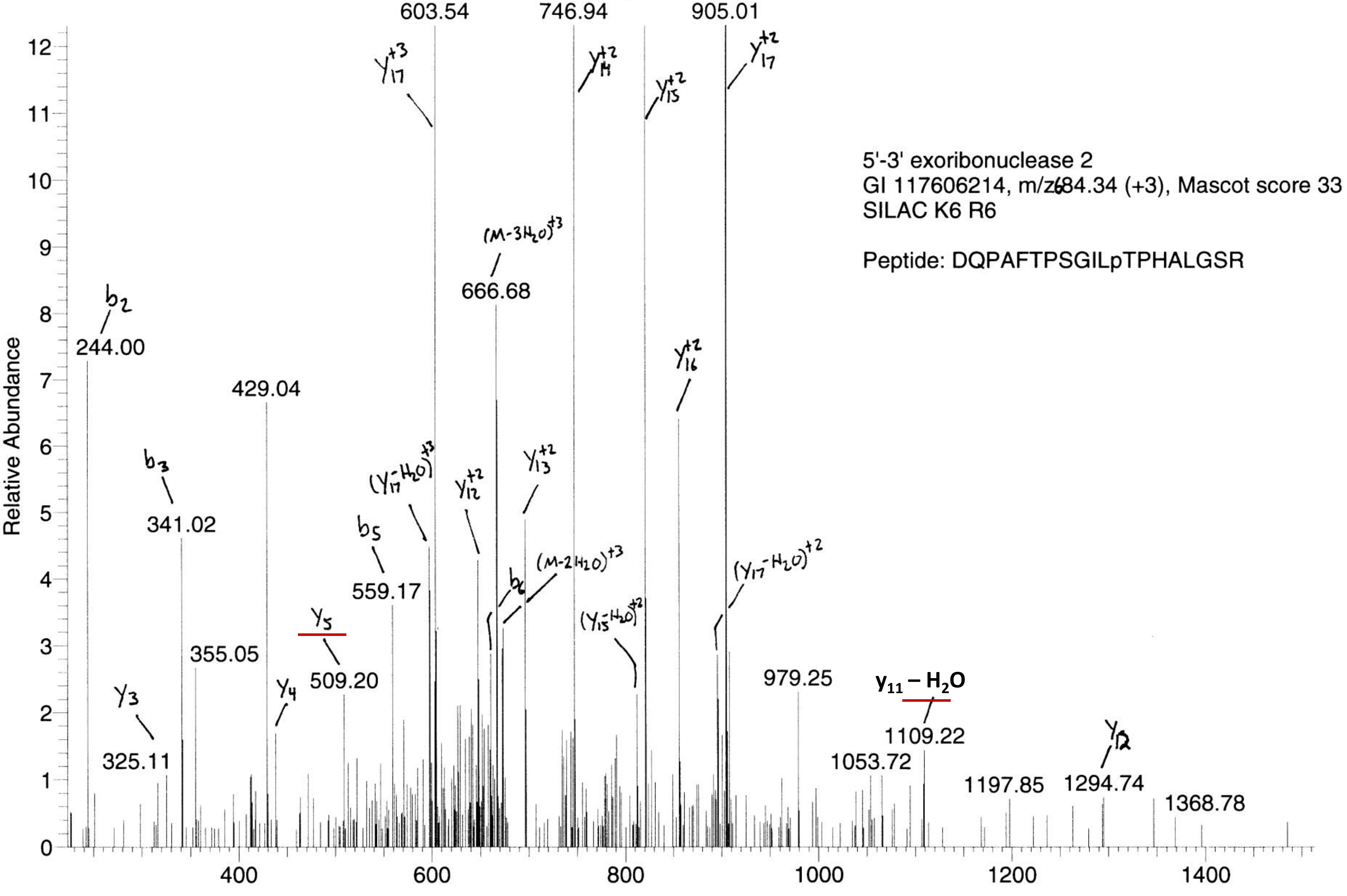
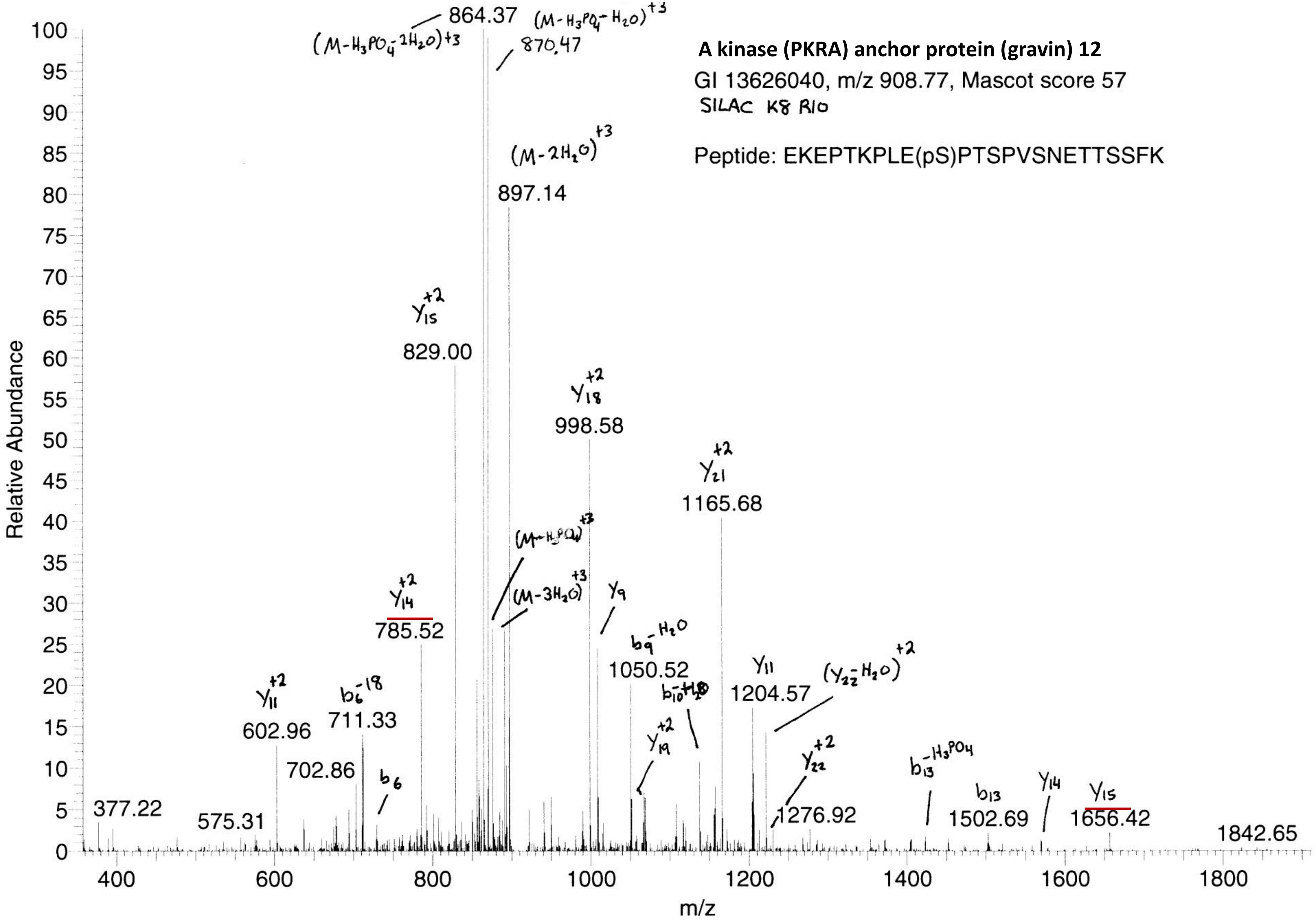
Peaks constraining the position of the phosphorylation site are underlined in red


5'-3' exoribonuclease 2
GI 117606214, m/z 684.34 (+3), Mascot score 33
SILAC K6 R6

Peptide: DQPAFTPSGILpTPHALGSR

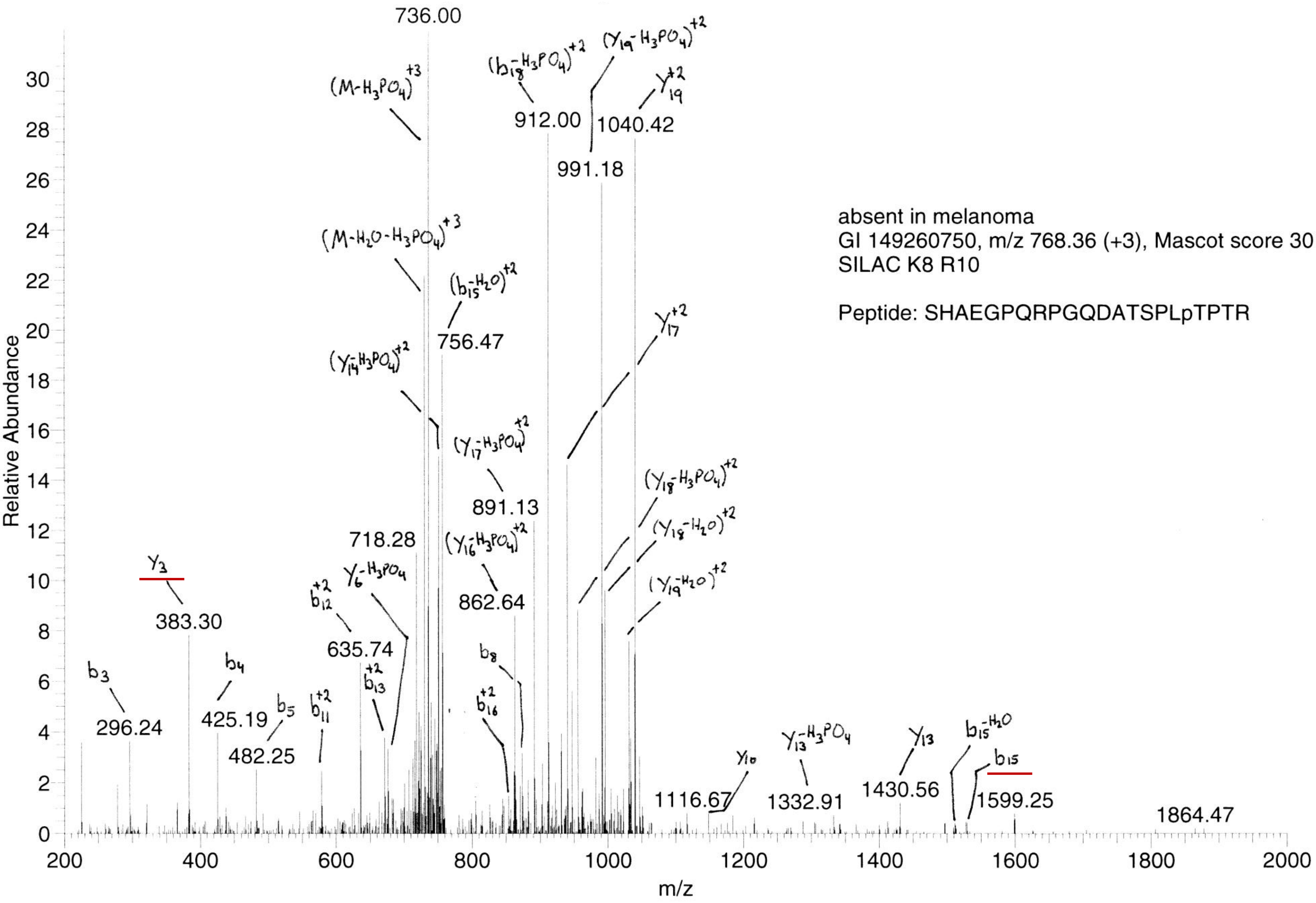


A kinase (PKRA) anchor protein (gravin) 12

GI 13626040, m/z 908.77, Mascot score 57

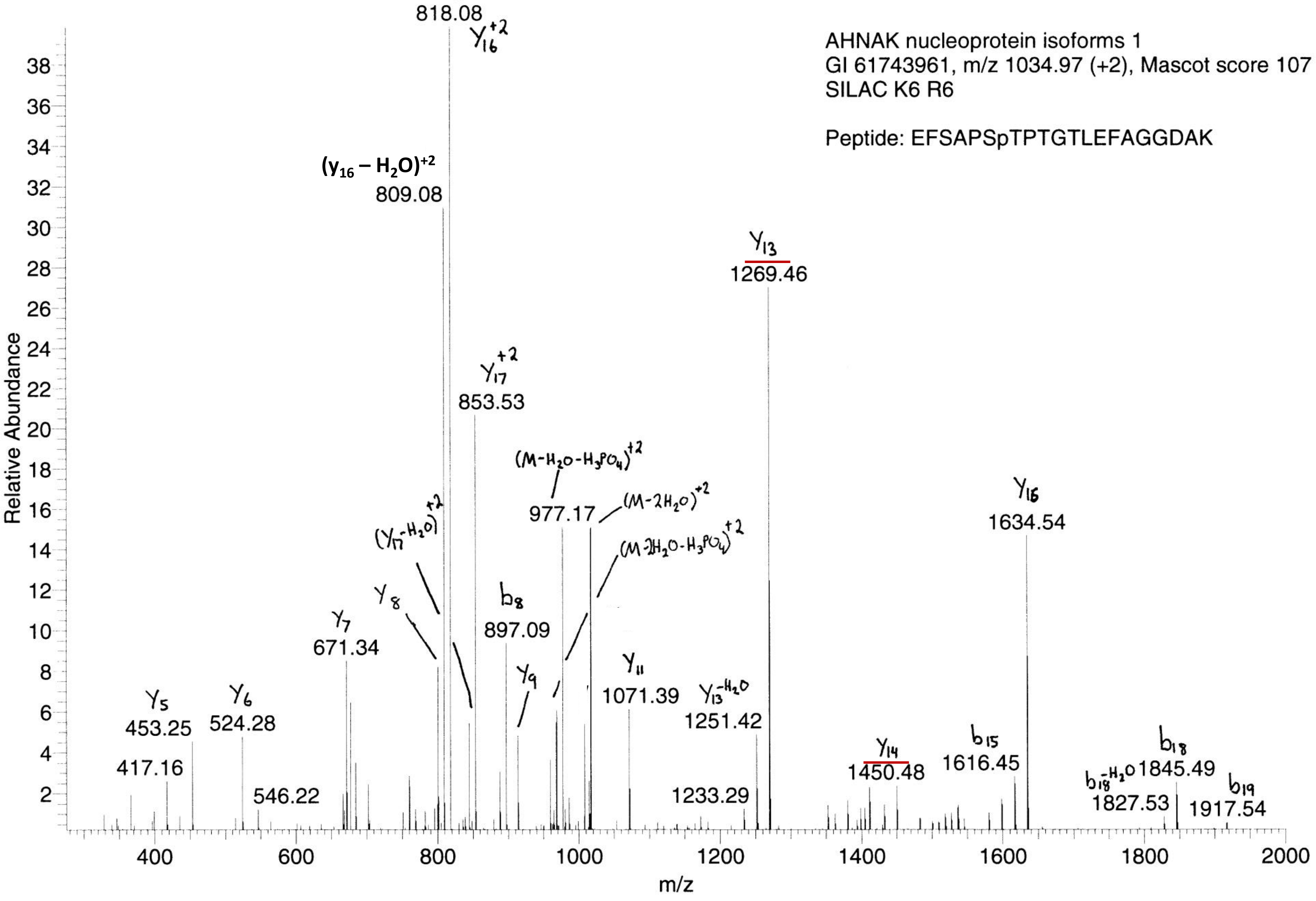
SILAC K8 R10

Peptide: EKEPTKPLE(pS)PTSPVSNETTSSFK



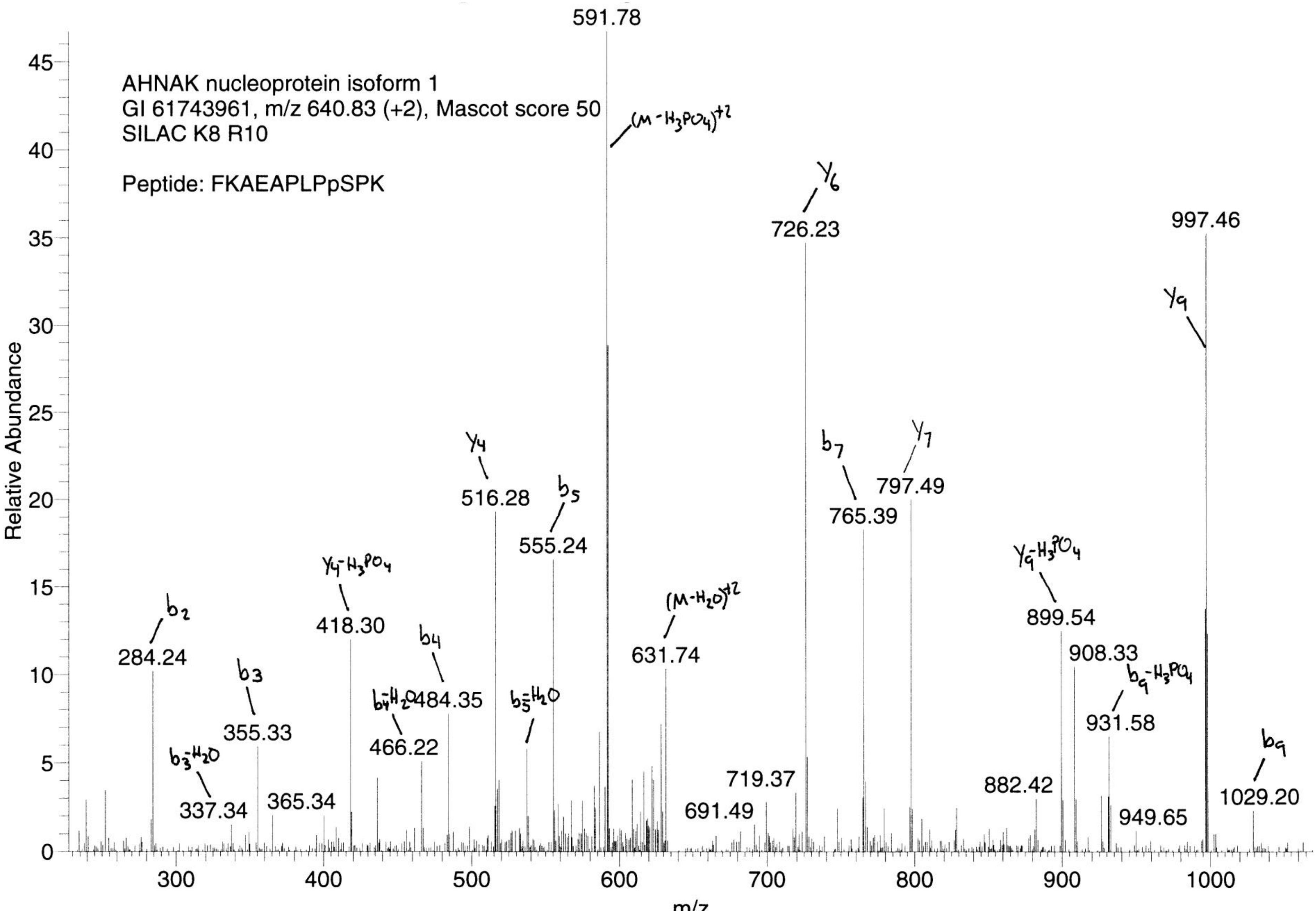
absent in melanoma
GI 149260750, m/z 768.36 (+3), Mascot score 30
SILAC K8 R10

Peptide: SHAEGPQRPGQDATSPLpTPTR



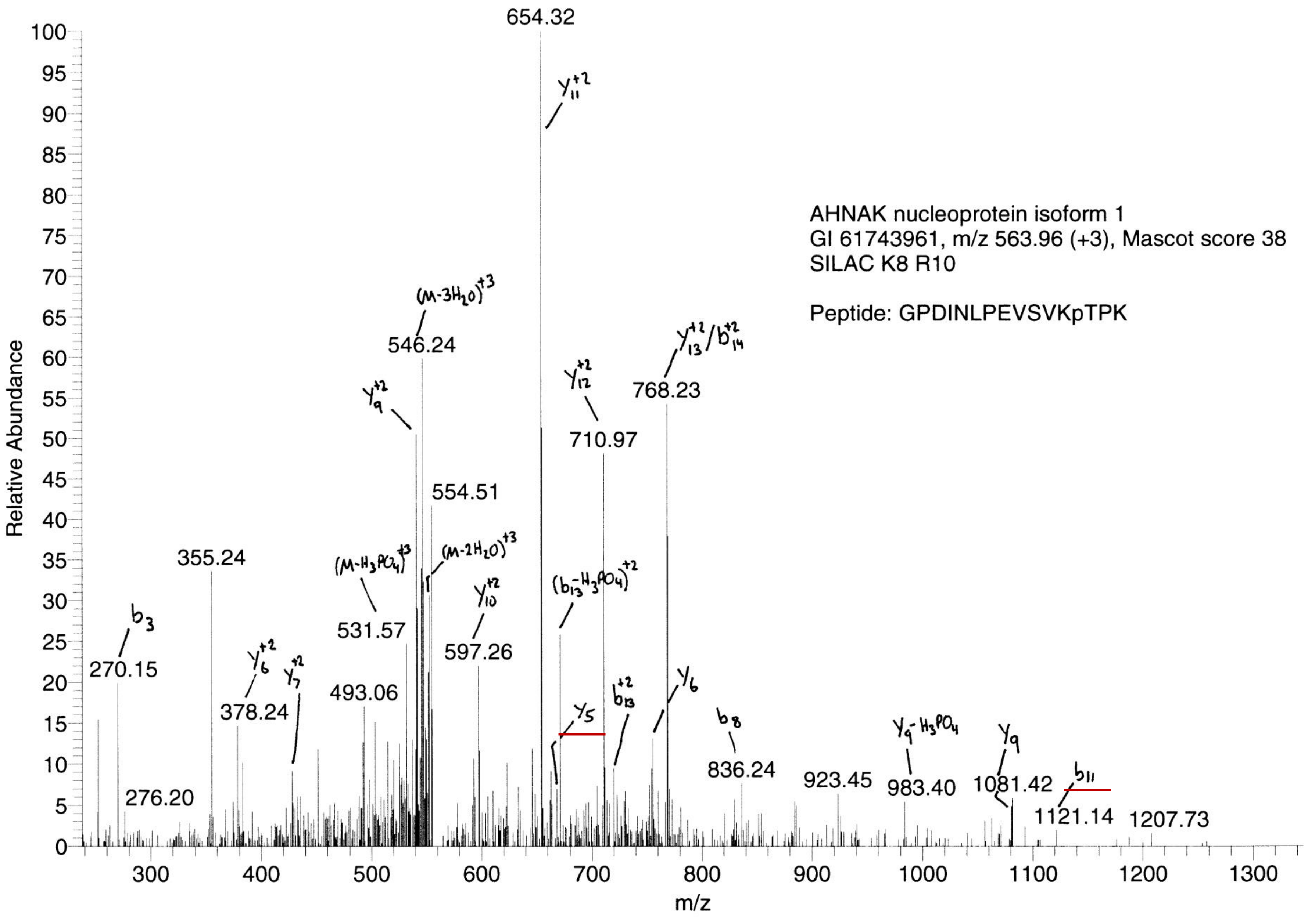
AHNAK nucleoprotein isoforms 1
GI 61743961, m/z 1034.97 (+2), Mascot score 107
SILAC K6 R6

Peptide: EFSAPSpTPTGTLEFAGGDAK



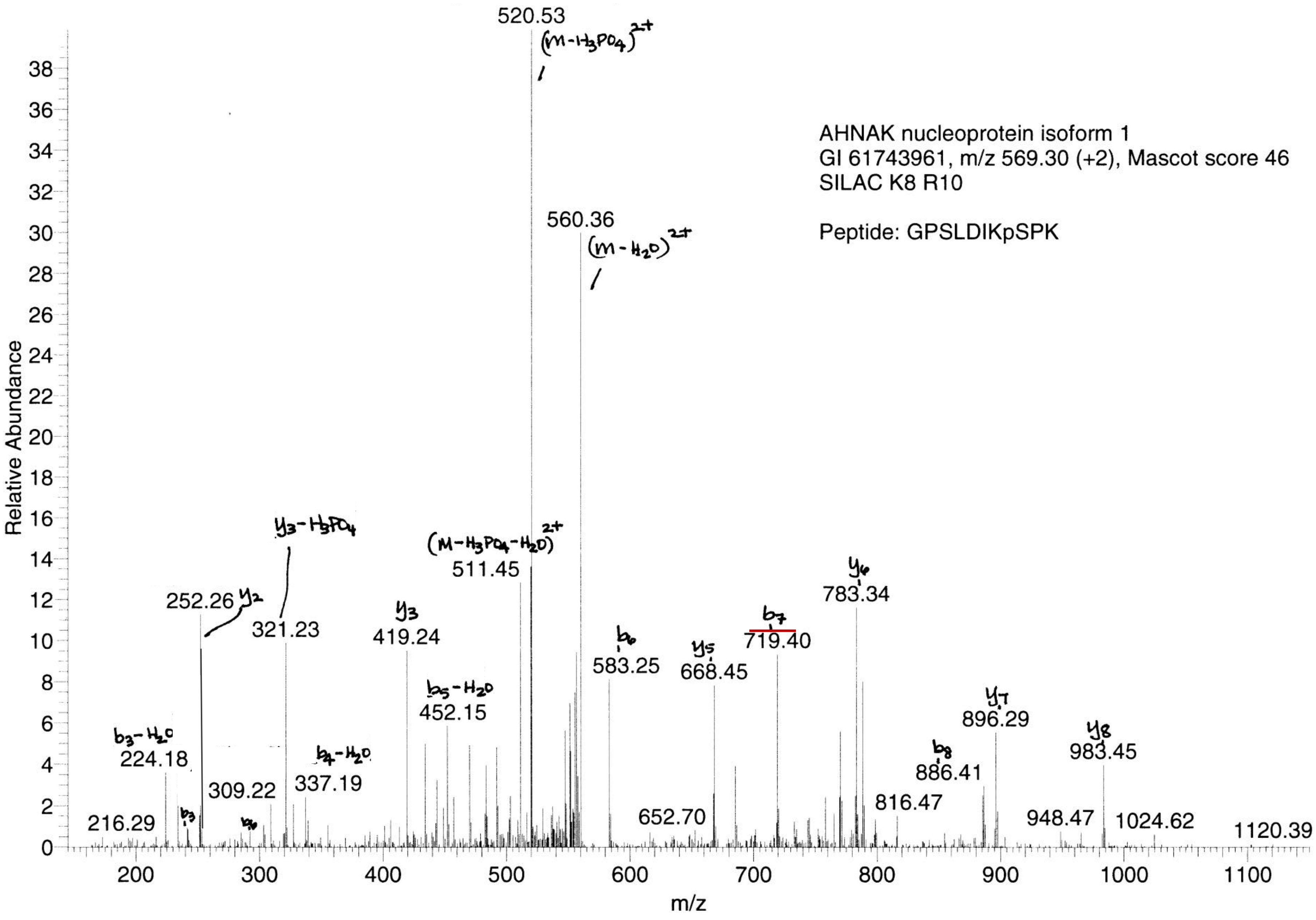
AHNAK nucleoprotein isoform 1
GI 61743961, m/z 640.83 (+2), Mascot score 50
SILAC K8 R10

Peptide: FKAEAPLPpSPK

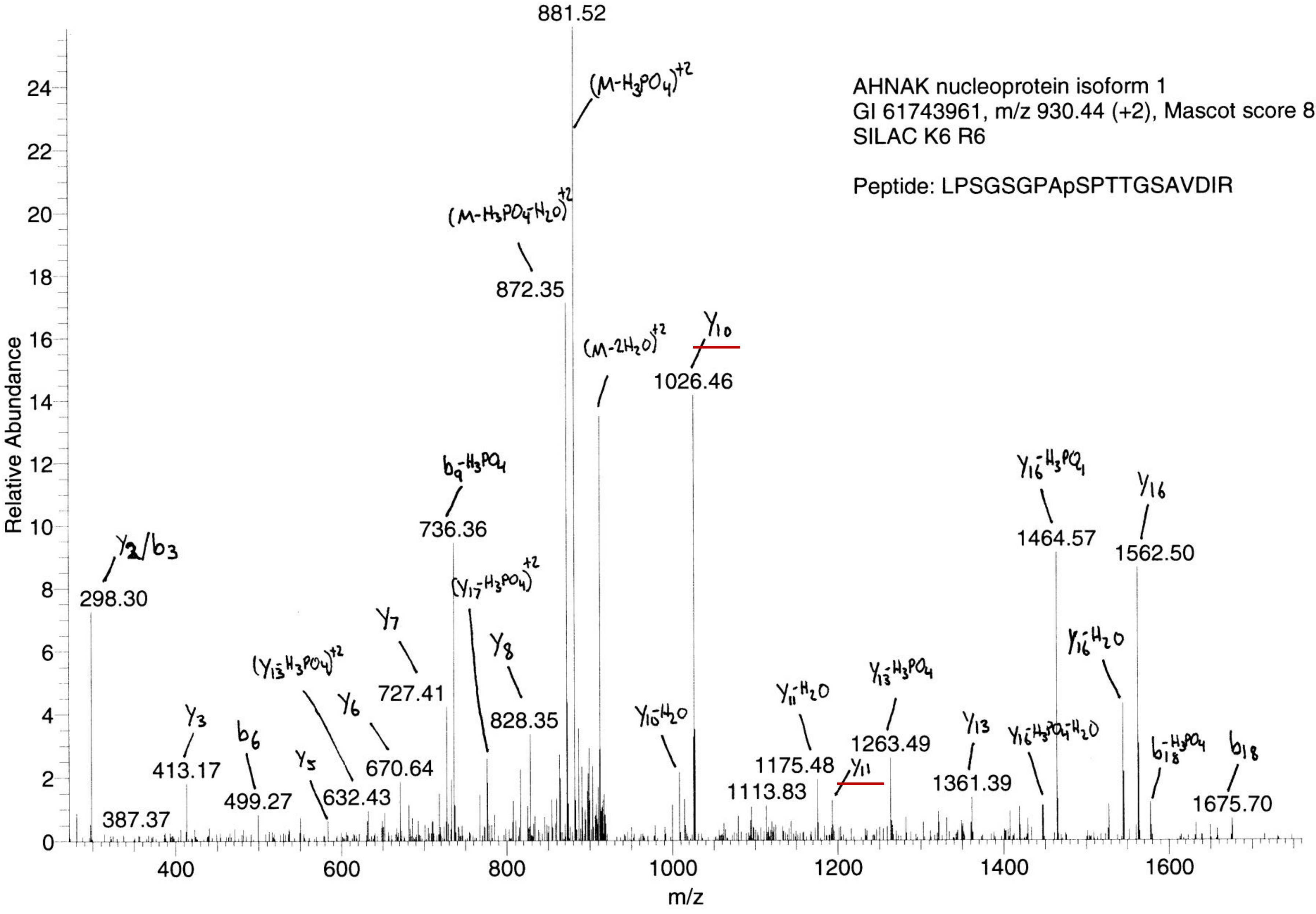


AHNAK nucleoprotein isoform 1
GI 61743961, m/z 563.96 (+3), Mascot score 38
SILAC K8 R10

Peptide: GPDINLPEVSVKpTPK

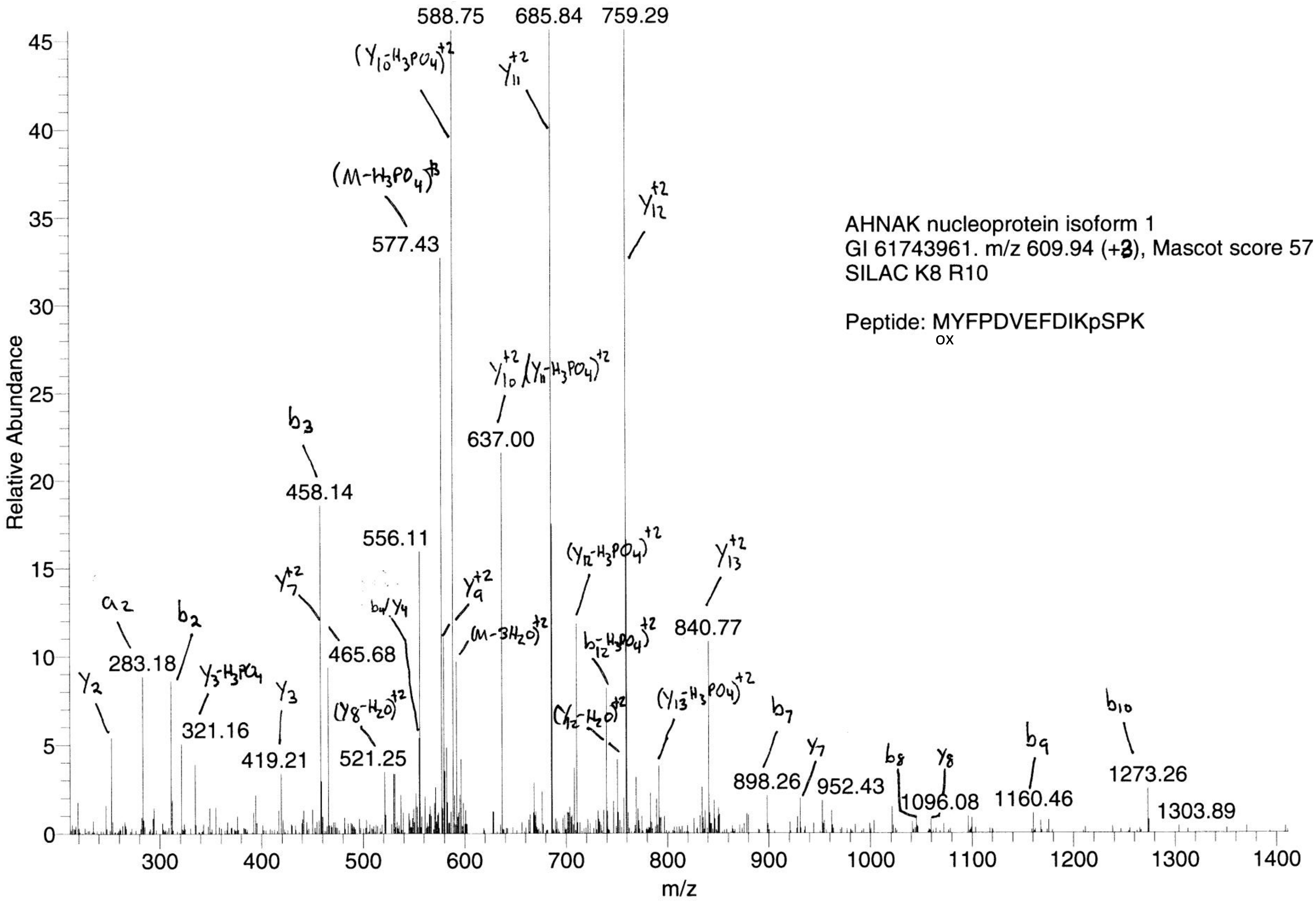

AHNAK nucleoprotein isoform 1
GI 61743961, m/z 569.30 (+2), Mascot score 46
SILAC K8 R10

Peptide: GPSLDIKpSPK



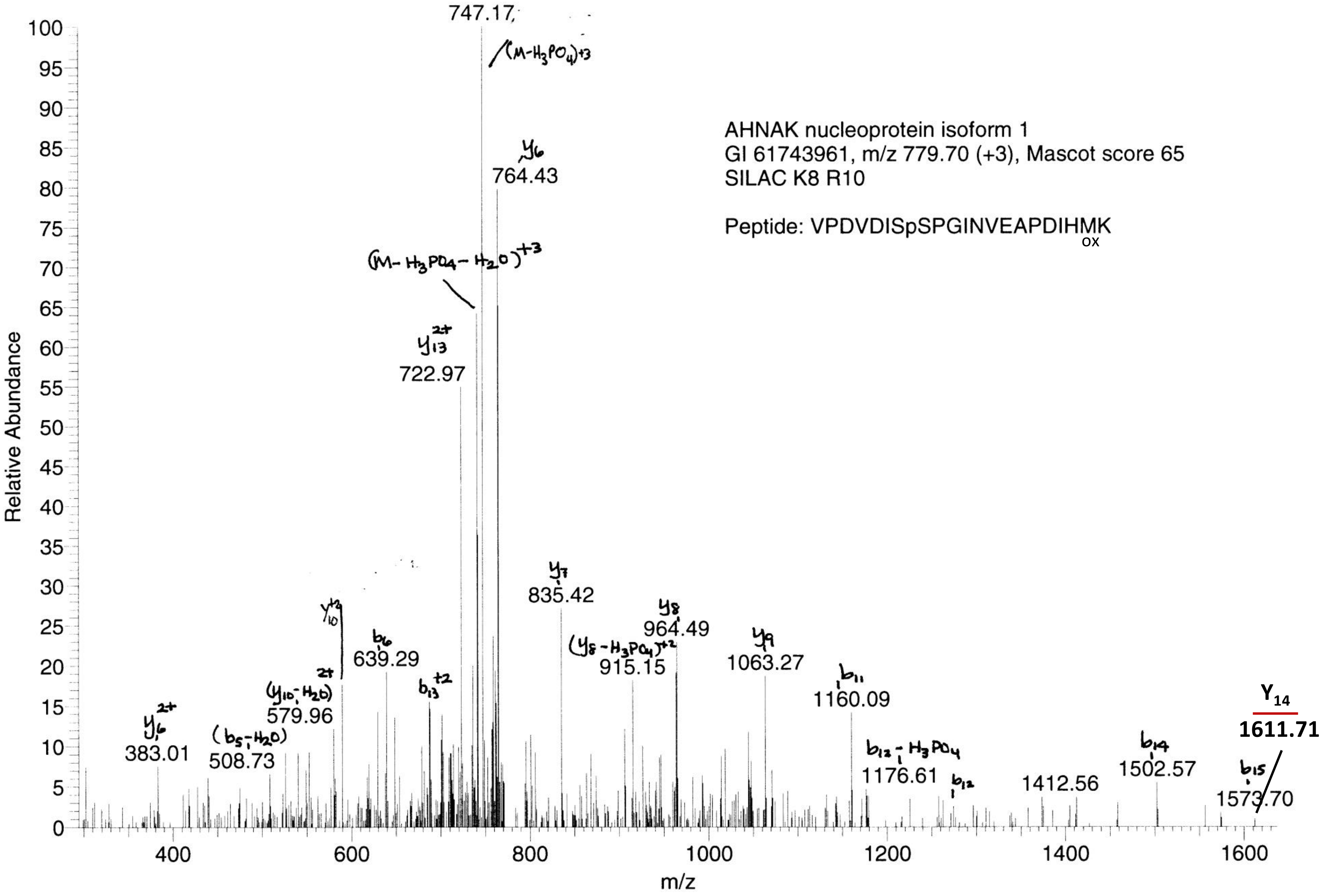
AHNAK nucleoprotein isoform 1
GI 61743961, m/z 930.44 (+2), Mascot score 89
SILAC K6 R6

Peptide: LPSGSGPApSPTTGSAVDIR



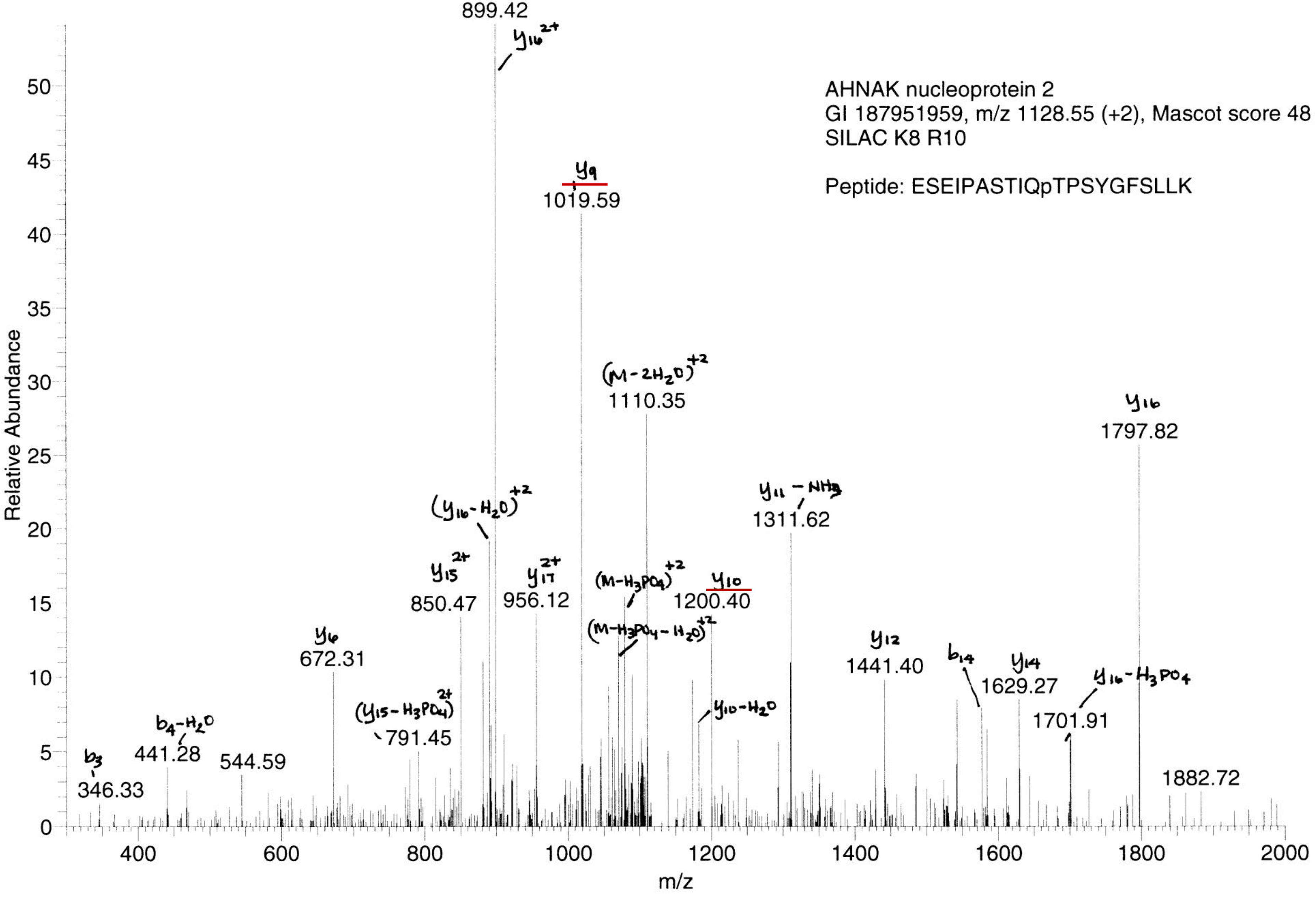
AHNAK nucleoprotein isoform 1
GI 61743961. m/z 609.94 (+3), Mascot score 57
SILAC K8 R10

Peptide: M_{ox}YFPDVEFDIKpSPK



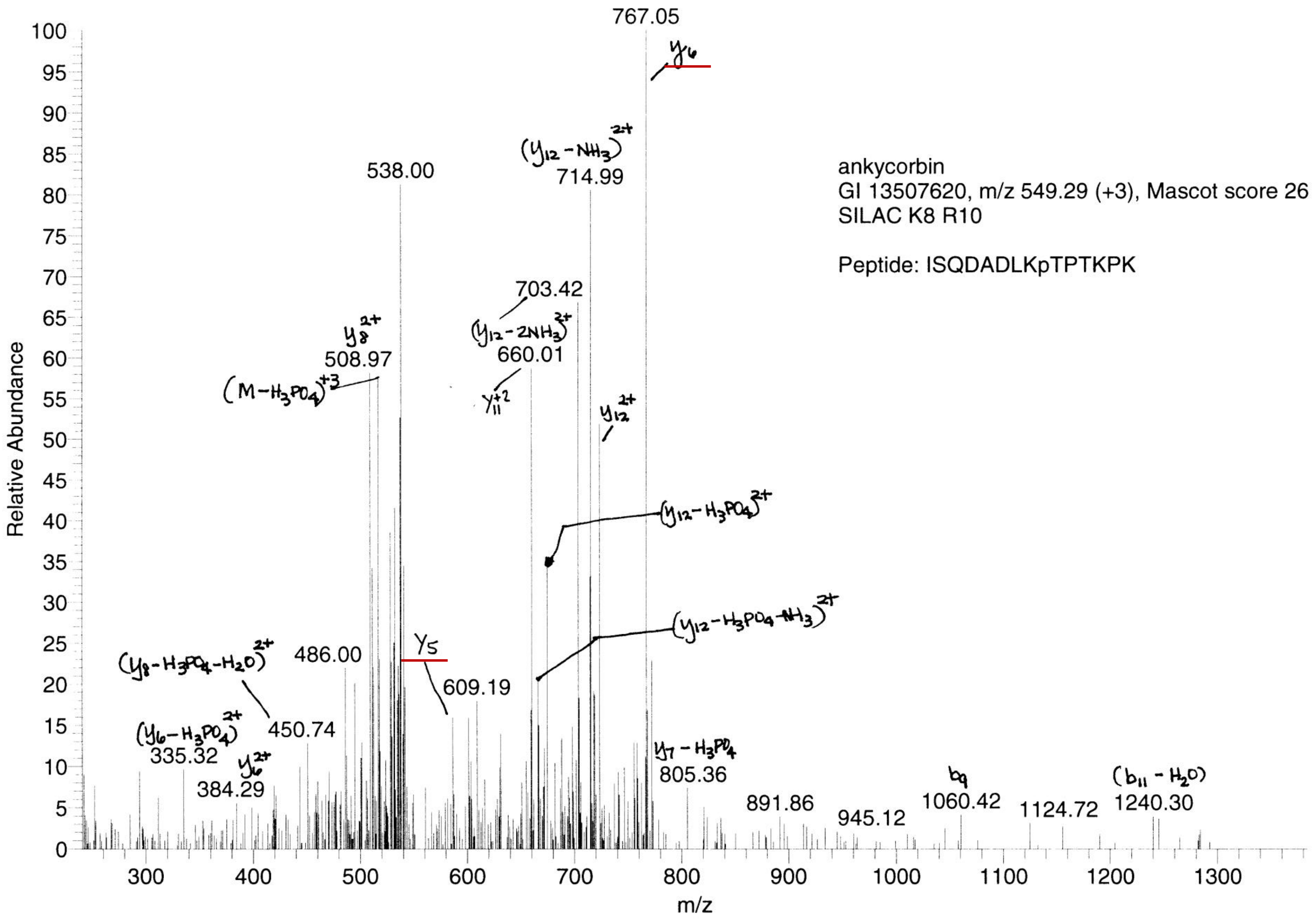
AHNAK nucleoprotein isoform 1
GI 61743961, m/z 779.70 (+3), Mascot score 65
SILAC K8 R10

Peptide: $VPDVDISpSPGINVEAPDIH\underset{ox}{M}K$



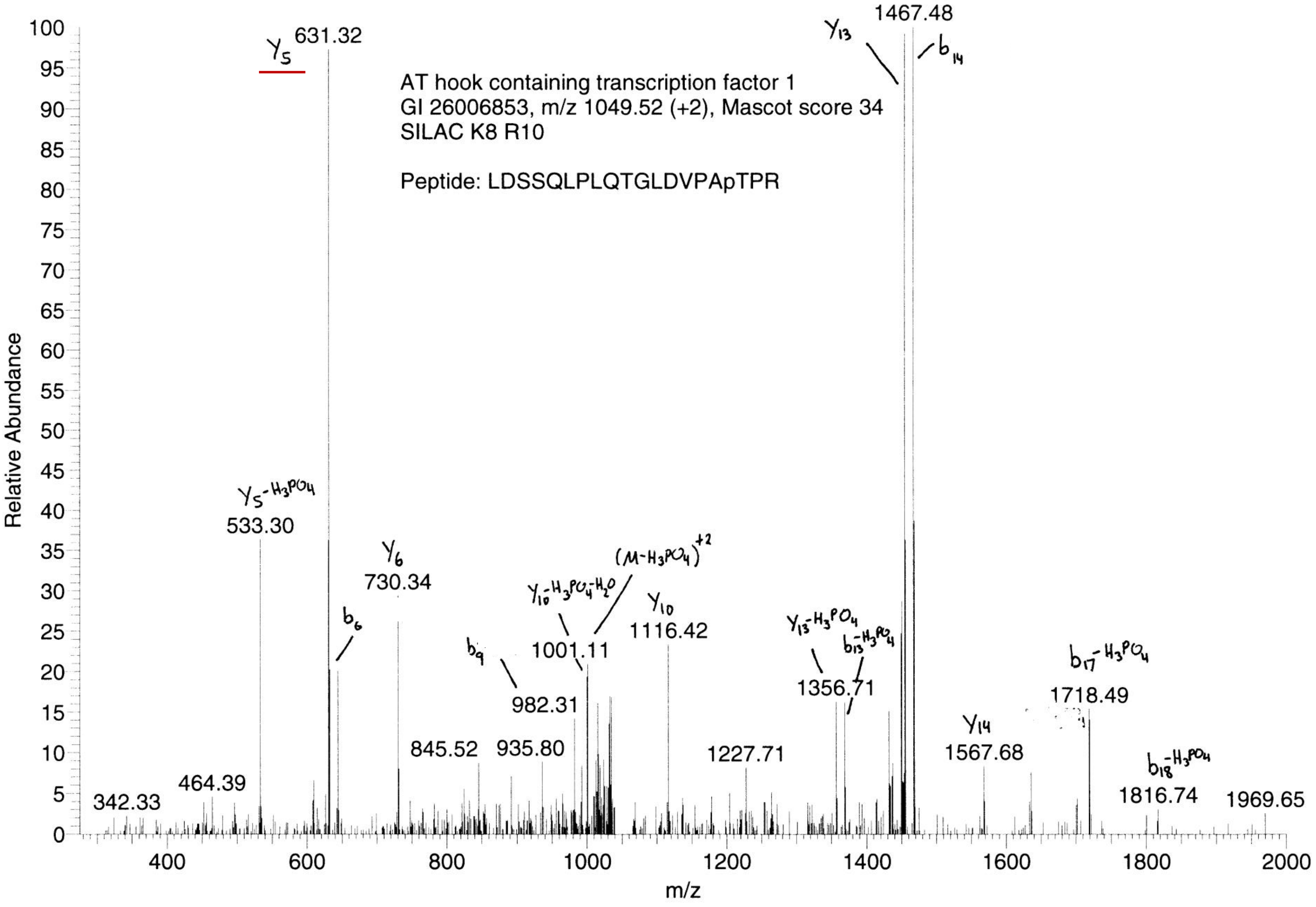
AHNAK nucleoprotein 2
GI 187951959, m/z 1128.55 (+2), Mascot score 48
SILAC K8 R10

