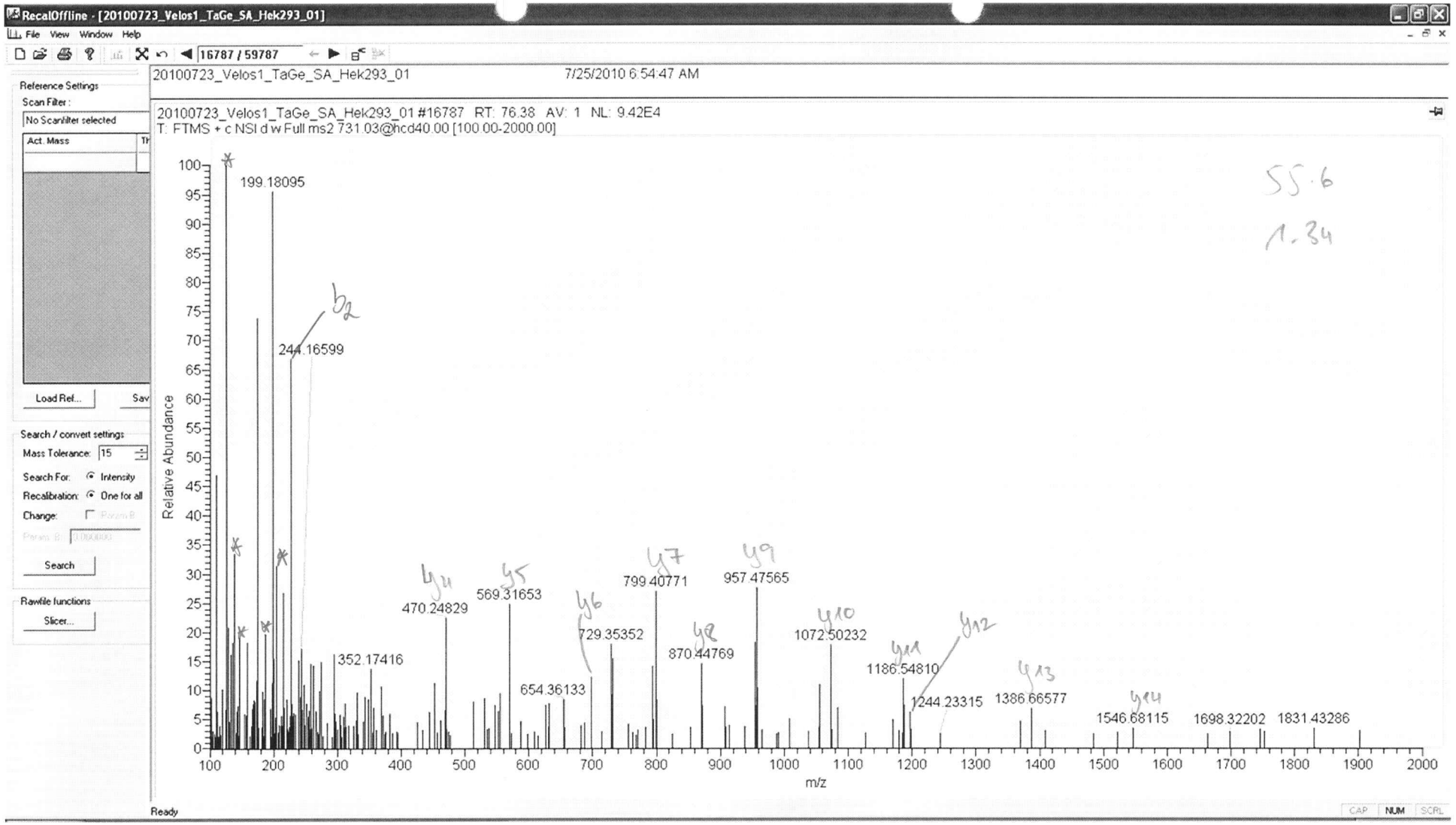
TMAVTPGTTtLPAtVK

y11

at least 1 more

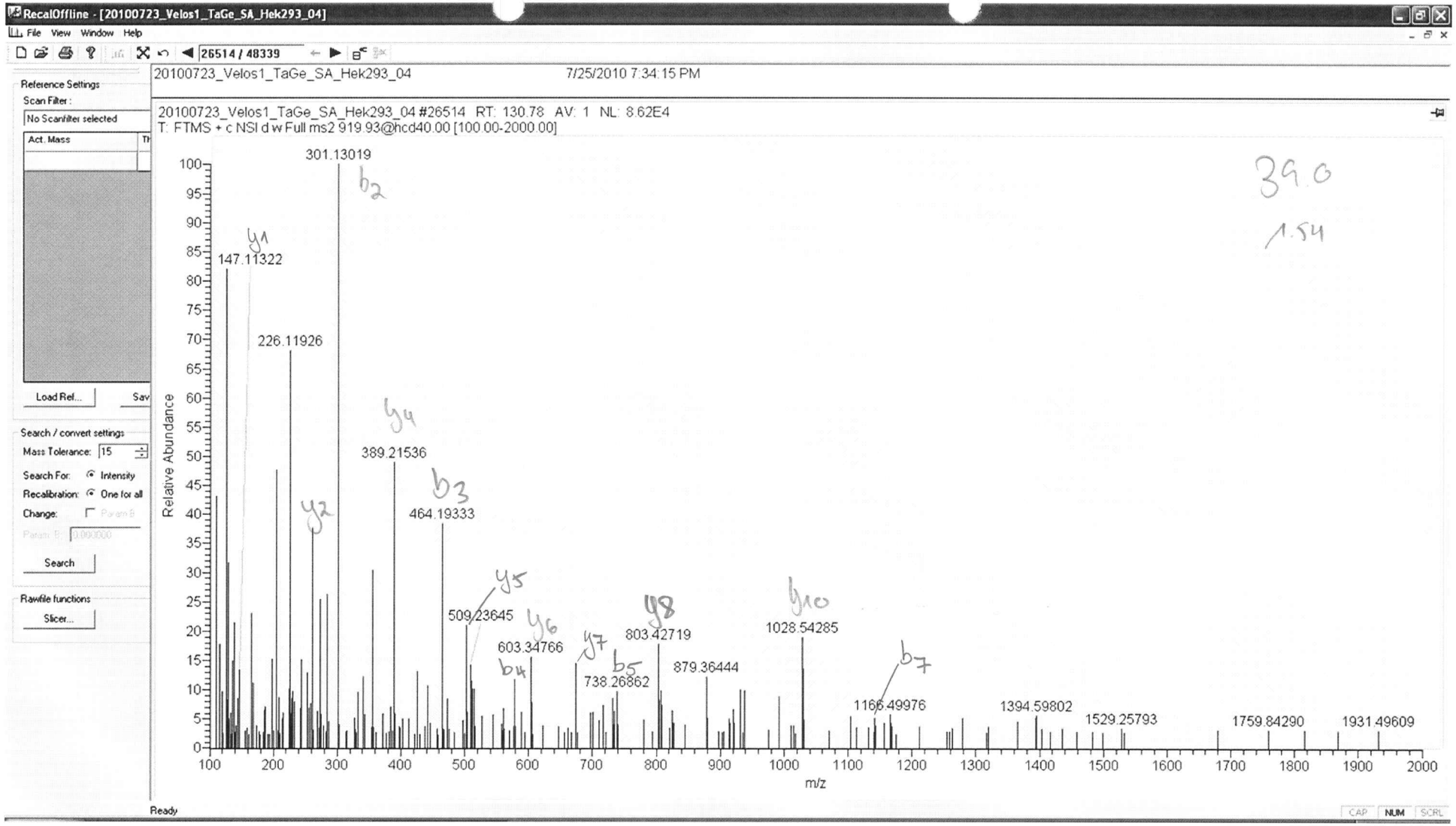
1 site @ T7, 8, 9 or T13

2nd site unknown



ILLTcSLNDSATEVtGHR

no site evidence

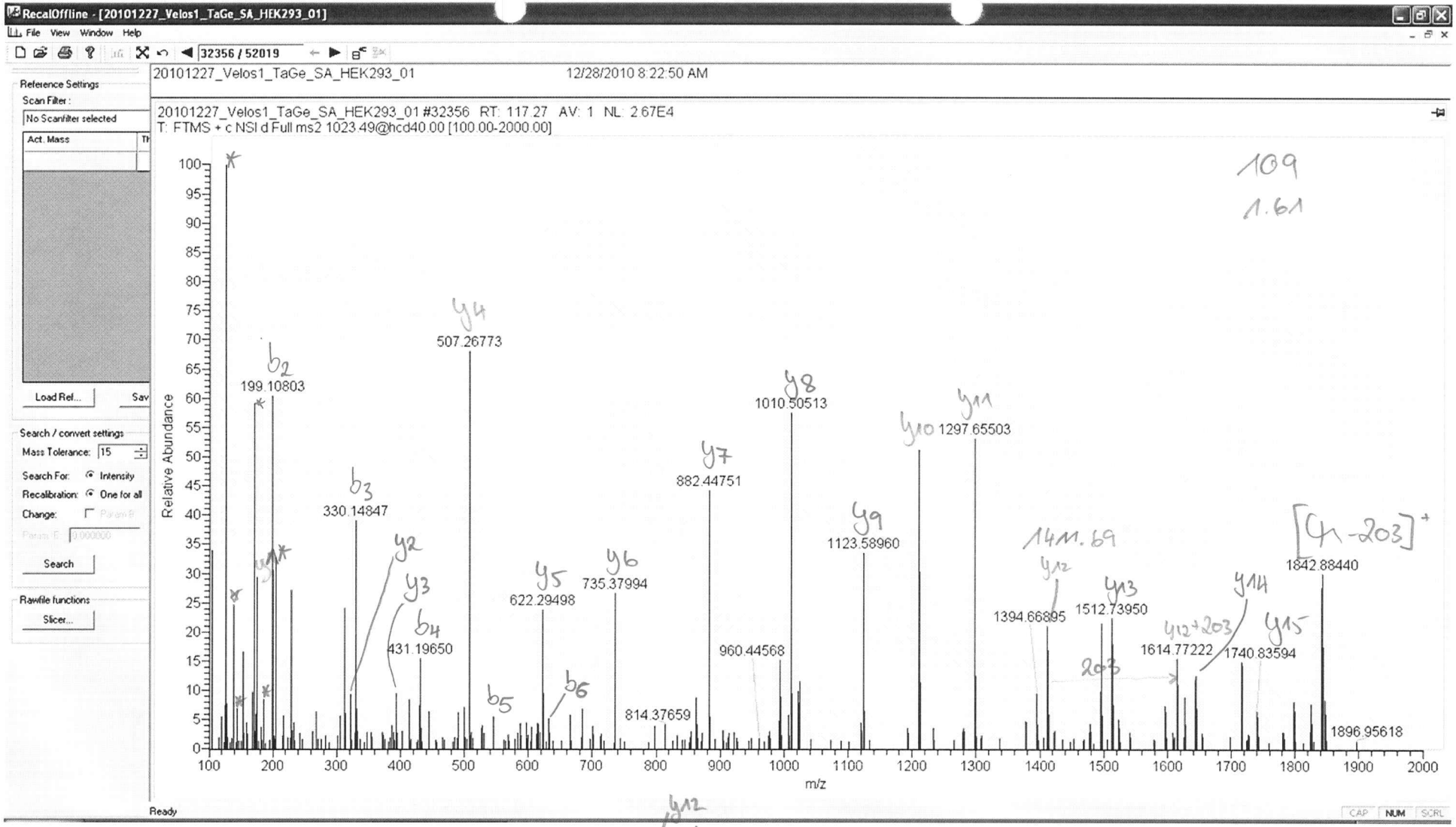


39.0

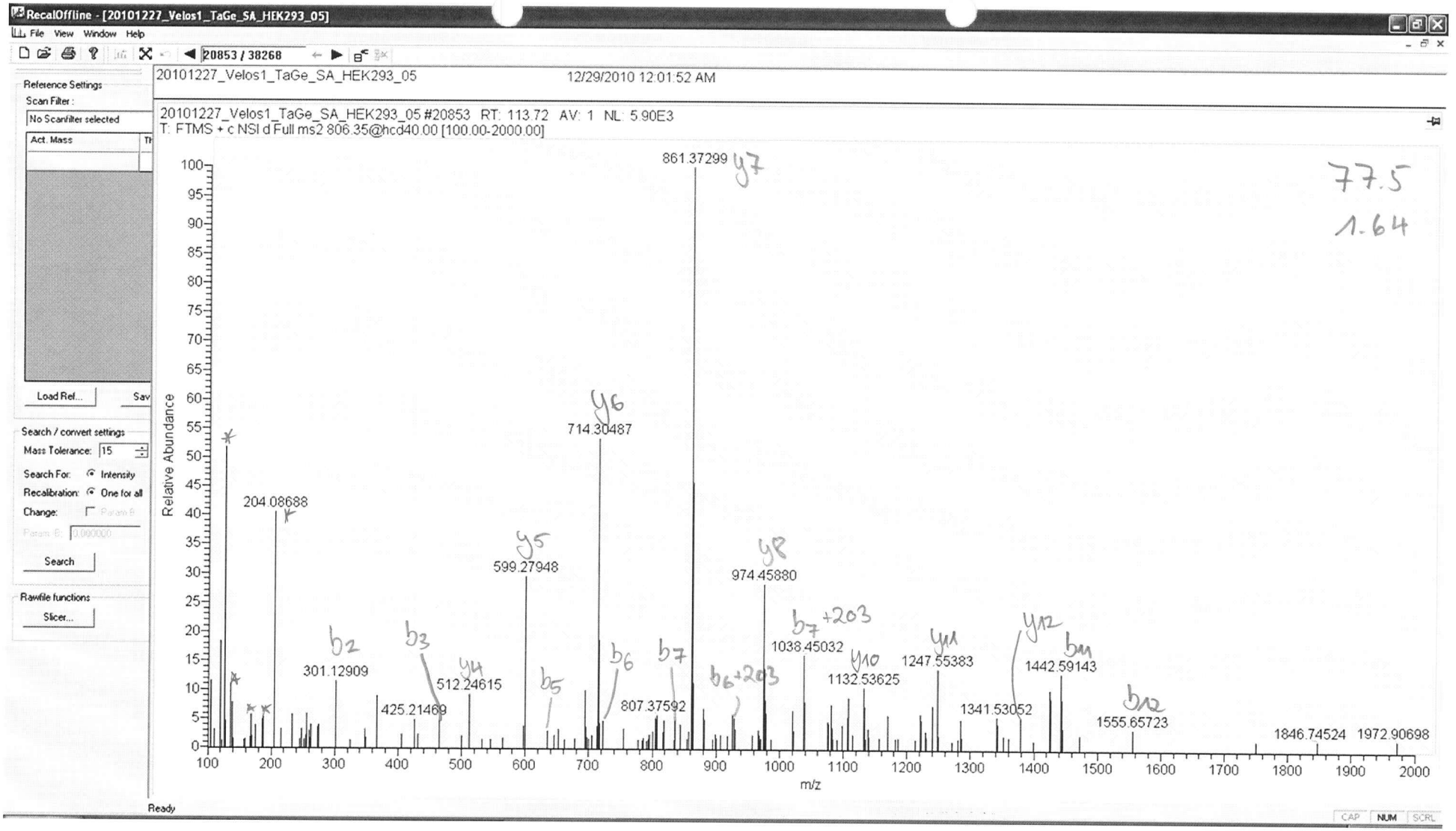
1.54

no site evidence

YHYNcsLLDGTQLFTSHDYGAPQEATLGANK



TPMTNSSIQFLDnAFR

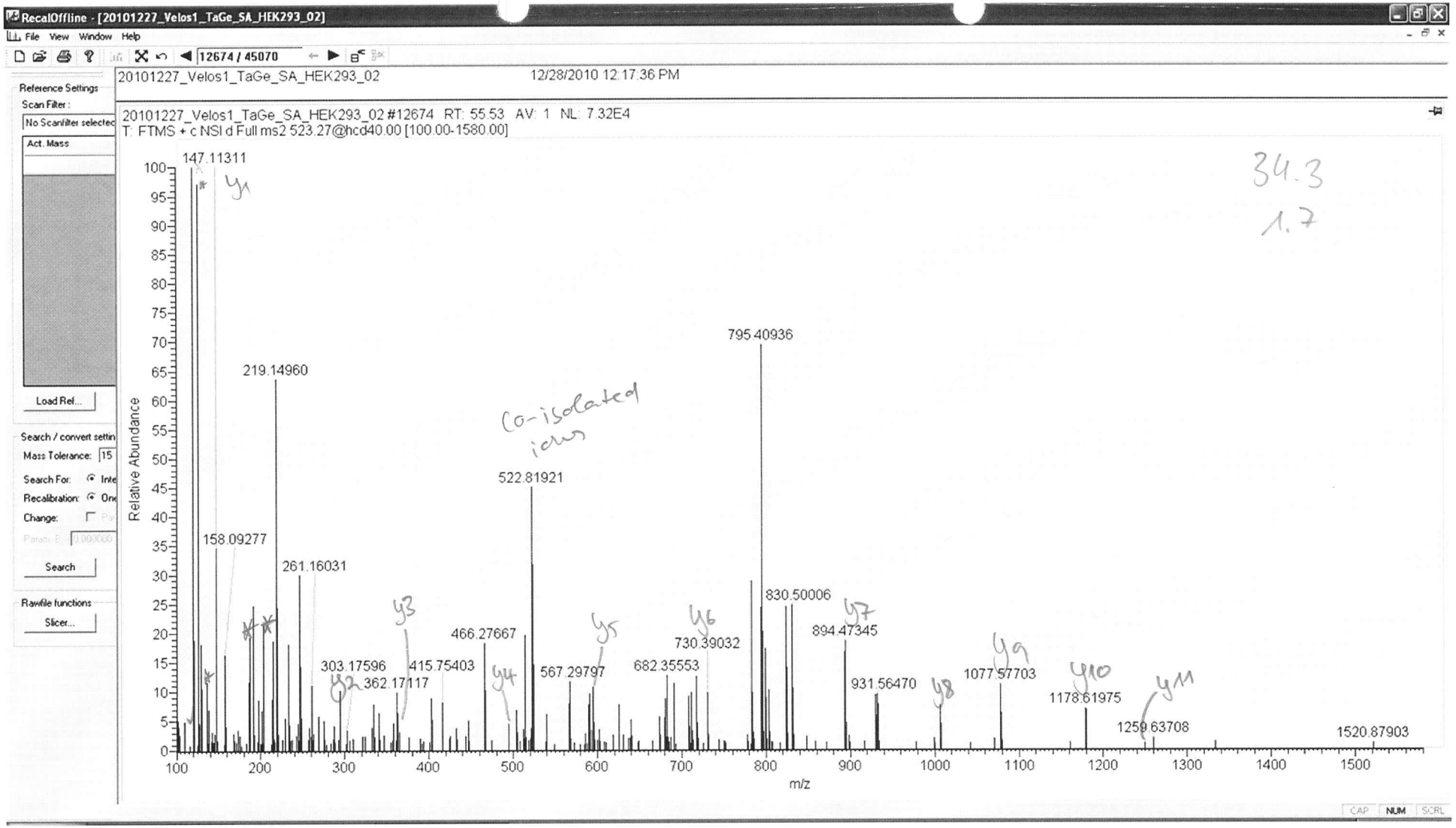


77.5
1.64

N4 or S6

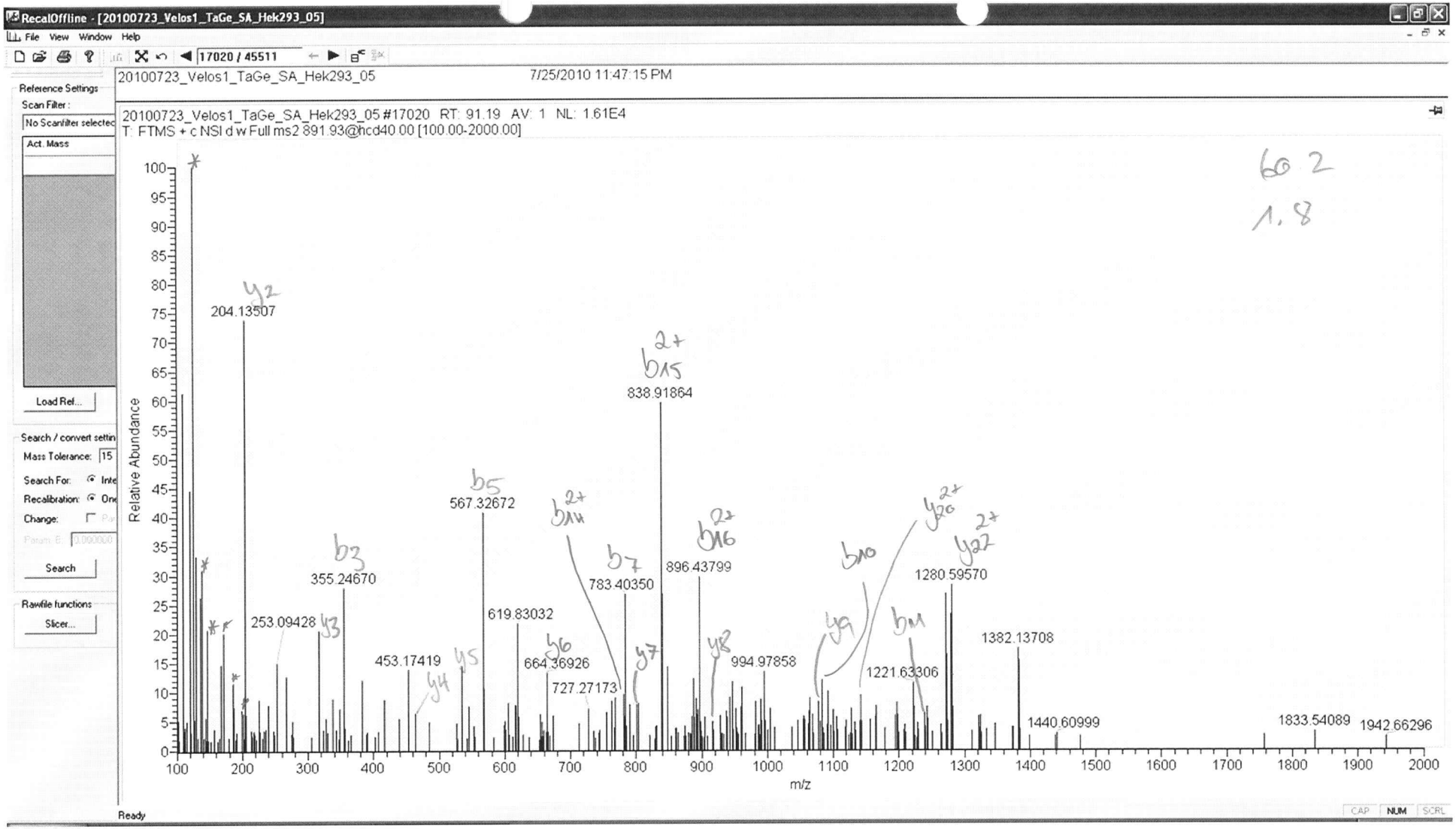
YHYNGsLMDGTLFDSSYSR

b2 b6 b7



NAtALYHVEAFK

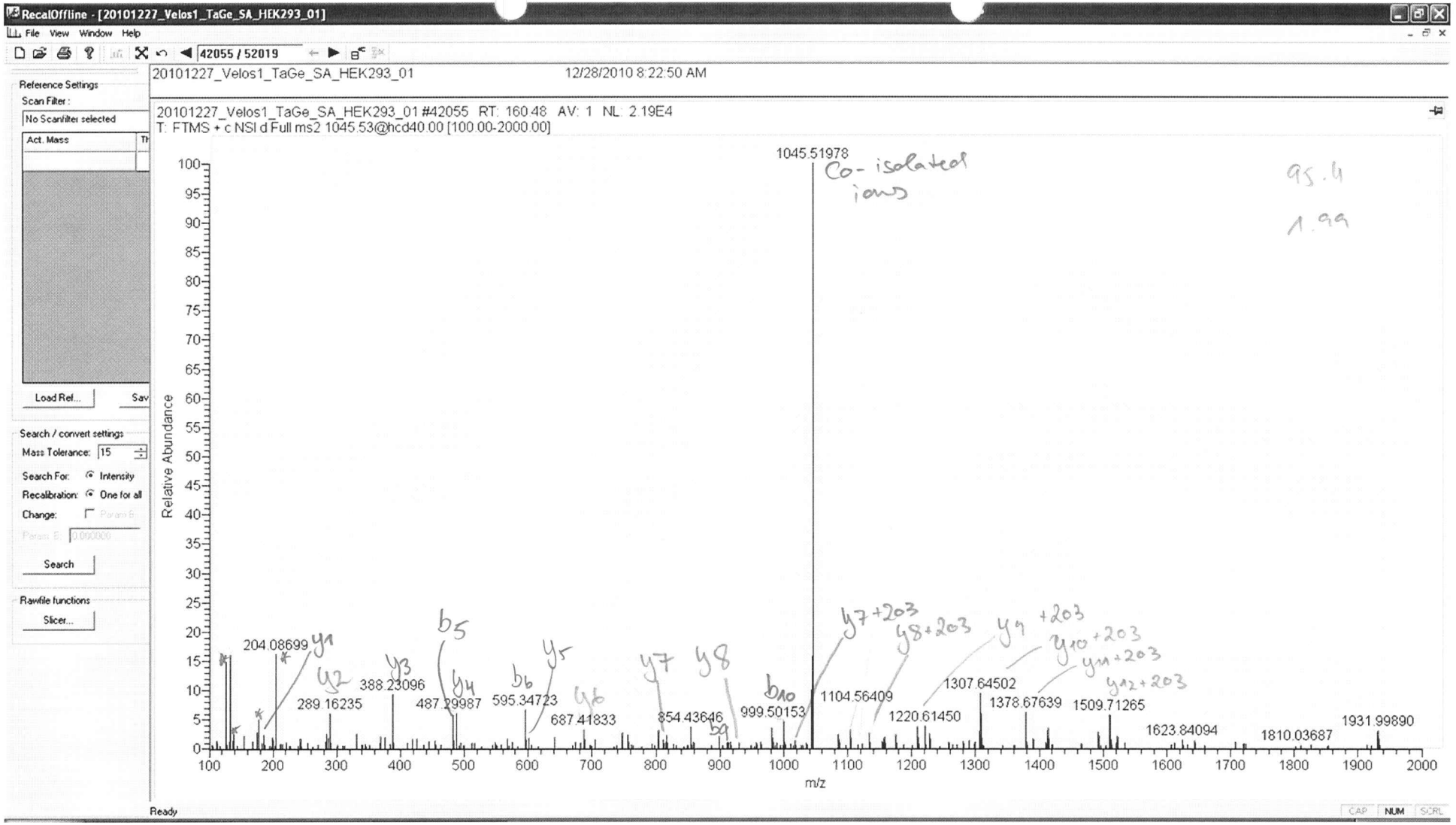
No site evidence



VVRPDSELGERPPEDNQsFQYDHEAFLGK

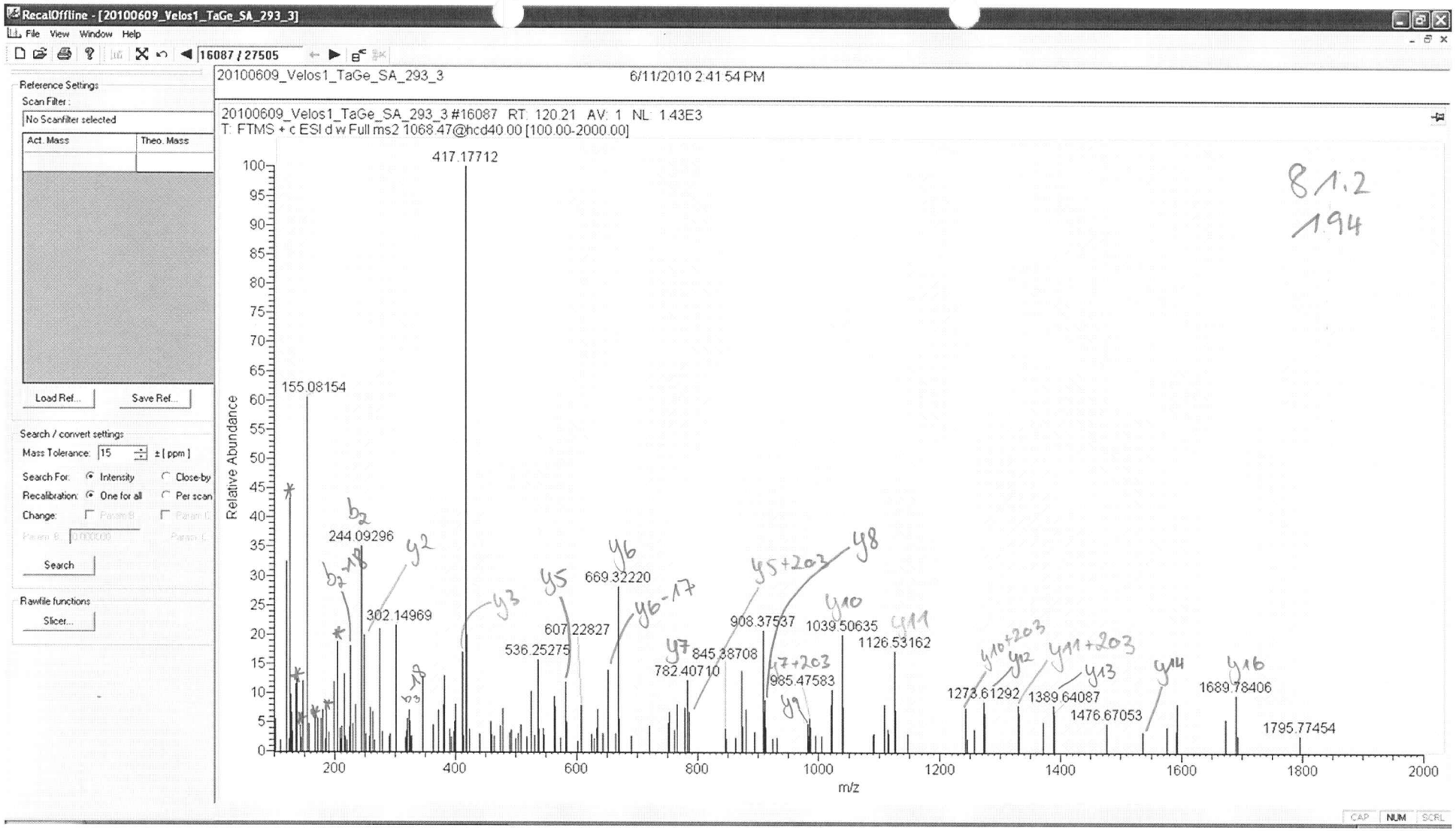
b3 b5 b7

no site evidence

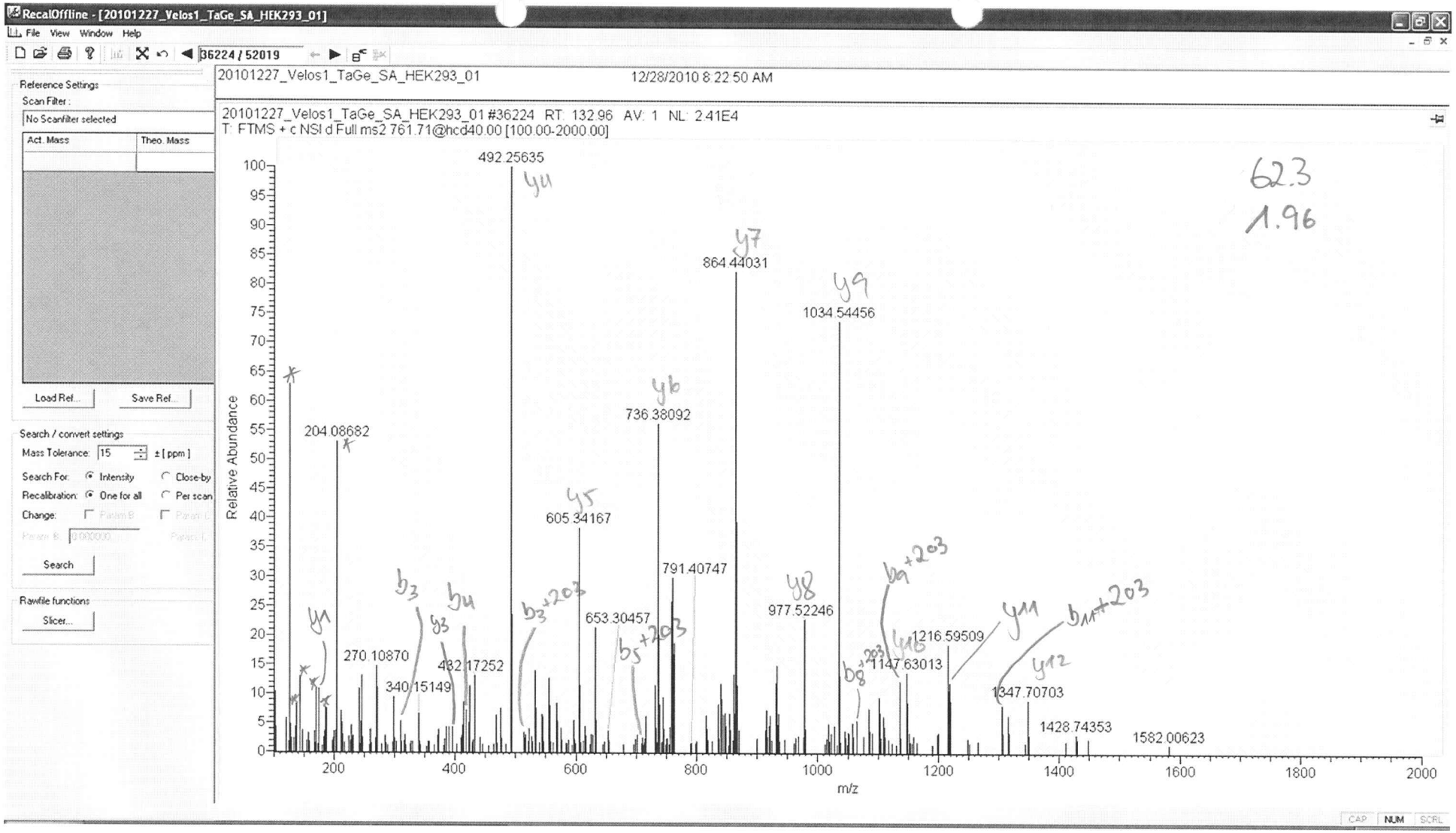


IDGPVISESTPIAETIMASSnESLVVNR

S23



ENPGFDFSGAEISGNYtK

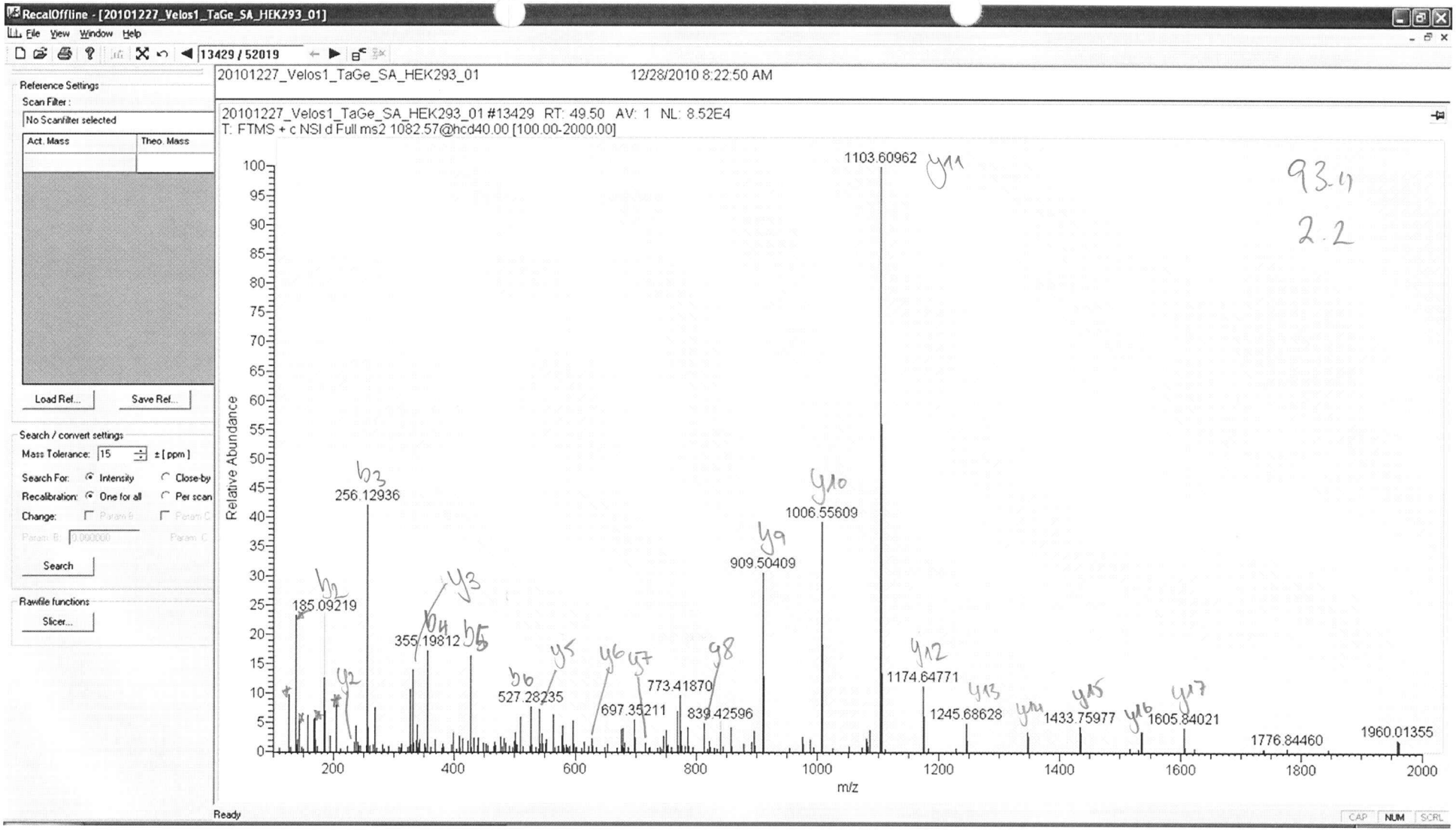


62.3
1.96

N30

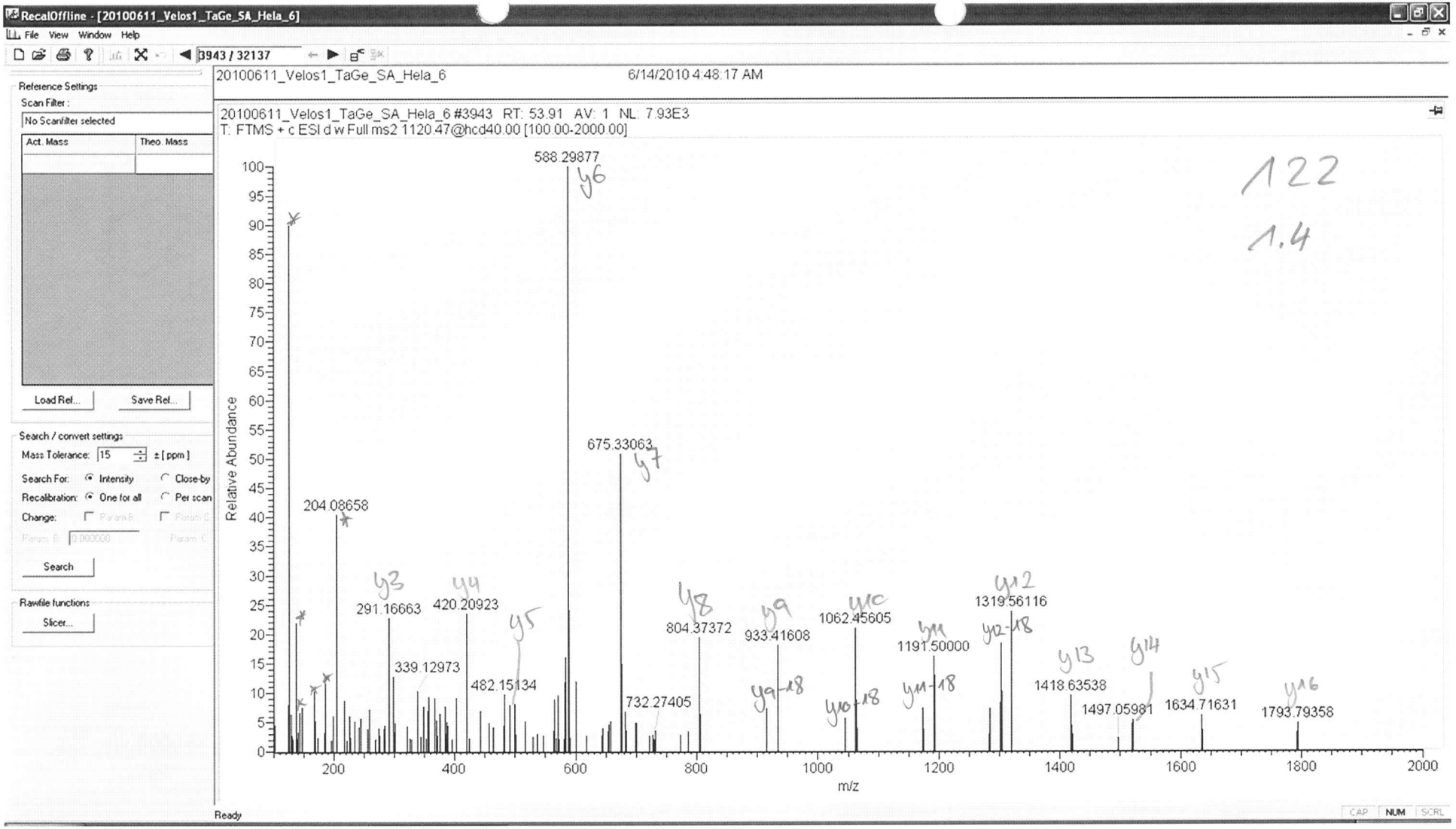
AMNTsQVEALGIQMLPGYR

b_3 b_5



SPAVATSTAAPPPPSSPLPsK

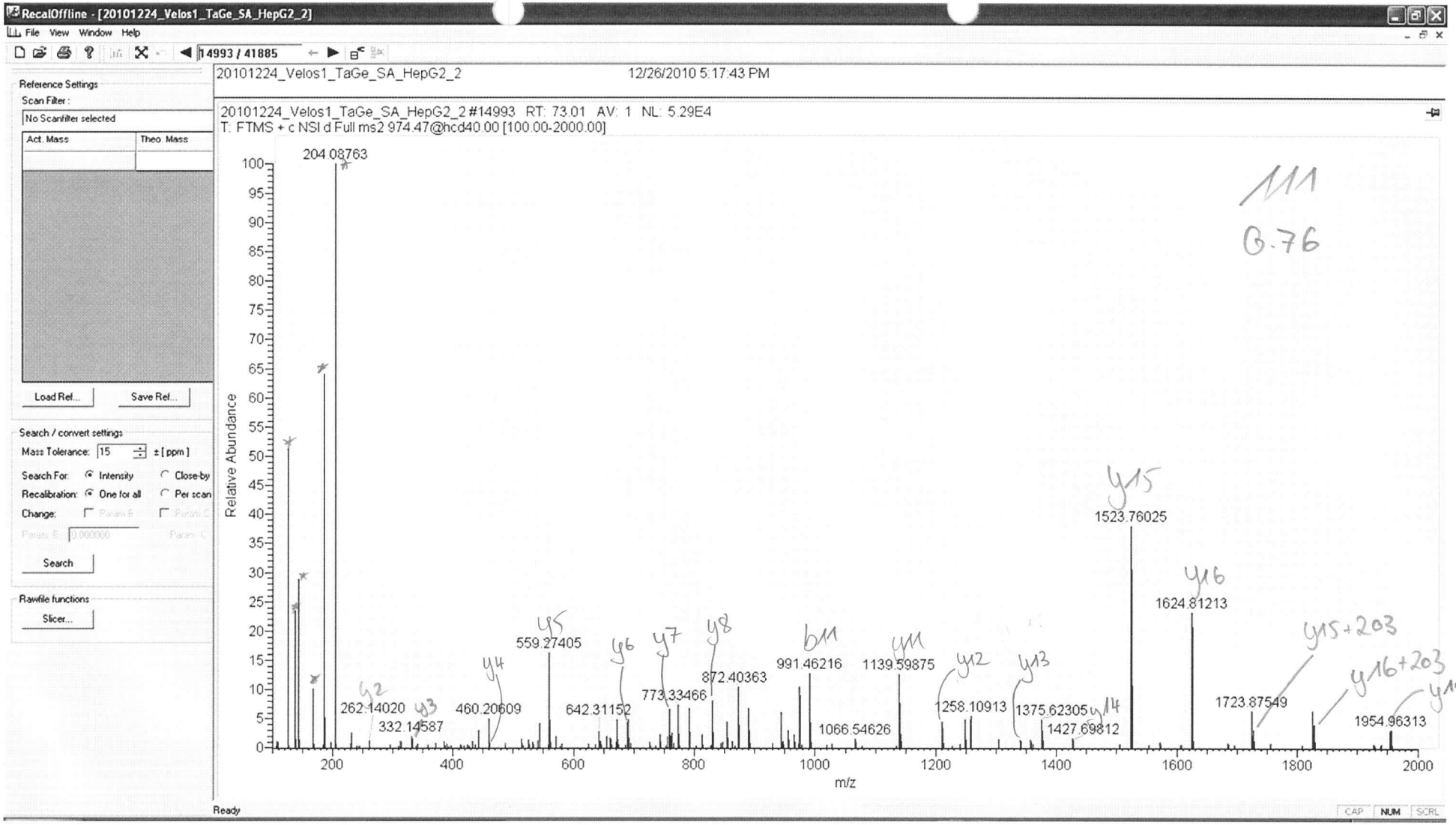
no site evidence



y7

ENGTDTVQEEEESPAEGsK

no site evidence

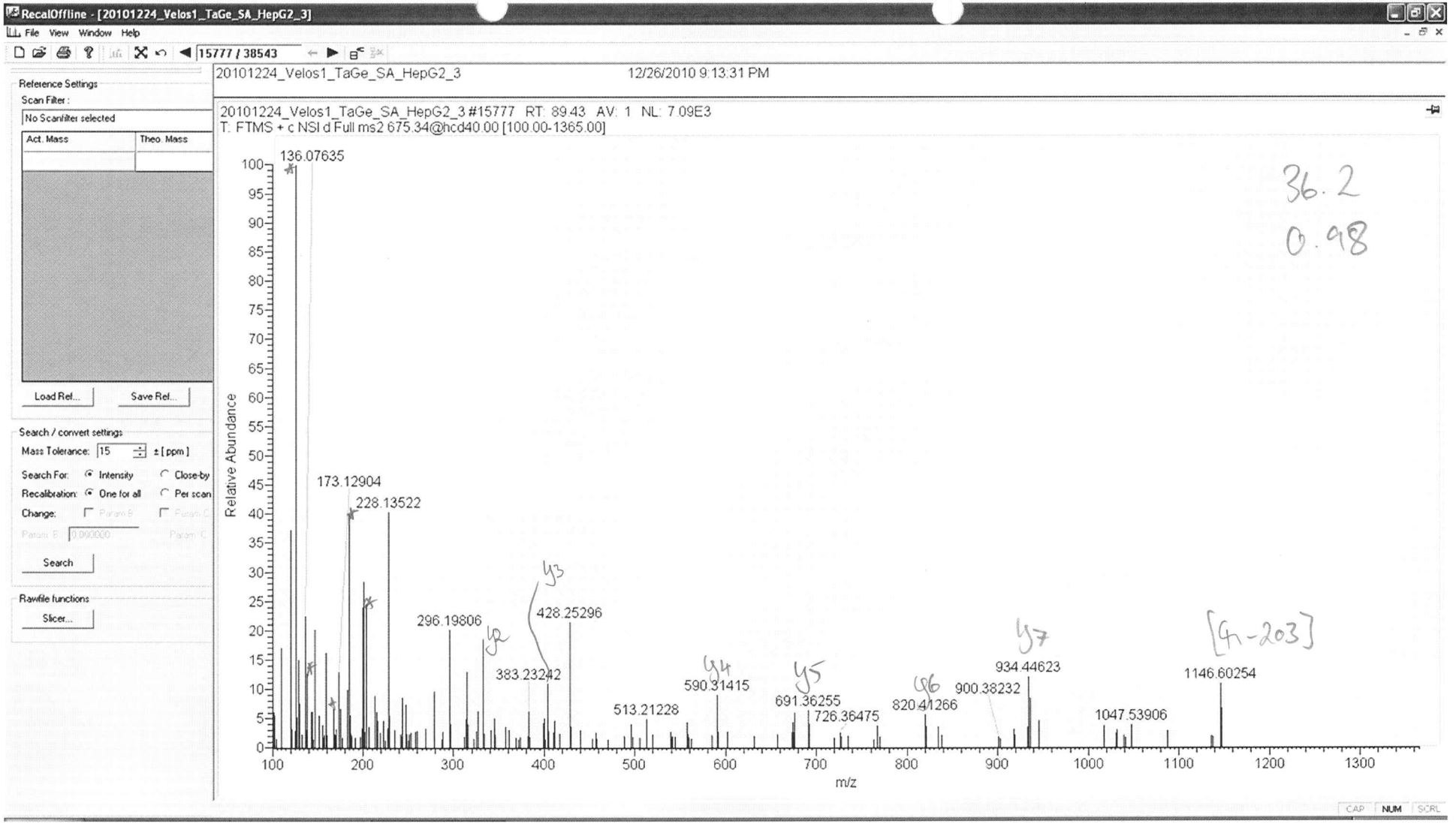


111
0.76

TETGATETVtPsEAPVLAAEPEADK

y15
b11

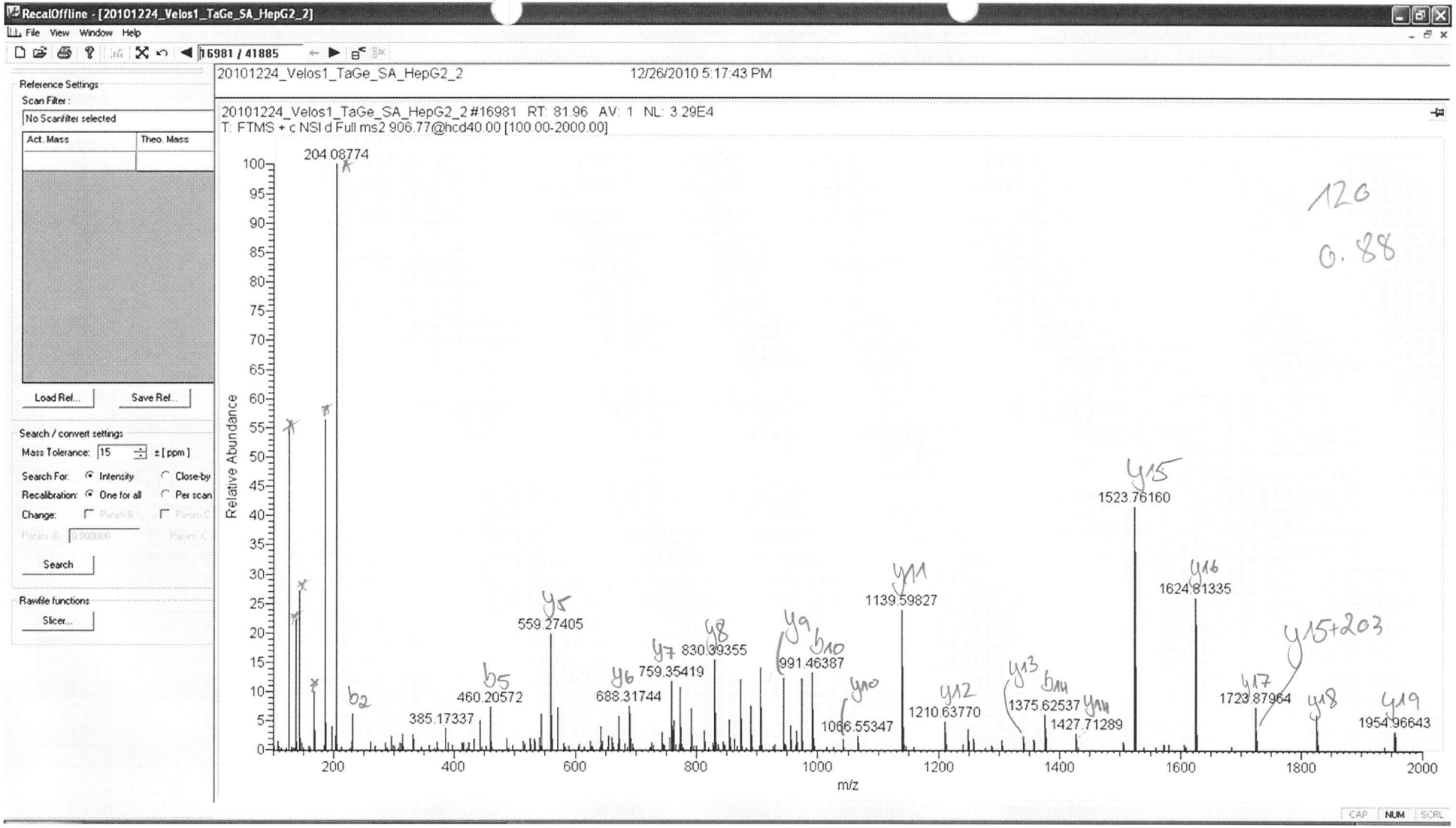
S12 and
2nd site ambiguous



36.2
0.98

VINEtWAWK

no site evidence



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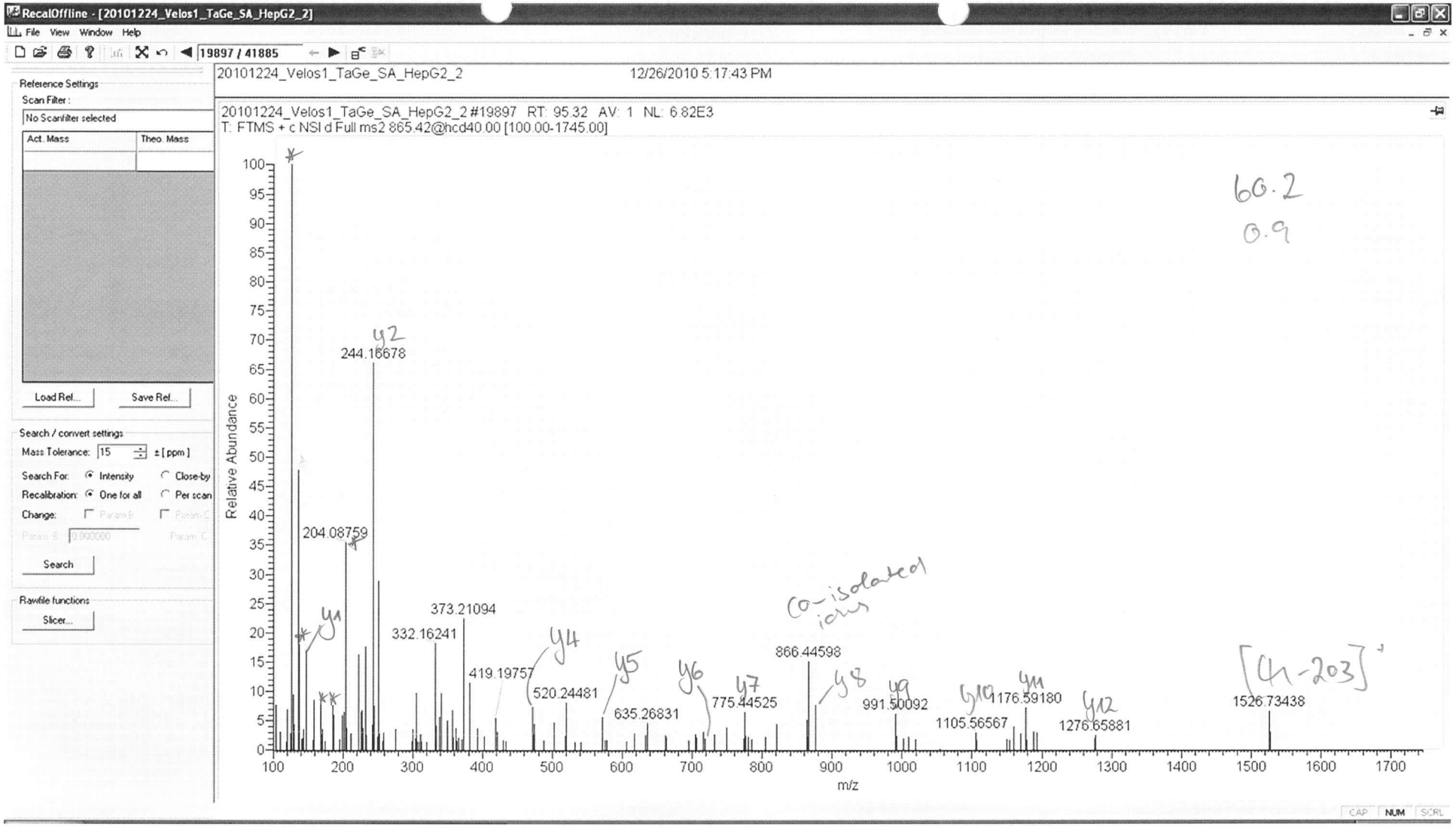
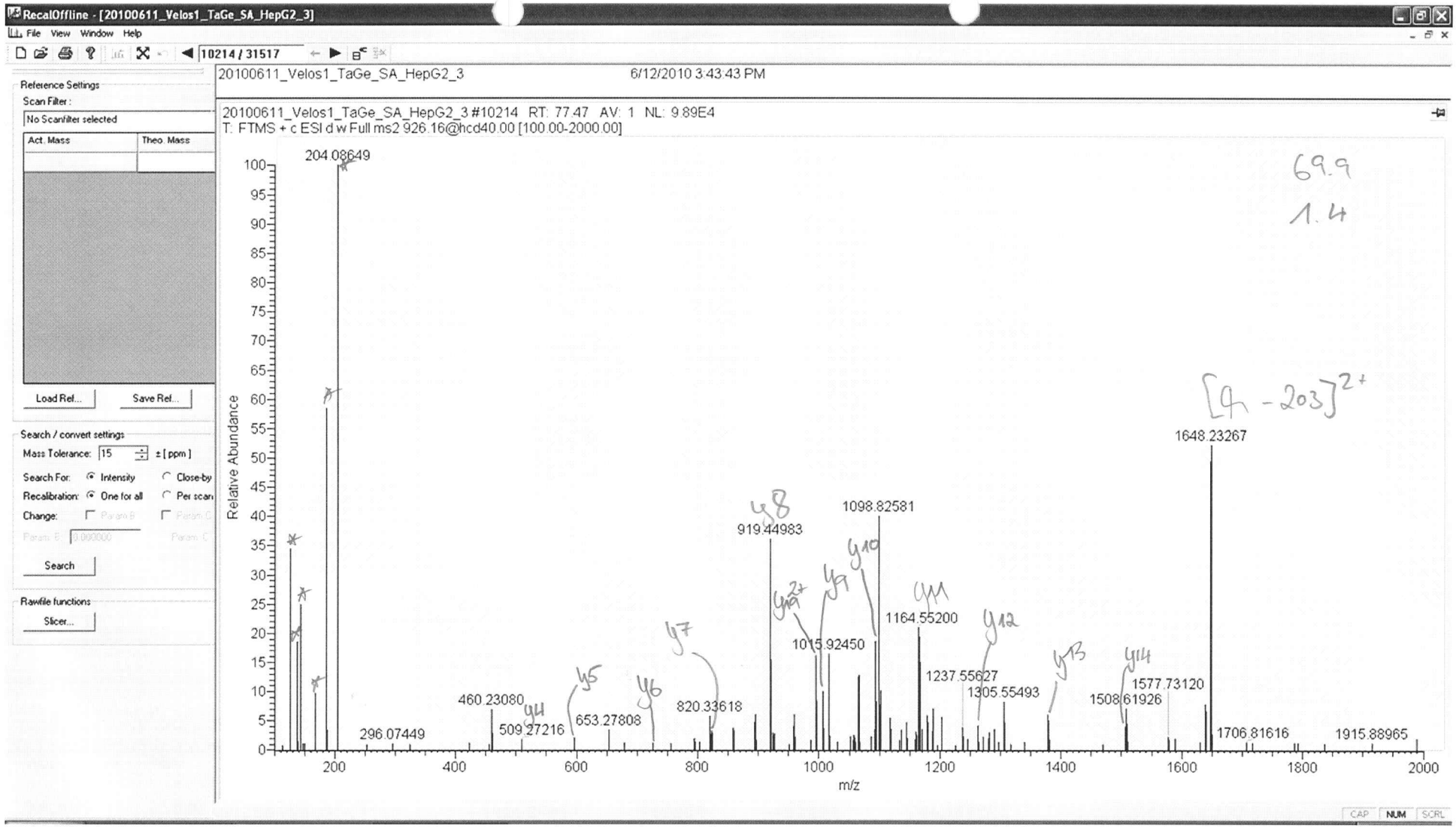


y10 y8

YSVANDtGFVDIPK

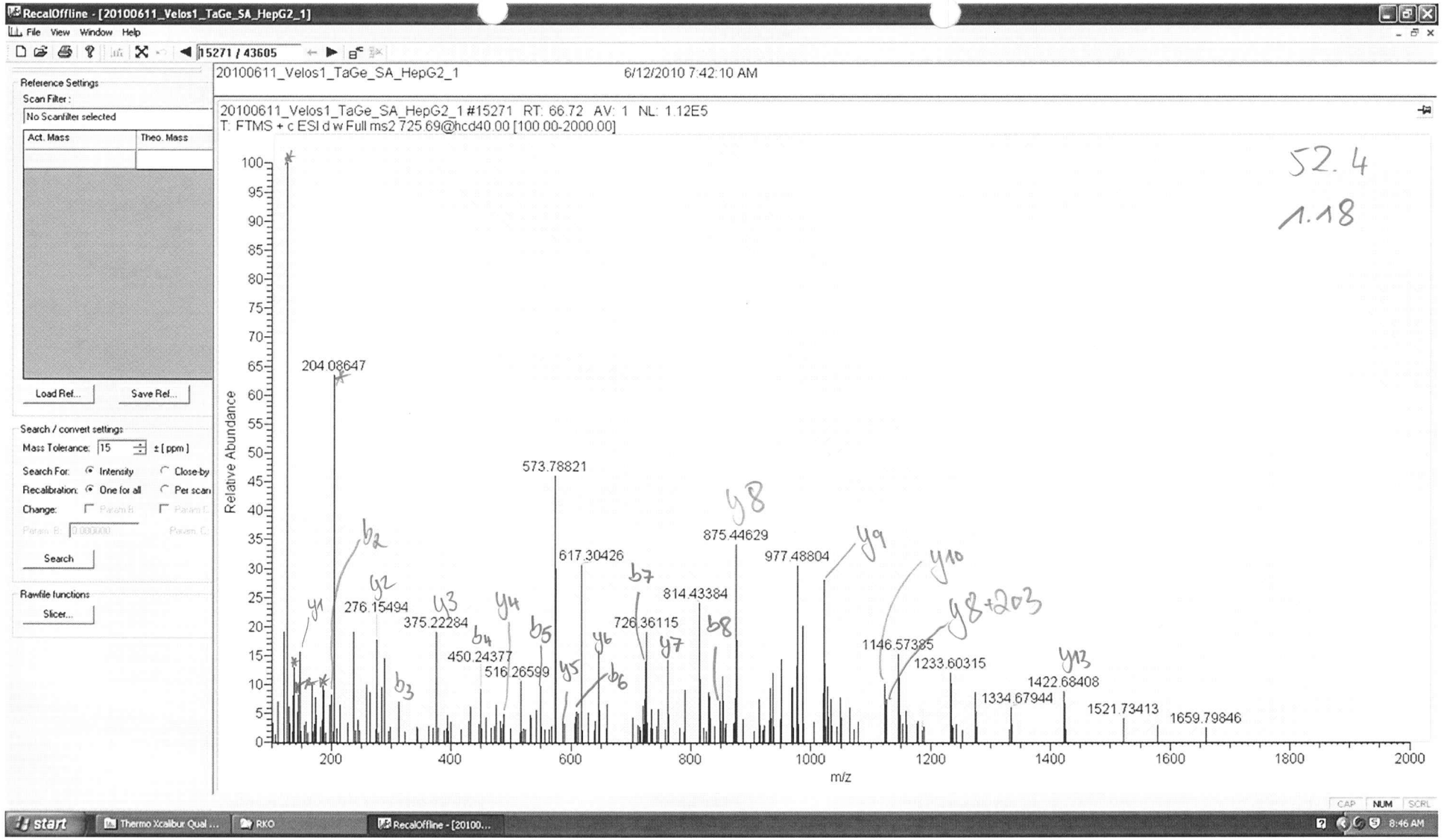
No site evidence



EFHHGPDPTDTAPGEQAQDVASsPPESsFQK

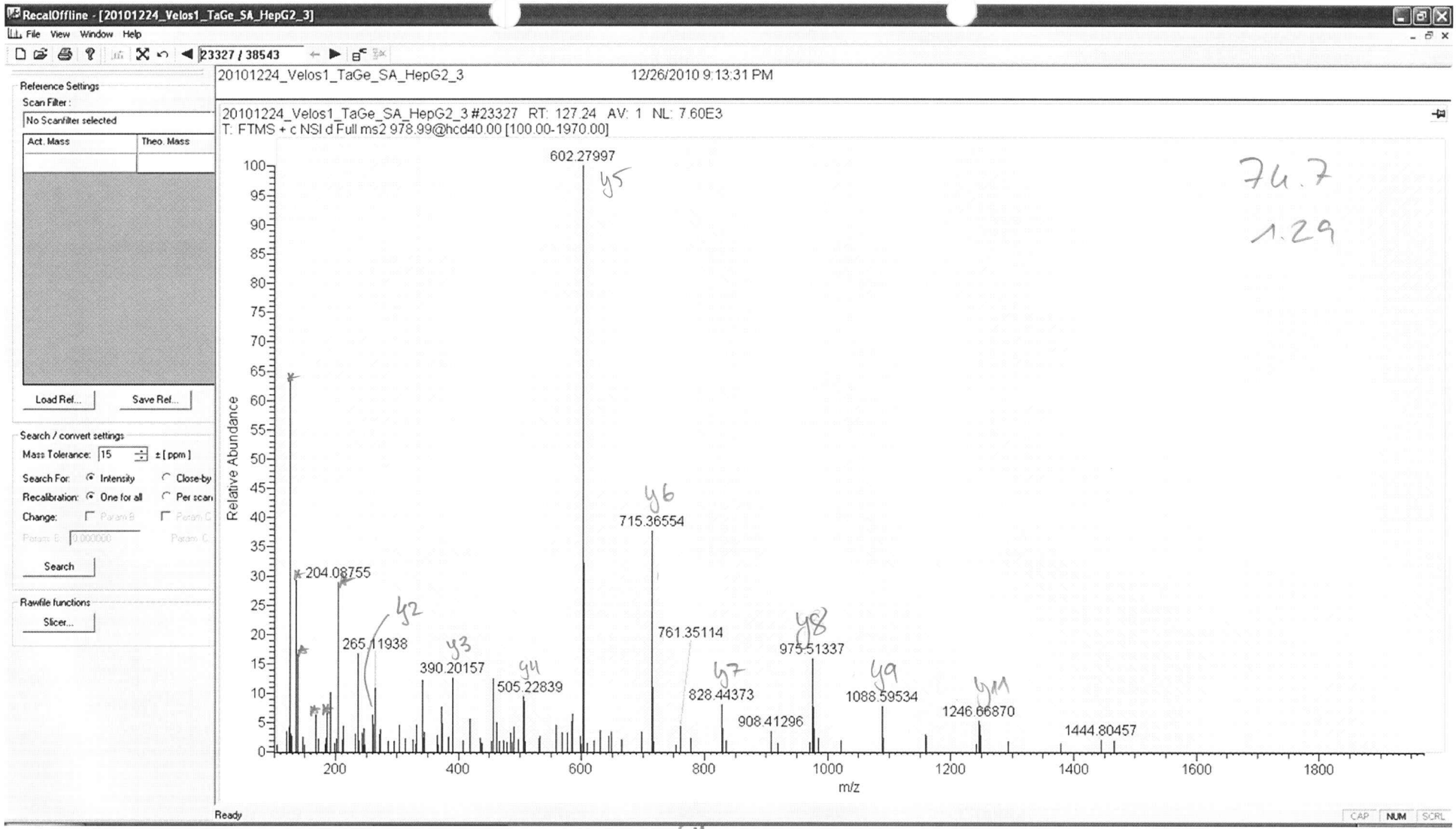
y8
y7

no site evidence



QAIHVGNQTFNDGtIVEK

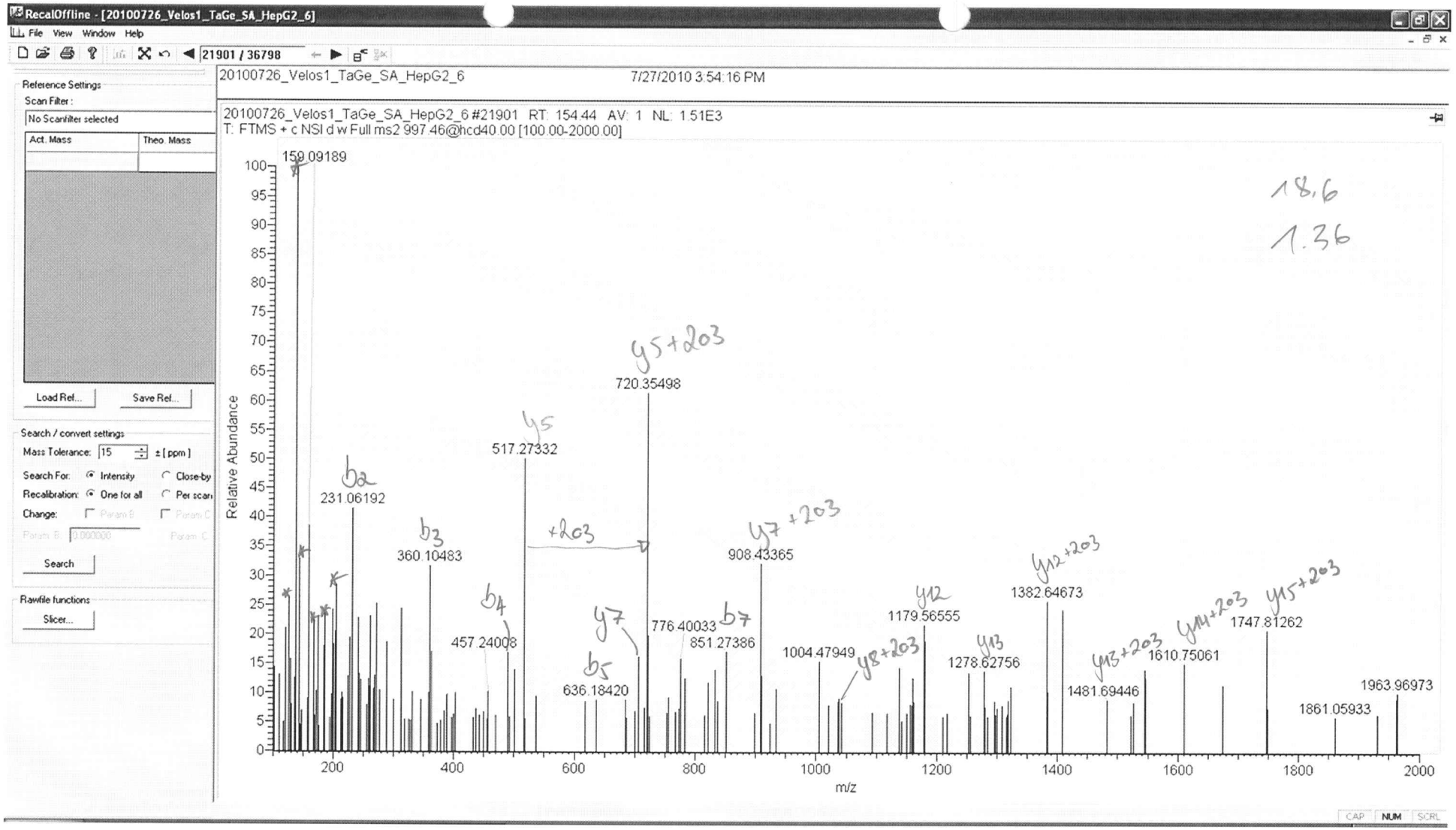
N11 or T14



74.7
1.29

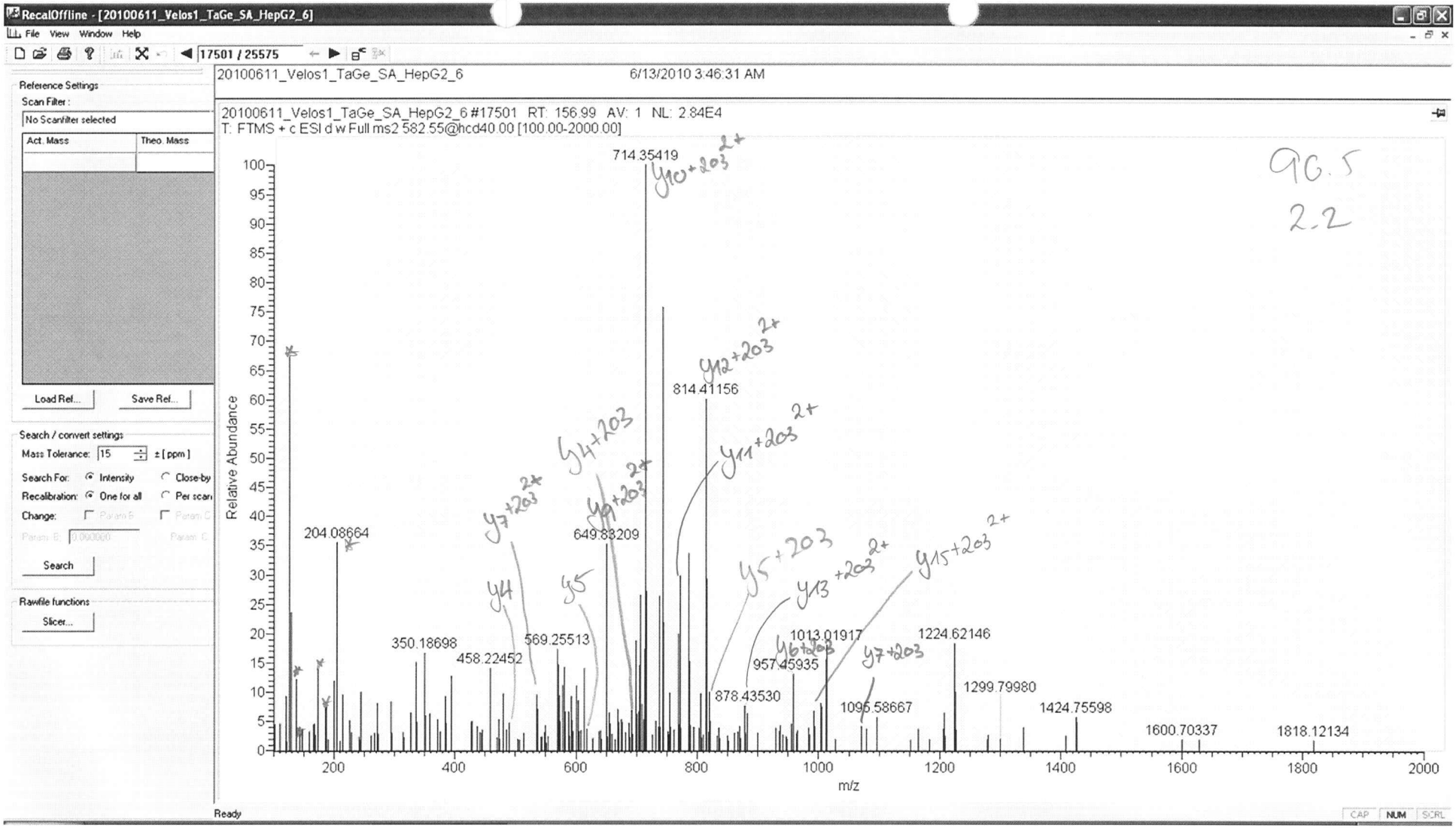
YTGNAsALFILPDQDK

no site evidence



DDEEmNTWIQAISSAISSDKHEVSASTQStPASSR

S33 or 34



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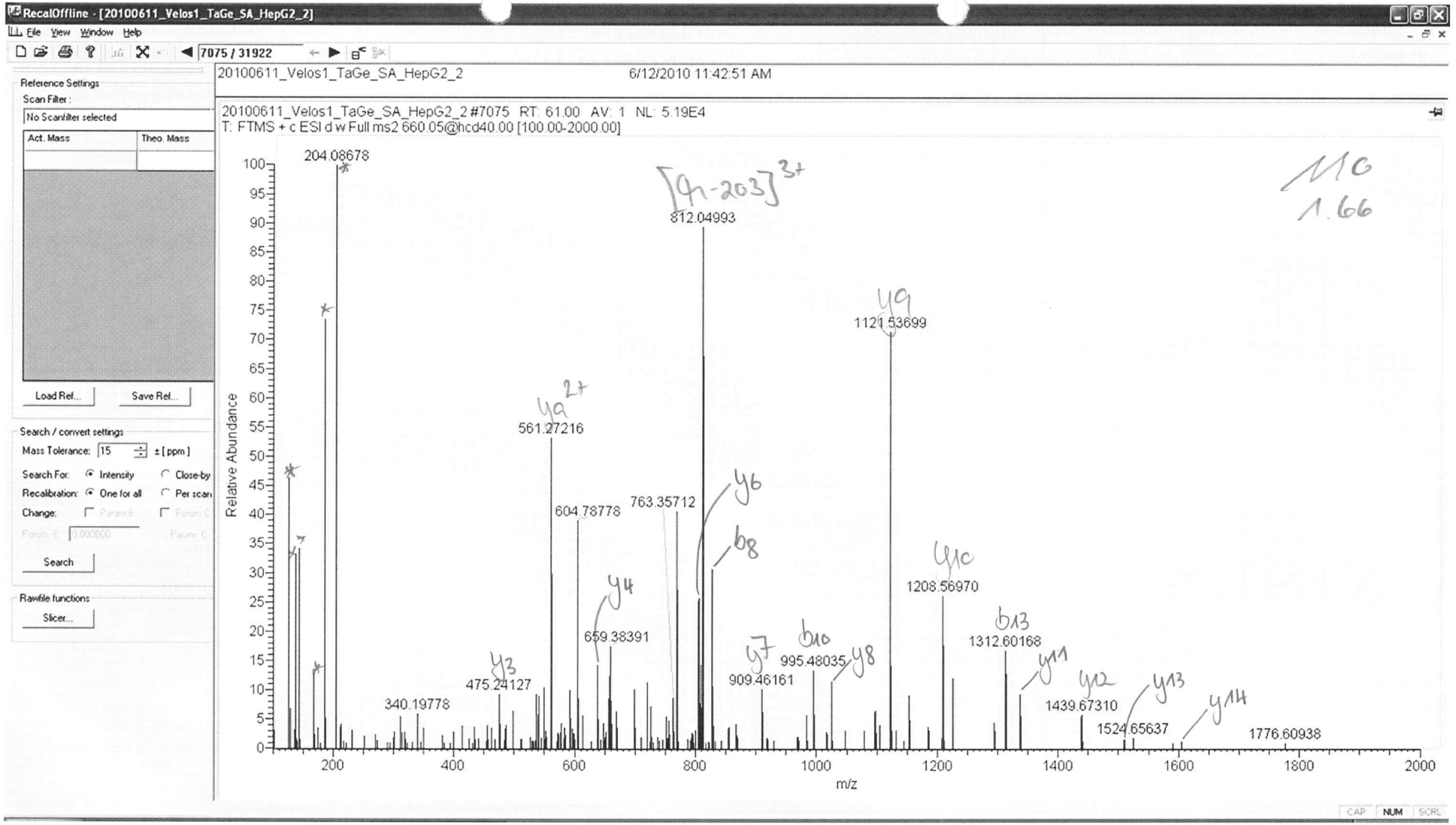
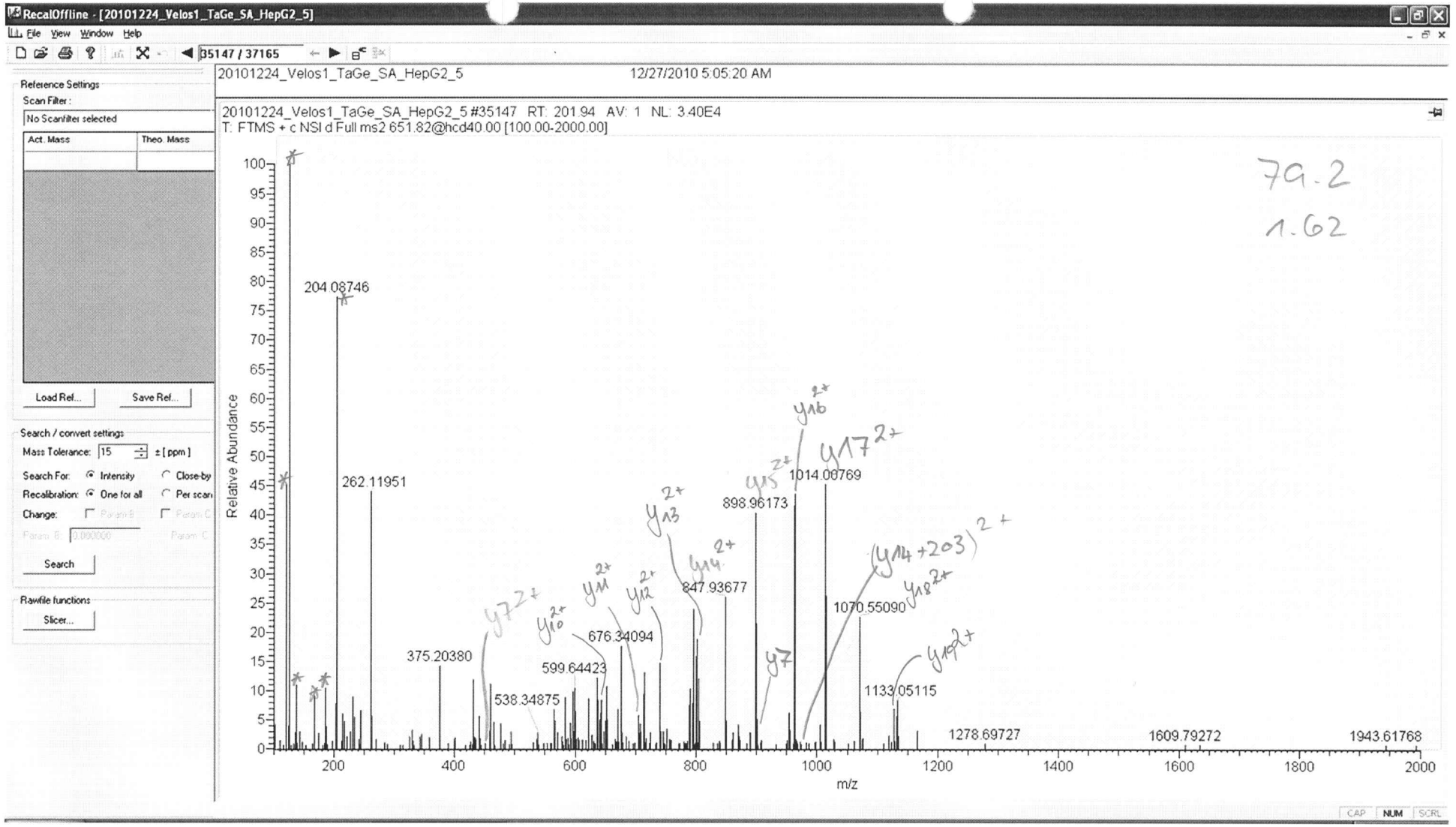


