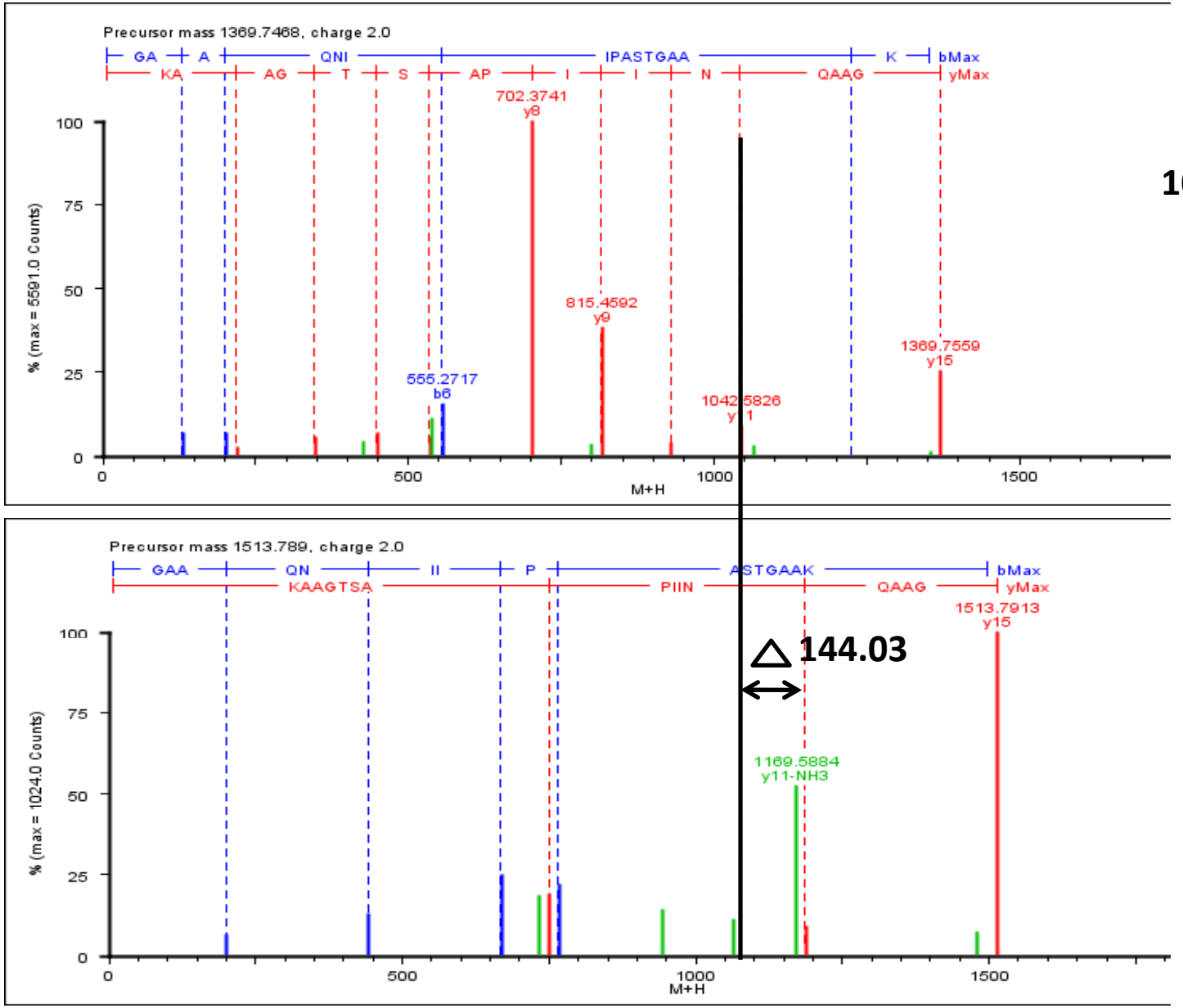
Supplemental Fig. S1: Manual annotation of AGE and ubiquitin modified peptides in the mass spectras of identified PRPs

Modifications and their corresponding ΔM listed as below:

1. Carboxy methyl lysine (CML) : +58.0055 Da
2. Carboxyethyllysine (CEL) : +72.0211 Da
3. Pyrraline (Pyr) : +108.0211 Da
4. 1-alkyl-2-formyl-3,4-glycosyl-pyrrole (AFGP) : +270.074 Da
5. Glycation (Gly): +162.02 Da
6. Imidazolone-A (ImiA): 144.03 Da
7. Methyl glyoxal lysine dimer (MOLD): +49.0078 Da
8. Crossline: +252.11 Da
9. Pentosidine (Pento): +58.03 Da
10. Ubiquitin (Ubi): +144.02 Da

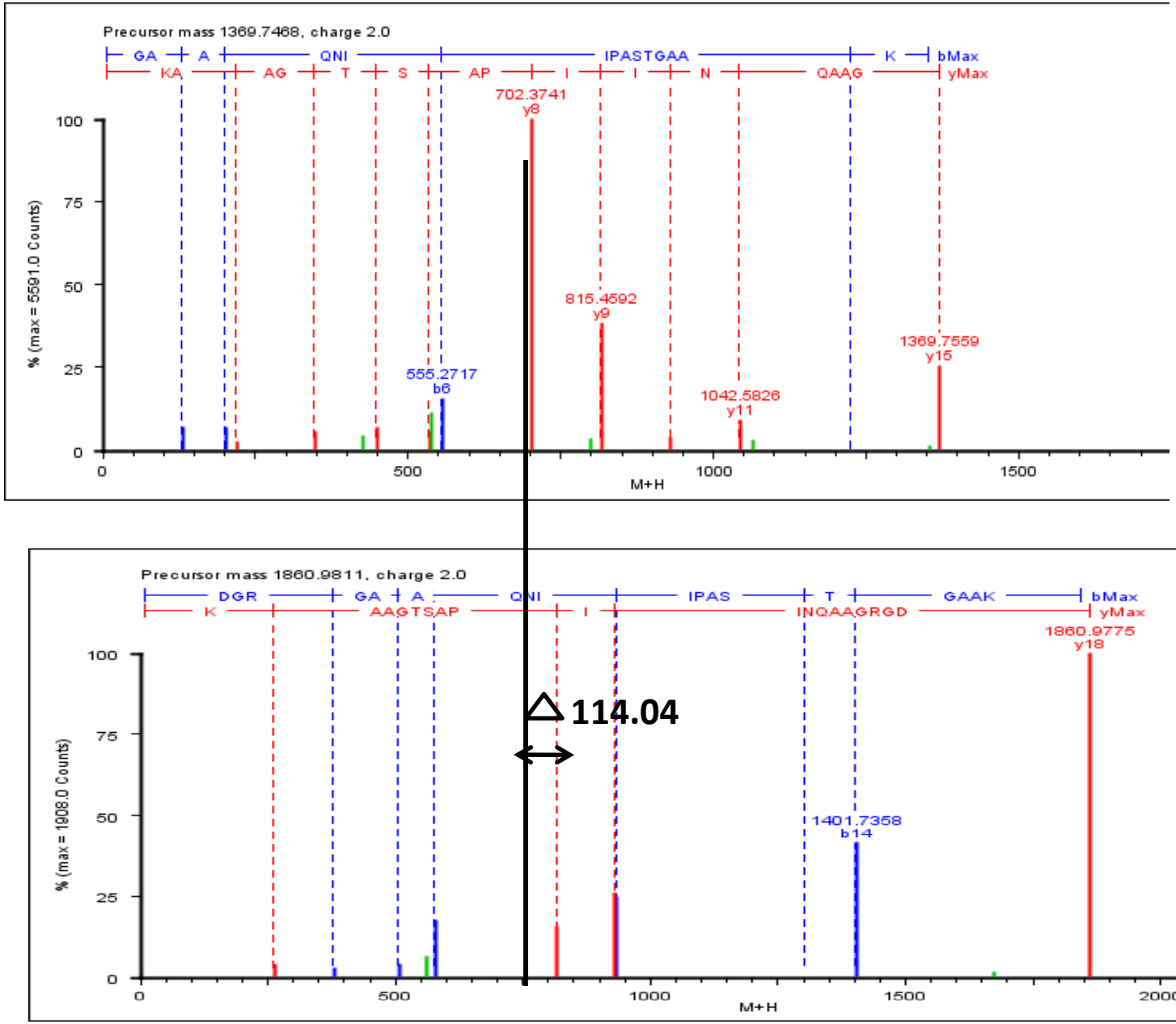
GAPDH



1042.5826

1186.6035

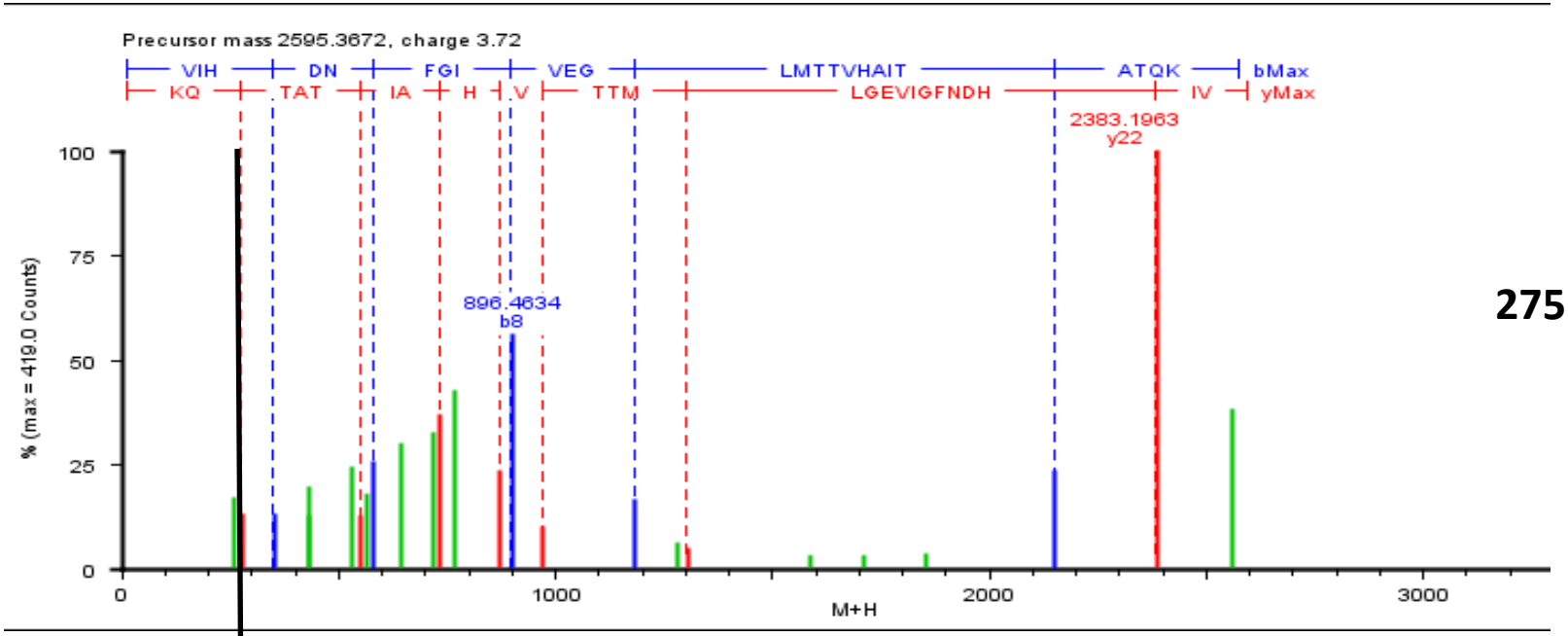
199-213 GAAQNIIPASTGAAK(ImiA) : 144.03



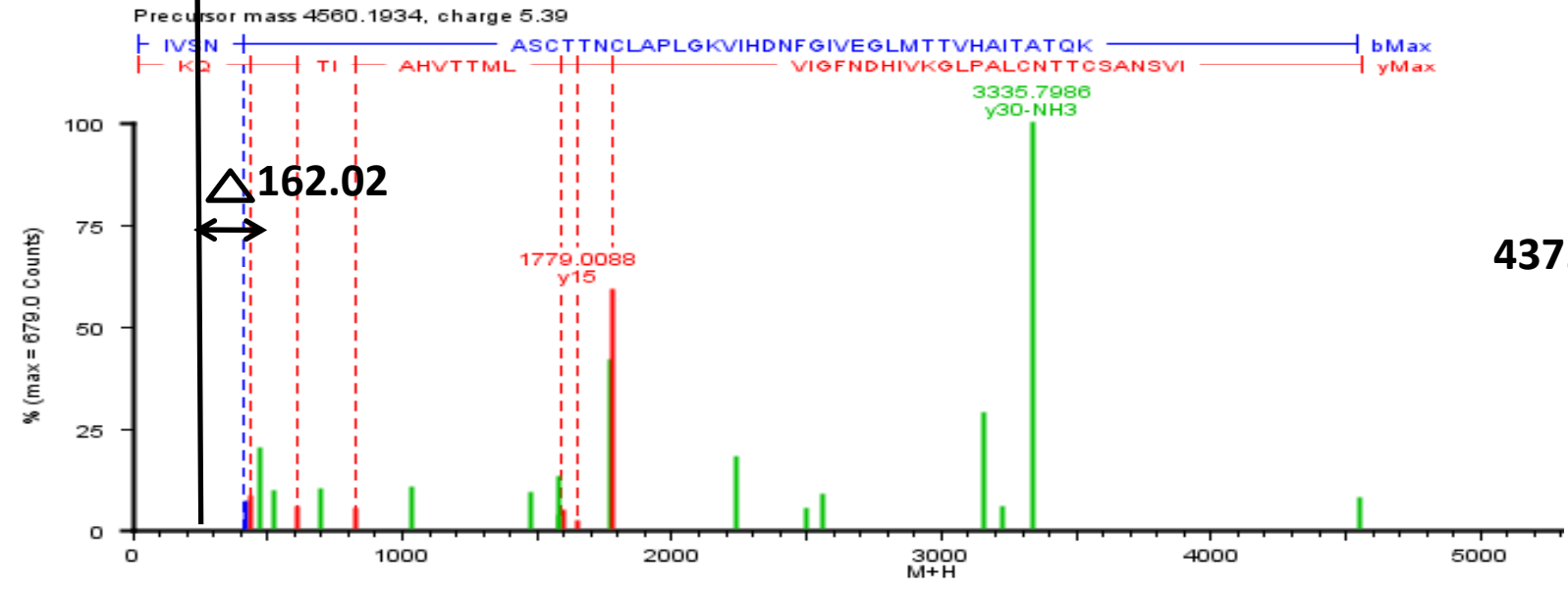
702.3741

816.4489

196-213 (R)DGRGAAQNIIPASTGAAK(Ubi)(A)

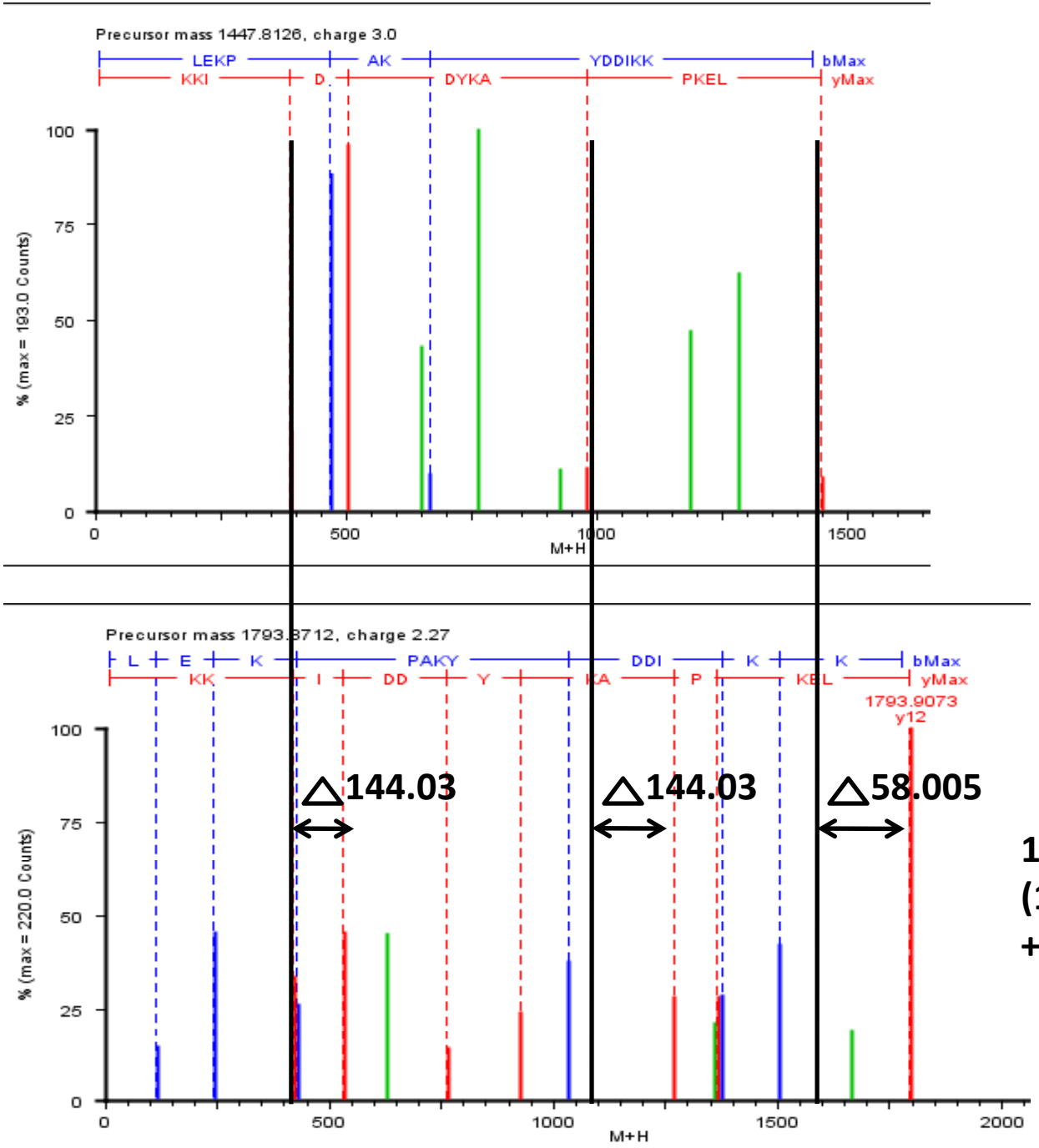


275.1764



437.1999

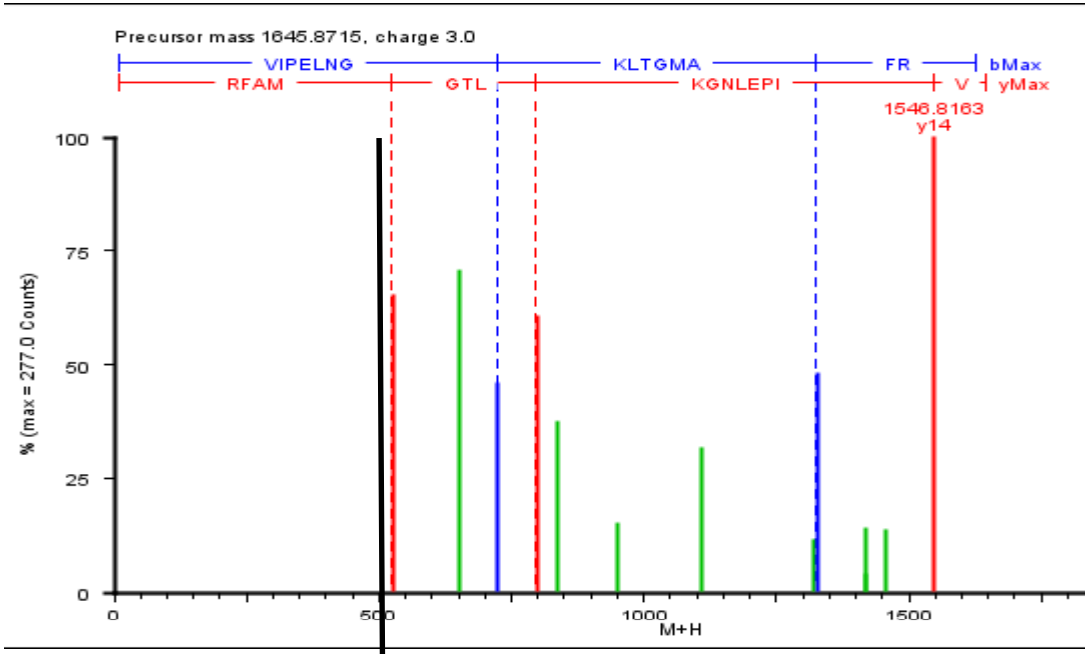
144-184 **IVSNASCTTNCLAPLGKVIHDNFGIVEGLMTTVHAITATQK(Gly) : 162.02**



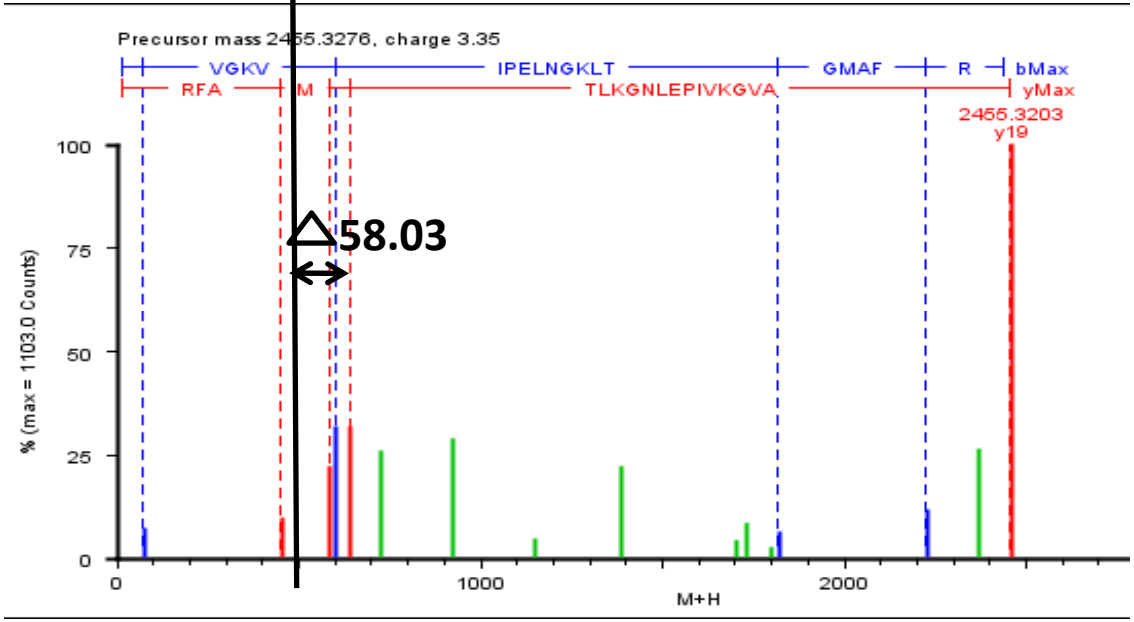
1447.8386

1793.9073: (1447.8386+144.03 +144.03+58.005)

247-258 (R)LEK(CML)PAK(ImiA)YDDIKK(ImiA)(V)

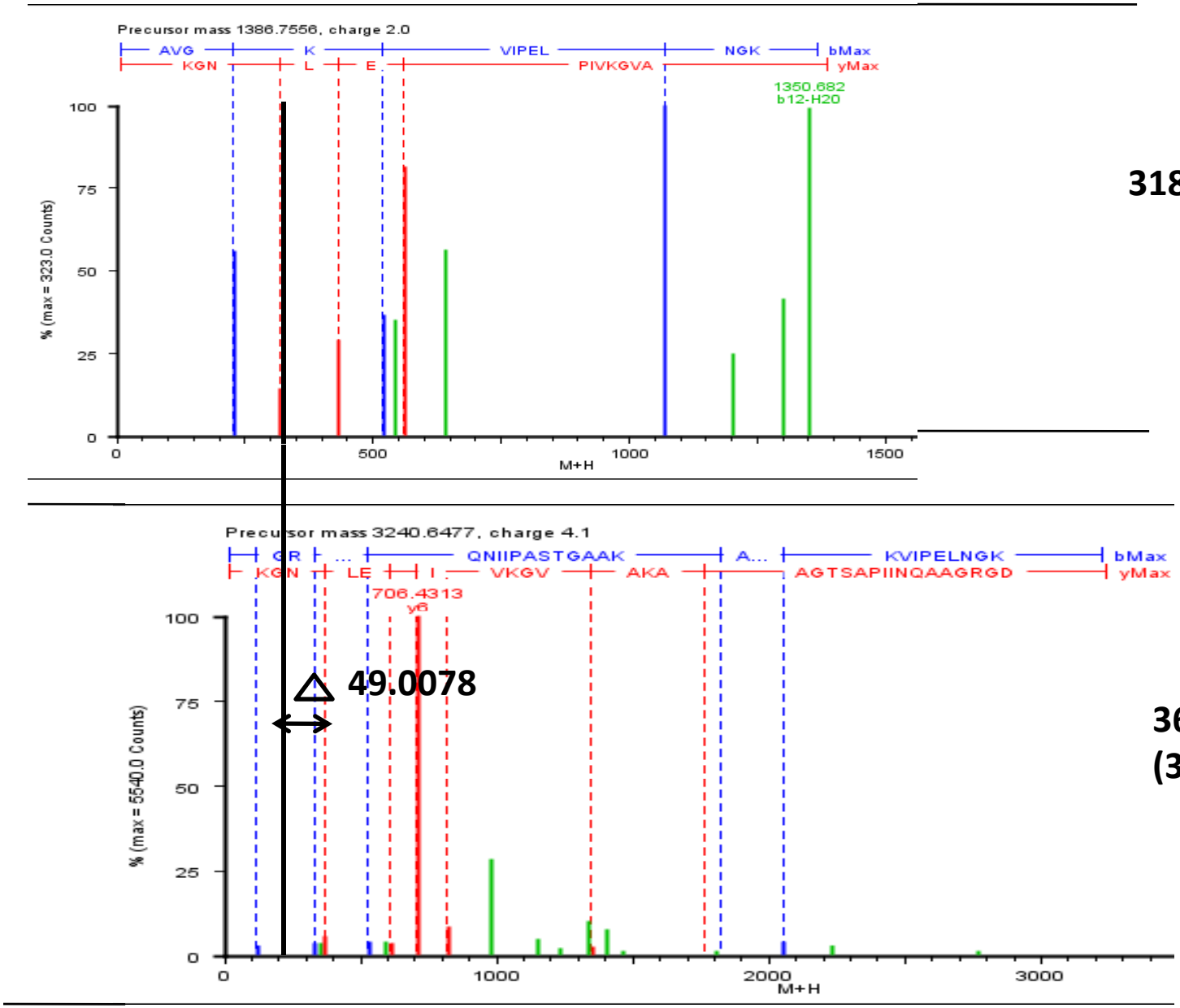


524.3024

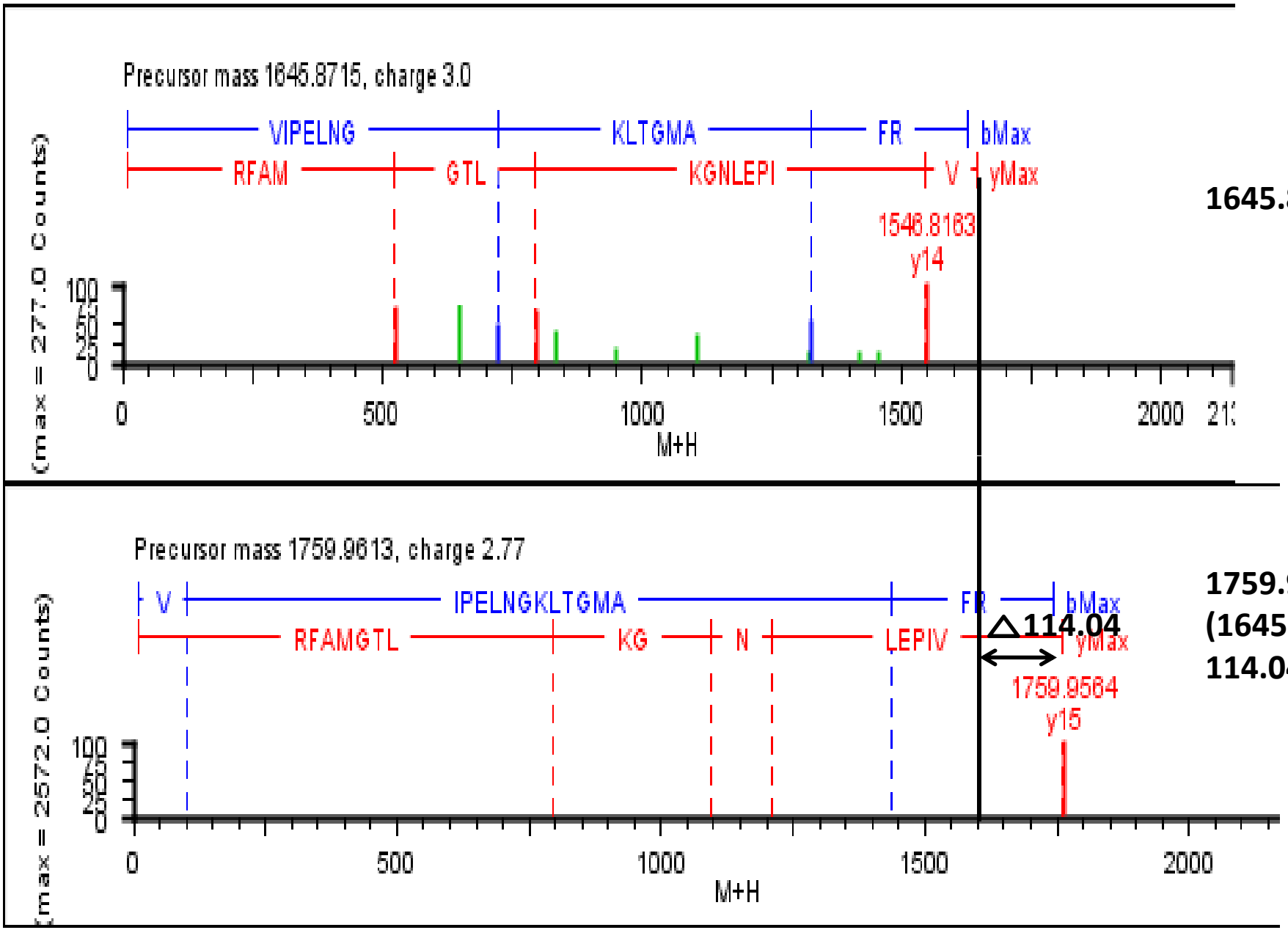


582.2783:
(524.3024+ 58.03)

214-232 ___(K)AVGKVIPELNGKLTGMAFR(Pento)(V)



(R)DGRGAAQNIIPASTGAAKAVGKVIPELNGK(MOLD)(L)

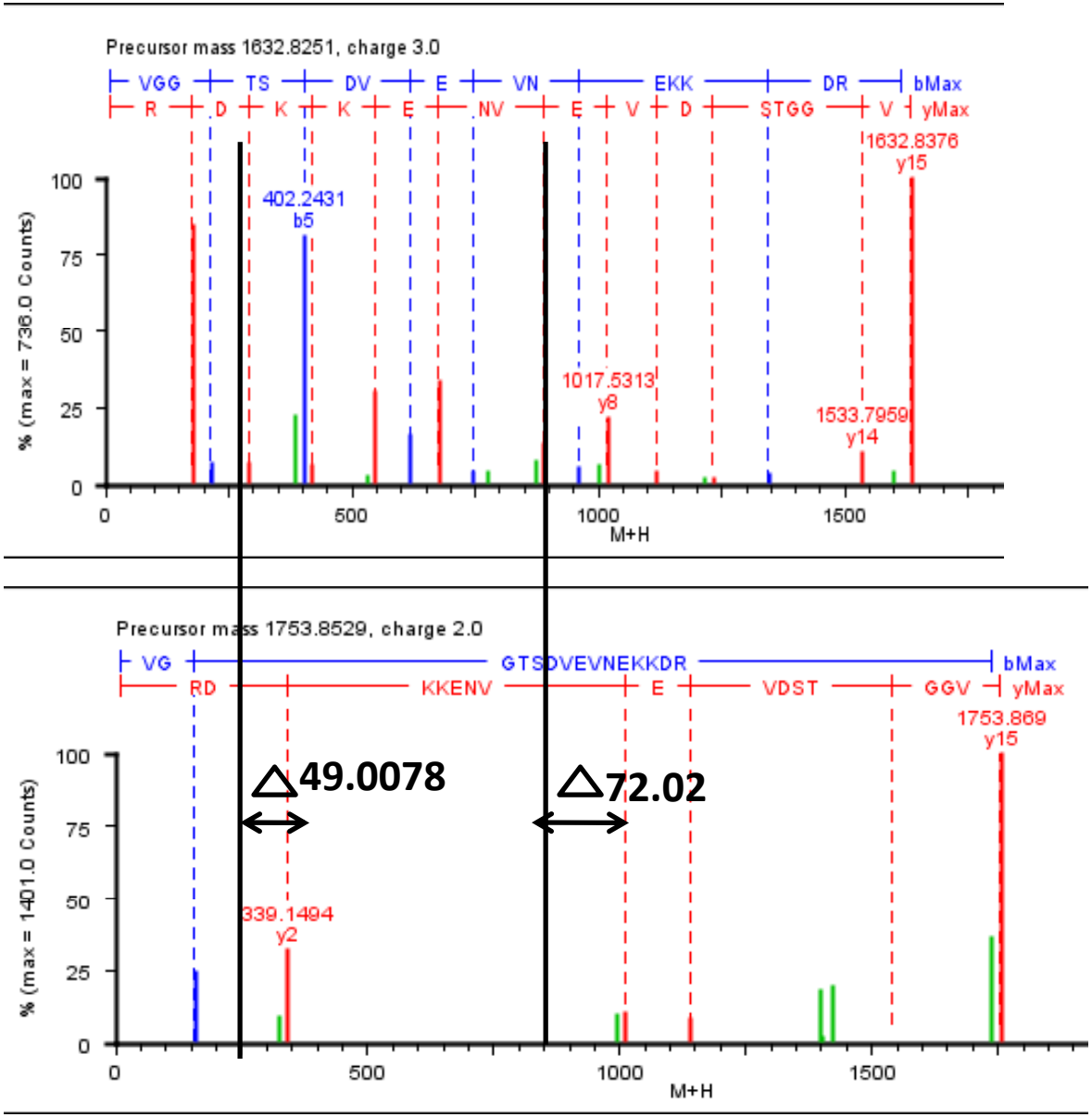


1645.8715

1759.9613: (1645.87+ 114.04)

218-232 (K)VIPELNGK(Ubi)LTGMAFR(V)

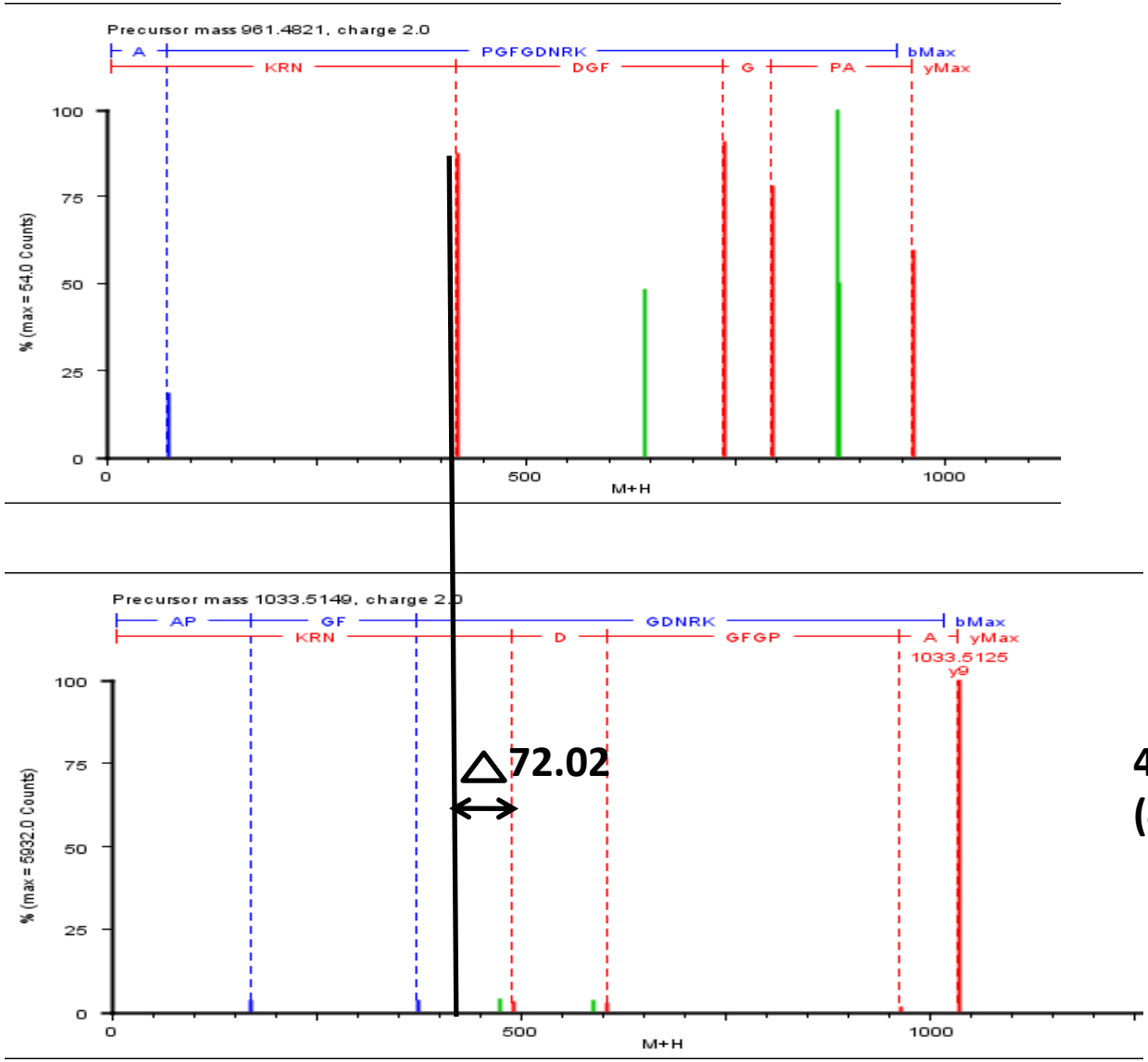
HSP60



888.4822

1009.5252:
(888.48+49.00+72.02)

406-420 (K)VGGTSDVEVNEK(CEL)KDR(MOLD)(V)

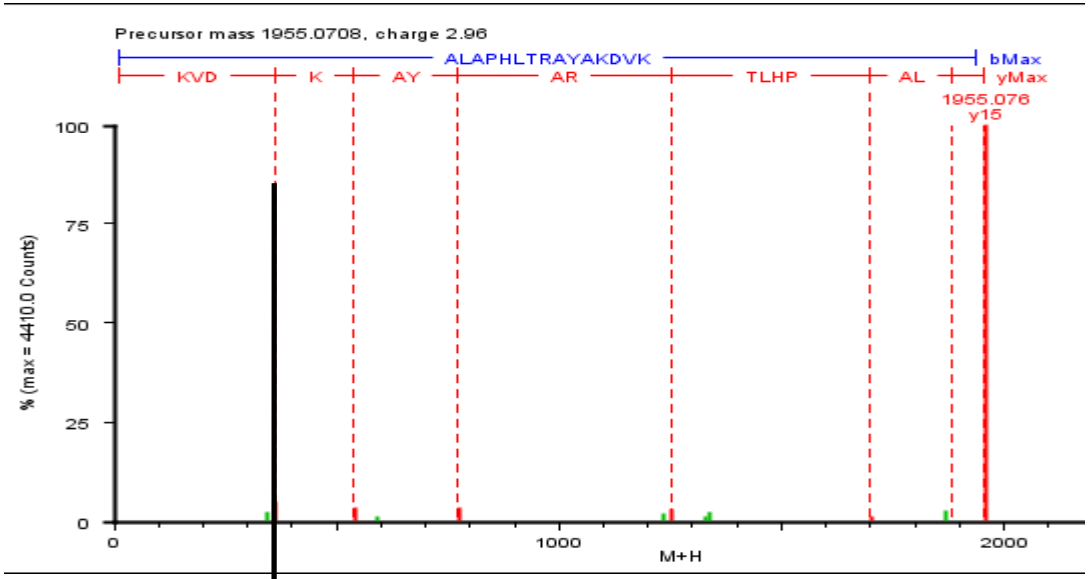


417.2319

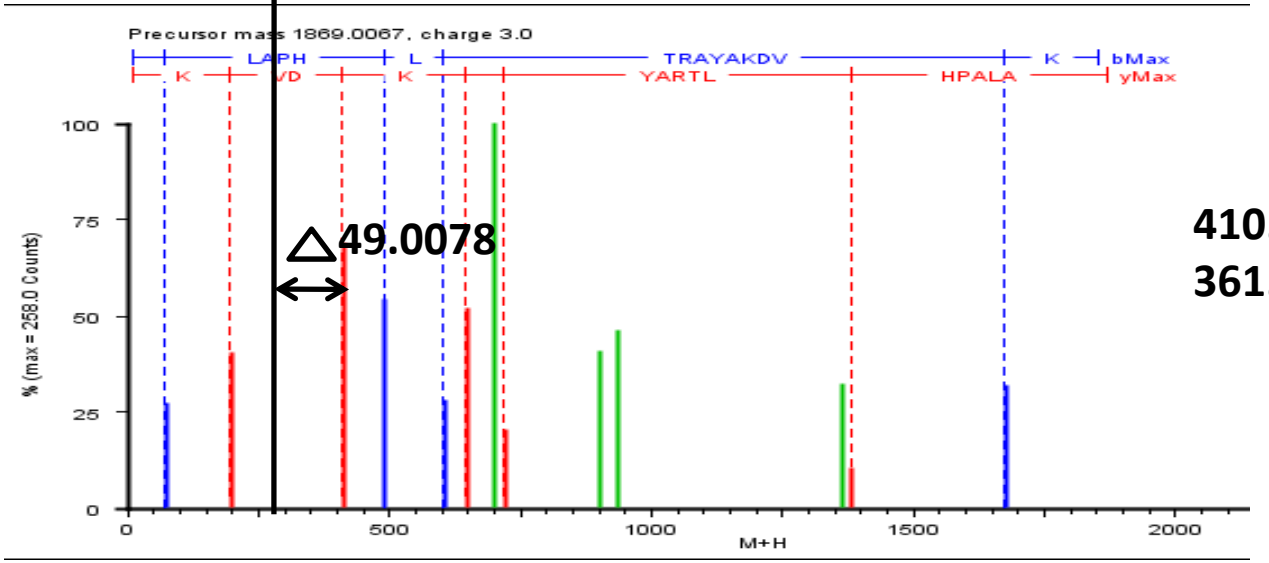
489.2734:
(417.23+72.02)

302-310

(K)APGFGDNRK(CEL)(N)



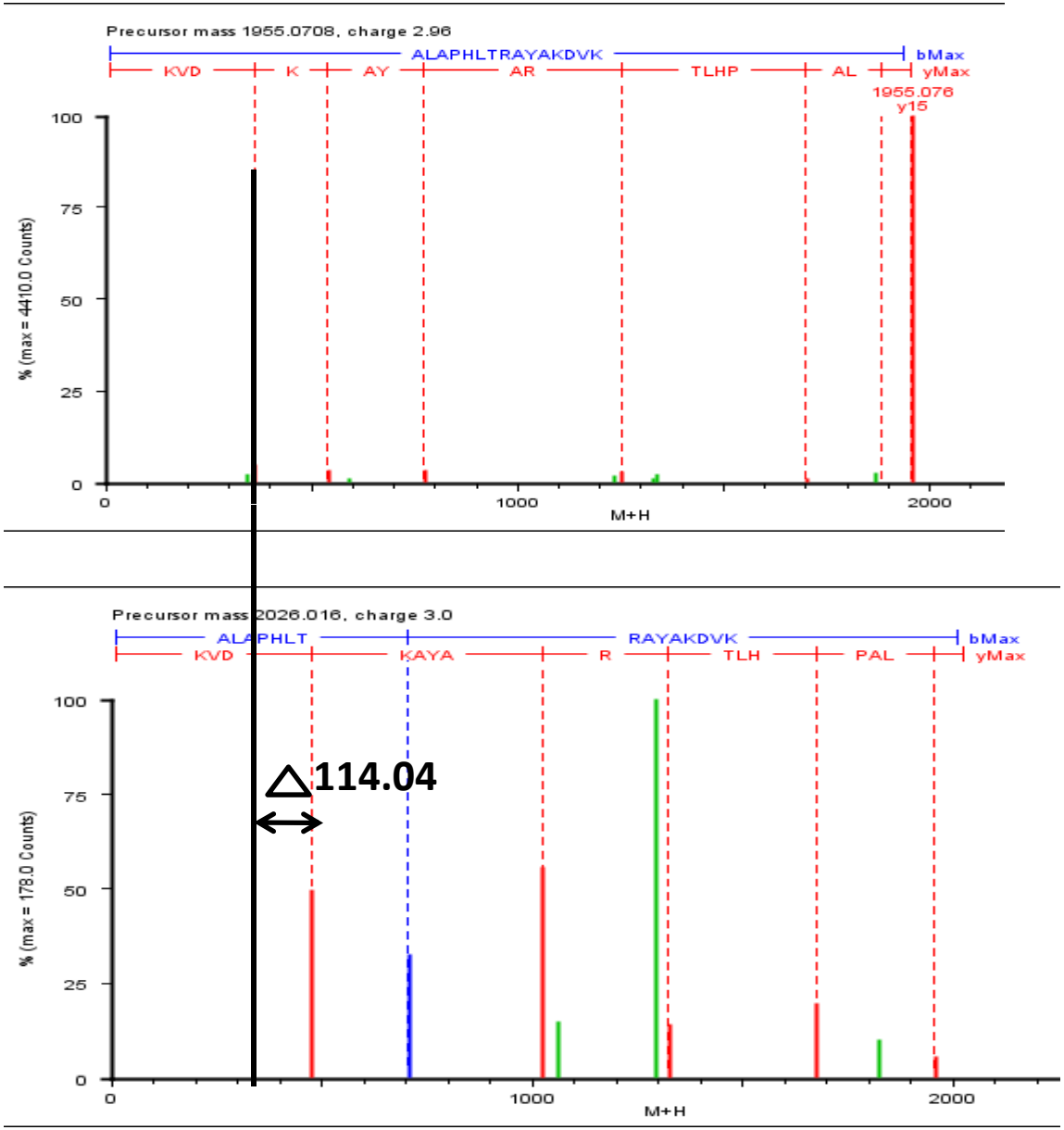
361.2075



410.2341:
361.20+ 49.00

17-31

(R)ALAPHLTRAYAKDVK(MOLD)(F)

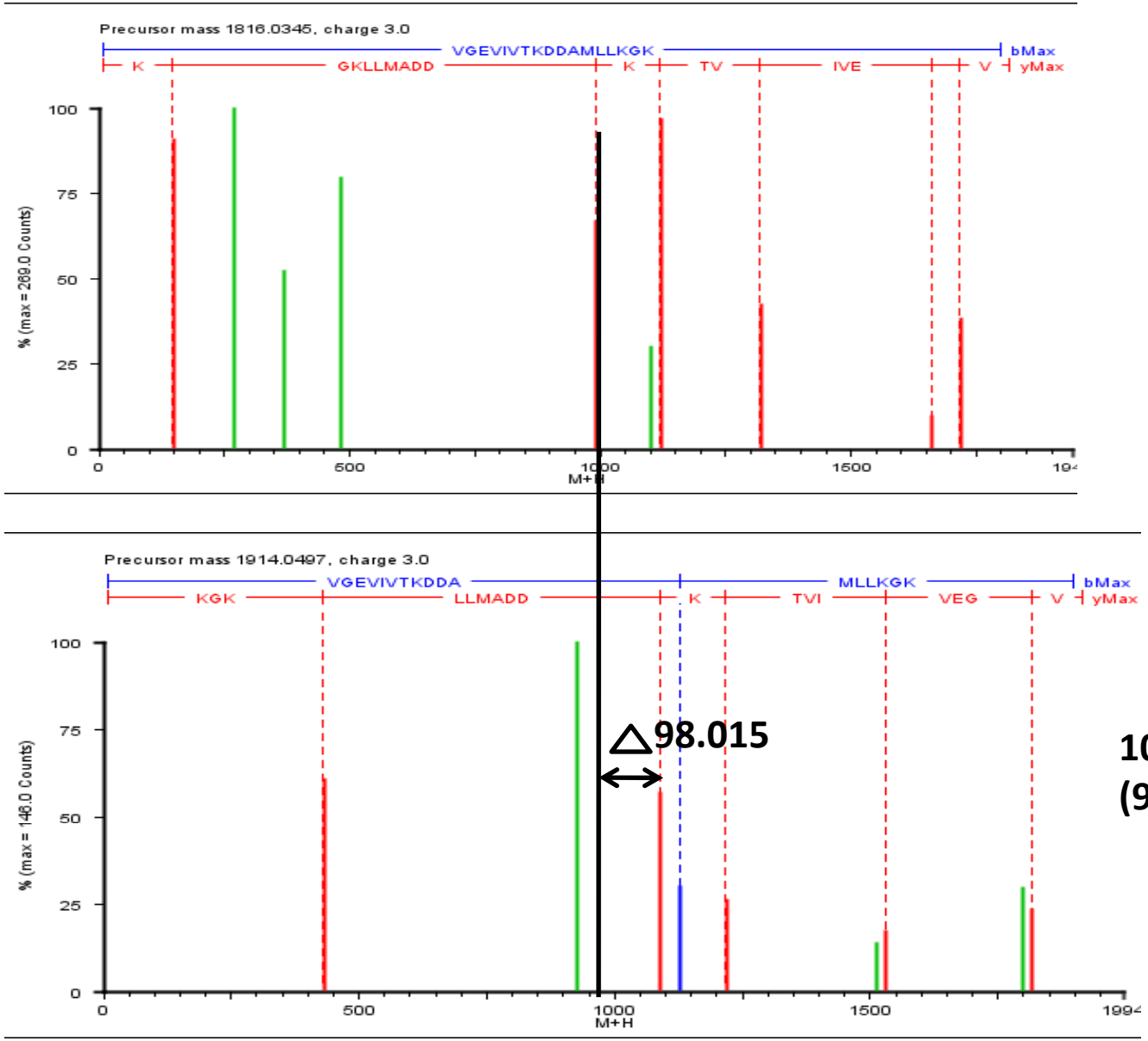


361.2075

475.2091:
(361.20+ 114.04)

17-31

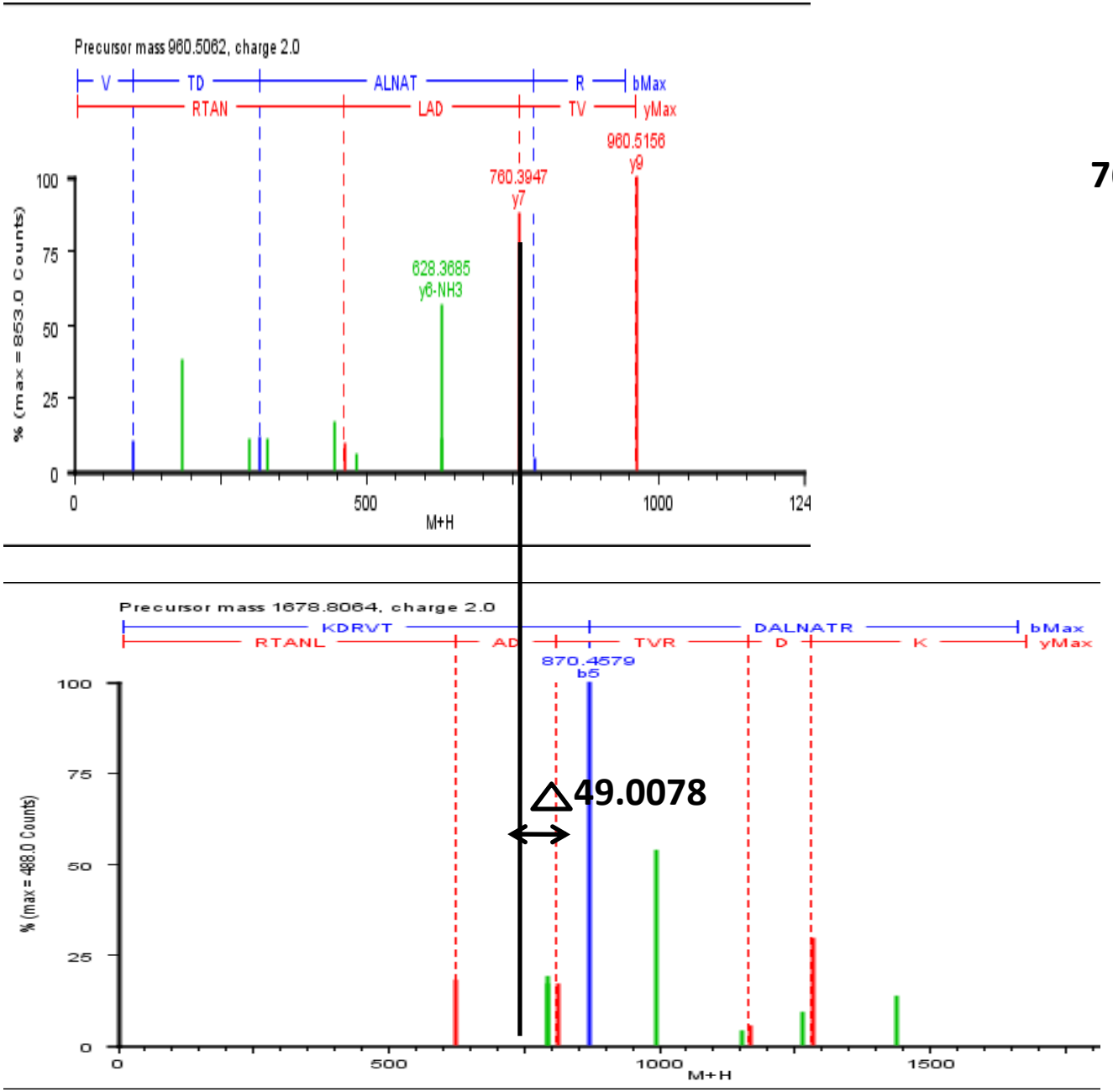
(R)ALAPHLTRAYAKDVK(Ubi)(F)



990.5292

1088.5643:
(990.52+49.00+49.0

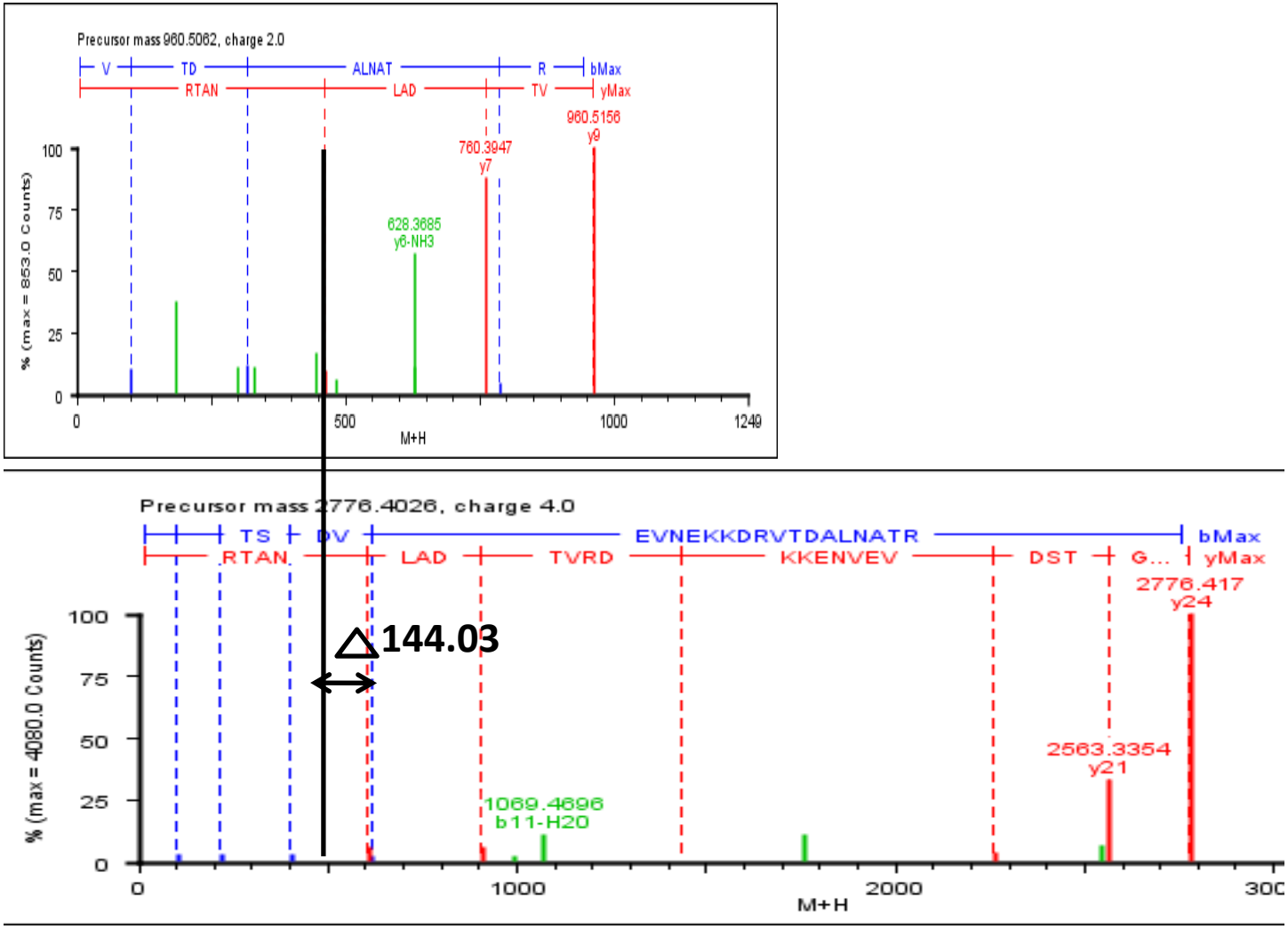
345-361 (K)VGEVIVTKDDAMLLK(MOLD)GK(MOLD)(G)



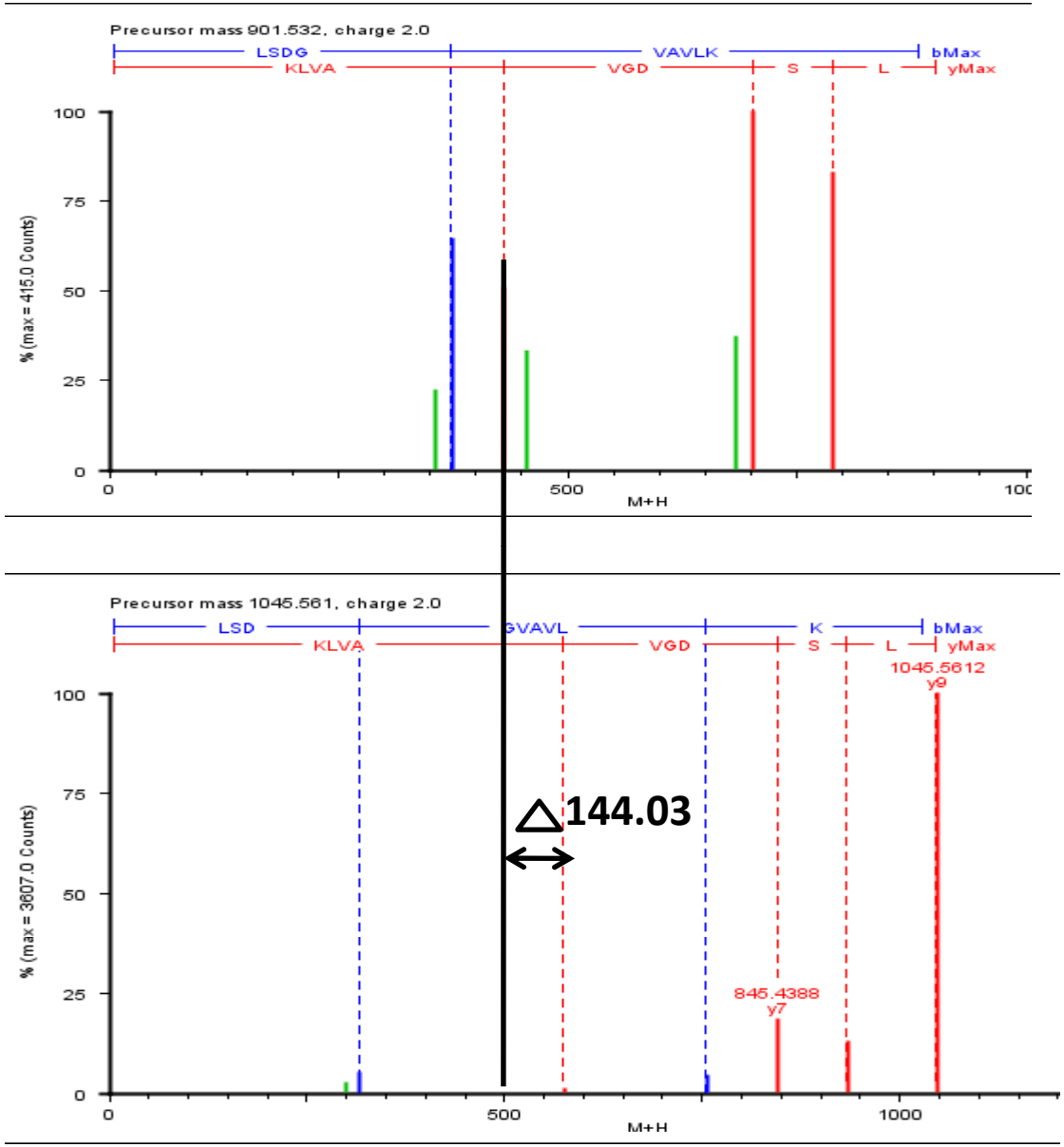
760.3947

809.3331:
(760.39+ 49.00)

- **418-429** (K)KDRVTDALNATR(MOLD)(A)



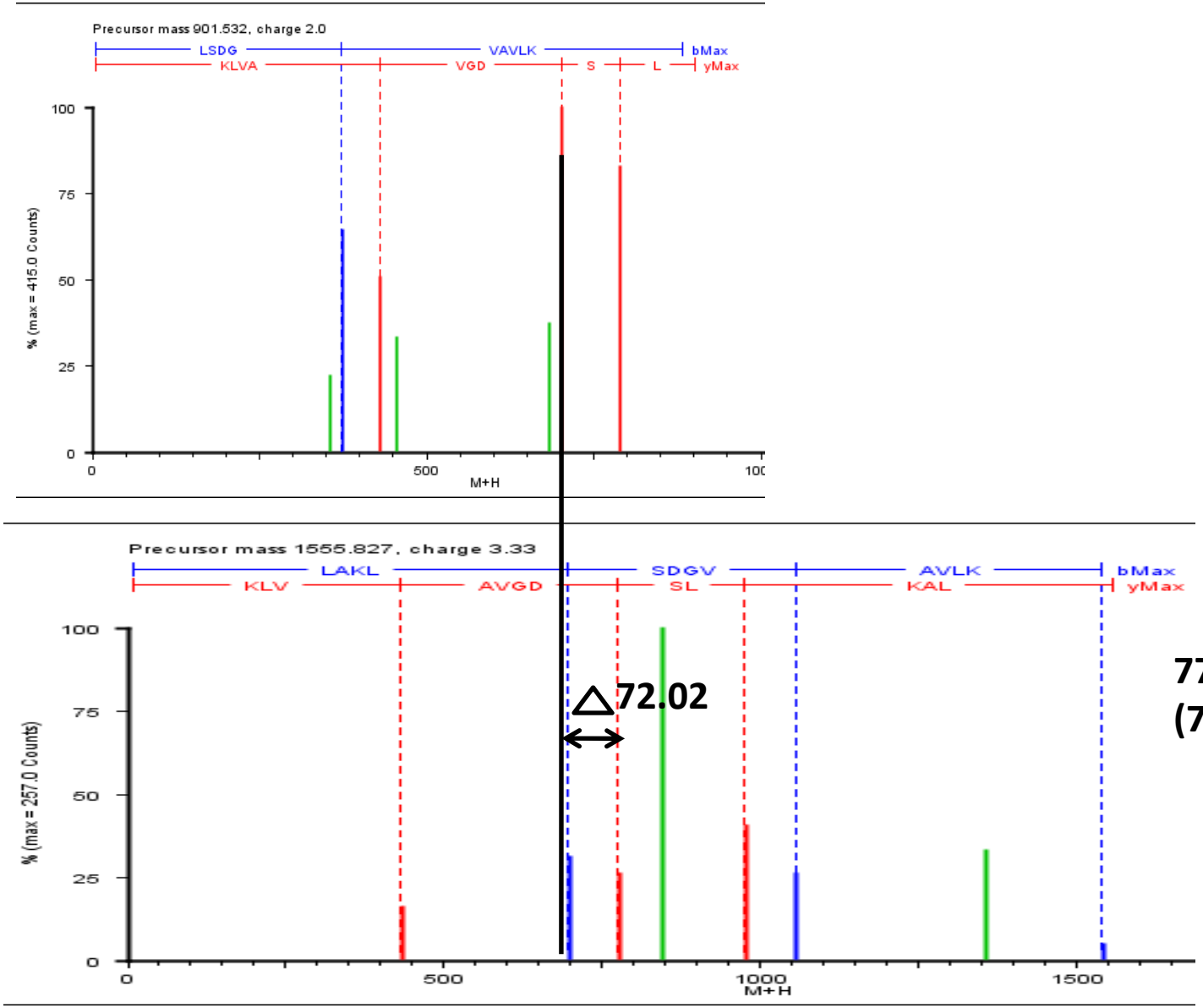
406-429 (K)VGGTSDVEVNEKKDRVTDALNATR(ImiA)(A)



430.3033

574.275:
(430.30+ 144.03)

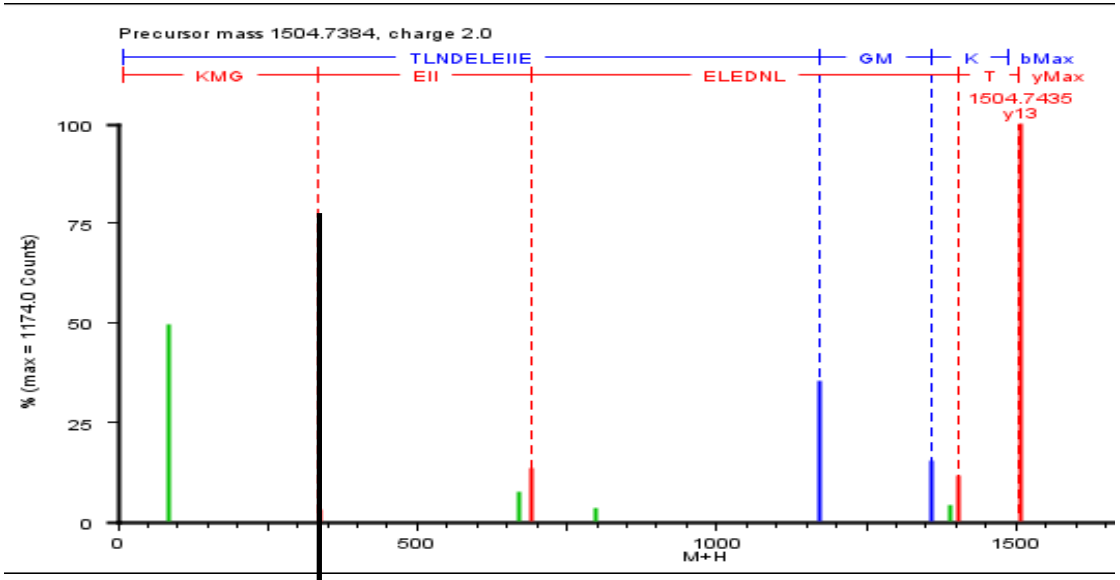
397-405 (K)LSDGVAVLK(ImiA)(V)



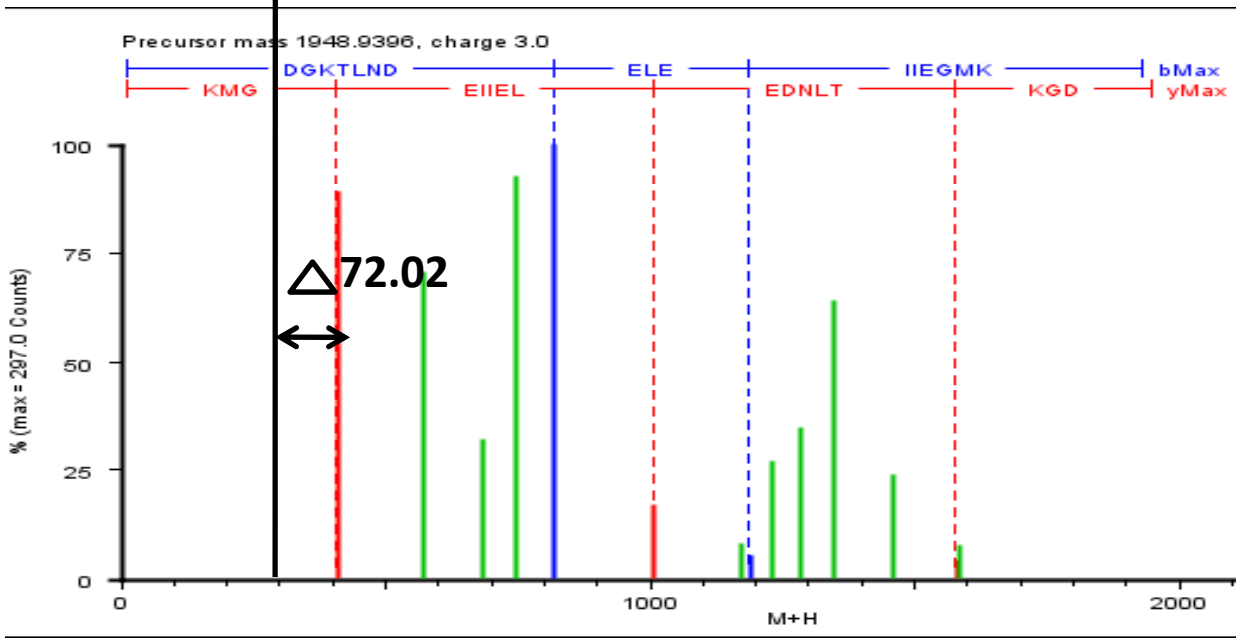
701.3756

773.3756:
(701.37+72.02)

394-405 (R)LAKLSDGVAVLK(CEL)(V)

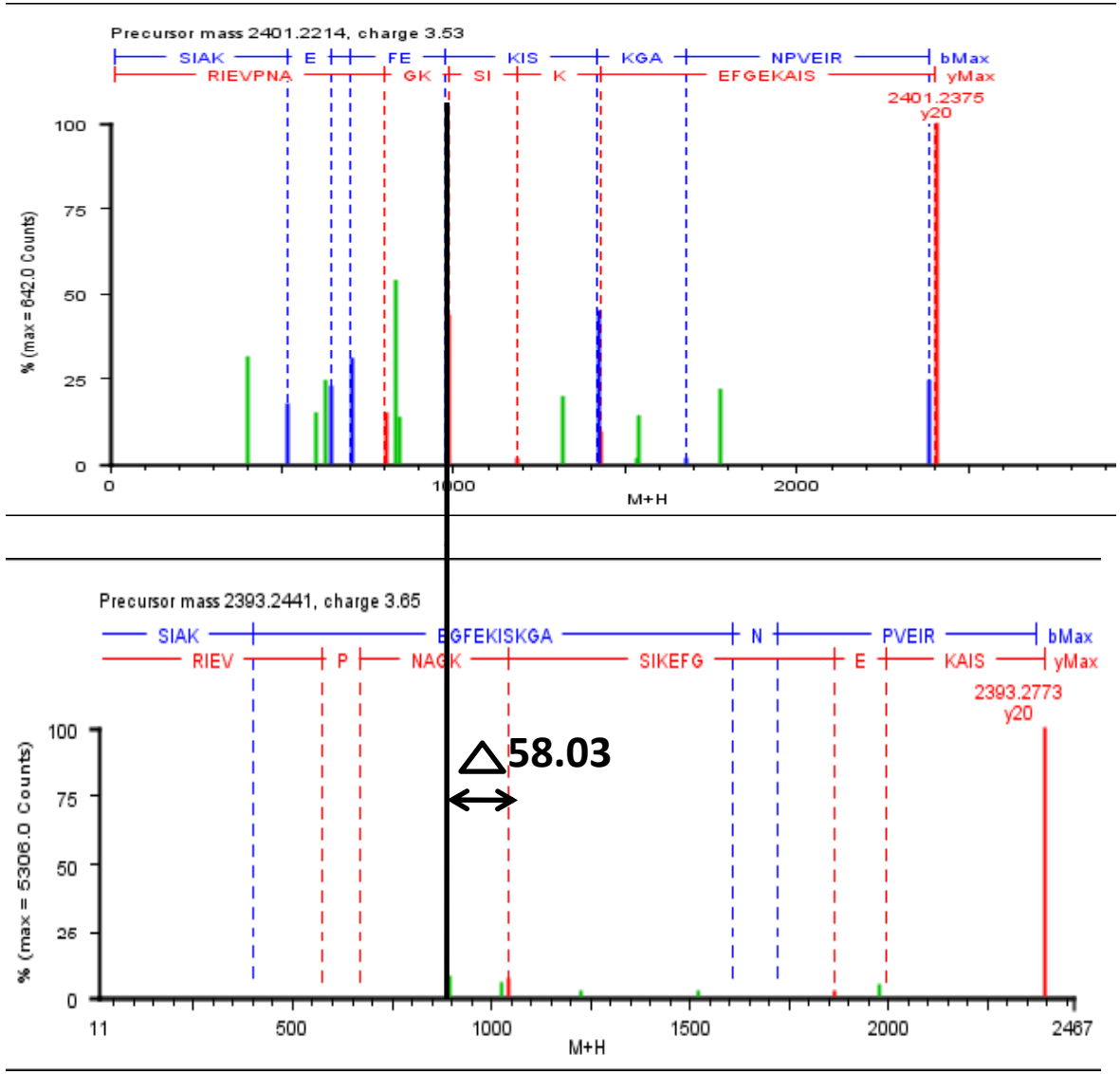


335.1418



407.189:
(335.14+ 72.02)

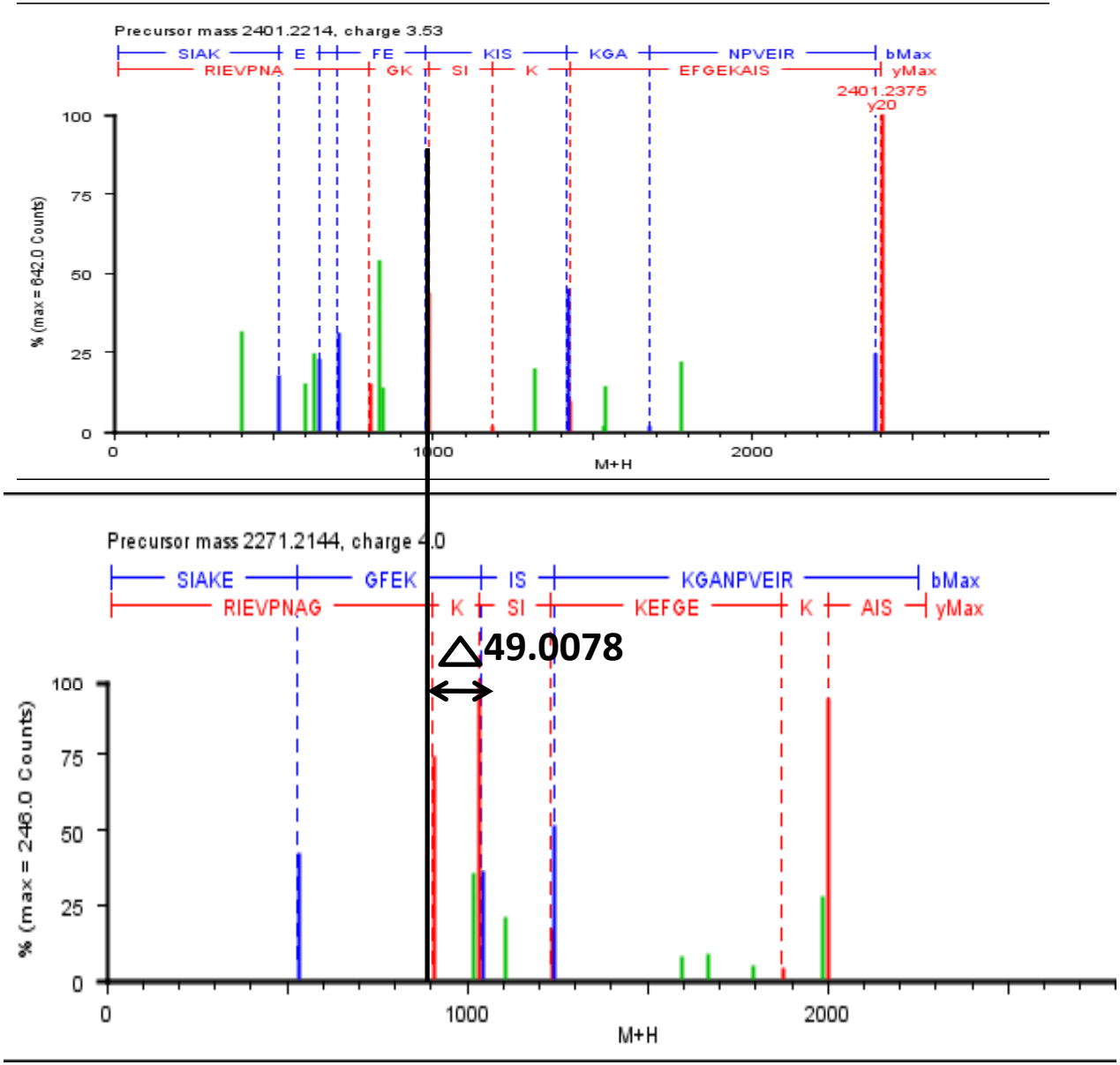
203-218 (K)DGKTLNDELEIIEGMK(CEL)(F)



983.4801

1041.4801

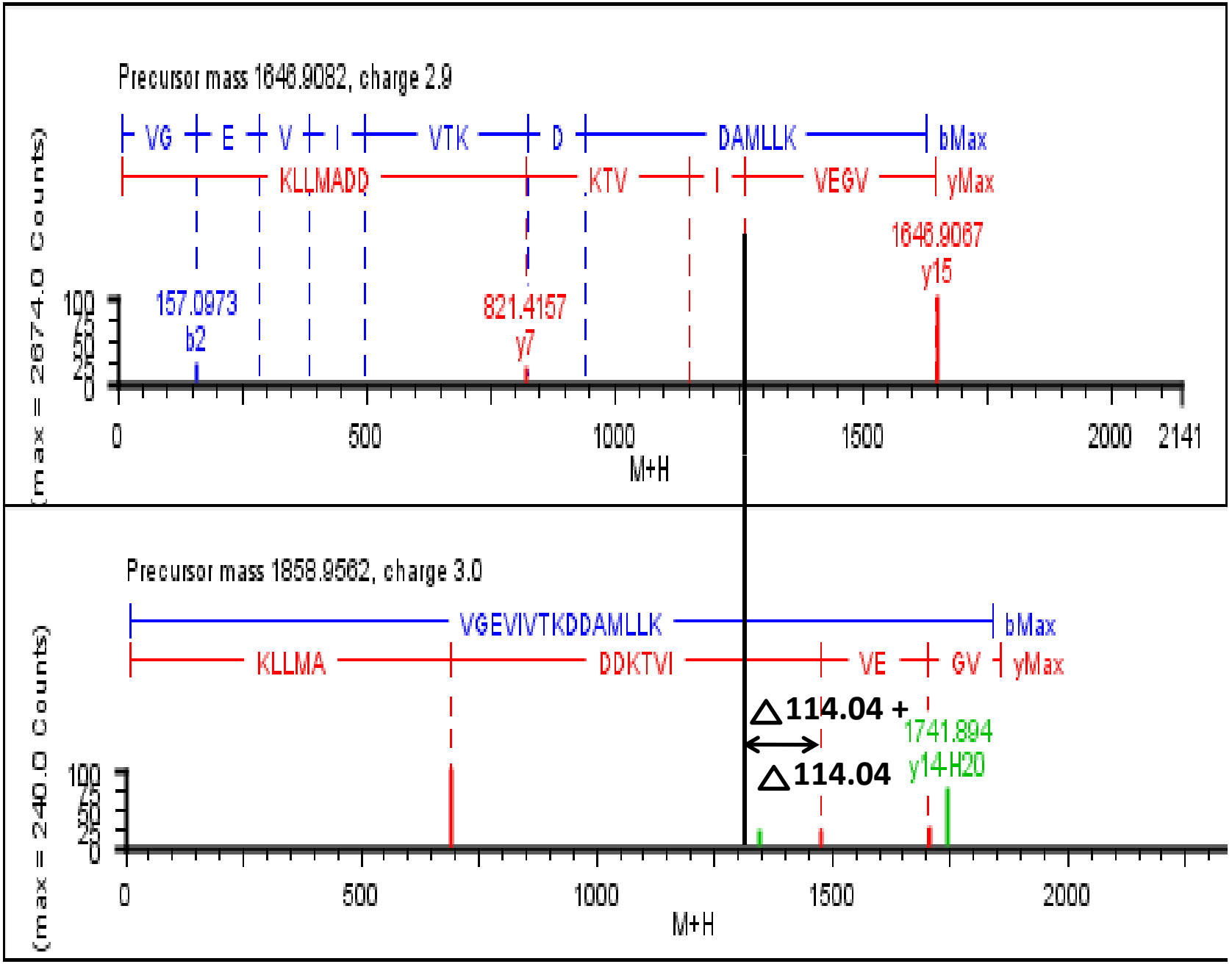
122-141 (R)SIAKEGFEKISKGANPVEIR(Pento)(R)



983.4801

1032.5952

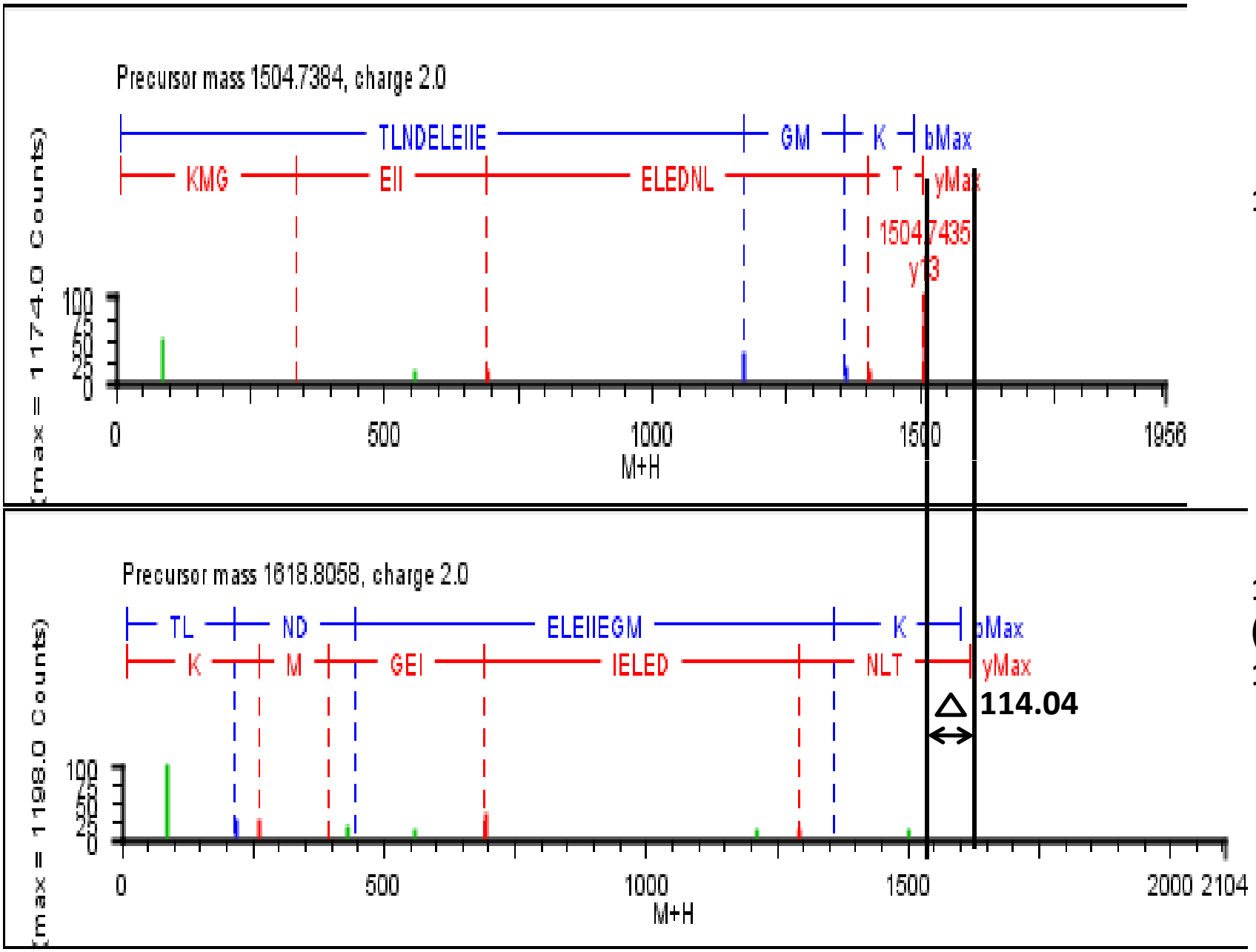
122-141 (R)SIAKEGFEKISKGANPVEIR(MOLD)(R)



1646.9067

1858.9562: (1646.90+ 114.04)

345-359 (K)VGEVIVTK(Ubi)DDAMLLK(Ubi)(G)