Peptide: ESEIPASTIQpTPSYGFSLLK



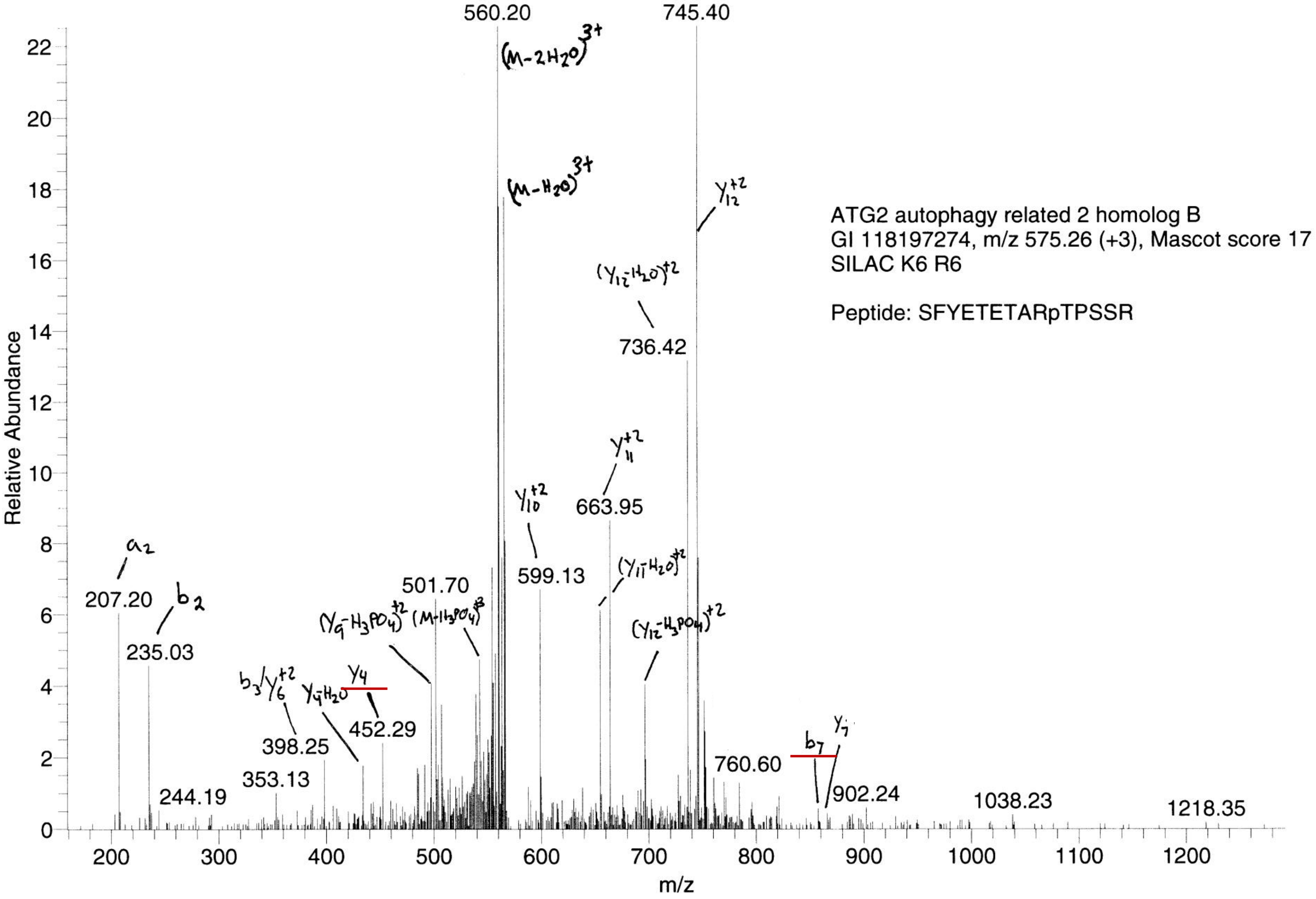
ankycorbin
GI 13507620, m/z 549.29 (+3), Mascot score 26
SILAC K8 R10

Peptide: ISQDADLKpTPTKPK



AT hook containing transcription factor 1
GI 26006853, m/z 1049.52 (+2), Mascot score 34
SILAC K8 R10

Peptide: LDSSQLPLQTGLDVPApTPR

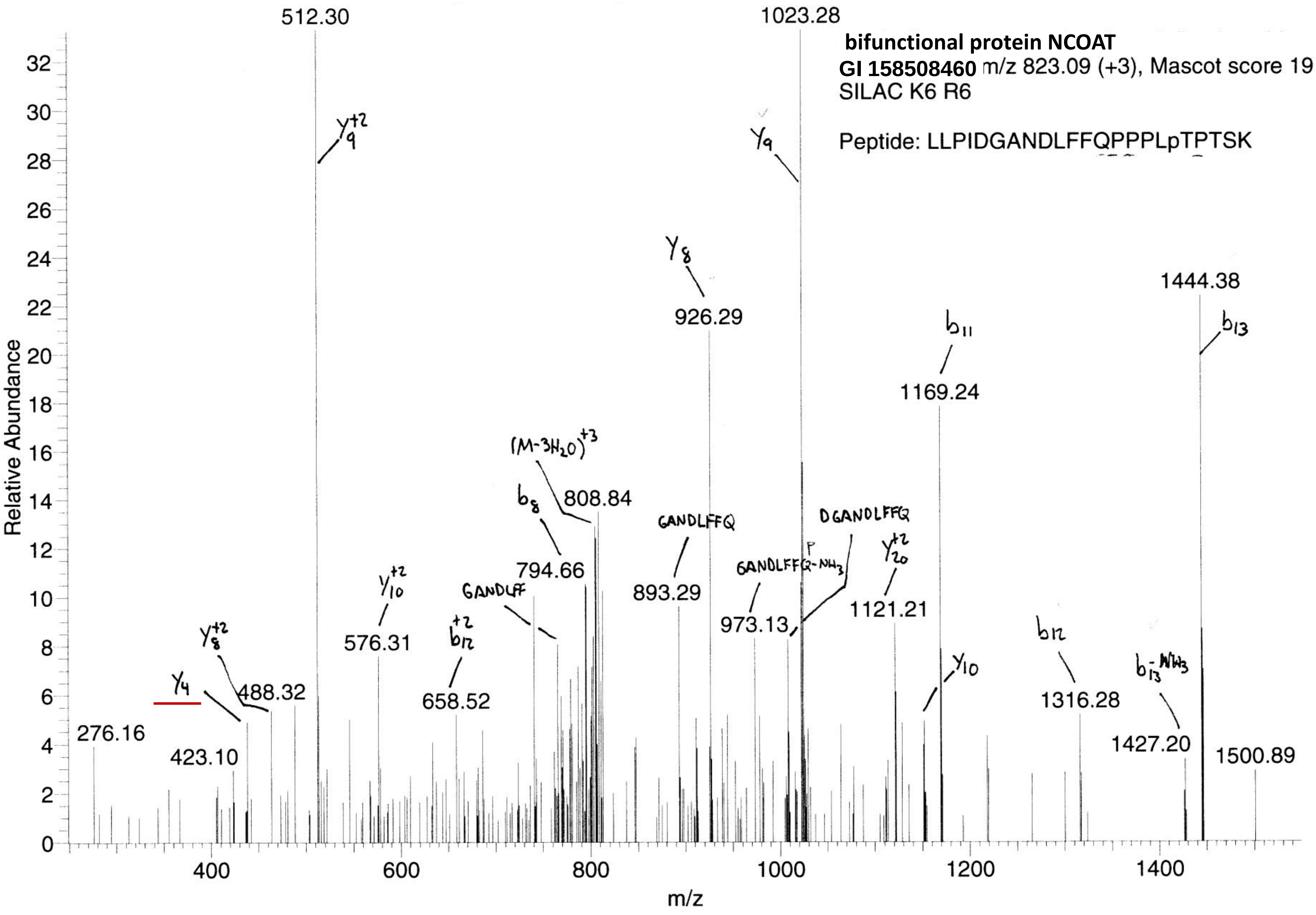


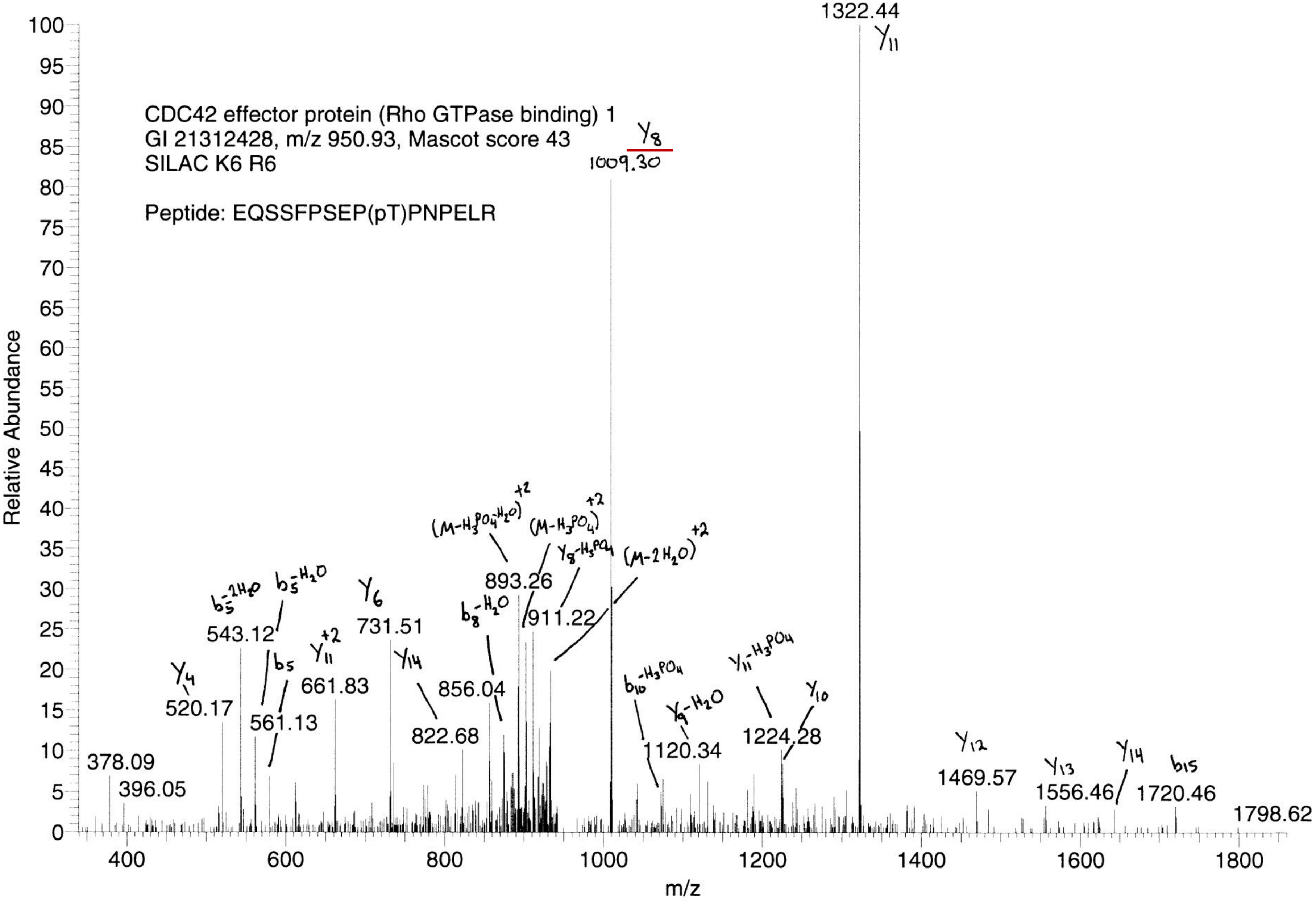
ATG2 autophagy related 2 homolog B
GI 118197274, m/z 575.26 (+3), Mascot score 17
SILAC K6 R6

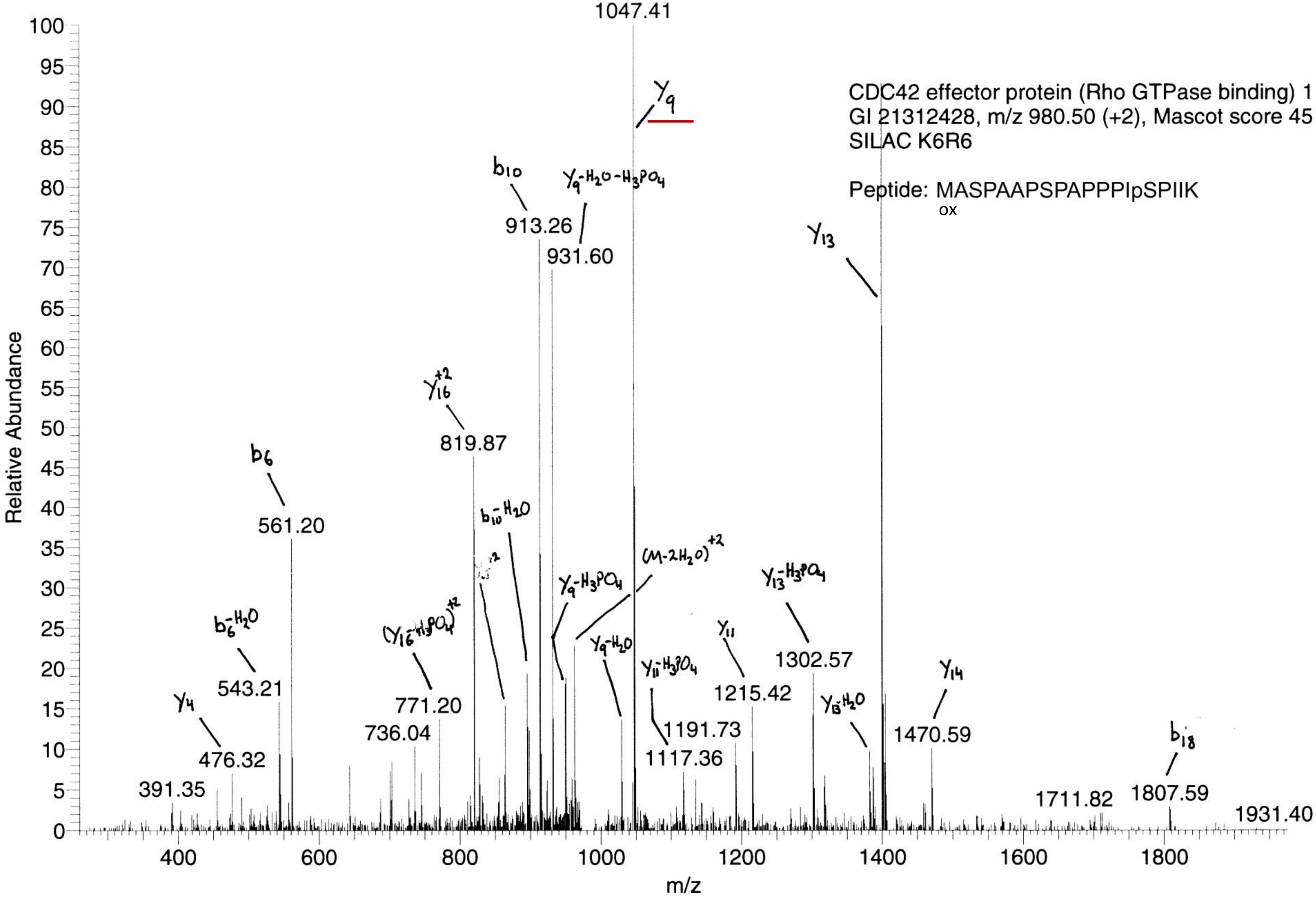
Peptide: SFYETETARpTPSSR

bifunctional protein NCOAT
GI 158508460 m/z 823.09 (+3), Mascot score 19
SILAC K6 R6

Peptide: LLPIDGANDLFFQPPPLpTPTSK

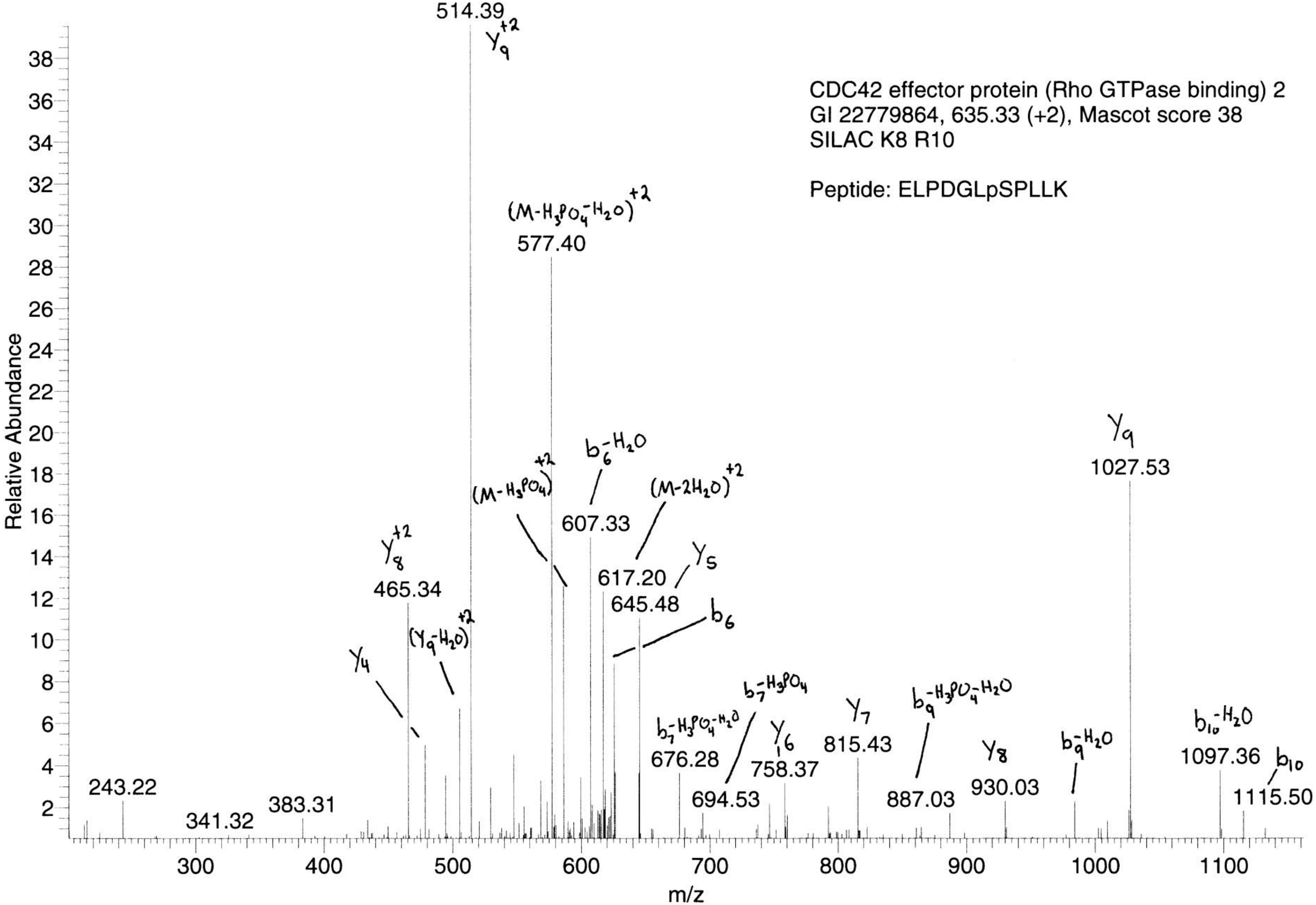



CDC42 effector protein (Rho GTPase binding) 1
GI 21312428, m/z 950.93, Mascot score 43
SILAC K6 R6
Peptide: EQSSFPSEP(pT)PNPELR
Relative Abundance
m/z
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
400
600
800
1000
1200
1400
1600
1800
1322.44
Y_{11}
Y_8
1009.30
378.09
396.05
Y_4
520.17
b_5-2H$_2$O
543.12
b_5-H$_2$O
b_5
561.13
Y_{11}^{+2}
661.83
Y_6
731.51
Y_{14}
822.68
b_8-H$_2$O
856.04
$(M-H_3PO_4-H_2O)^{+2}$
893.26
$(M-H_3PO_4)^{+2}$
Y_8-H$_3$PO$_4$
911.22
$(M-2H_2O)^{+2}$
b_{10}-H$_3$PO$_4$
Y_9-H$_2$O
1120.34
Y_{11}-H$_3$PO$_4$
Y_{10}
1224.28
Y_{12}
1469.57
Y_{13}
1556.46
Y_{14}
b_{15}
1720.46
1798.62



CDC42 effector protein (Rho GTPase binding) 1
GI 21312428, m/z 980.50 (+2), Mascot score 45
SILAC K6R6

Peptide: MASPAAPSPAPPPIpSPIIK
ox



CDC42 effector protein (Rho GTPase binding) 2
GI 22779864, 635.33 (+2), Mascot score 38
SILAC K8 R10

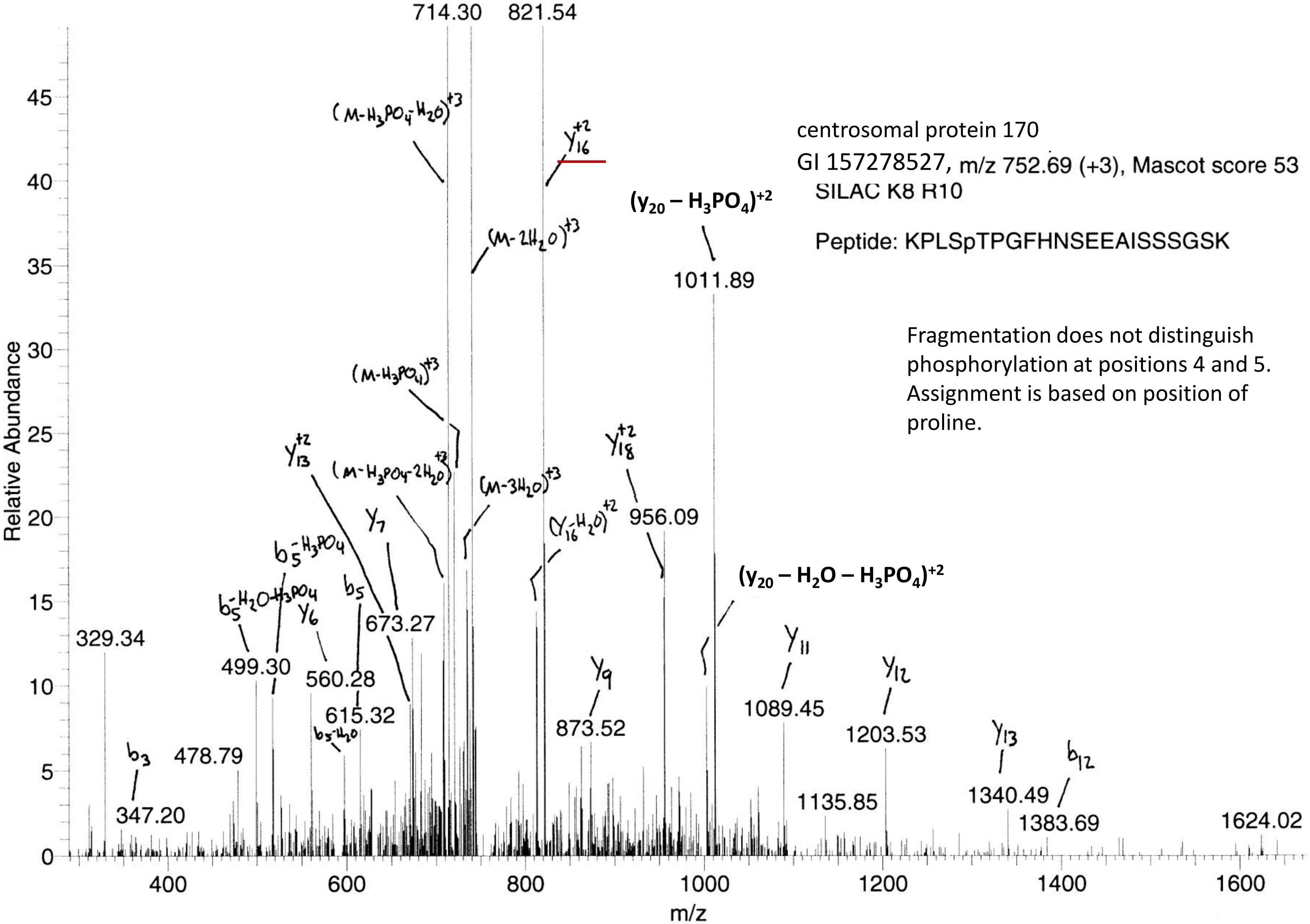
Peptide: ELPDGLpSPLLK

centrosomal protein 170

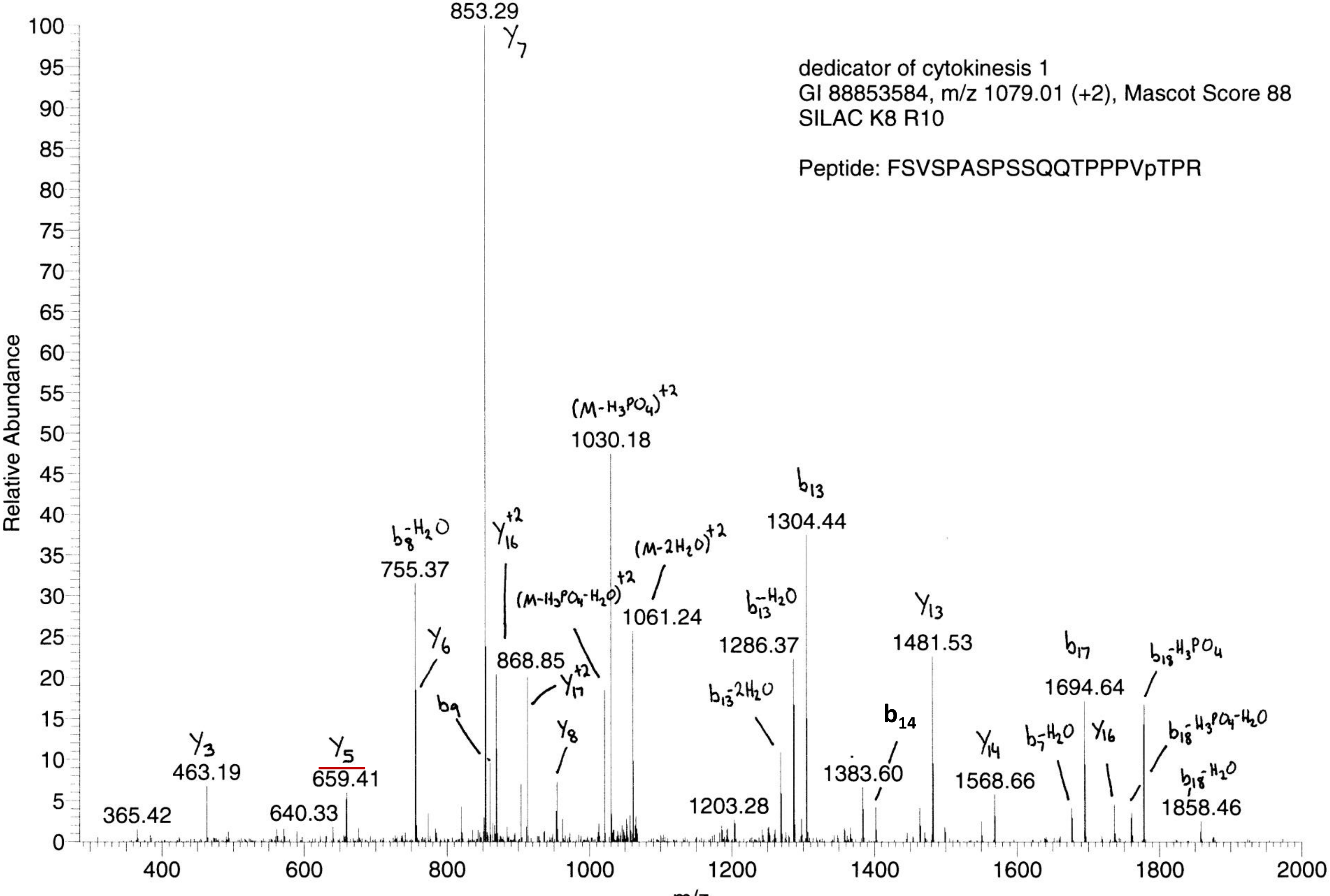
GI 157278527, m/z 752.69 (+3), Mascot score 53

SILAC K8 R10

Peptide: KPLSpTPGFHNSEEAISSSGSK

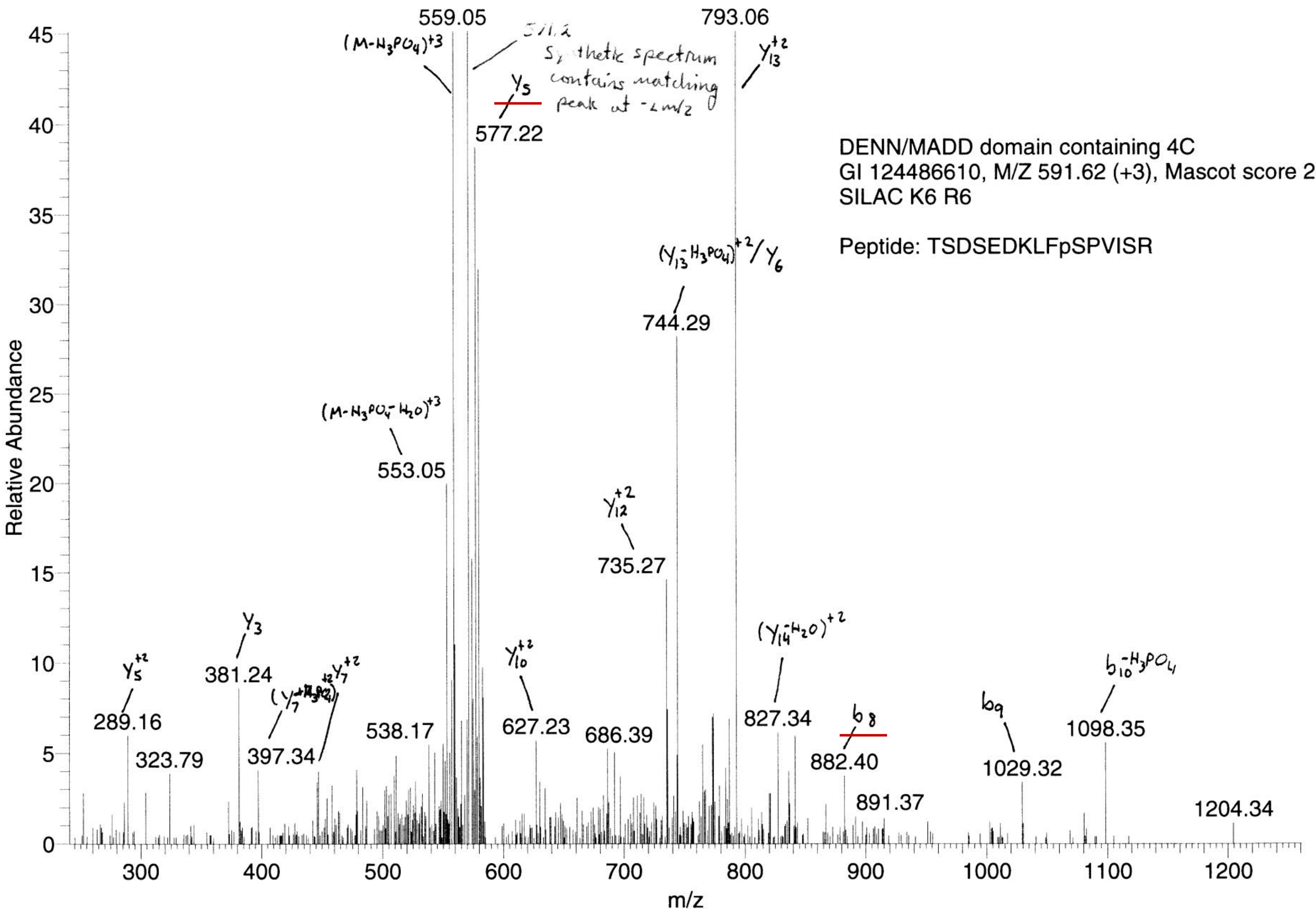


Fragmentation does not distinguish phosphorylation at positions 4 and 5. Assignment is based on position of proline.



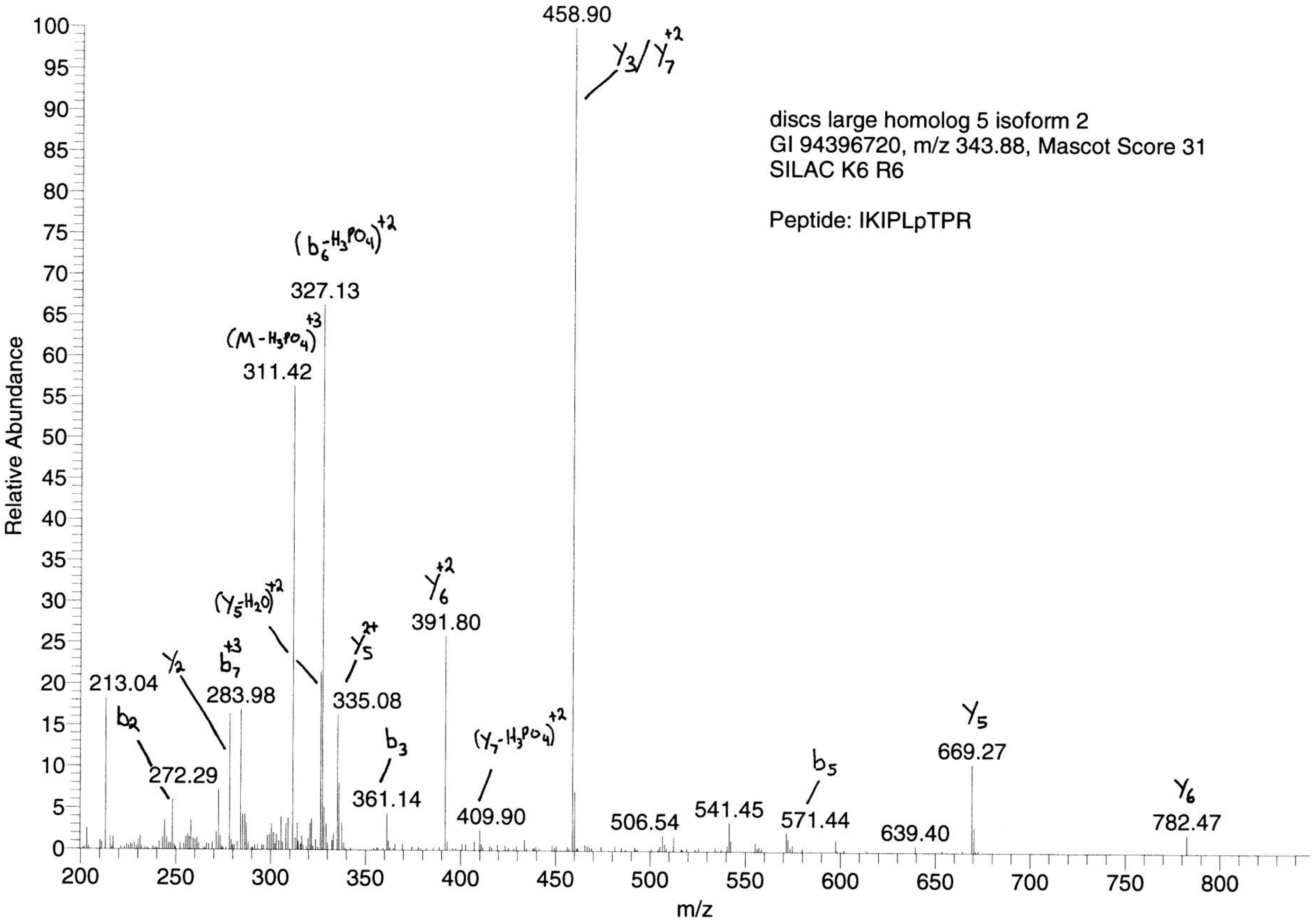
dedicator of cytokinesis 1
GI 88853584, m/z 1079.01 (+2), Mascot Score 88
SILAC K8 R10

Peptide: FSVSPASPSSQQTPPPVpTPR


DENN/MADD domain containing 4C
GI 124486610, M/Z 591.62 (+3), Mascot score 26
SILAC K6 R6

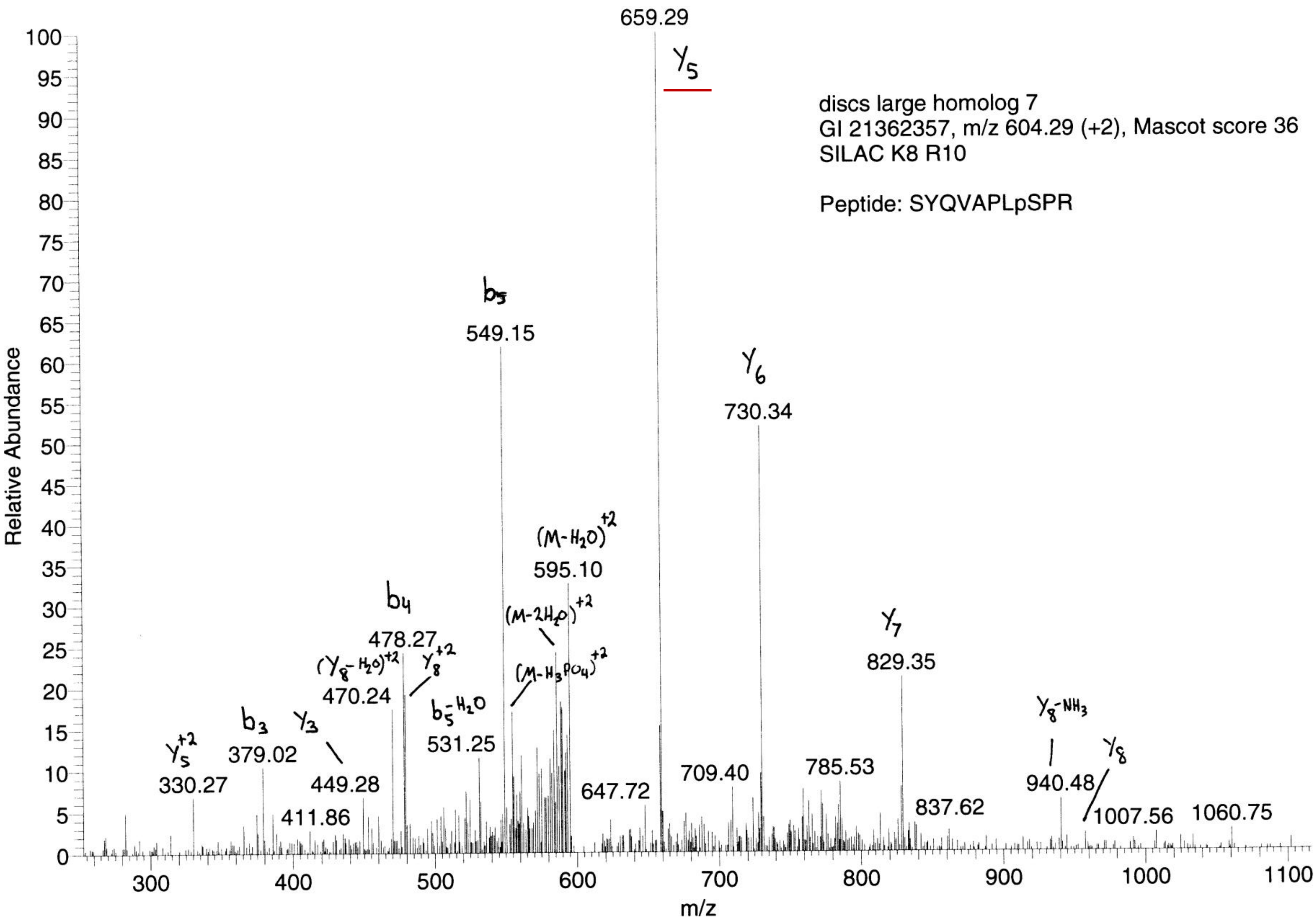
Peptide: TSDSEDKLFpSPVISR

571.2
Synthetic spectrum
contains matching
peak at ~2 m/z



discs large homolog 5 isoform 2
GI 94396720, m/z 343.88, Mascot Score 31
SILAC K6 R6

Peptide: IKIPLpTPR



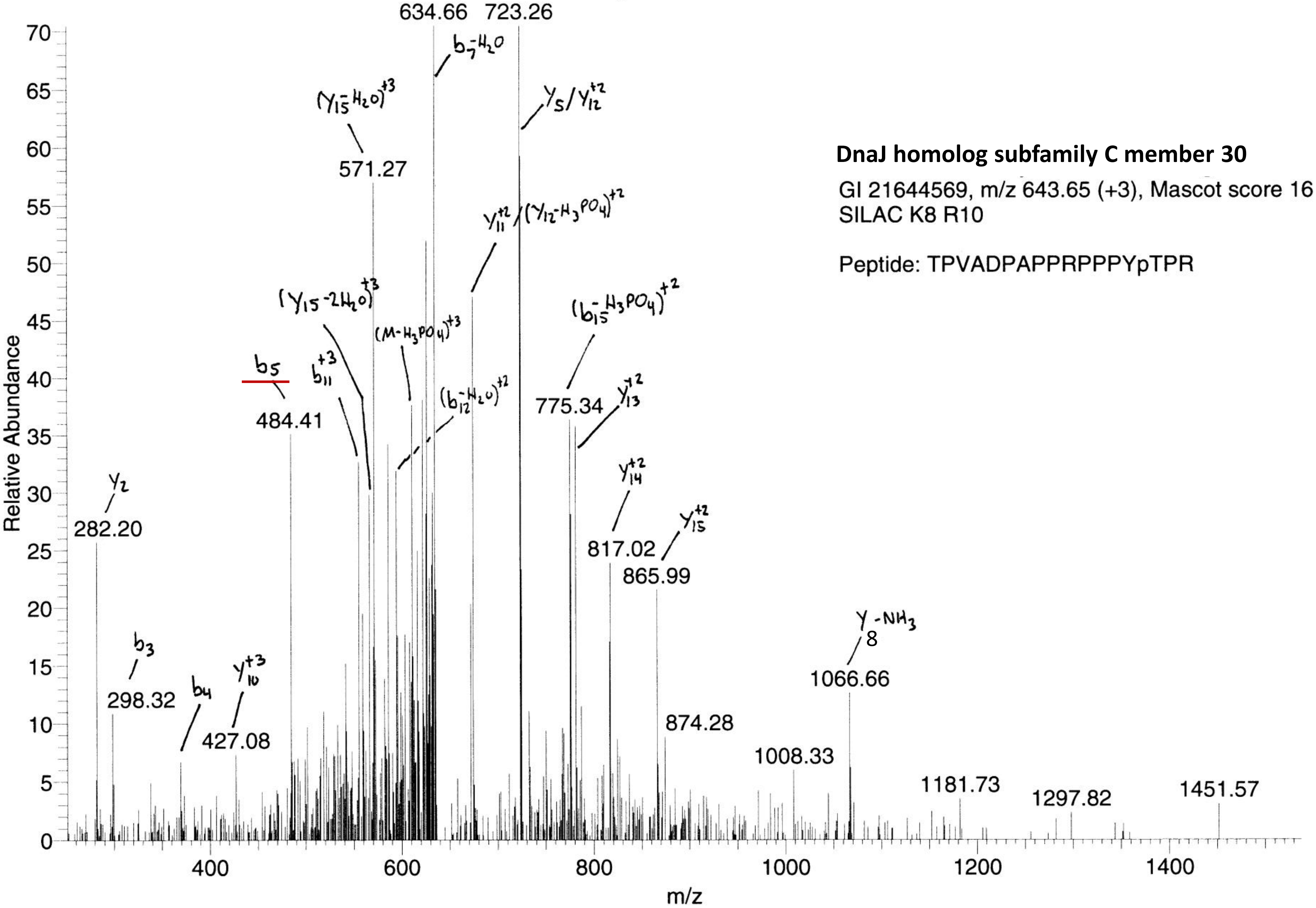
discs large homolog 7
GI 21362357, m/z 604.29 (+2), Mascot score 36
SILAC K8 R10