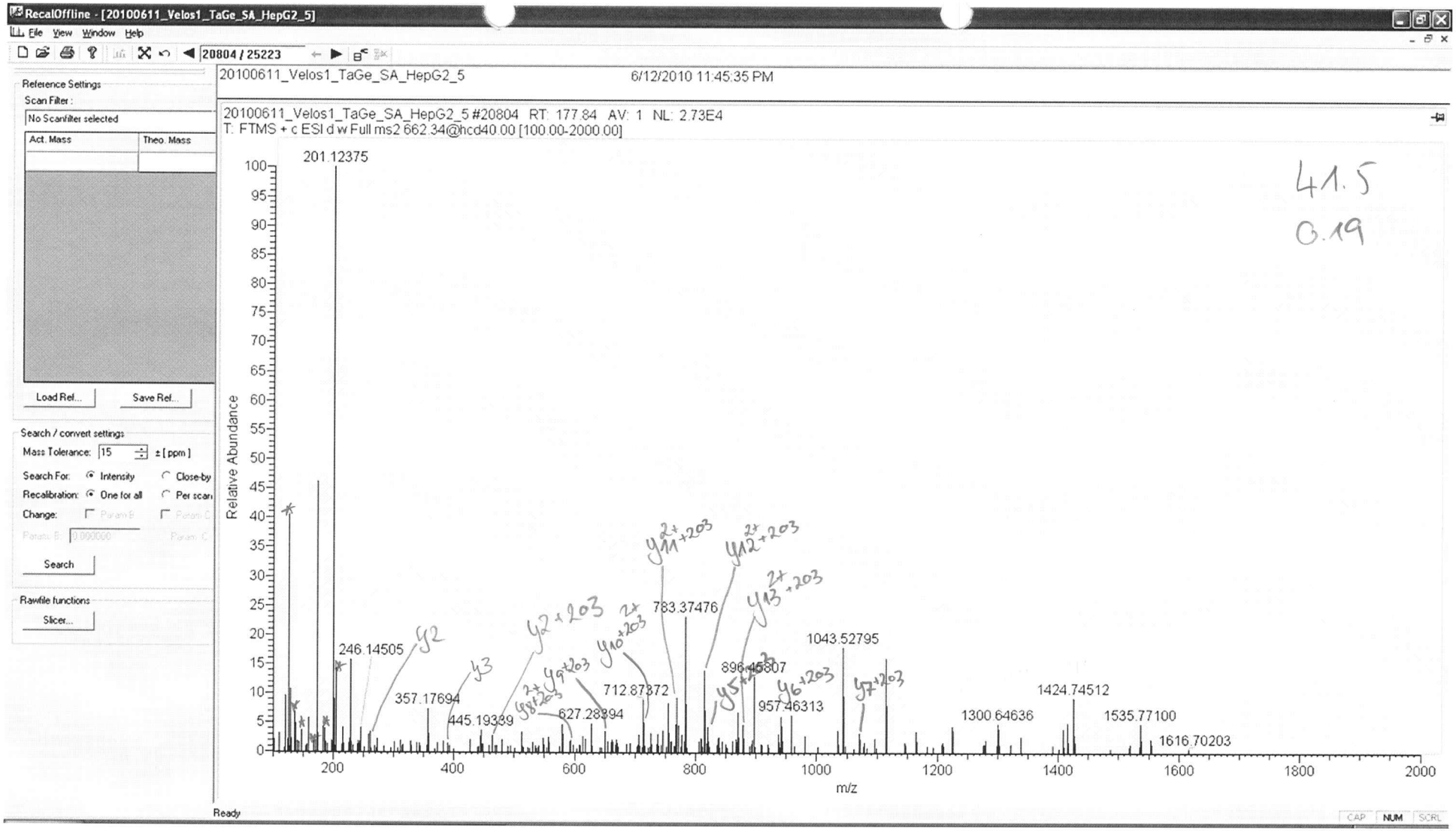
GAPNKEETPATESPDtGLYYHR

no site evidence



FNLTETSEAEIHQsFQHLLR

S7 or S14

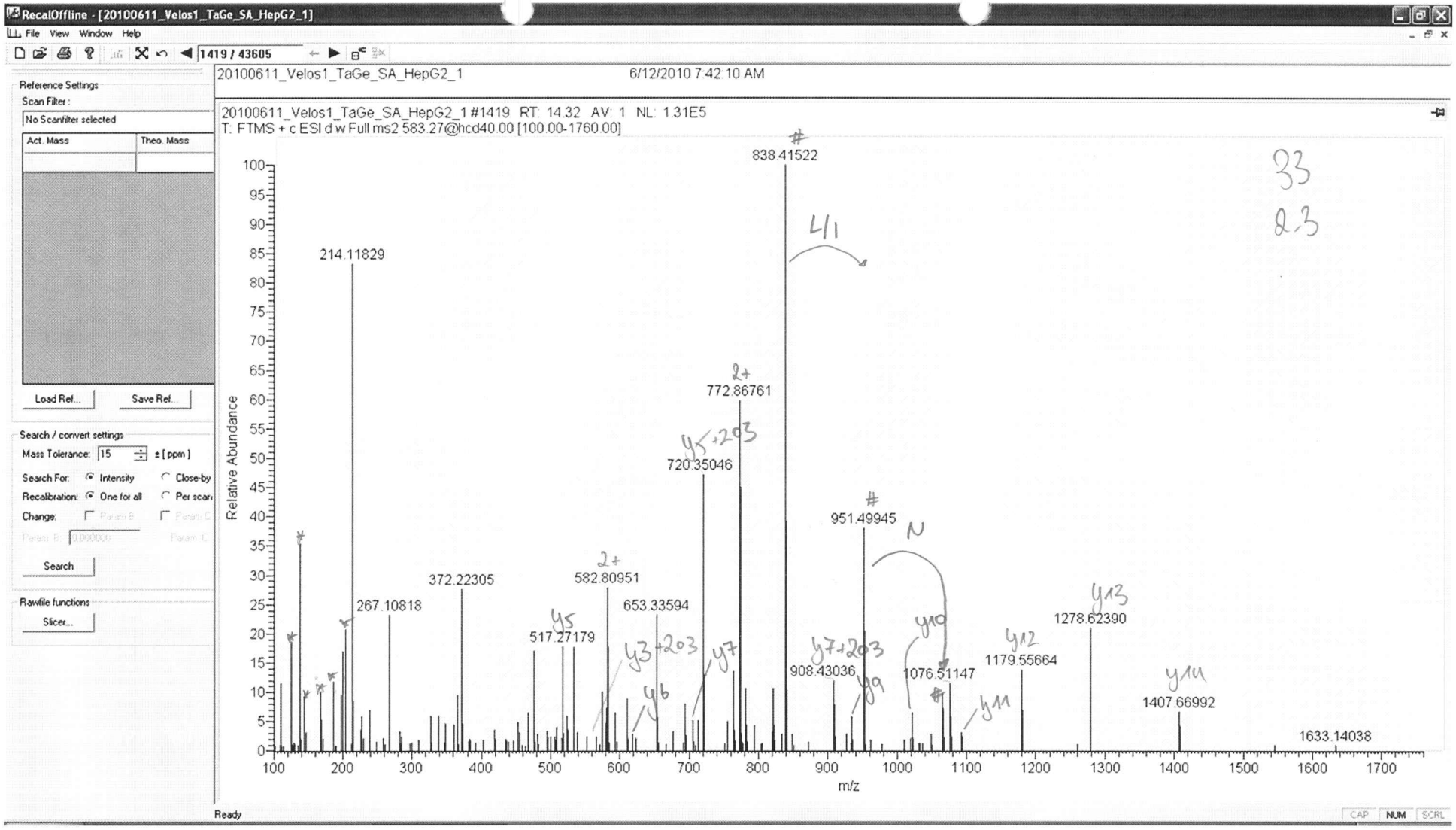


41.5

0.19

DLQSLEDILHQVEnK

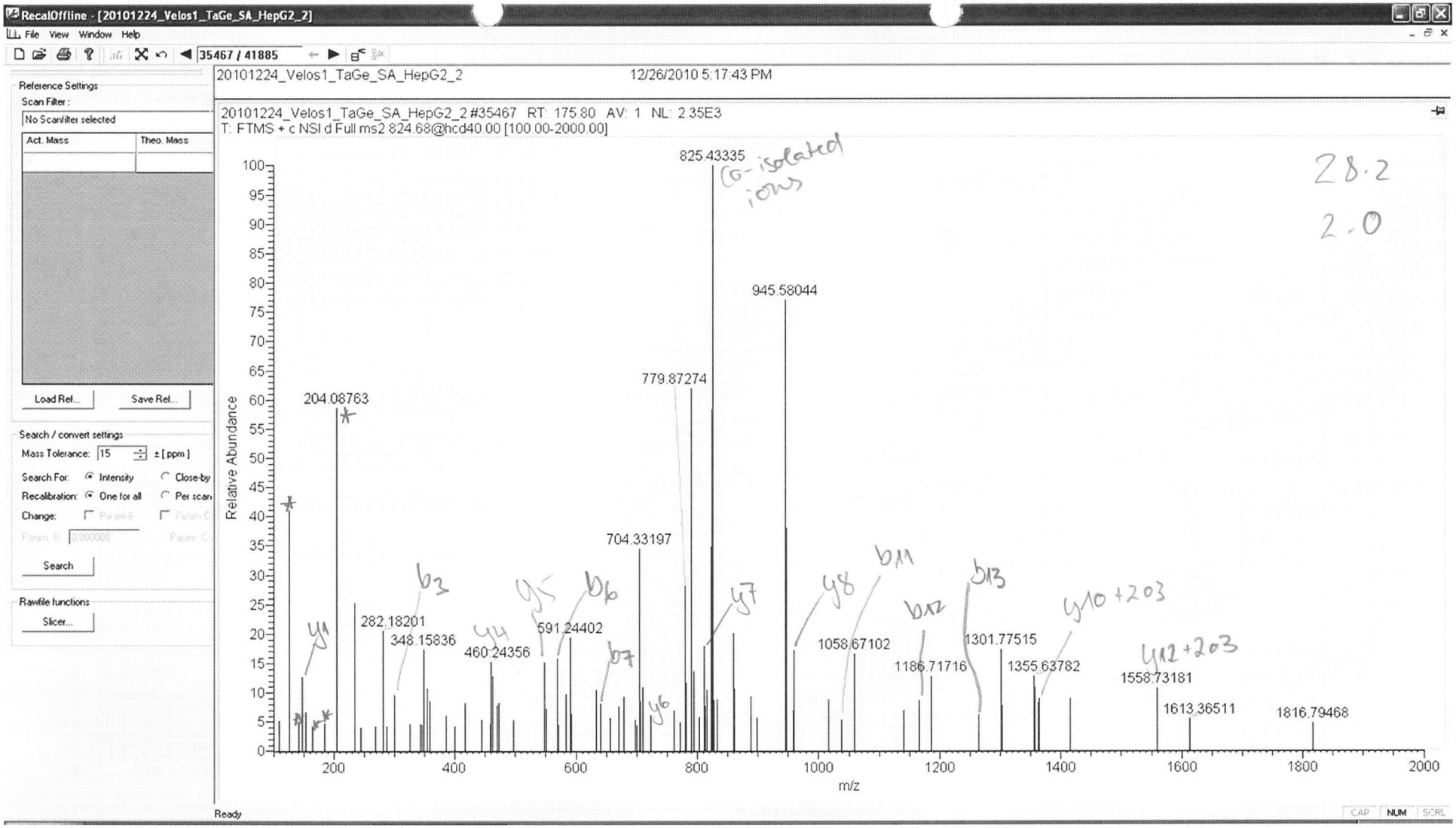
N 14



hEVSASTQSTPASsR

Site : S13 or S14

chimeric spectrum; 2nd ion series



28.2

2.0

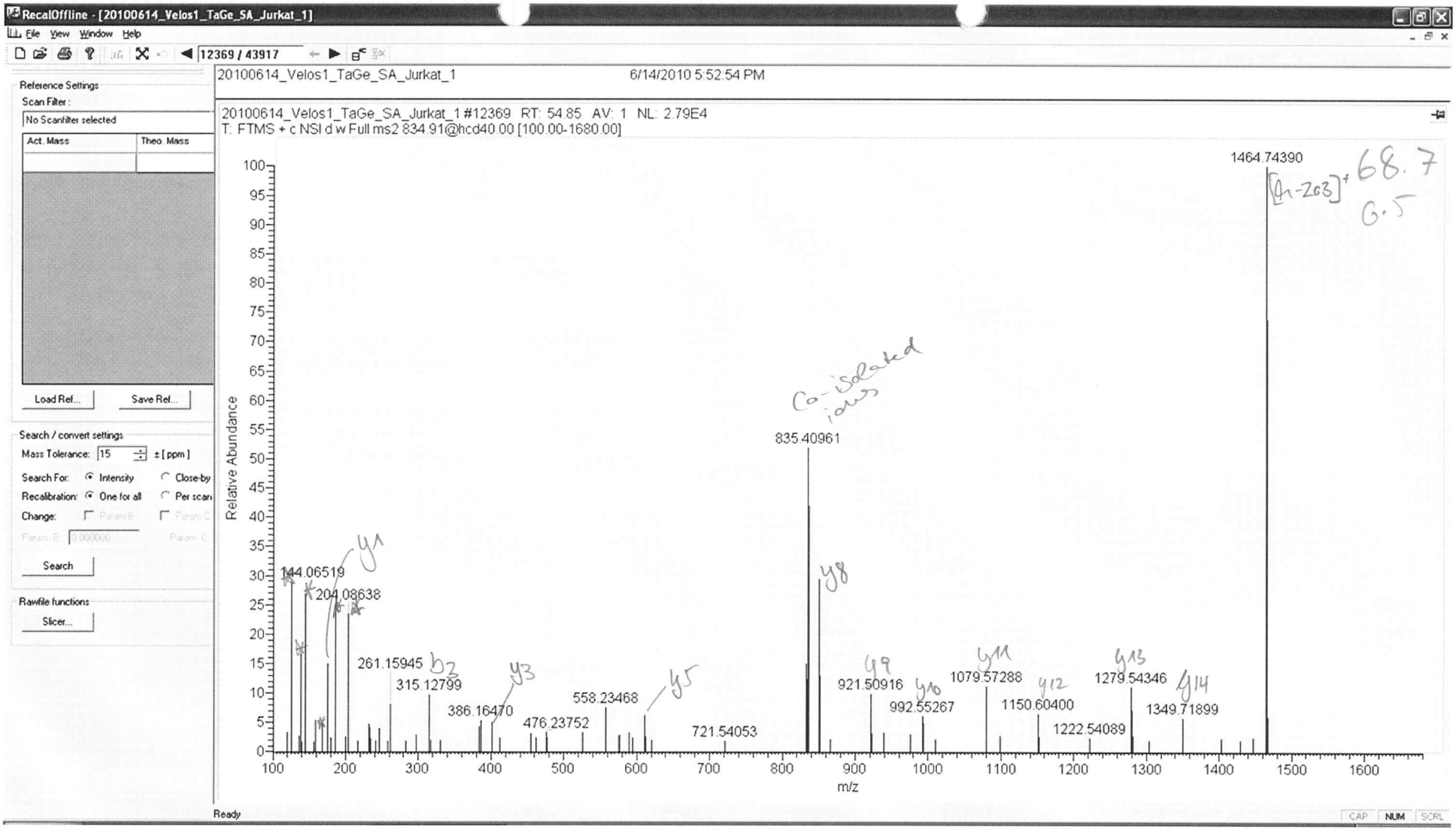
co-isolated ions

b3 y5 b6 y1 y4 b7 y6 y7 y8 b11 b12 b13 y10+203 y12+203

y12 y10 y4

VTVLGVATAPQQVLSNGVPVSnFTYSPDTK

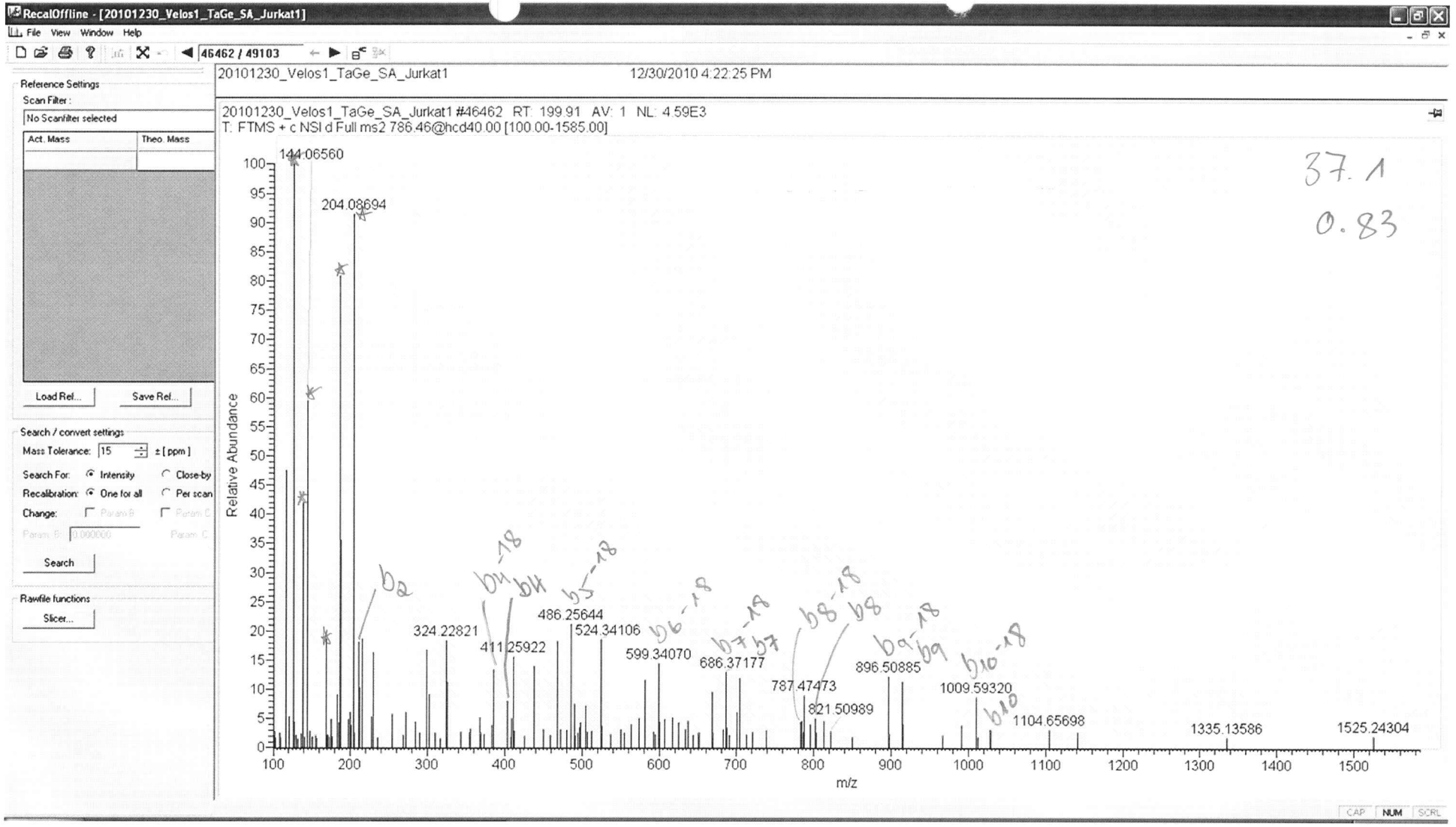
S21 or N22



y8 y5

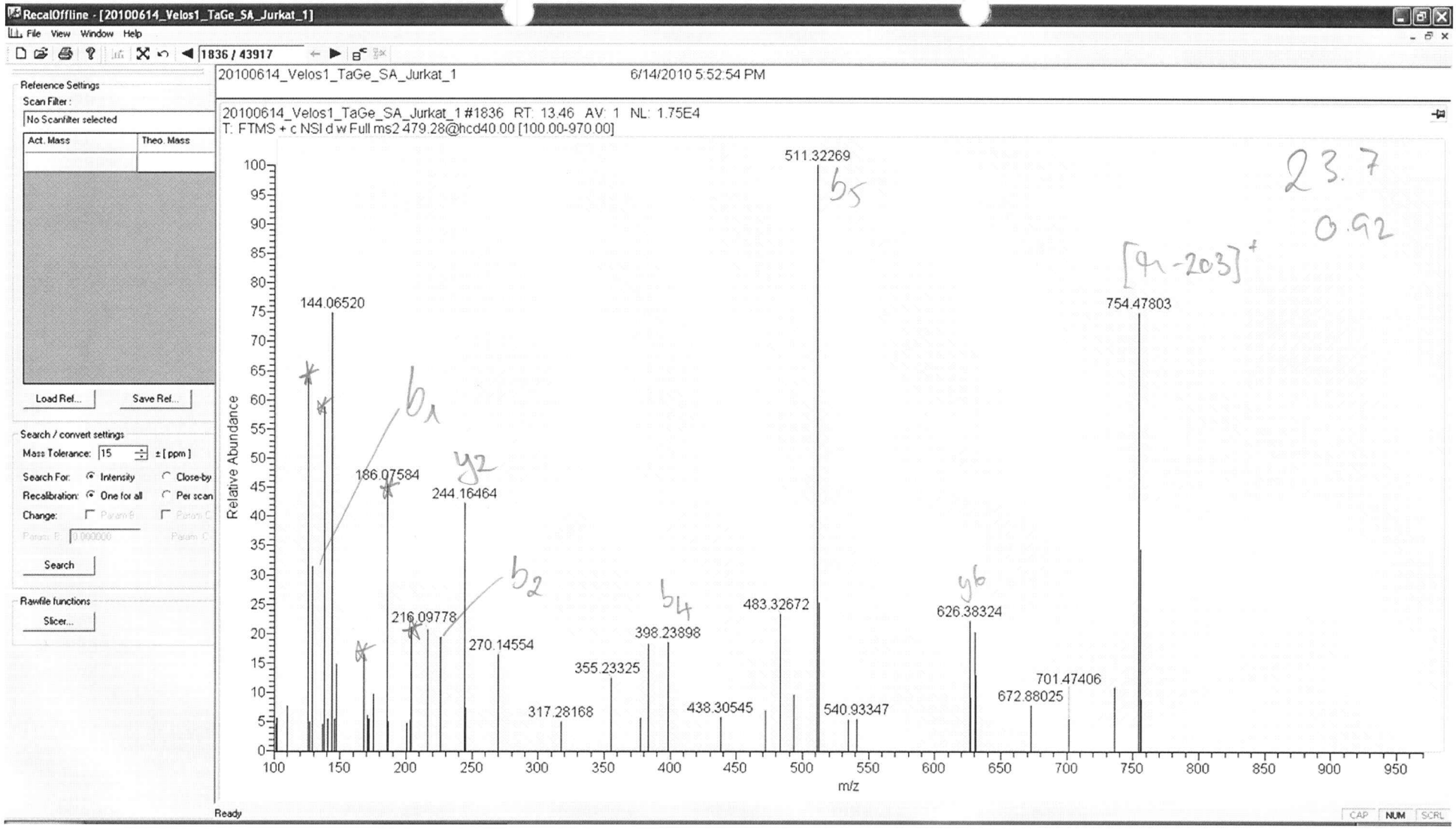
DAQAsAAPAAPLPER

S5



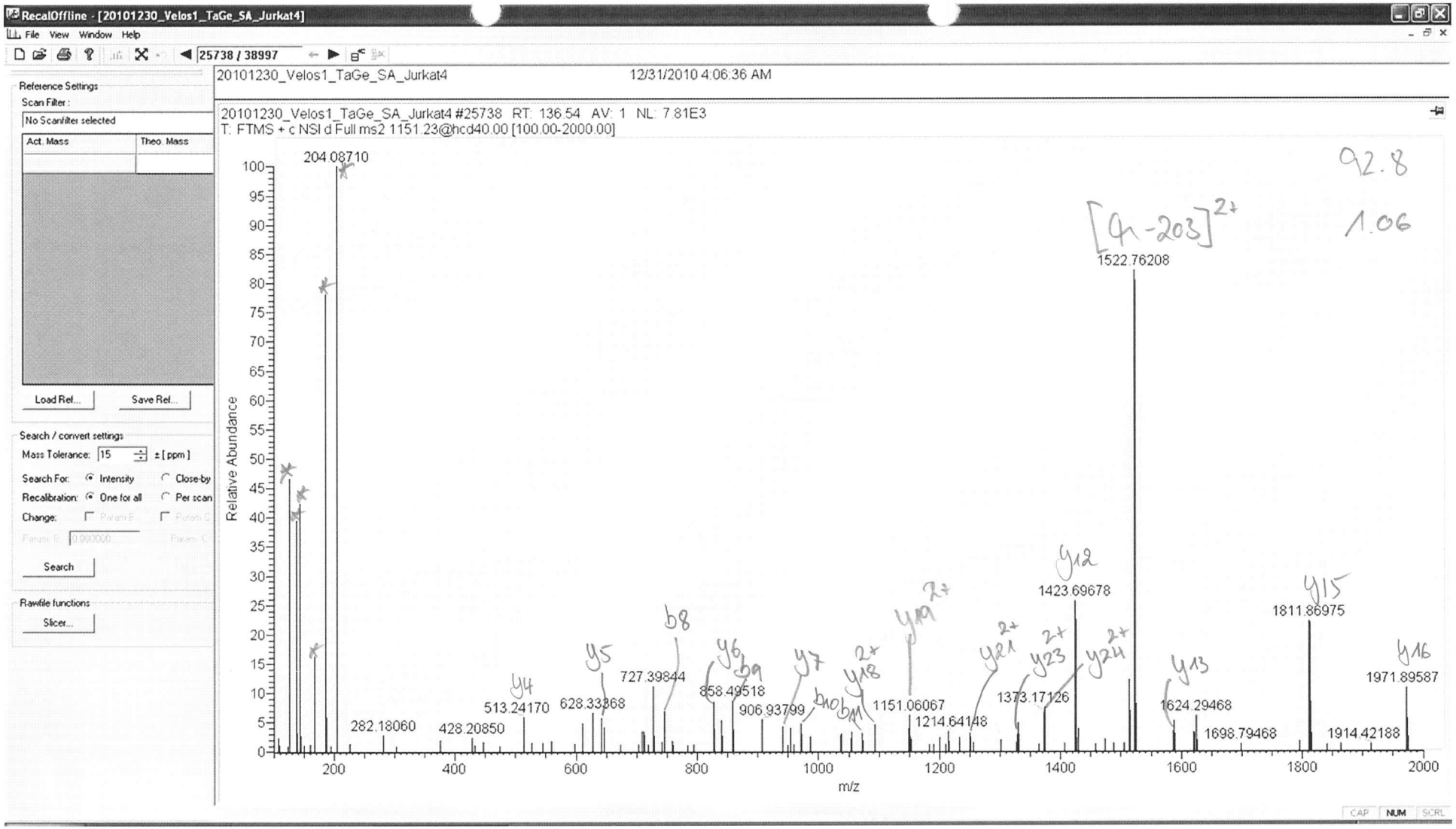
TIStTISPLLLIP

No site evidence


RecalOffline - [20100614_Velos1_TaGe_SA_Jurkat_1]
File View Window Help
1836 / 43917
Reference Settings
Scan Filter :
No Scanfilter selected
Act. Mass
Theo. Mass
Load Ref...
Save Ref...
Search / convert settings
Mass Tolerance: 15 ± [ppm]
Search For: Intensity Close-by
Recalibration: One for all Per scan
Change:
Search
Rawfile functions
Slicer...
20100614_Velos1_TaGe_SA_Jurkat_1
6/14/2010 5:52:54 PM
20100614_Velos1_TaGe_SA_Jurkat_1 #1836 RT: 13.46 AV: 1 NL: 1.75E4
T: FTMS + c NSI d w Full ms2 479.28@hcd40.00 [100.00-970.00]
Relative Abundance
m/z
511.32269
754.47803
144.06520
186.07584
244.16464
216.09778
270.14554
317.28168
355.23325
398.23898
438.30545
483.32672
540.93347
626.38324
672.88025
701.47406
b5
b1
b2
b4
y2
y6
[M-203]+
23.7
0.92
Ready
CAP
NUM
SCRL