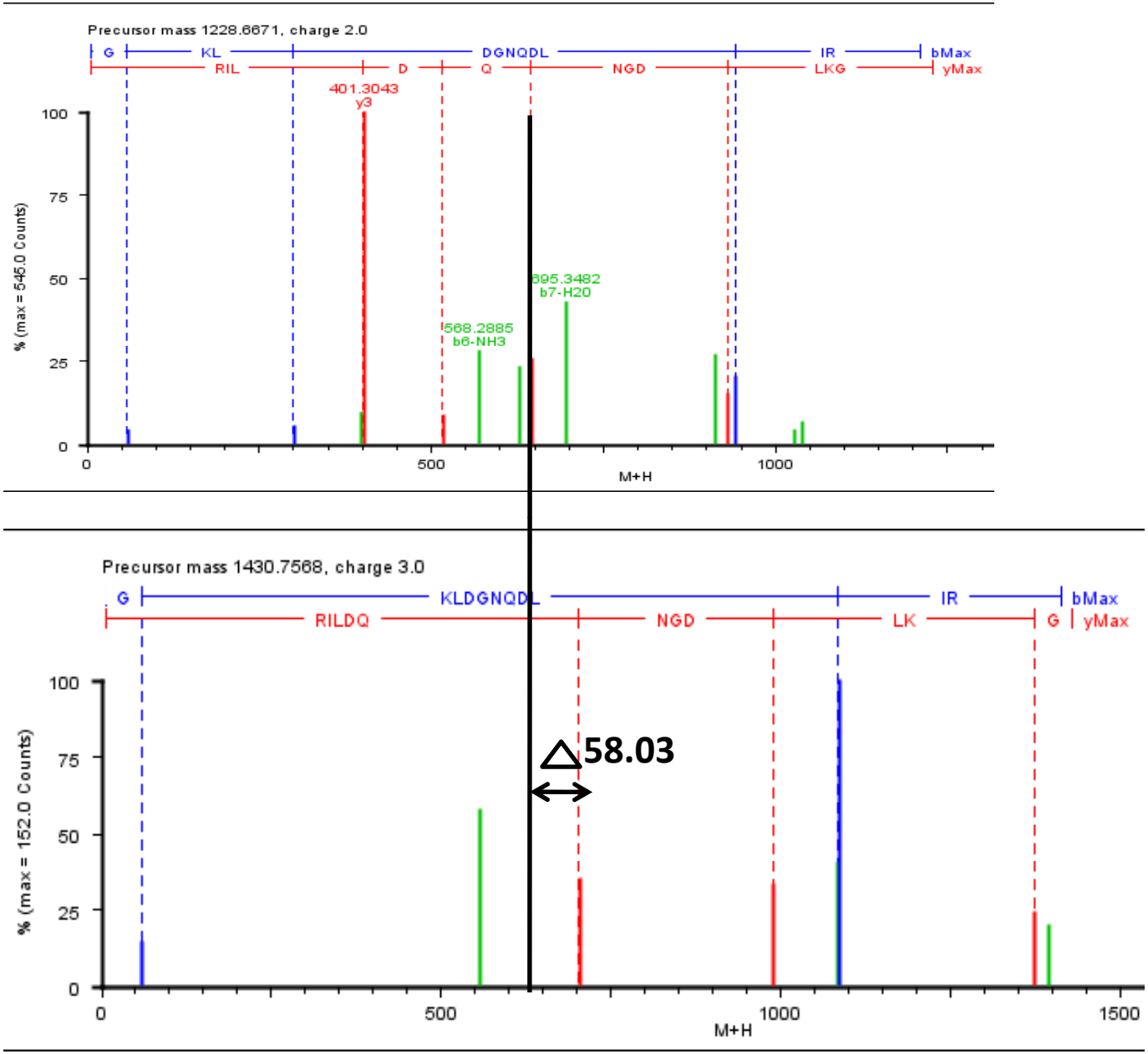


1504.7384

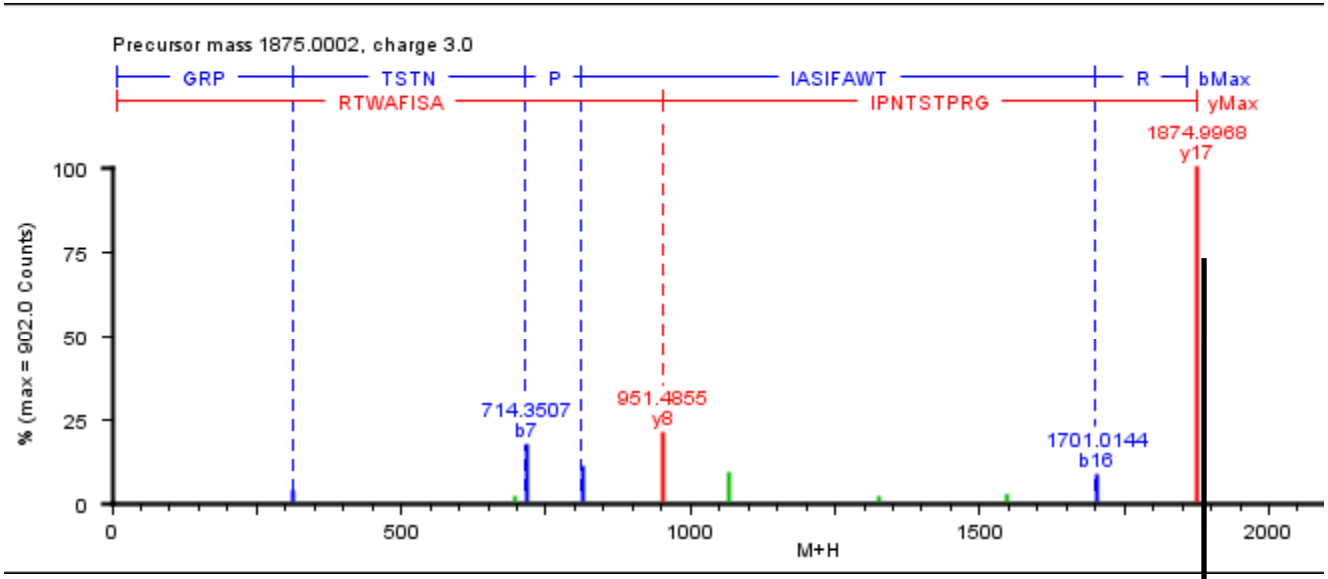
1618.8058: (1504.73+ 114.04)

206-218 (K)TLNDELEIIEGMK(Ubi)(F)

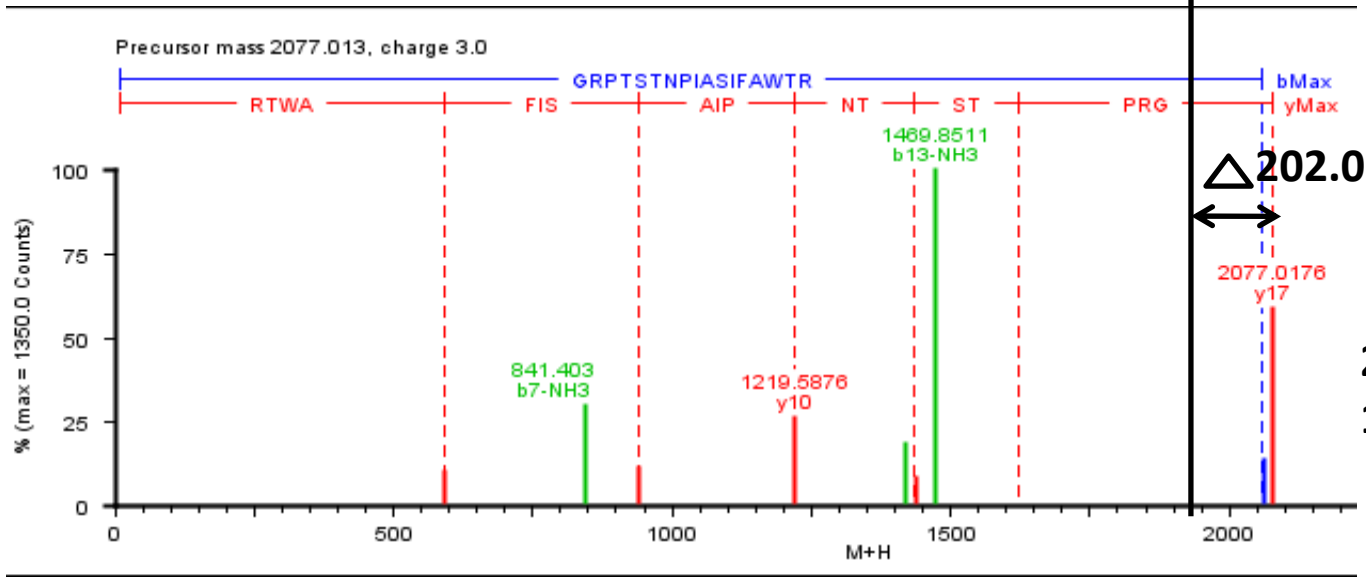
ICDH



383-393 (R)GKLDGNQDLIR(Pento)(F)

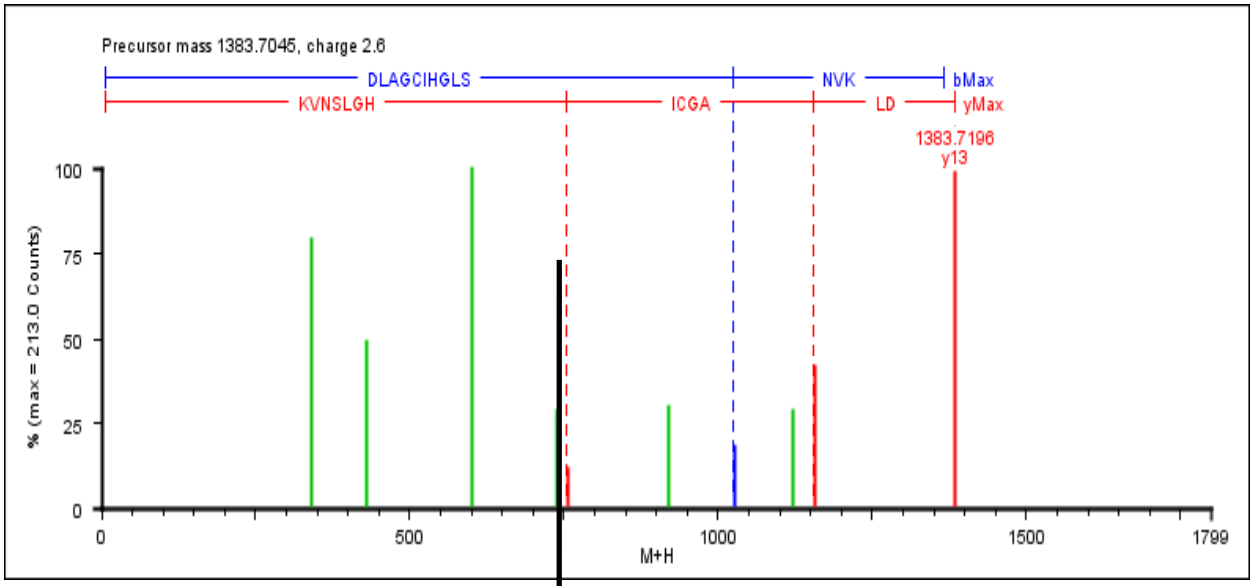


1874.9968

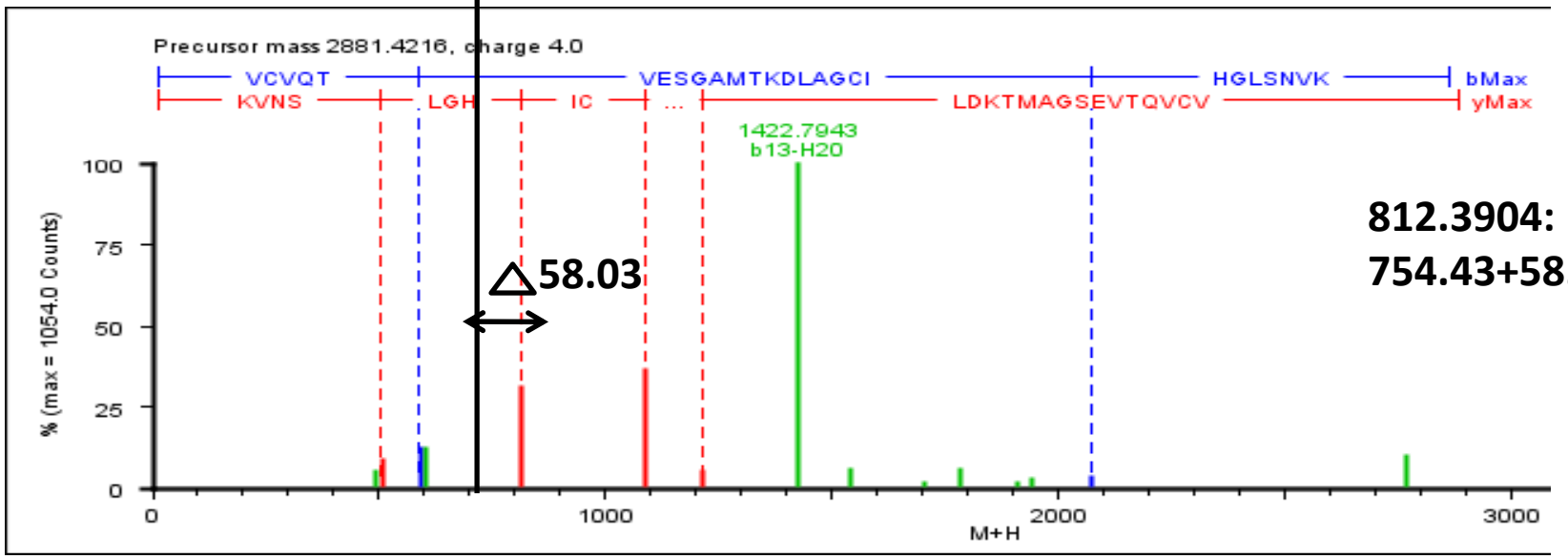


2077.0178:
1874.999+202.02

361-377 (K)GR(ImiA)PTSTNPIASIFAWTR(Pento)(G)

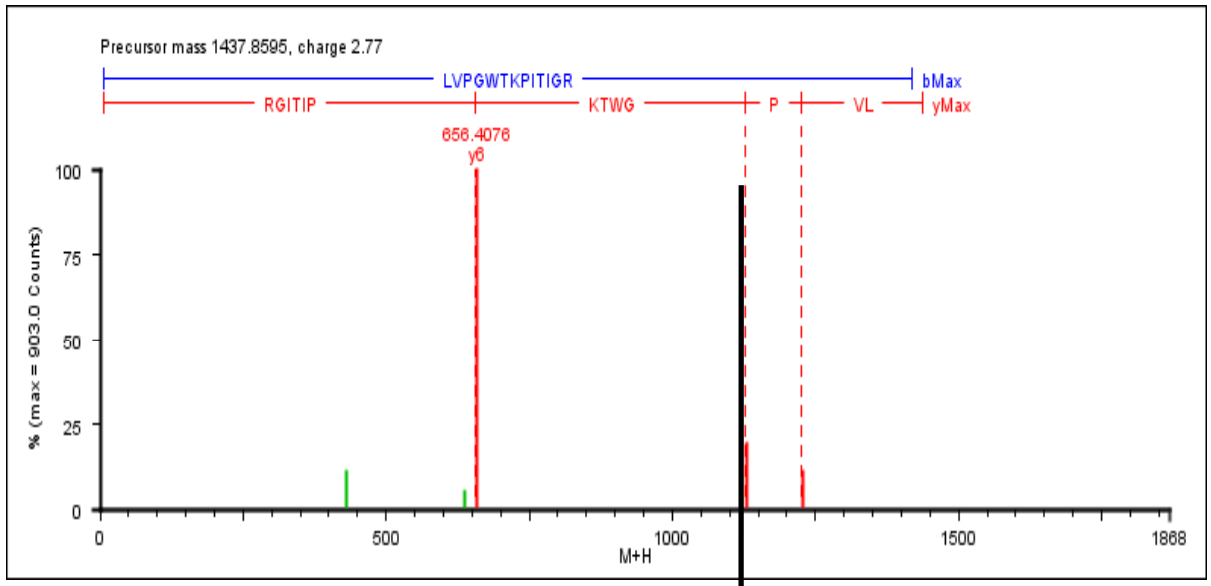


754.4303

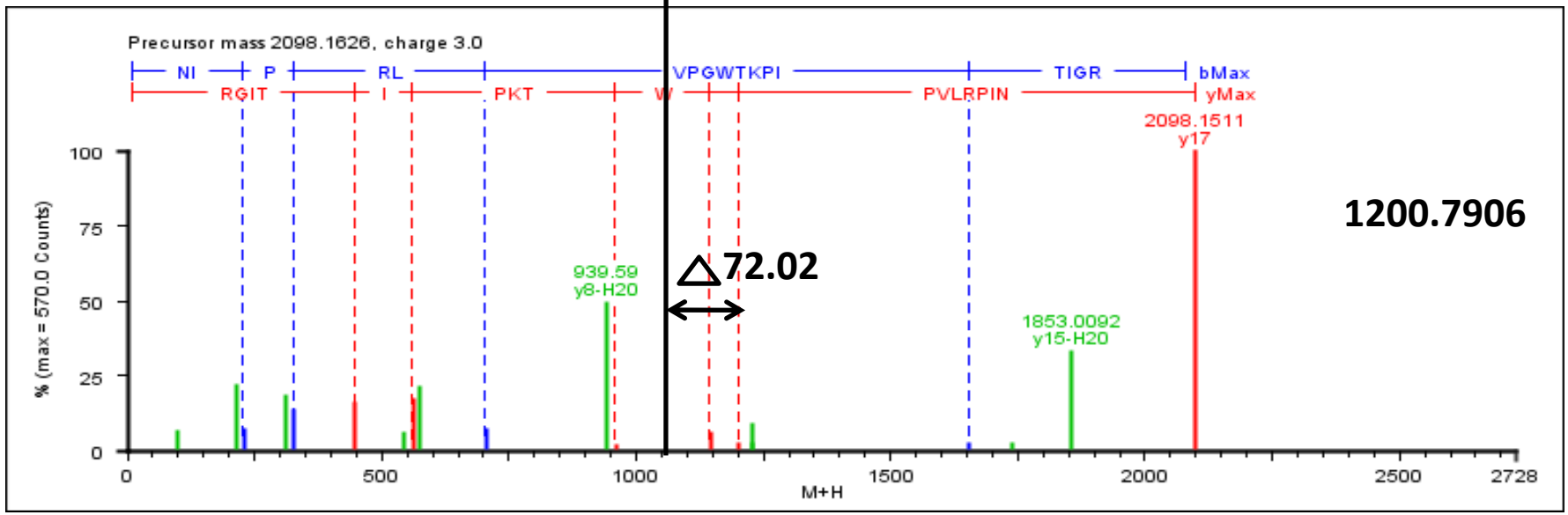


812.3904:
754.43+58.03

401-426 (K)VCVQTVESGAMTKDLAGCIHGLSNVK(Pento)(L)

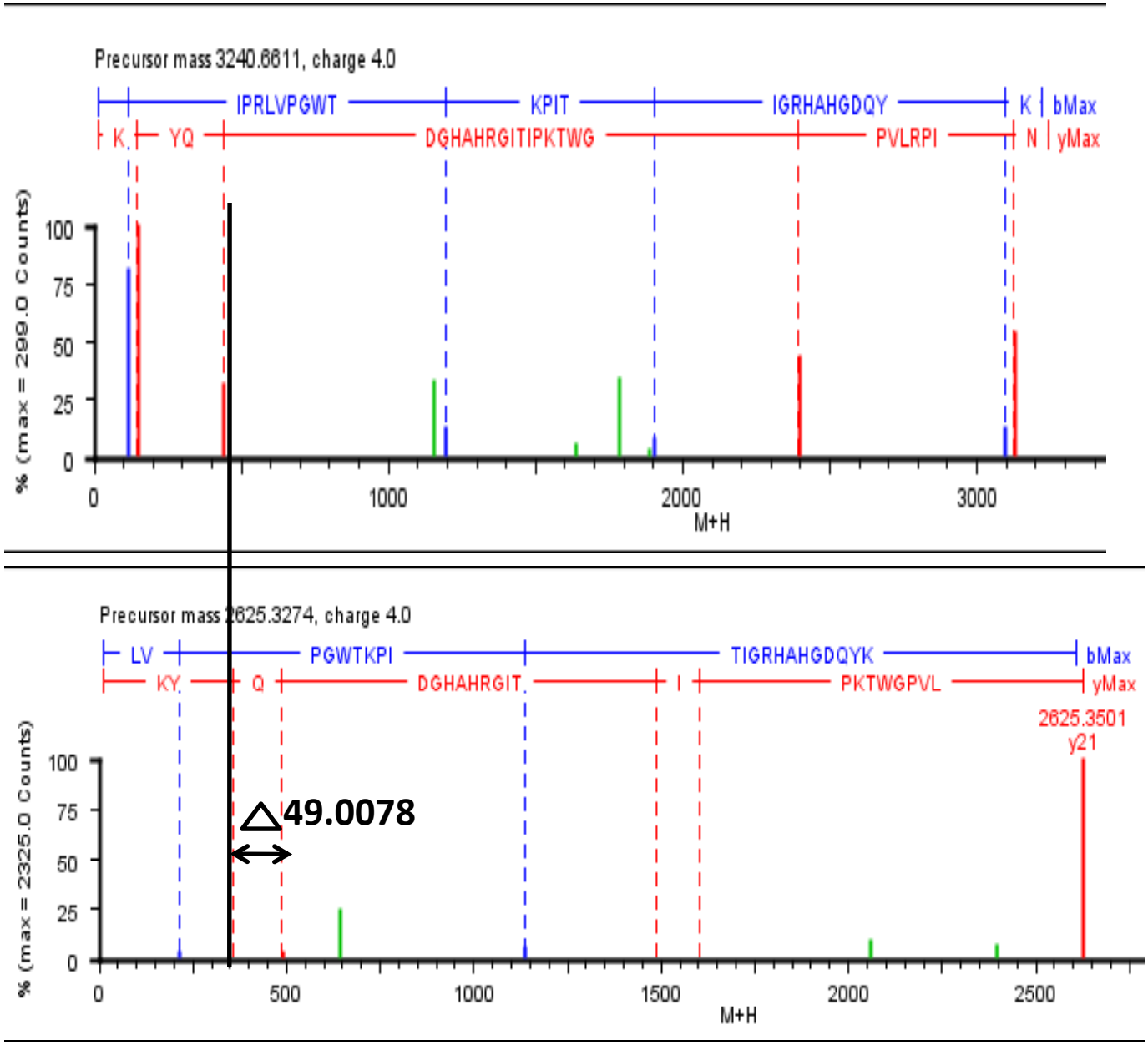


1128.6216



1200.7906

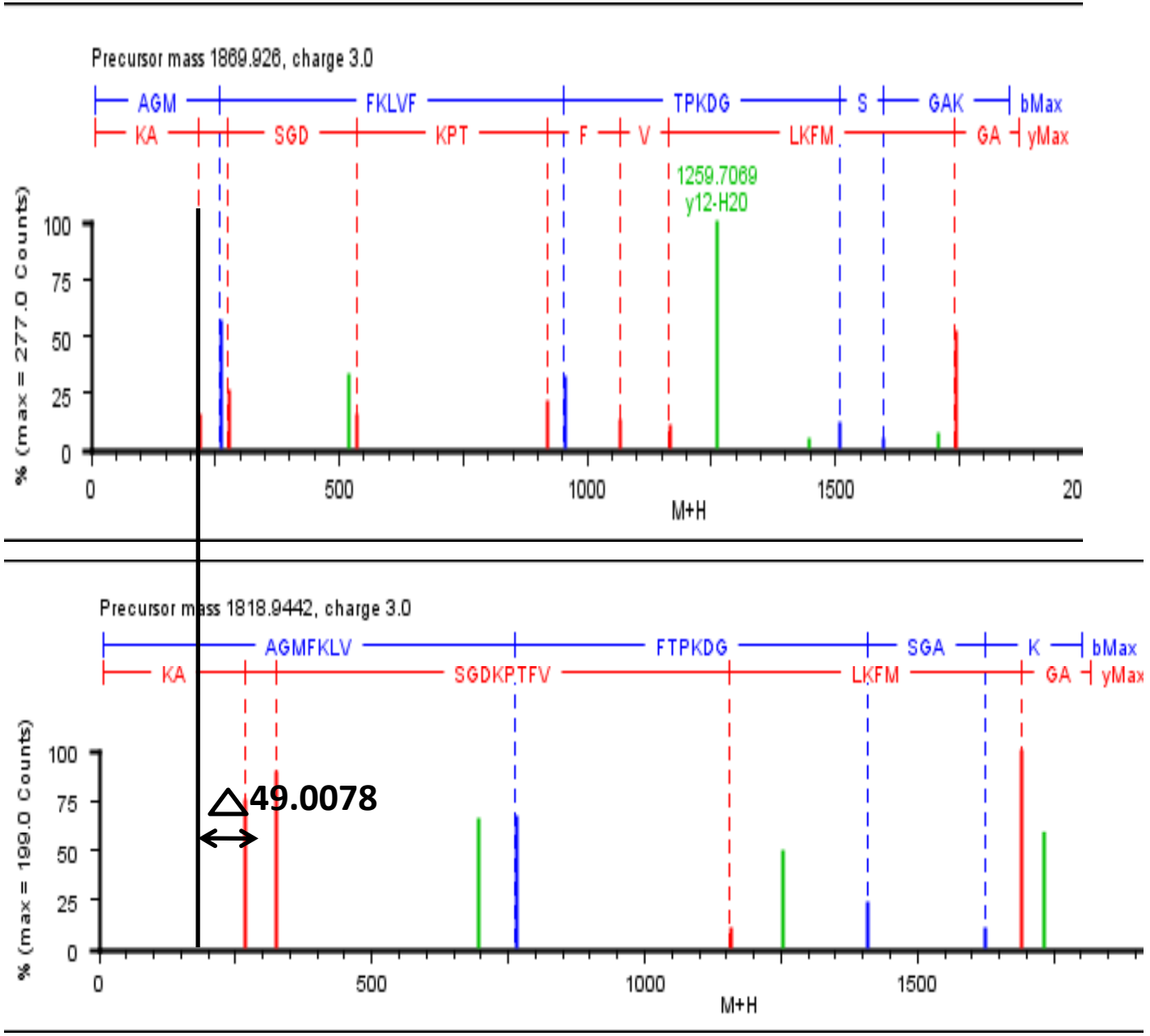
156-172 (K)NIPRLVPGWTKPITIGR(CEL)(H)



438.2404

487.2357

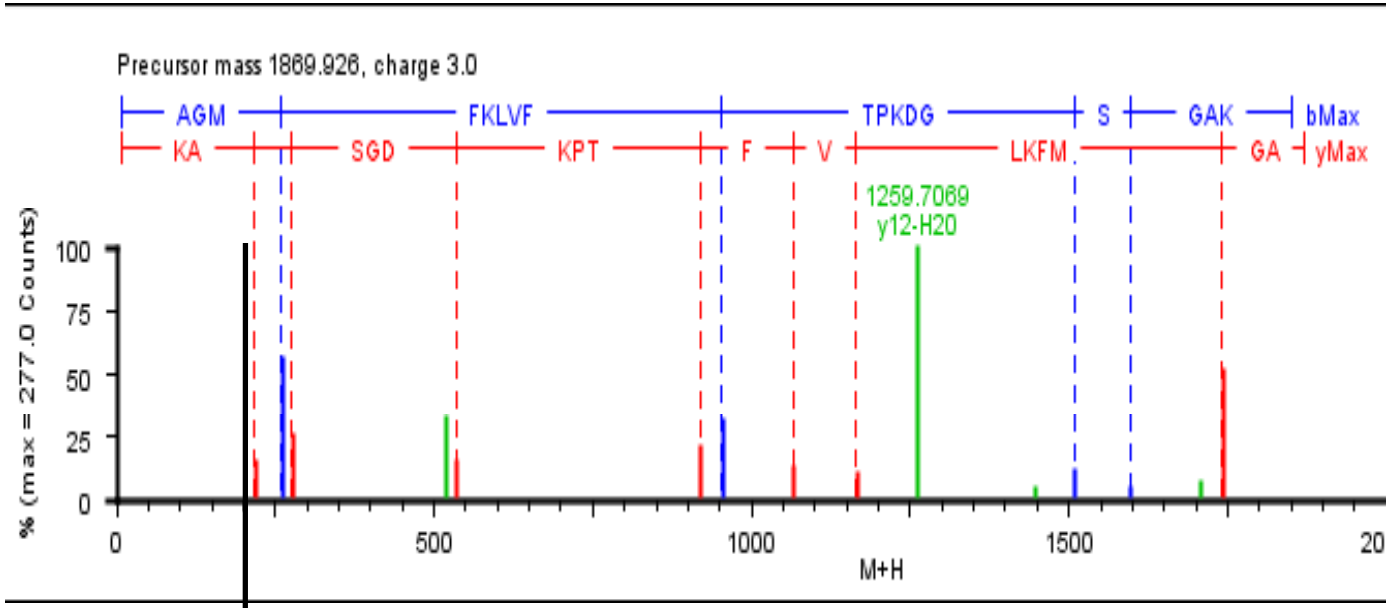
160-180 (R)LVPGWTKPITIGRHAHGDQYK(MOLD)(A)



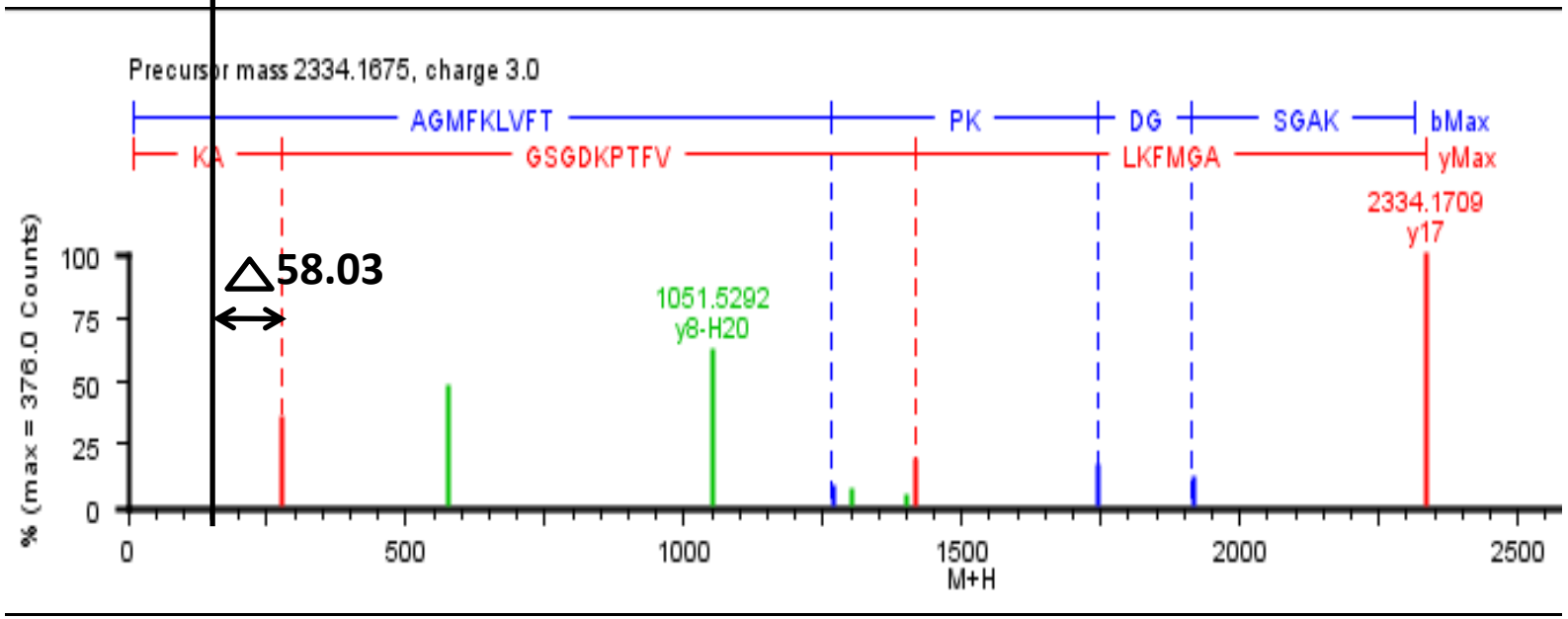
218.1401

267.1448

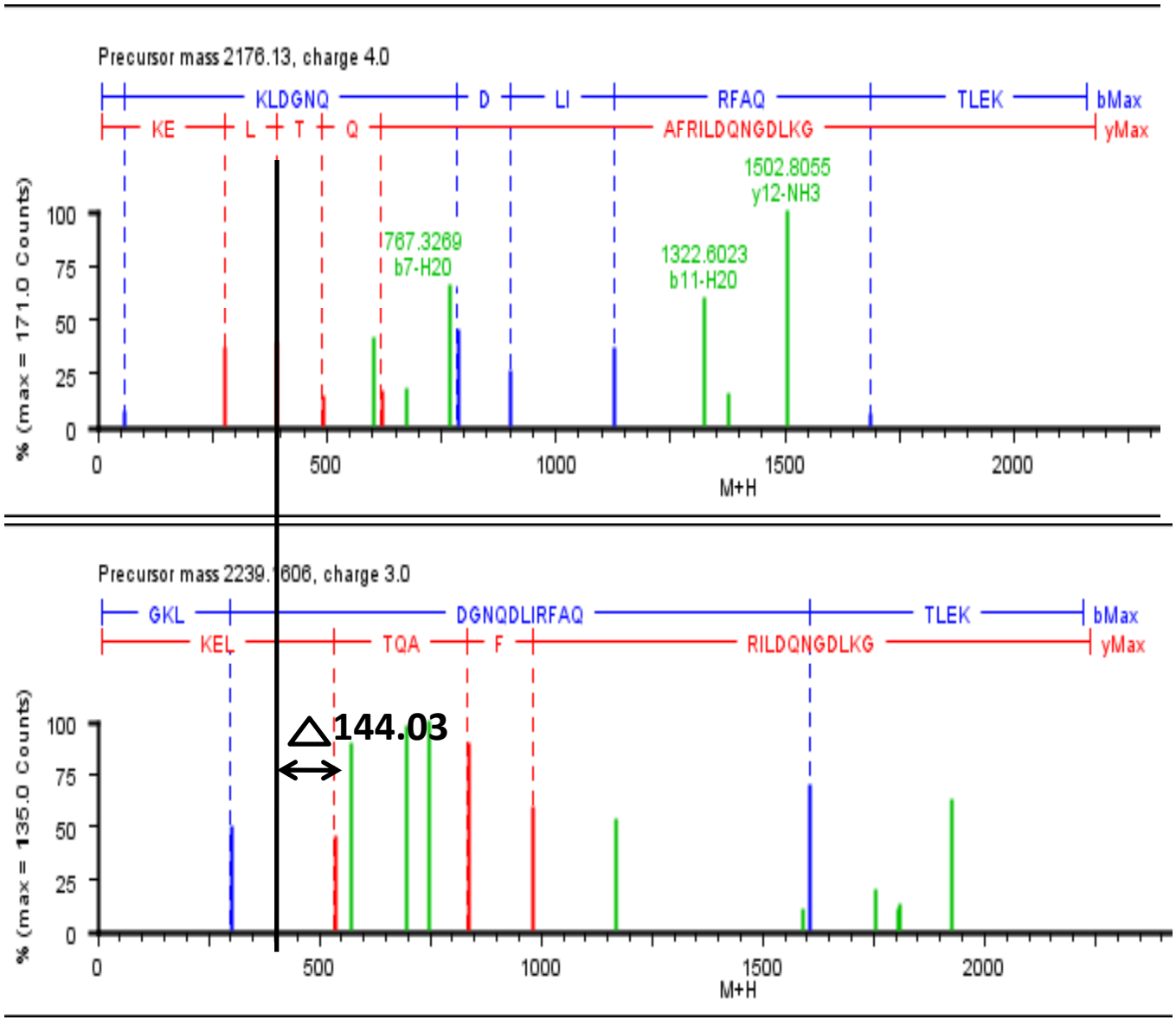
189-205 (R)AGMFKLVFTPKDGSGAK(MOLD)(E)



218.1401



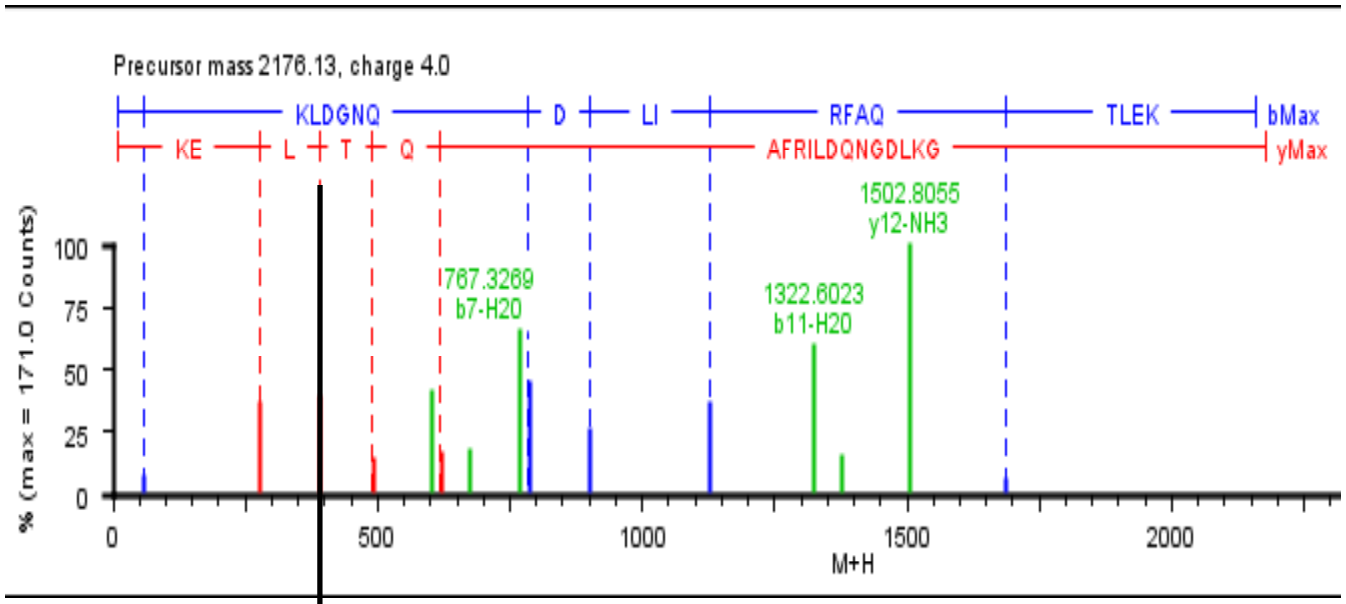
276.1783



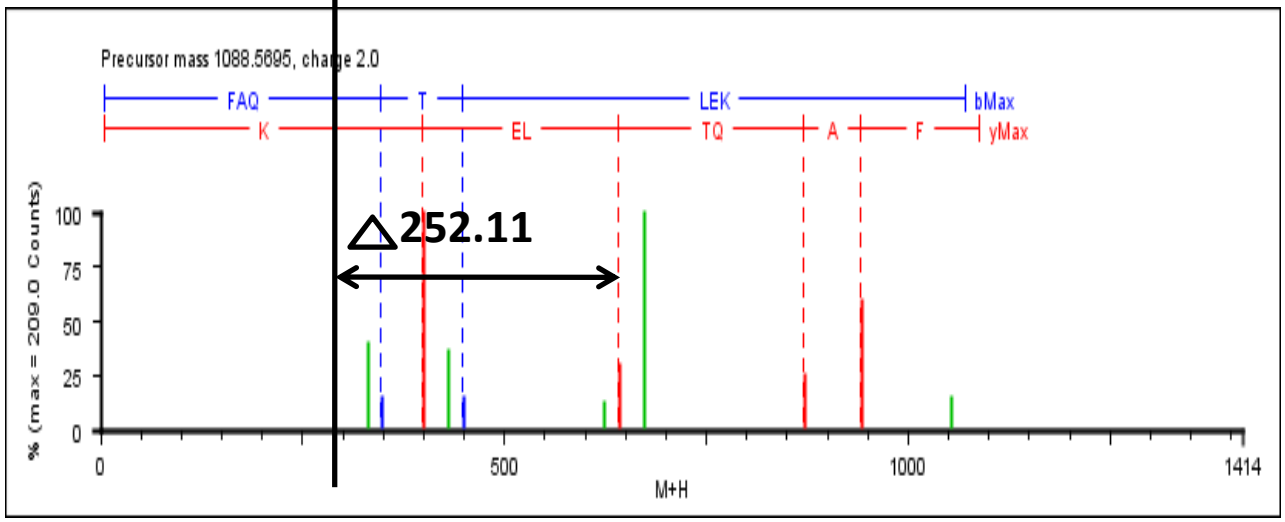
389.2382

533.2373

383-400 (R)GKLDGNQDLIRFAQTLEK(ImiA)(V)

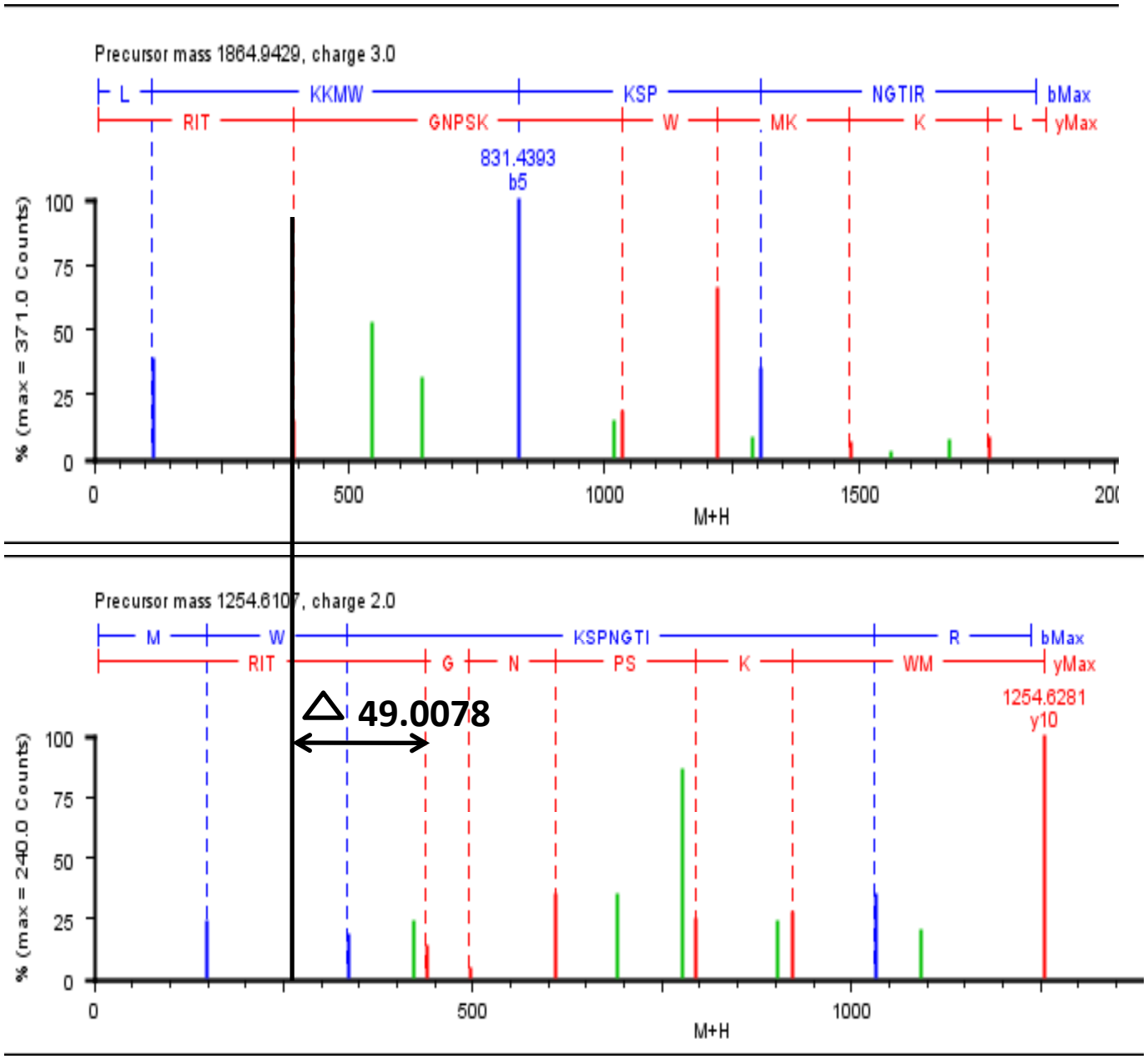


389.2382



641.3063

394-400 (R)FAQTLEK(Crossline)(V)

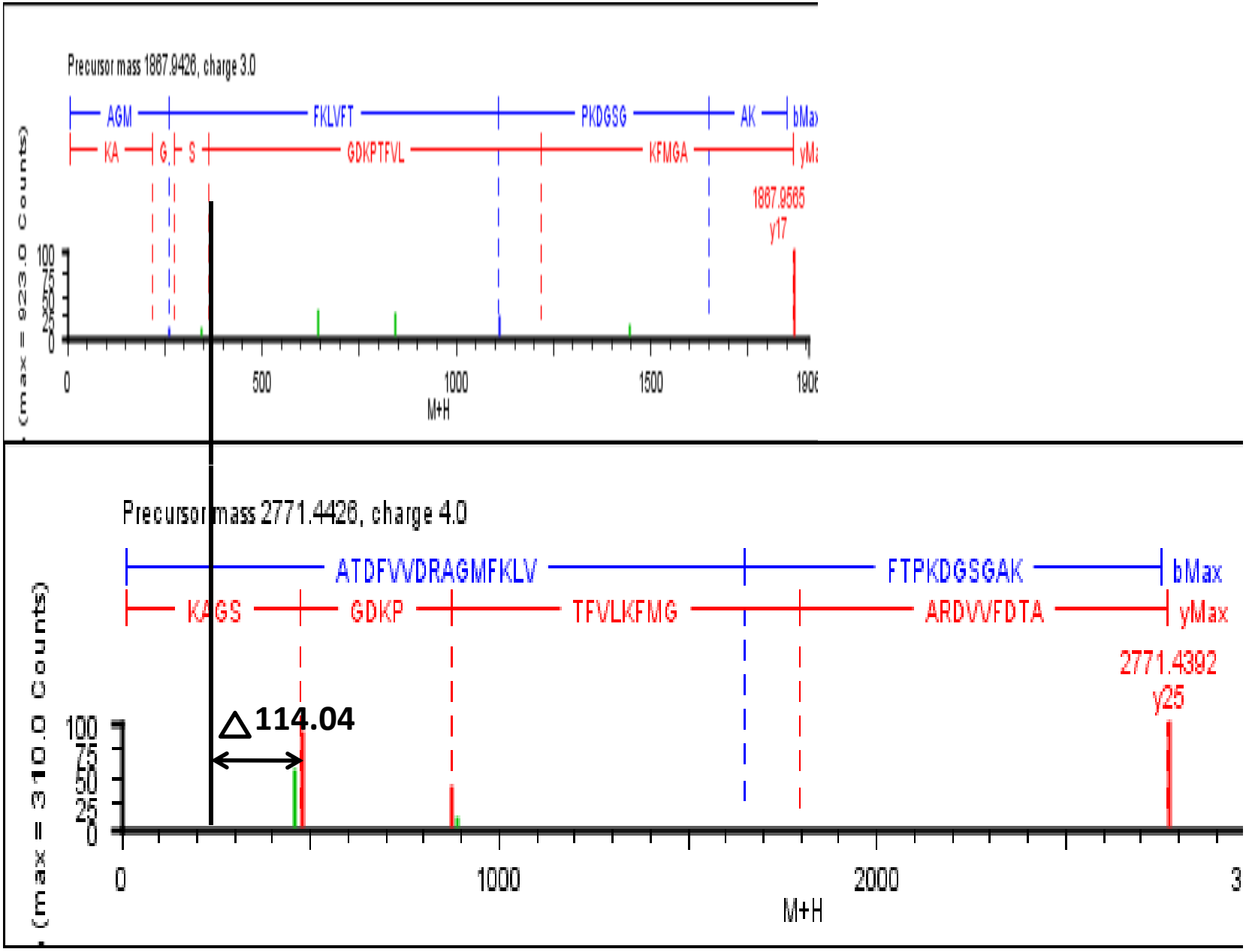


389.2232

438.2558

131-140

(K)MWKSPNGTIR(MOLD)(N)

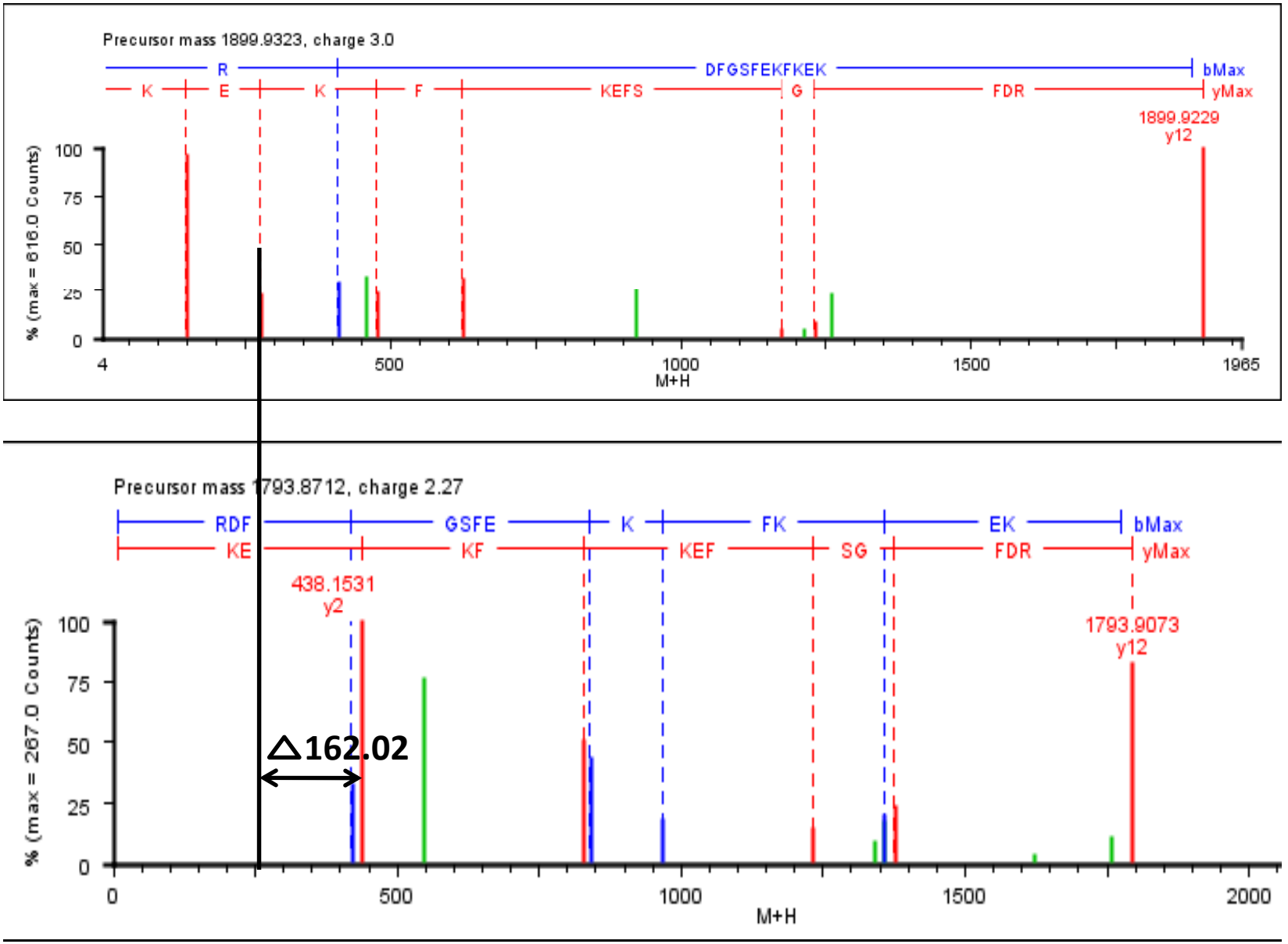


362.1801

476.2037: (362.18+ 114.04)

181-205 (K)ATDFVVDRAGMFKLVFTPKDGSGAK(Ubi)(E)

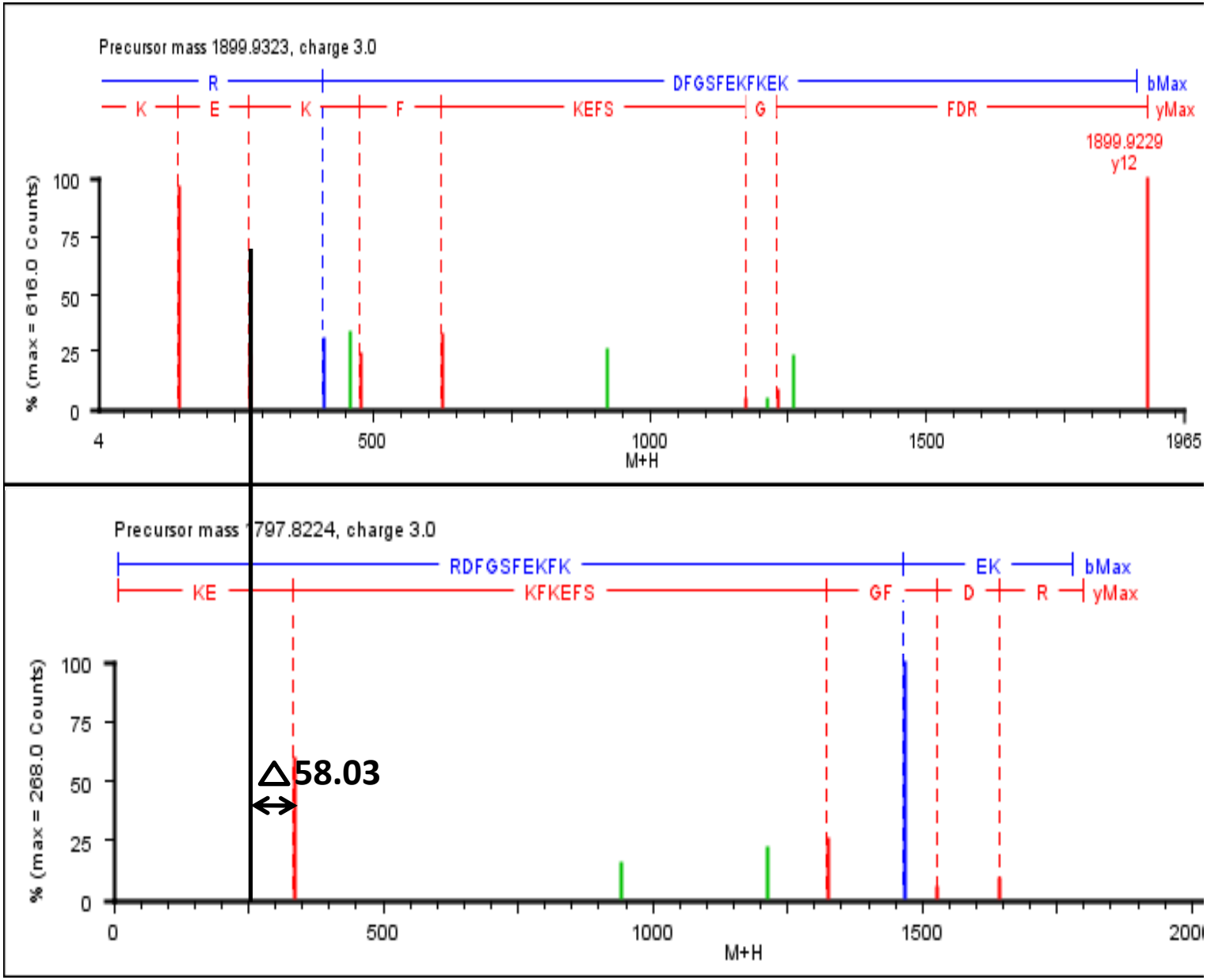
SOD



276.1479

438.1531: (276.1479 +162)

123-134 (K)RDFGSFEKFKEK(Gly)(L)

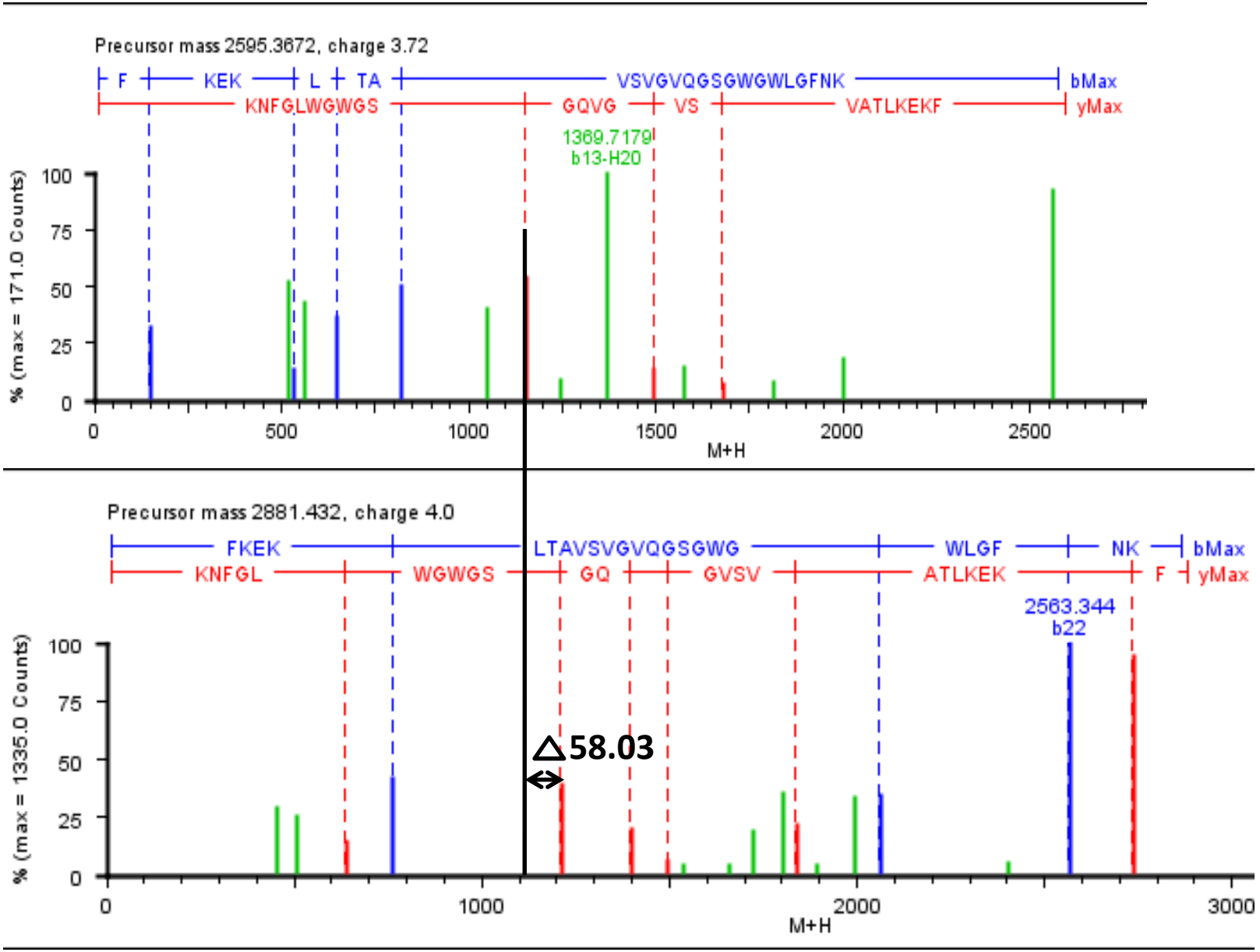


276.1479

334.1845: (276.1479 + 58)

123-134

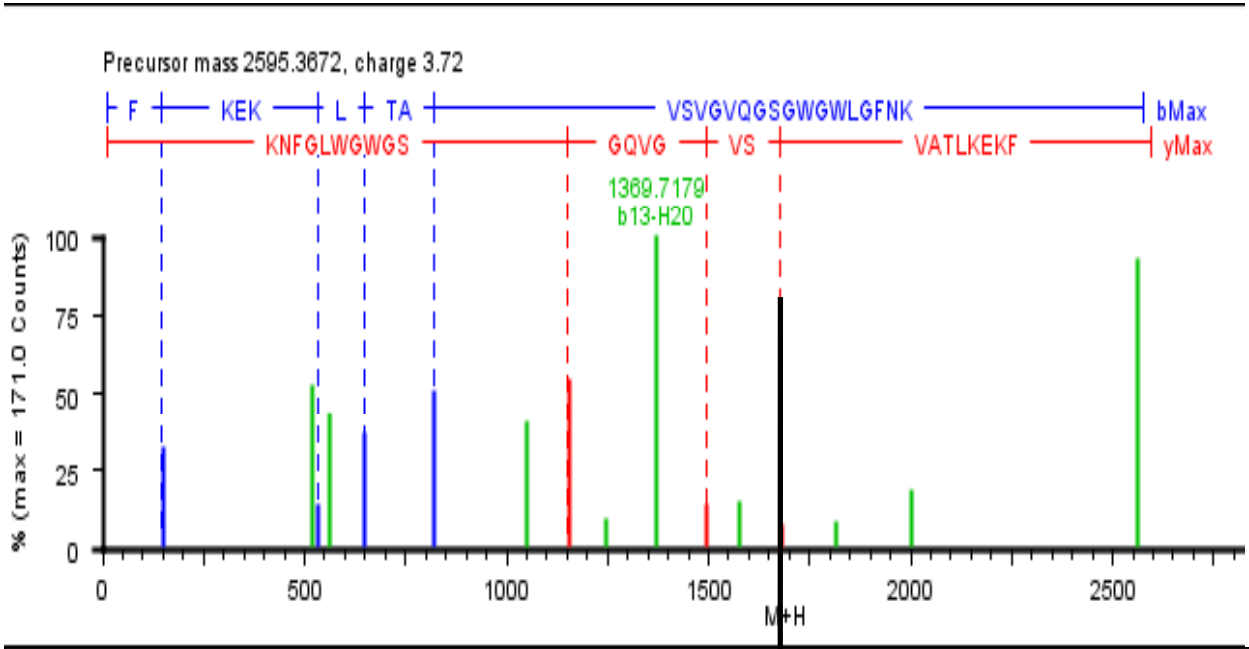
(K)RDFGSFEKFKEK(Pento)(L)



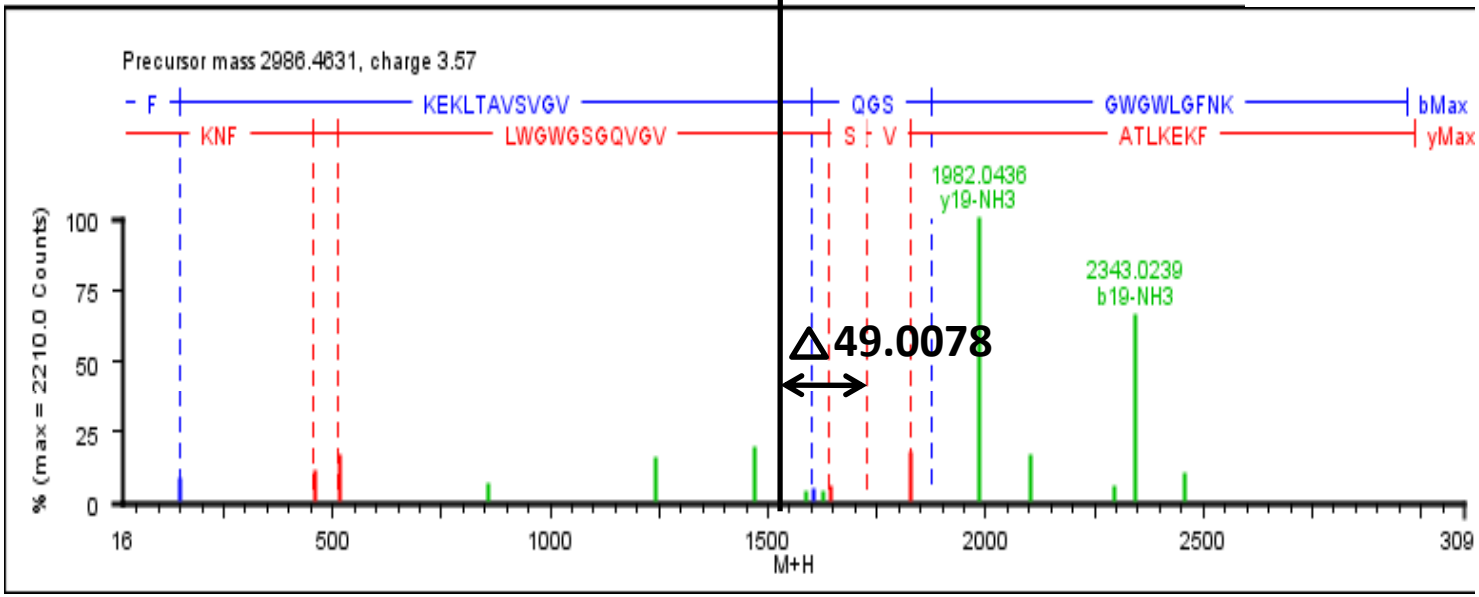
1151.567

1209.5673: (1151.567+58

131-154 (K)FKEKLTAVSVGVQGSGWGWLGFNK(Pento)(E)

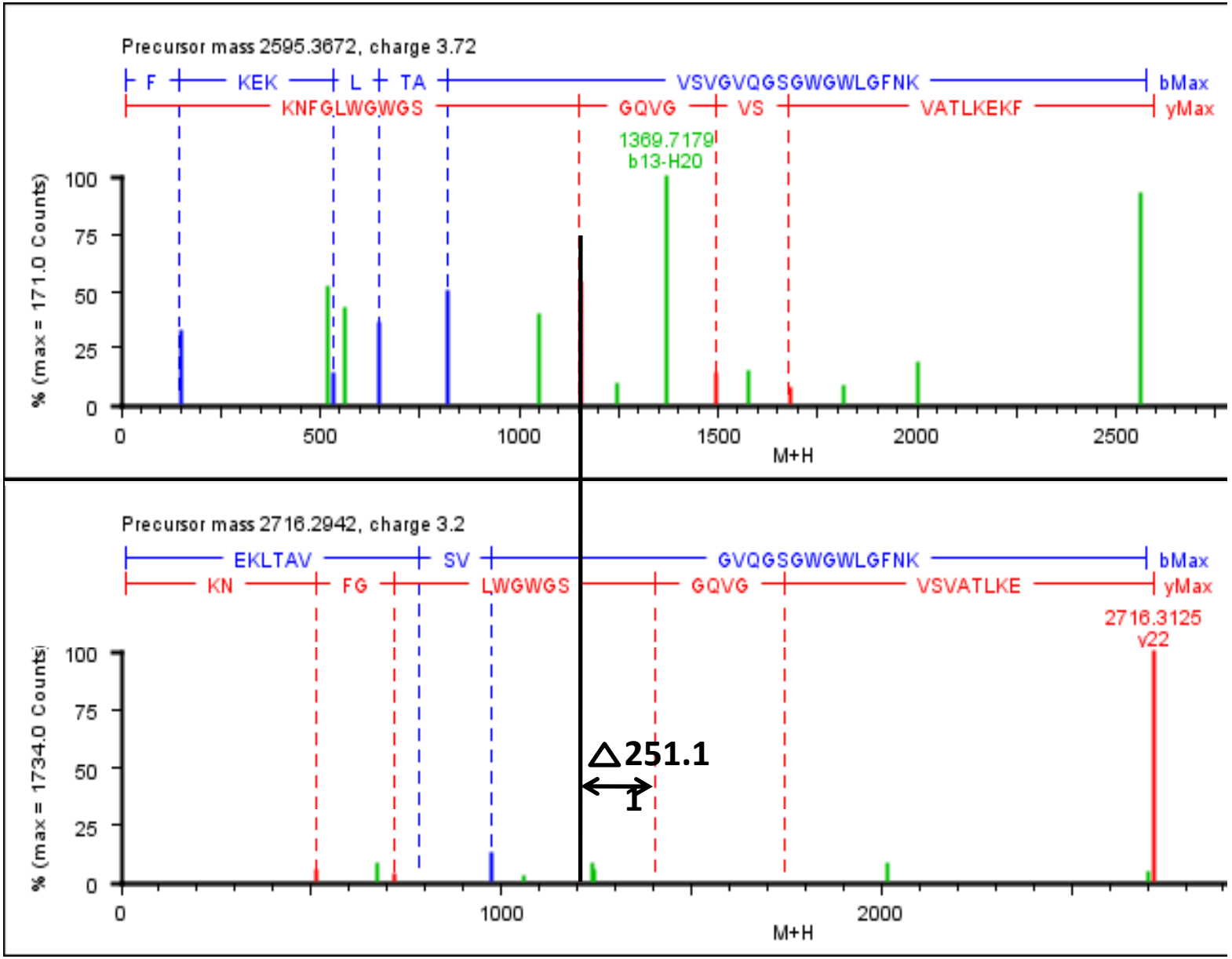


1678.9824



1727.8658:
(1678.98+ 49)

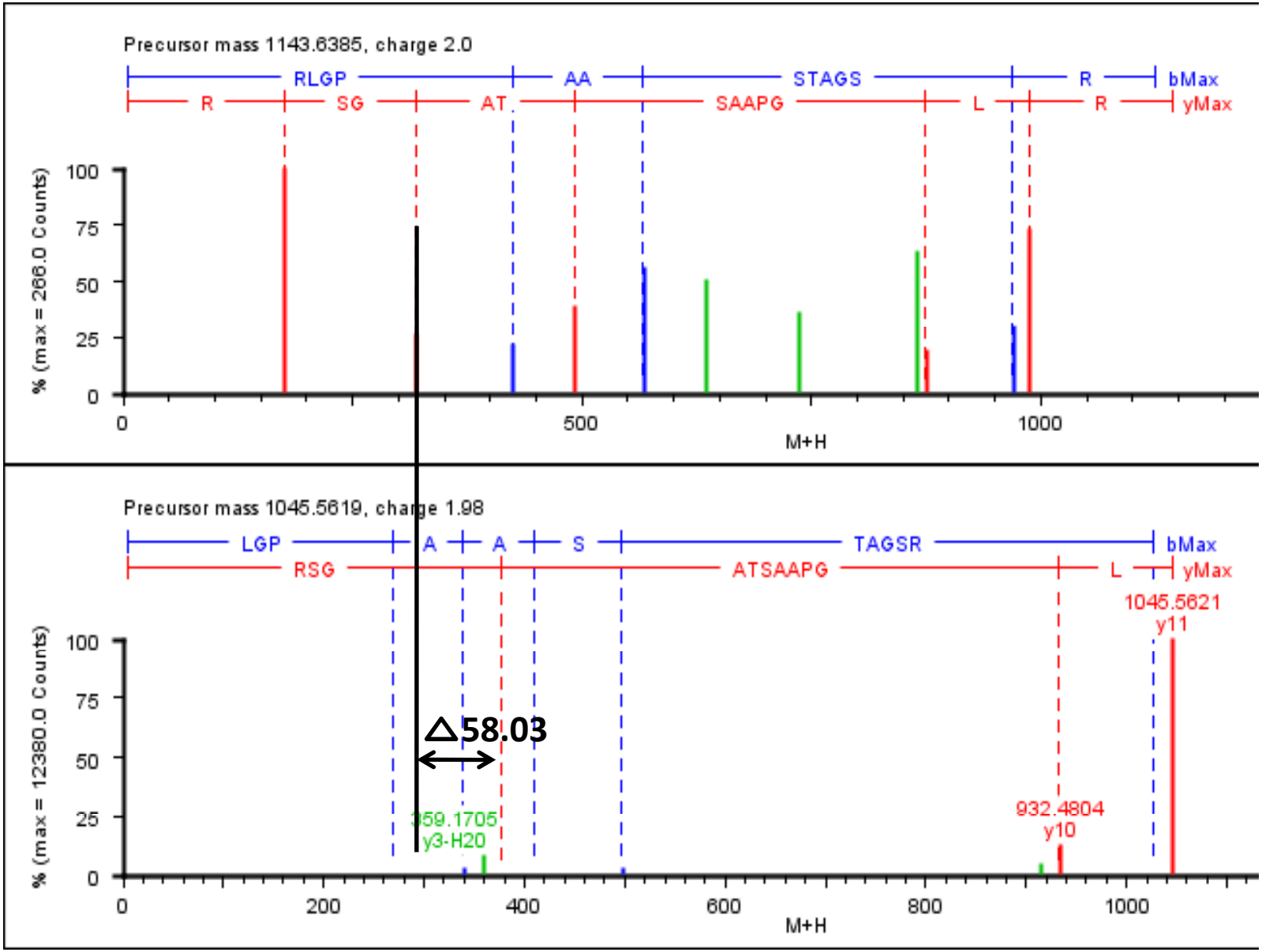
131-154 (K)FKEKLTAVSVGVQGSGWGWLGFNK(MOLD)(E)



1151.567

1403.5505:
(1151.567+252)

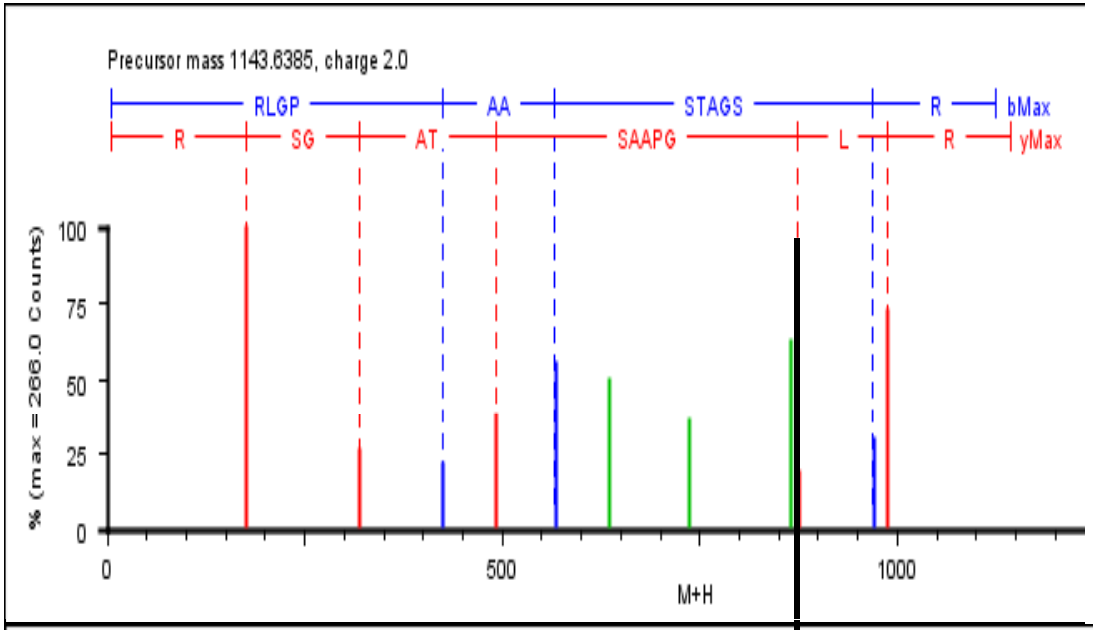
133-154 (K)EKLTAVSVGVQGSGWGWLGFNK(Crossline)(E)



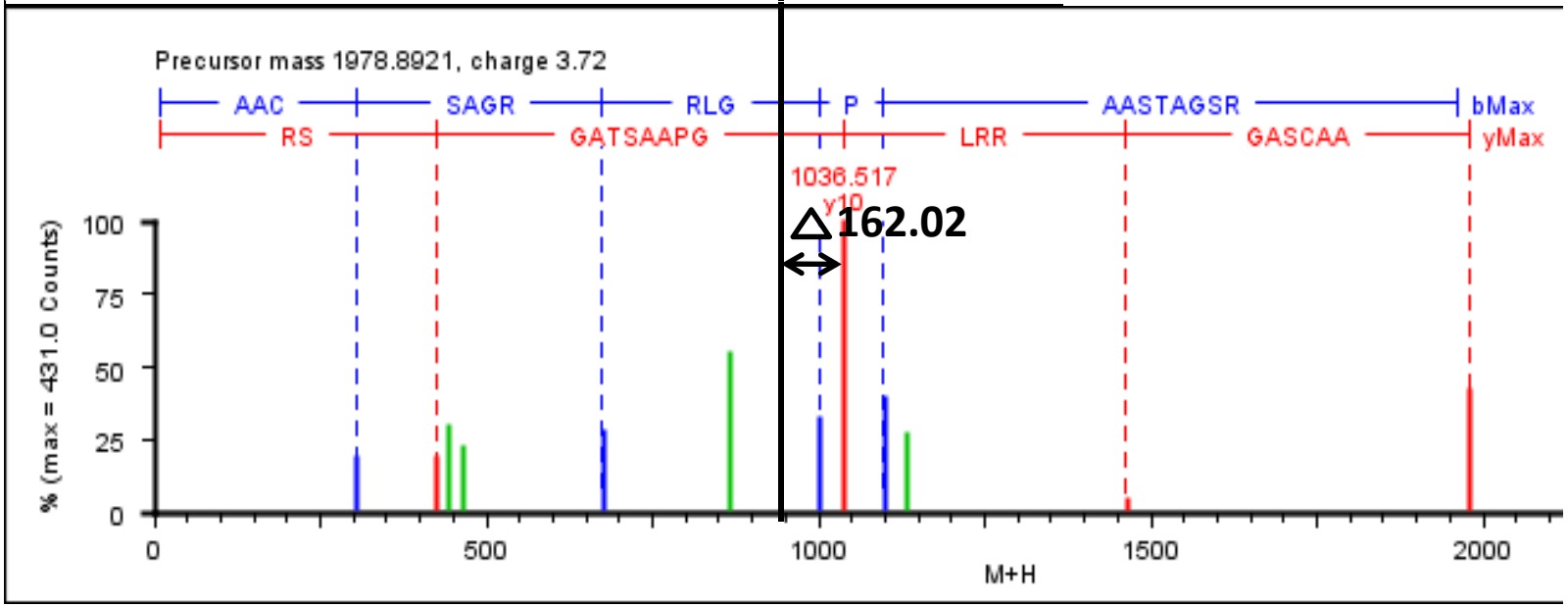
319.1342

377.1741:
(319.1342+58.03

13-23 (R)LGPAASTAGSR(Pento)(H)

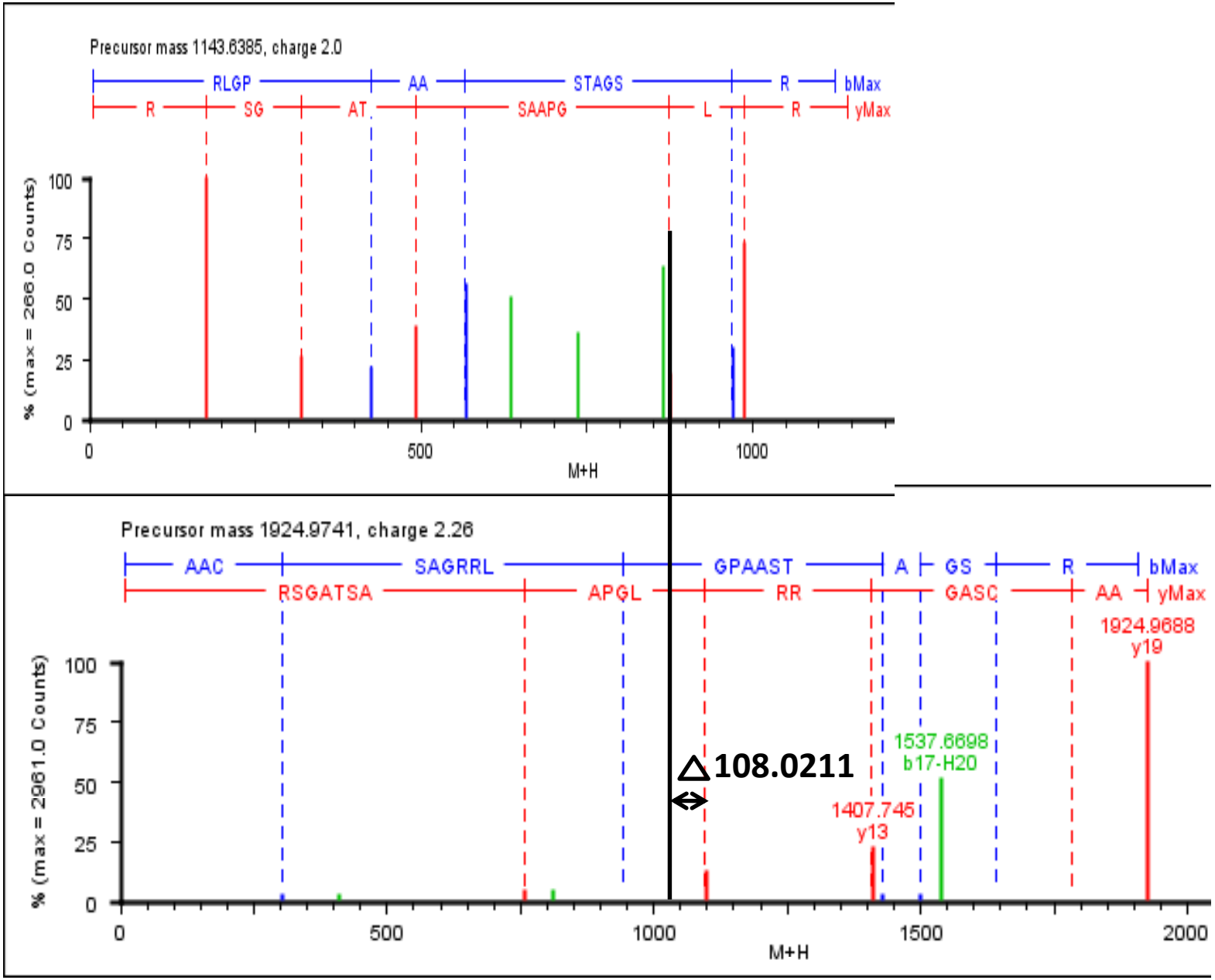


874.487



1036.517:
(874.487+162.0

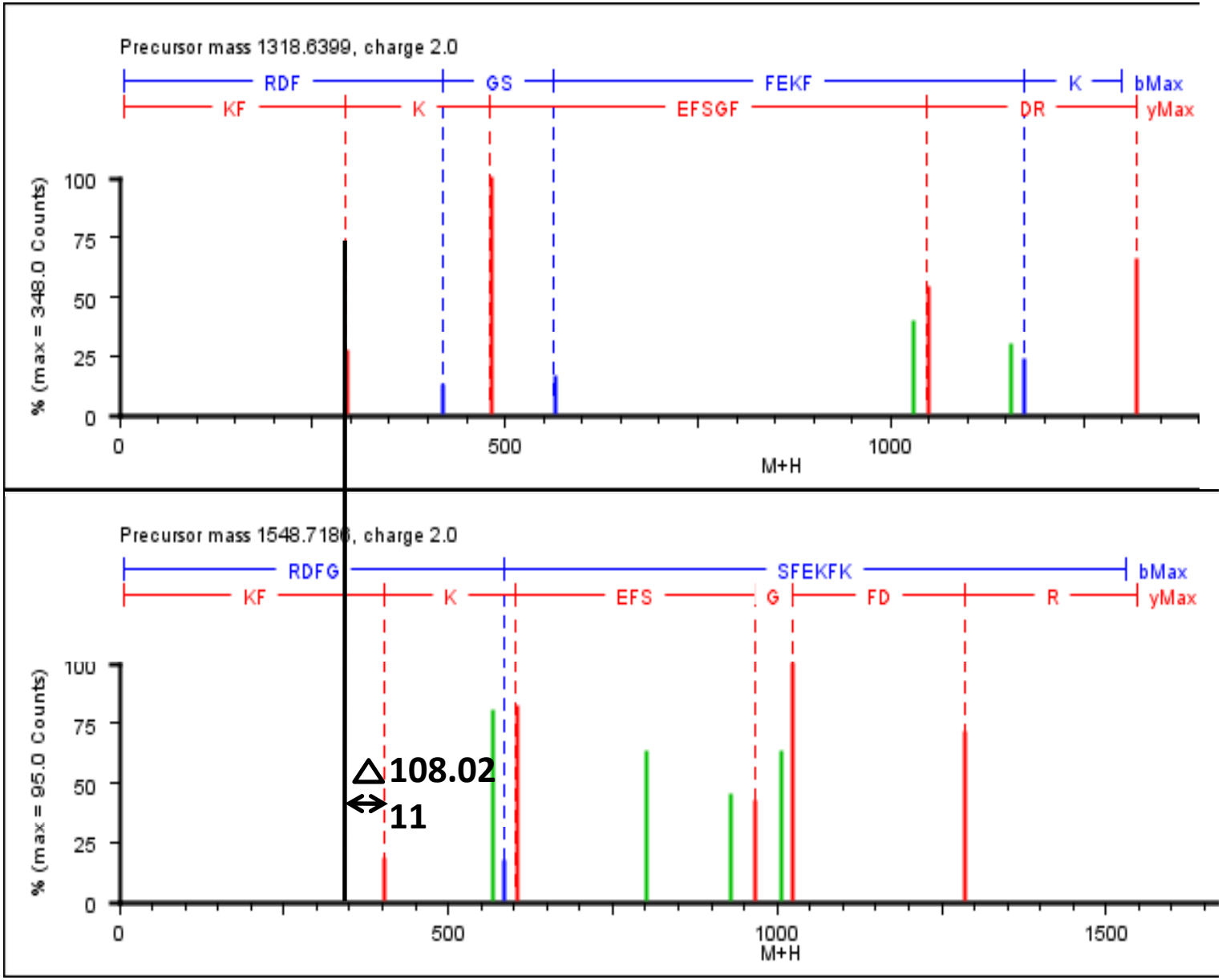
5-23 (R)AACSAGRRLGPAASTAGSR(Gly)(H)



987.52

1095.53: (987.5205 +108.02)

5-23 (R)AACSAGRRLGPAASTAGSR(Pyr)(H)

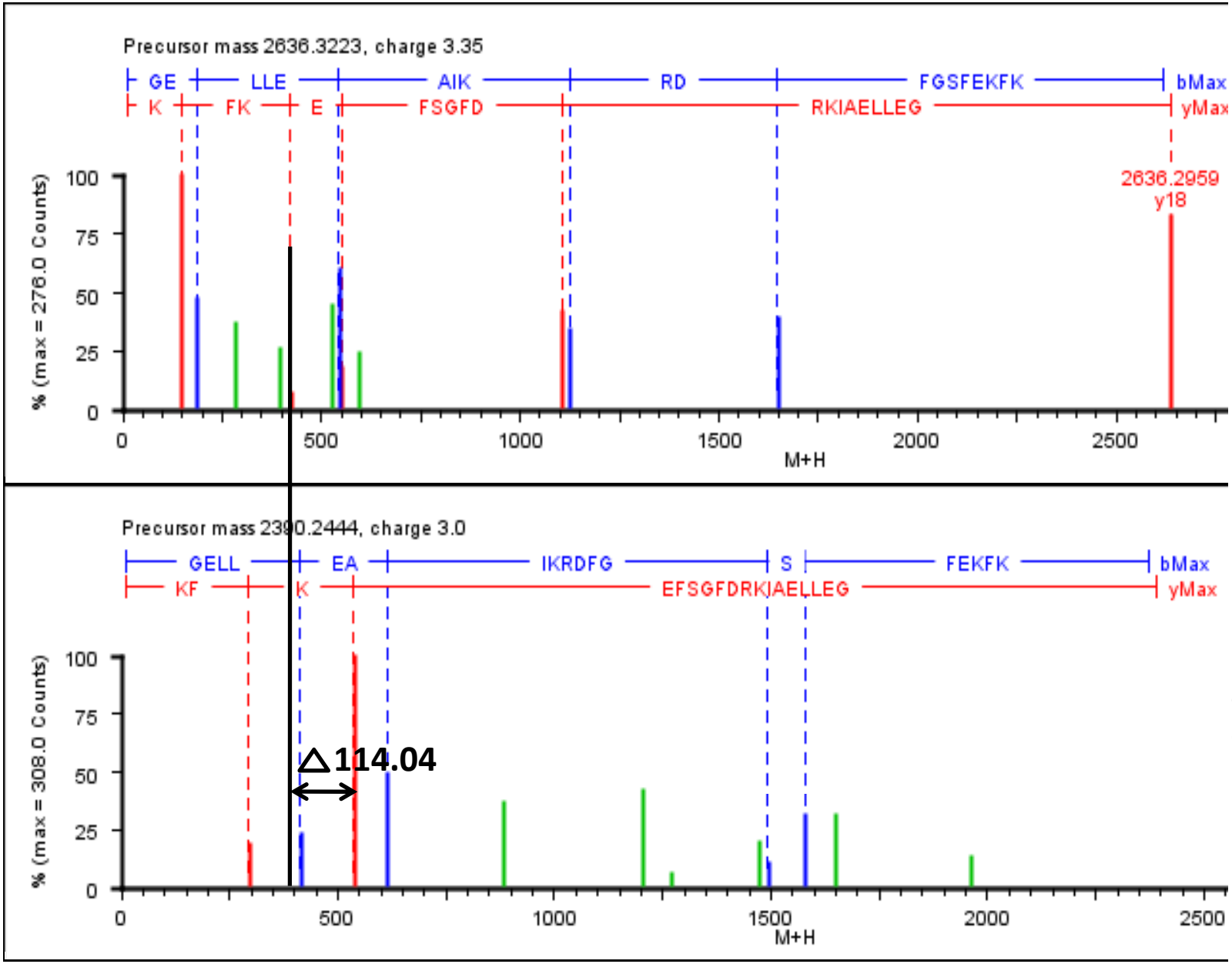


294.189

402.2085:
(294.189+108)