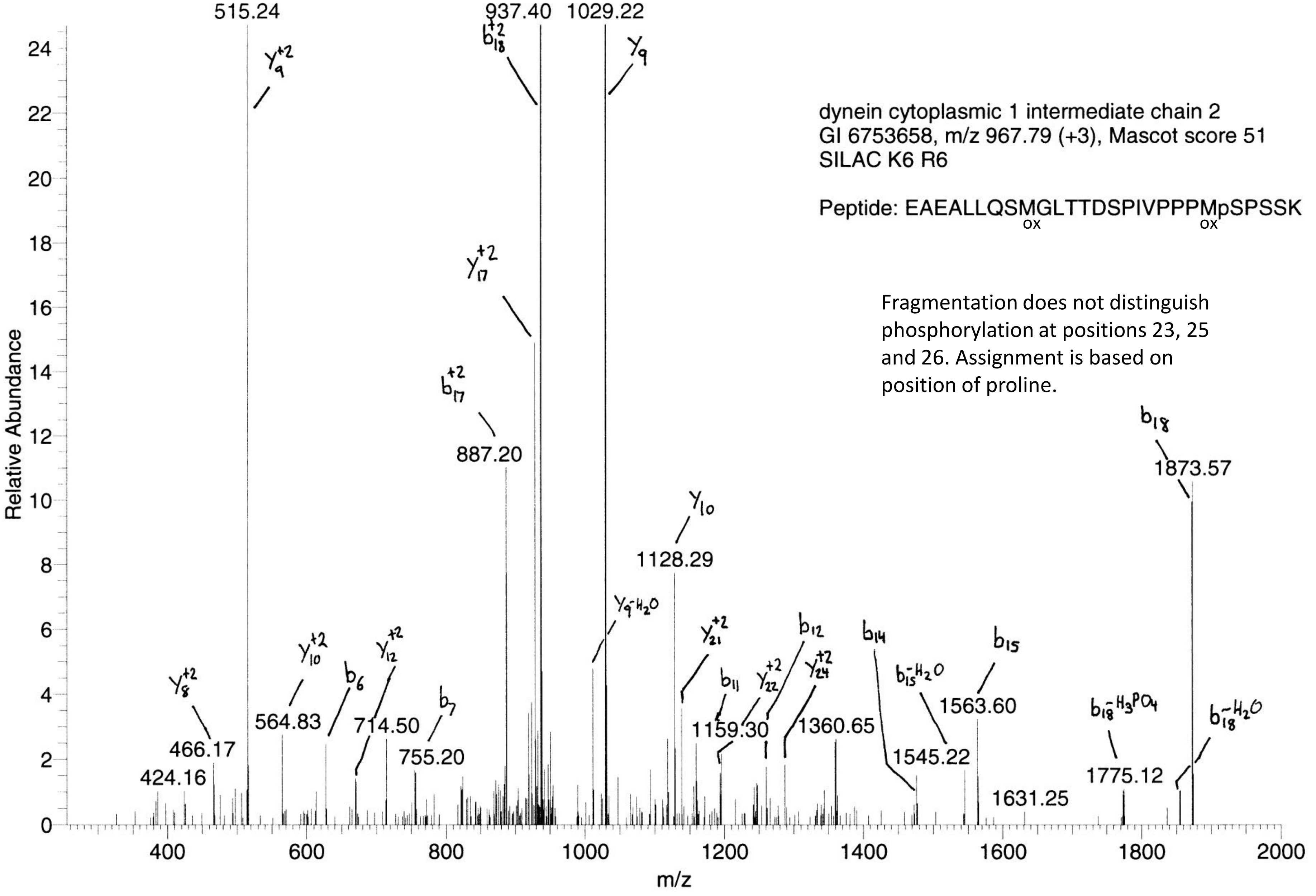
Peptide: SYQVAPLpSPR

DnaJ homolog subfamily C member 30

GI 21644569, m/z 643.65 (+3), Mascot score 16
SILAC K8 R10

Peptide: TPVADPAPPRPPPYpTPR

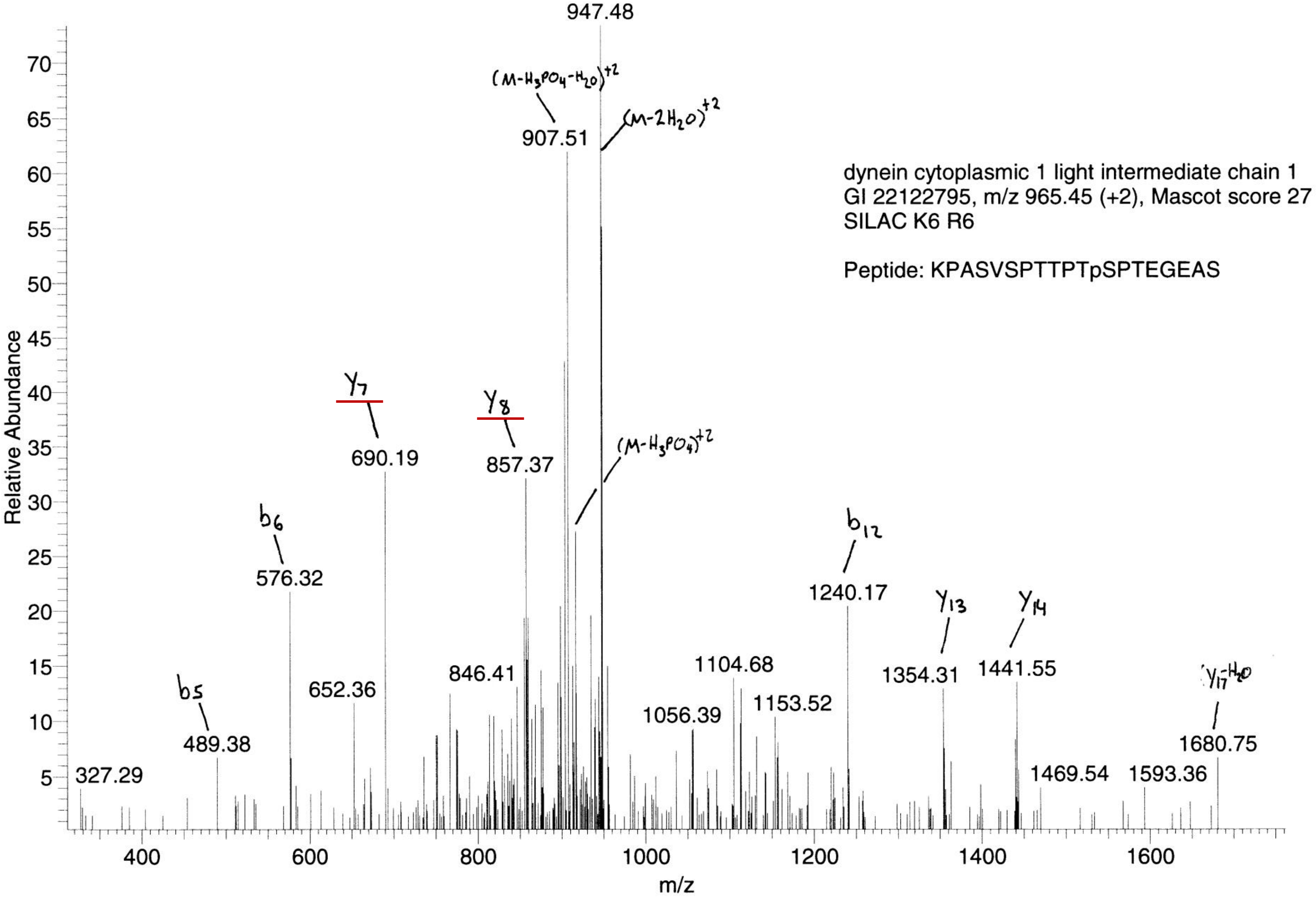




dynein cytoplasmic 1 intermediate chain 2
GI 6753658, m/z 967.79 (+3), Mascot score 51
SILAC K6 R6

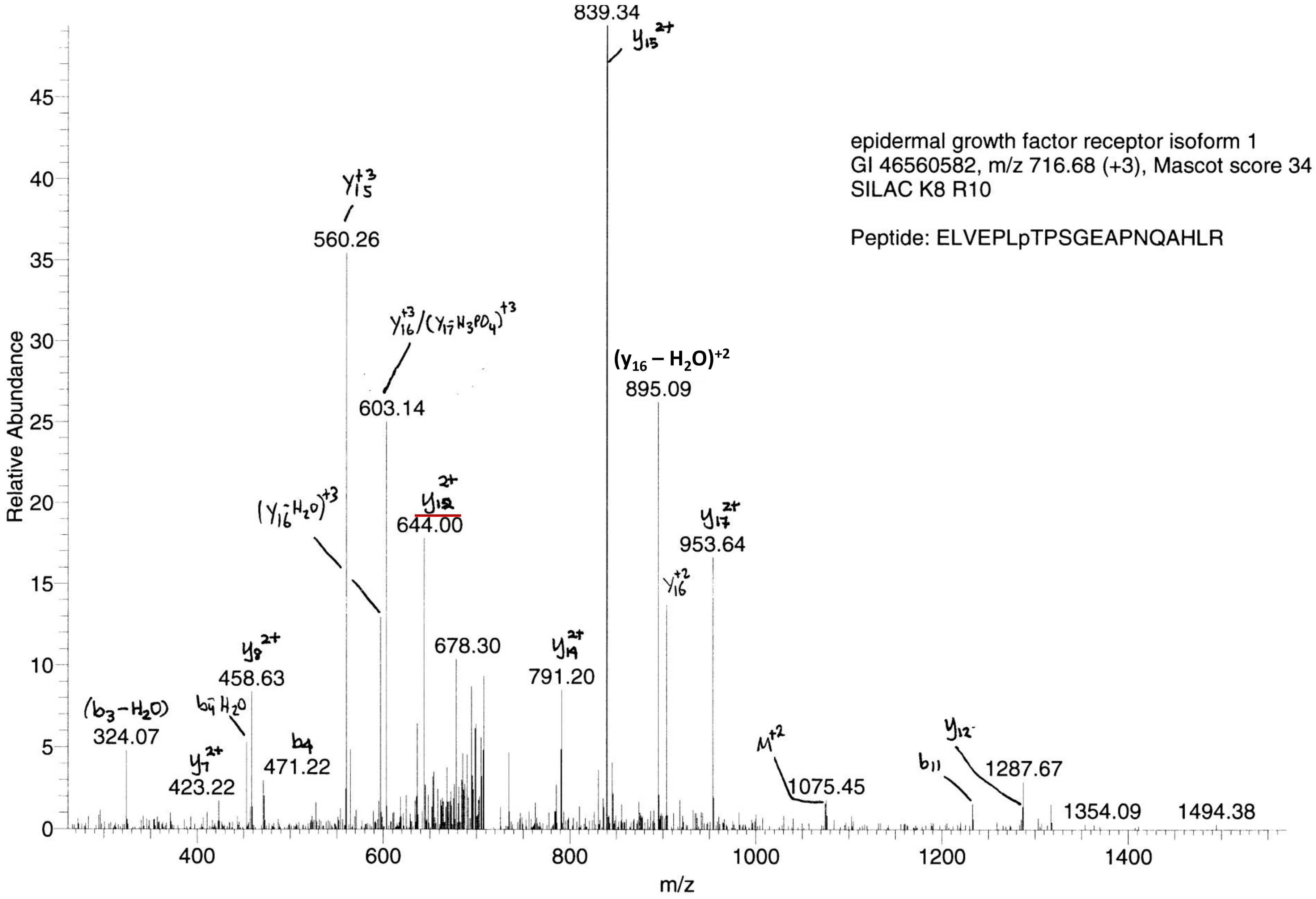
Peptide: EAEALLQSM_{ox}GLTTDSPIVPPPM_{ox}pSPSSK

Fragmentation does not distinguish phosphorylation at positions 23, 25 and 26. Assignment is based on position of proline.



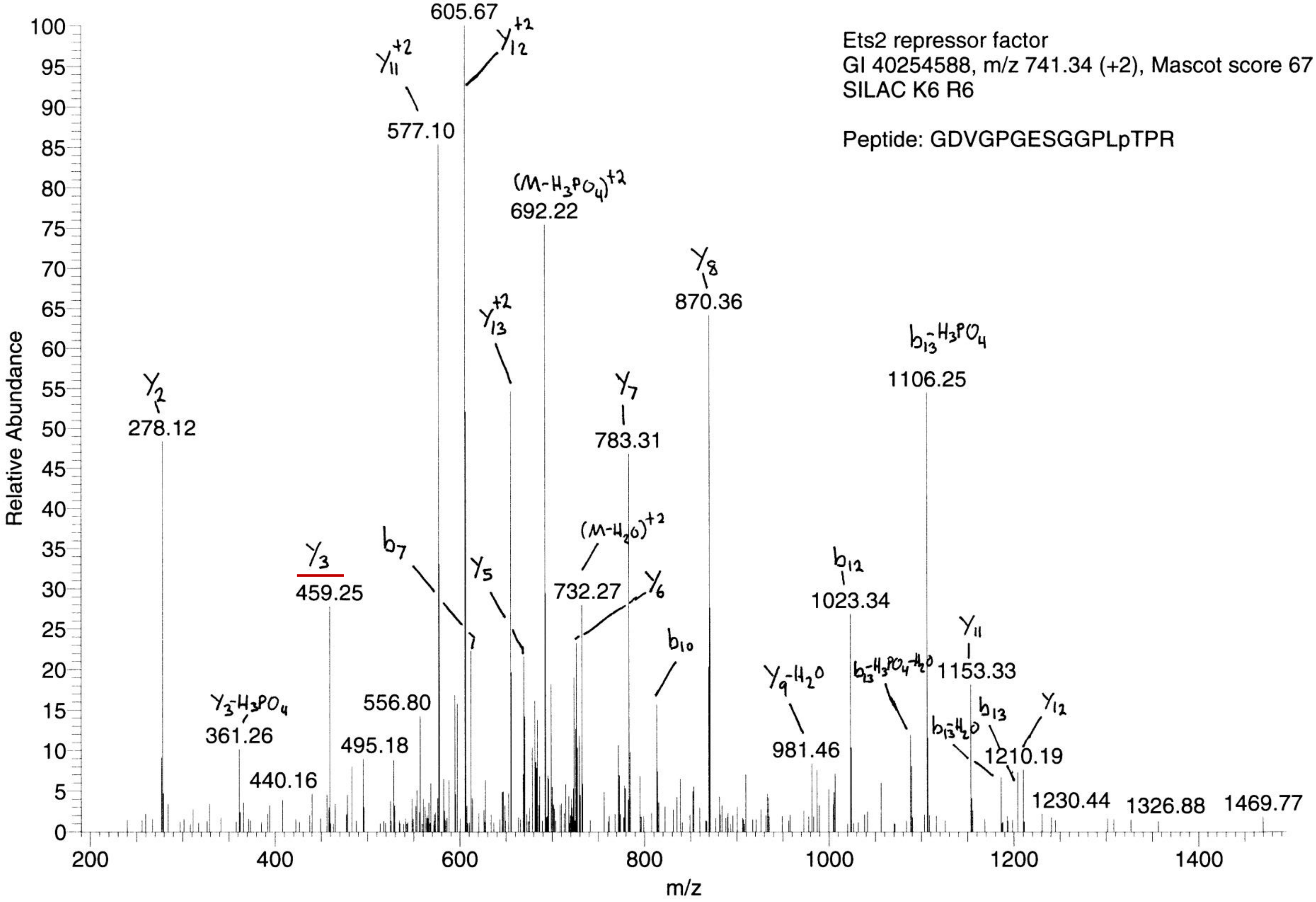
dynein cytoplasmic 1 light intermediate chain 1
GI 22122795, m/z 965.45 (+2), Mascot score 27
SILAC K6 R6

Peptide: KPASVSPTTPTpSPTEGEAS



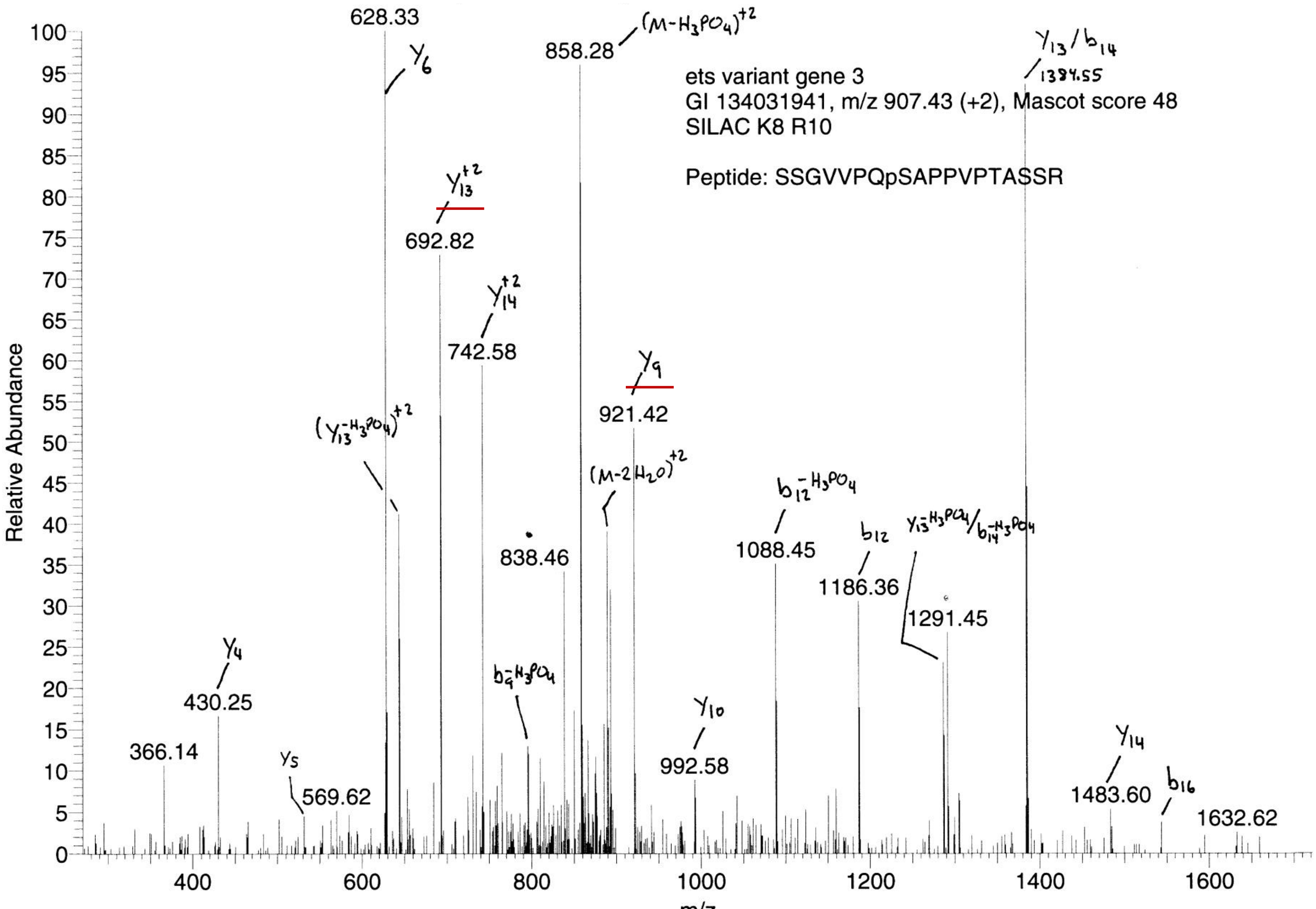
epidermal growth factor receptor isoform 1
GI 46560582, m/z 716.68 (+3), Mascot score 34
SILAC K8 R10

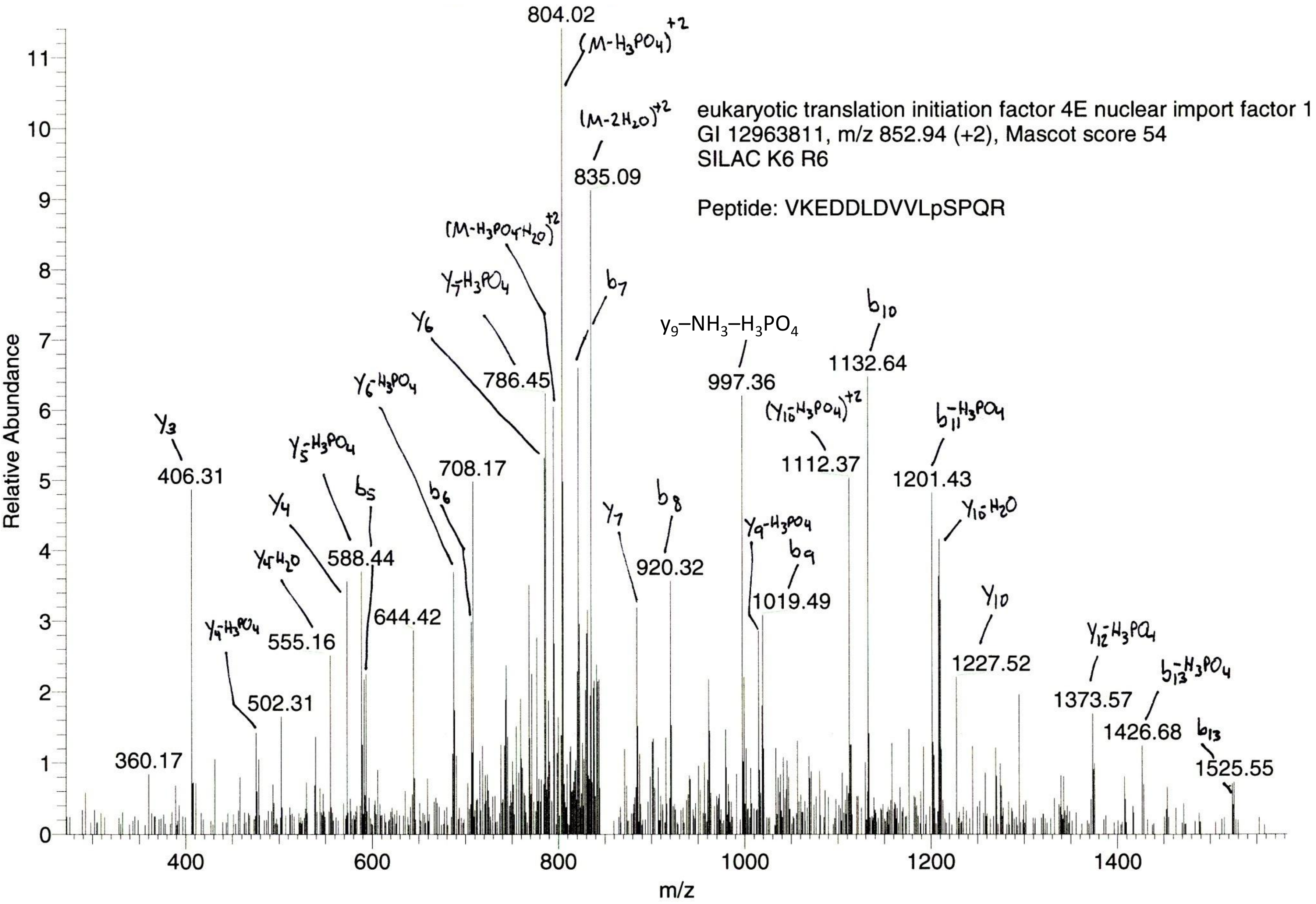
Peptide: ELVEPLpTPSGEAPNQAHLR



Ets2 repressor factor
GI 40254588, m/z 741.34 (+2), Mascot score 67
SILAC K6 R6

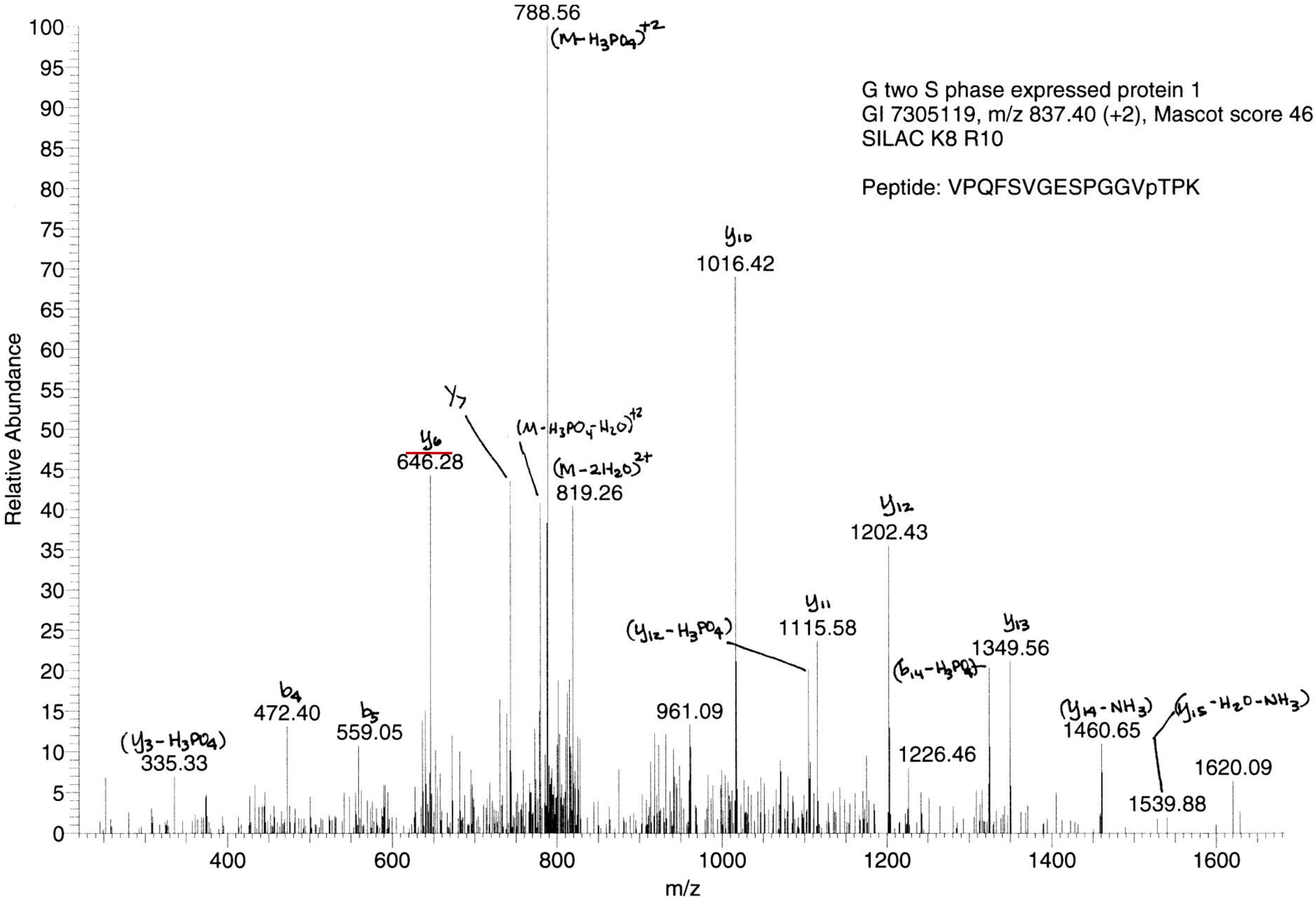
Peptide: GDVGPGESGGPLpTPR


ets variant gene 3
GI 134031941, m/z 907.43 (+2), Mascot score 48
SILAC K8 R10
Peptide: SSGVVPQpSAPPVPTASSR
Relative Abundance
m/z
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
400
600
800
1000
1200
1400
1600
628.33
Y6
858.28
(M-H3PO4)+2
Y13/b14
1384.55
Y13+2
692.82
Y14+2
742.58
Y9
921.42
(Y13-H3PO4)+2
(M-2H2O)+2
838.46
b12-H3PO4
1088.45
b12
1186.36
Y13-H3PO4/b14-H3PO4
1291.45
Y4
430.25
366.14
Y5
569.62
b9-H3PO4
Y10
992.58
Y14
1483.60
b16
1632.62



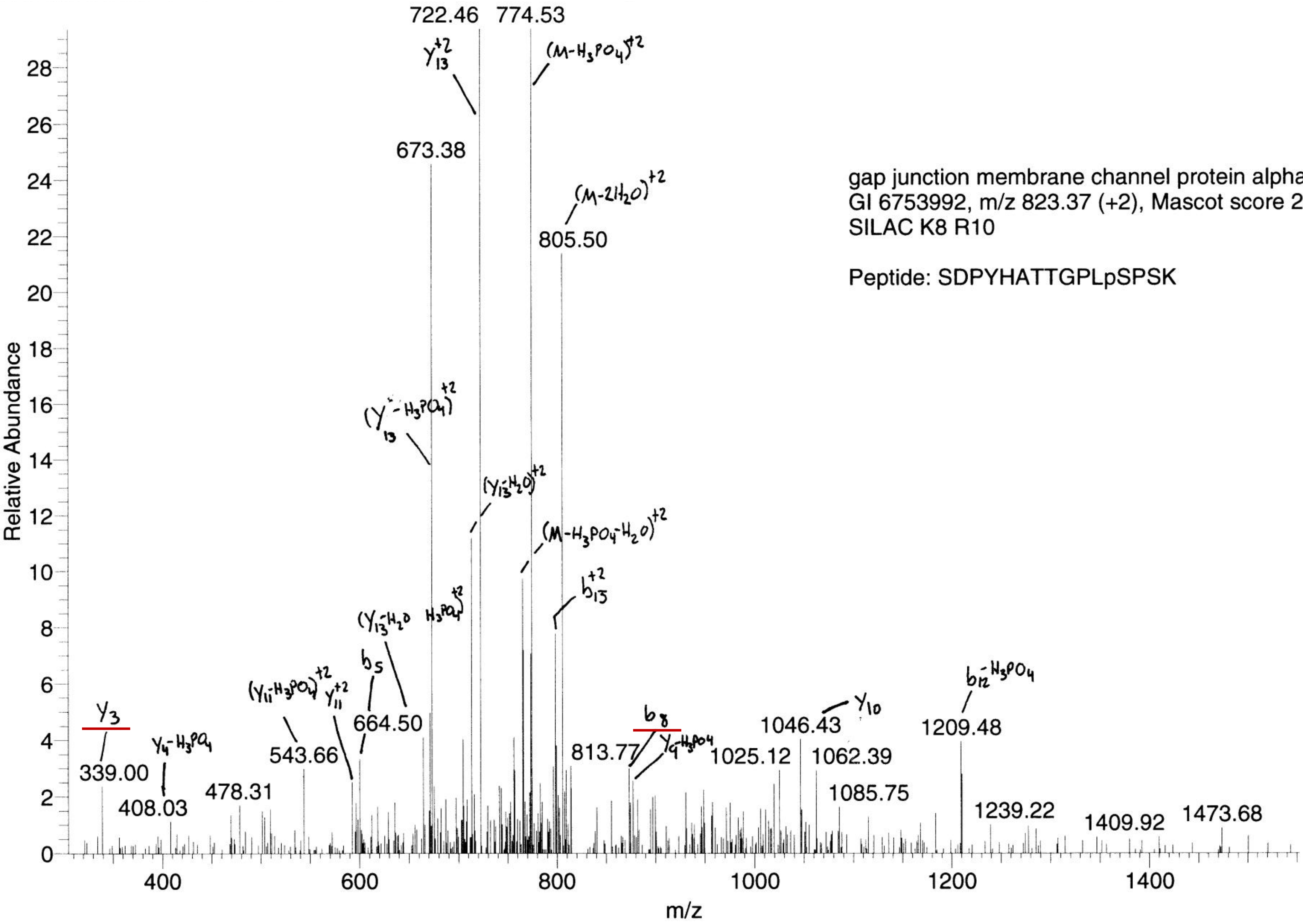
eukaryotic translation initiation factor 4E nuclear import factor 1
GI 12963811, m/z 852.94 (+2), Mascot score 54
SILAC K6 R6

Peptide: VKEDDLDVVLpSPQR



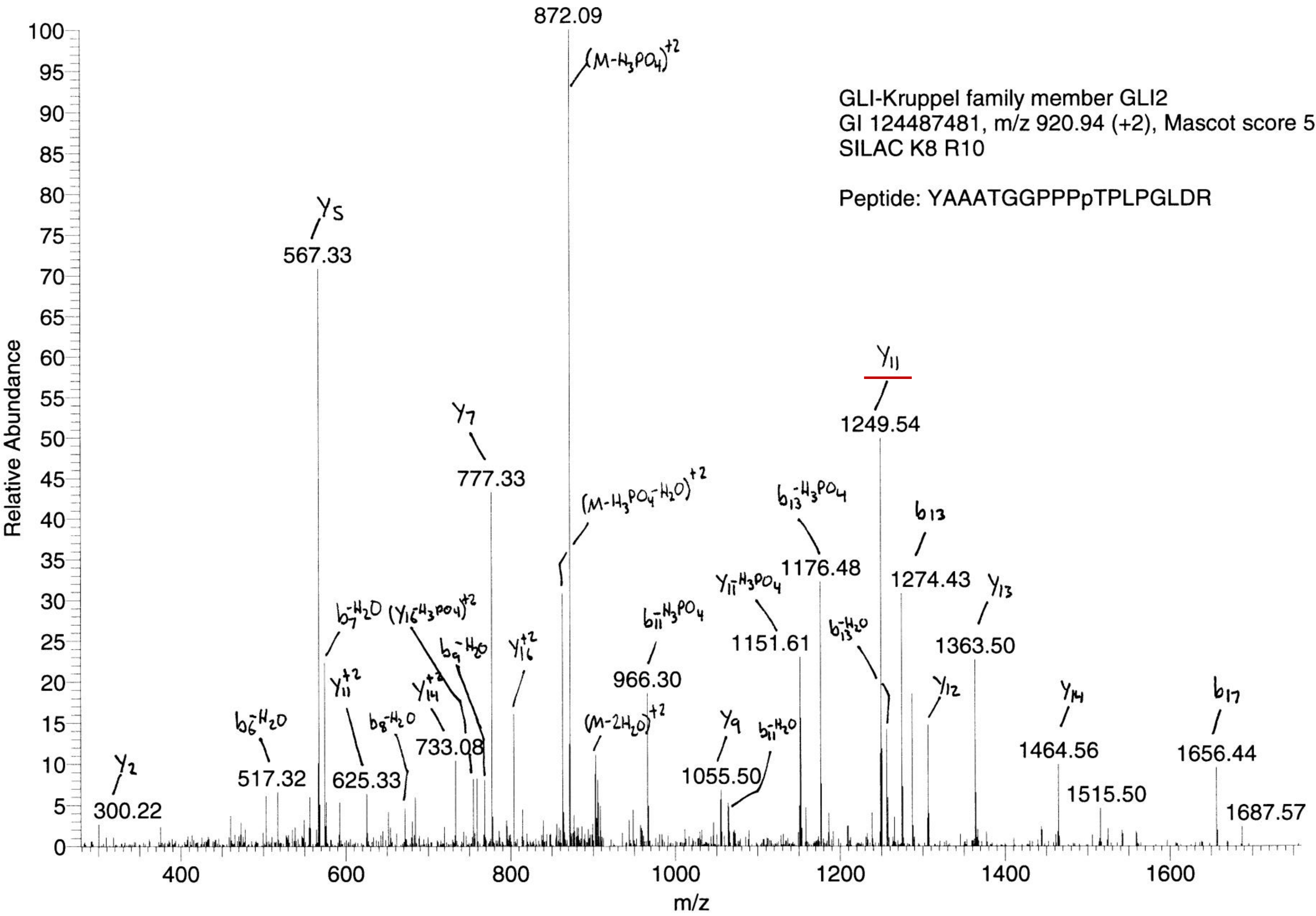
G two S phase expressed protein 1
GI 7305119, m/z 837.40 (+2), Mascot score 46
SILAC K8 R10

Peptide: VPQFSVGESPGGVpTPK



gap junction membrane channel protein alpha 1
GI 6753992, m/z 823.37 (+2), Mascot score 20
SILAC K8 R10

Peptide: SDPYHATTGPLpSPSK



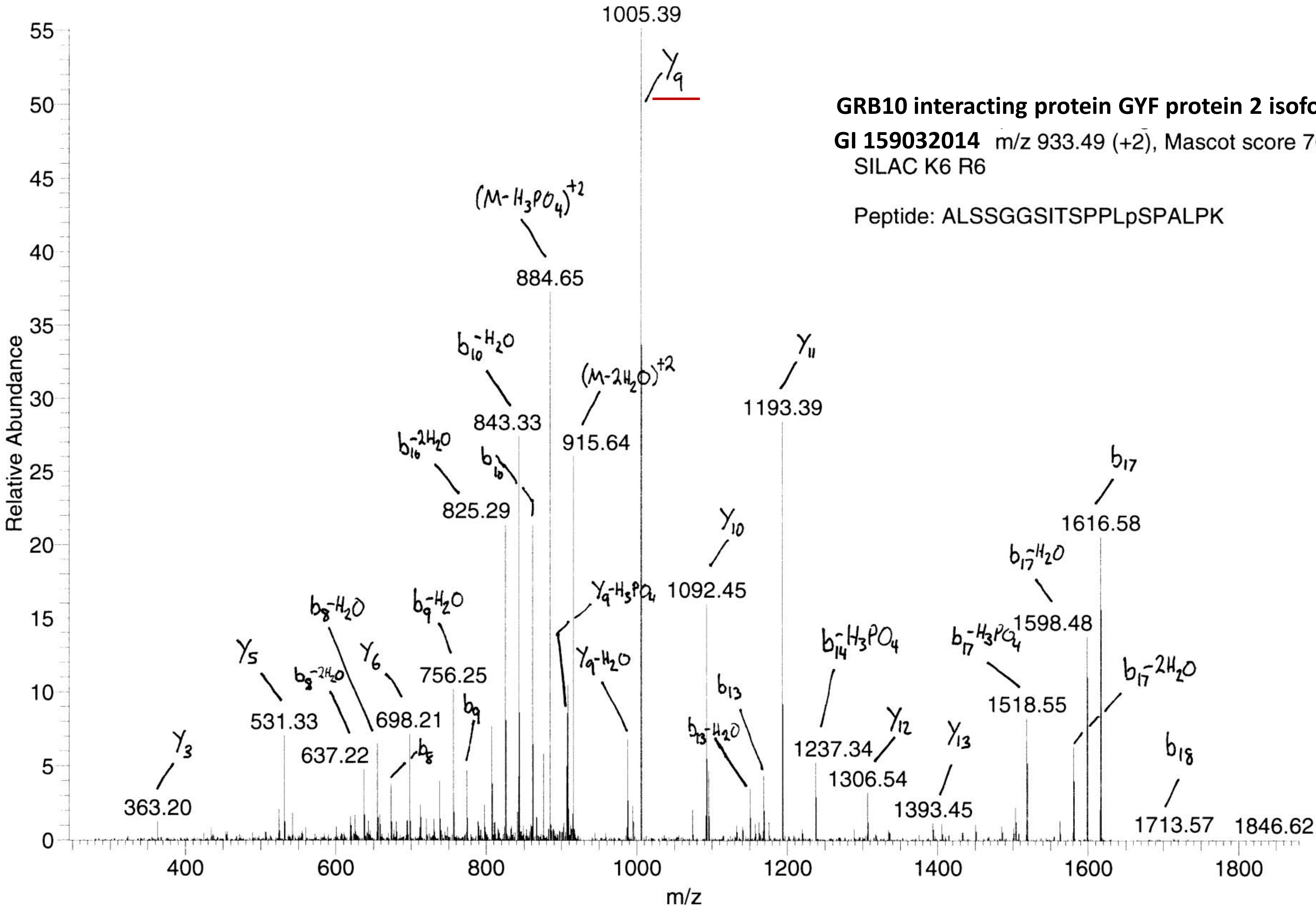
GLI-Kruppel family member GLI2
GI 124487481, m/z 920.94 (+2), Mascot score 56
SILAC K8 R10

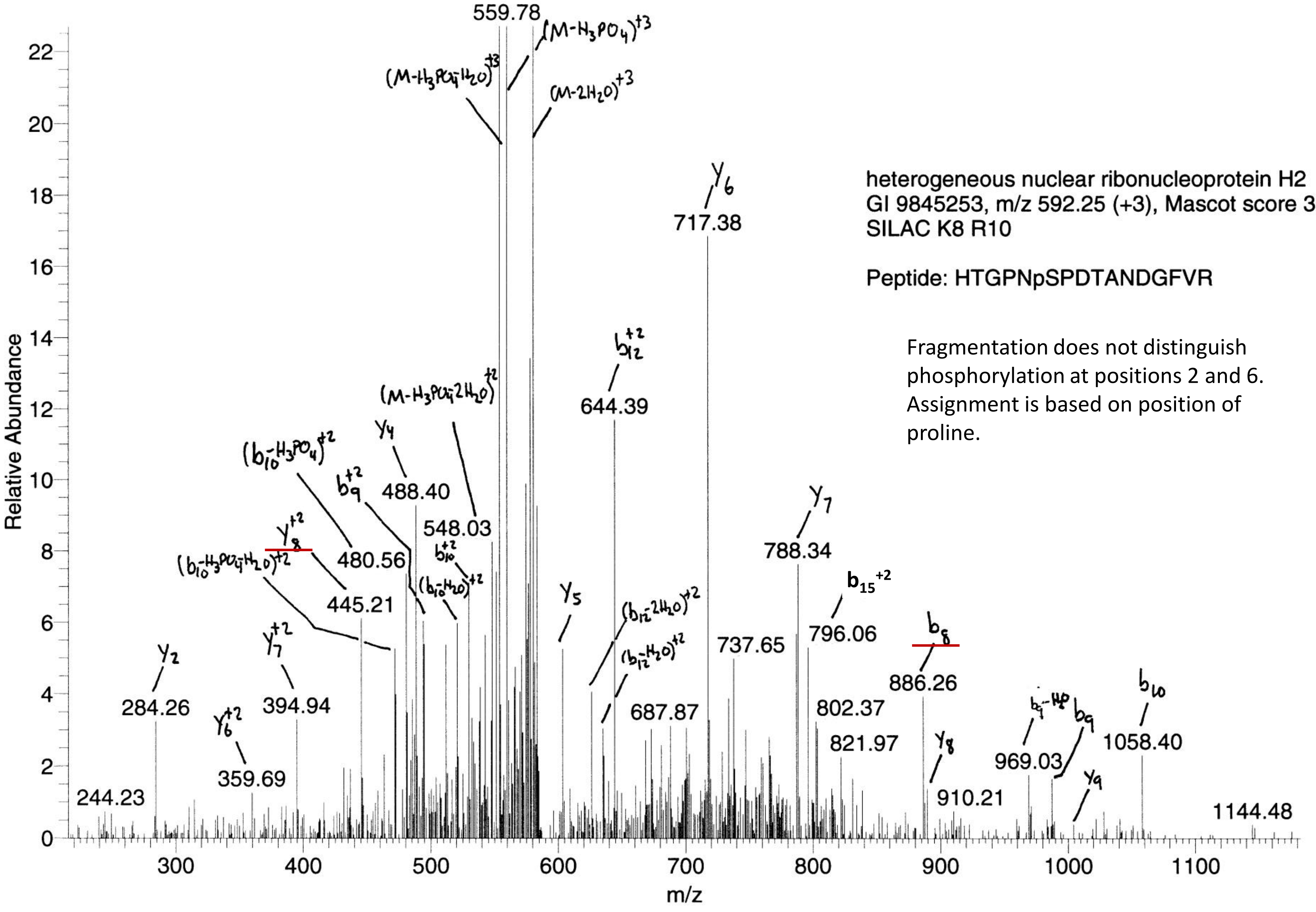
Peptide: YAAATGGPPPpTPLPGLDR

GRB10 interacting protein GYF protein 2 isoform a

GI 159032014 m/z 933.49 (+2), Mascot score 76
SILAC K6 R6

Peptide: ALSSGGSITSPPLpSPALPK

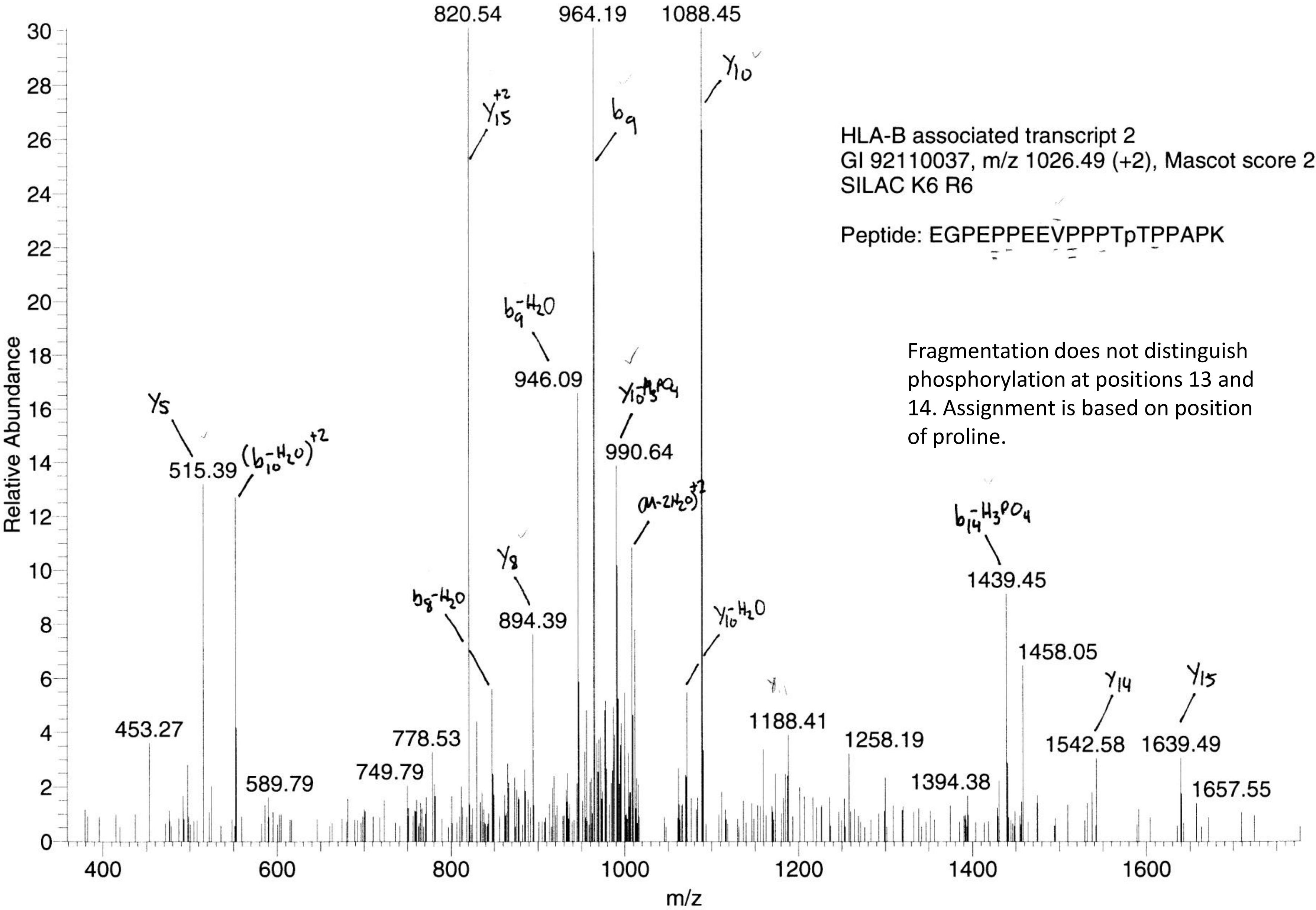




heterogeneous nuclear ribonucleoprotein H2
GI 9845253, m/z 592.25 (+3), Mascot score 33
SILAC K8 R10

Peptide: HTGPNpSPDTANDGFVR

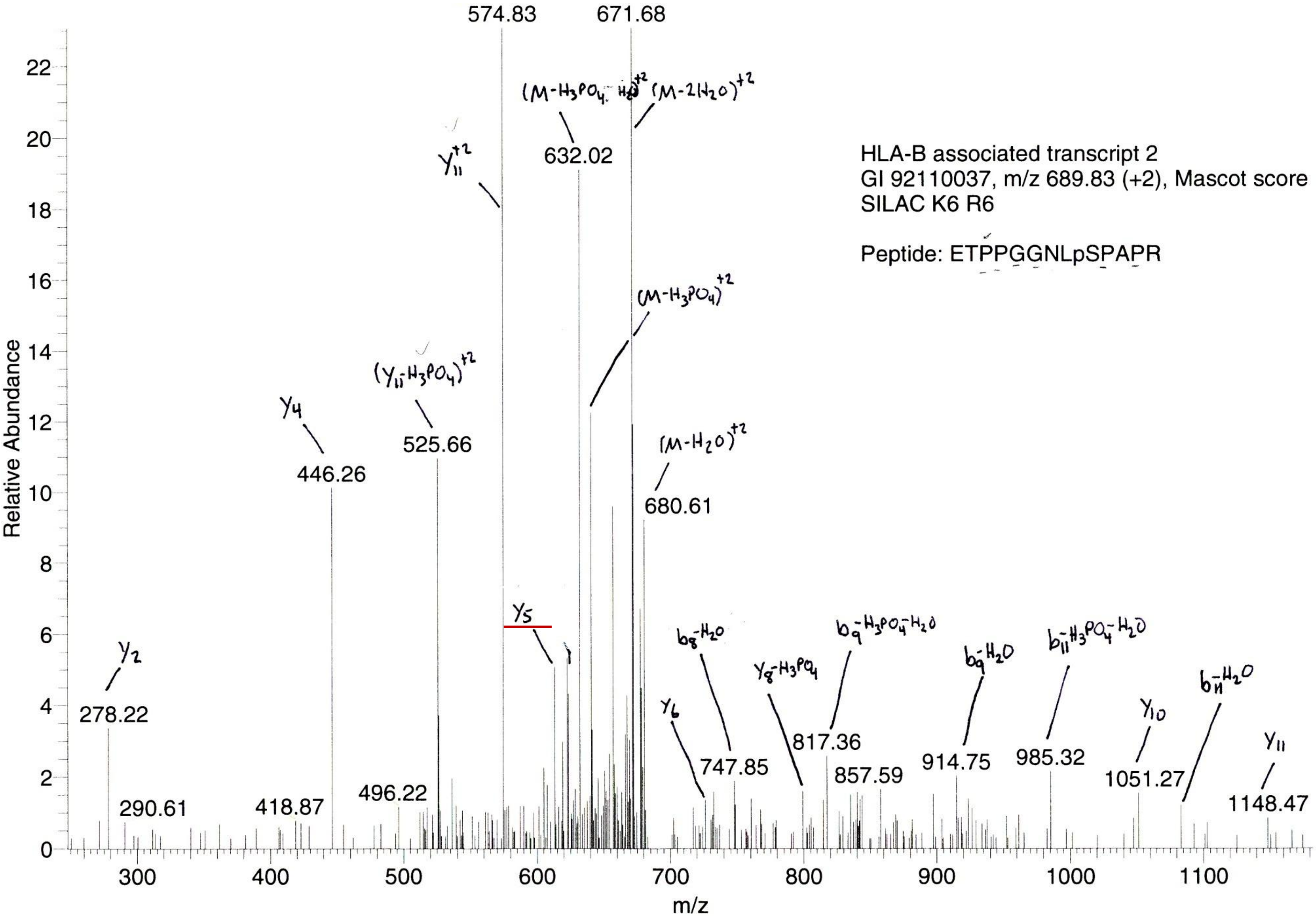
Fragmentation does not distinguish phosphorylation at positions 2 and 6. Assignment is based on position of proline.