KPtAIPK

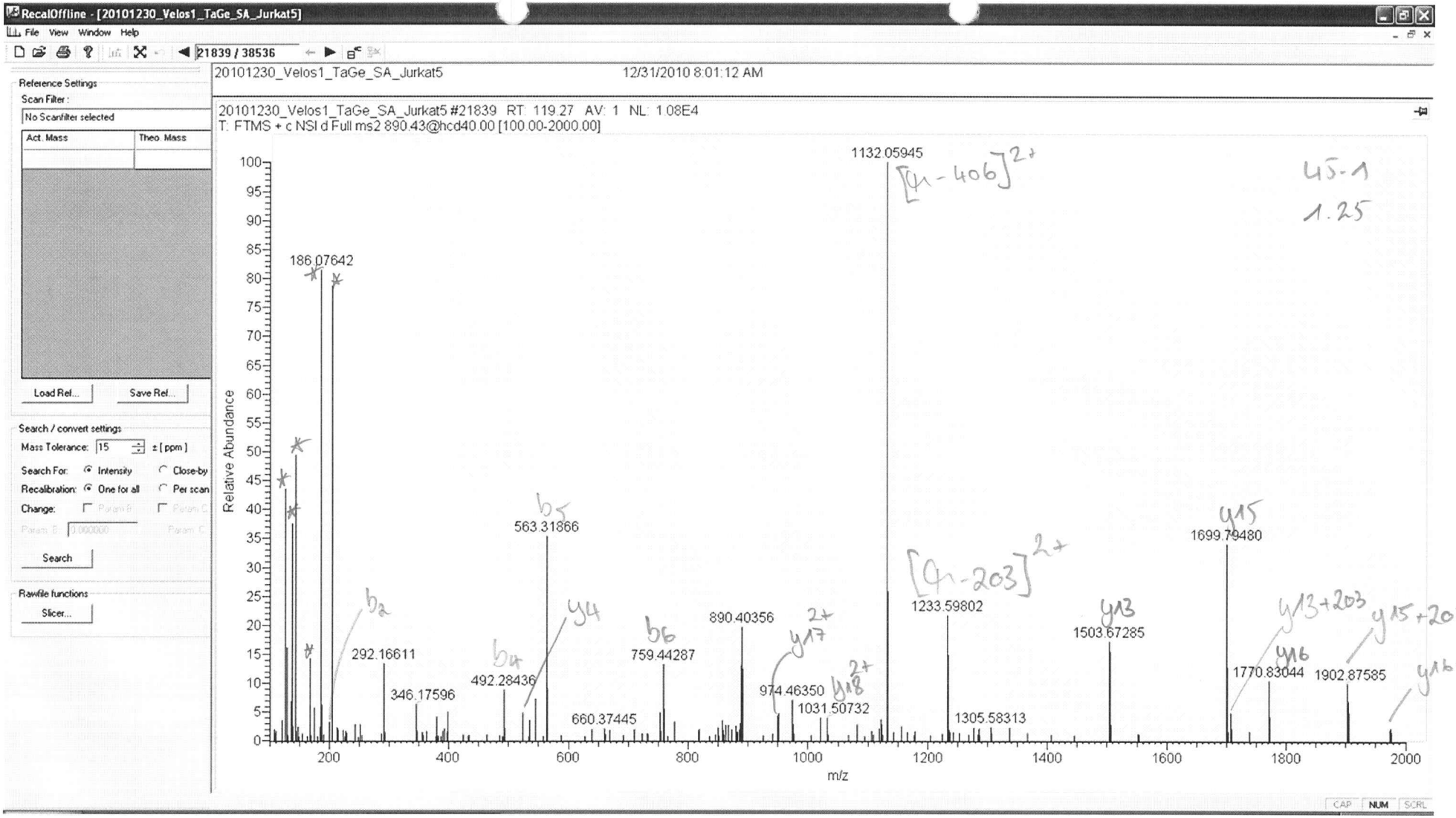
+3



VSISGTTVILTcPQYPGsEILWQHnDK

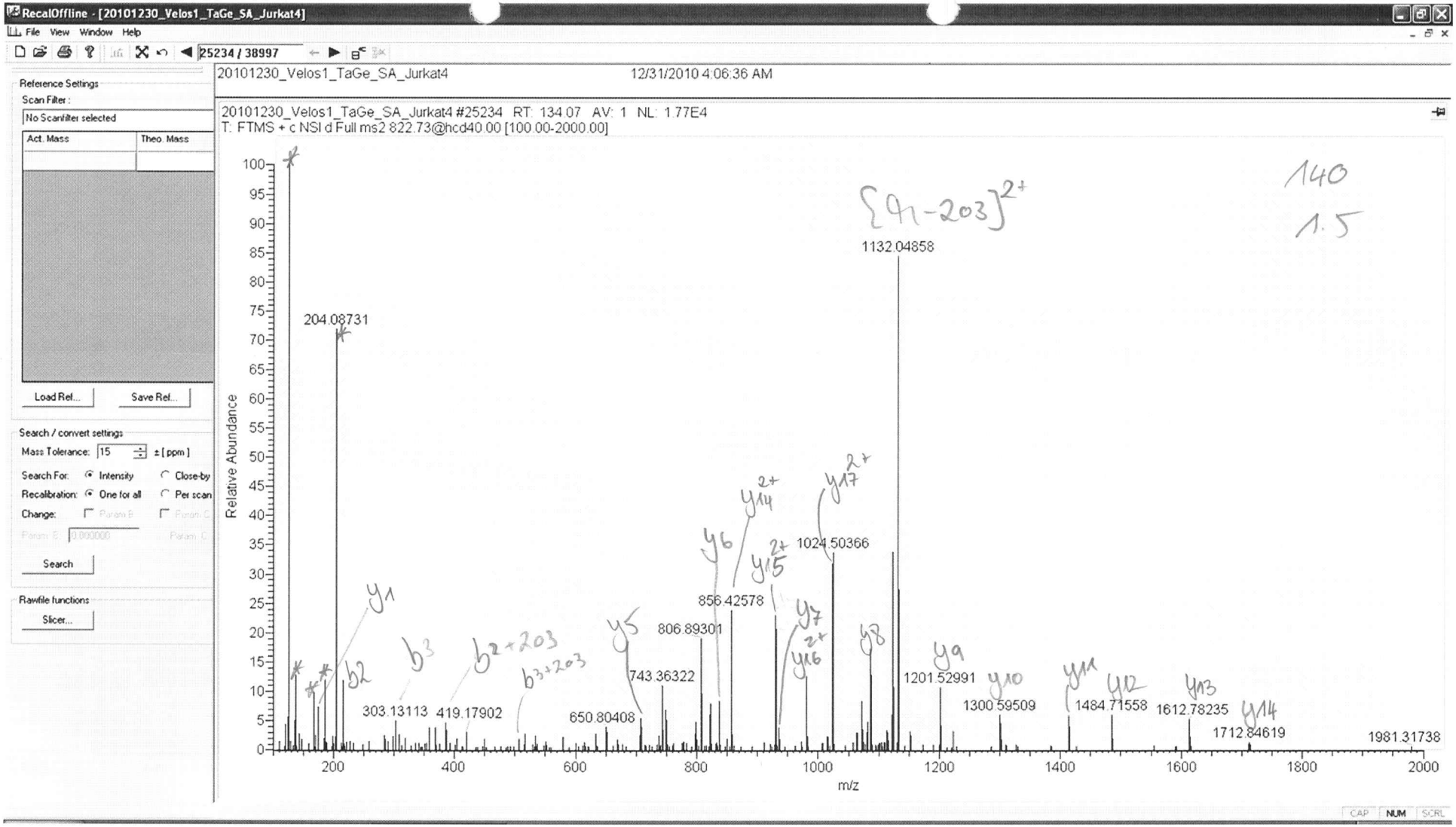
y15 y12

no site evidence

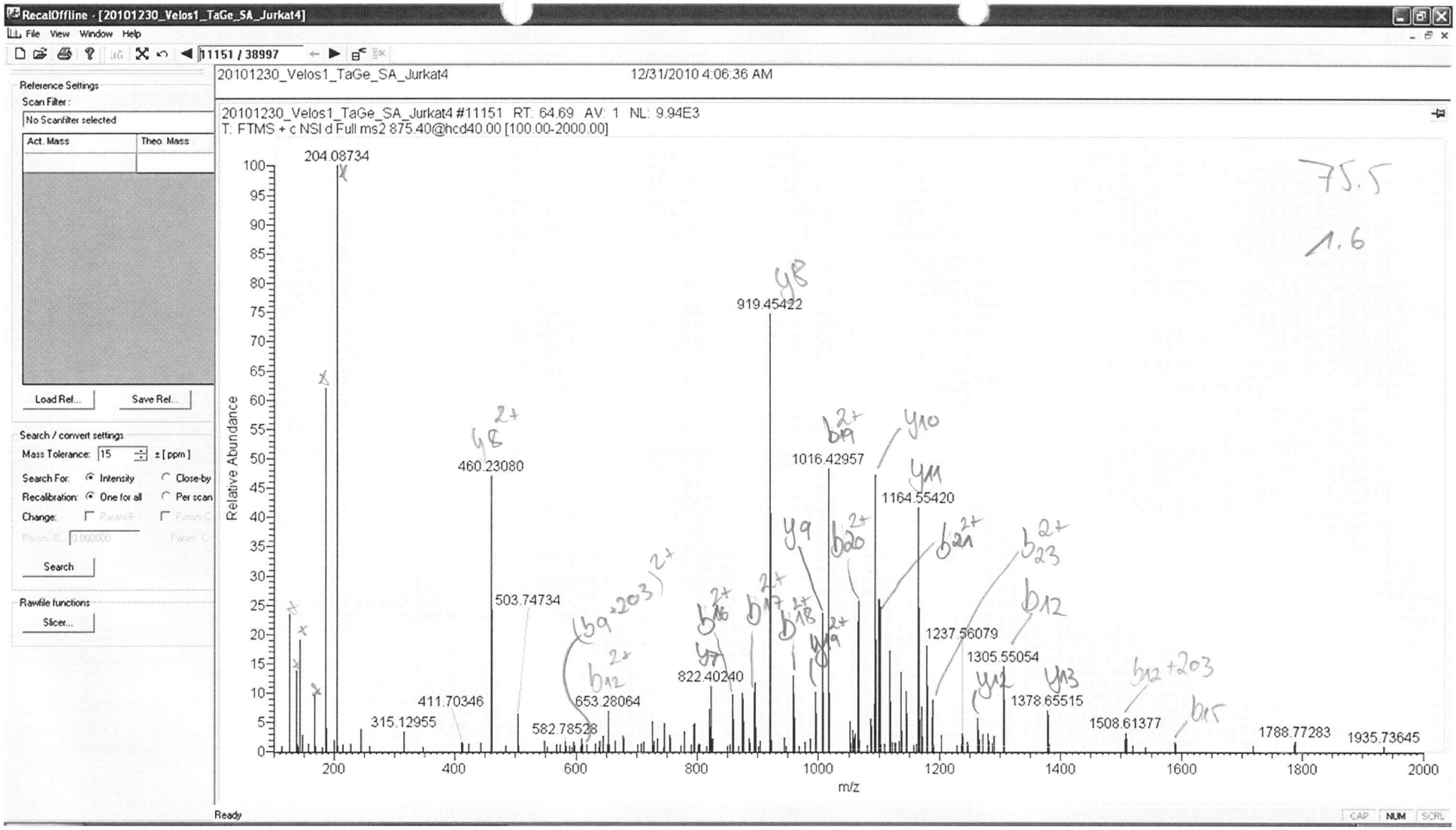


VTYKAPVPtGEVYFADsFDR

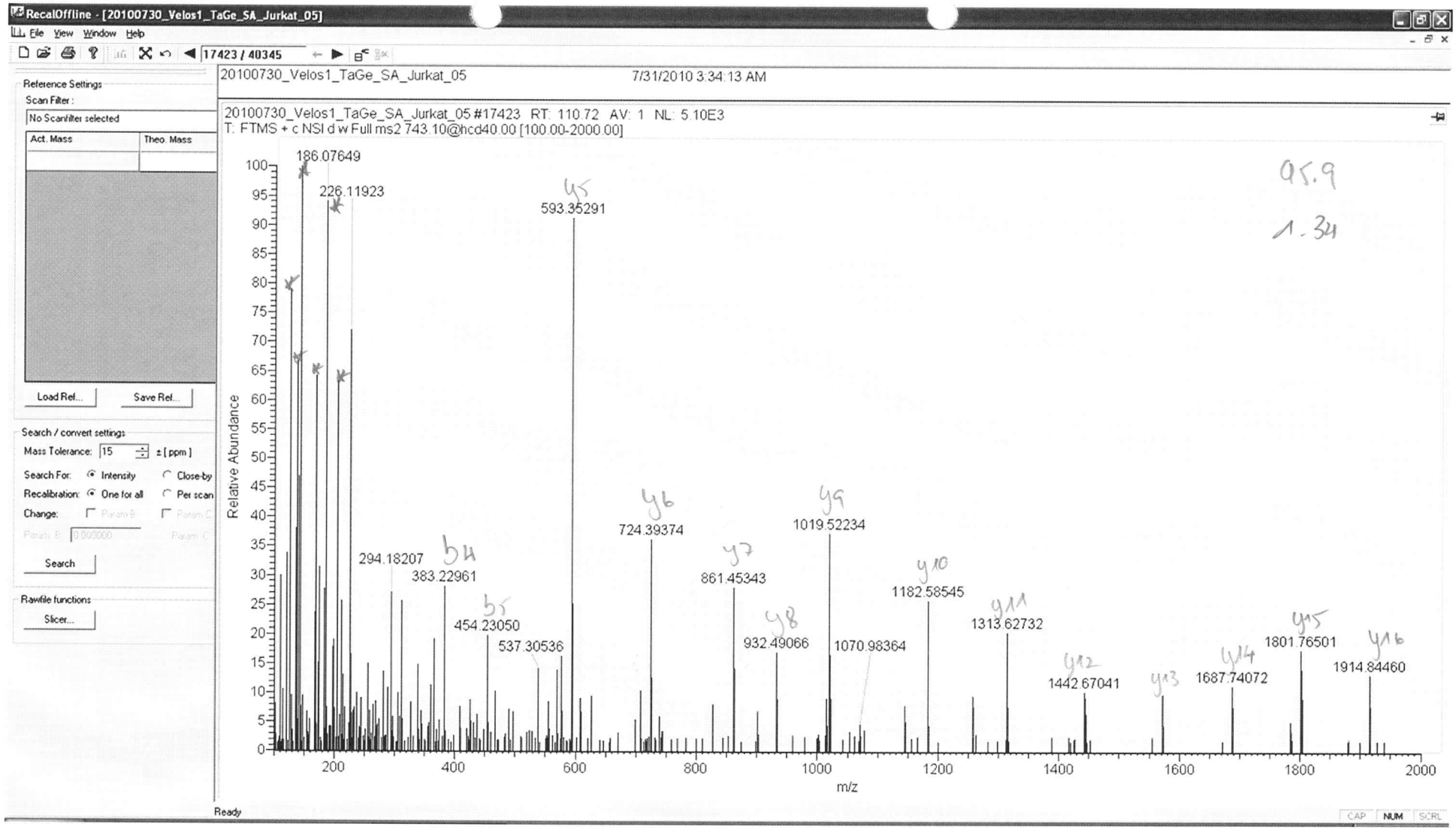
T9 and S17



TNStFVQALVEHVKEEcDR

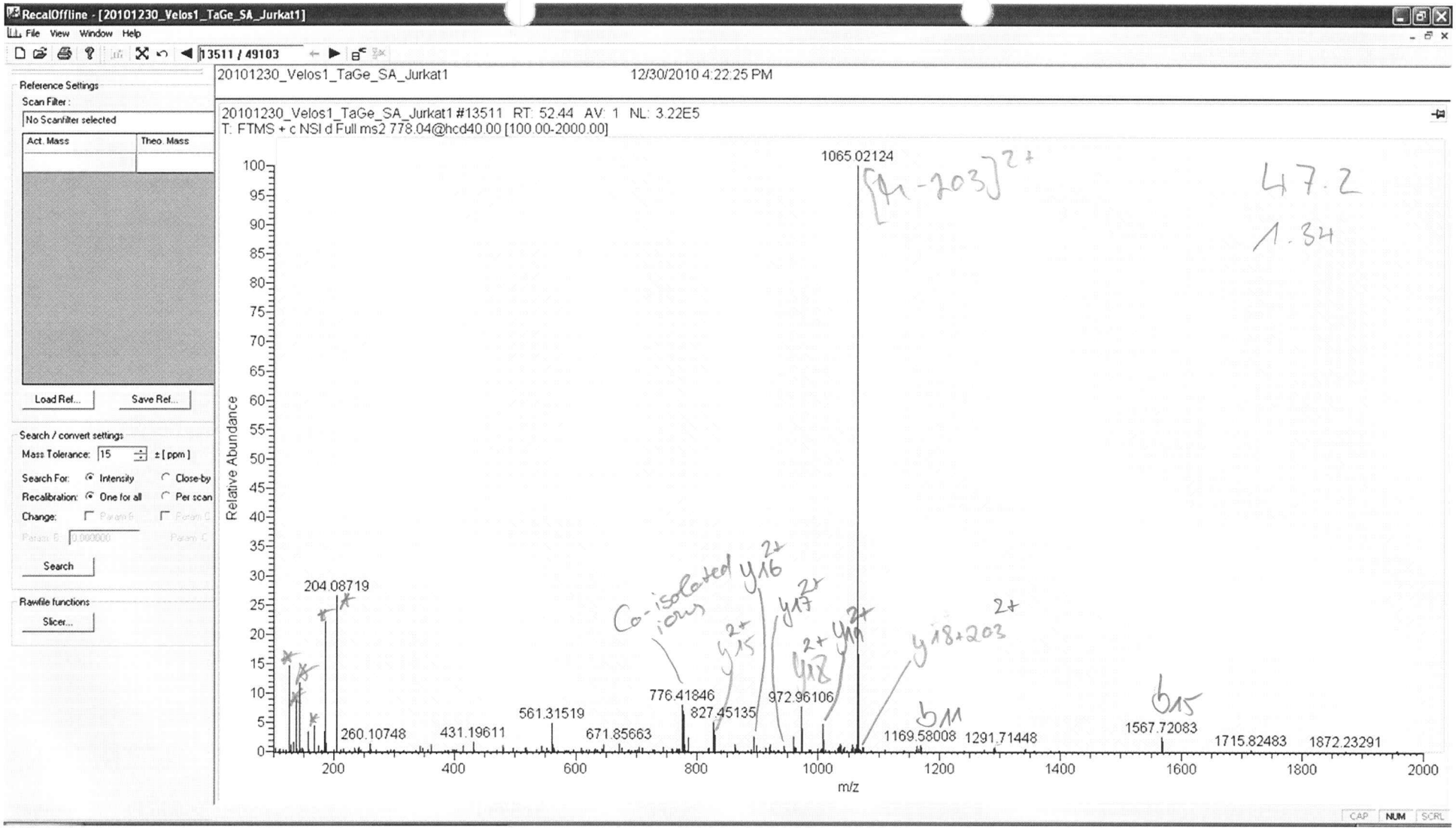


EFHHGPDPTDTAPGEQAQDVASSPPESsFQK



APLTATAPQLDDEEMYsAHMPAHLR

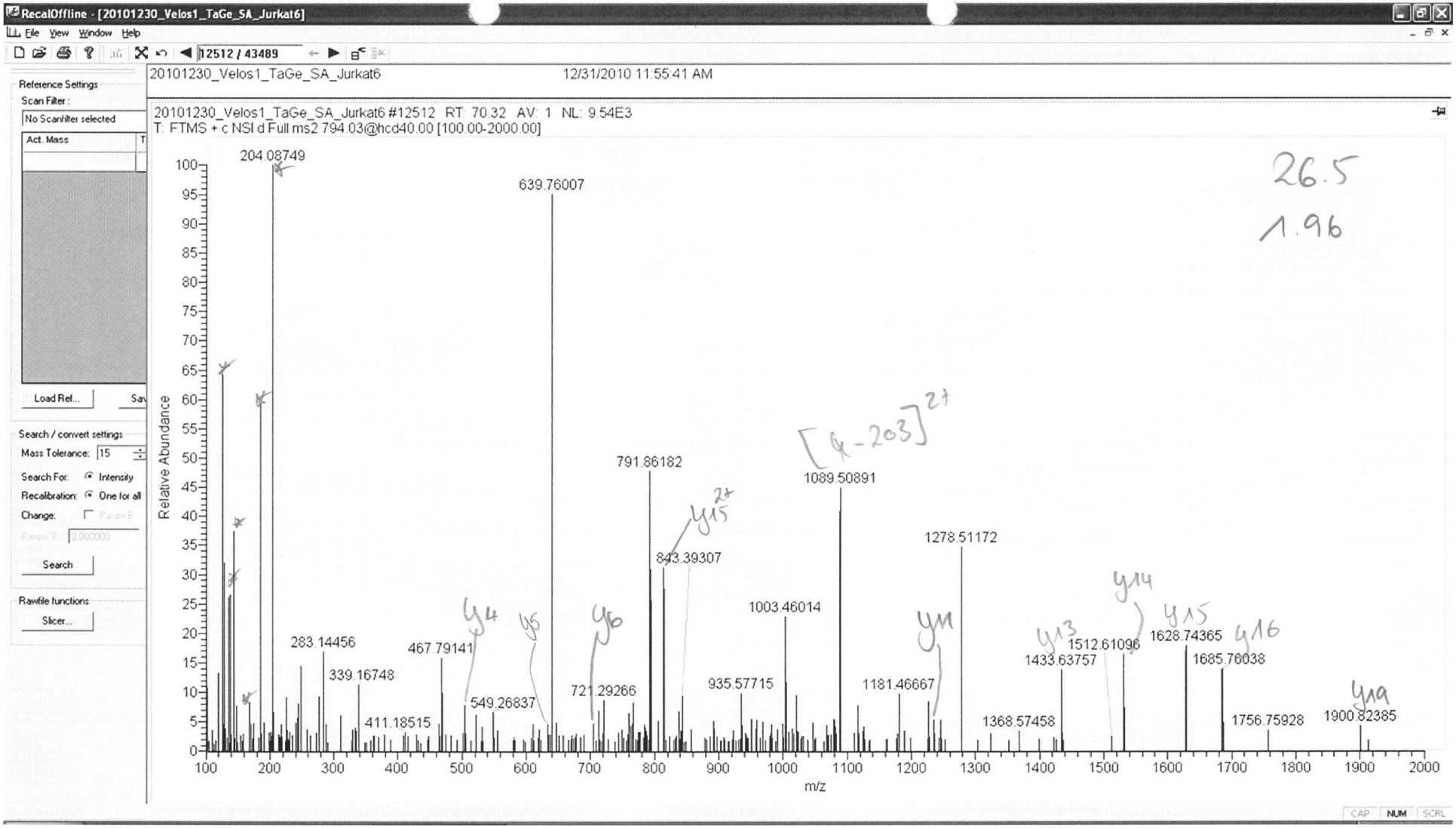
no site evidence



y19 y15

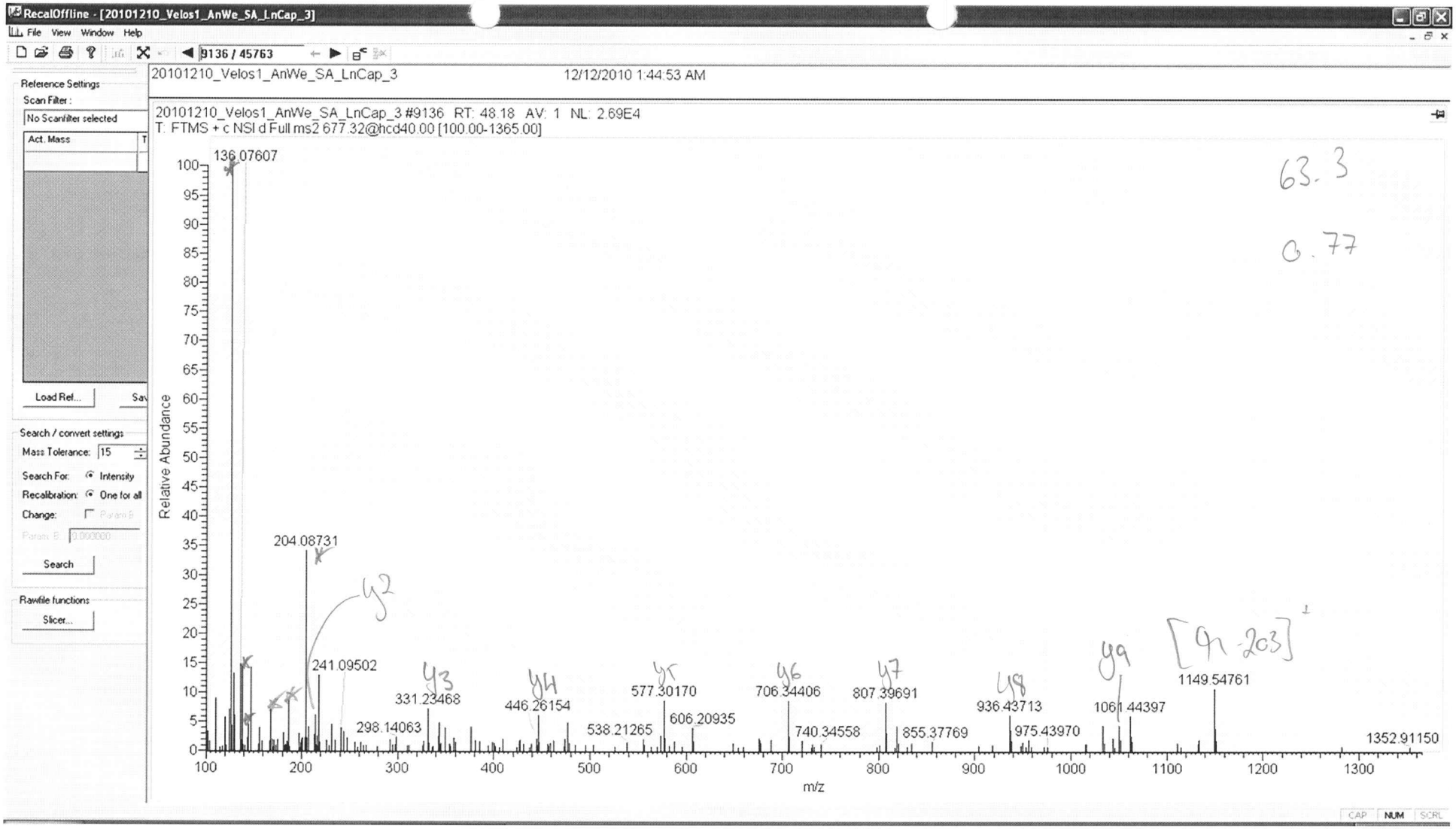
No site evidence

LAGTEsPVREEPGEDFPAAR



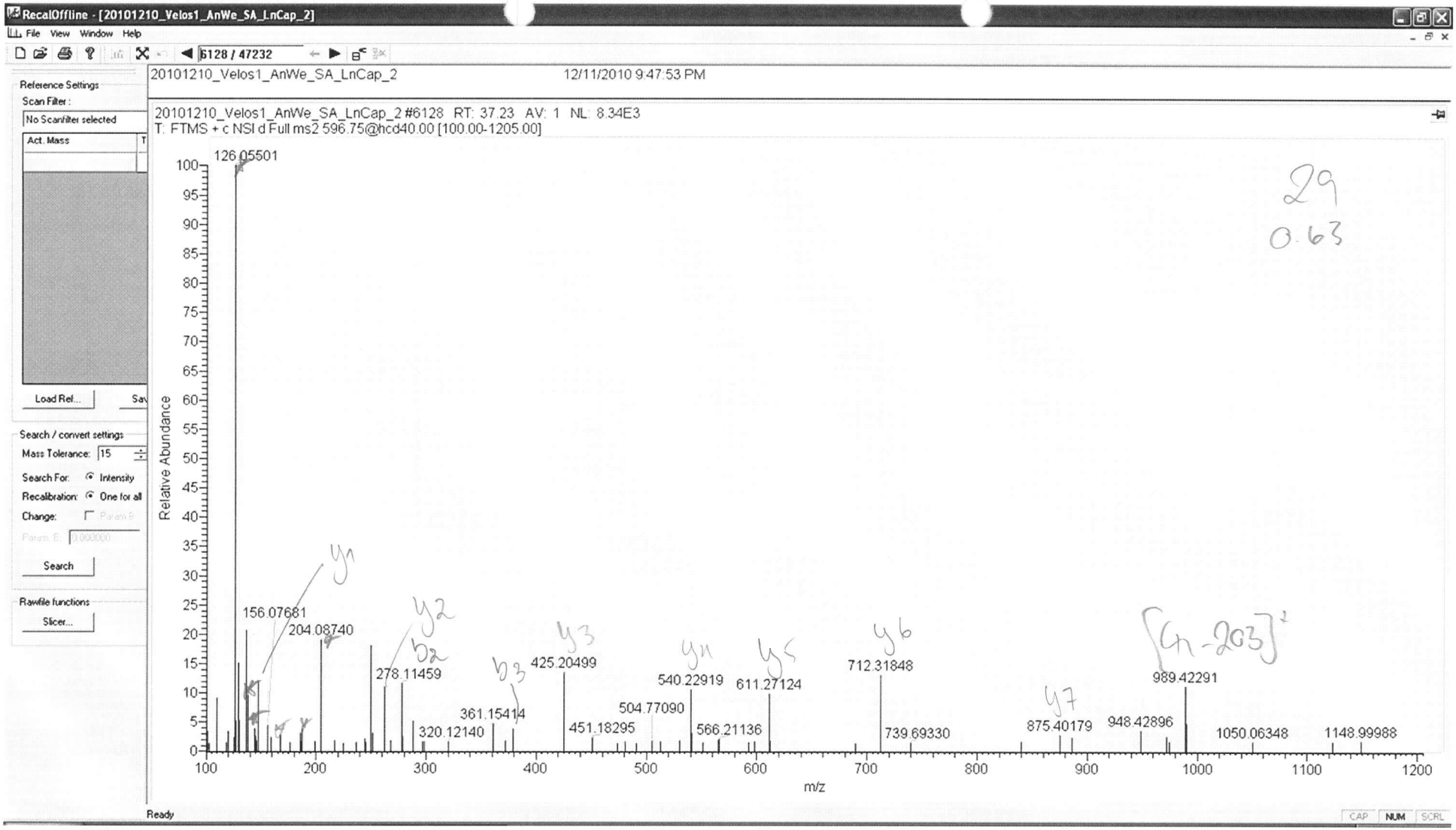
LYGsAGPPPTGEEDTAEKDEL

no site evidence



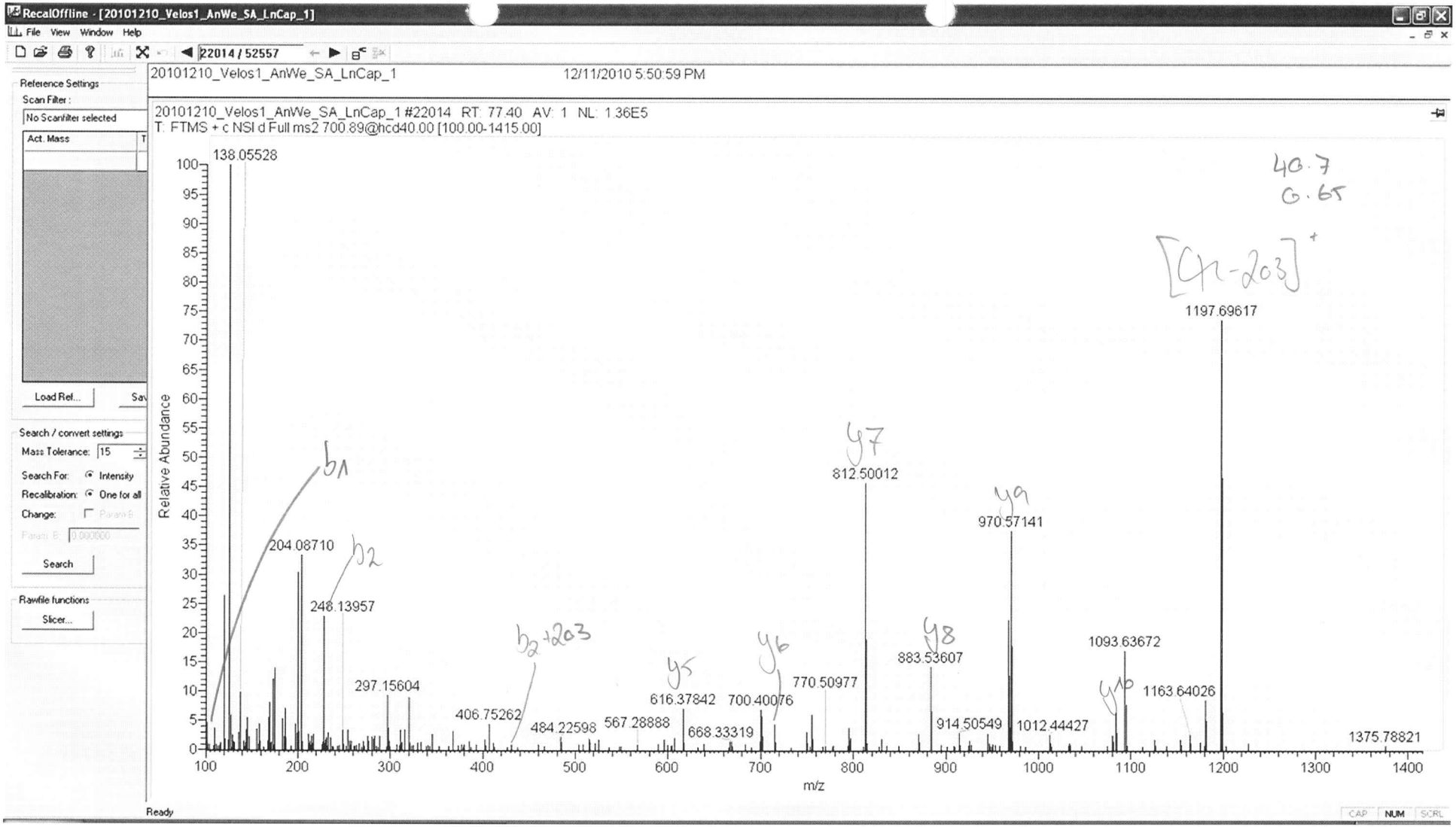
VNEtEMDIAK

no site evidence

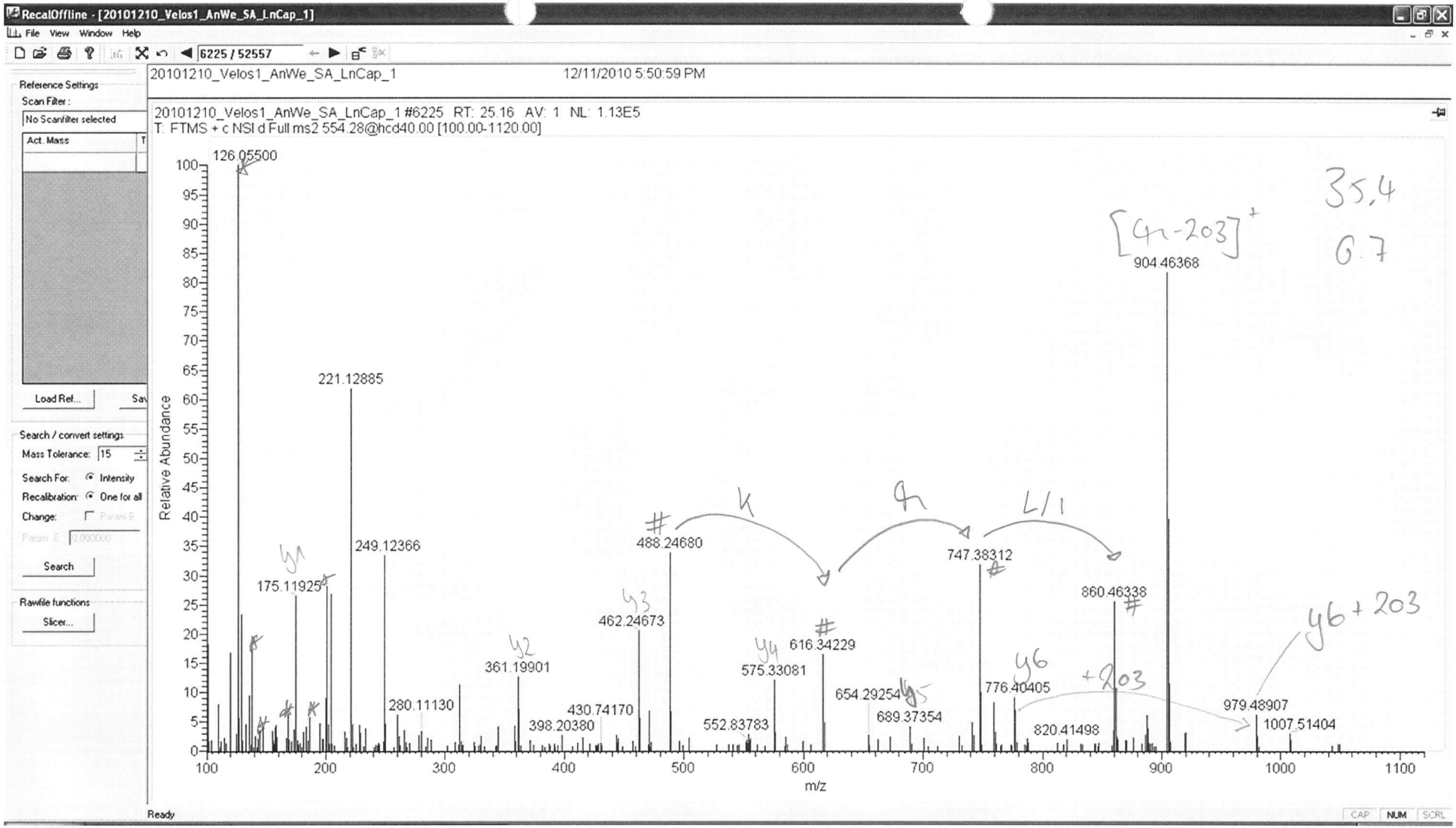


NYtADYDK

no site evidence



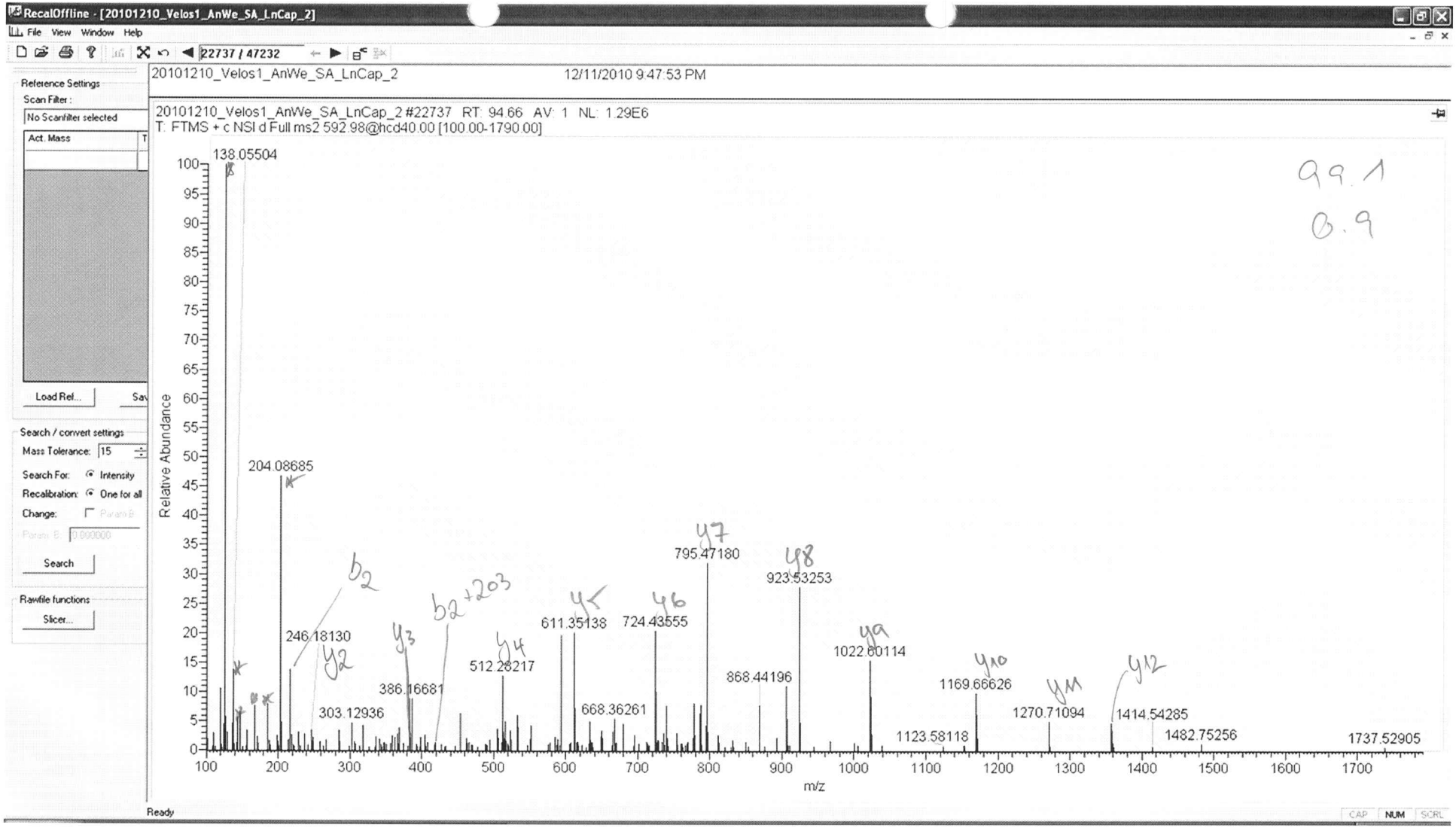
NLSAPVTLnLR



GASNLtWR

53

chimeric spectrum; ion series from co-isolated precursor



99.1

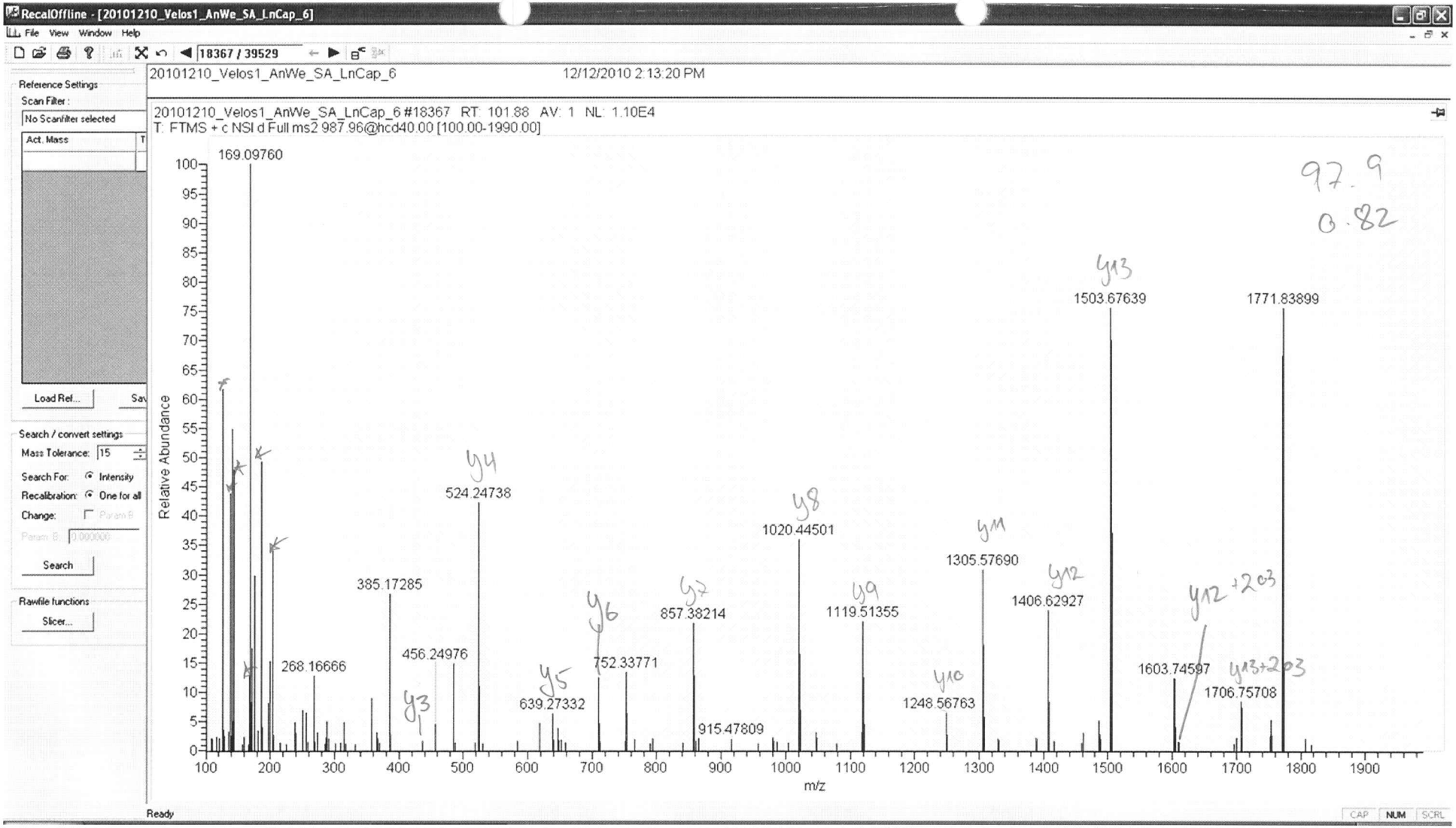
0.9

TNStFVQALVEHVK

N2

b2

F1

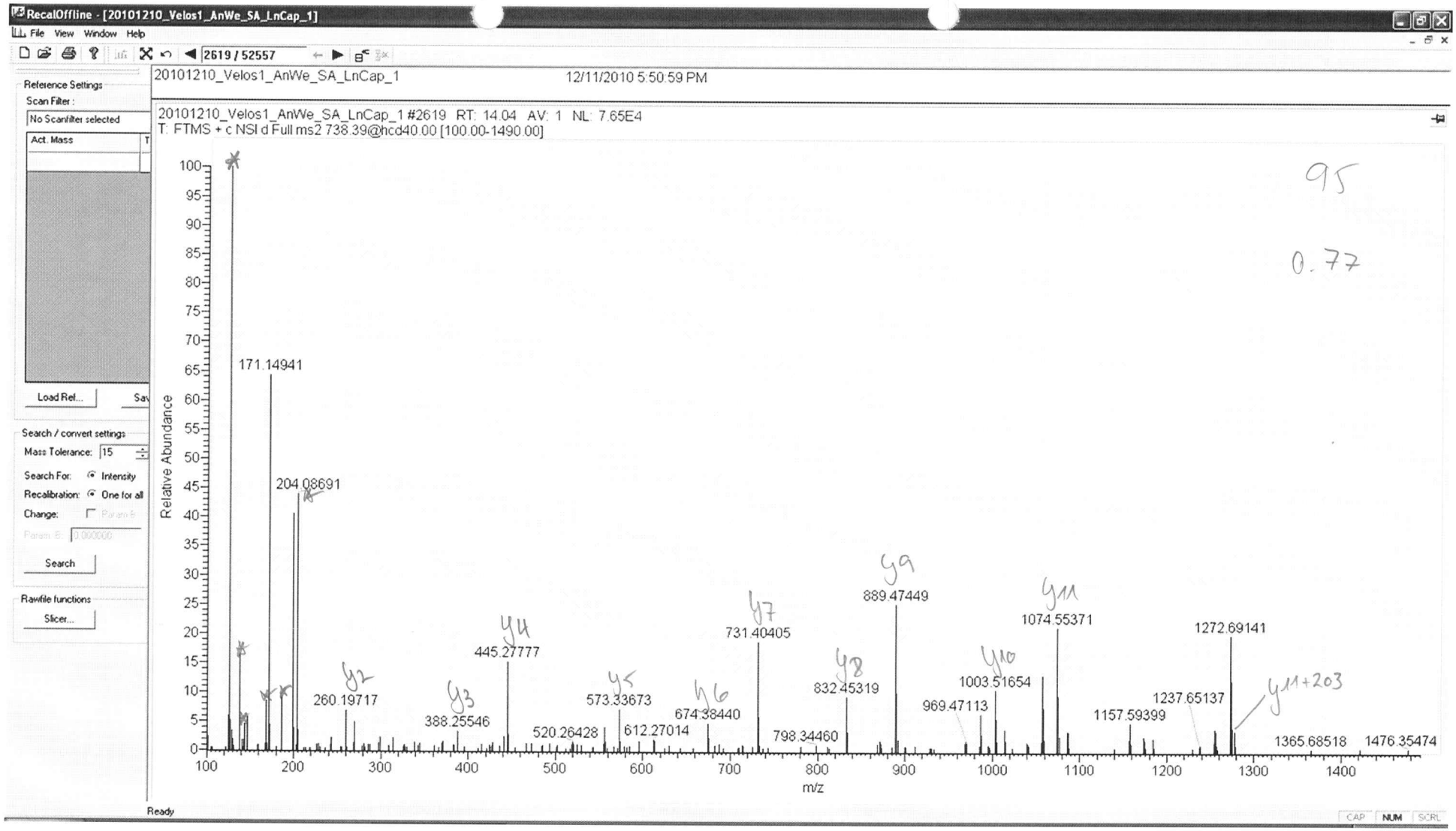


97.9
0.82

y13 y12

APVPTGEVYFADsFDR

T5

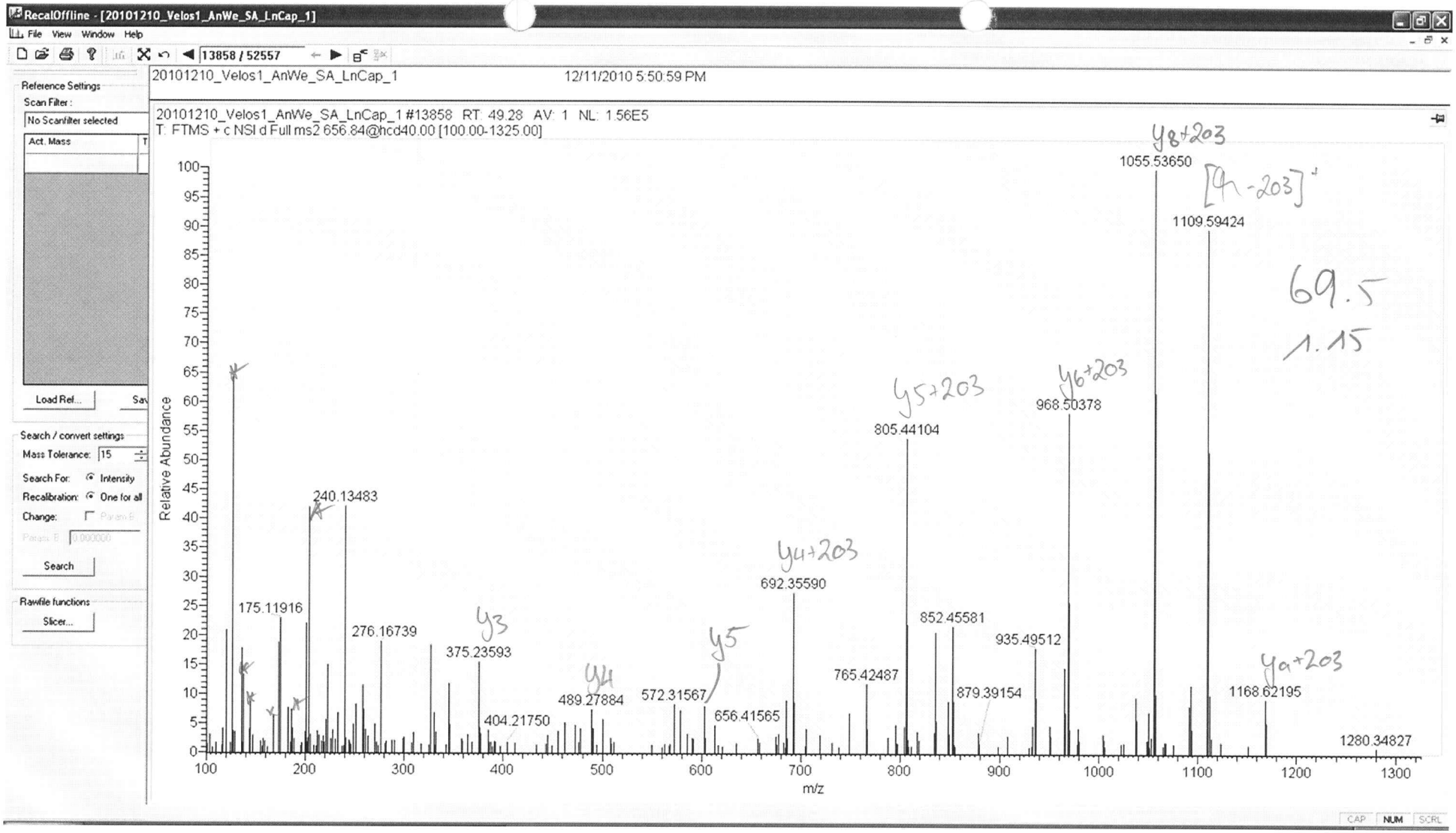


95

0.77

VVANGTGtQGQLK

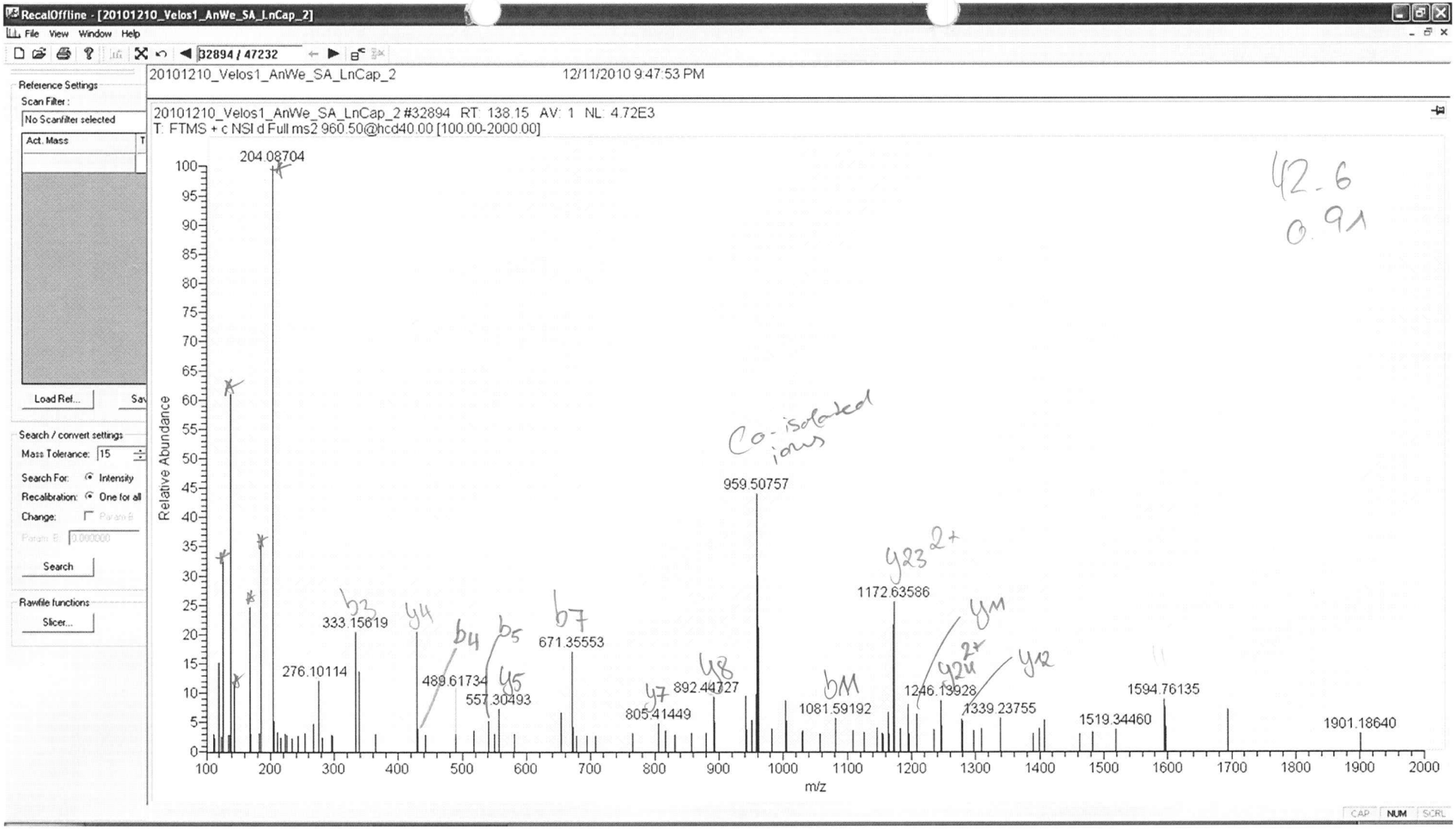
No site evidence



y5
y4
y3

GSLSYLnVTR

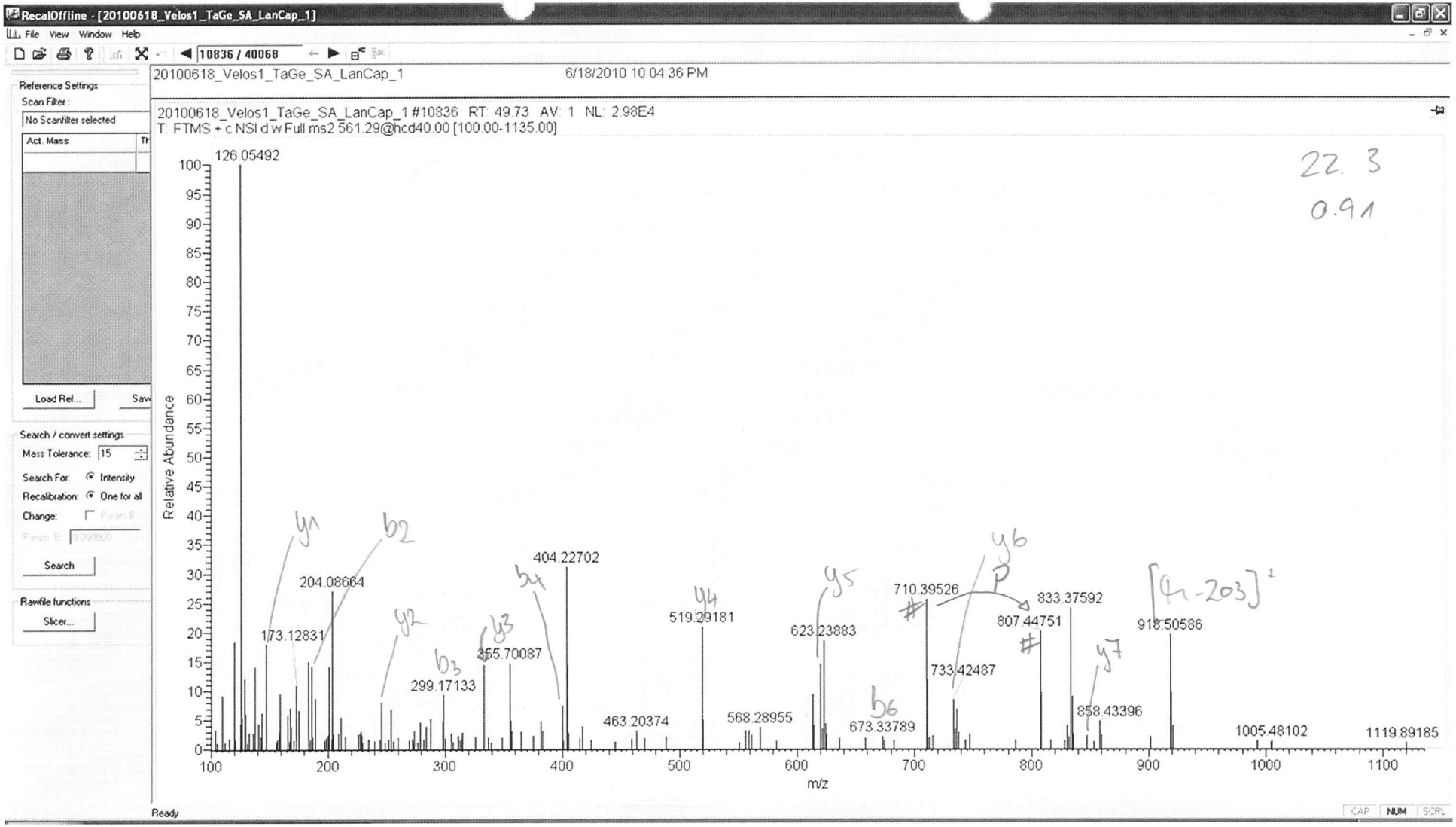
N 7



y23

NAFPLGAPTLVTSQATTLSTFQPAnK

no site evidence

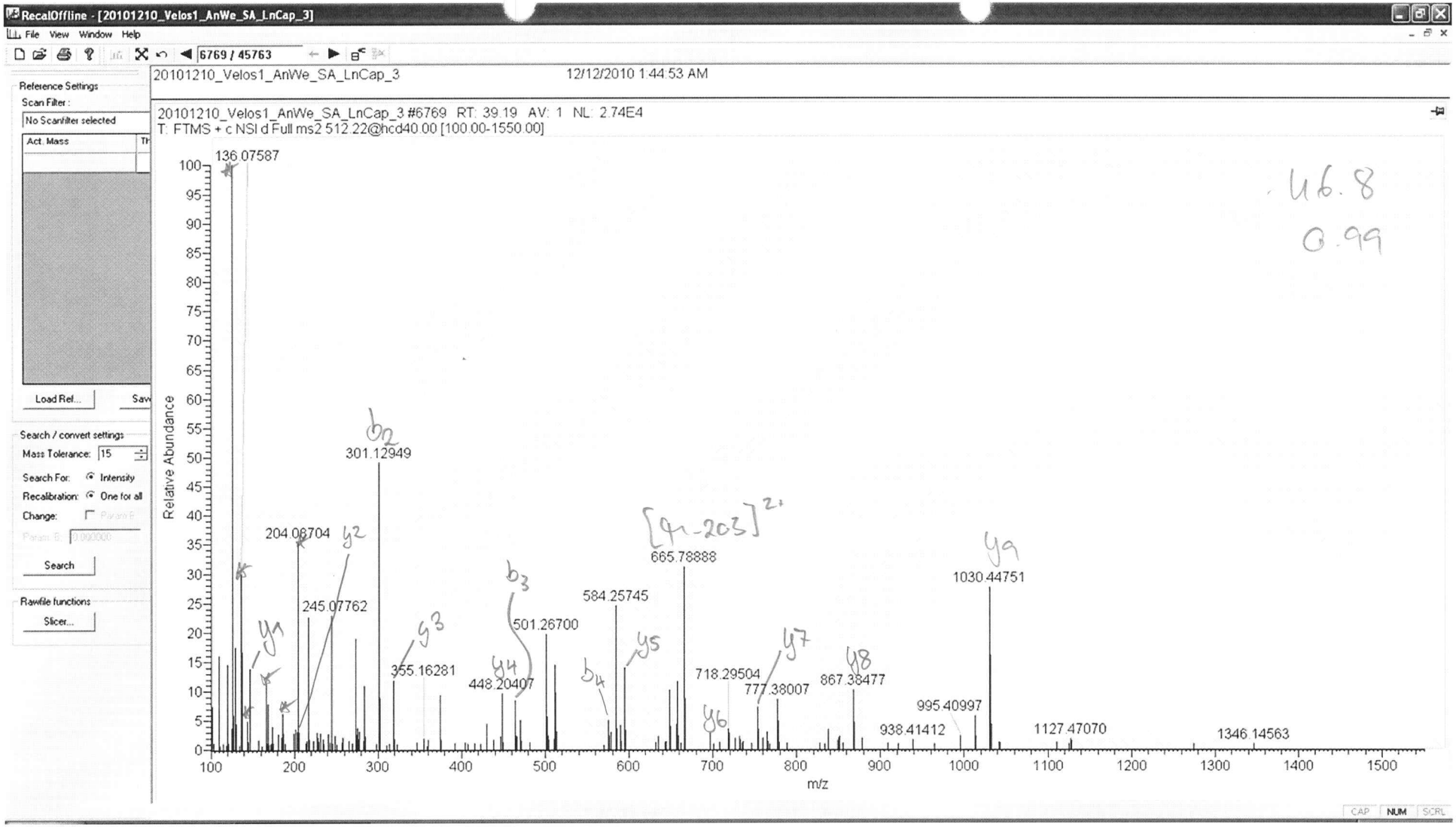


22.3
0.91

ANLTWsVK

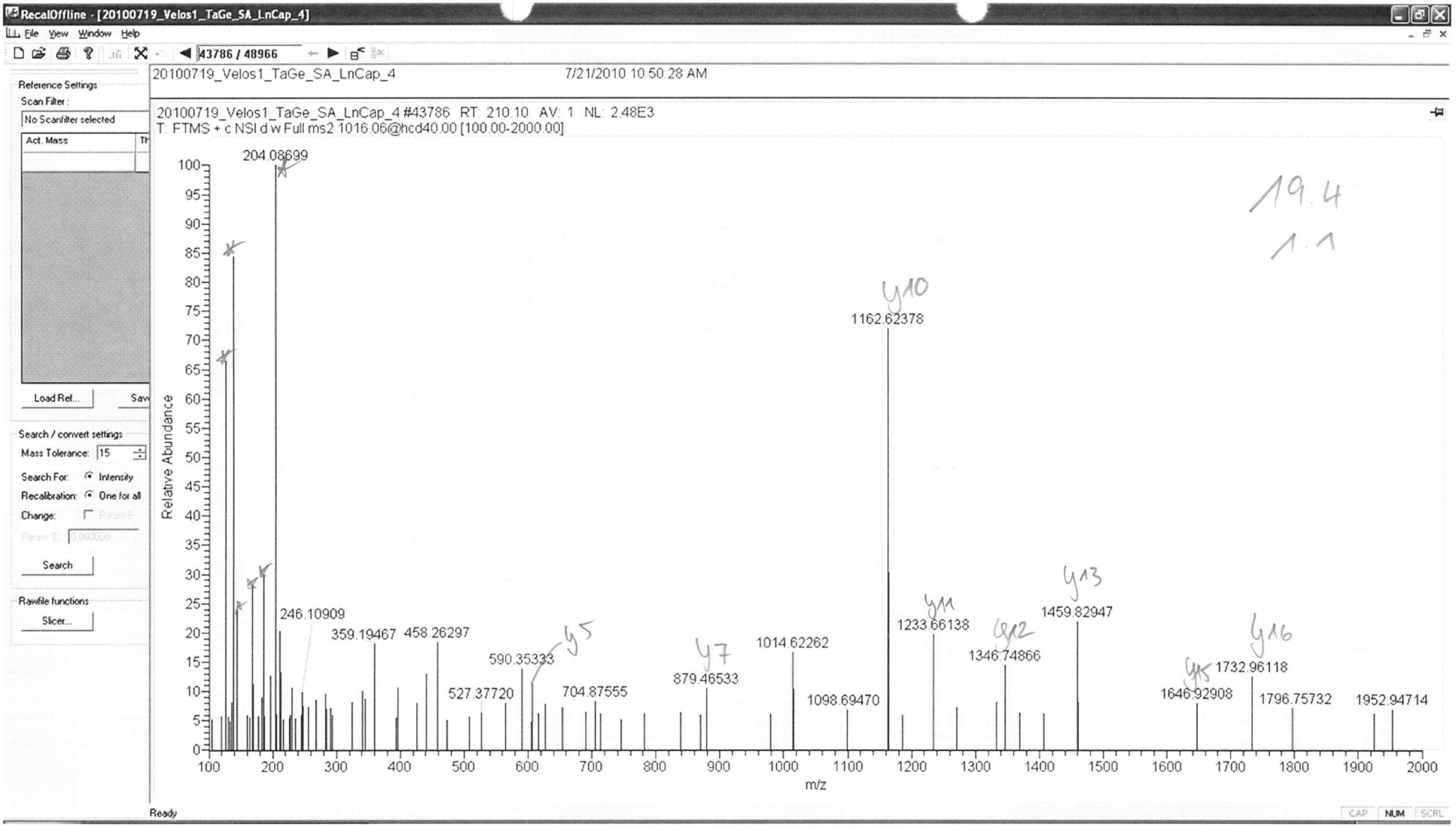
no site evidence

chimeric spectra; peaks from 2nd ion series



YHYNGtFEDGK

77

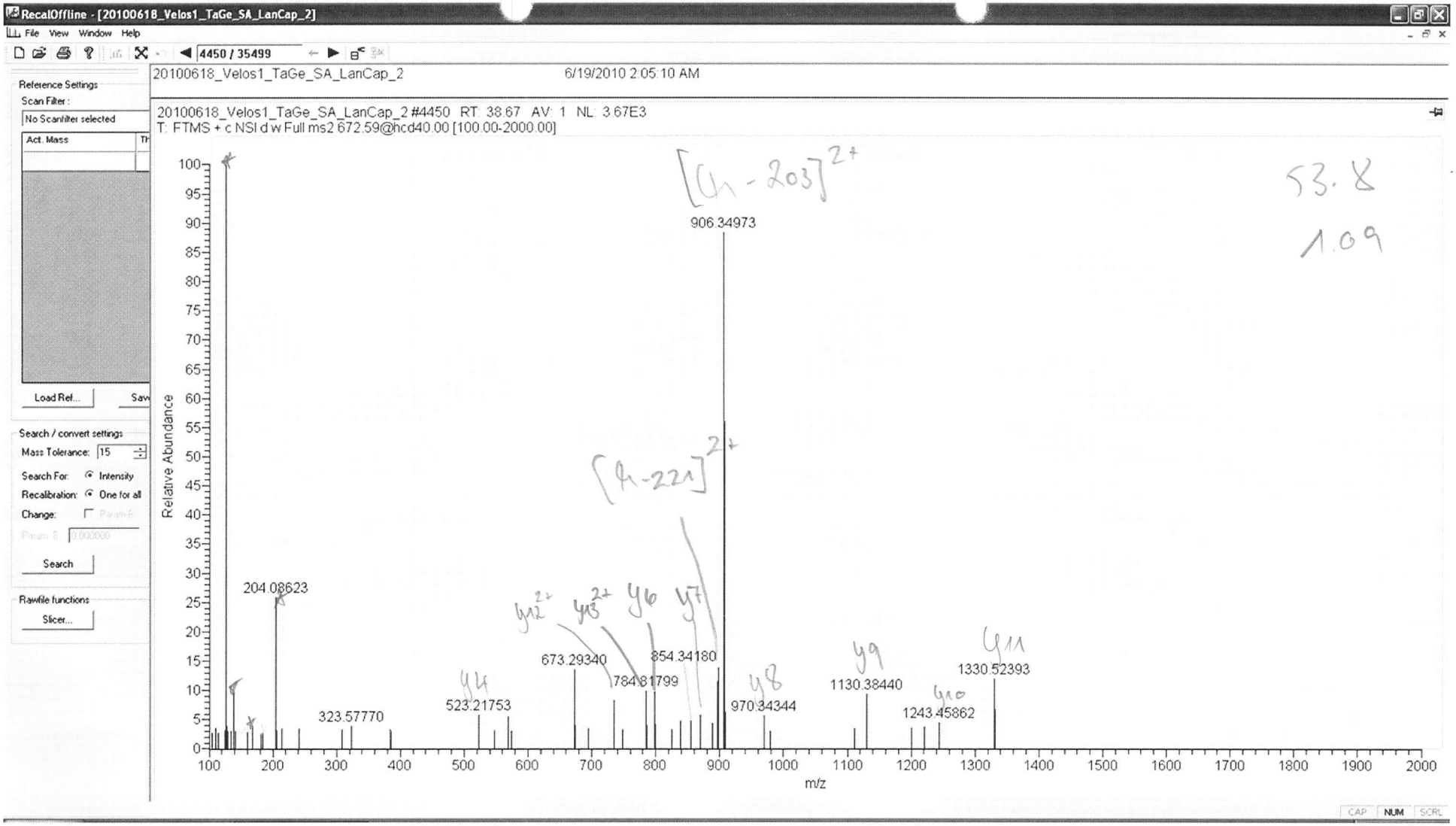


19.4
1.1

y13 y10 y7 y5

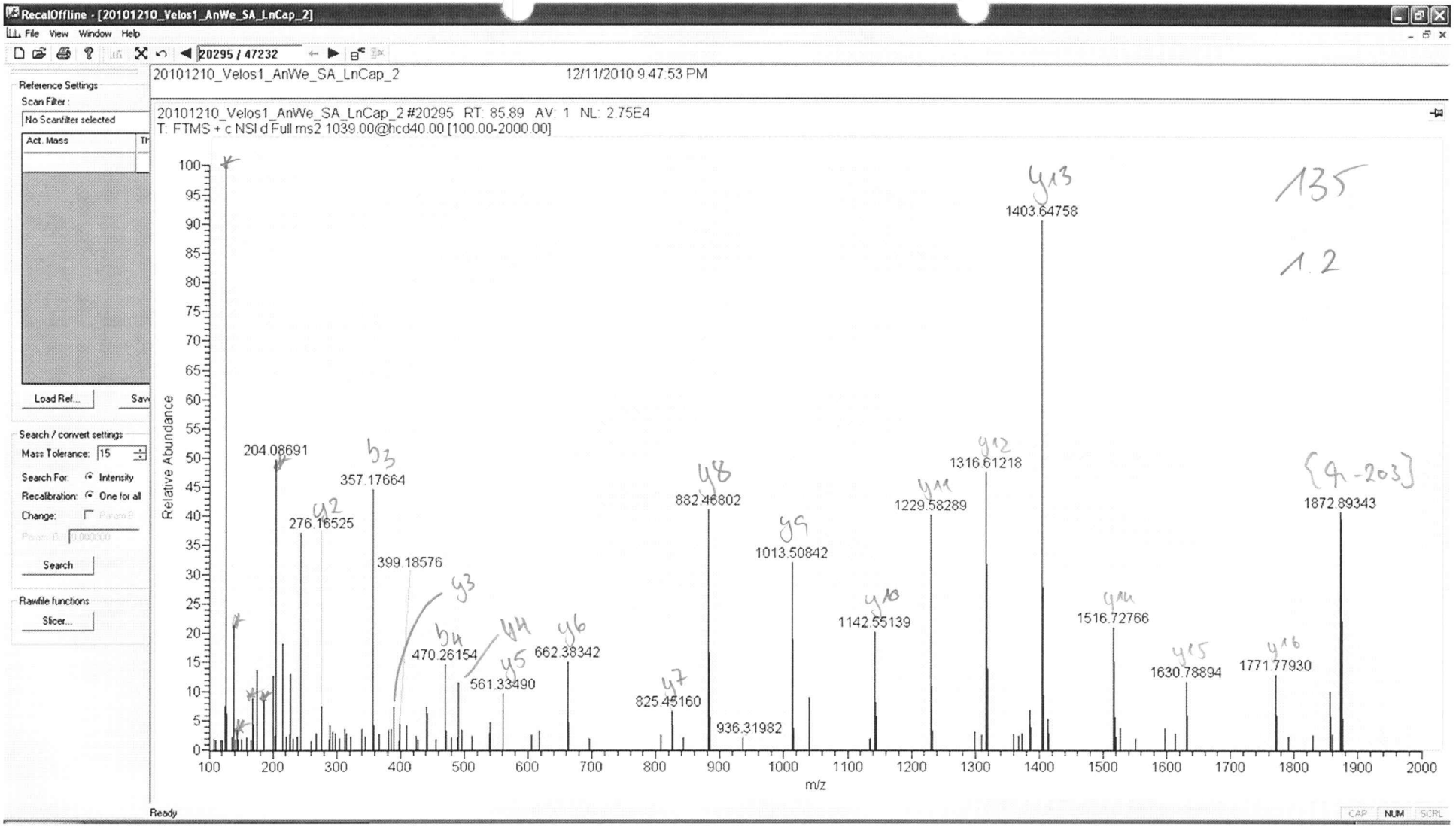
VLSSAIPVAGAPLVTATTTAVSSVLLAPSVFQQtVtR

no site evidence



no site evidence

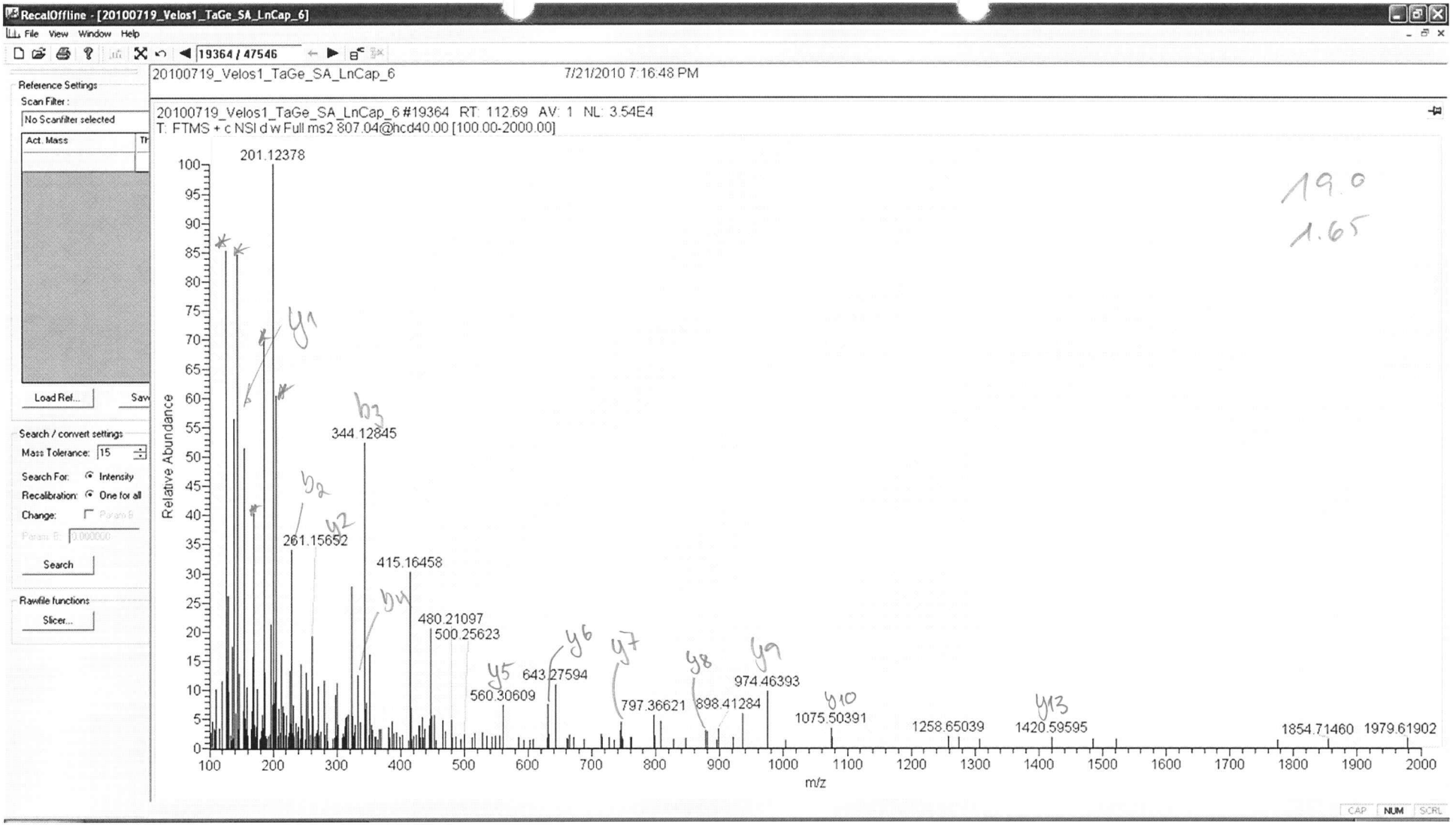
NETHSIcTAcDEscK



no site evidence

LENLSSSEMGYTATLtR

80

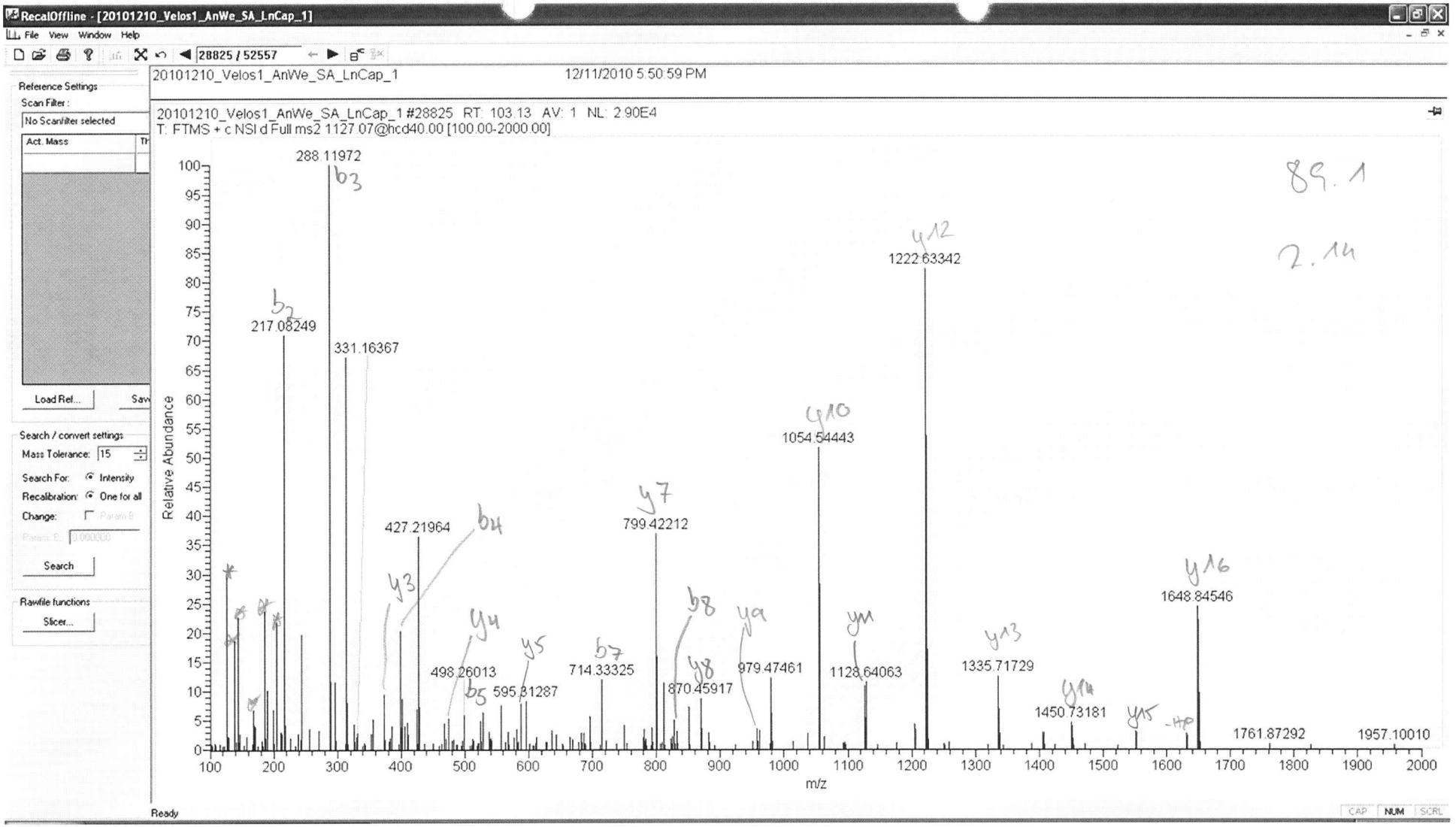


y9

DLDPGPVTTEDTPMDAIDAnK

b3

no strong evidence

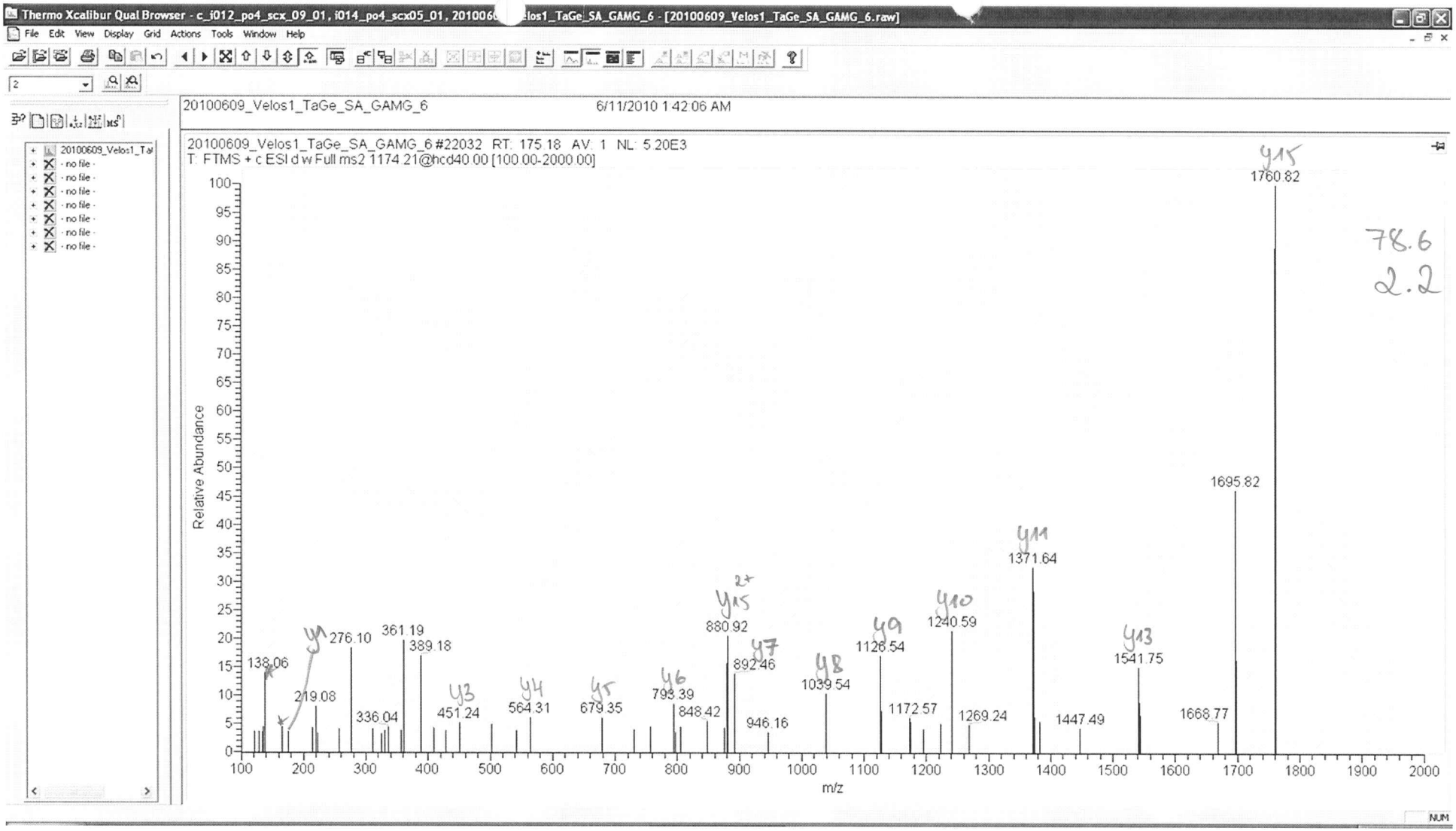


89.1

2.14

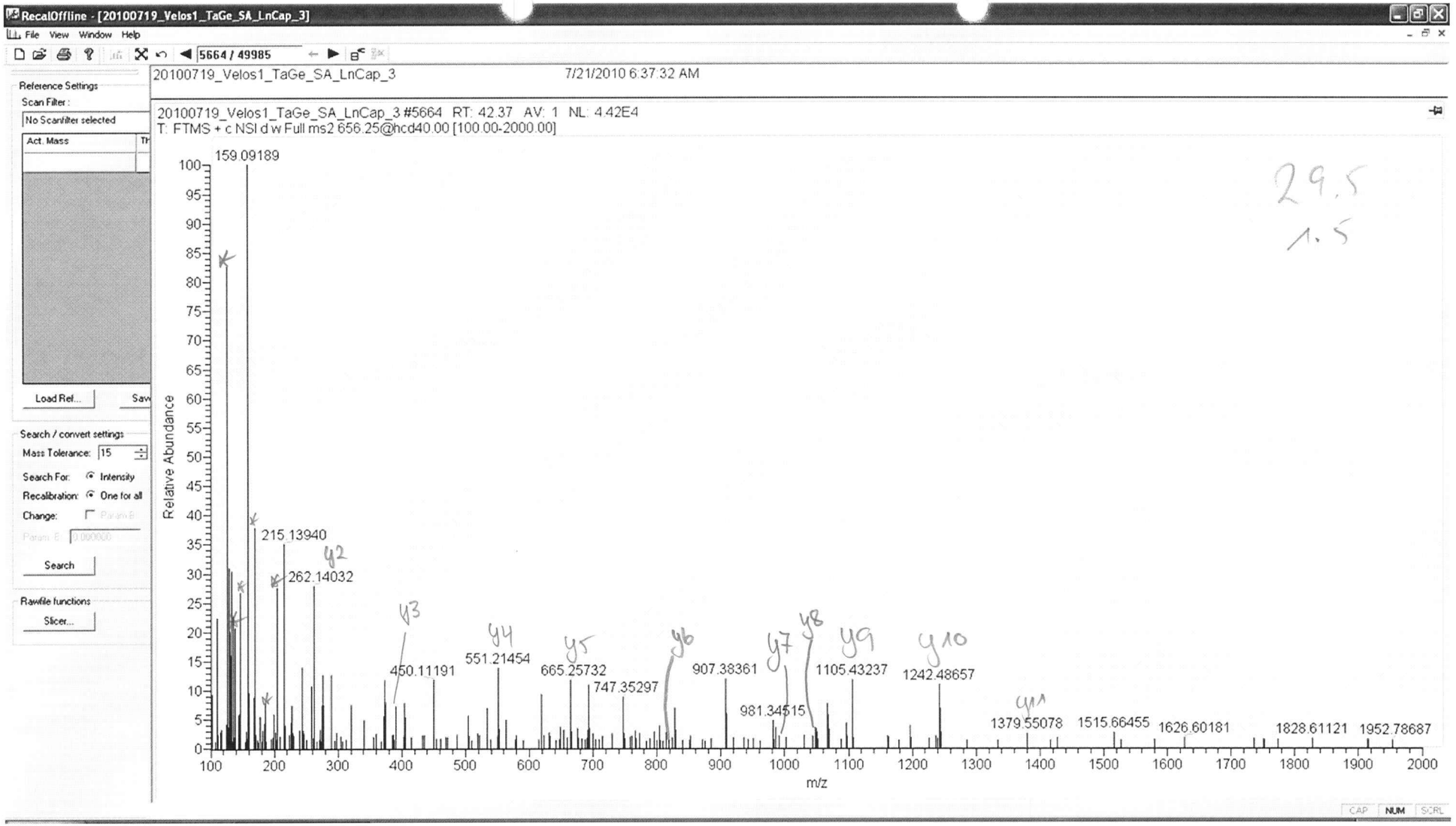
no fit evidence

SEALPTDLPAPSAPDLtEPK



No site evidence

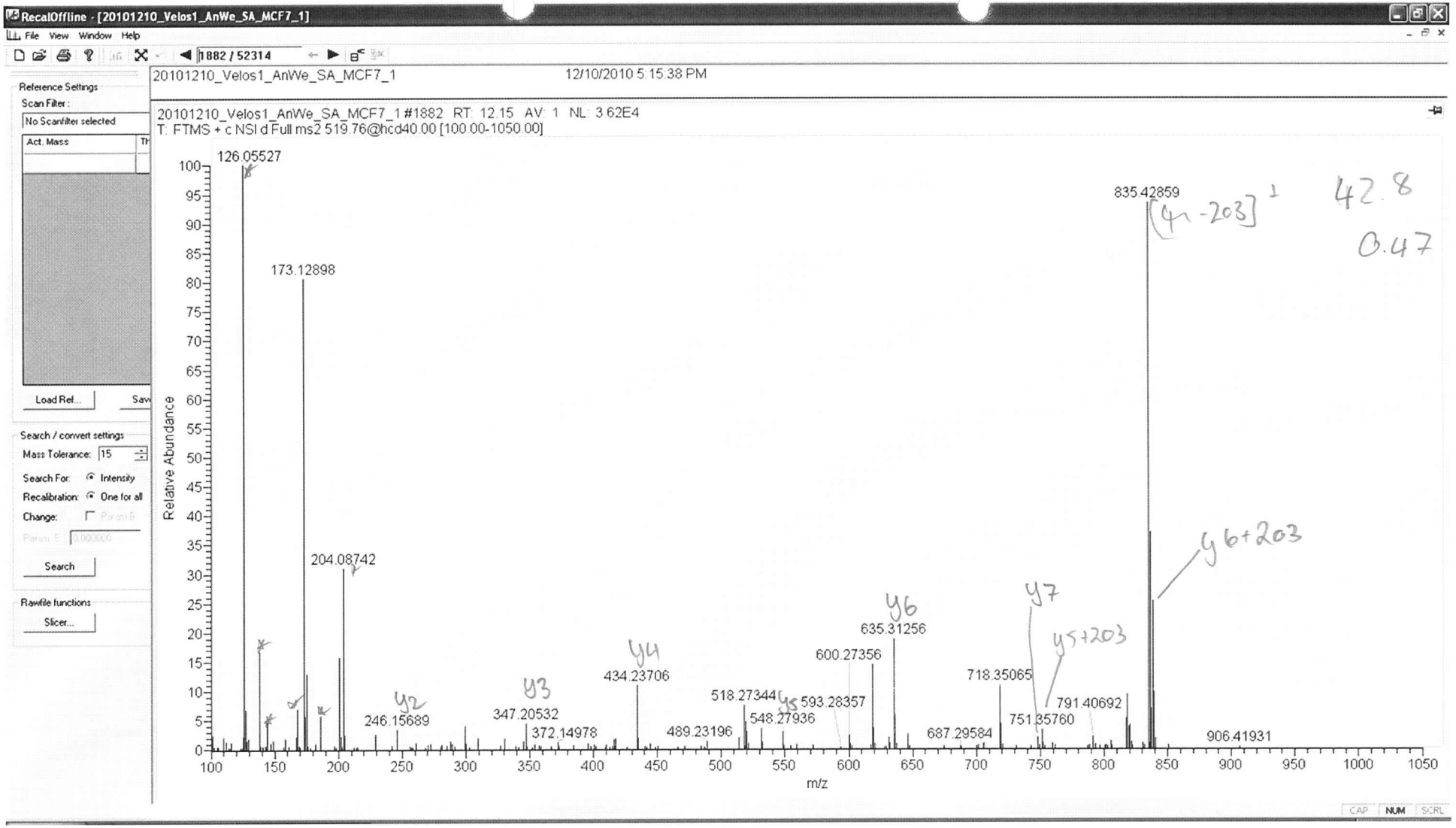
QVHPDtGIssKAMGImNSFVNDIFER



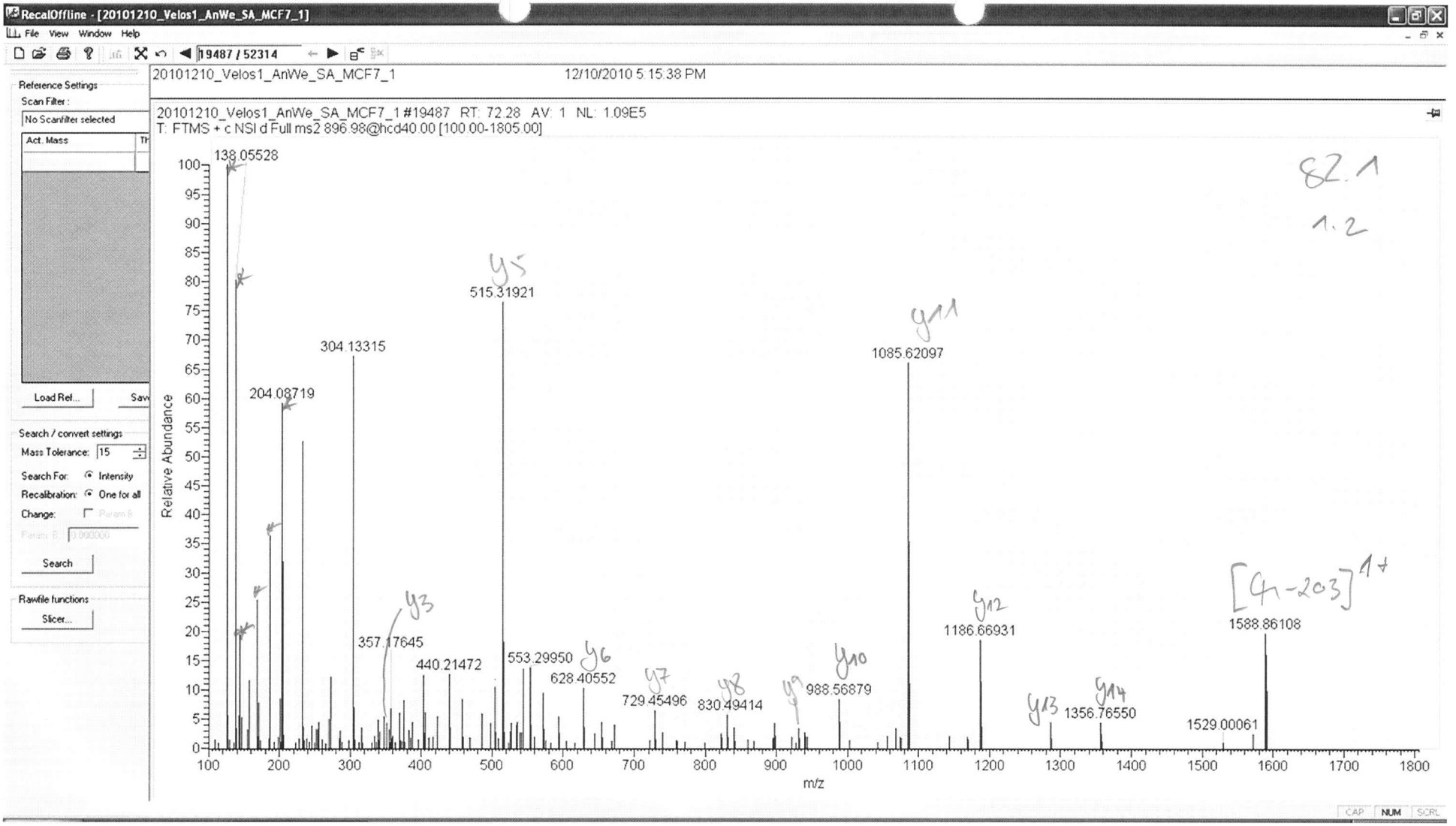
y10
y9

WGQNCscHHGGYYncEDK

no site evidence


RecalOffline - [20101210_Velos1_AnWe_SA_MCF7_1]
File View Window Help
1882 / 52314
20101210_Velos1_AnWe_SA_MCF7_1
12/10/2010 5:15:38 PM
Reference Settings
Scan Filter:
No Scanfilter selected
Act. Mass
Load Ref...
Search / convert settings
Mass Tolerance: 15
Search For: Intensity
Recalibration: One for all
Change:
Search
Rawfile functions
Slicer...
20101210_Velos1_AnWe_SA_MCF7_1 #1882 RT: 12.15 AV: 1 NL: 3.62E4
T: FTMS + c NSI d Full ms2 519.76@hcd40.00 [100.00-1050.00]
Relative Abundance
m/z
126.05527
173.12898
204.08742
246.15689
347.20532
372.14978
434.23706
489.23196
518.27344
548.27936
593.28357
600.27356
635.31256
687.29584
718.35065
751.35760
791.40692
835.42859
906.41931
y2
y3
y4
y5
y6
y7
y5+203
y6+203
[y1-203]1+
42.8
0.47
CAP NUM SCRL

SLSnSTAR



82.1

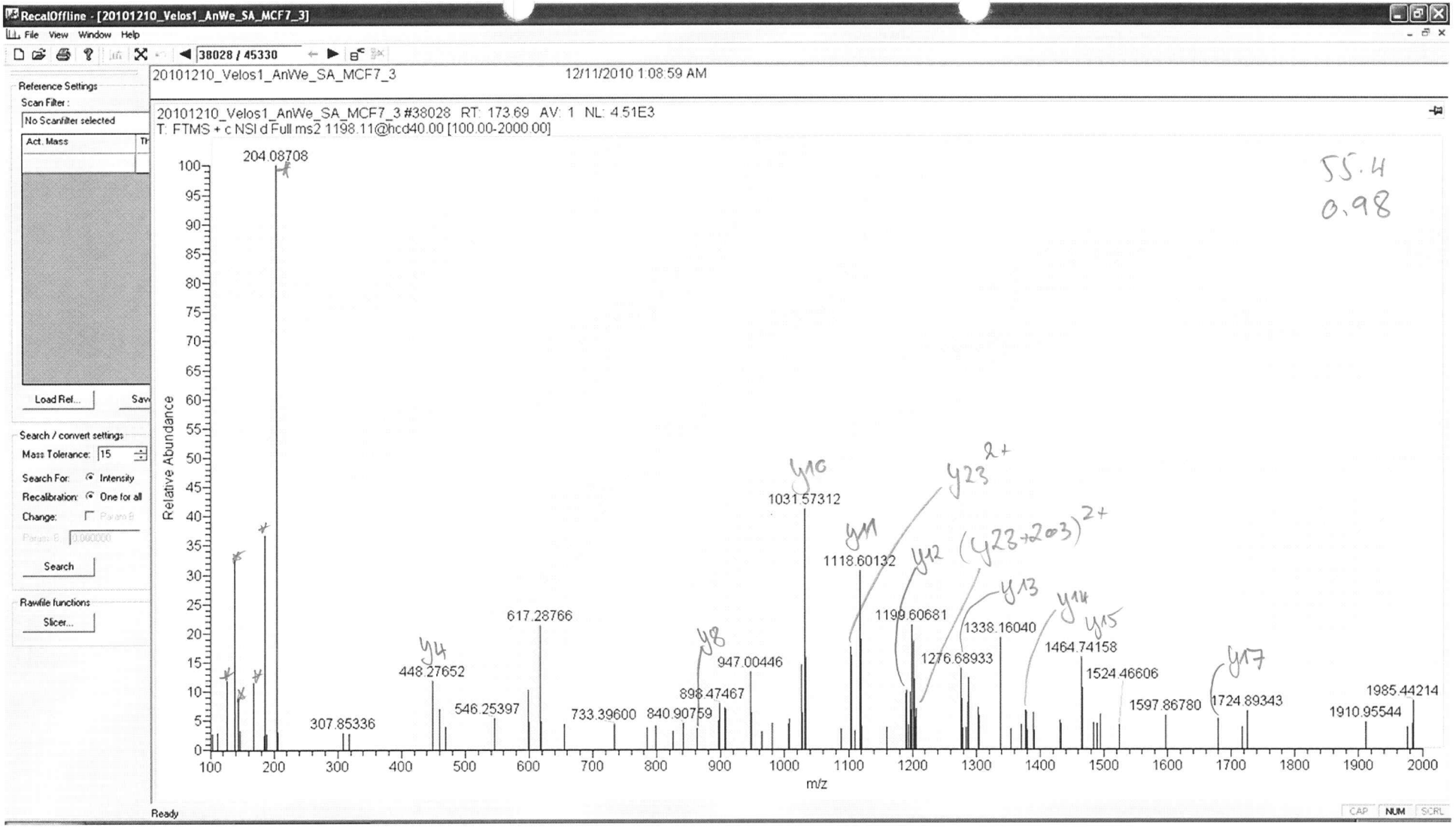
1.2

No site evidence

TMAVTPGTTTLPAtVK

y11 y5

88

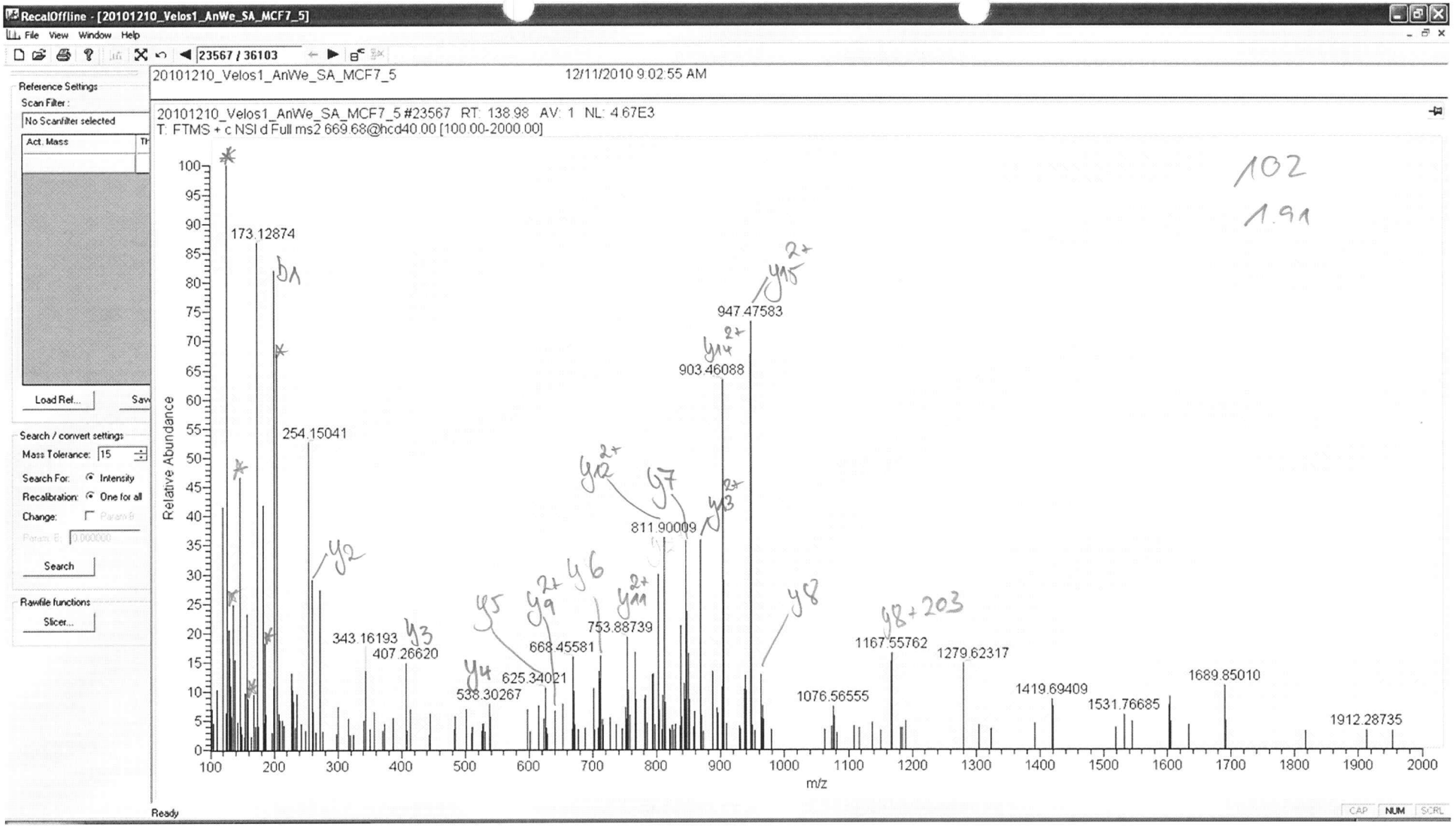


55.4
0.98

TQTQSAPALQGLSSLLQsVTGNPVPASEAASQSTSA
SPANTTVSTIK

y23
y10

site @
S27, 31, 33
T34, S35 or 37



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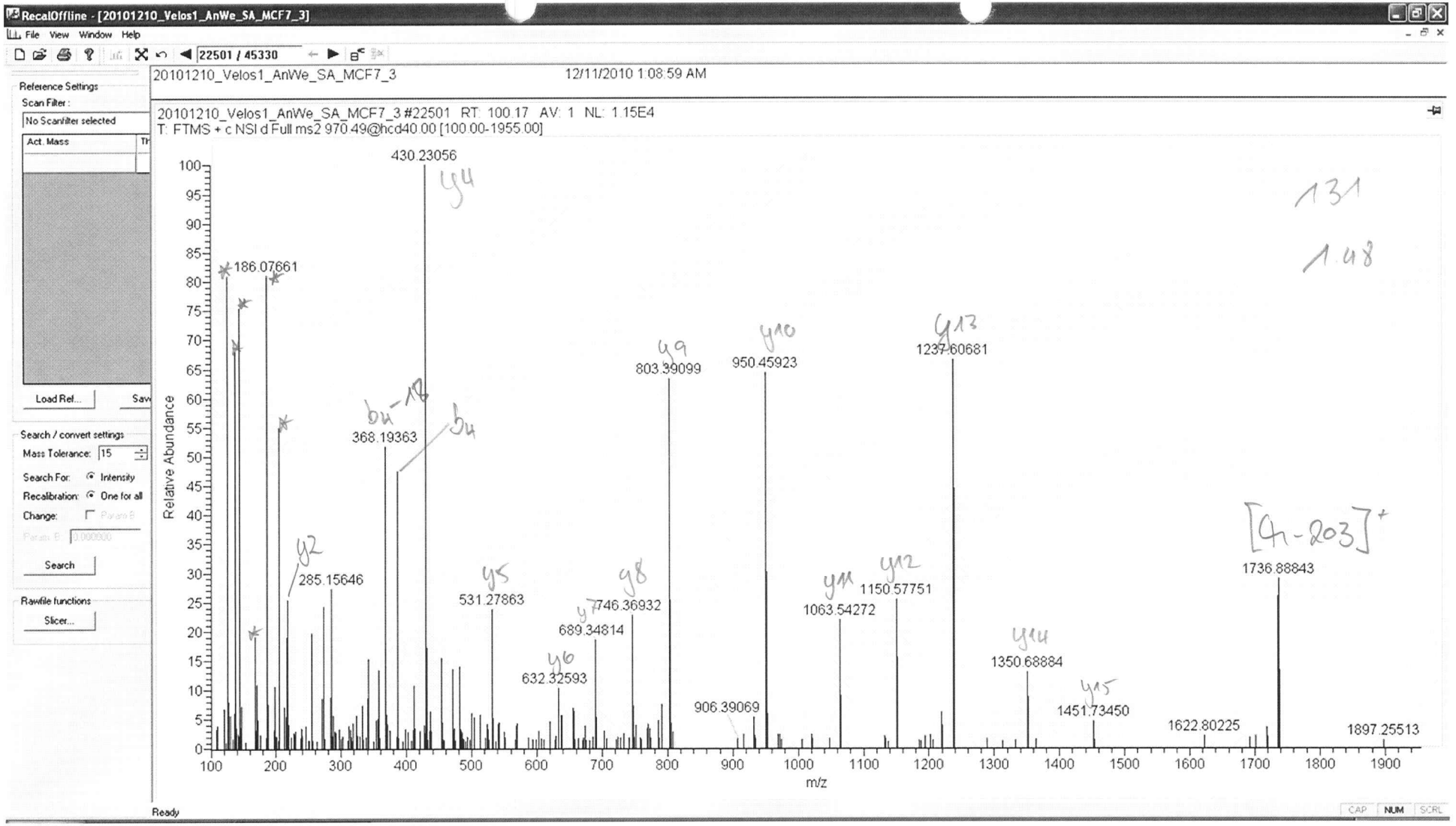

131

1.48

[4-203]+

no site evidence

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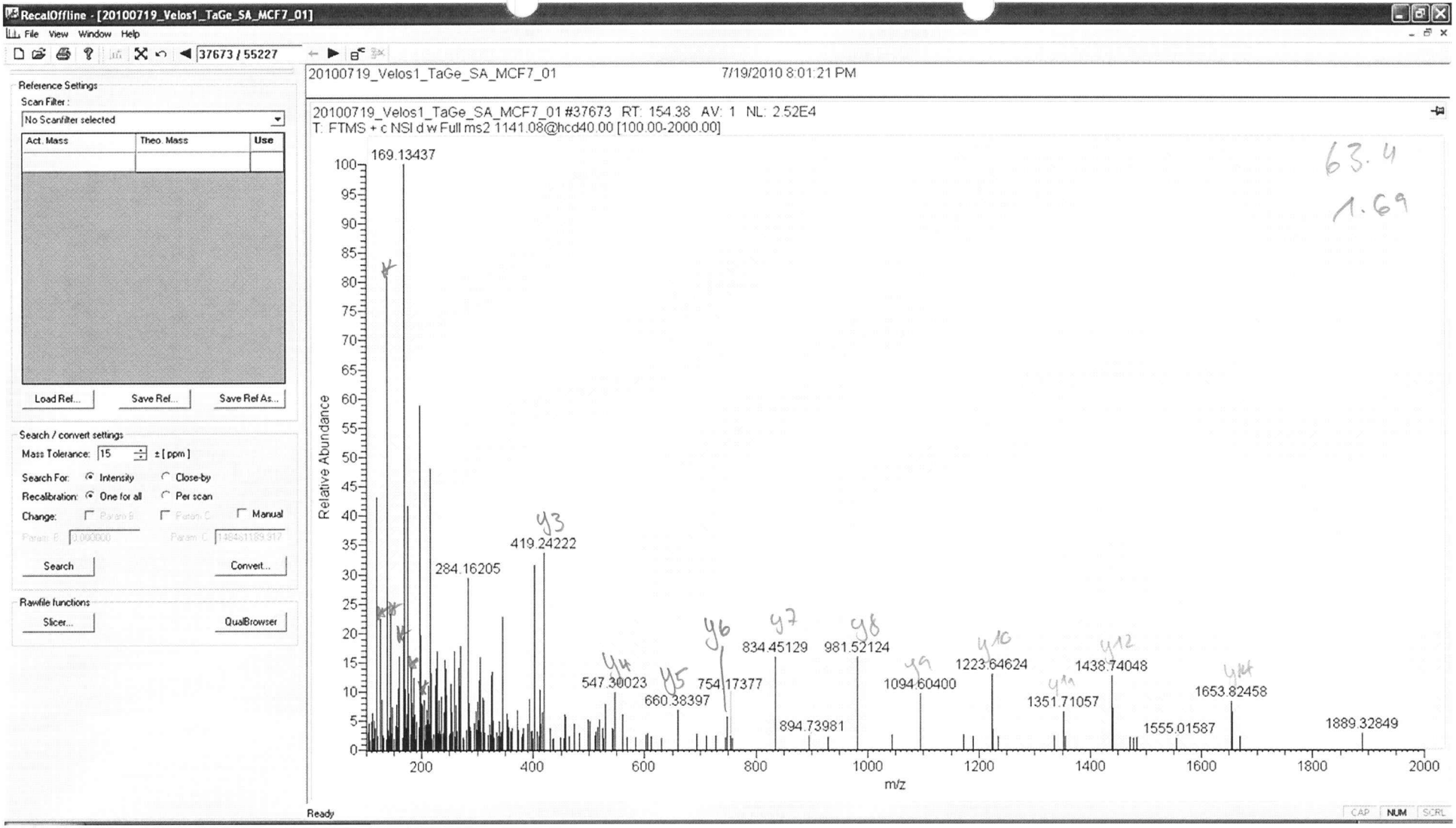
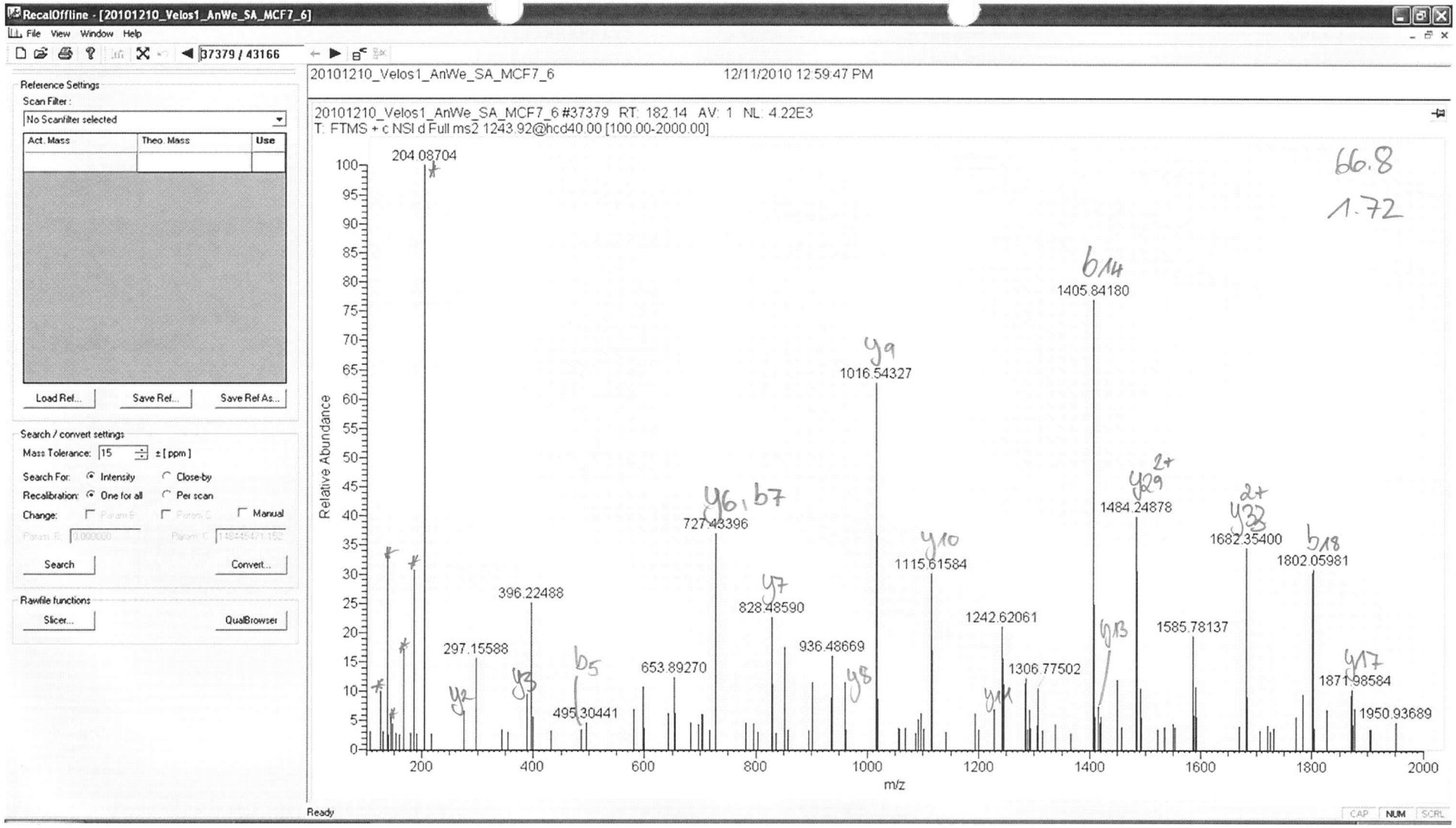


63.4

1.69

No site evidence

GGLPVSQSQEIFSsLQPFR



66.8

1.72

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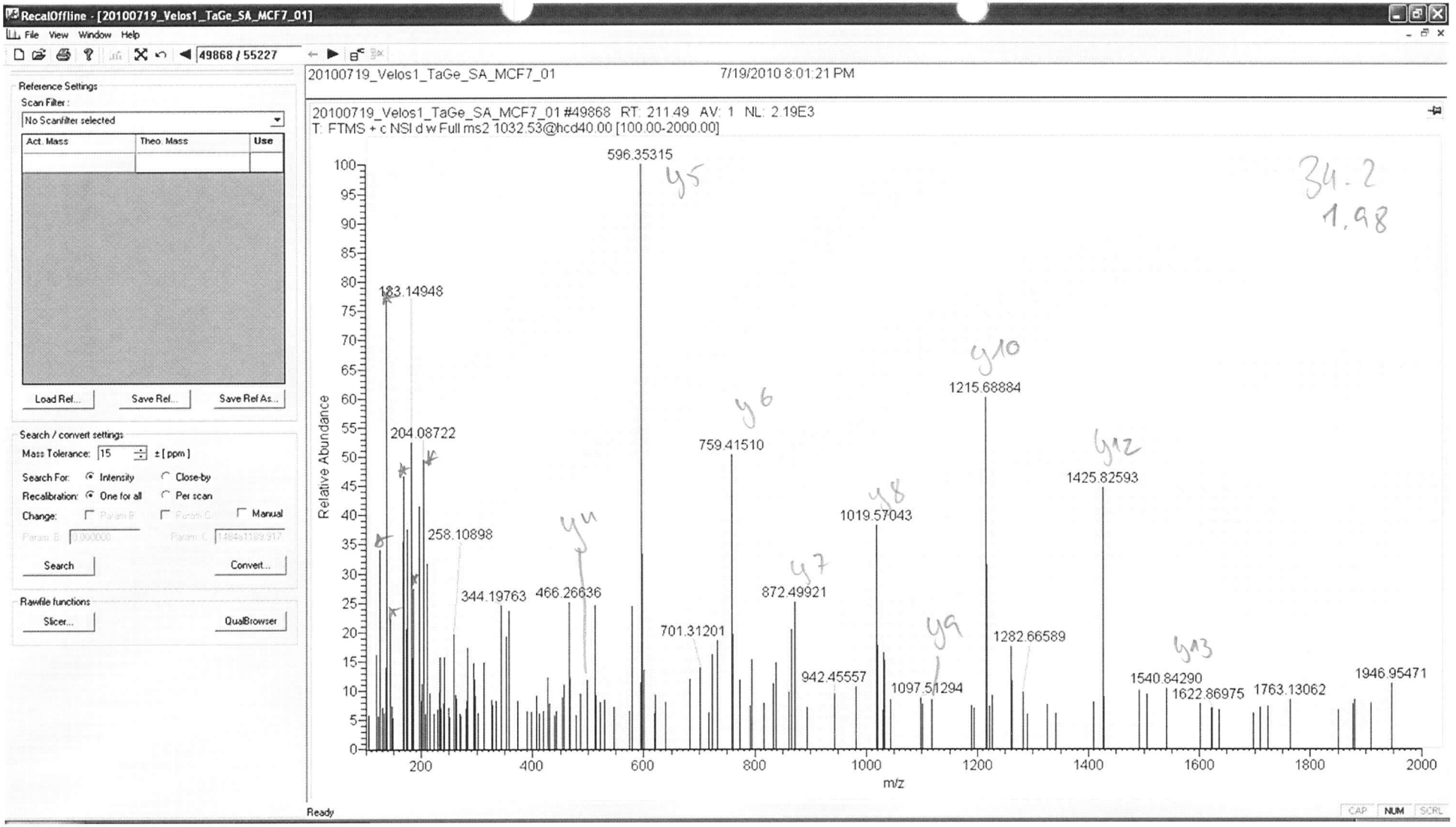
no site evidence

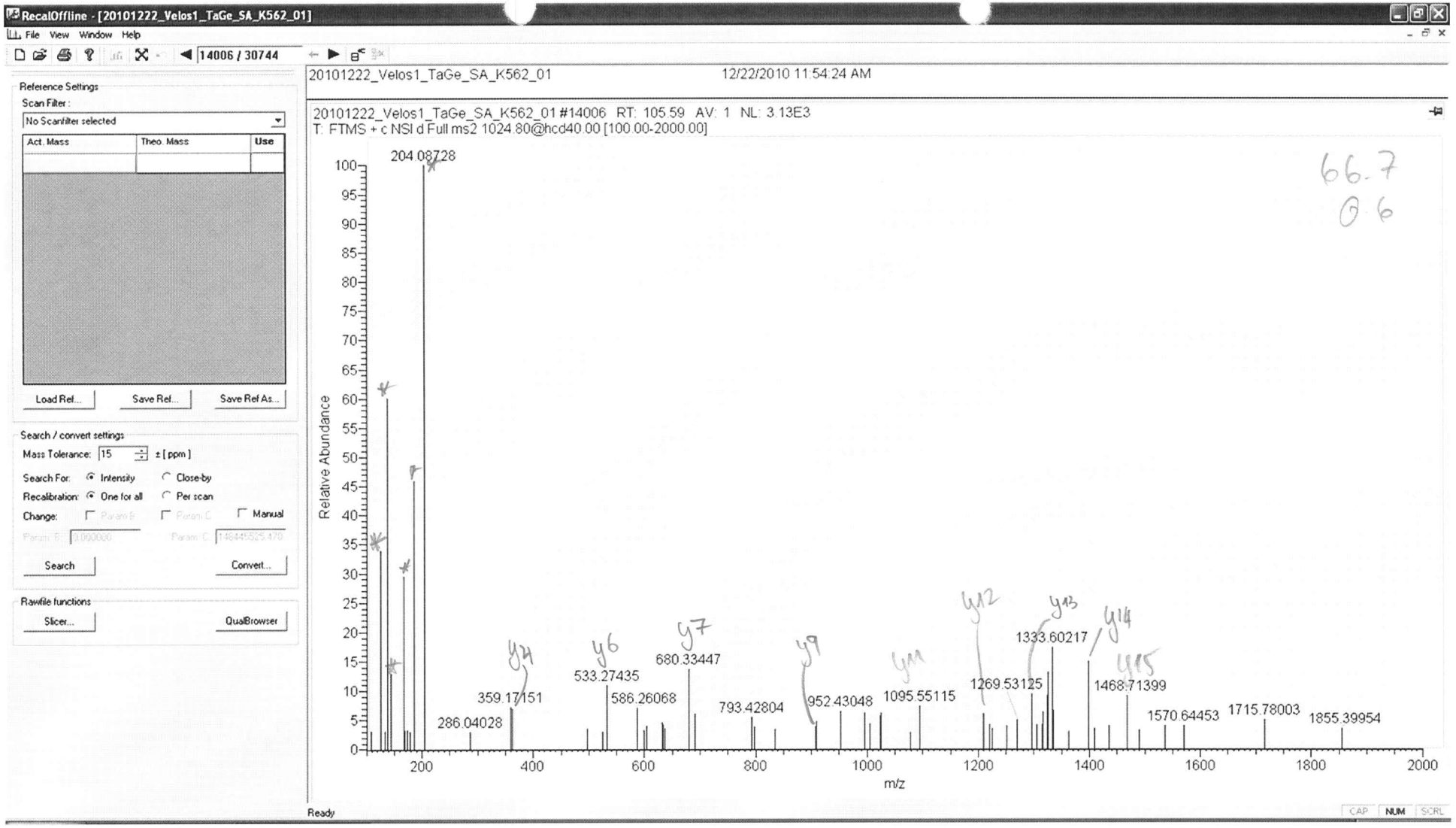


34.2
1.98

TVPVsSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQR

R

No site evidence



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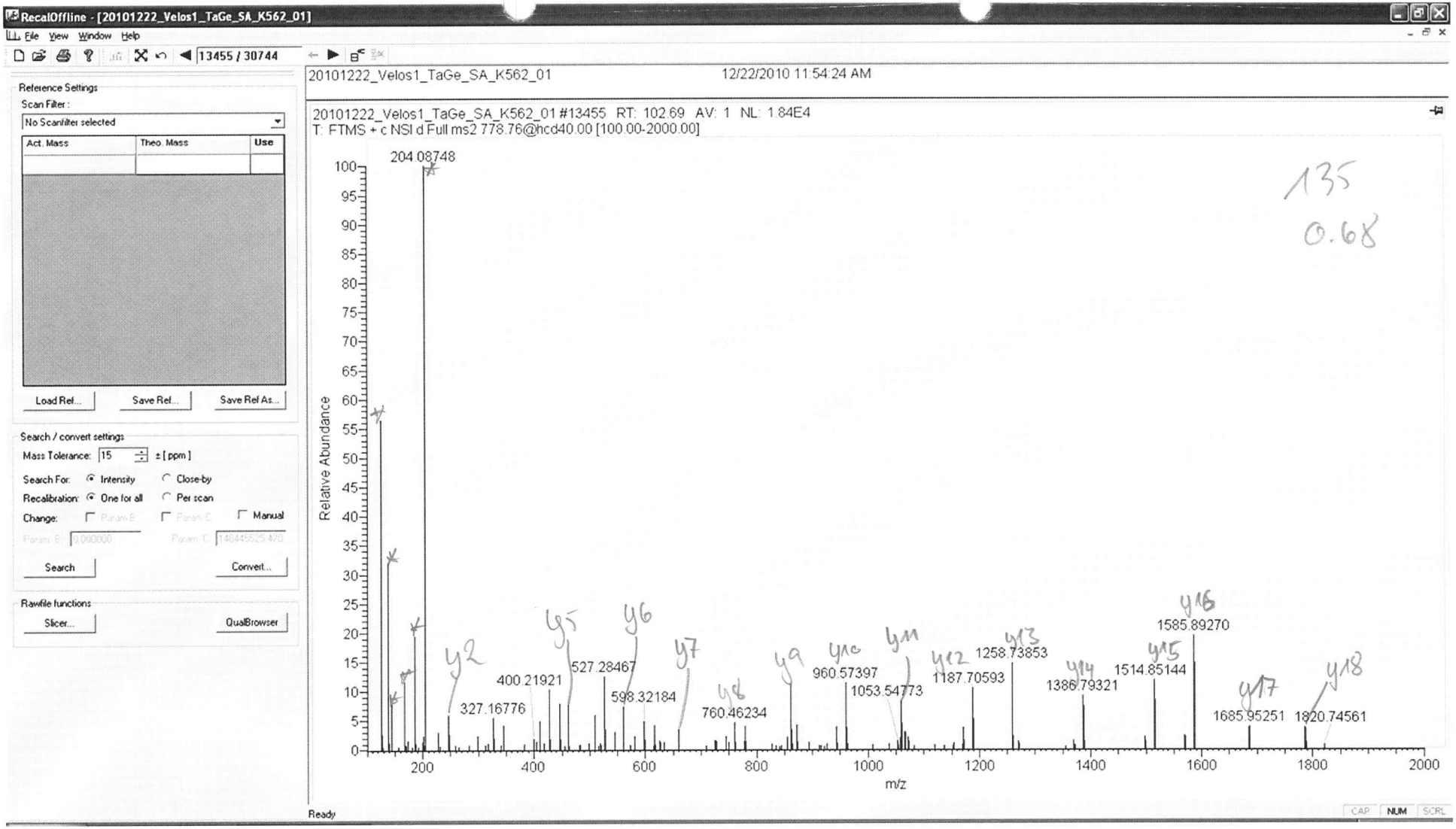
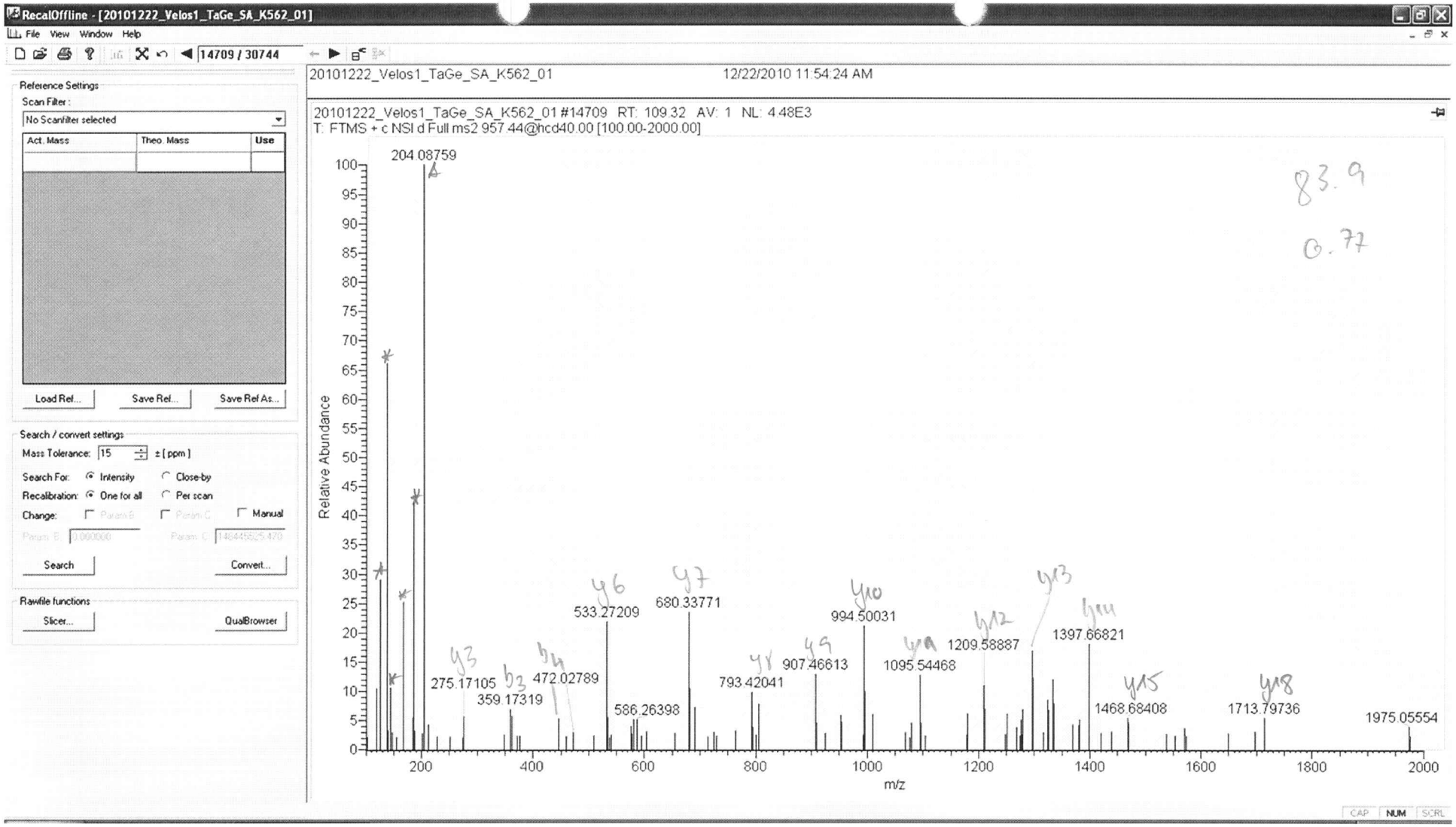