123-132

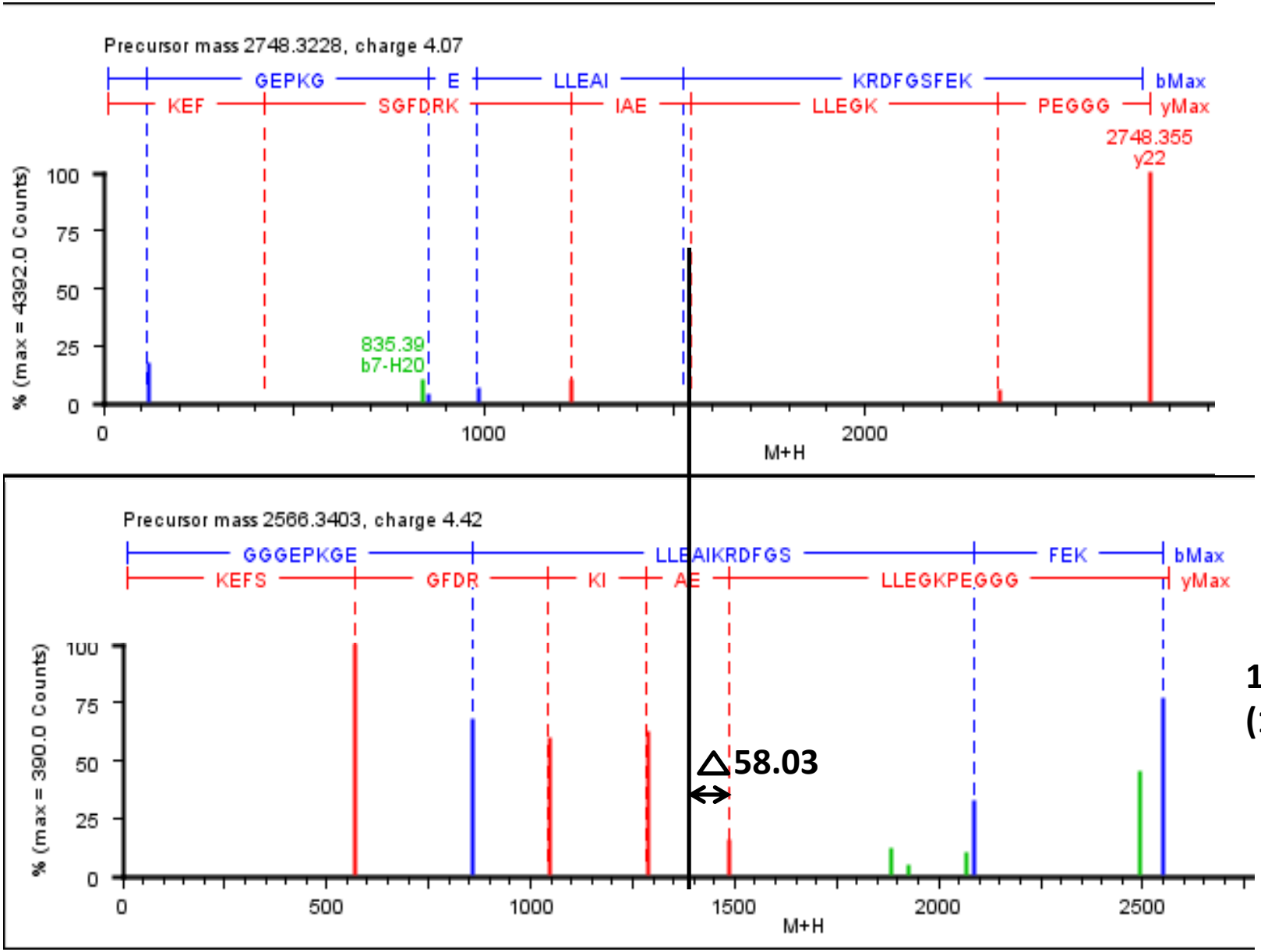
(K)RDFGSFEKFK(Pyr)(E)



422.2997

536.2785:
(422.29+ 114.04)

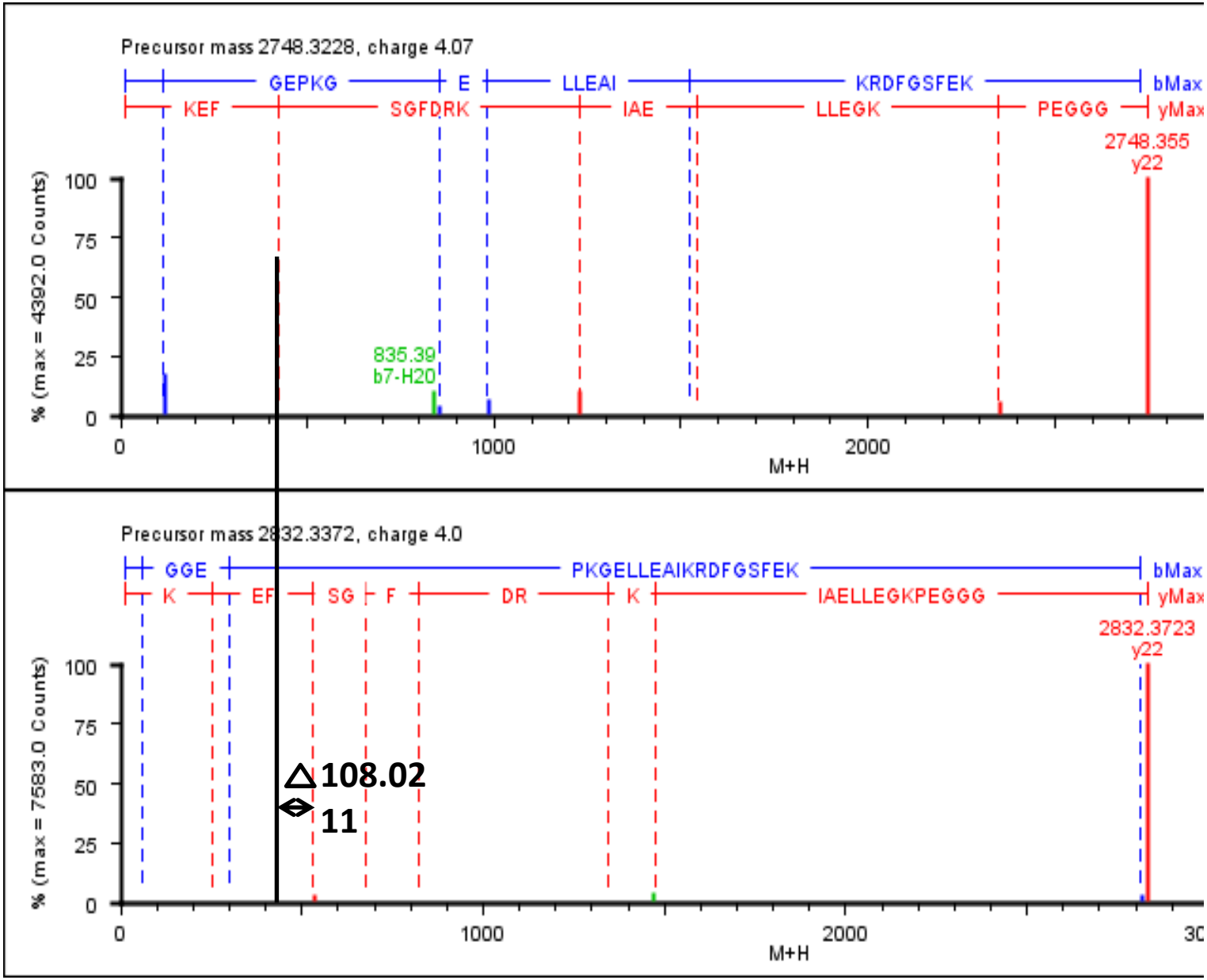
115-132 (K)GELLEAIKRDFGSFEK(Ubi)FK(E)



1484.8413

1540.7725:
(1484.84+ 58.03)

109-130 (K)GGGEPKGELLEAIKRDFGSFEK(Pento)(F)

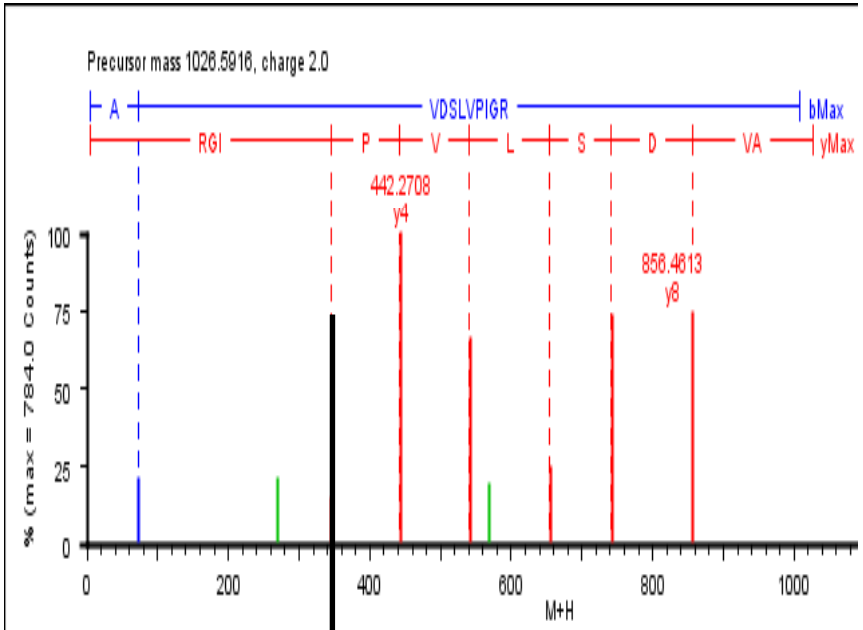


423.1844

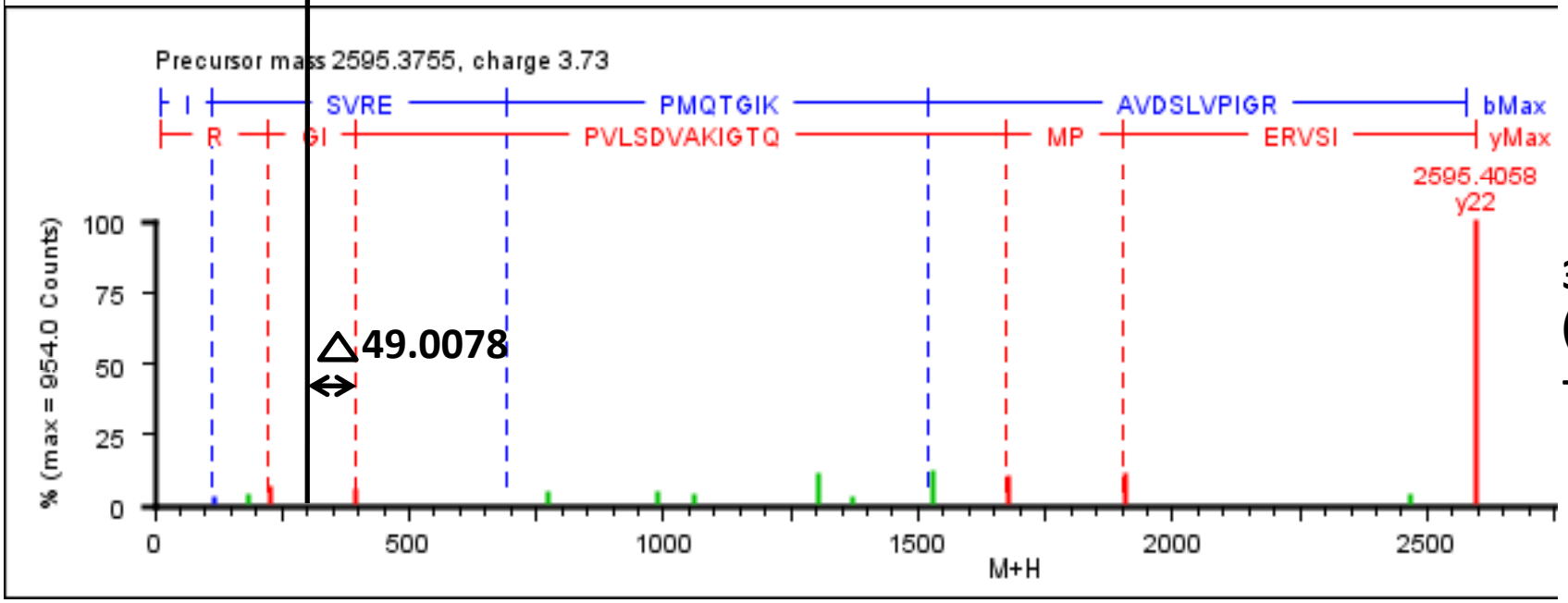
531.676:
(423.1844+108.0

109-130 (K)GGGEPKGELLEAIKRDFGSFEK(Pyr)(F)

ATP Alpha

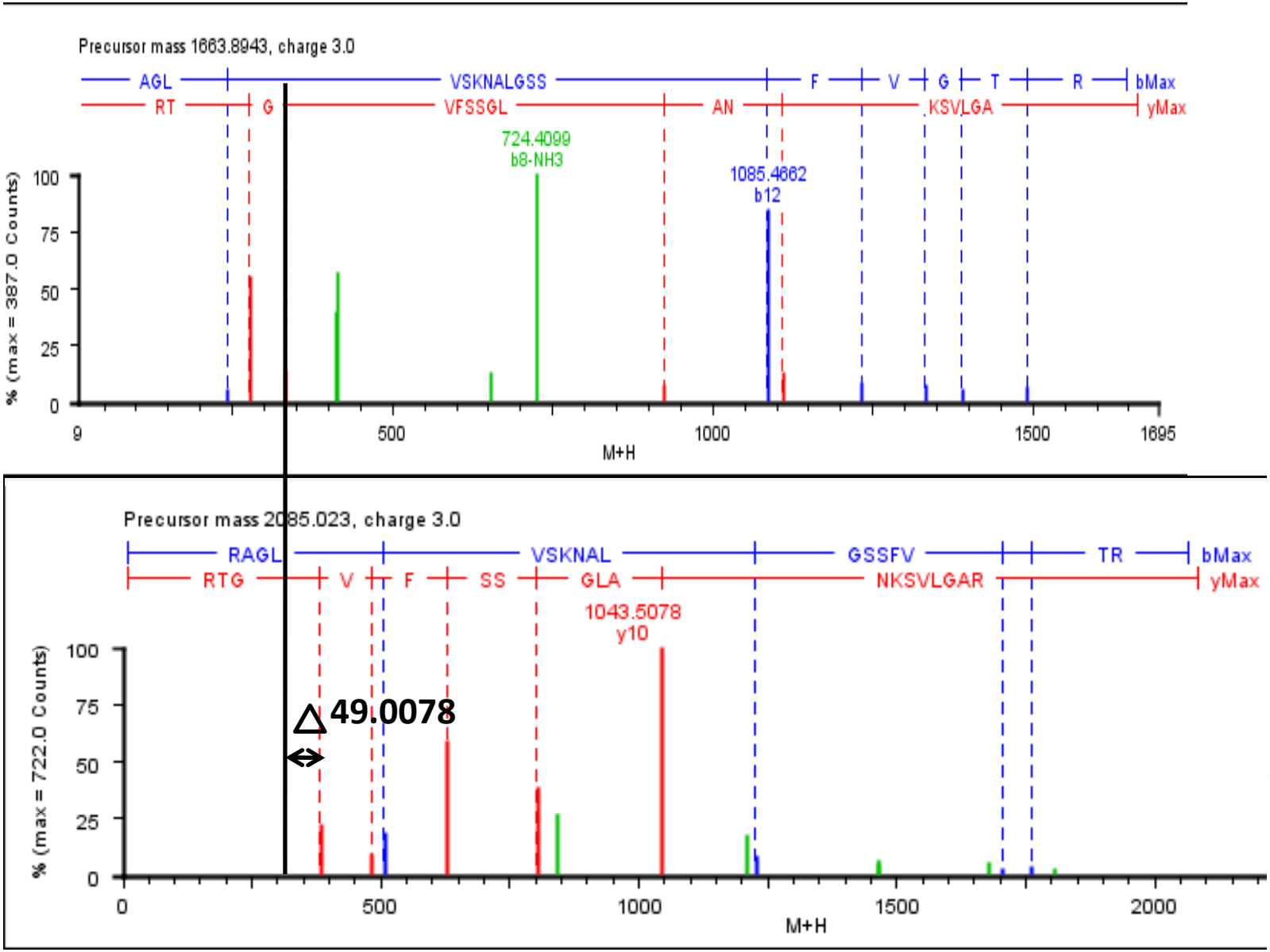


345.2166



394.2203: (345.2166 + 49.00)

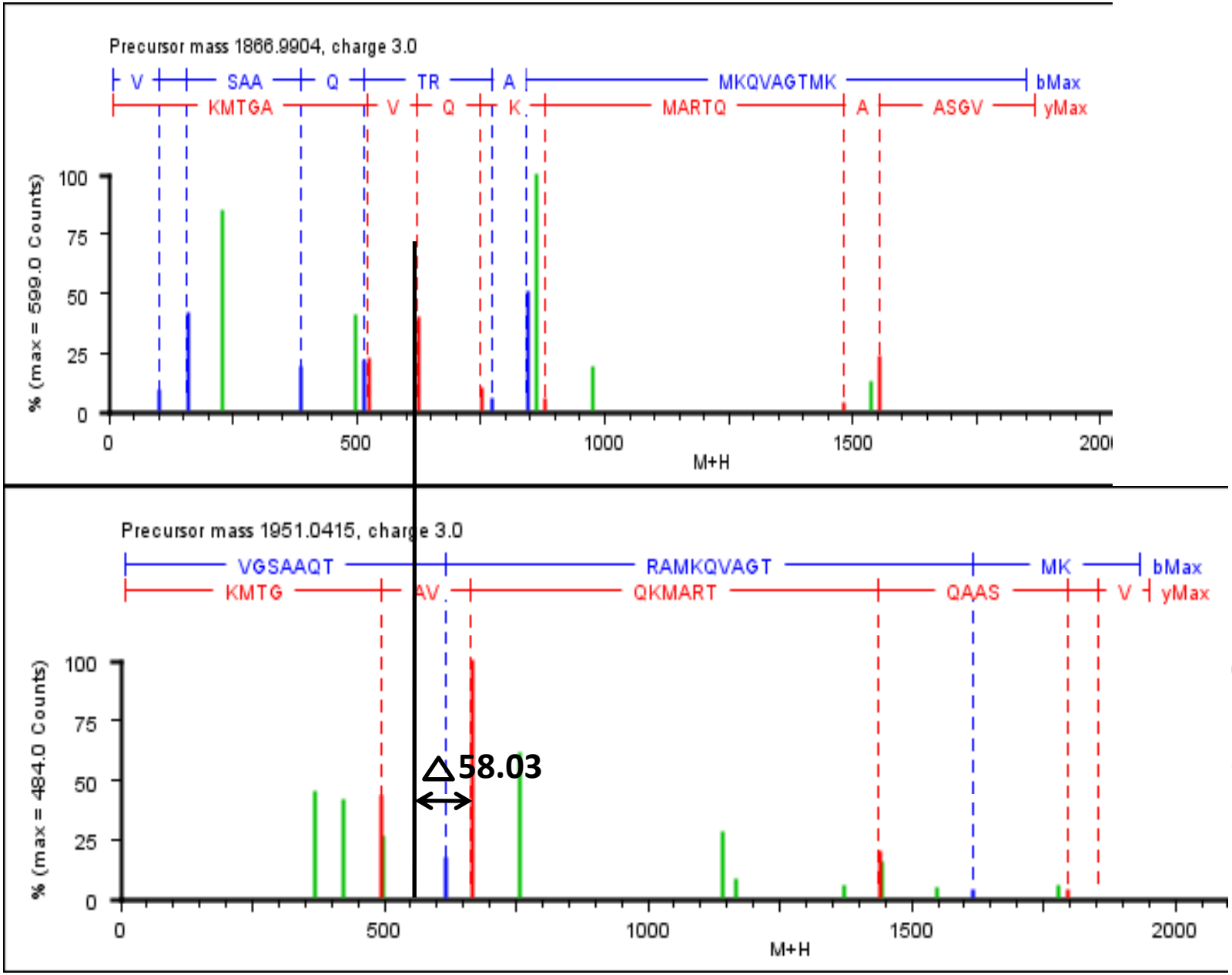
195-204 (R)ISVREPMQTGIKAVDSLVPIGR(MOLD)(G)



333.2027

382.1598: (333.2027 + 49.00)

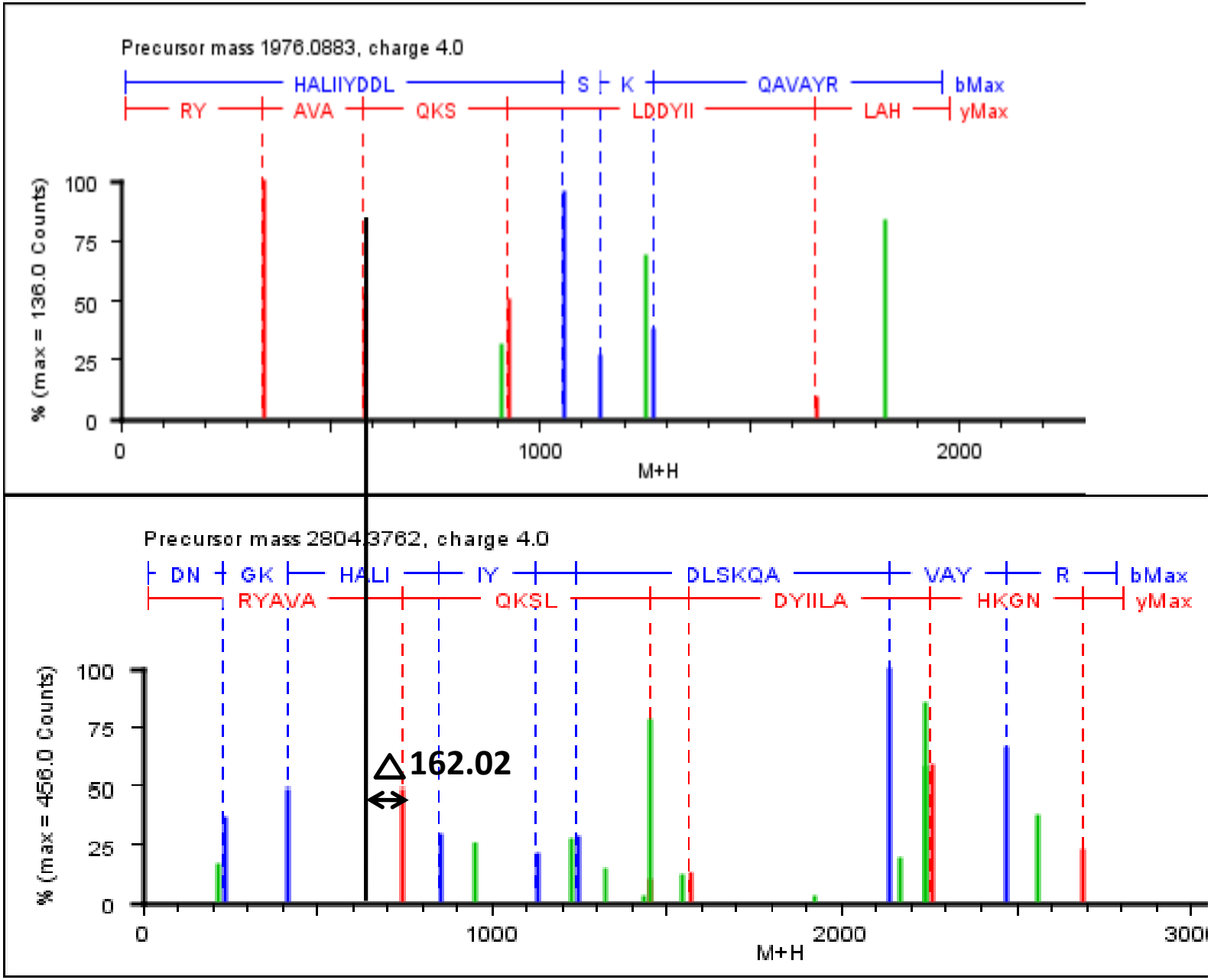
18-34 (R)RAGLVSKNALGSSFVGTR(MOLD)(N)



607.3415

664.3415: (607.34+ 58.03)

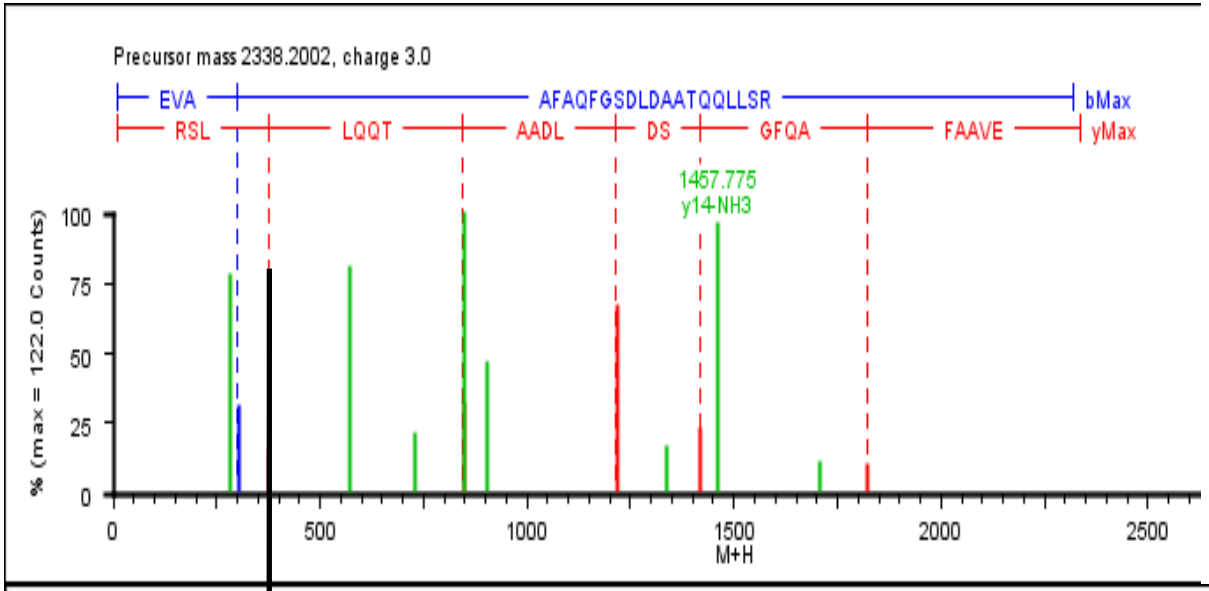
417-434 (R)VGSAAQTRAMKQVAGTMK(MOLD)(L)



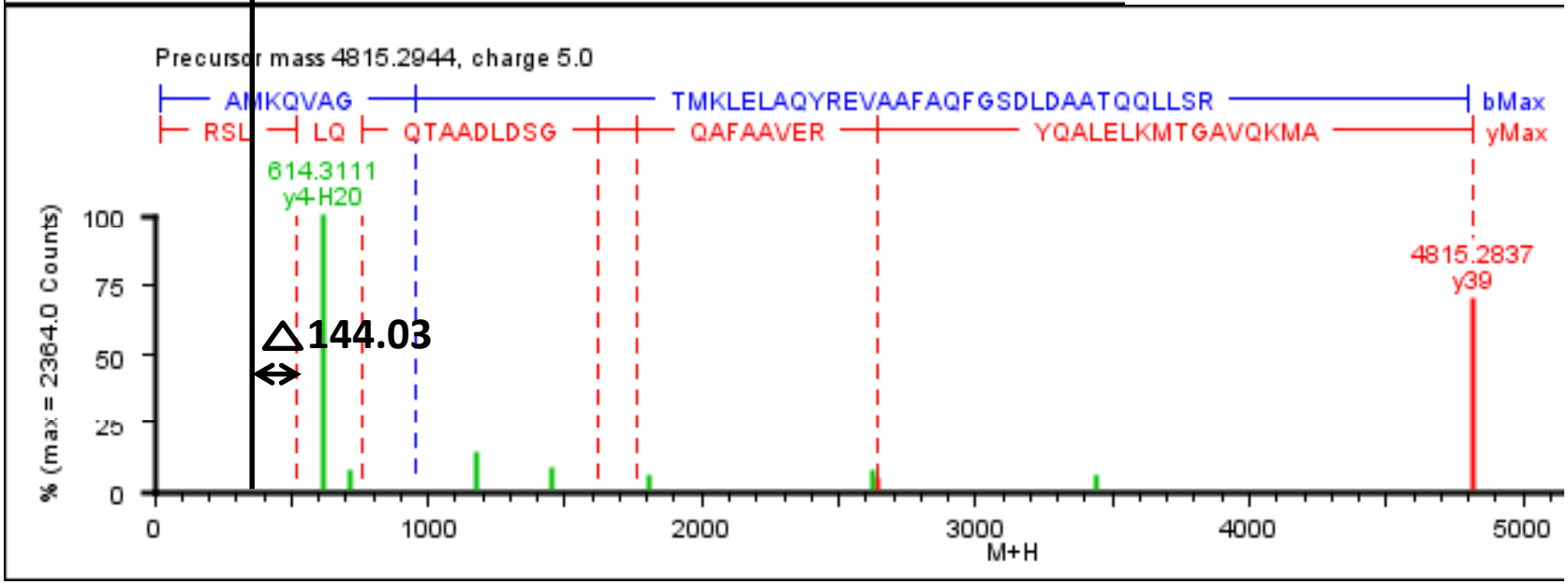
579.3374

741.3374: (579.2902 + 162.02

306-322 (K)HALIIYDDLSKQAVAYR(Gly)(Q)

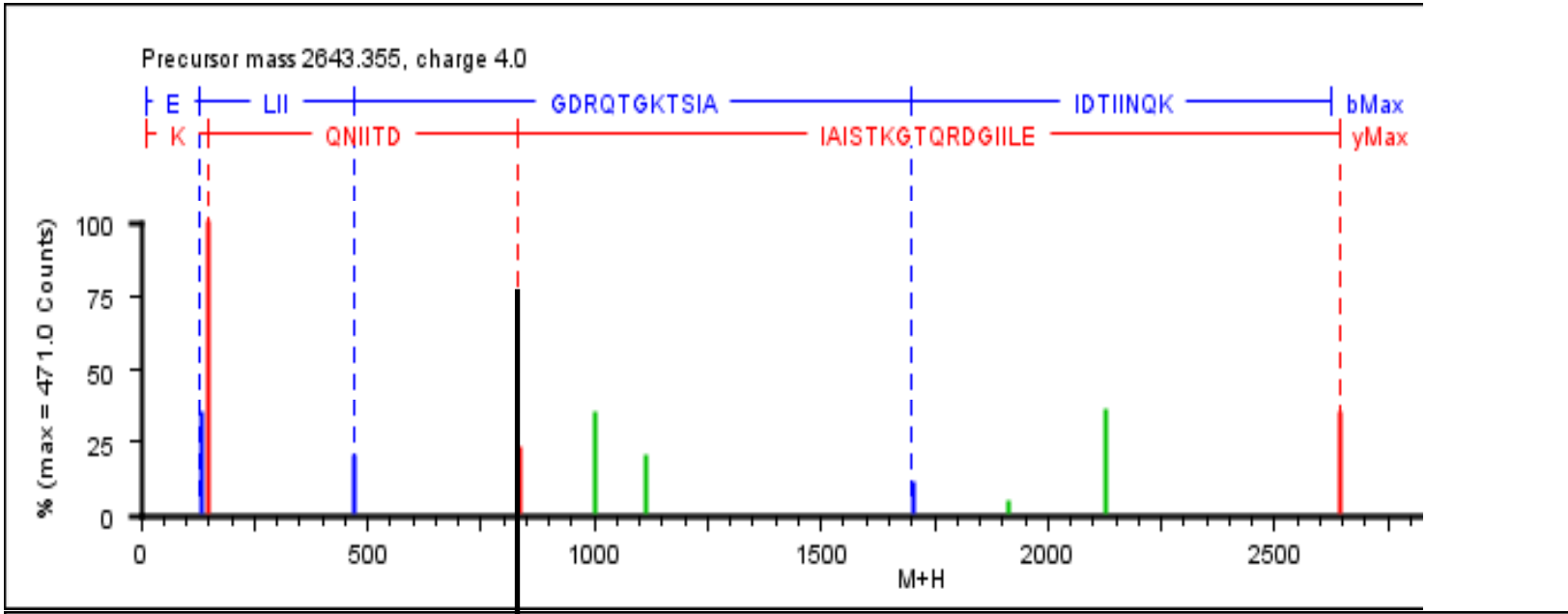


375.2097

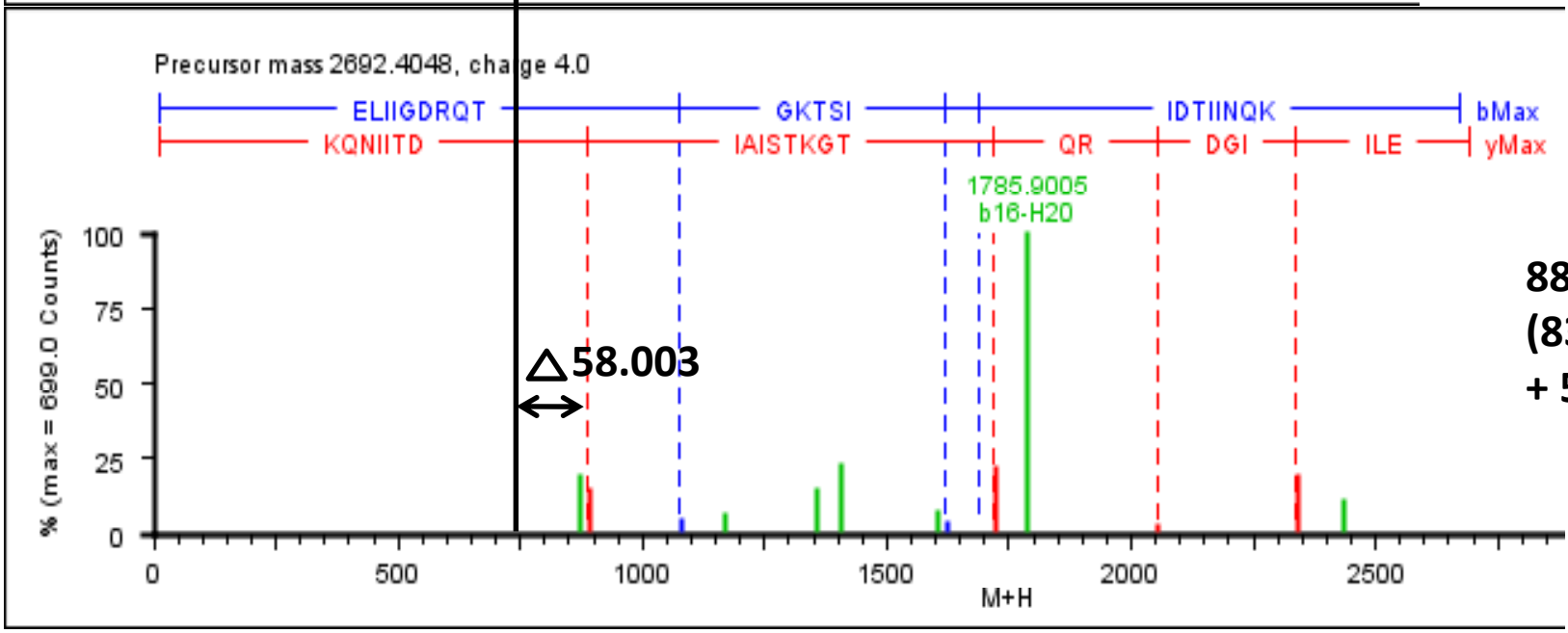


519.2749: (375.20 +144.03)

425-463 (R)AMKQVAGTMKLELAQYREVAAFAQFGSDLDAATQQLLSR(ImiA)(G)

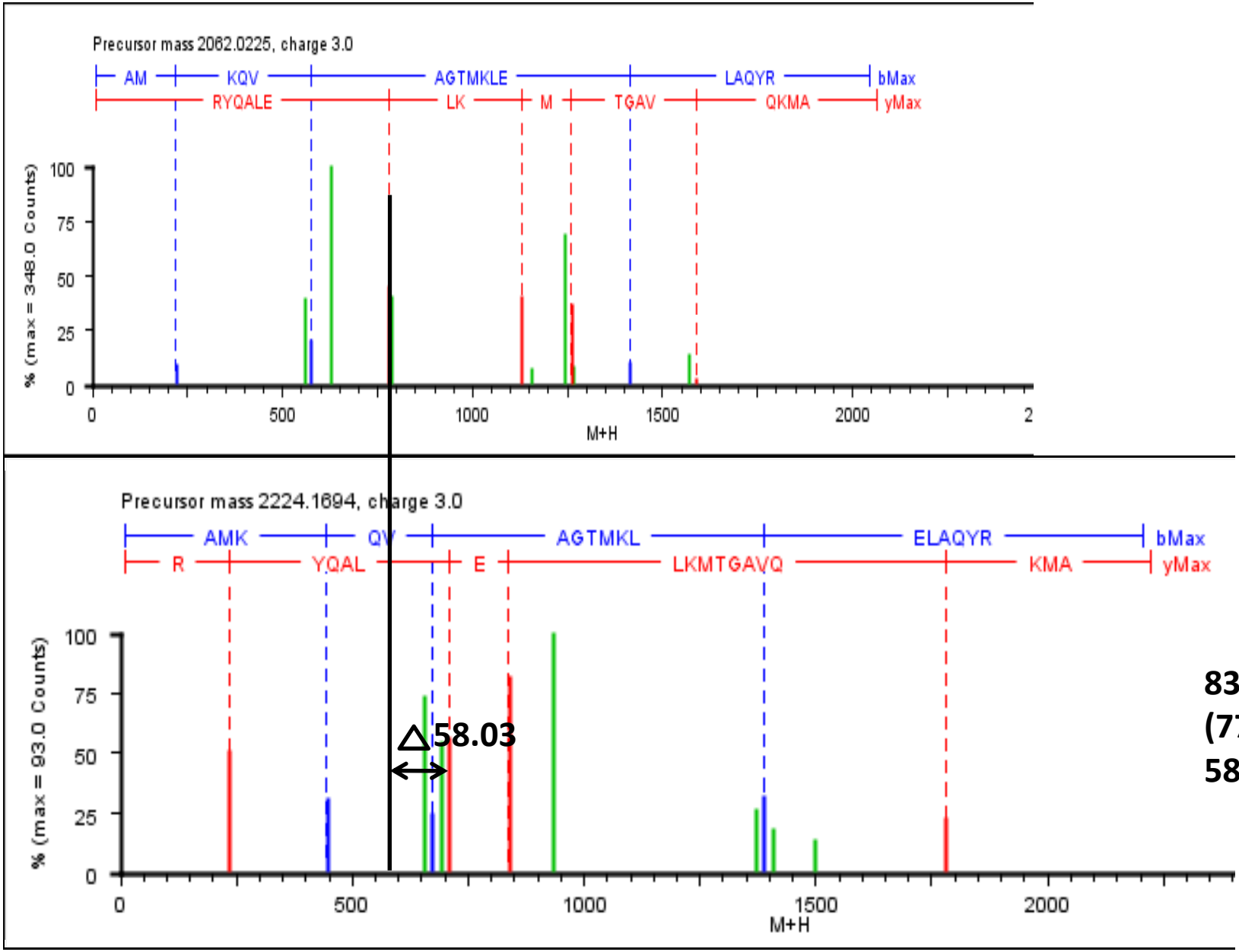


831.4121



889.399: (831.4121 + 58.003

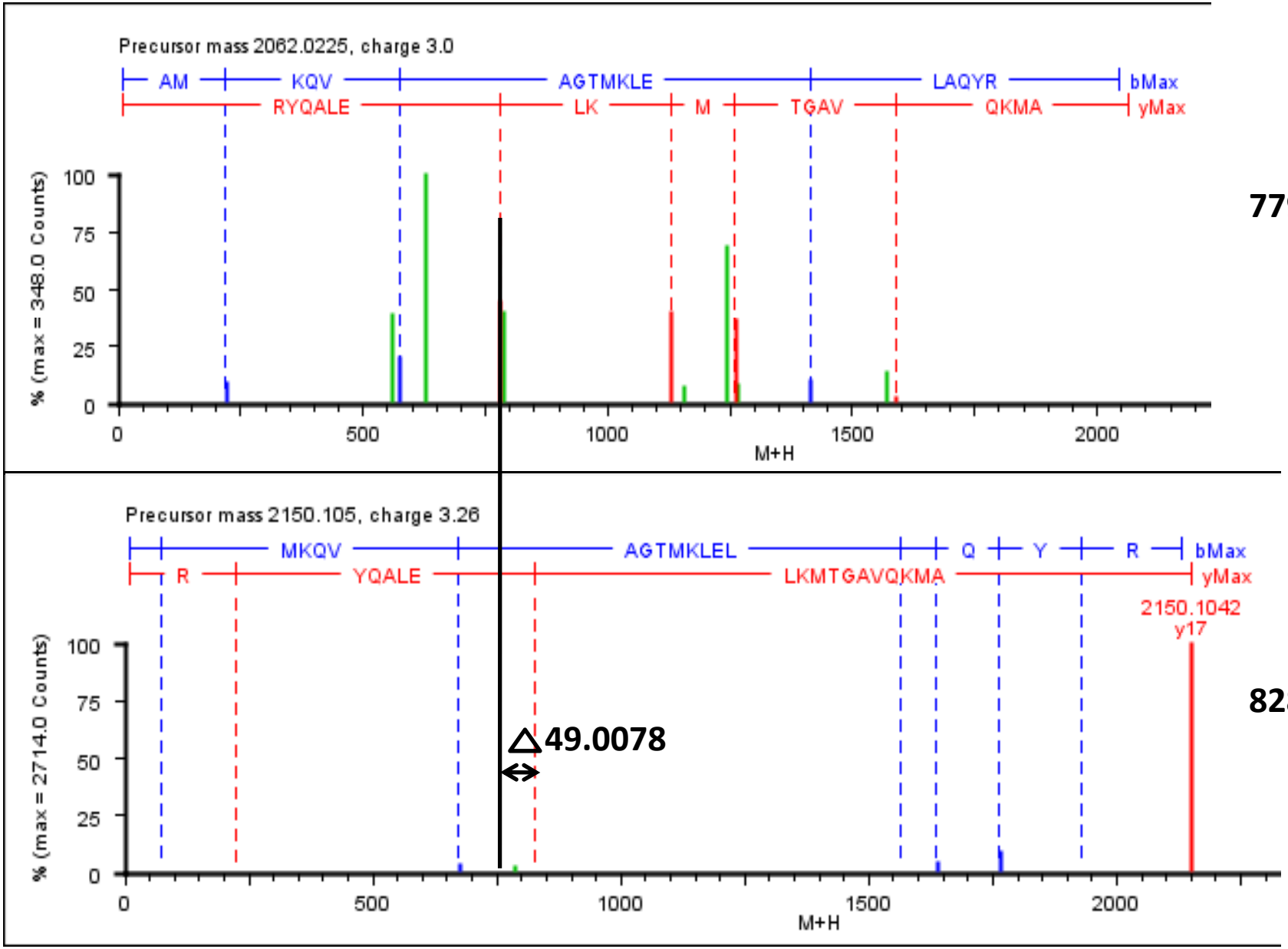
375.2097 (R)ELIIGDRQTGKTSIAIDTIINQK(CML)(R)



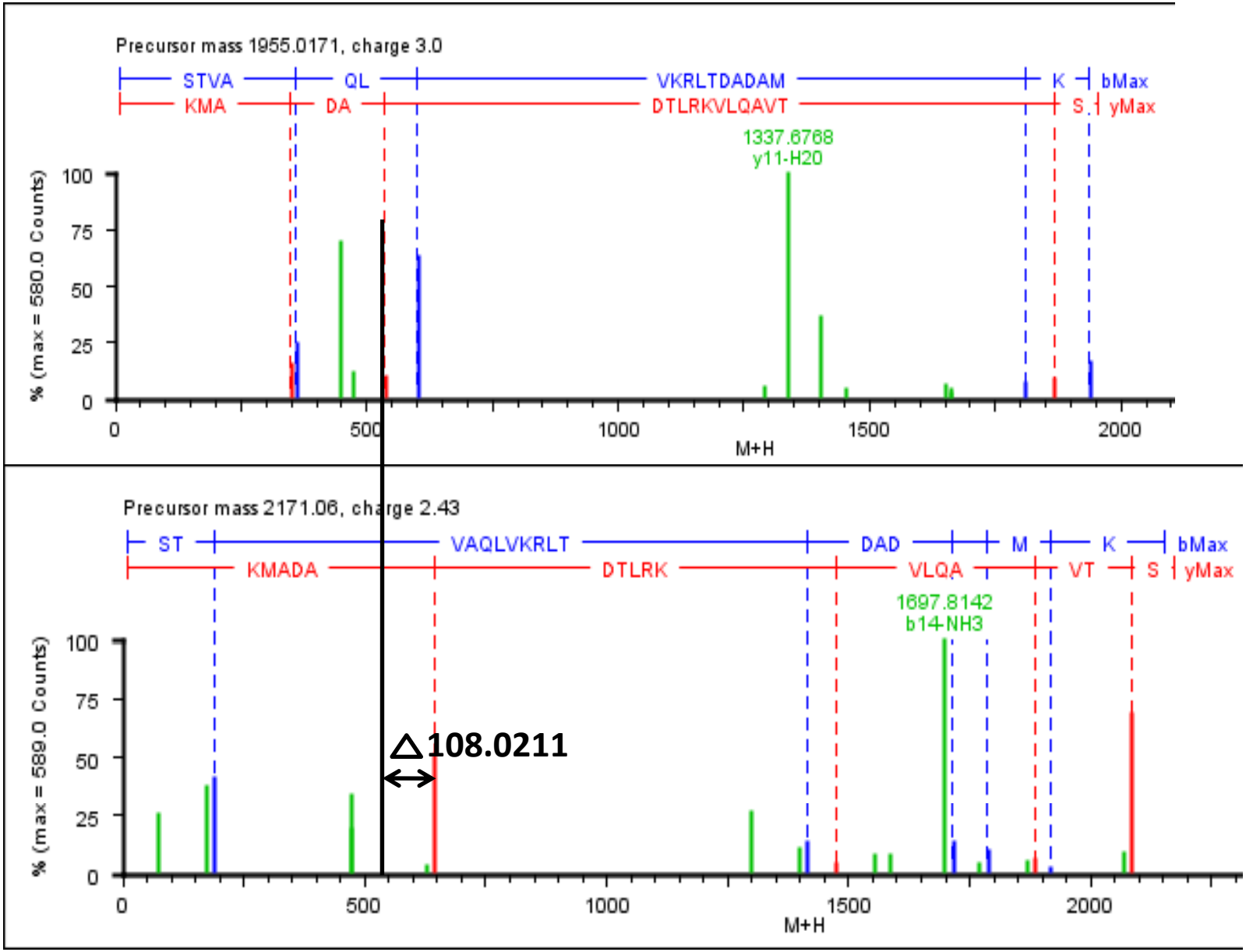
779.33

837.4419: (779.33+ 58.03)

831.4121 (R)AMKQVAGTMKLELAQYR(Pento)(E)



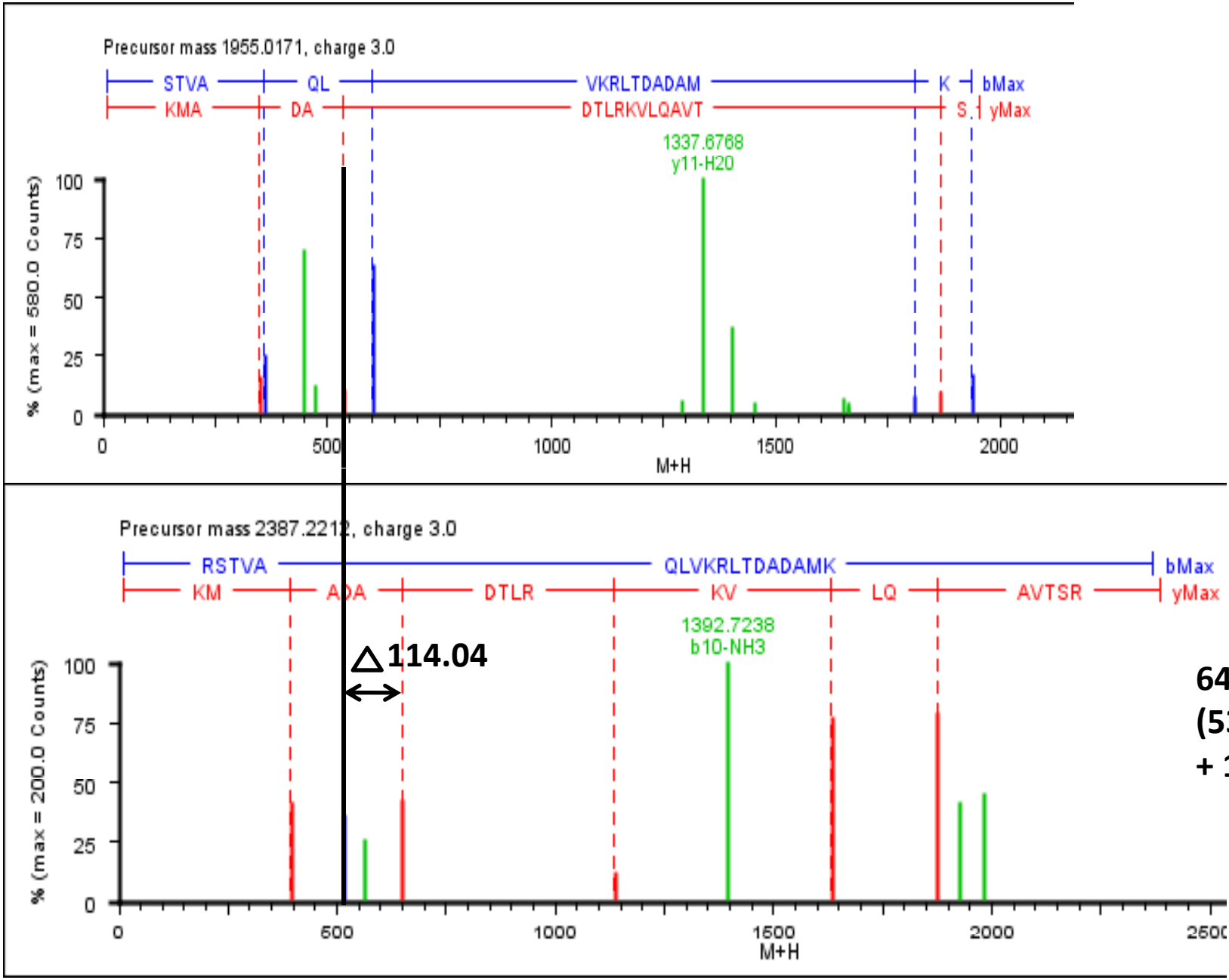
425-441 (R)AMKQVAGTMKLELAQYR(MOLD)(E)



535.2043

643.2515: (535.20+ 108.02)

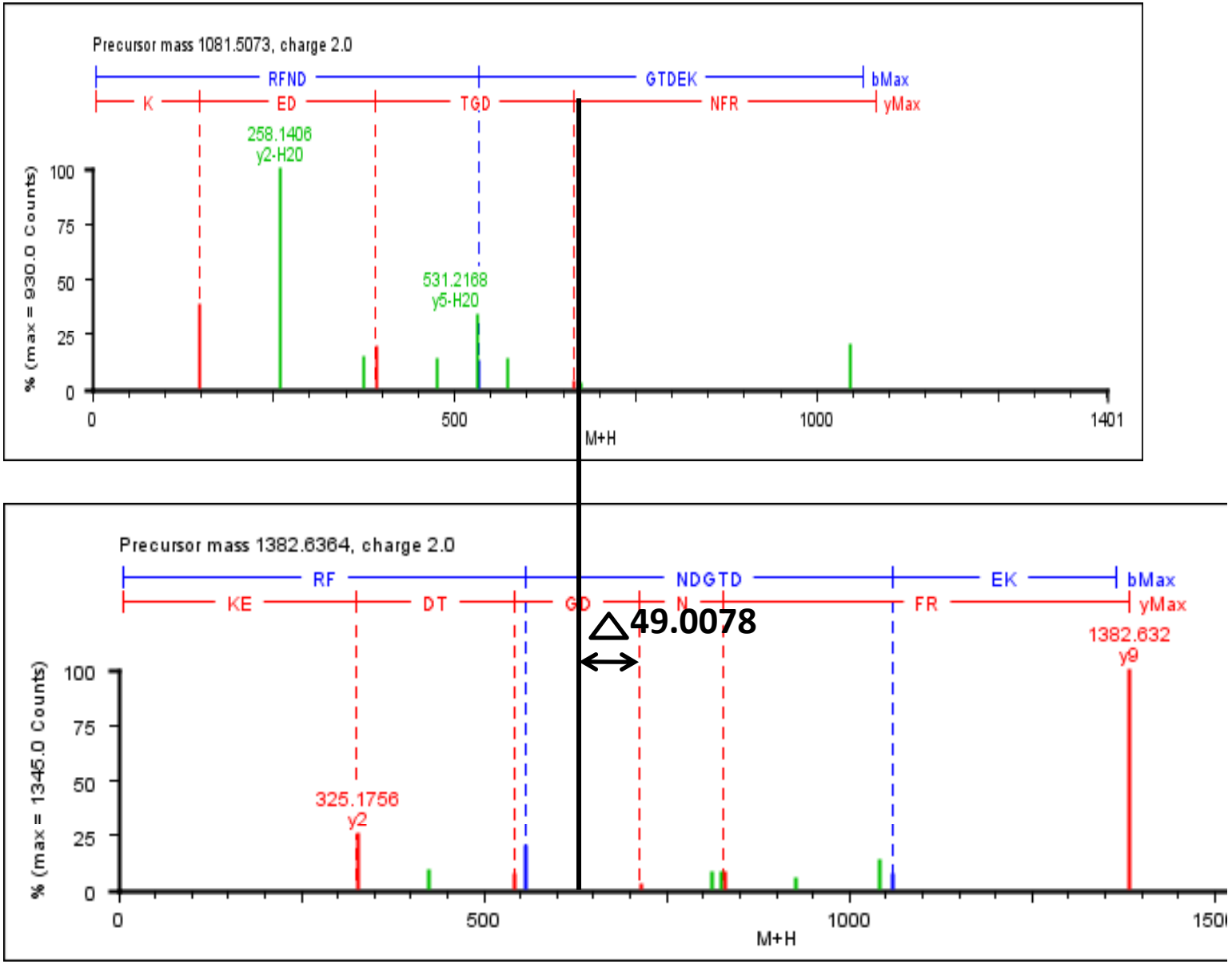
254-270 (R)STVAQLVKRLTDADAMK(Pyr)(Y)



535.2043

649.2541: (535.2043 + 114.04)

253-270 (K)RSTVAQLVKRLTDADAMK(Ubi)(Y)

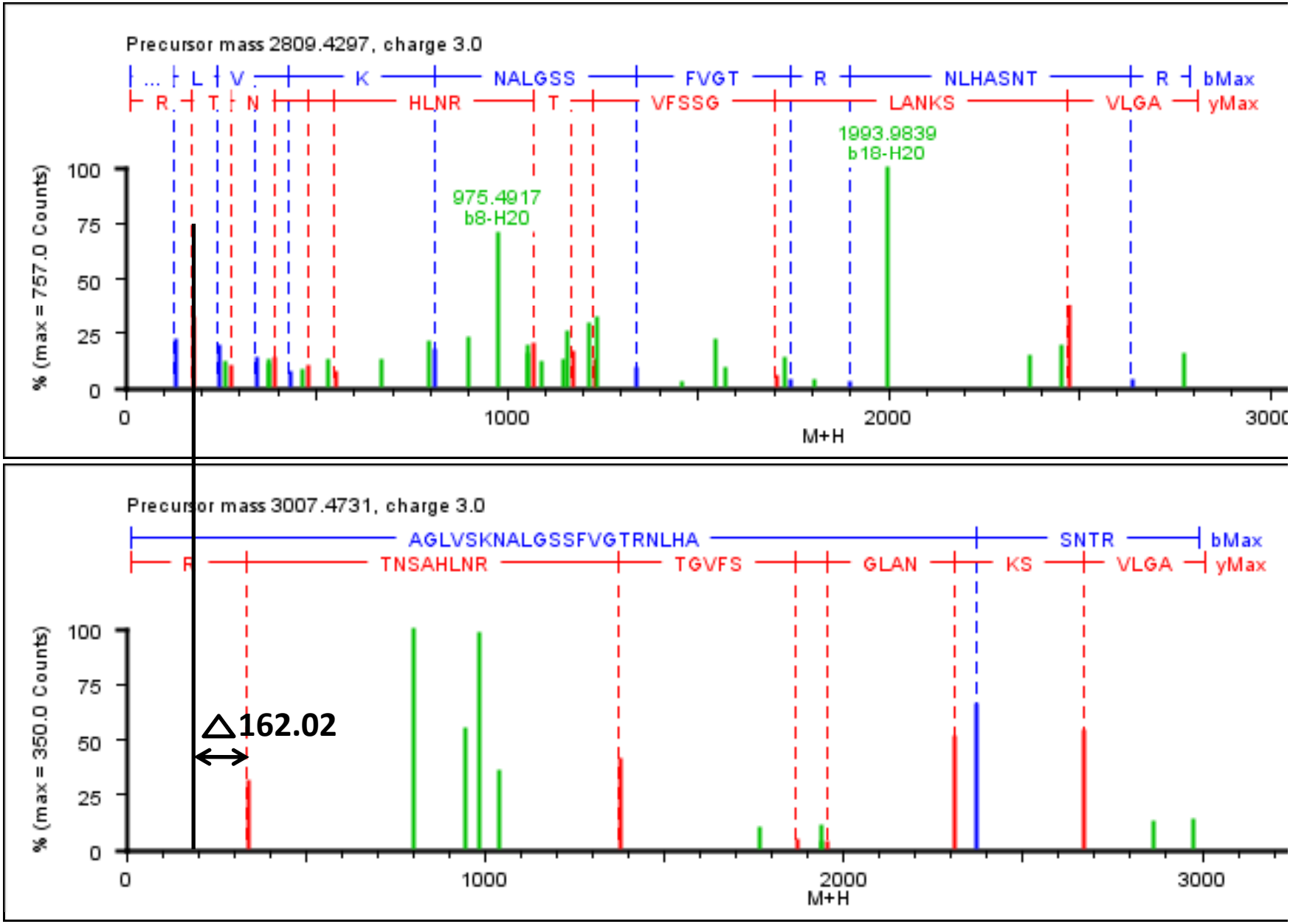


664.3463

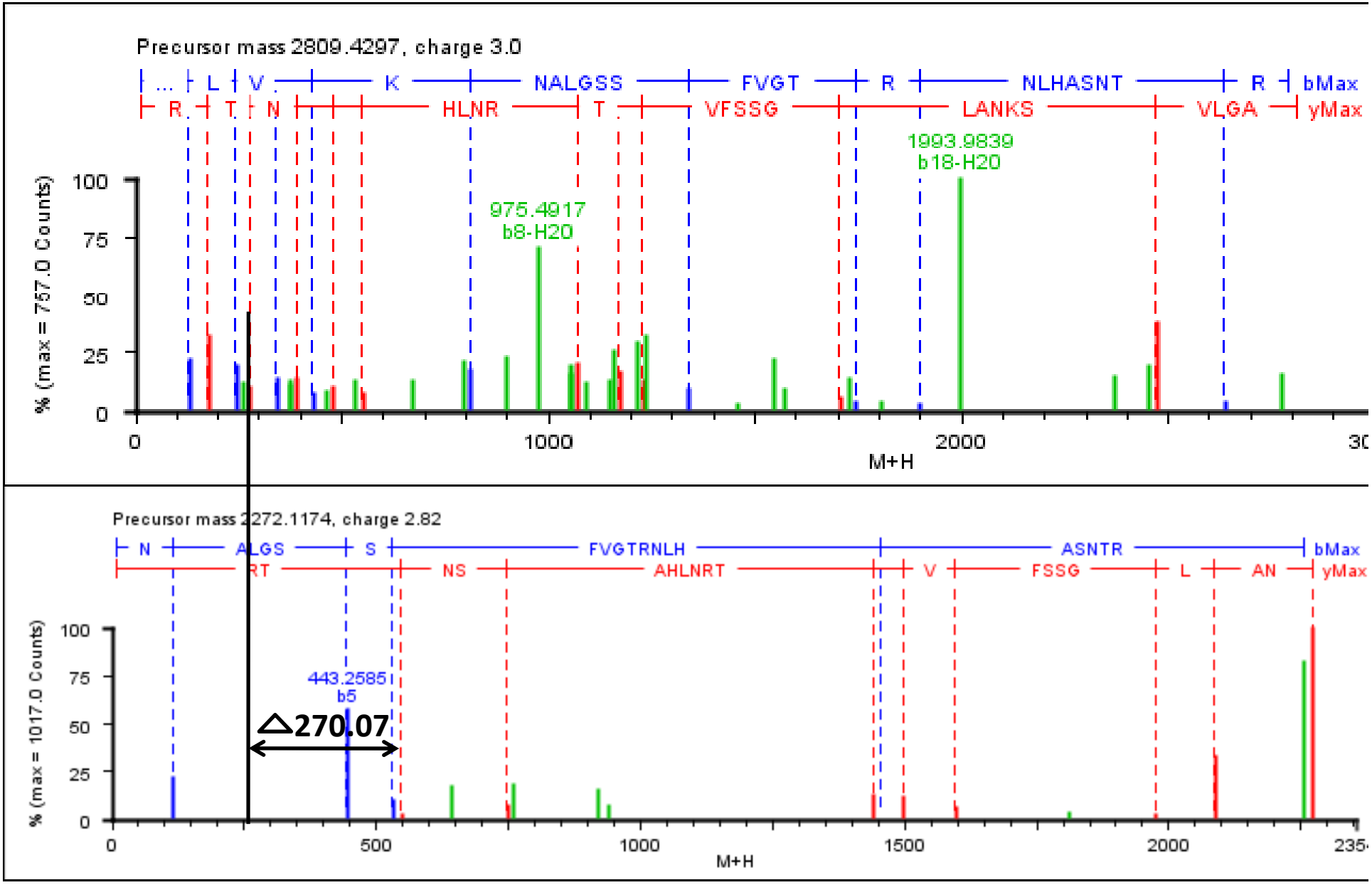
713.3528:
(664.34+ 49.00

231-239

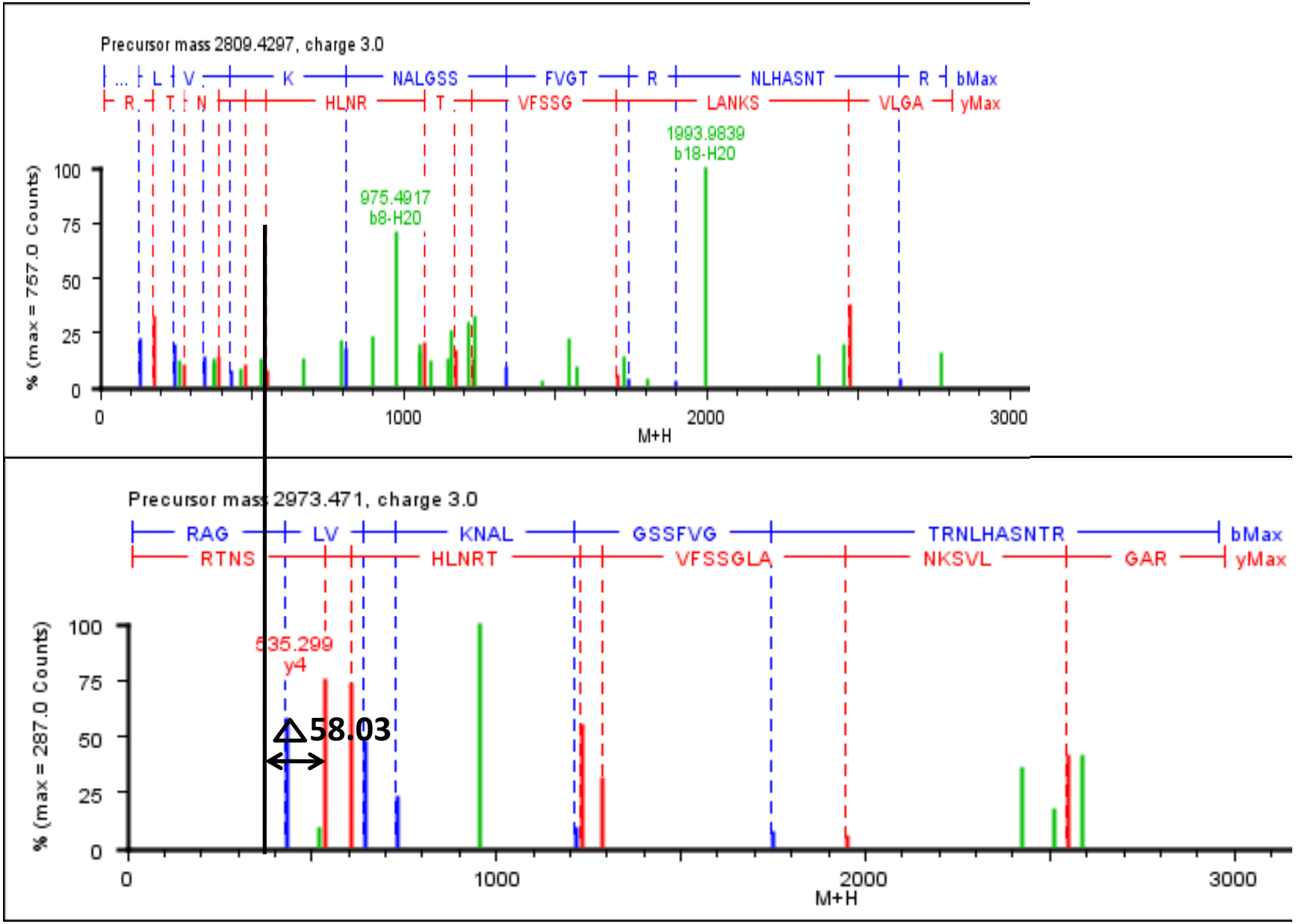
(K)RFNDGTDEK(MOLD)(K)



18-42 (R)AGLVSKNALGSSFVGTRNLHASNTR(Gly)(L)

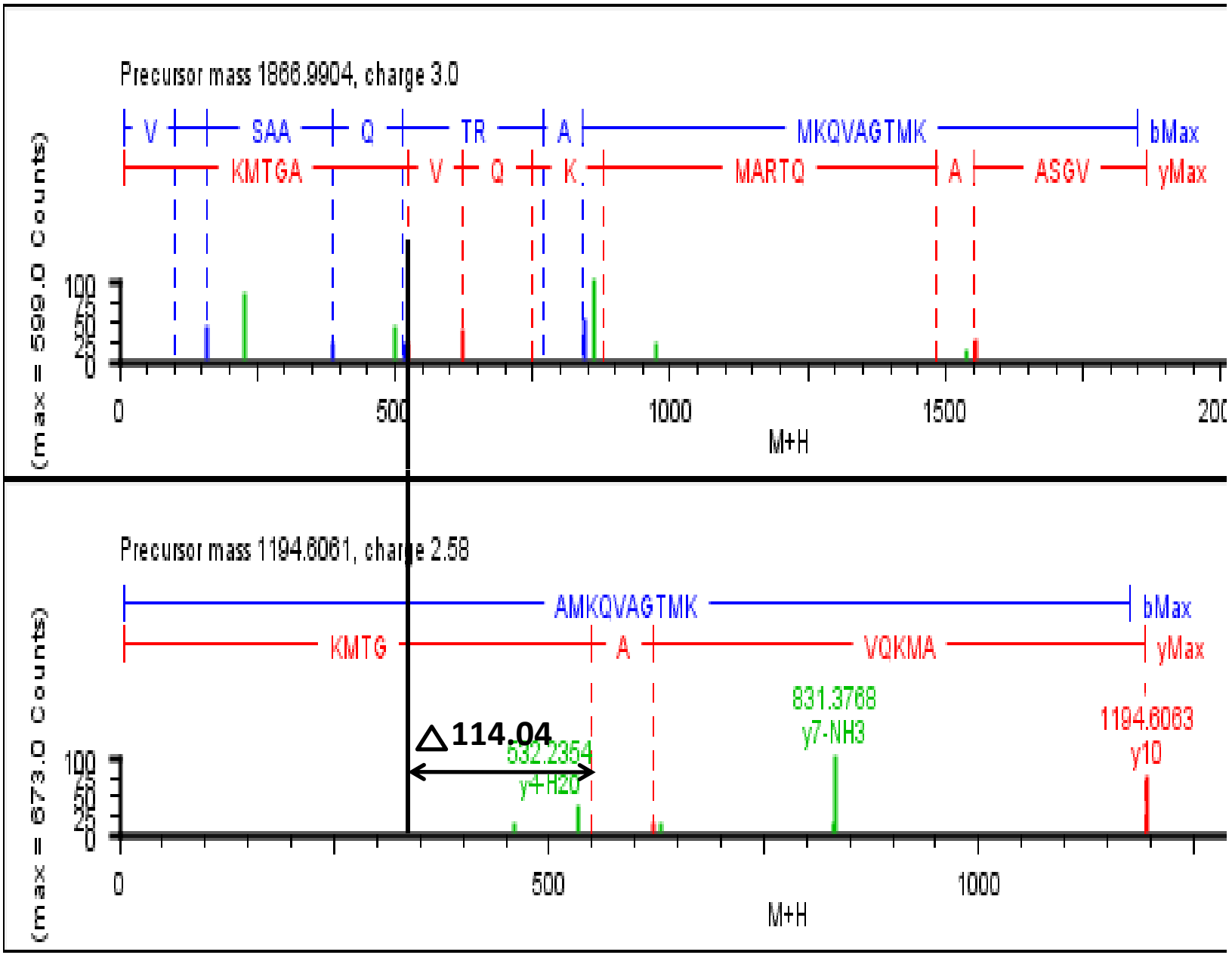


24-42 (K)NALGSSFVGTRNLHASNTR(AFGP)(L)



17-42

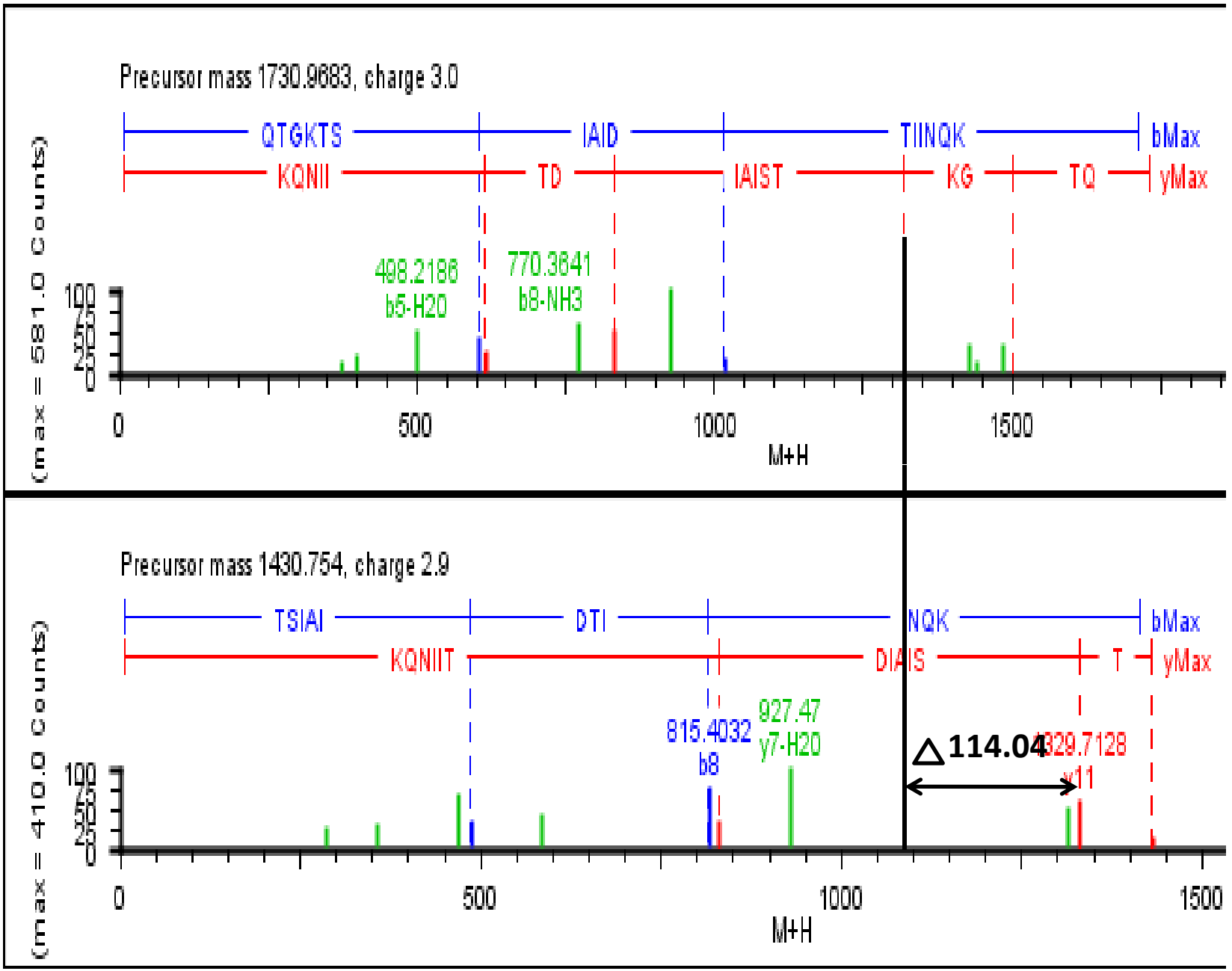
(R)RAGLVSKNALGSSFVGTRNLHASNTR(Pento)(L)



523.2258

621.3326: (523.22+ 114.04)

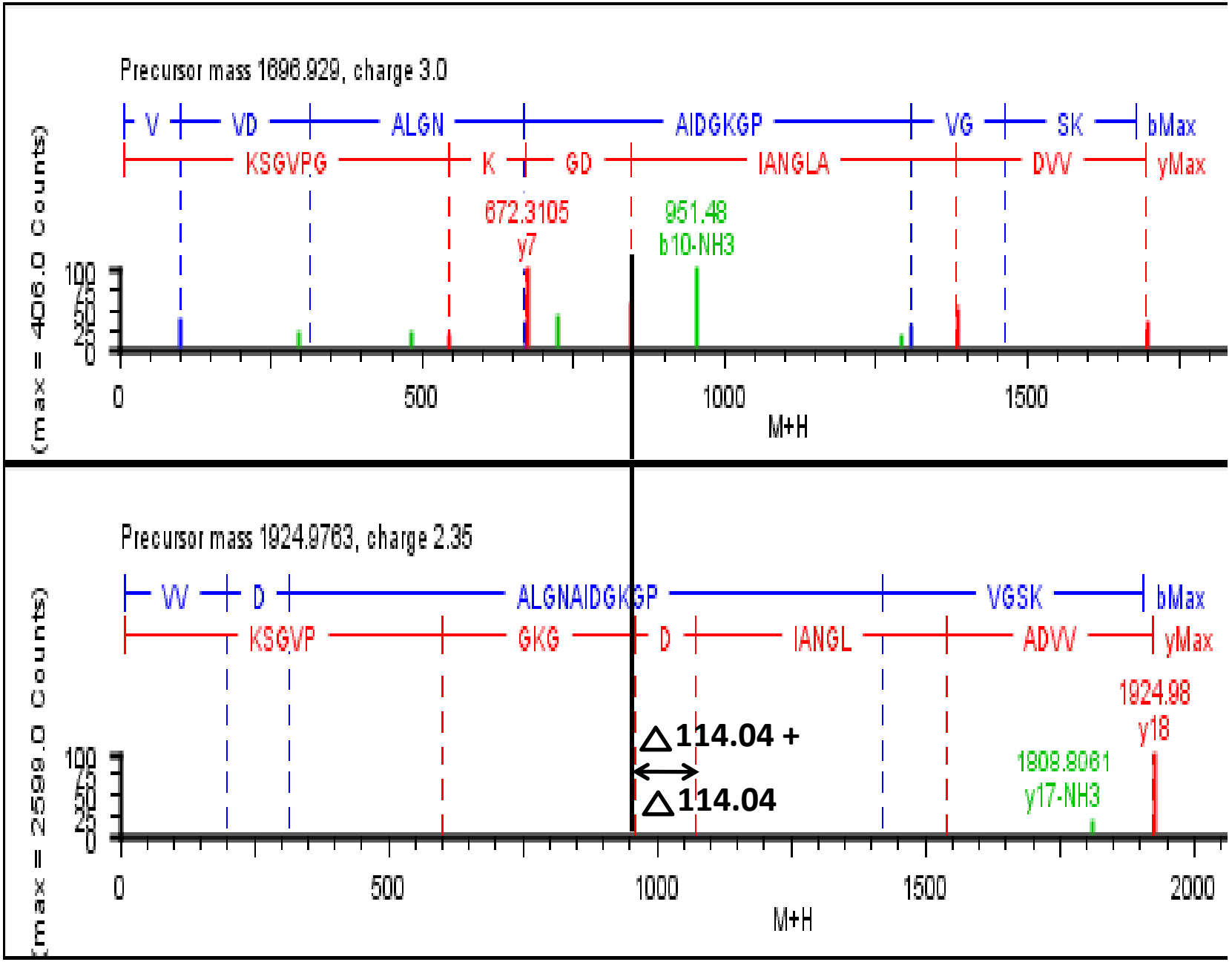
425-434 (R)AMKQVAGTMK(Ubi)(L)



1316.9087

1430.754: (1316.90+ 114.04)

219-230 (K)TSIAIDTIINQK(Ubi)(R)

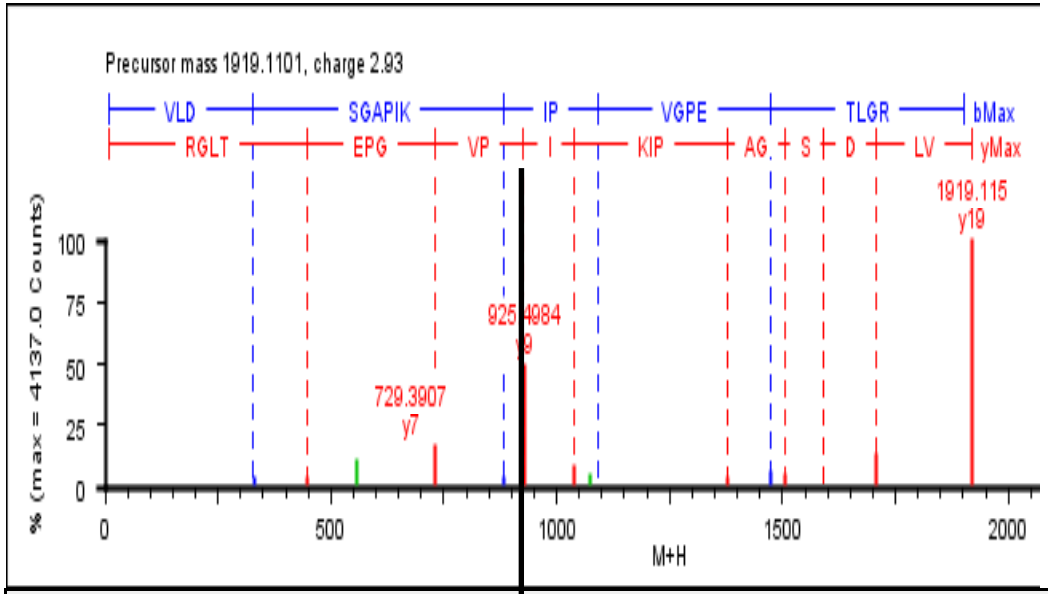


844.4328

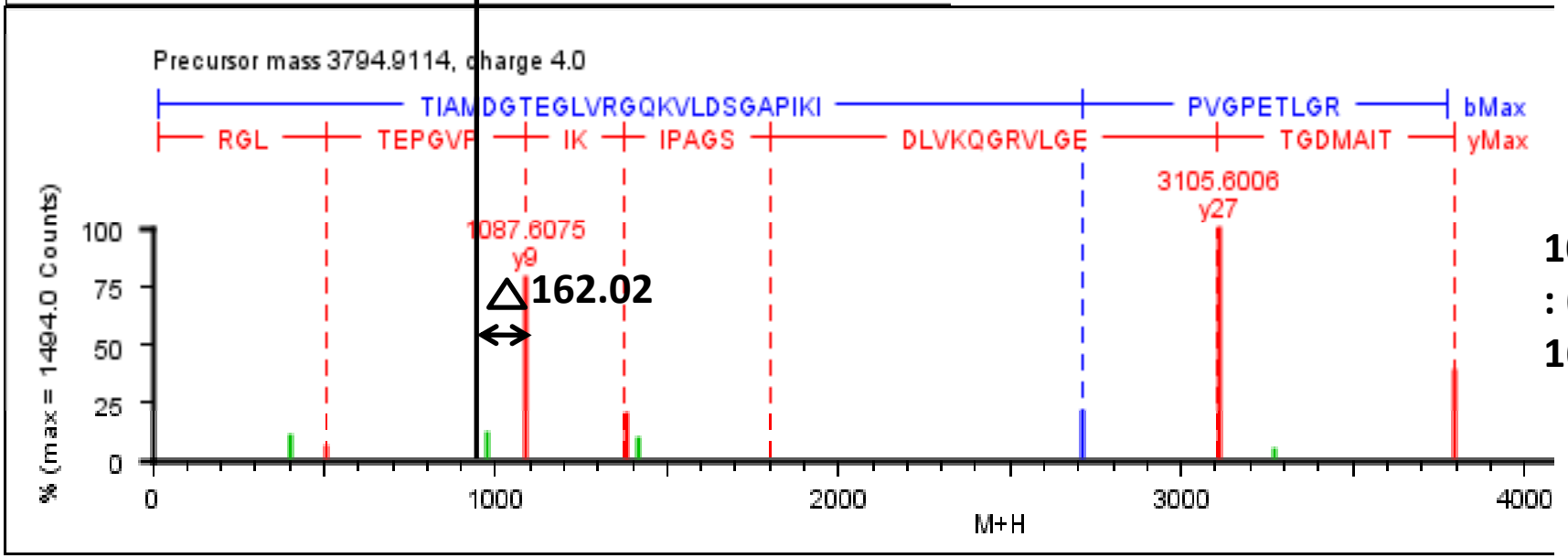
1072.6128 : (844.43+ 144.04+ 144.04)

150-167 (R)VVDALGNAIDGK(ubi)GPVGSK(Ubi)(I)

ATP beta

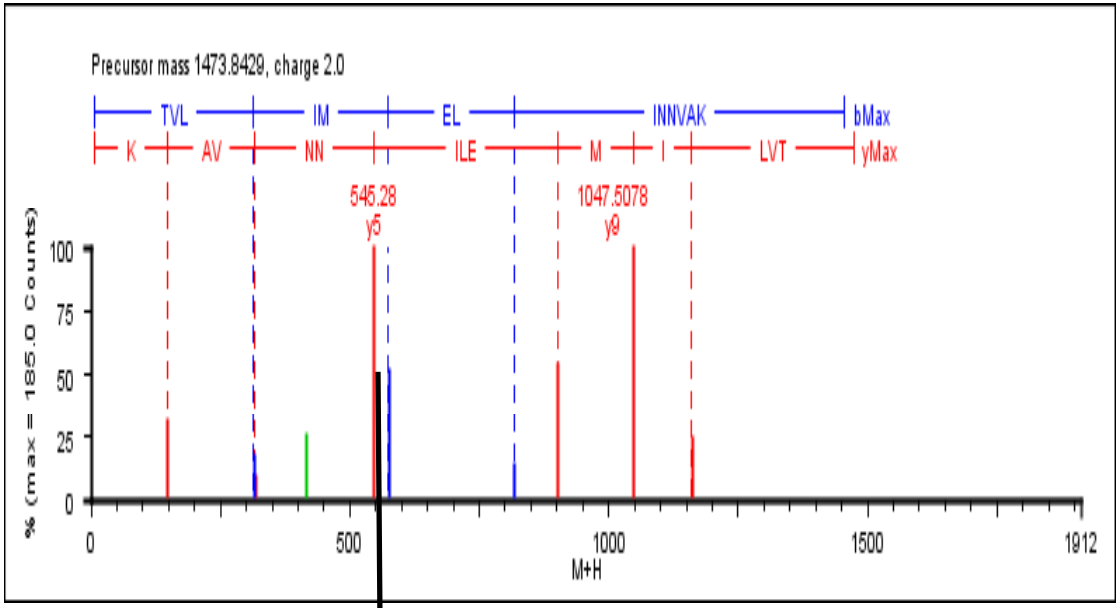


925.4984

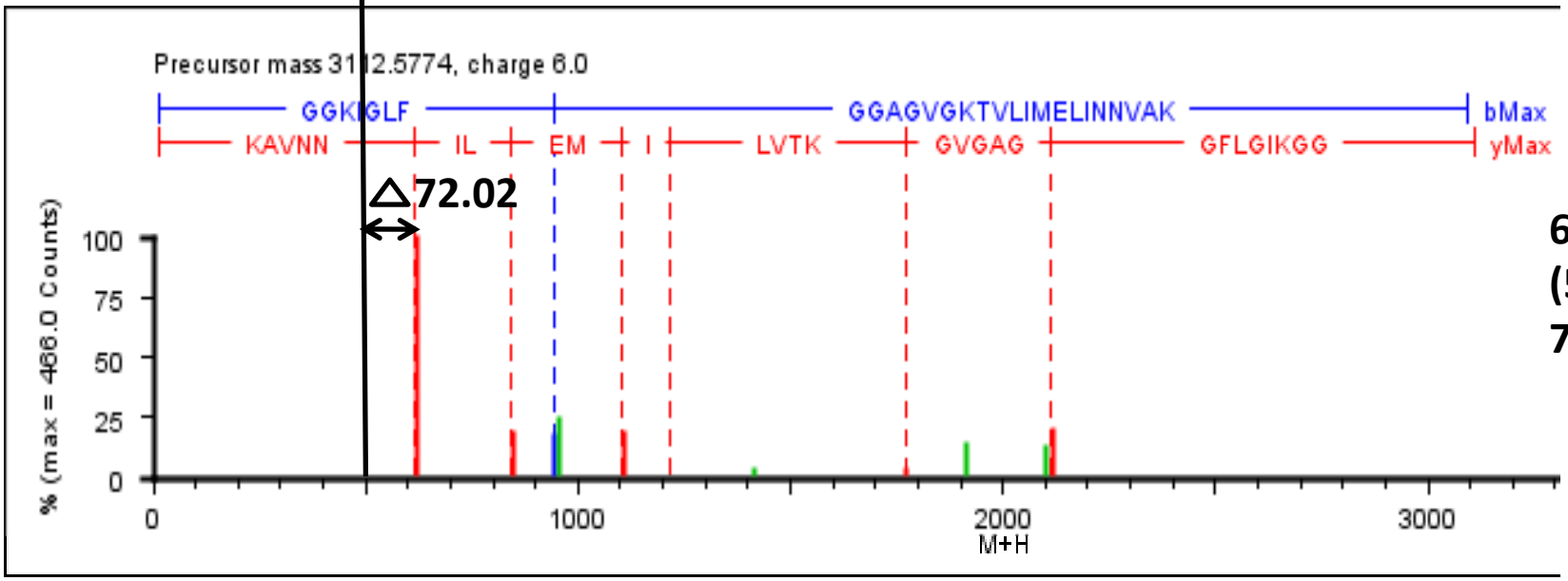


1087.6075 : (925.49+ 162.02)