HLA-B associated transcript 2
GI 92110037, m/z 1026.49 (+2), Mascot score 20
SILAC K6 R6

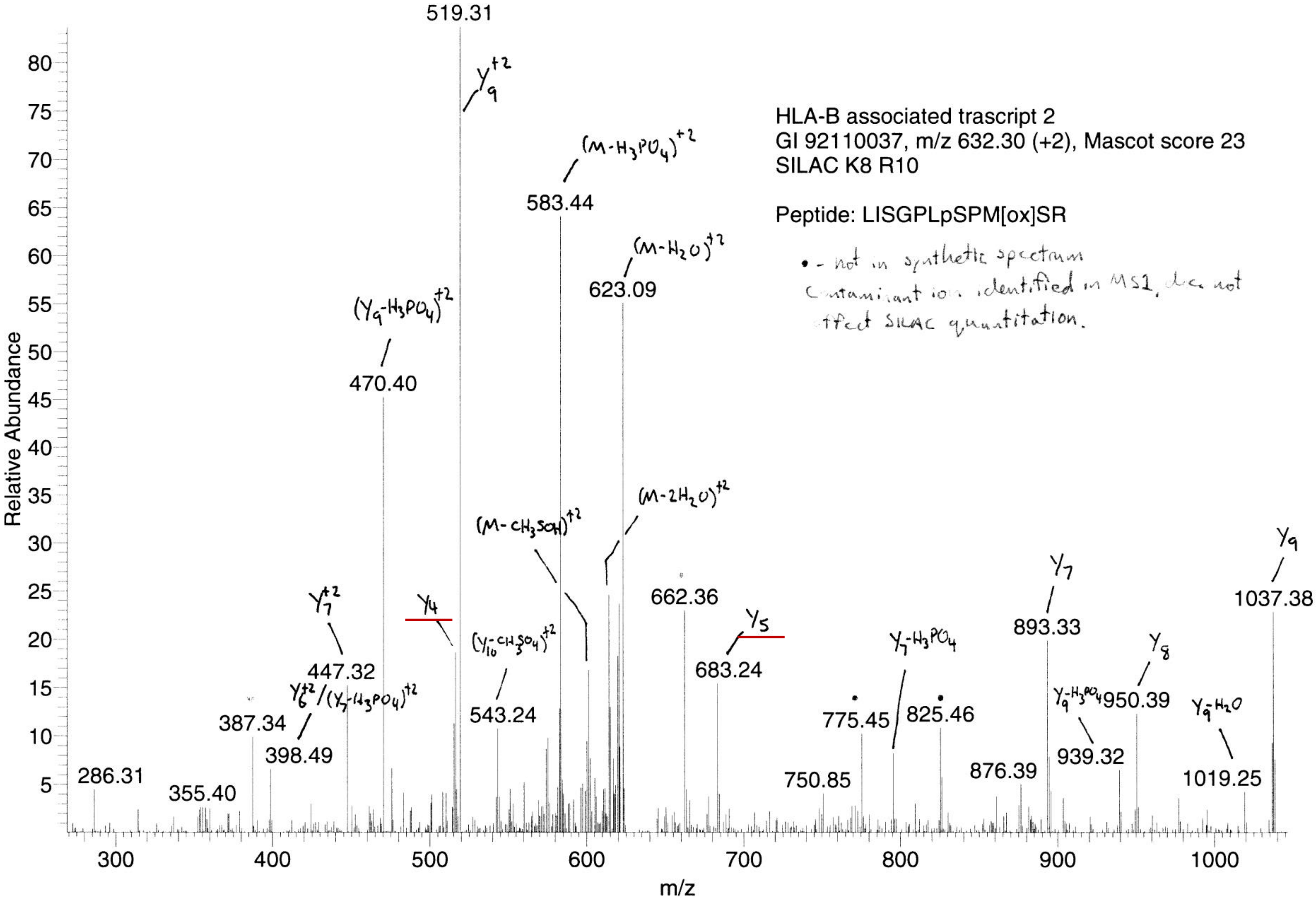
Peptide: EGPEPPEEVPPPTpTPPAPK

Fragmentation does not distinguish phosphorylation at positions 13 and 14. Assignment is based on position of proline.



HLA-B associated transcript 2
GI 92110037, m/z 689.83 (+2), Mascot score 19
SILAC K6 R6

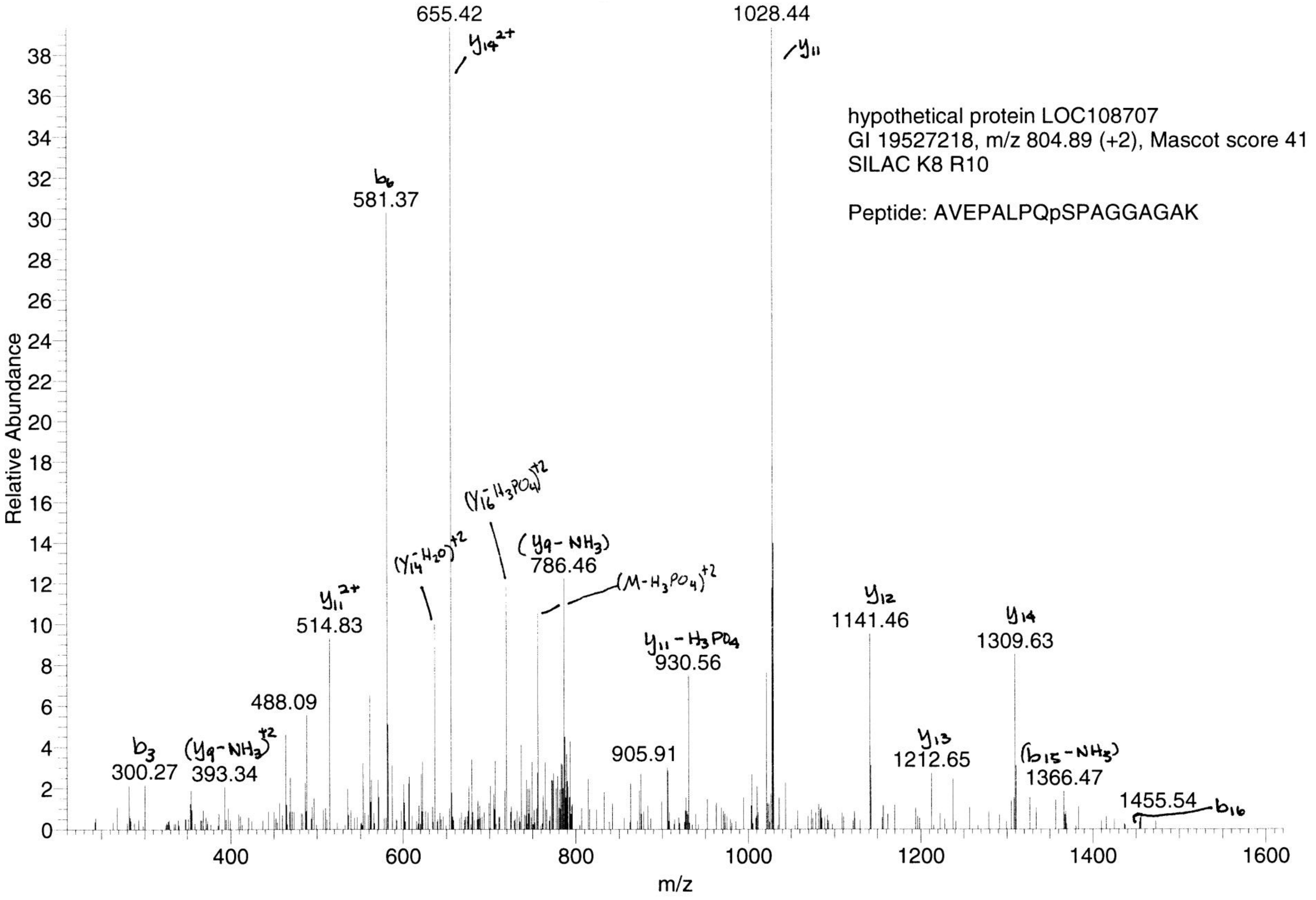
Peptide: ETPPGGNLpSPAPR



HLA-B associated trascript 2
GI 92110037, m/z 632.30 (+2), Mascot score 23
SILAC K8 R10

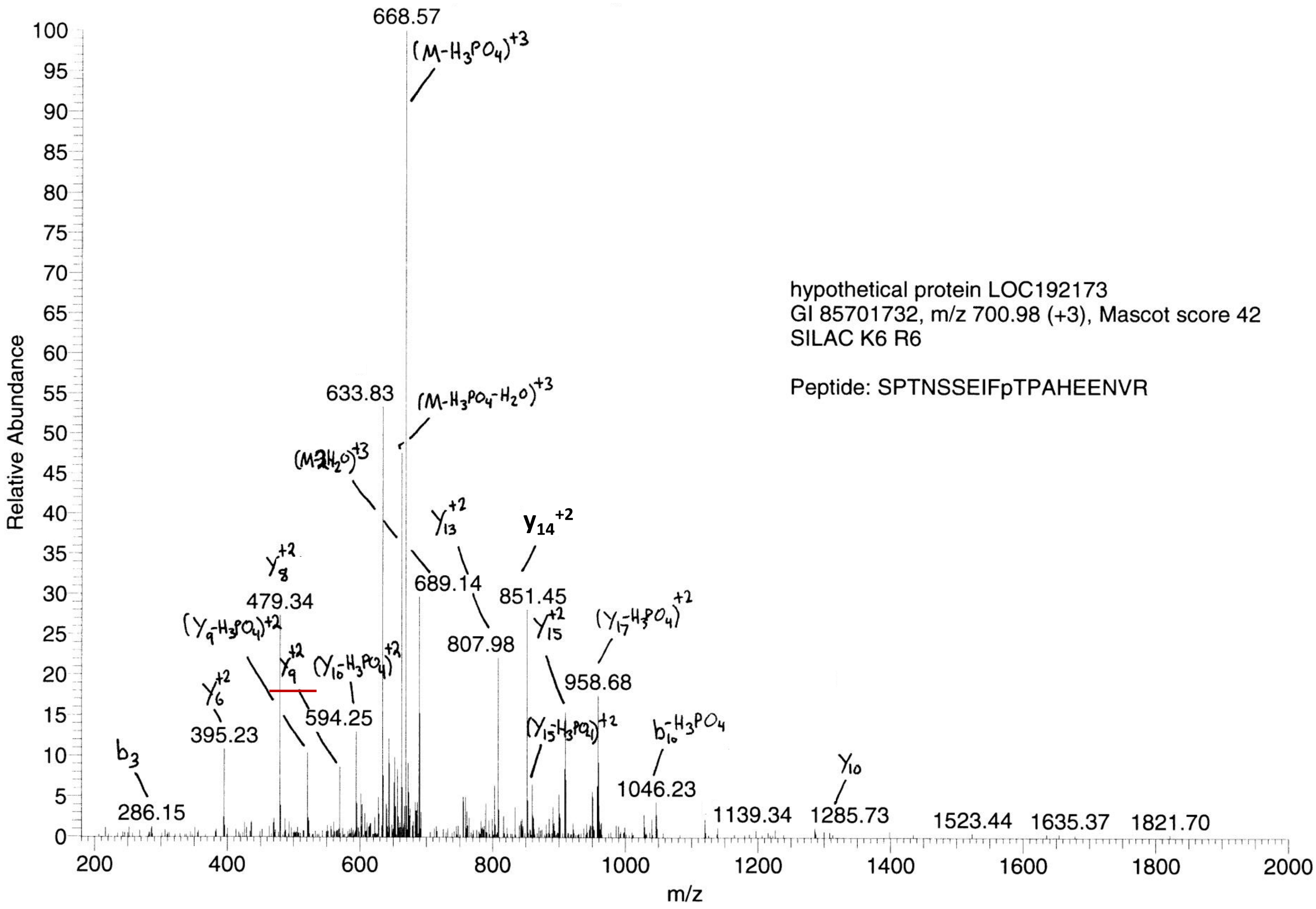
Peptide: LISGPLpSPM[ox]SR

• - not in synthetic spectrum
Contaminant ion identified in MS1, does not affect SILAC quantitation.



hypothetical protein LOC108707
GI 19527218, m/z 804.89 (+2), Mascot score 41
SILAC K8 R10

Peptide: AVEPALPQpSPAGGAGAK

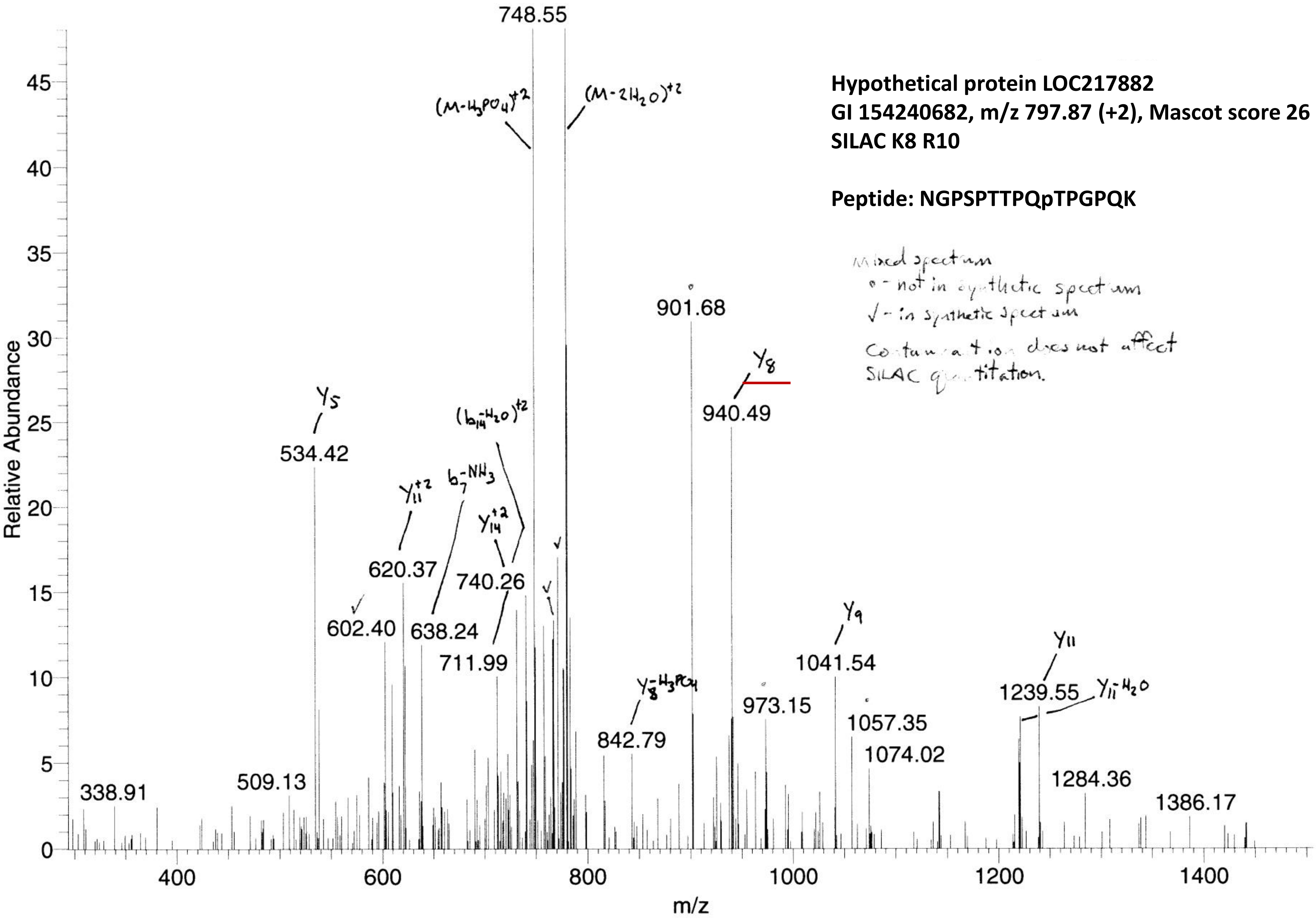


hypothetical protein LOC192173
GI 85701732, m/z 700.98 (+3), Mascot score 42
SILAC K6 R6

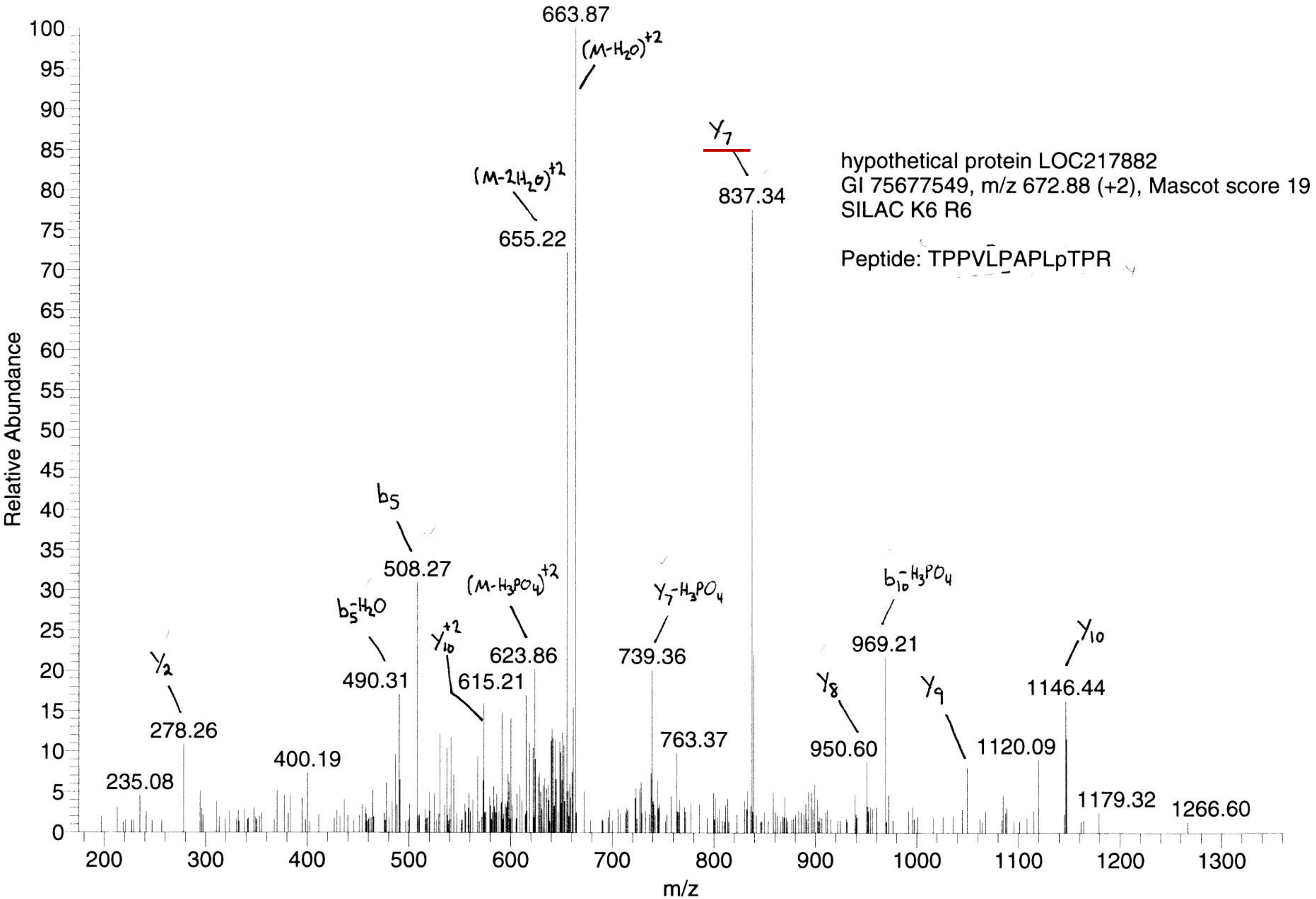
Peptide: SPTNSSEIFpTPAHEENVR

Hypothetical protein LOC217882
GI 154240682, m/z 797.87 (+2), Mascot score 26
SILAC K8 R10

Peptide: NGPSPTTPQpTPGPQK

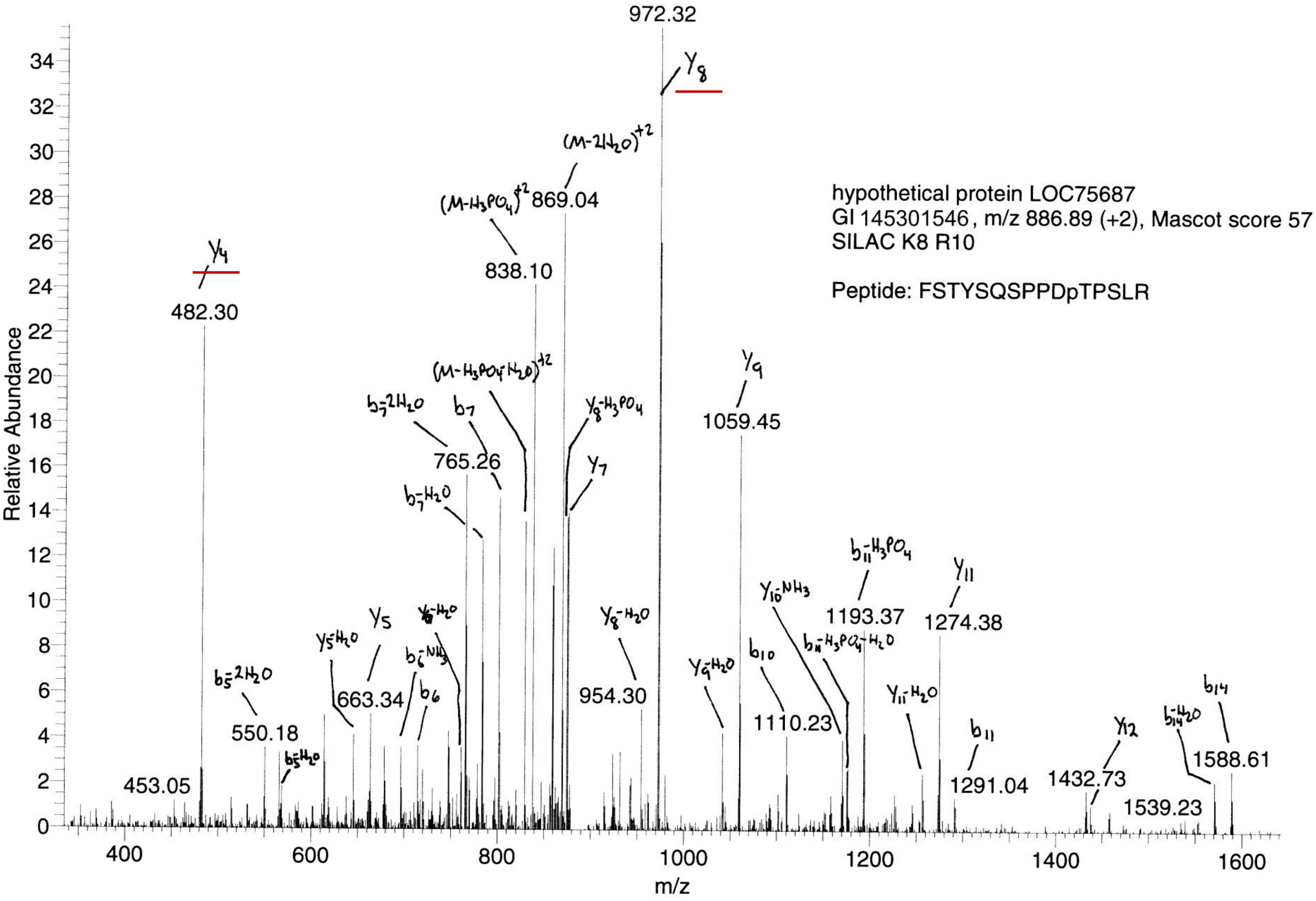


Mixed spectrum
○ - not in synthetic spectrum
√ - in synthetic spectrum
Contamination does not affect SILAC quantitation.



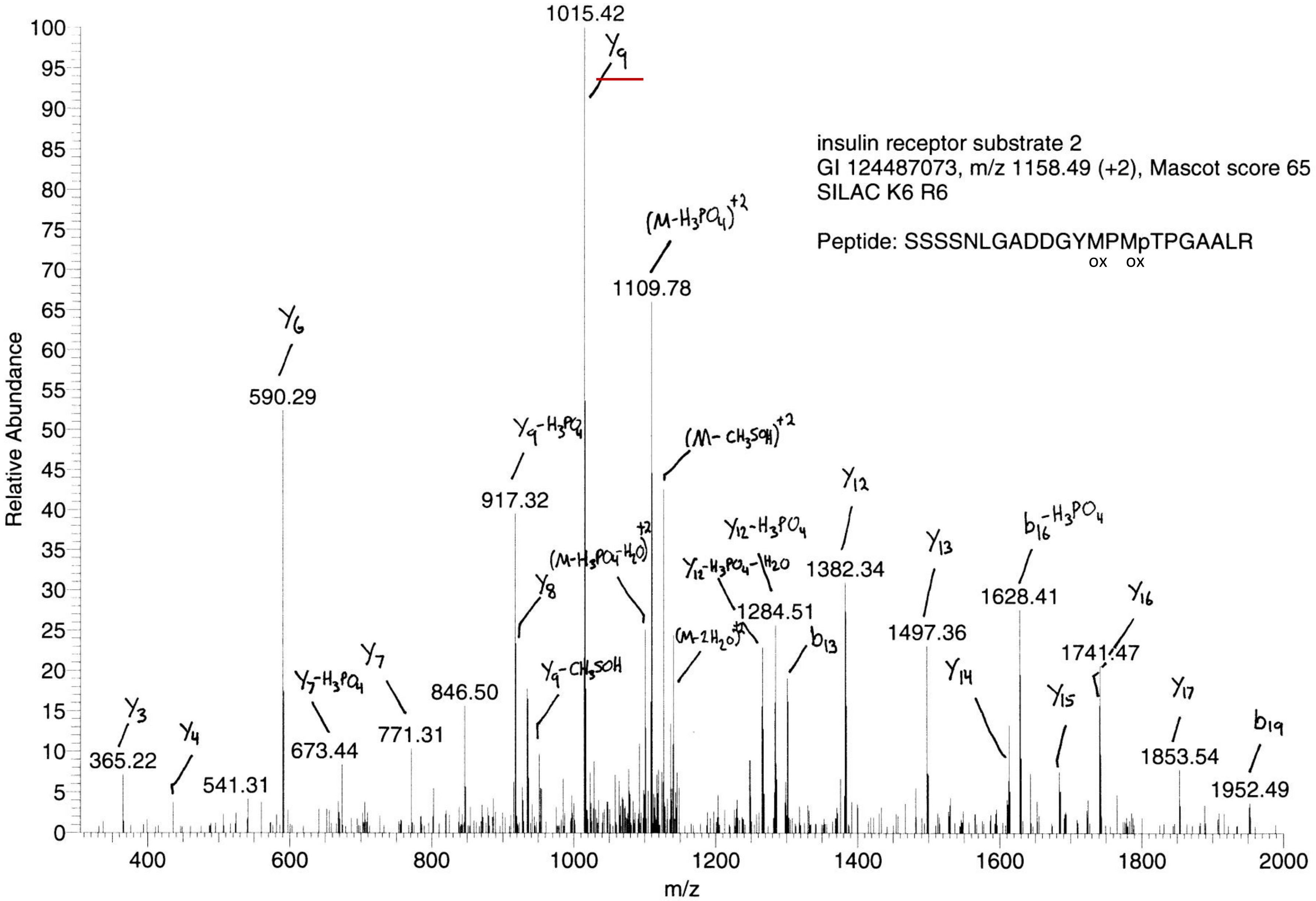
hypothetical protein LOC217882
GI 75677549, m/z 672.88 (+2), Mascot score 19
SILAC K6 R6

Peptide: TPPVLPAPLpTPR



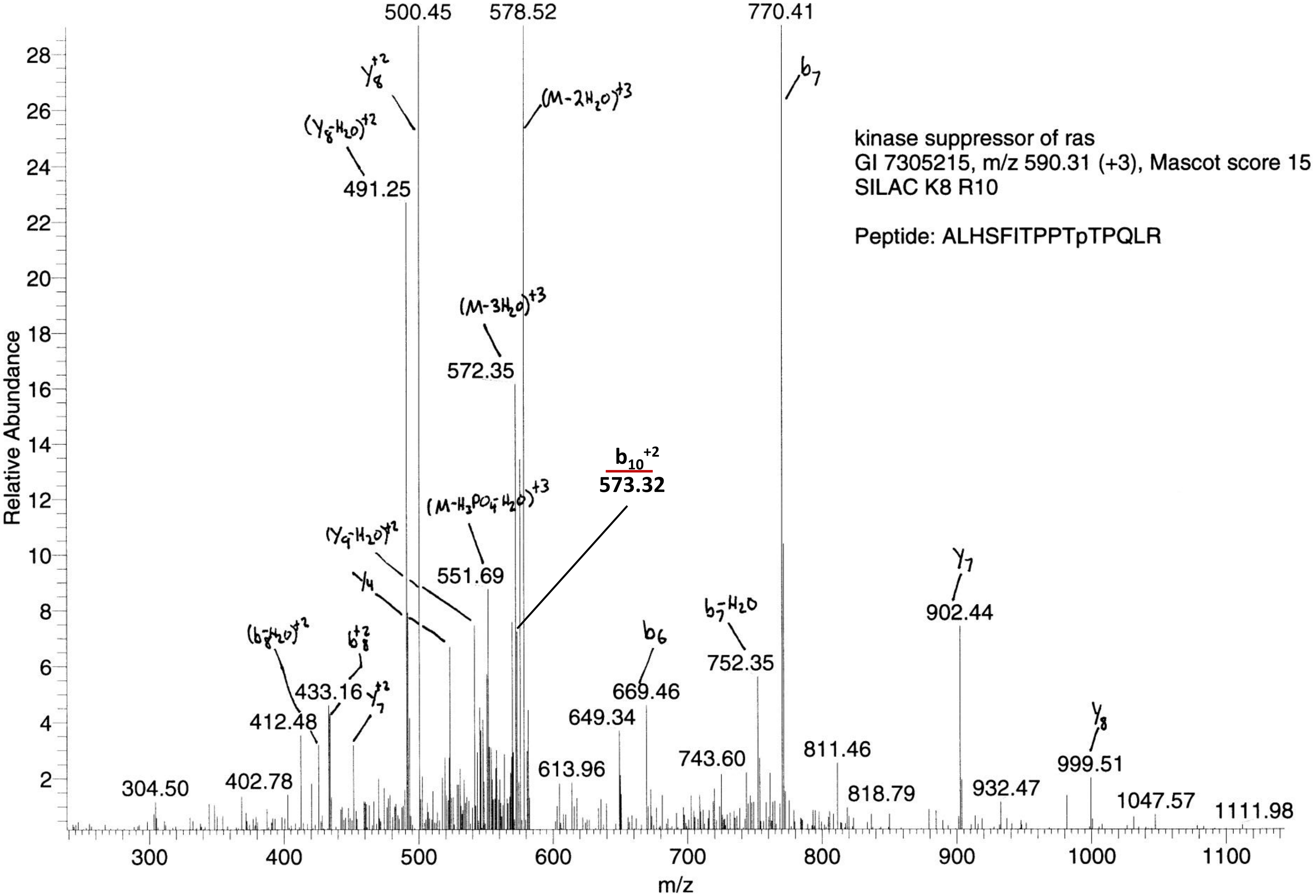
hypothetical protein LOC75687
GI 145301546, m/z 886.89 (+2), Mascot score 57
SILAC K8 R10

Peptide: FSTYSQSPPDpTPSLR



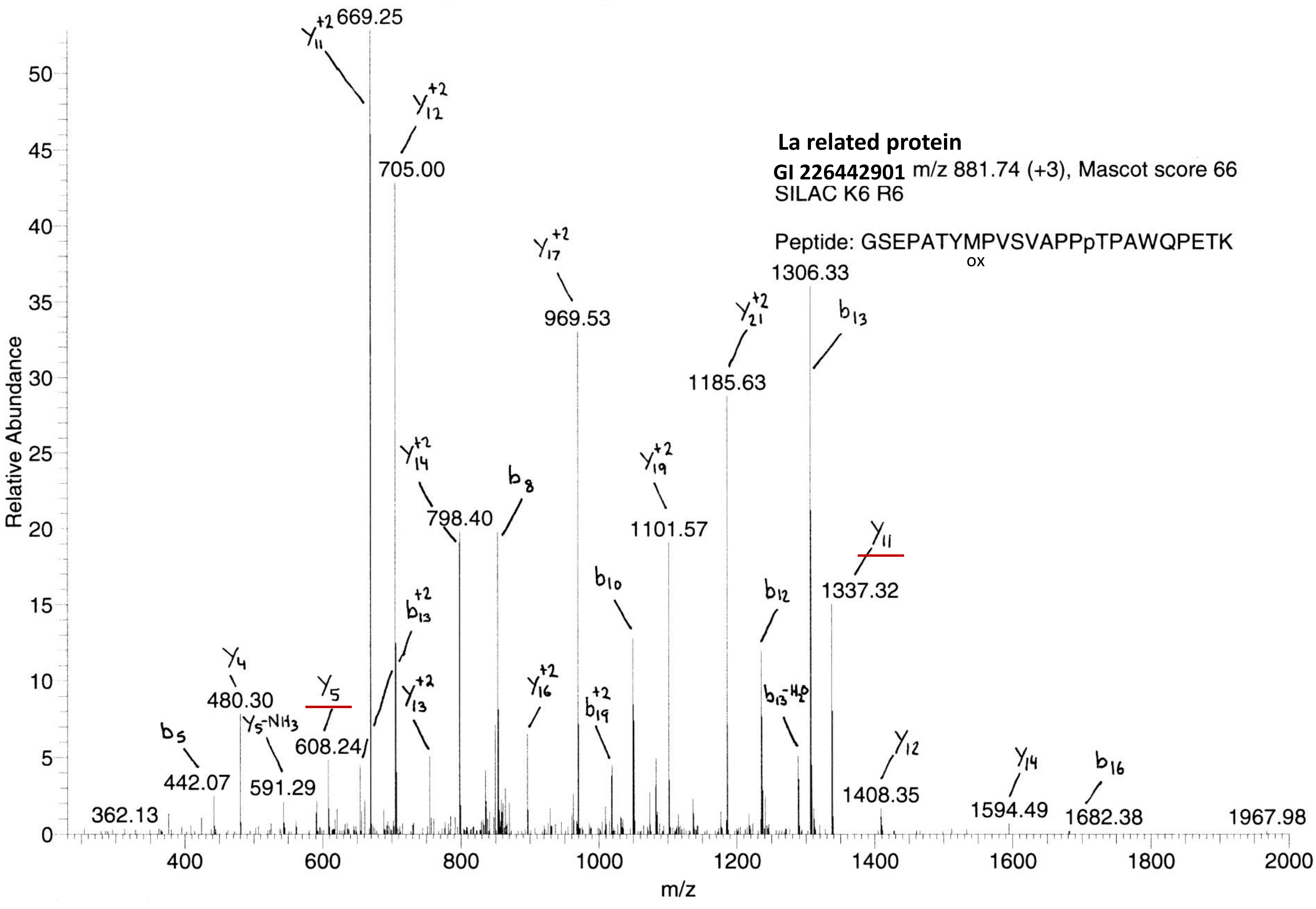
insulin receptor substrate 2
GI 124487073, m/z 1158.49 (+2), Mascot score 65
SILAC K6 R6

Peptide: SSSSNLGADDGYMPMpTPGAALR
ox ox



kinase suppressor of ras
GI 7305215, m/z 590.31 (+3), Mascot score 15
SILAC K8 R10

Peptide: ALHSFITPPTpTPQLR

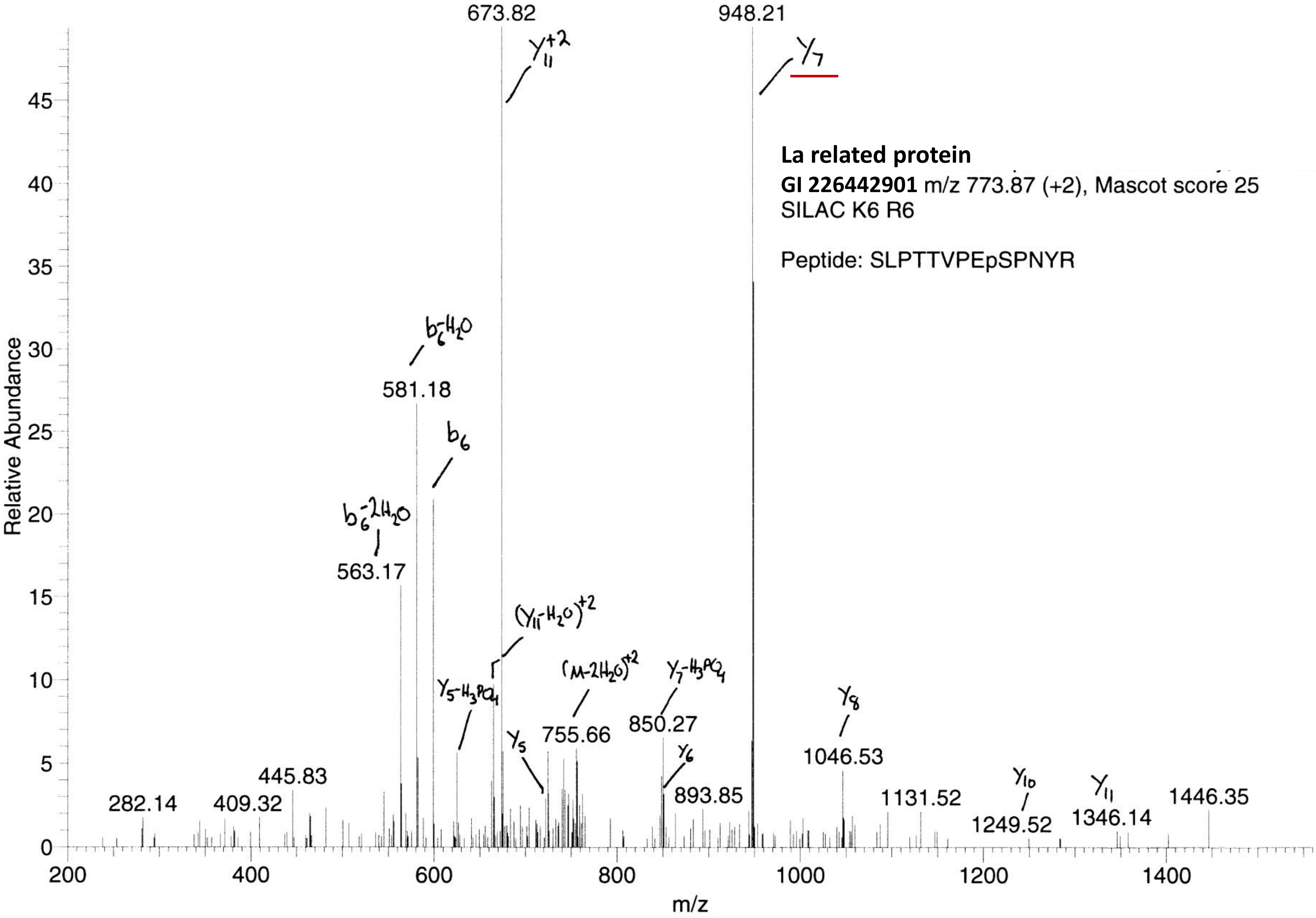


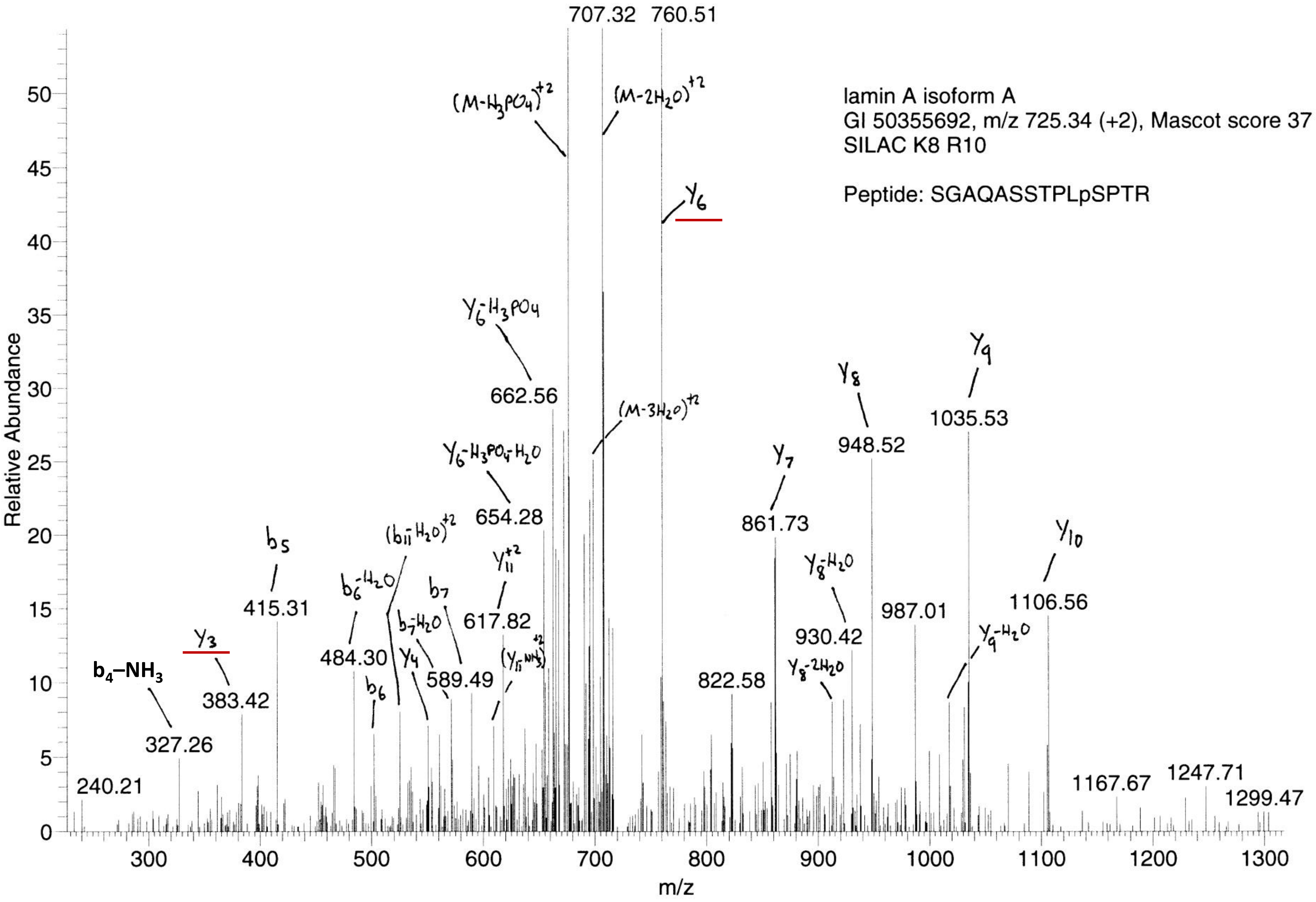
La related protein
GI 226442901 m/z 881.74 (+3), Mascot score 66
SILAC K6 R6

Peptide: GSEPATYM$_{ox}$PVSVAPPpTPAWQPETK

La related protein
GI 226442901 m/z 773.87 (+2), Mascot score 25
SILAC K6 R6

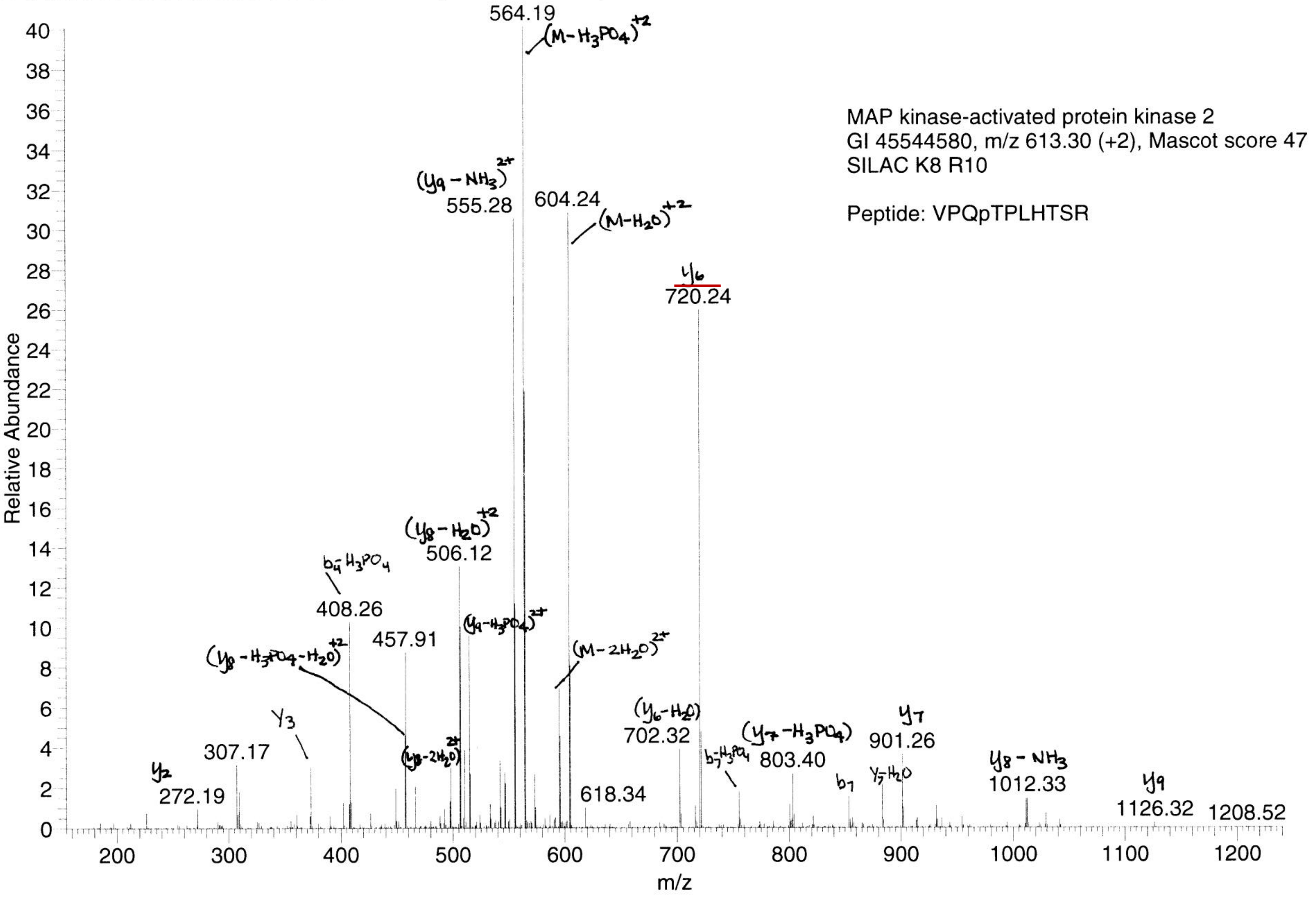
Peptide: SLPTTVPEpSPNYR





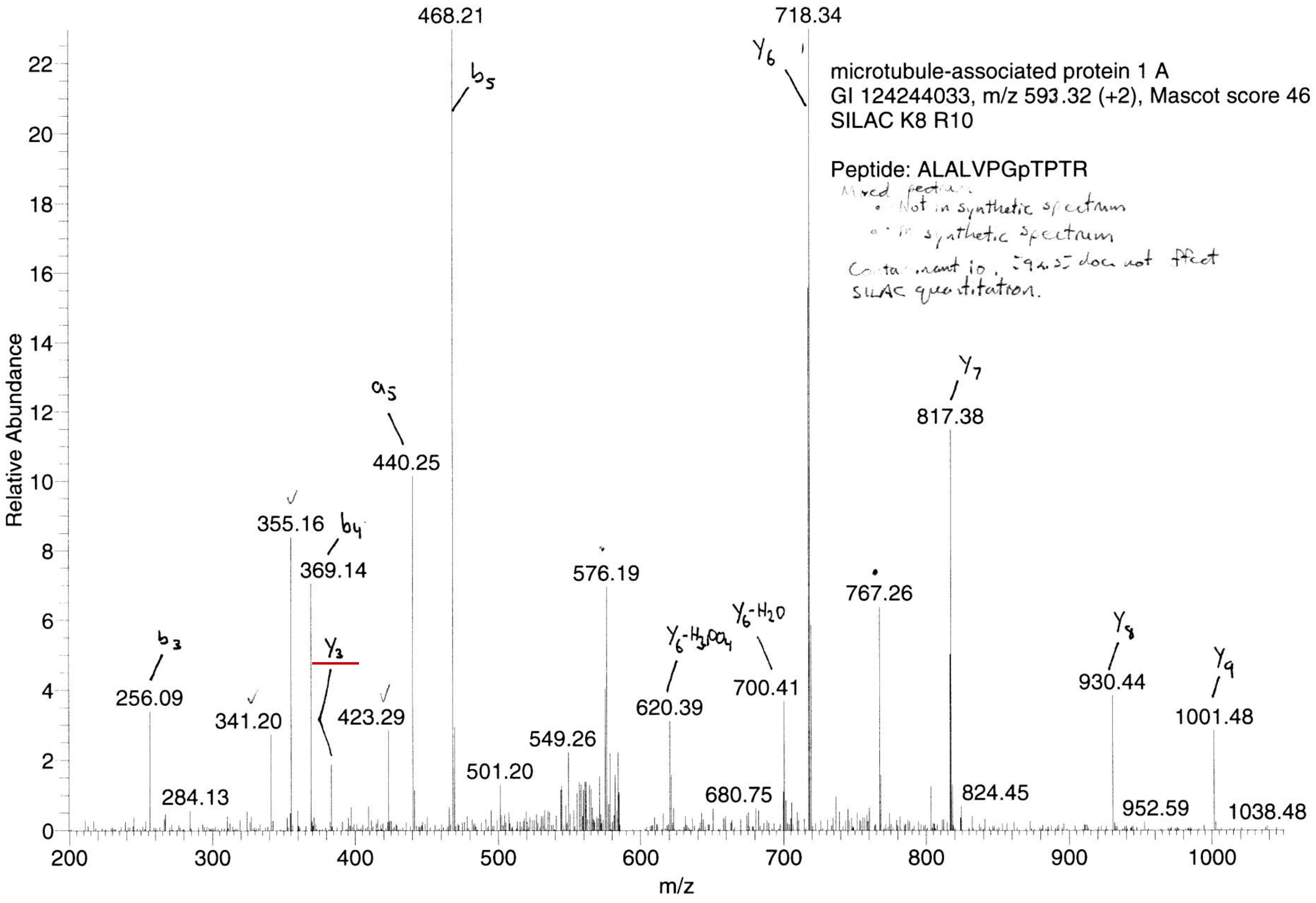
lamin A isoform A
GI 50355692, m/z 725.34 (+2), Mascot score 37
SILAC K8 R10