135
0.68

No site evidence

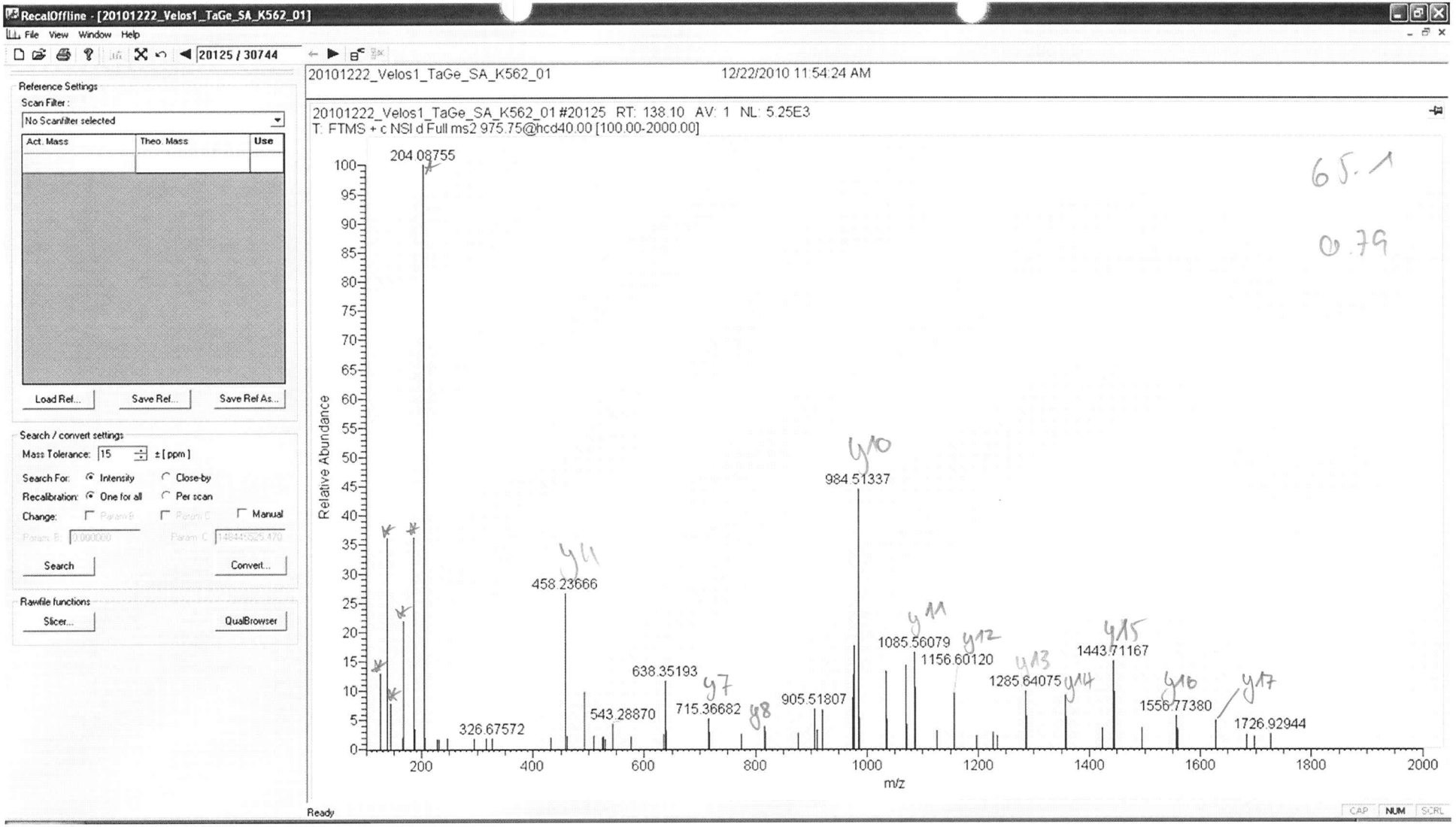
y9
y8

SGTVtVAQQAQVVTTVVGGVTK



NPFSSASGGFGStATSNTSNLFGNSGAK

no site evidence



65.1

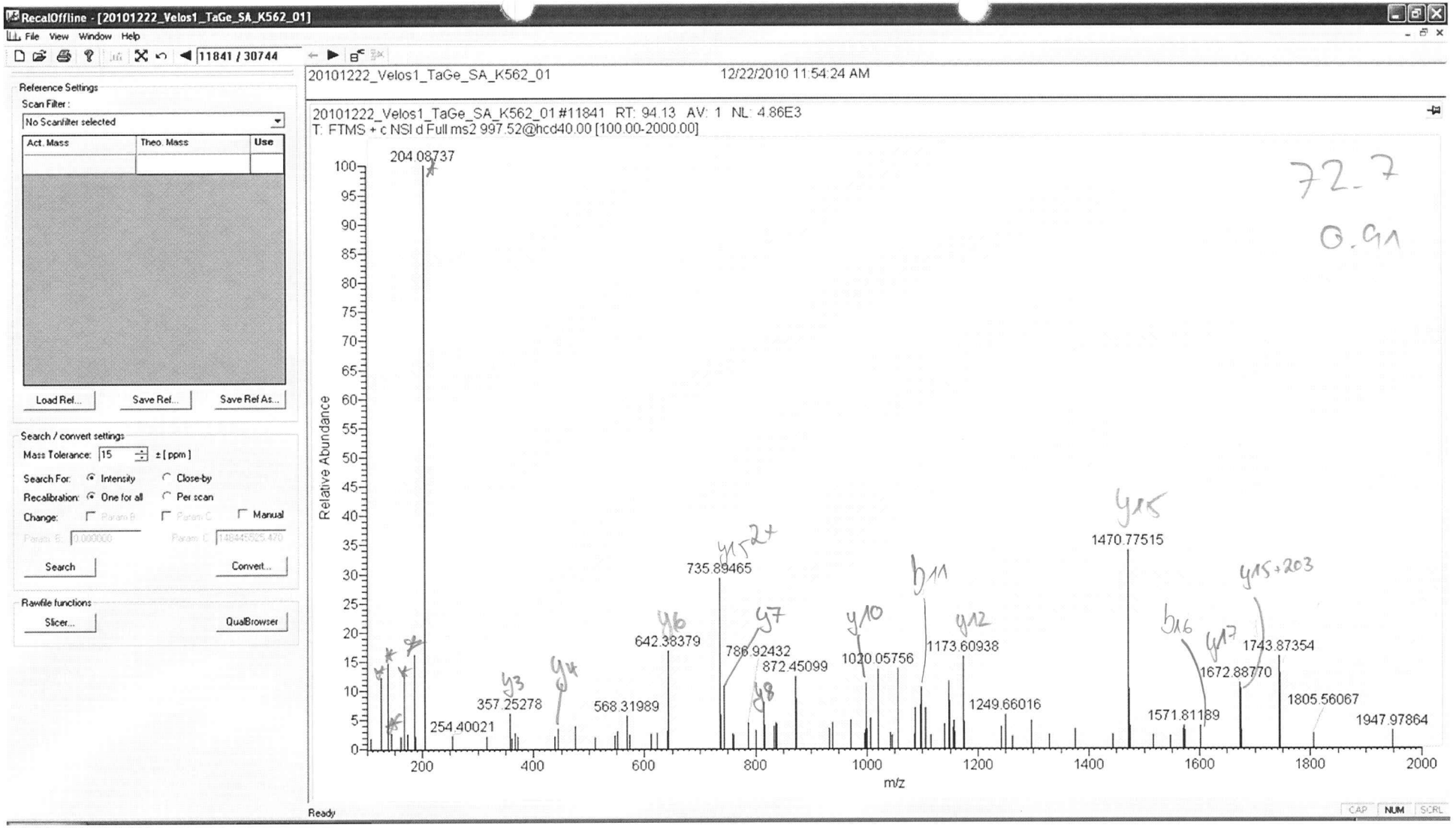
0.79

EPVLAQPAVSNSGTAASSTSLVALSAEATPATtGVPDAR

y10 y7 y4

no site evidence

9a



72.7

0.91

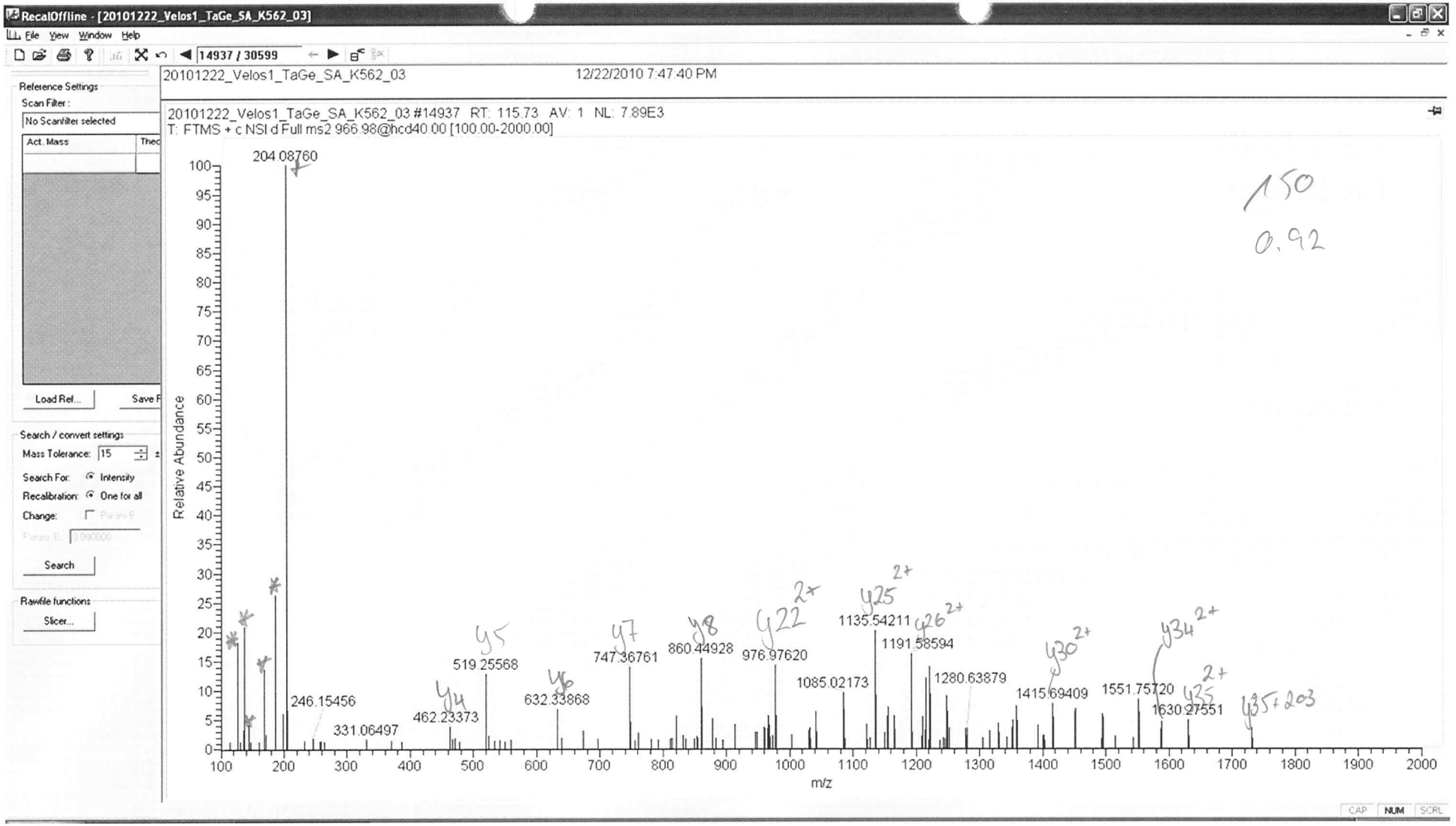
TKPLASVTNANTSSTQAAPVAVTTPTVSSGQATPTsPIK

y15

b11 b12

no site evidence

100



150

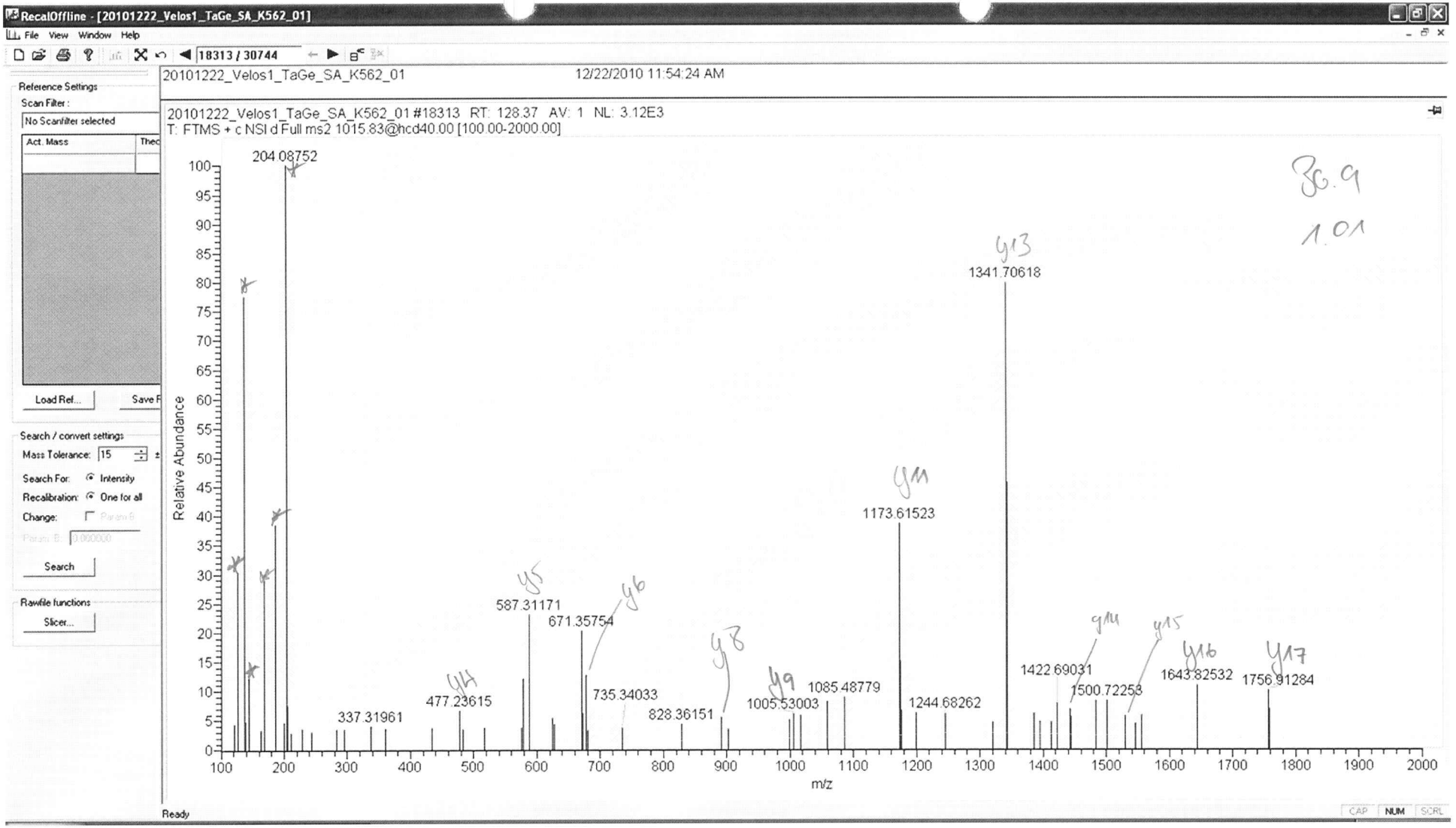
0.92

S5

y35 y34

VVTTSANSANGYILTSQGAAGGSHDAAGAAVLDLGsEAR

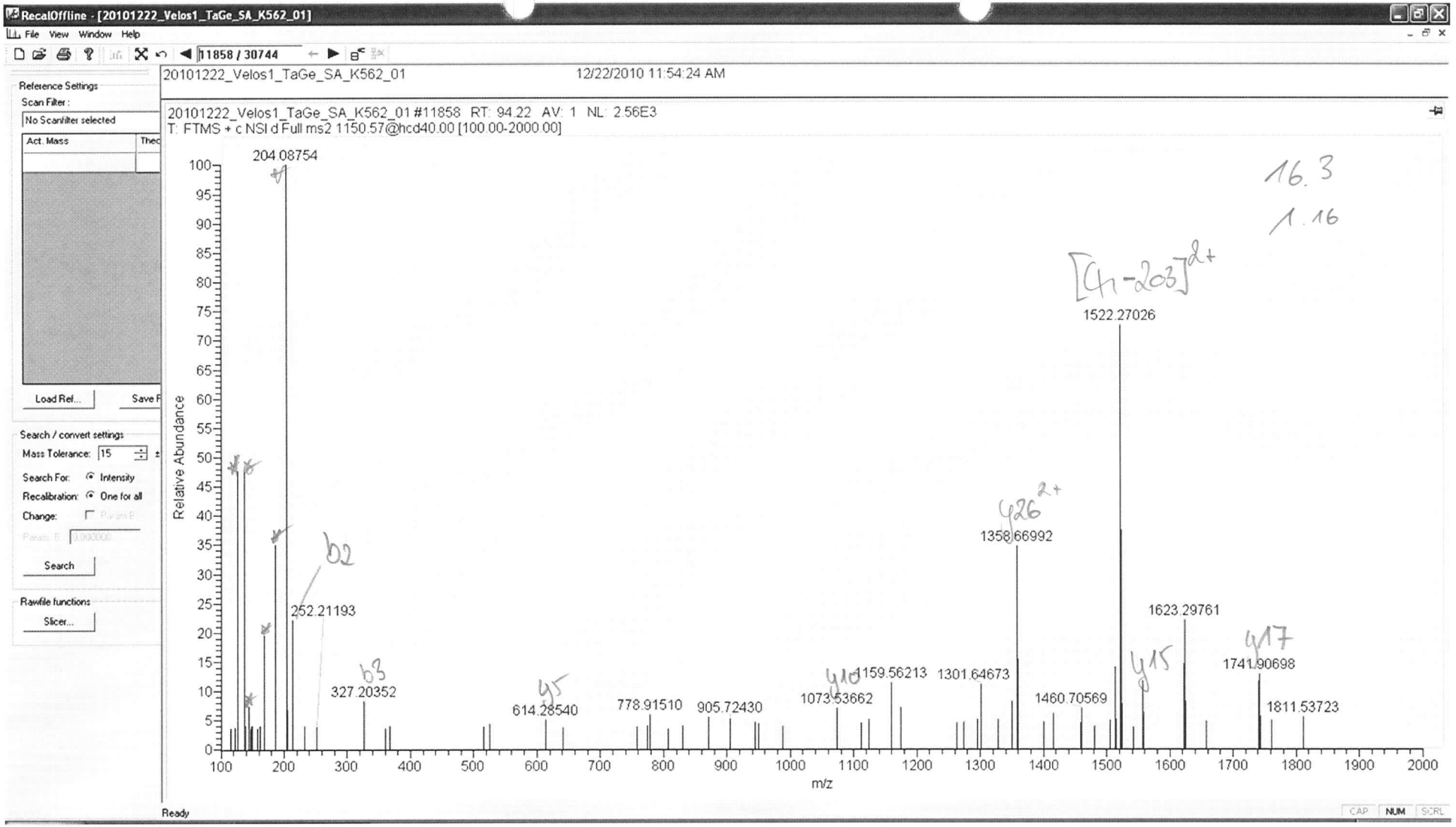
101



SSSAGFSFGTGVINSTPAPANTIVTSEnK

y4

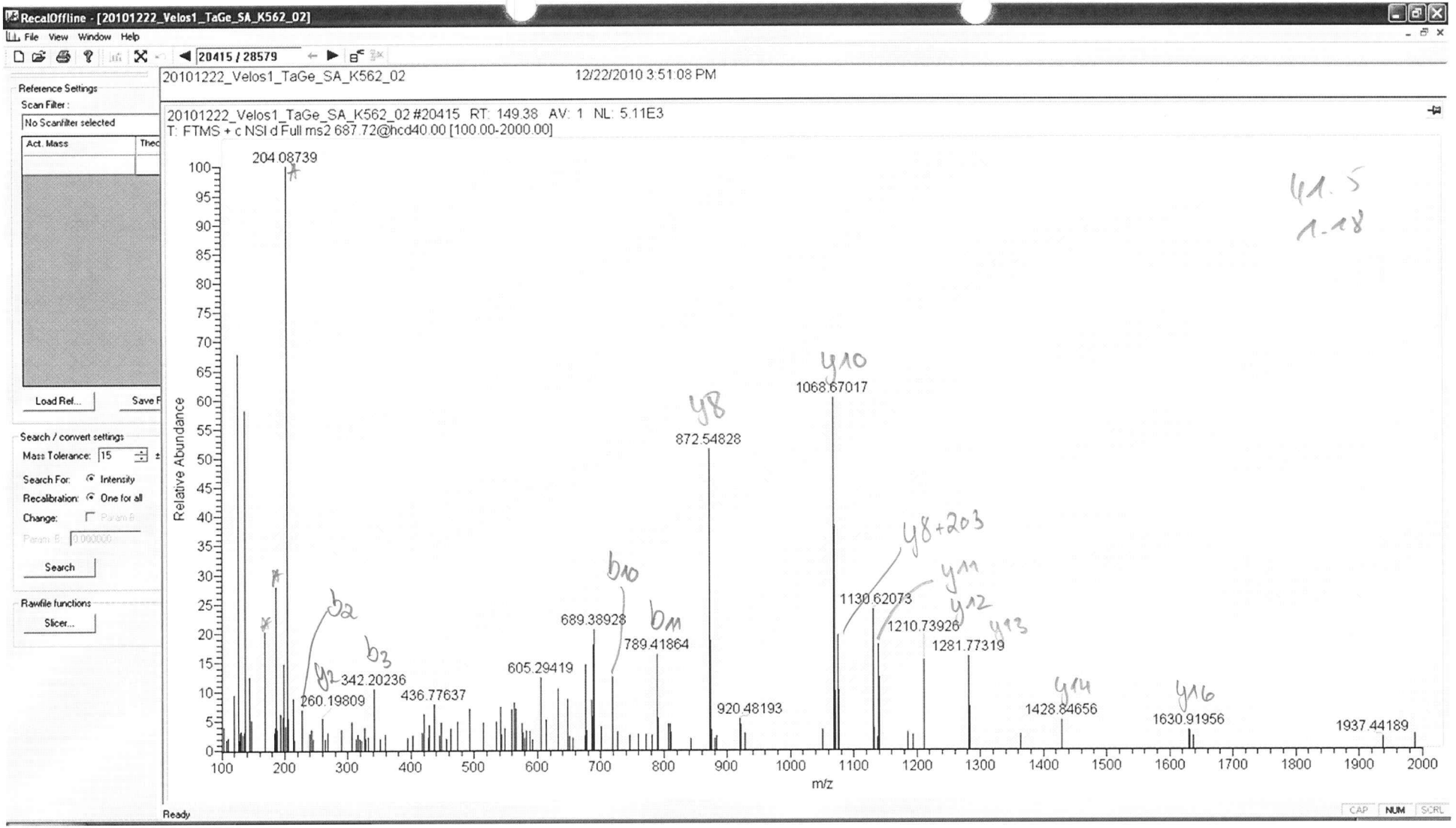
no site evidence



y26 y17 y15 y5

VNLPTTVSNFNNPSPSVVTATTSVHEsnK

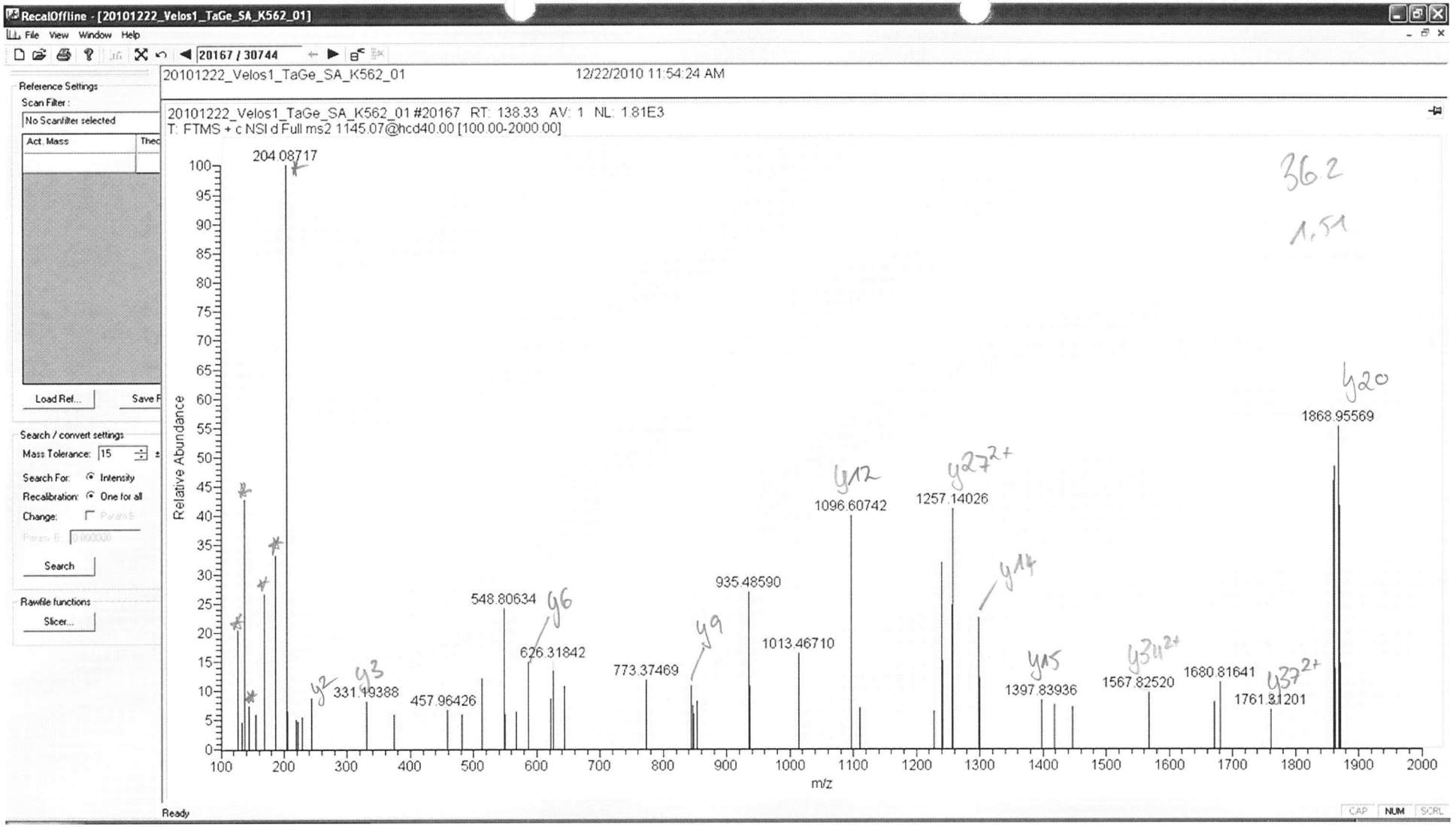
No site evidence



y8

ILDSFAAAPVPTTtLVLK

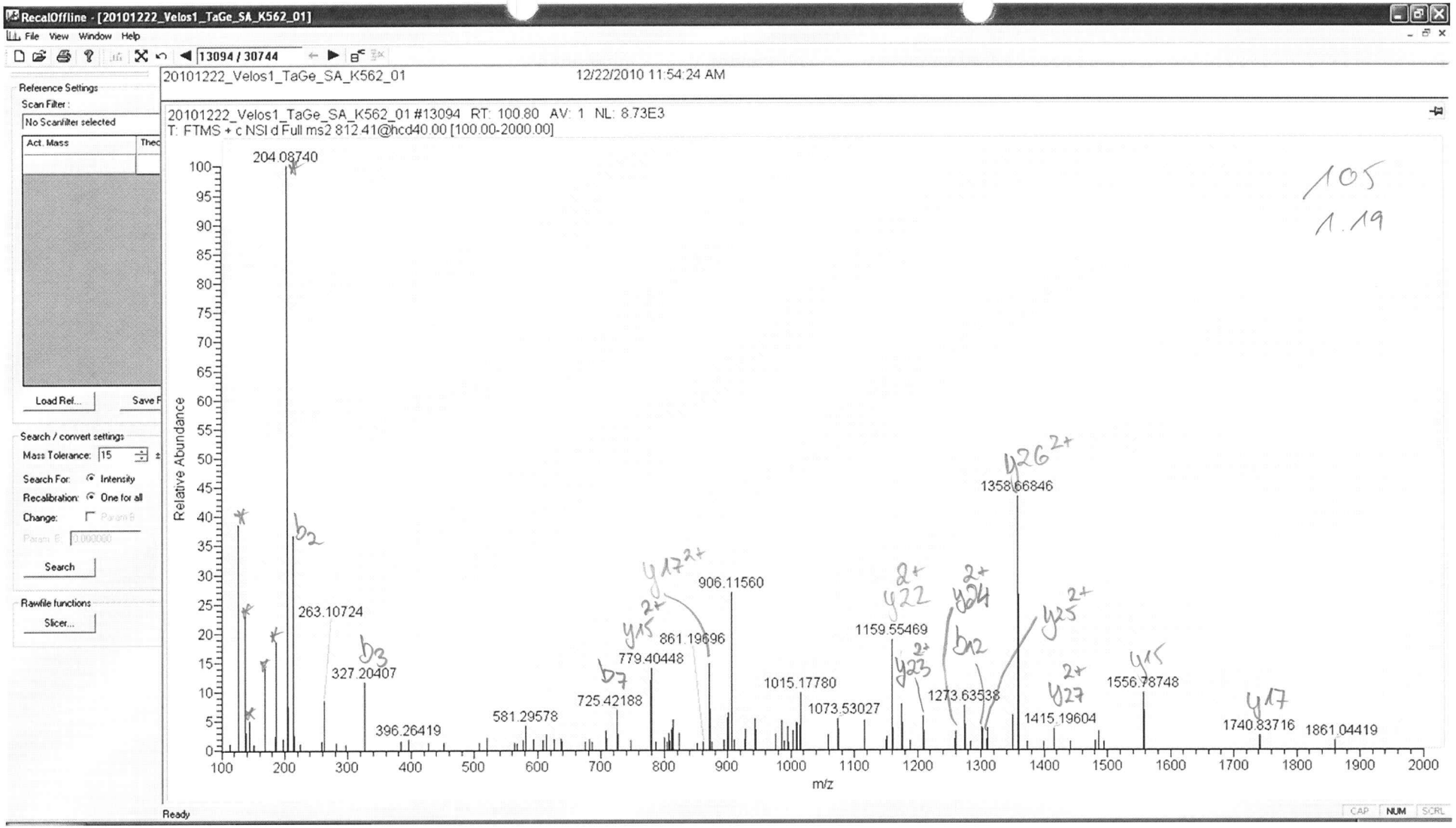
T 12, 13 or 14



SAAPAPISAScPEPPIGSAVPTSSASIPVTSSVSDPGVGSISPAsPK

y20 y12 y2

no site evidence

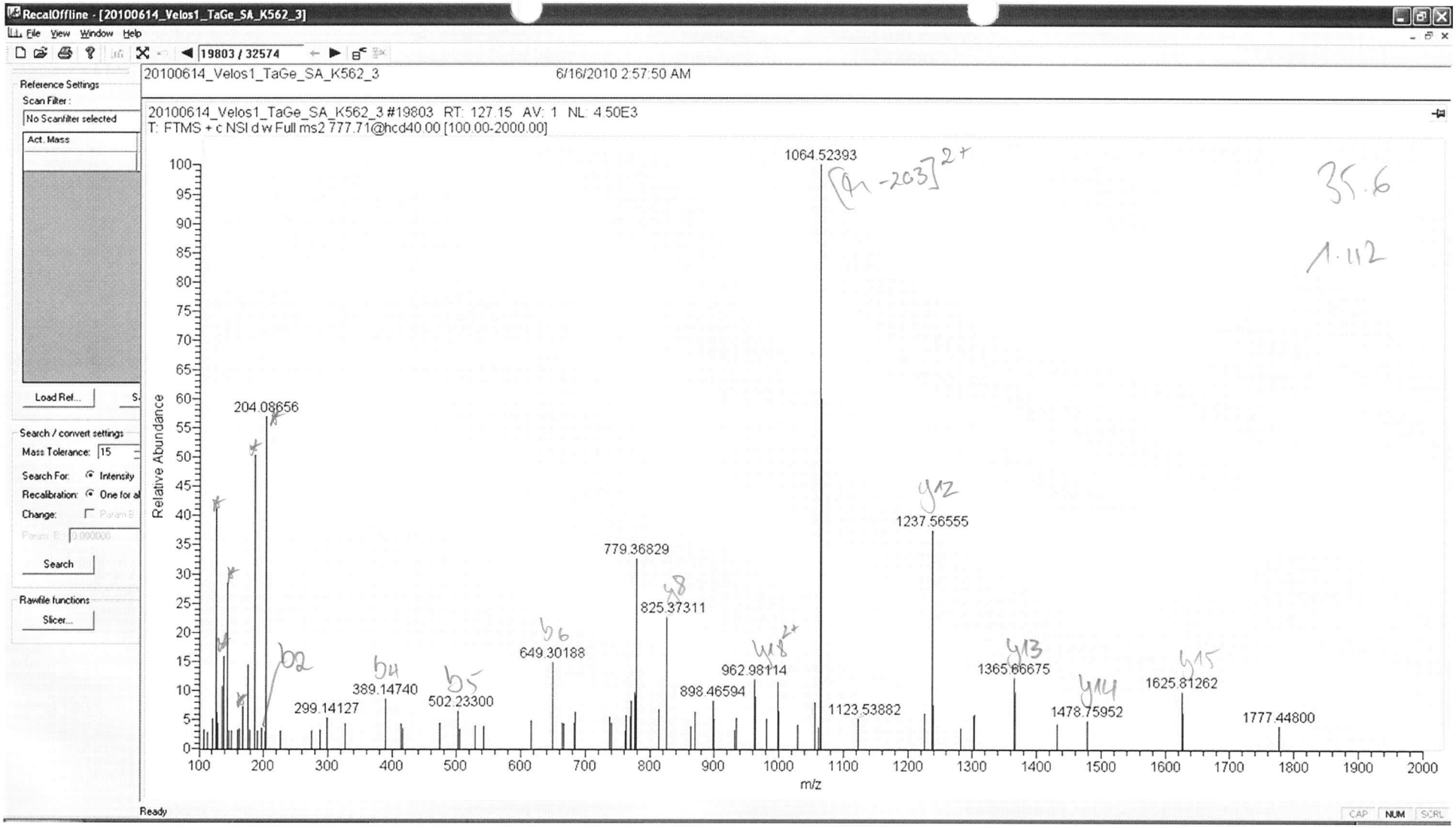


105
1.19

y26 y17 y15

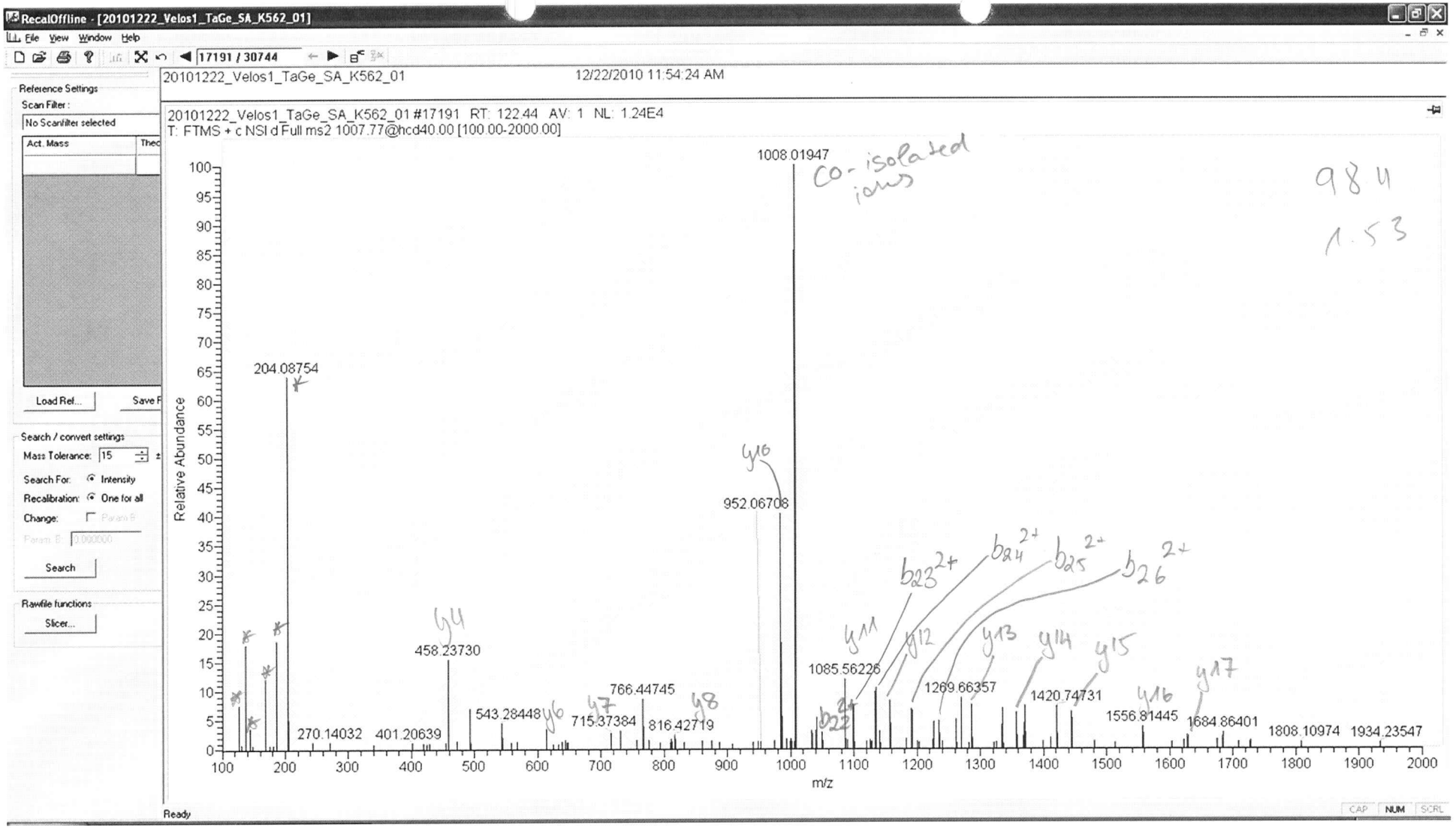
VNLPTTVSNFNNPSPSVVTATTSVHESnK

no site evidence



AMEGIFIKPSVEPsAGHDEL

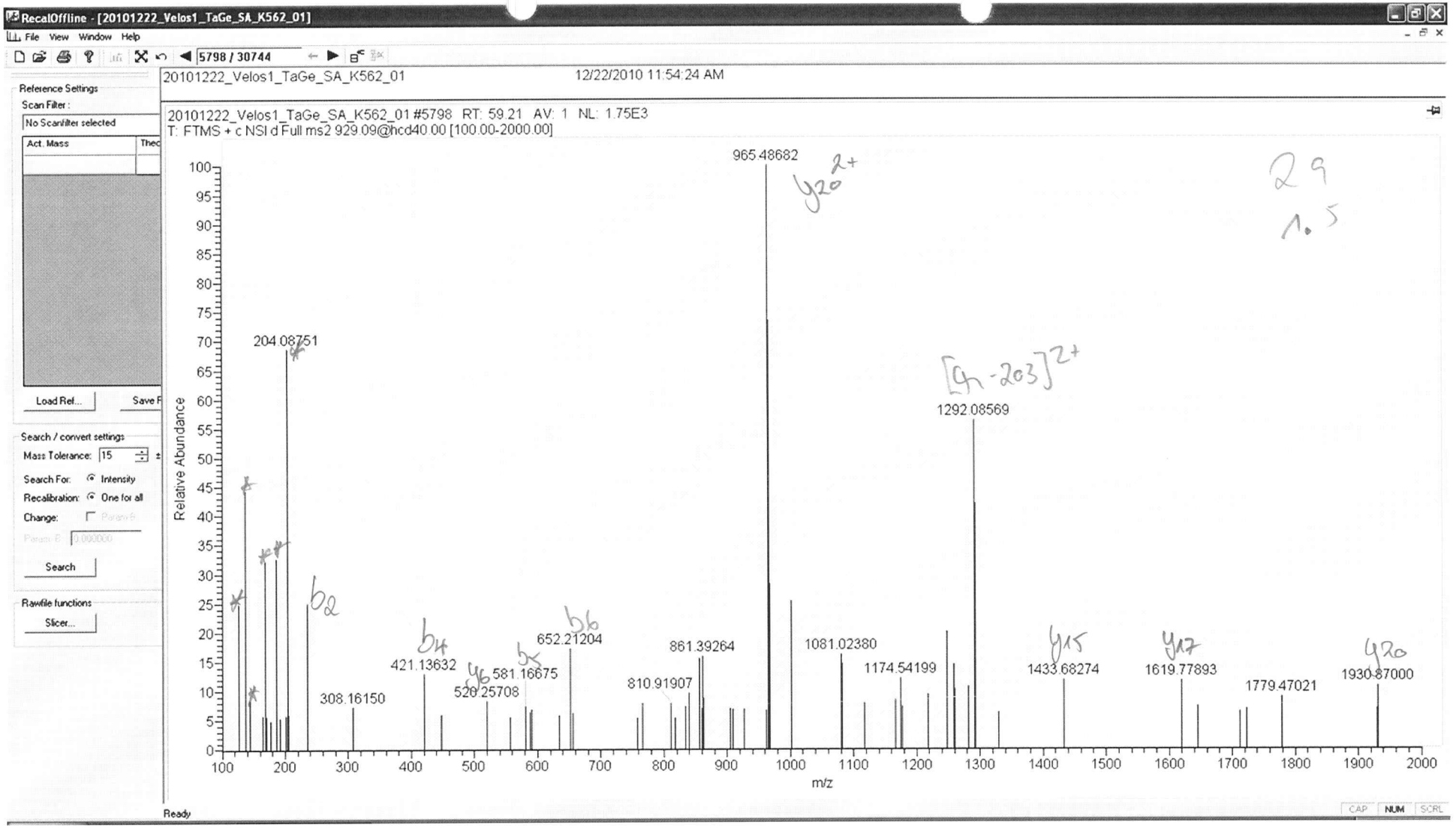
No site evidence



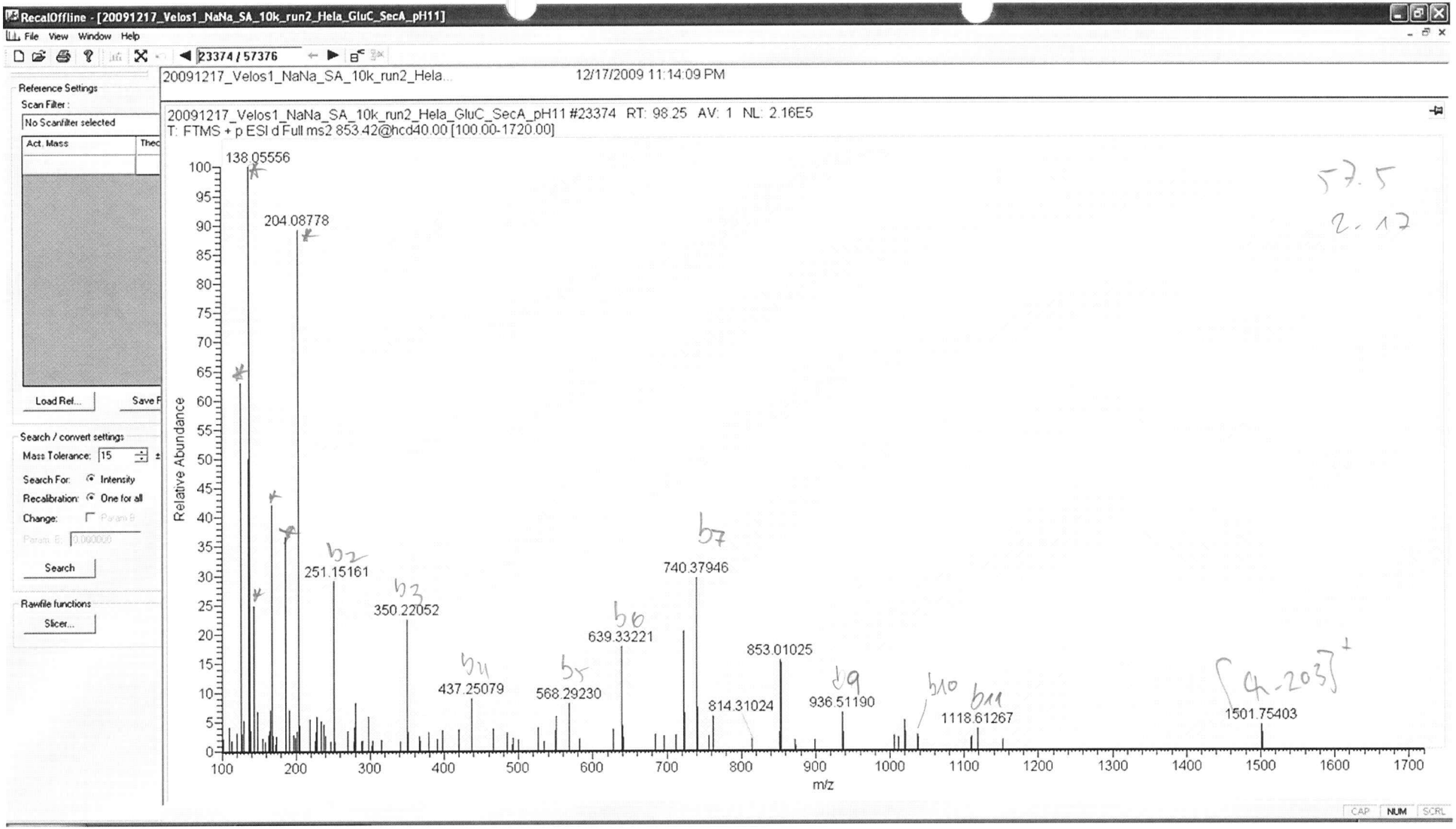
KEPVLAQPAVSNSGTAASSTSLVALSAEATPATtGVPDAR

y4

no site evidence



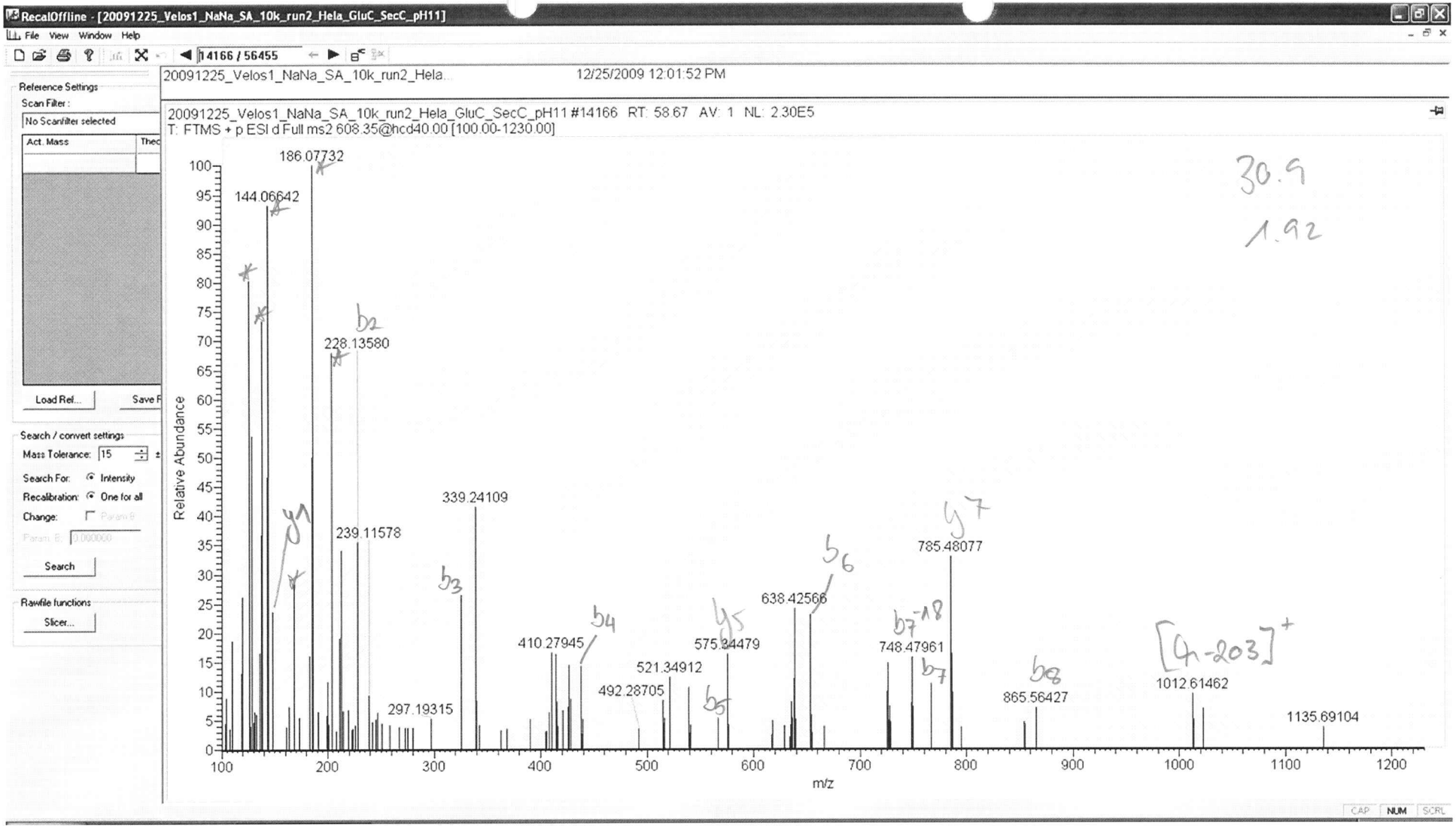
mSGEcAPNVSVSVSTSHTTISGGGsR



no further evidence

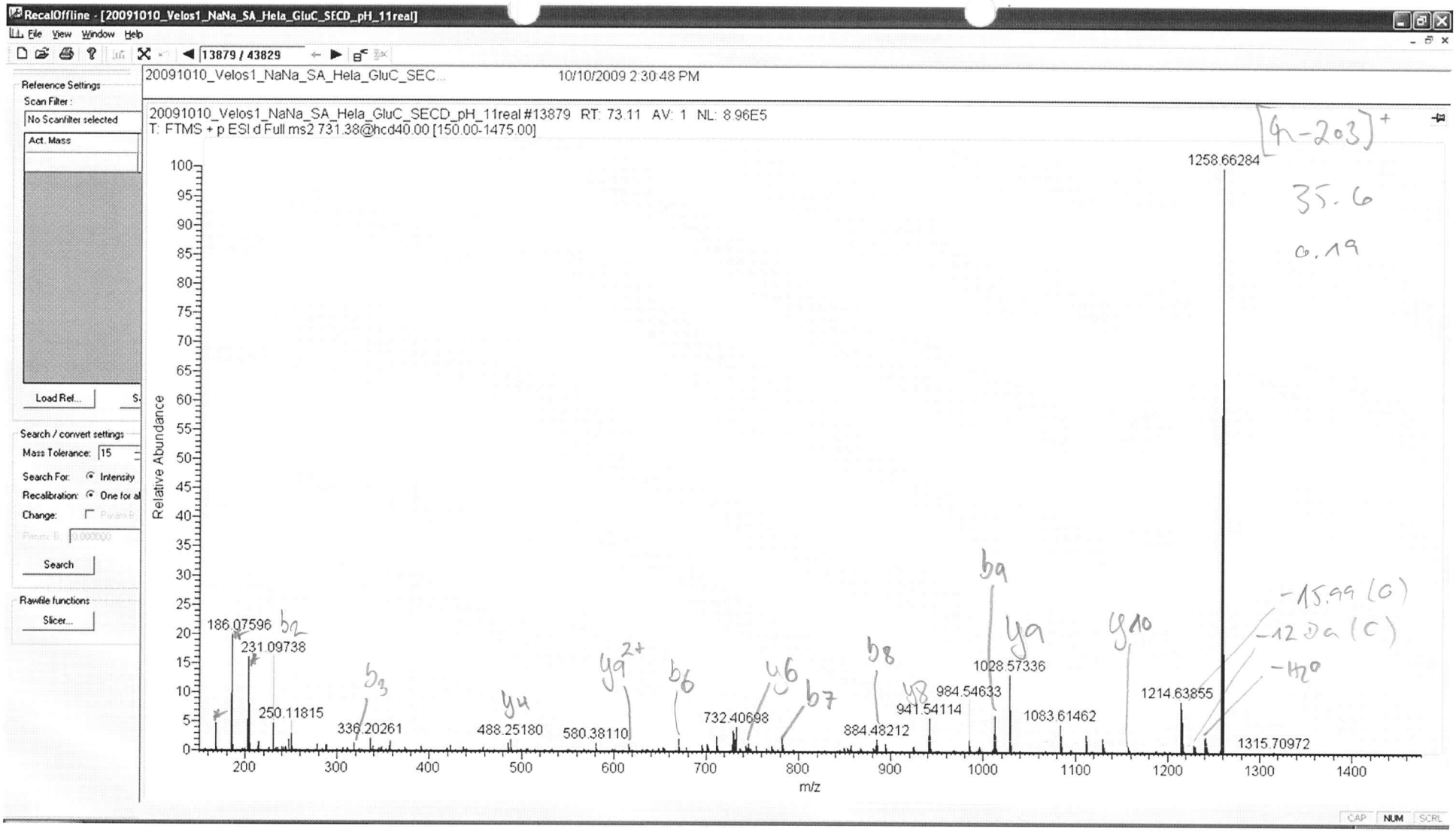
IHVSMATPVtVSME

mc



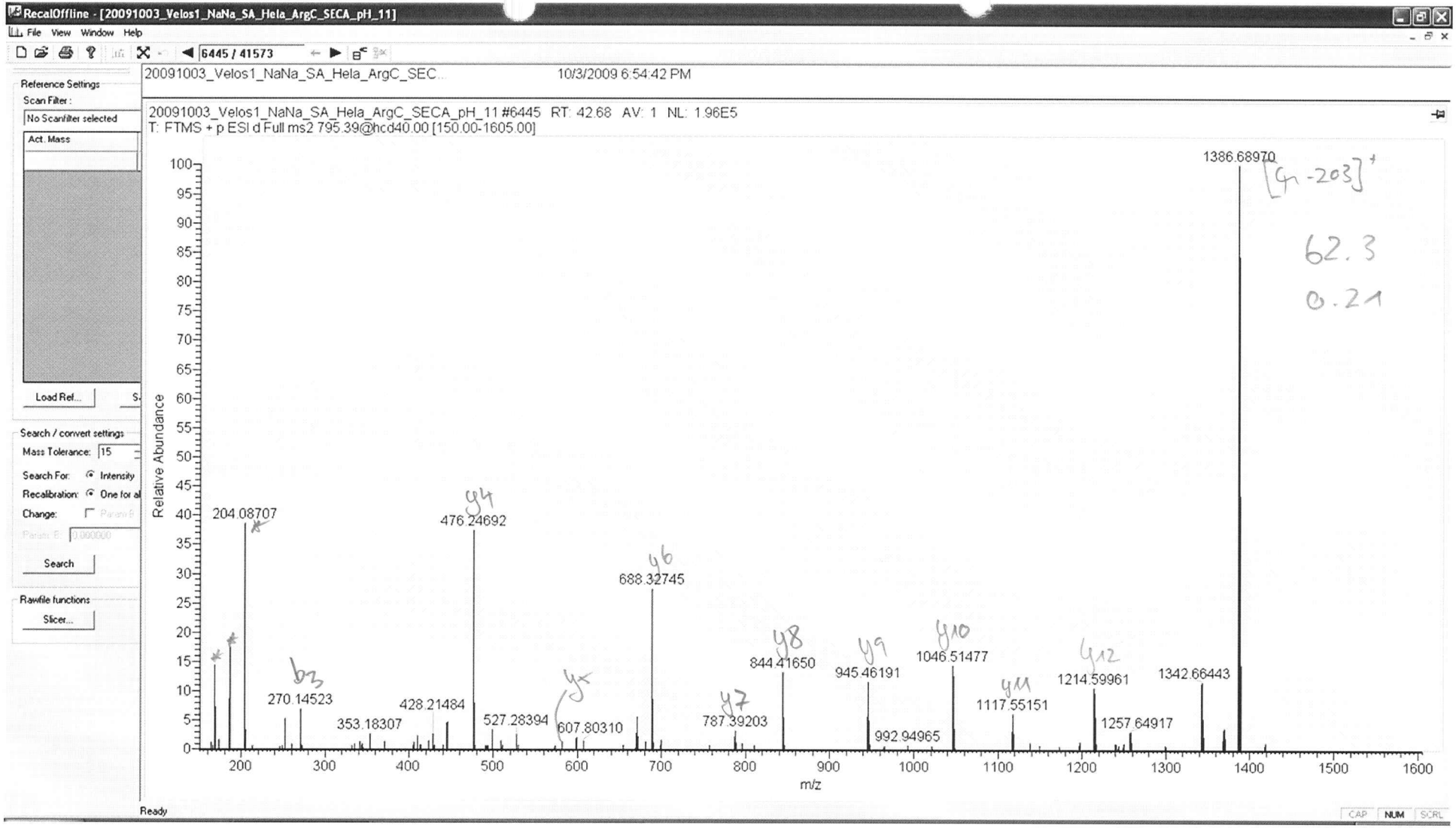
LNPLKsIVE

No phospho evidence



no site evidence

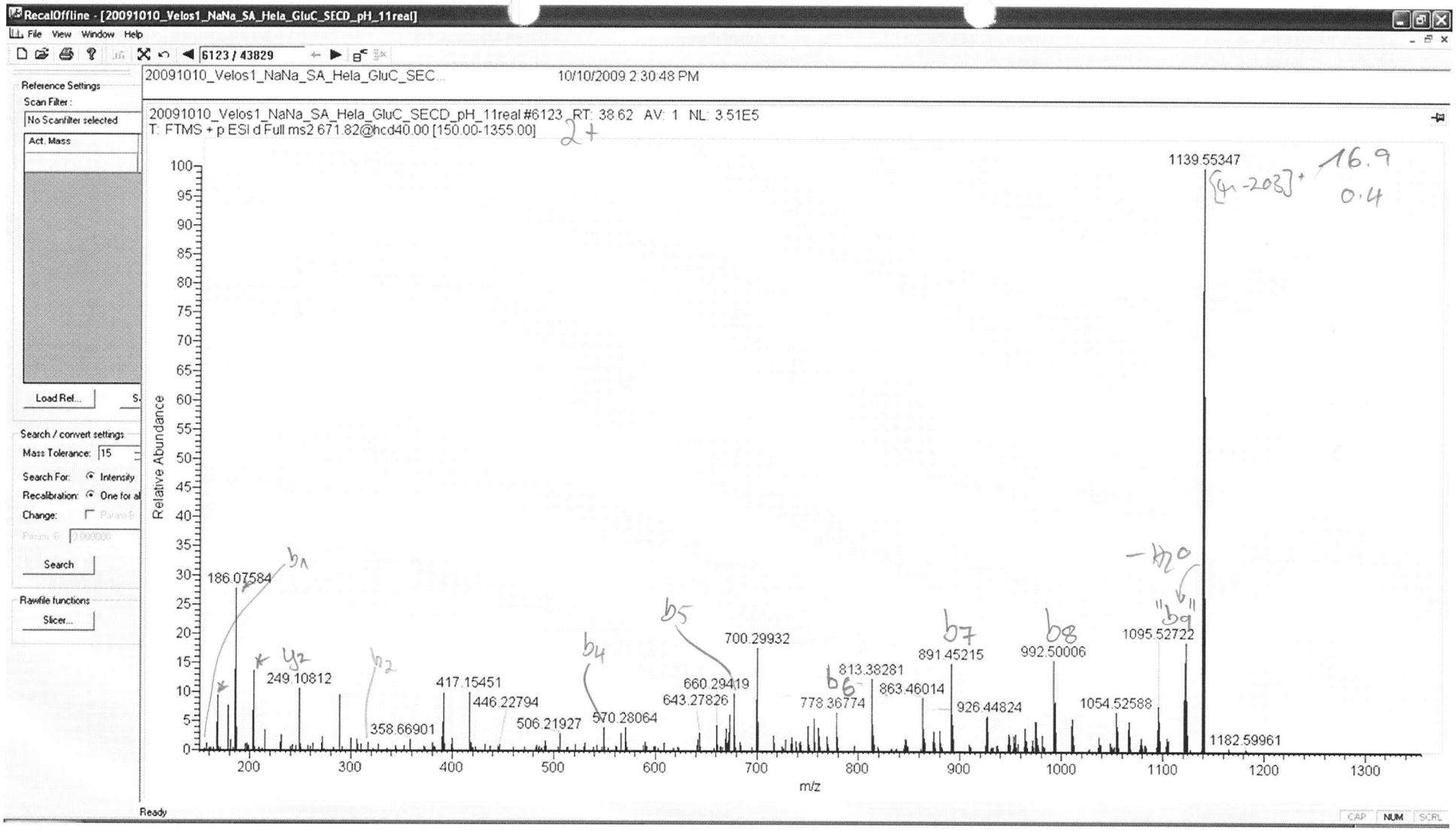
TESPVRtLQVE



no site evidence

ATPATTGVPDARtE

111

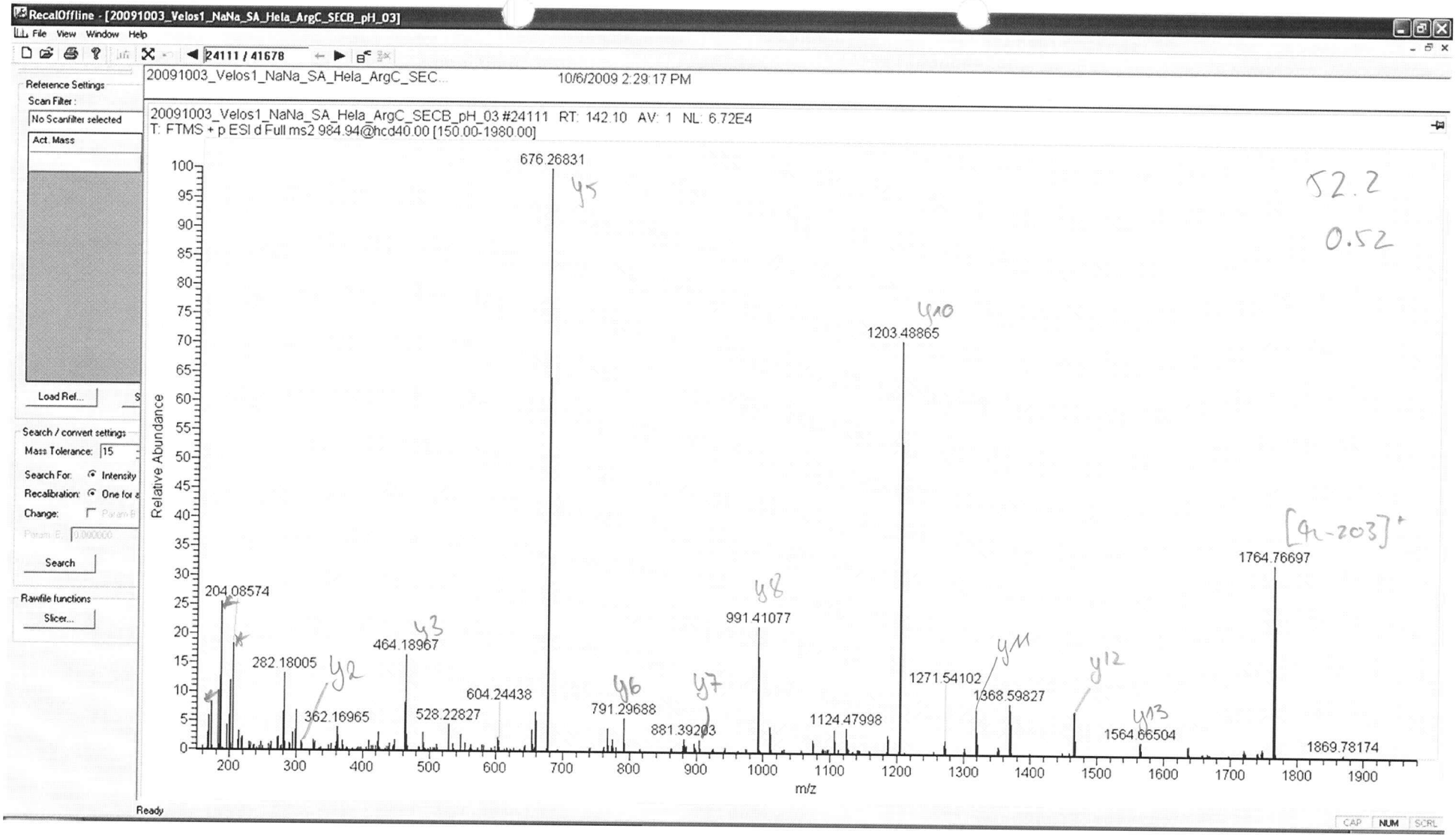


no site evidence

y2

RcTMKTLtE

b8

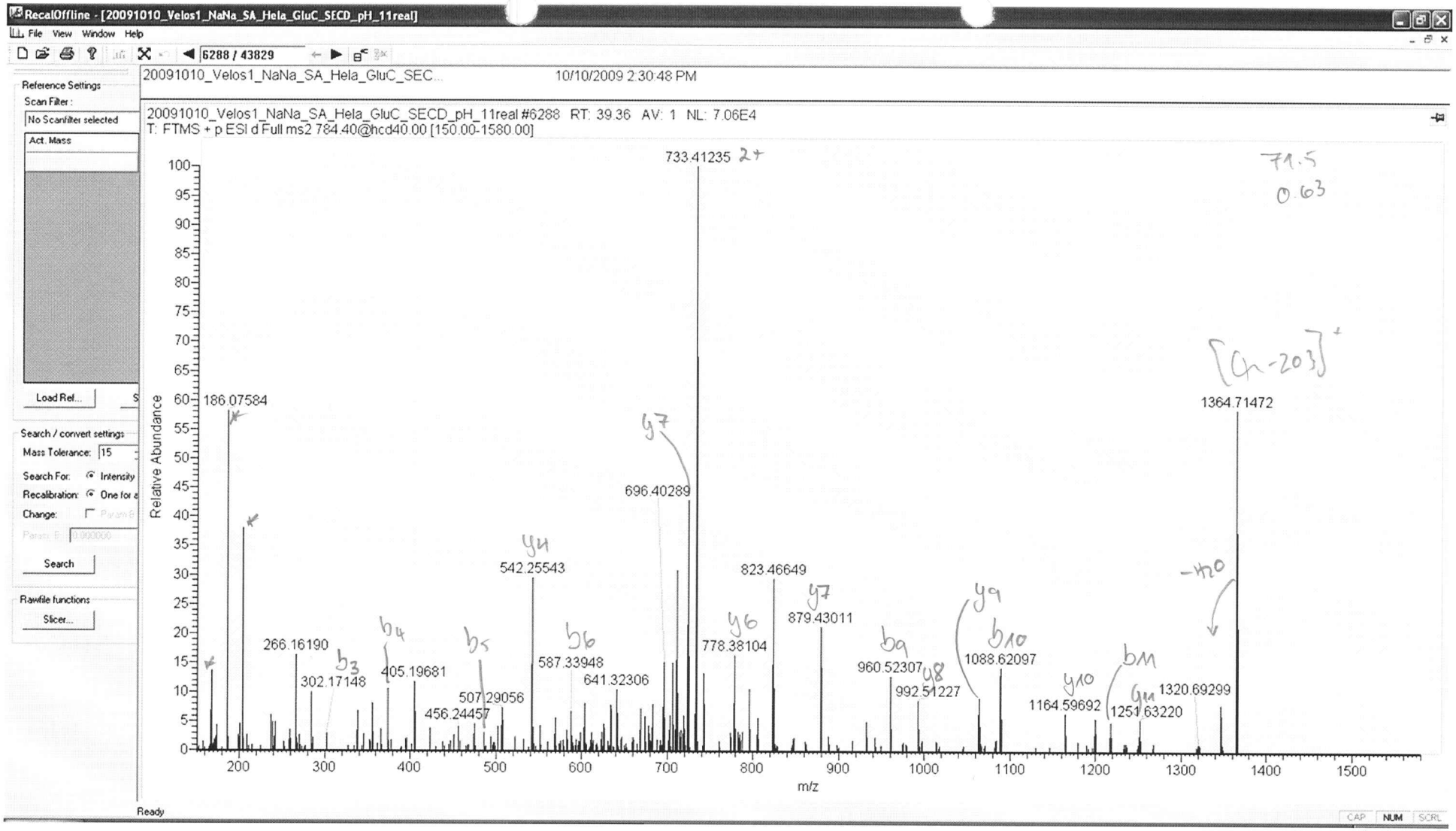


no site evidence

y10 y5 y3

VTVFDPDsLDPDRcE

116



71.5
0.63

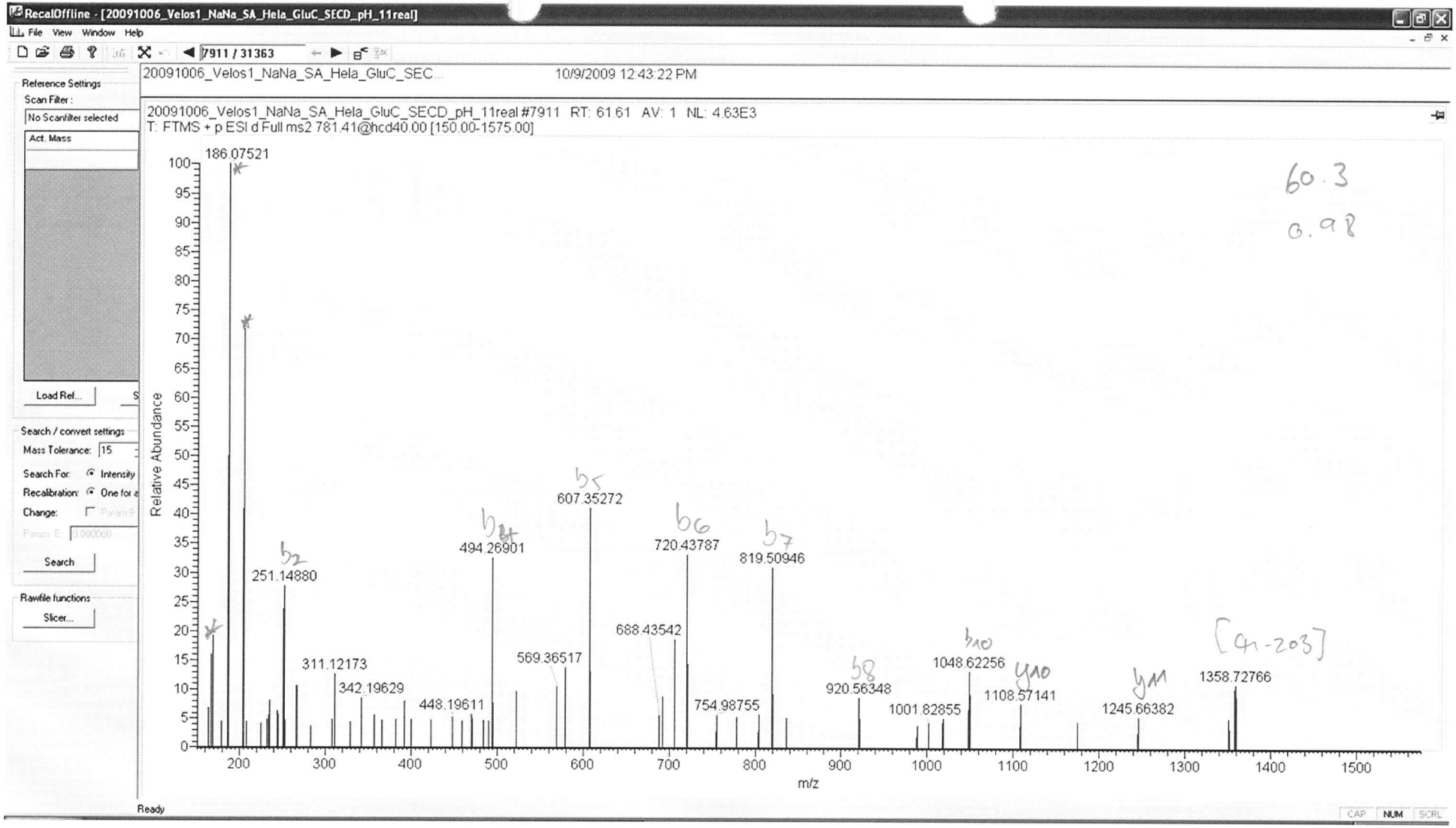
$[M-2O3]^+$

$-H_2O$

no site evidence

LSTAItHVHKEE

b_9



60.3

0.98

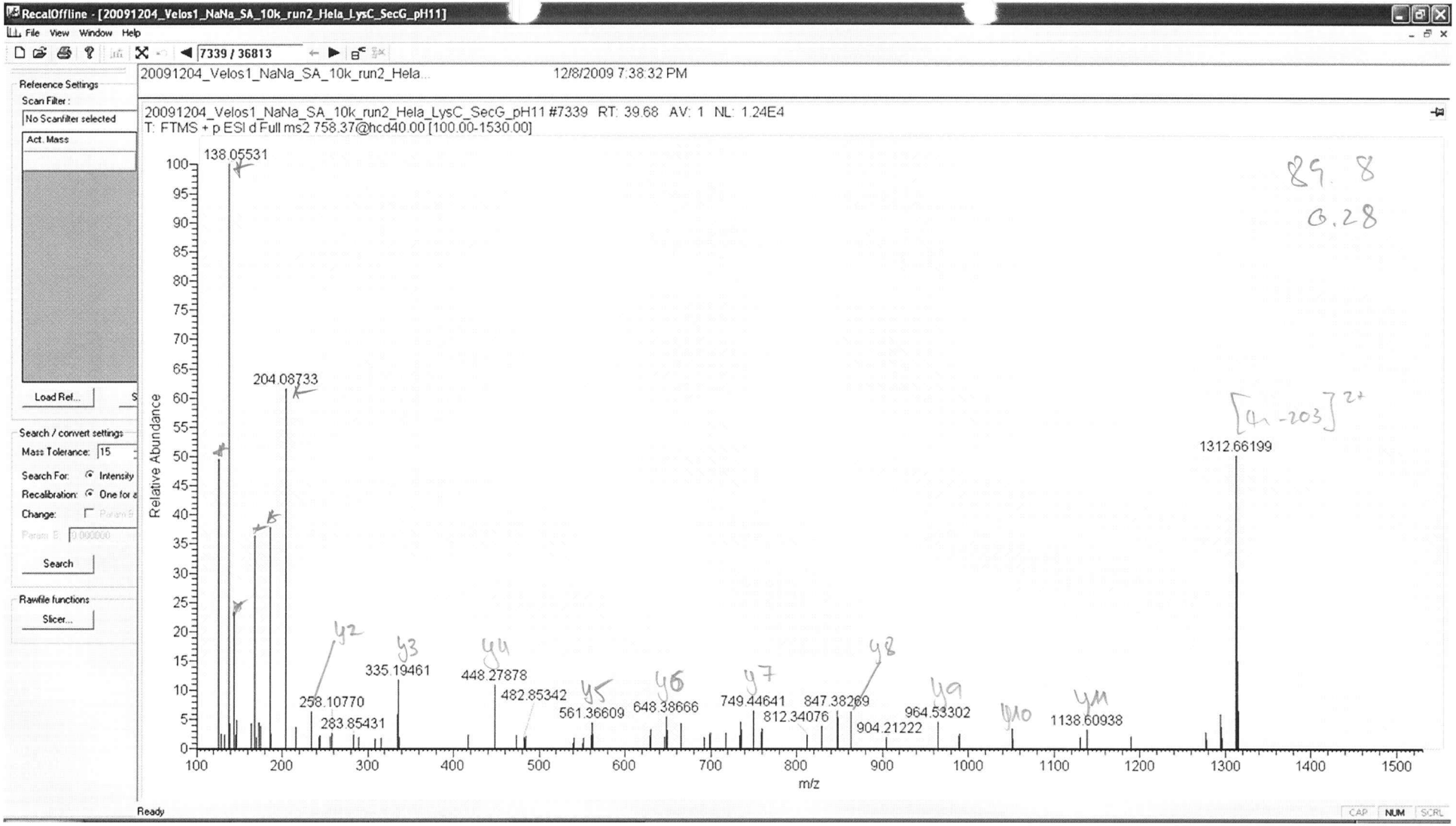
b5 b6 b7 b2 b4 b8 b10 y10 y11 [M-203]