125-143 (R)TIAMDGTEGLVRGQKVLDSGAPIKIPVGPETLGR(Gly)(I)

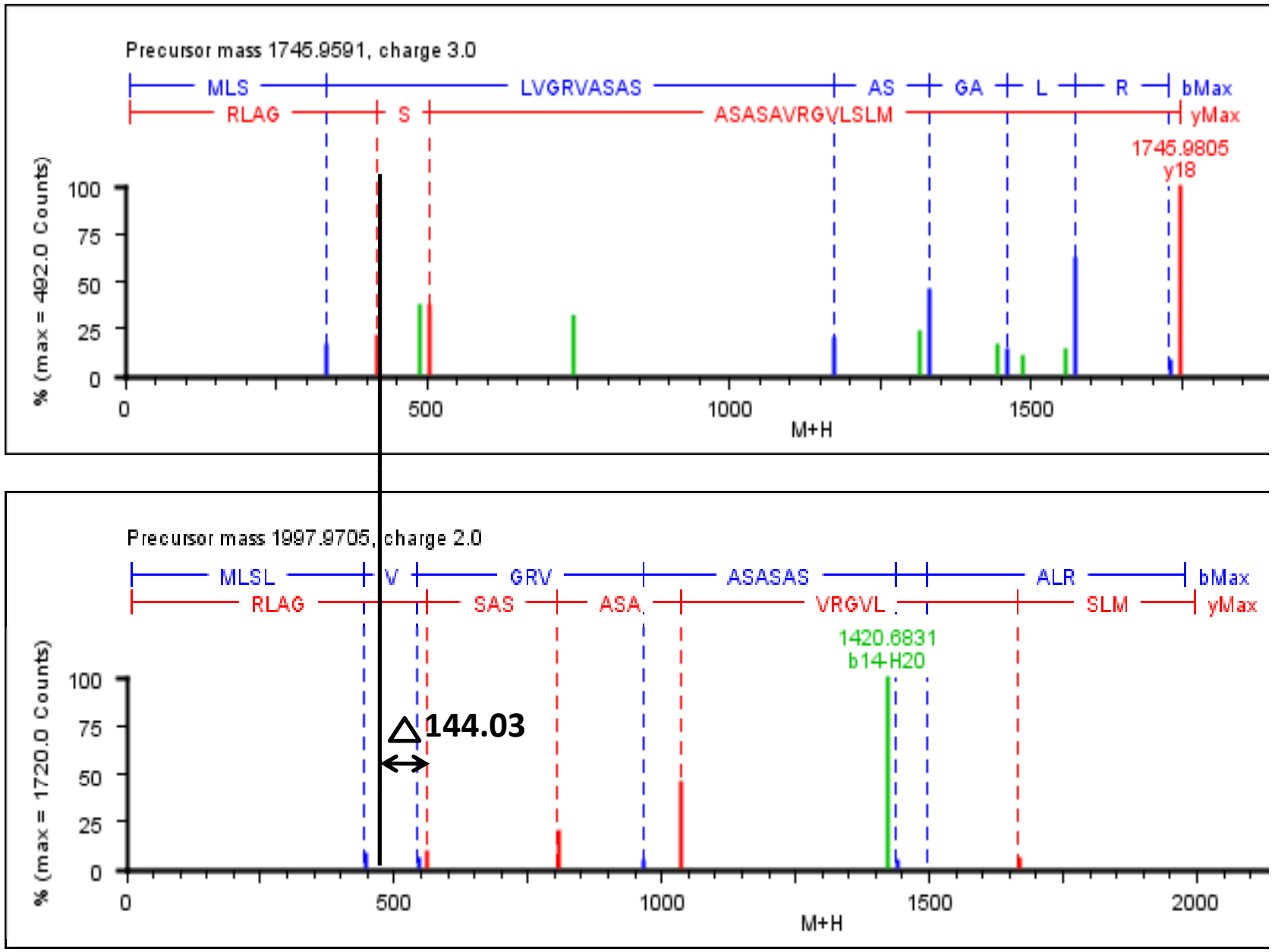


545.28



617.3039: (545.28+ 72.02)

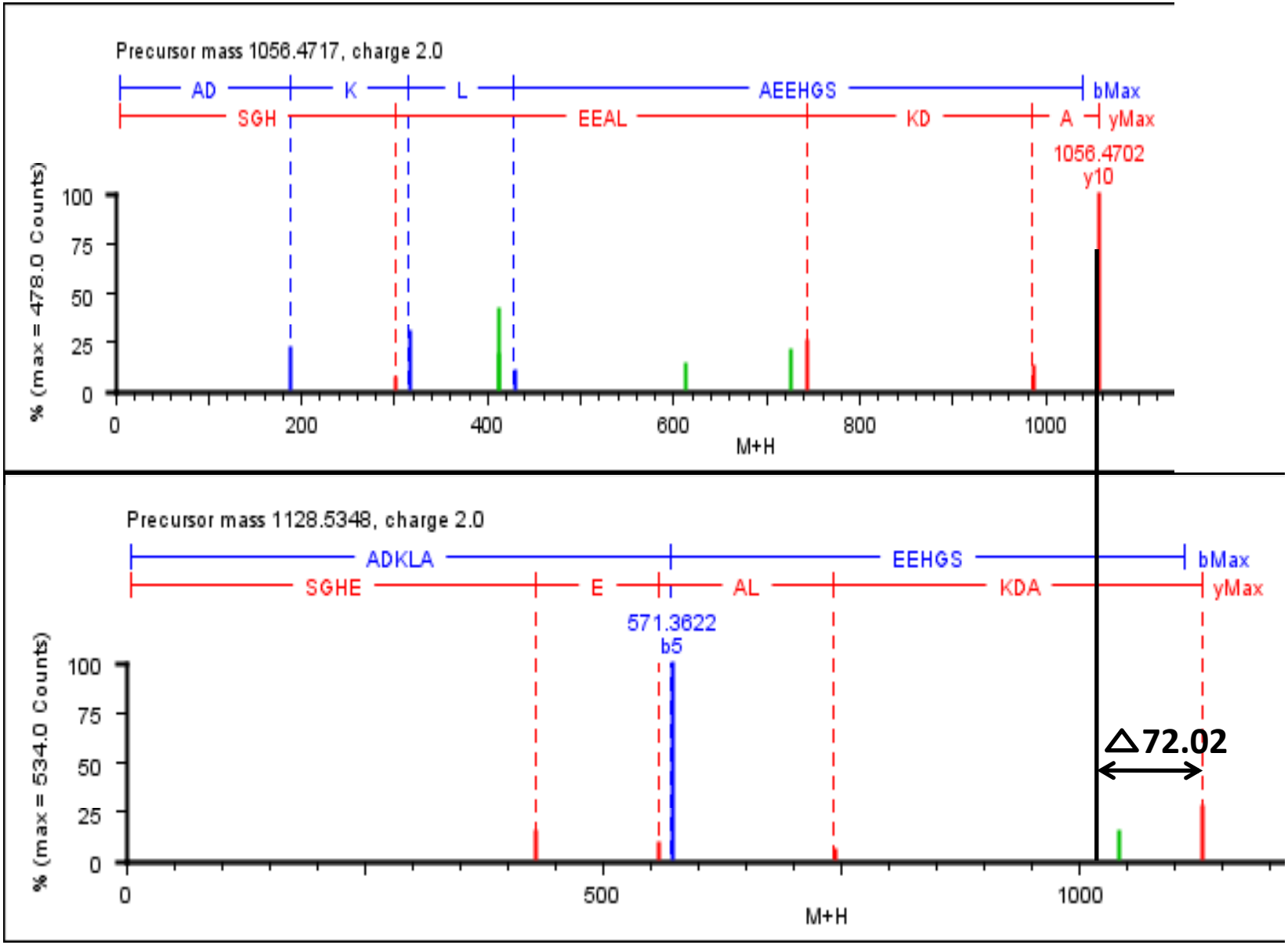
213-225 (K)TVLIMELINNVAK(CEL)(A)



416.2748

560.264: (416.2748 + 144.03)

1-18 (-)MLSLVGRVASASASGALR(ImiA)(G)

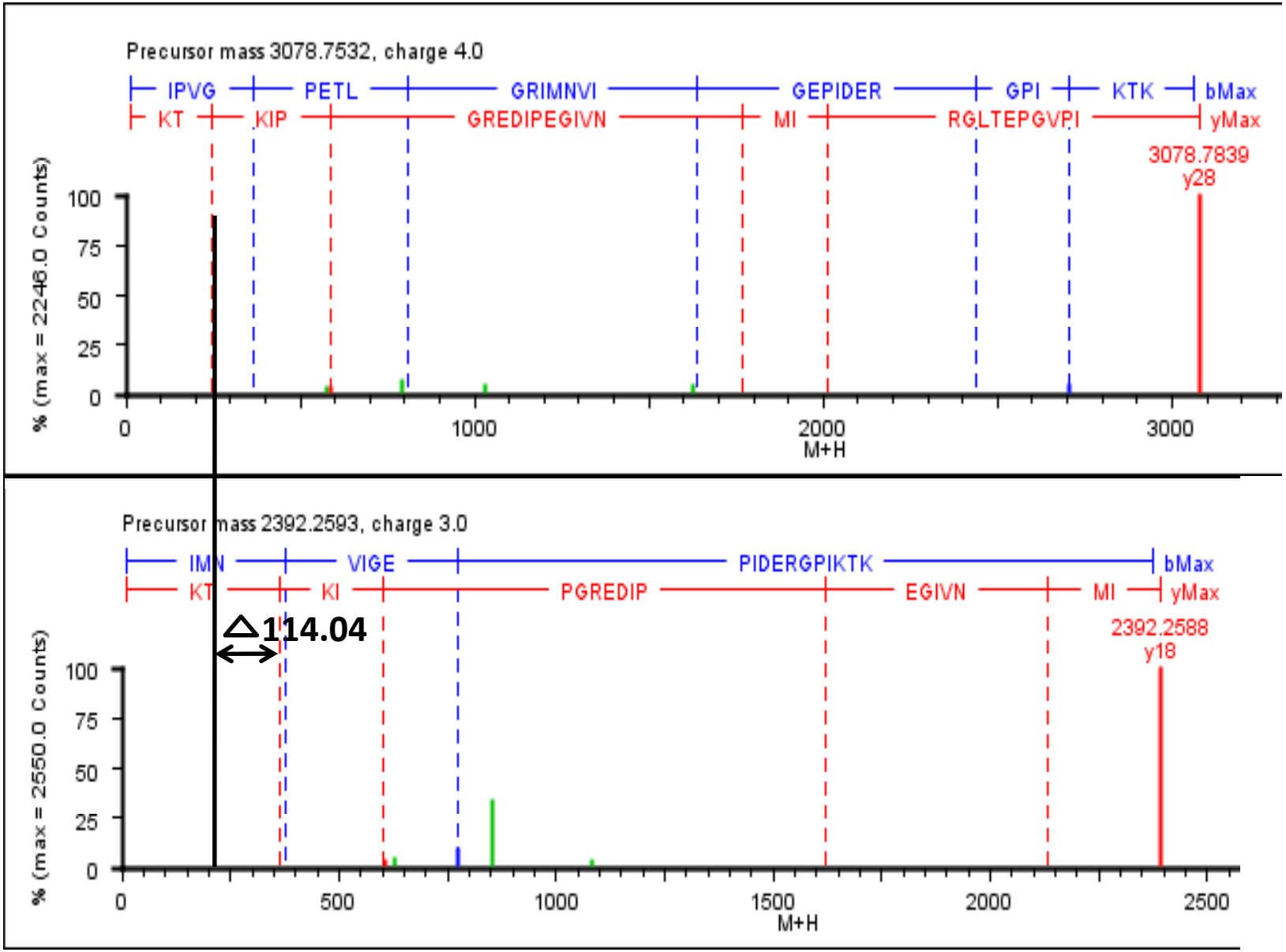


1056.4702

1128.5419: (1056.4702+ 72.02

520-529

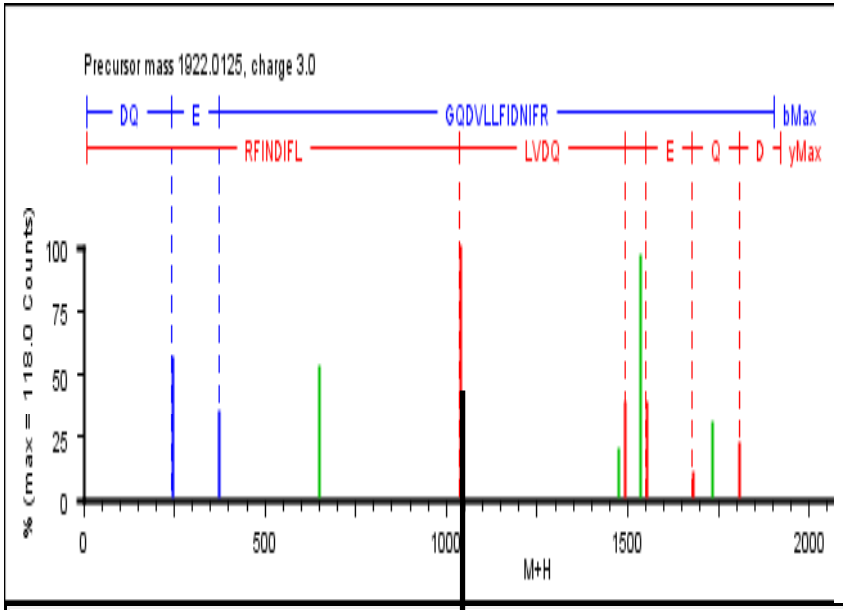
(K)ADK(CEL)LAEEHGS(-)



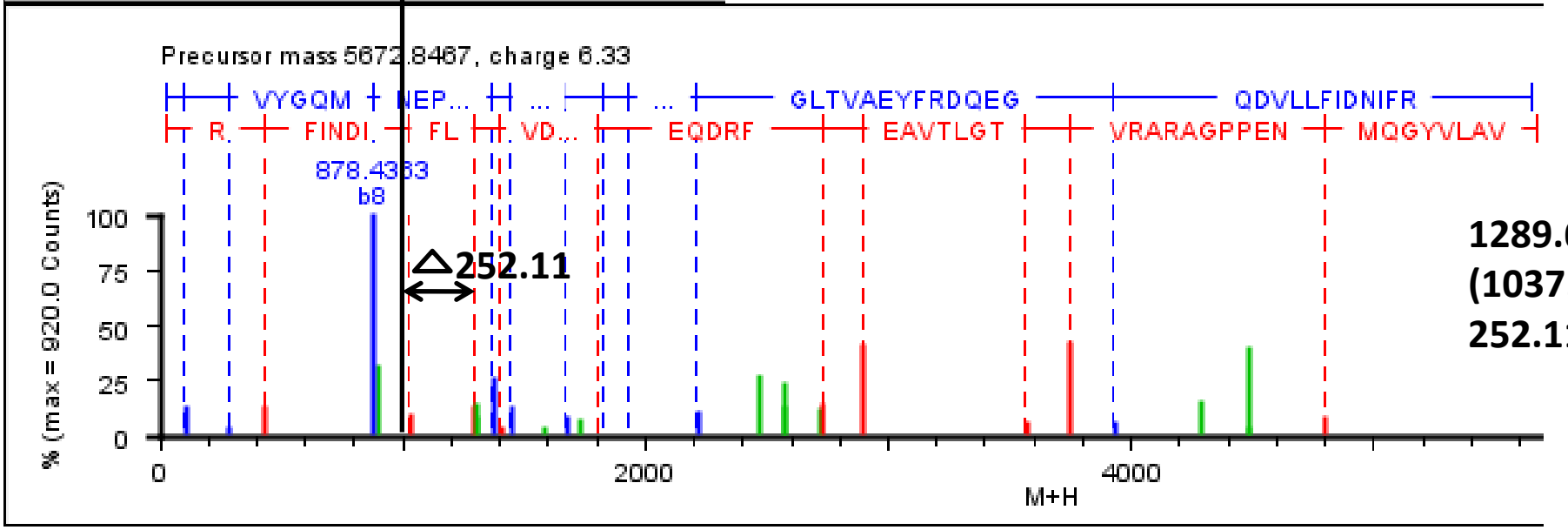
248.1532

362.2053: (248.15+ 114.04)

134-161 (R)IMNVIGEPIDERGPIKTK(Ubi)(Q)

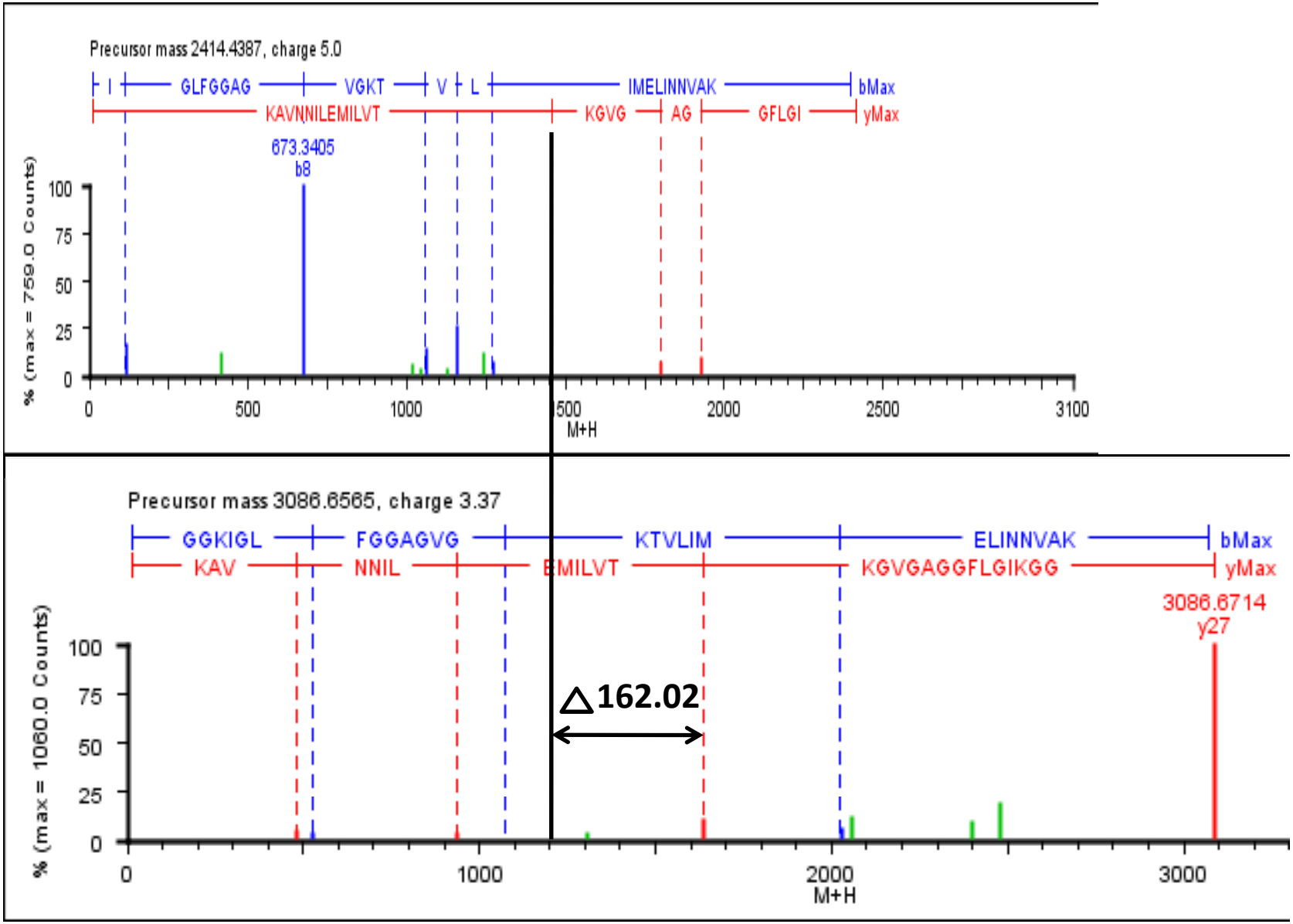


1037.5018



1289.6475: (1037.50+ 252.11)

265-310 (K)VALVYGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFR(Crossline)(F)

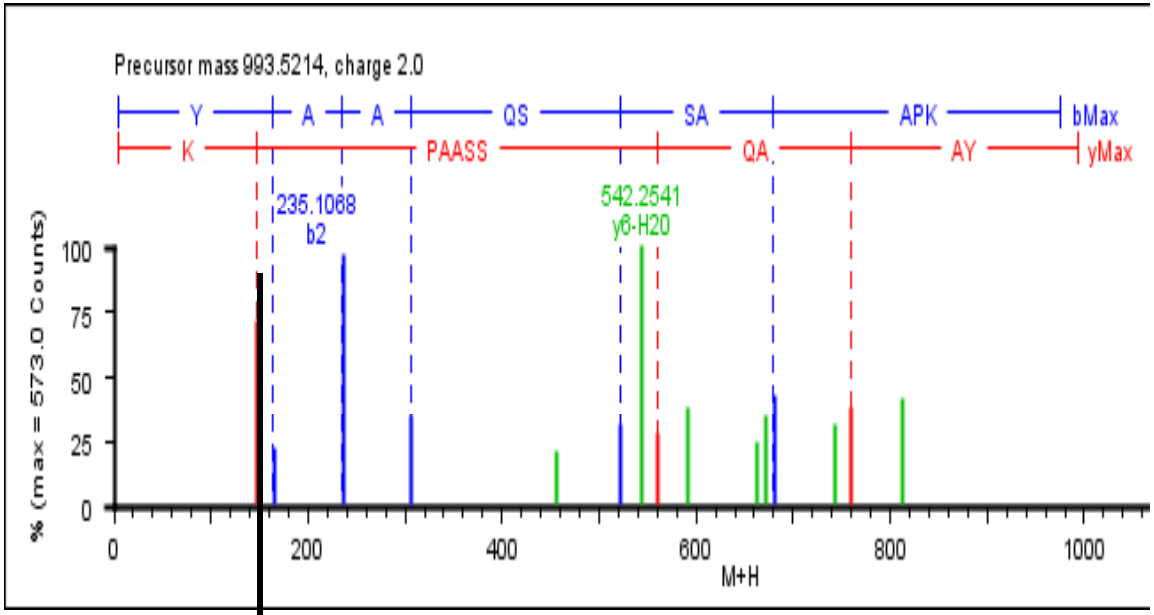


1457.8594

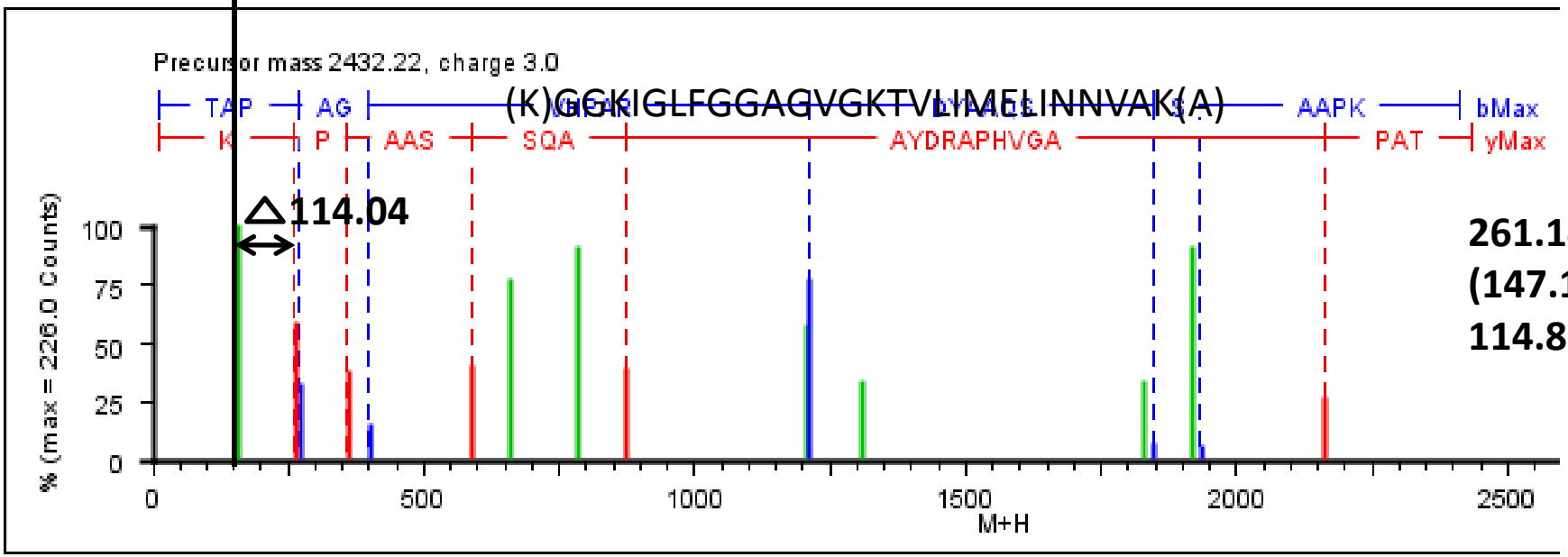
1635.78: (1457.85+ 162.02)

202-225

(K)IGLFGGAGVGKTVLIMELINNVAK(Gly)(A)



147.1094



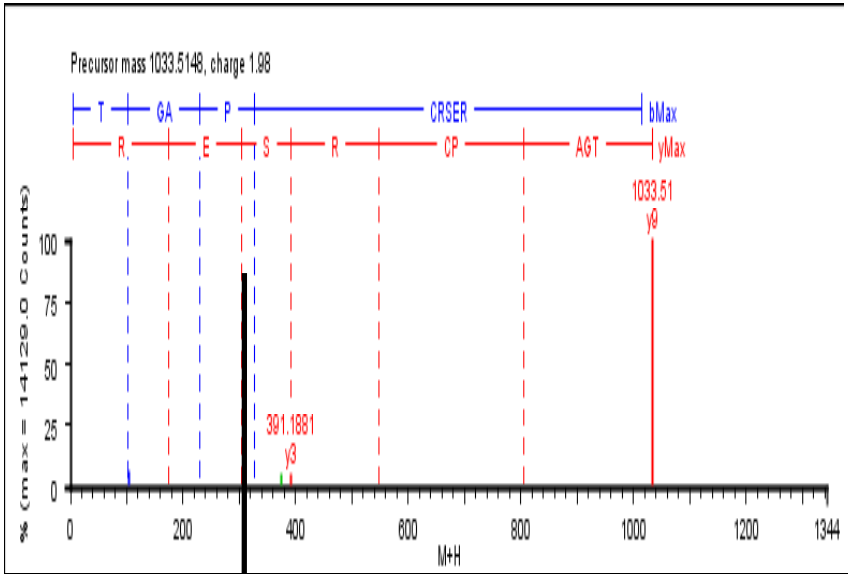
(K)GGKIGLFGGAGVGKTVLIMELINNVAK(A)

261.1413: (147.10+ 114.85)

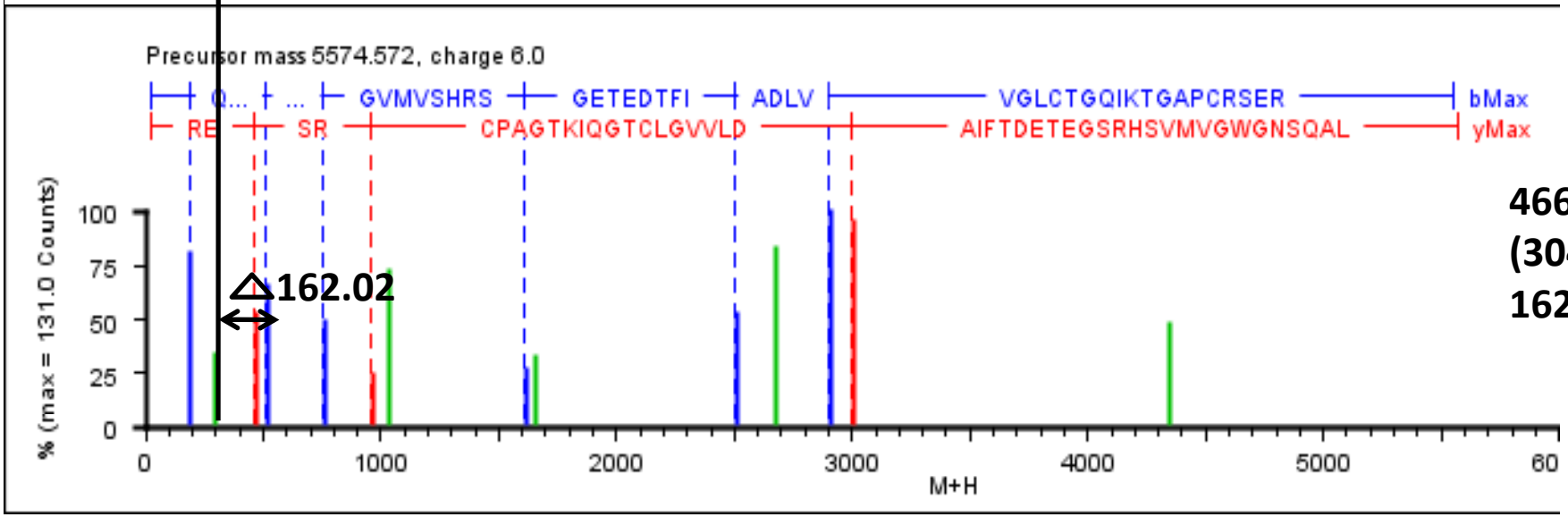
35-55

(R)TAPAGVHPARDYAAQSSAAPK(Ubi)(A)

Enolase

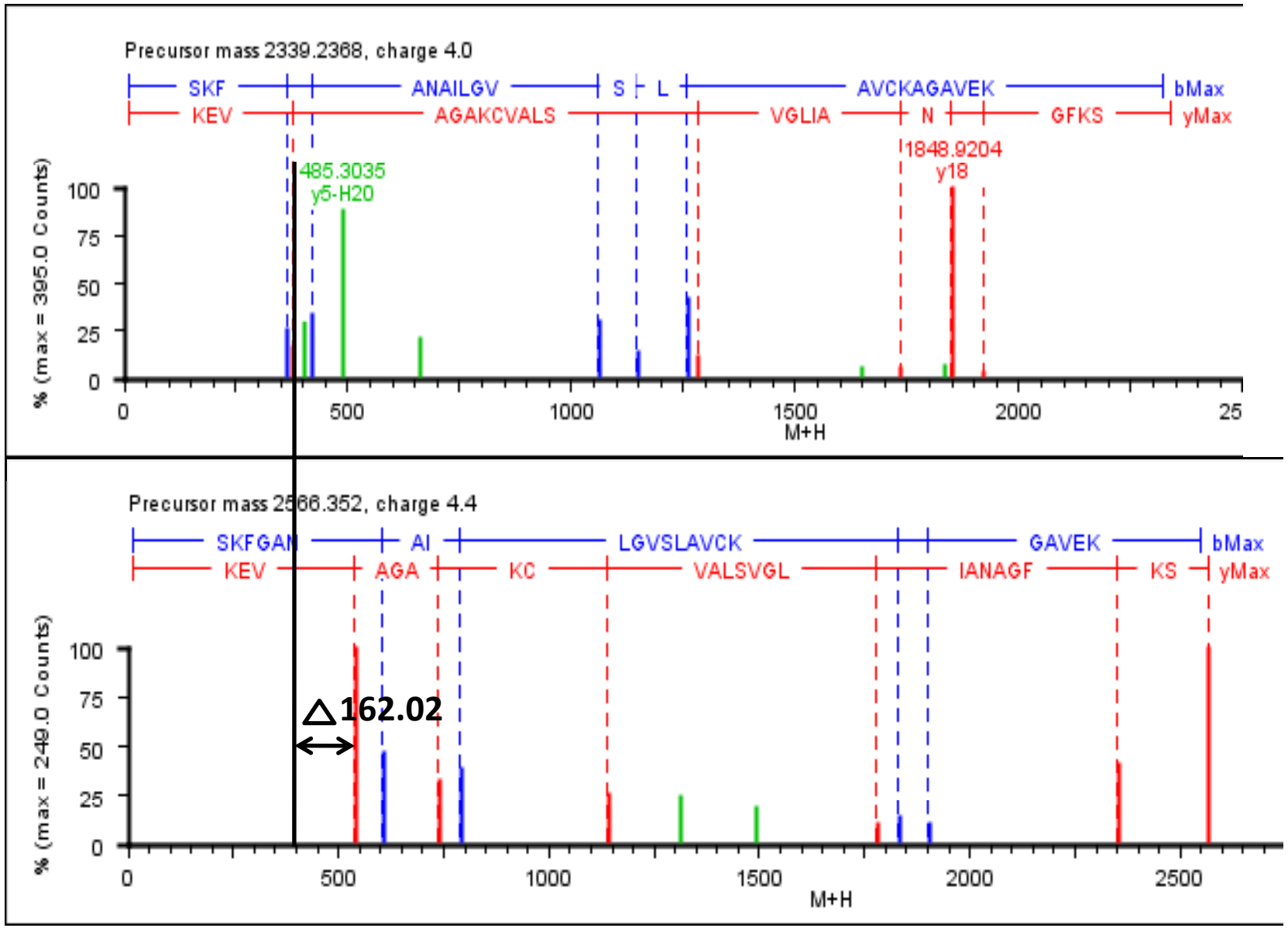


304.1511



466.1734: (304.15+ 162.02)

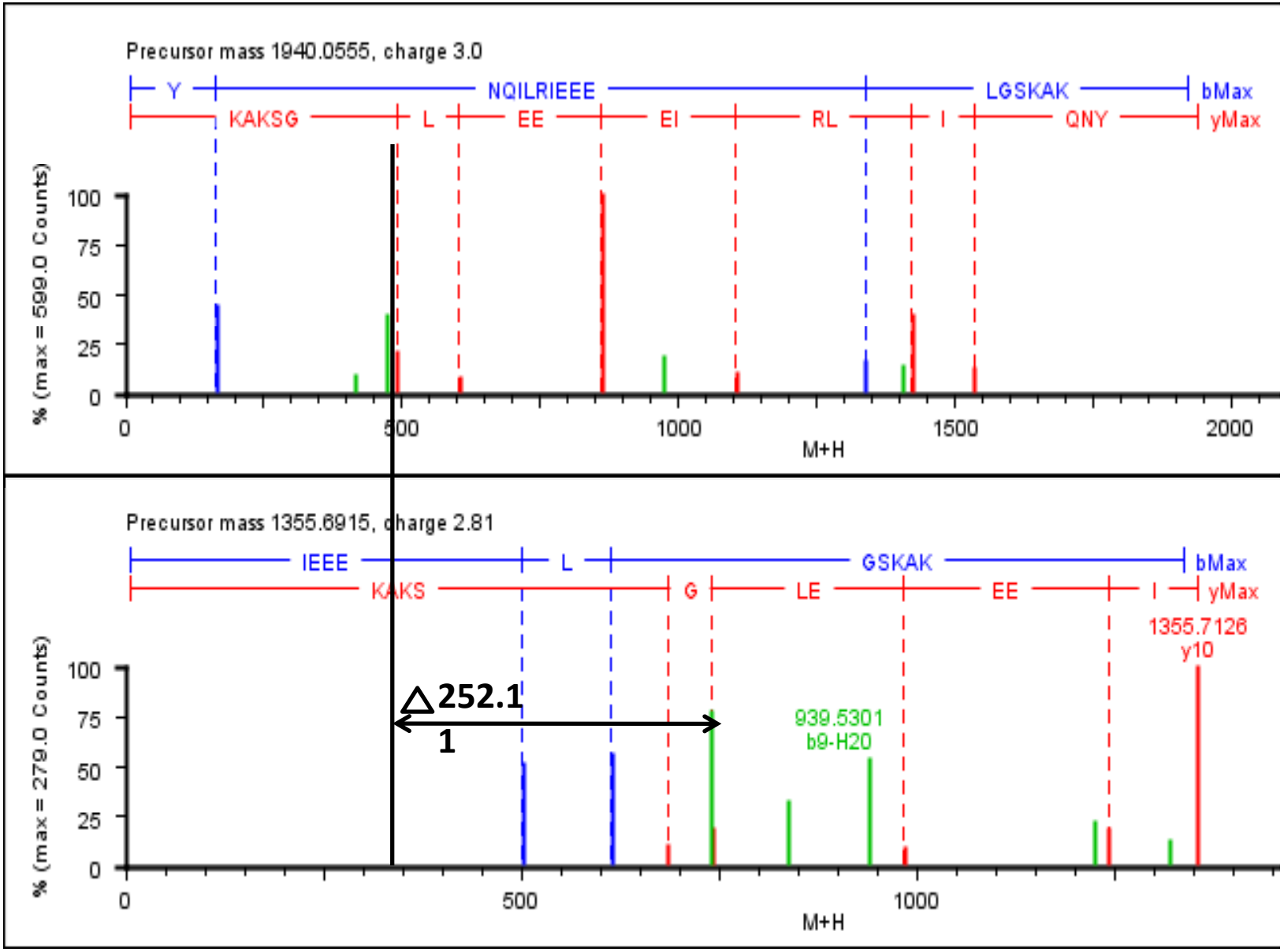
356-403 (K)LAQSNGWGVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSER(Gly)(L)



375.2169

537.2874: (375.21+ 162.02)

104-126 (K)SKFGANAILGVSLAVCKAGAVEK(Gly)(G)

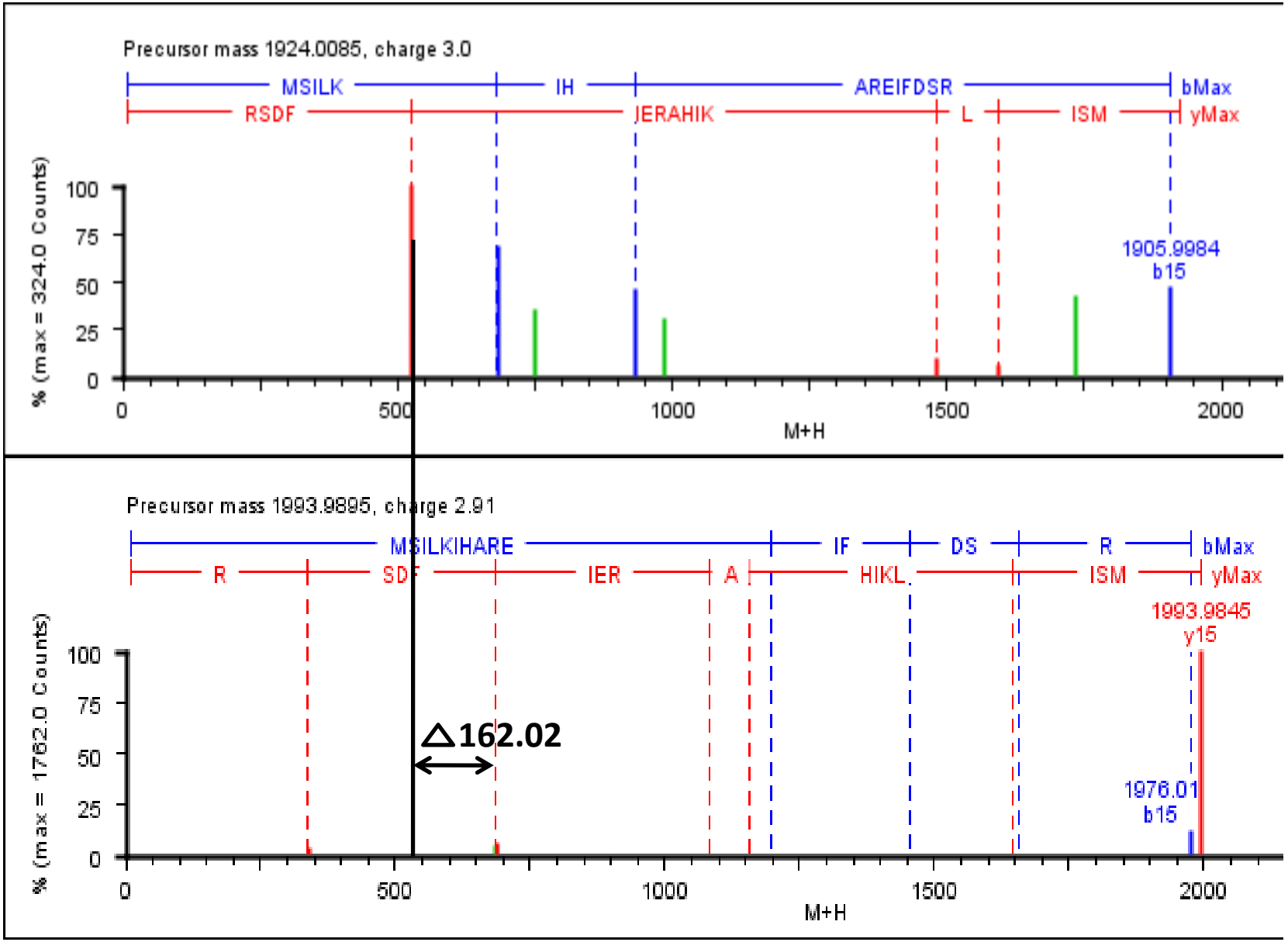


490.2533

742.4358

413-422

(R)IEEELGSKAK(Crossline)(F)

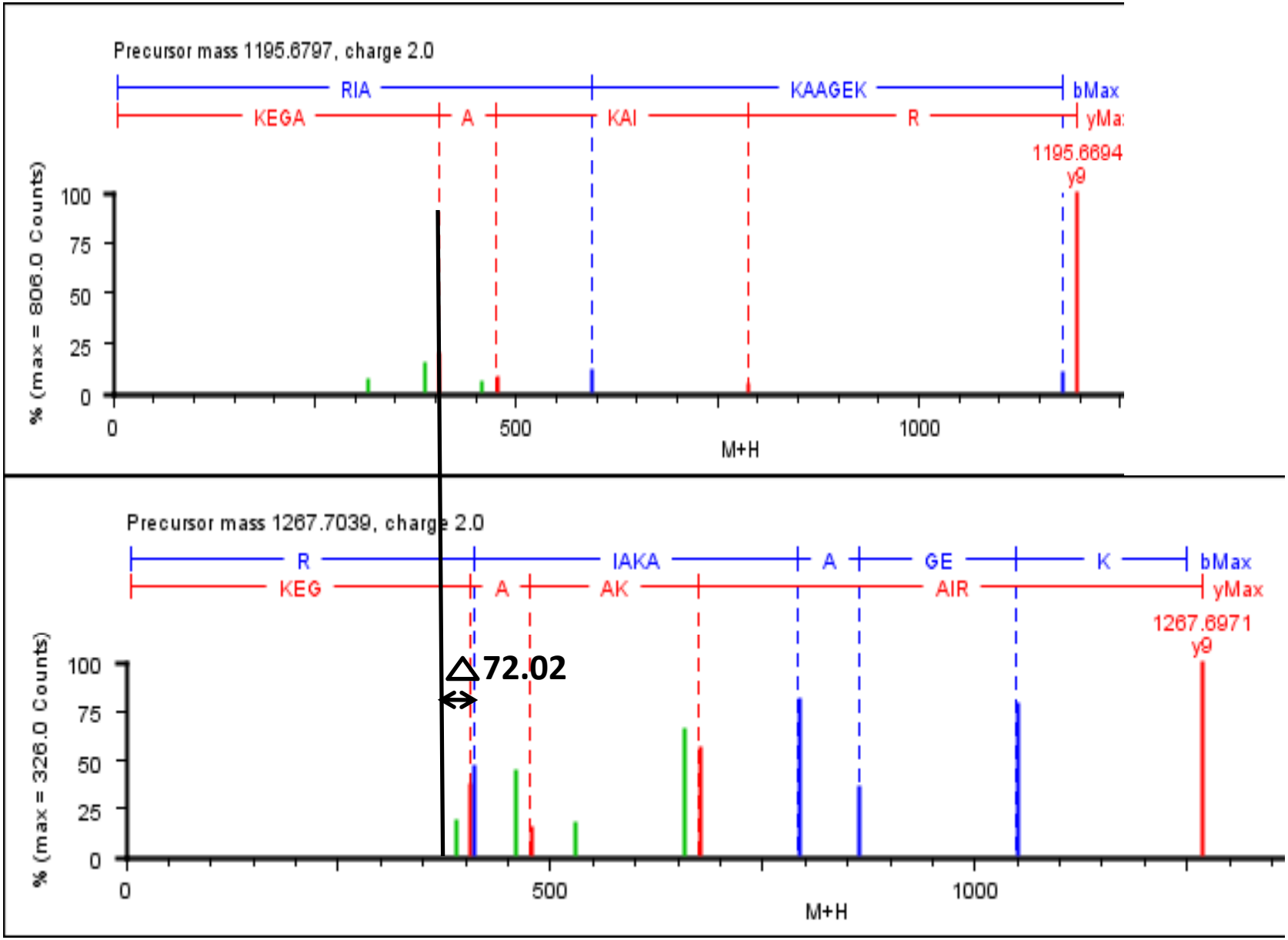


524.2554

686.2645: (524.2554 + 162.02)

1-15

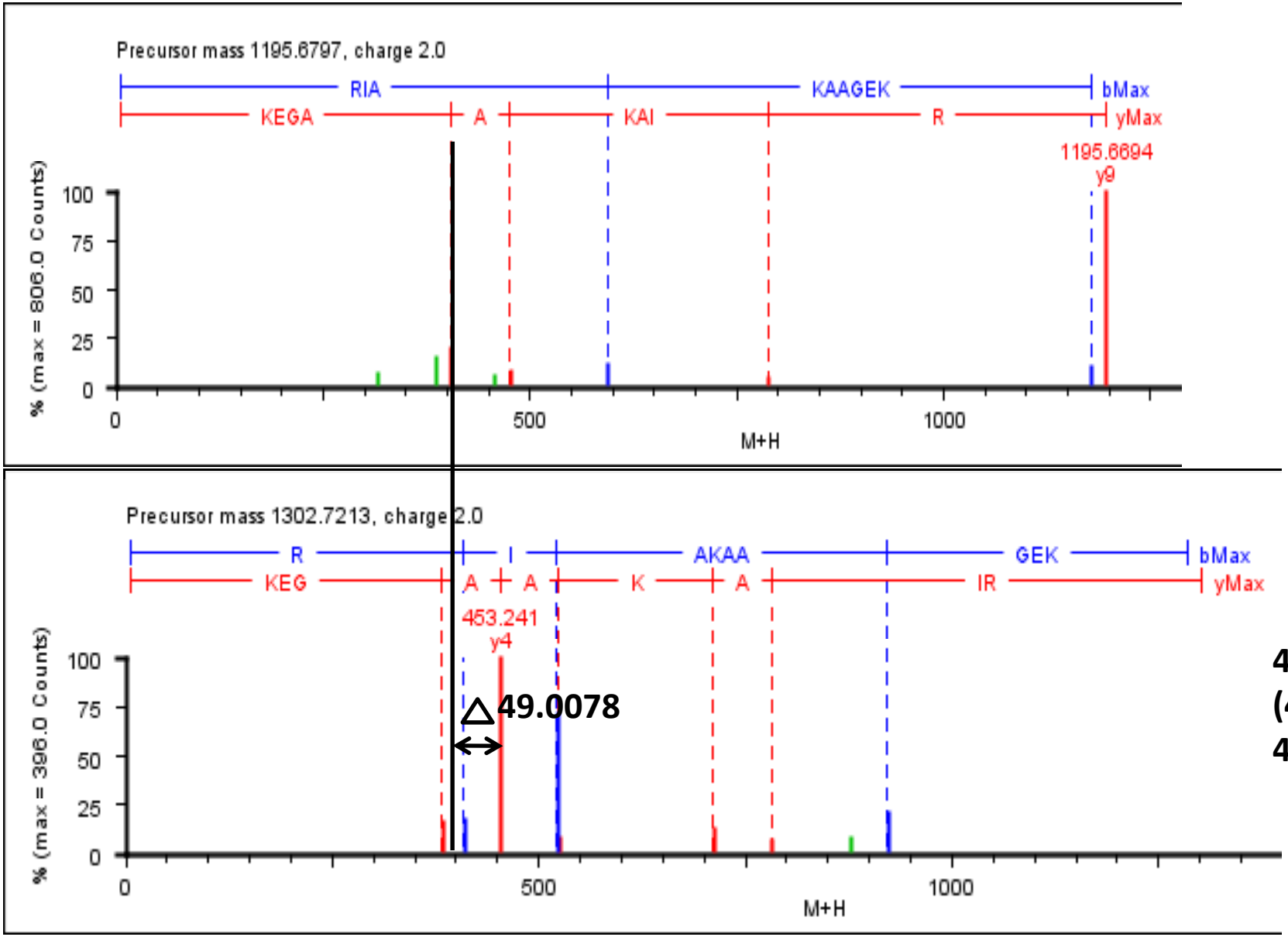
(-)MSILKIHAREIFDSR(Gly)(G)



404.2195

476.262: (404.21+ 72.02)

327-335 (K)RIAKAAGEK(CEL)(S)

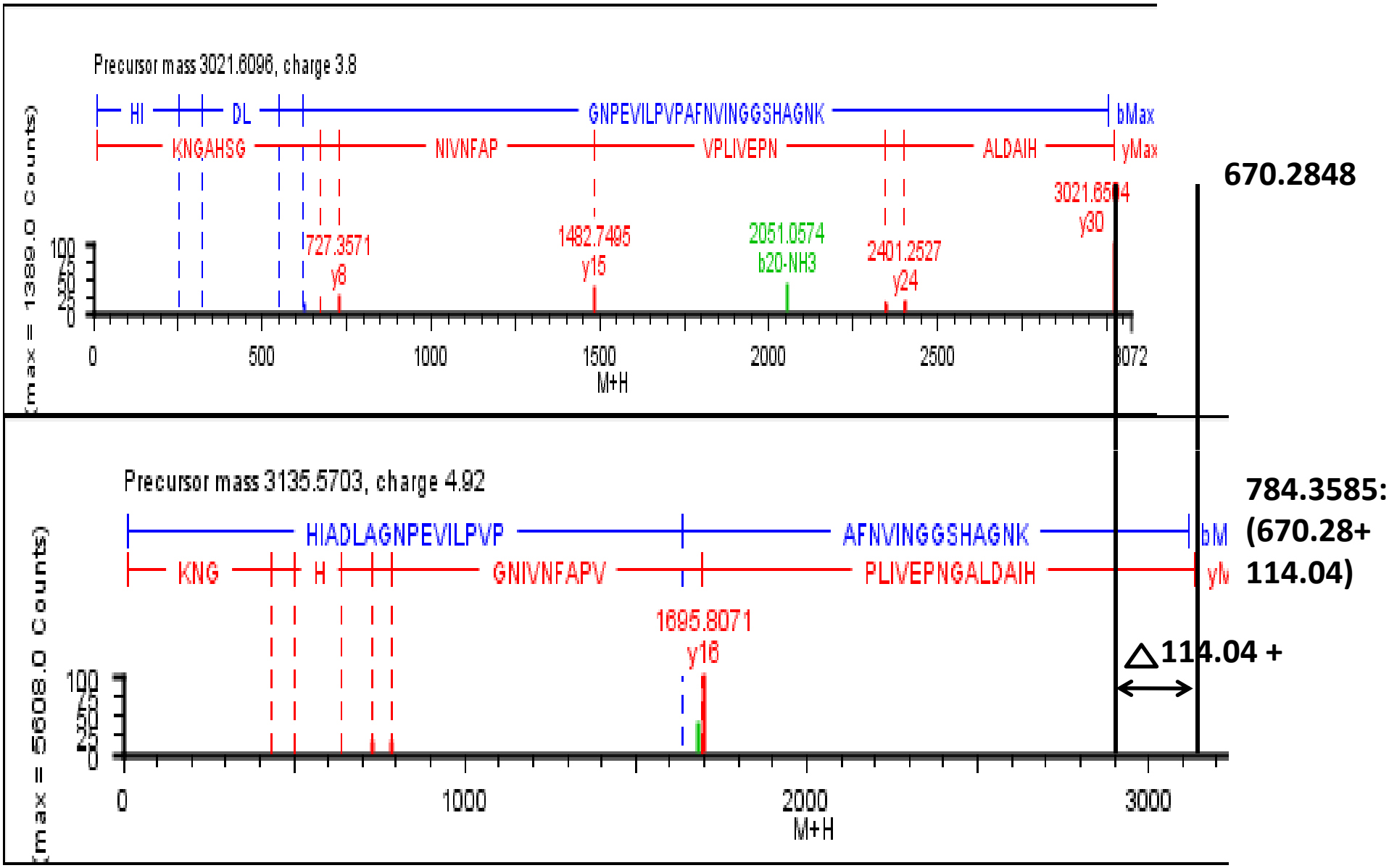


404.2195

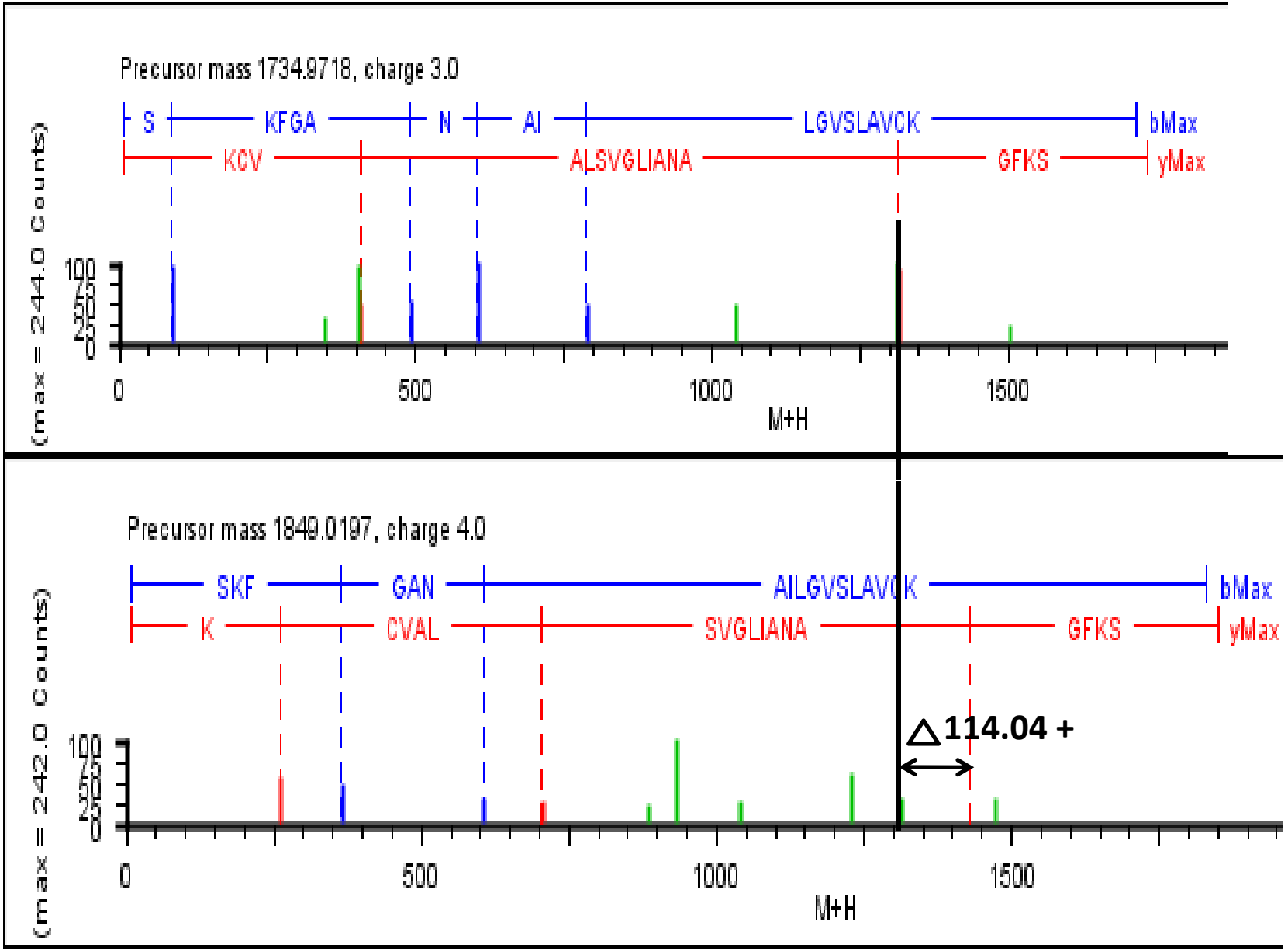
453.241: (404.21+ 49.00)

327-335

(K)RIAKAAGEK(MOLD)(S)



133-162 (R)HIADLAGNPEVILPVPAFNVINGGSHAGNK(Ubi)(L)

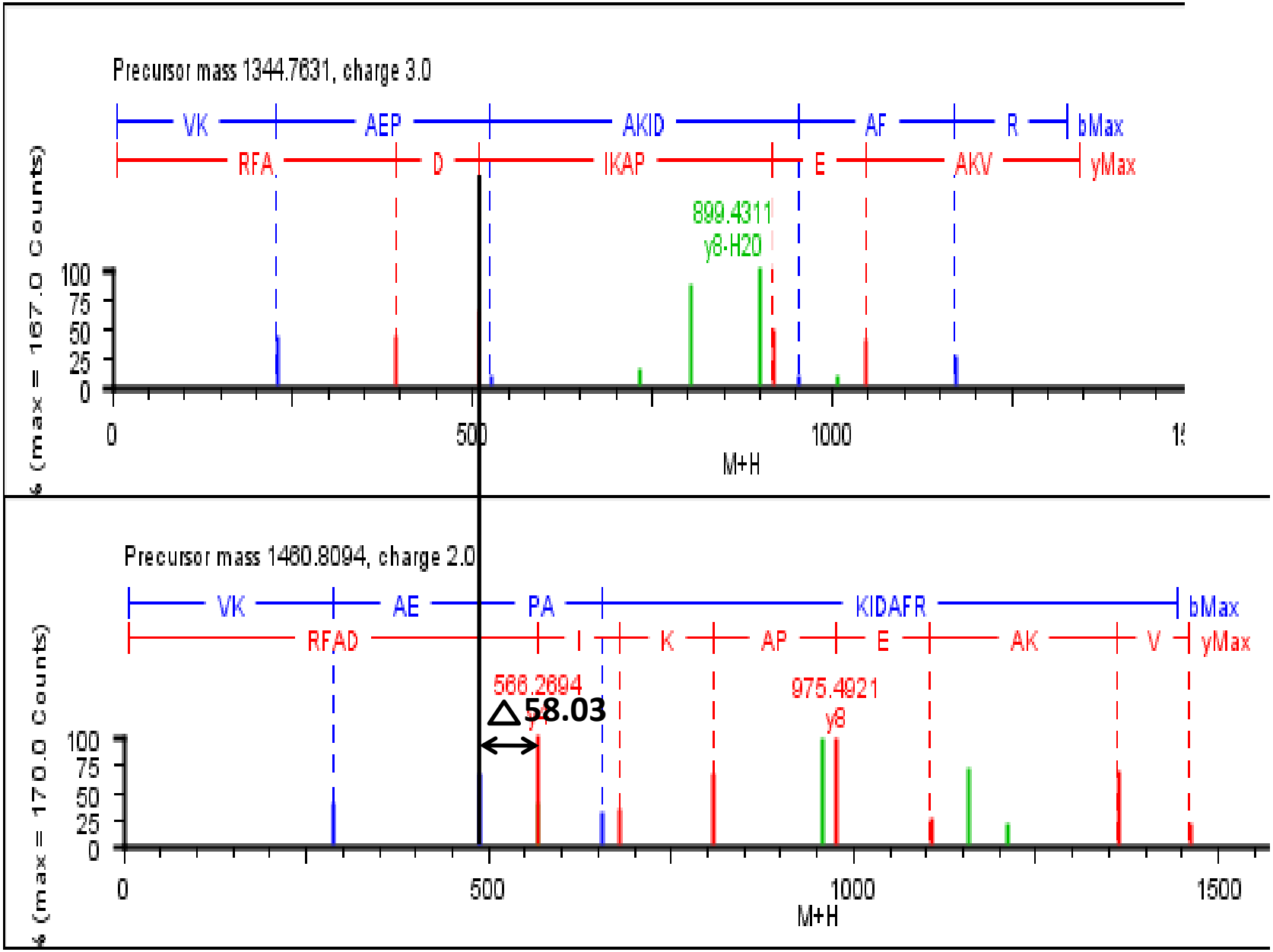


1315.6705

1429.7592: (1315.67+ 114.04)

104-120 (K)SKFGANAILGVSLAVCK(Ubi)(A)

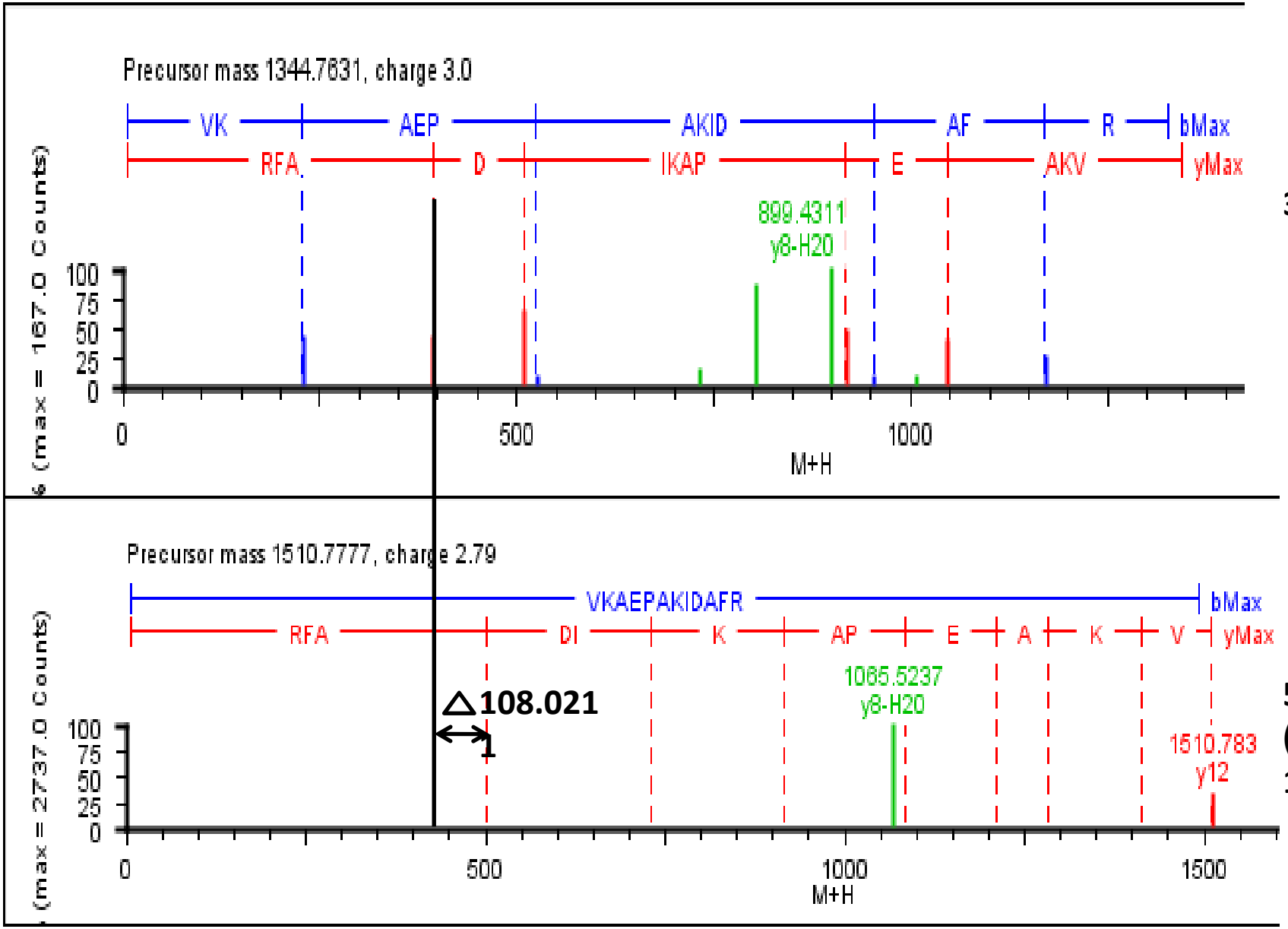
PGK



508.2894

566.2694: (508.28+ 58.03)

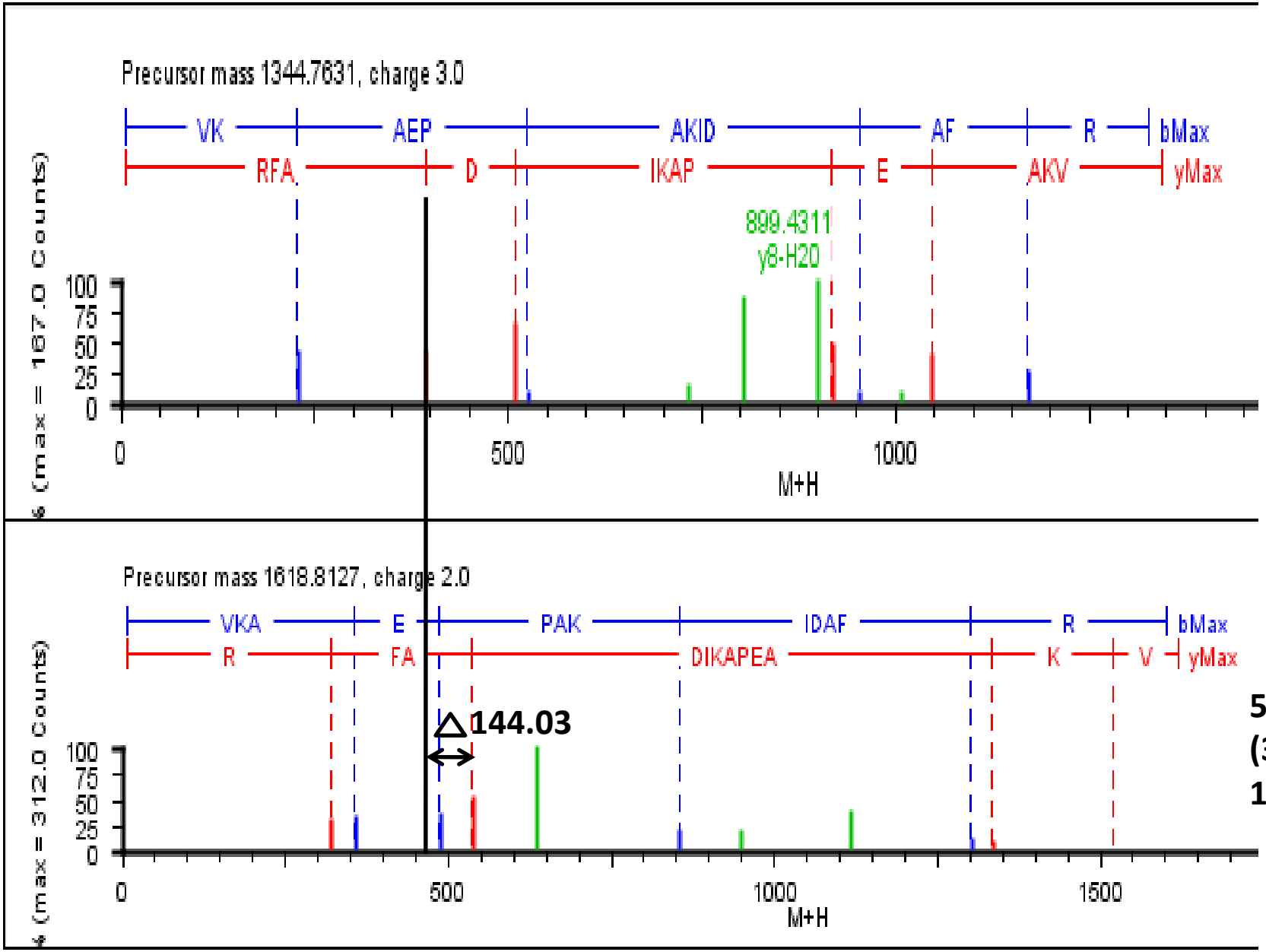
140-151 (K)VKAEPAKIDAFR(Pento)(A)



393.2415

501.2251: (393.24+ 108.02)

140-151 (K)VKAEPAKIDAFR(Pyr)(A)

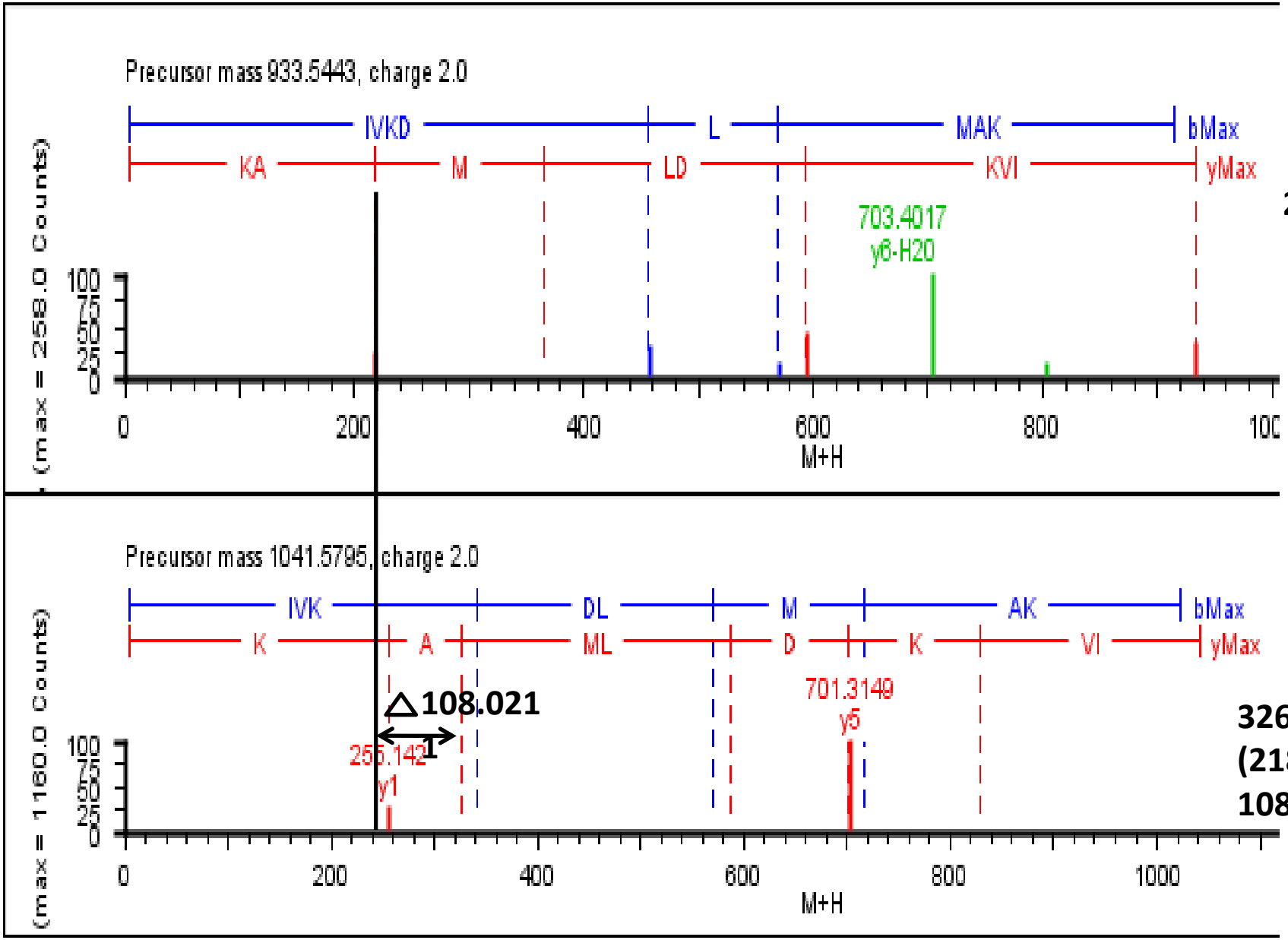


393.2415

537.2731: (393.24+ 144.03)

140-151

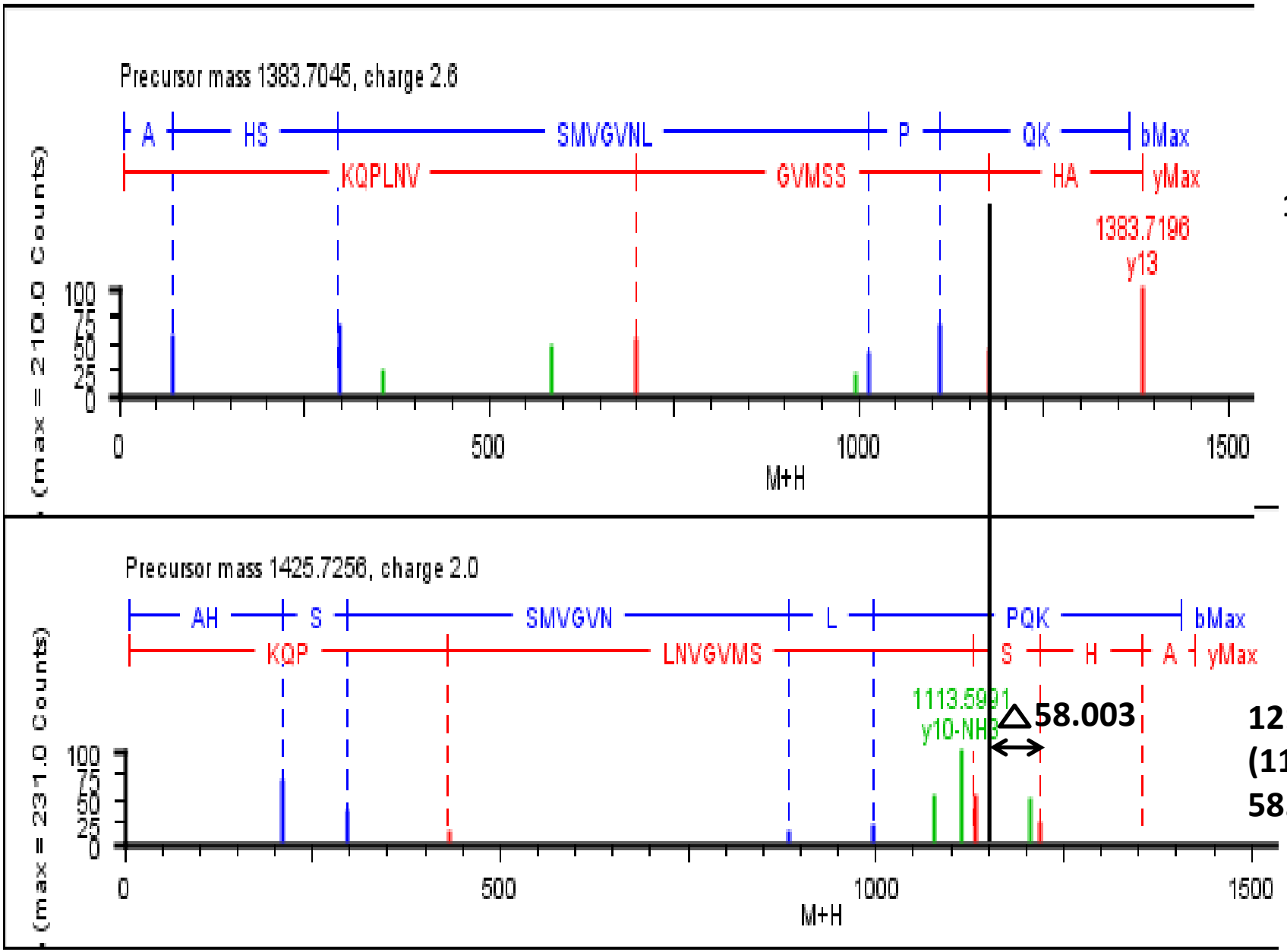
(K)VKAEPAKIDAFR(ImiA)(A)



218.1501

326.1721: (218.15+ 108.02)

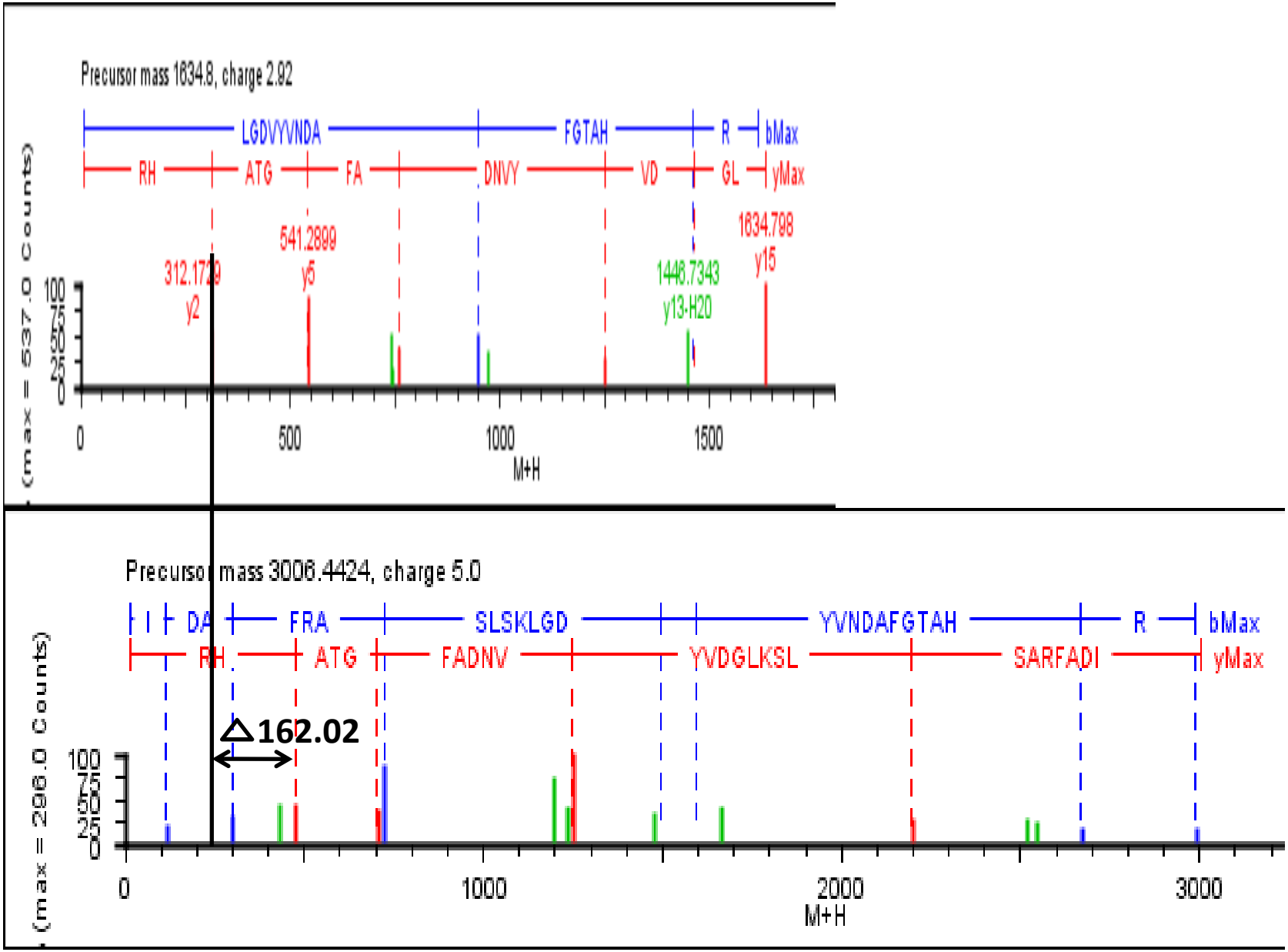
265-272 (K)IVKDLMAK(Pyr)(A)



1175.579

1217.6604: (1175.579+ 58.03)

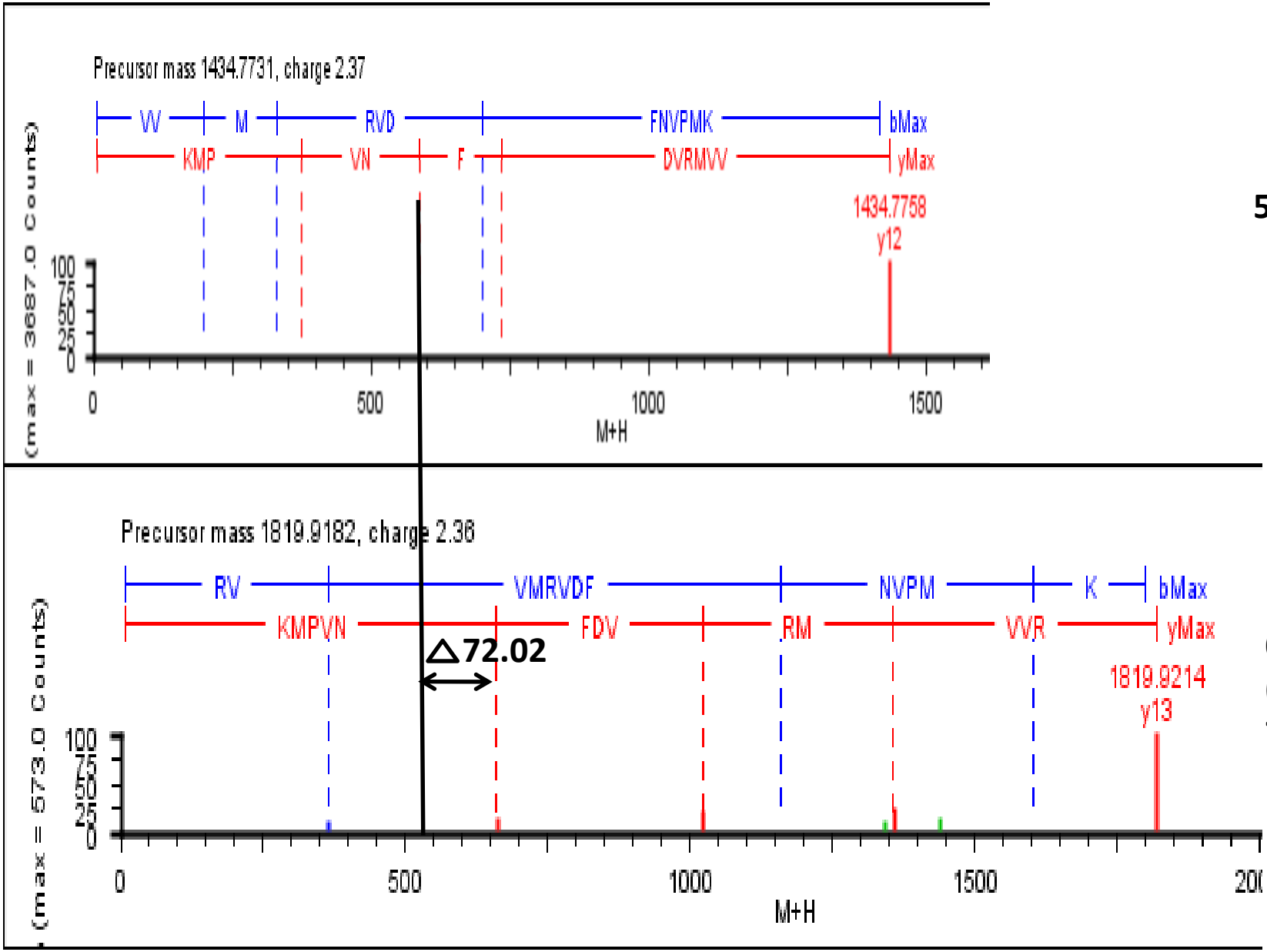
172-184 (R)AHSSMVGVNLPQK(CML)(A)



312.1729

474.1729: (312.1729 + 162.02)

157-171 (K)LGDVYVNDAFGTAHR(Gly)(A)