Peptide: SGAQASSTPLpSPTR



MAP kinase-activated protein kinase 2
GI 45544580, m/z 613.30 (+2), Mascot score 47
SILAC K8 R10

Peptide: VPQpTPLHTSR

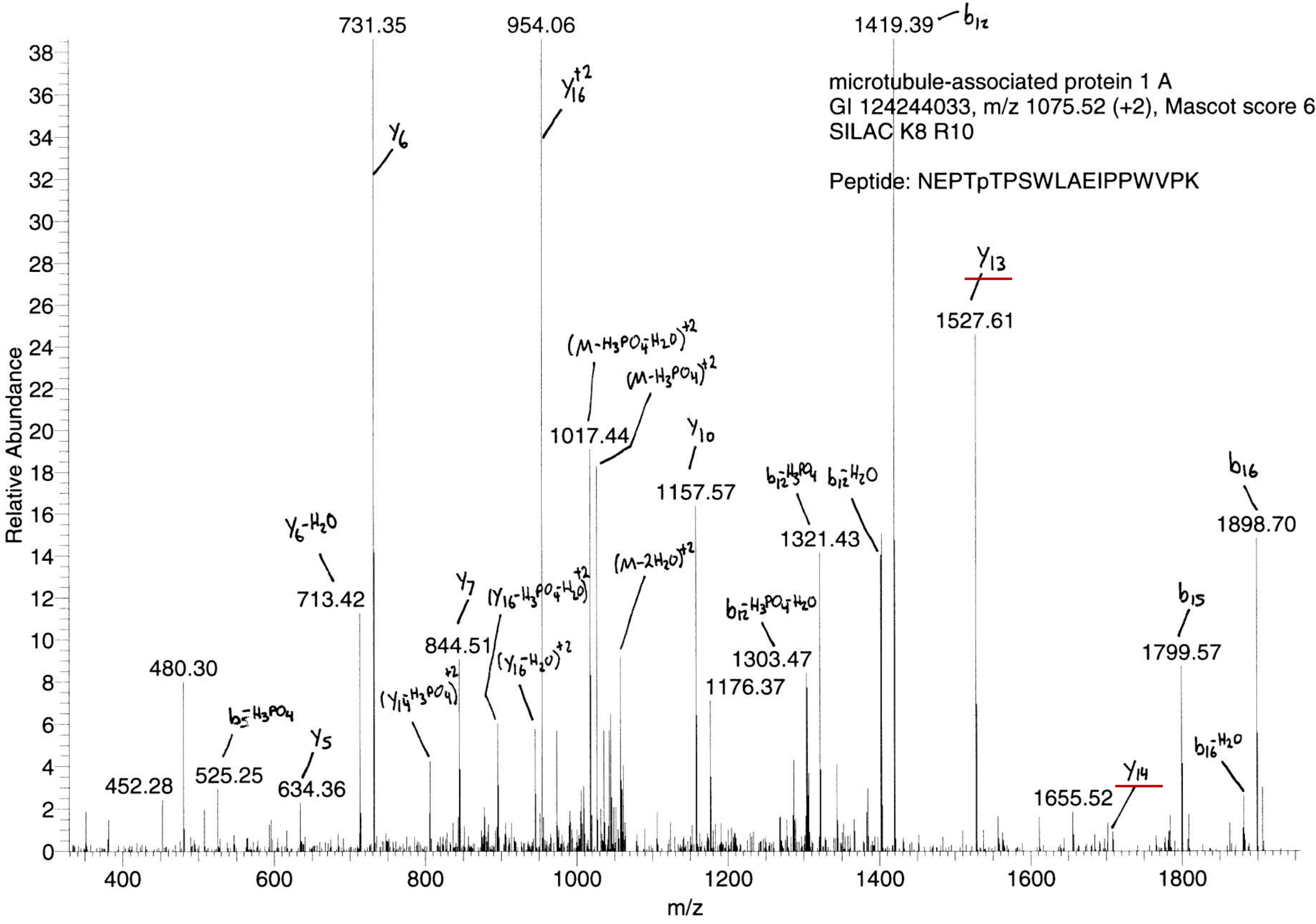


microtubule-associated protein 1 A
GI 124244033, m/z 593.32 (+2), Mascot score 46
SILAC K8 R10

Peptide: ALALVPGpTPTR

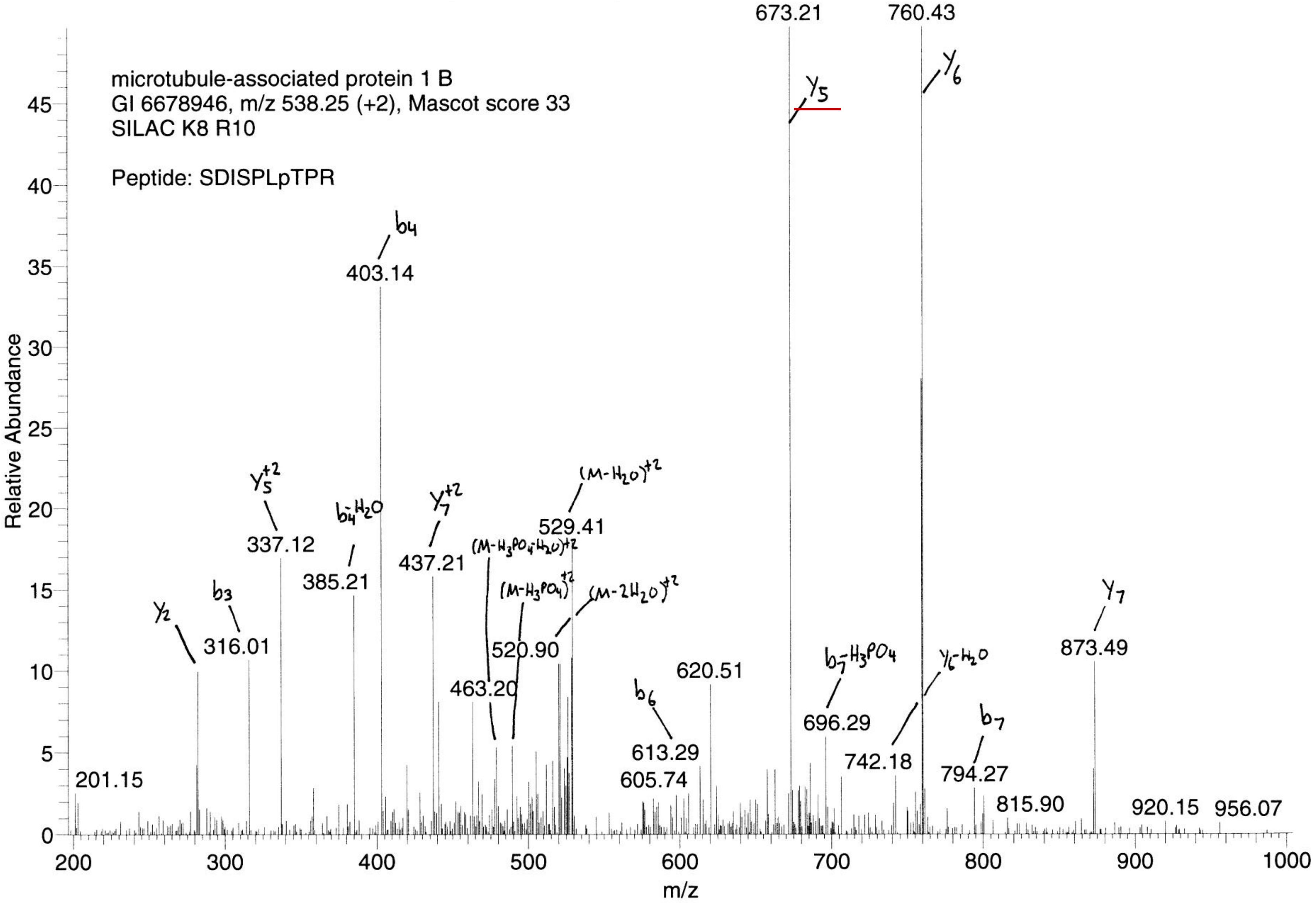
Mixed spectrum:
- • Not in synthetic spectrum
- ✓ in synthetic spectrum

Contaminant ion, 592.35 does not affect SILAC quantitation.



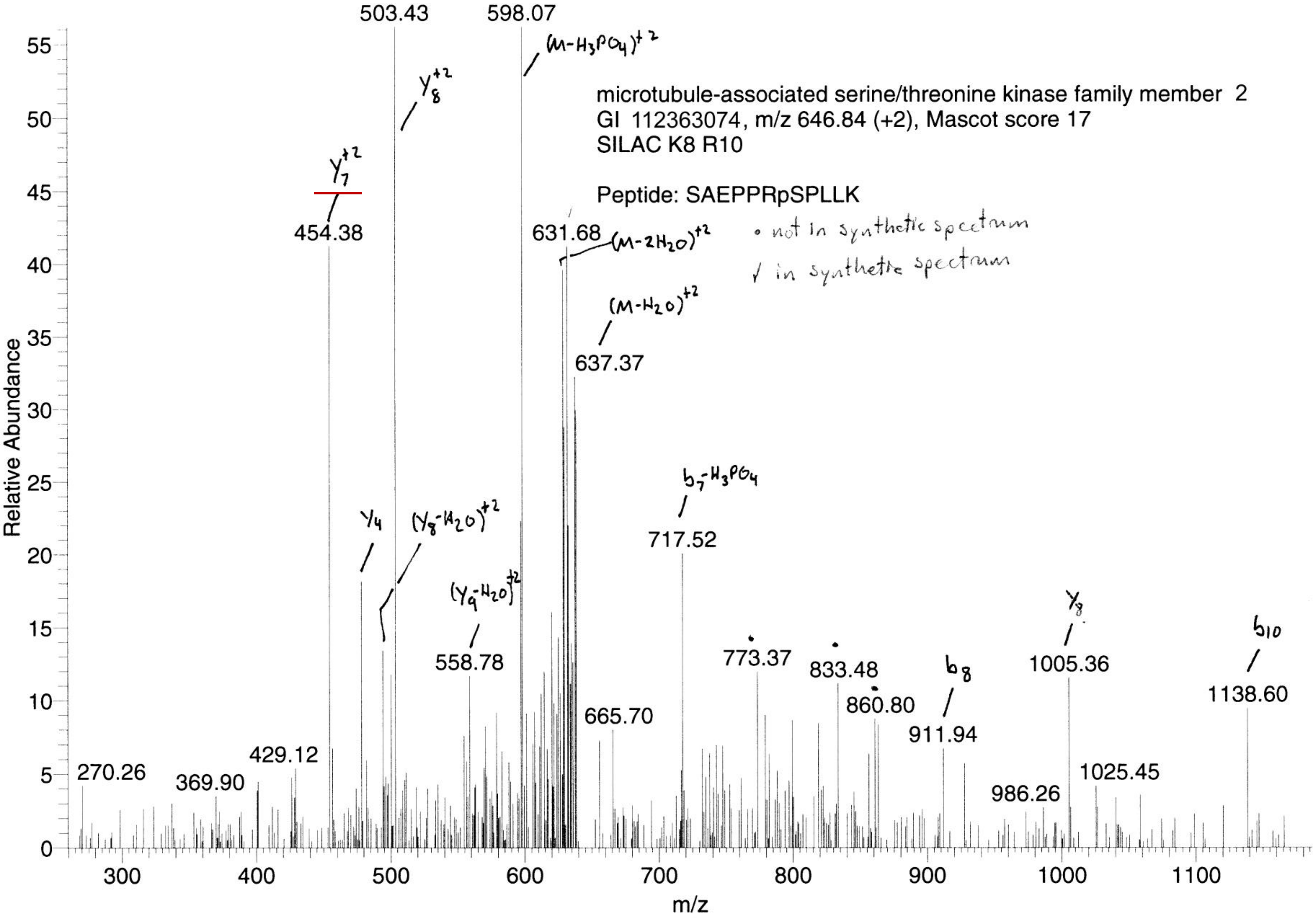
microtubule-associated protein 1 A
GI 124244033, m/z 1075.52 (+2), Mascot score 68
SILAC K8 R10

Peptide: NEPTpTPSWLAEIPPWVPK



microtubule-associated protein 1 B
GI 6678946, m/z 538.25 (+2), Mascot score 33
SILAC K8 R10

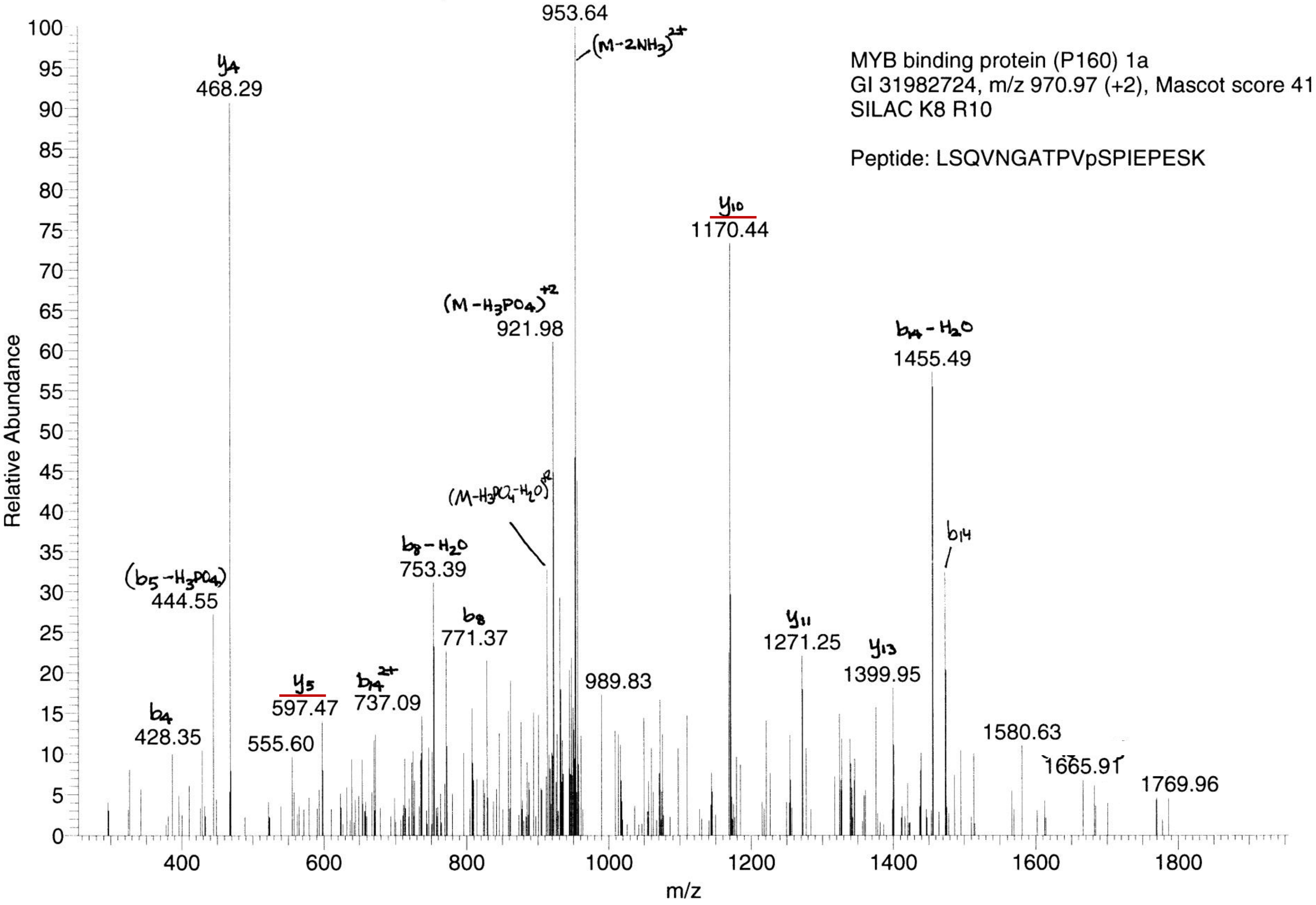
Peptide: SDISPLpTPR



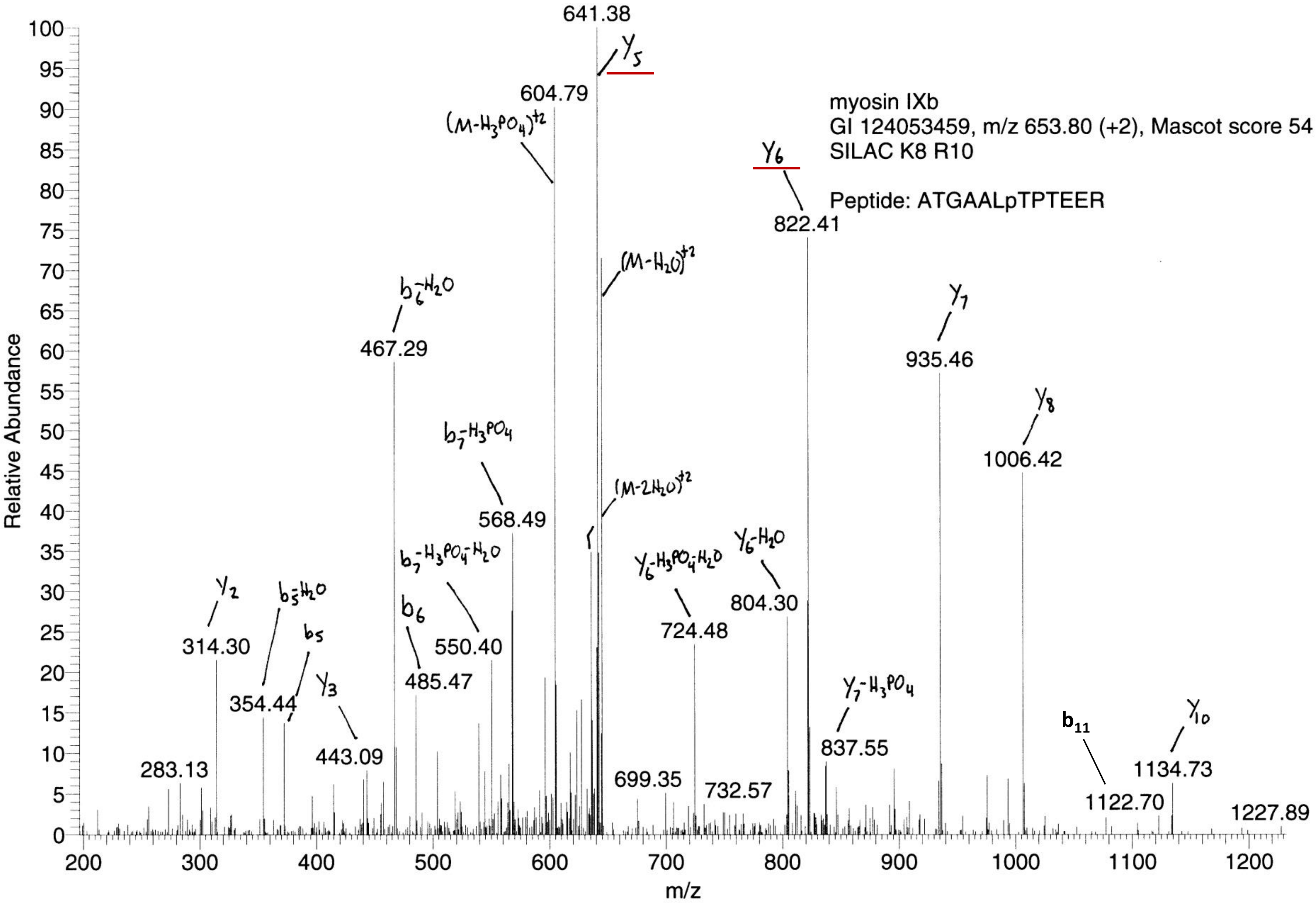
microtubule-associated serine/threonine kinase family member 2
GI 112363074, m/z 646.84 (+2), Mascot score 17
SILAC K8 R10

Peptide: SAEPPRpSPLLK

• not in synthetic spectrum
✓ in synthetic spectrum

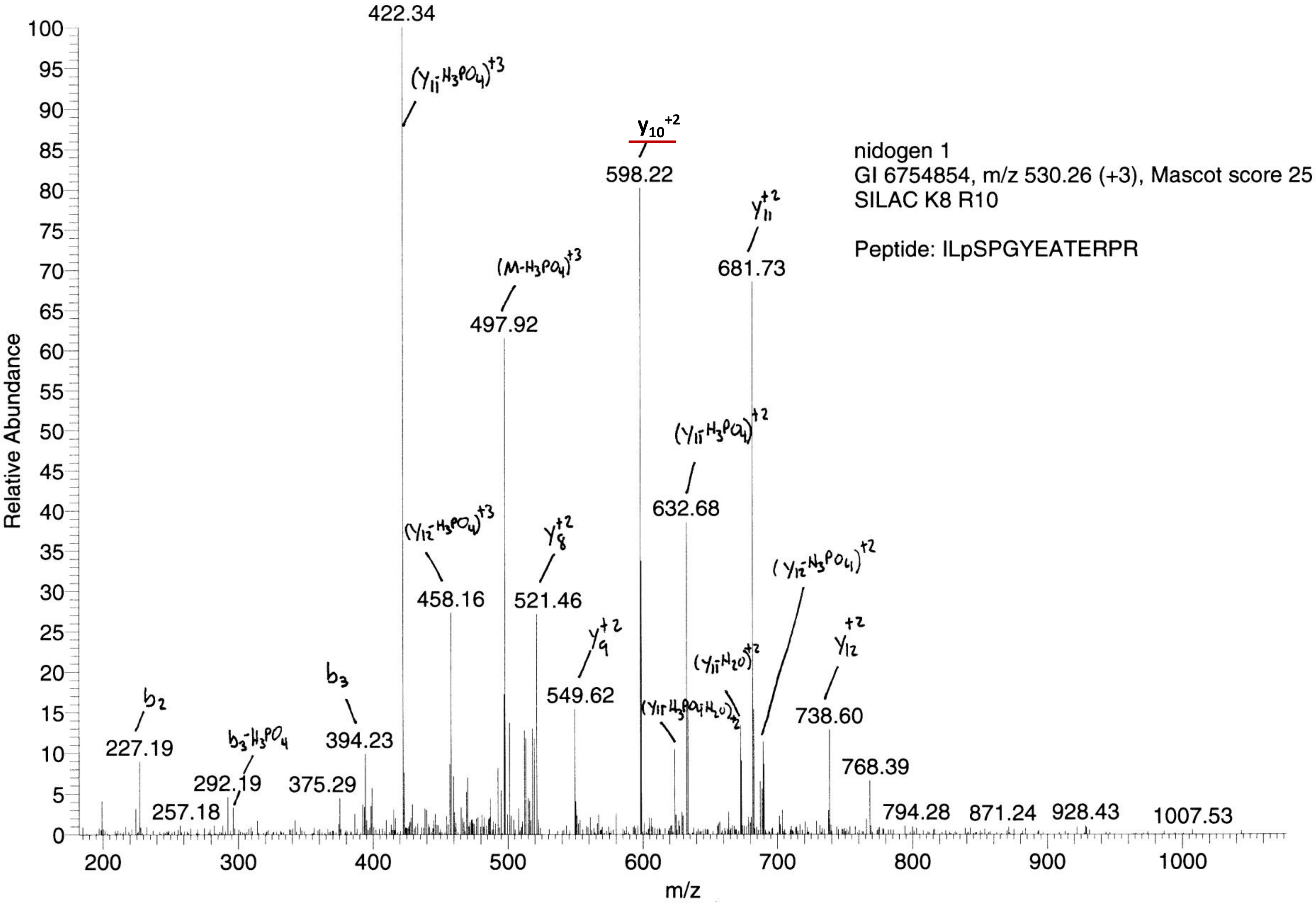

MYB binding protein (P160) 1a
GI 31982724, m/z 970.97 (+2), Mascot score 41
SILAC K8 R10

Peptide: LSQVNGATPVpSPIEPESK

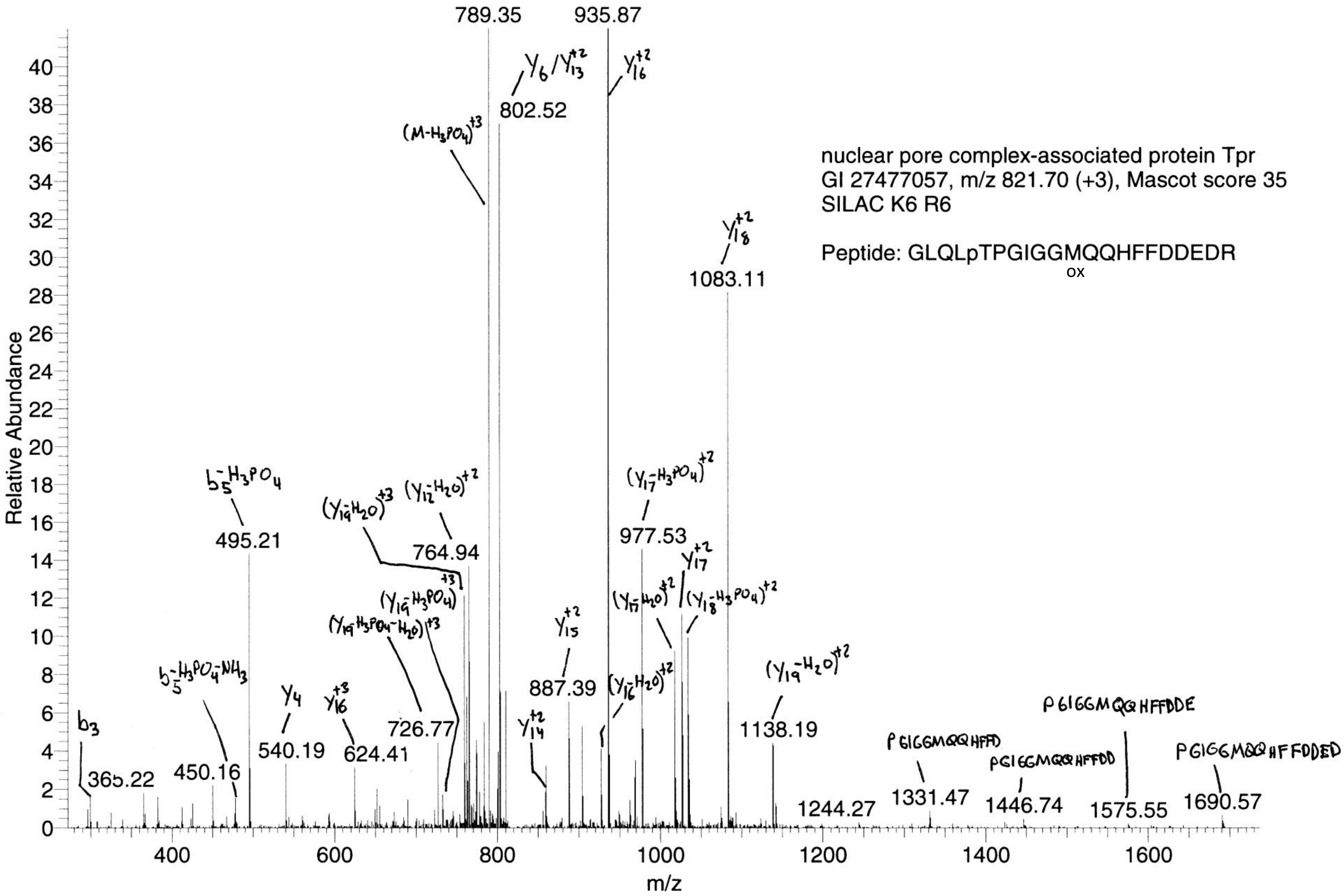


myosin IXb
GI 124053459, m/z 653.80 (+2), Mascot score 54
SILAC K8 R10

Peptide: ATGAALpTPTEER

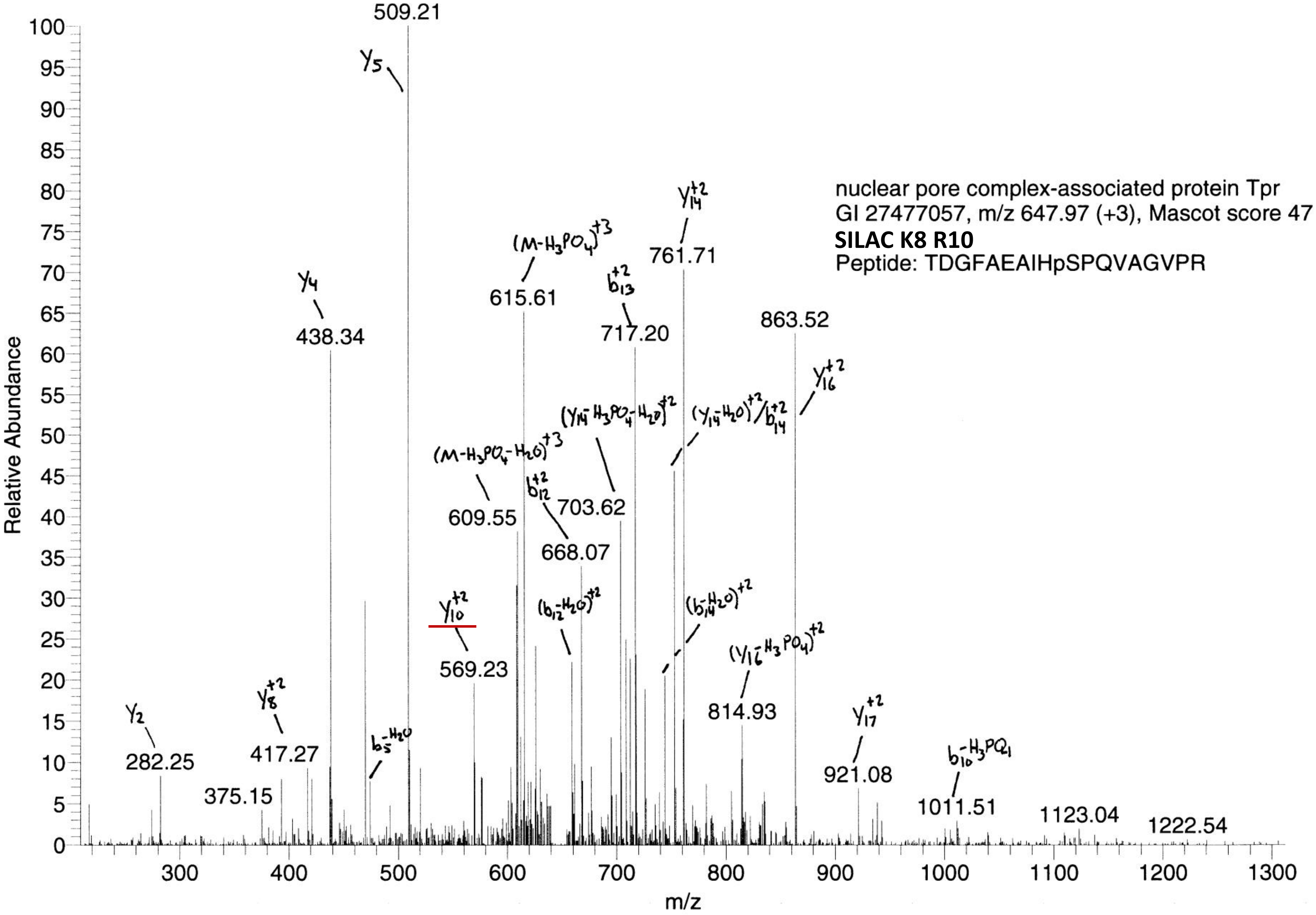

nidogen 1
GI 6754854, m/z 530.26 (+3), Mascot score 25
SILAC K8 R10

Peptide: ILpSPGYEATERPR

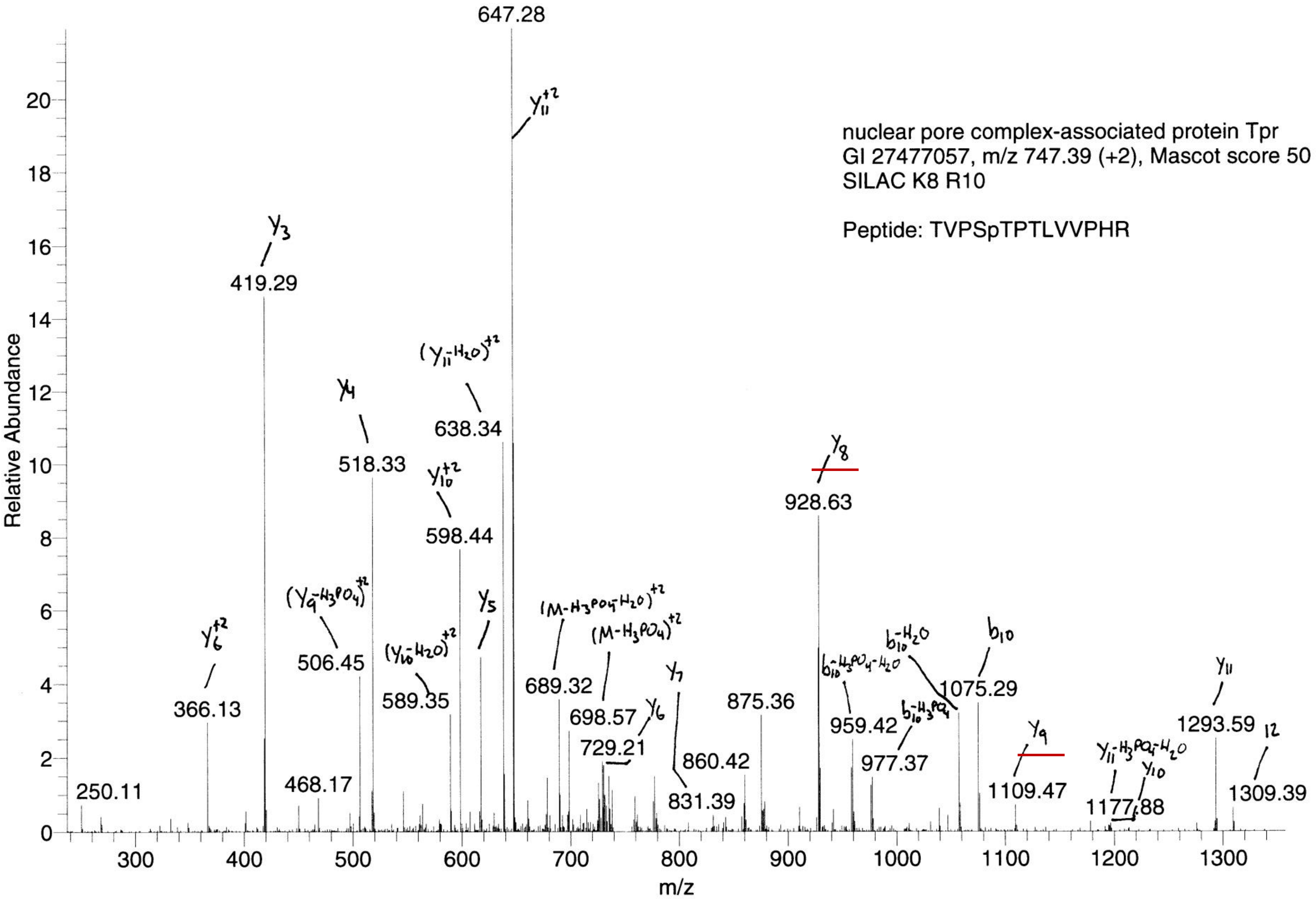


nuclear pore complex-associated protein Tpr
GI 27477057, m/z 821.70 (+3), Mascot score 35
SILAC K6 R6

Peptide: GLQLpTPGIGG$\underset{\text{ox}}{\text{M}}$QQHFFDDEDR

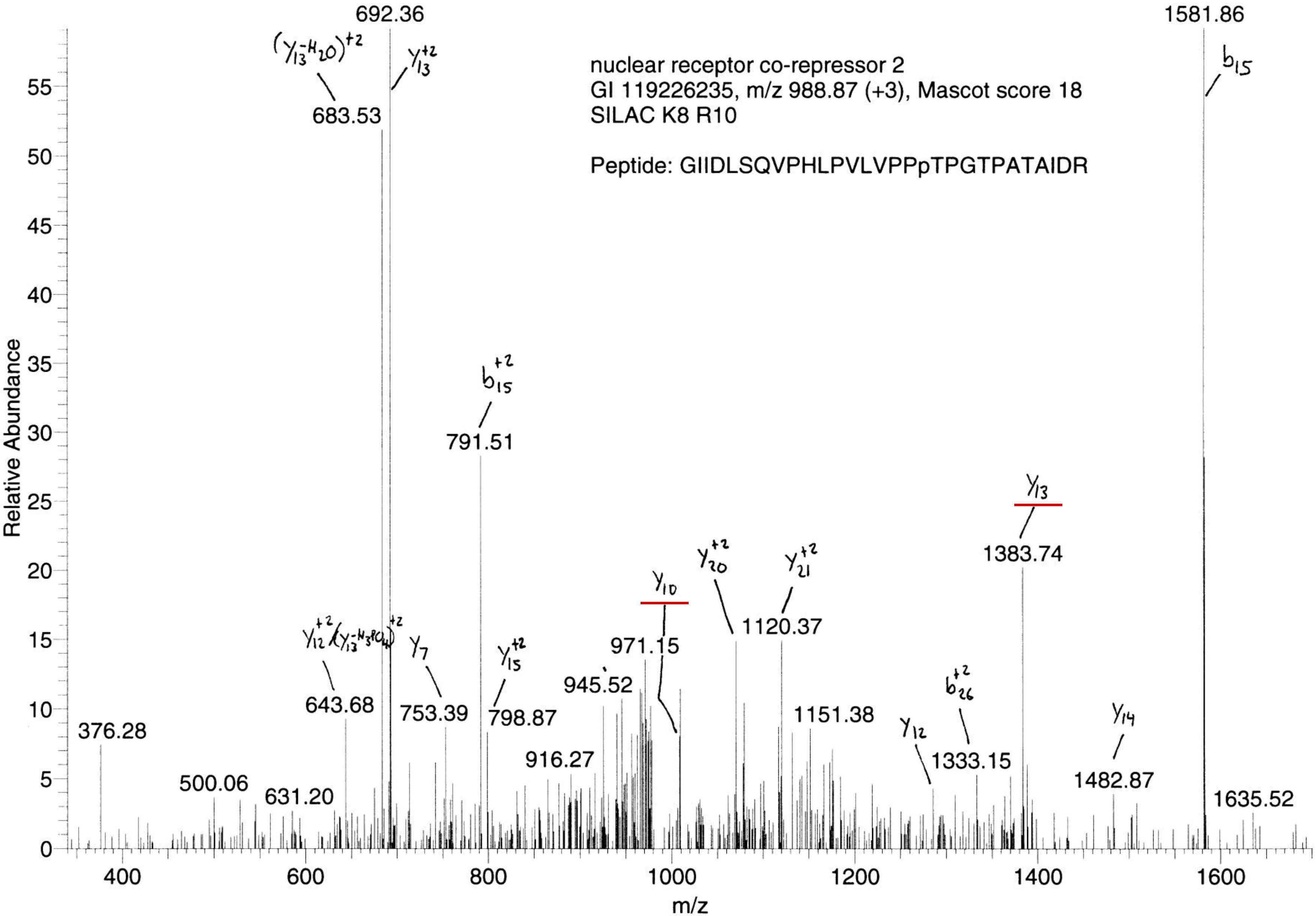


nuclear pore complex-associated protein Tpr
GI 27477057, m/z 647.97 (+3), Mascot score 47
SILAC K8 R10
Peptide: TDGFAEAIHpSPQVAGVPR



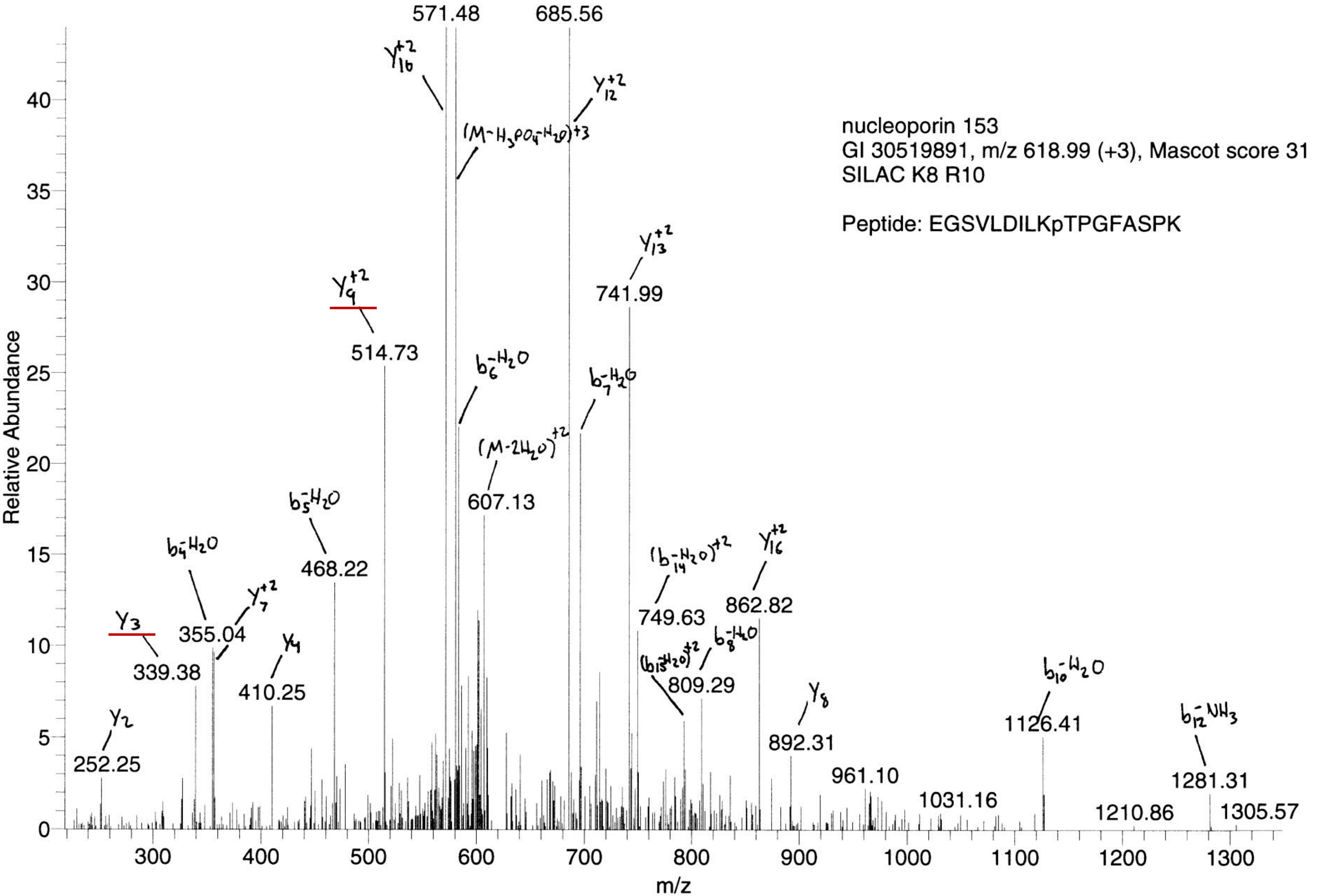
nuclear pore complex-associated protein Tpr
GI 27477057, m/z 747.39 (+2), Mascot score 50
SILAC K8 R10

Peptide: TVPSpTPTLVVPHR



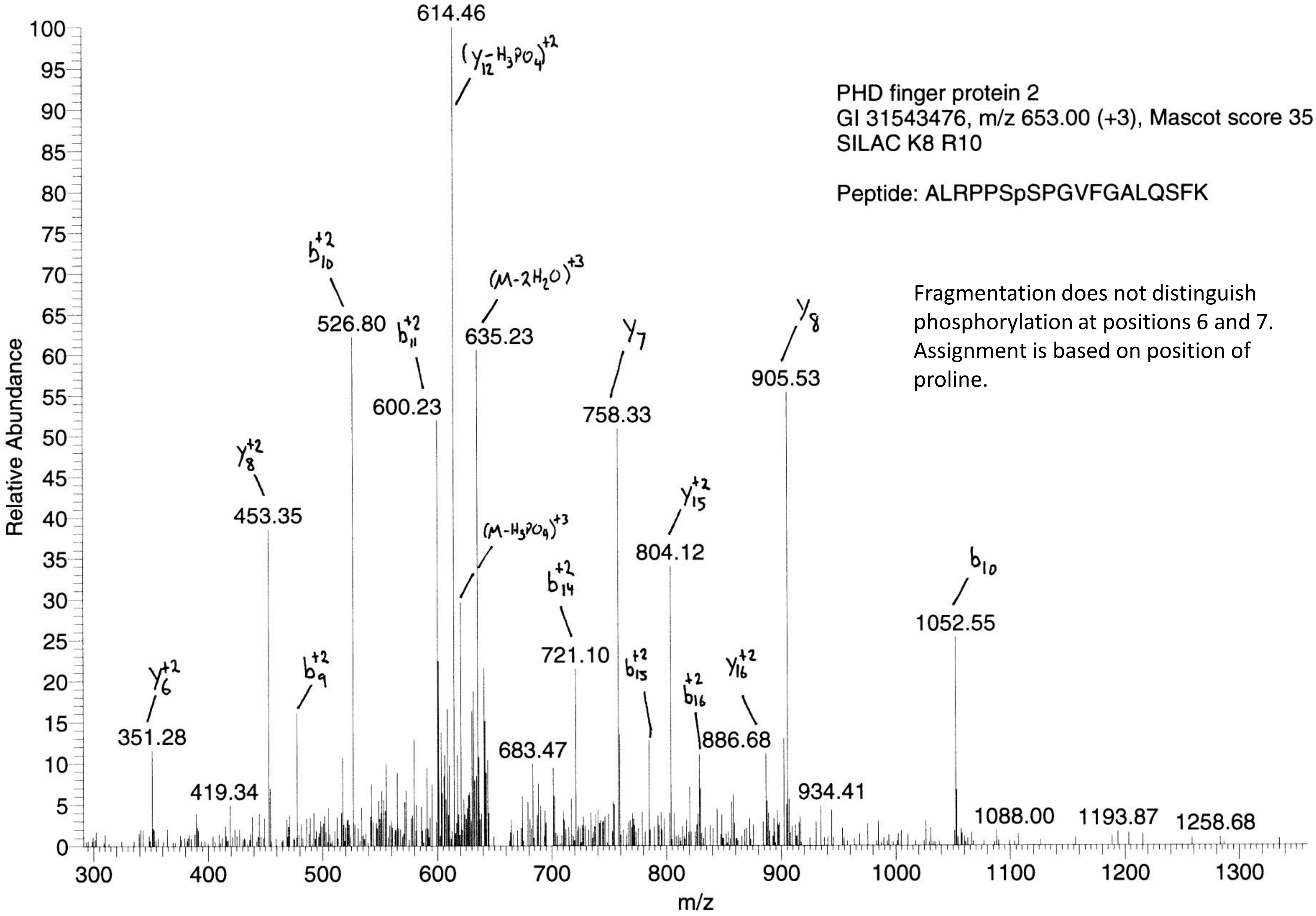
nuclear receptor co-repressor 2
GI 119226235, m/z 988.87 (+3), Mascot score 18
SILAC K8 R10