T8

IHKDLLVtGAYE

y11 b10

11 9



89.8

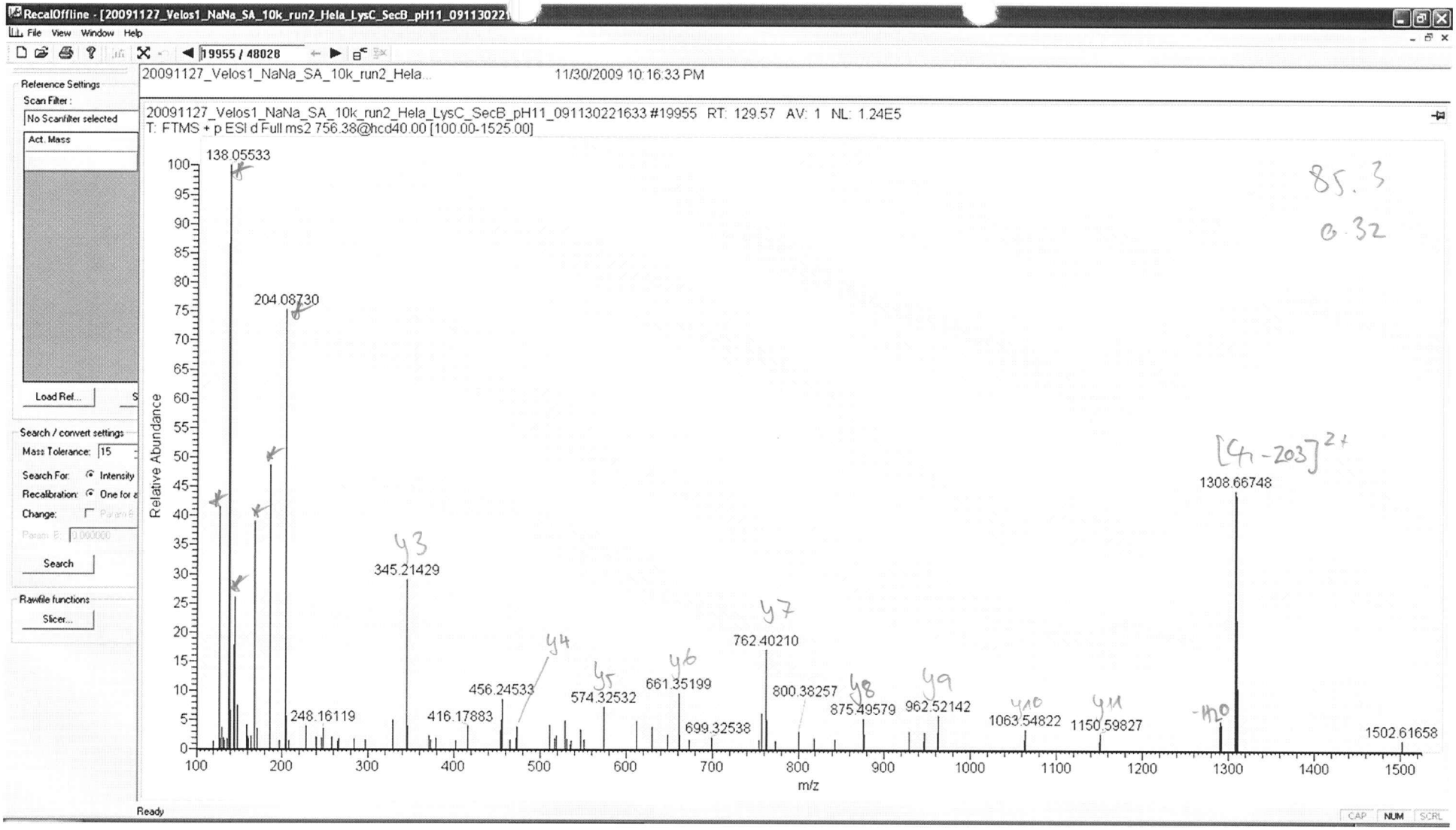
0.28

No site evidence

120

SSSSTNTSLLTsK

y4

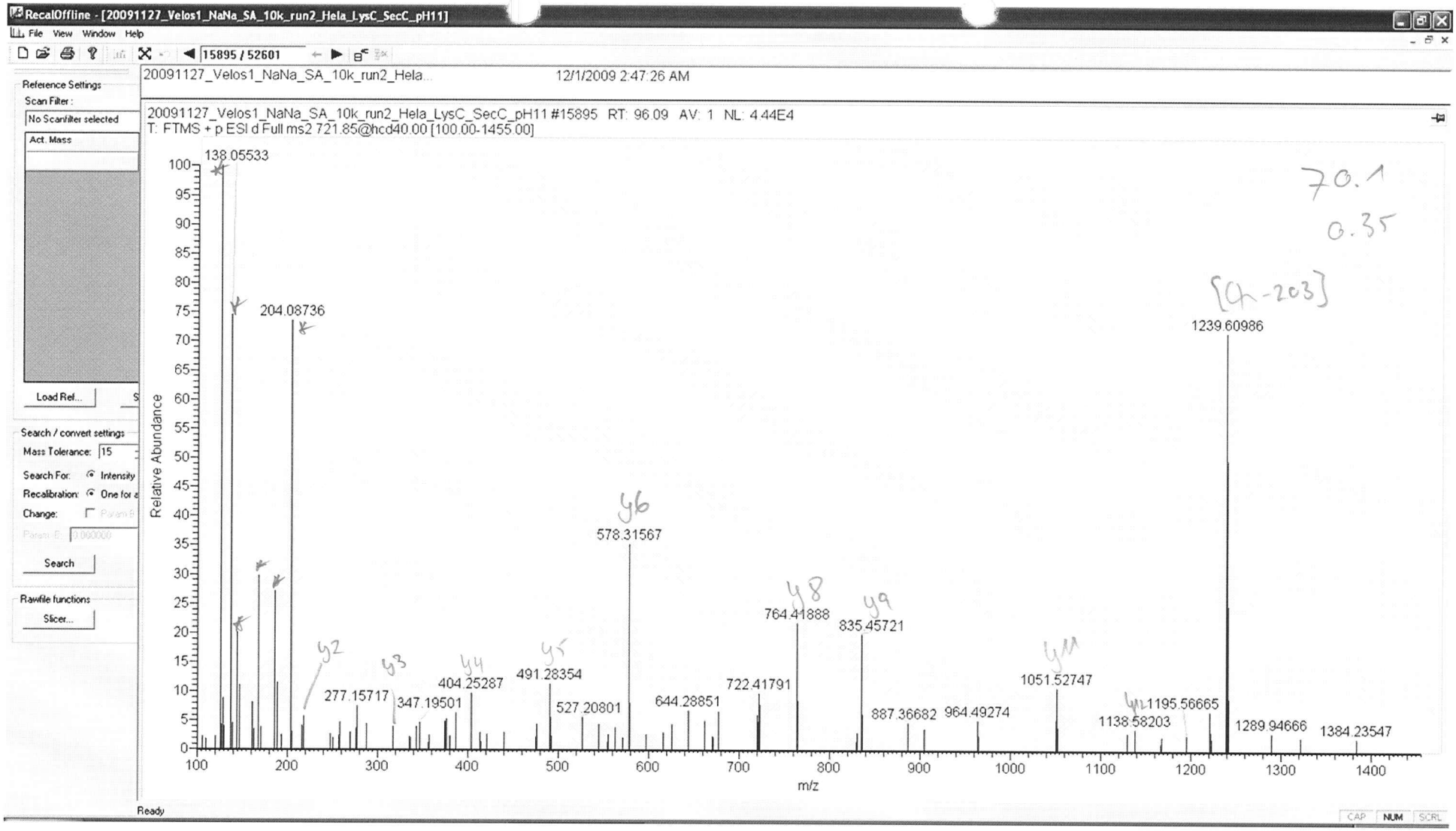


no site evidence

y11

AsSTSLTSTQPTK

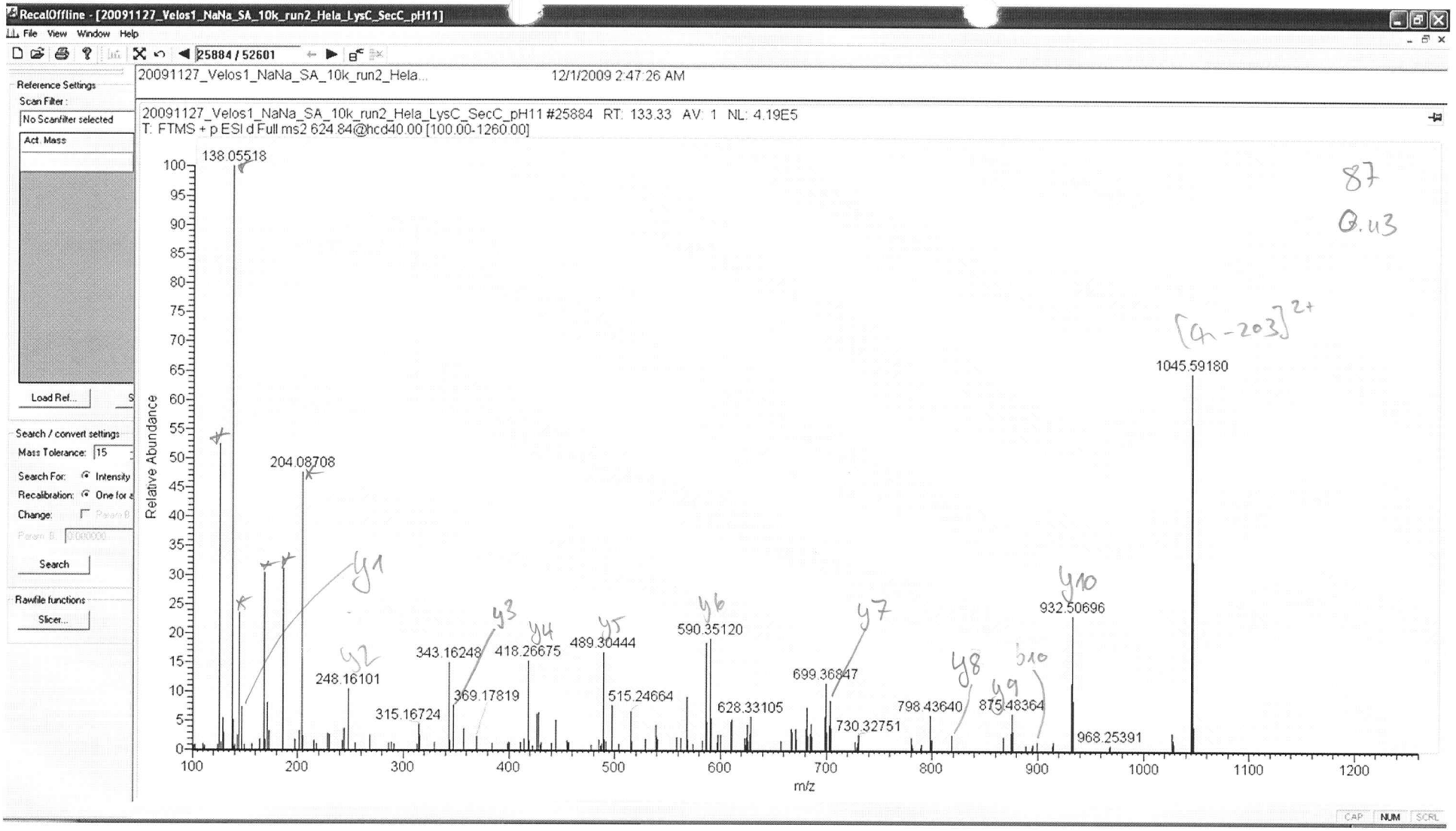
21



y6

TSSEASVSSsVAK

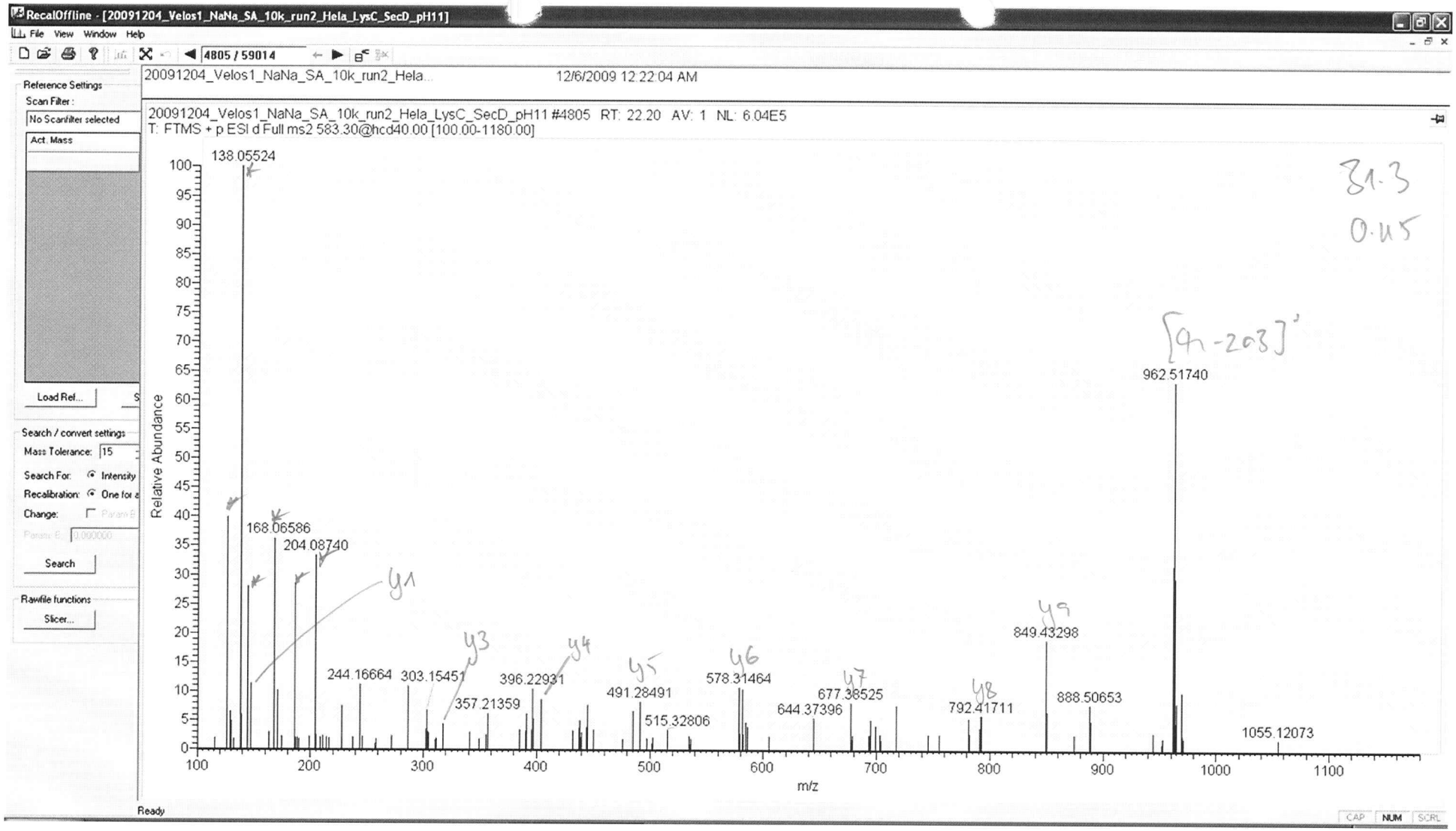
no site evidence



No glitch evidence

IGGDLTAAVtK

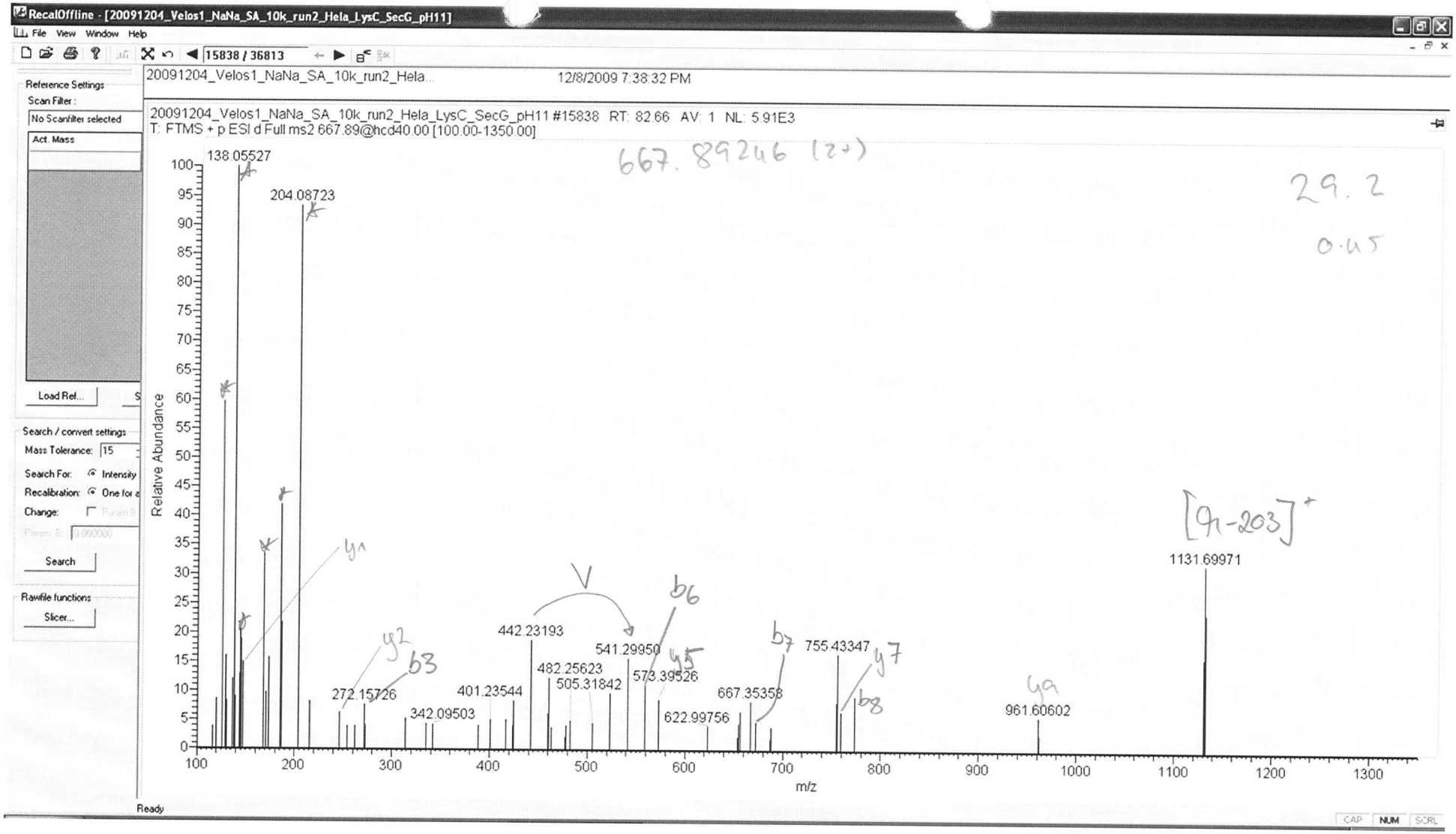
123



no 8i4 evidence

IGDVSSsAVK

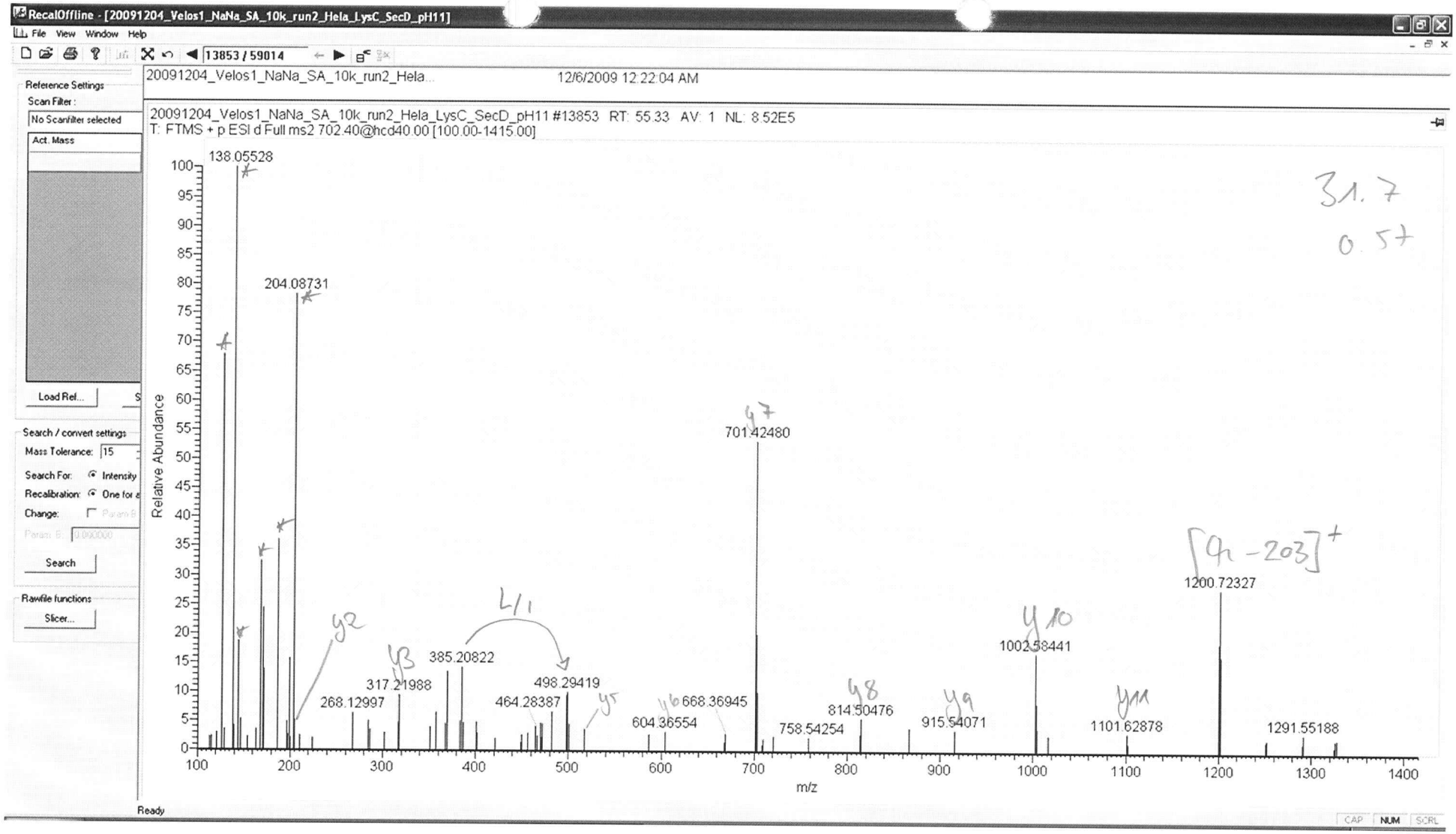
124



y9 y7 y5

VATTSVItIVK

No Site evidence



31.7

0.5+

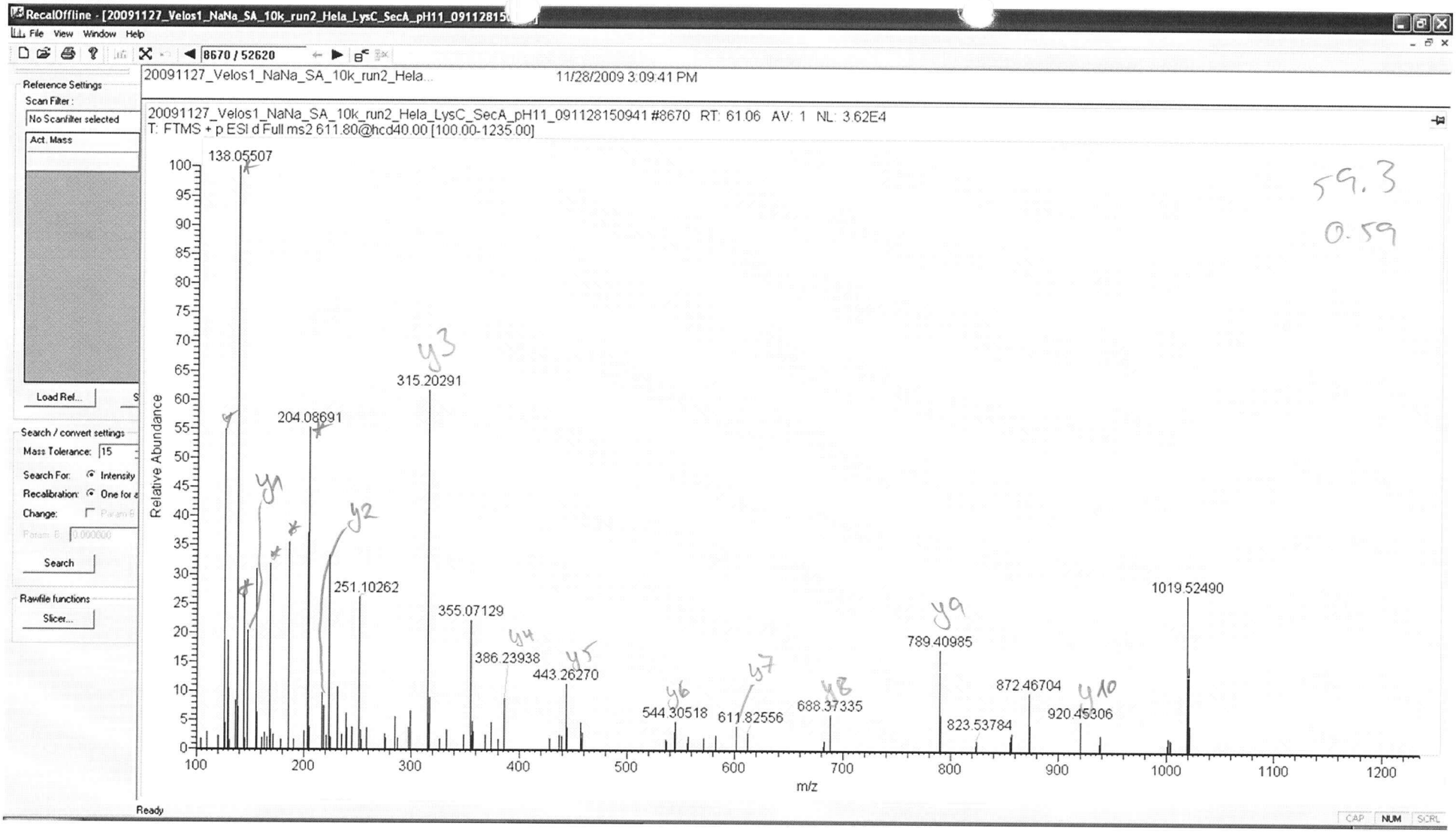
$[y_4 - 203]^+$

No Site evidence

y7

VVSTLPStVLGK

126



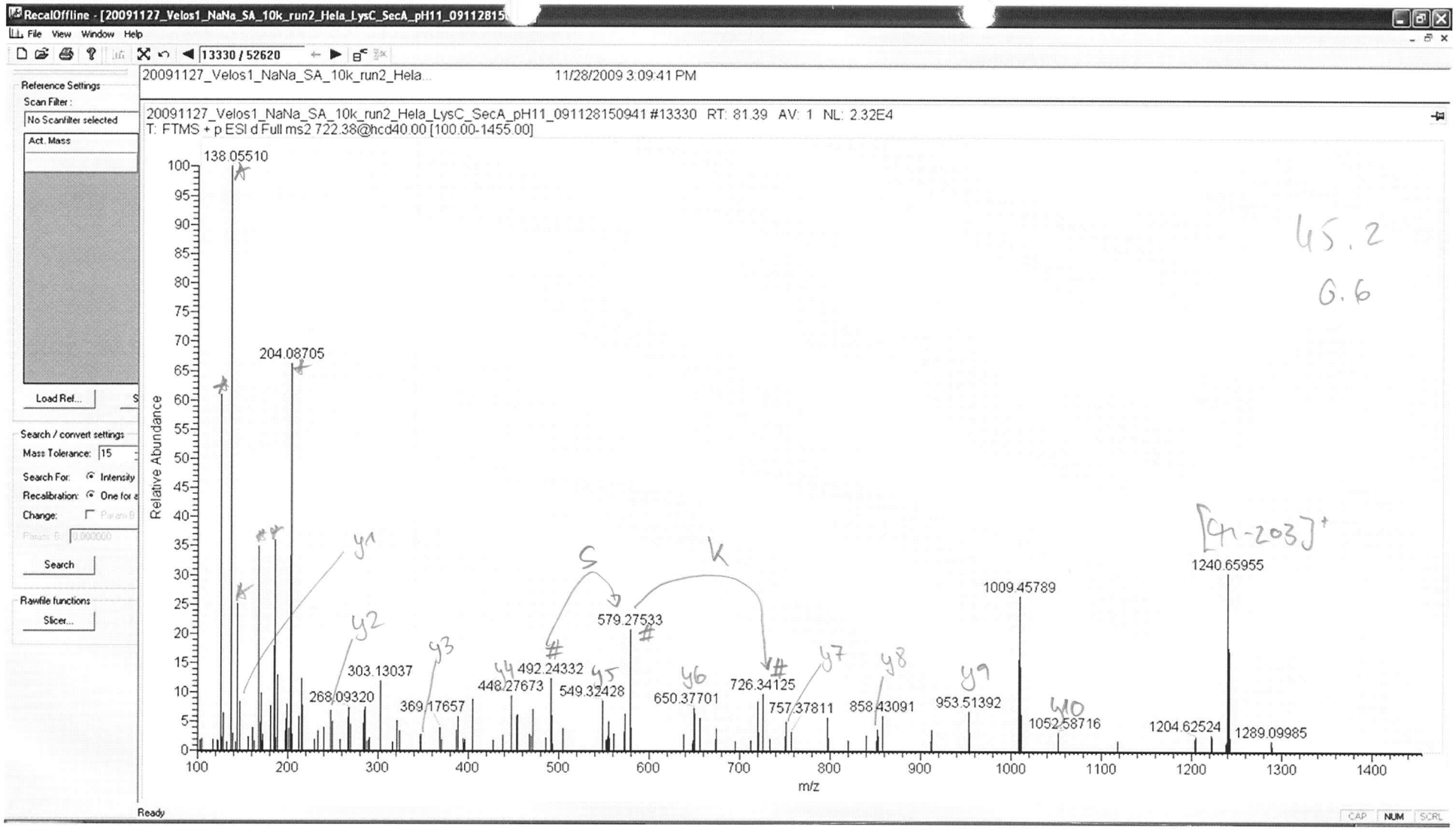
59.3

0.59

no site evidence

VMTSGtGAPAK

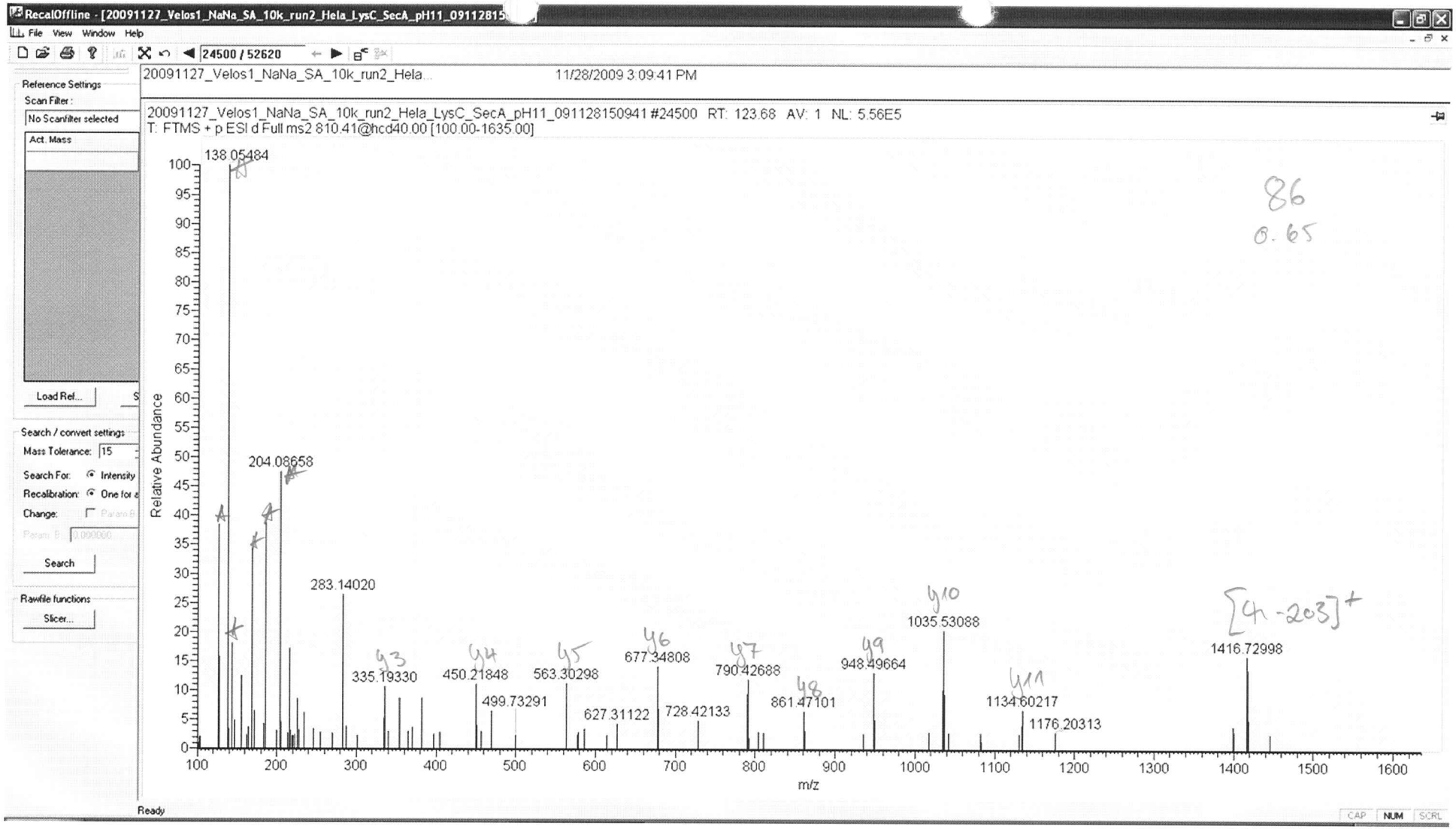
127



STVTTTTTTVtK

No Site evidence

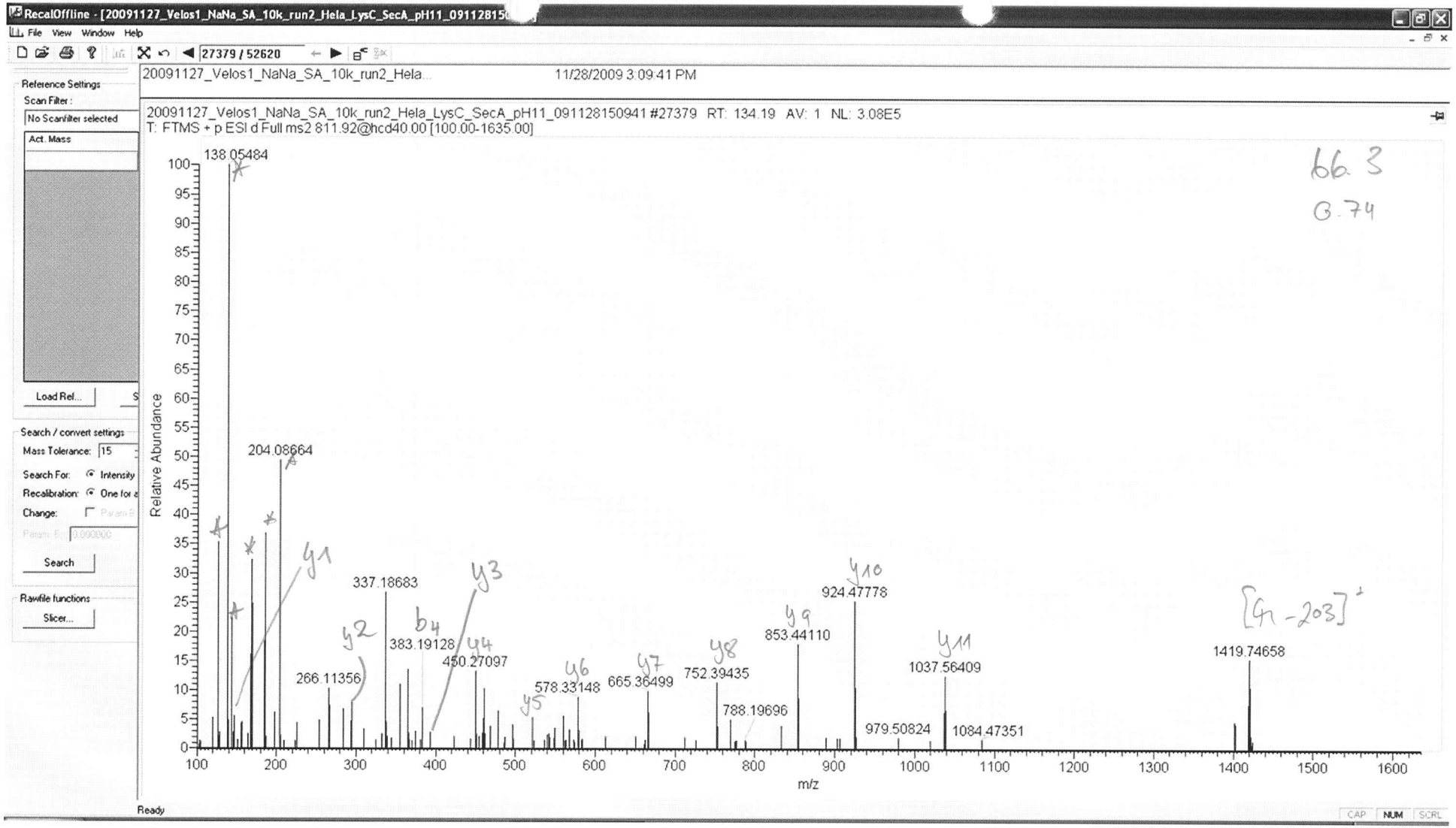
Chimeric Spectra: Second ion series of Co-isolated precursor 128