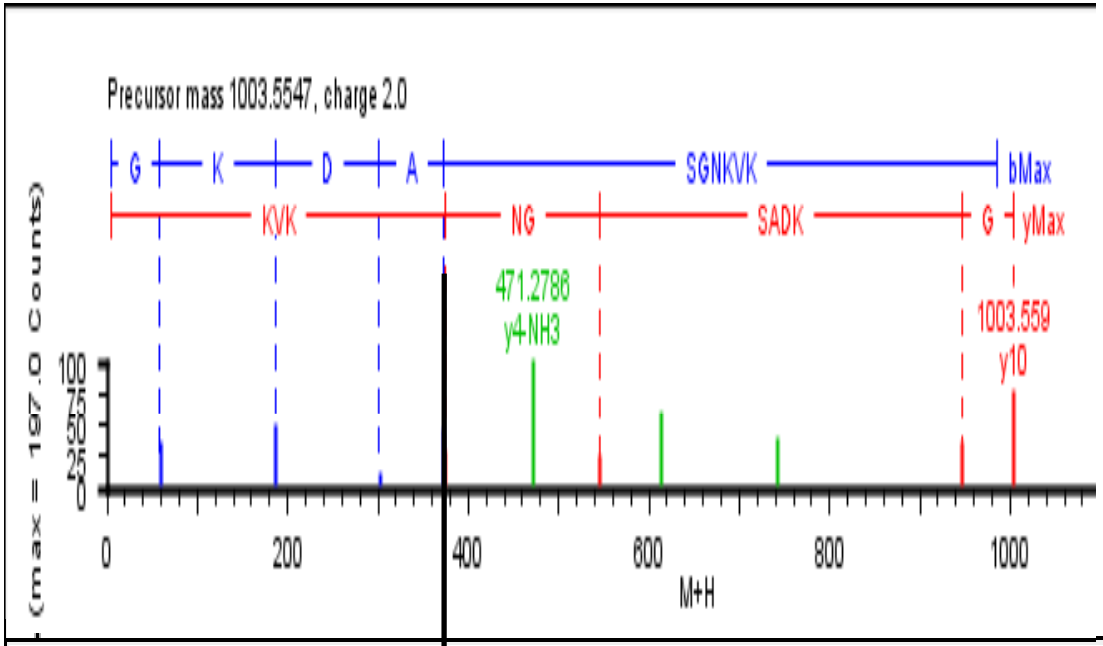


588.2782

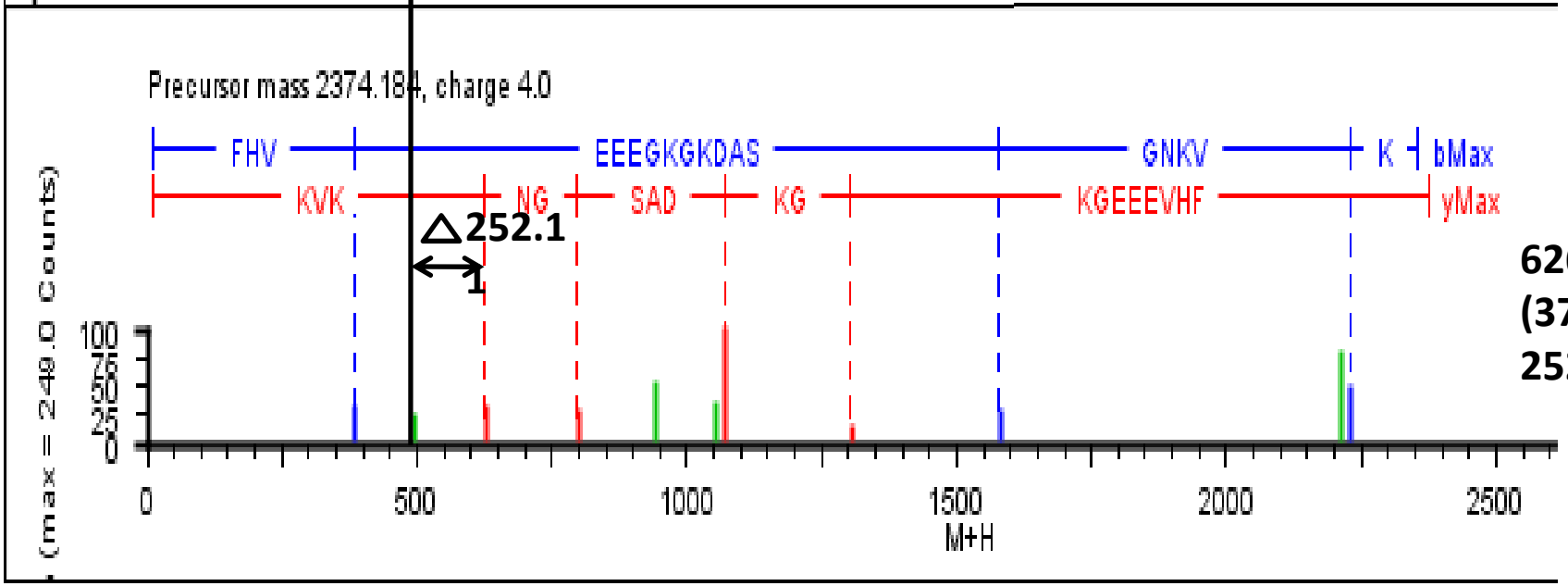
660.3208: (588.27+ 72.02)

19-30

(R)VVMRVDFNVPMK(CEL)(N)

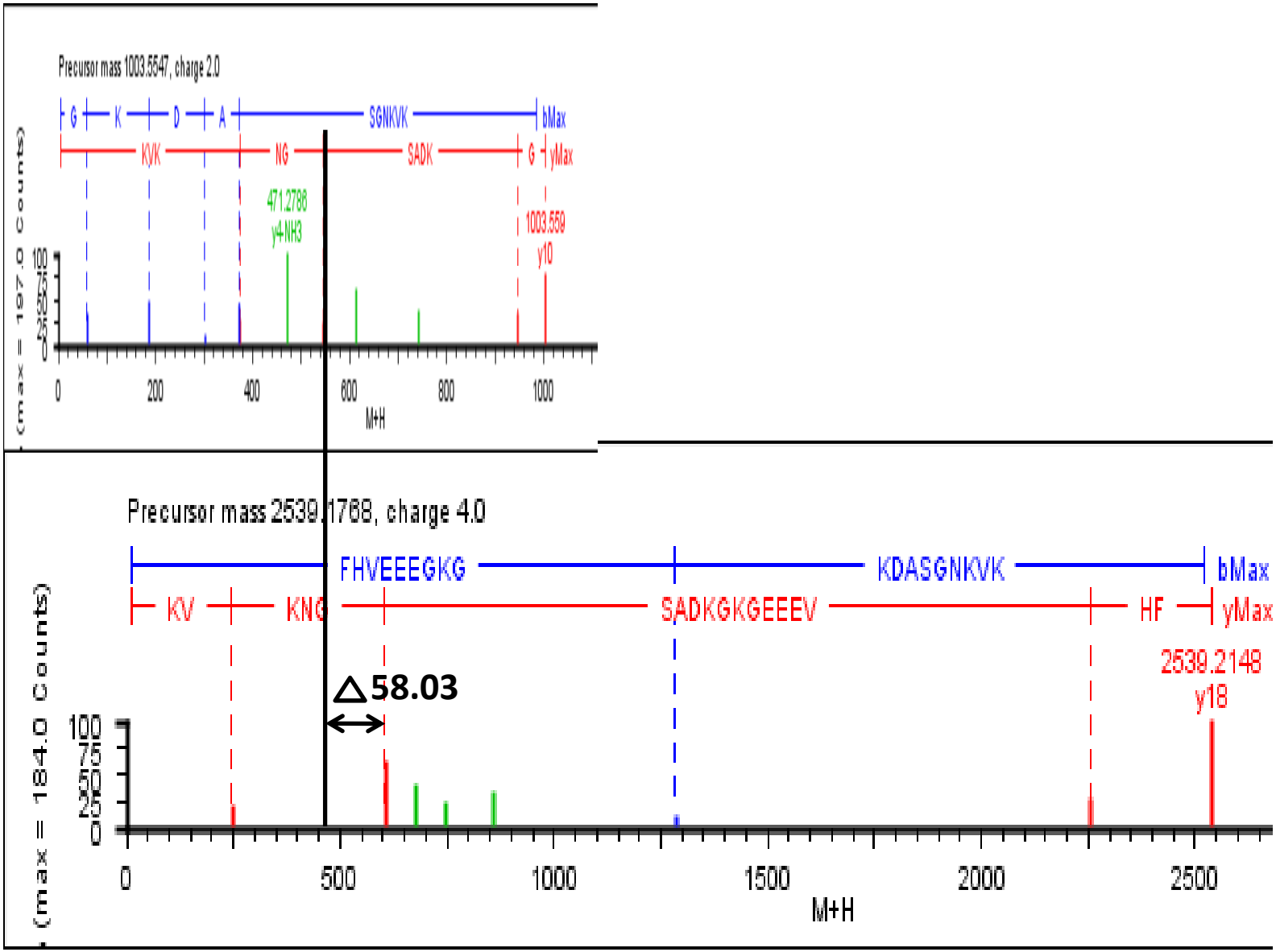


374.2361



626.3456: (374.23+ 252.1)

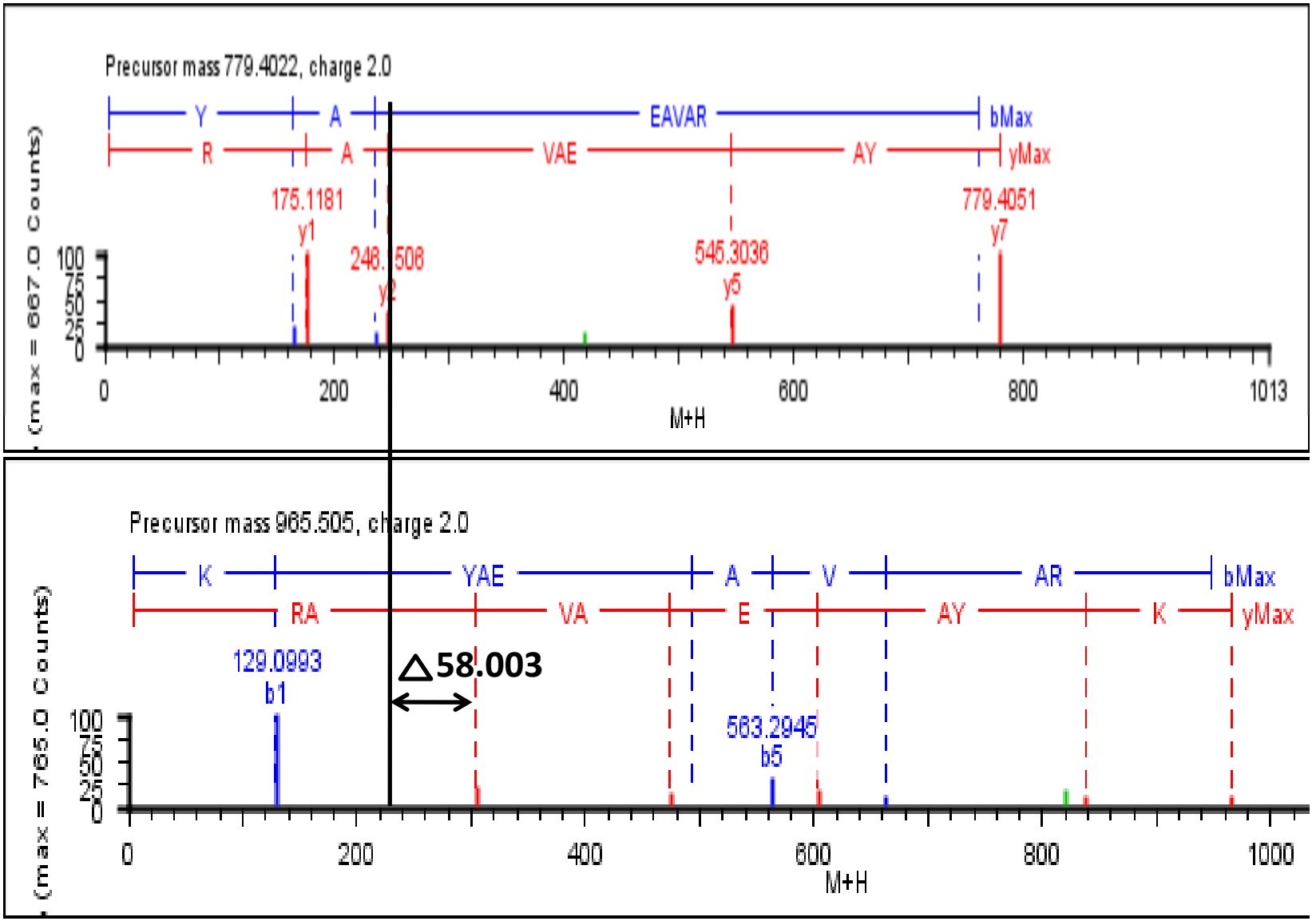
124-141 (R)FHVEEEGKGKDASGNK(Crossline)VK(A)



545.309

603.3259: (545.30+ 58.03)

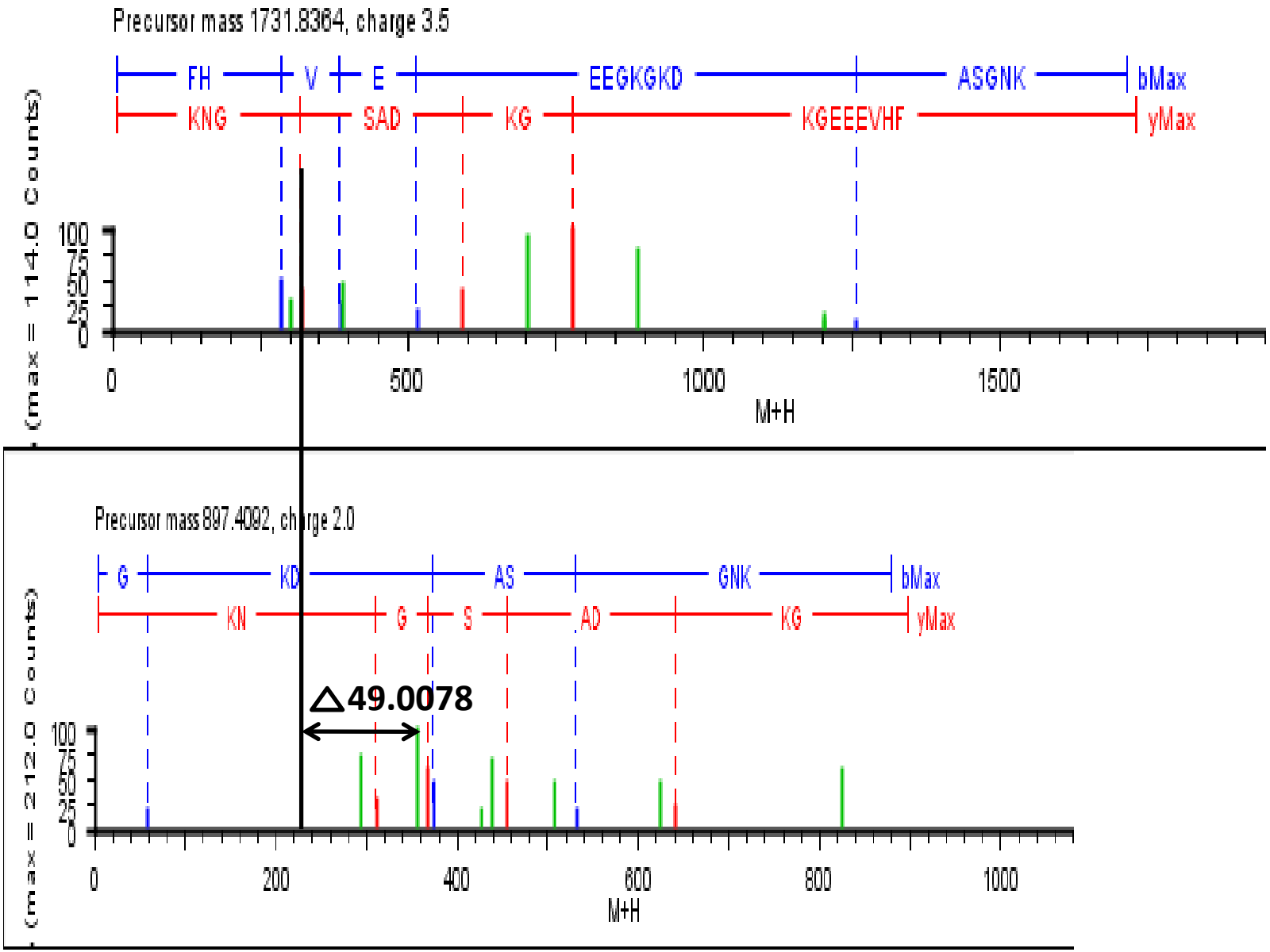
124-141 (R)FHVEEEGKGKDASGNK(Pento)VK(A)



246.1506

304.1746: (246.15+ 58.003)

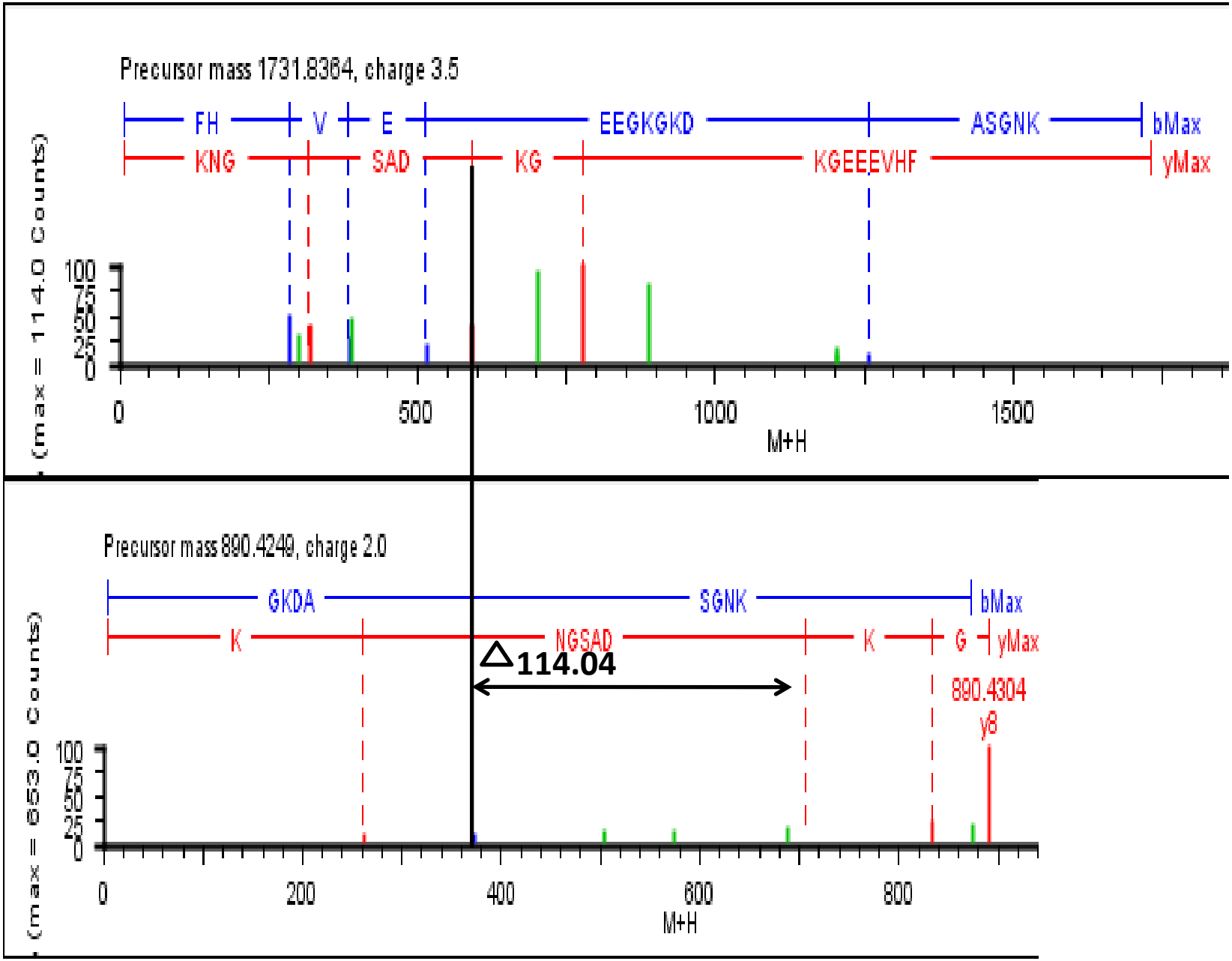
324-330 (K)YAEAVAR(CML)(A)



318.1321

367.194

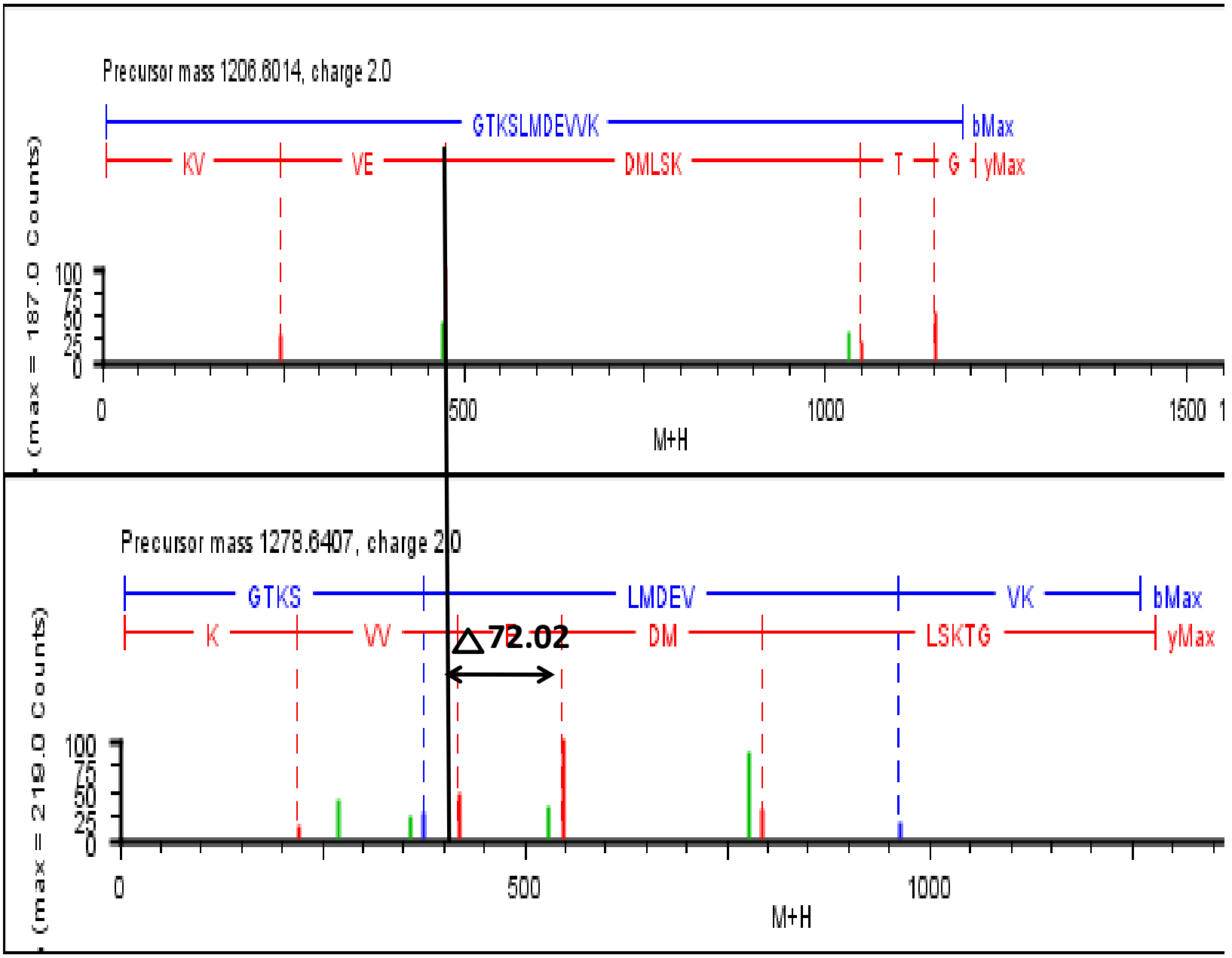
124-139 (R)FHVEEEGK(MOLD)GKDASGNK(V)



591.3358

705.3616: (591.33+ 114.04)

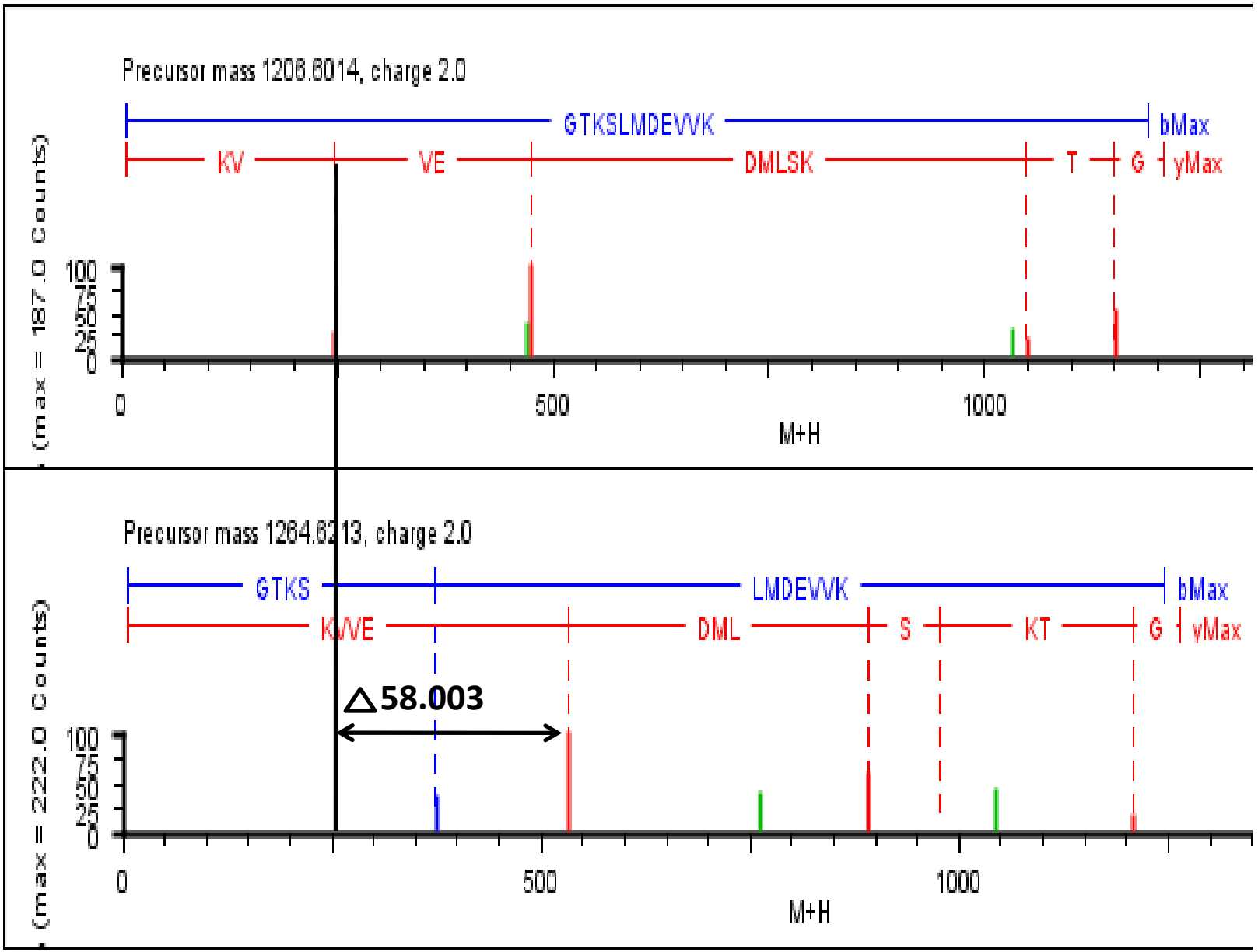
124-139 (R)FHVEEEGK(Ubi)GKDASGNK(V)



474.2409

546.271: (474.24+ 72.02)

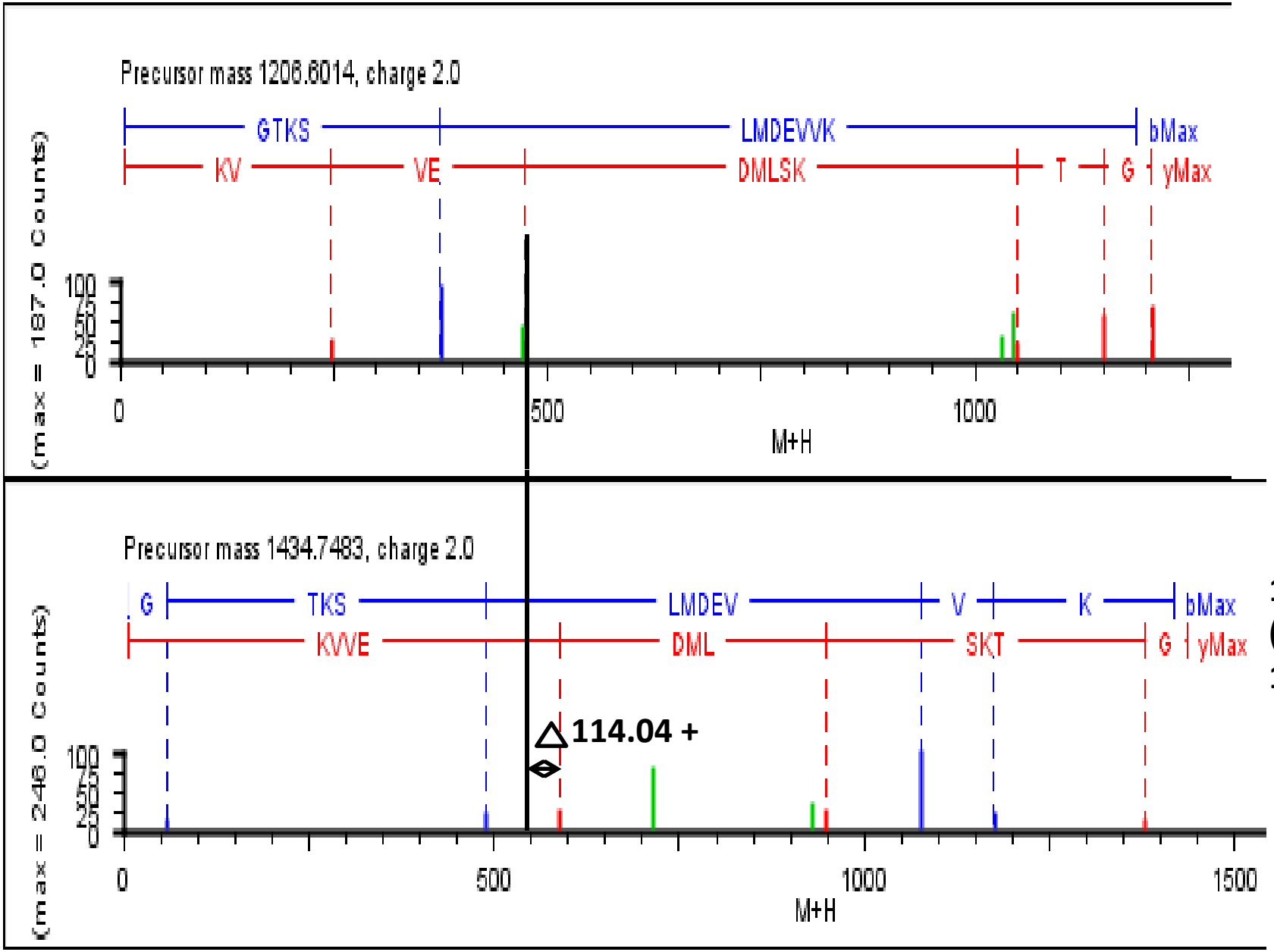
351-361 (R)GTKSLMDEVVK(CEL)(A)



474.2409

532.263: (474.2409 + 58.003)

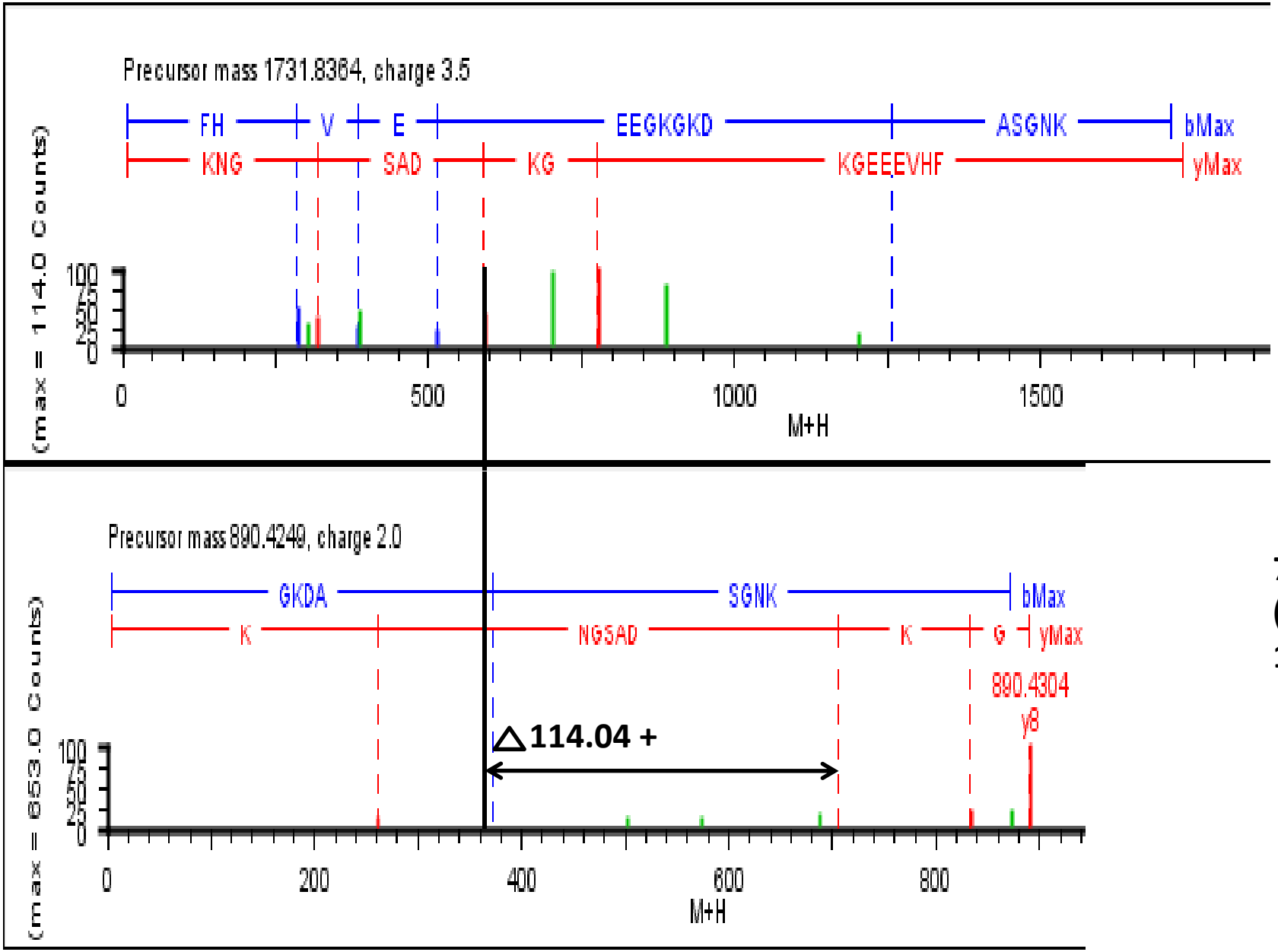
351-361 (R)GTKSLMDEVVK(CML)(A)



1149.5447

1377.6901: (1149.54+ 114.04)

351-361 (R)GTK(Ubi)SLMDEVVK(Ubi)(A)

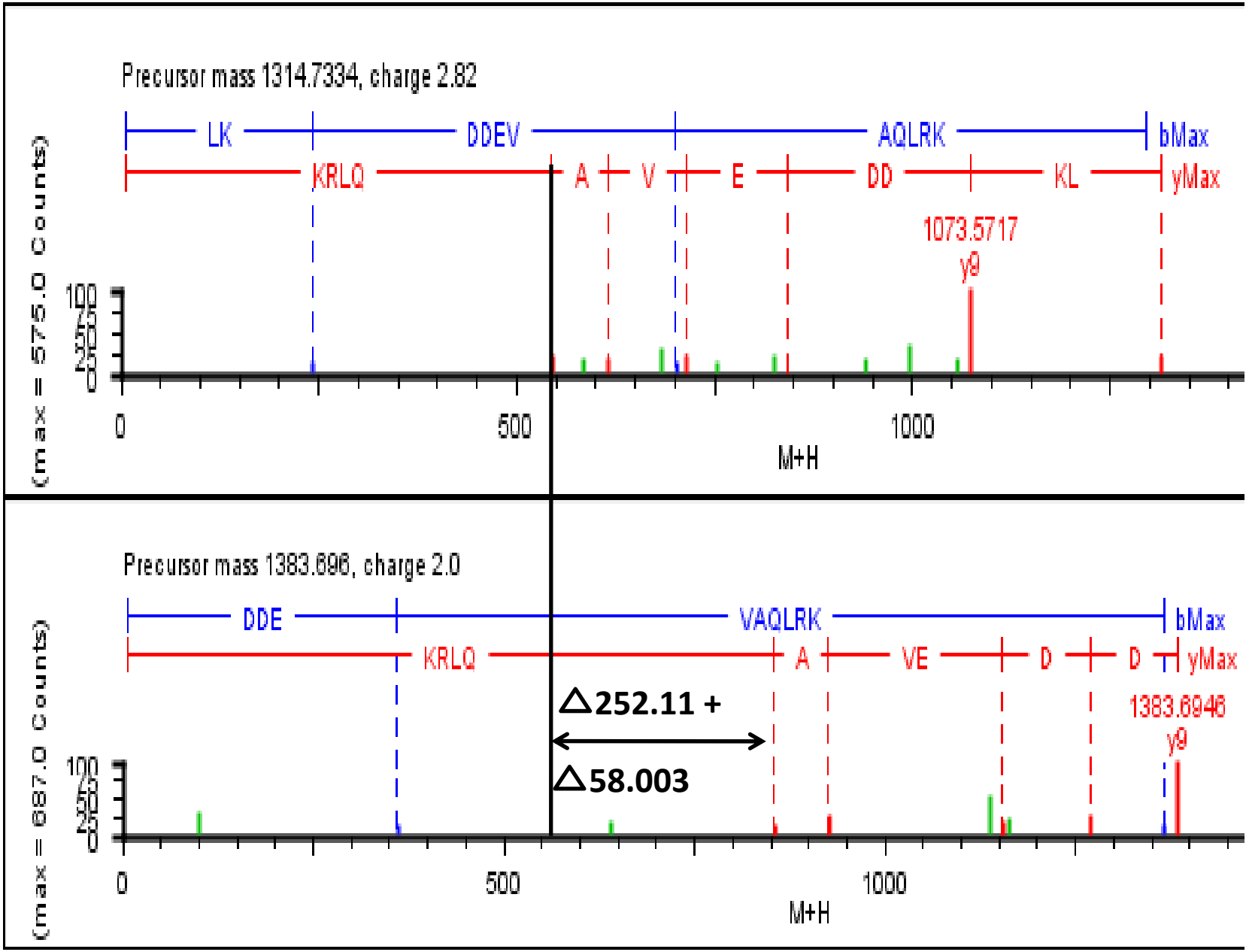


591.3356

705.3616: (591.33+ 114.04)

132-139 (K)GKDASGNK(Ubi)(V)

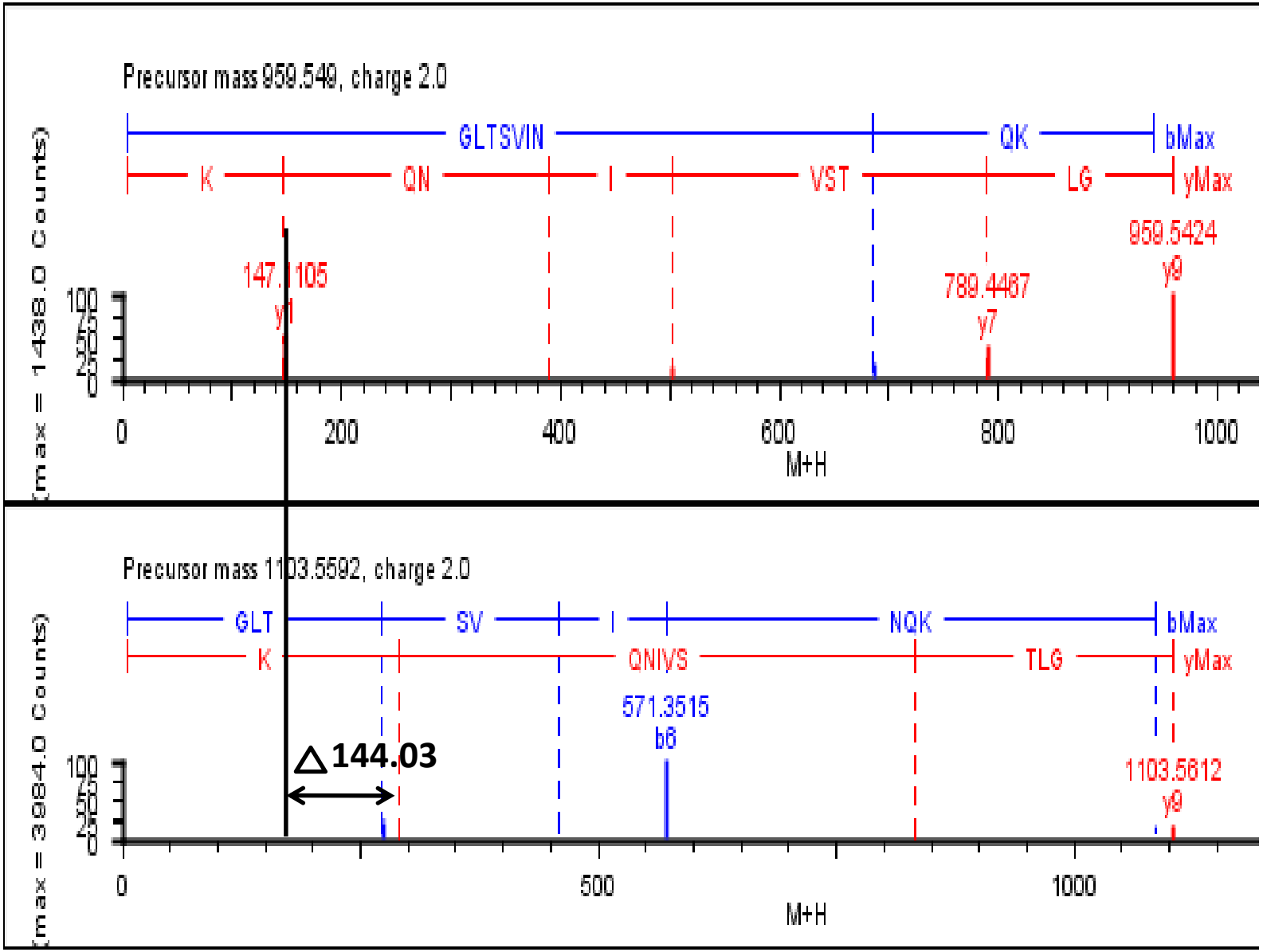
LDH



544.3514

854.481: (544.35+ 58.003+ 252.11)

309-319 (K)LKDDEVAQLR(Crossline)K(CML)(S)

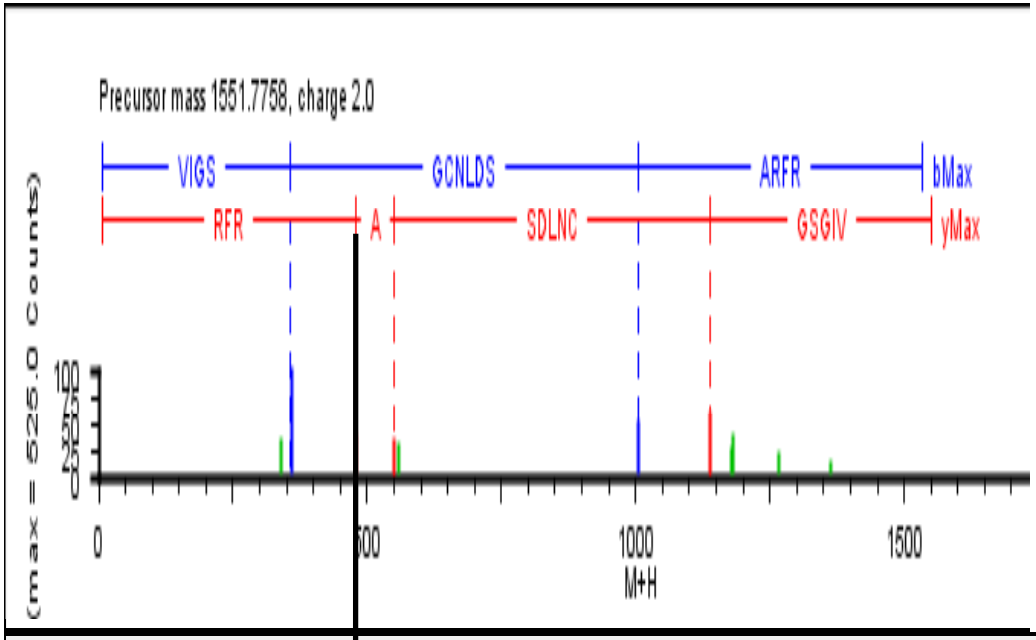


147.1105

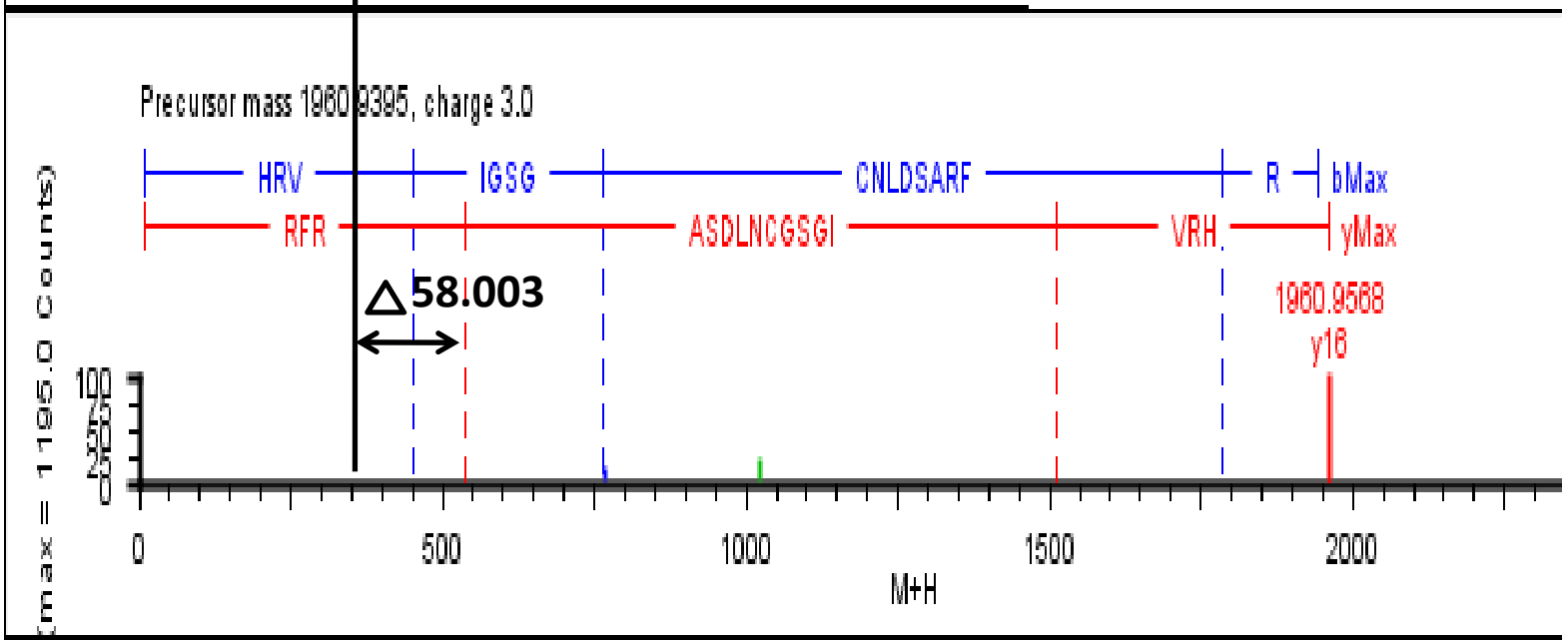
291.156: (147.11+ 144.03)

300-308

(R)GLTSVINQK(ImiA)(L)

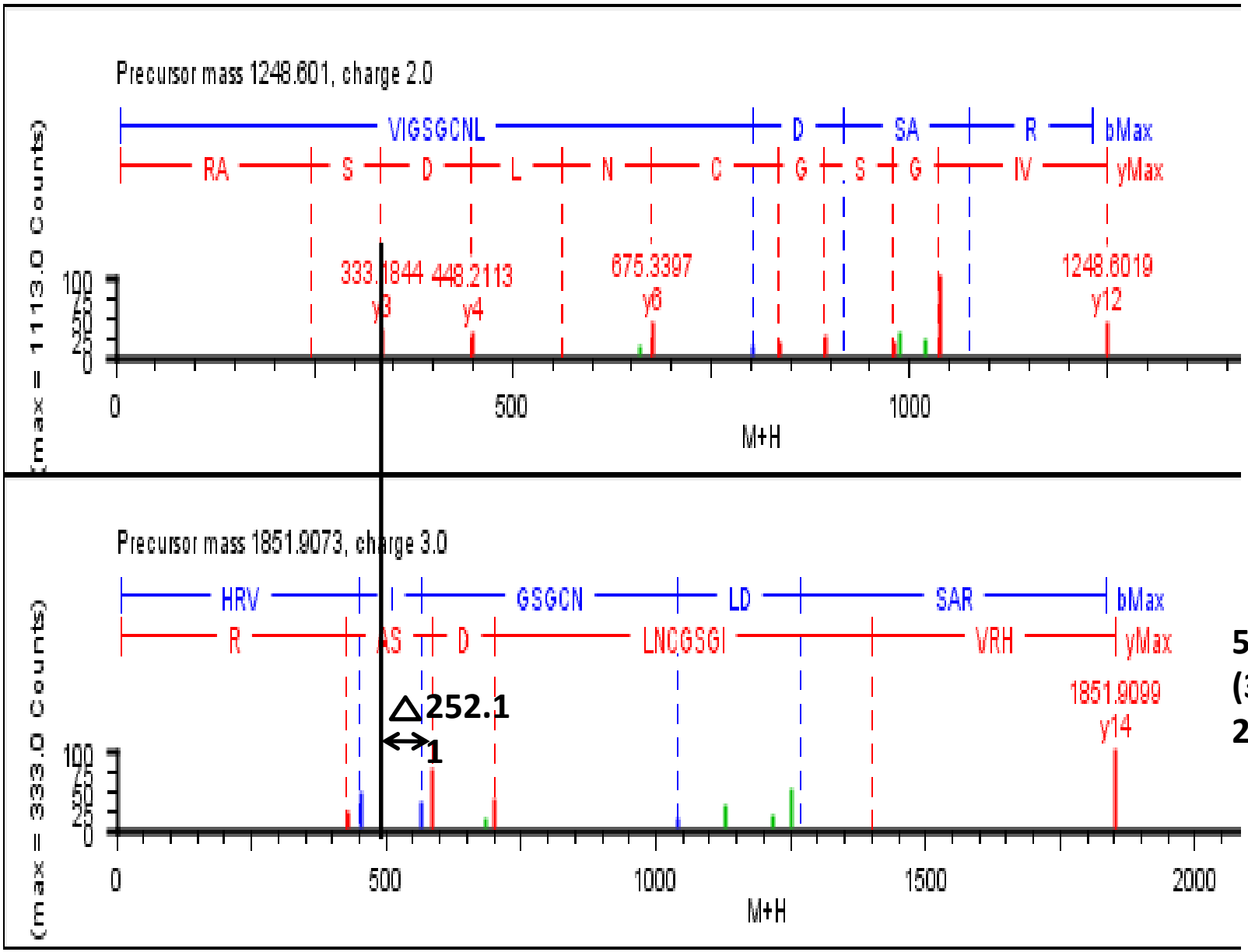


478.2678



536.3219: (478.29+ 58.003)

159-172 (R)VIGSGCNLDSARFR(CML)(Y)

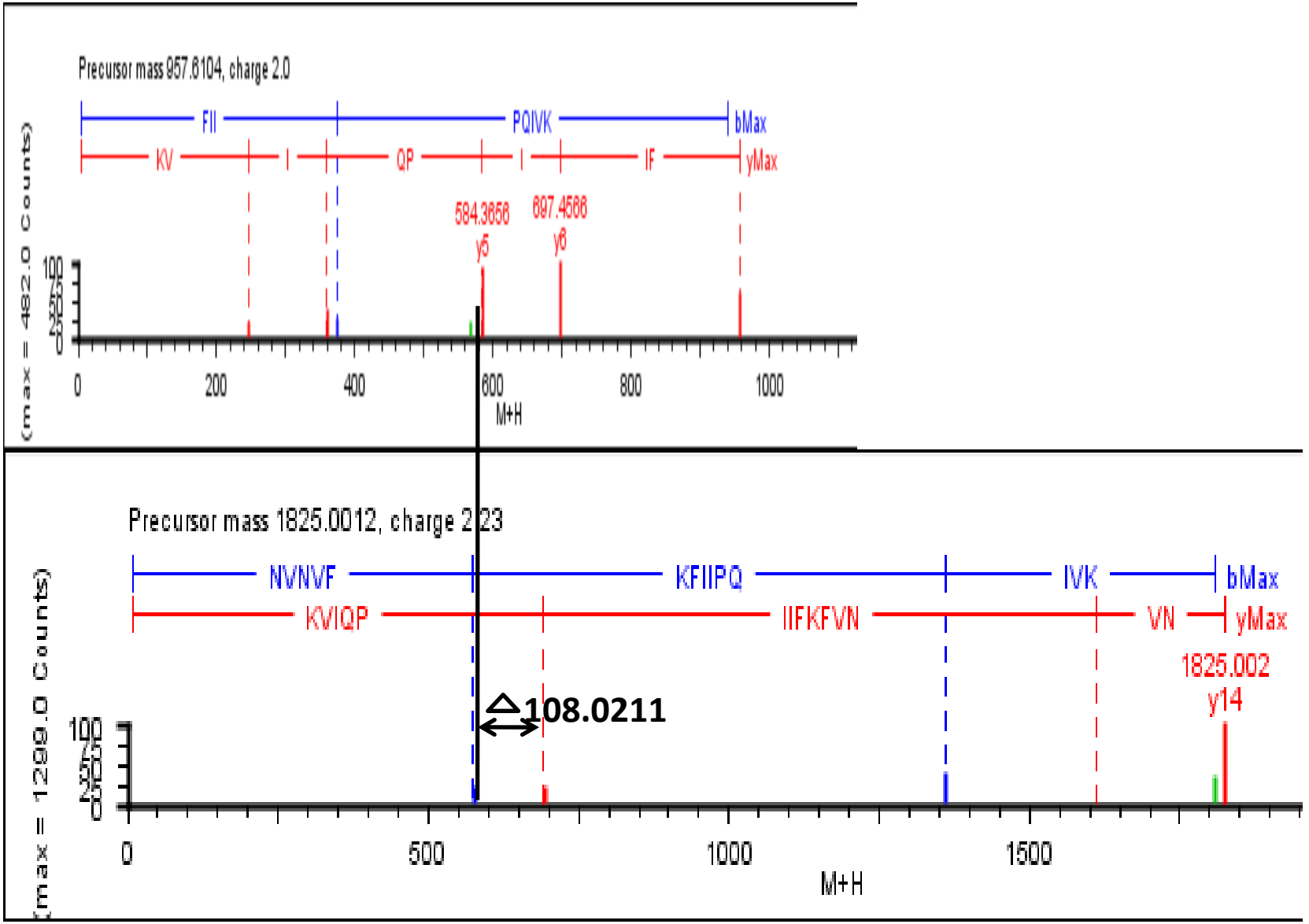


333.1844

585.3293: (333.18+ 252.1)

159-170

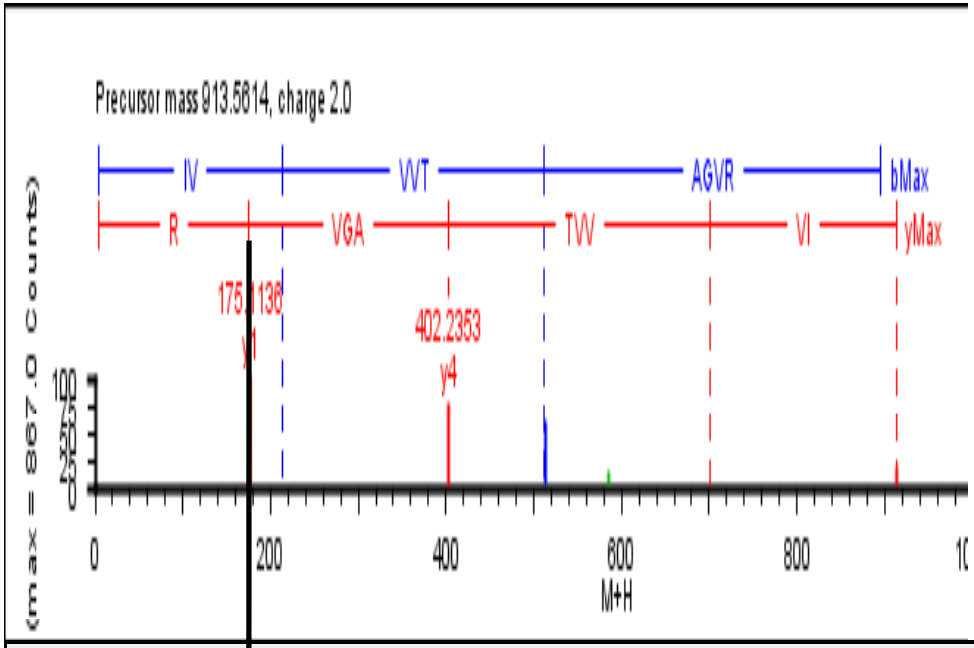
(K)HRVIGSGCNLDSAR(Crossline)(F)



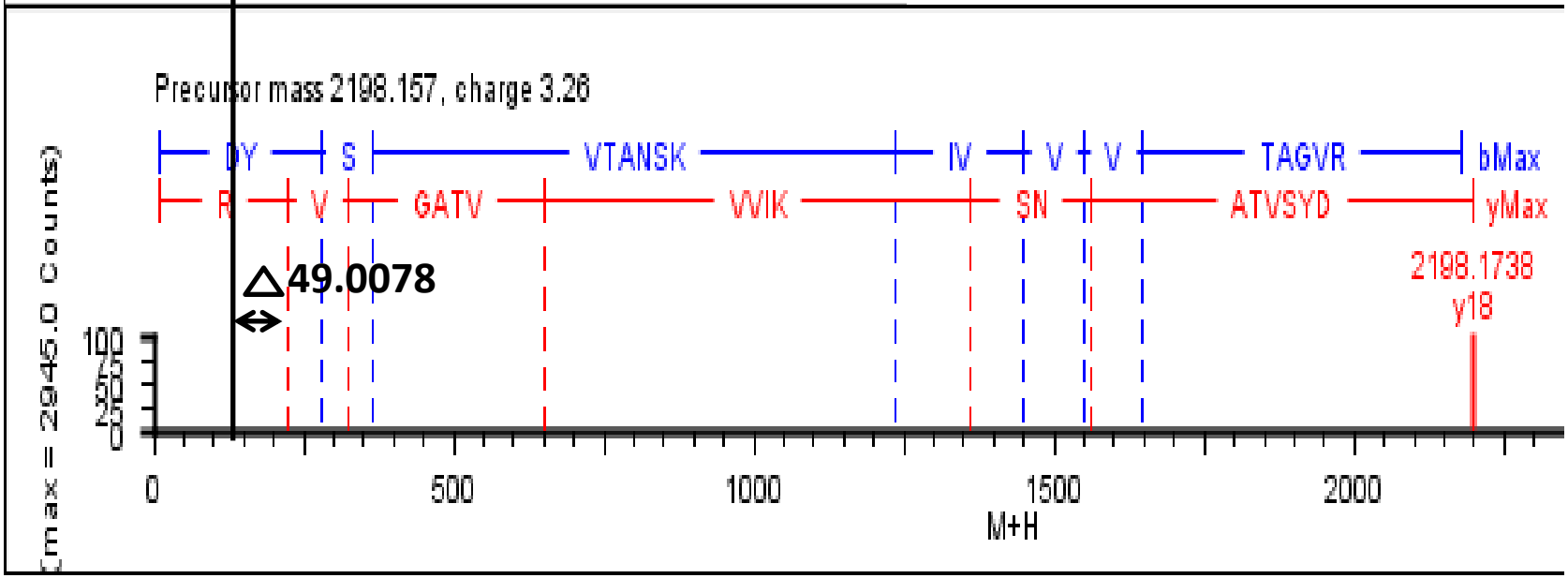
584.3656

692.3466: (584.36+ 108.02)

120-127 (R)NVNVFKFIIPQIVK(Pyr)(Y)



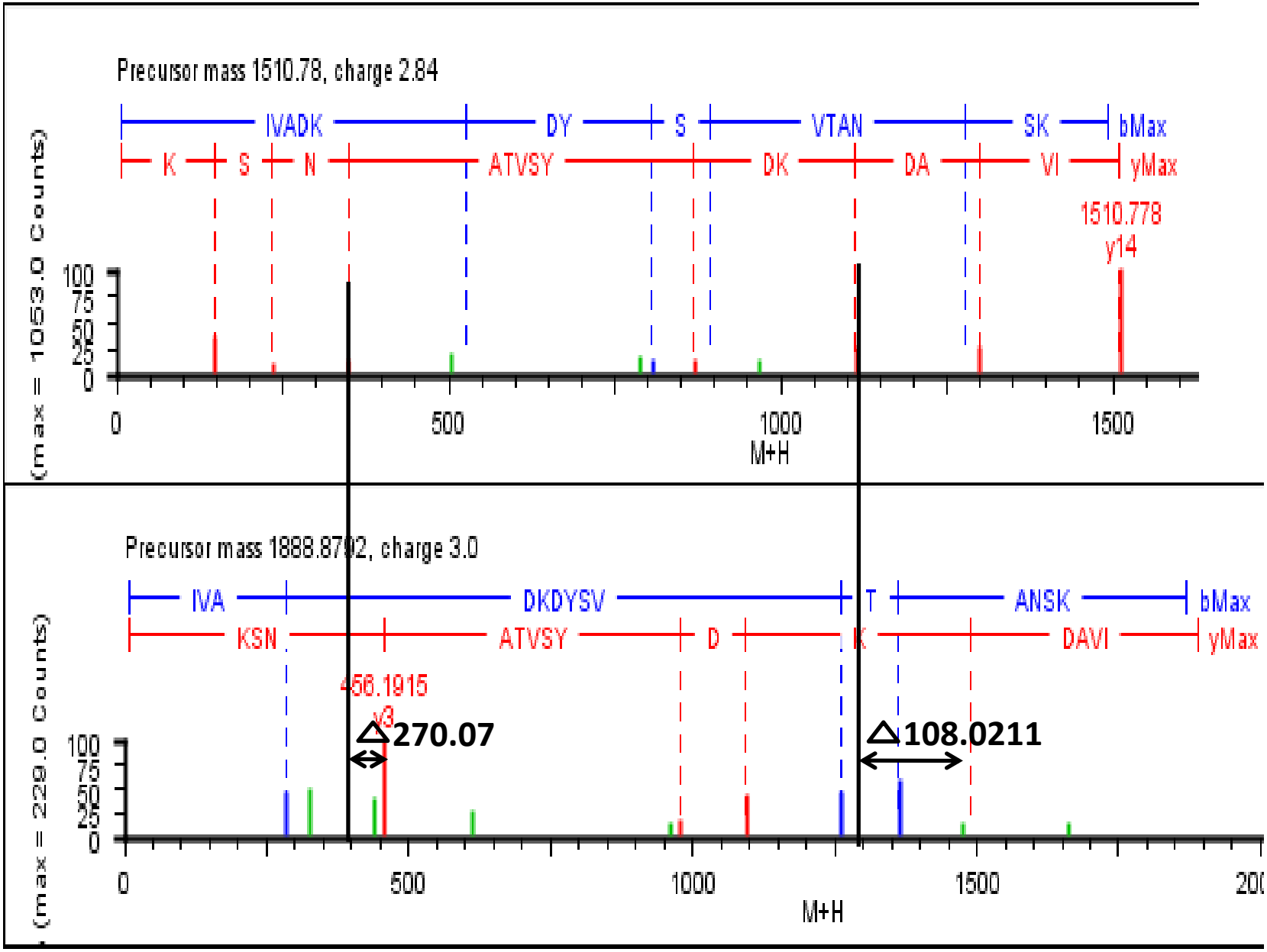
175.1136



224.1228: (175.11+ 49.00)

83-100

(K)DYSVTANSKIVVVTAGVR(MOLD)(Q)

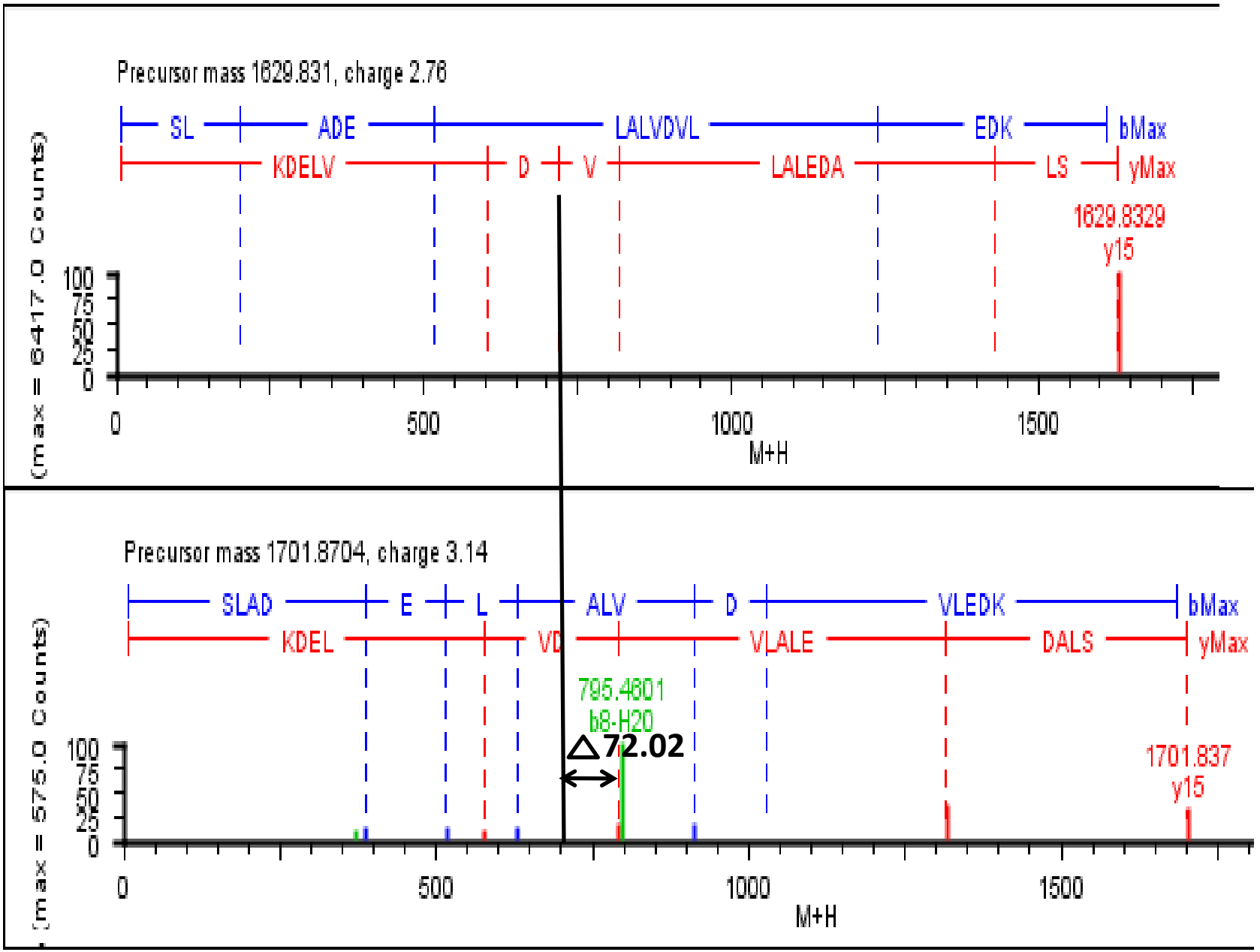


1112.5748

1490.6512: (1112.5748+ 270.07+ 108.02)

78-91

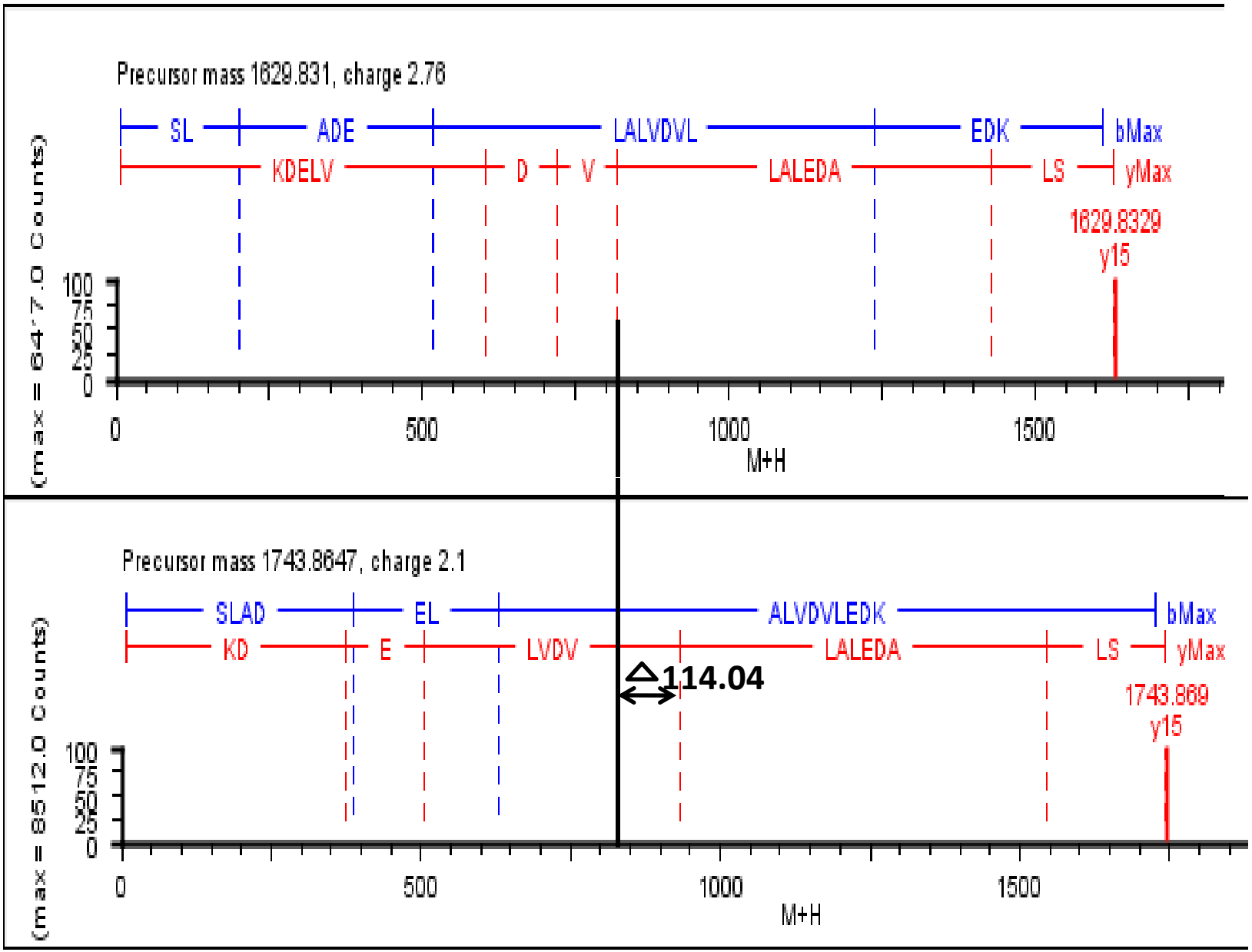
(K)IVADK(AFGP)DYSVTANSK(Pyr)(I)



718.3266

790.3942: (718.32+ 72.02)

44-58 (K)SLADELALVDVLEDK(CEL)(L)

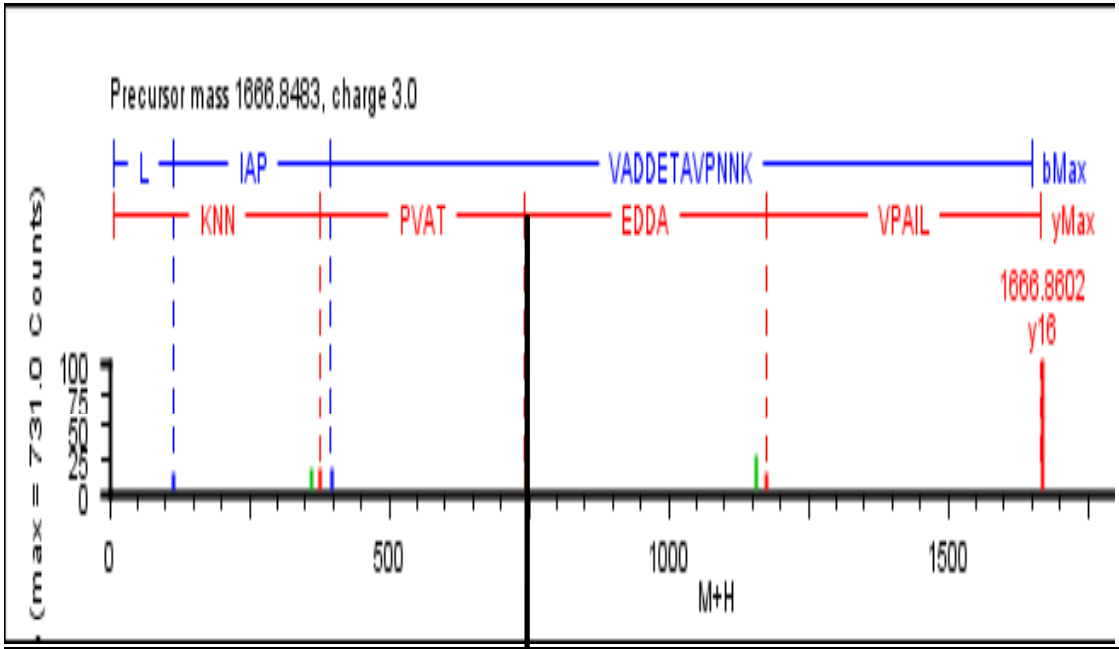


817.404

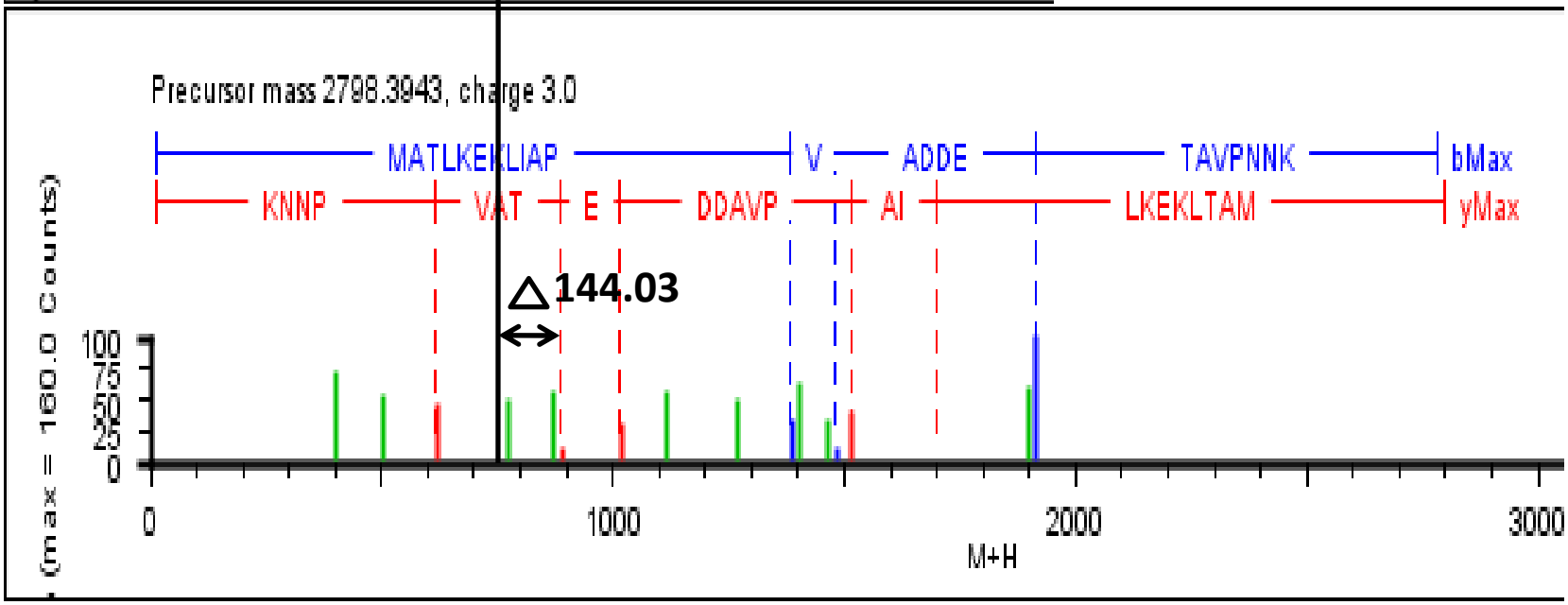
931.4877: (817.40+ 114.04)

44-58

(K)SLADELALVDVLEDK(Ubi)(L)



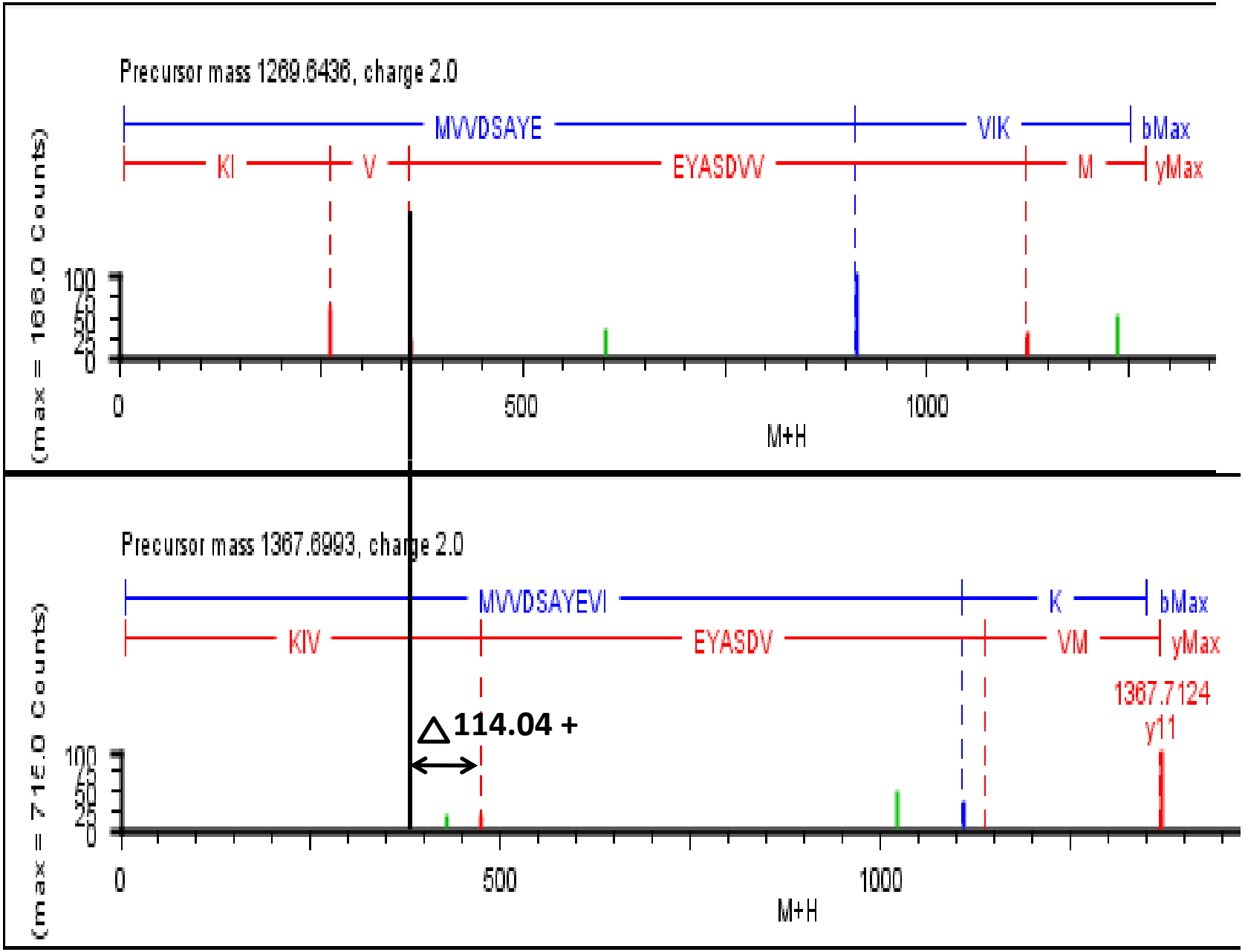
743.3833



887.4383: (743.38+ 144.03)

1- 23

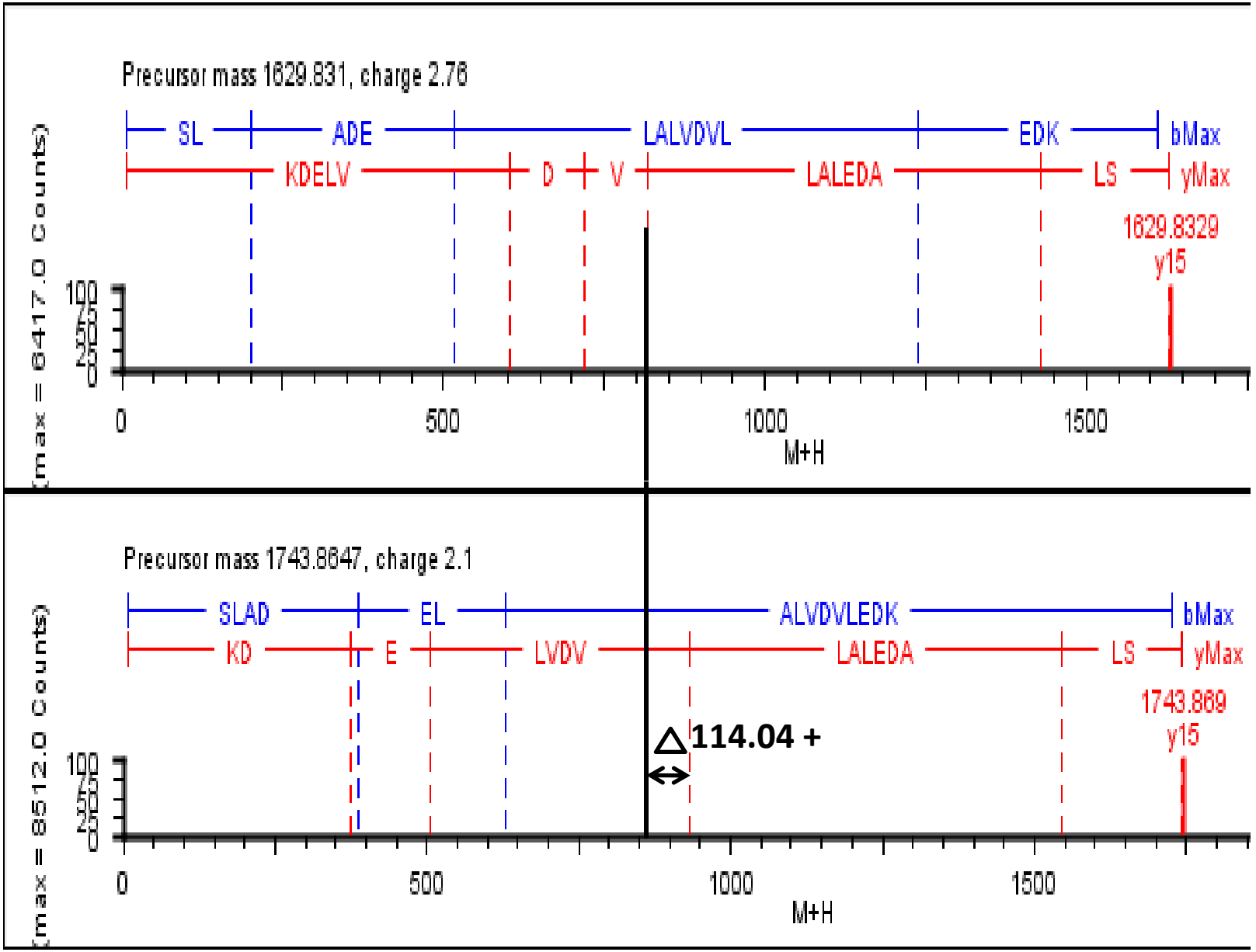
(-)MATLKEKLIAPVADDETAVPNNK(ImiA)(I)



359.2397

473.3243: (359.23+ 114.04)

234-244 (K)MVVDSAYEVIK(Ubi)(L)



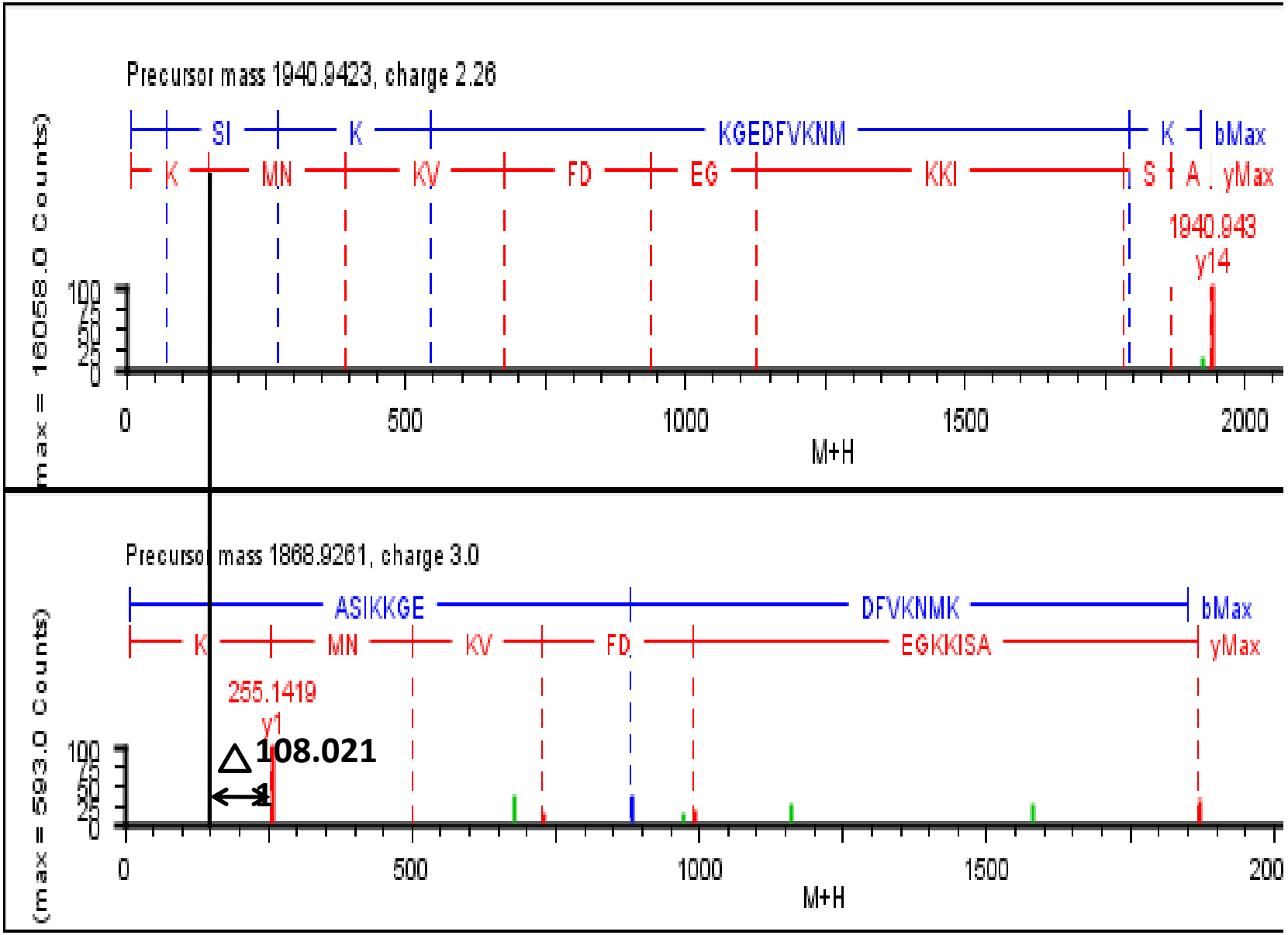
817.404

931.4877: (817.404+ 114.04)