Peptide: GIIDLSQVPHLPVLVPPpTPGTPATAIDR



nucleoporin 153
GI 30519891, m/z 618.99 (+3), Mascot score 31
SILAC K8 R10

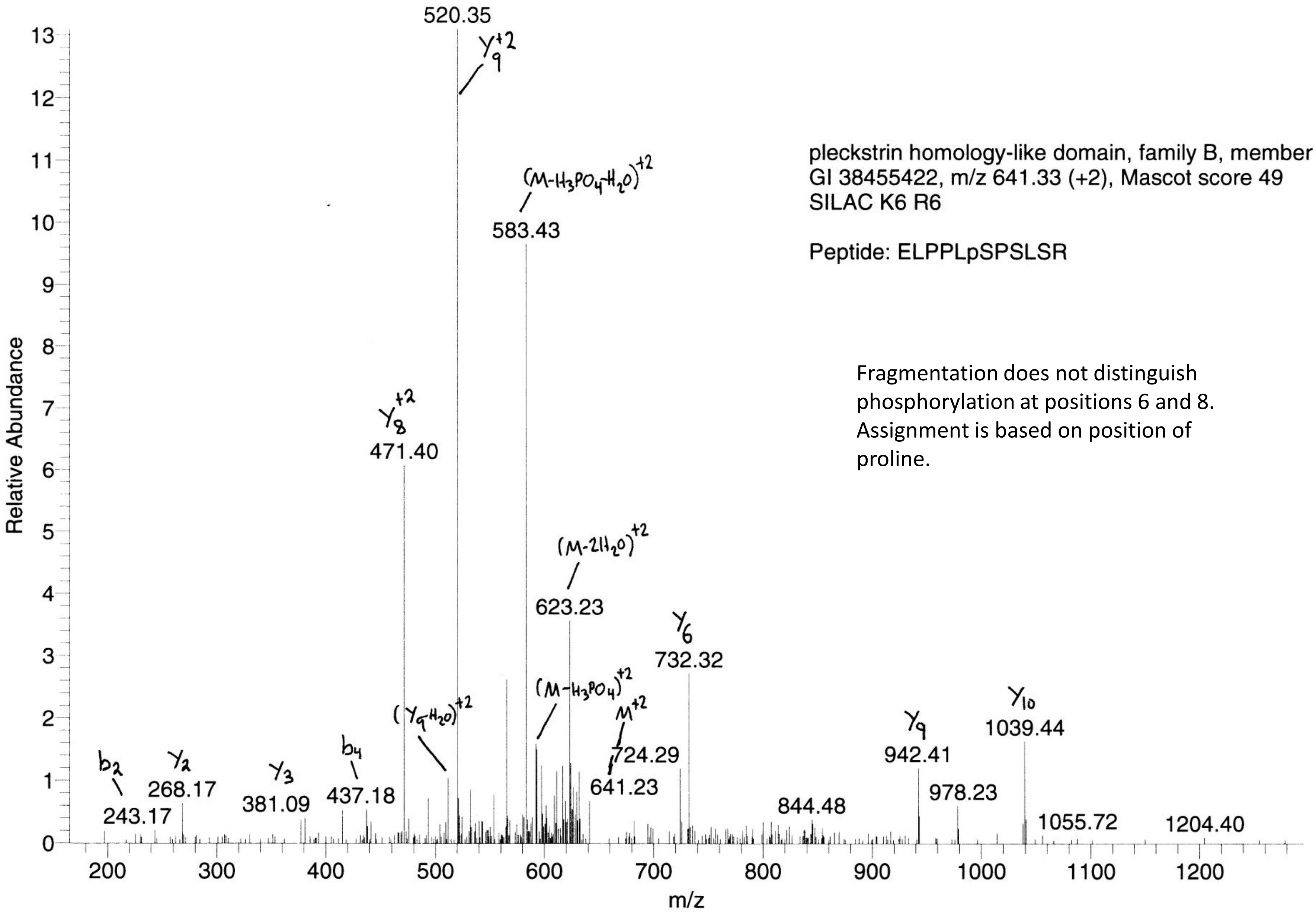
Peptide: EGSVLDILKpTPGFASPK



PHD finger protein 2
GI 31543476, m/z 653.00 (+3), Mascot score 35
SILAC K8 R10

Peptide: ALRPPSpSPGVFGALQSFK

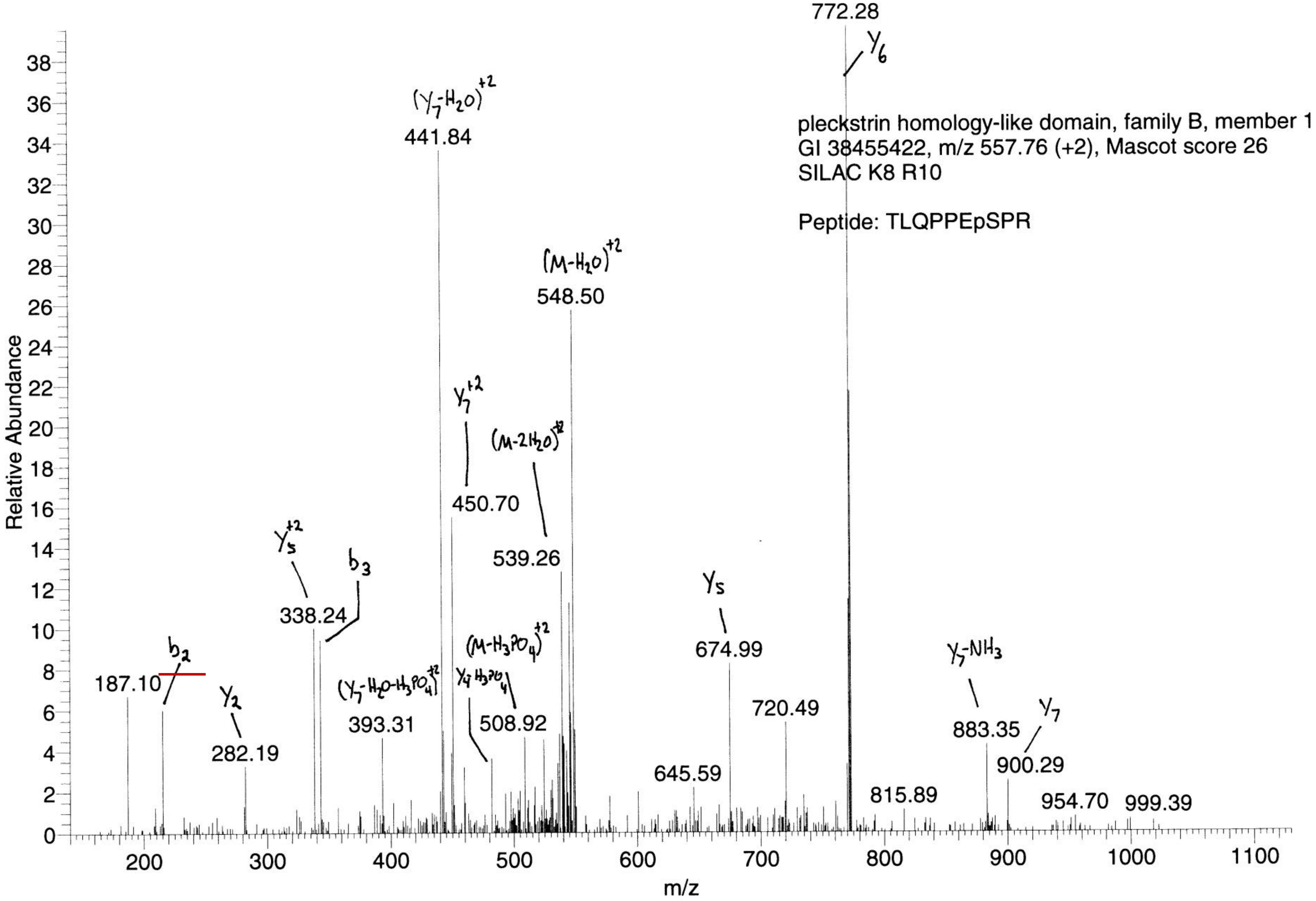
Fragmentation does not distinguish phosphorylation at positions 6 and 7. Assignment is based on position of proline.



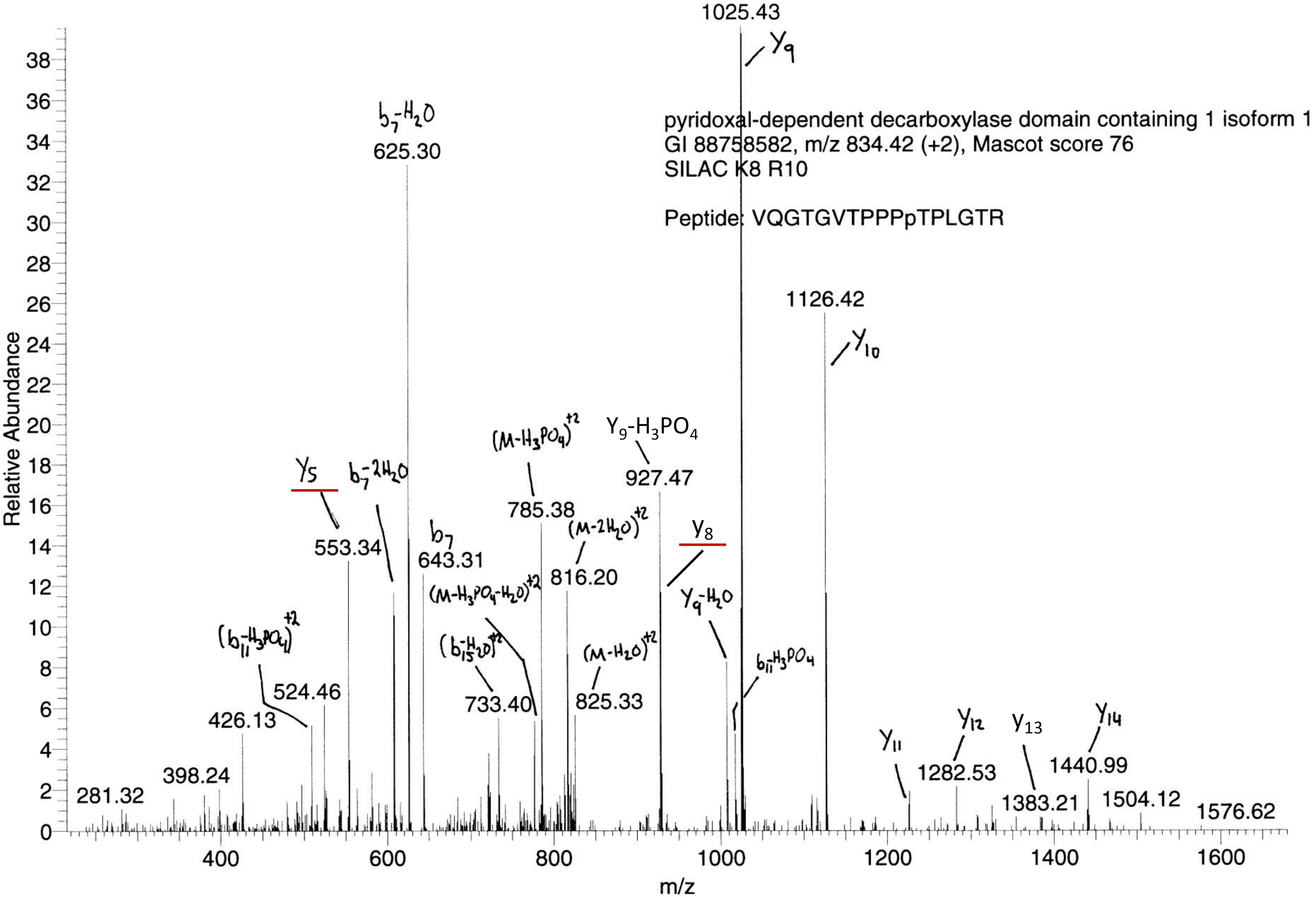
pleckstrin homology-like domain, family B, member 1
GI 38455422, m/z 641.33 (+2), Mascot score 49
SILAC K6 R6

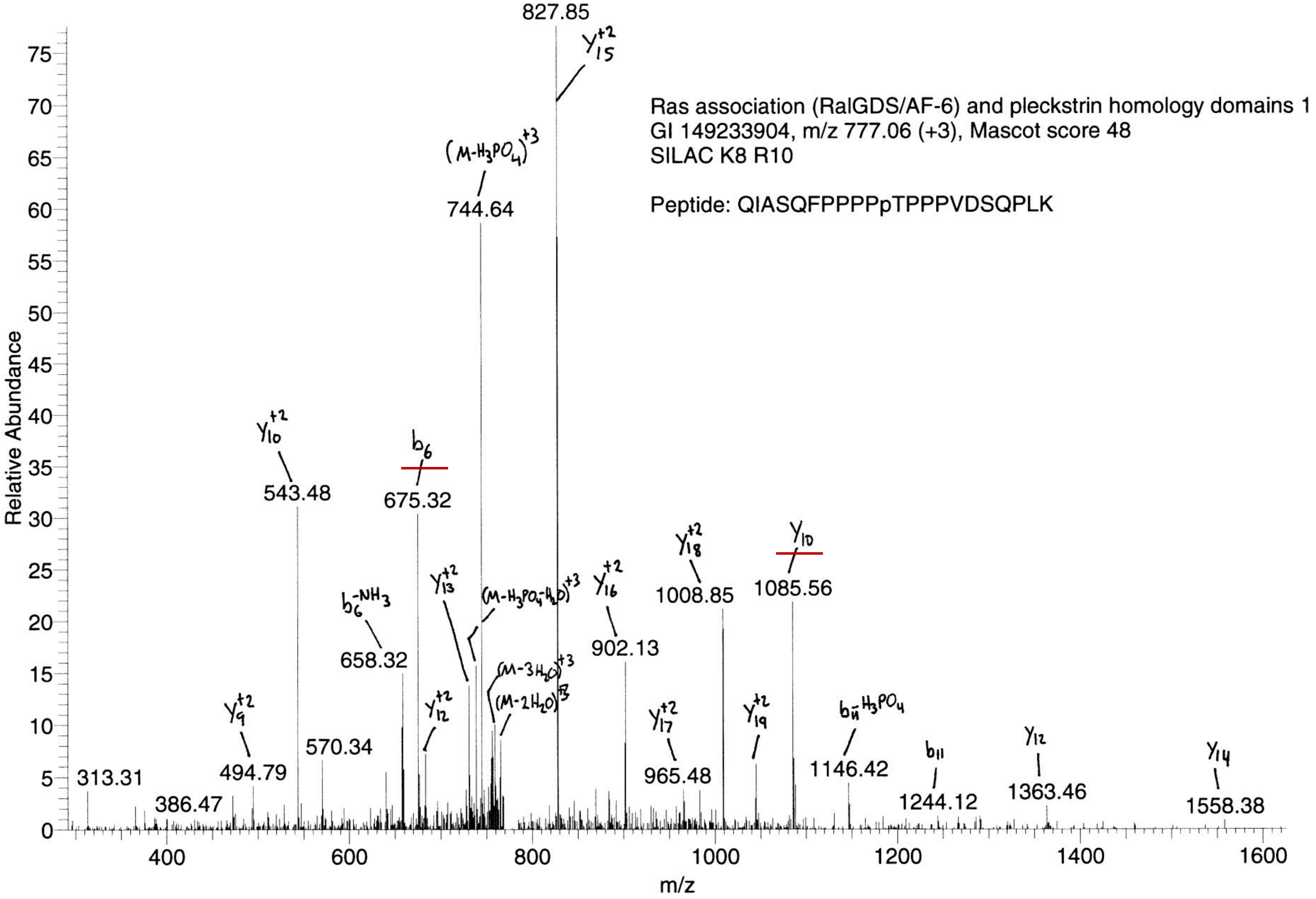
Peptide: ELPPLpSPSLSR

Fragmentation does not distinguish phosphorylation at positions 6 and 8. Assignment is based on position of proline.


pleckstrin homology-like domain, family B, member 1
GI 38455422, m/z 557.76 (+2), Mascot score 26
SILAC K8 R10

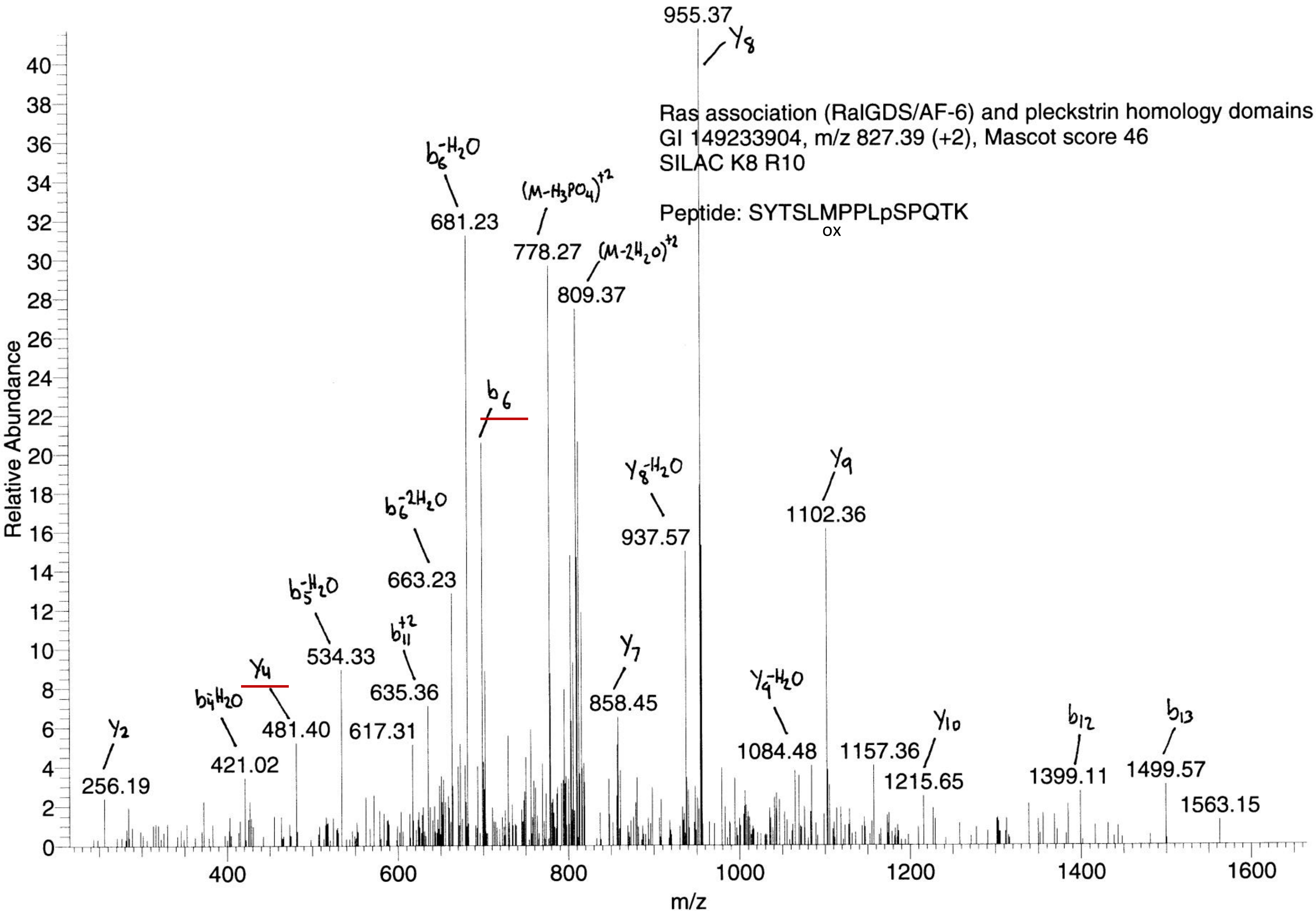
Peptide: TLQPPEpSPR


pyridoxal-dependent decarboxylase domain containing 1 isoform 1
GI 88758582, m/z 834.42 (+2), Mascot score 76
SILAC K8 R10
Peptide: VQGTGVTPPPpTPLGTR
Relative Abundance
m/z
1025.43 y_9
625.30 b_7-H_2O
1126.42 y_{10}
927.47 y_9-H_3PO_4
785.38 $(M-H_3PO_4)^{+2}$
816.20 $(M-2H_2O)^{+2}$
825.33 $(M-H_2O)^{+2}$
553.34 y_5
b_7-$2H_2O$
643.31 b_7
y_8
y_9-H_2O
b_{11}-H_3PO_4
$(M-H_3PO_4-H_2O)^{+2}$
733.40 $(b_{15}-H_2O)^{+2}$
524.46
426.13 $(b_{11}-H_3PO_4)^{+2}$
398.24
281.32
y_{11}
1282.53 y_{12}
1383.21 y_{13}
1440.99 y_{14}
1504.12
1576.62
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38
400 600 800 1000 1200 1400 1600



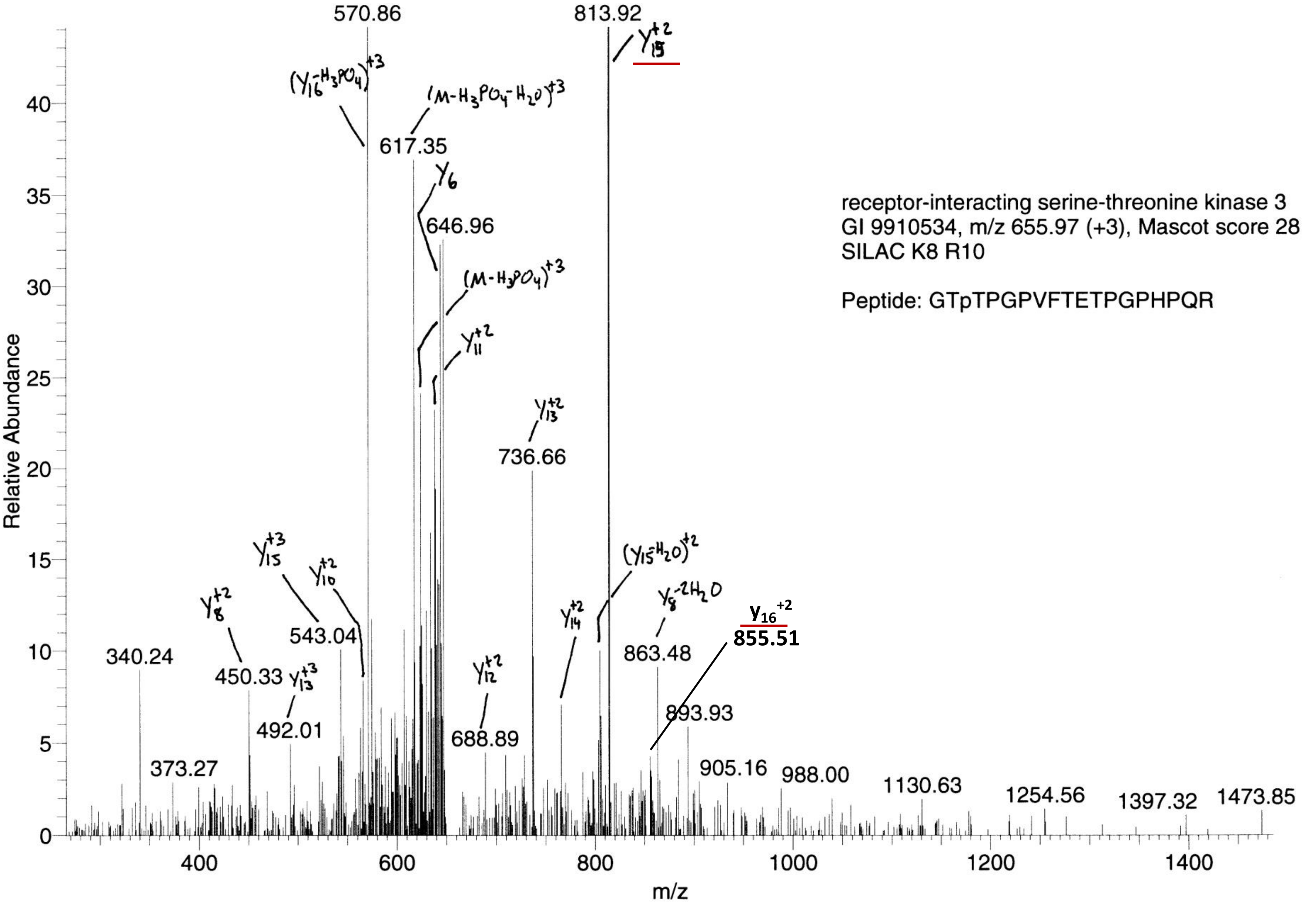
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
GI 149233904, m/z 777.06 (+3), Mascot score 48
SILAC K8 R10

Peptide: QIASQFPPPPpTPPPVDSQPLK



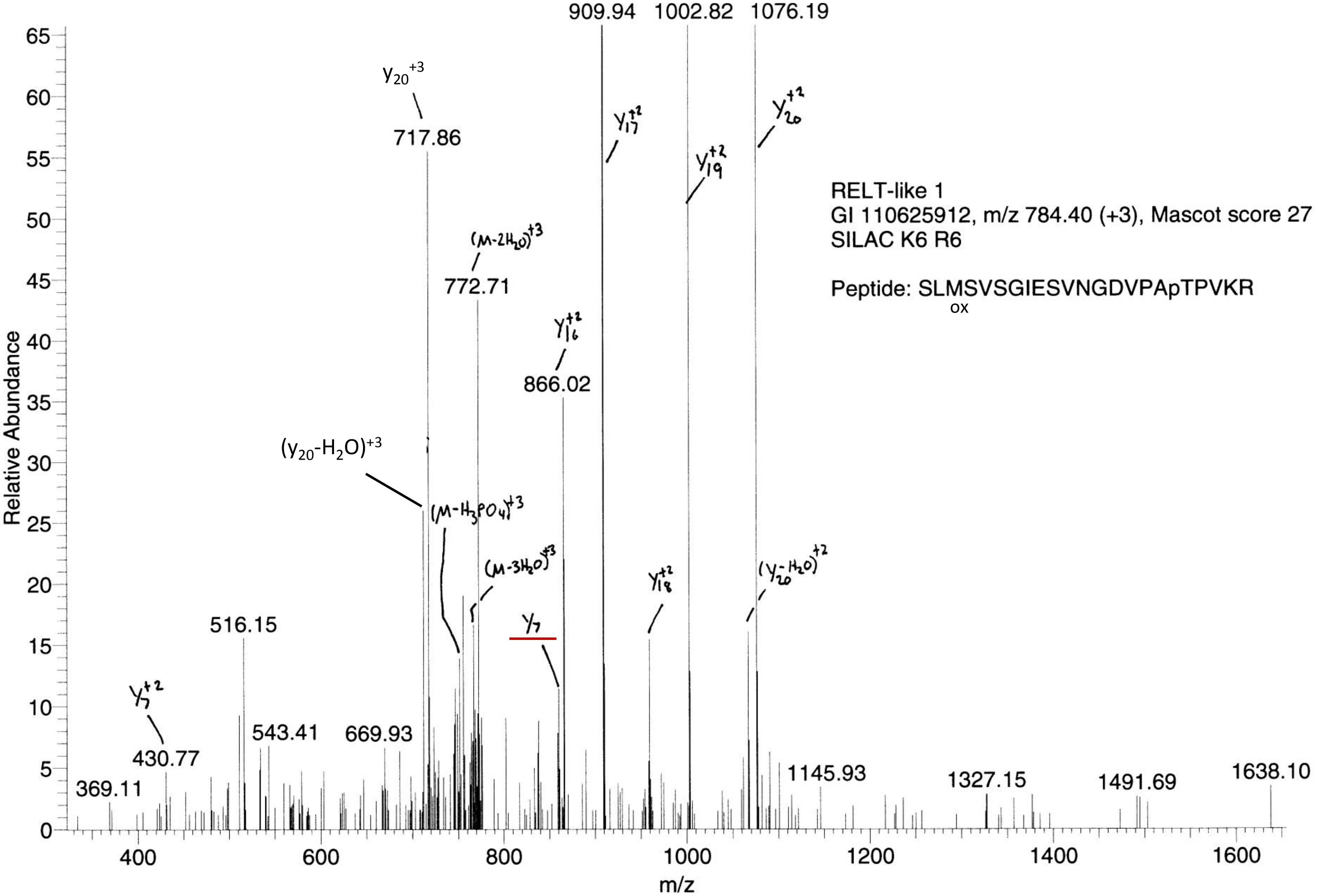
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
GI 149233904, m/z 827.39 (+2), Mascot score 46
SILAC K8 R10

Peptide: SYTSLM_{ox}PPLpSPQTK



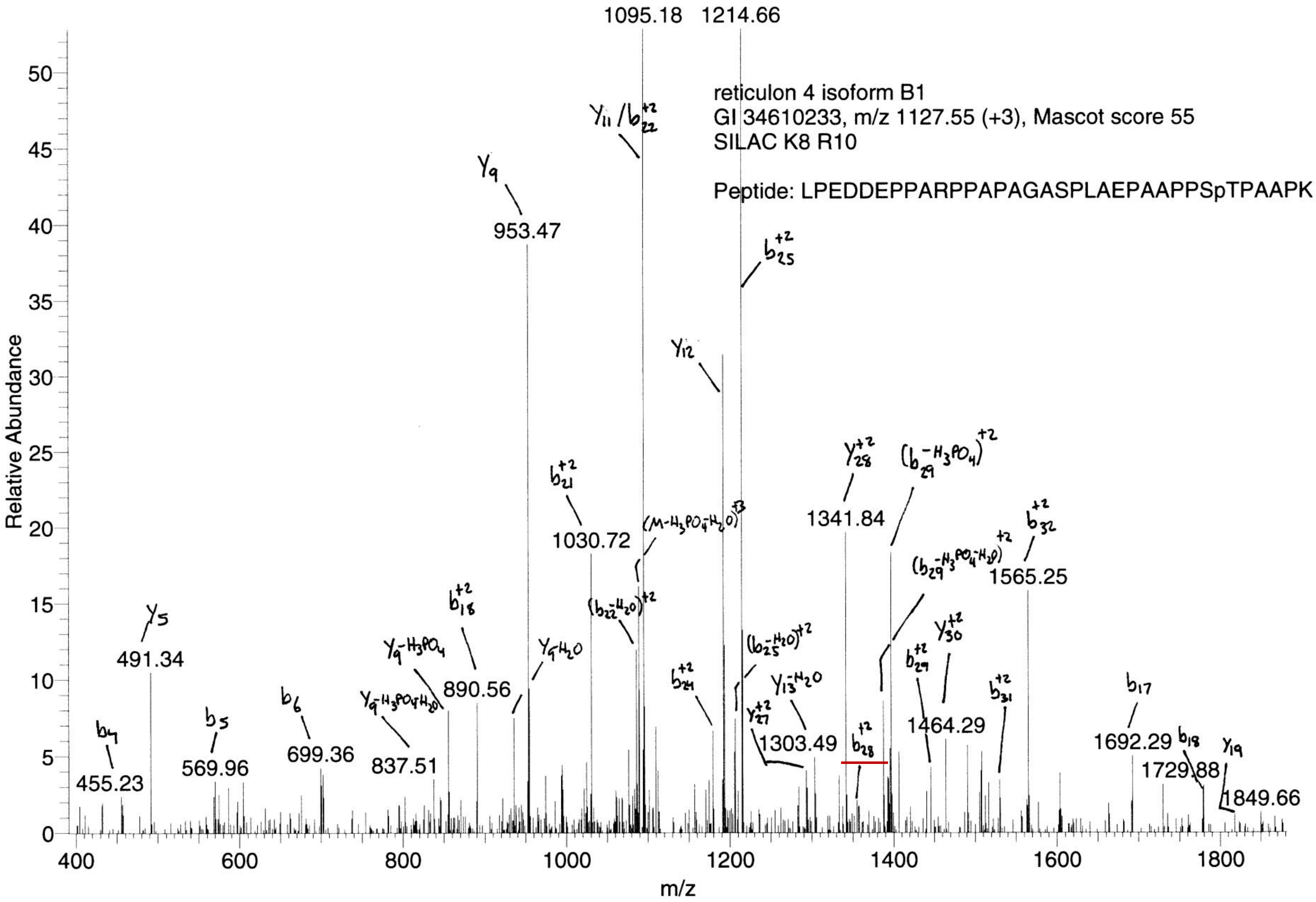
receptor-interacting serine-threonine kinase 3
GI 9910534, m/z 655.97 (+3), Mascot score 28
SILAC K8 R10

Peptide: GTpTPGPVFTETPGPHPQR

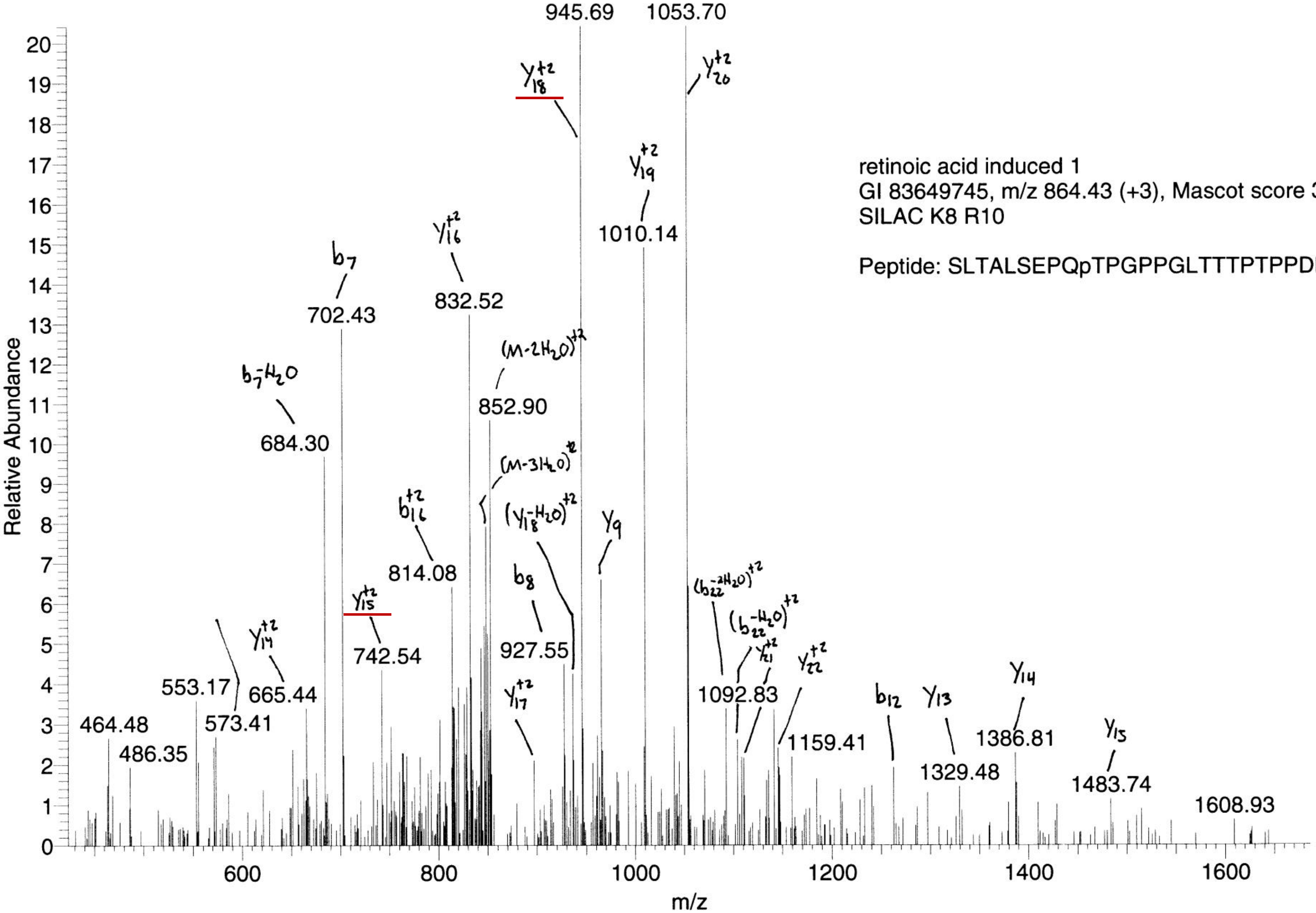


RELT-like 1
GI 110625912, m/z 784.40 (+3), Mascot score 27
SILAC K6 R6

Peptide: SLM$_{ox}$SVSGIESVNGDVPApTPVKR

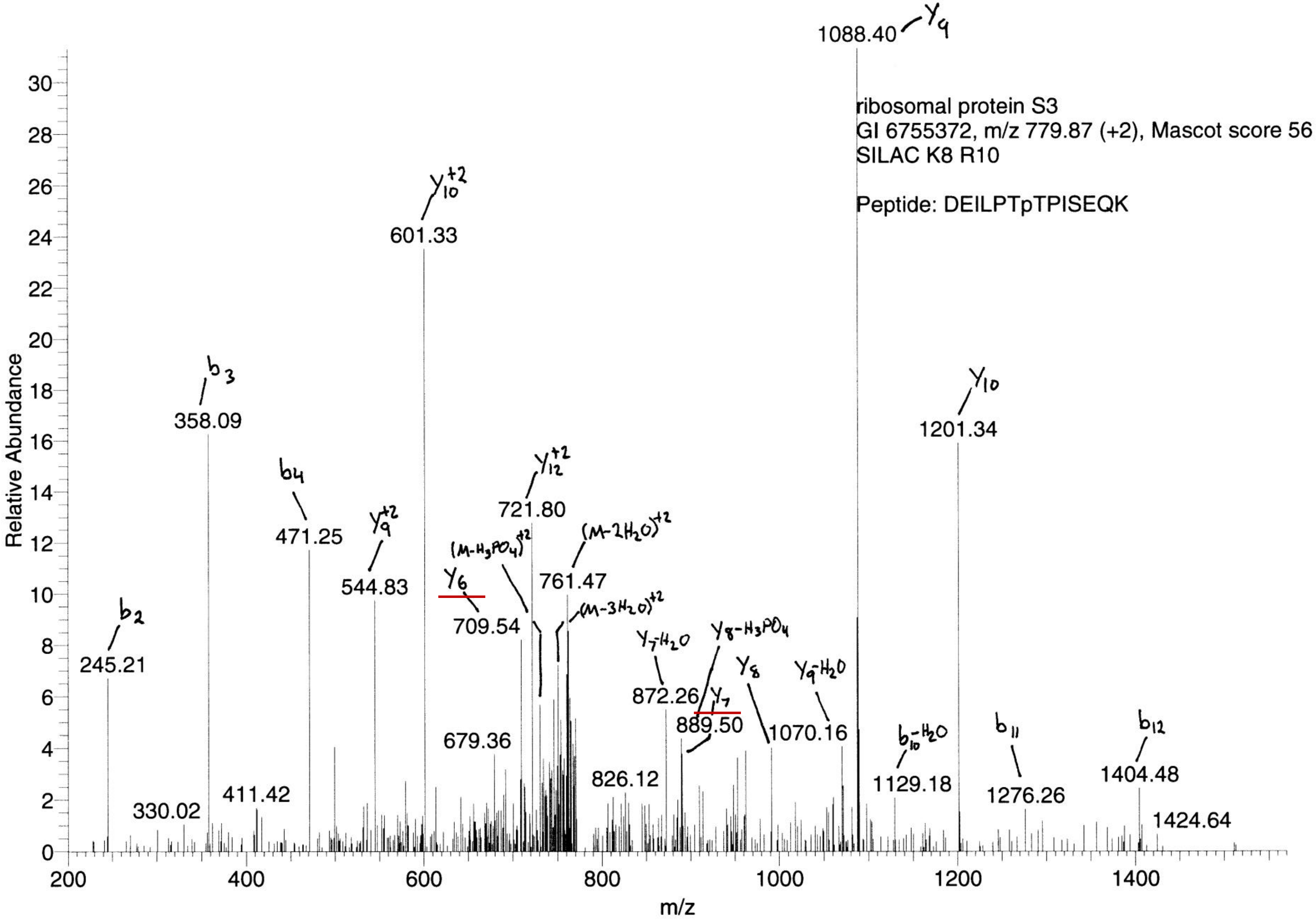

reticulon 4 isoform B1
GI 34610233, m/z 1127.55 (+3), Mascot score 55
SILAC K8 R10

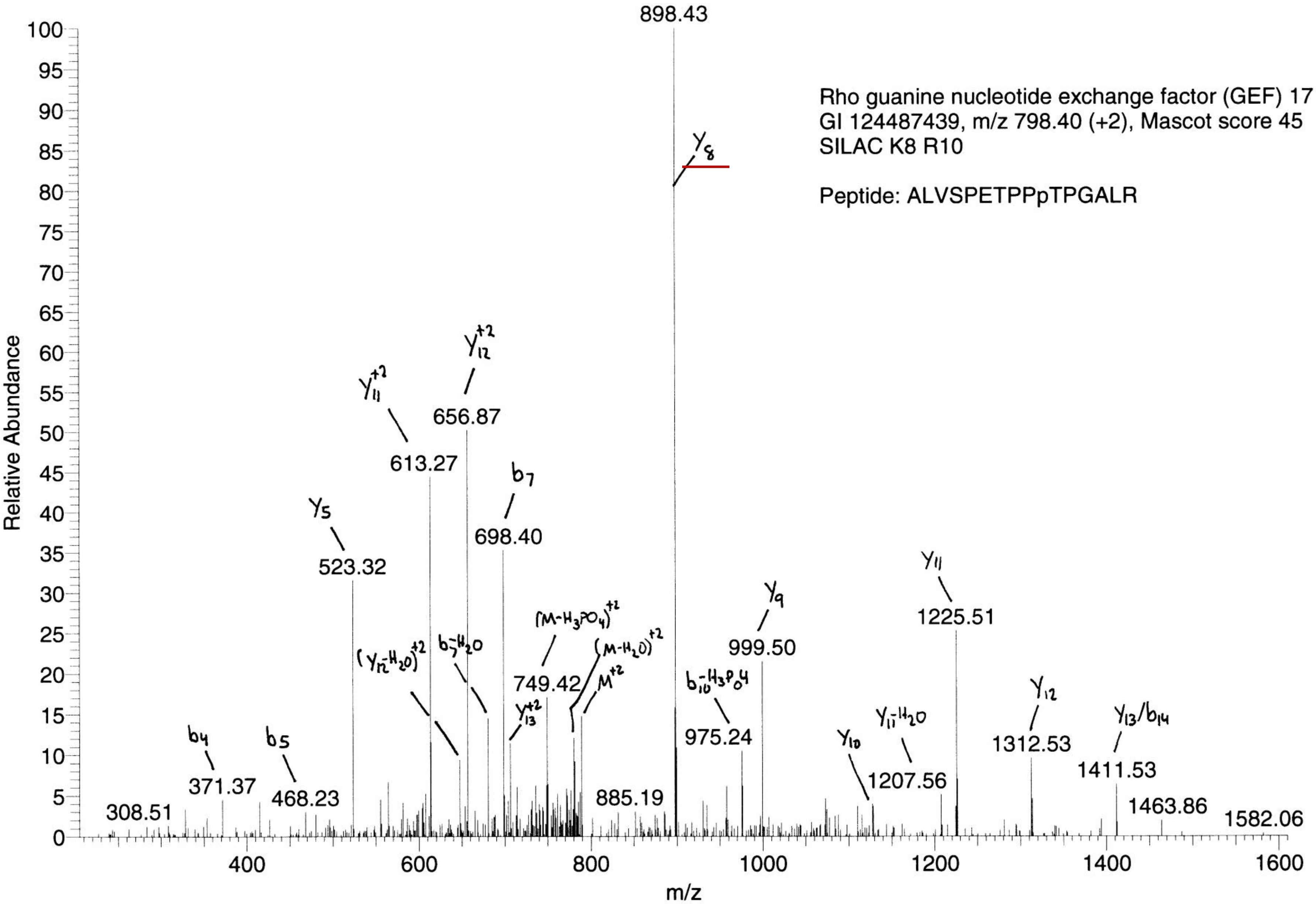
Peptide: LPEDDEPPARPPAPAGASPLAEPAAPPSpTPAAPK



retinoic acid induced 1
GI 83649745, m/z 864.43 (+3), Mascot score 38
SILAC K8 R10

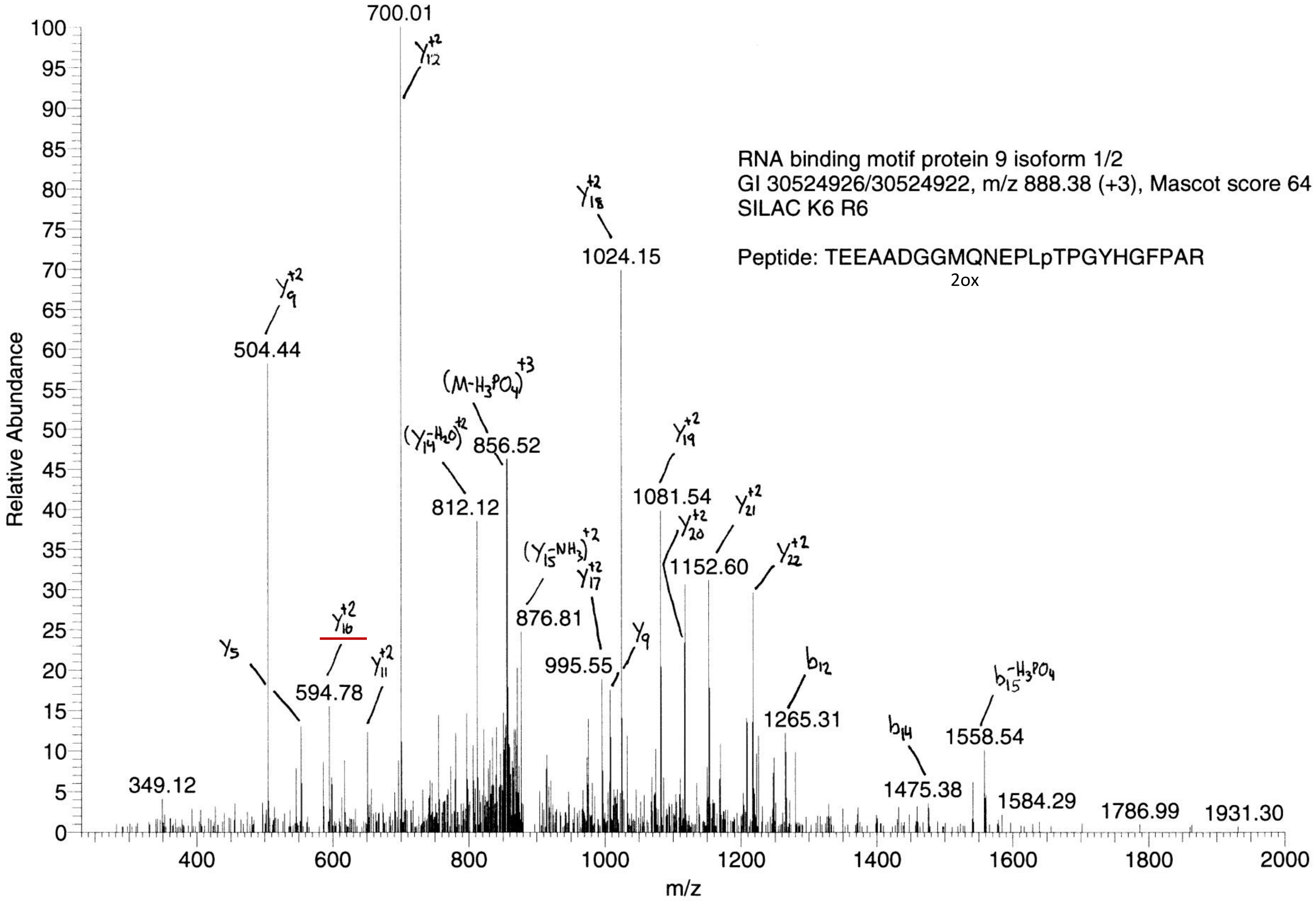
Peptide: SLTALSEPQpTPGPPGLTTTPTPPDK


ribosomal protein S3
GI 6755372, m/z 779.87 (+2), Mascot score 56
SILAC K8 R10
Peptide: DEILPTpTPISEQK
Relative Abundance
m/z
0
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
200
400
600
800
1000
1200
1400
245.21
b_2
330.02
358.09
b_3
411.42
471.25
b_4
544.83
y_9^{+2}
601.33
y_{10}^{+2}
679.36
709.54
y_6
$(M-H_3PO_4)^{+2}$
721.80
y_{12}^{+2}
761.47
$(M-2H_2O)^{+2}$
$(M-3H_2O)^{+2}$
826.12
872.26
y_7-H_2O
889.50
y_7
$y_8-H_3PO_4$
y_8
1070.16
y_9-H_2O
1088.40
y_9
1129.18
$b_{10}-H_2O$
1201.34
y_{10}
1276.26
b_{11}
1404.48
b_{12}
1424.64