no site evidence

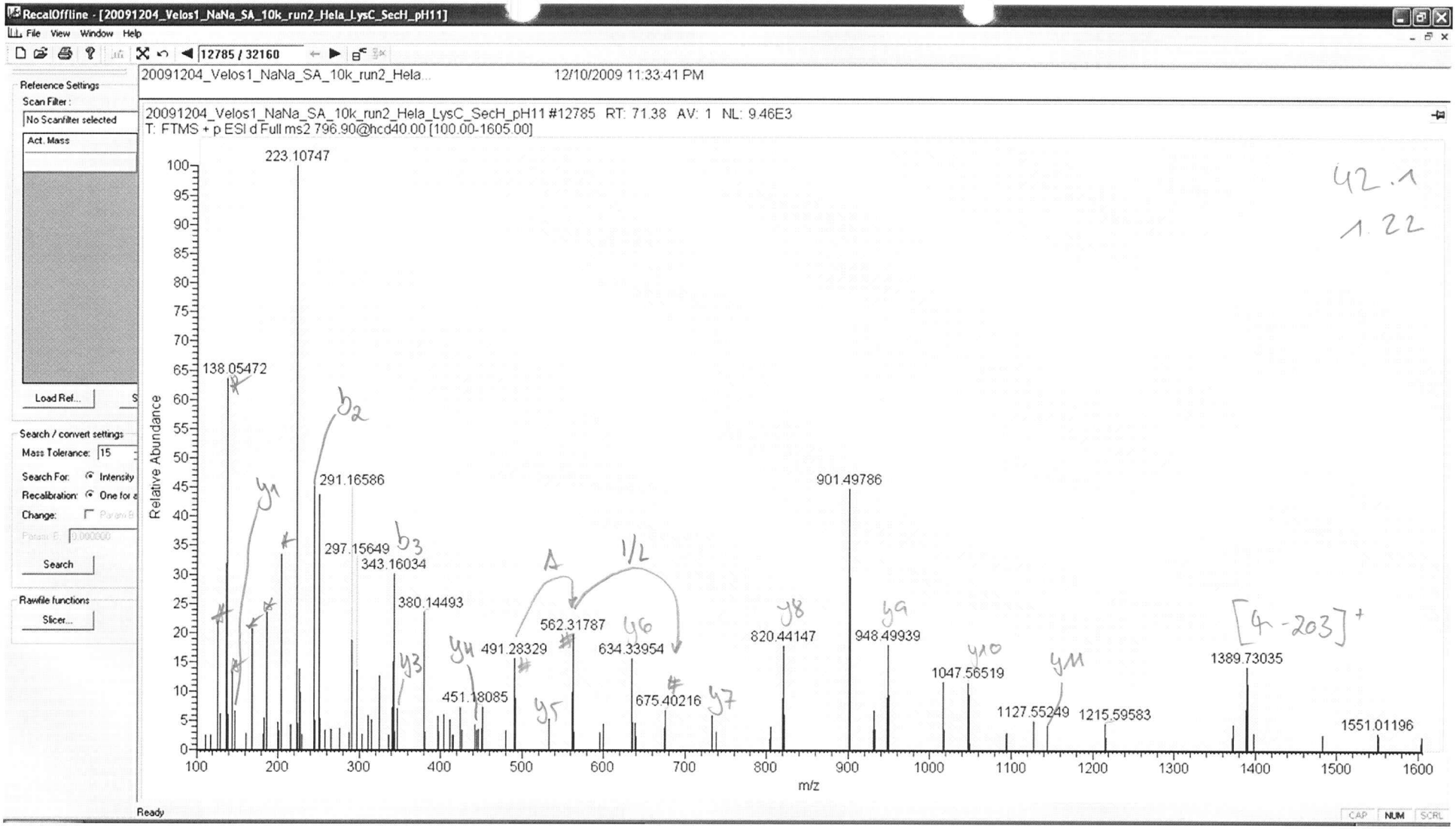
GPQVSSALNLDTsK

129



no site evidence

EGPVLATSsGAGVFK



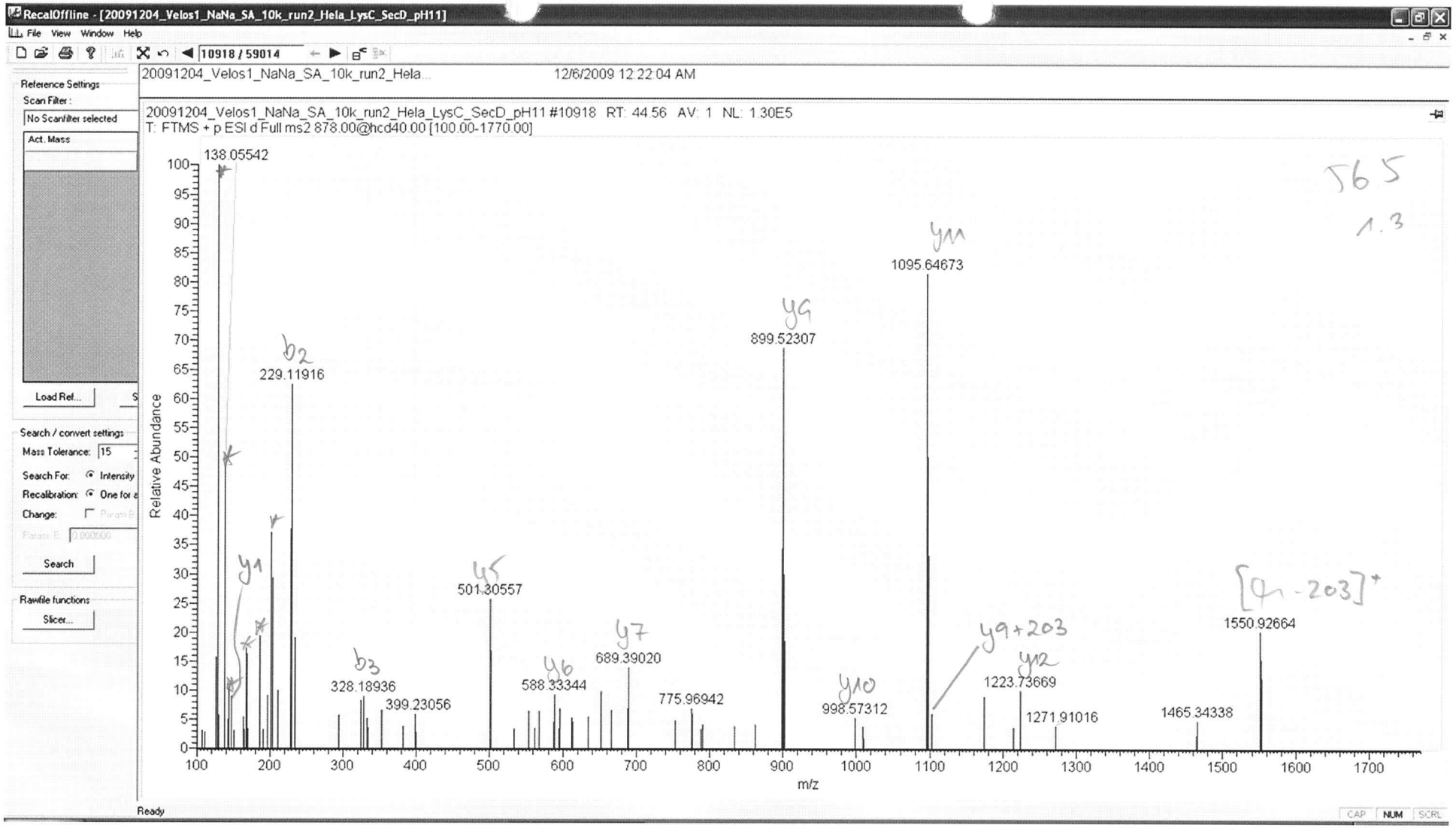
42.1
1.22

No site evidence

ENVVQSVTsVAEK

chimeric spectrum: 2nd ion series from co-isolated precursor

131



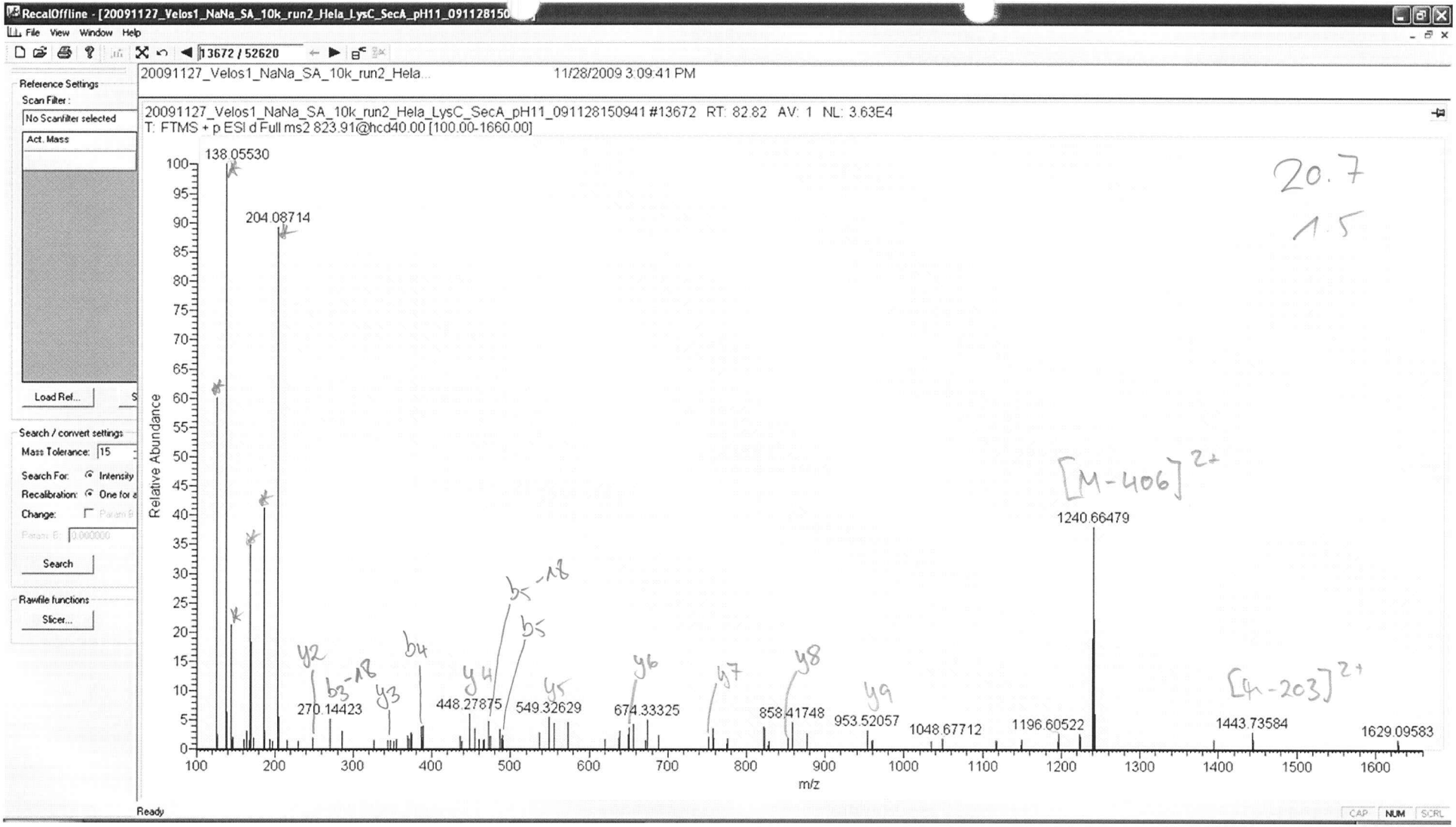
T65

1.3

y11 y9 y5

EVVKPVPITSPAVsK

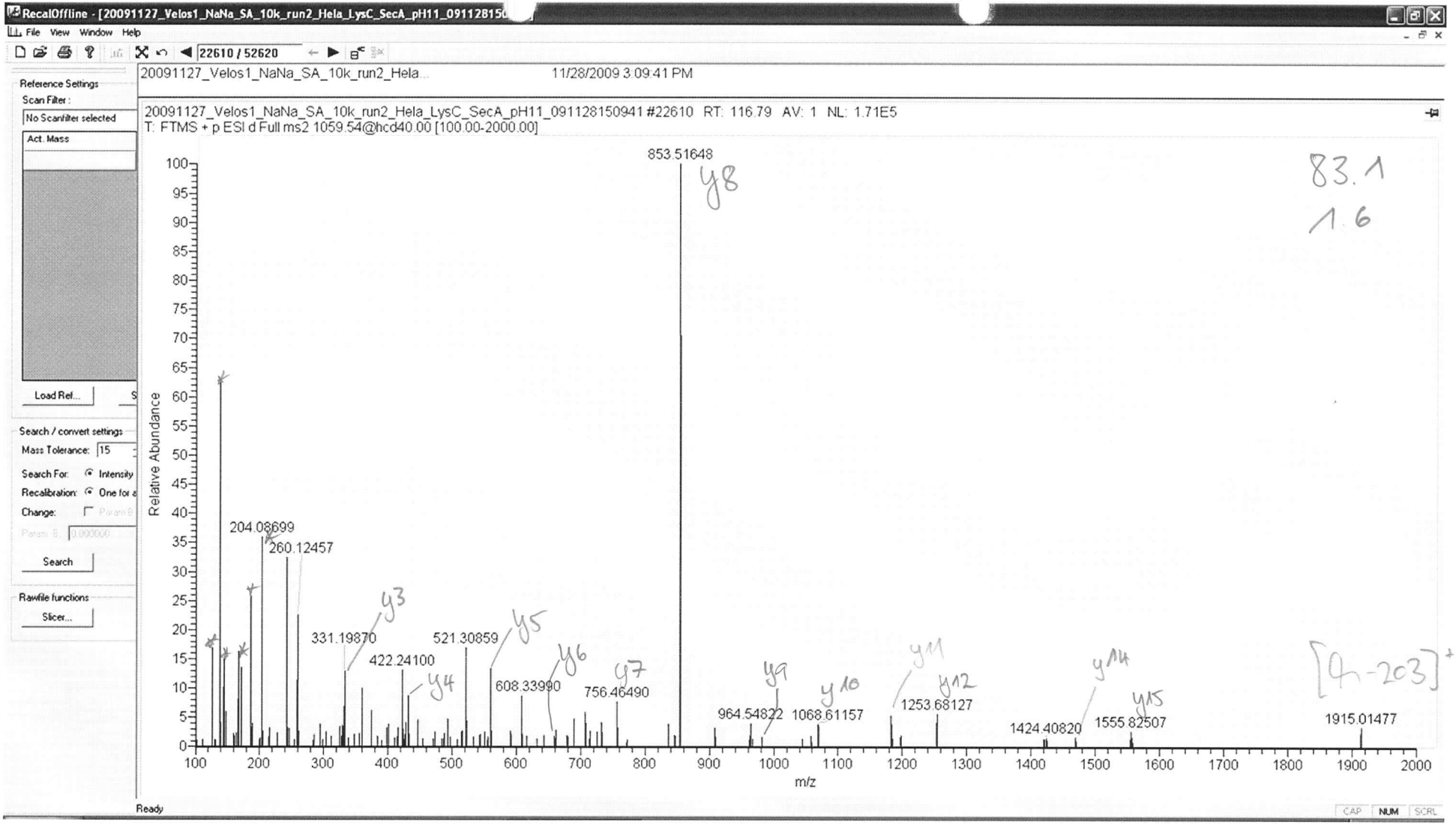
T9 or S10



no site evidence

STVTTTTTtVtK

133

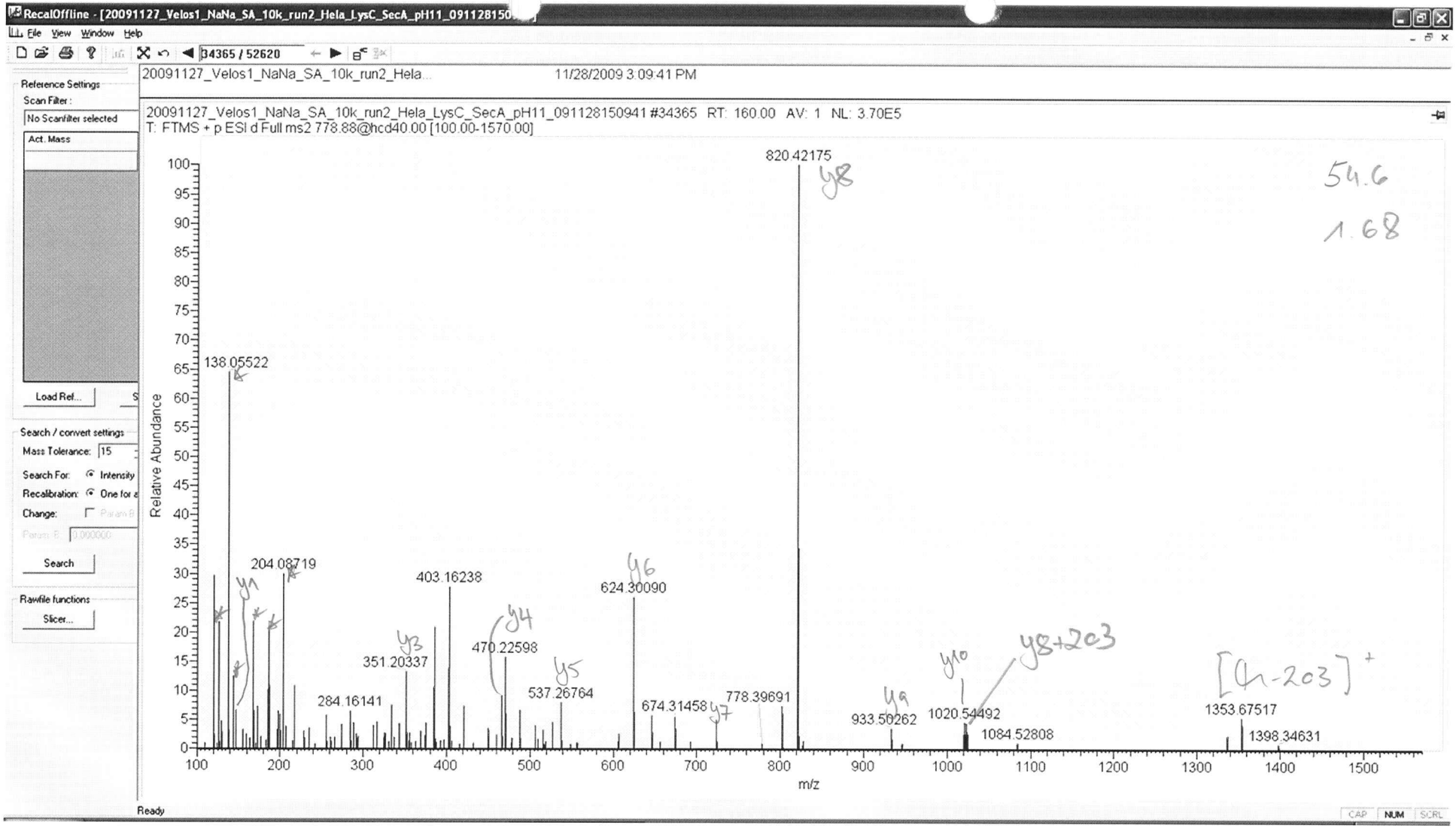


no site evidence

y8

TSAVSSQANSQPPVQVsVK

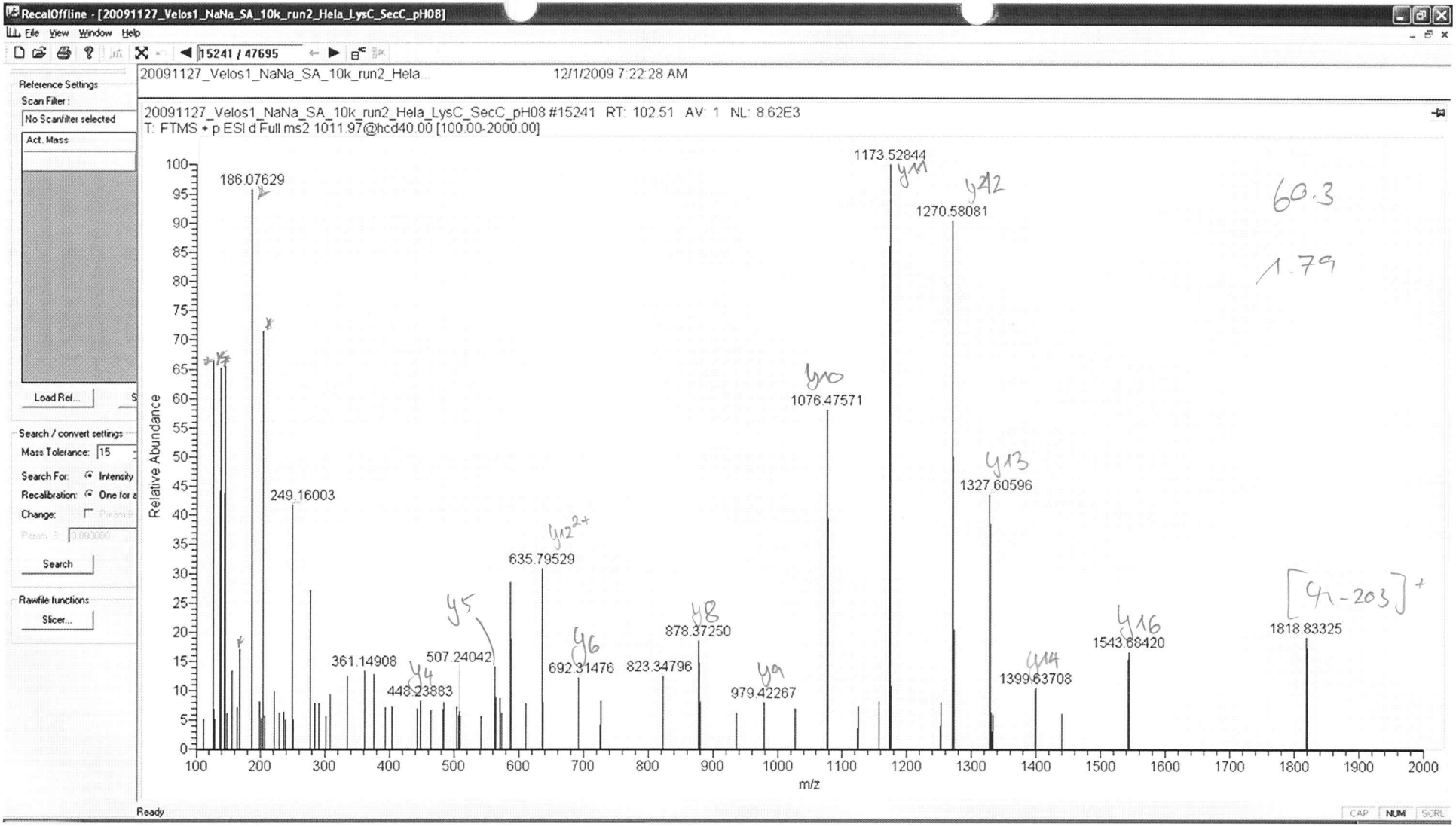
134



y8

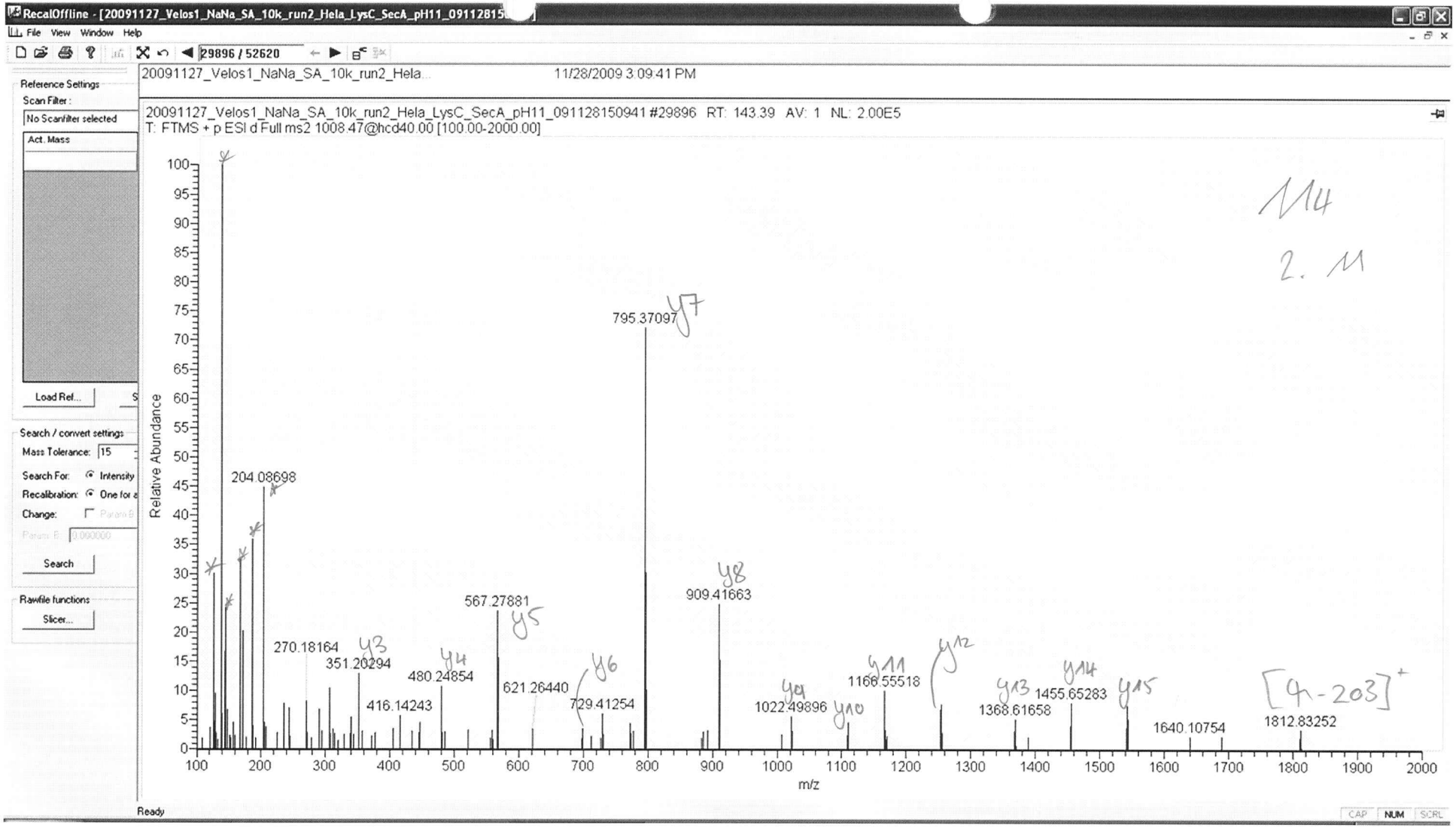
S8

EGFSIPVsADGFK



no site evidence

LYGsAGPPPTGEEDTAEK



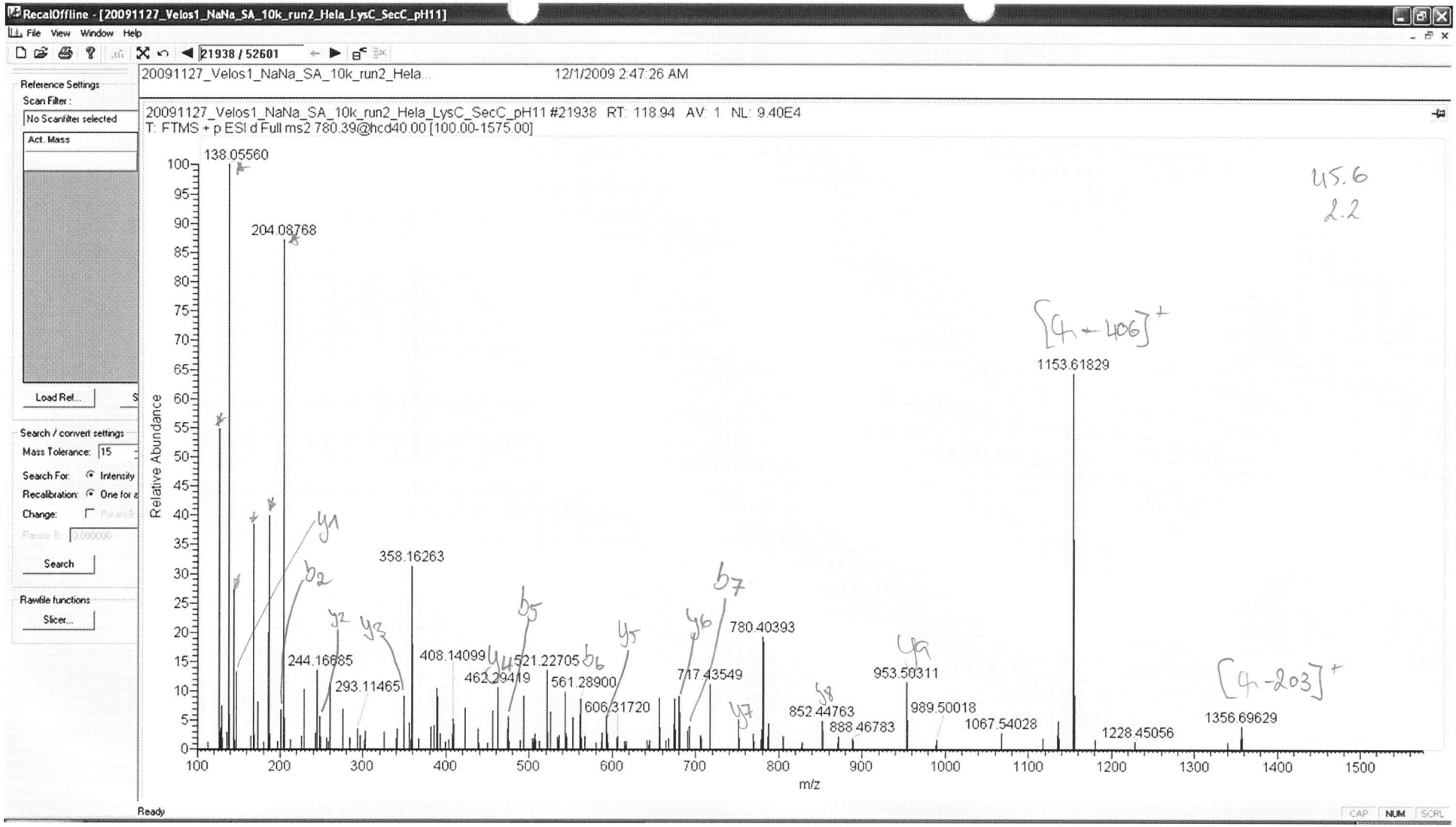
114

2. 11

y12 y7

IGVSSDSGSINPMsEGFK

No site evidence



45.6
2.2

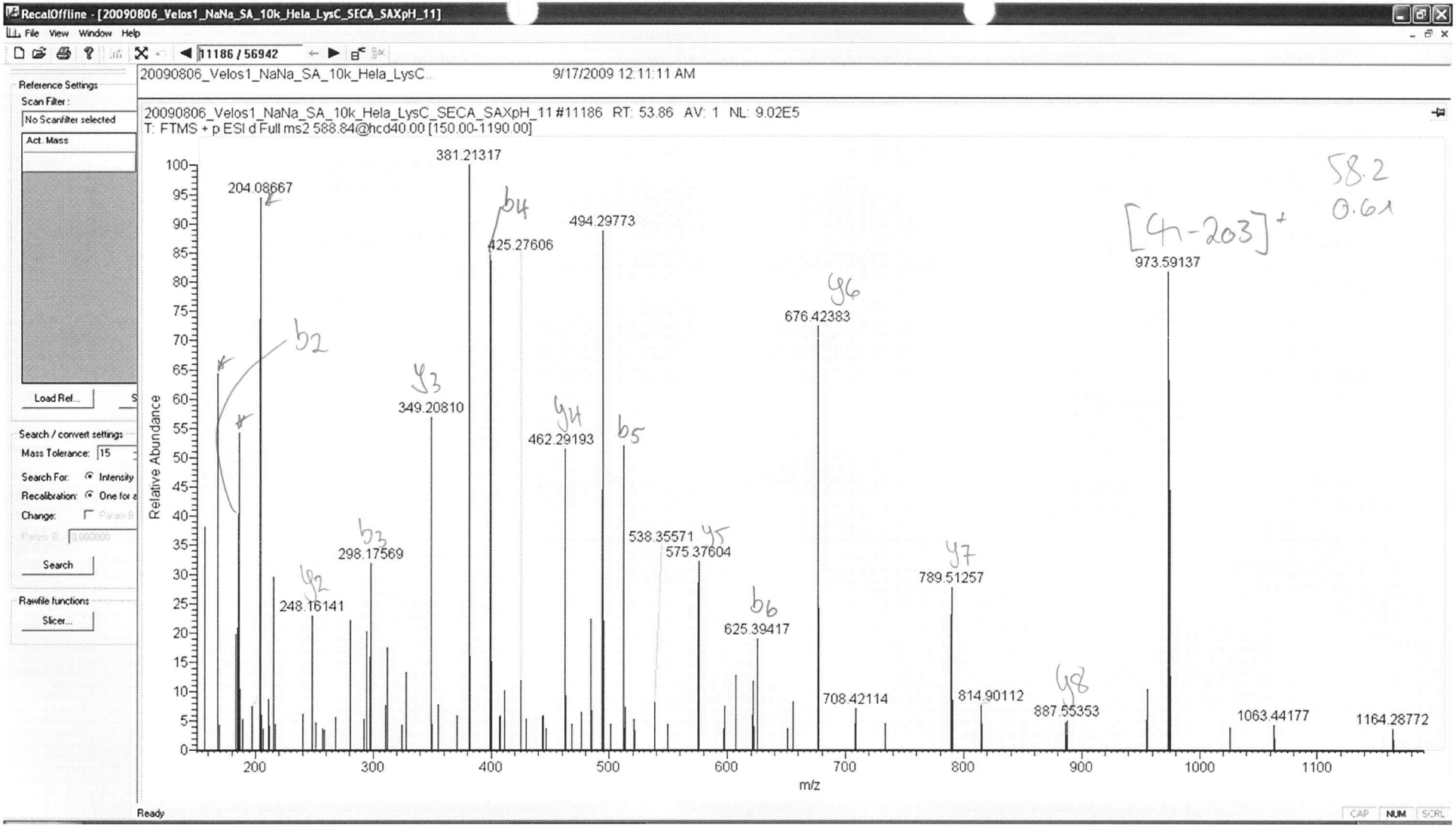
[4-406]+

[4-203]+

No site evidence

TVTTASMIttK

138



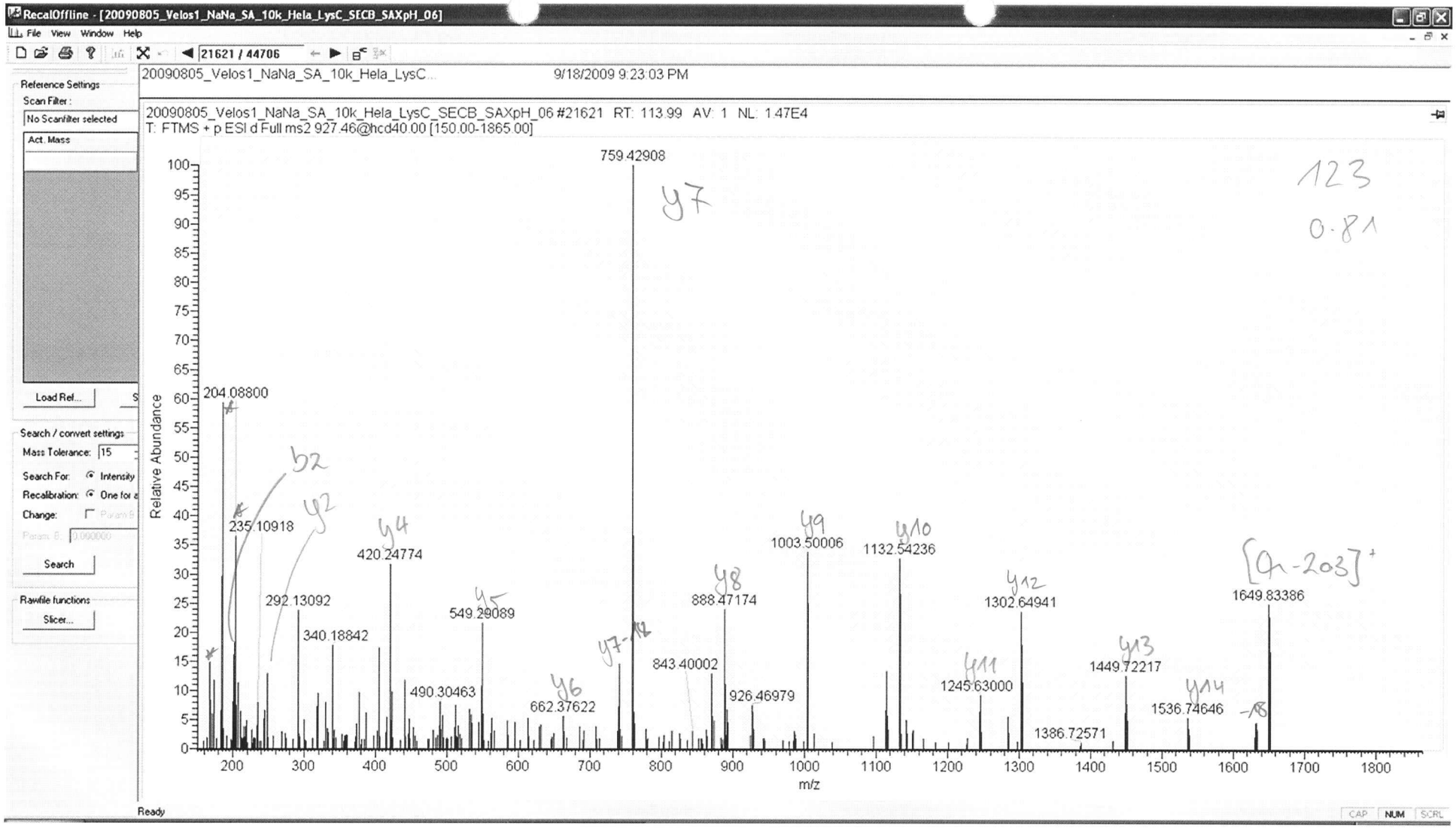
58.2
0.61

[4-203]+

No site evidence

SPITIITtK

139

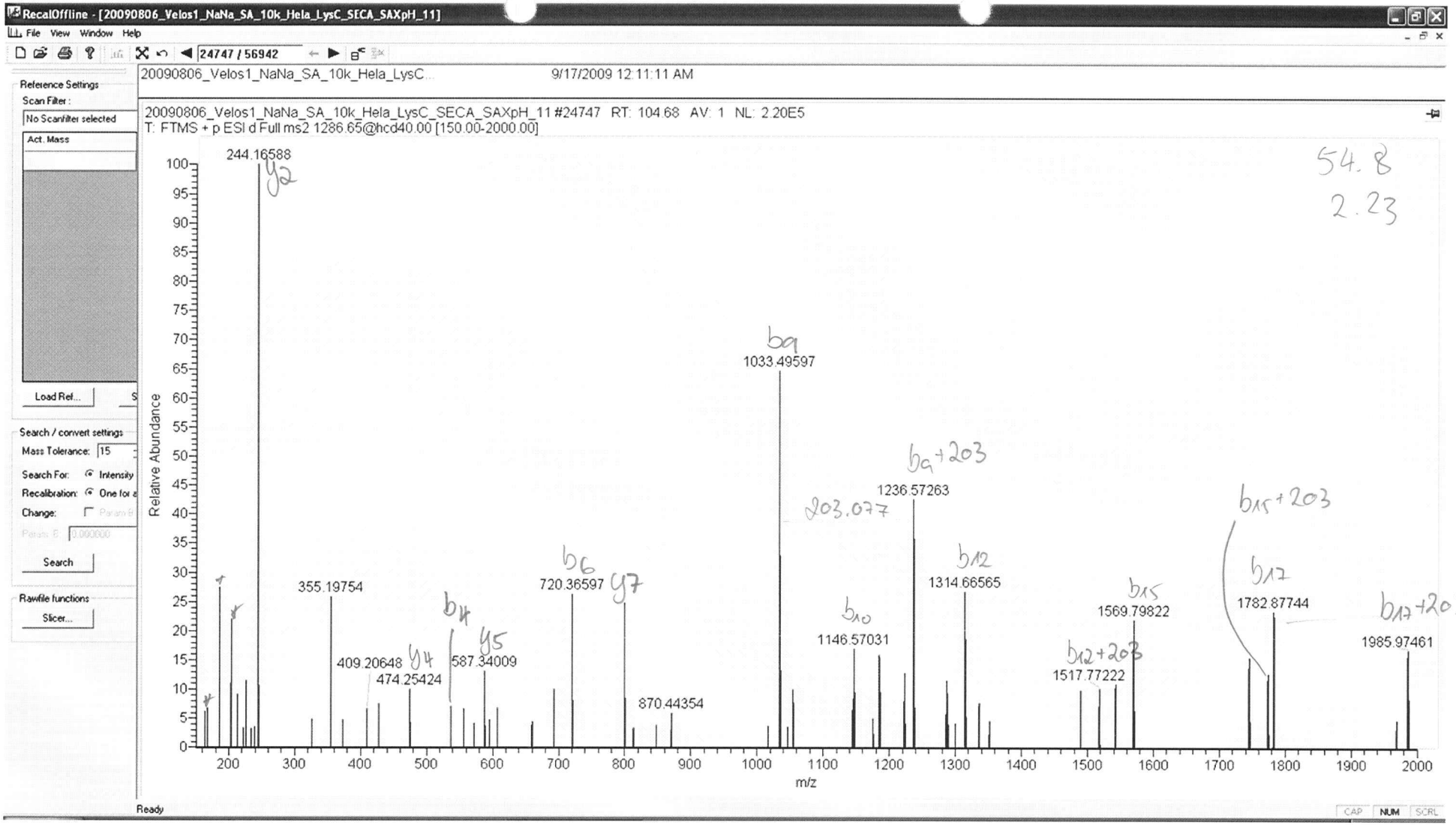


y7 y4 y2

LSFGLEDEPLETAtK

no site evidence

1 1 0



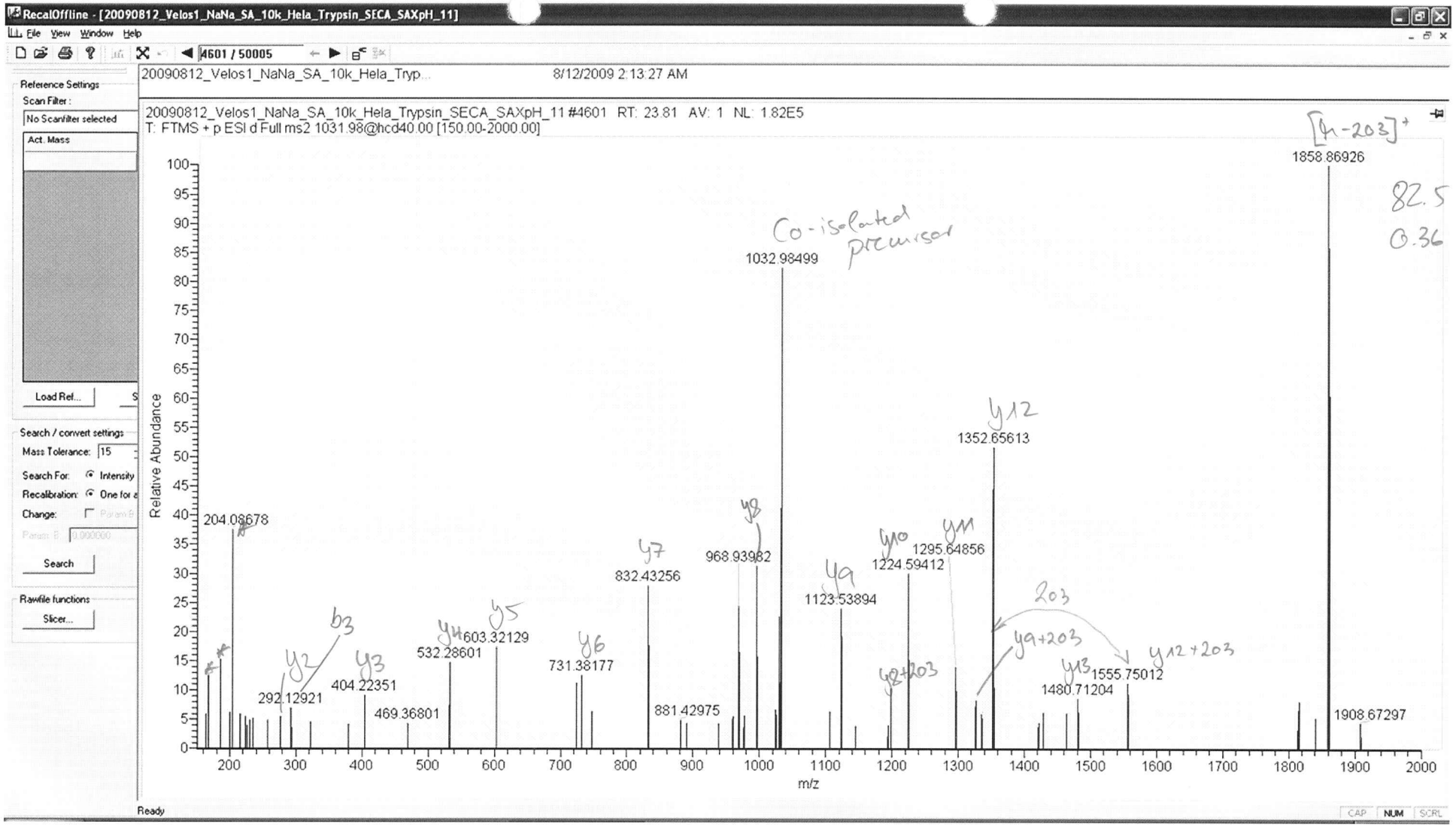
54.8

2.23

YRSEALPtDLPAPSAPDLTEPK

T8

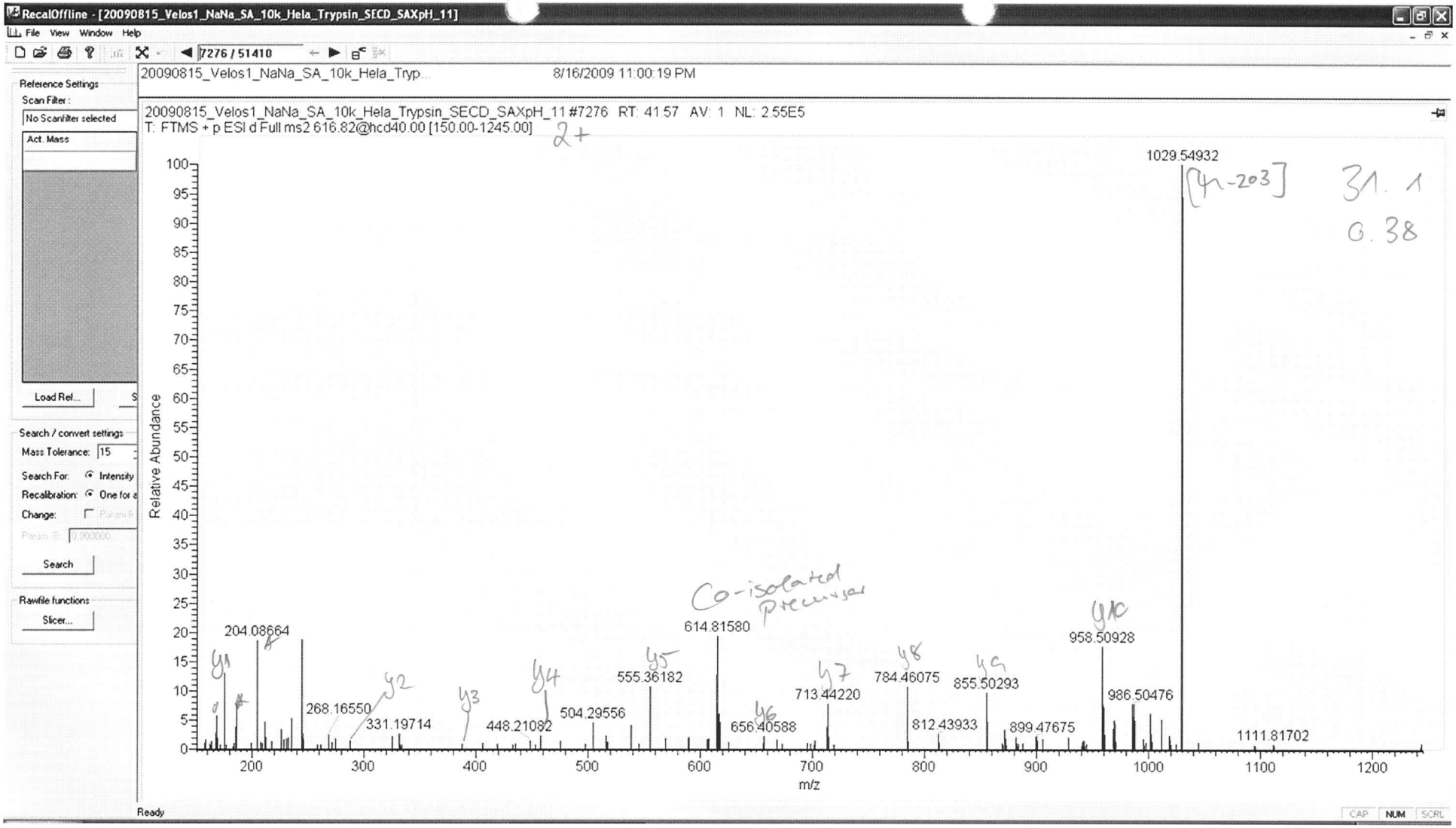
141



y12 y9 y8 y7

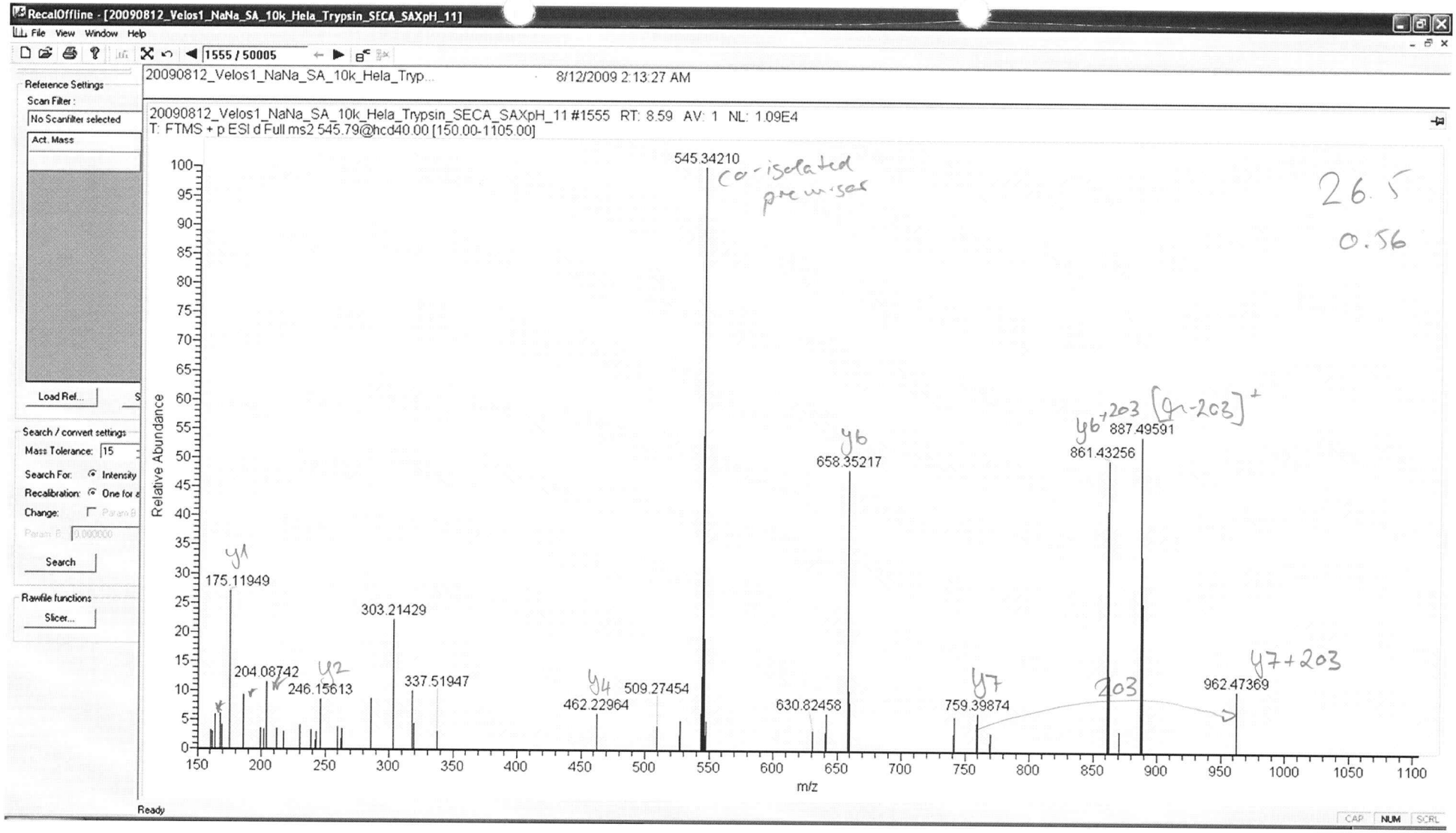
AGYSQGATQYTQAQQtR

TM or T16



T6

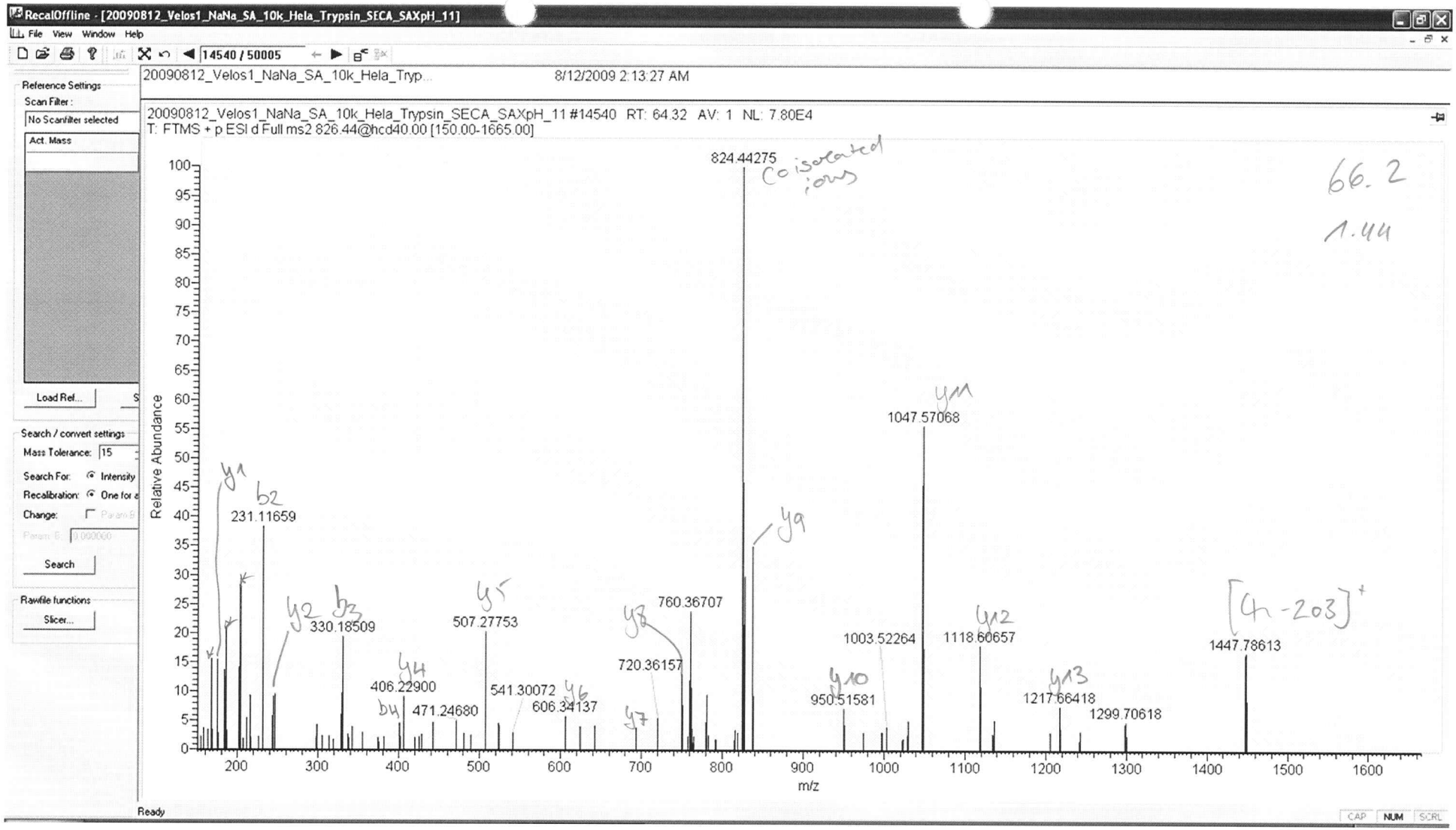
ACAAGtPAVIR



y6

KTPVsEAR

144

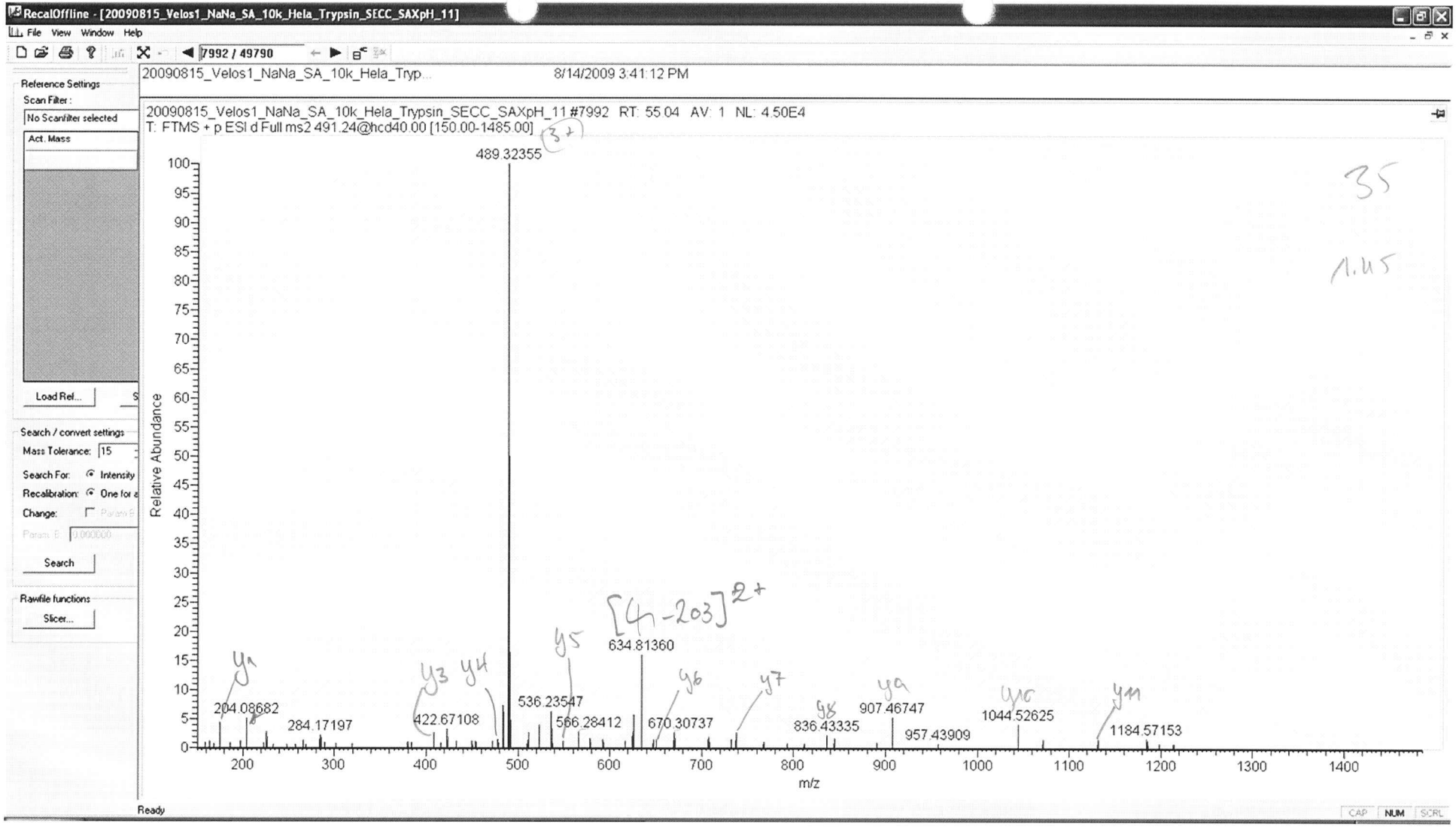


no site evidence

y11 y8 y5

VMVAPISGSVTTGtK

1 of 5



35

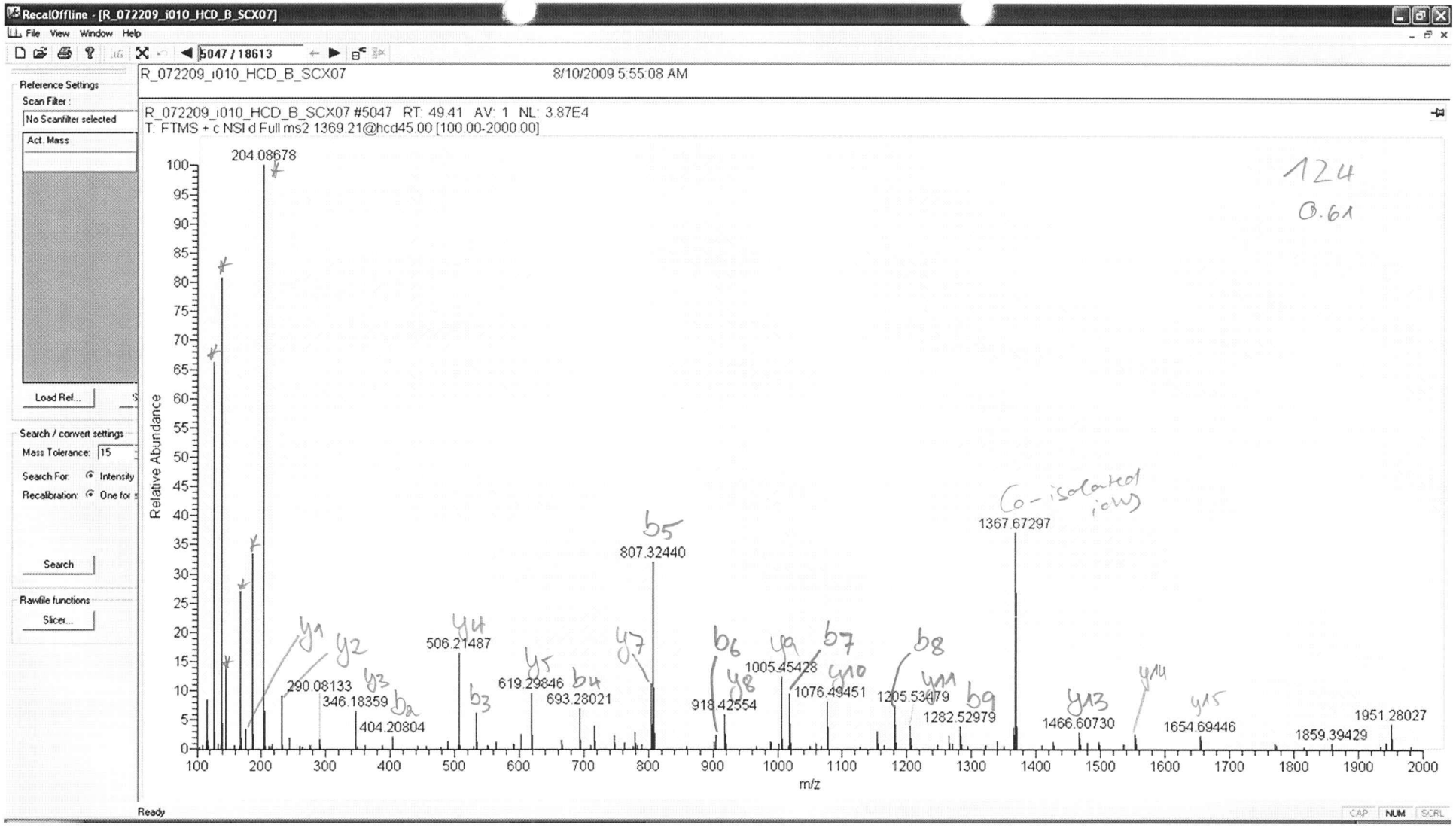
1.45

$[4-203]^{2+}$

No site evidence

HSHAVSTAAMtR

146



124

0.61

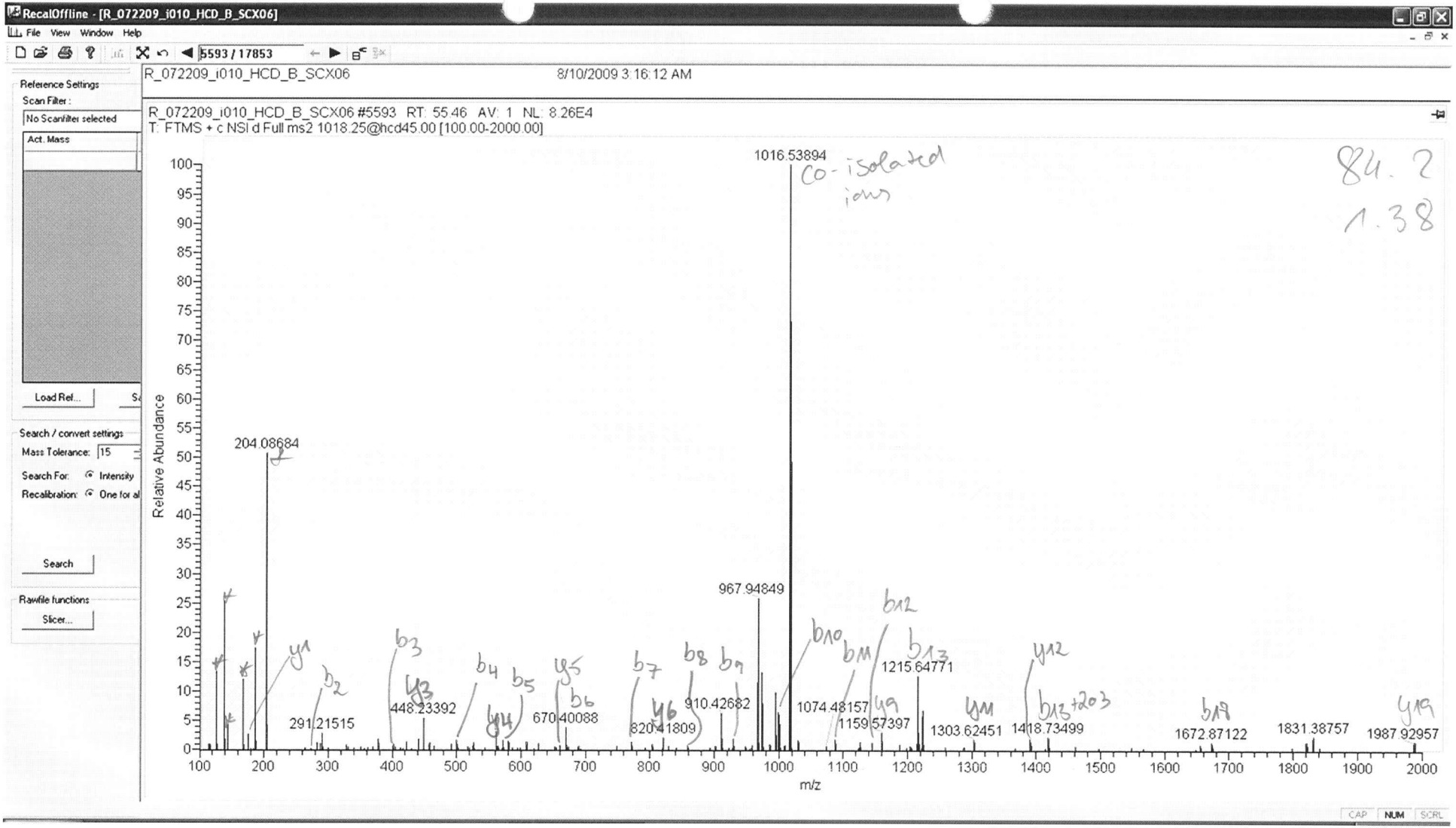
No site evidence

N-terminal: iTRAQ4plex

y9

vcEcNPNYTGsAcDcSLDTSTcEASNGQIcNGR

148

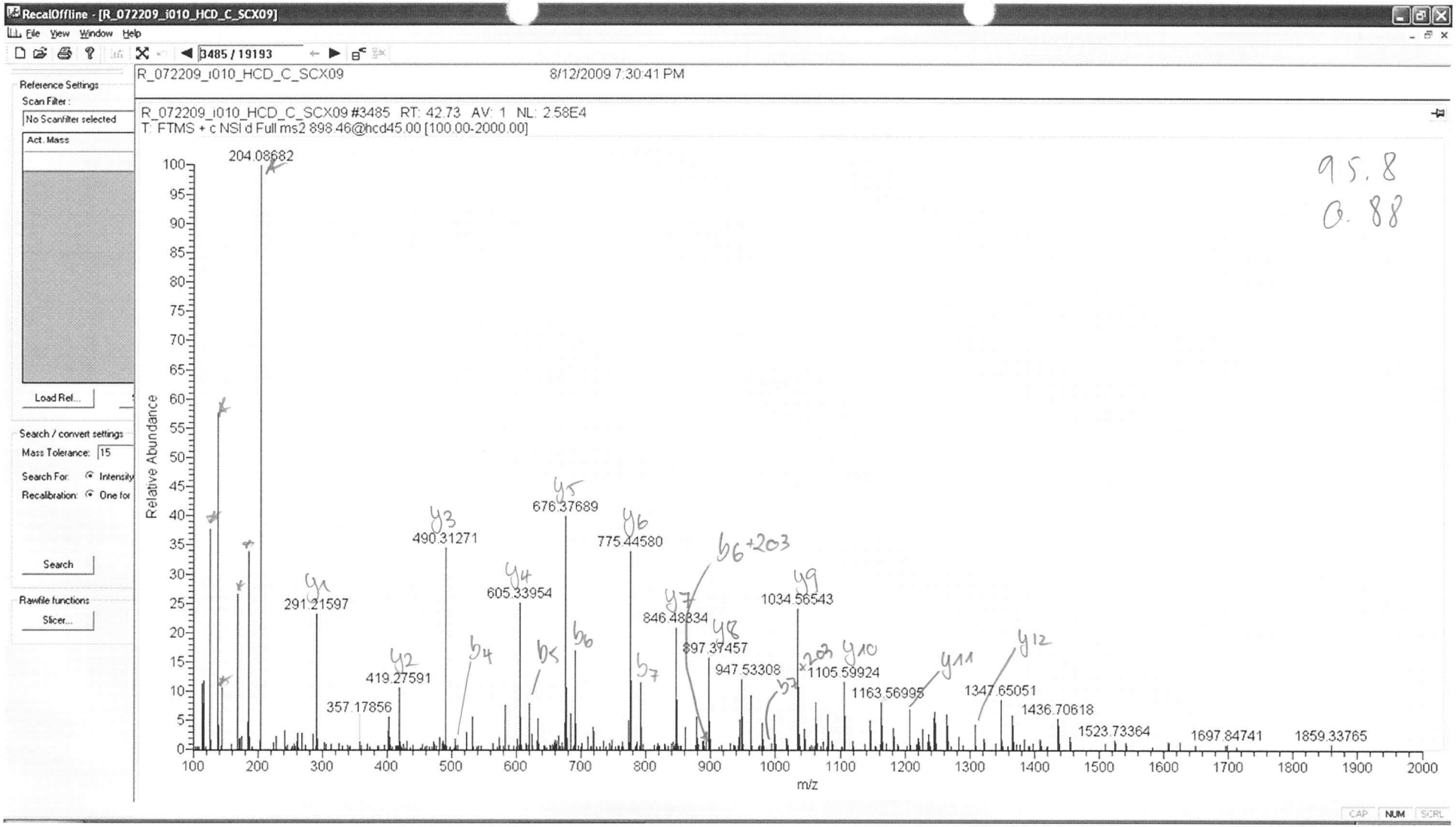


1 site @ T7, S8 or S11 !
2nd site unknown.
N-terminal iTRAQ4plex

qGAVAVTSAASGAPTTSAPAPSSSASsGPnQcVIcLR

y19 y9 b13

T7
S8
S11



95.8
0.88

gTTTNATStTTTTASTAVADAQk

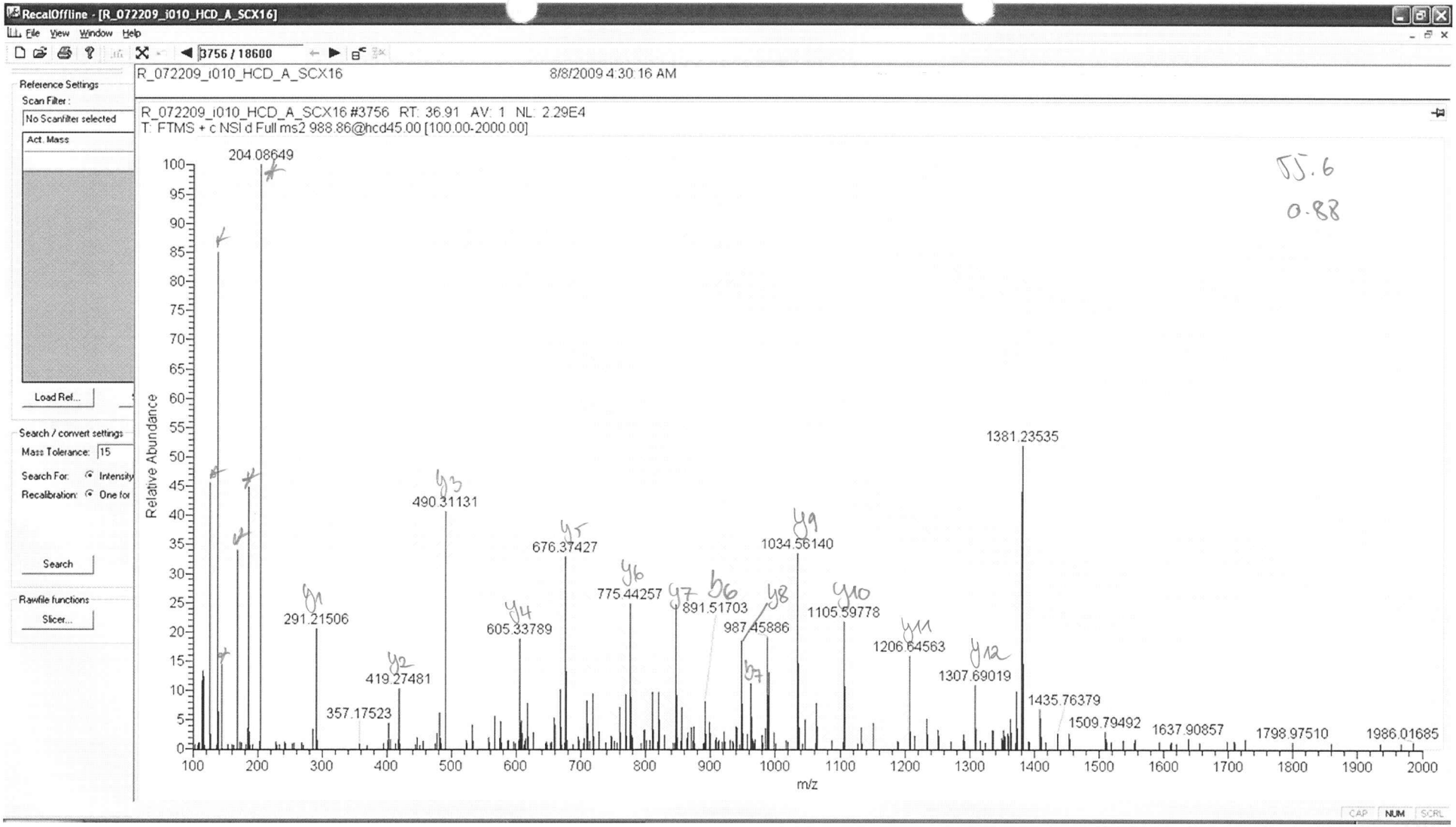
y9 y8

b6 b7

no site evidence

N-terminus + K23: iTRAQ 4plex

152



55.6

0.88

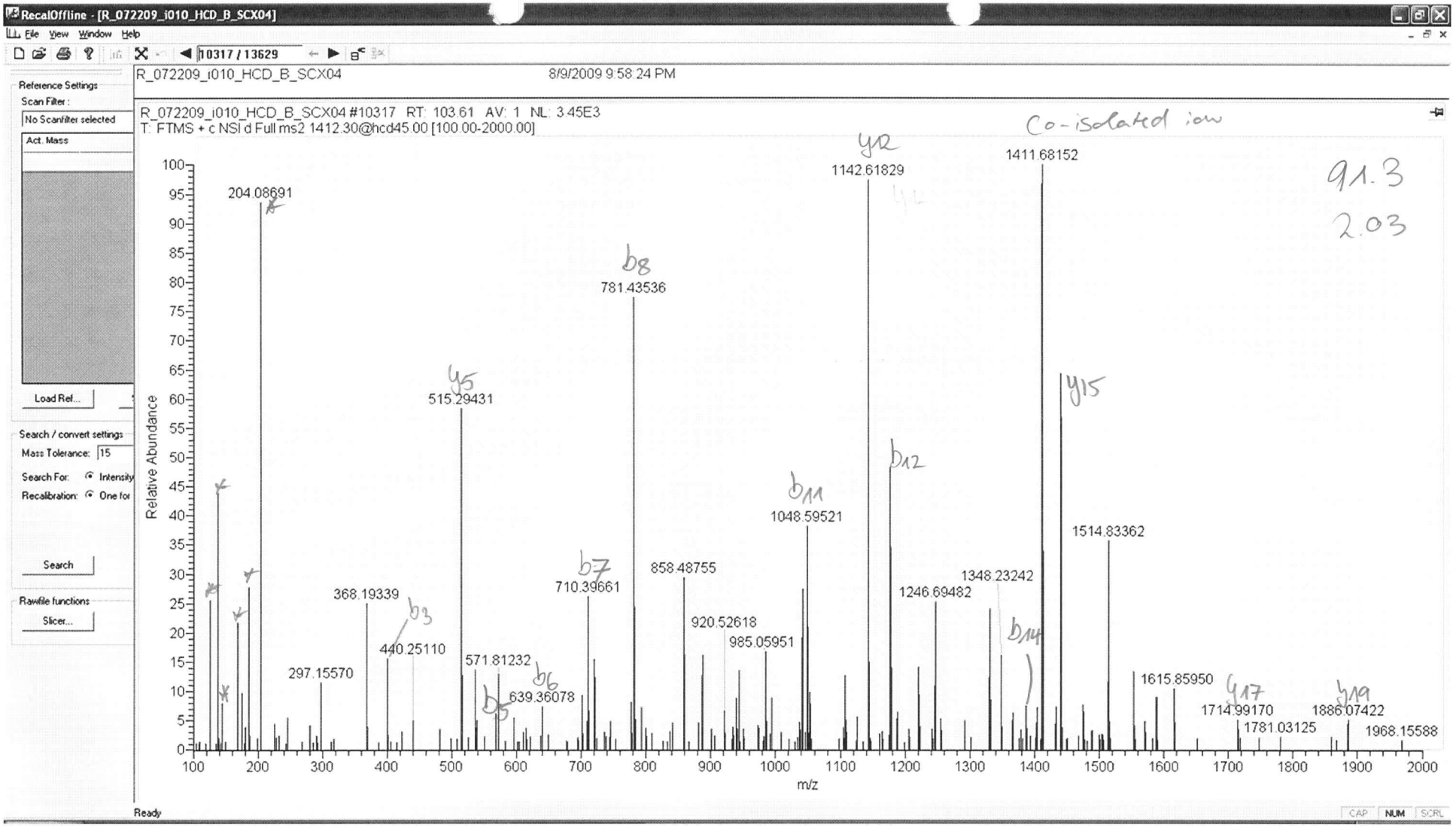
kGTTTNATSTTTTTAStAVADAQk

b_6

No site evidence

N-term, K1, K24: iTRAQ4plex

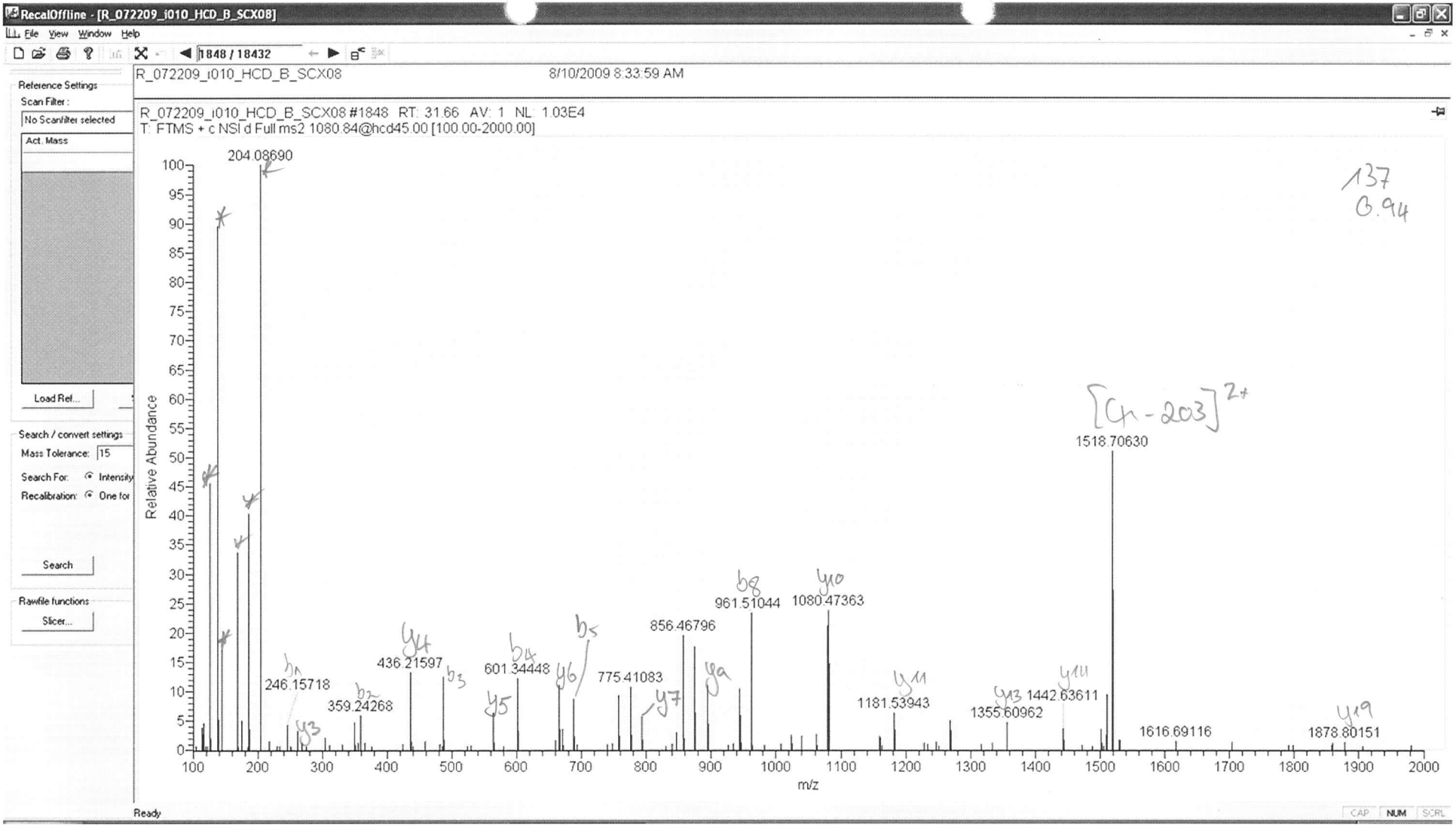
153



no site evidence

SPAPAAAAPAVQPLTQVGITLLPQAAPAPPTTTTTIQVLPTVPGSSIsVPtAAR

N-term. : iTRAQ4plex



137
0.94

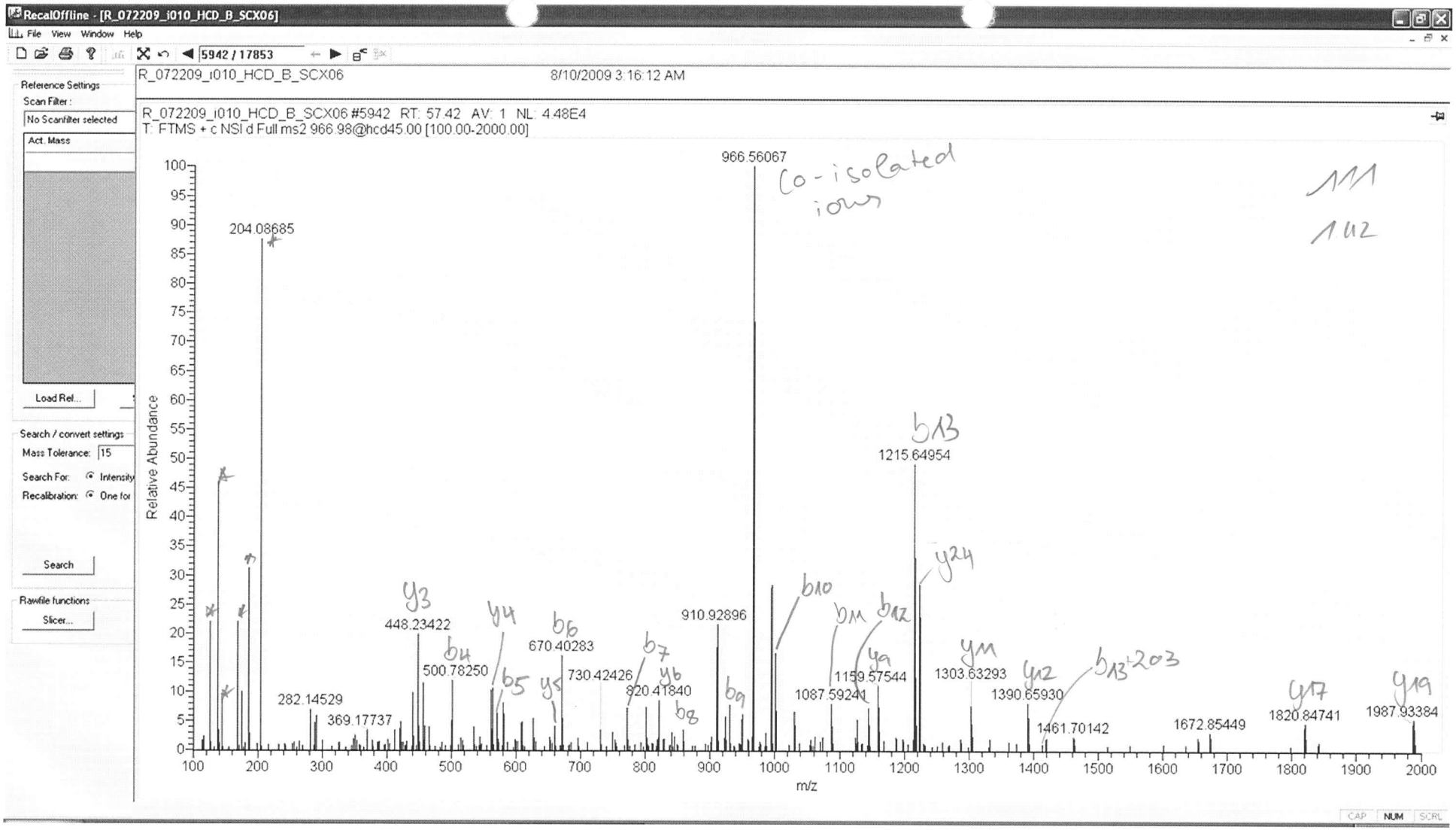
No site evidence

N-term. iTRAQ 4plex

tIQNSSVSPTSSSSSSSSTGETQTQSSsR

b4 b8

155



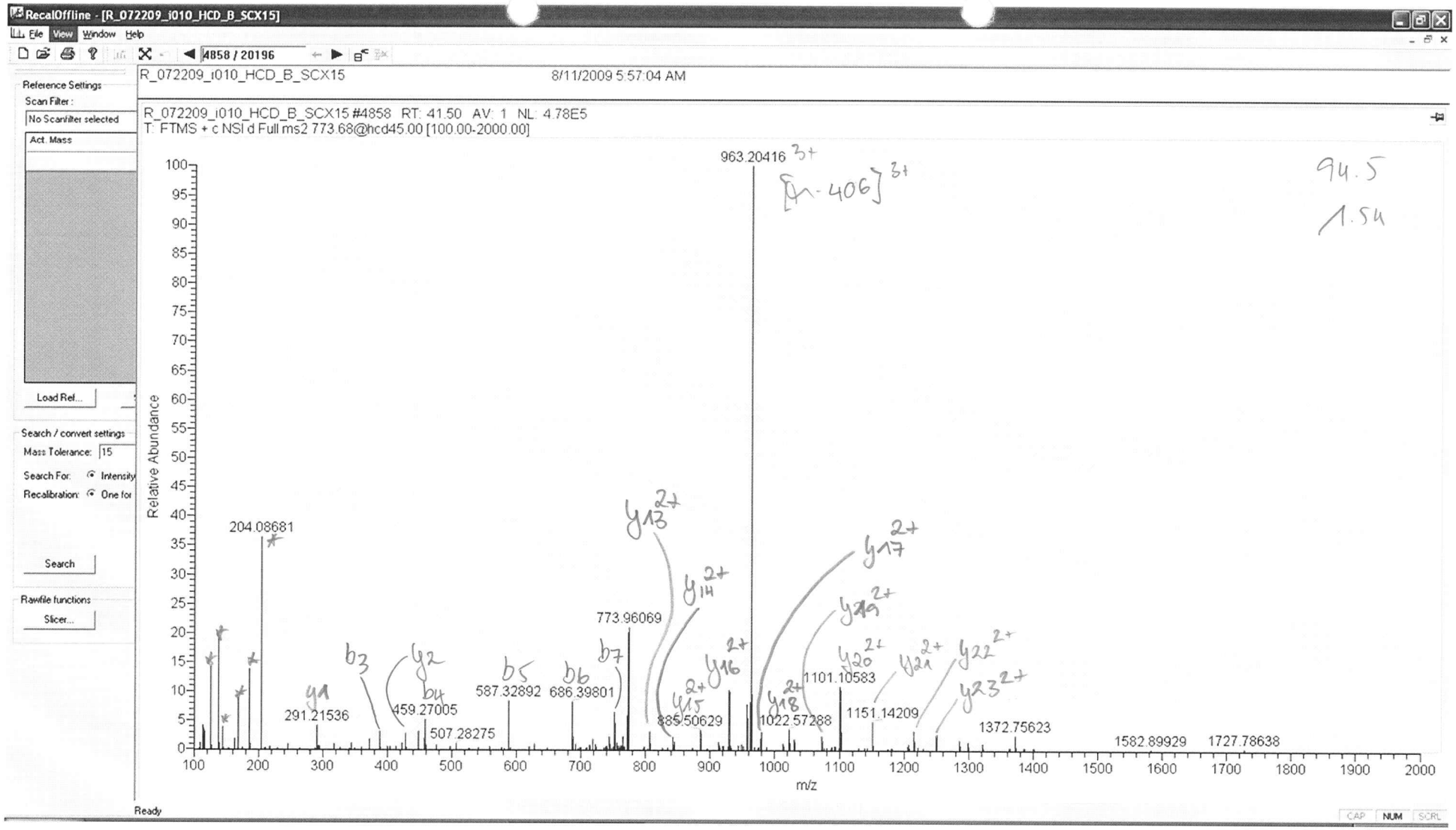
qGAVAVTSAASGAPTTSAPAPSSSASSGPnQcVIcLR

y24

bM b13

T7, S8, SM

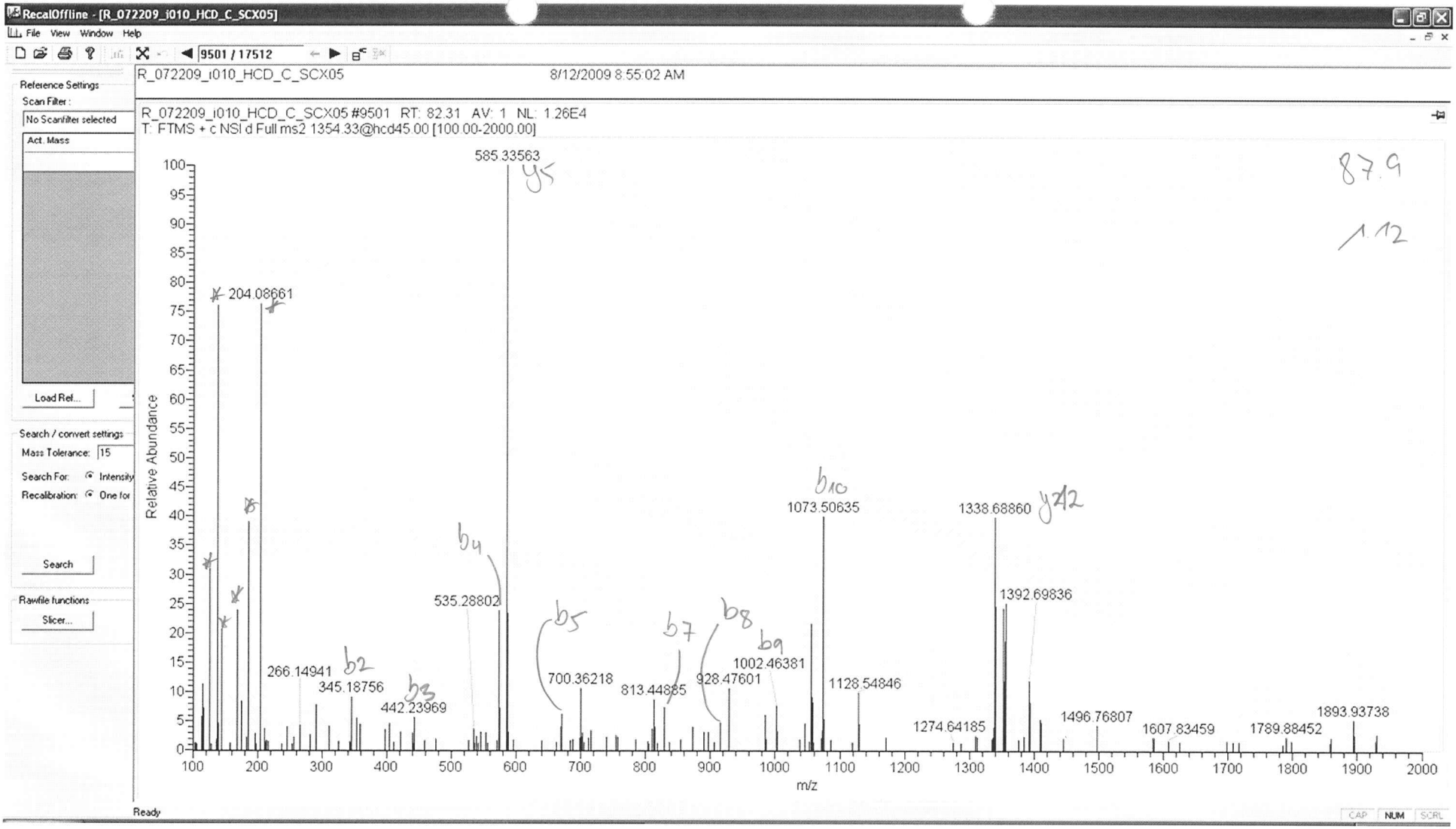
N-term. iTRAQ4plex



no Site evidence

TAAAQVGTSVSSATNTStRPIItVHK

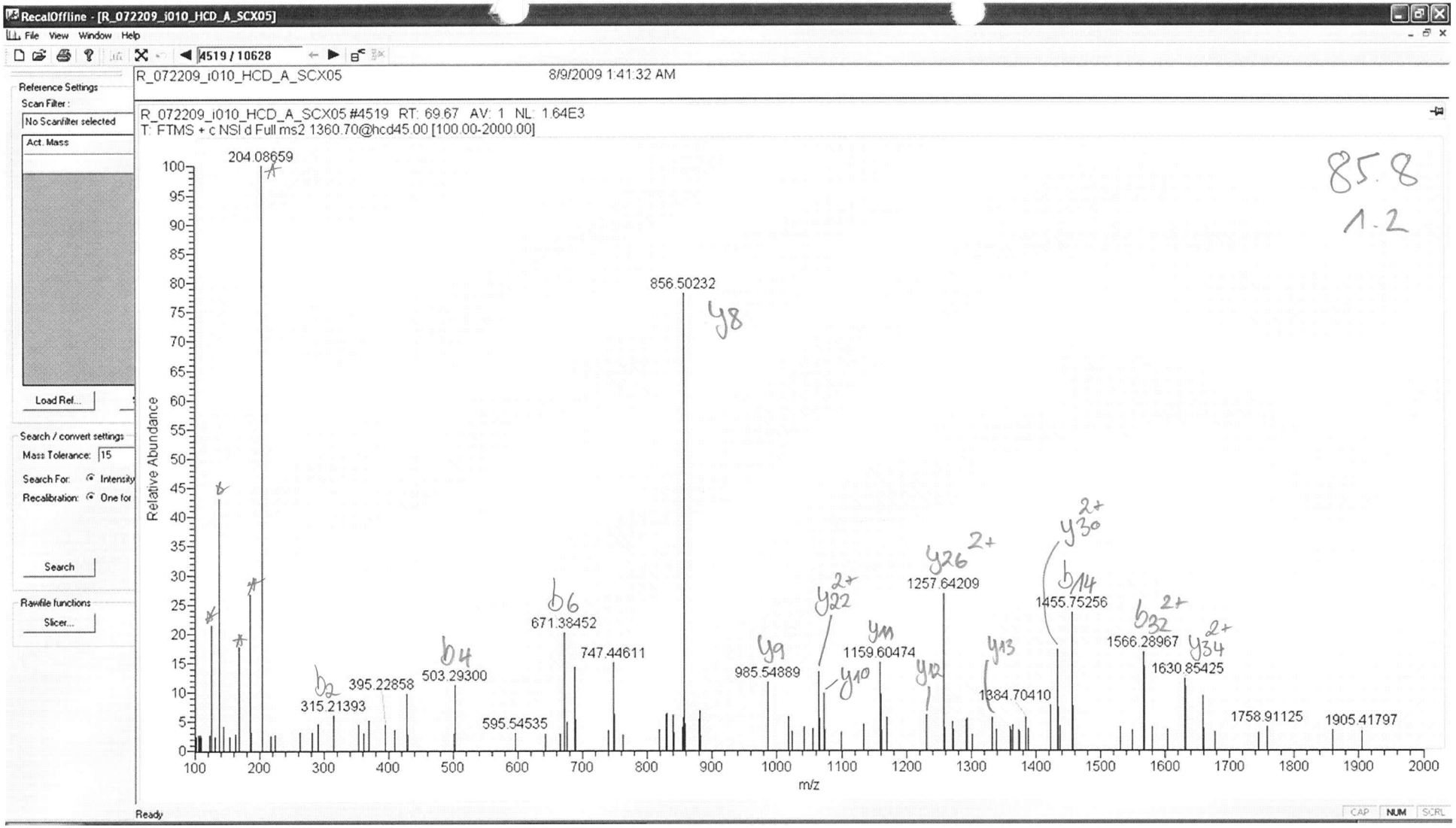
N-term., K26 iTRAQ4plex



aEPMPSASSAPPASSLYSSPVNSsAPLAEDIDPELAR

No further evidence

N-term. iTRAQ4plex



858
1.2

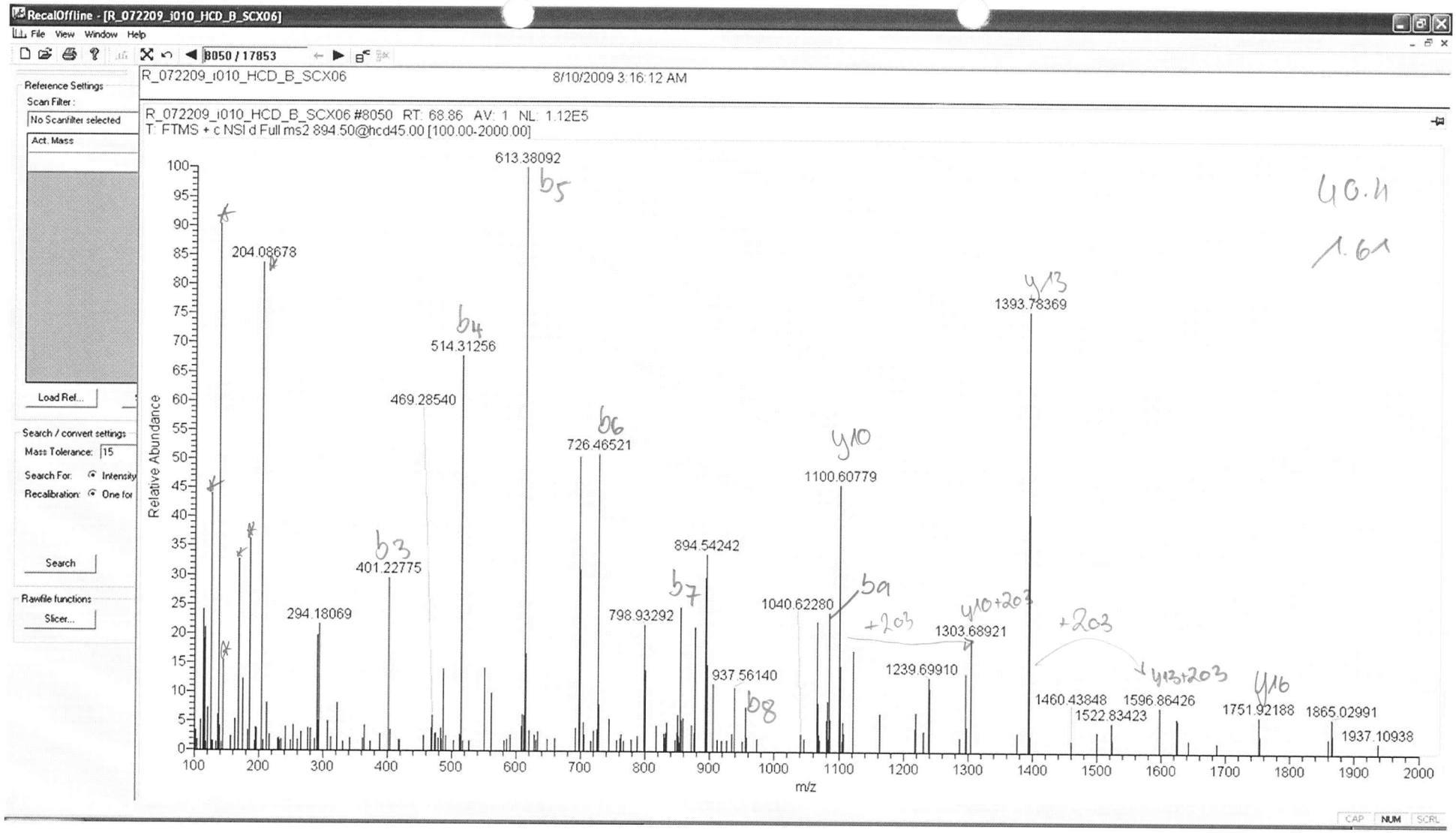
No site evidence

aVSTPAPATTQQSAPASTTAVTSSTTTTVAQAPTPVPALAPTSTPASITPASATASsEPAPAsAAk

b4 b6 b32 y26 y8

N-ter., K66 : iTRAQ4plex

159



AANIVIQtEPPVPVSINSNITR

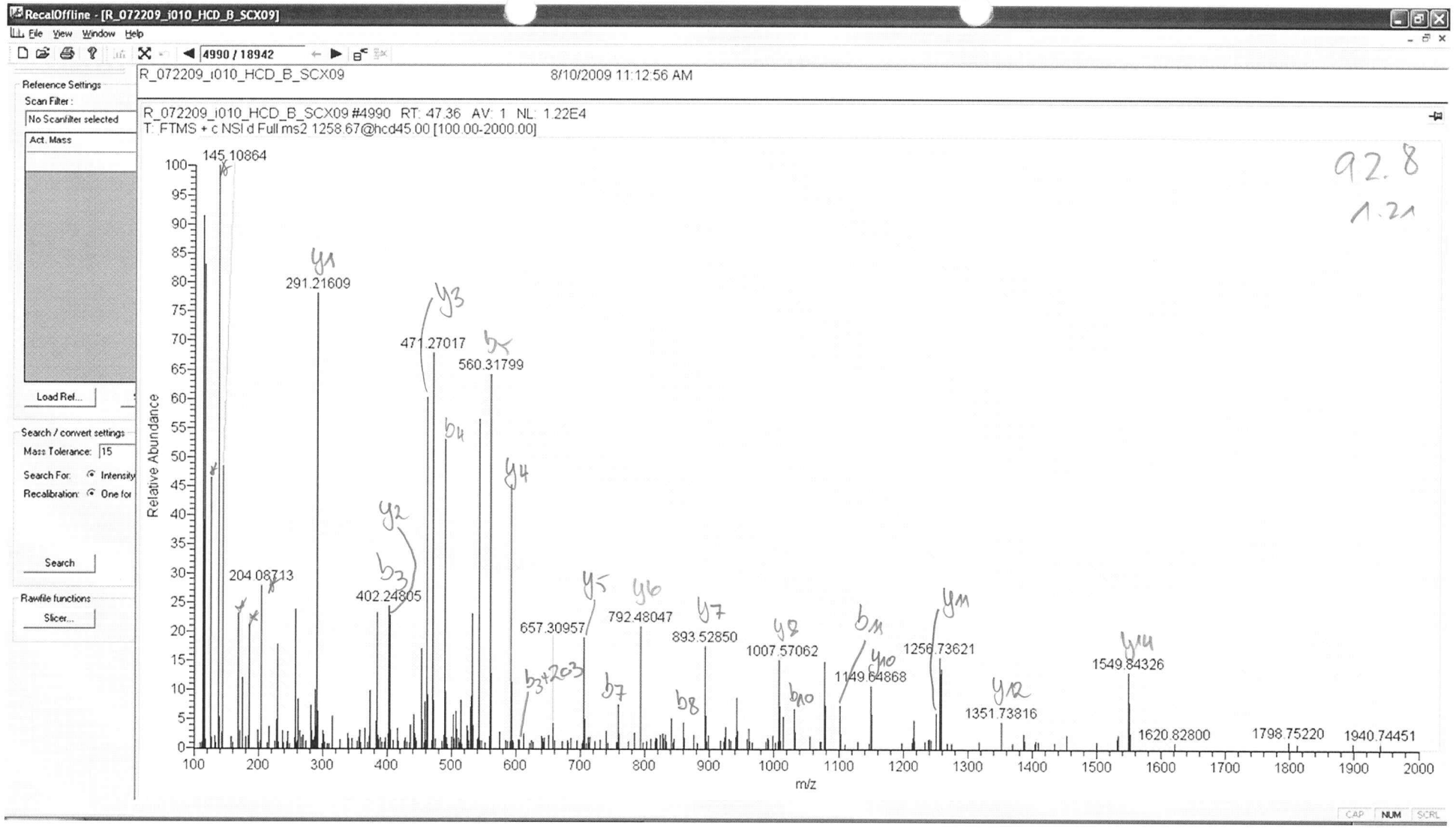
y13 y10

b9

S15, N17, S18, N19 or T21

N-term. iTRAQ4plex

160

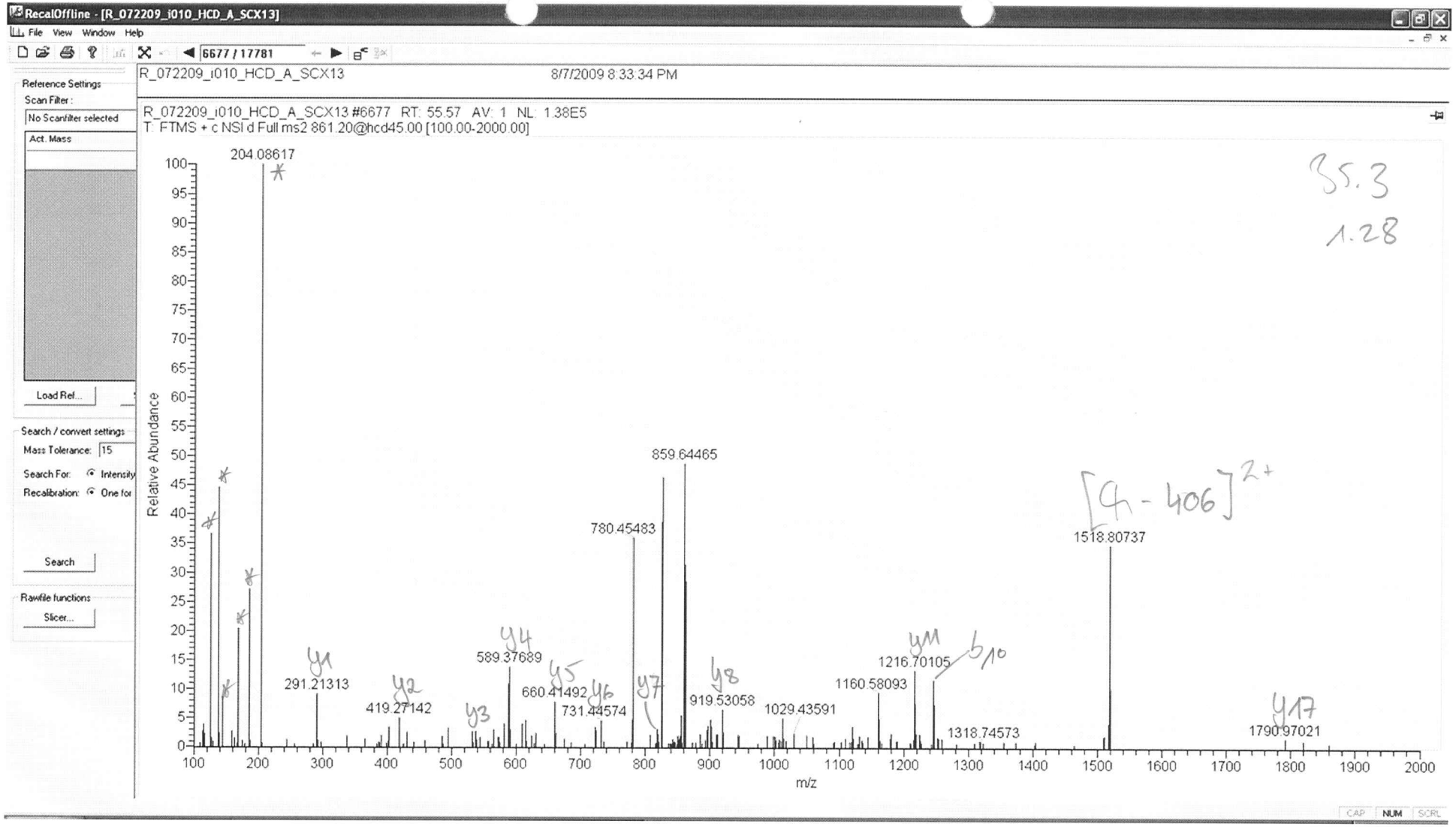


iGSSAPTTTAANtsLMGIk

S3 ; 2nd site : unknown

N-term., K19 ; iTRAQ 4plex

161

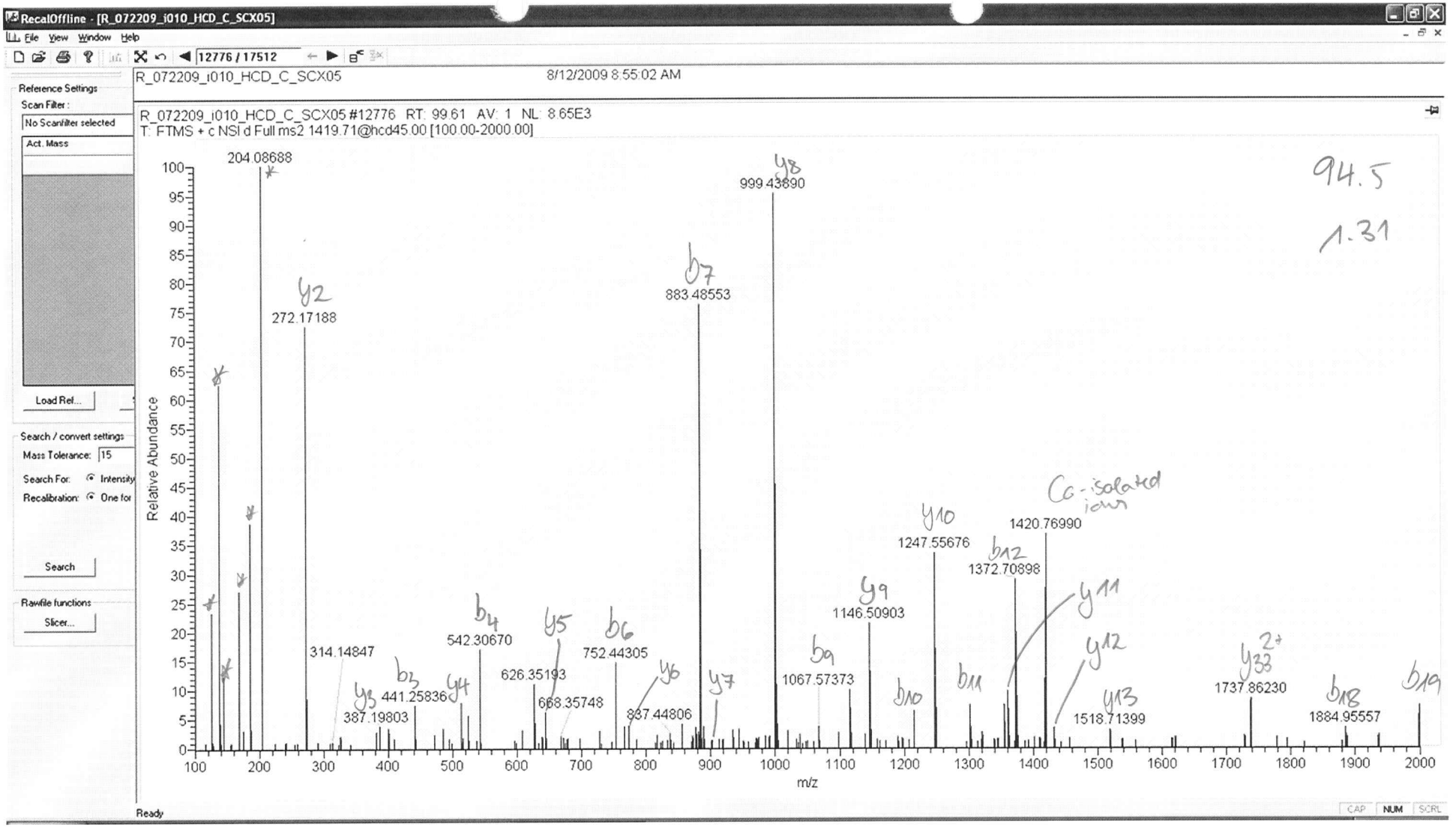


rQDDLISSSVPSTTSTPTVtsAAGLQk

y17 y11 b10

No Site evidence

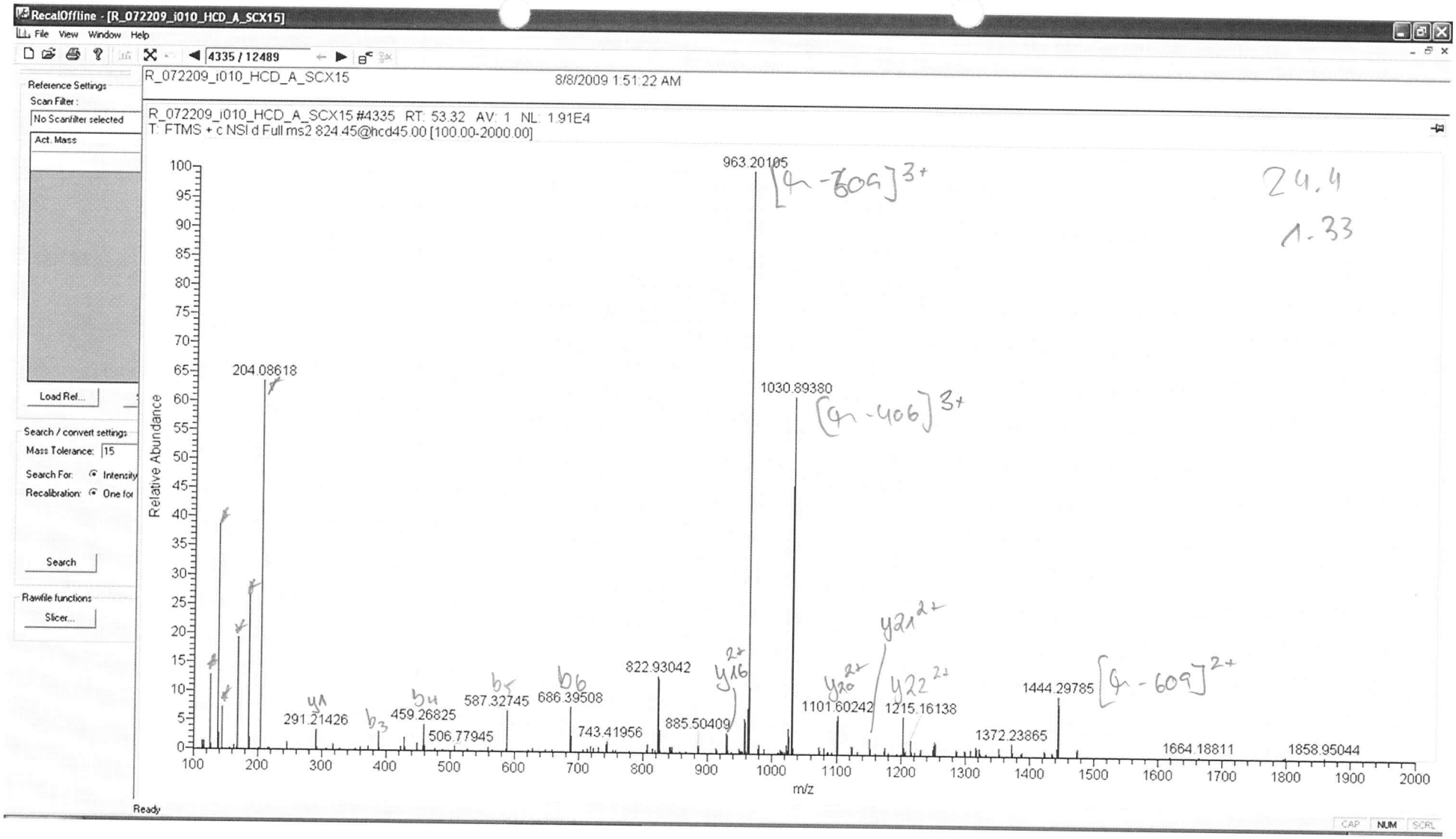
N-term., K27 iTRAQ4plex



y10
y8

aPQTPLMPSFSAPSGTGLLPTPITQQASLTSLAQGTGTTSAItFPEEQEDPR

N-term. iTRAQ 4plex



24.4

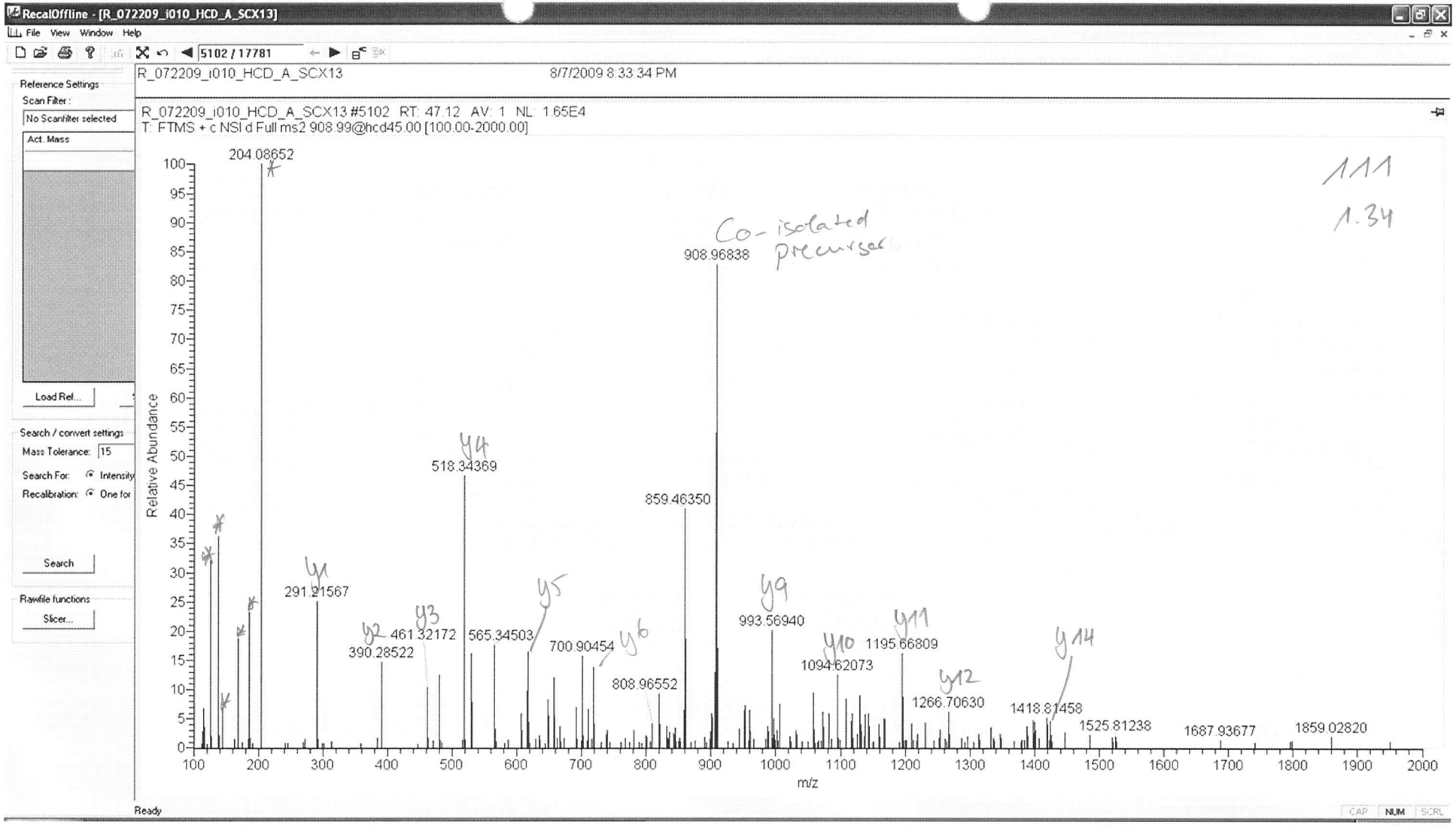
1.33

tAAAQVGTSVSSATNTStRPIItVHk

no Site evidence

N-term., K26: iTRAQ4plex

165

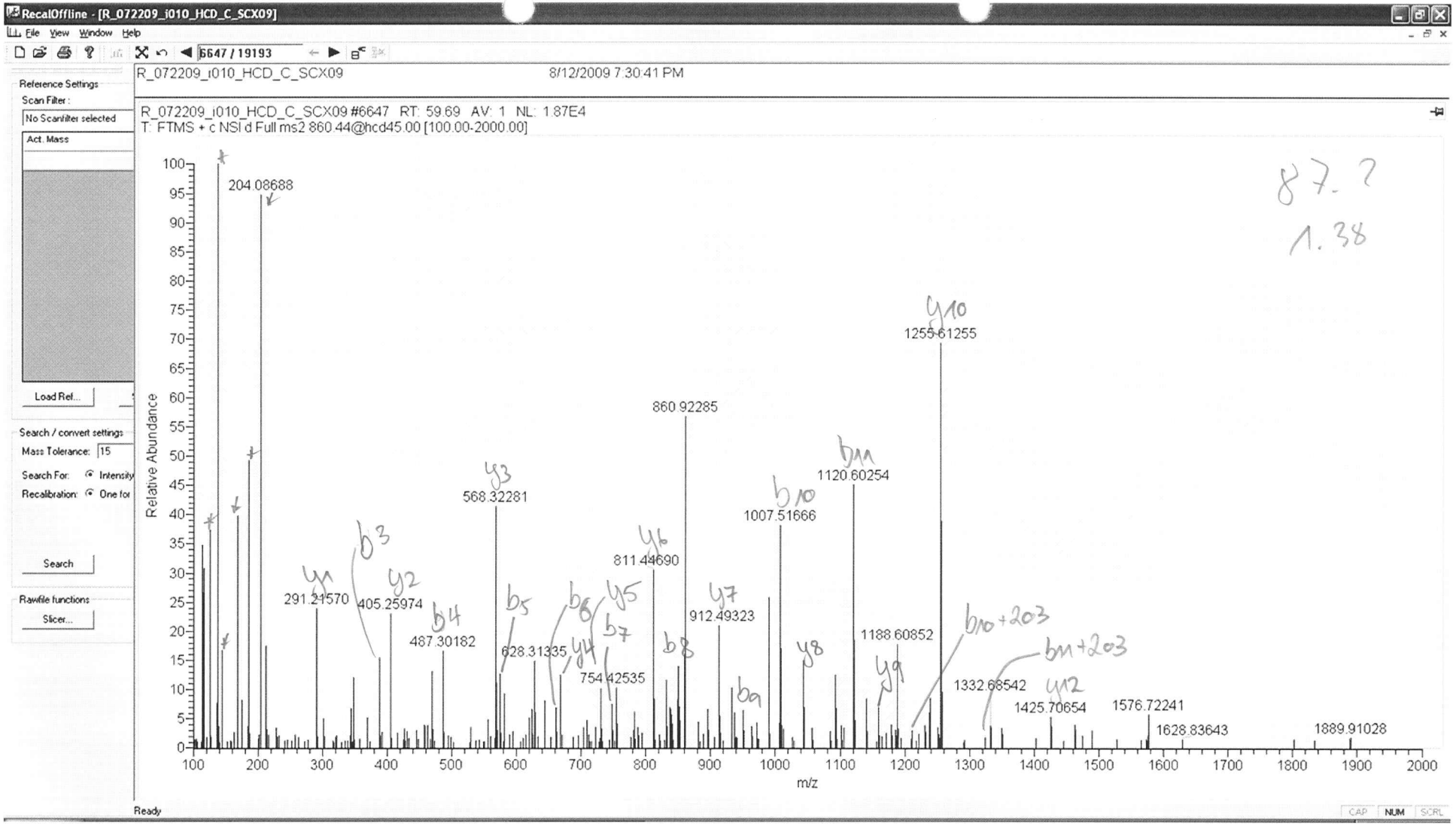


No site evidence

N-term, K1, K31 : iTRAQ4plex

kTEALQVATTSPTANTTGTATTSSTtVGAVk

166



87.7
1.38

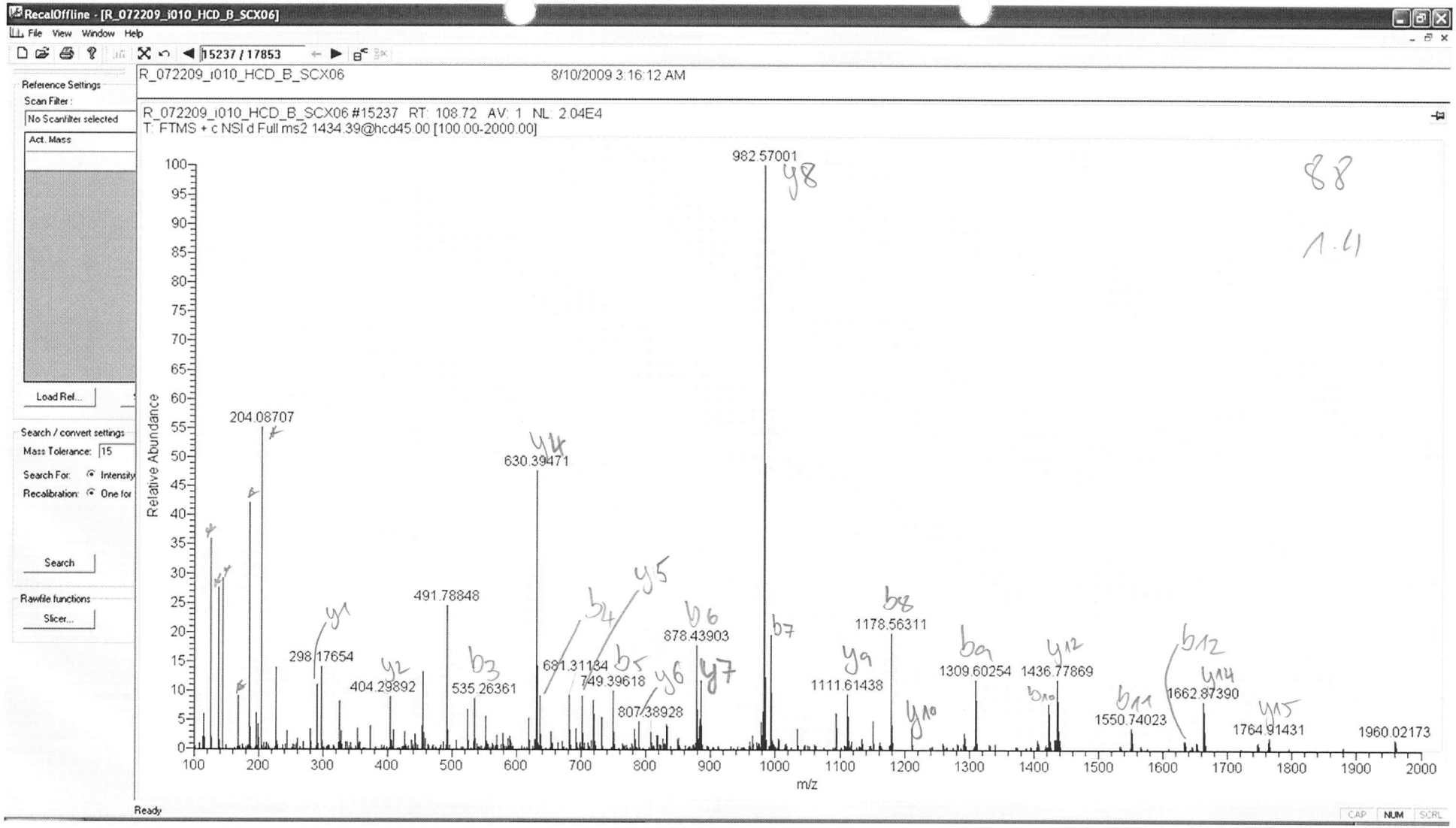
S3, S5, S6, S7, T8 or T9

N-term, K21 : iTRAQ 4plex

167

gVSVSSSTTGLPDMTGSVYnk

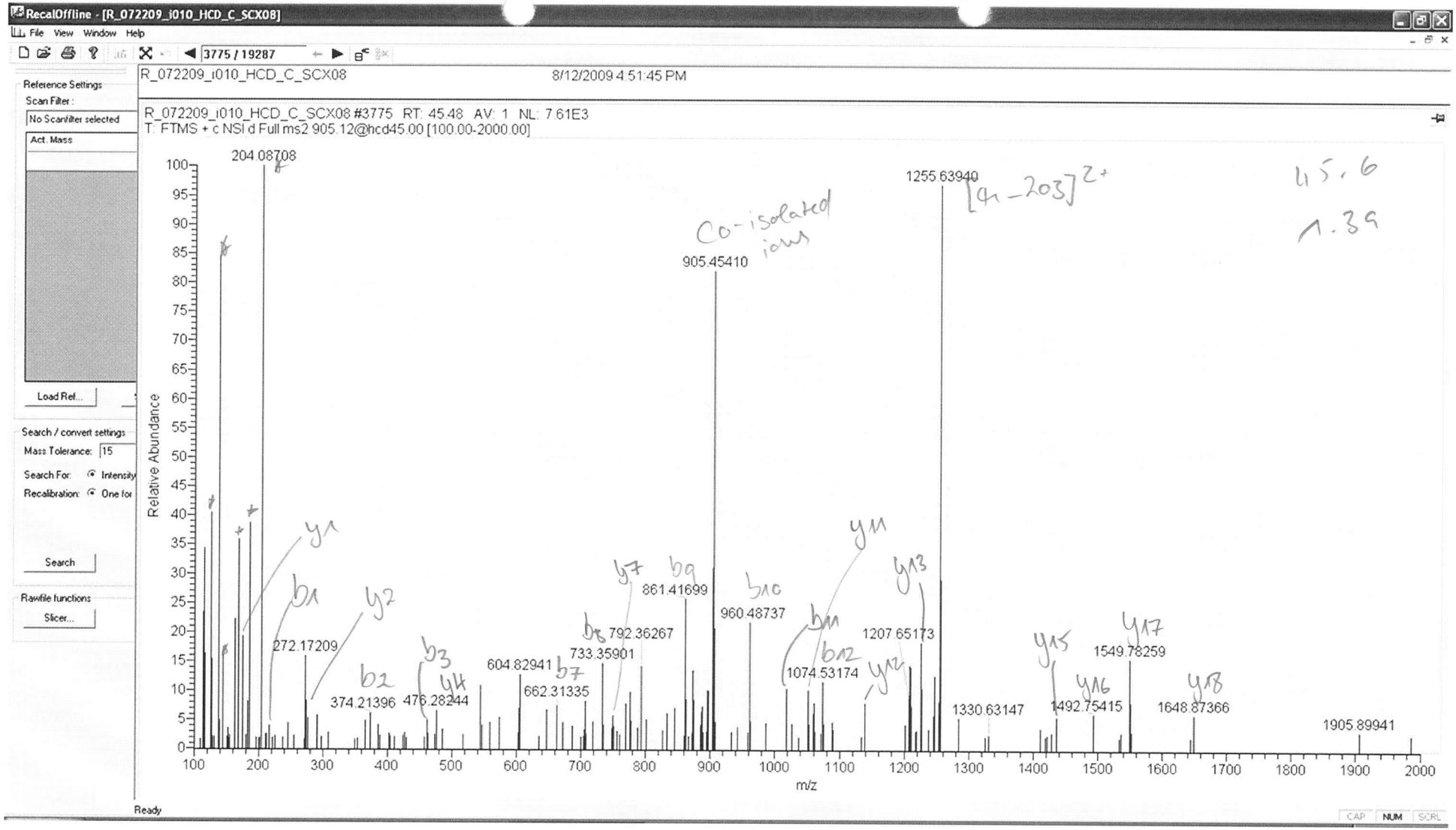
b10
b11



No site evidence
N-term., K33 : iTRAQ4plex

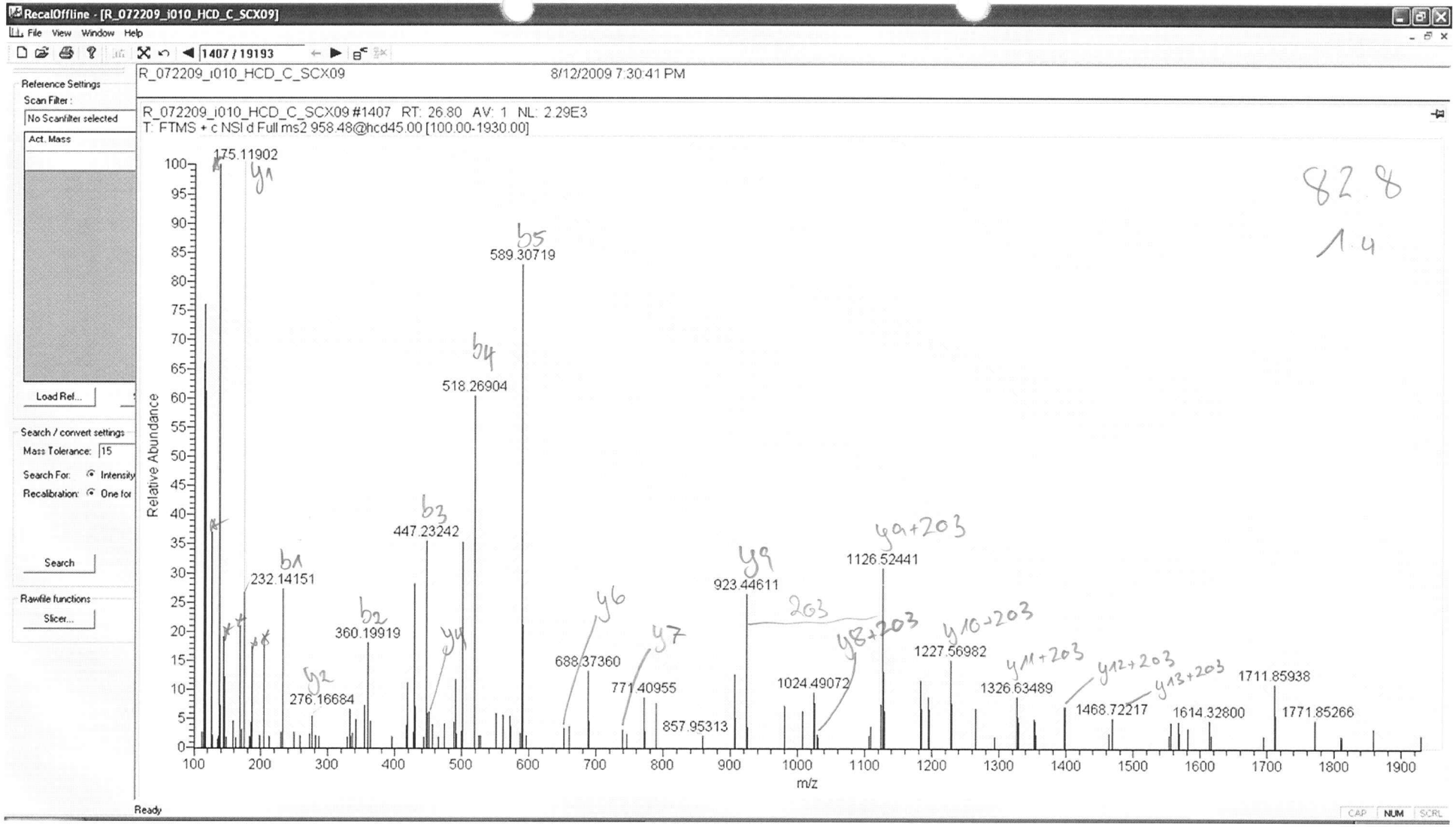
dFQTLENWMLQTLNEEPVTPEPEVEPPsAPELk

168



no further evidence
N-term. iTRAQ4plex

aSASGSGAQVGGPISSGSSASSVTVtR



828

1.4

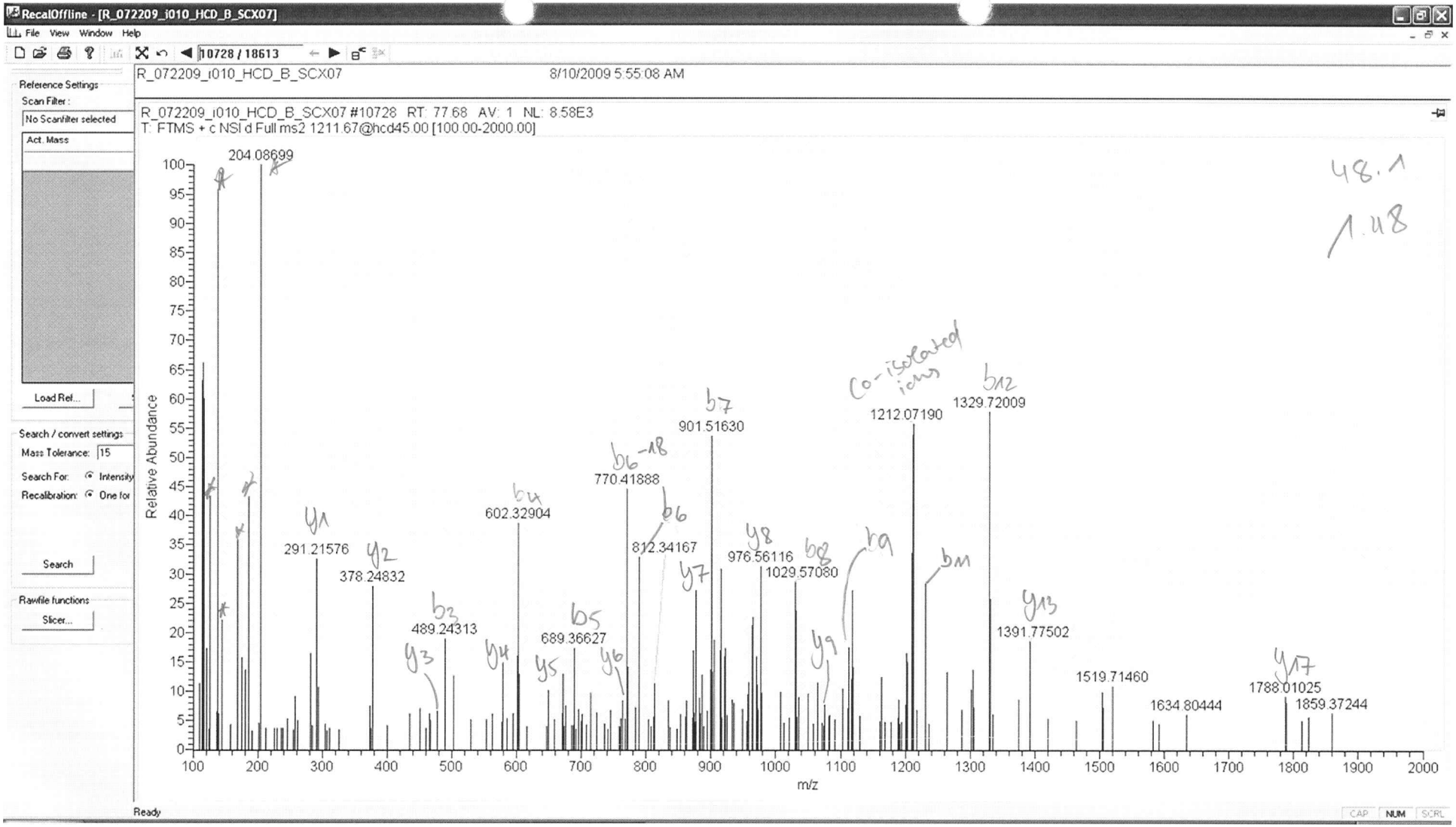
sQSAAVTPSSTTSStR

y9 y8

S9

N-term. iTRAQ4plex

170



48.1

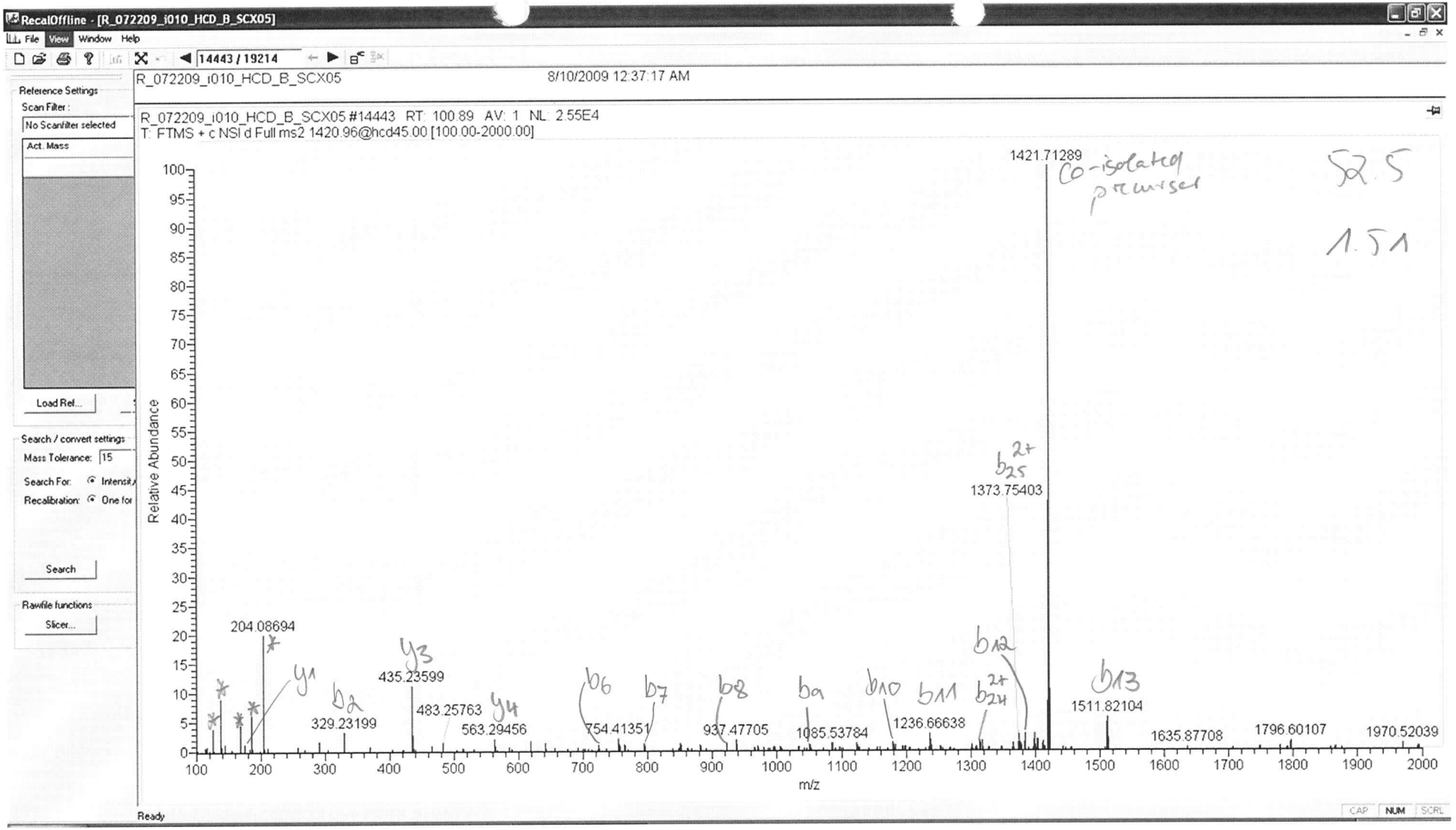
1.48

No site evidence

N-term, K32 : iTRAQ4plex

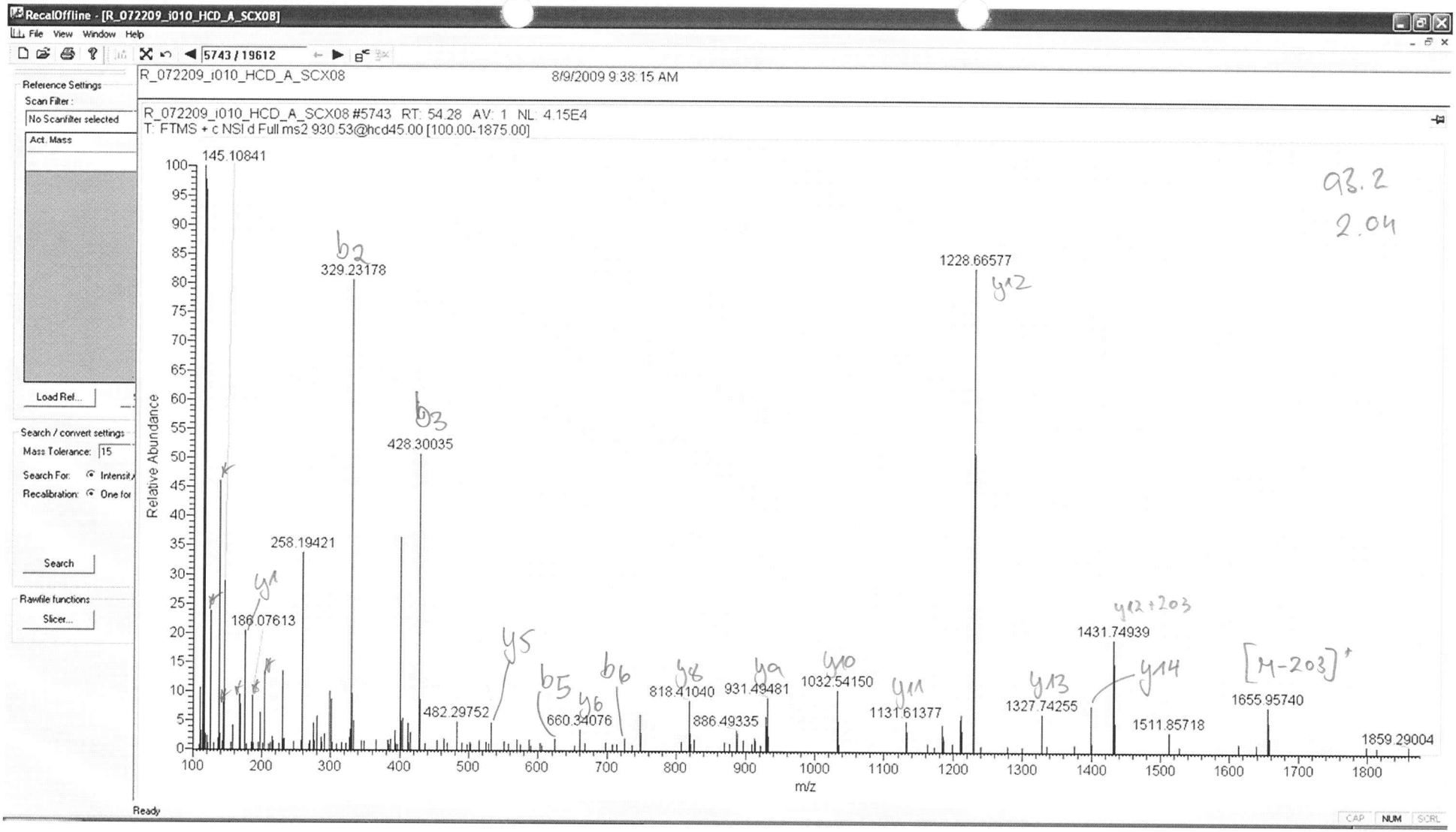
171

tNEISVIQSGGVPTLPVSLGATSVVNNATVsk