44-58

(K)SLADELALVDVLEDK(Ubi)(L)

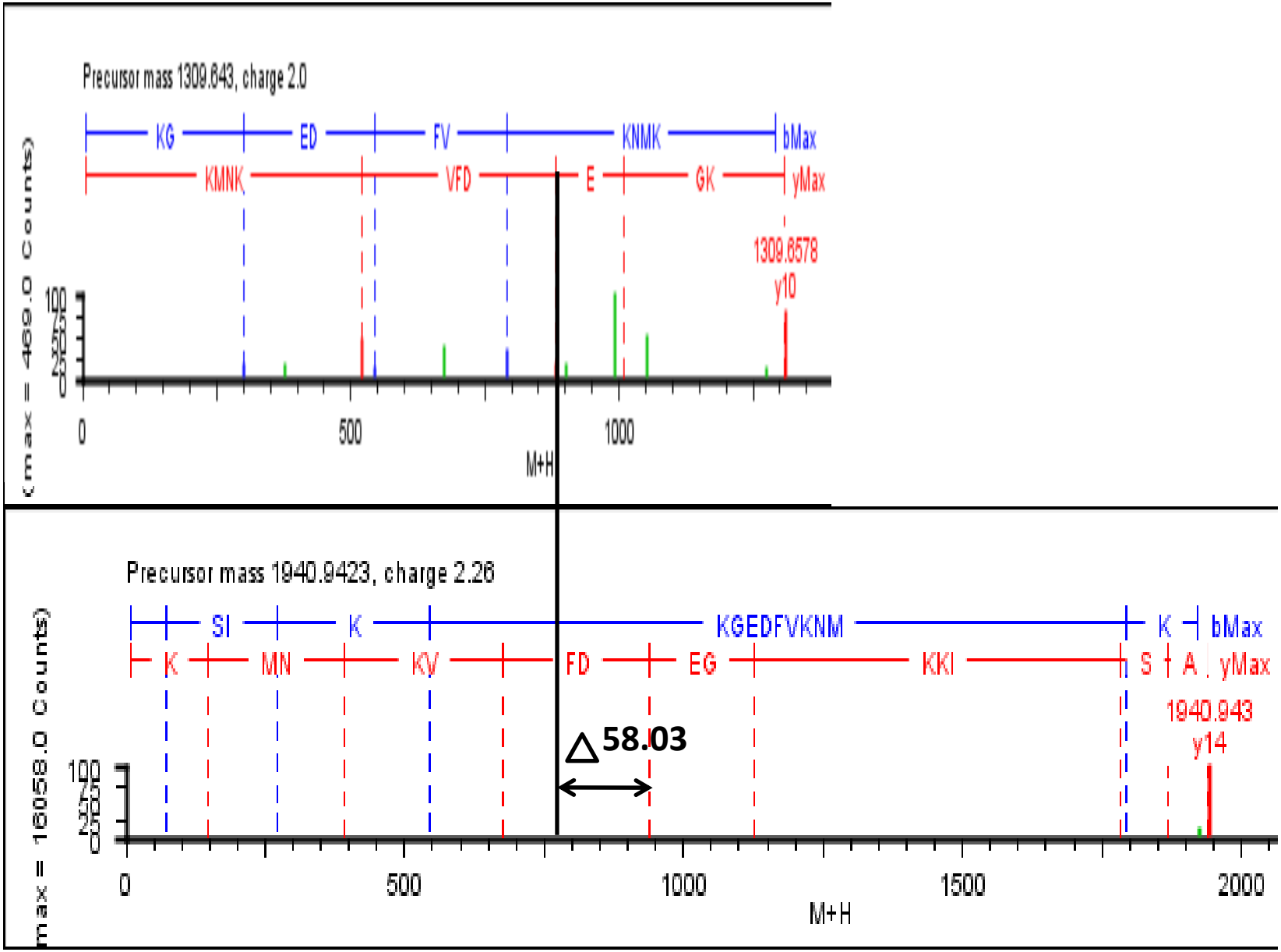
MDH



147.1099

255.1419: (147.10+ 108.02)

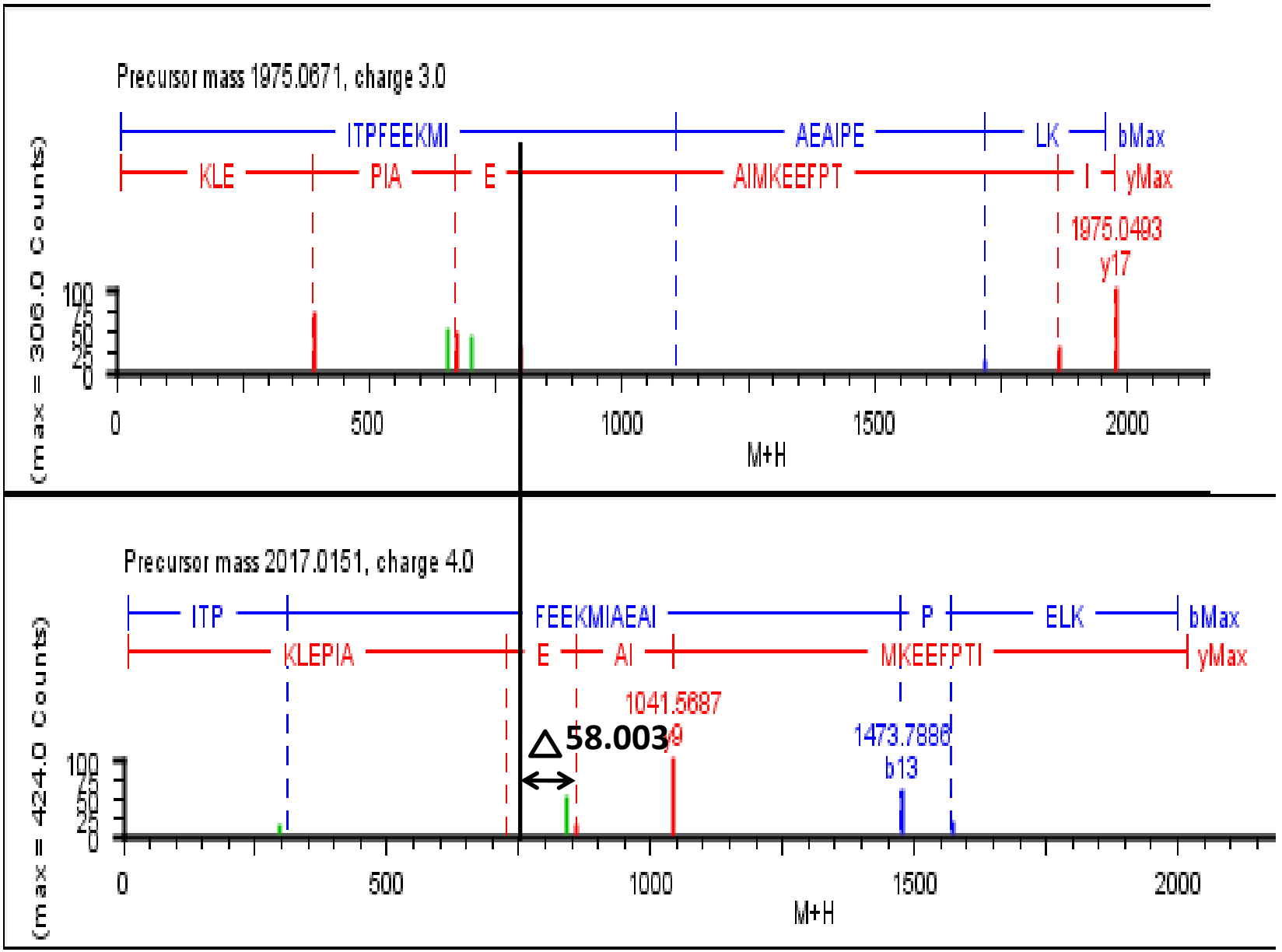
325-338 (K)ASIKKGEDFVKNMK(Pyr)(-)



881.4461

939.4362: (881.44+ 58.03)

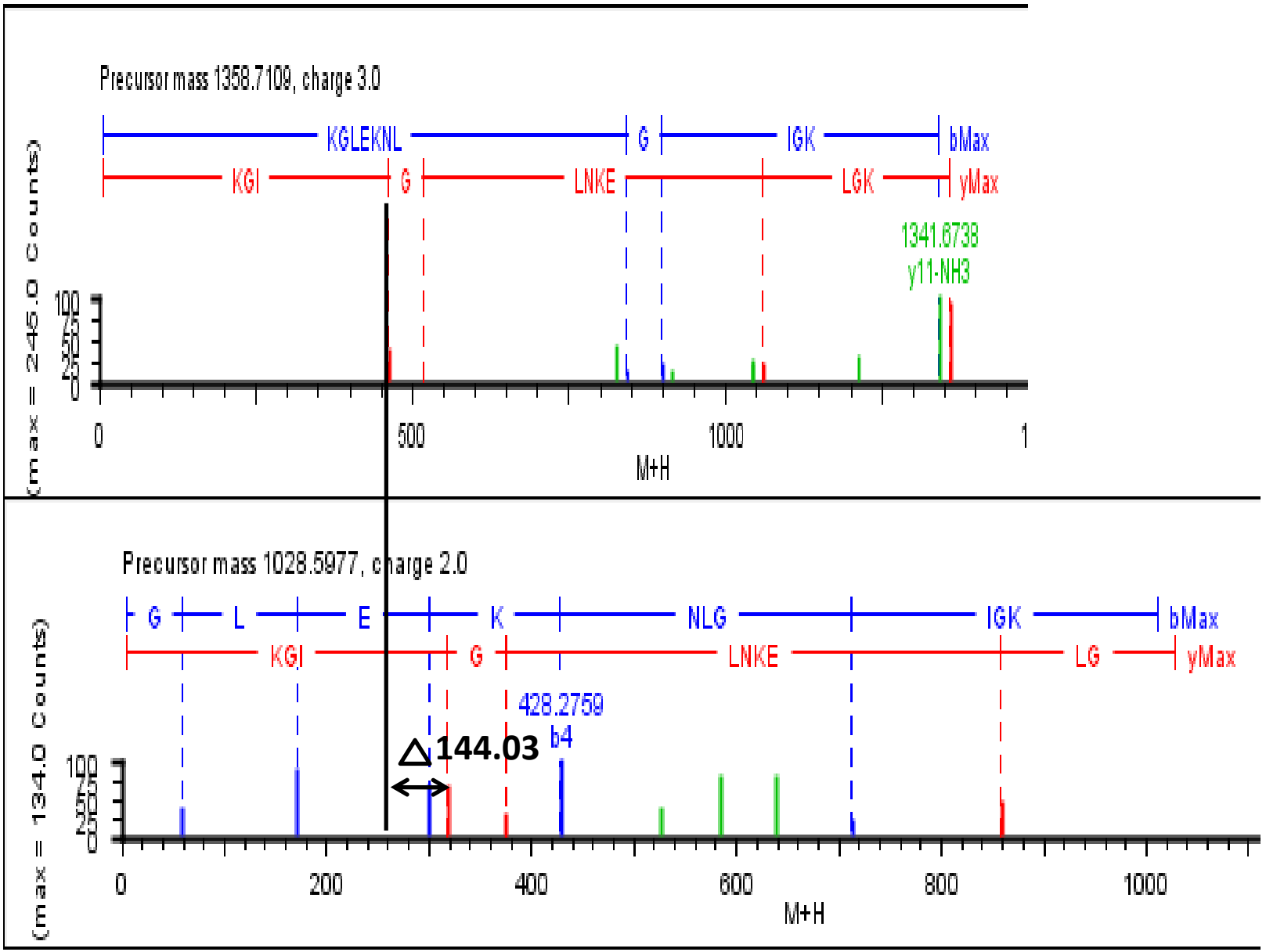
329-338 (K)KGEDFVKNMK(Pento)(-)



670.363

728.4481: (670.36+ 58.003)

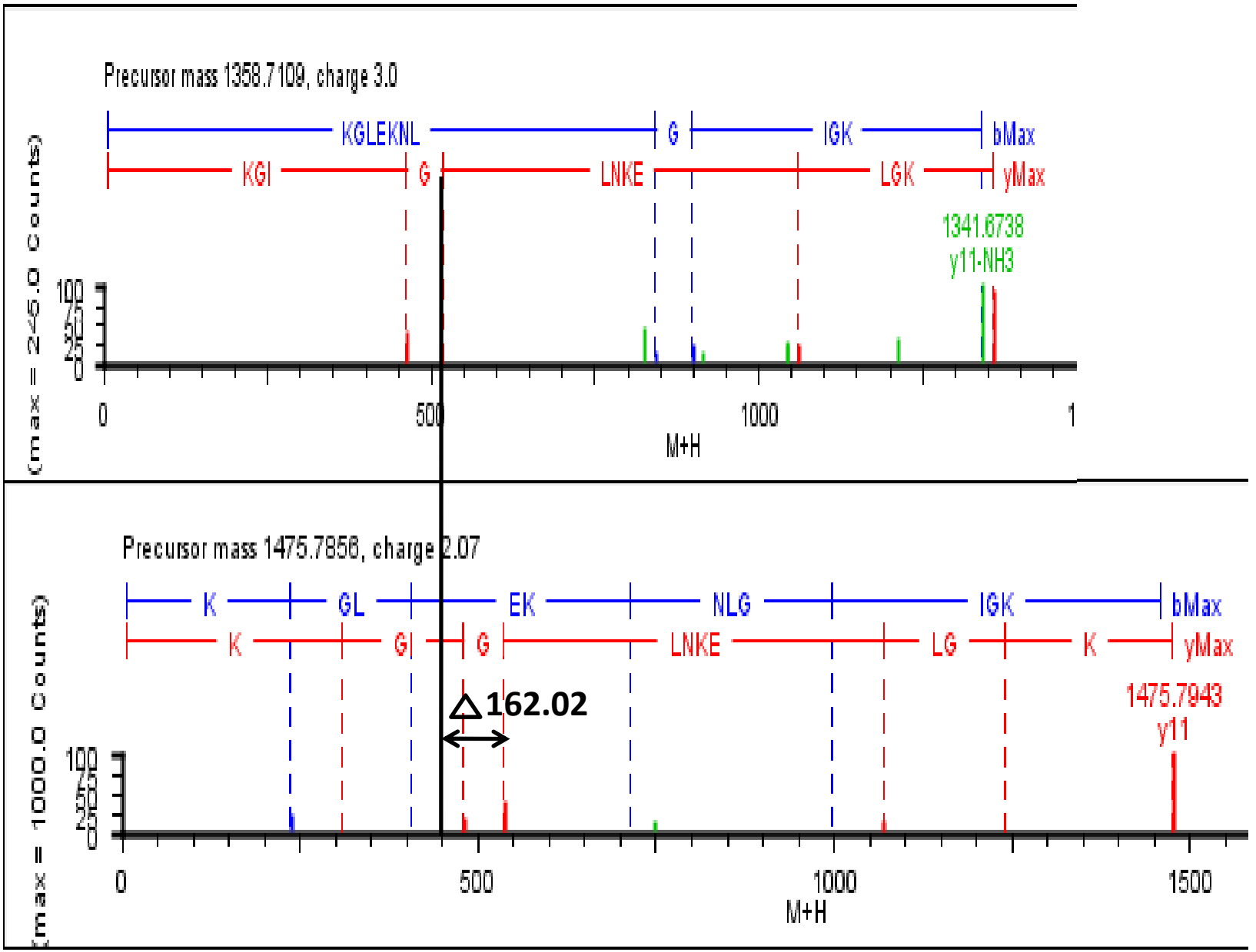
308-324 (K)ITPFEEKMIAEAIPELK(CML)(A)



317.1725

461.245: (317.17+ 144.03)

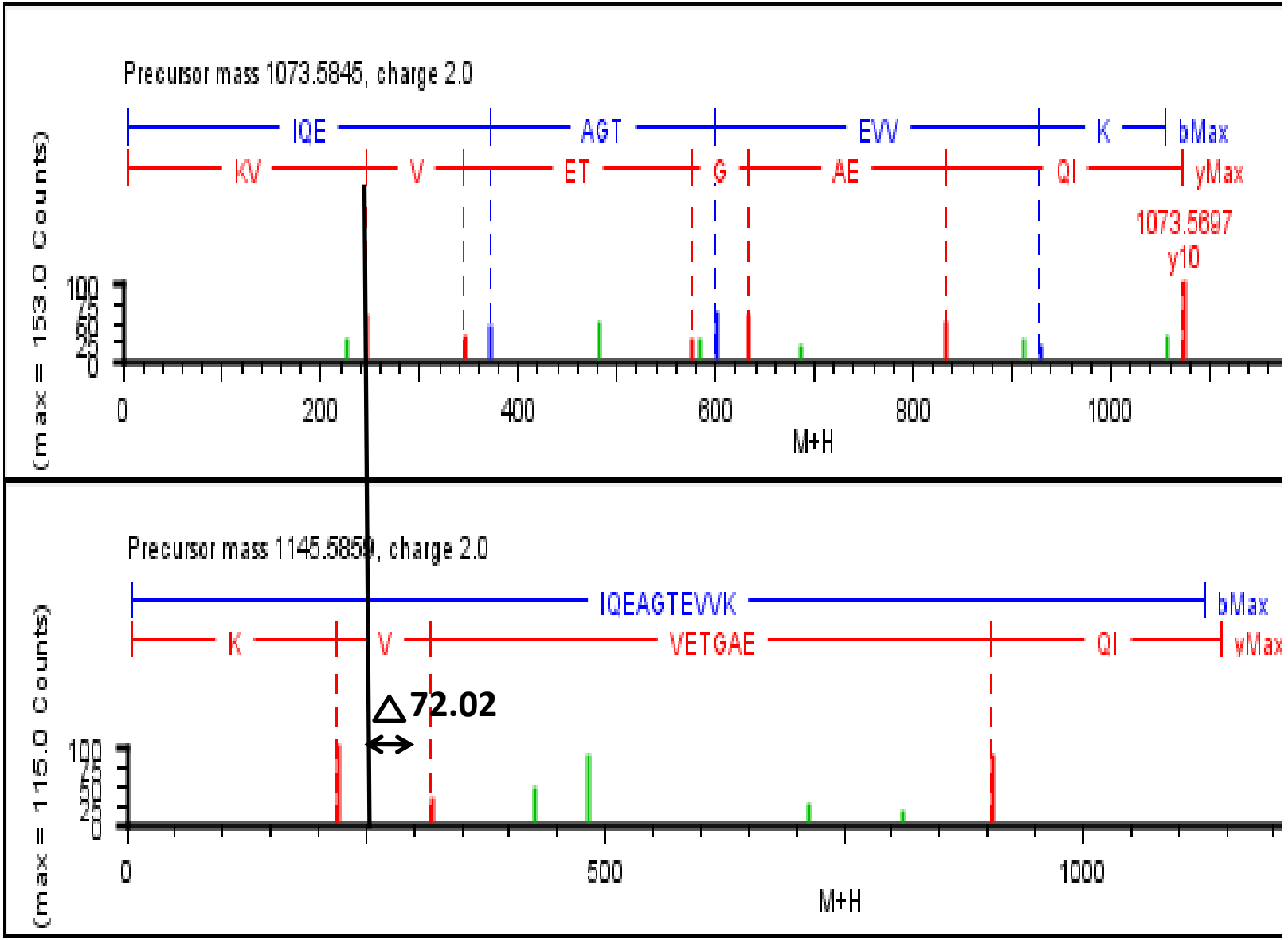
297-307 (K)KGLEKNLGIGK(ImiA)(I)



317.1725

479.2264: (317.17+ 162.02)

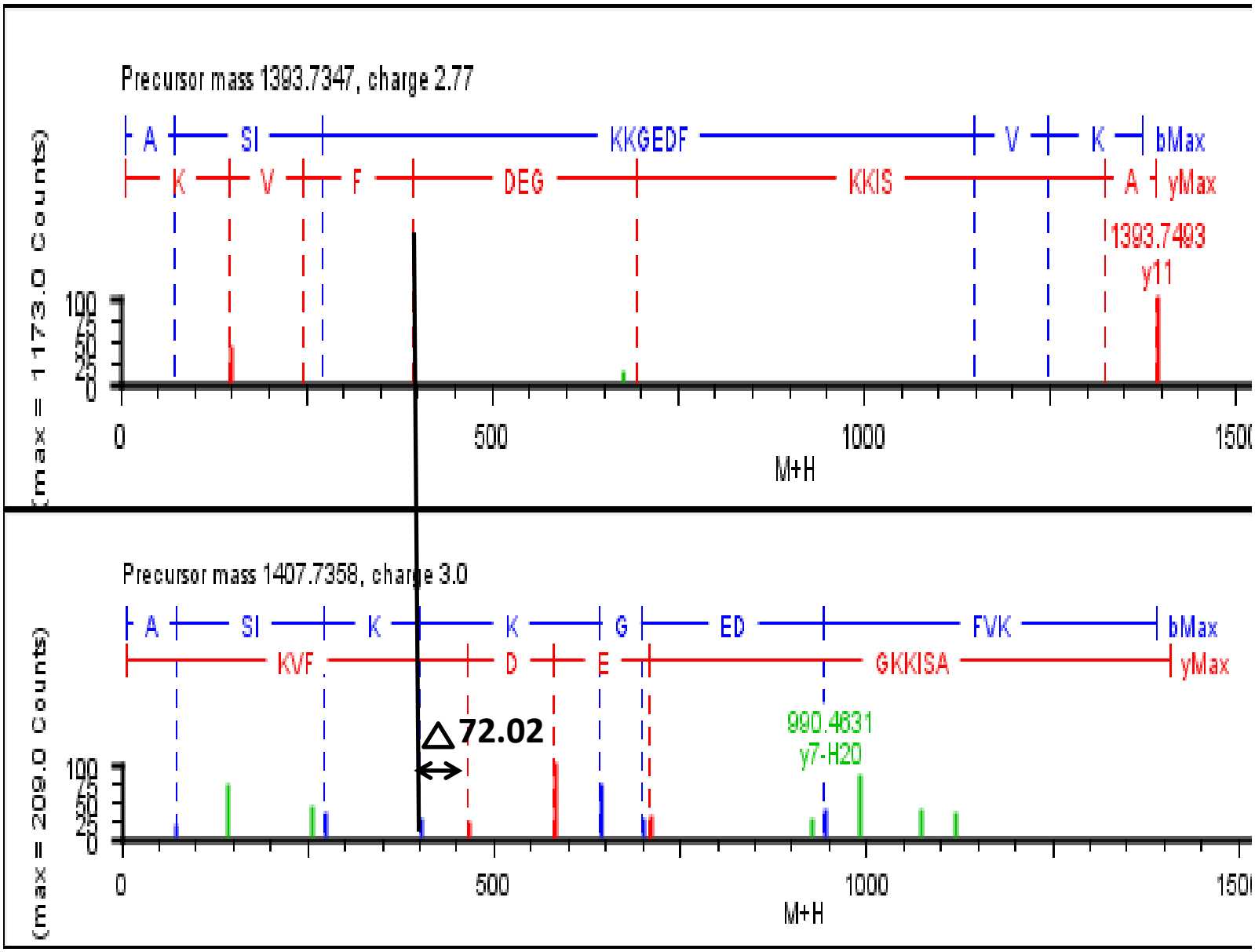
297-307 (K)KGLEKNLGIGK(Gly)(I)



246.1697

318.2058: (246.16+ 72.02)

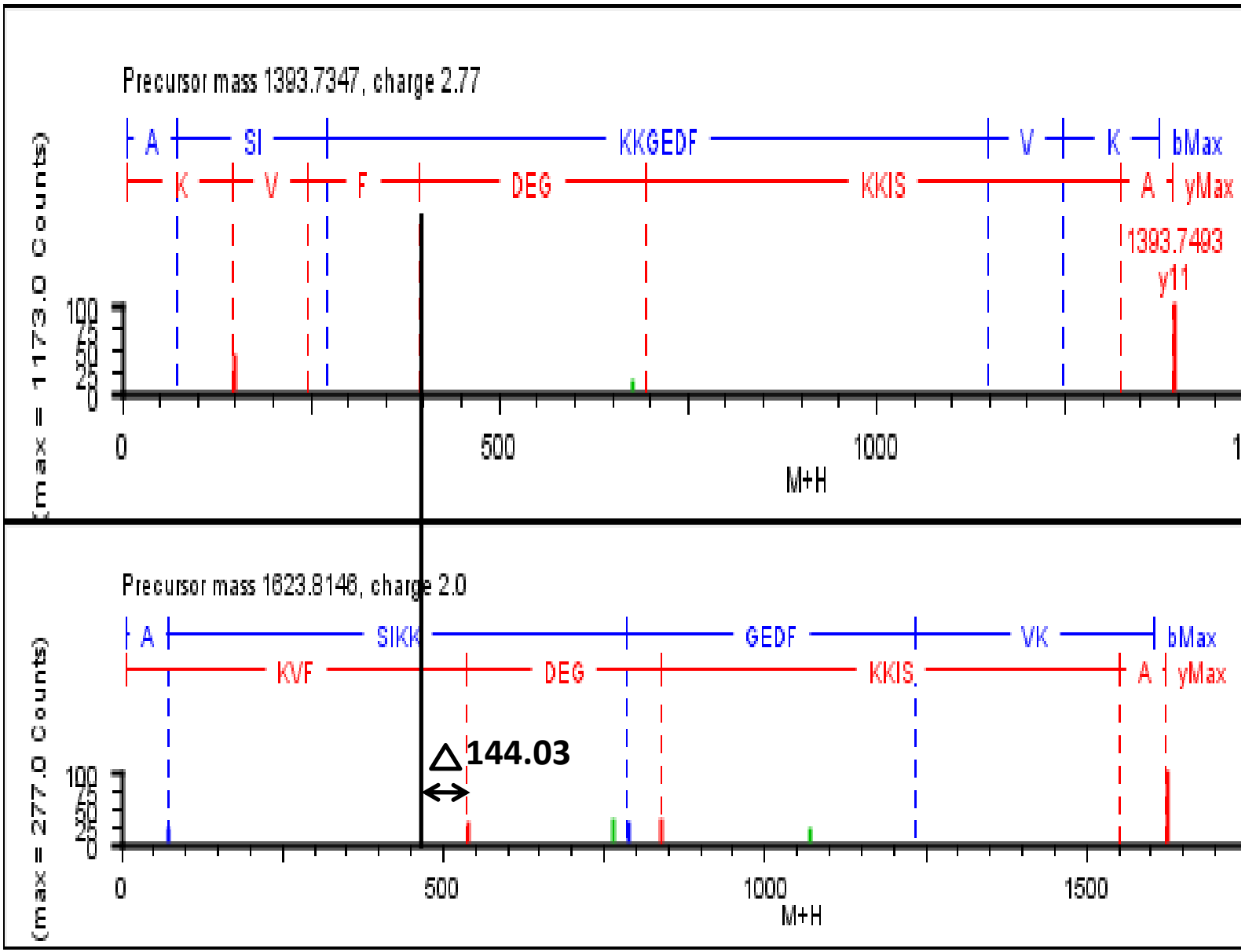
230-239 (R)IQEAGTEVVK(CEL)(A)



393.2541

465.2833: (393.25+ 72.02)

325-335 (K)ASIKKGEDFVK(CEL)(N)

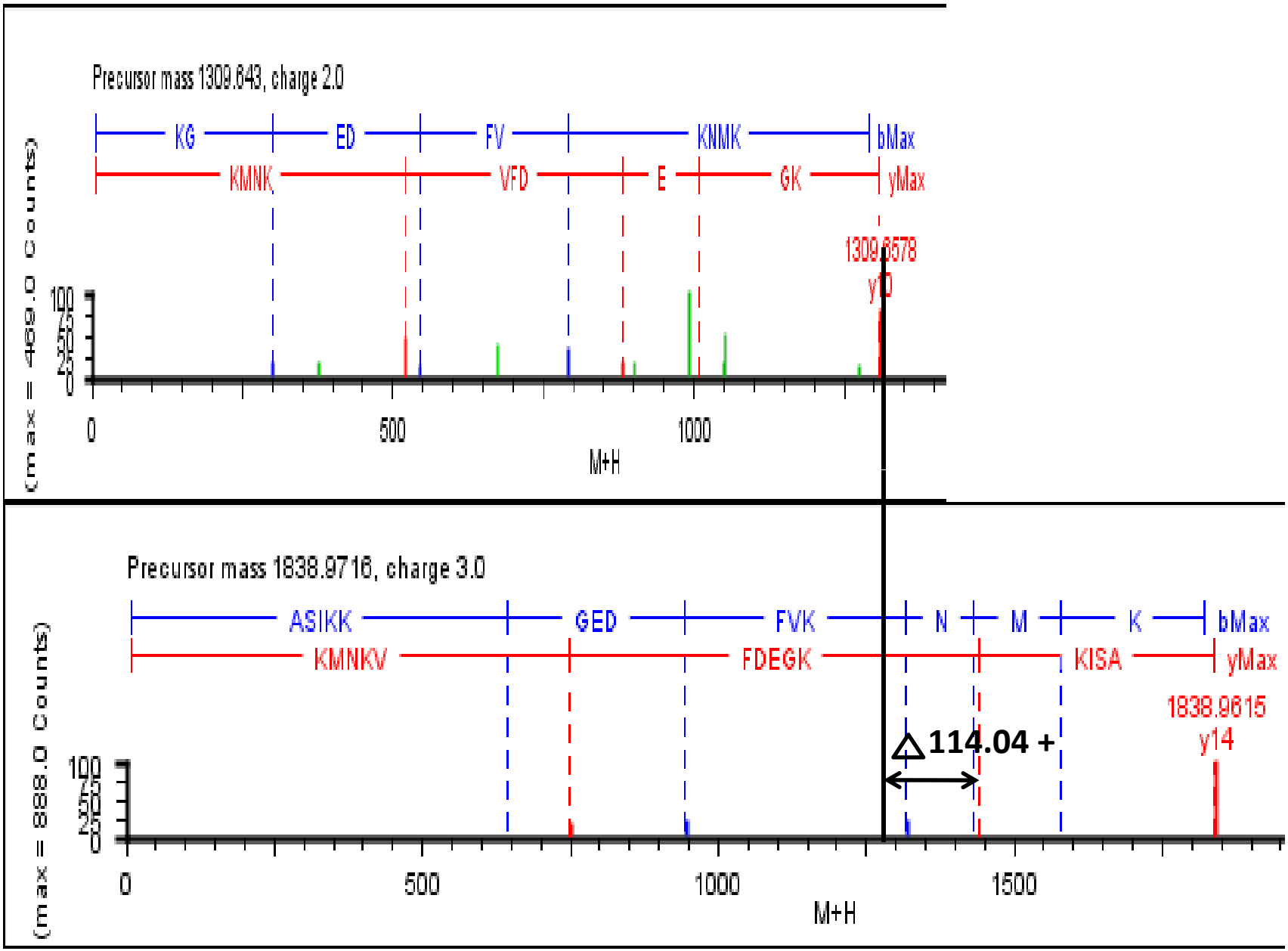


393.2541

537.2552: (393.25+ 144.03)

325-335

(K)ASIKKGEDFVK(ImiA)(N)

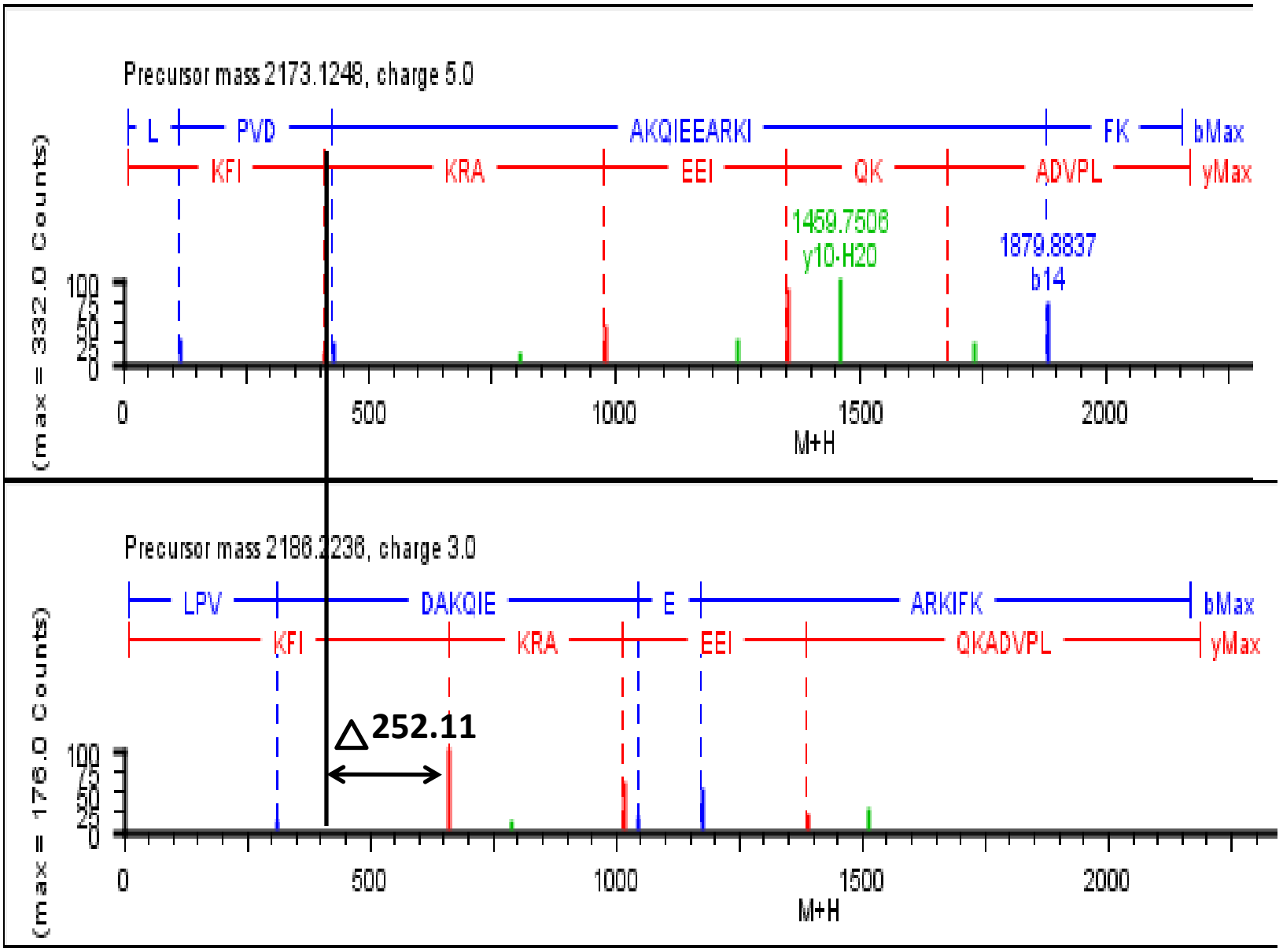


1309.6578

1439.7446 (1309.65+ 114.04)

325-338 (K)ASIKKGEDFVKNMK(Ubi)(-)

GST

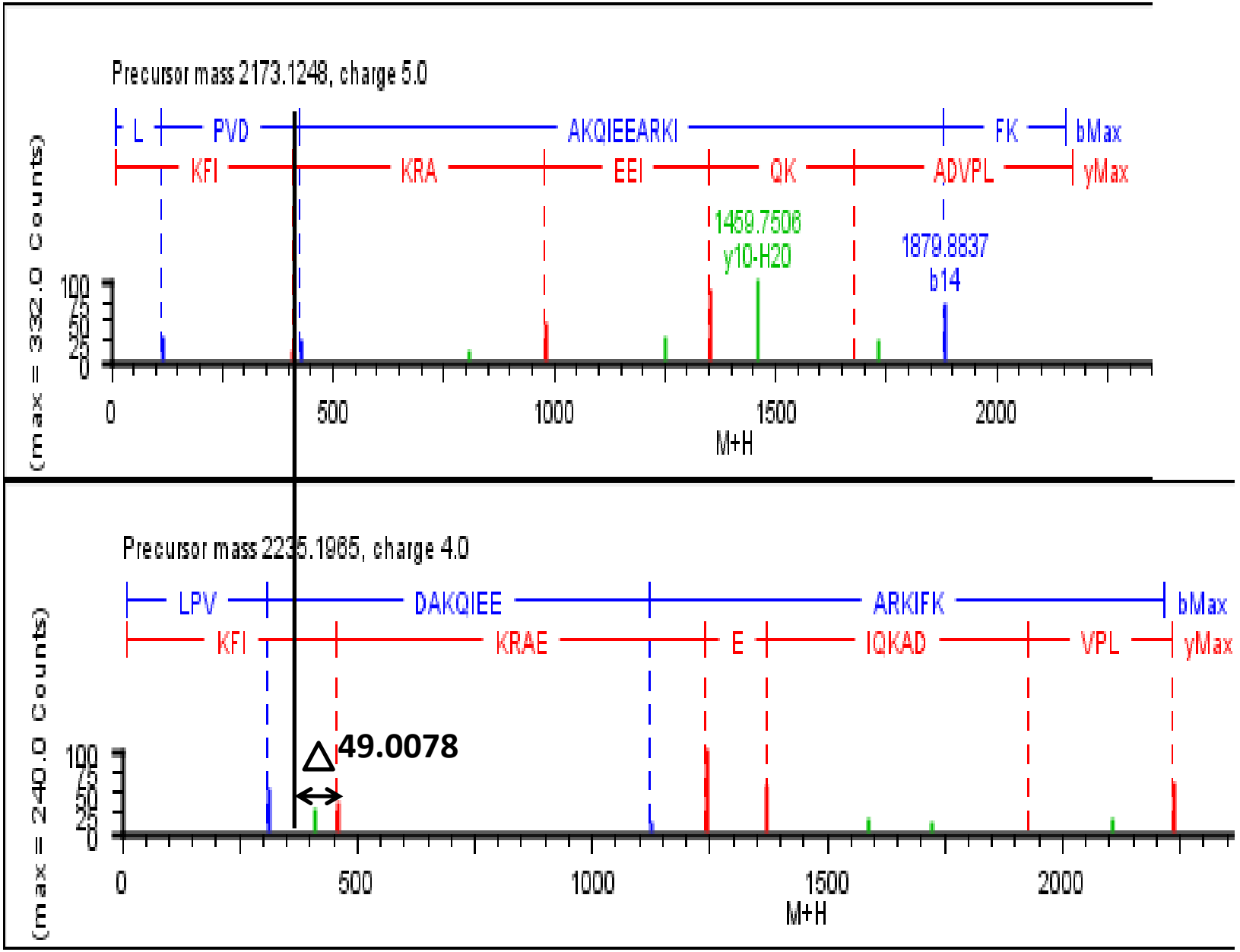


407.269

659.3647: (407.269+ 252.11)

206-221

(K)LPVDAKQIEEARKIFK(Crossline)(F)

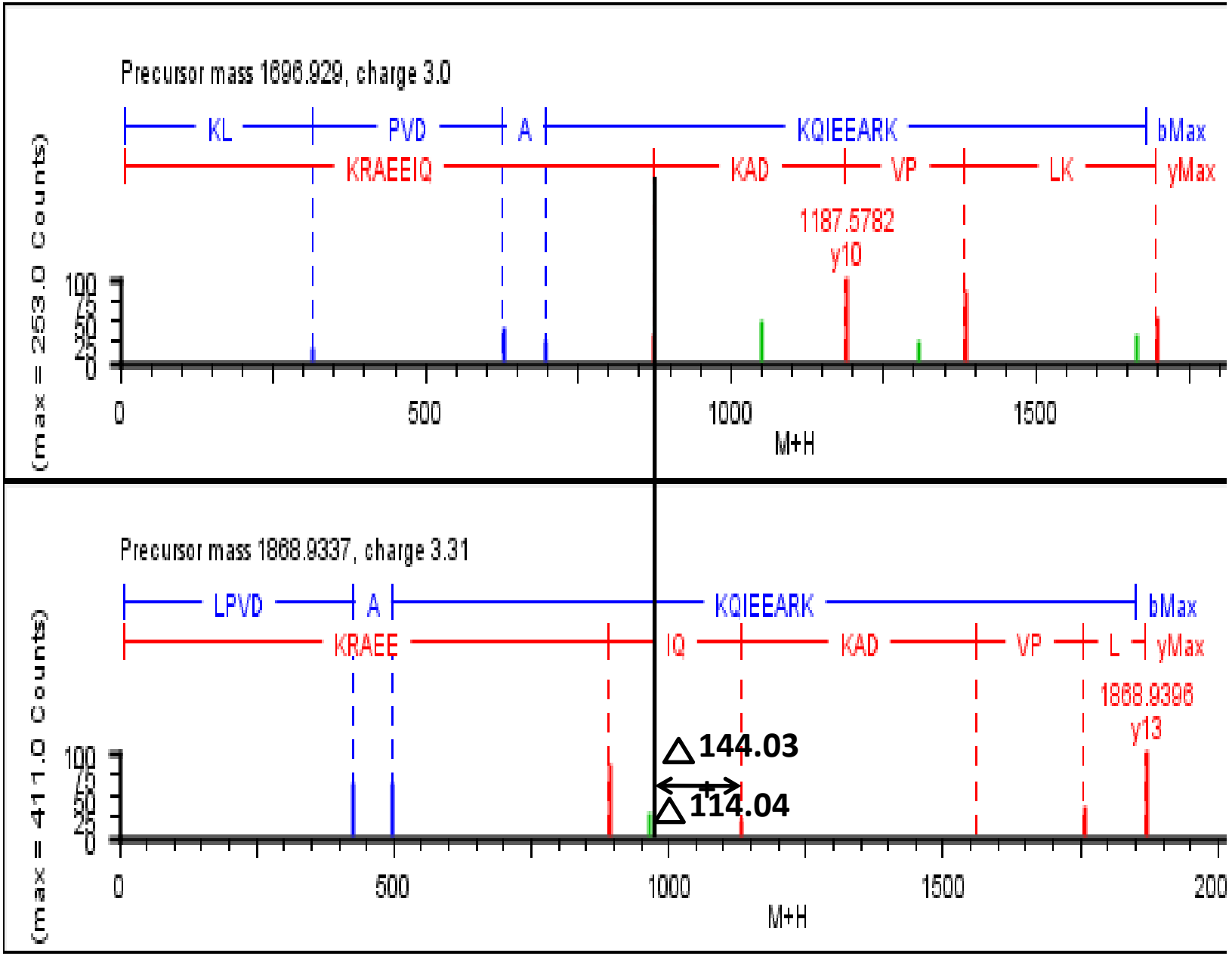


407.269

456.3085:(407.269+ 49.00)

206-221

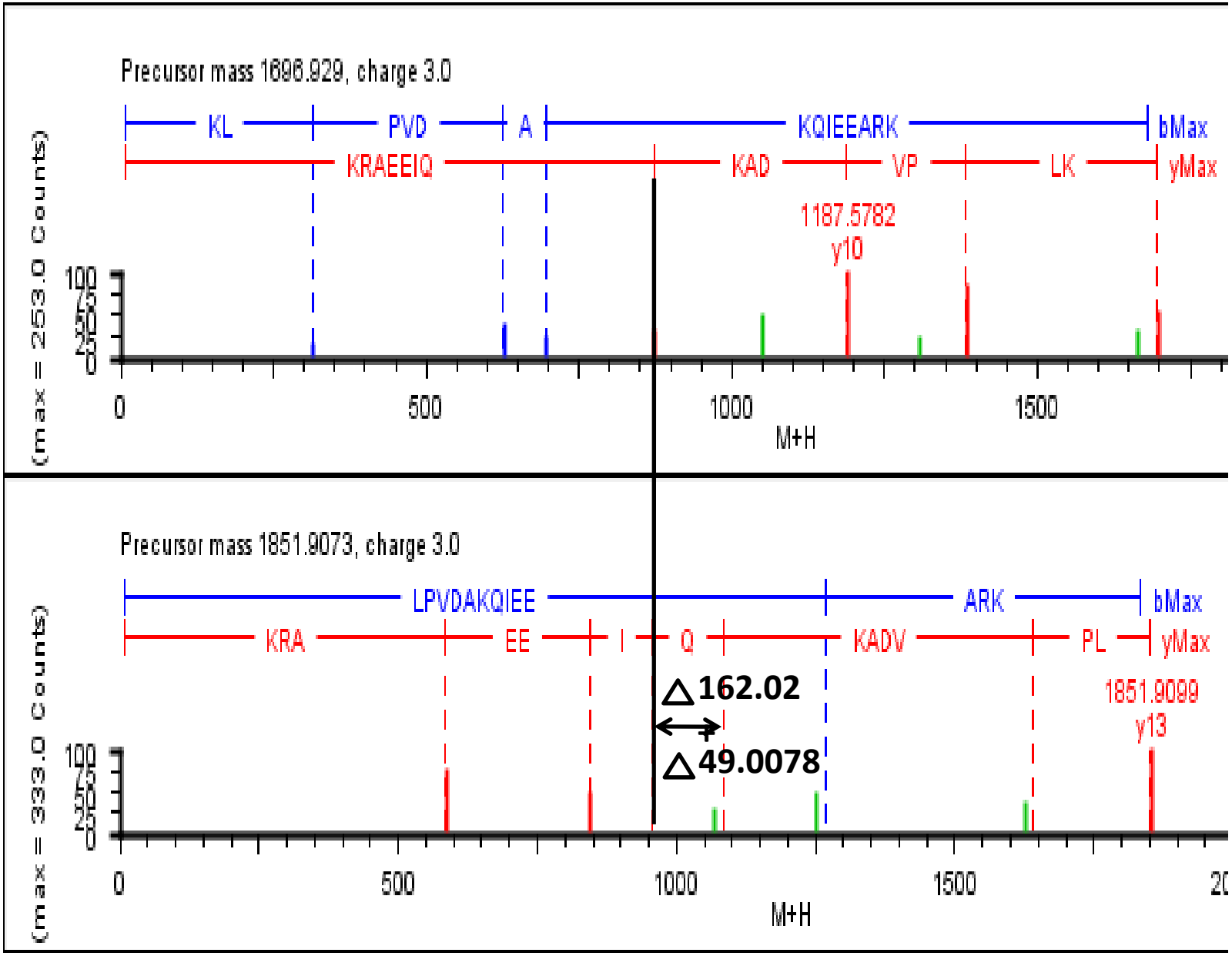
(K)LPVDAKQIEEARKIFK(MOLD)(F)



873.4067

1131.4565 : (873.40+ 144.03+ 114.04)

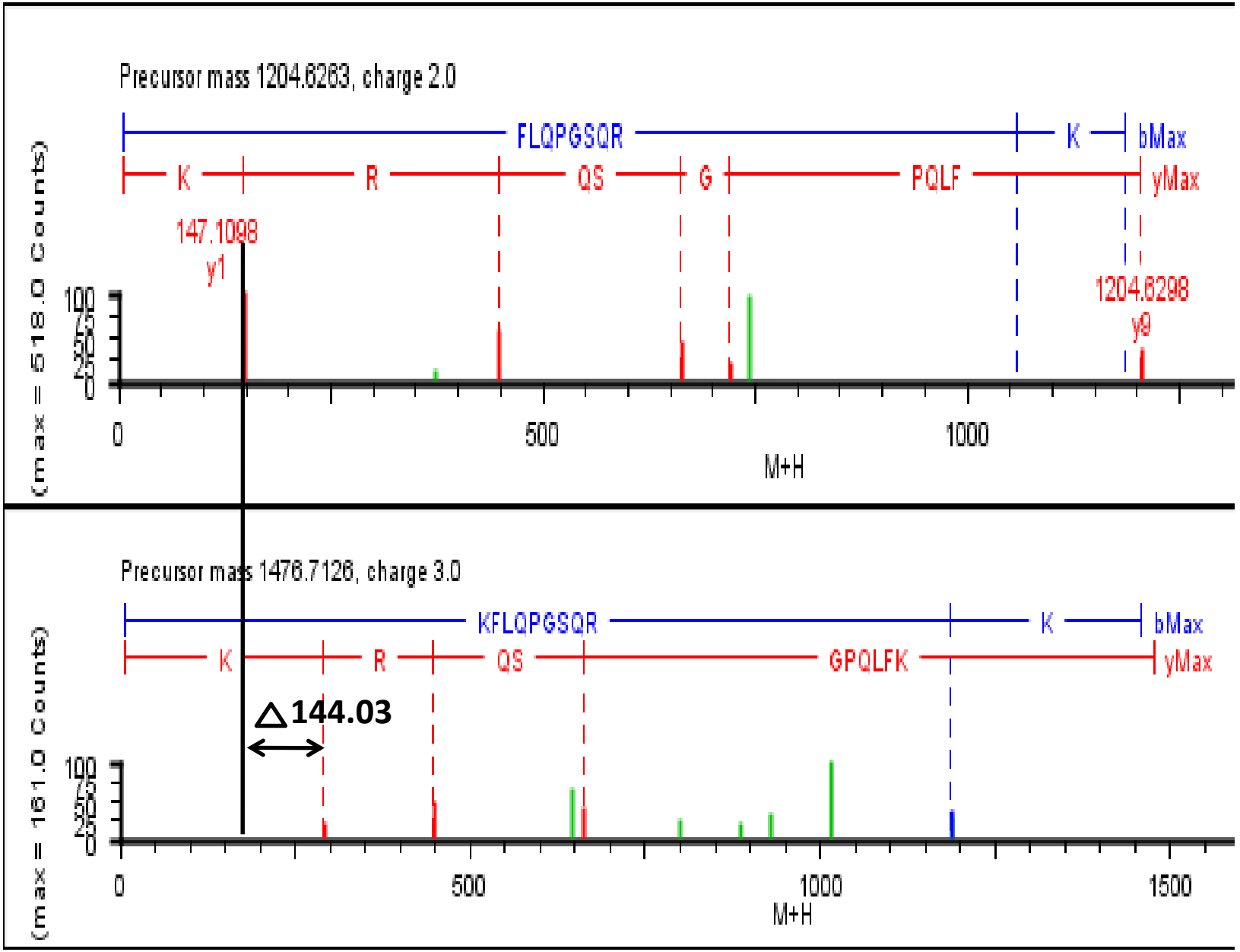
205-218 (R)KLPVDAKQIEEAR(ImiA)K(Ubi)(I)



873.4067

1084.4537 : (873.40+ 162.02+ 49.0078)

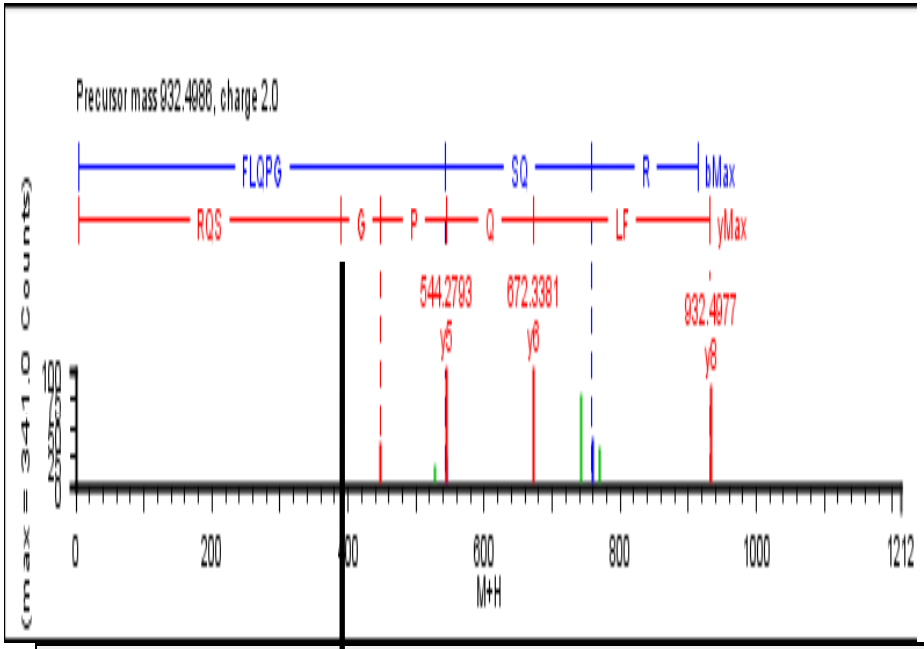
206-218 (K)LPVDAKQIEEAR(Gly)K(MOLD)(I)



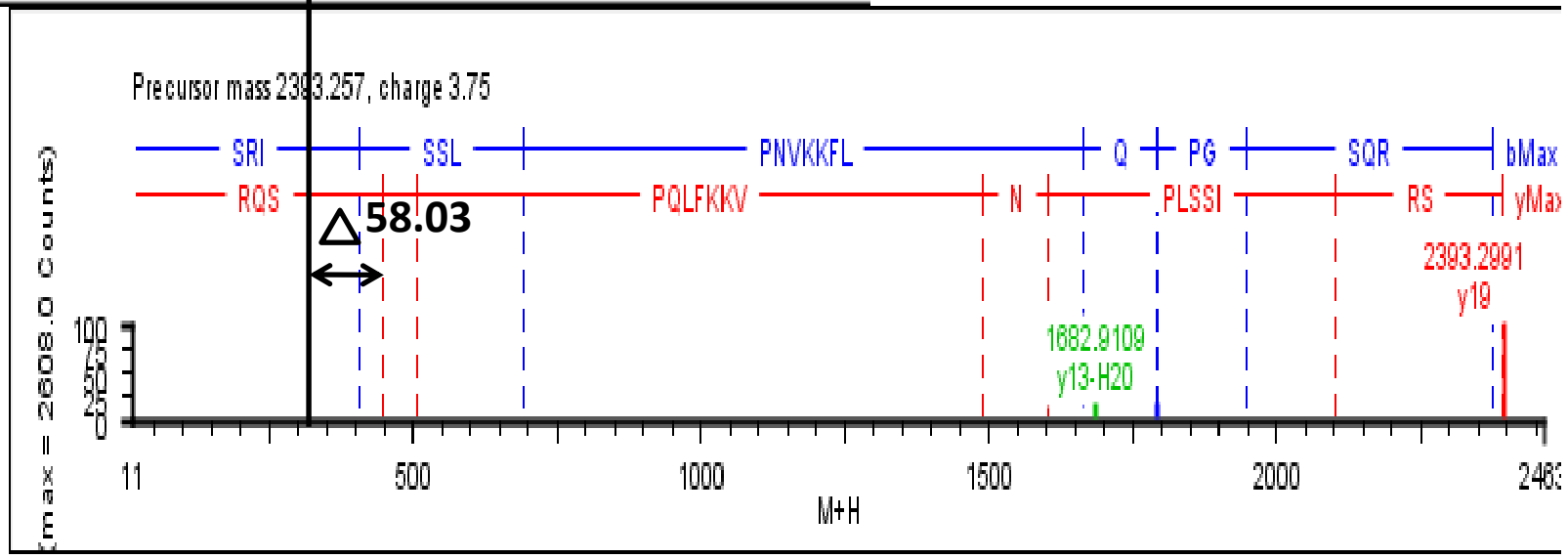
147.1098

291.1473: (147.1098 + 144.03)

196-205 (K)KFLQPGSQRK(ImiA)(L)



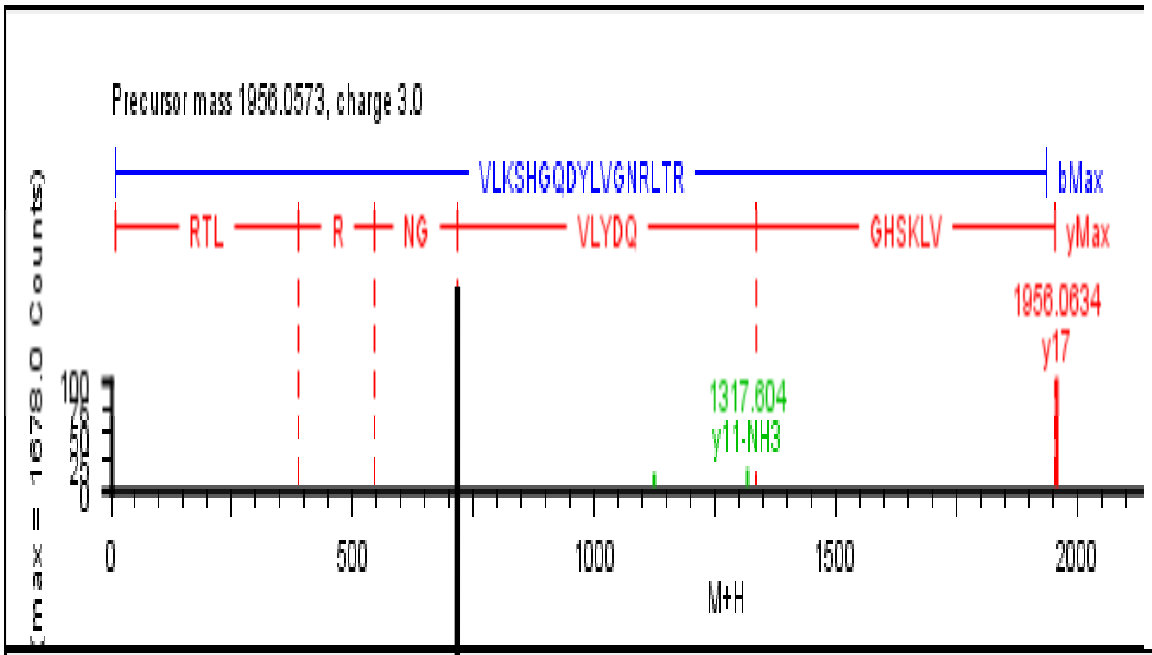
447.2205



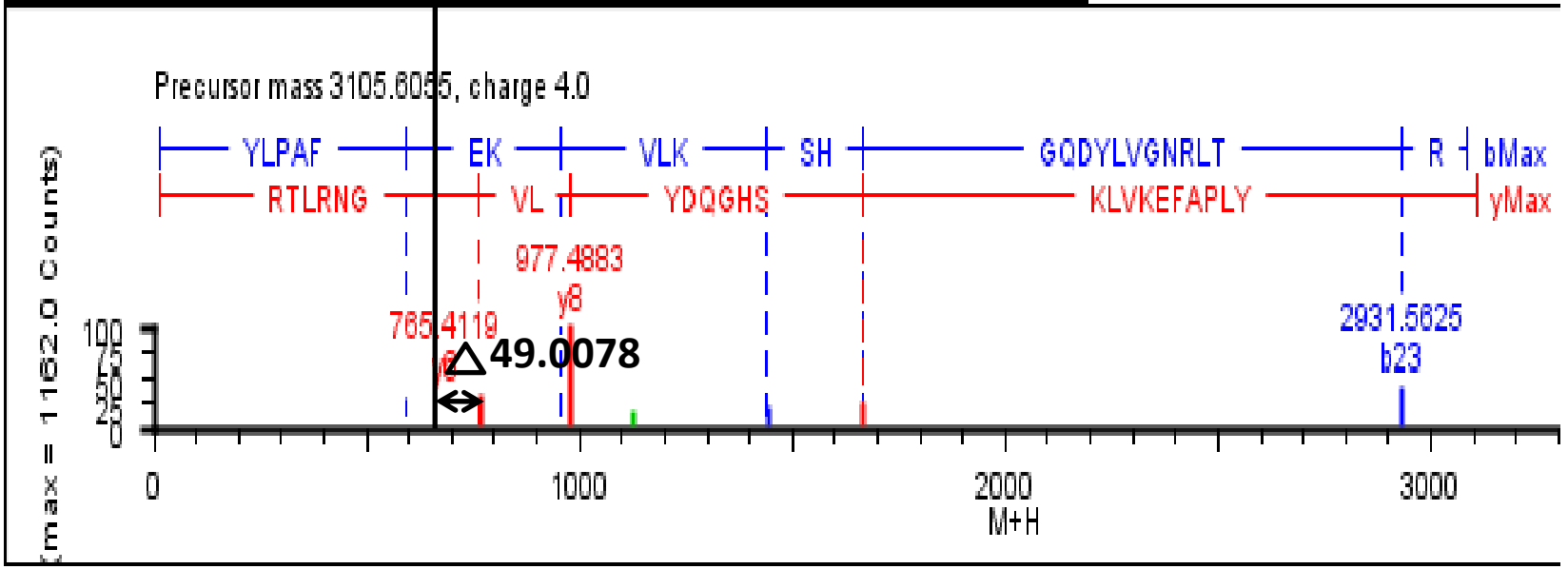
505.232: (447.22+ 58.03)

186-204

(K)SRISSLPNVKKFLQPGSQR(Pentosidine)(K)



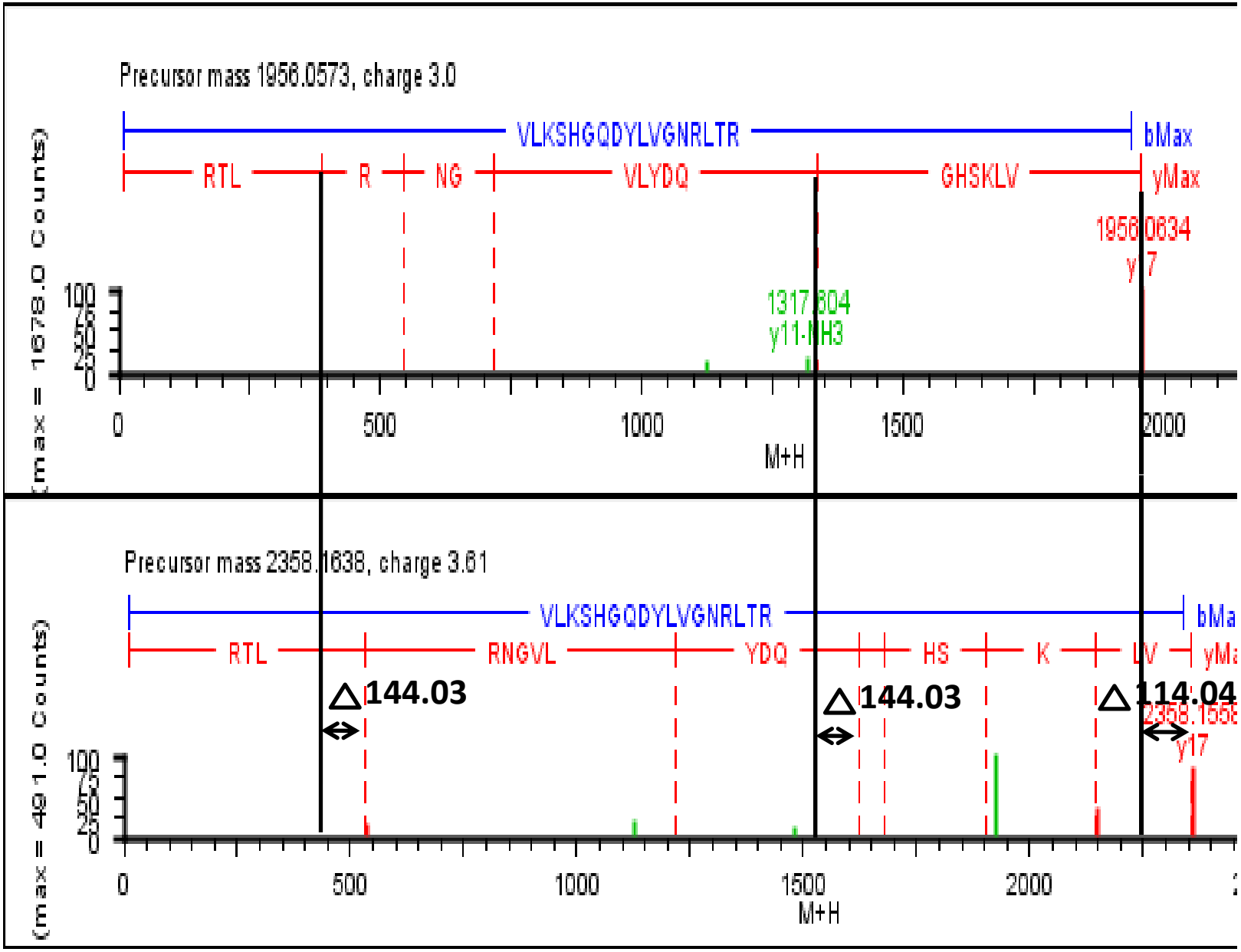
716.3885



765.4119: (716.38+ 49.00)

132-155

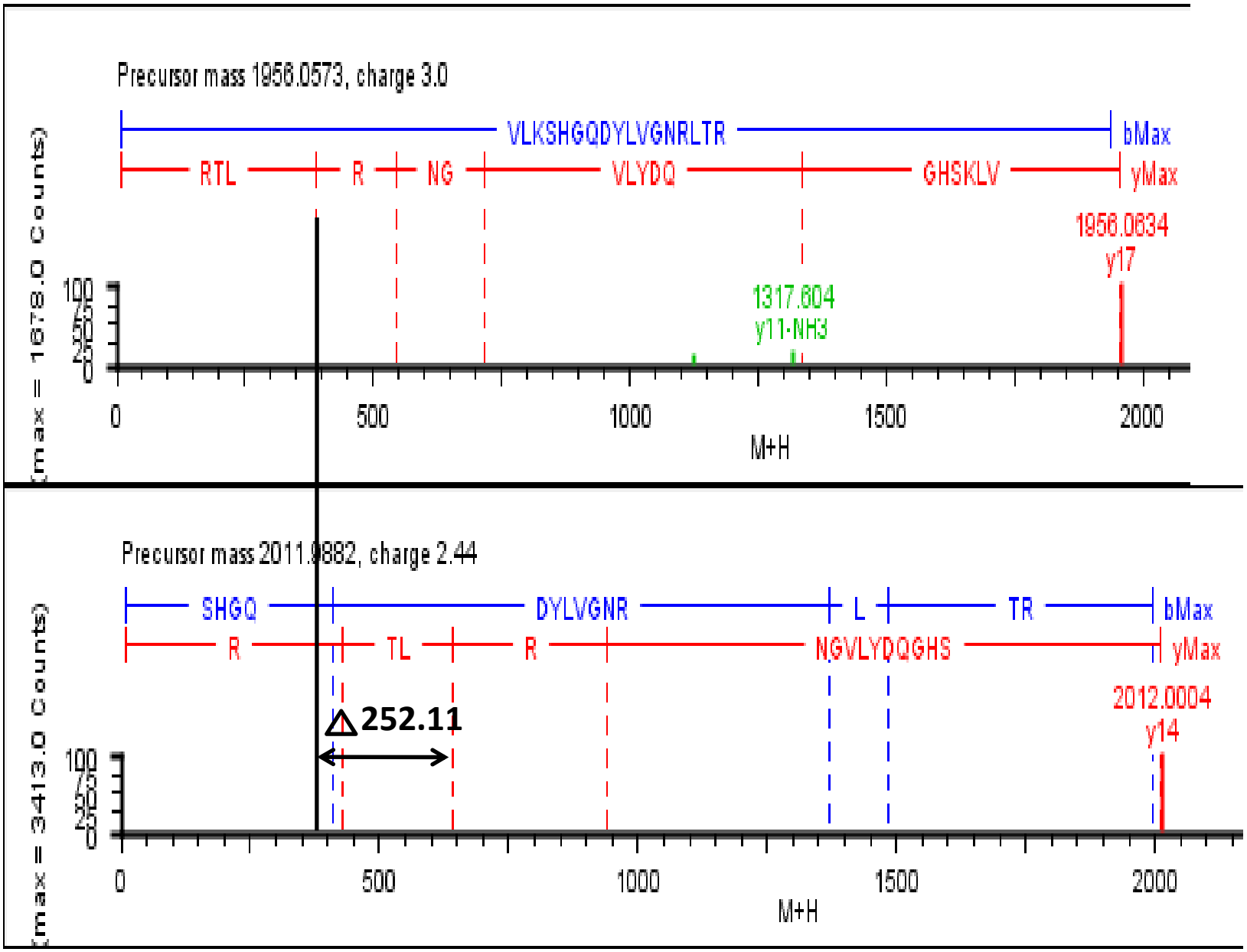
(R)YLPAFEKVLKSHGQDYLVGNR(MOLD)LTR((V)



1956.0634

2358.1558: (1956.06+ 114.04+ 144.03+ 144.03)

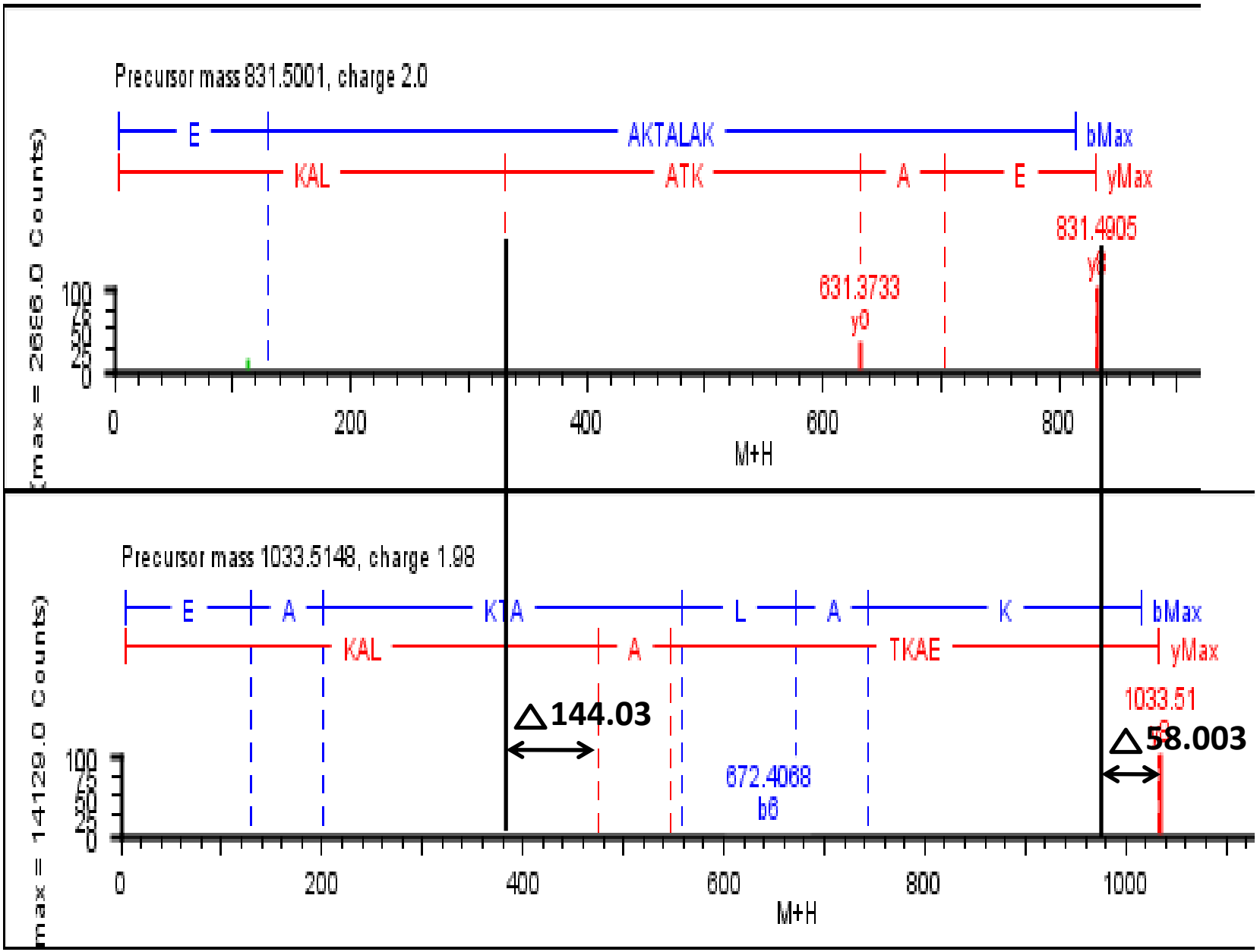
139-155 (K)VLK(Ubi)SHGQDYLVGNR(ImiA)LTR(ImiA)(V)



389.2514

641.3743: (389.25+ 252.11)

142-155 (K)SHGQDYLVGNRLTR(Crossline)(V)

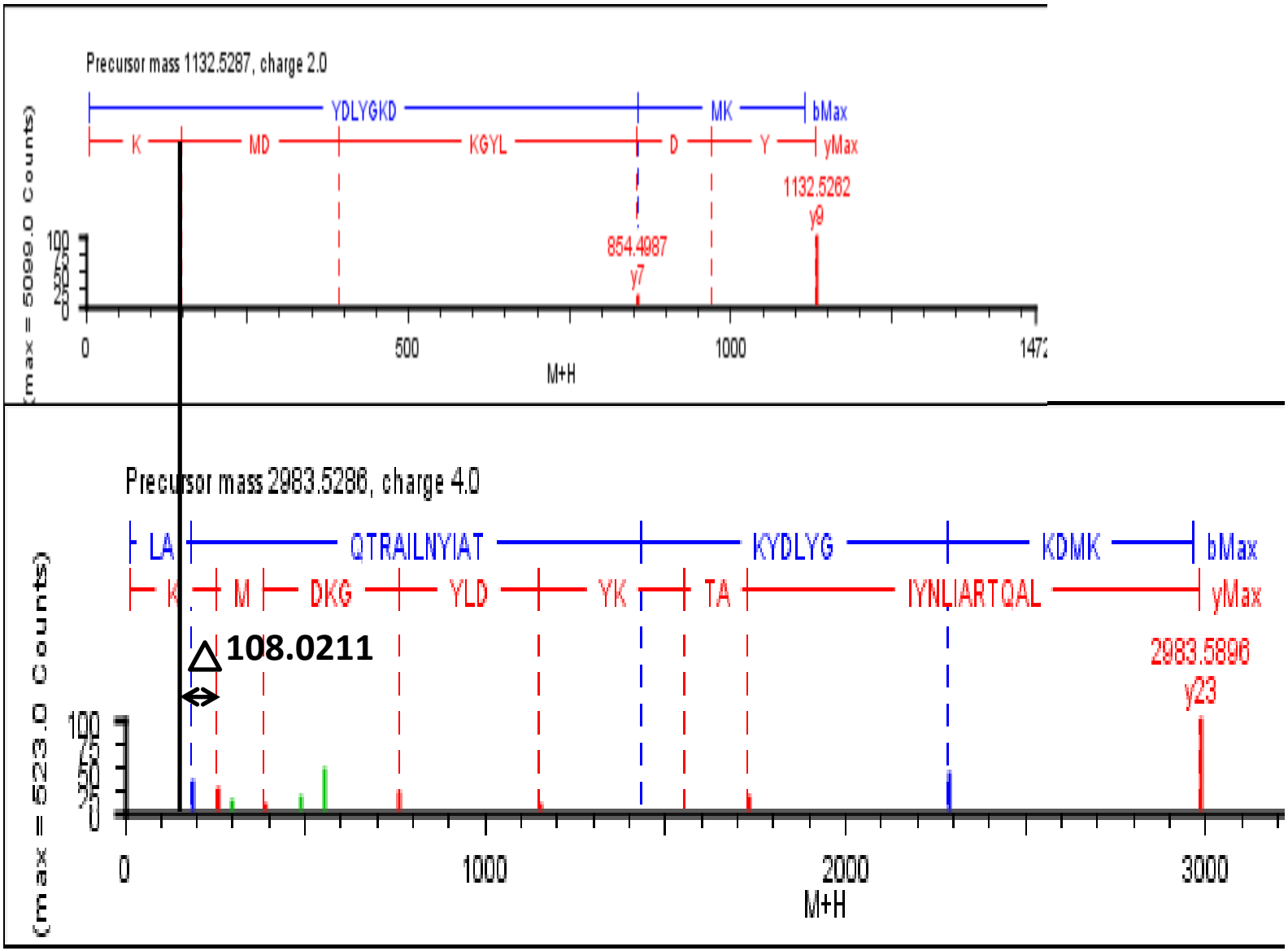


831.4905

1033.51: (831.49+ 144.03)

118-125

(K)EAK(CML)TALAK(ImiA)(D)

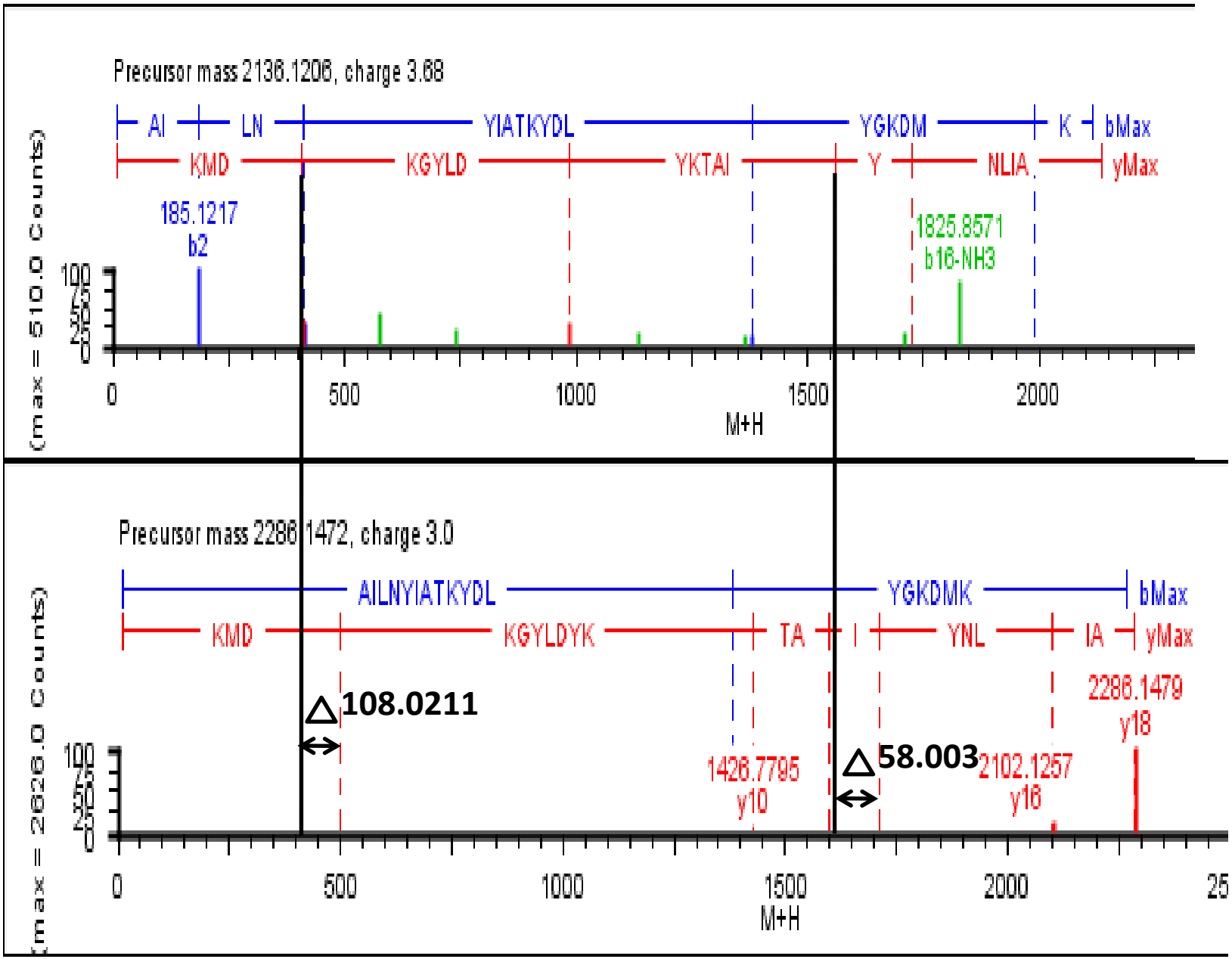


147.11

255.1422: (147.11+ 108.02)

79-87

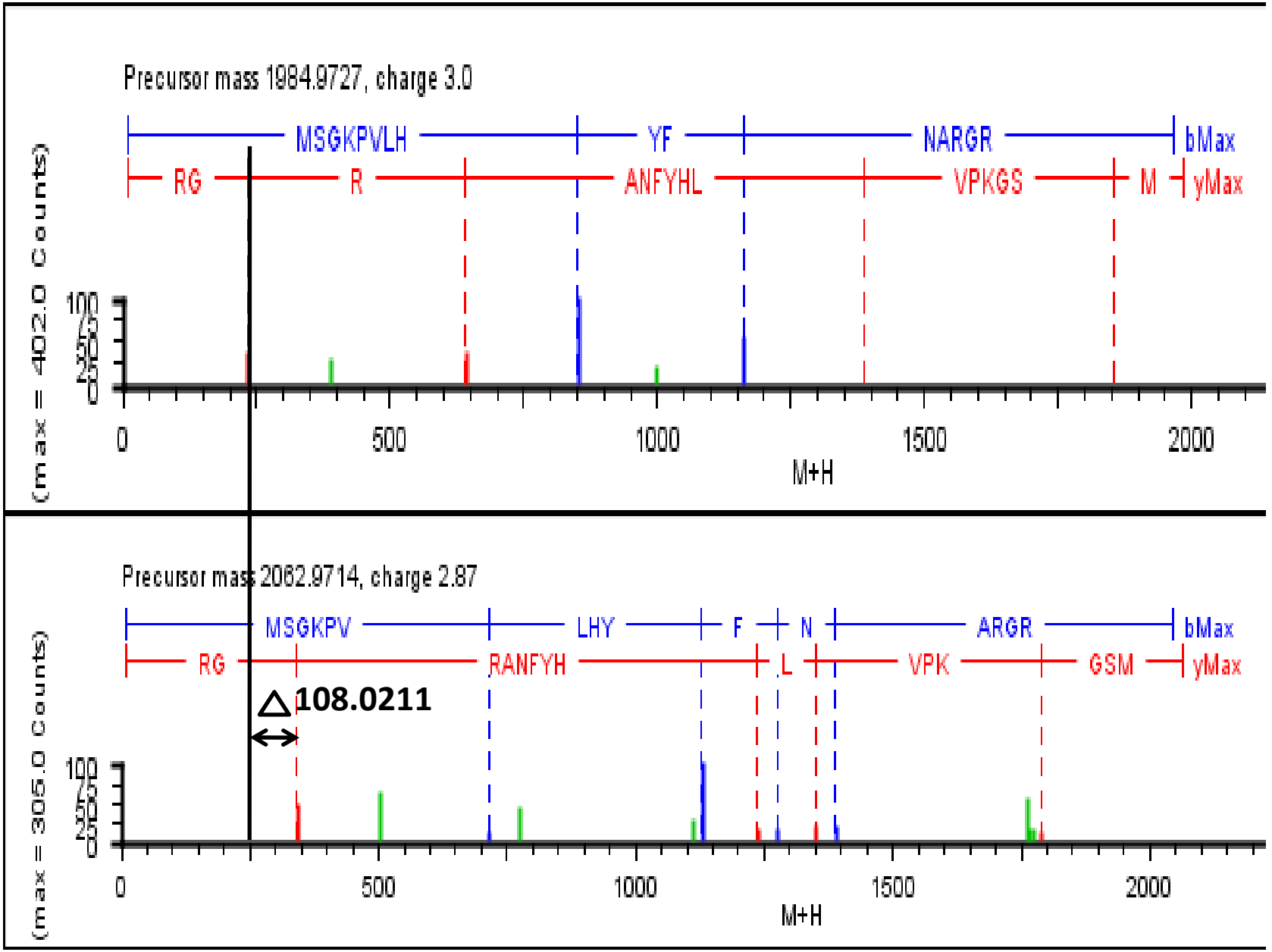
(K)YDLYGKDMK(Pyr)(E)



1561.6608

1711.8083: (1561.66+ 108.02)

70-87 (R)AILNYIATKYDLYGK(CML)DMK(Pyr)(E)

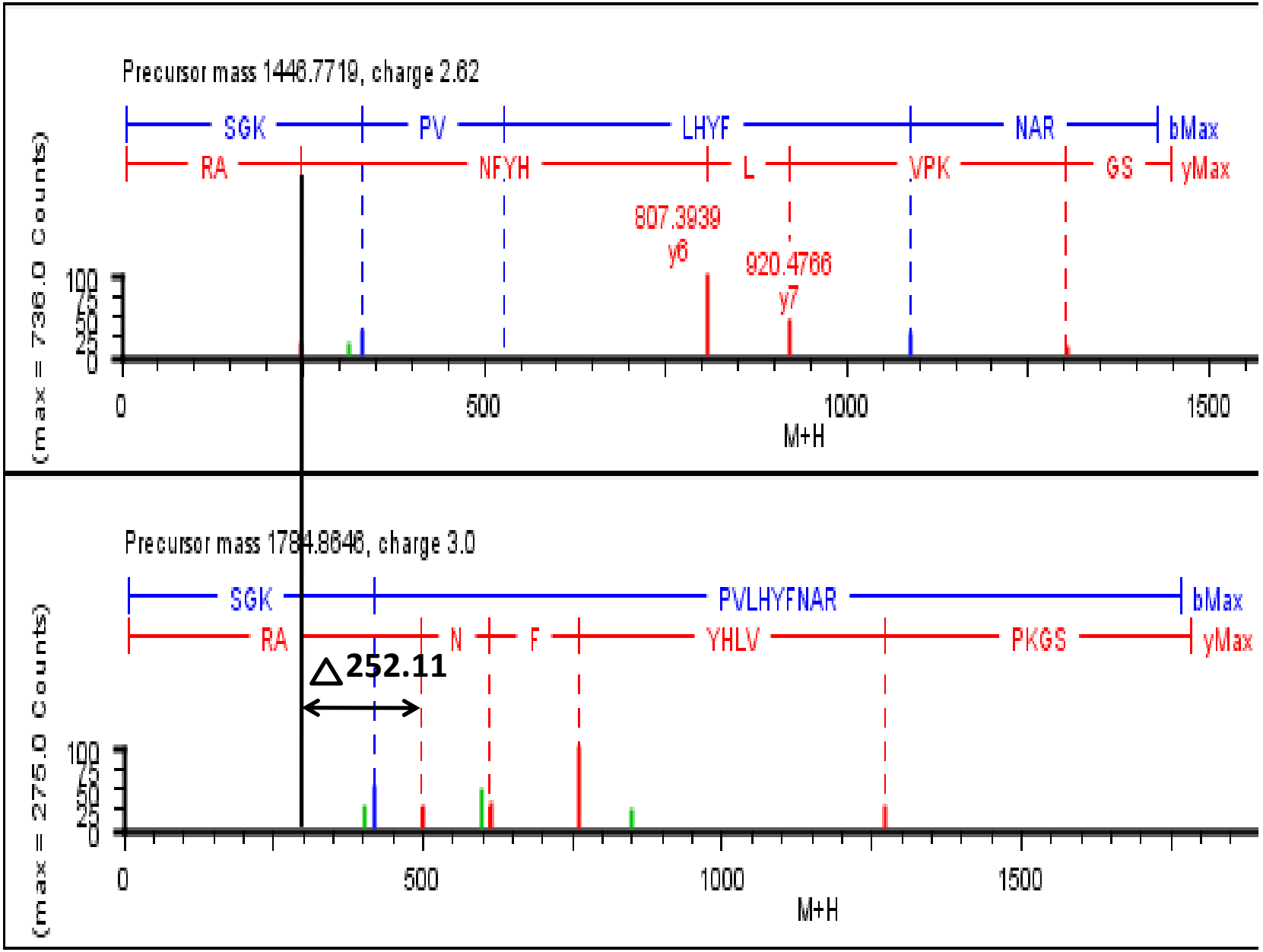


232.1293

340.1729: (232.12+ 108.02)