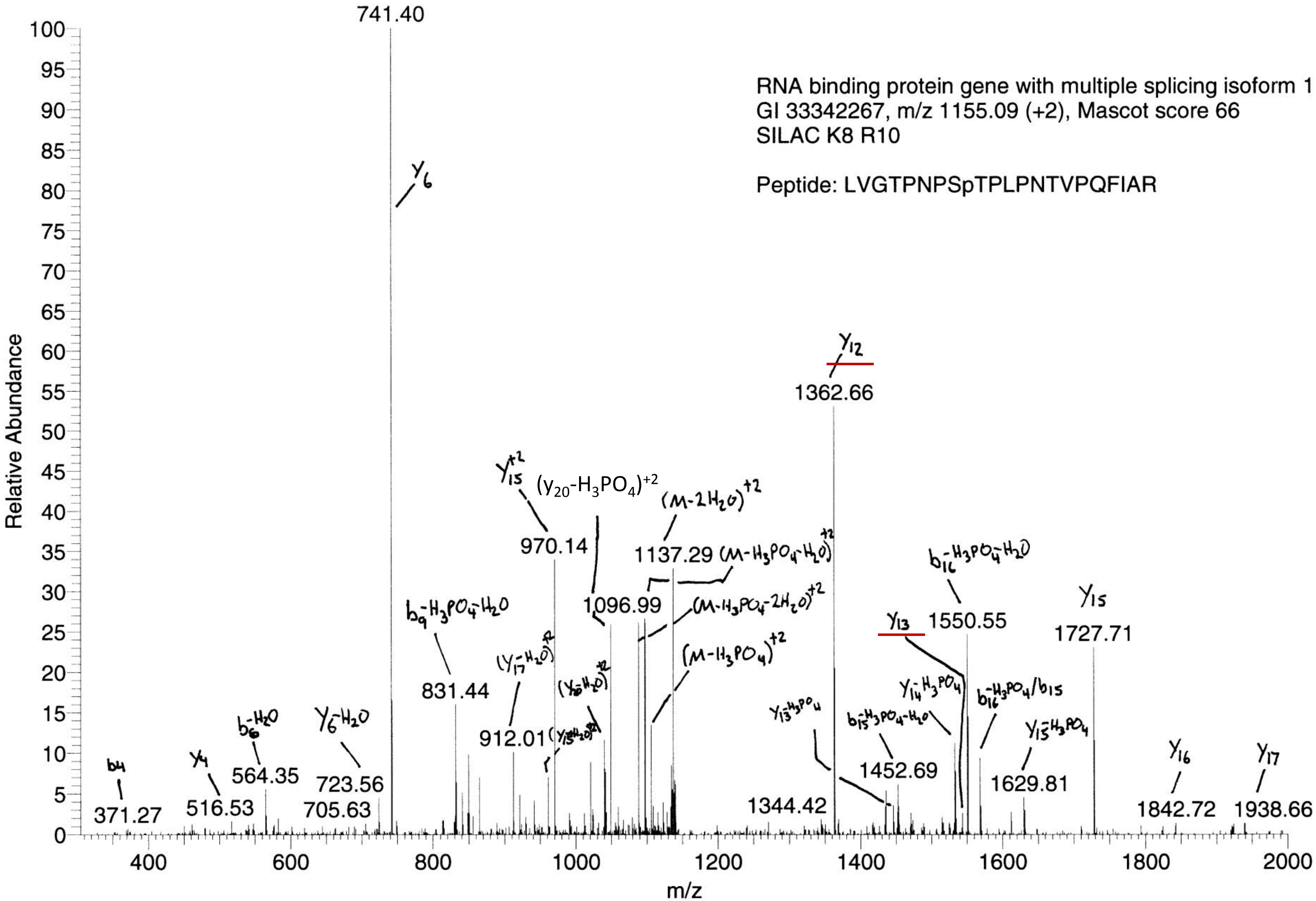
Rho guanine nucleotide exchange factor (GEF) 17
GI 124487439, m/z 798.40 (+2), Mascot score 45
SILAC K8 R10

Peptide: ALVSPETPPpTPGALR



RNA binding motif protein 9 isoform 1/2
GI 30524926/30524922, m/z 888.38 (+3), Mascot score 64
SILAC K6 R6

Peptide: TEEAADGGMQNEPLpTPGYHGFPAR
2ox


RNA binding protein gene with multiple splicing isoform 1
GI 33342267, m/z 1155.09 (+2), Mascot score 66
SILAC K8 R10
Peptide: LVGTPNPSpTPLPNTVPQFIAR
741.40
y6
1362.66
y12
y15+2
970.14
(y20-H3PO4)+2
(M-2H2O)+2
1137.29
(M-H3PO4-H2O)+2
1096.99
(M-H3PO4-2H2O)+2
(M-H3PO4)+2
b9-H3PO4-H2O
831.44
(y17-H2O)+2
912.01
(y18-H2O)+2
(y15-H2O)+2
b4
371.27
y4
516.53
b6-H2O
564.35
y6-H2O
723.56
705.63
y13-H3PO4
1344.42
b15-H3PO4-H2O
1452.69
y13
y14-H3PO4
b16-H3PO4-H2O
1550.55
b16-H3PO4/b15
y15-H3PO4
1629.81
y15
1727.71
y16
1842.72
y17
1938.66
Relative Abundance
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
400
600
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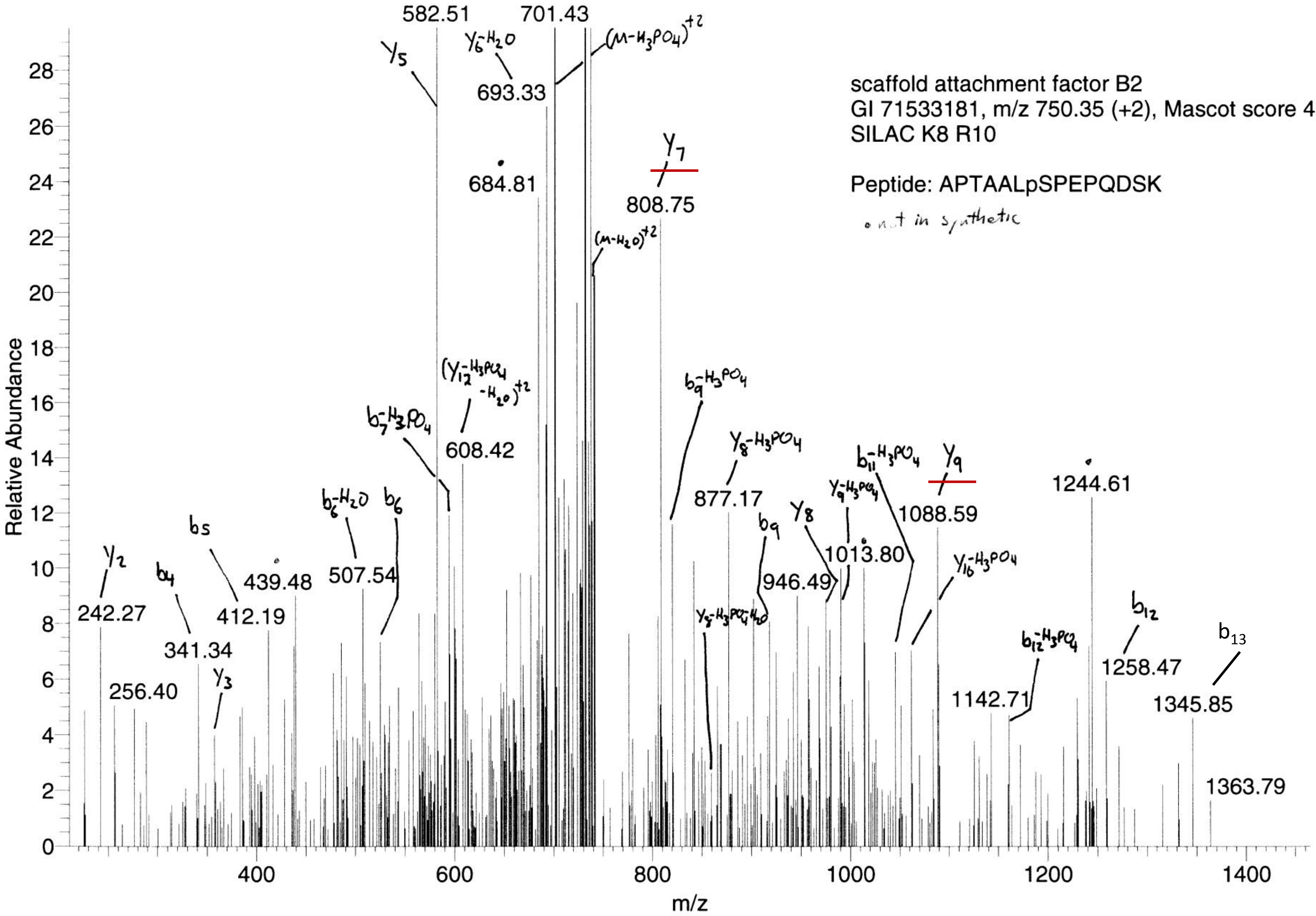
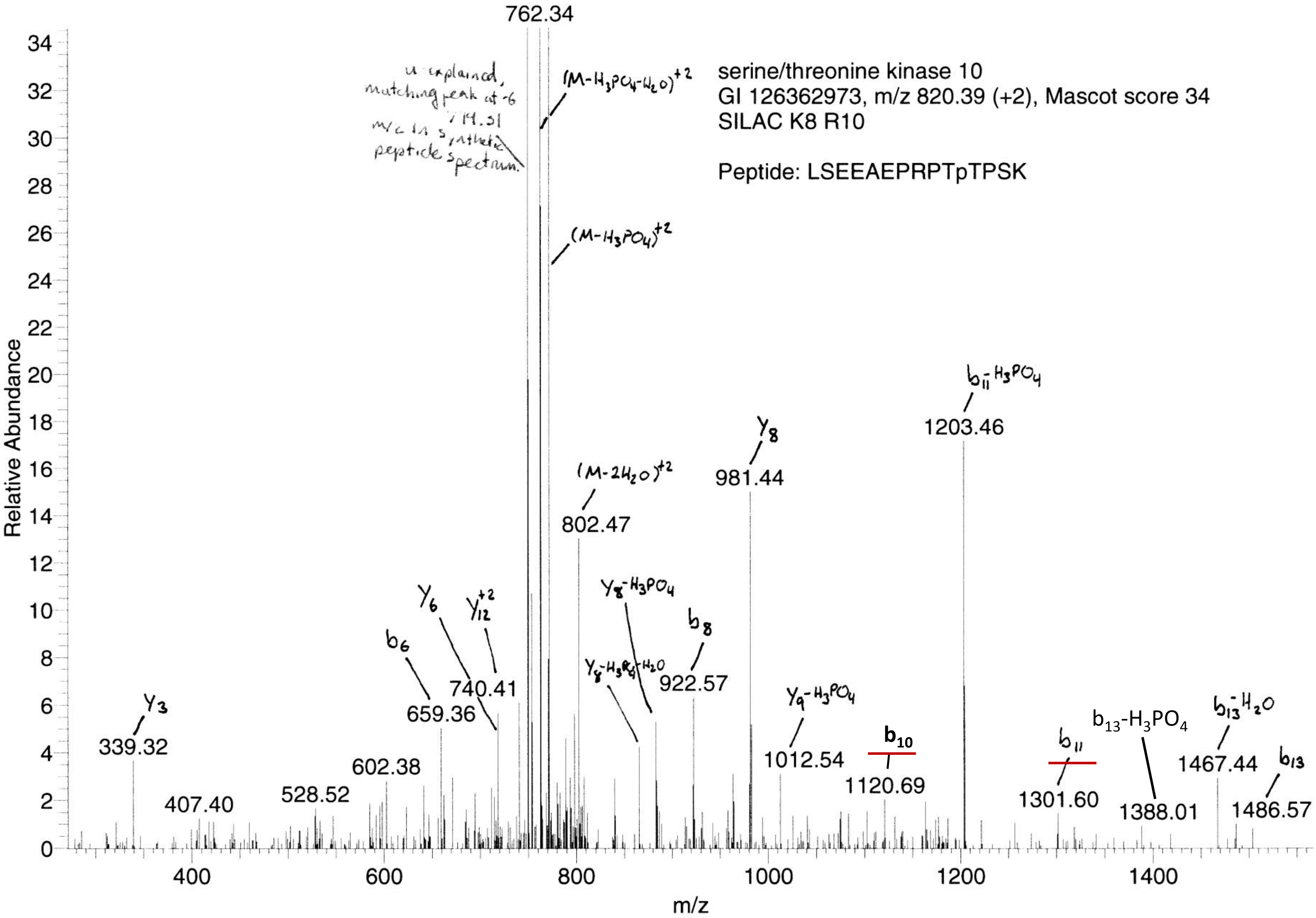
1200
1400
1600
1800
2000
m/z



scaffold attachment factor B2
GI 71533181, m/z 750.35 (+2), Mascot score 48
SILAC K8 R10

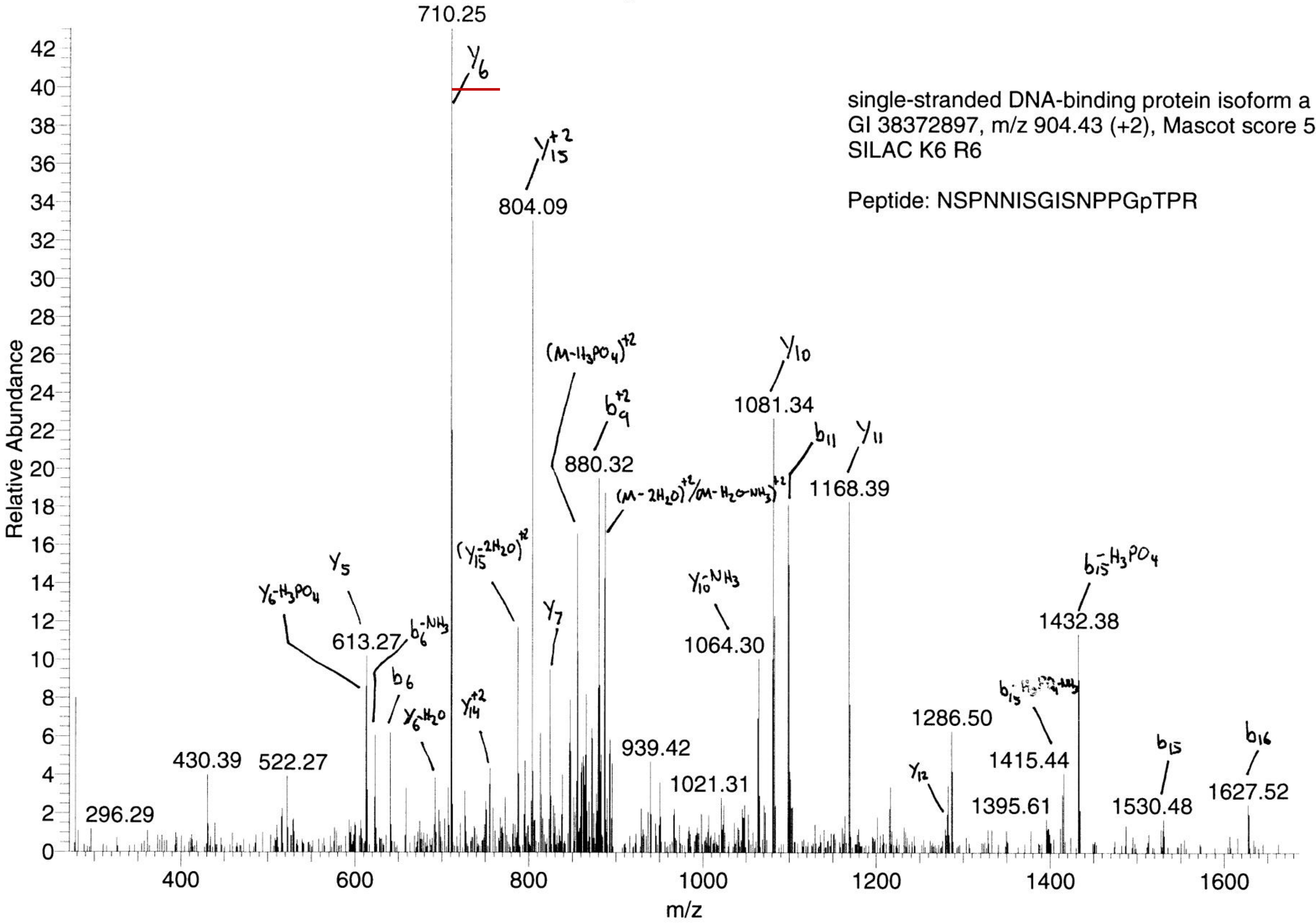
Peptide: APTAALpSPEPQDSK

• not in synthetic



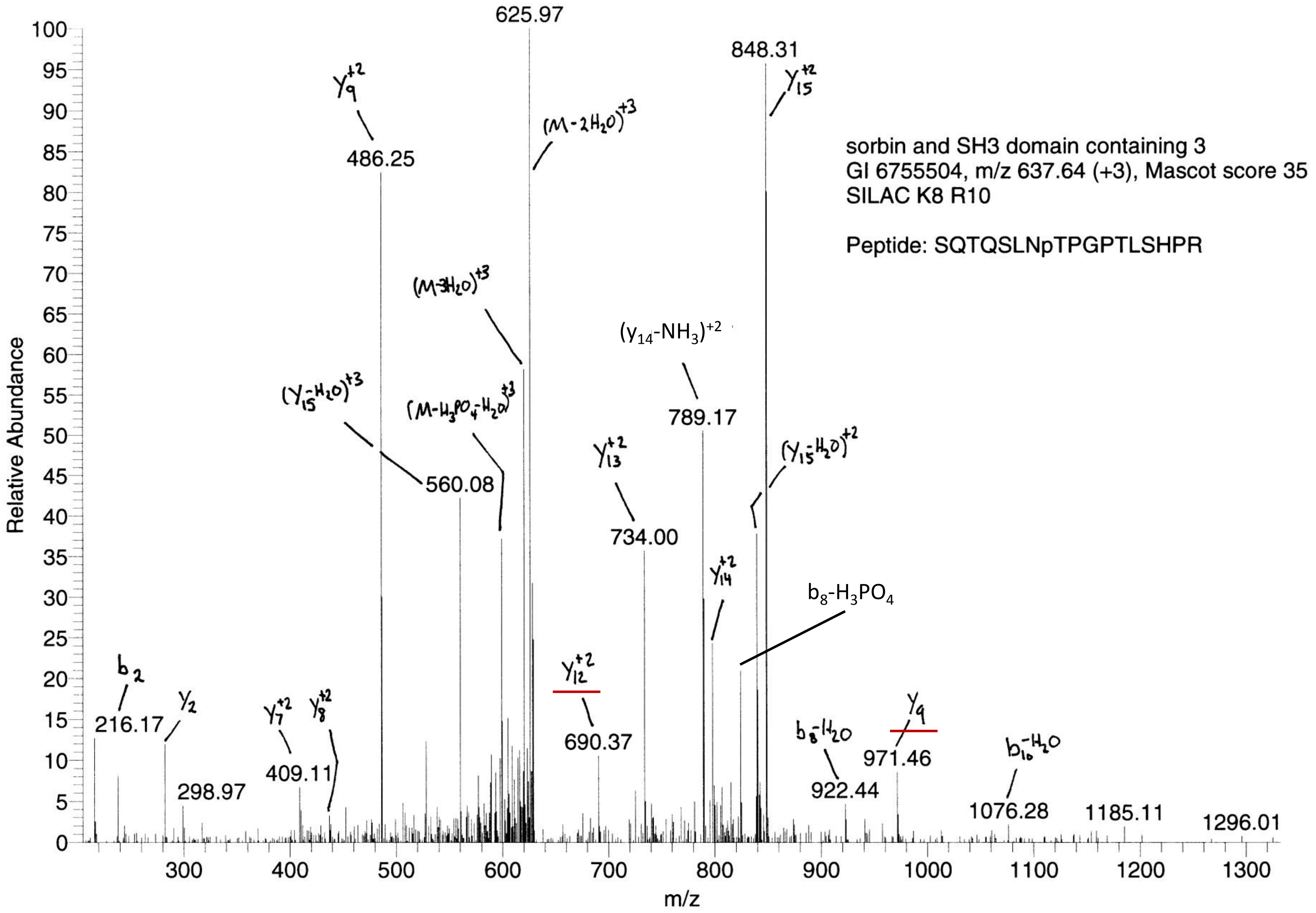
serine/threonine kinase 10
GI 126362973, m/z 820.39 (+2), Mascot score 34
SILAC K8 R10

Peptide: LSEEAEPRPTpTPSK



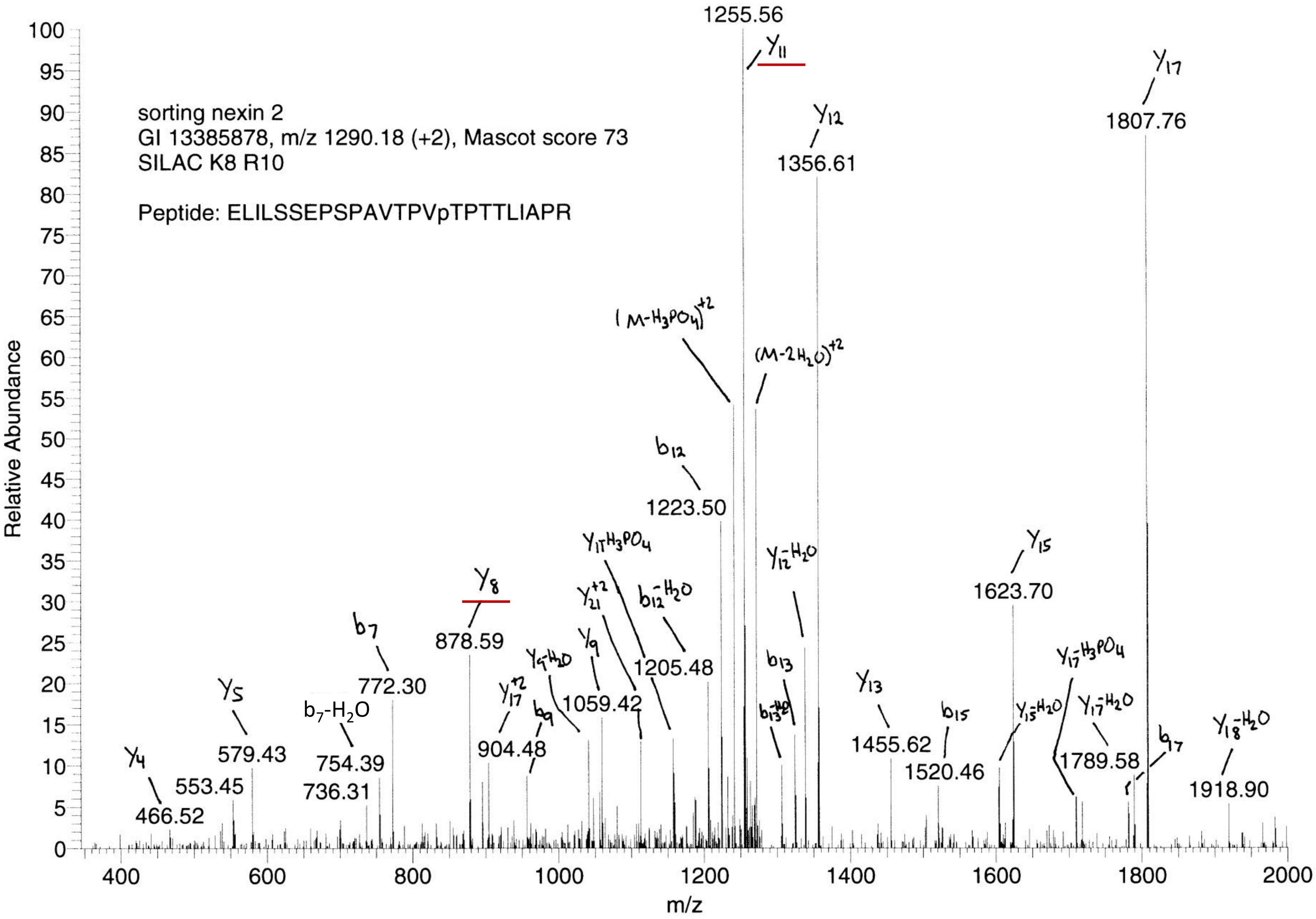
single-stranded DNA-binding protein isoform a
GI 38372897, m/z 904.43 (+2), Mascot score 54
SILAC K6 R6

Peptide: NSPNNISGISNPPGpTPR



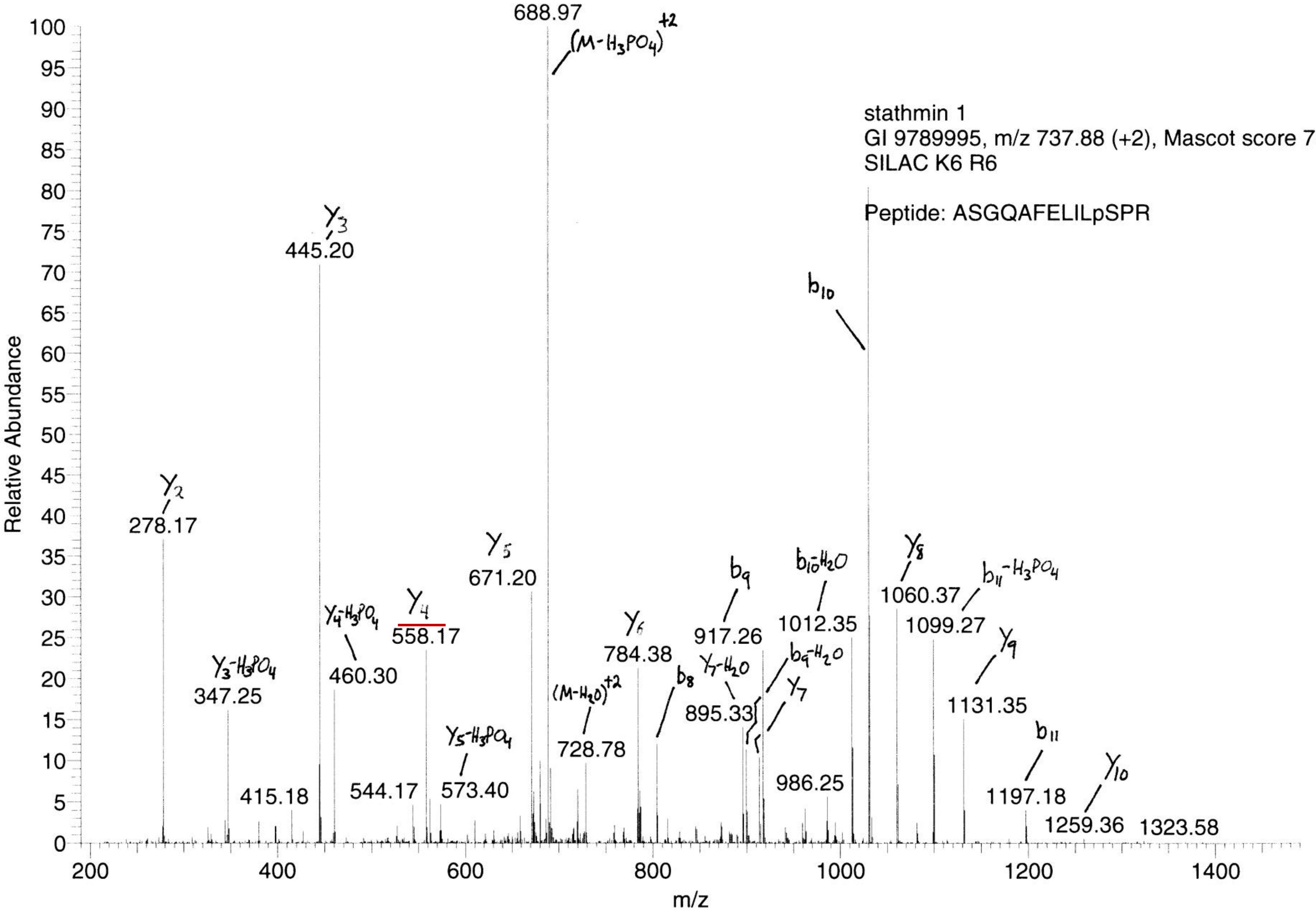
sorbin and SH3 domain containing 3
GI 6755504, m/z 637.64 (+3), Mascot score 35
SILAC K8 R10

Peptide: SQTQSLNpTPGPTLSHPR



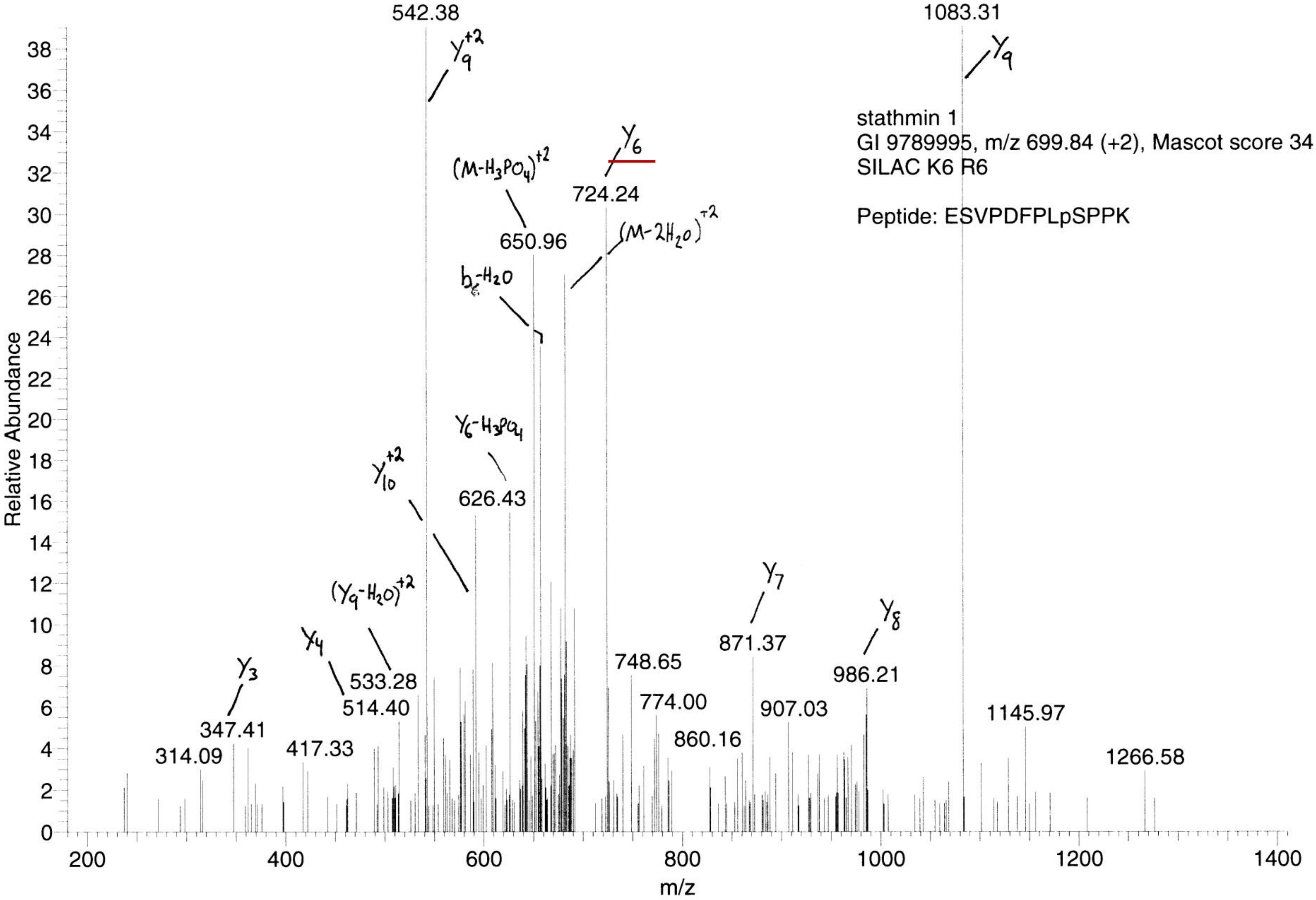
sorting nexin 2
GI 13385878, m/z 1290.18 (+2), Mascot score 73
SILAC K8 R10

Peptide: ELILSSEPSPAVTPVpTPTTLIAPR



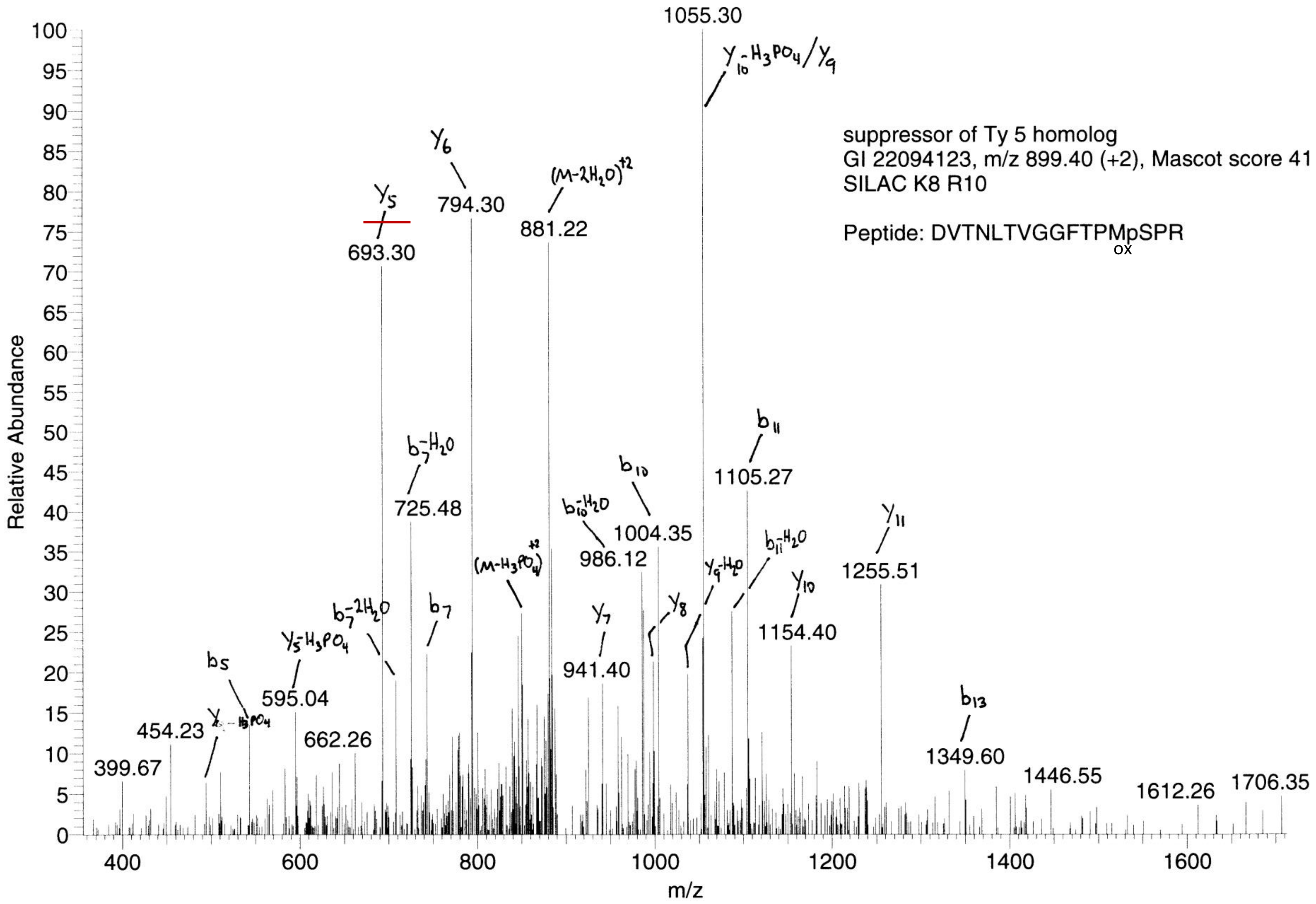
stathmin 1
GI 9789995, m/z 737.88 (+2), Mascot score 76
SILAC K6 R6

Peptide: ASGQAFELILpSPR



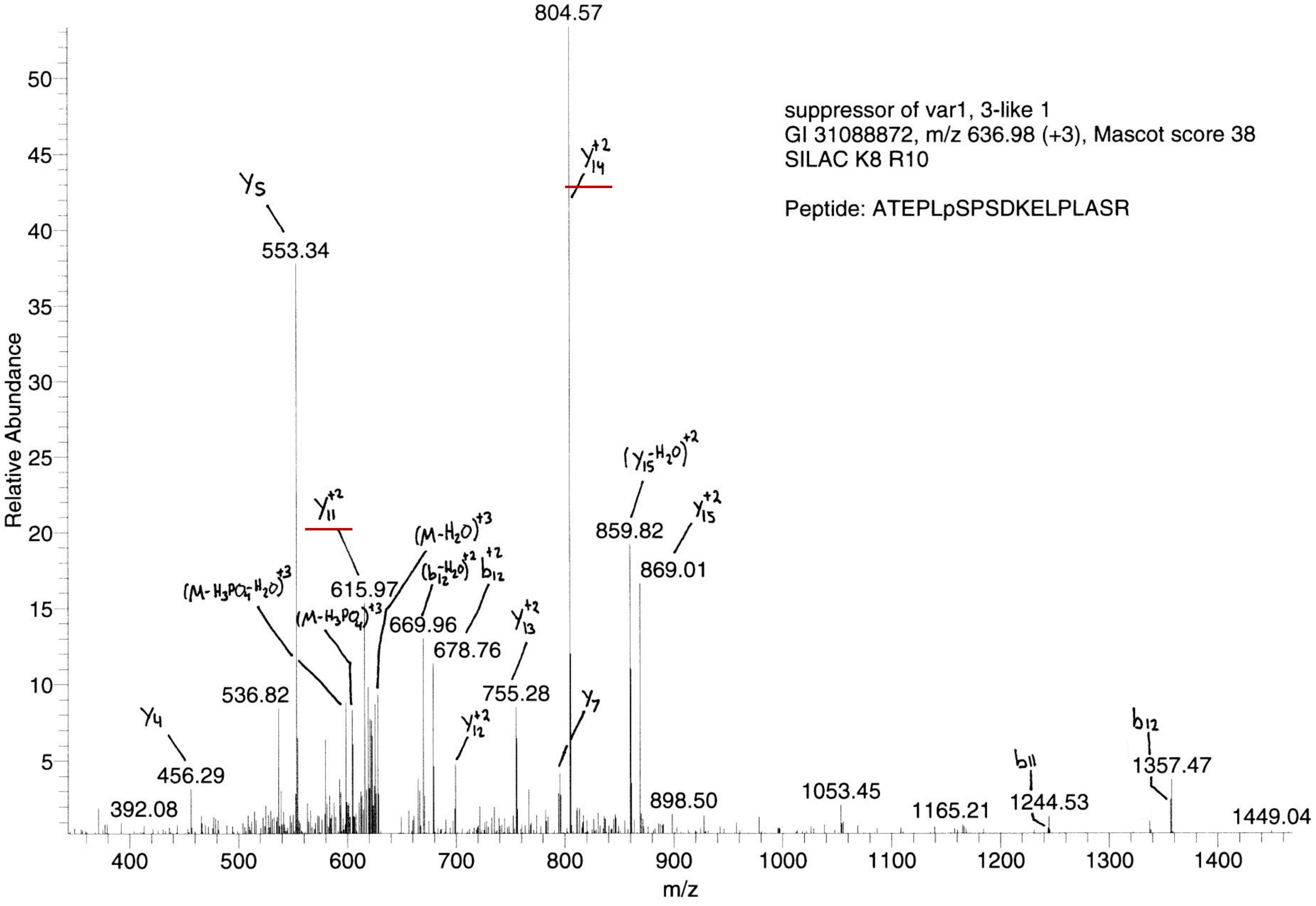
stathmin 1
GI 9789995, m/z 699.84 (+2), Mascot score 34
SILAC K6 R6

Peptide: ESVPDFPLpSPPK

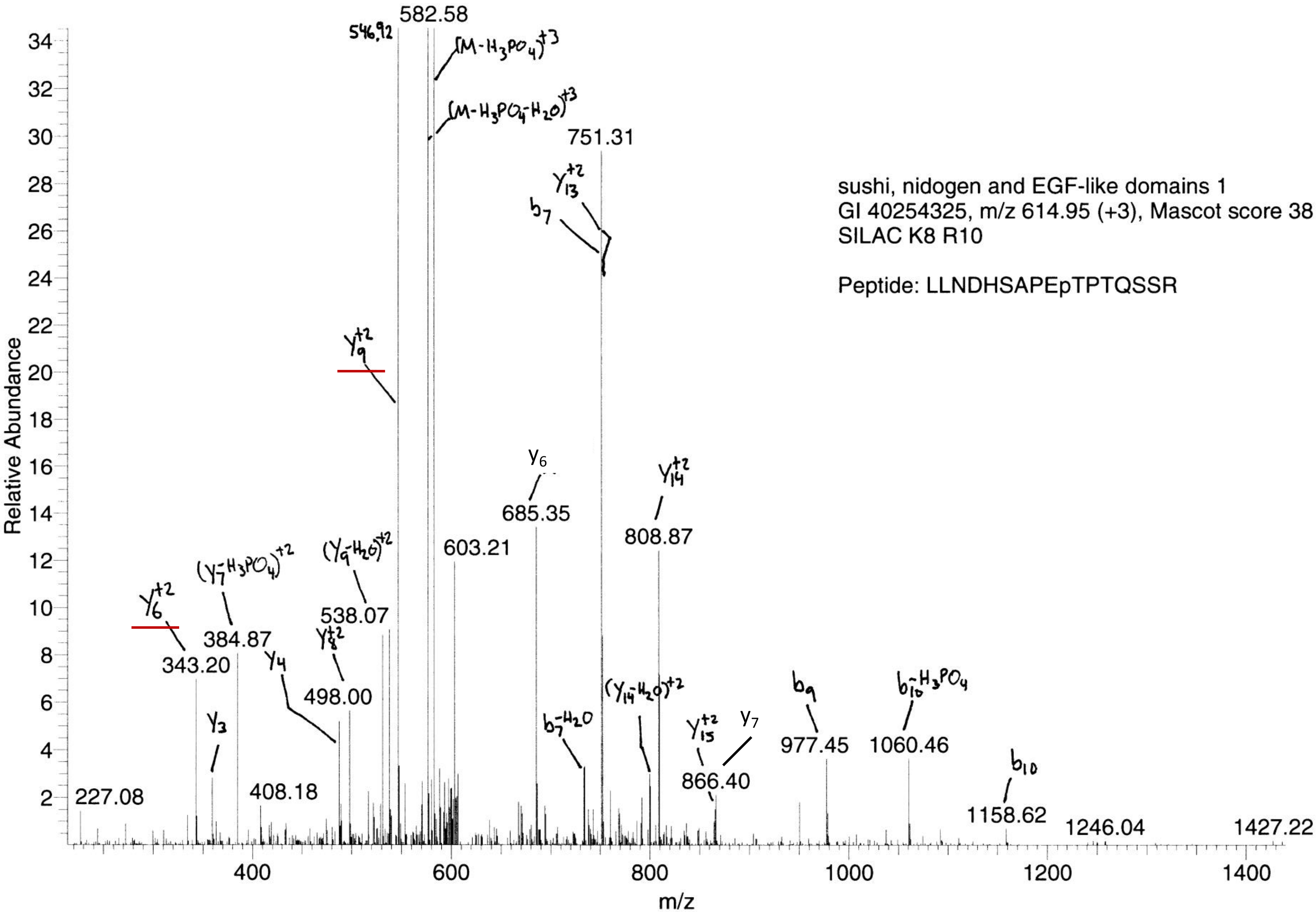


suppressor of Ty 5 homolog
GI 22094123, m/z 899.40 (+2), Mascot score 41
SILAC K8 R10

Peptide: DVTNLTVGGFTPM_{ox}pSPR

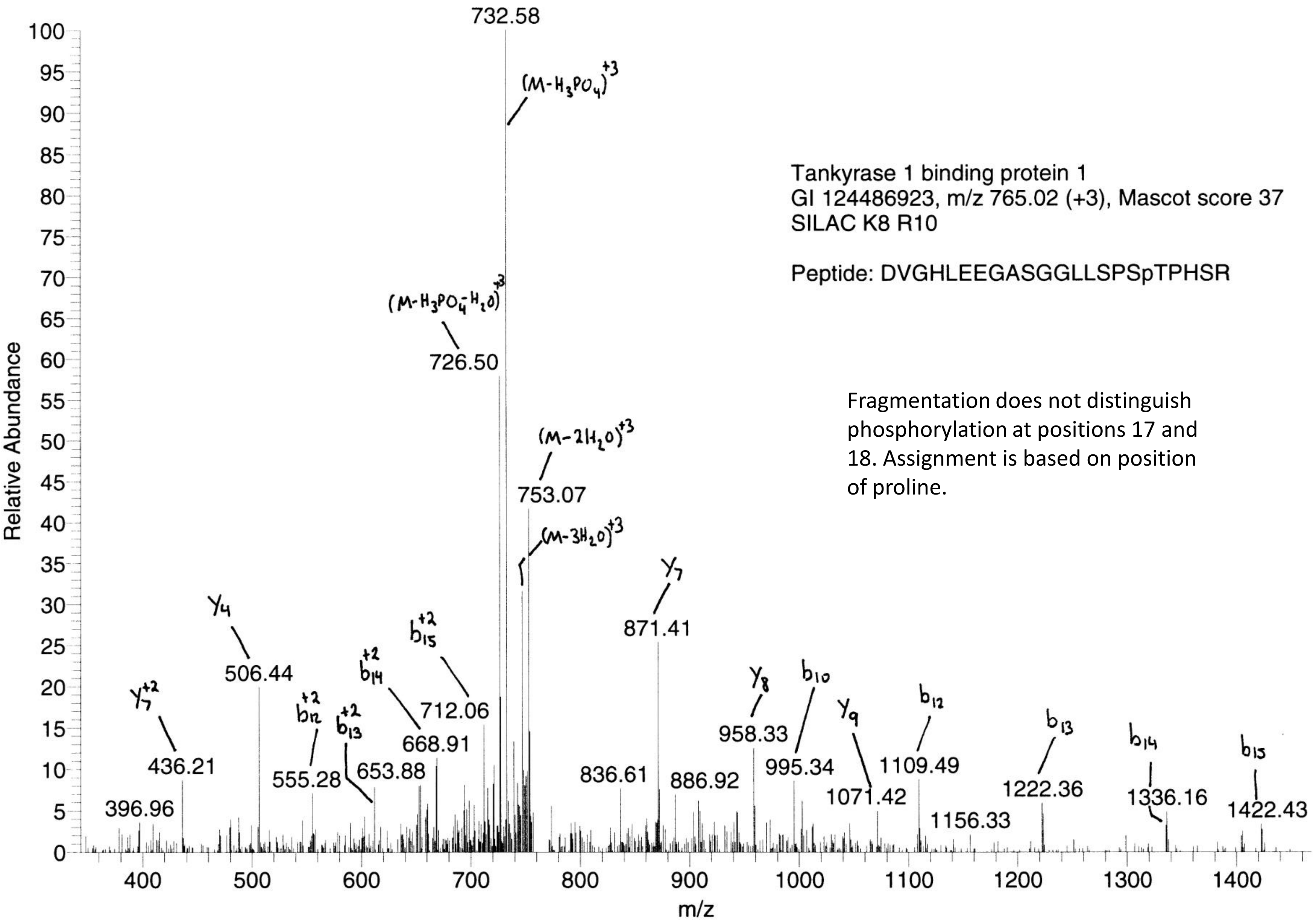

suppressor of var1, 3-like 1
GI 31088872, m/z 636.98 (+3), Mascot score 38
SILAC K8 R10