lAPPSLAQQQGFQPGLSQPTSVQQIPIPIYAPLQGQHQAQLSLGAGPAVSQAQELFSSsLQPYR

N-term: iTRAQ4plex



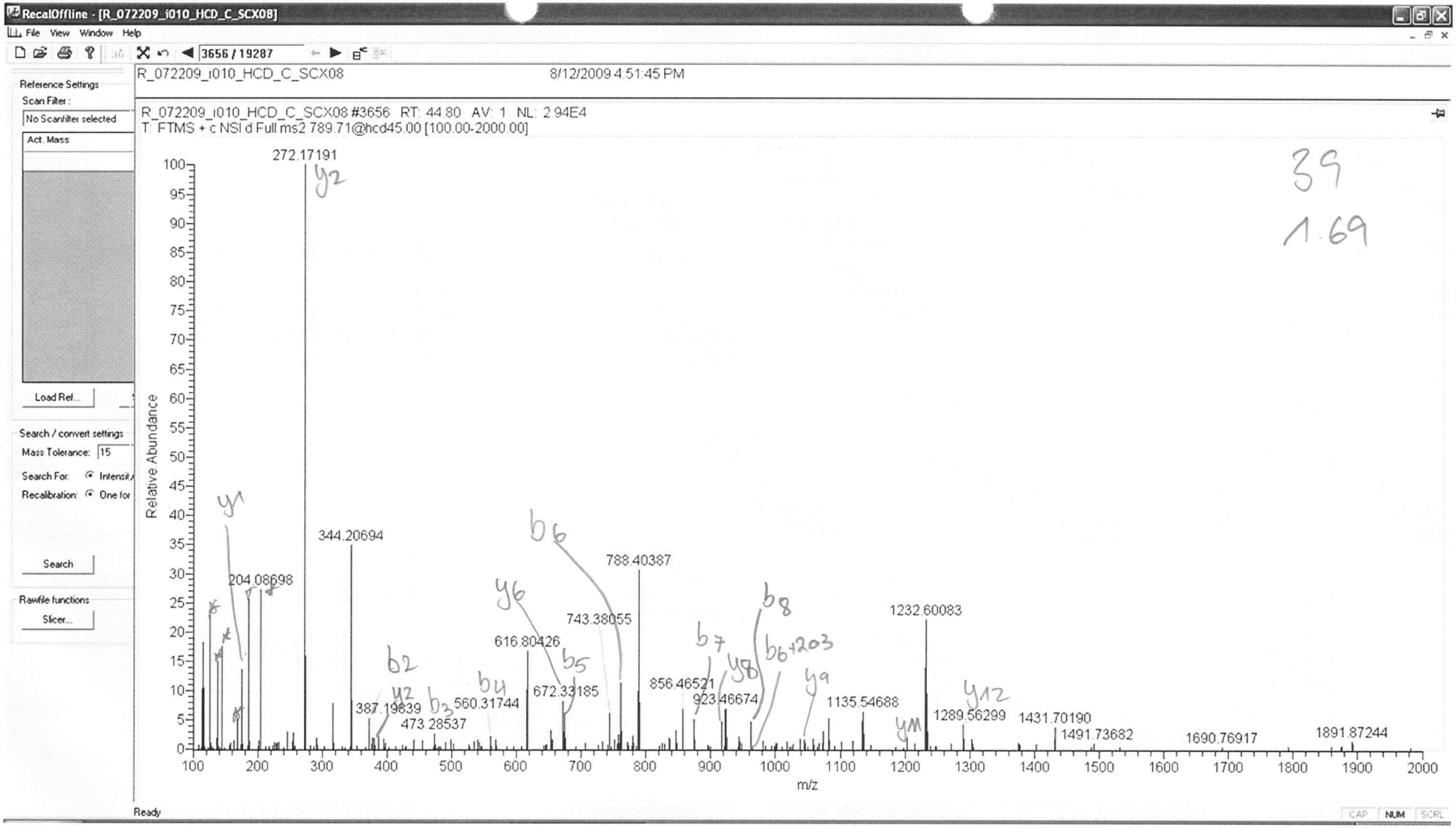
y12

lAVPVTLASQQAGtR

No 2nd evidence

N-term: iTRAQ4plex

176



39

1.69

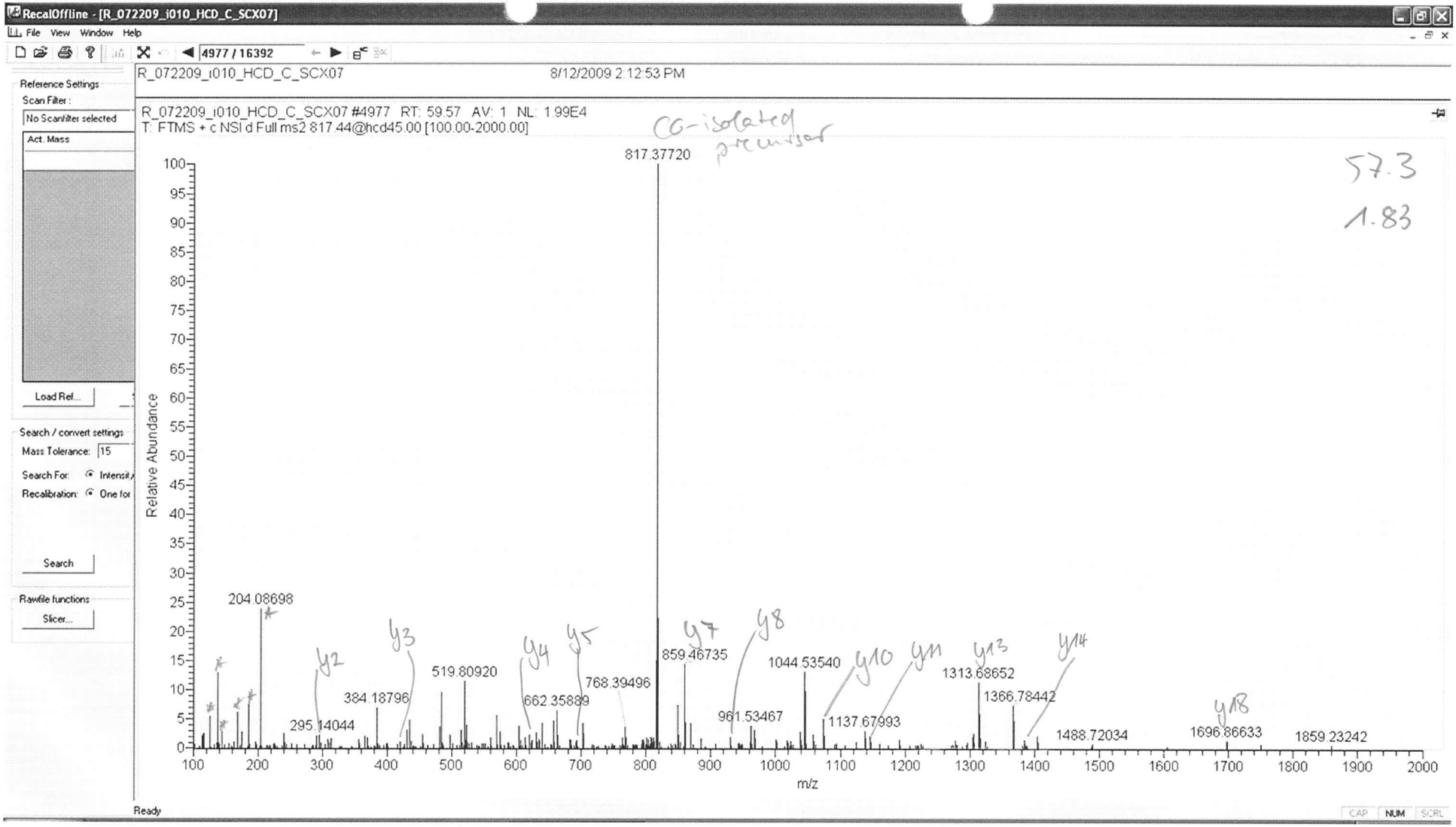
qVTSNSLsGTQEDGLDDPR

b6

T3, S4, N5 or S6

N-term : iTRAQ 4plex

177



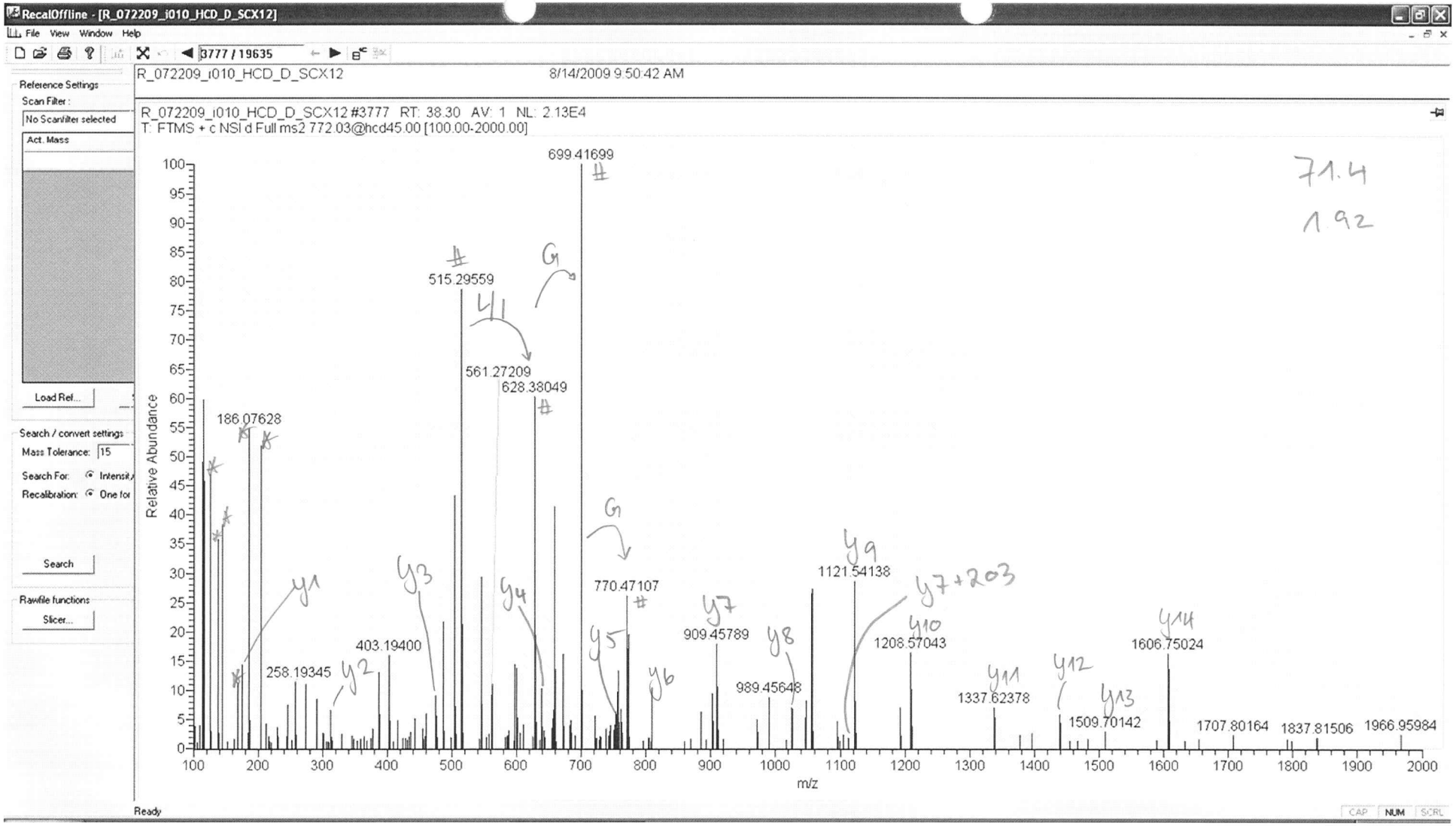
No Site evidence

N-term., K33: iTRAQ4plex

lASVPAGGAVAVSAAPGSAAPAAGsAPAAAEEk

y7

178



71.4

192

N-term : iTRAQ 4plex

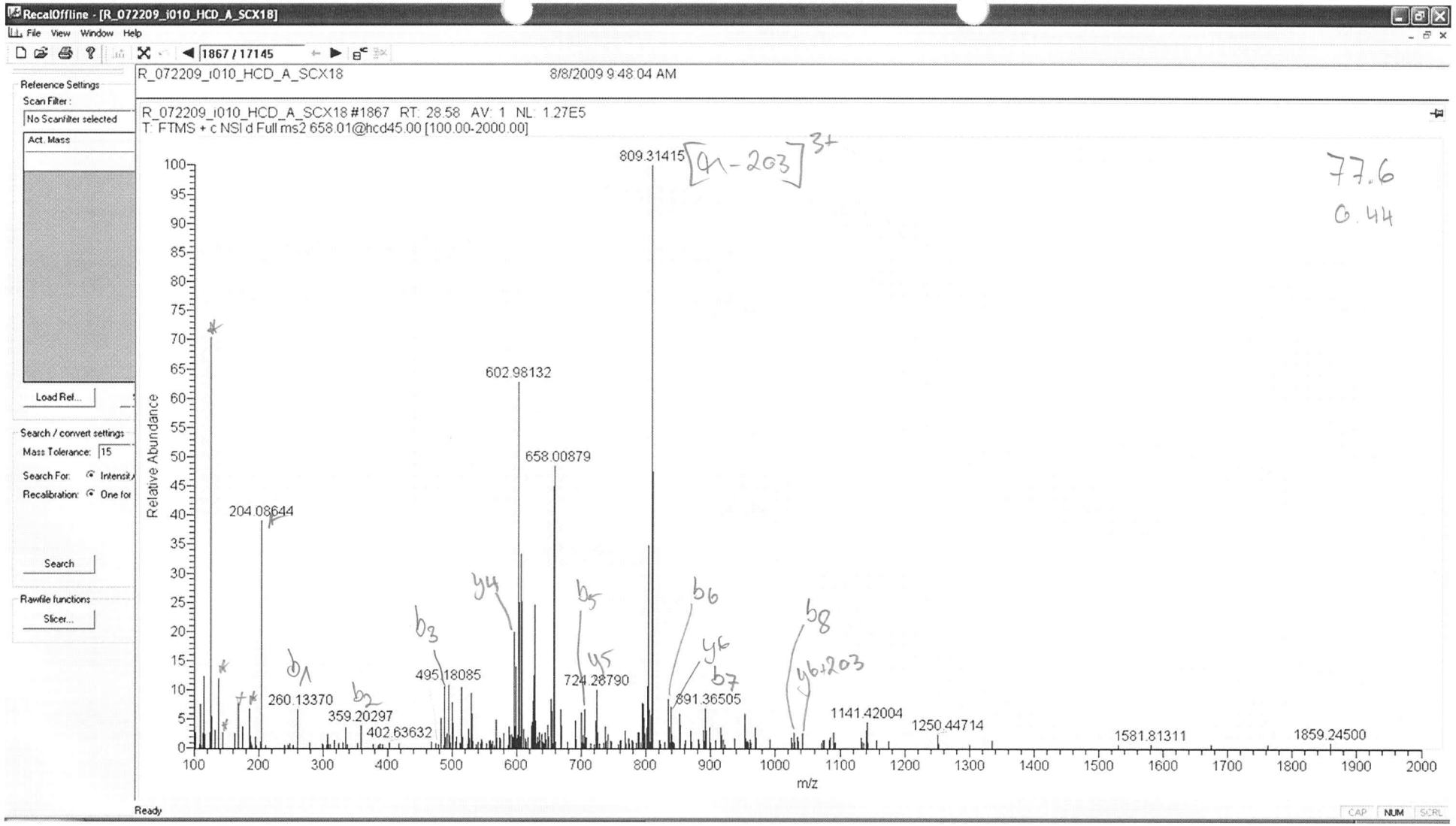
T11

eETPATESPDtGLYYHR

y7

Chimeric spectrum; 2nd ion series from co-isolated precursor

179

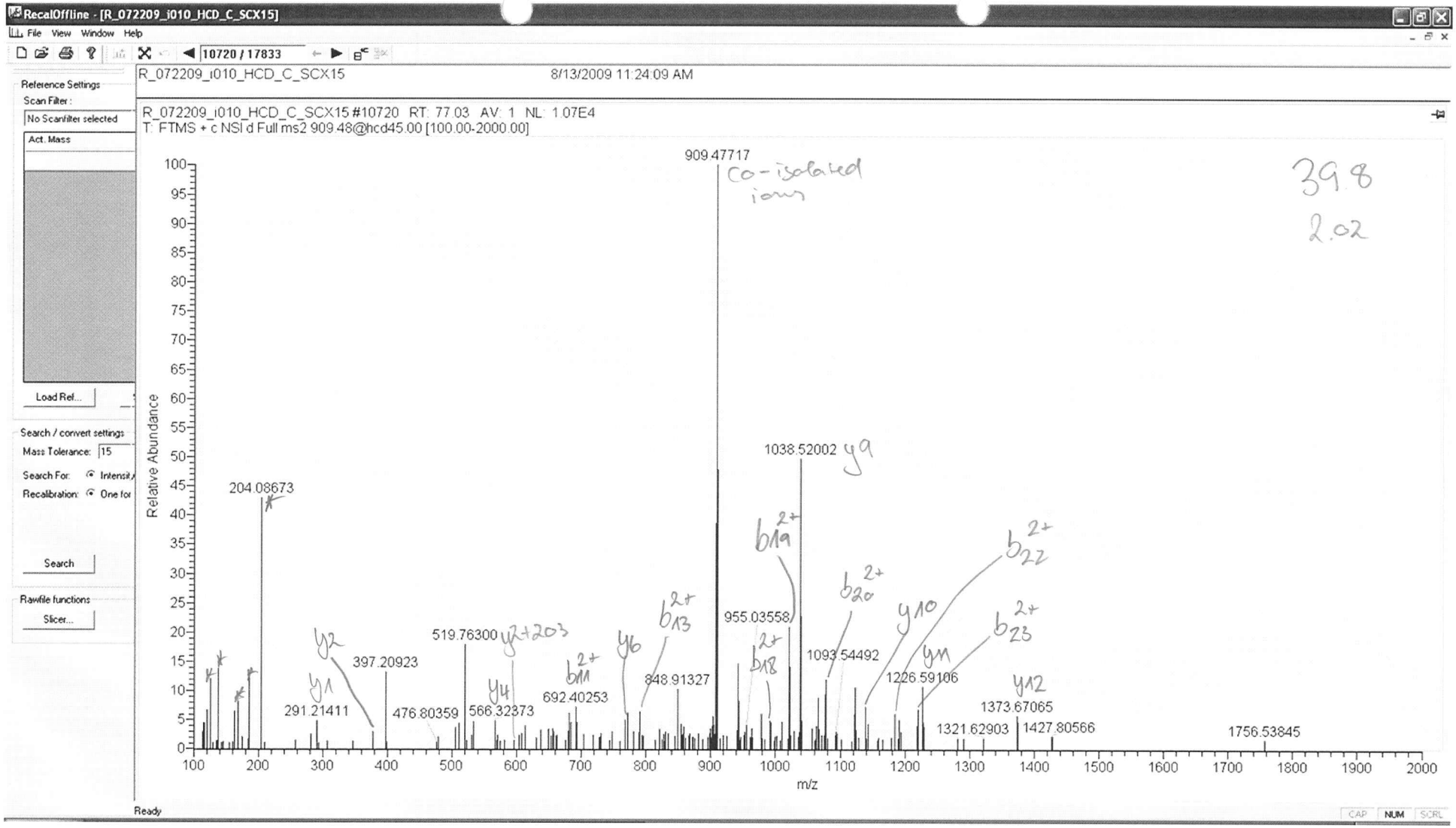


dVEcGEGHFcHDNQtccR

y6 y5 y4

NA3
N-term. :TRAQ4plex

180



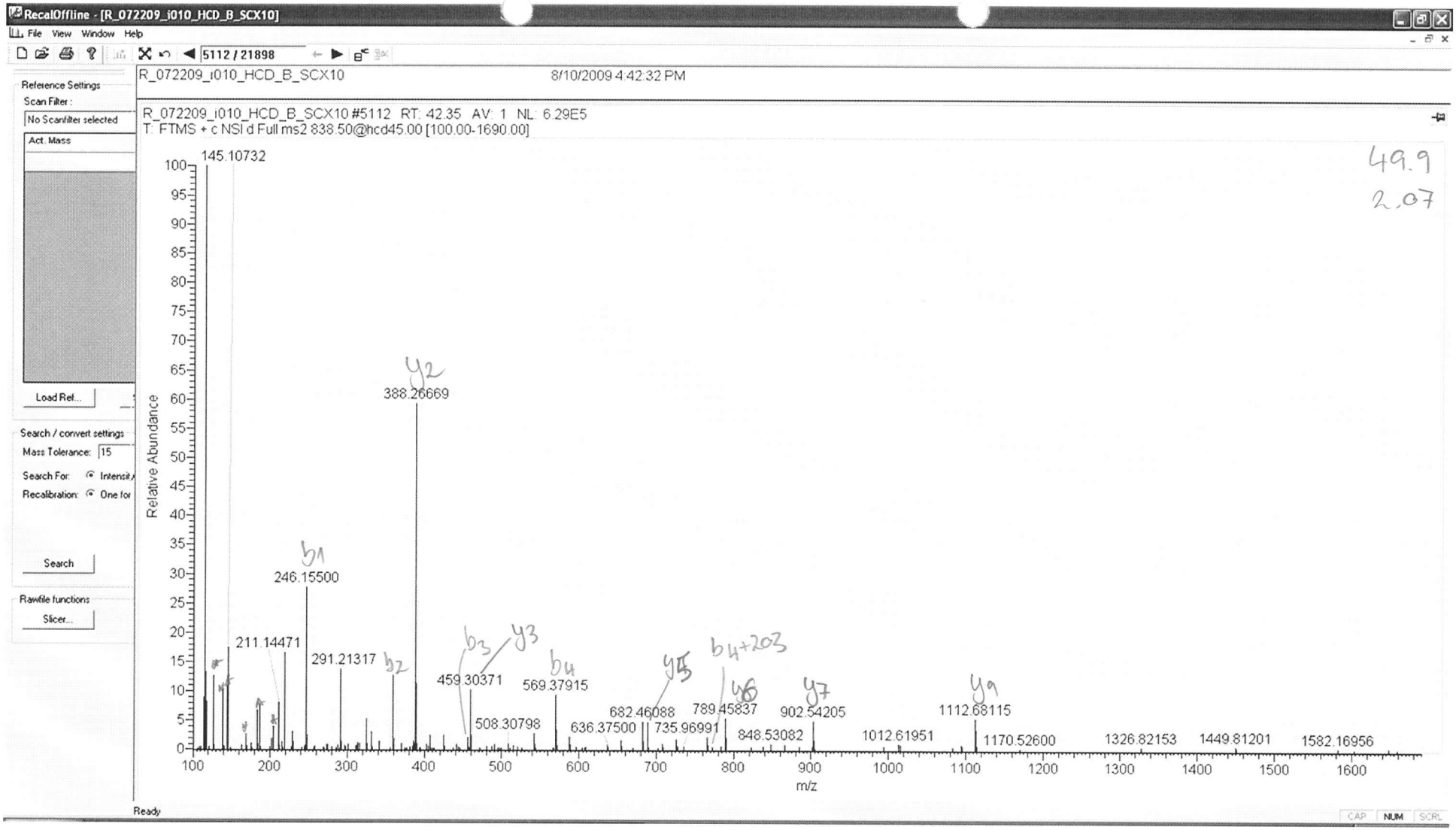
kPHTSLTTAASPVSTSAGGIMtAPAIDIFSTPSSSNSTSk

y9 y2

S39

N-term, K1, K40 : iTRAQ4plex

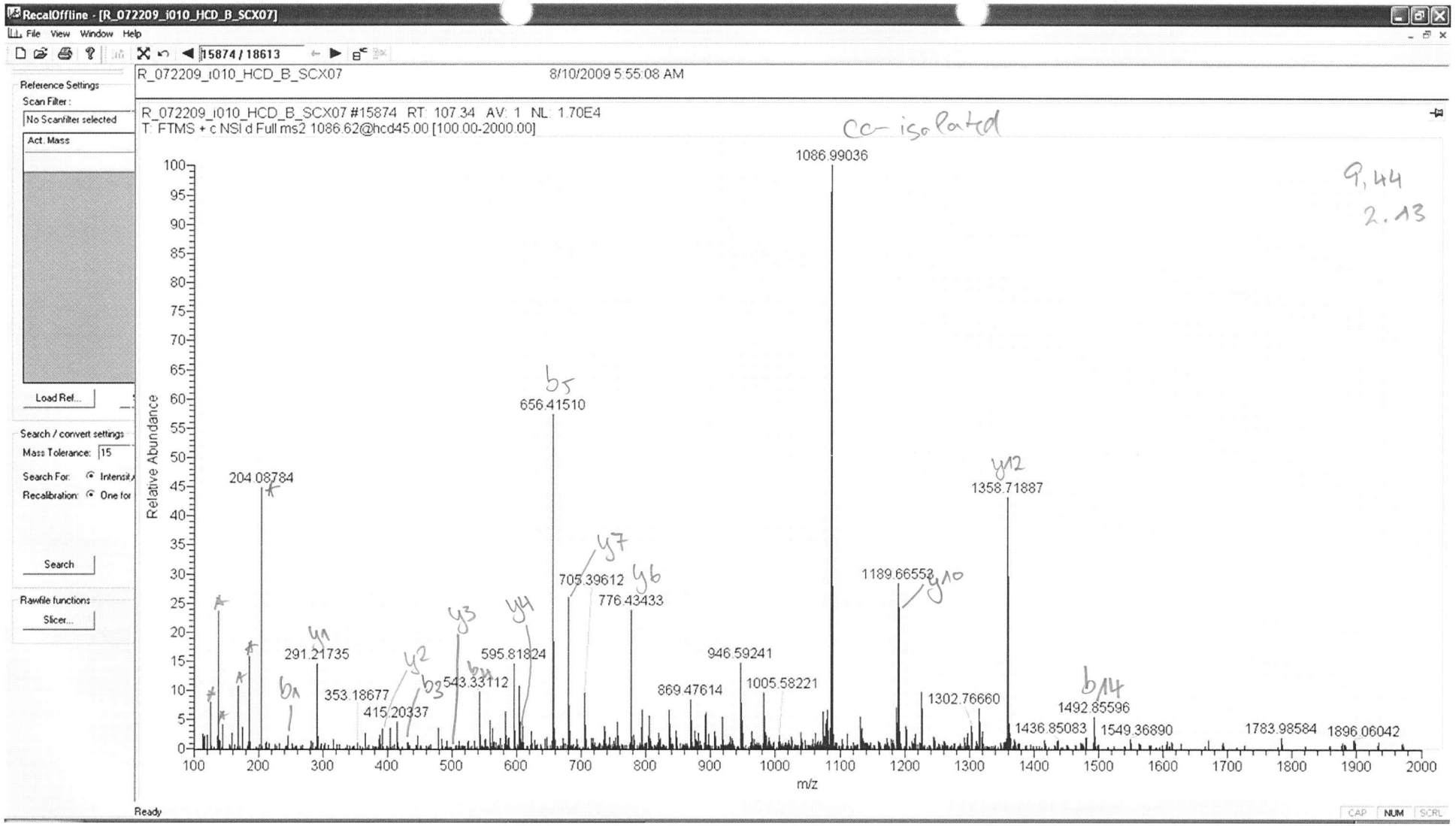
181



49.9
2.07

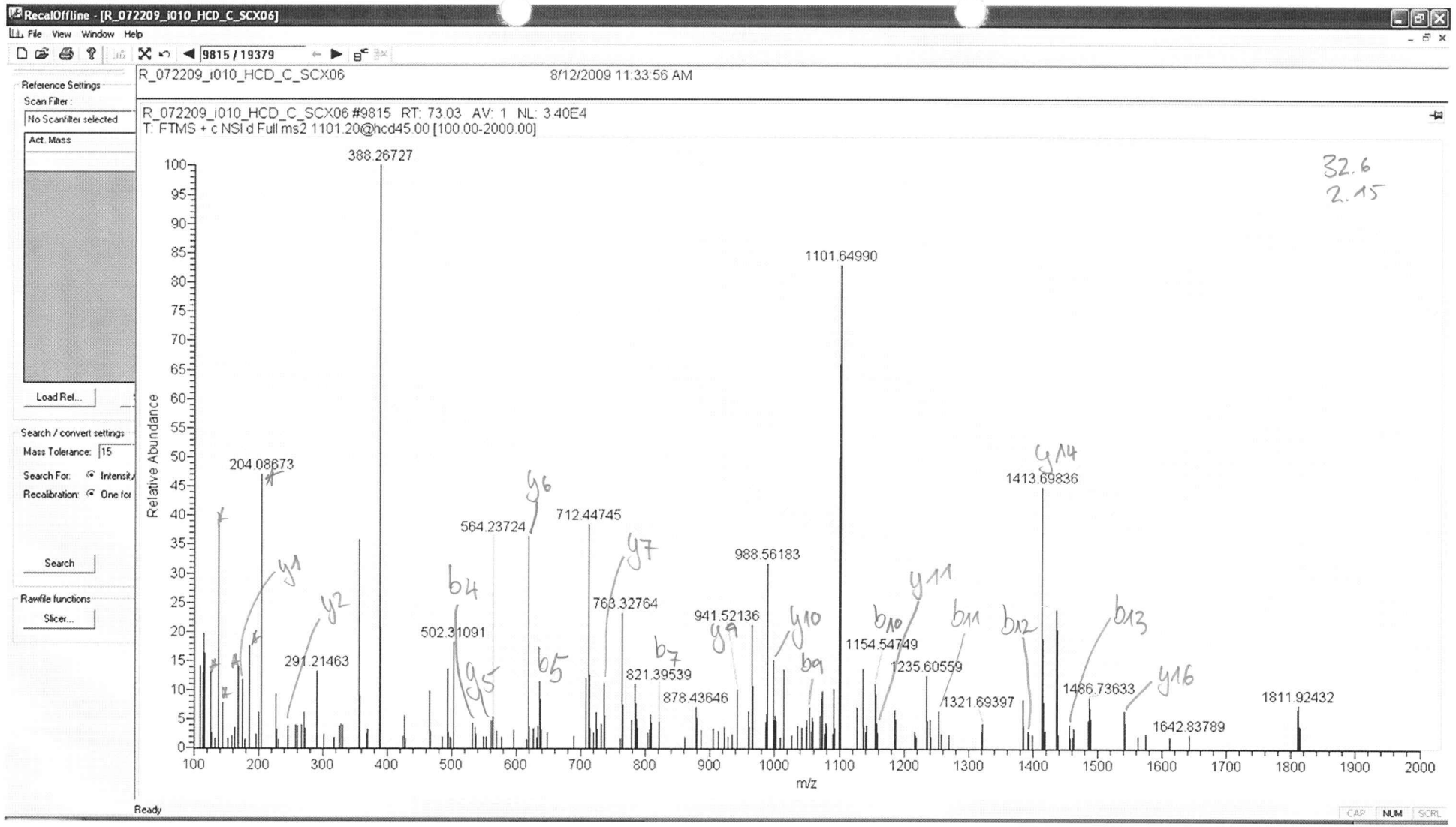
tLPILTtQAPk
b4

T1 ;
2nd site unknown
b-term., V.11 : iTRAQ4plex
182



tPSLLPPLGLSQSGPPGLLPSPSFDSkPPTTLLGLIPAP
SMVPATDtk

No Site evidence
N-term., K27, K48:
iTRAQ 4plex

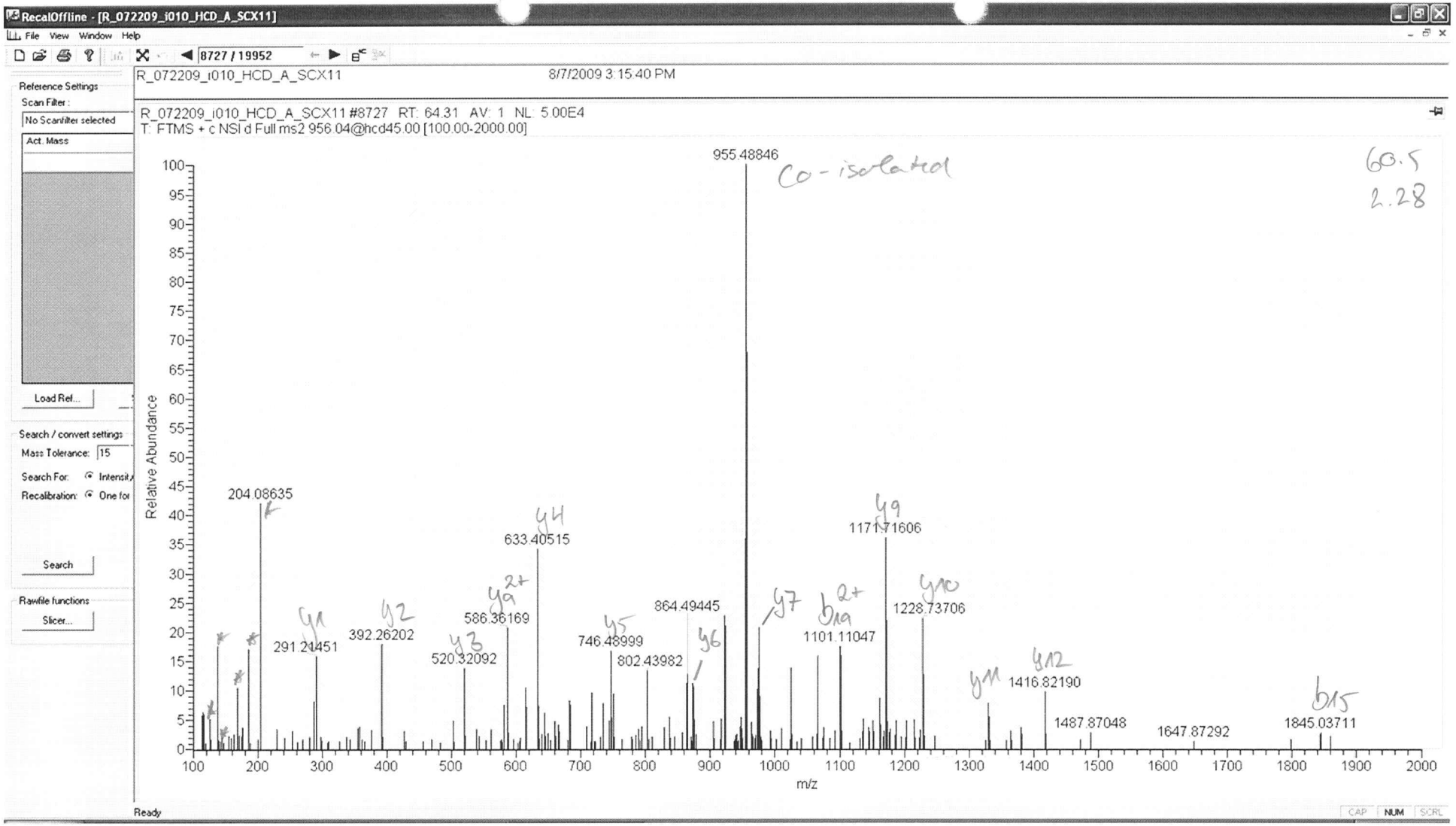


32.6
2.15

No site evidence
N-term : TRAQ4plex

qTSATSTTMTVMATGAPcsAGPLLGPSMAR

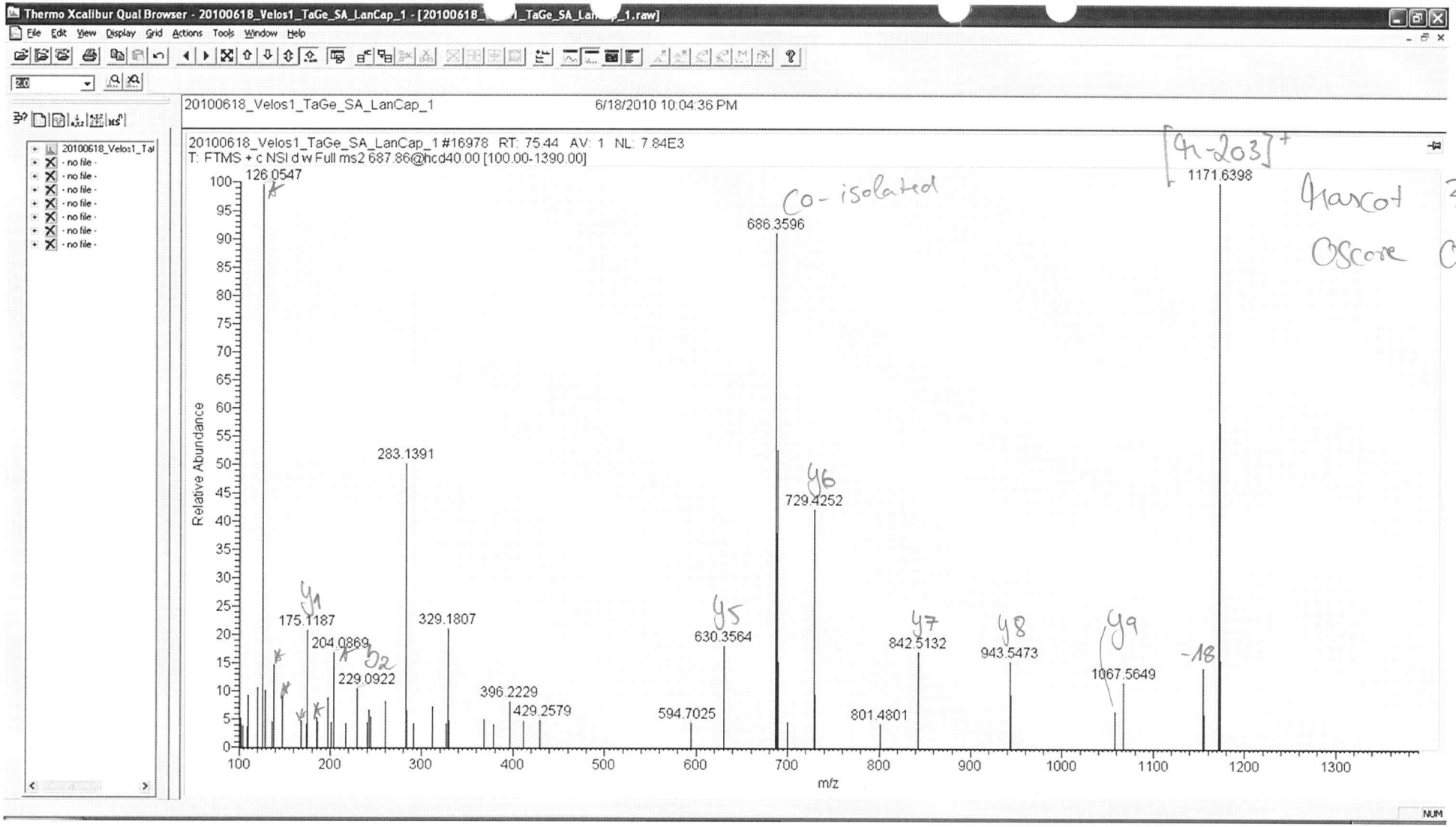
y14 y9

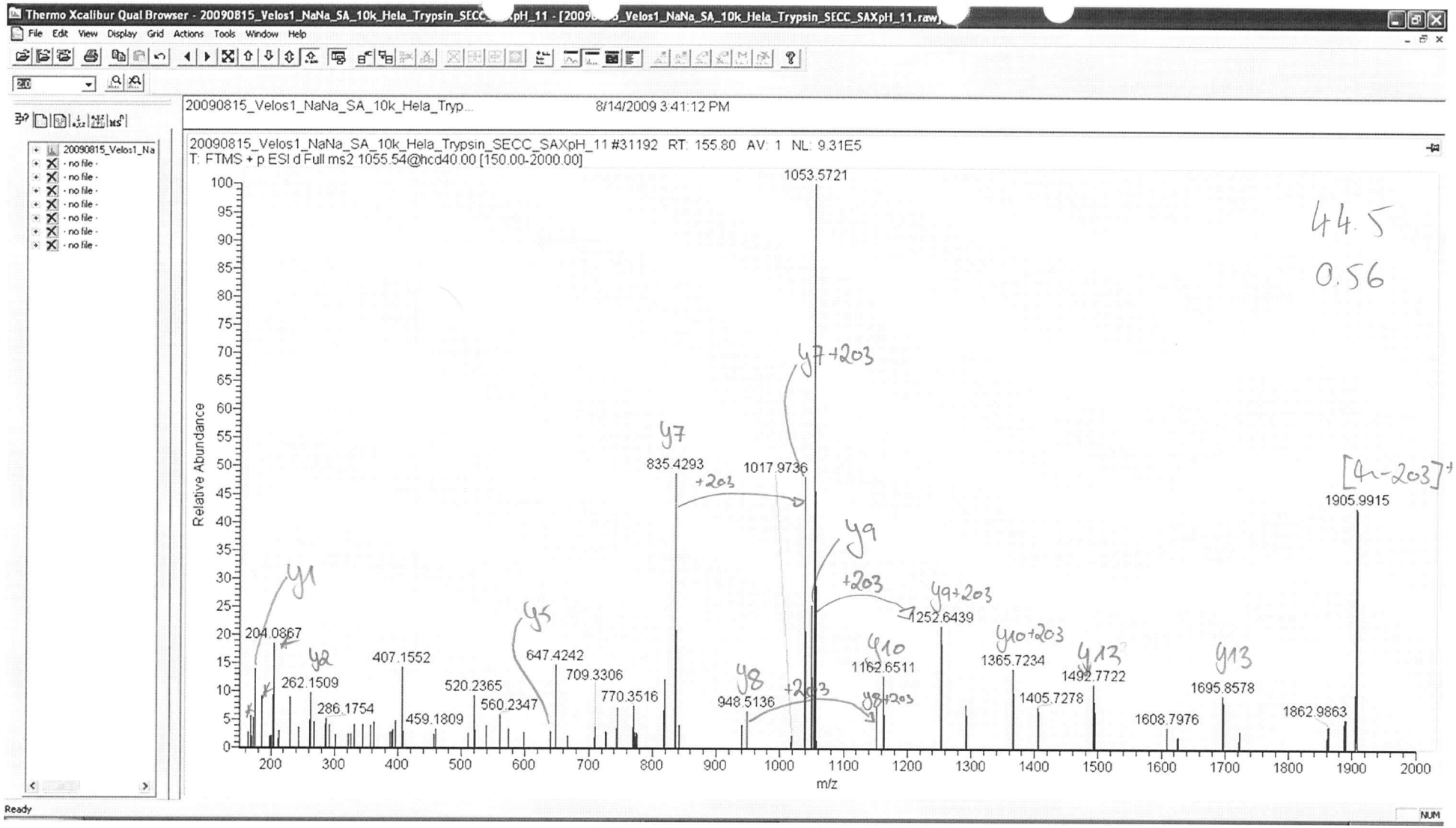


vMSVVQTkPVQTSAVTGQASTGPVTQIIQtk

No site evidence
N-term, K8, K31: iTRAQ4plex

185


Thermo Xcalibur Qual Browser - 20100618_Velos1_TaGe_SA_LanCap_1
File Edit View Display Grid Actions Tools Window Help
20100618_Velos1_TaGe_SA_LanCap_1 6/18/2010 10:04:36 PM
20100618_Velos1_TaGe_SA_LanCap_1 #16978 RT: 75.44 AV: 1 NL: 7.84E3
T: FTMS + c NSI d w Full ms2 687.86@hcd40.00 [100.00-1390.00]
[M-203]+
1171.6398
Co-isolated
686.3596
126.0547
283.1391
729.4252
175.1187
204.0869
329.1807
630.3564
842.5132
943.5473
1067.5649
-18
229.0922
396.2229
429.2579
594.7025
801.4801
Relative Abundance
m/z
Marcot 38
Oscore 0.66
No site evidence
NNTIVnELVR
186



44.5

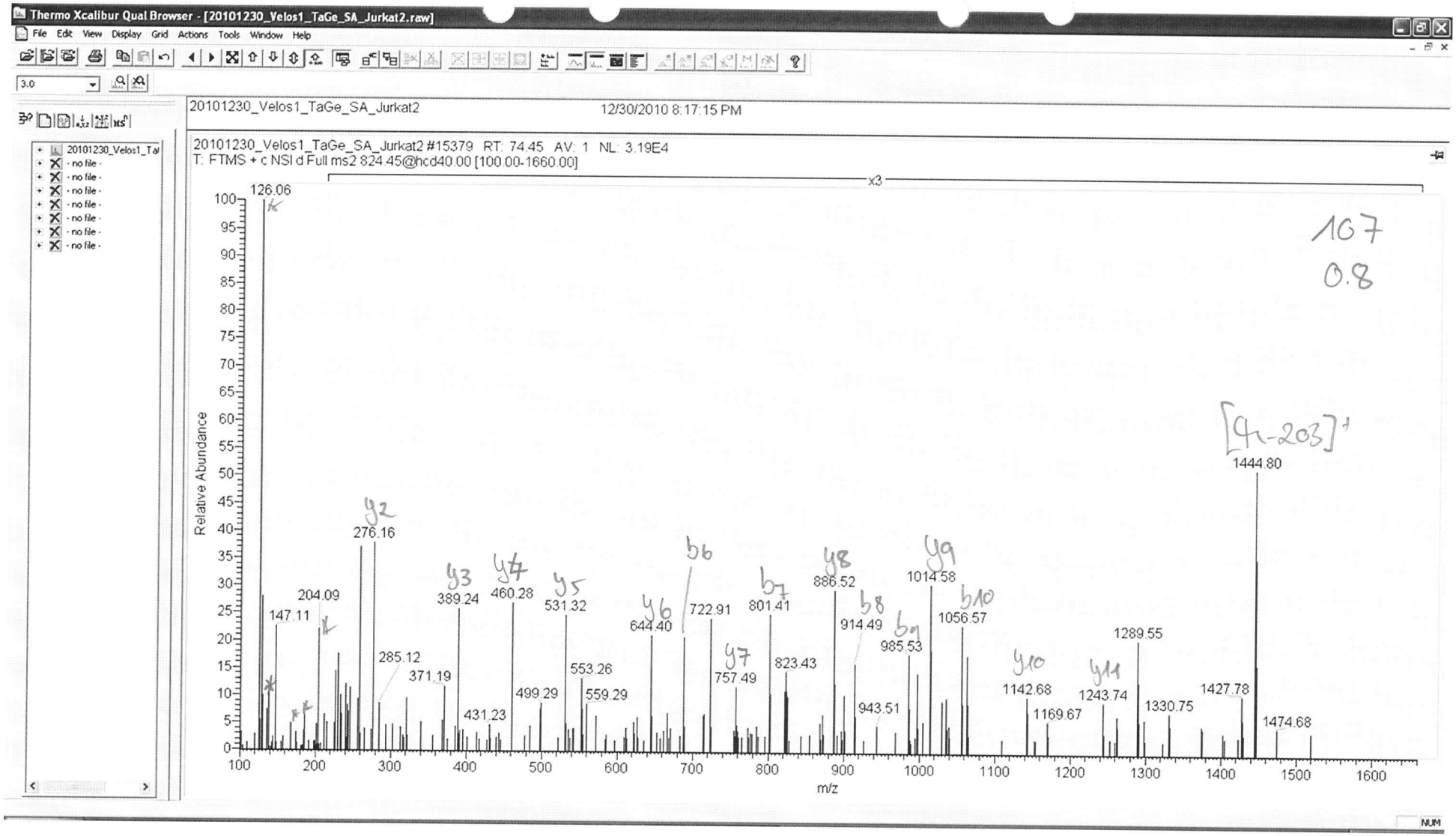
0.56

T13 or S16

y7

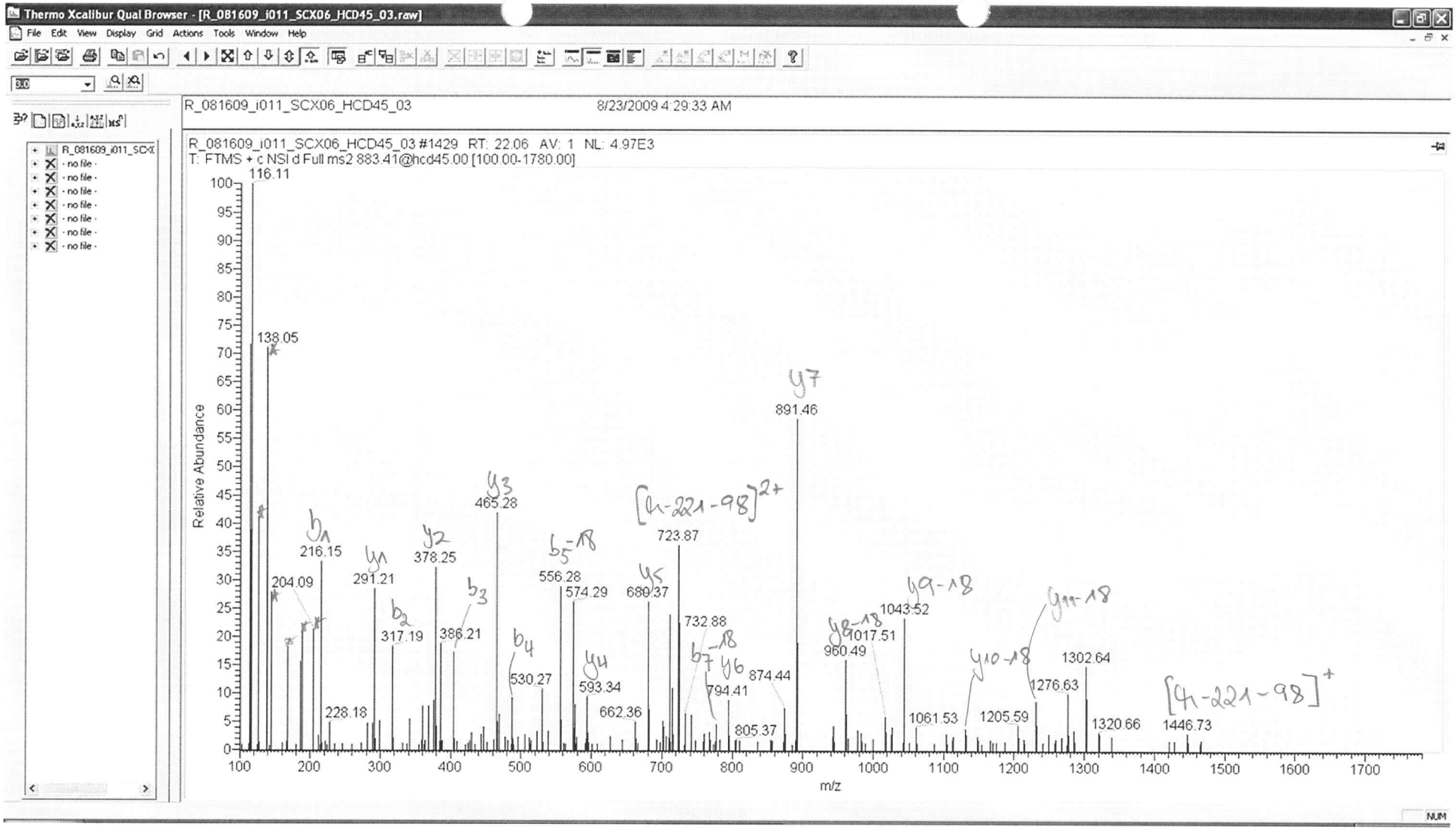
LATQSNEITIPVTFEsR

187



No site evidence

NStKQEILAALEK



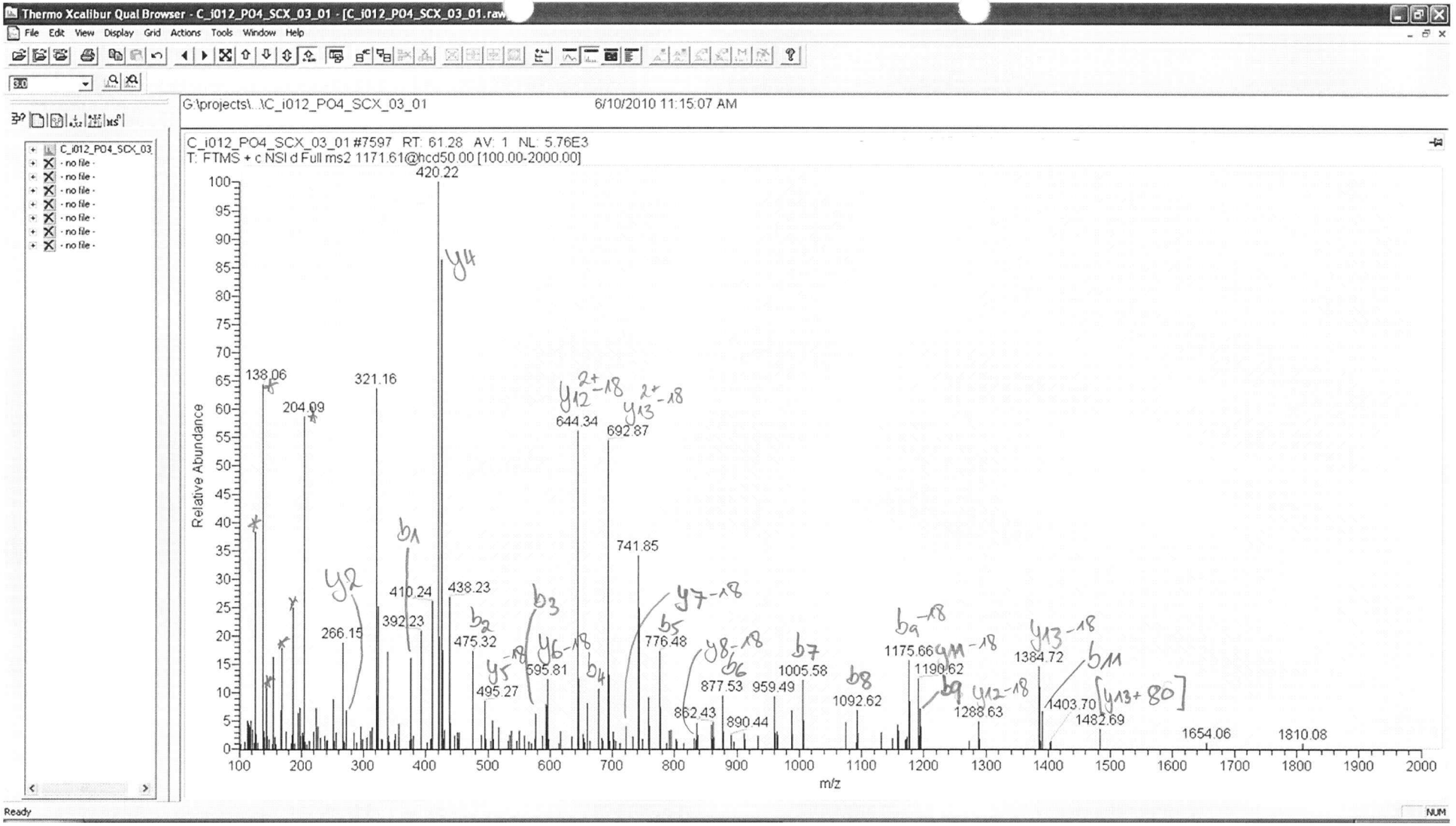
189: aTSTsPNSQSsk

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 77.7, Oscore = 1.78)

No site evidence for OGlcNAc

S5: phospho

N-term, K12: iTRAQ4plex

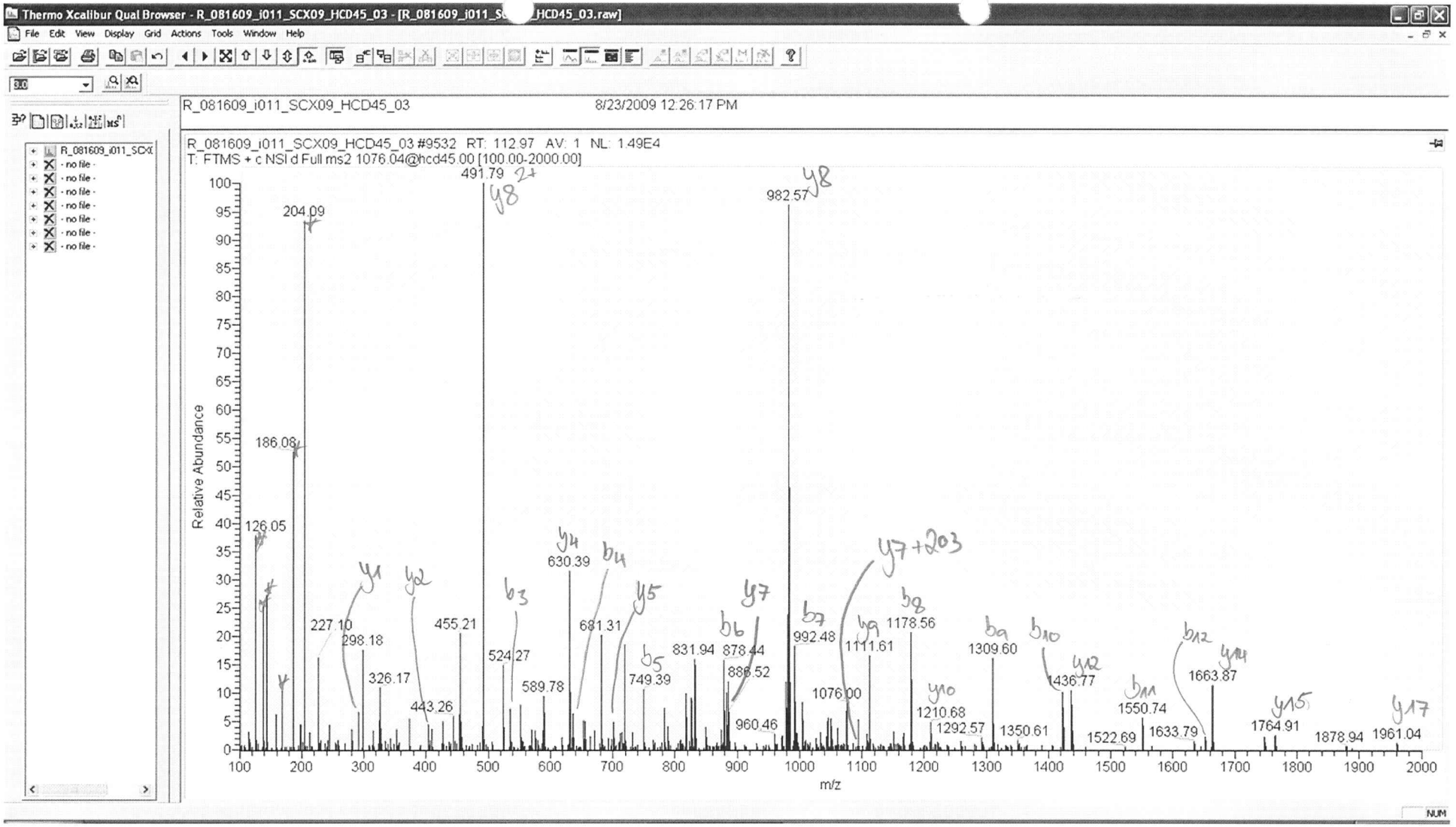


S25: phospho GlcNAc site unknown

N-term iTRAQ8plex

190: aVTTVTQSTPVPGPsVPPPEELQVsPGPR

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 65.8, Oscore = 1.83)

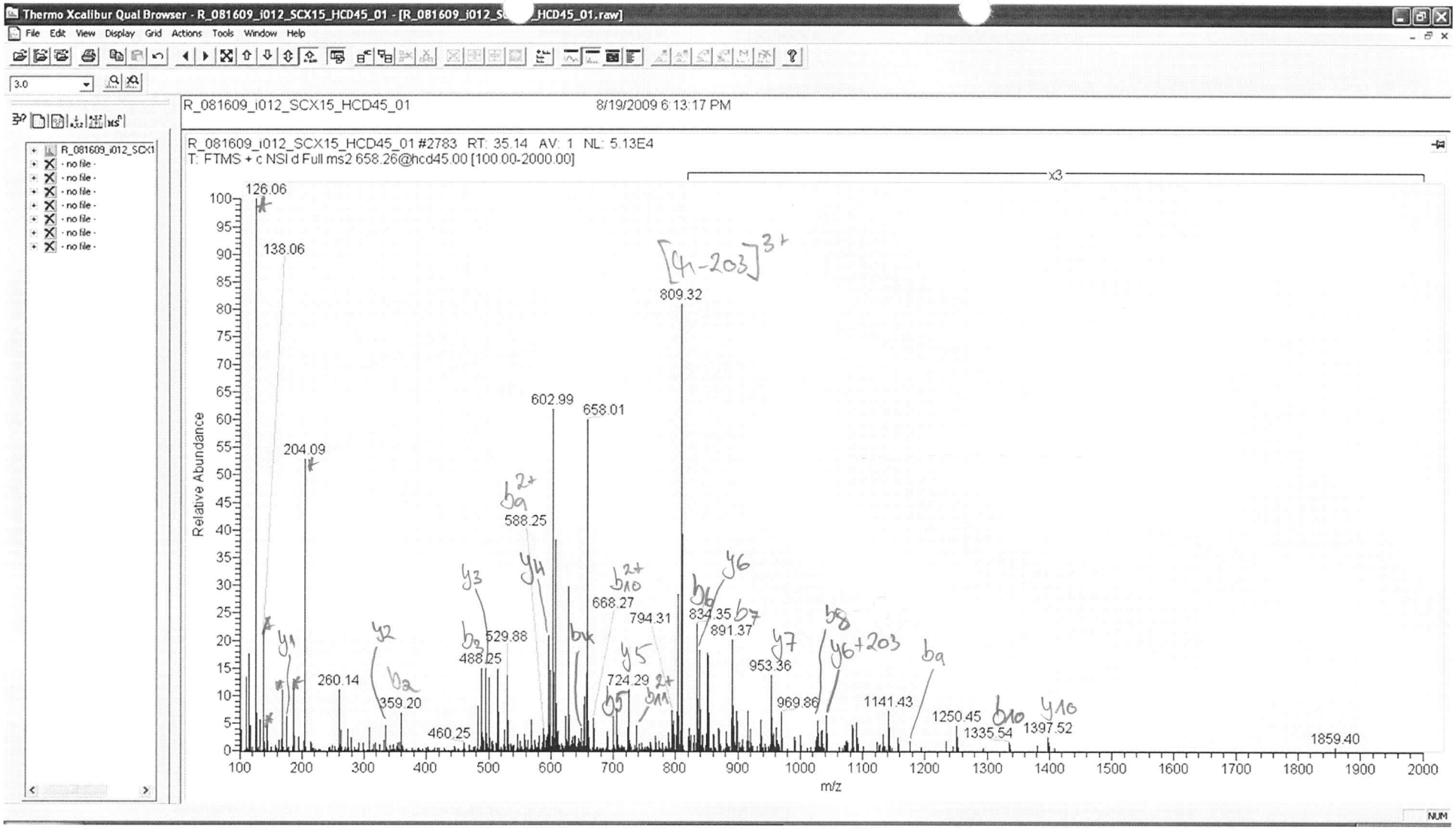


S28 : OGlcNAc

N-term., K33 : iTRAQ8plex

191: dFQTLENWMLQTLNEEPVTPEPEVEPPsAPELk

(1 O-GlcNAc site, 0 phospho-site, Mascot score = 86.3, Oscore = 1.53)

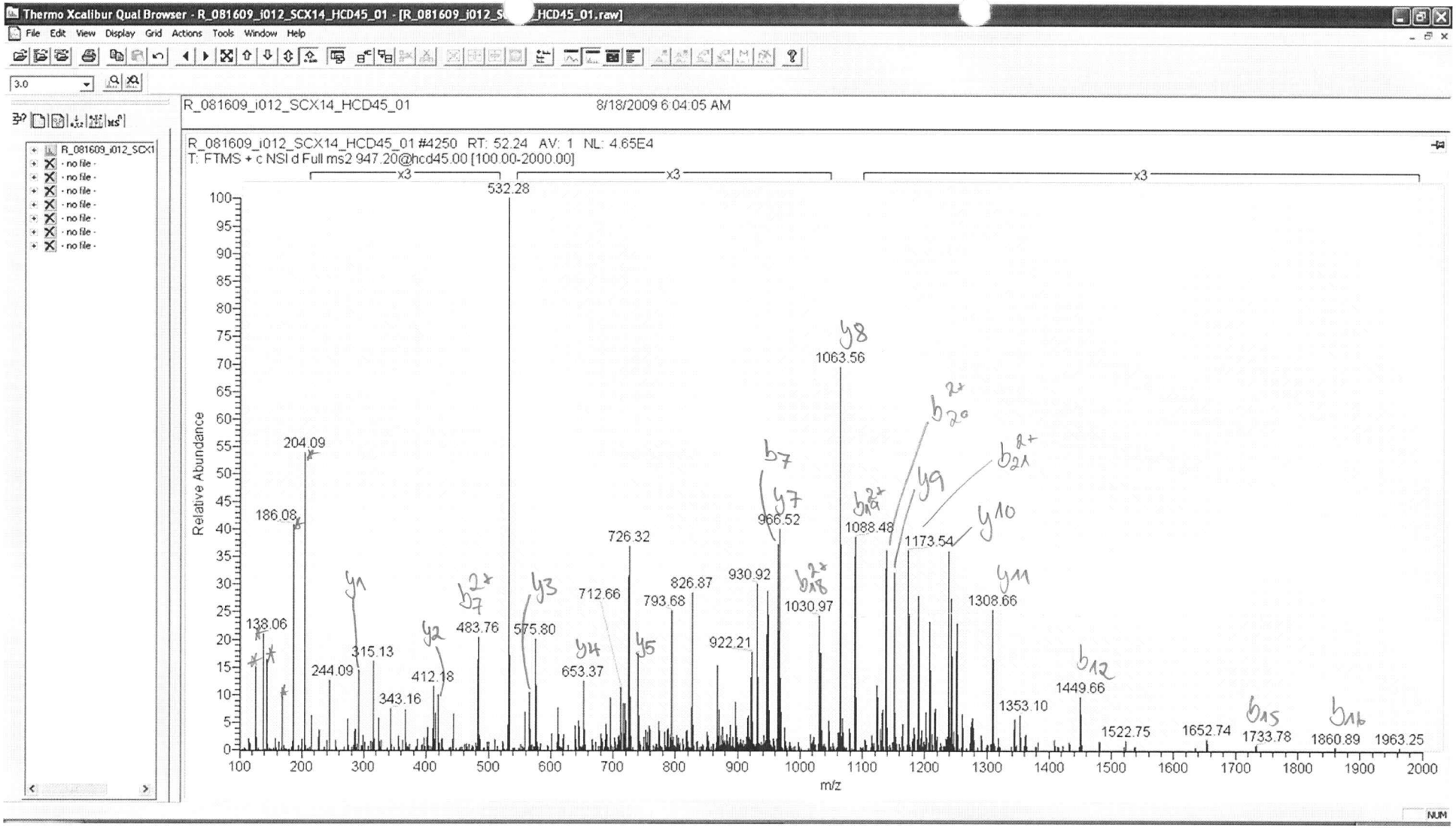


N13 : GlcNAc

N-term, iTRAQ4plex

192: dVEcGEGHFcHDNQtccR

(1 O-GlcNAc site, 0 phospho-site, Mascot score = 76.4, Oscore = 1.79)

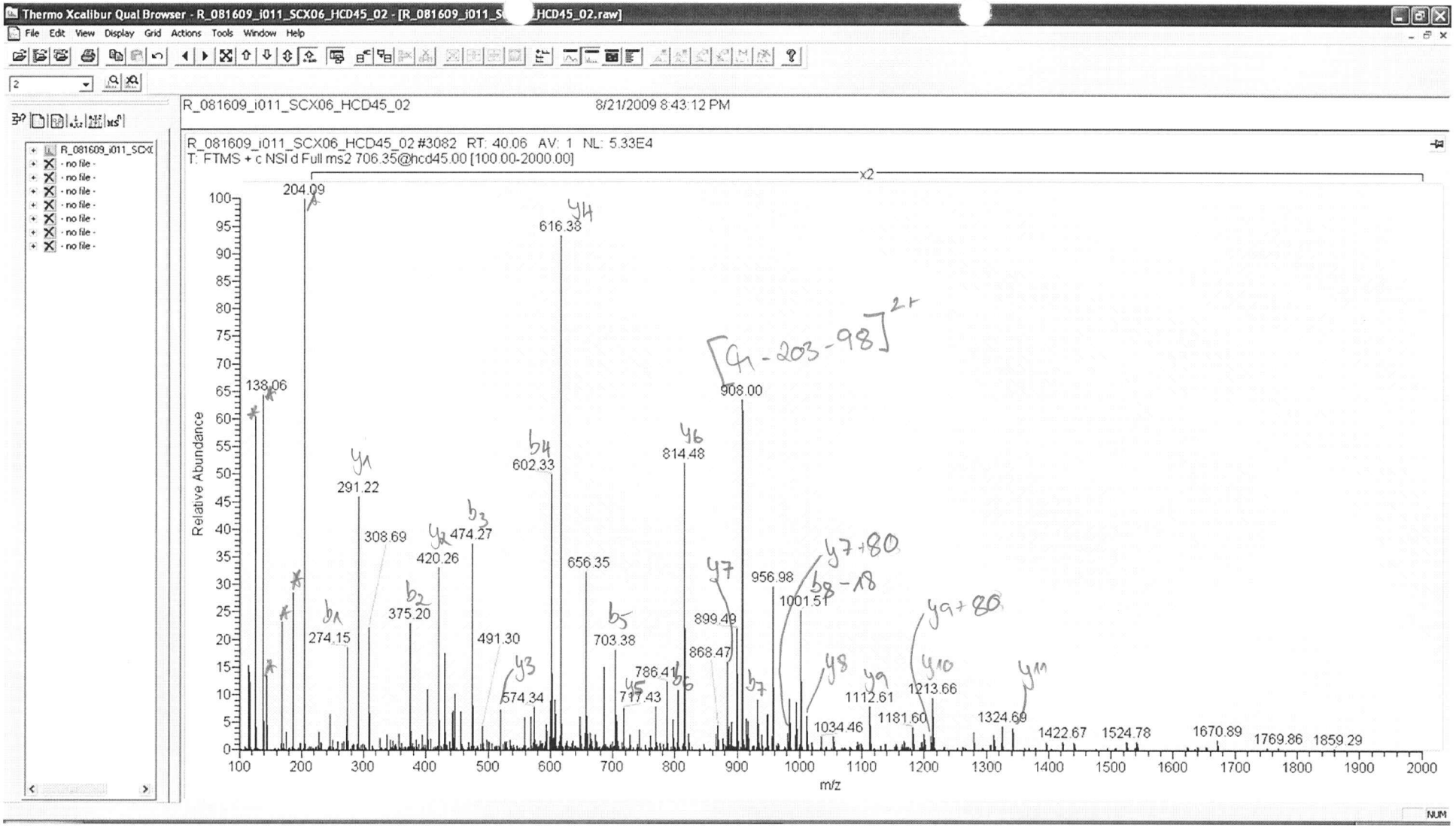


No site evidence

N-term., K31: iTRAQ4plex

193: eFHHGPDPTDTAPGEQAQDVASSPPESsFQk

(1 O-GlcNAc site, 0 phospho-site, Mascot score = 68.8, Oscore = 1.71)

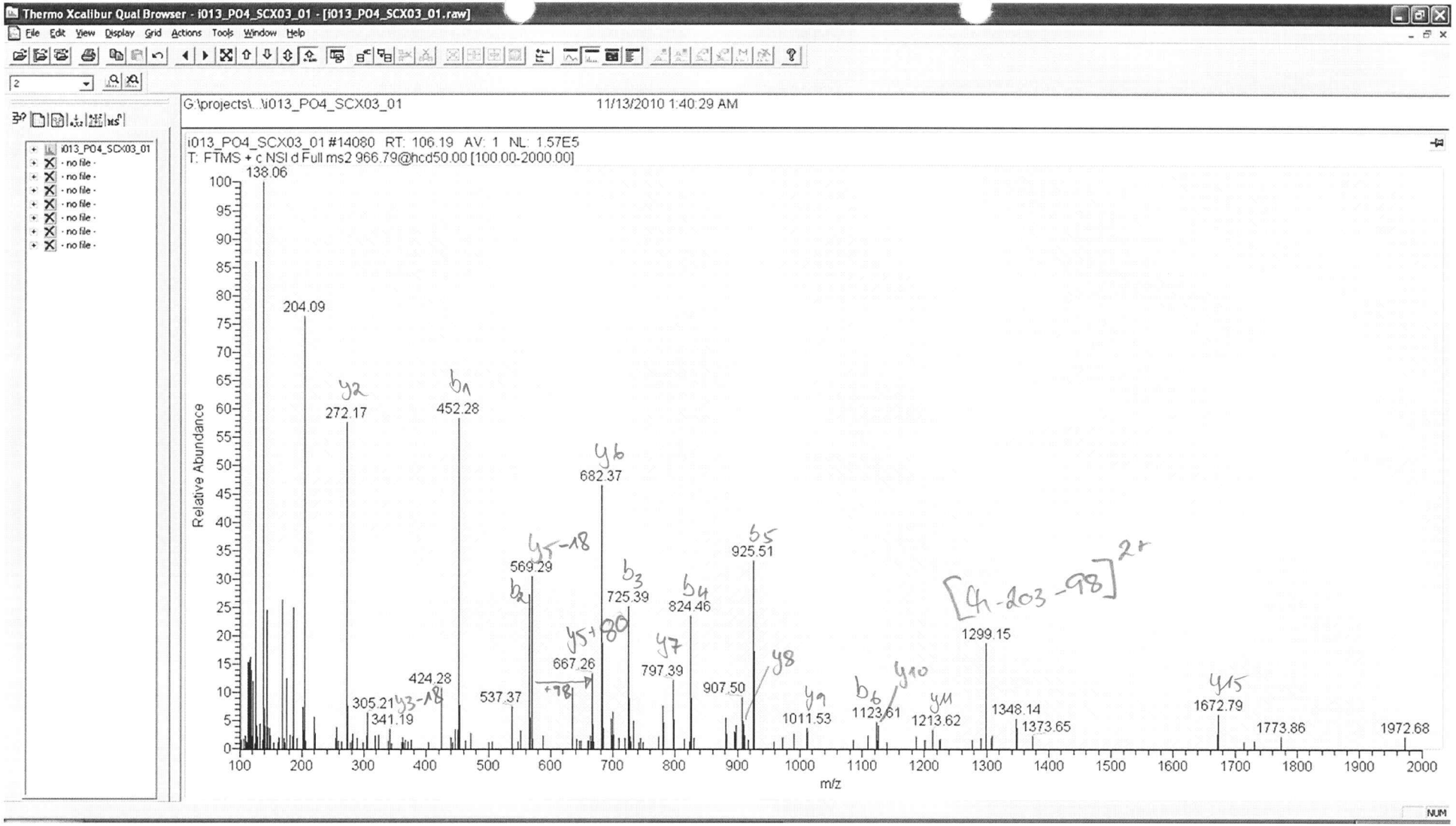


S8 : phospho
OGlcNAc site unknown

N-term., K14 : iTRAQ 4plex

194: eTVQTtQsPTPVEk

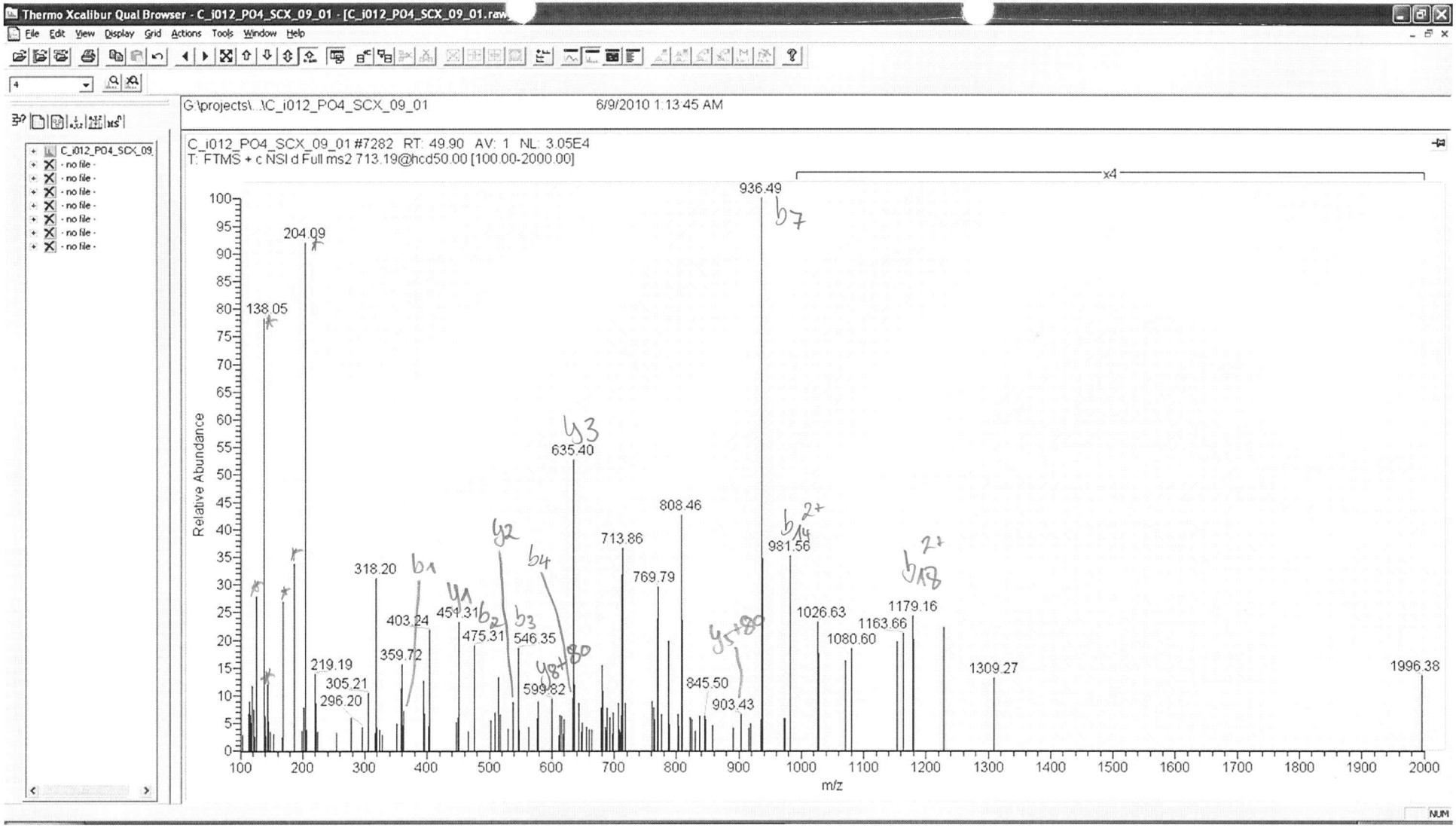
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 63.5, Oscore = 0.91)



S18 : phospho
OGlcNAc site unknown

N-term. iTRAQ 8plex

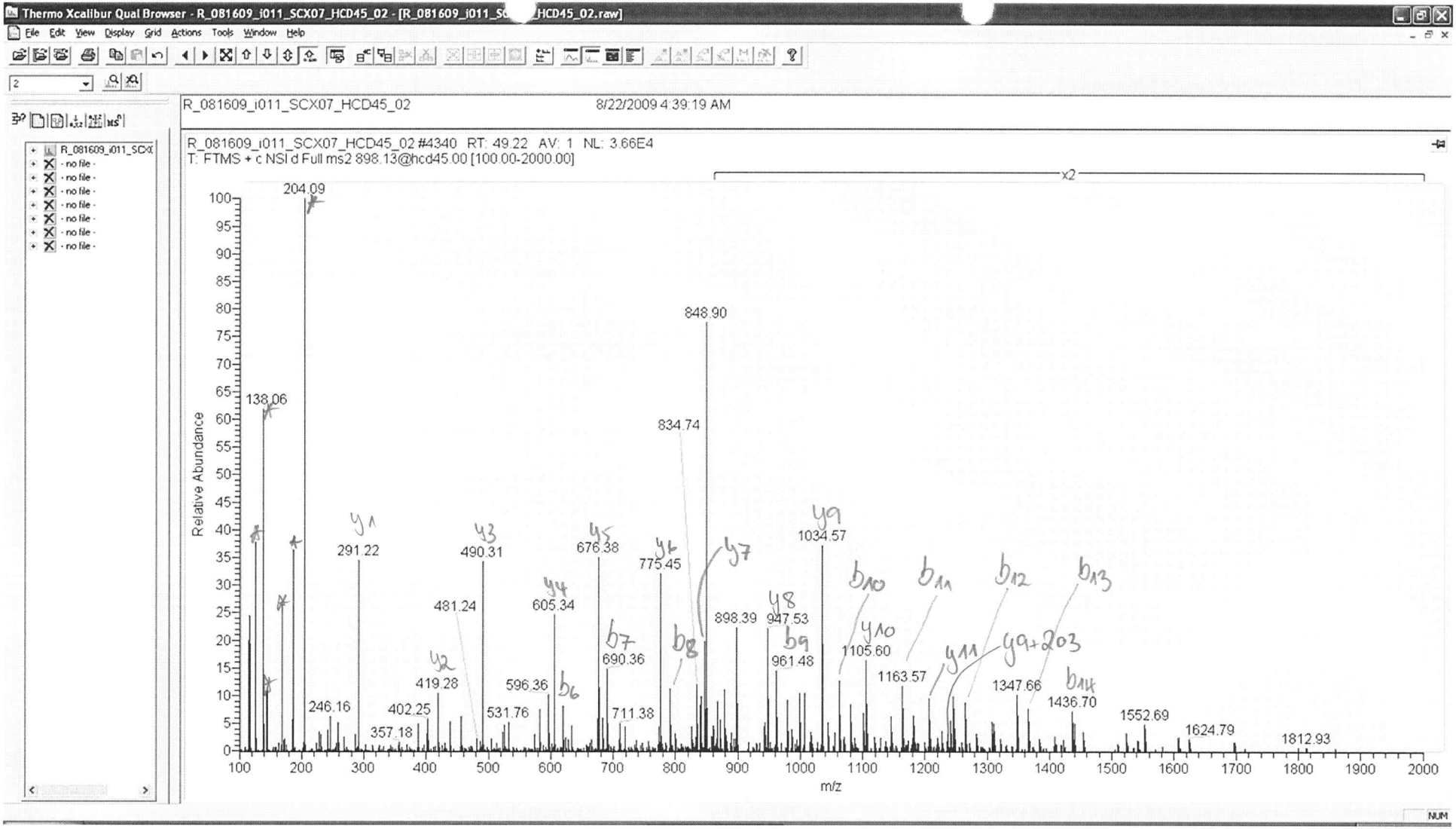
195: fIcVTPTTcSNtIDLPMsPR
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 78, Oscore = 0.87)



No site evidence for O-GlcNAc phospho @ S20 or T21
N-term., K14, K24 iTRAQ 8plex

196: gIASTSDPPTANIkPTPVVStPsk

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 31.5, Oscore = 1.72)

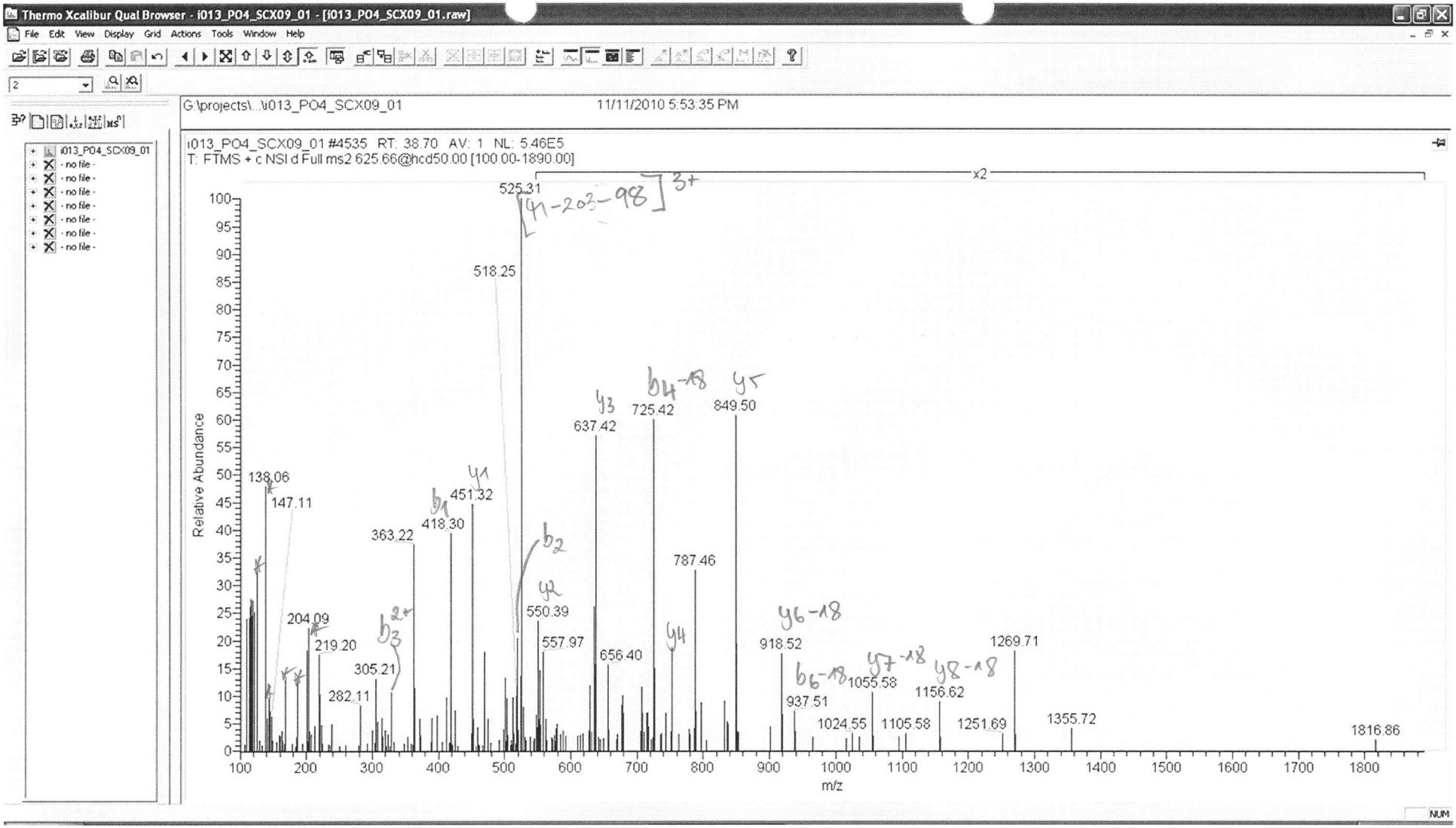


S15 or T16 : OGlcNAc

N-term, K23 iTRAQ 4 plex

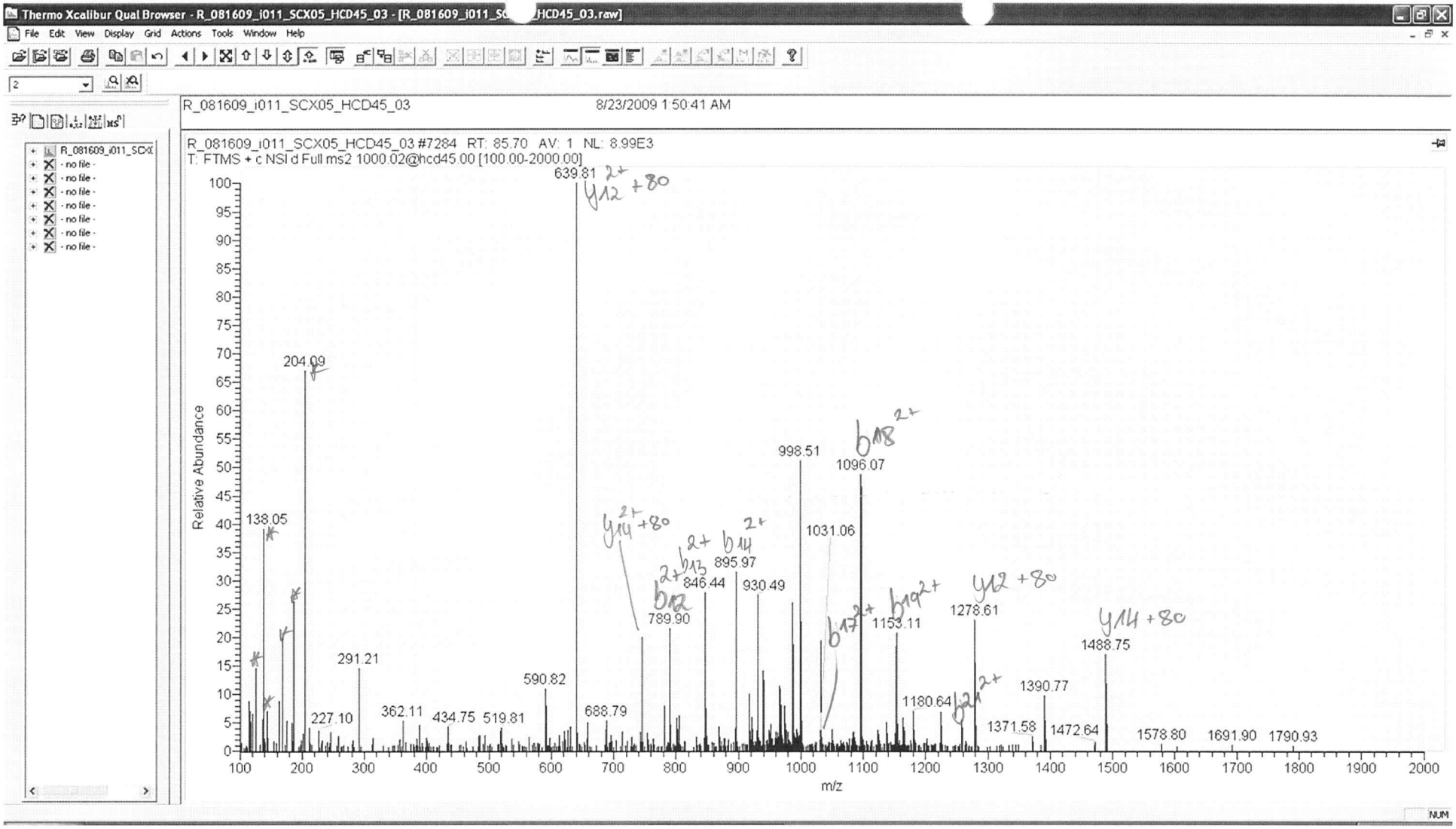
197: gTTTNATStTTTTASTAVADAQk

(1 O-GlcNAc site, 0 phospho-site, Mascot score = 90.5, Oscore = 1.23)



No site evidence for OglcNAc
S4: phospho
N-term, K9: iTRAQ8plex

199: iTHsPDsVk
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 37.8, Oscore = 2.04)



No site evidence for OGlcNAc

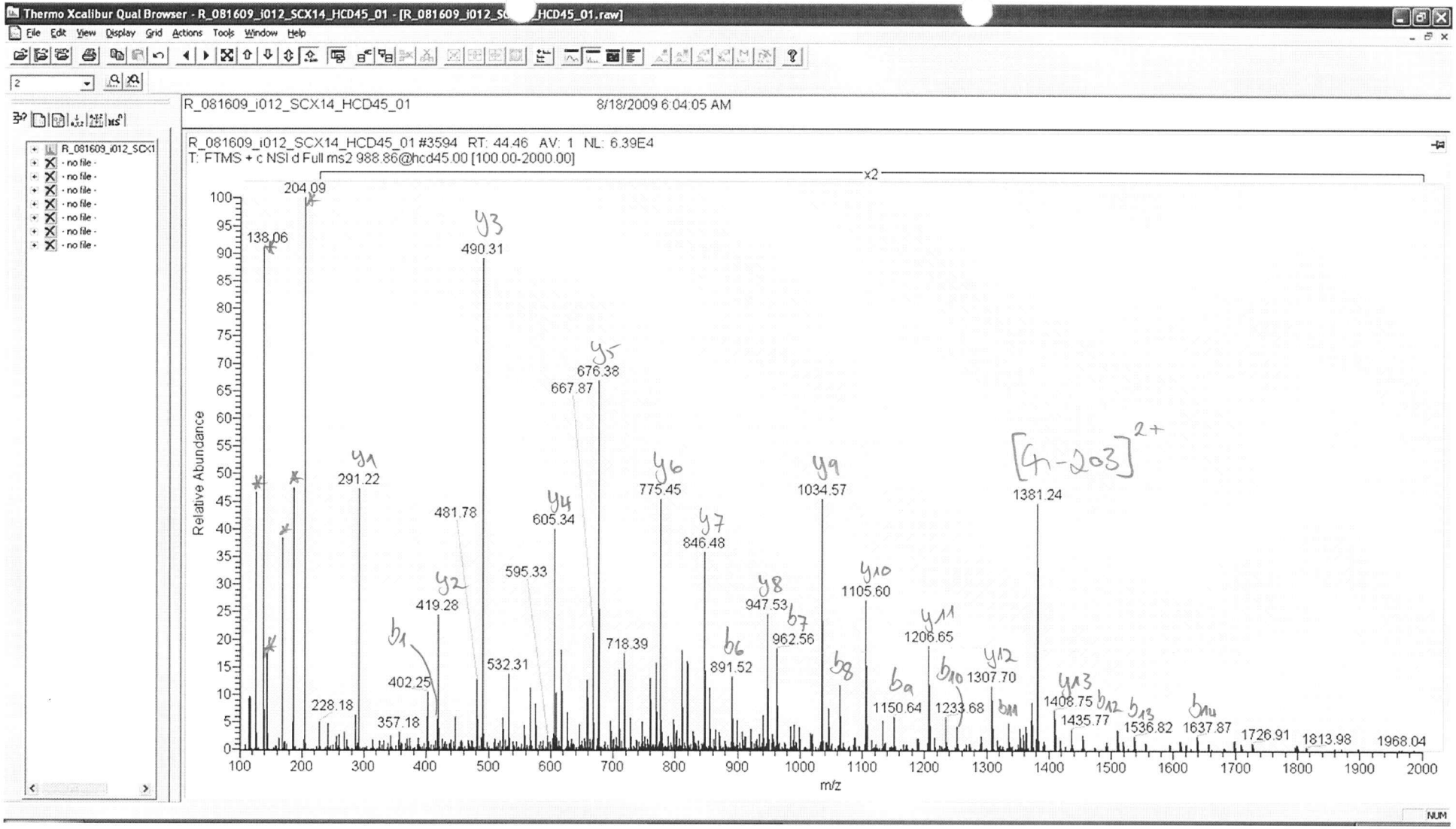
S24, T26, T27, S29 or S30 : phospho

K1, N-ter. : iTRAQ4plex

y14 y12

200: kEQEGQtSETTAIVSIAELPLPPSPTTVSsVAR

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 33, Oscore = 1.95)