1-15

(-)MSGKPVLHYFNARGR(Pyr)(M)

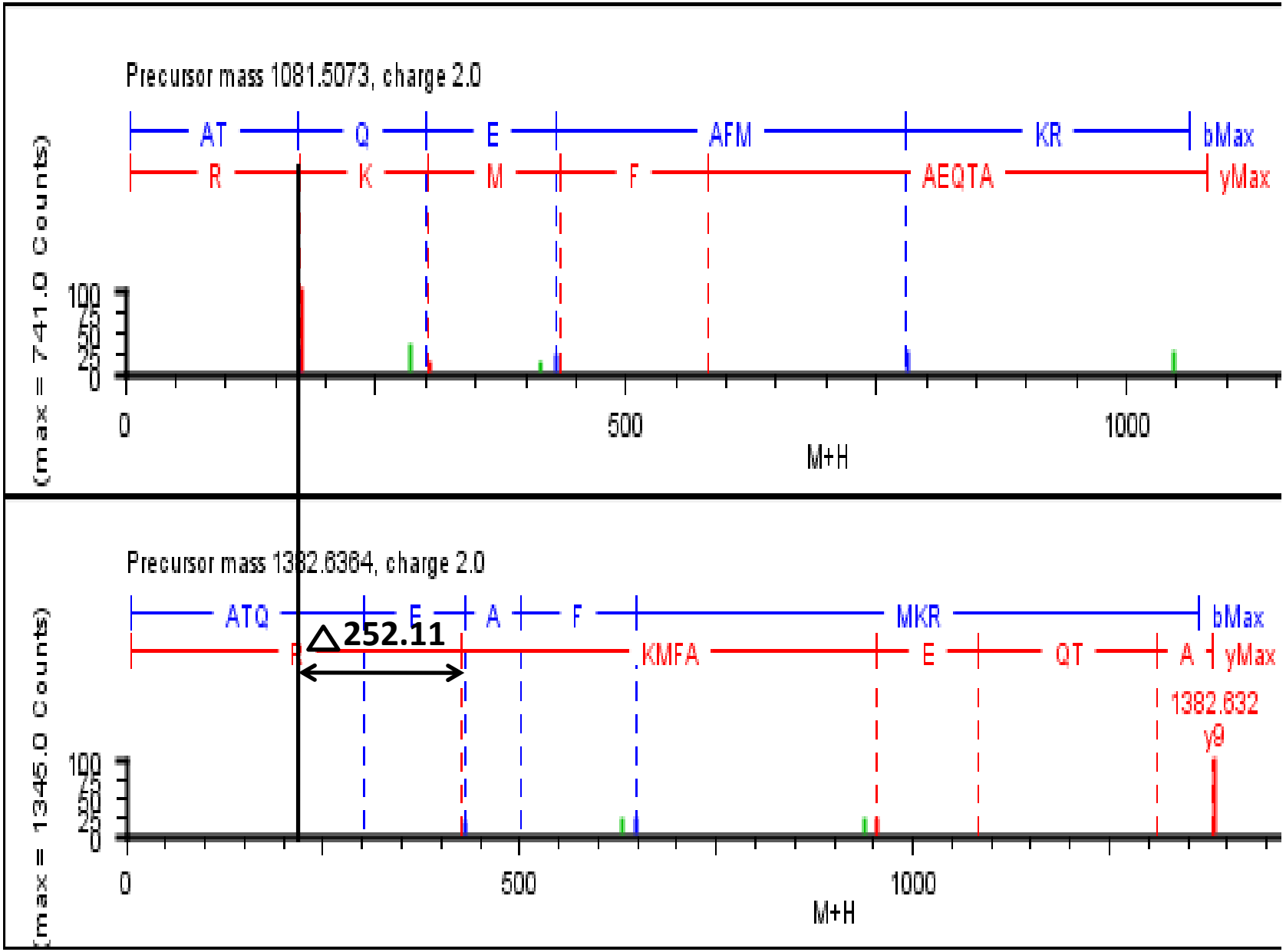


246.1561

498.2607: (246.15+ 252.1)

2-13 (M)SGKPVLHYFNAR(Crossline)(G)

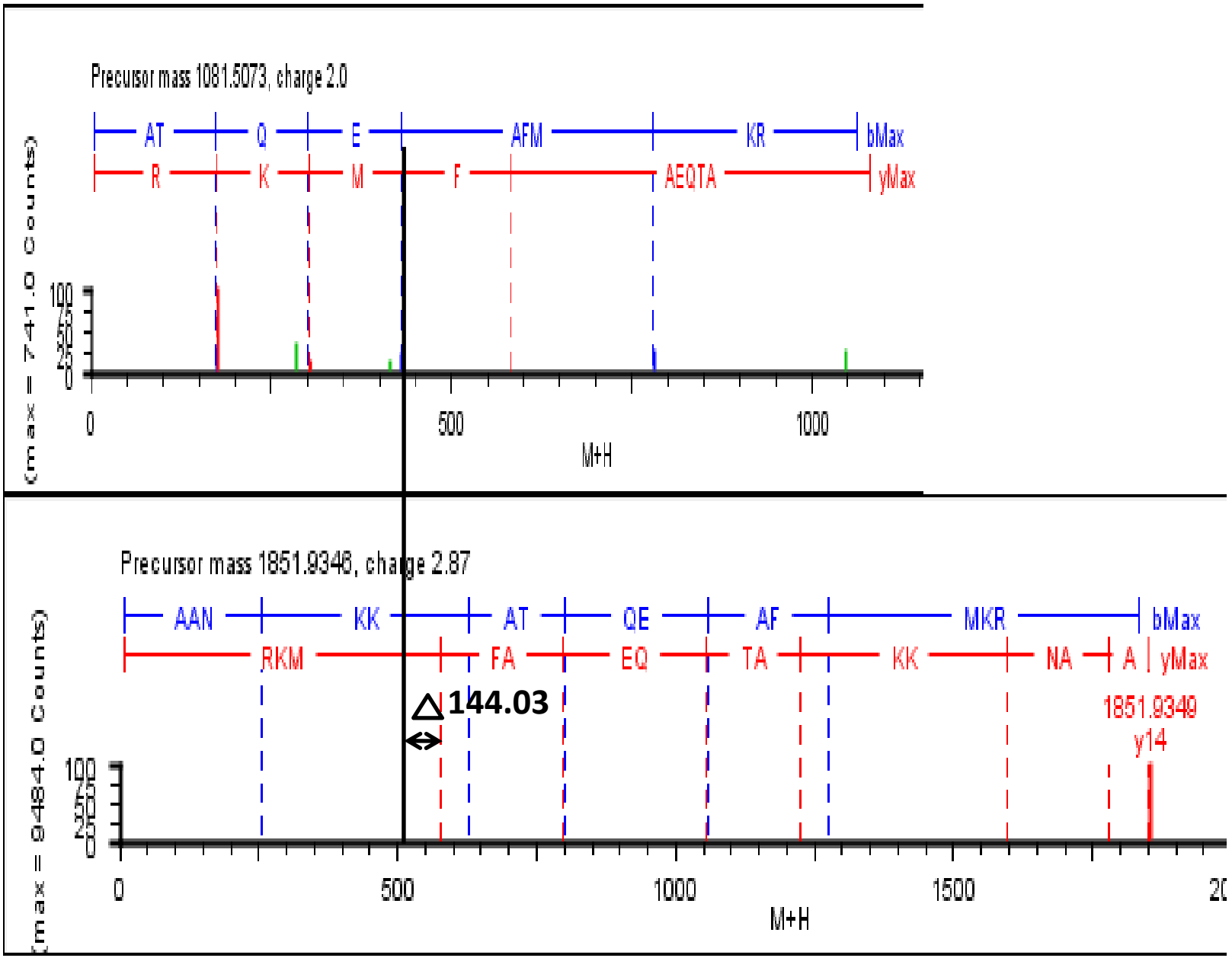
FBPA



175.1177

427.2141: (175.11+ 252.1)

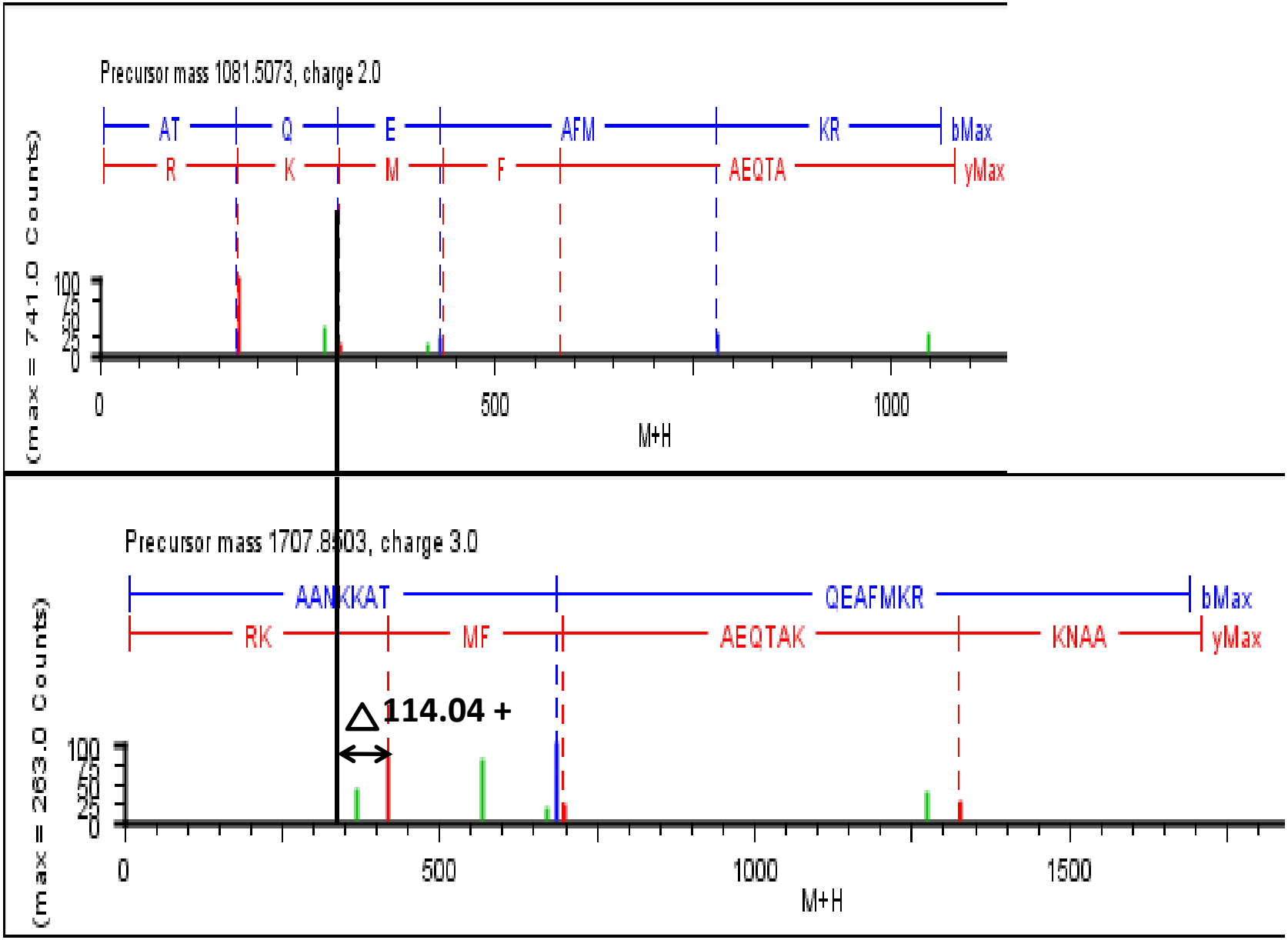
323-331 (K)ATQEAFMKR(Crossline)(A)



434.2673

578.2823: (434.26+ 144.03)

318-331 (K)AANKKATQEAFMK(ImiA)R(A)

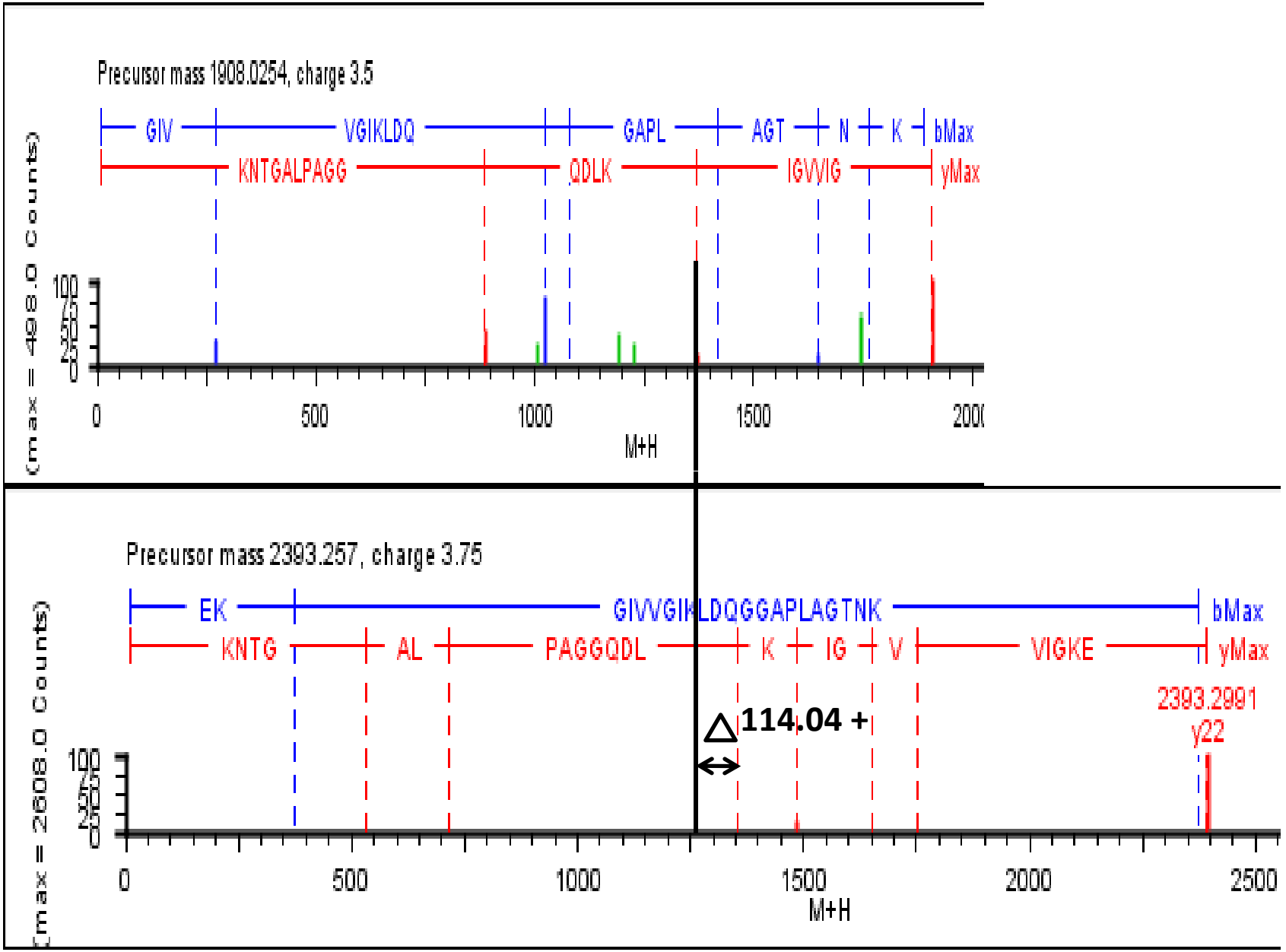


303.2136

417.2569: (303.21+ 114.04)

318-331

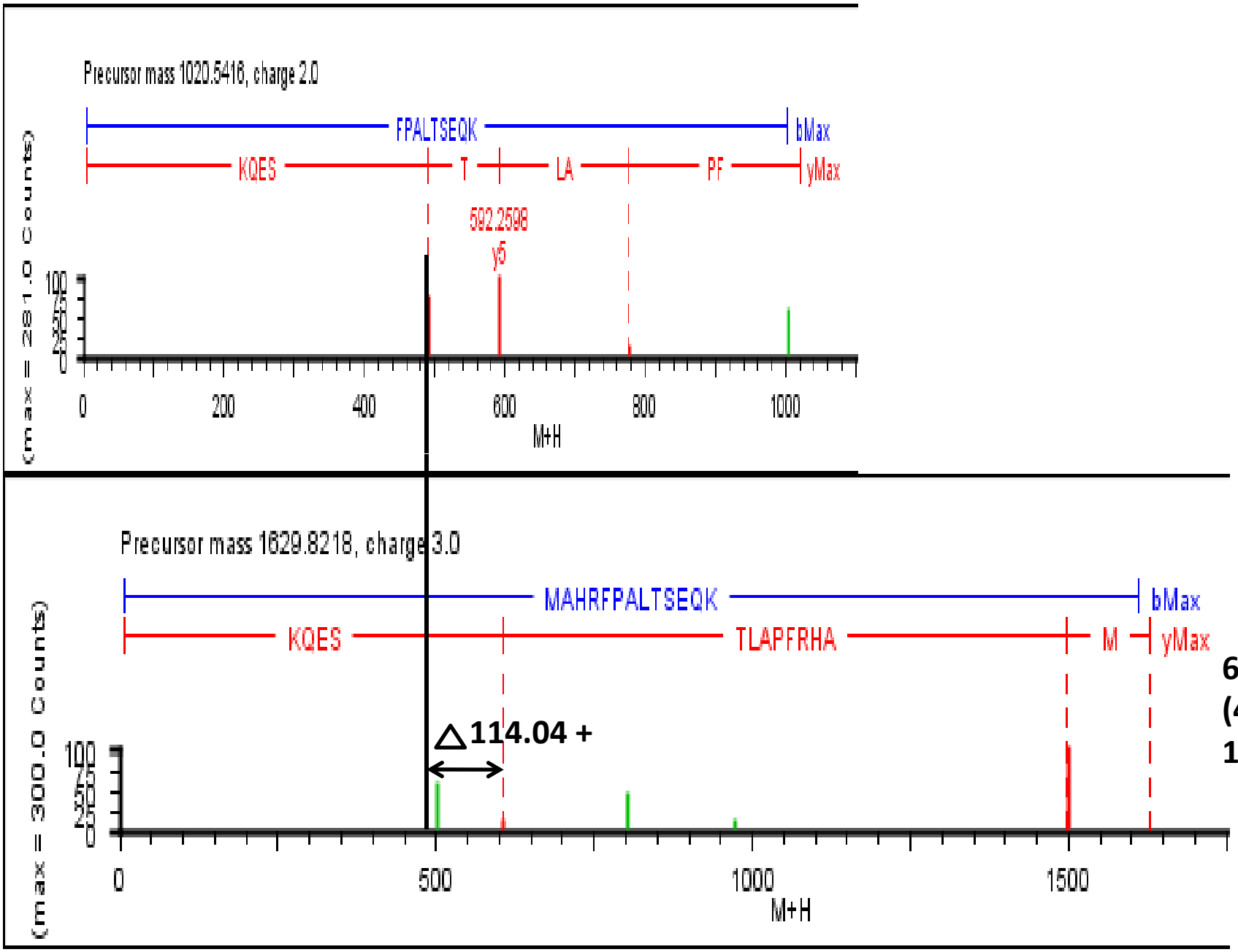
(K)AANKKATQEAFMK(Ubi)R(A)



1369.3607

1483.7935: (1369.36+ 114.04)

100-121 (K)EKGIVVGIKLDQGGAPLAGTNK(Ubi)(E)

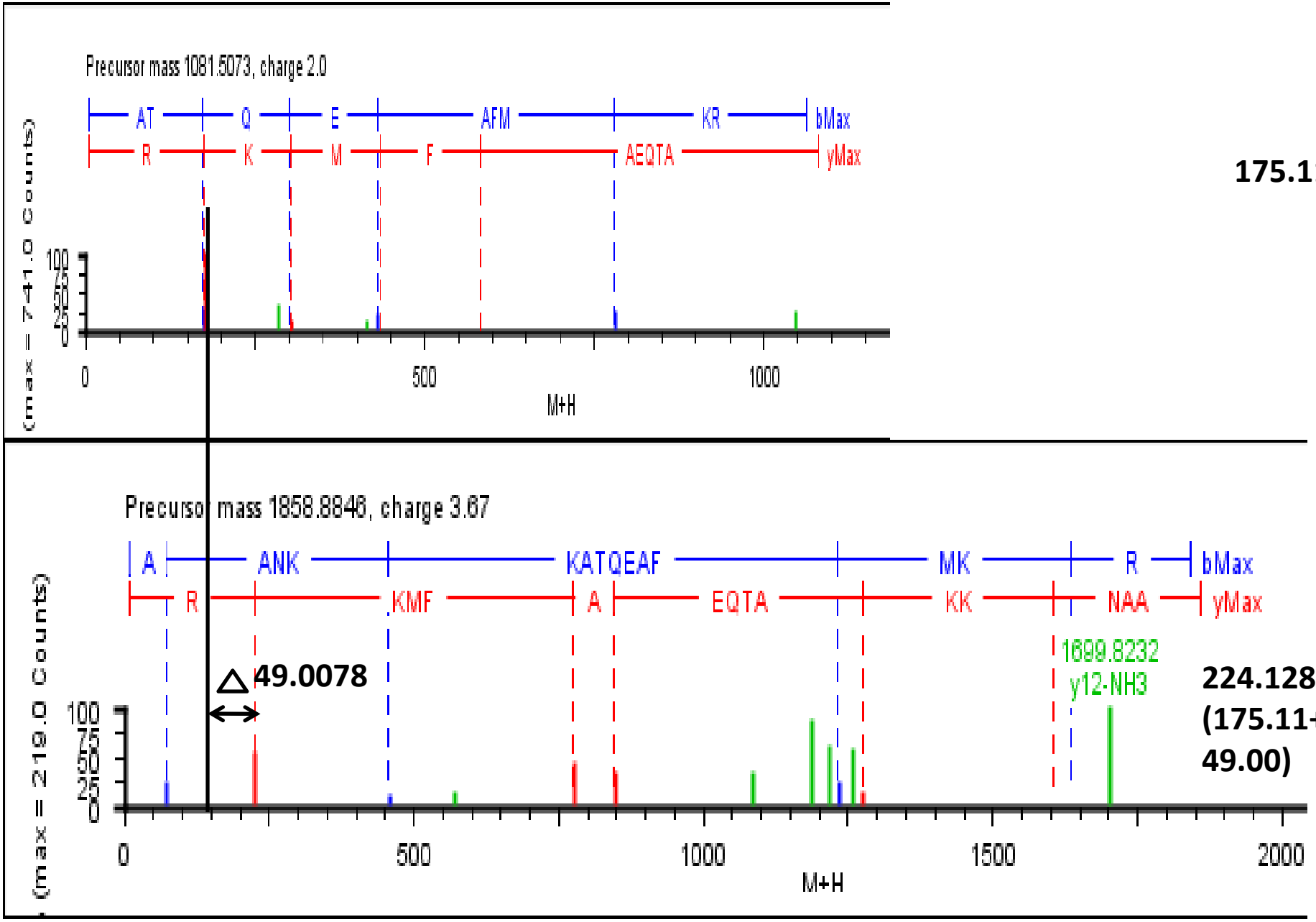


491.2249

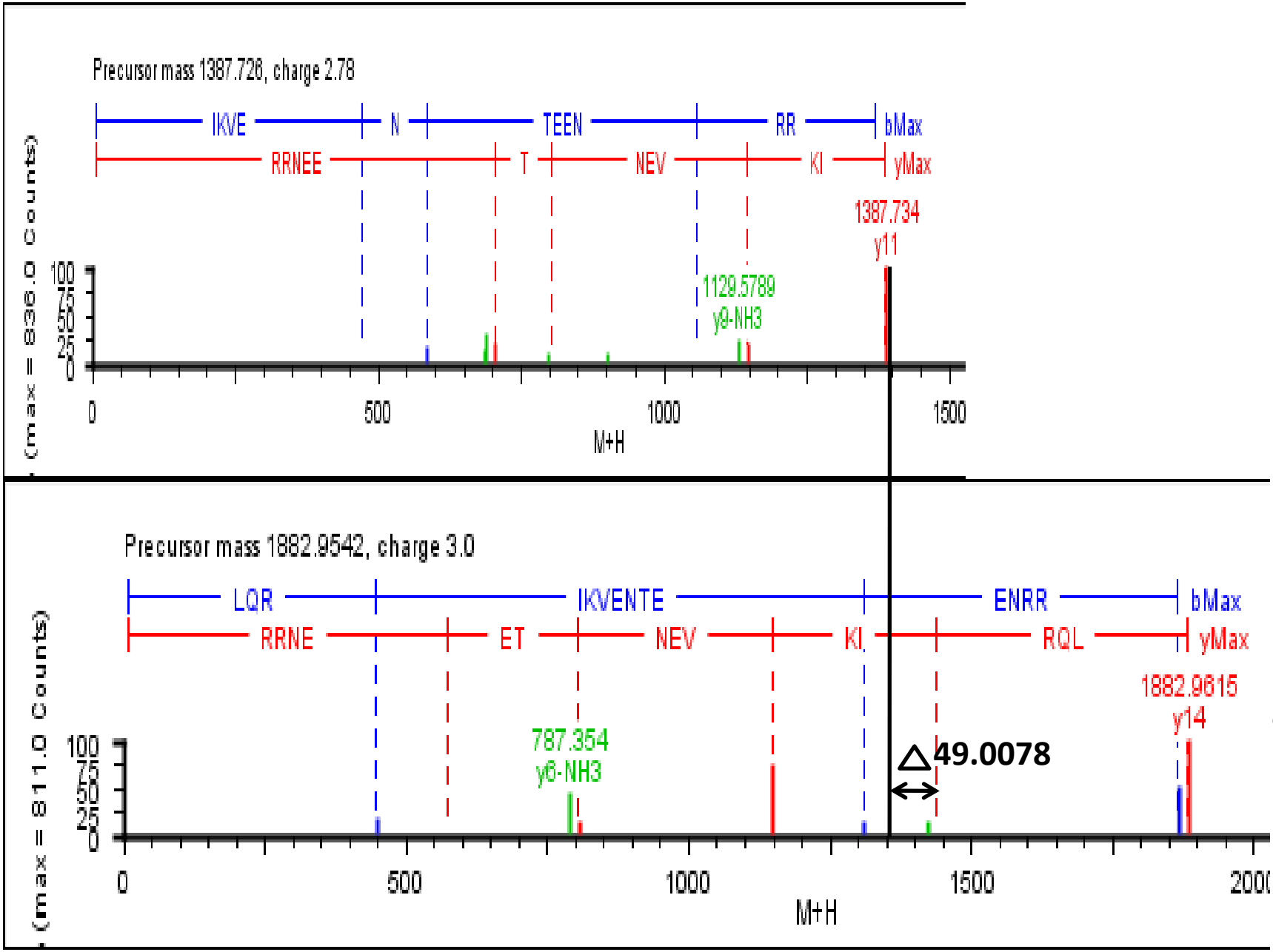
605.2387: (491.22+ 114.04)

1- 13

(-)MAHRFPALTSEQK(Ubi)(K)



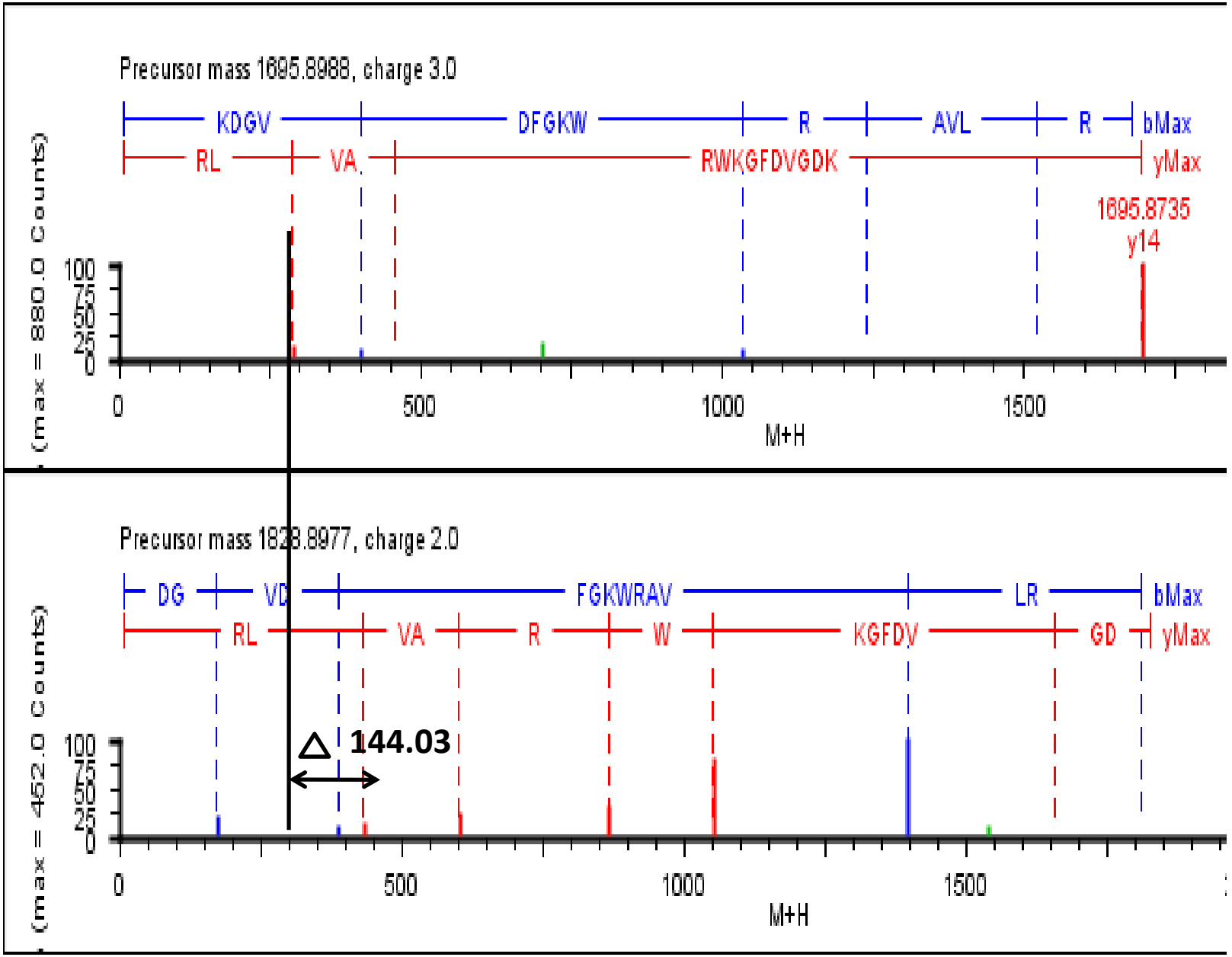
318-331 (K)AANKKATQEAFMKR(MOLD)(A)



1387.734

1436.6107 (1387.734-49.00)

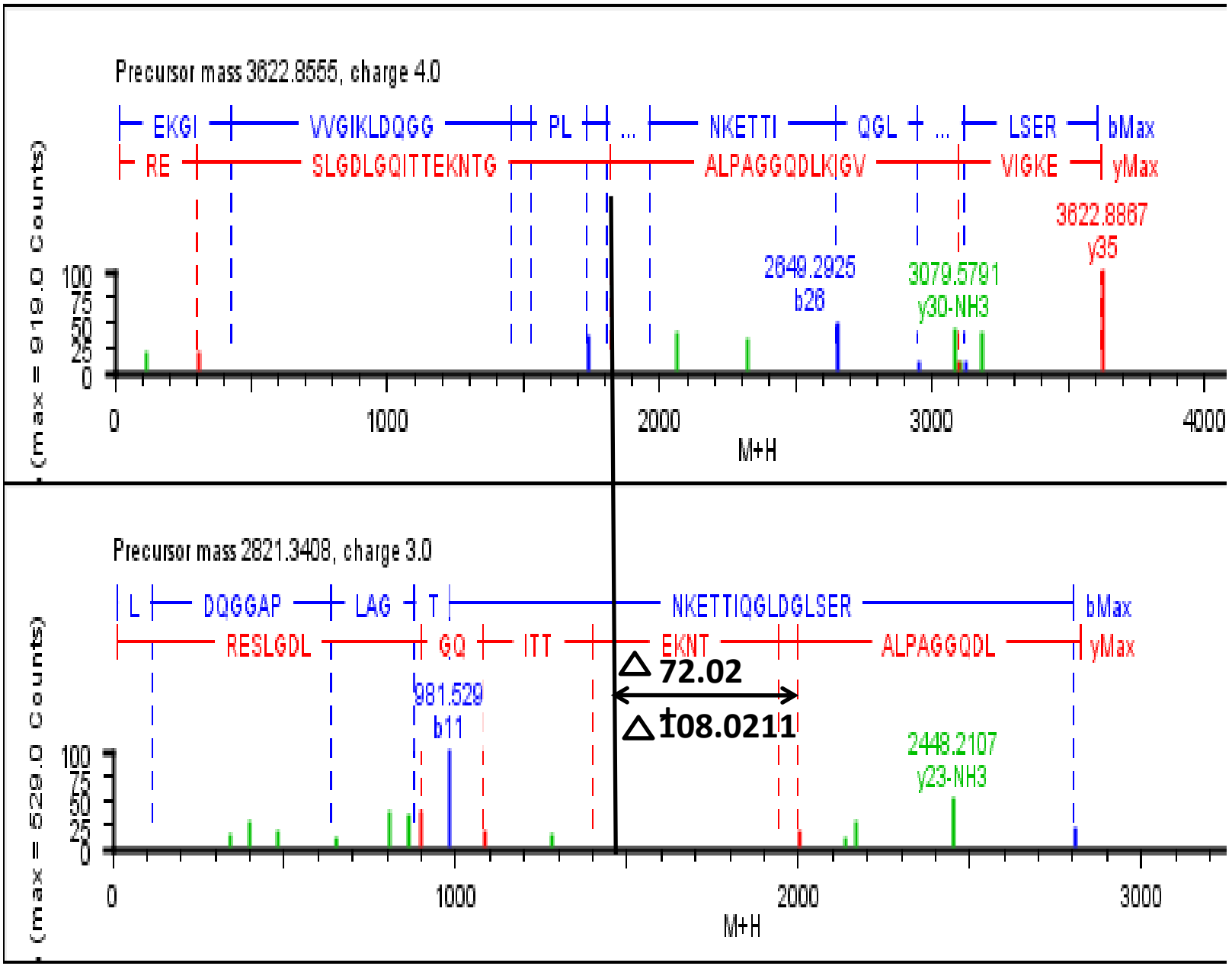
44-57 (R)LQRIK(MOLD)VENTEENRR(Q)



288.2013

432.2314: (288.20+ 144.03)

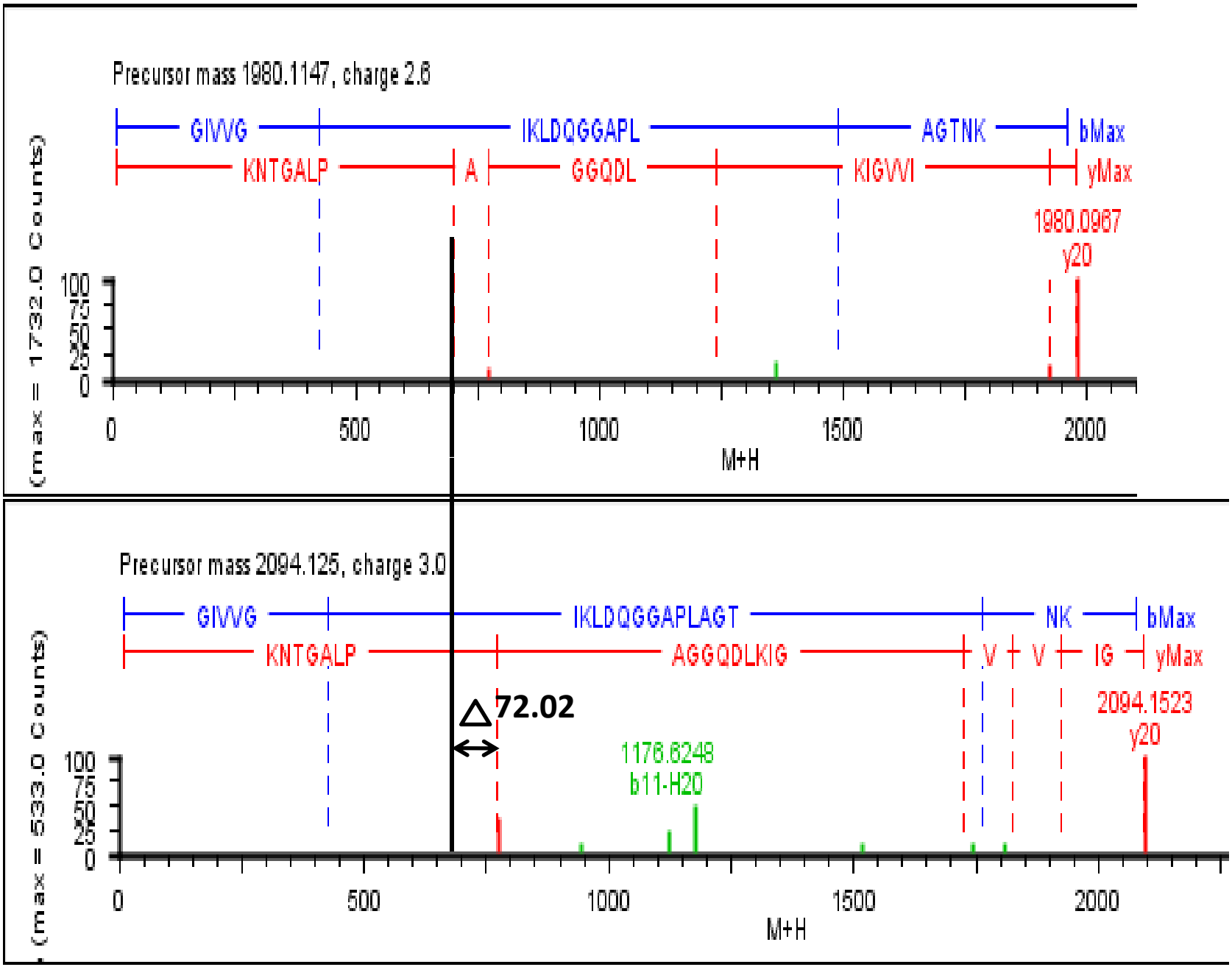
141-153 (K)DGVDFGKWRAVLR(ImiA)(I)



1818.9491

1999.0198: (1818.94+ 72.02+ 108.02

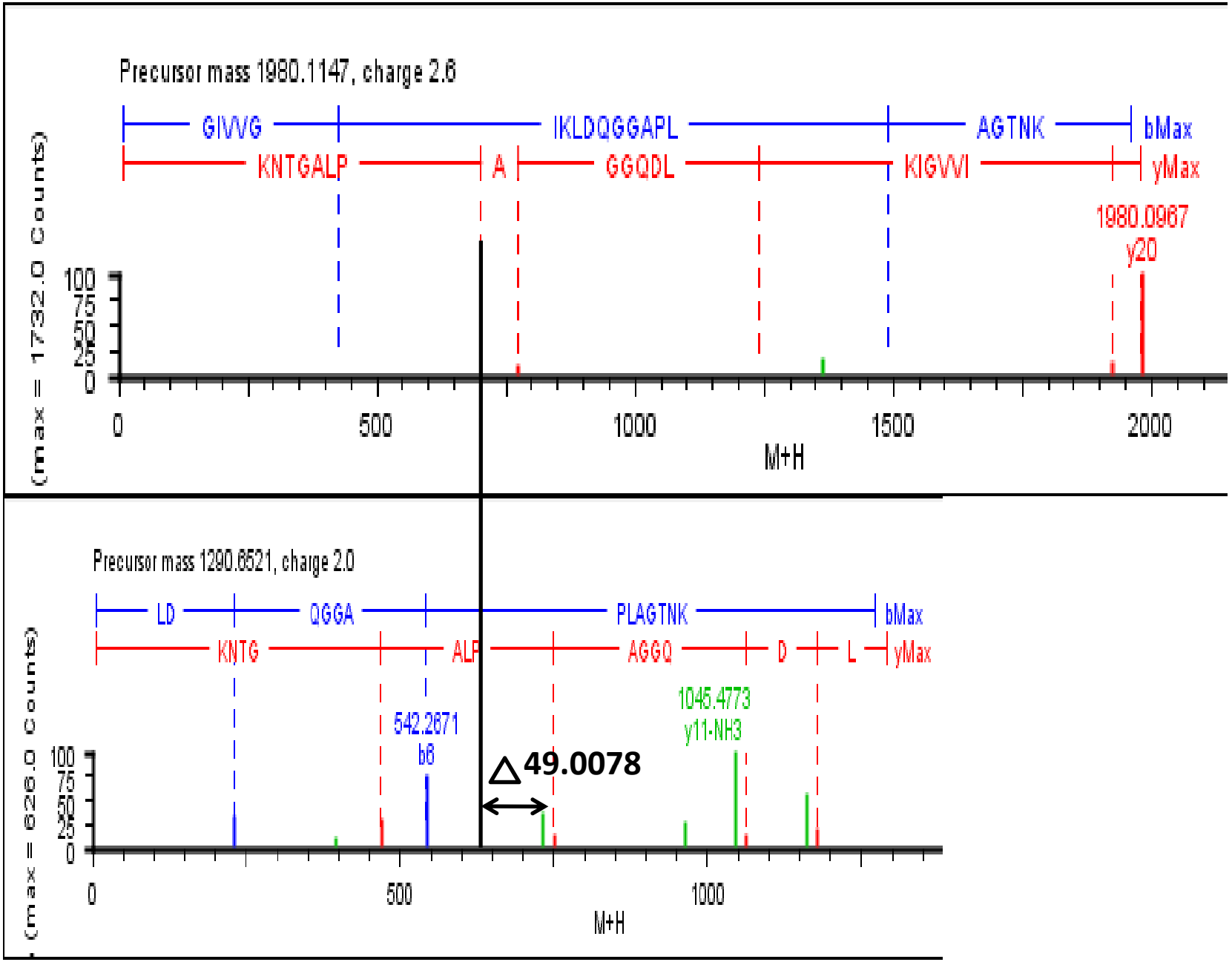
109-134 (K)LDQGGAPLAGTNK(CEL)ETTIQGLDGLSER(Pyr)(C)



700.3675

772.462: (700.36+ 72.02)

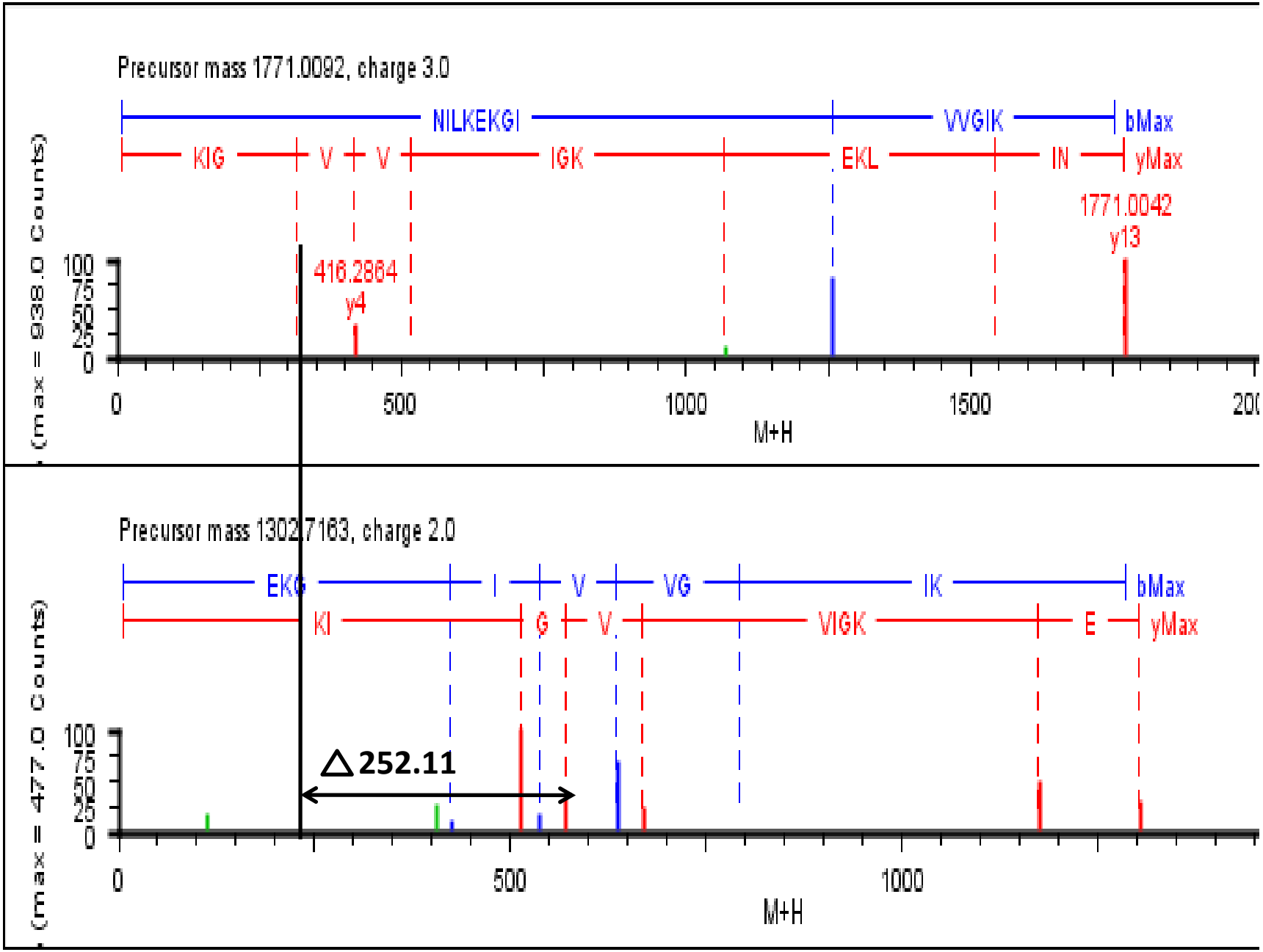
102-121 (K)GIVVGIKLDQGGAPLAGTNK(CEL)(E)



700.3675

749.4335: (700.36+ 49.00)

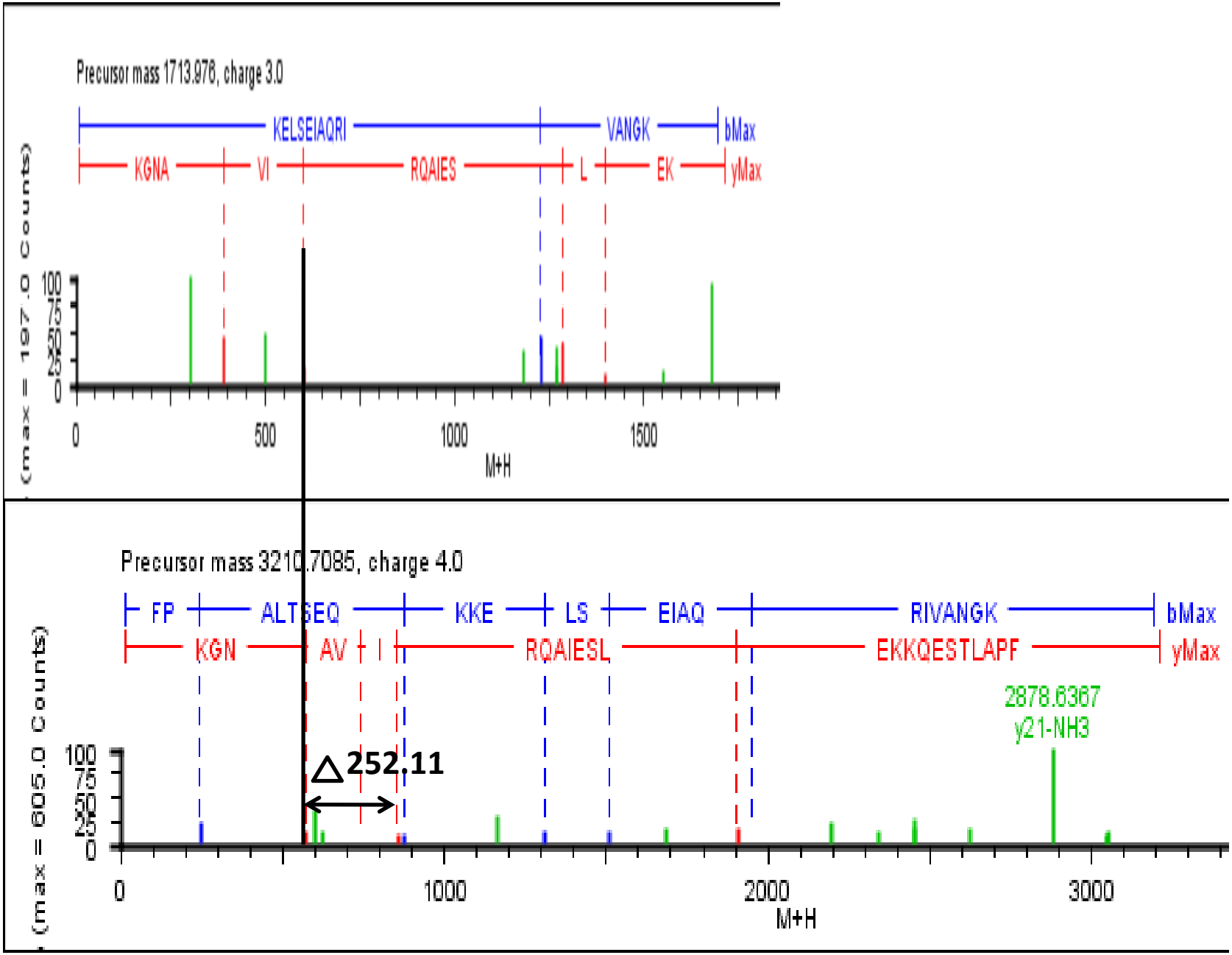
109-121 (K)LDQGGAPLAGTNK(MOLD)(E)



317.202

569.2986:
(317.201+
252.11)

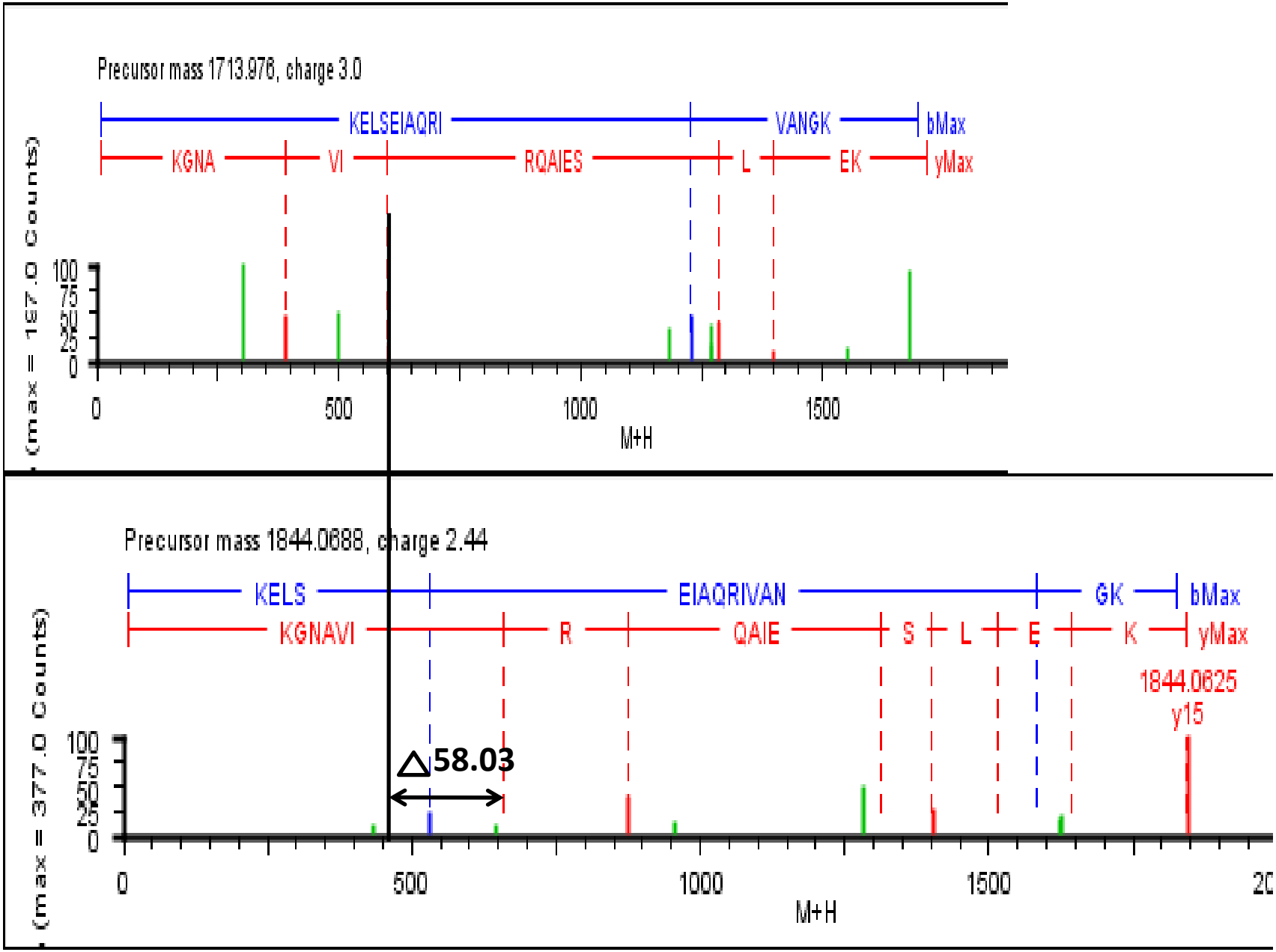
100-108 (K)EKGIVVGIK(Crossline)(L)



601.3851

853.466: (601.38+ 252.1)

5-28 (R)FPALTSEQKKELSEIAQRIVANGK(Crossline)(G)

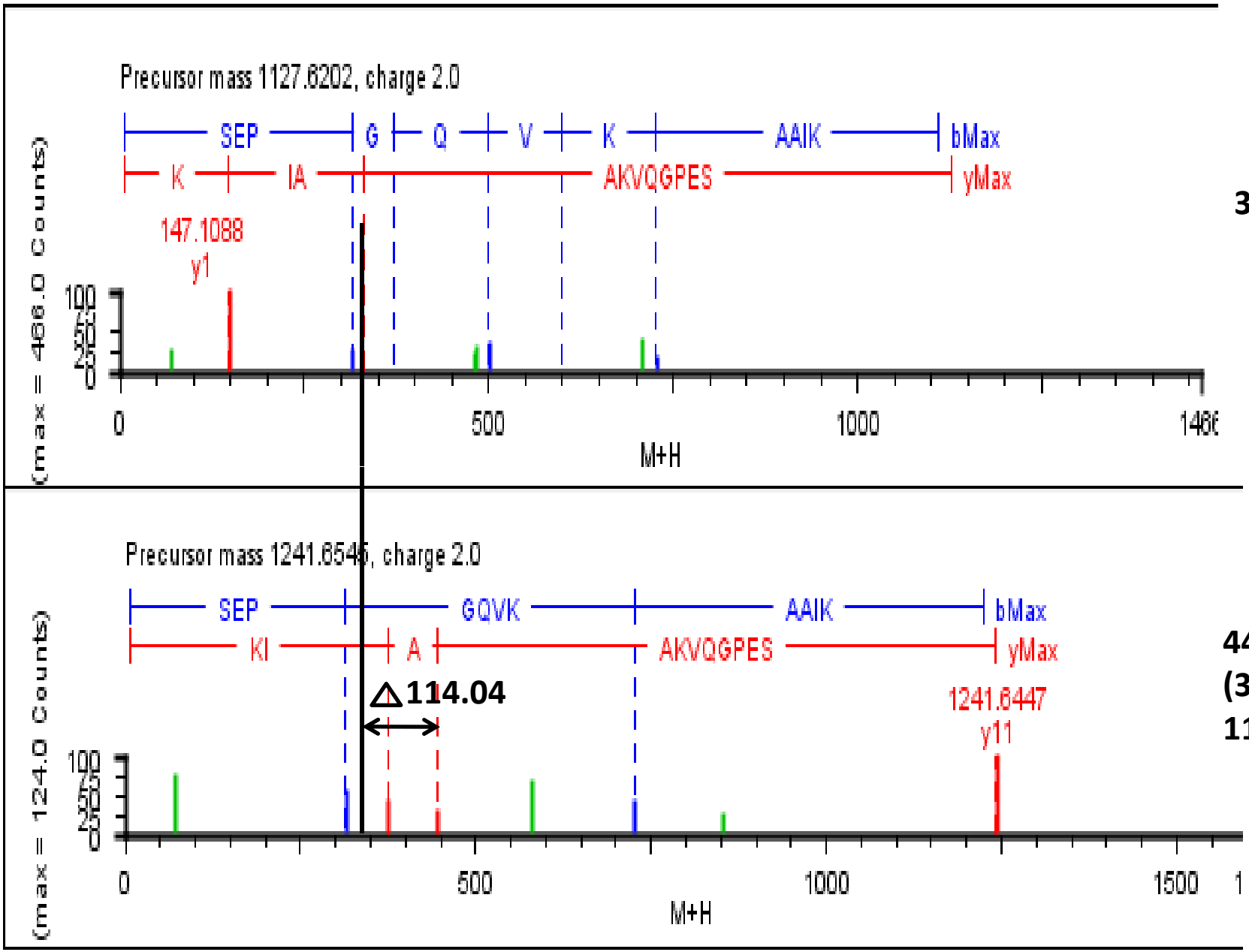


601.3851

659.4387: (601.38+ 58.03)

14-28 (K)KELSEIAQRIVANGK(Pento)(G)

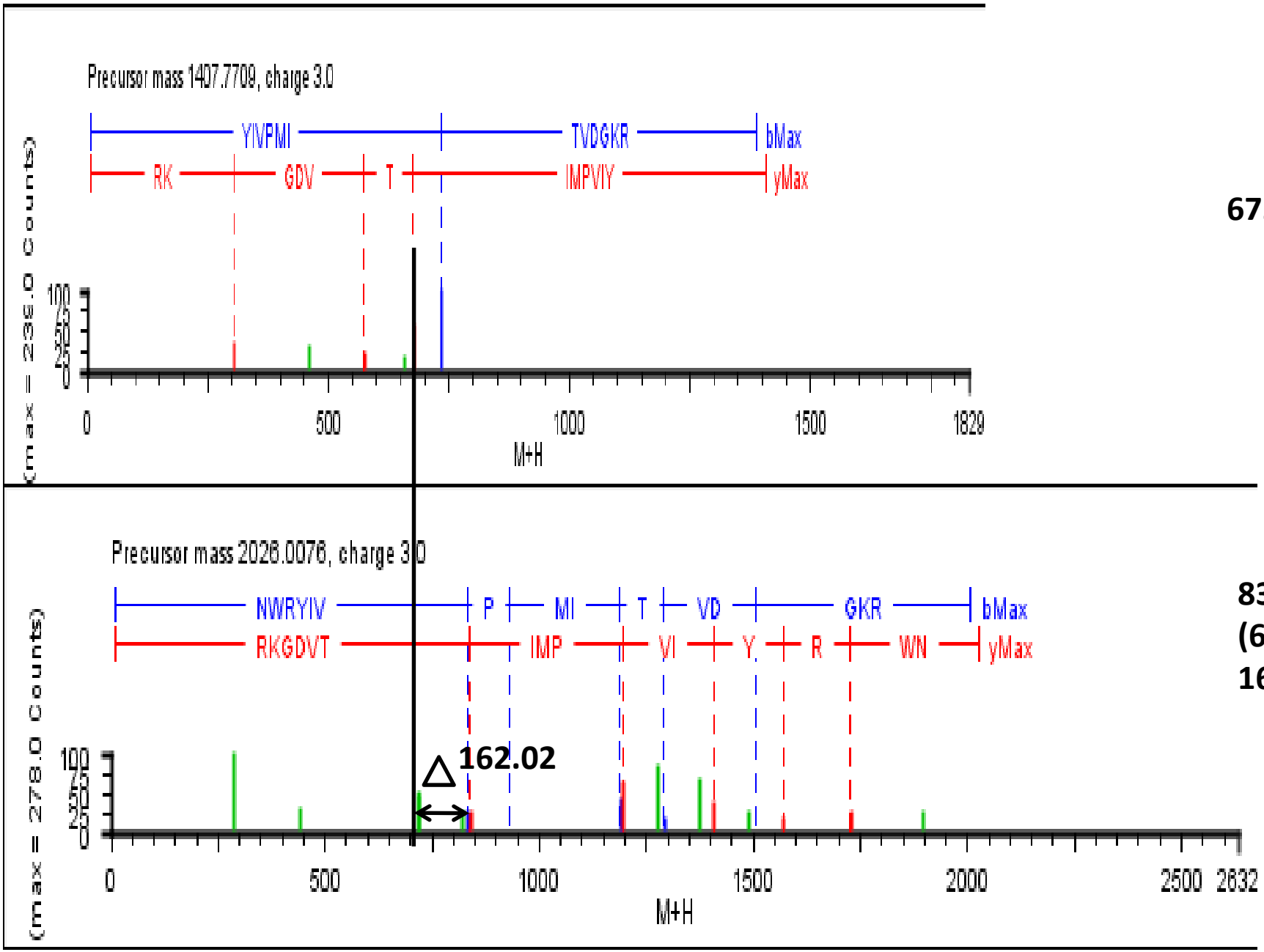
ADH



331.2106

445.2547: (331.21+ 114.04)

24-34 (K)SEPGQVKAAIK(Ubi)(Y)

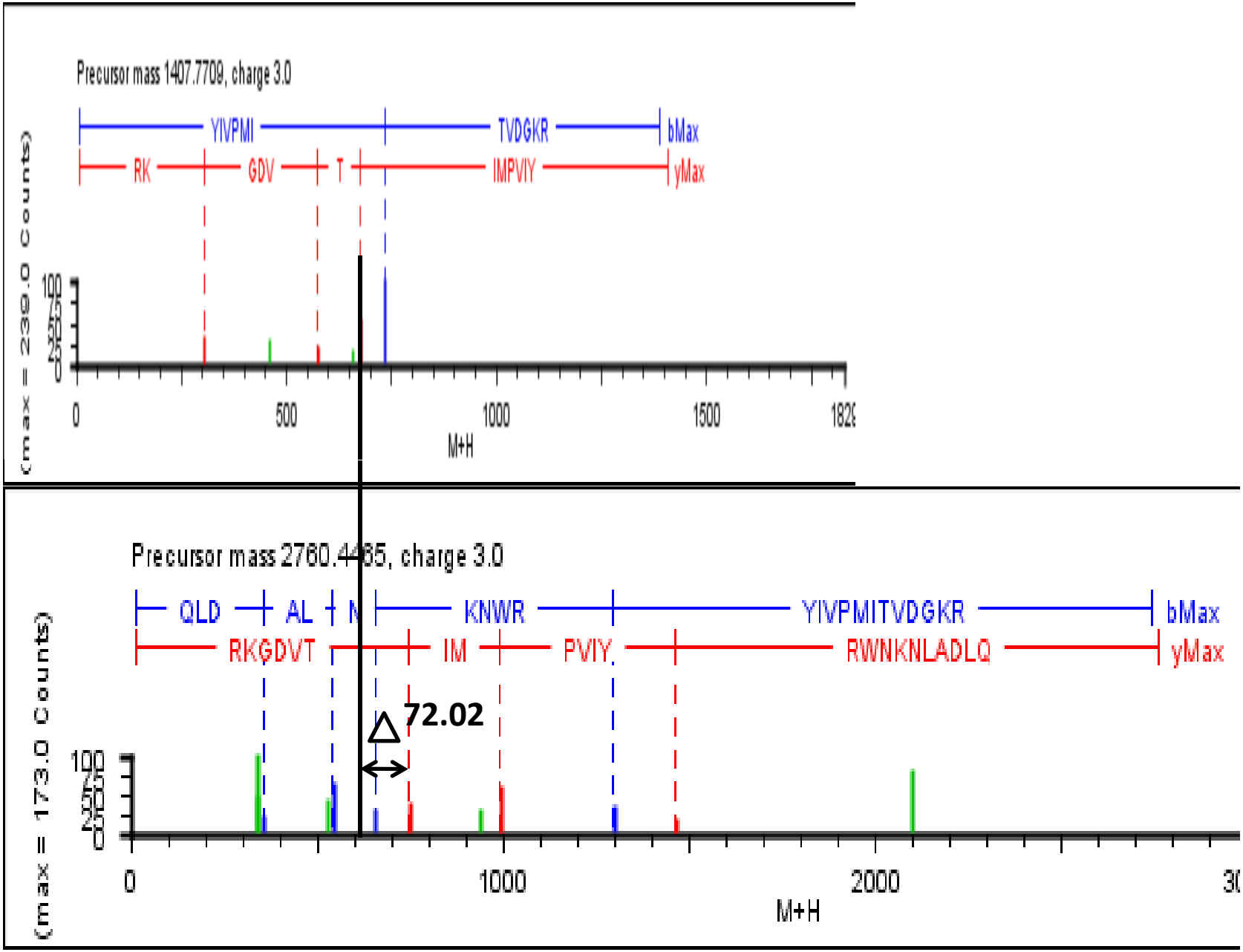


675.3715

837.4258: (675.37+ 162.02)

295-309

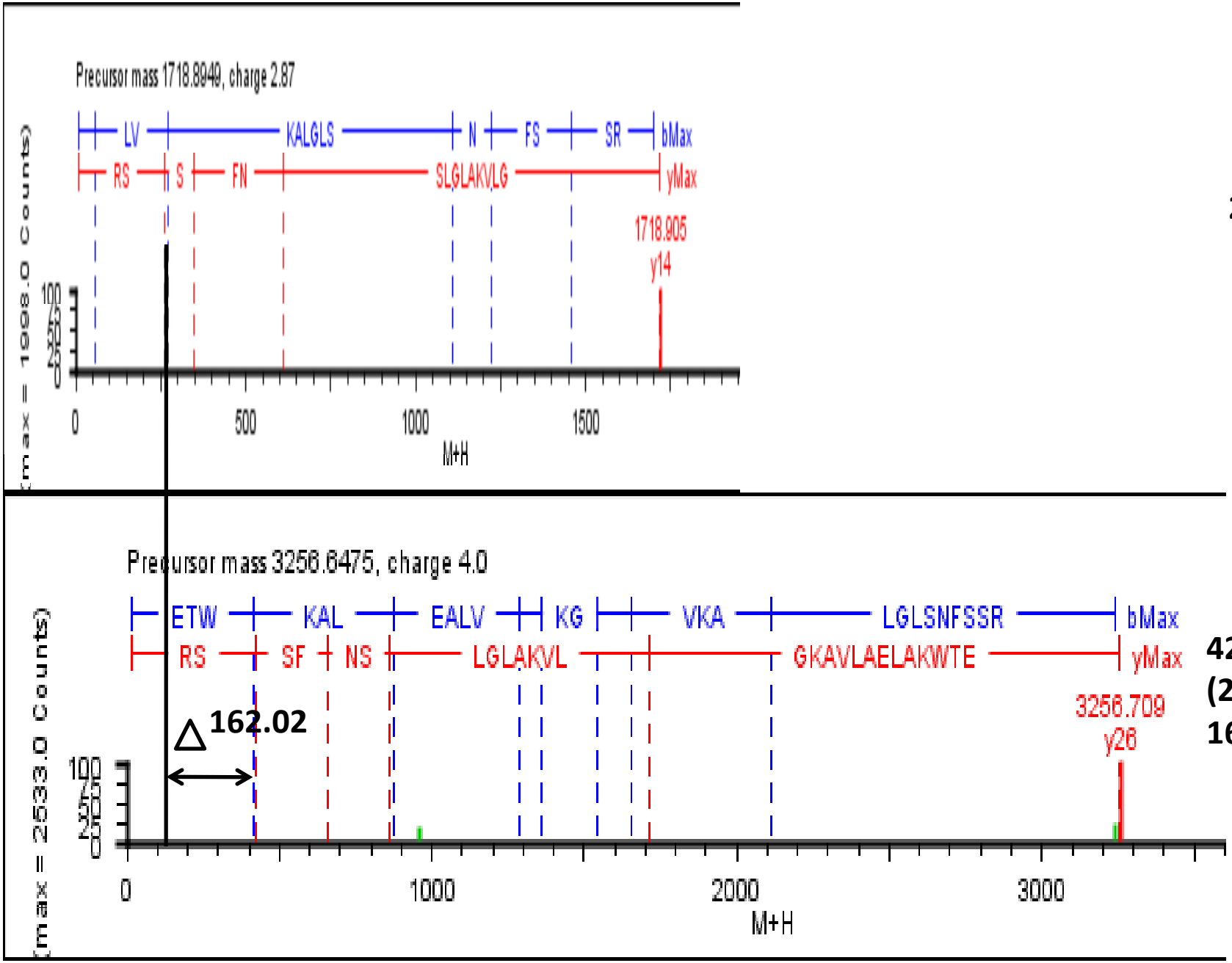
(K)NWRYIVPMITVDGKR(Gly)(V)



675.3715

74.4246: (675.37+ 72.02)

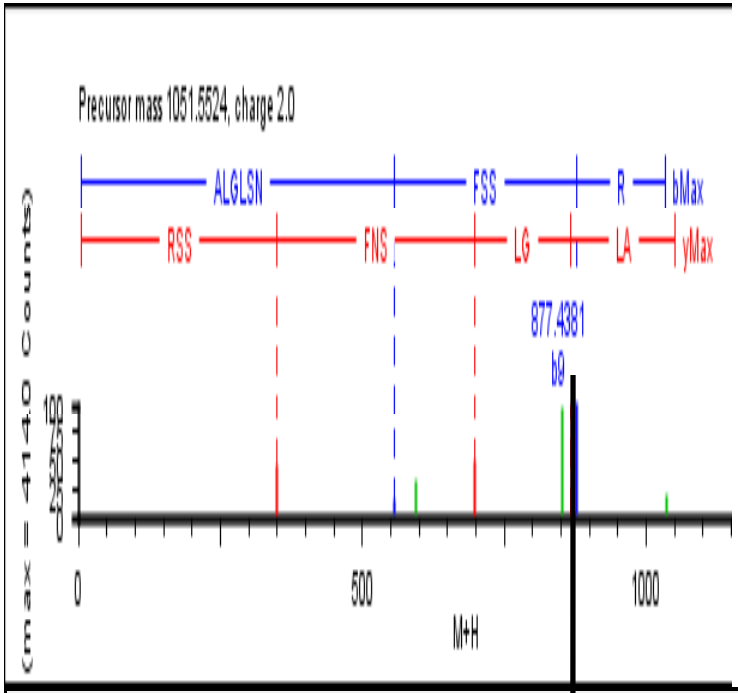
288-309 (K)QLDALNKNWRYIVPMITVDGK(Cel)R(V)



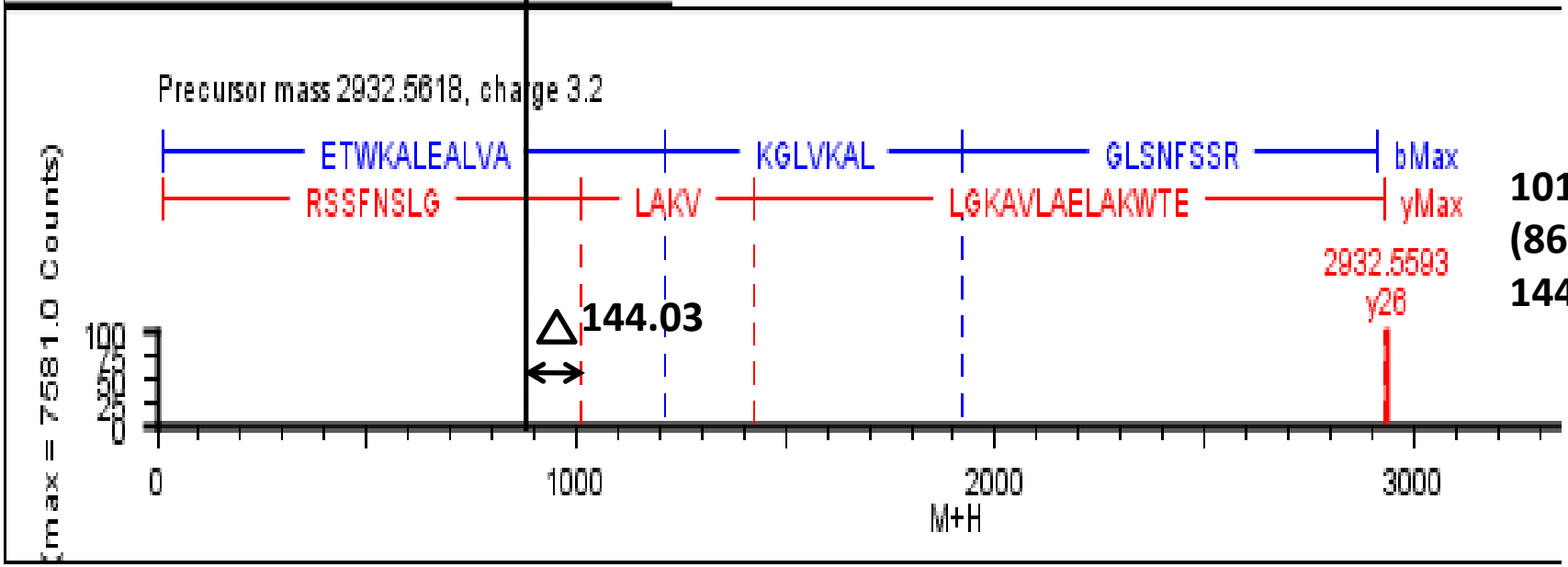
262.158

424.1726: (262.15+ 162.02)

142-167 (K)ETWKALEALVAKGLVKALGLSNFSSR(Gly)(Q)



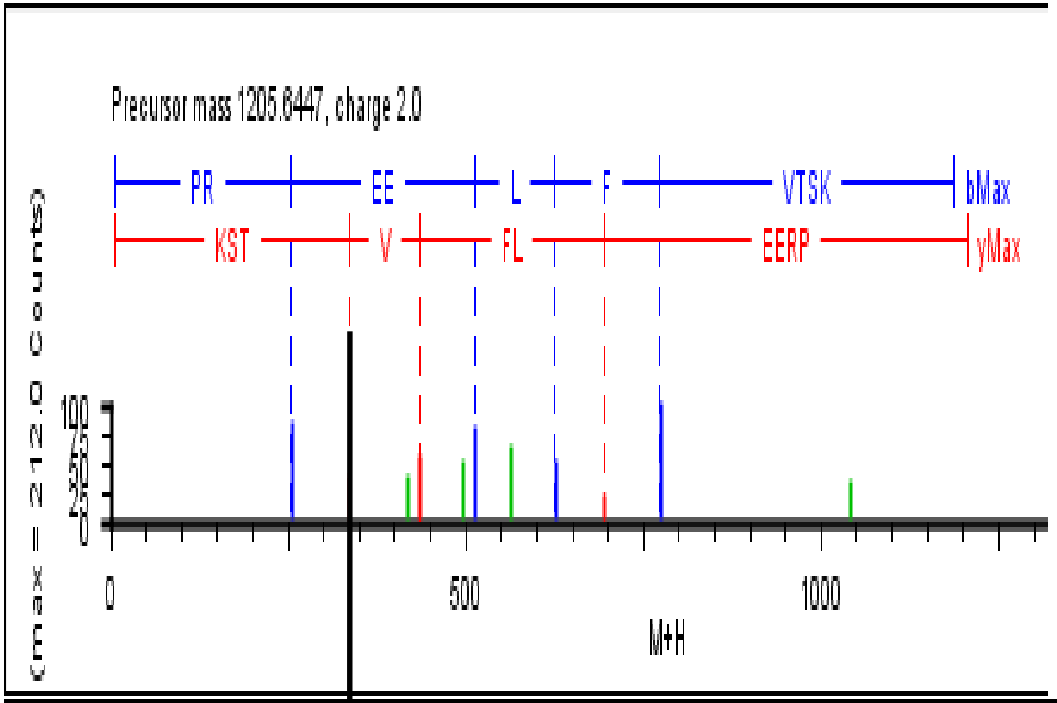
867.4374



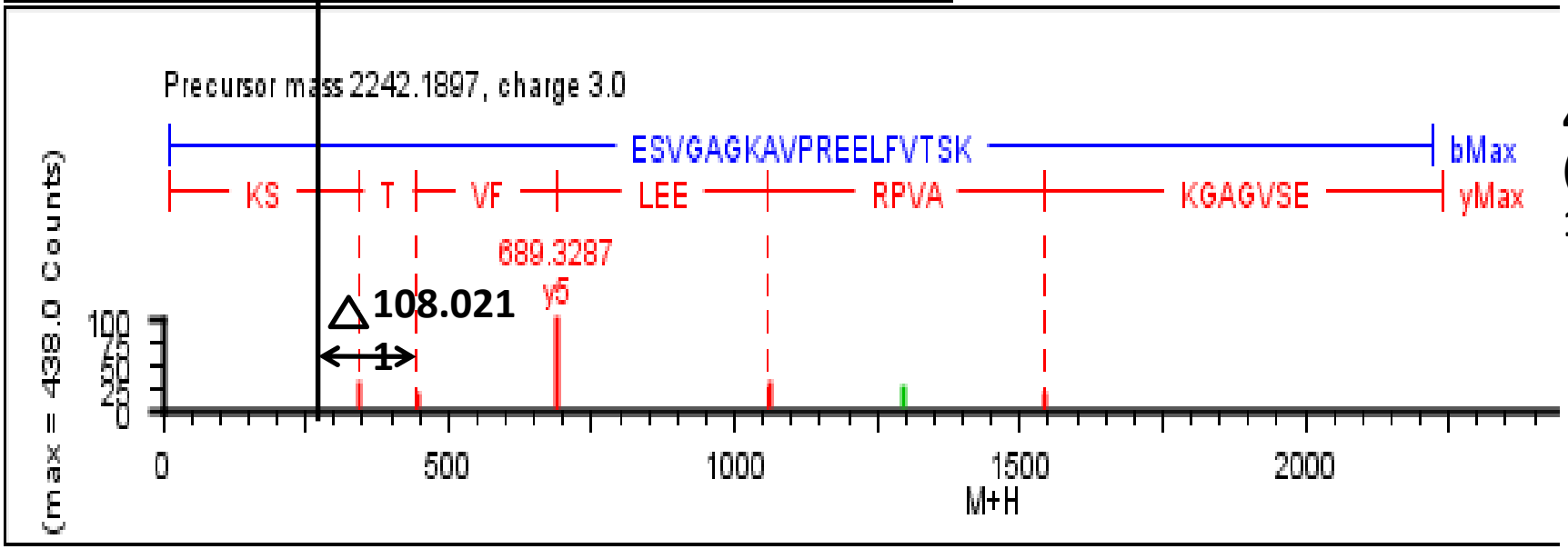
1011.5593: (867.43+ 144.03)

142-167

(K)ETWKALEALVAKGLVKALGLSNFSSR(ImiA)(Q)

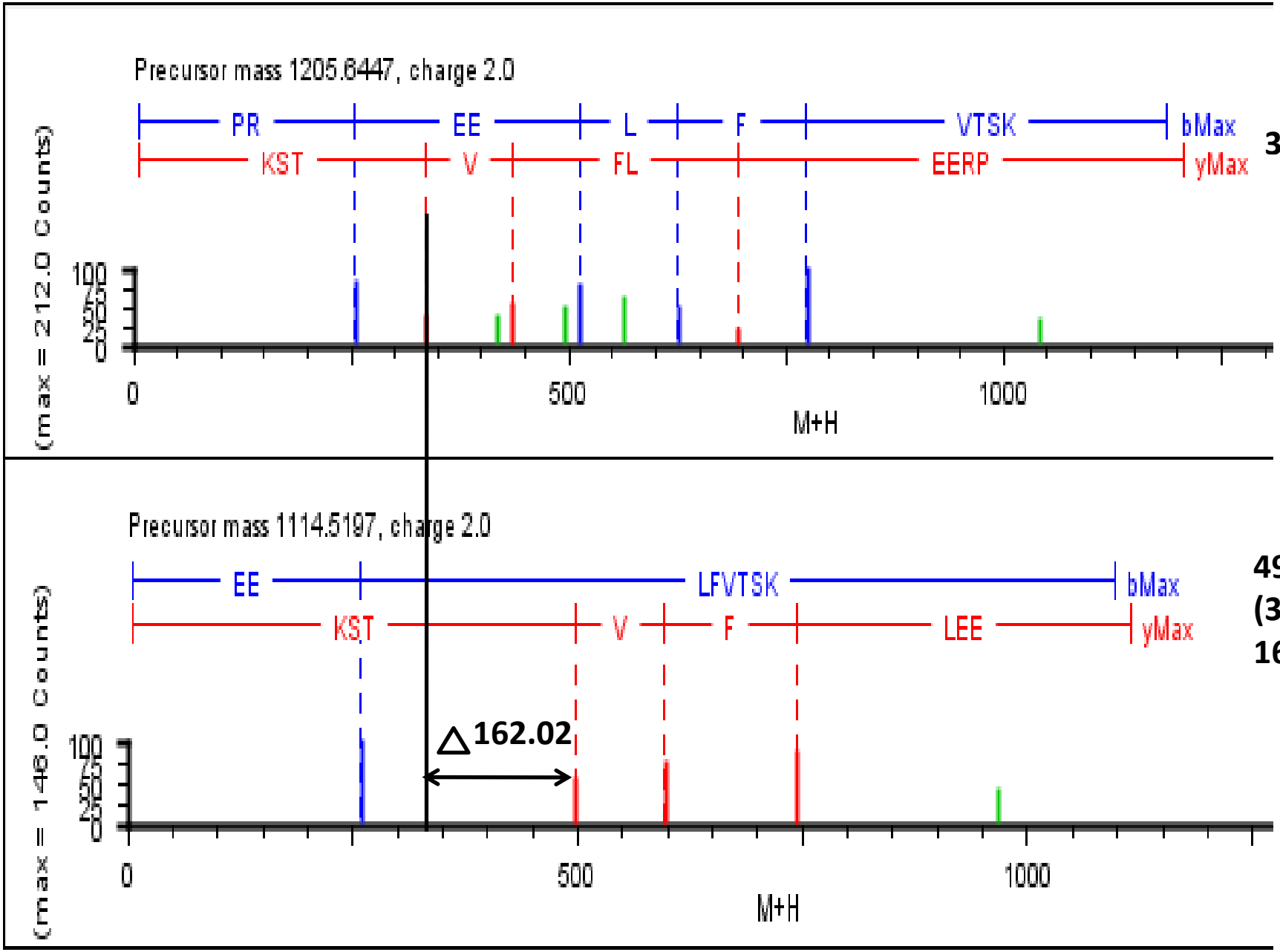


335.1957



443.1832: (335.19+ 108.02)

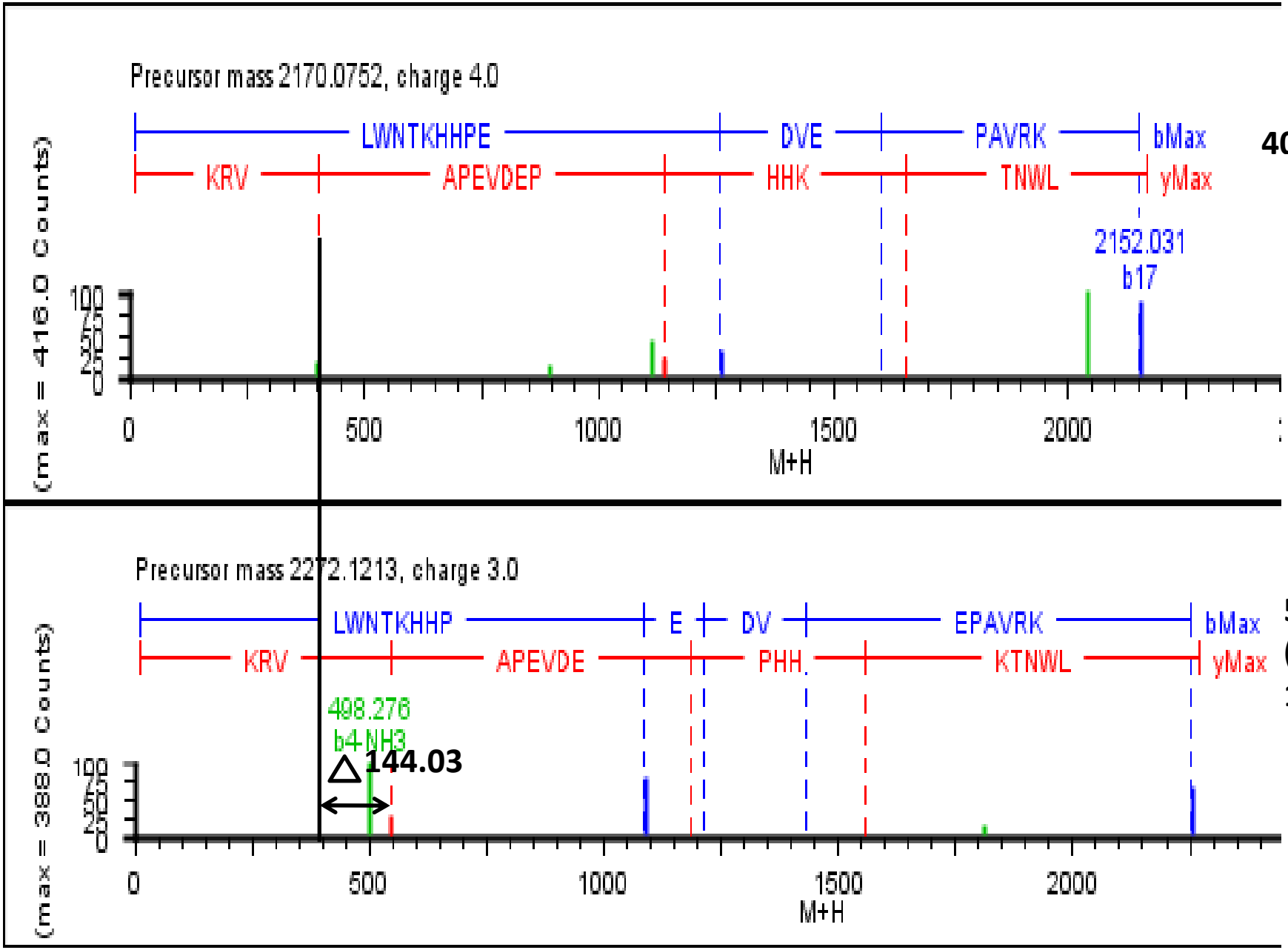
62-80 (K)ESVGAGKAVPREELFVTSK(Pyr)(L)