Peptide: ATEPLpSPSDKELPLASR



sushi, nidogen and EGF-like domains 1
GI 40254325, m/z 614.95 (+3), Mascot score 38
SILAC K8 R10

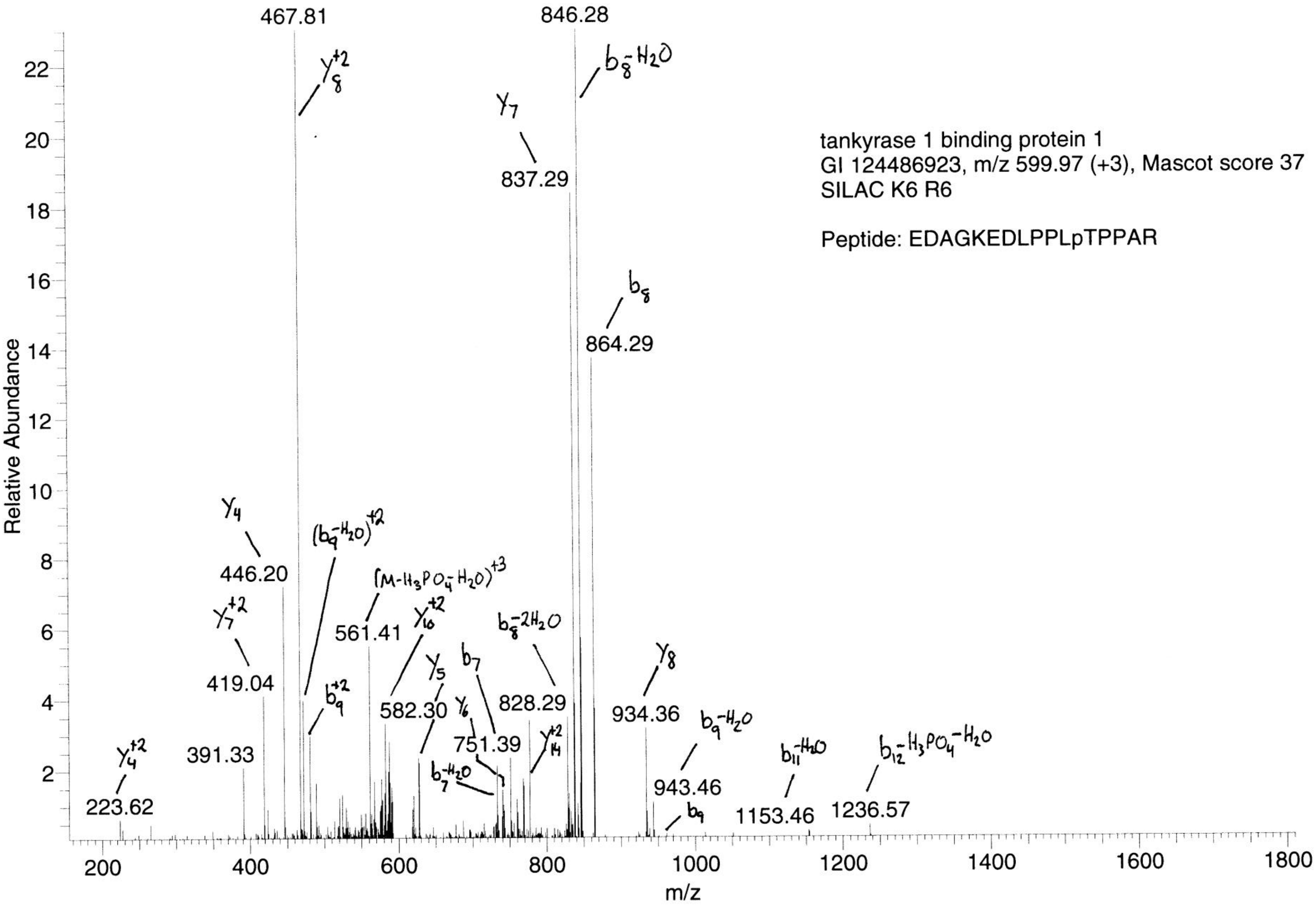
Peptide: LLNDHSAPEpTPTQSSR



Tankyrase 1 binding protein 1
GI 124486923, m/z 765.02 (+3), Mascot score 37
SILAC K8 R10

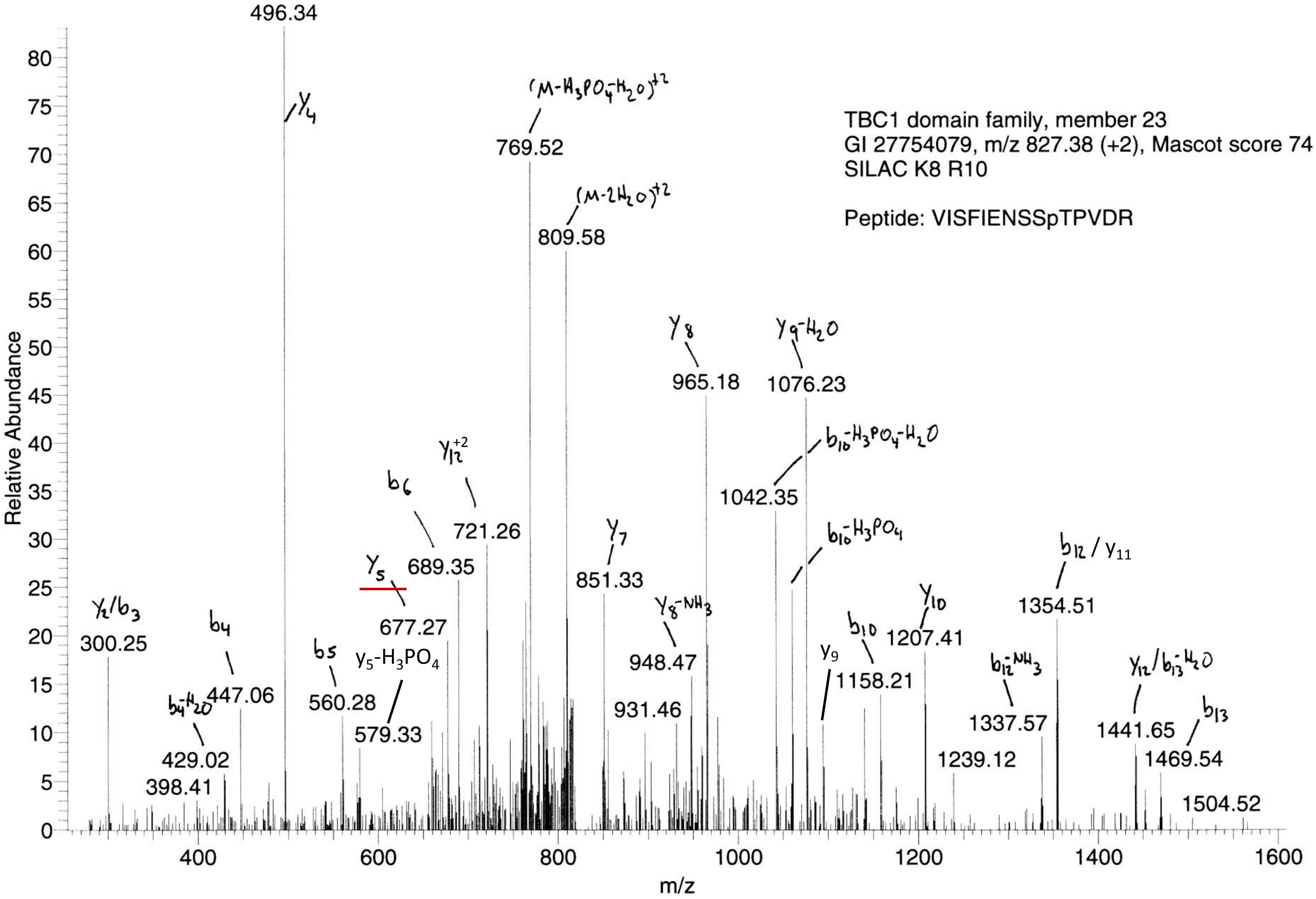
Peptide: DVGHLEEGASGGLLSPSpTPHSR

Fragmentation does not distinguish phosphorylation at positions 17 and 18. Assignment is based on position of proline.



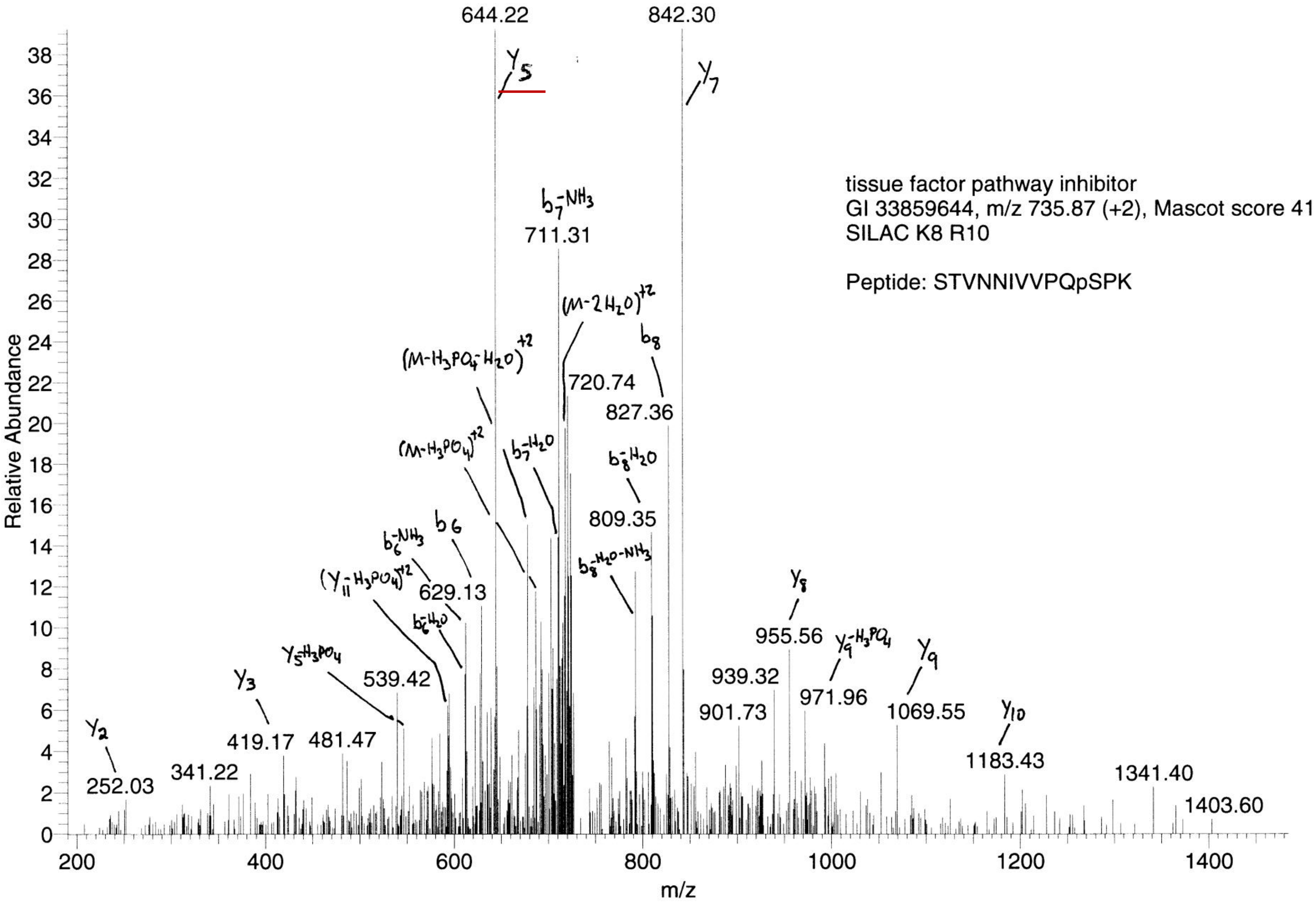
tankyrase 1 binding protein 1
GI 124486923, m/z 599.97 (+3), Mascot score 37
SILAC K6 R6

Peptide: EDAGKEDLPPLpTPPAR



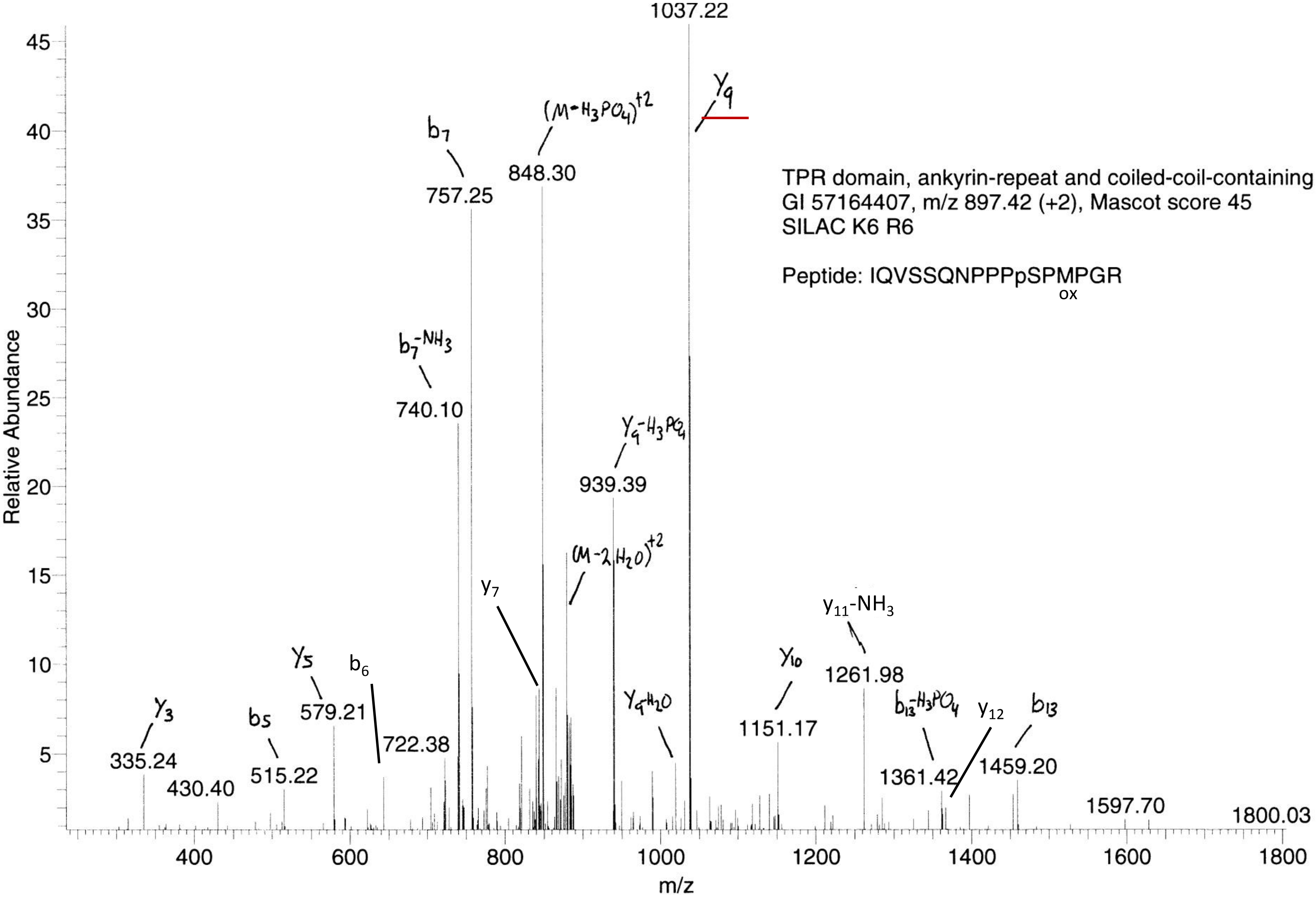
TBC1 domain family, member 23
GI 27754079, m/z 827.38 (+2), Mascot score 74
SILAC K8 R10

Peptide: VISFIENSSpTPVDR



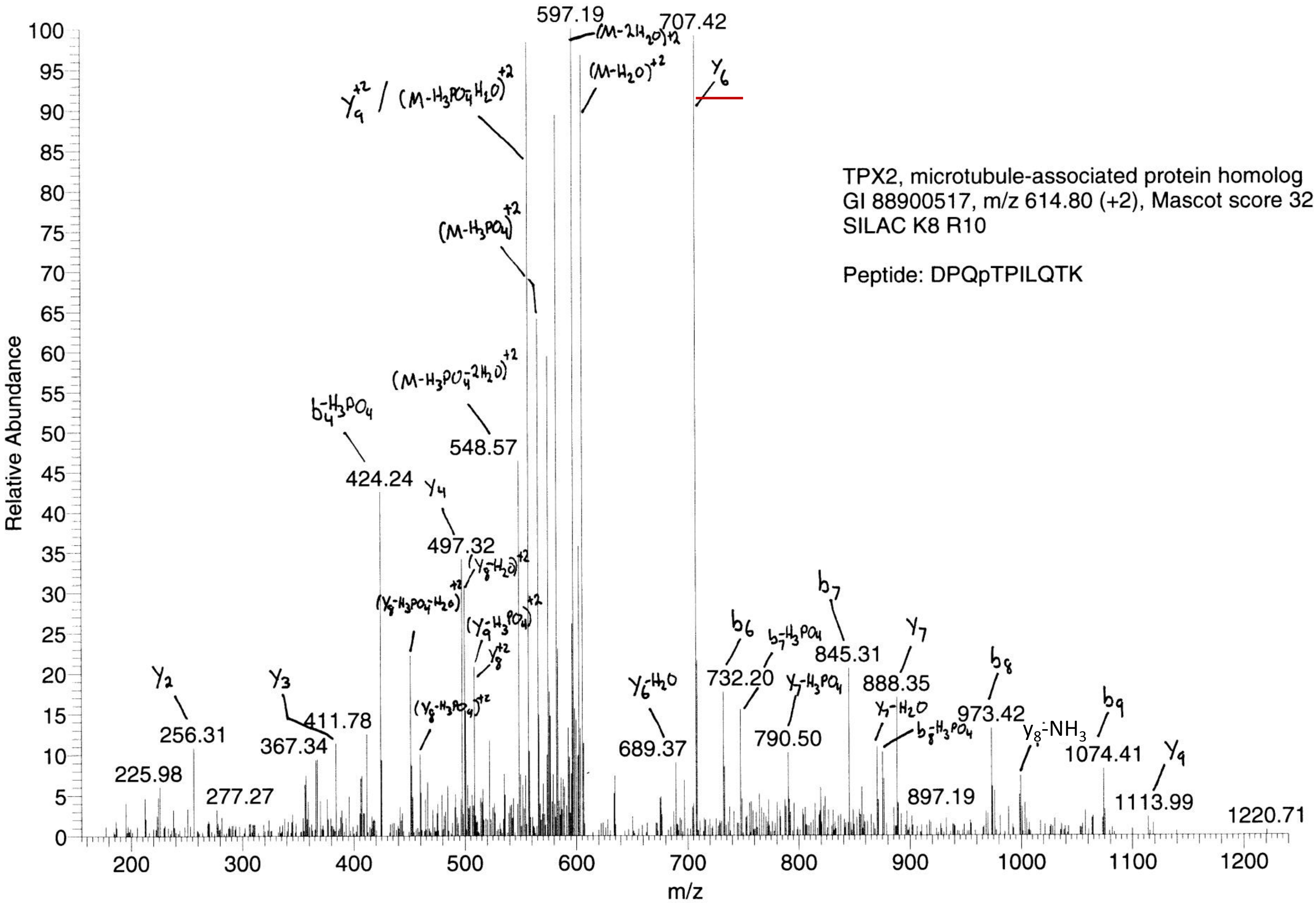
tissue factor pathway inhibitor
GI 33859644, m/z 735.87 (+2), Mascot score 41
SILAC K8 R10

Peptide: STVNNIVVPQpSPK



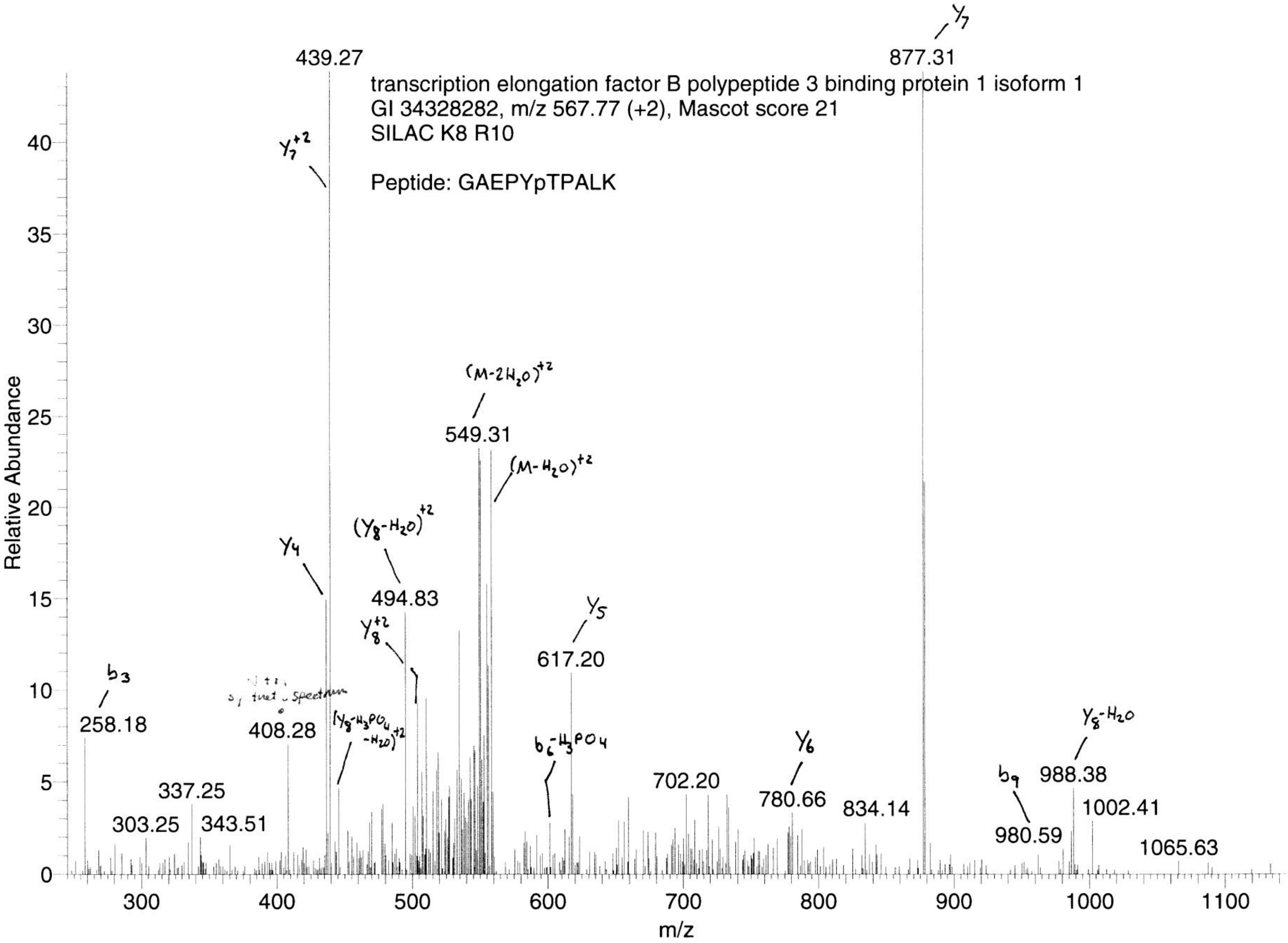
TPR domain, ankyrin-repeat and coiled-coil-containing
GI 57164407, m/z 897.42 (+2), Mascot score 45
SILAC K6 R6

Peptide: IQVSSQNPPPpSPM_{ox}PGR



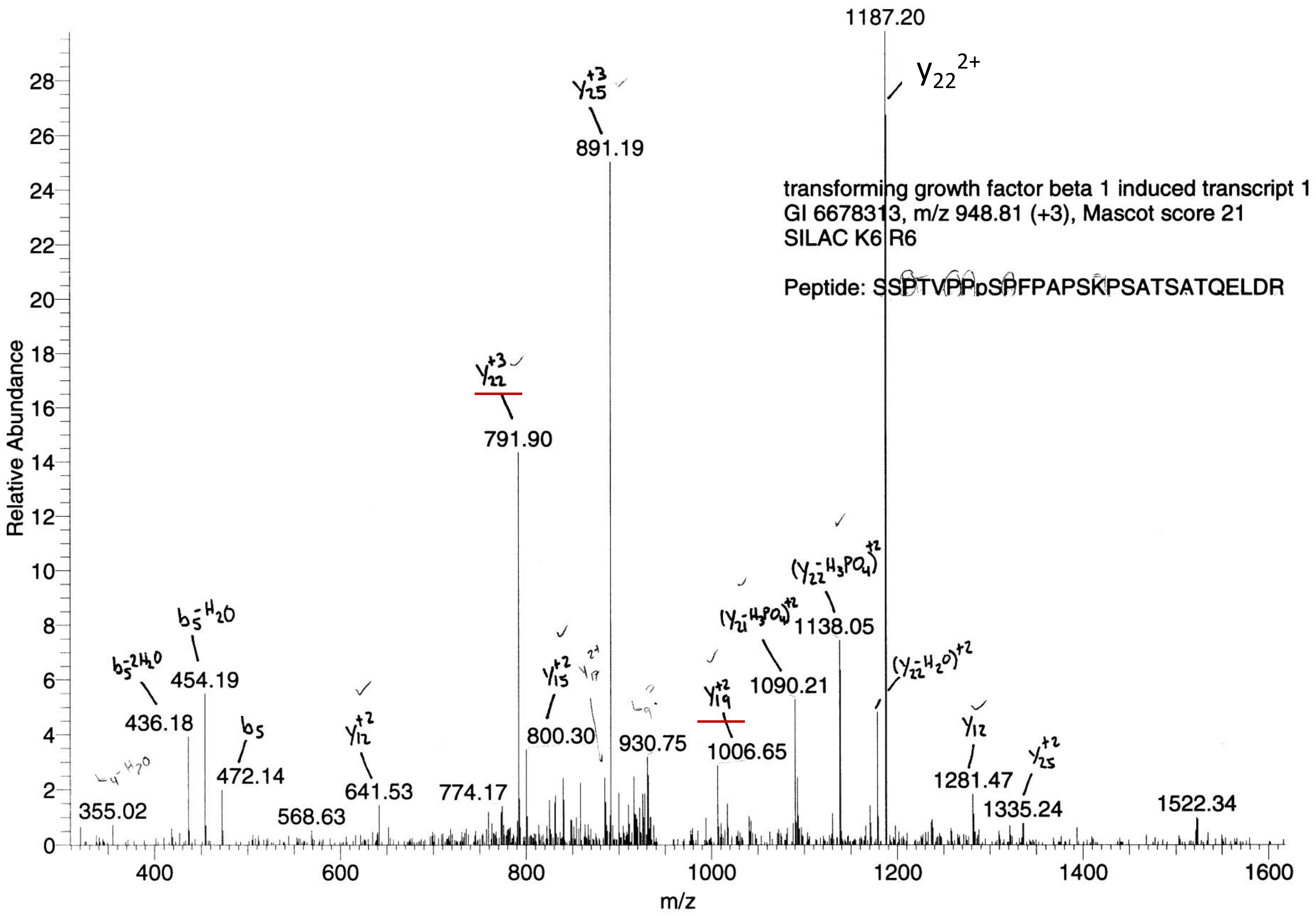
TPX2, microtubule-associated protein homolog
GI 88900517, m/z 614.80 (+2), Mascot score 32
SILAC K8 R10

Peptide: DPQpTPILQTK



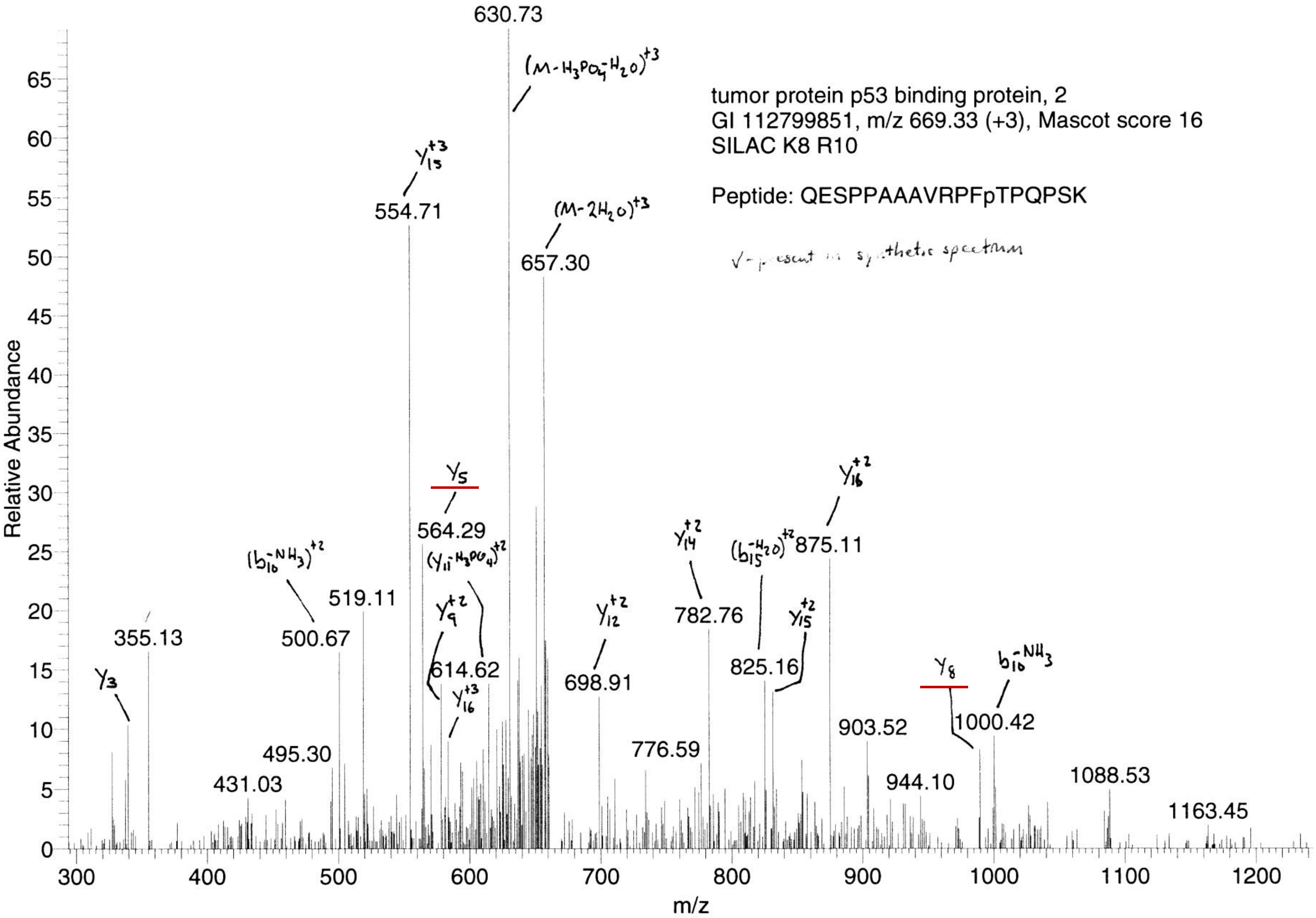
transcription elongation factor B polypeptide 3 binding protein 1 isoform 1
GI 34328282, m/z 567.77 (+2), Mascot score 21
SILAC K8 R10

Peptide: GAEPYpTPALK



transforming growth factor beta 1 induced transcript 1
GI 6678313, m/z 948.81 (+3), Mascot score 21
SILAC K6 R6

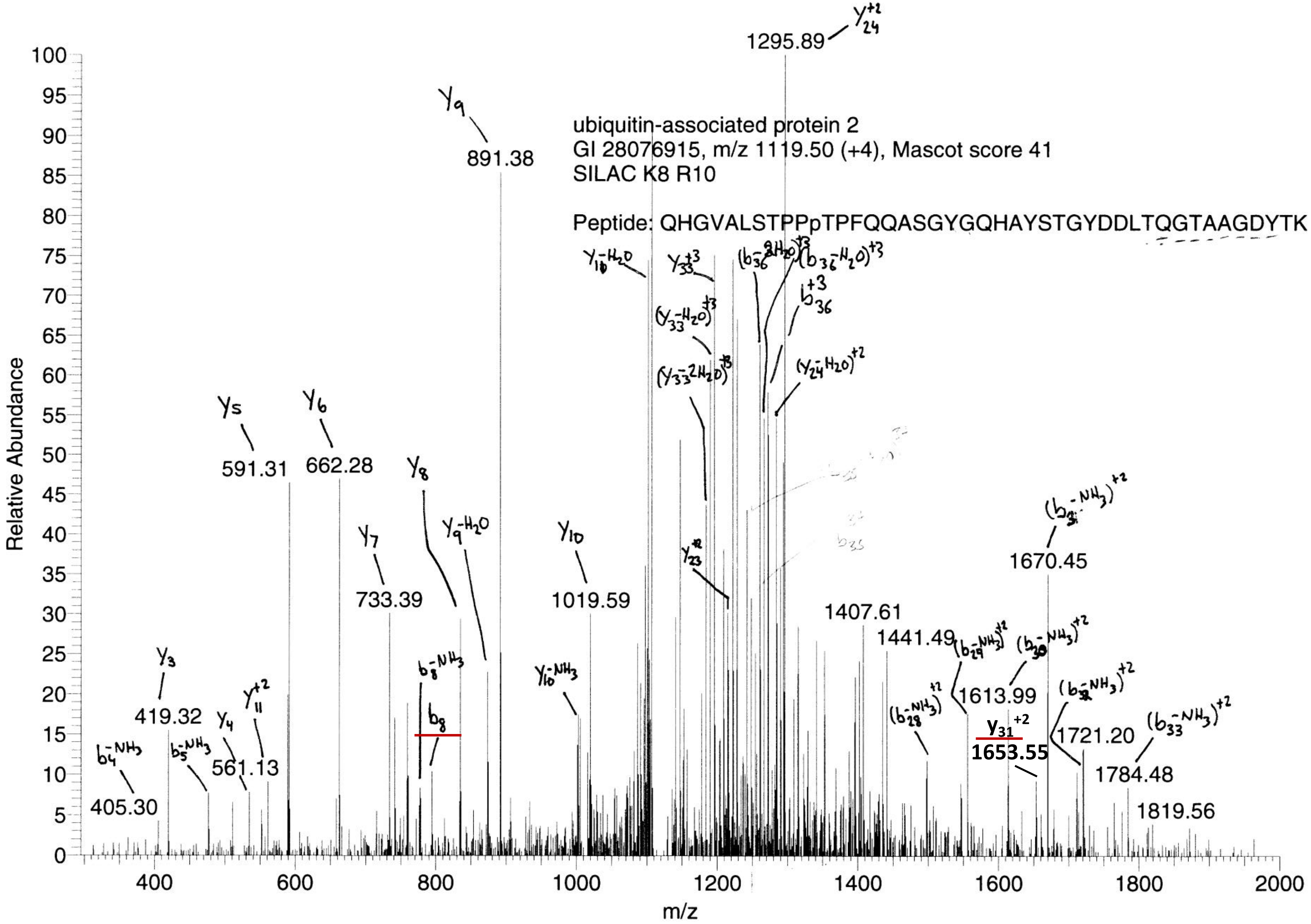
Peptide: SSPTVPPpSPFPAPSKPSATSATQELDR

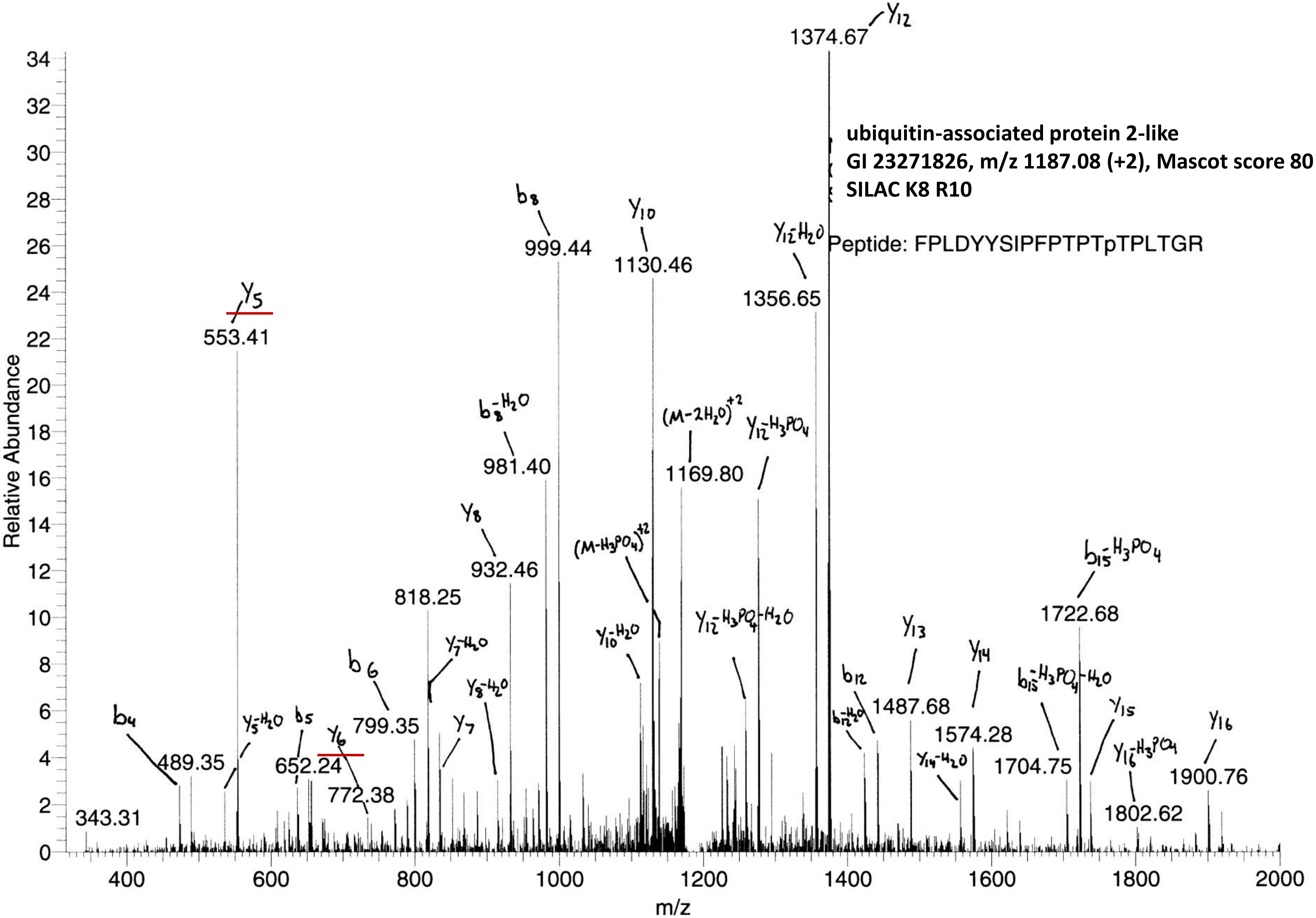


tumor protein p53 binding protein, 2
GI 112799851, m/z 669.33 (+3), Mascot score 16
SILAC K8 R10

Peptide: QESPPAAAVRPFpTPQPSK

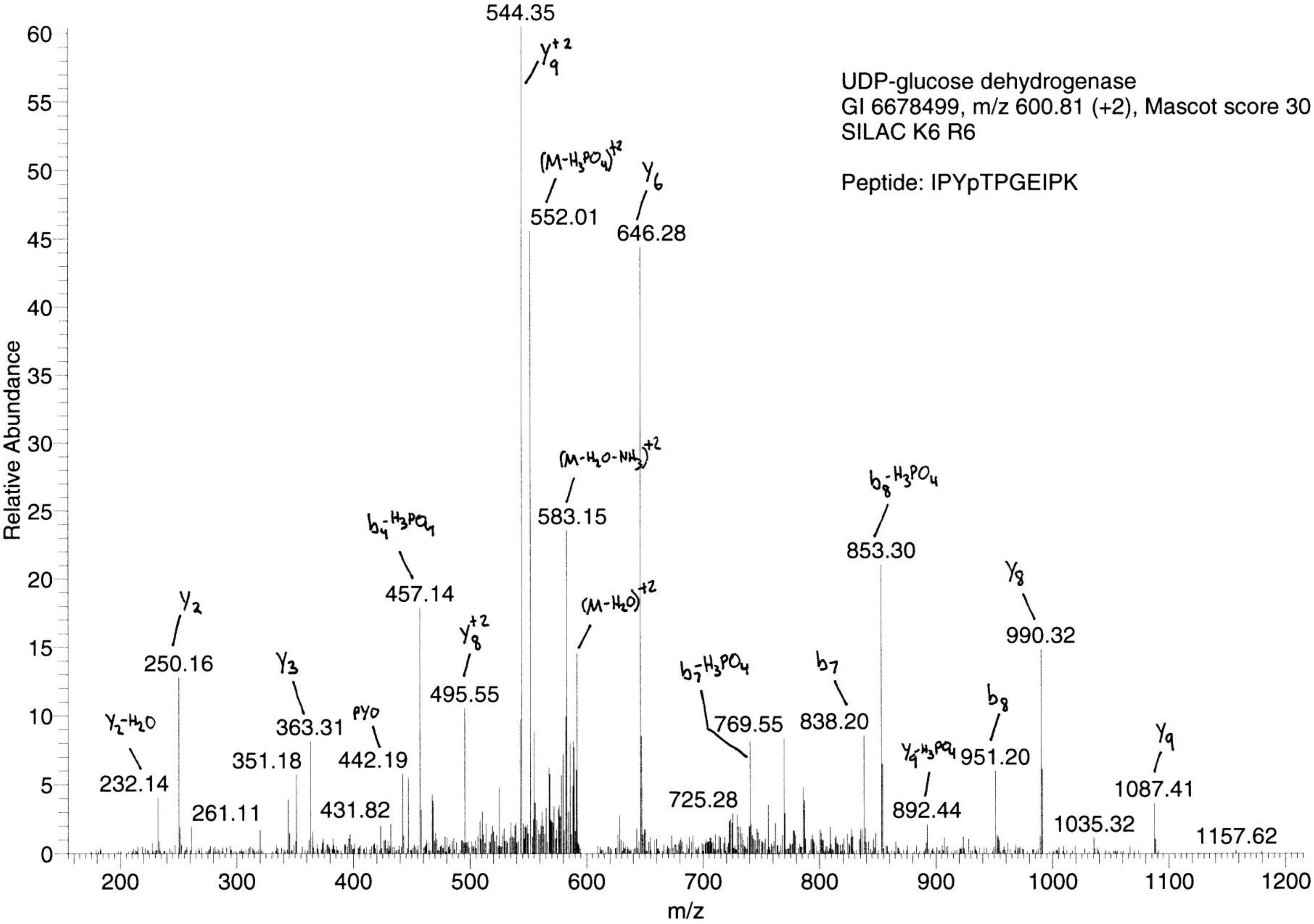
√- present in synthetic spectrum


ubiquitin-associated protein 2
GI 28076915, m/z 1119.50 (+4), Mascot score 41
SILAC K8 R10
Peptide: QHGVALSTPPpTPFQQASGYGQHAYSTGYDDLTQGTAAGDYTK
Relative Abundance
m/z
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
400
600
800
1000
1200
1400
1600
1800
2000
405.30
419.32
561.13
591.31
662.28
733.39
891.38
1019.59
1295.89
1407.61
1441.49
1613.99
1653.55
1670.45
1721.20
1784.48
1819.56
b4-NH3
y3
b5-NH3
y4
y11+2
y5
y6
y7
y8
b8-NH3
b8
y9-H2O
y9
y10-NH3
y10
y10-H2O
y33+3
(y33-H2O)+3
(y33-2H2O)+3
y23+2
(b36-2H2O)+3
(b36-H2O)+3
b36+3
(y24-H2O)+2
y24+2
b35
(b28-NH3)+2
(b29-NH3)+2
(b30-NH3)+2
y31+2
(b31-NH3)+2
(b32-NH3)+2
(b33-NH3)+2



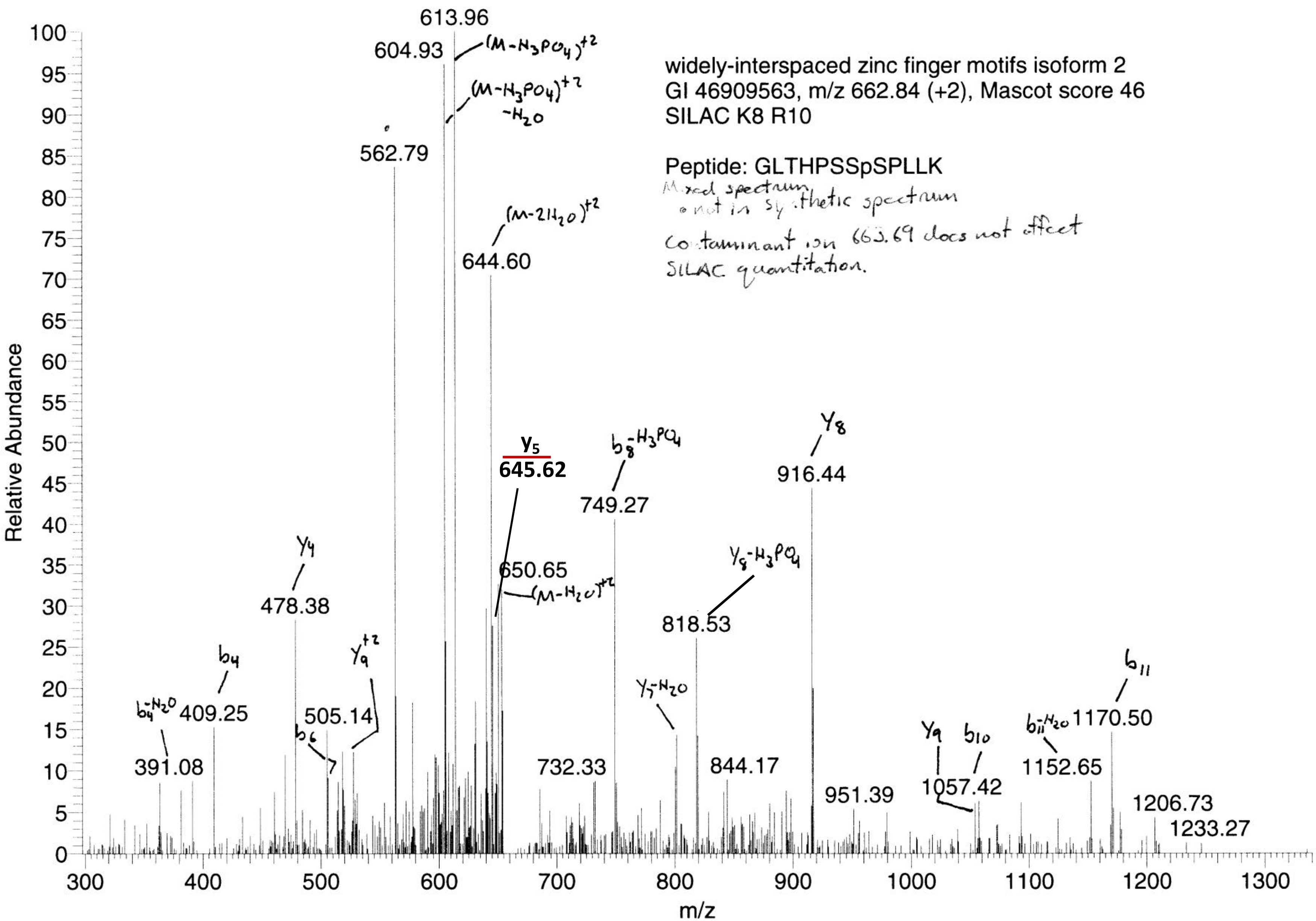
ubiquitin-associated protein 2-like
GI 23271826, m/z 1187.08 (+2), Mascot score 80
SILAC K8 R10

Peptide: FPLDYYSIPFPTPTpTPLTGR



UDP-glucose dehydrogenase
GI 6678499, m/z 600.81 (+2), Mascot score 30
SILAC K6 R6

Peptide: IPYpTPGEIPK



widely-interspaced zinc finger motifs isoform 2
GI 46909563, m/z 662.84 (+2), Mascot score 46
SILAC K8 R10

Peptide: GLTHPSSpSPLLK

Mixed spectrum
• not in synthetic spectrum

Contaminant ion 663.69 does not affect SILAC quantitation.