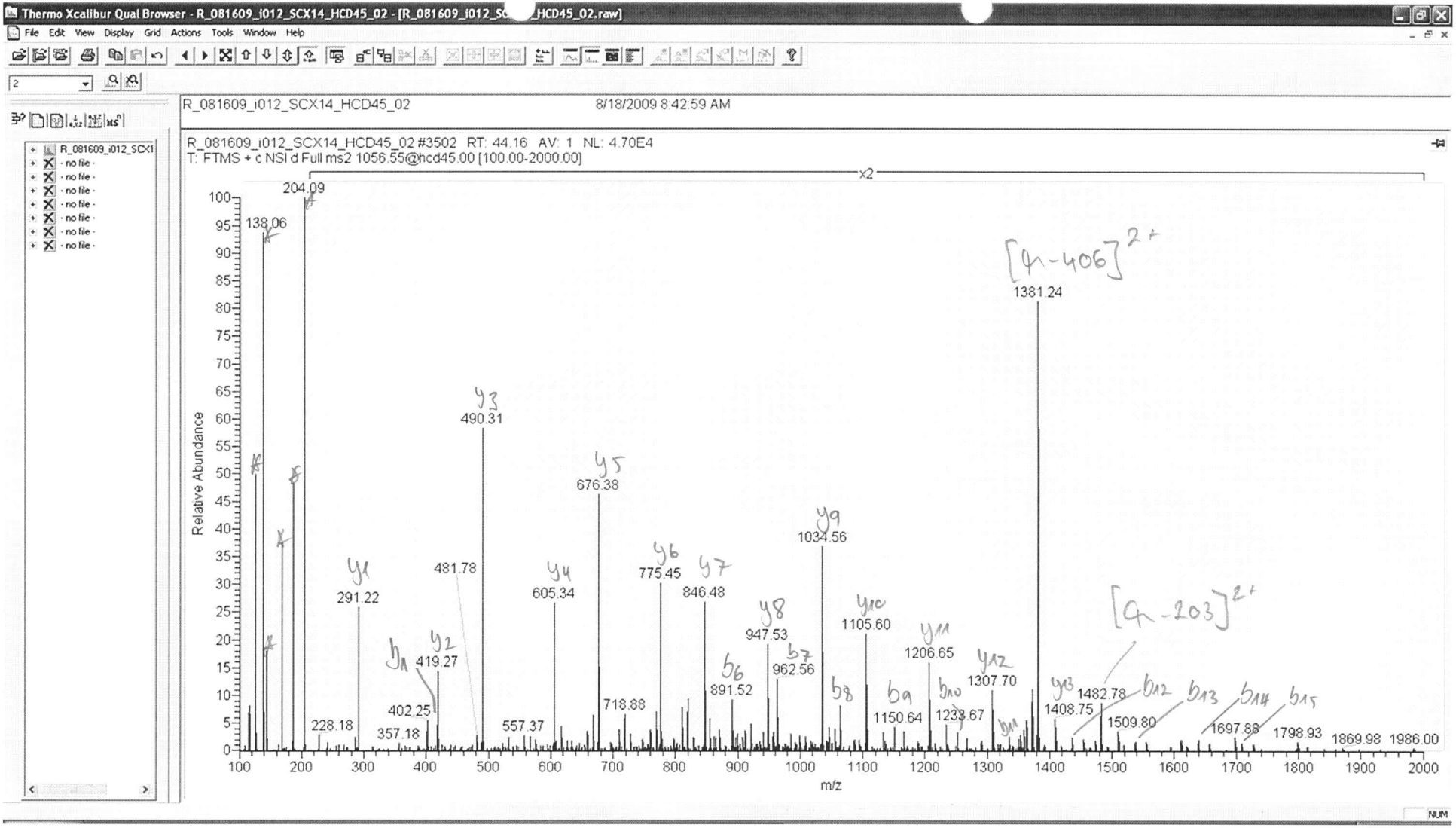


No site evidence

K-term., K1, K24 : iTRAQ4plex

201: kGTTTNATSTtTTTASTAVADAQk

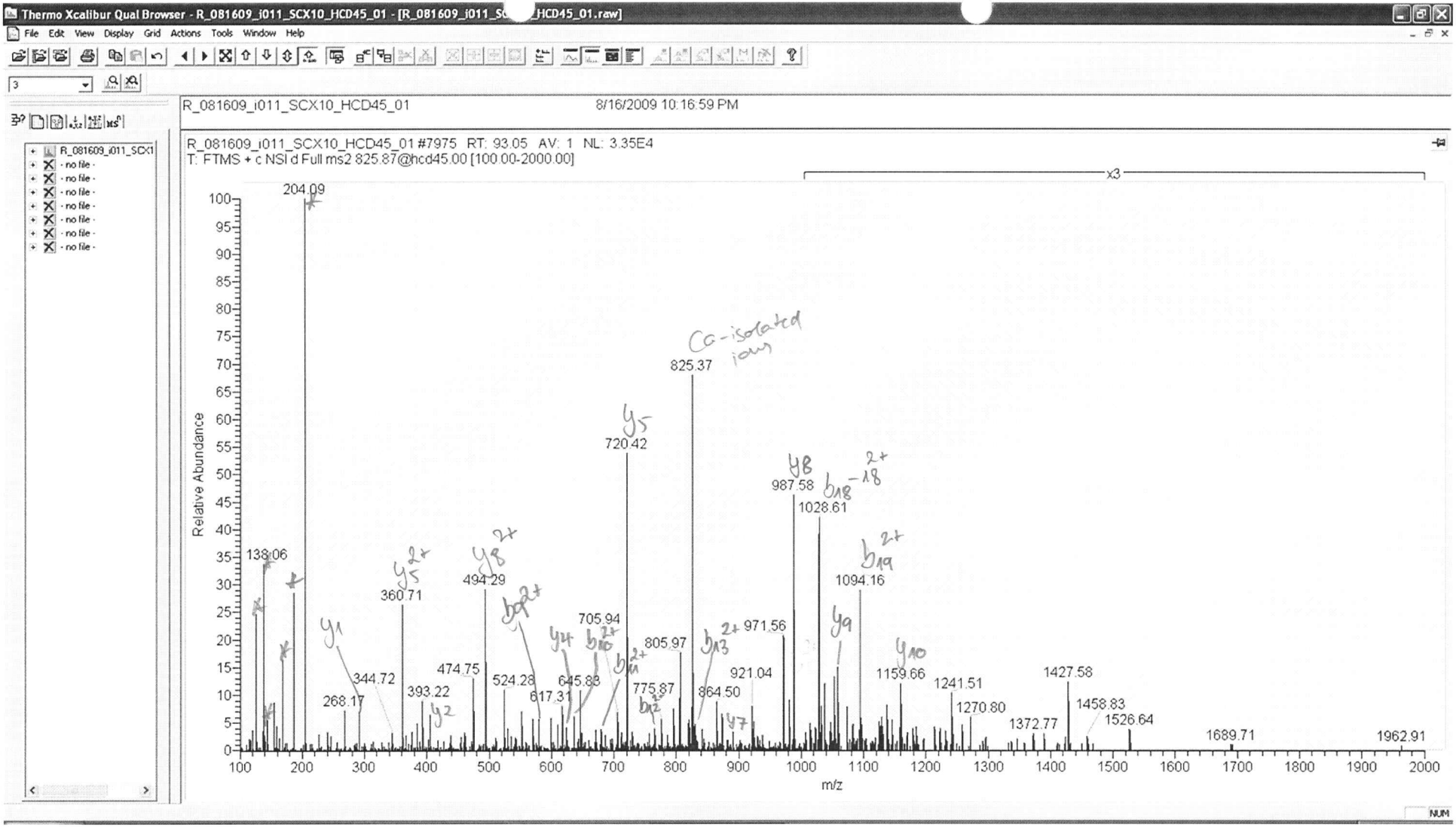
(1 O-GlcNAc site, 0 phospho-site, Mascot score = 120, Oscore = 0.86)



no site evidence found
N-term, K1, K24: iTRAQ4plex

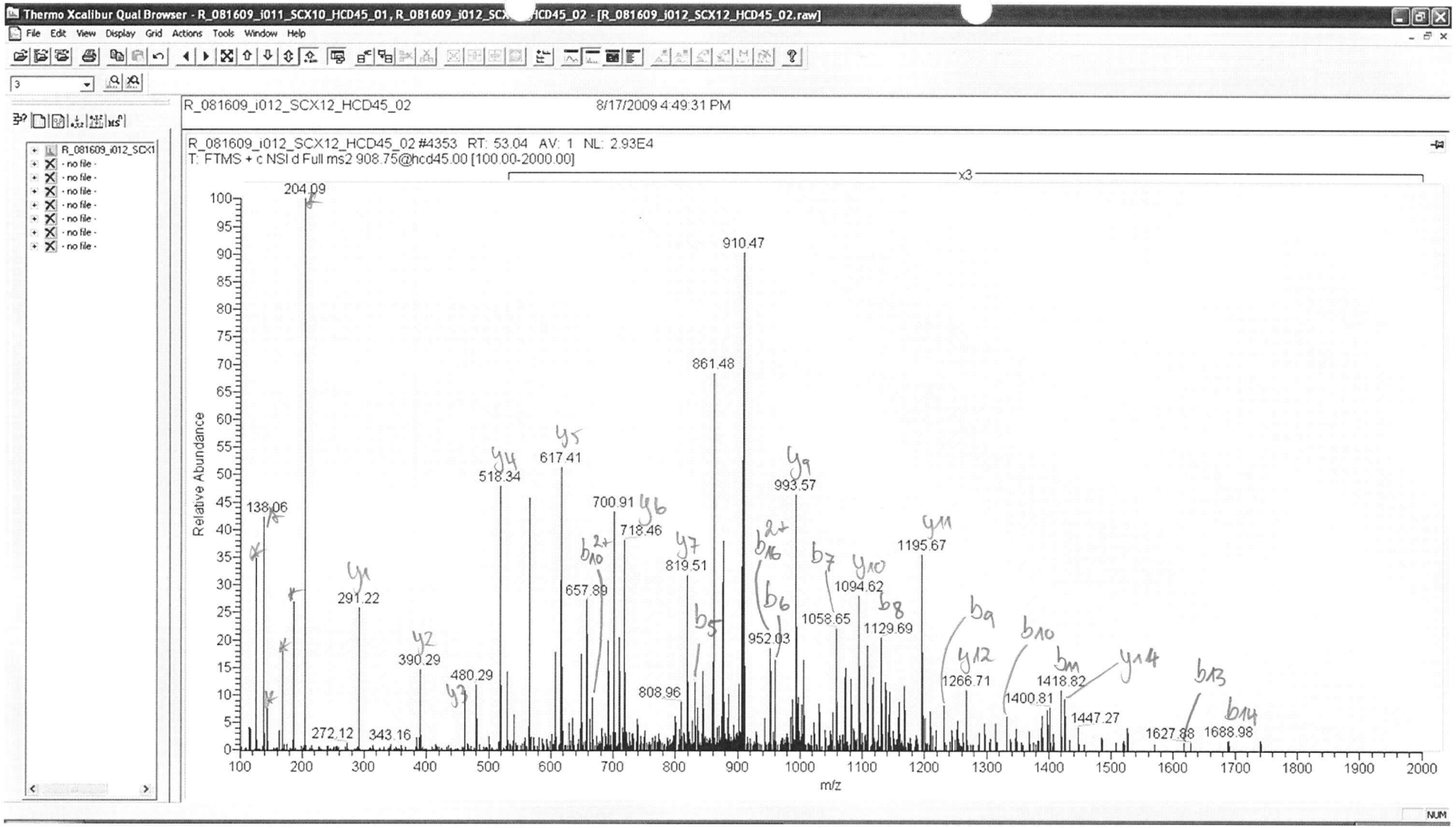
202: kGTTTNATStTTTTAsTAVADAQk

(2 O-GlcNAc site, 0 phospho-site, Mascot score = 115, Oscore = 0.95)



No site evidence found
N-term., K1, K36 : iTRAQ4plex

203: kPLVASTTALSATESLTLLSTSAGTATAPGLPAFnk
(1 O-GlcNAc site, 0 phospho-site, Mascot score = 49.8, Oscore = 1.40)

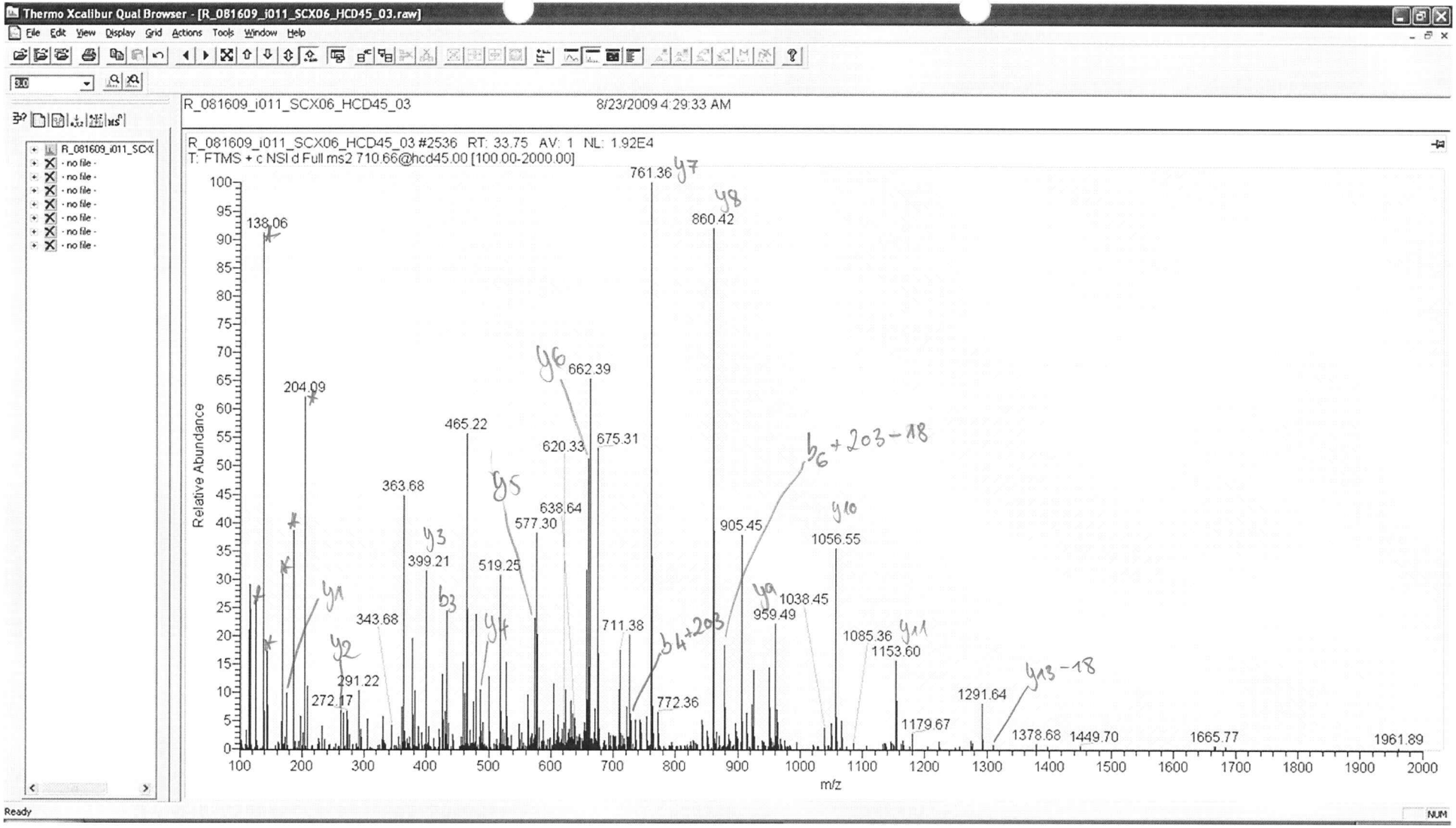


no site evidence

N-term, K1, K31: iTRAQ4plex

204: kTEALQVATTSPTANTTGTATTSSTtVGAVk

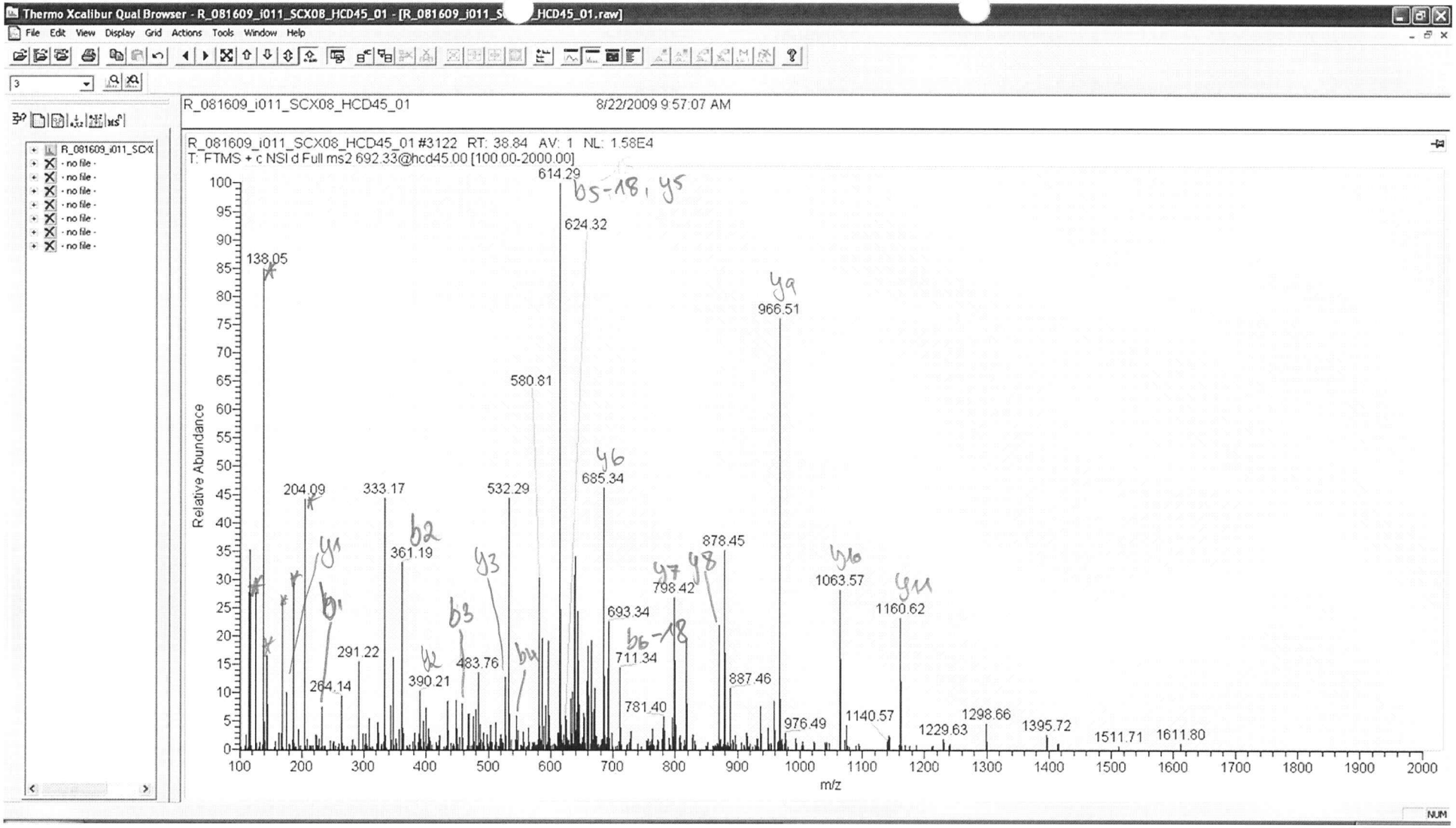
(1 O-GlcNAc site, 0 phospho-site, Mascot score = 126, Oscore = 1.00)



S4: OGlcNAc
S5 or S6: phospho
N-term.: iTRAQ4plex

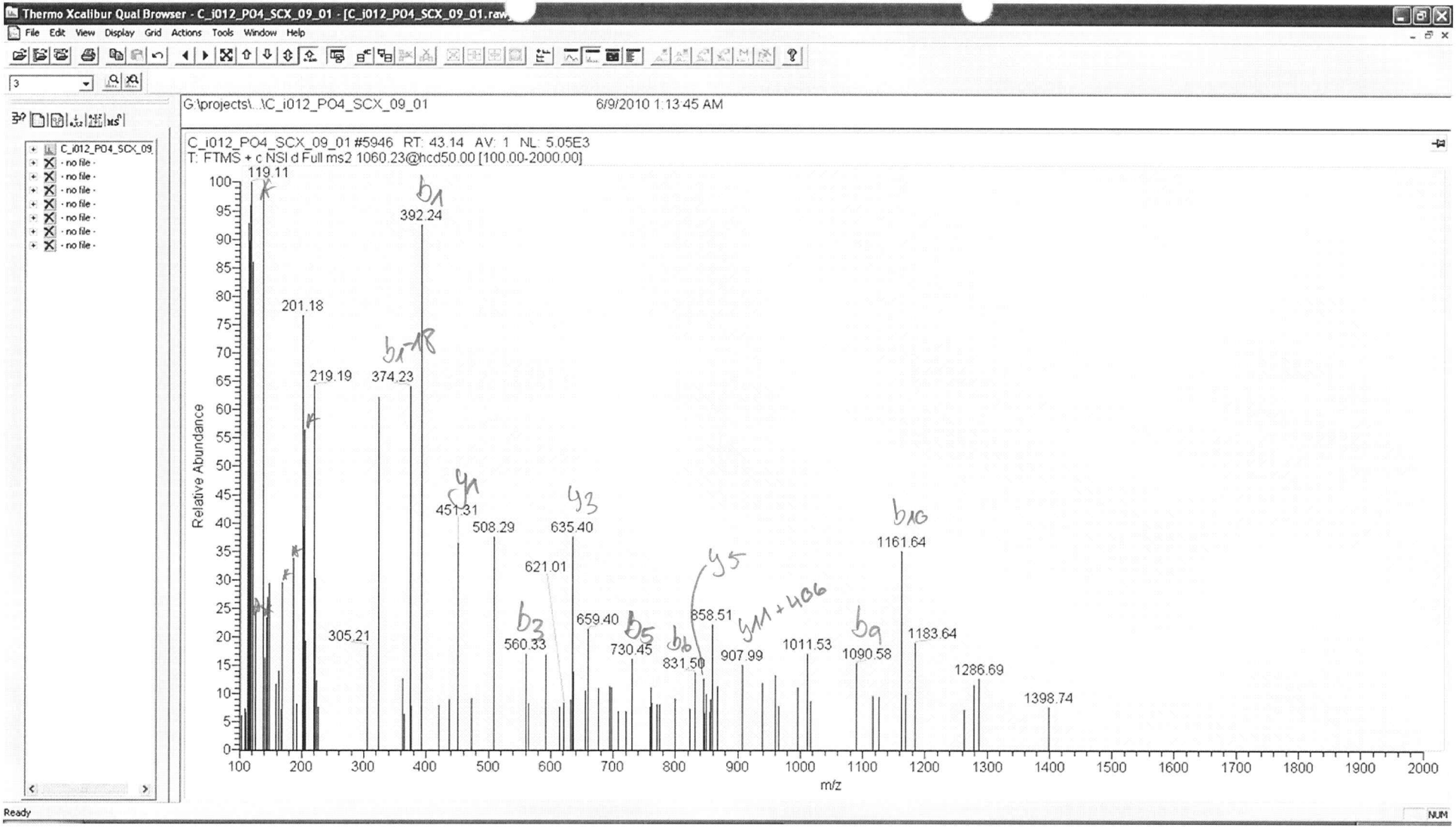
y13
y11
b4
b6

208: sEASSsPPVVTSSSHSR
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 58.3, Oscore = 1.92)



209: sEPSsPPPAIASHsQR

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 54.9, Oscore = 1.99)

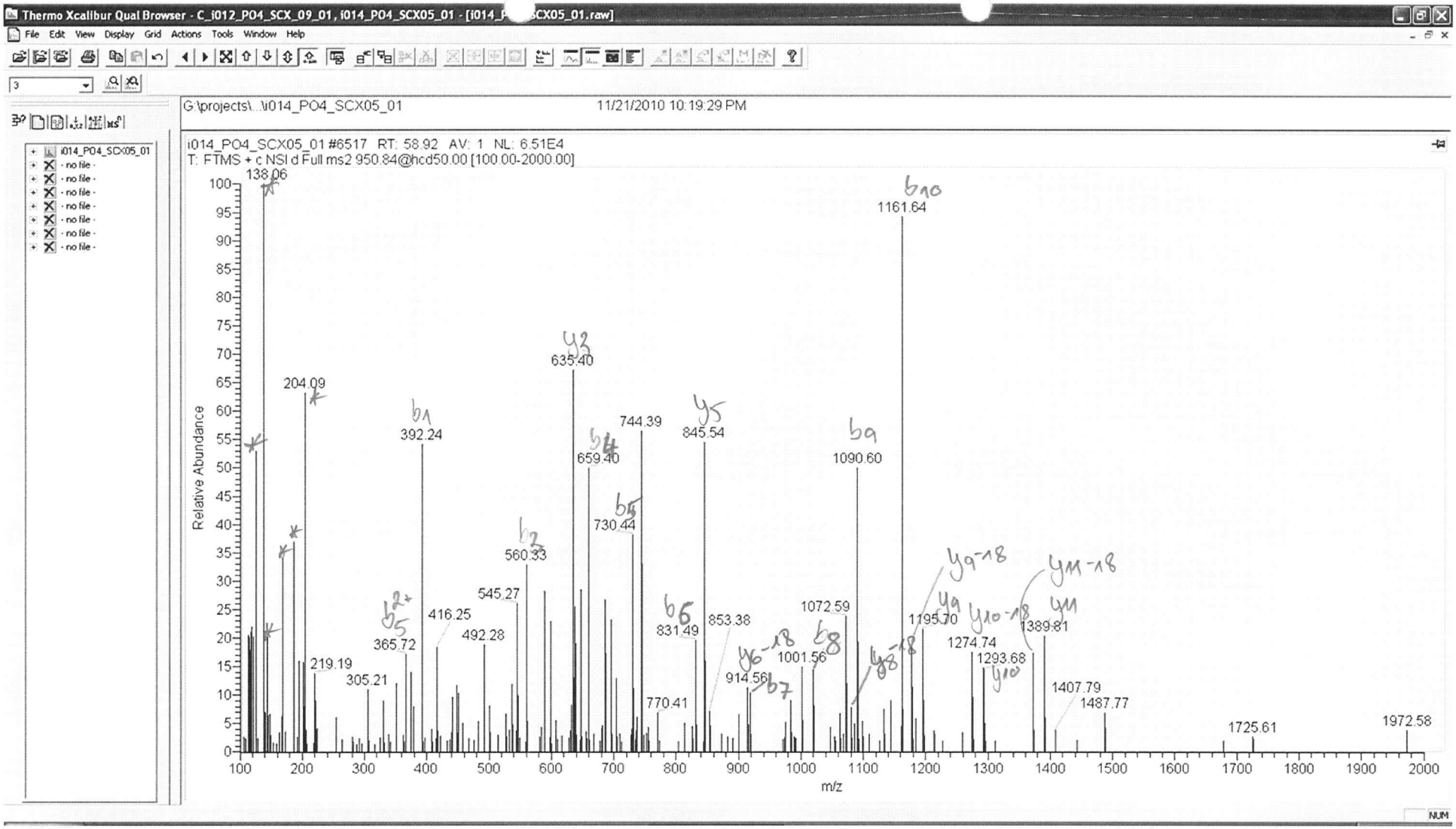


2 OGlcNAc sites at S15, 16 and/or 20

N-term., K21 : iTRAQ 8plex

210: sPAVATStAAPPPPssPLPSk

(3 O-GlcNAc site, 0 phospho-site, Mascot score = 17.5, Oscore = 1.81)



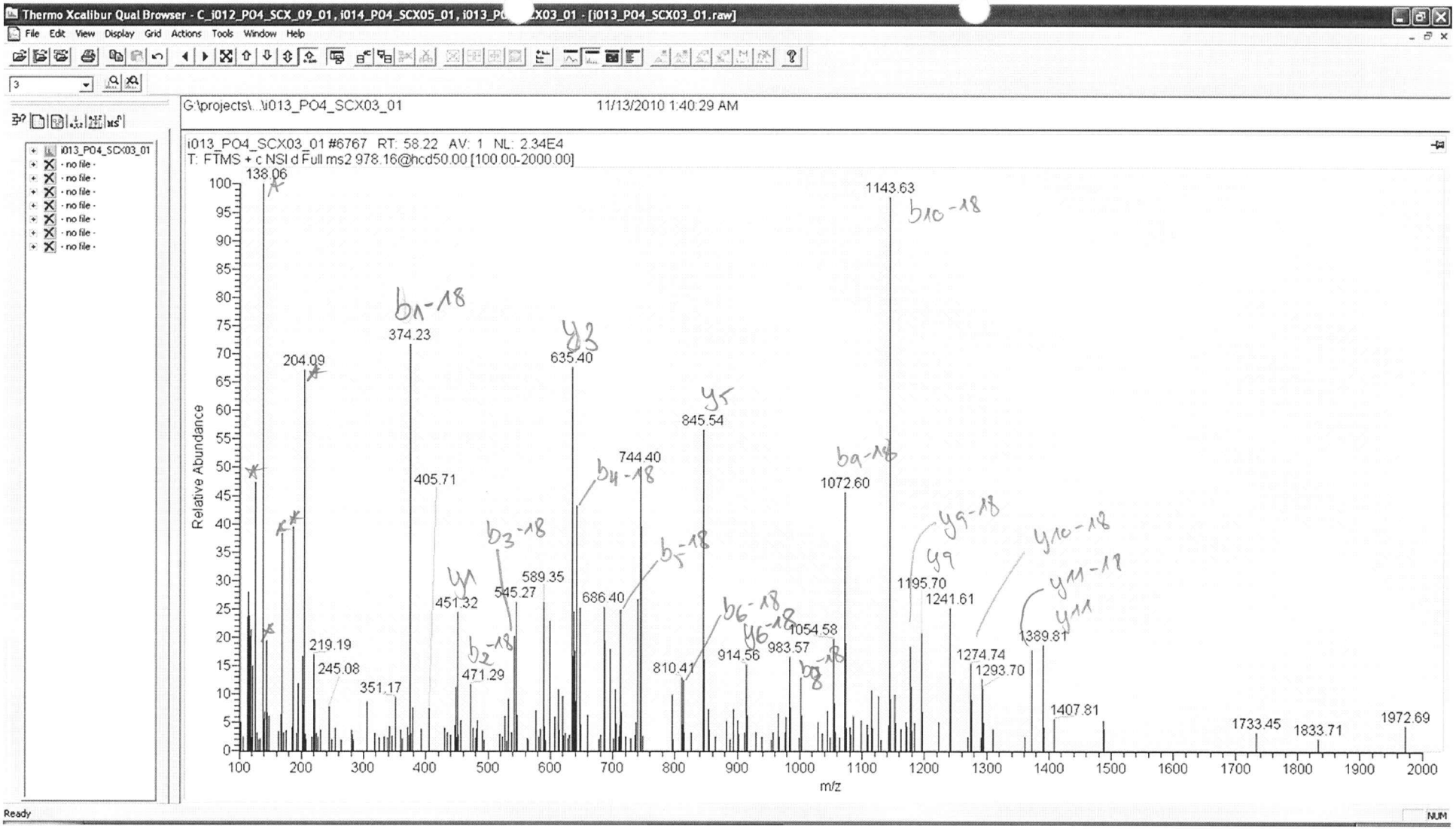
S16 : phospho

OGlcNAc site : unknown

N-term, K21 : iTRAQ8plex

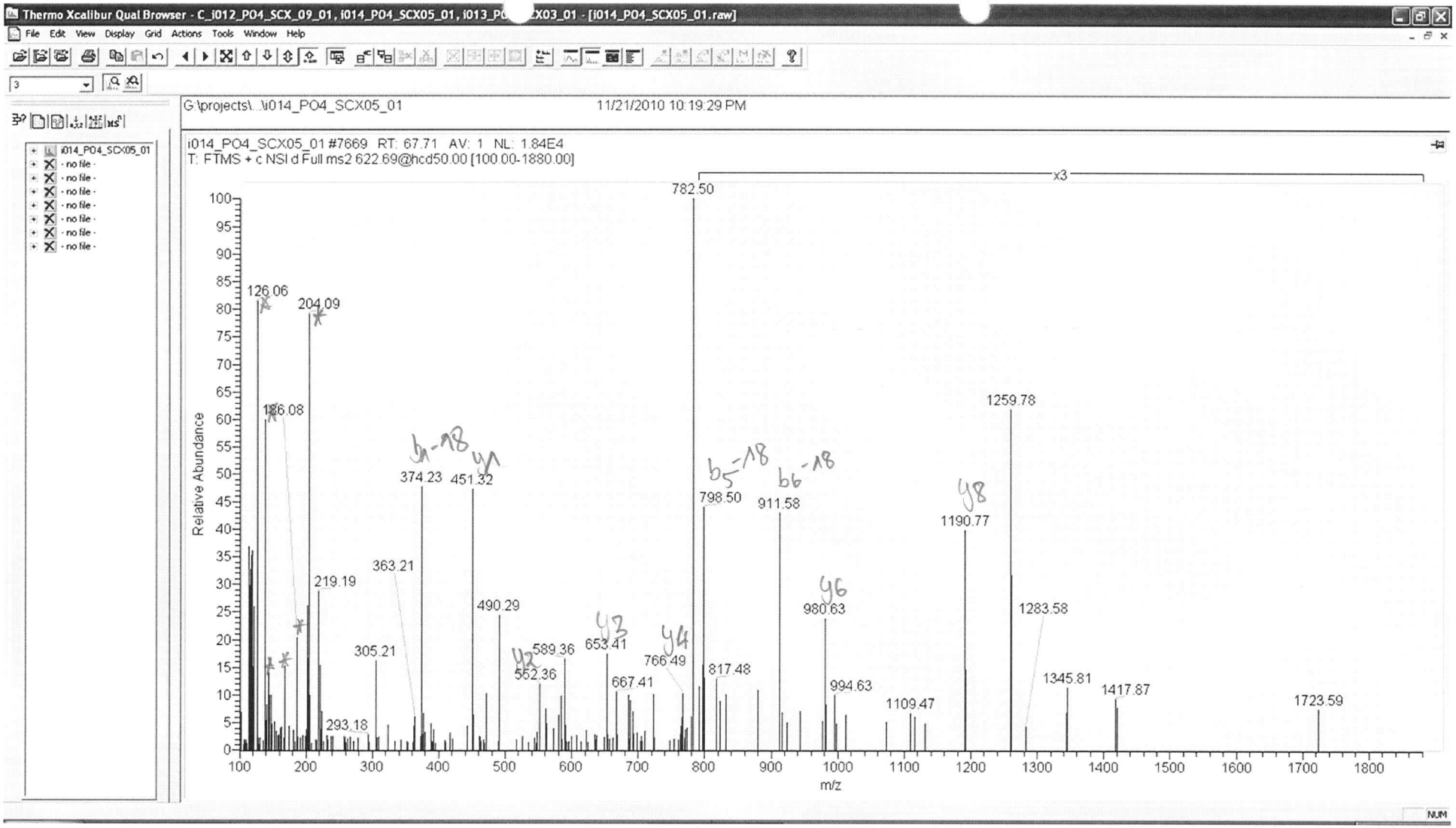
211: sPAVATStAAPPPPSsPLPSk

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 56.9, Oscore = 1.74)



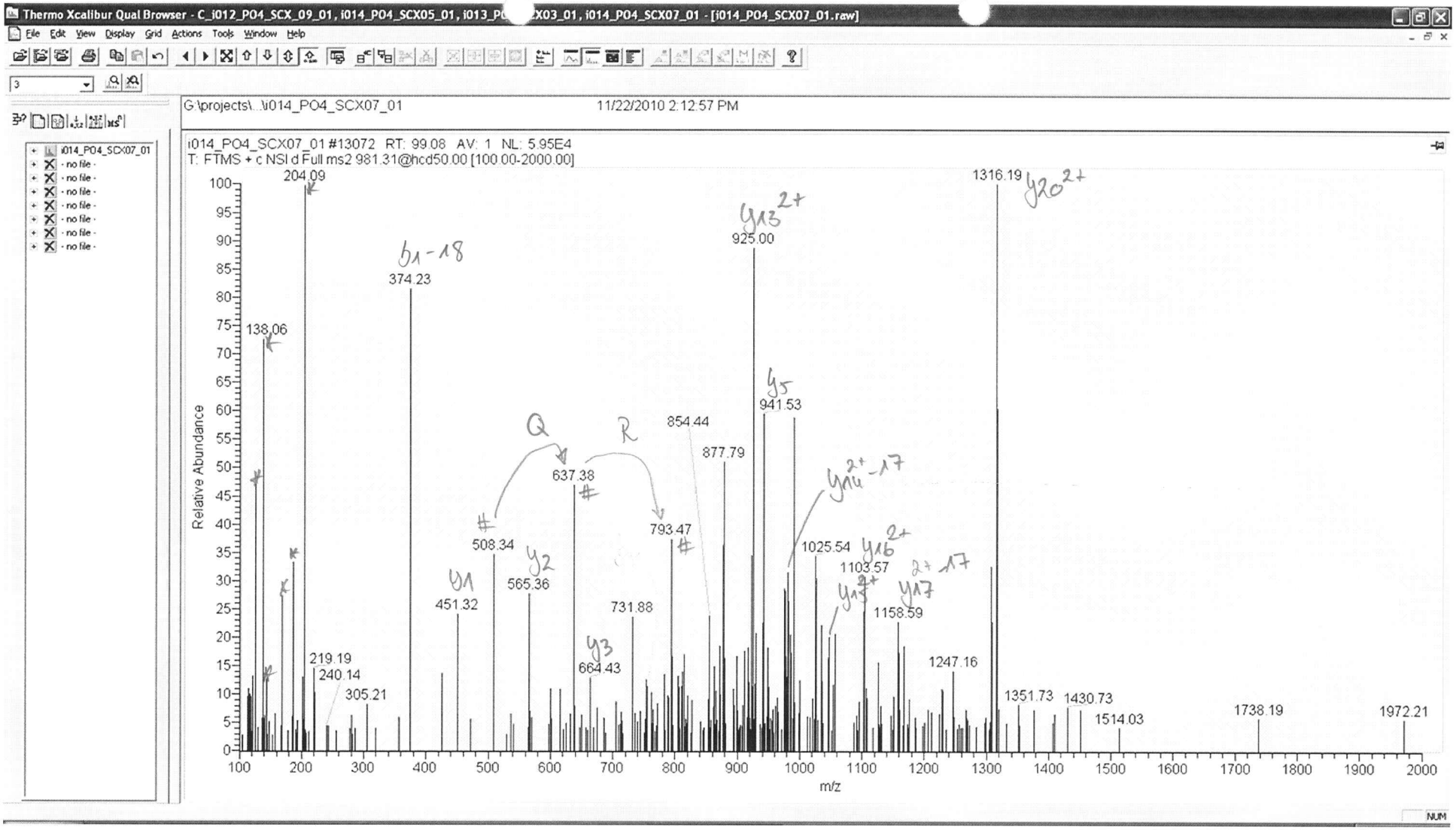
S1: phospho
S16: phospho
O-GlcNAc site unknown
N-term., K21 iTRAQ8plex

212: sPAVAtSTAAPPPPSsPLPsk
(1 O-GlcNAc site, 2 phospho-site, Mascot score = 58, Oscore = 1.72)



S1 : phospho
OGlcNAc site unknown
N-term, K9 iTRAQ8plex

213: sPITIITtk
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 24.6, Oscore = 1.29)

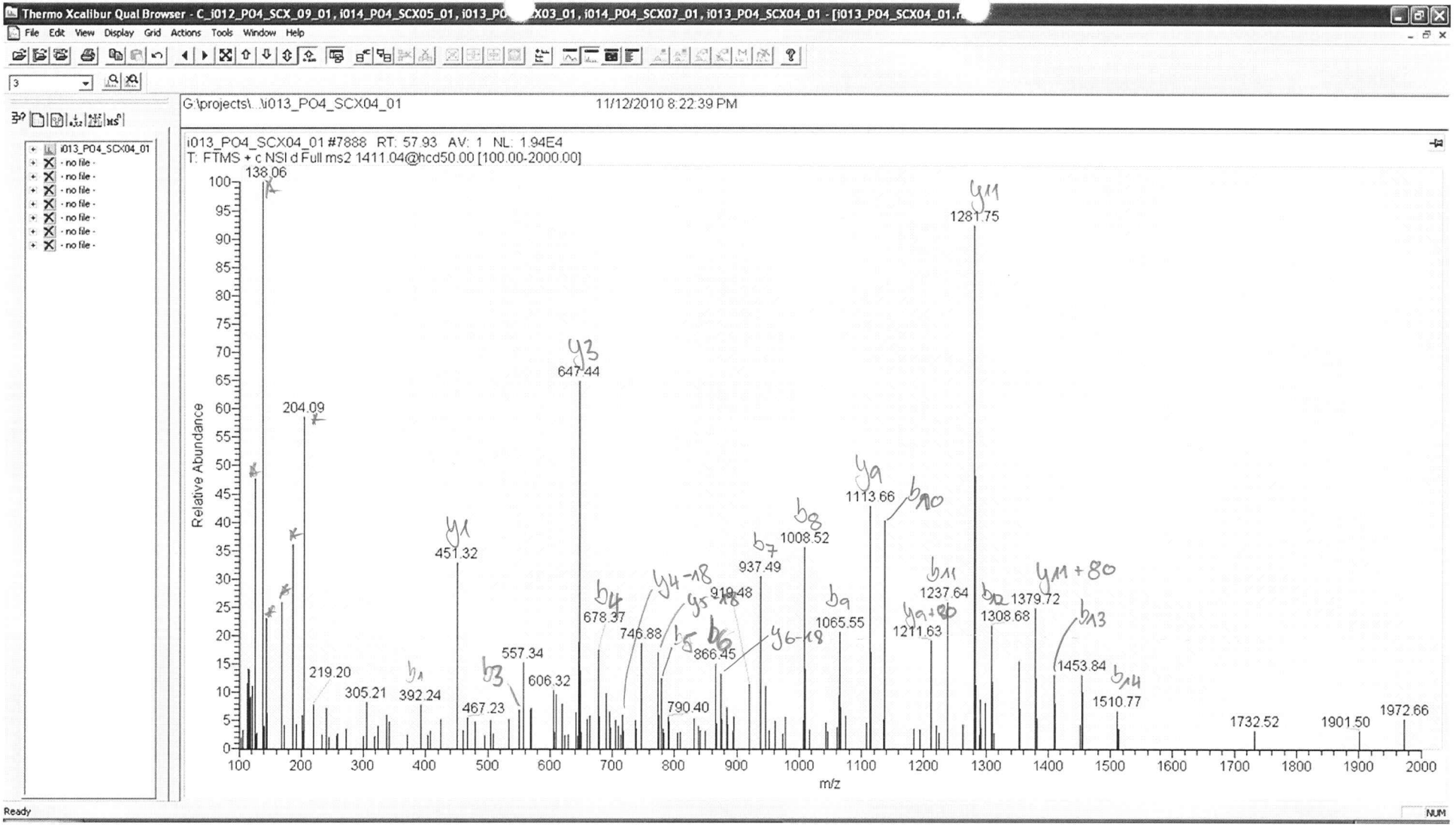


S1 : phospho
OGlcNAc : unknown

214: sPPVQPHTPVtISLGTAPSLQNNQPVEFNHAINYVNk
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 35.3, Oscore = 2.16)

chimeric spectra; 2nd ion series

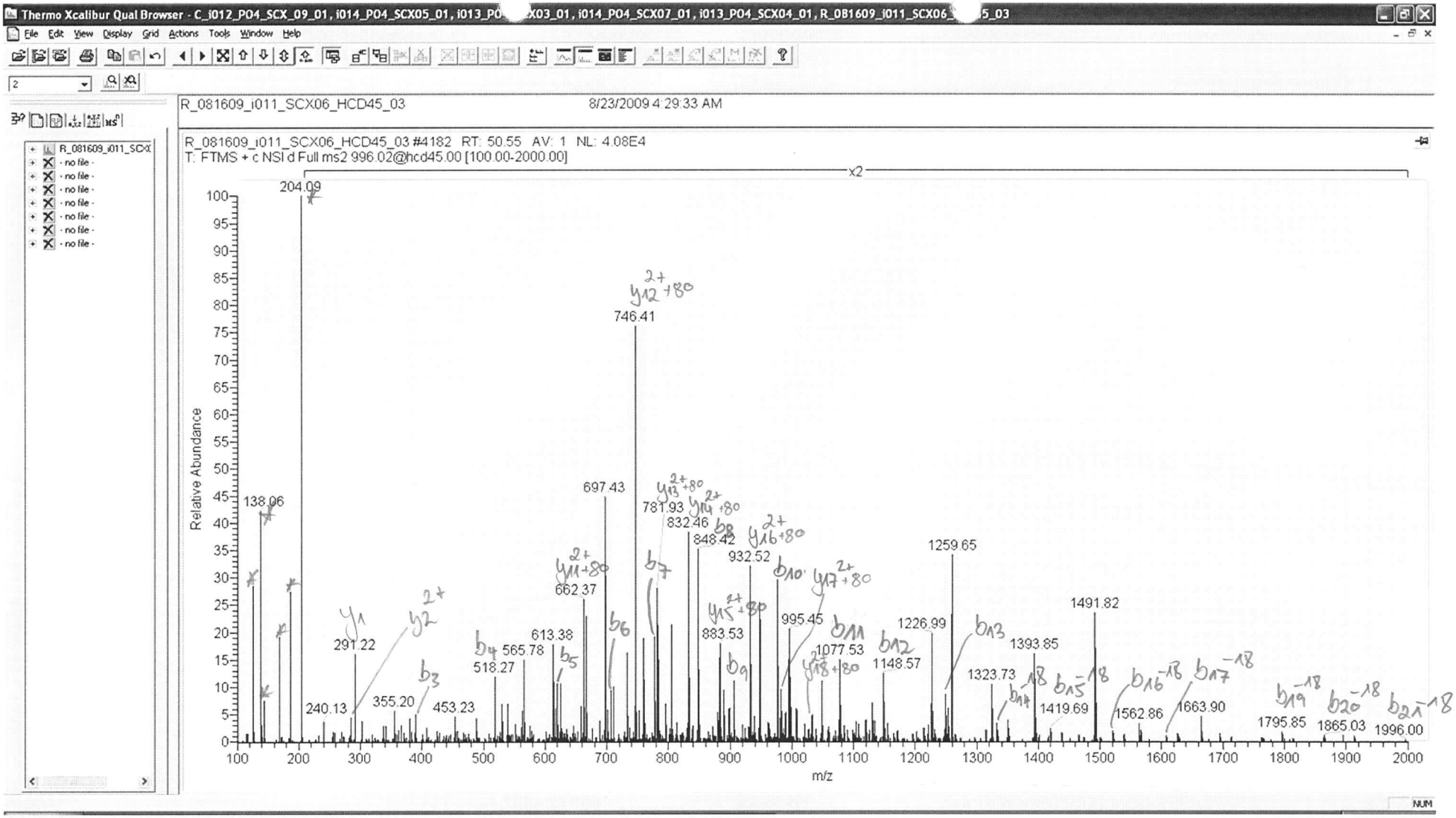
N-term, V37 : iTRAQ8plex



S32 : phospho
OglcNAc unknown
N-term., K35 : iTRAQ8plex

215: sSAQTSAAGATATTsTSSTVtVTAPAPAATGsPVk

(2 O-GlcNAc site, 1 phospho-site, Mascot score = 133, Oscore = 1.43)



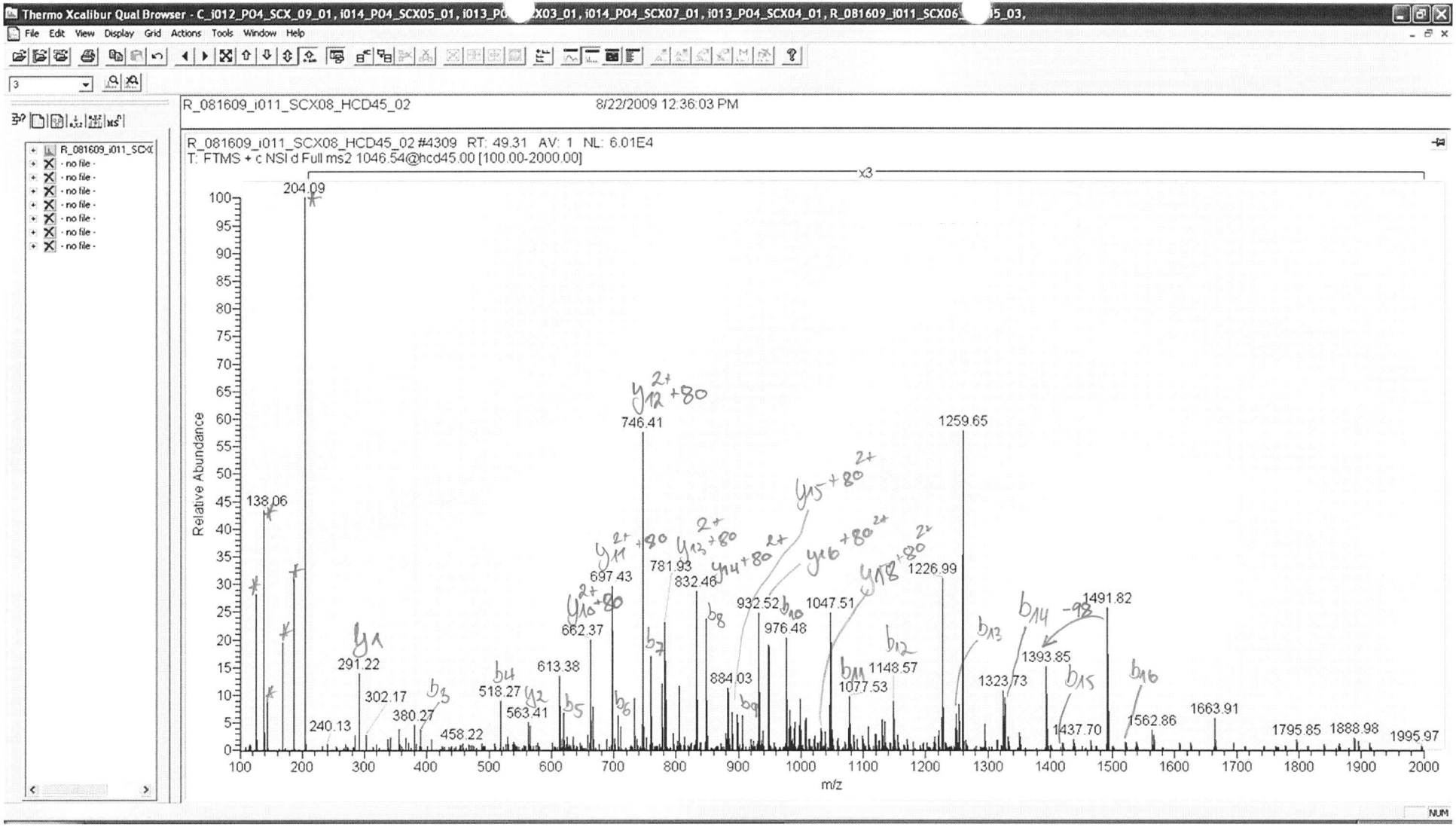
S32: phospho

OglcNAc site unknown

N-term., K35, K36: iTRAQ4plex

216: sSAQTSAAGATATTtSTSSTVTVTAPAPAATGsPVkk

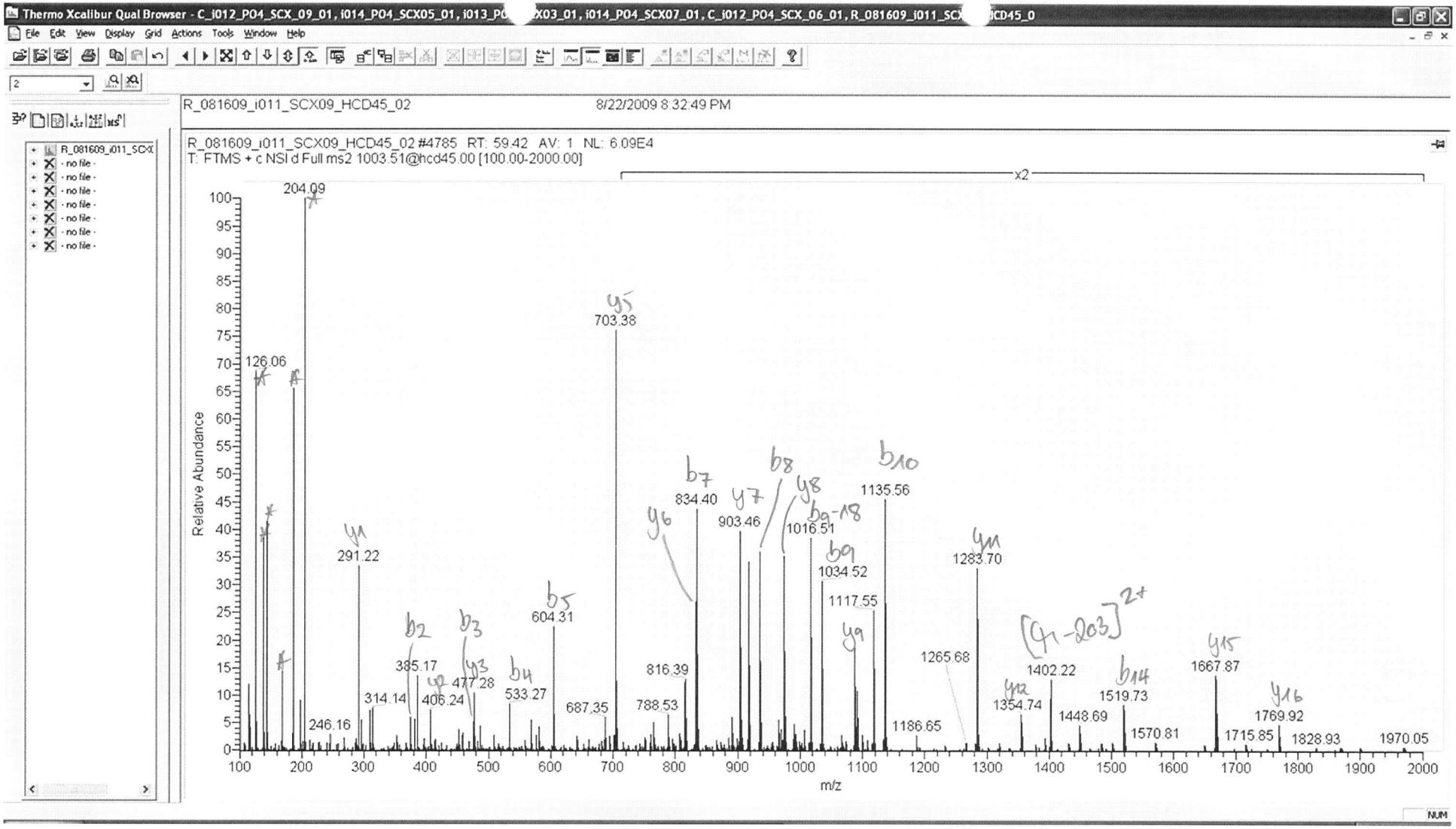
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 152, Oscore = 1.05)



S32 : phospho
OGlcNAc sites unknown

N-term, K35, K36 :
iTRAQ4plex

217: sSAQTSAAGATATTtSTsSTVTVTAPAPAATGsPVkk
(2 O-GlcNAc site, 1 phospho-site, Mascot score = 127, Oscore = 0.81)

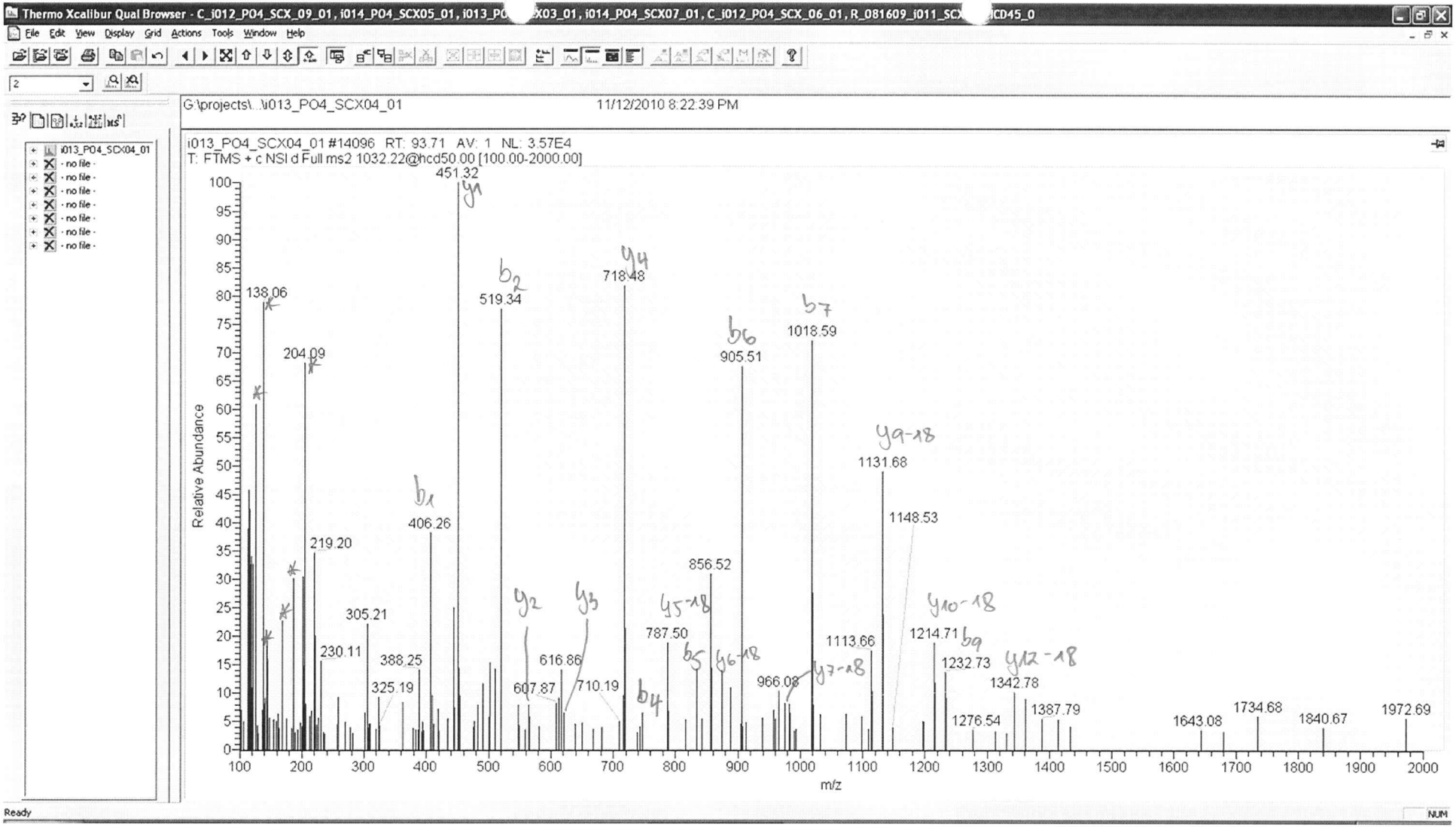


OGlcNAc Site
Number

N-term, 425 : iTRAQ4plex

219: tETGATETVTPsEAPVLAAEPEADk

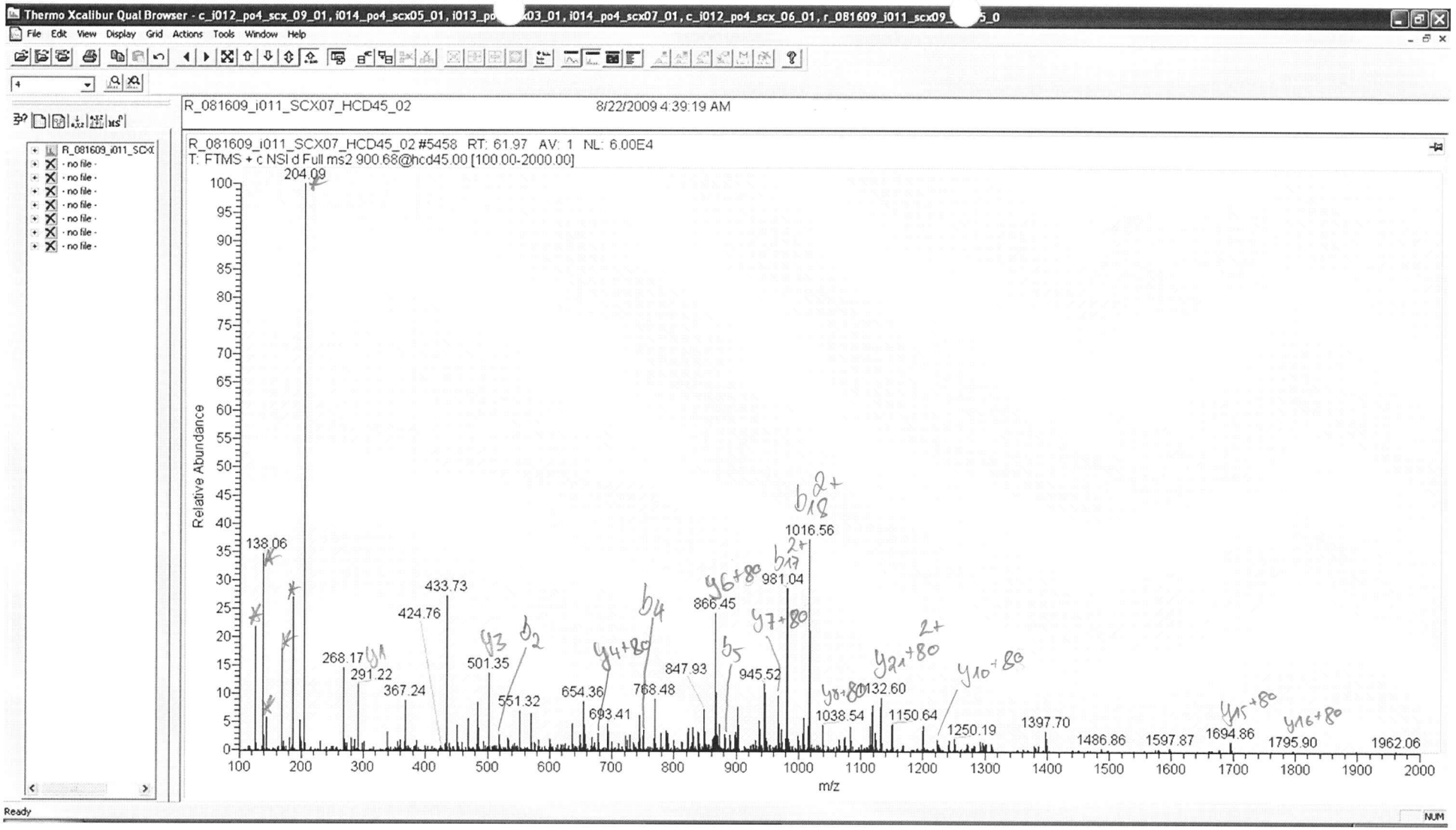
(1 O-GlcNAc site, 0 phospho-site, Mascot score = 85.1, Oscore = 1.08)



S19 : phospho
OGlcNAc unknown
N-term, K23 : iTRAQ 8plex

220: tIPMSAIITQAGATGVTssPGIk

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 64, Oscore = 1.92)



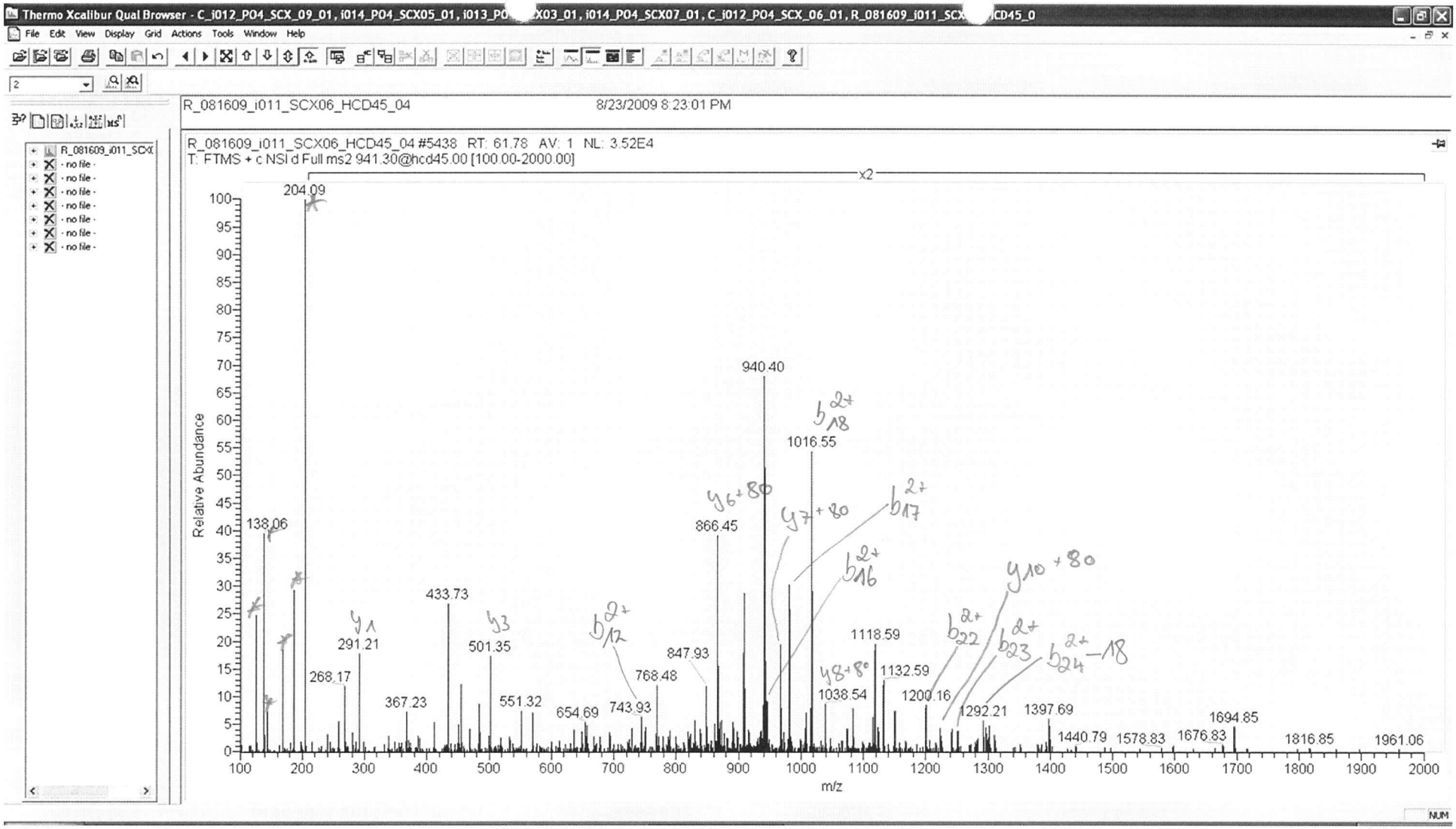
S36: phospho

OGlcNAc unknown

N-term, K2, K39: iTRAQ4plex

221: tkPLASVTNANTSSTQAAPVAVTTPTVSSGQATPtsPIk

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 71.4, Oscore = 1.27)



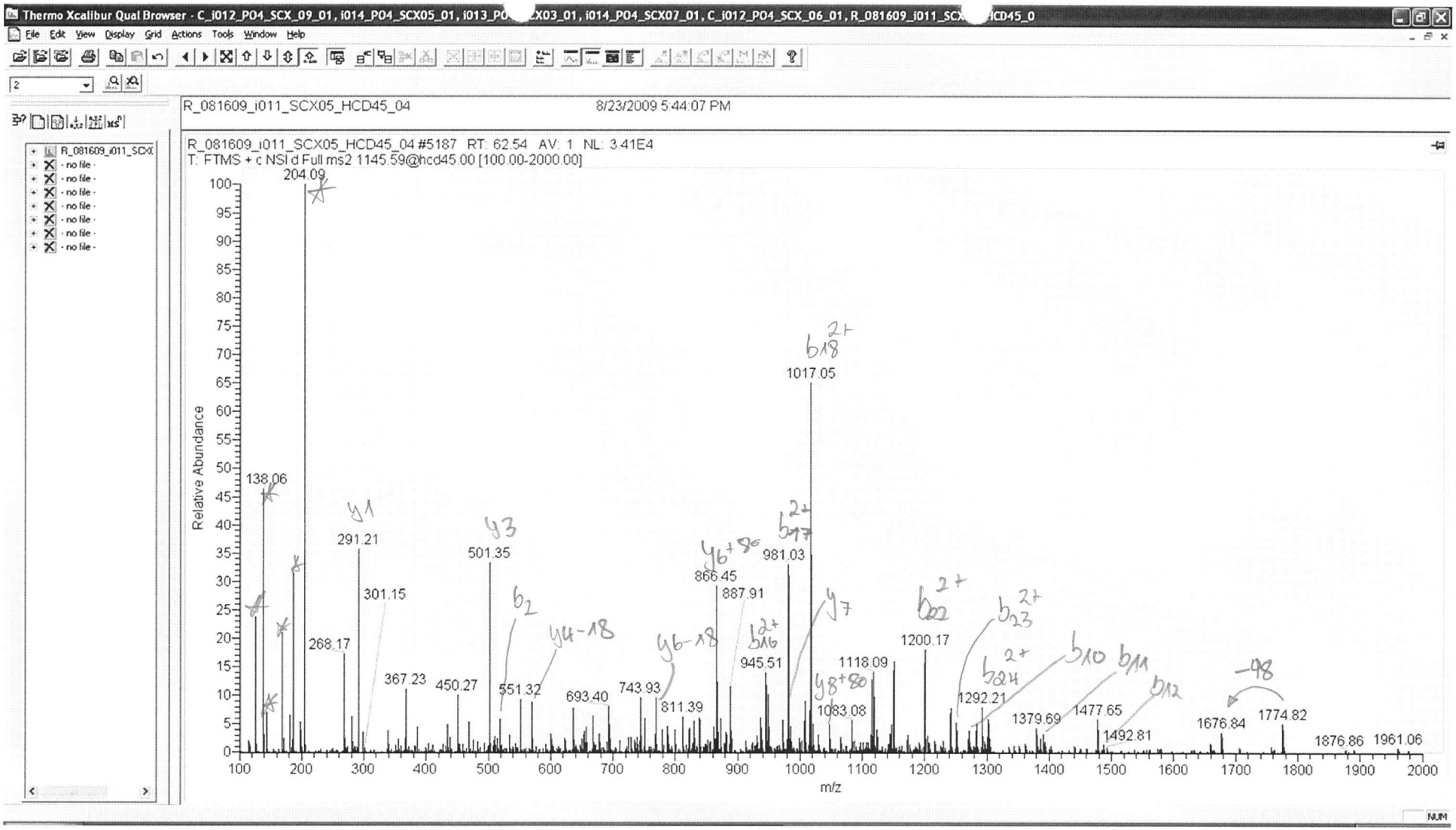
T24 : phospho

OGlcNAc site unknown

N-term, K2, K39 : iTRAQ4plex

222: tkPLASVTNANTSSTQAAPVAVTtPTVSsGQATPTsPIk

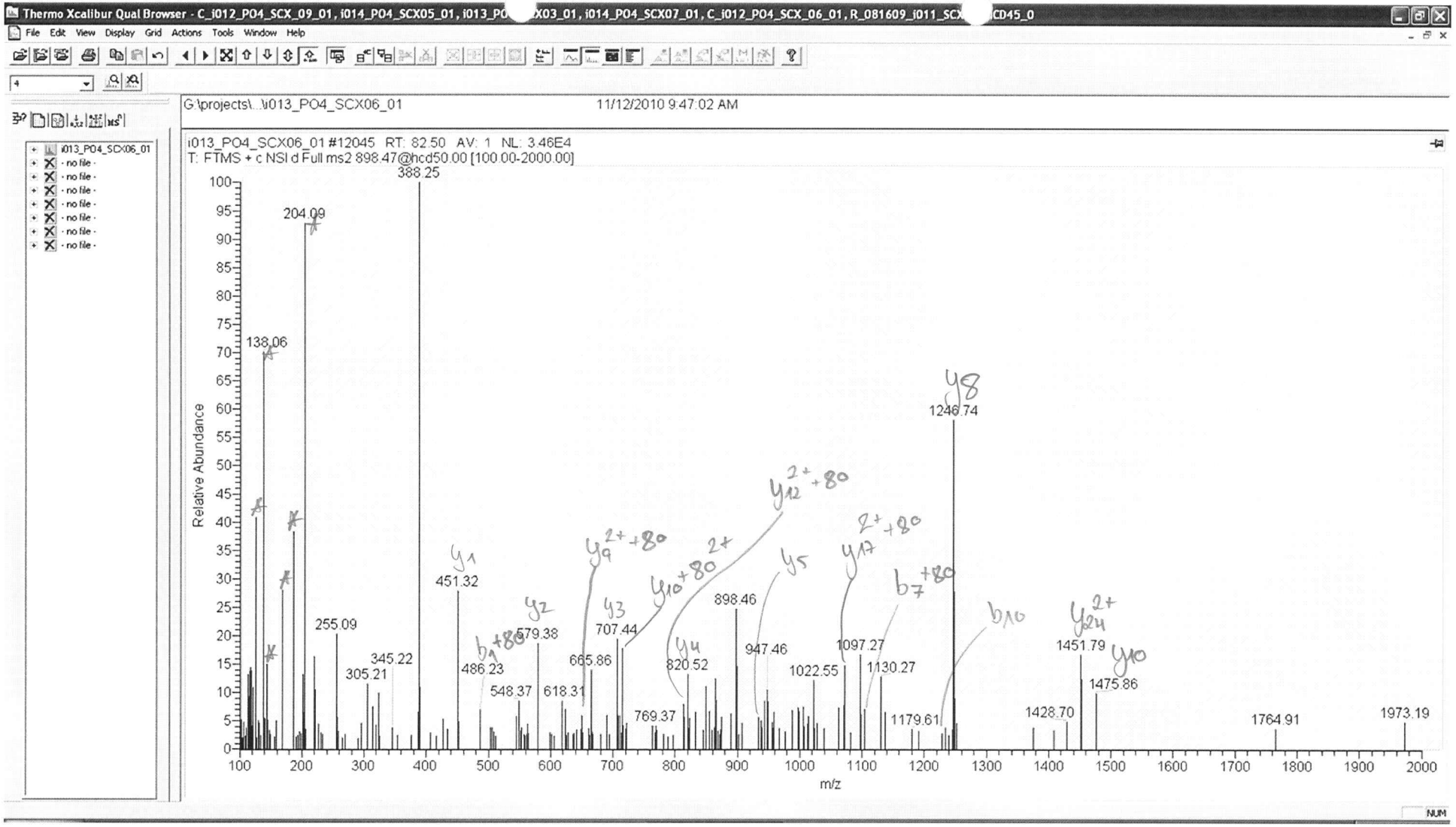
(2 O-GlcNAc site, 1 phospho-site, Mascot score = 47.2, Oscore = 0.95)



S36 : phospho
2nd phospho-site and
OGlcNAc site unknown
N-term., K2, K39: iTRAQ4-plex

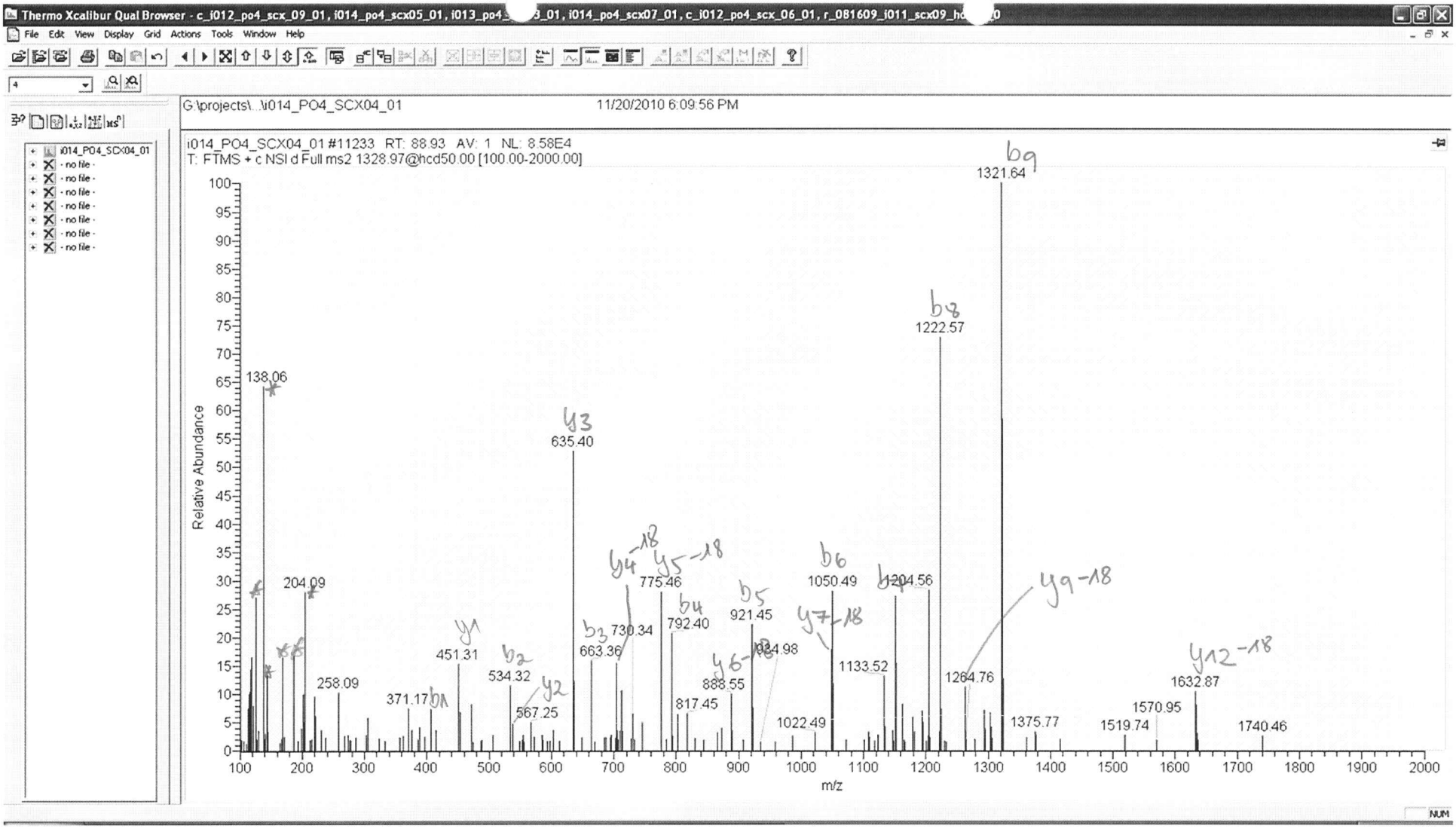
223: tkPLASVTNANTSSTQAAPVAVTTPTVSsGQAtPTsPIk

(1 O-GlcNAc site, 2 phospho-site, Mascot score = 98, Oscore = 1.41)



T1: phospho
OGlcNAc site unknown
N-term, K25: iTRAQ8plex

225: tPPTANHPVEPVTSVTQPsELLQQk
(1 O-GlcNAc site, 1 phospho-site, Mascot score = 25.8, Oscore = 1.48)



S26: phospho

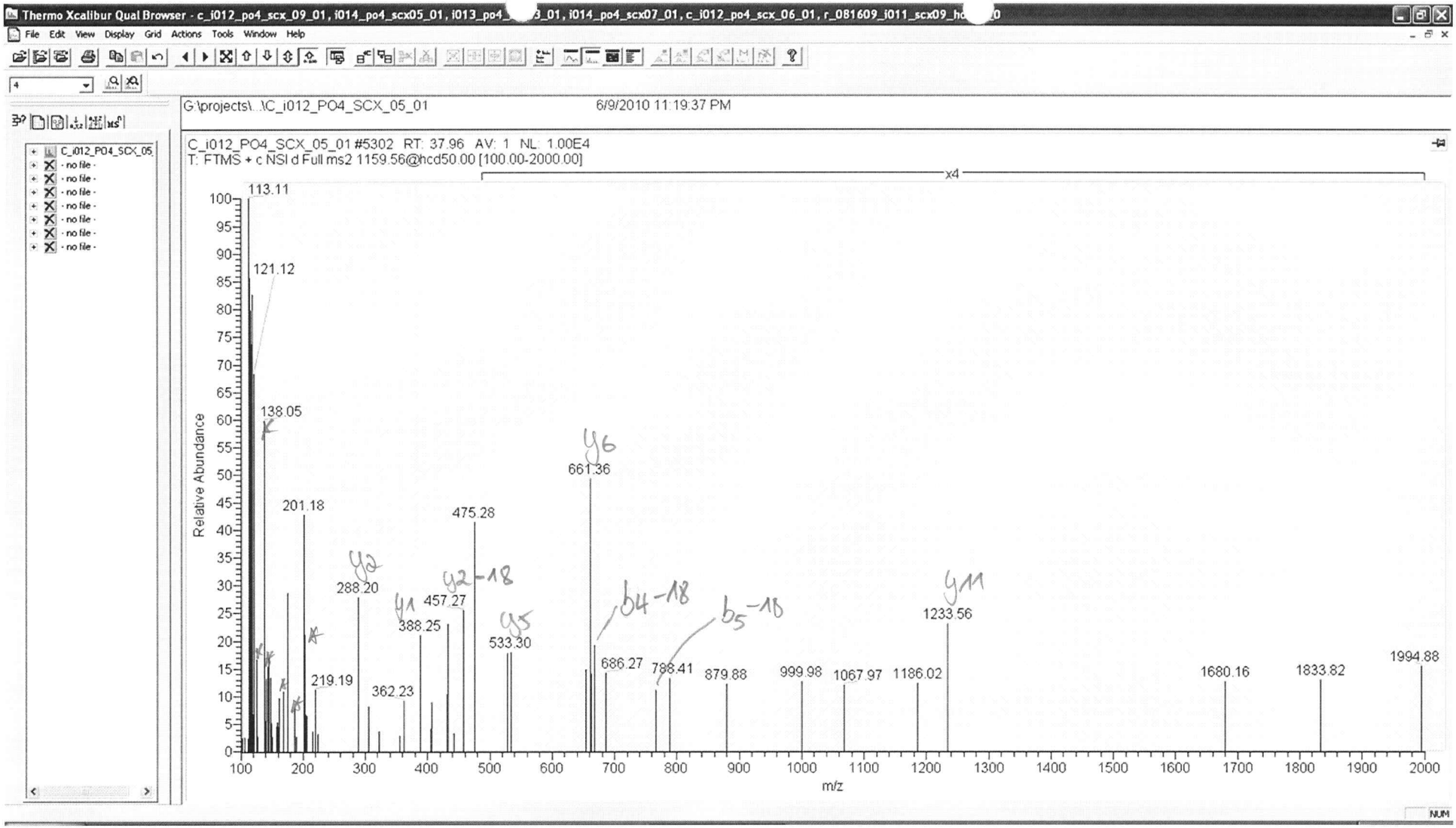
OGlcNAc Site unknown

N-term., K29: iTRAQ8plex

y4

227: tQEEEETAVPTSQGTGTPcLTLcLAsPsk

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 69, Oscore = 1.79)

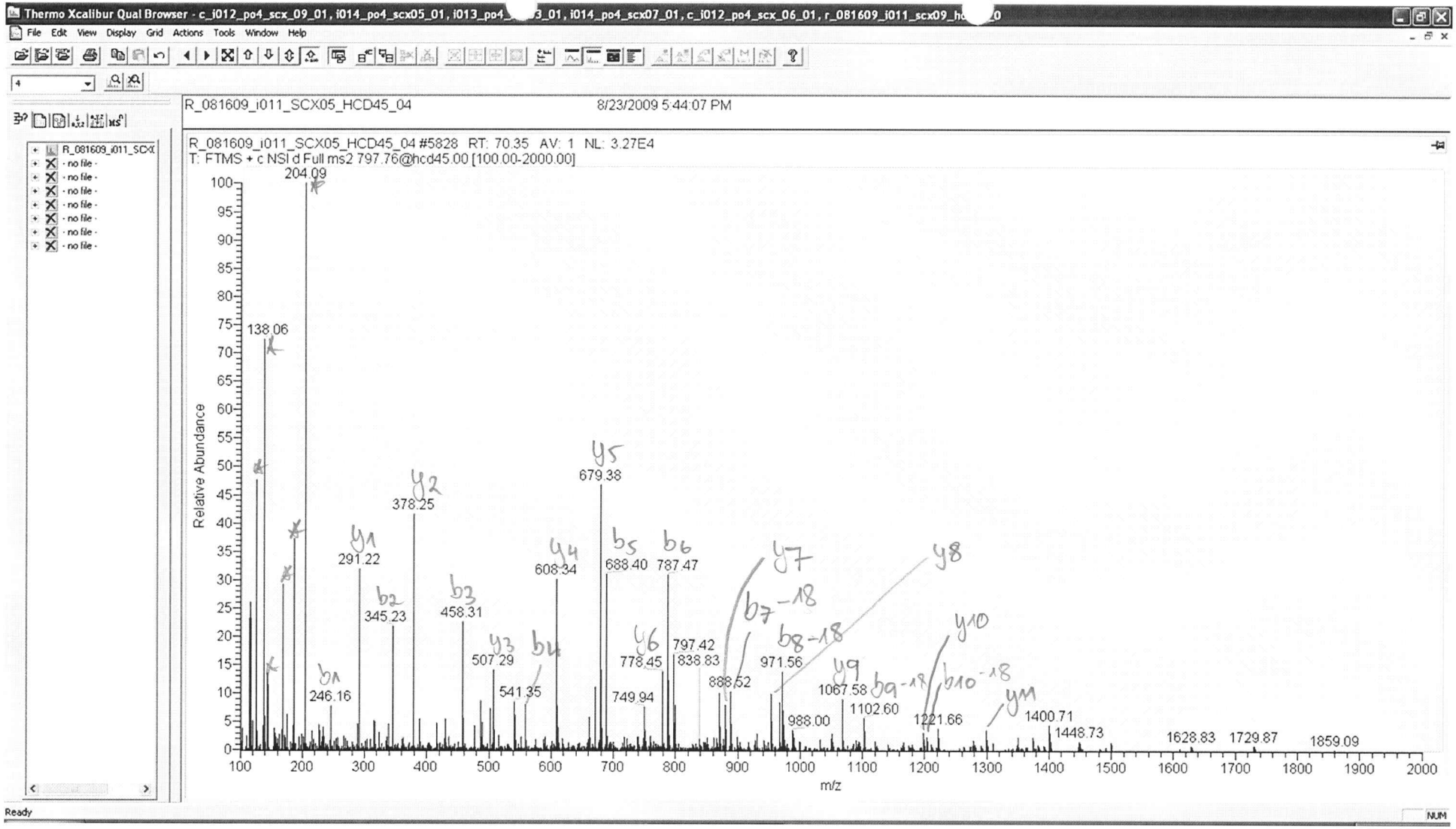


S2: phospho OGlcNAc site unknown

b-ion : iTRAQ 8plex

228: tsPLVSQNNEQGSTLR

(1 O-GlcNAc site, 1 phospho-site, Mascot score = 10.8, Oscore = 2.13)



OGlcNAc site unknown

N-term, K18: iTRAQ4plex

229: tVItEVTTMTSTVATESk

(1 O-GlcNAc site, 0 phospho-site, Mascot score = 90, Oscore = 0.97)