335.1957

497.1933: (335.19+ 162.02)

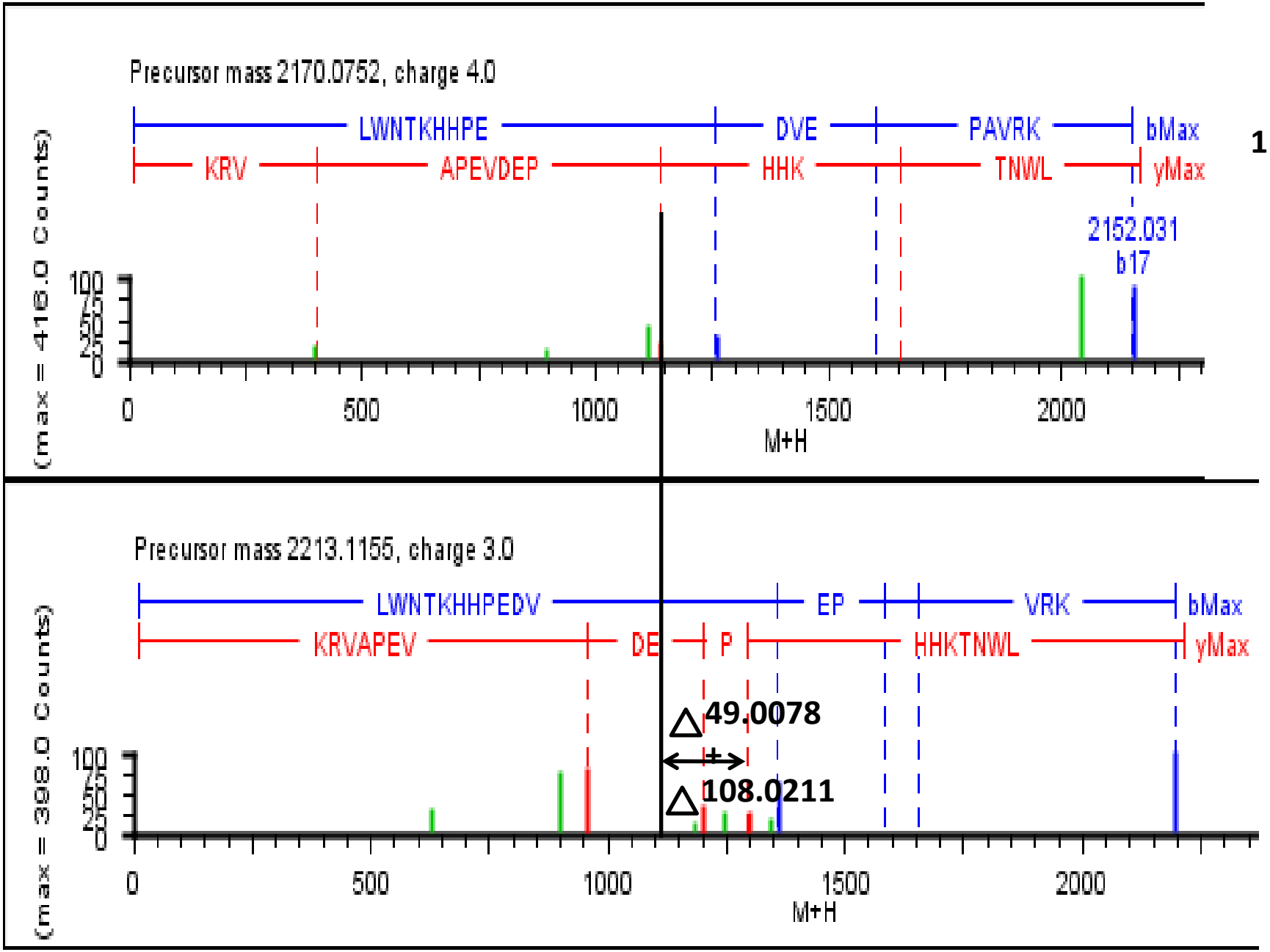
73-80 (R)EELFVTSK(Gly)(L)



402.2854

546.2994
(402.28+
144.03)

81-97 (K)LWNTKHHPEDVEPAVRK(ImiA)(T)

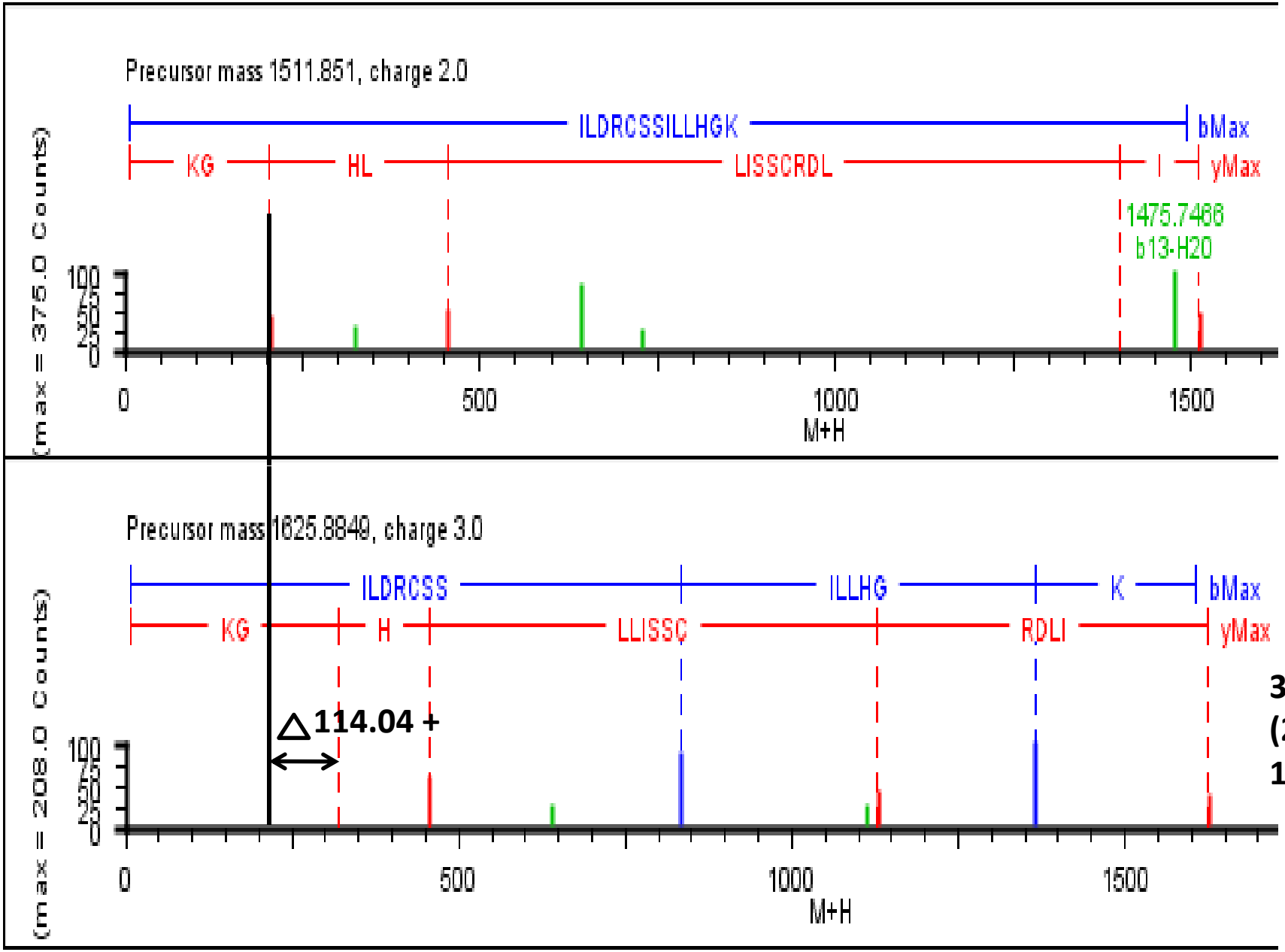


1139.5957

1296.633!
(1139.59+
49.00+
108.02)

81-97 (K)LWNTKHHPEDVEPAVR(MOLD)K(Pyr)(T)

NaKT

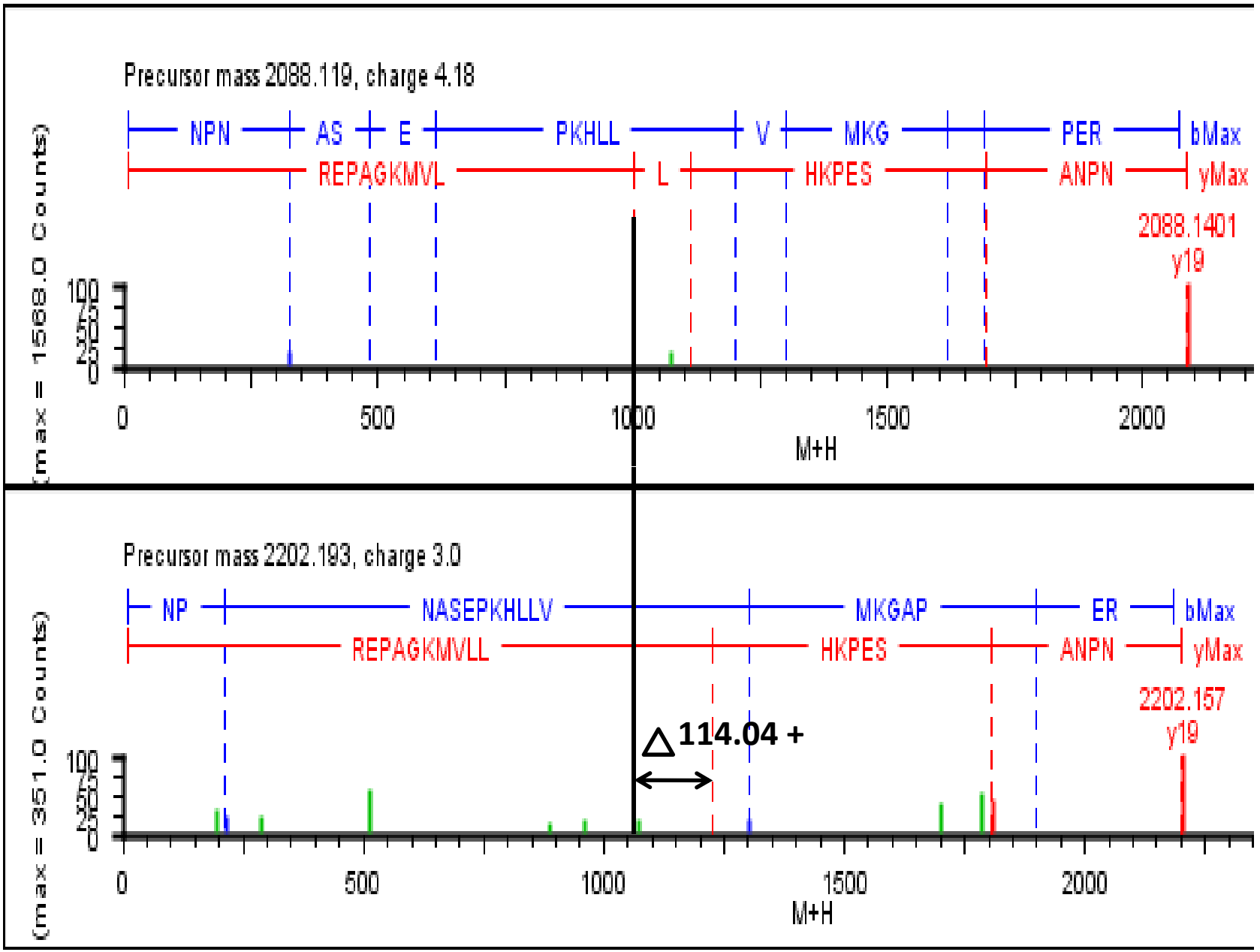


204.1403

318.1632: (204.14+ 114.04)

514-526

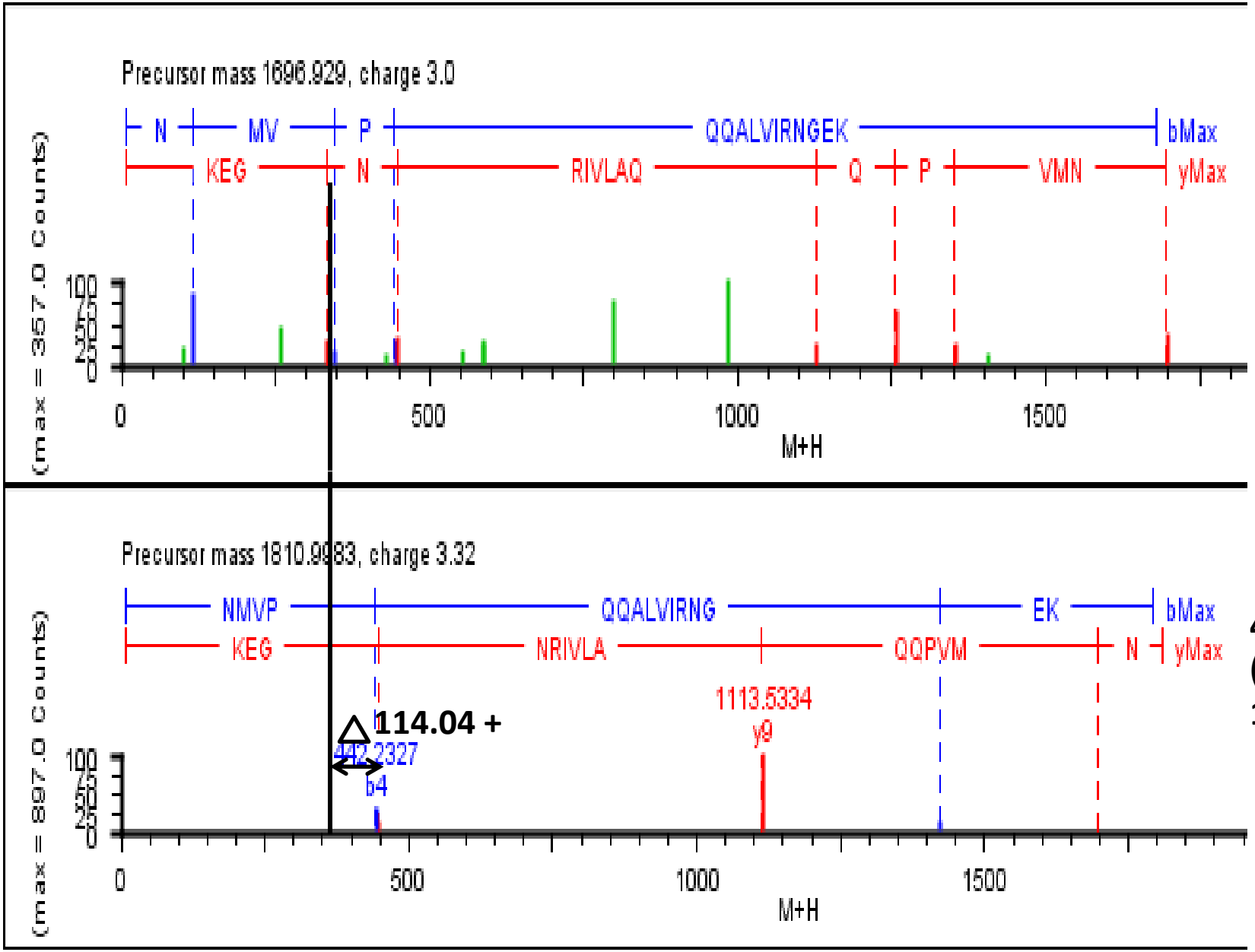
(R)ILDRCSSILLHGK(Ubi)(E)



1113.6058

1227.7126: (1113.6+ 114.04)

495-513 (K)HLLVMK(Ubi)GAPER(I)

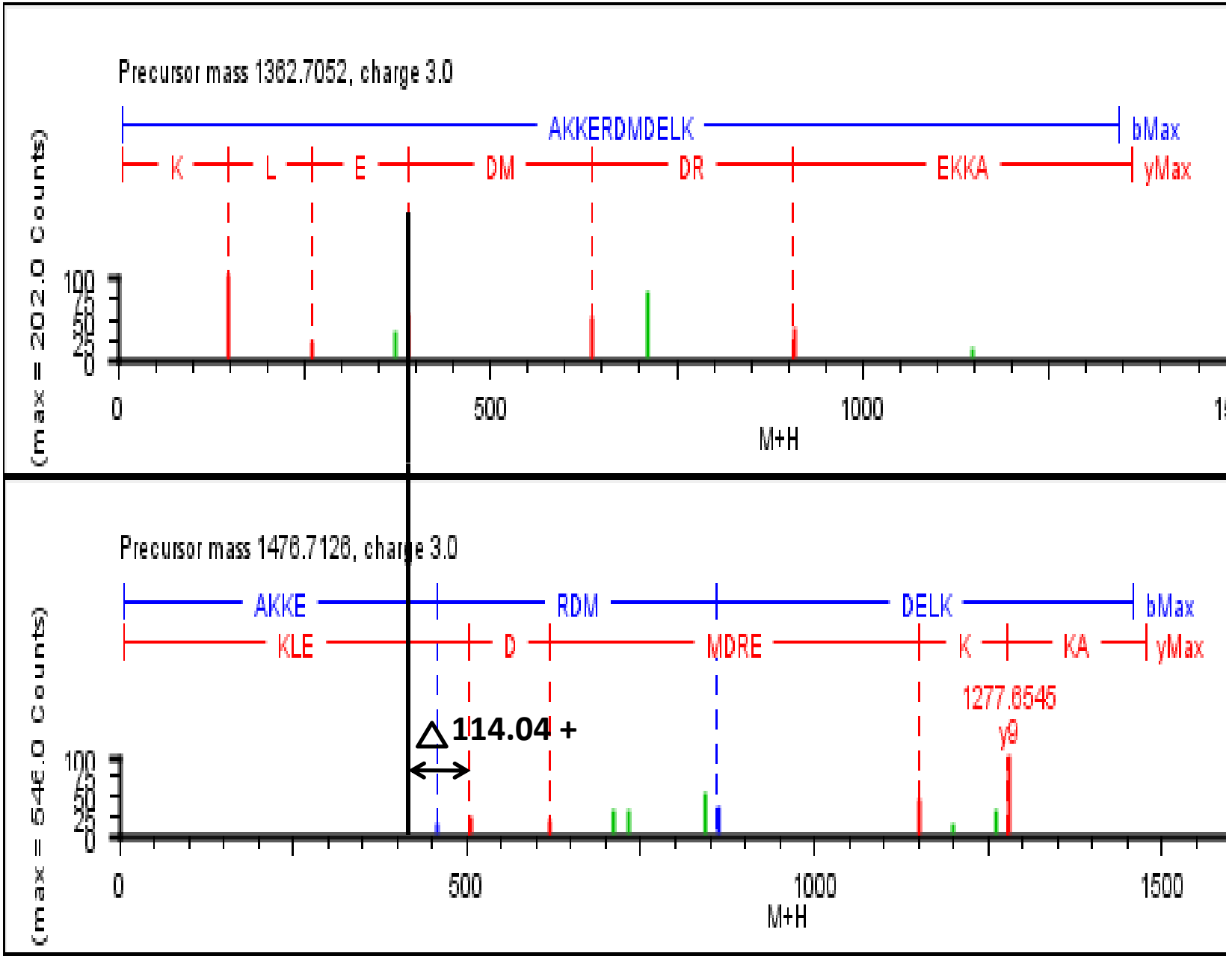


333.1433

447.2488: (333.14+ 114.04)

163-177

(K)NMVPQQALVIRNGEK(Ubi)(M)

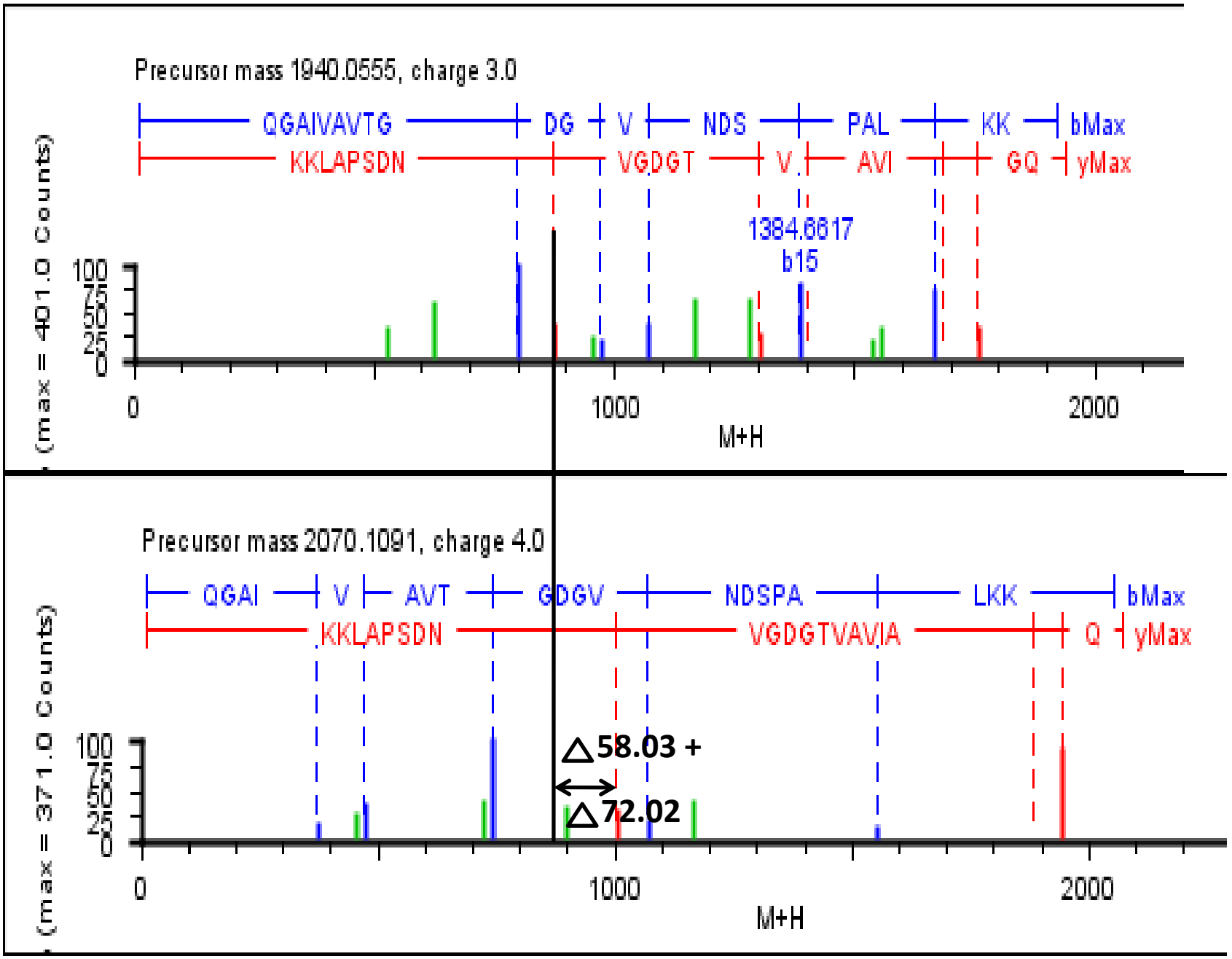


389.202

503.2875: (389.20+ 114.04)

26-36

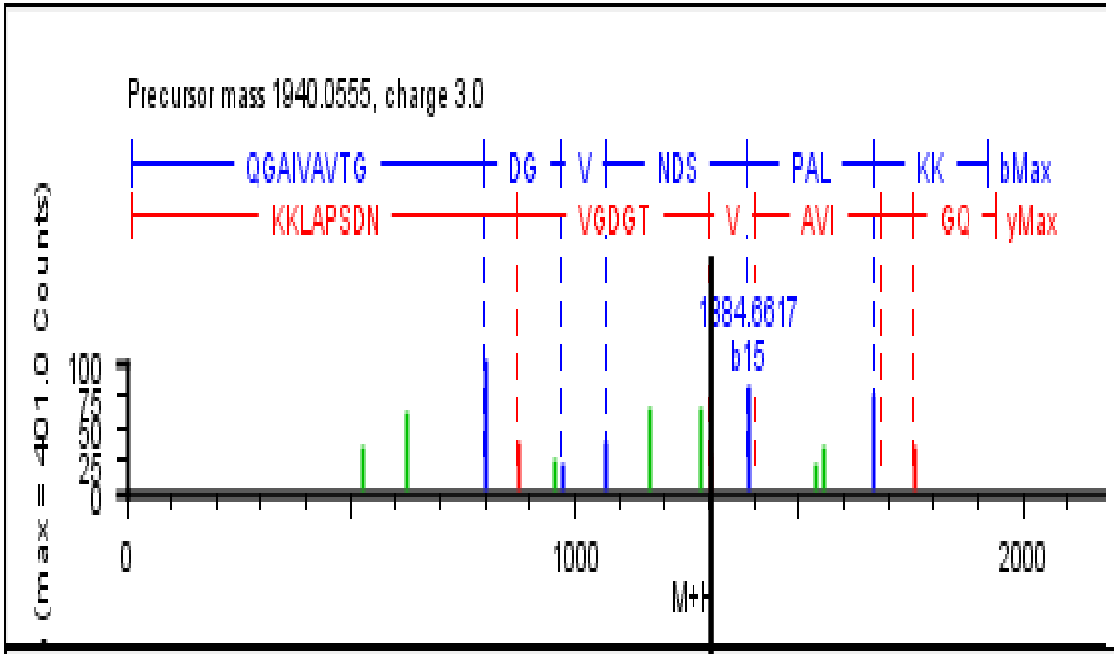
(K)AKKERDMDELK(Ubi)(K)



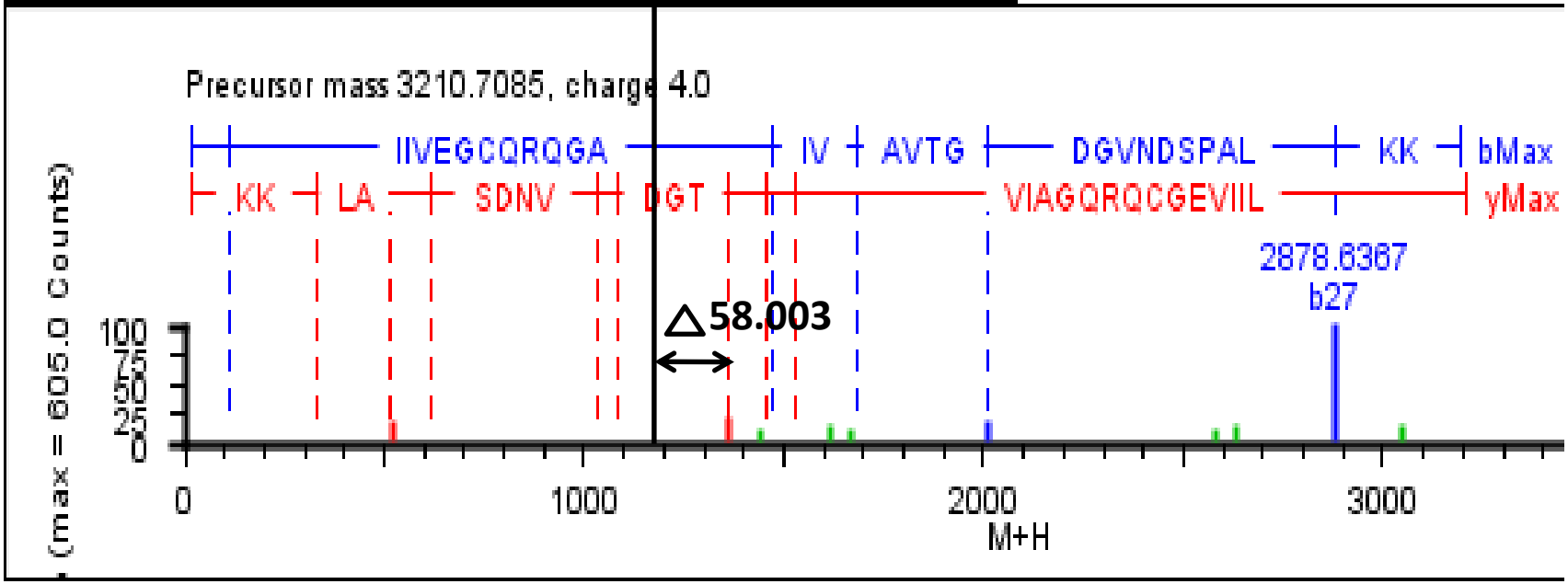
872.4454

1002.4733 (872.44+ 72.02+ 58.02)

708-727 (R)QGAIVAVTGDGVNDSPALK(CEL)K(Pento)(A)

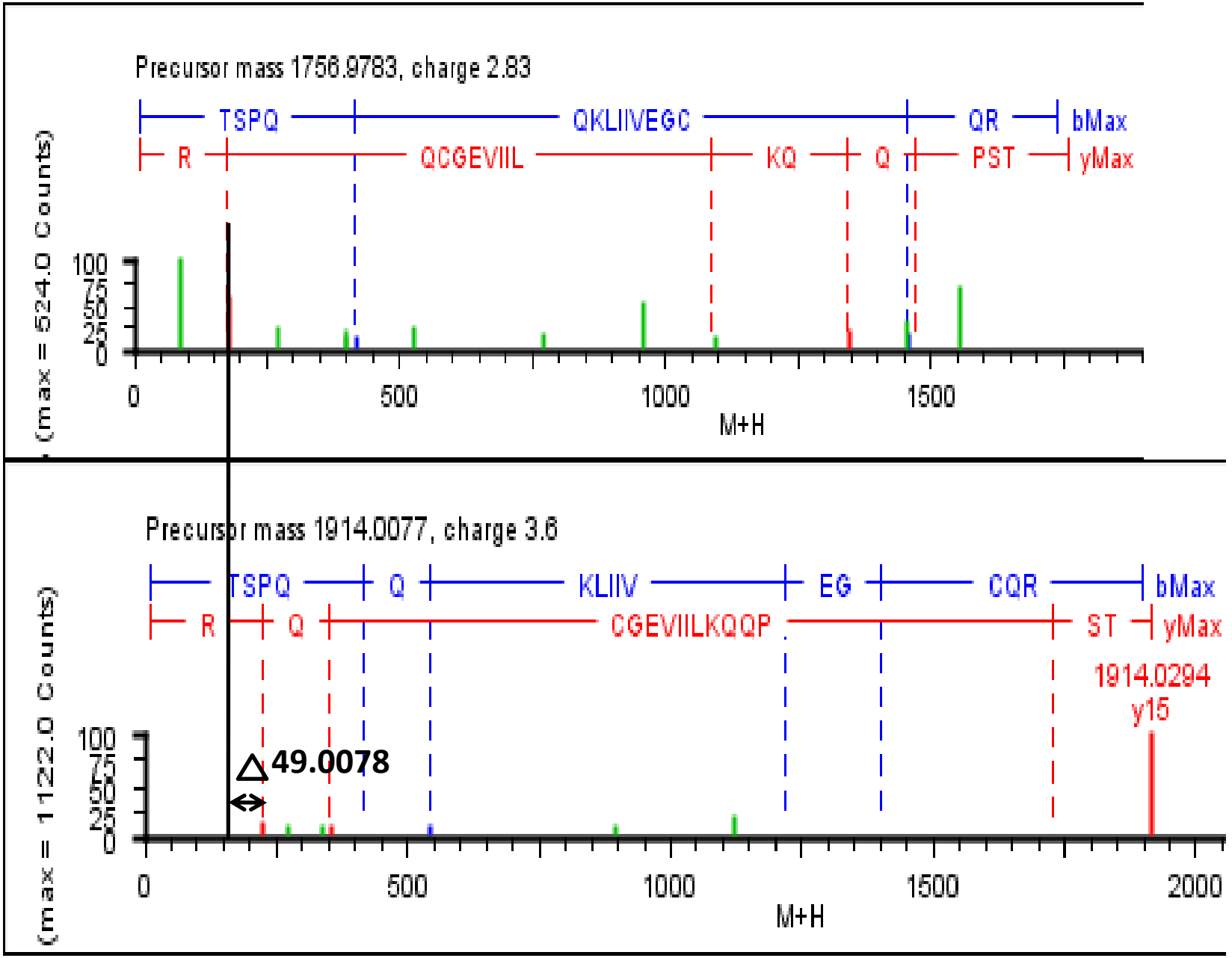


1301.5514



1359.5514: (1301.55+ 58.00)

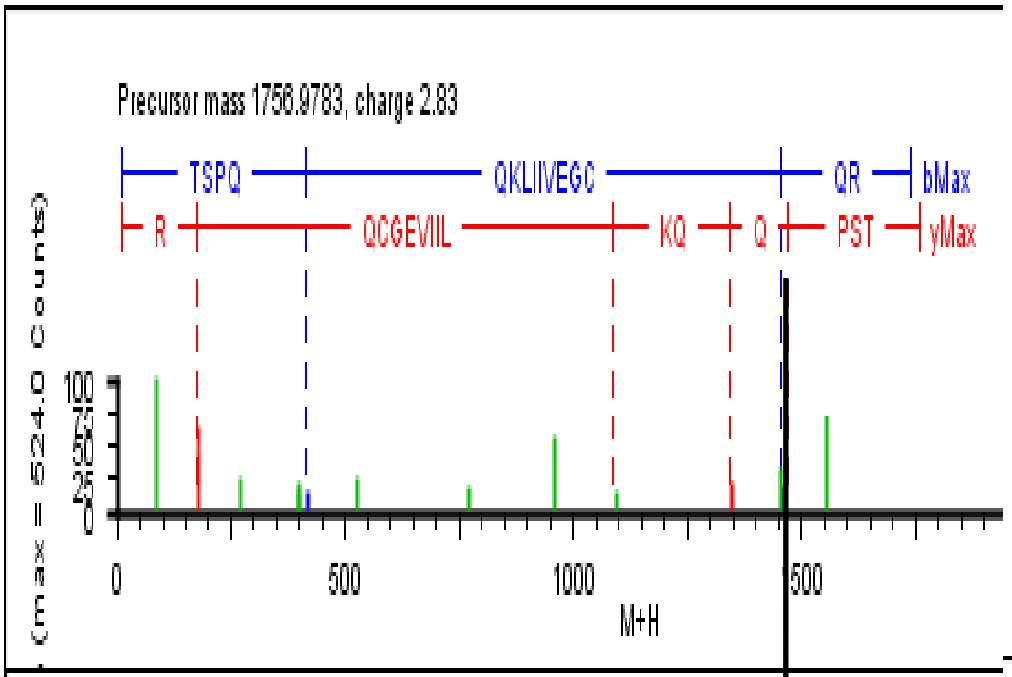
699-727 (K)LIIVEGCQRQGAIVAVTGDGVNDSPALK(CML)K(A)



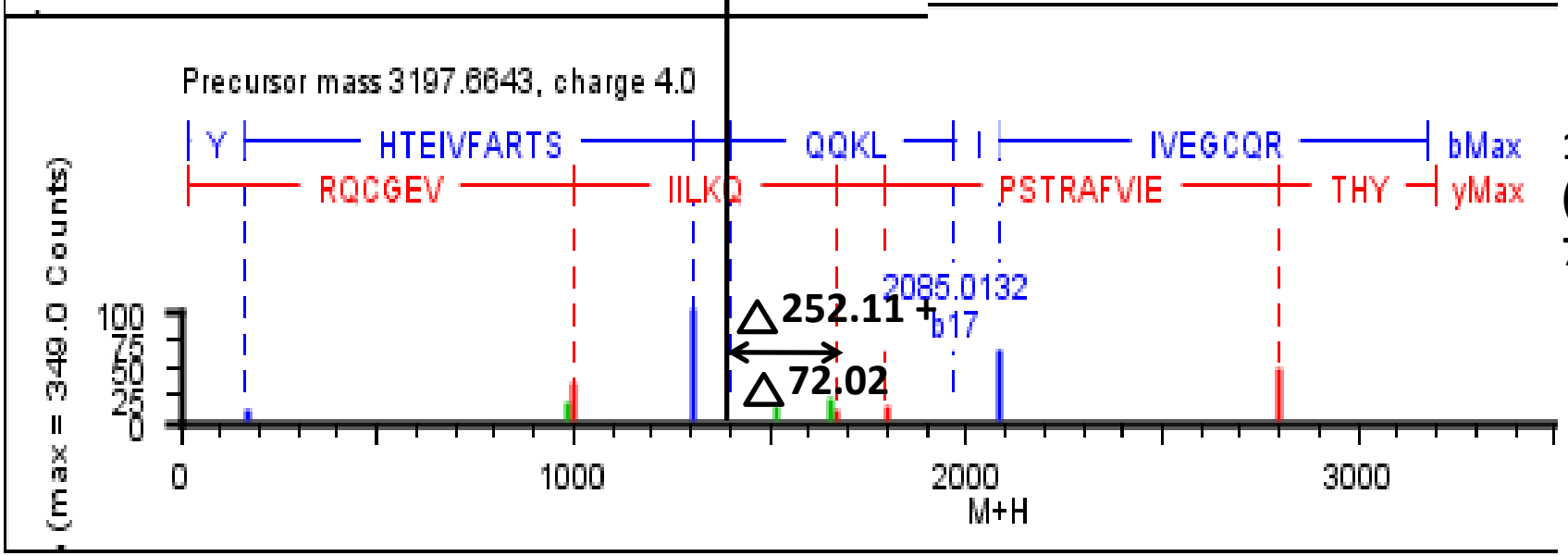
175.1153

224.1323: (175.11+ 49.00)

693-707 (R)TSPQQKLIIVEGCQR(MOLD)(Q)

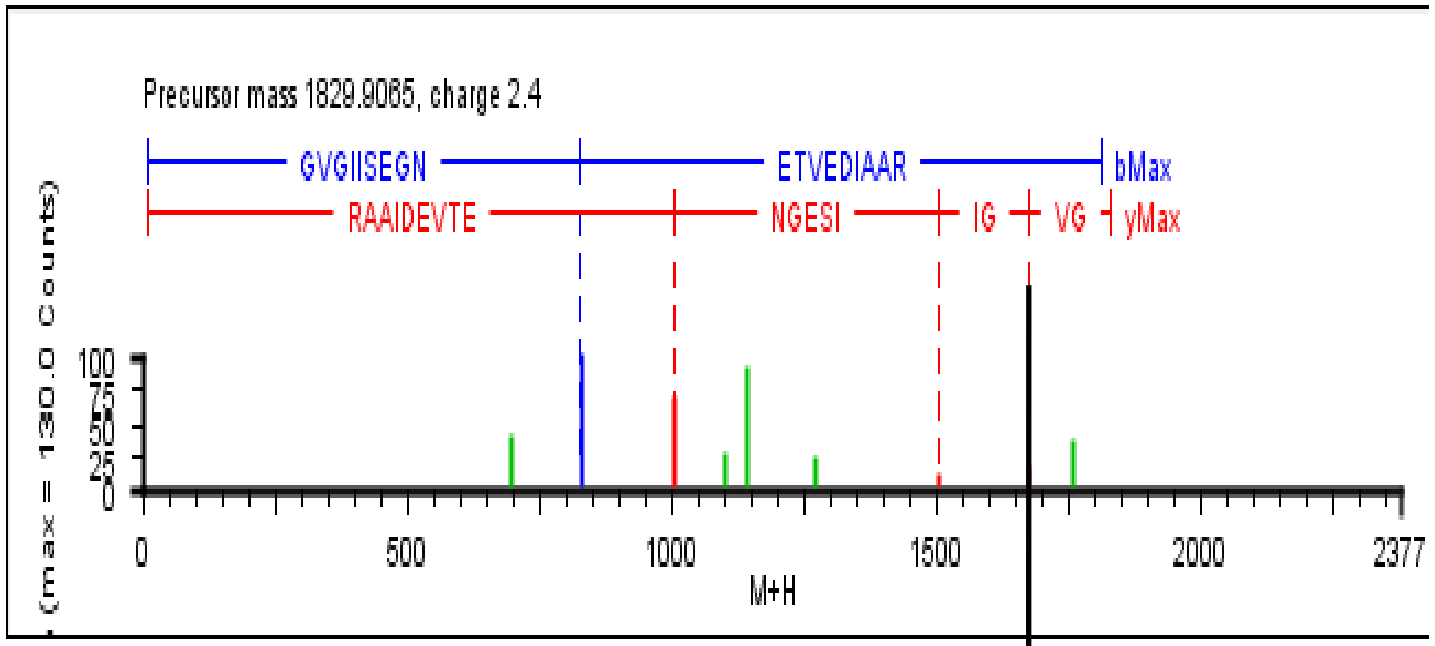


1343.5881

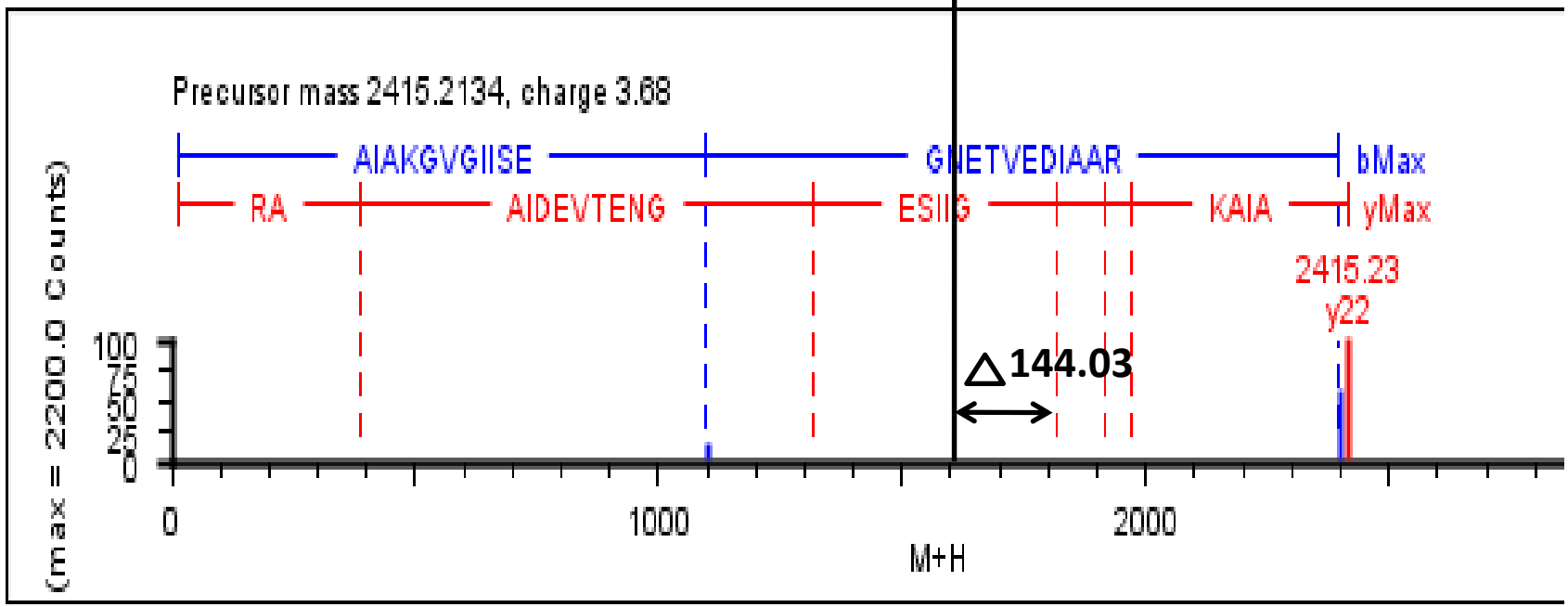


1667.7557: (1343.58+ 72.02+ 252.

684-707 (R)YHTEIVFARTSPQQK(CEL)LIIVEGCQR(Crossline)(Q)

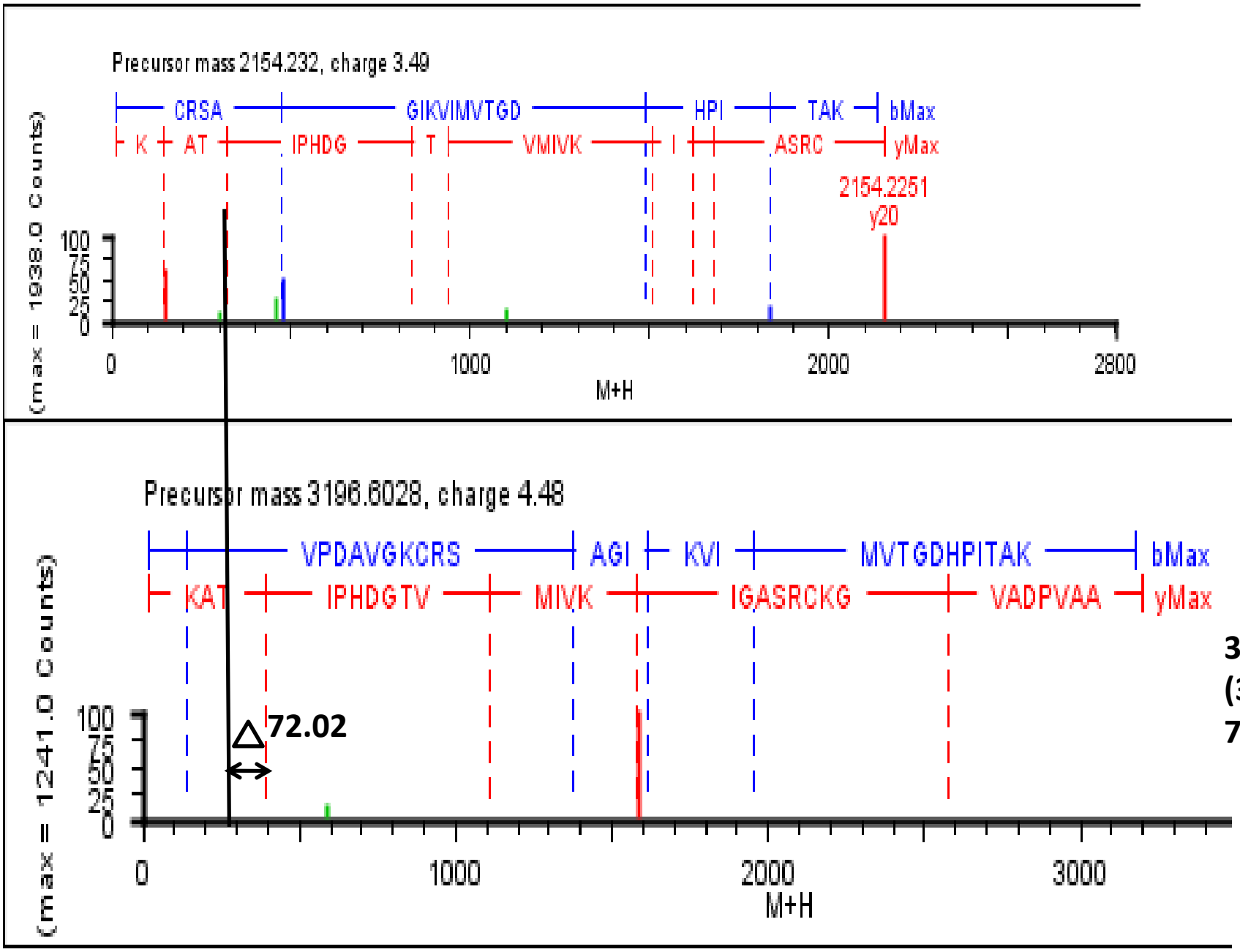


1673.829



1817.7036: (1673.82+ 144.03)

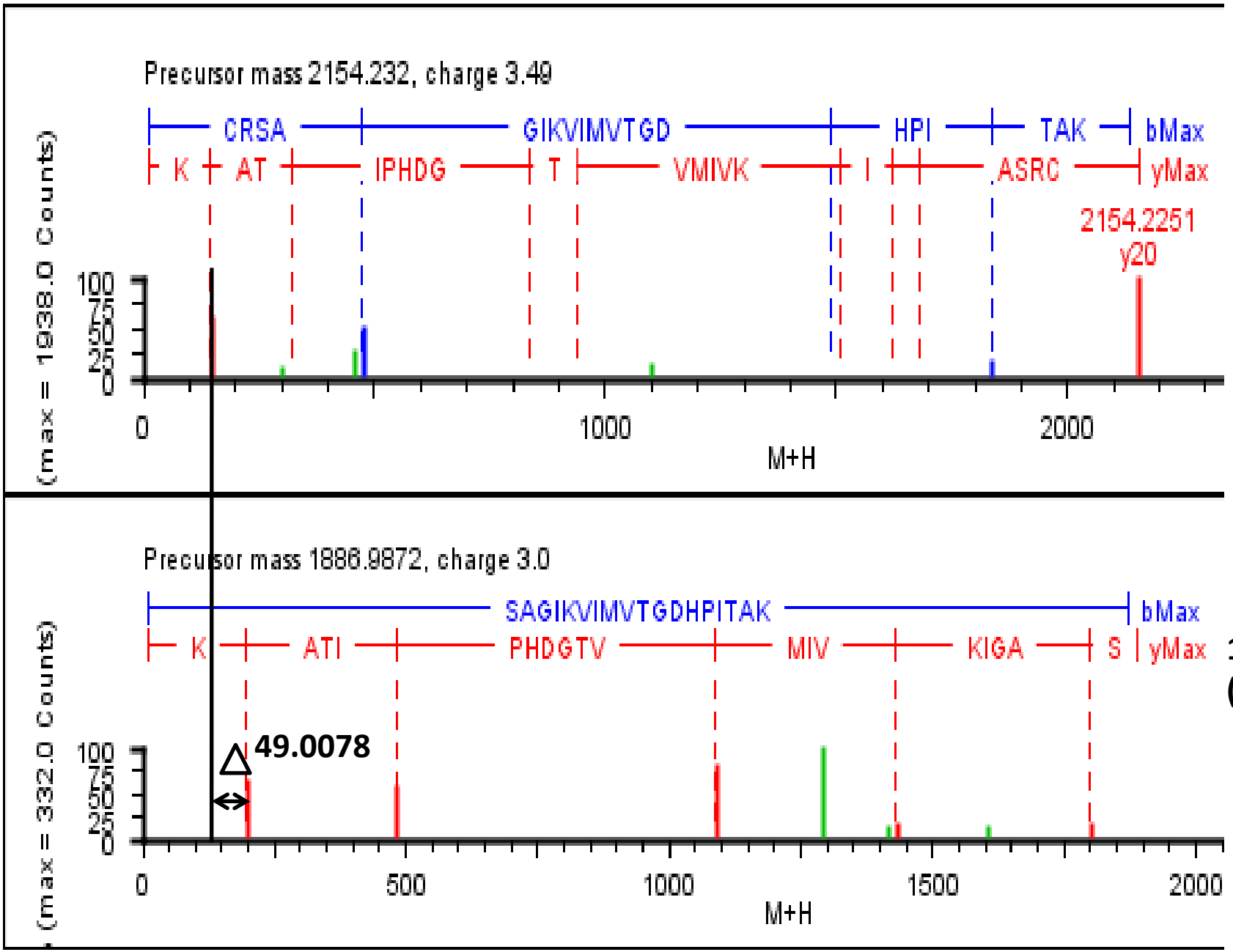
626-647 (K)AIAKGVGIISEGNETVEDIAAR(ImiA)(L)



319.1606

391.2183: (319.16+ 72.02)

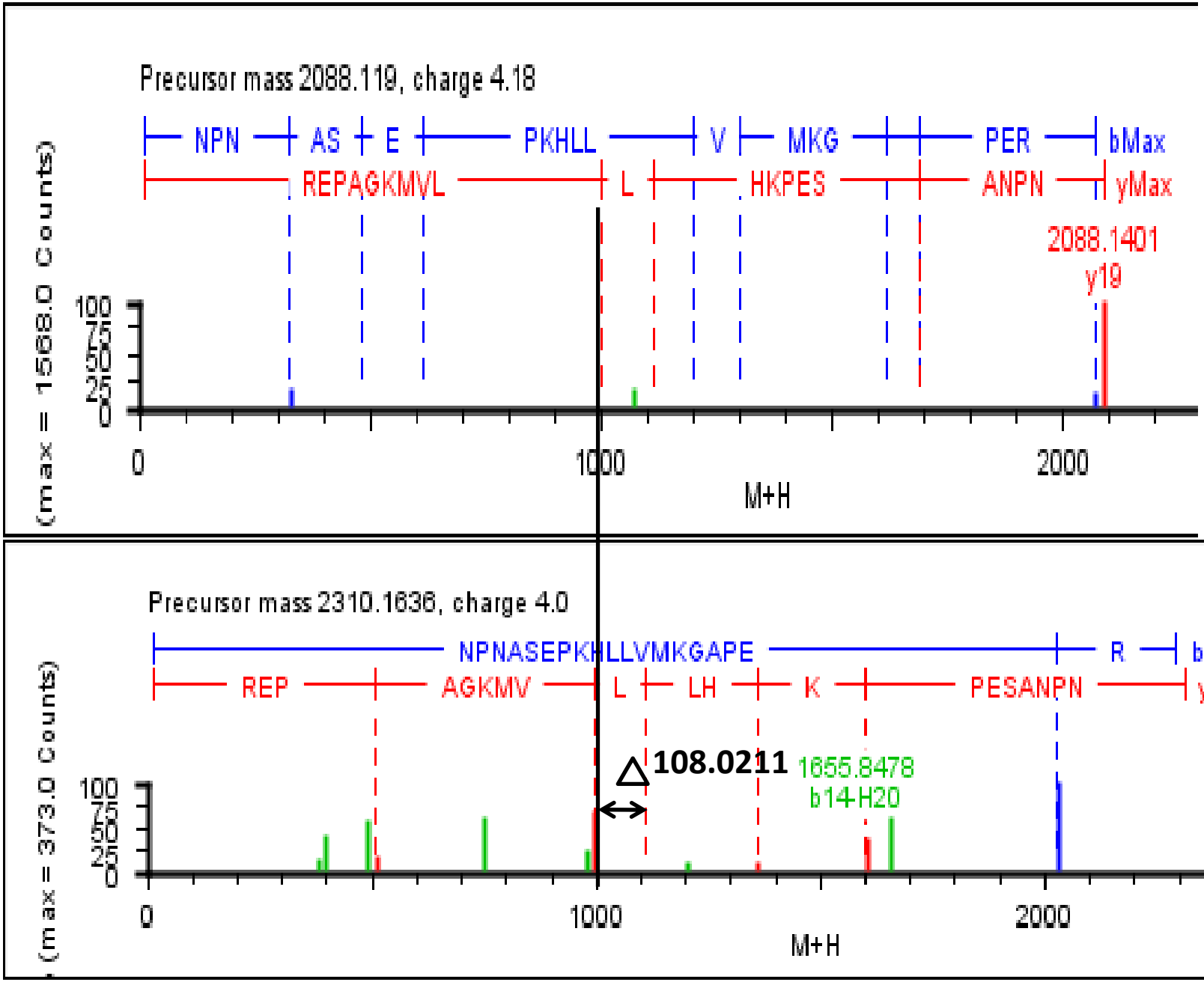
597-625 (R)AAVPDAVGKCRSAGIKVIMVTGDHPITAK(CEL)(A)



147.1094

196.1161:
(147.1+ 49.0

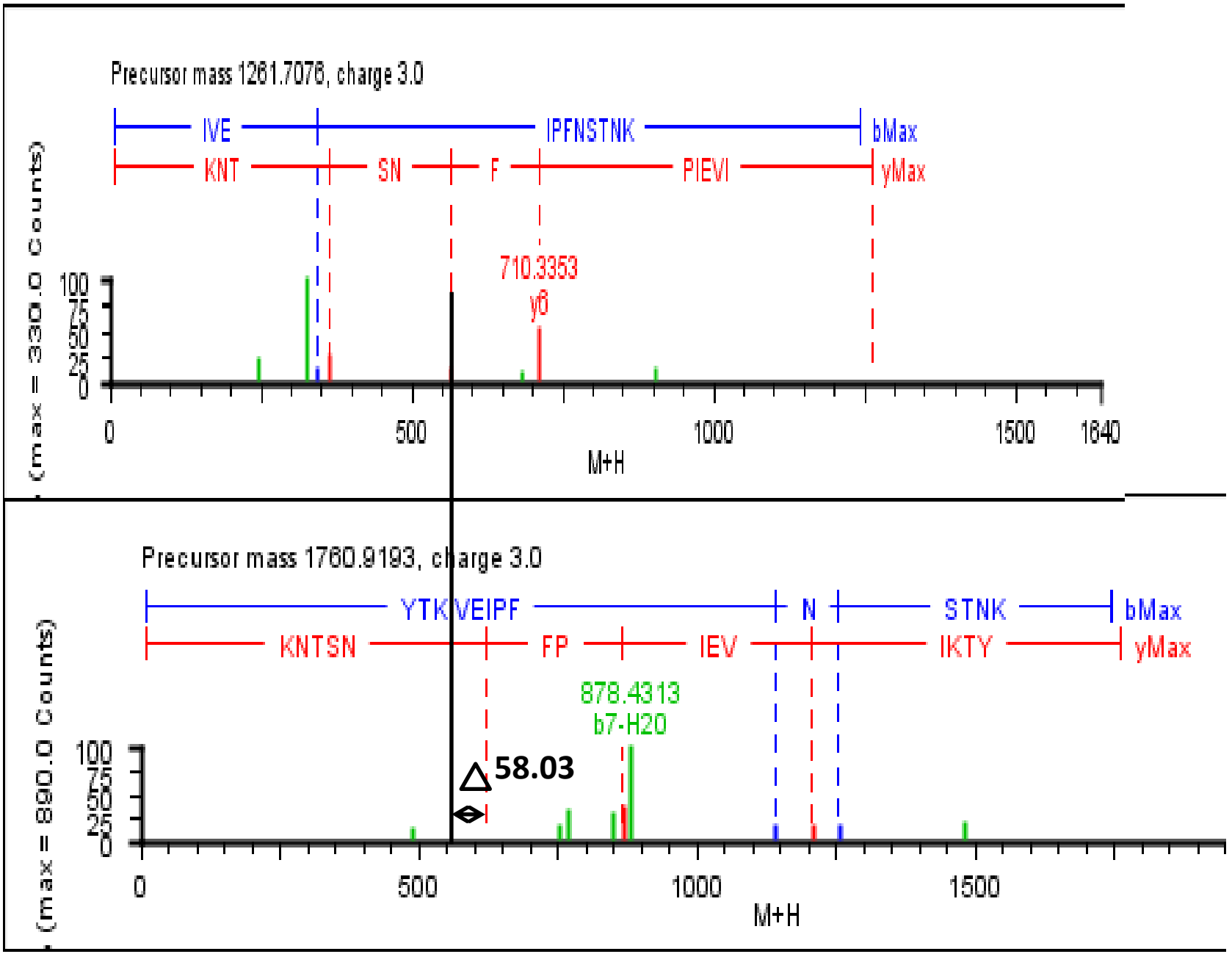
608-625 (R)SAGIKVIMVTGDHPITAK(MOLD)(A)



1000.6045

1108.4863: (1000.6+ 108.02)

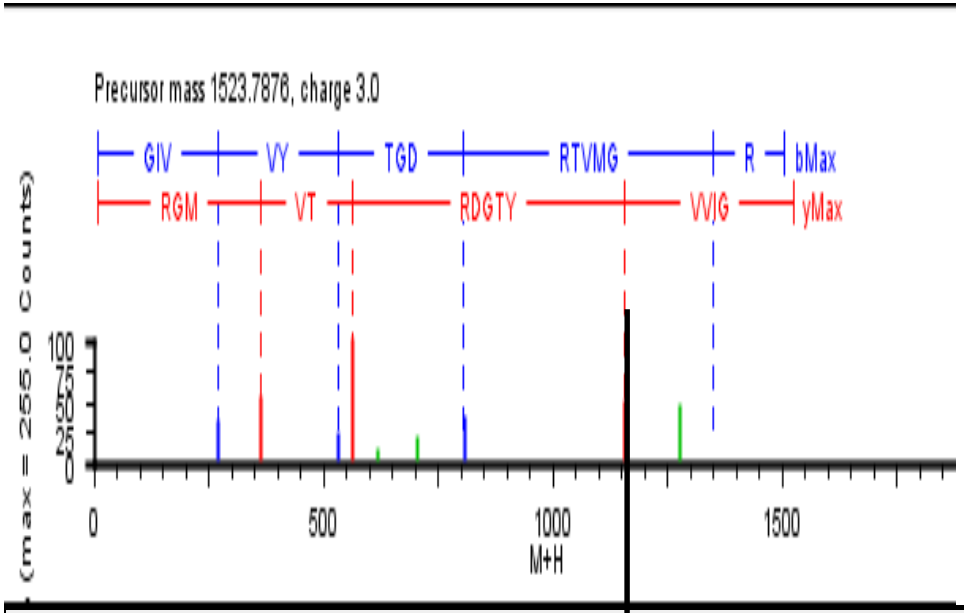
495-513 (K)NPNASEPKHLLVMKGAPER(Pyr)(I)



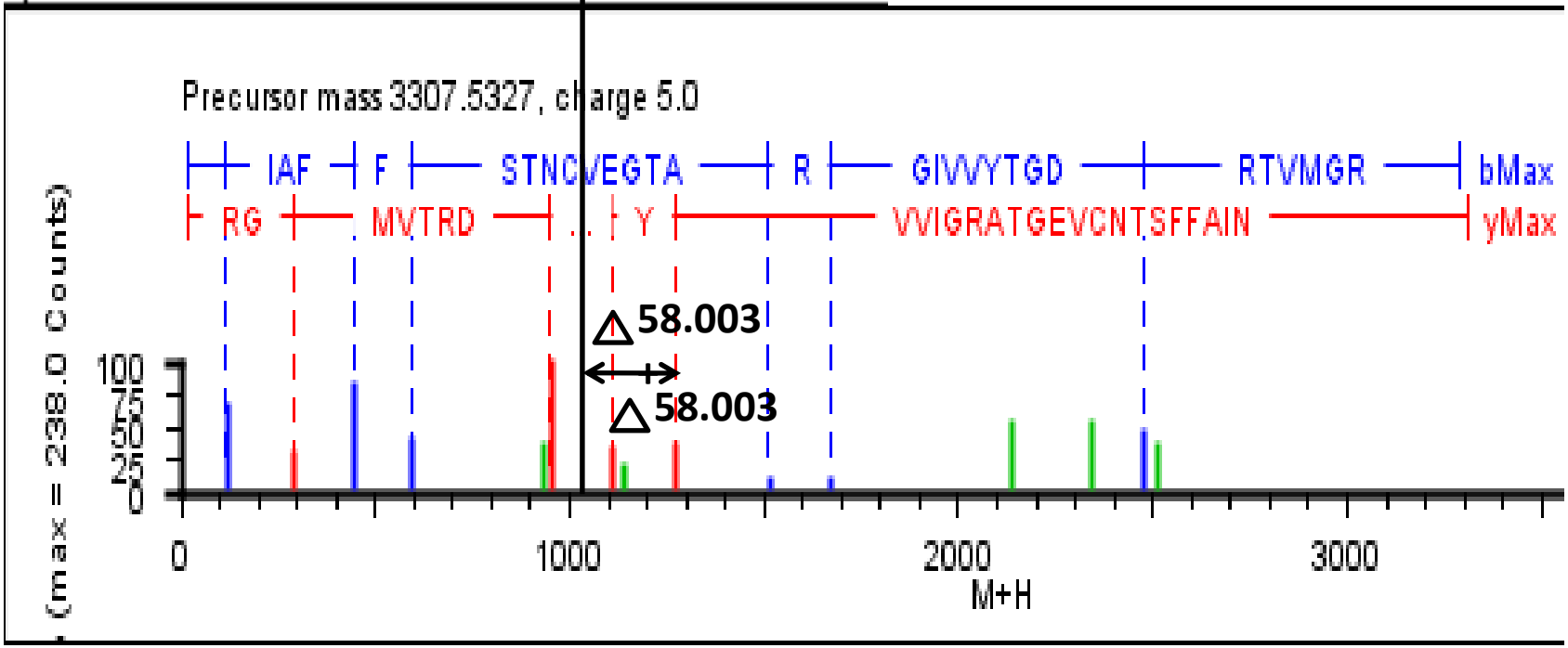
563.3173

621.349: (563.31+ 58.03)

474-487 (K)YTKIVEIPFNSTNK(Pento)(Y)

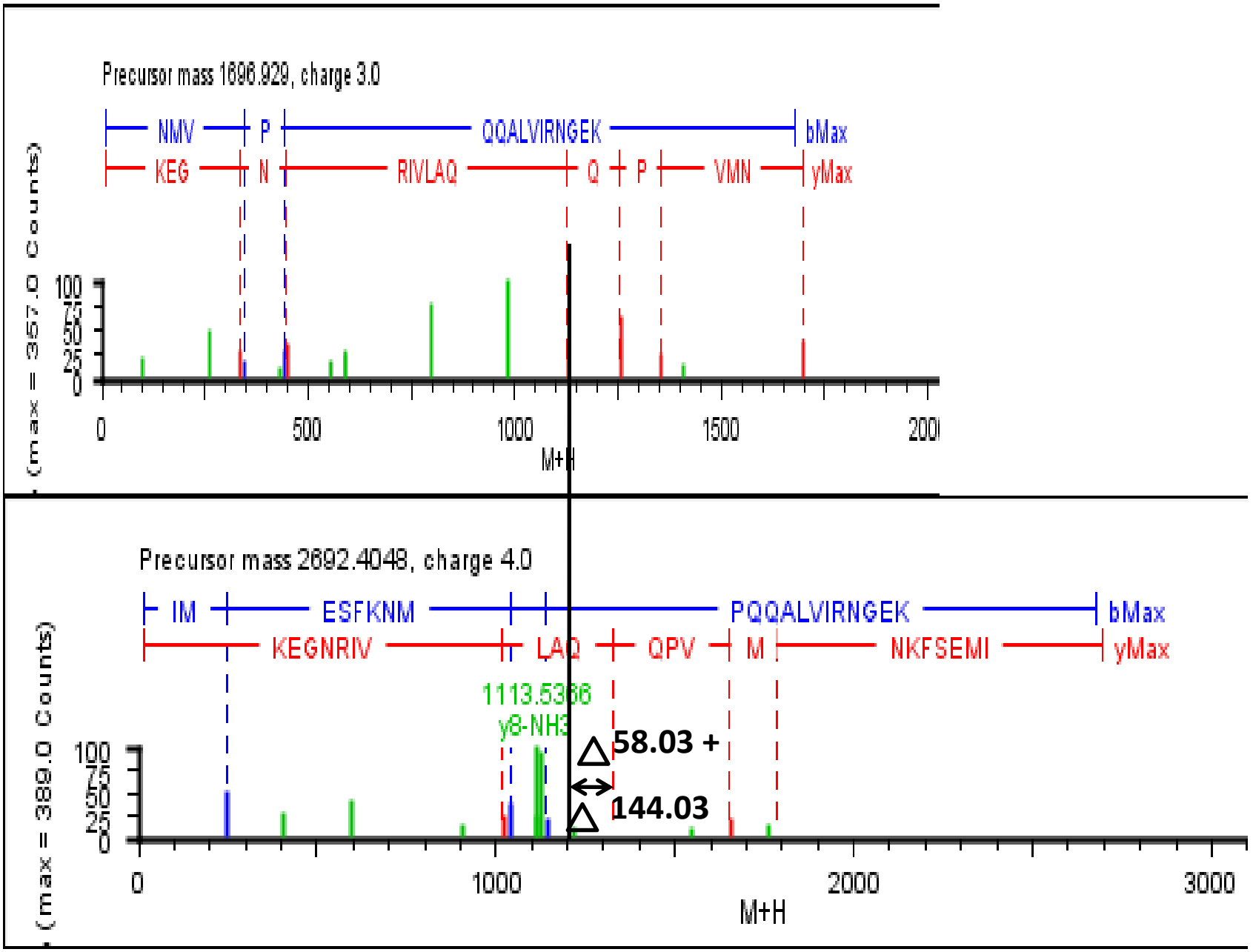


1155.5348



1271.5724: (1155.53+ 58.0035+ 58.003)

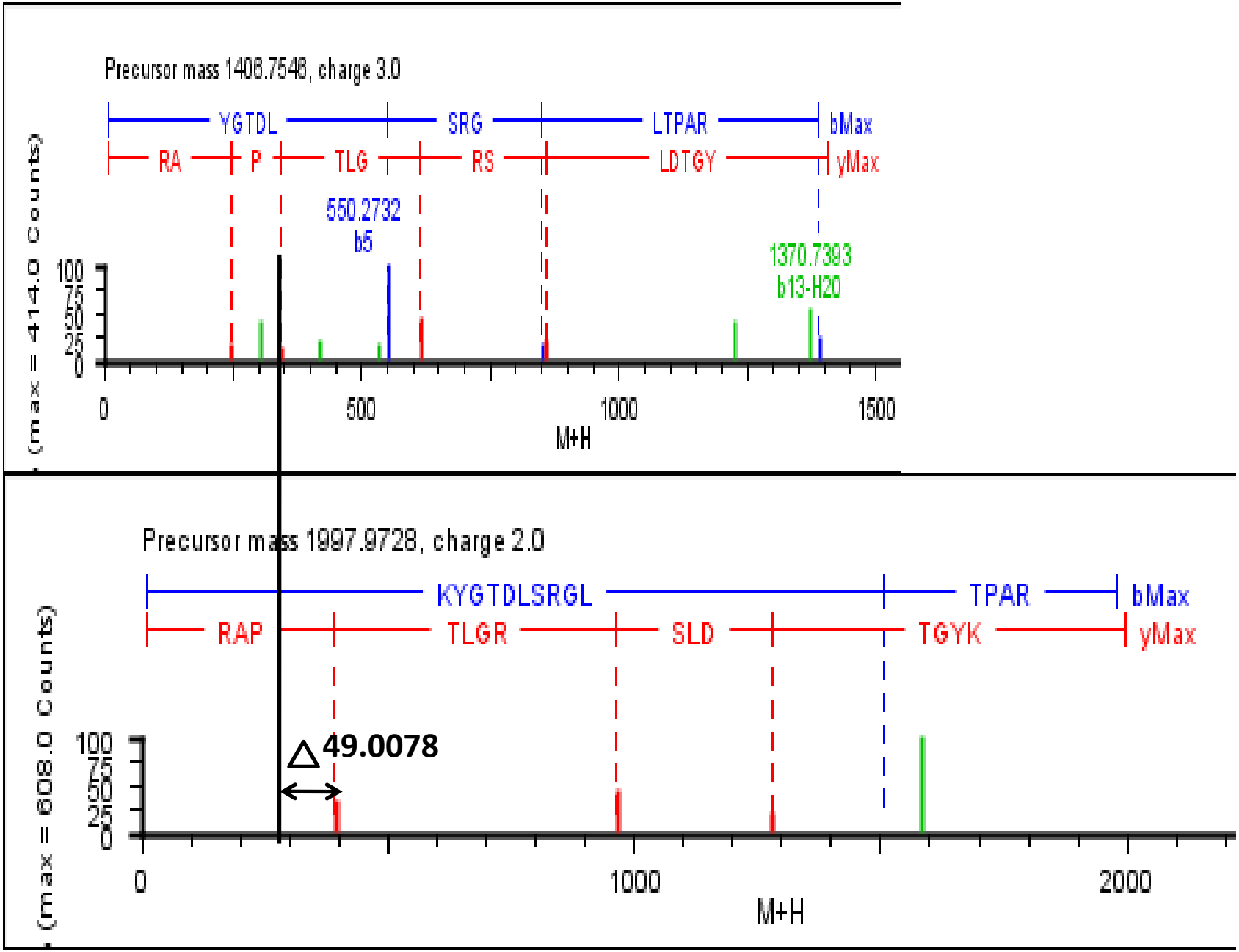
241-269 (R)NIAFFSTNCVEGTARGIVVYTGDR(CML)TVMGR(CML)(I)



1127.5831

1329.738: (1127.58+ 58.03+ 144.03)

163-177 (K)NMVPQQALVIR(Pento)NGEK(ImiA)(M)

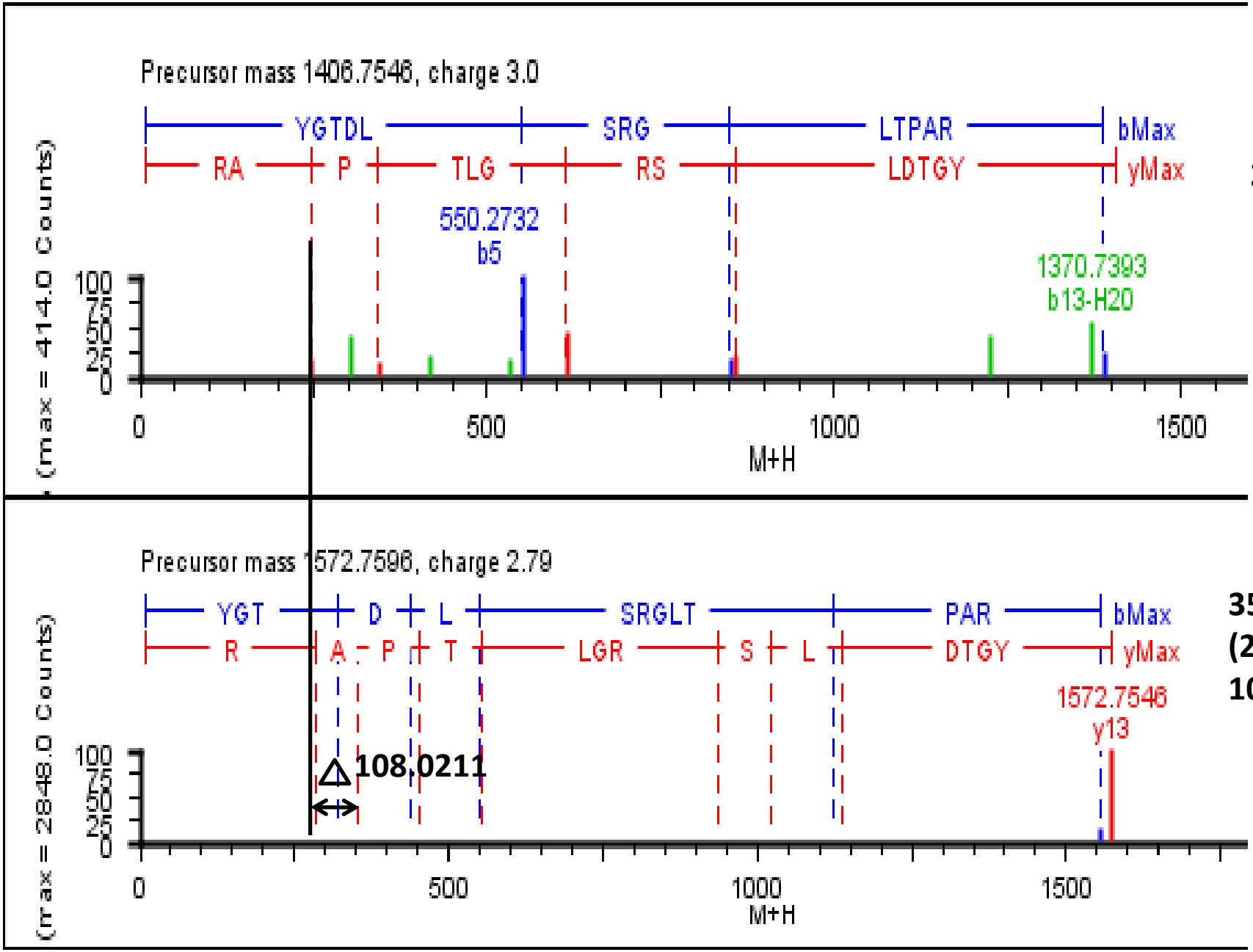


343.1896

392.214: (343.18+ 49.00)

54-67

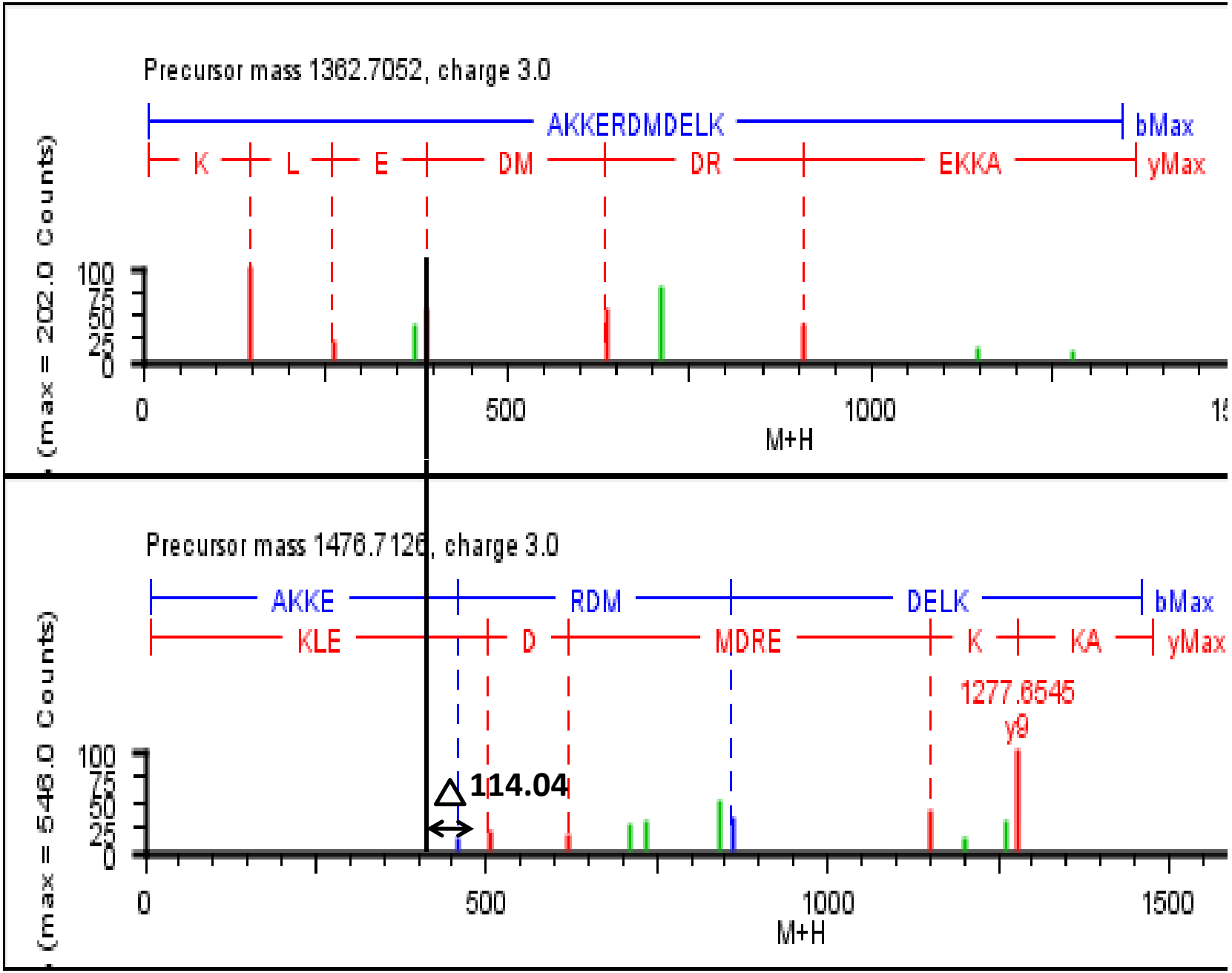
(R)KYGTDLSRGLTPAR(MOLD)(A)



246.1511

354.1745: (246.15+ 108.02)

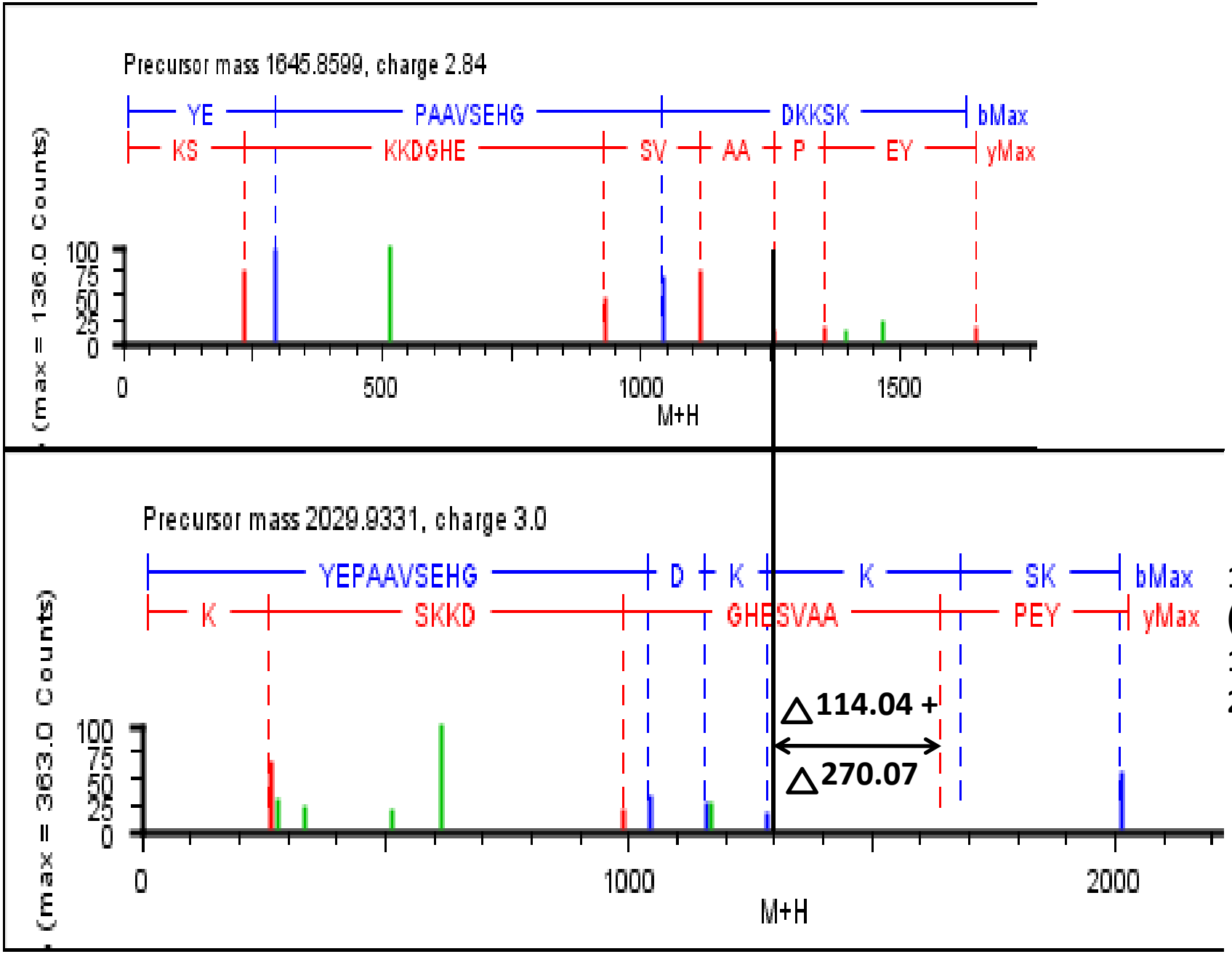
55-67 (K)YGTDLSRGLTPAR(Pyr)(A)



389.202

503.2875: (389.20+ 114.04)

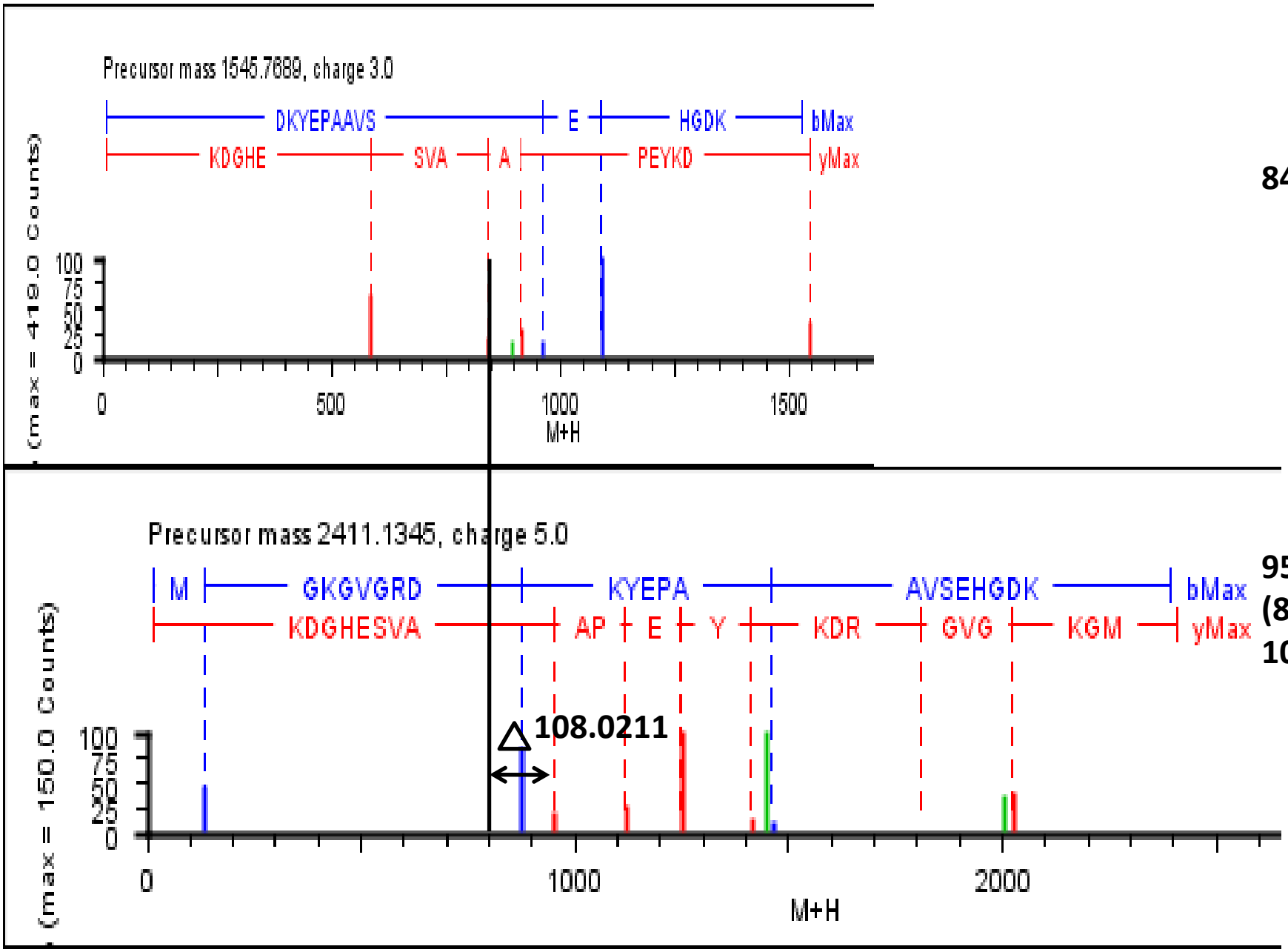
26-36 (K)AKKERDMDELK(Ubi)(K)



1256.5714

1640.8994: (1256.57+ 114.04+ 270.07)

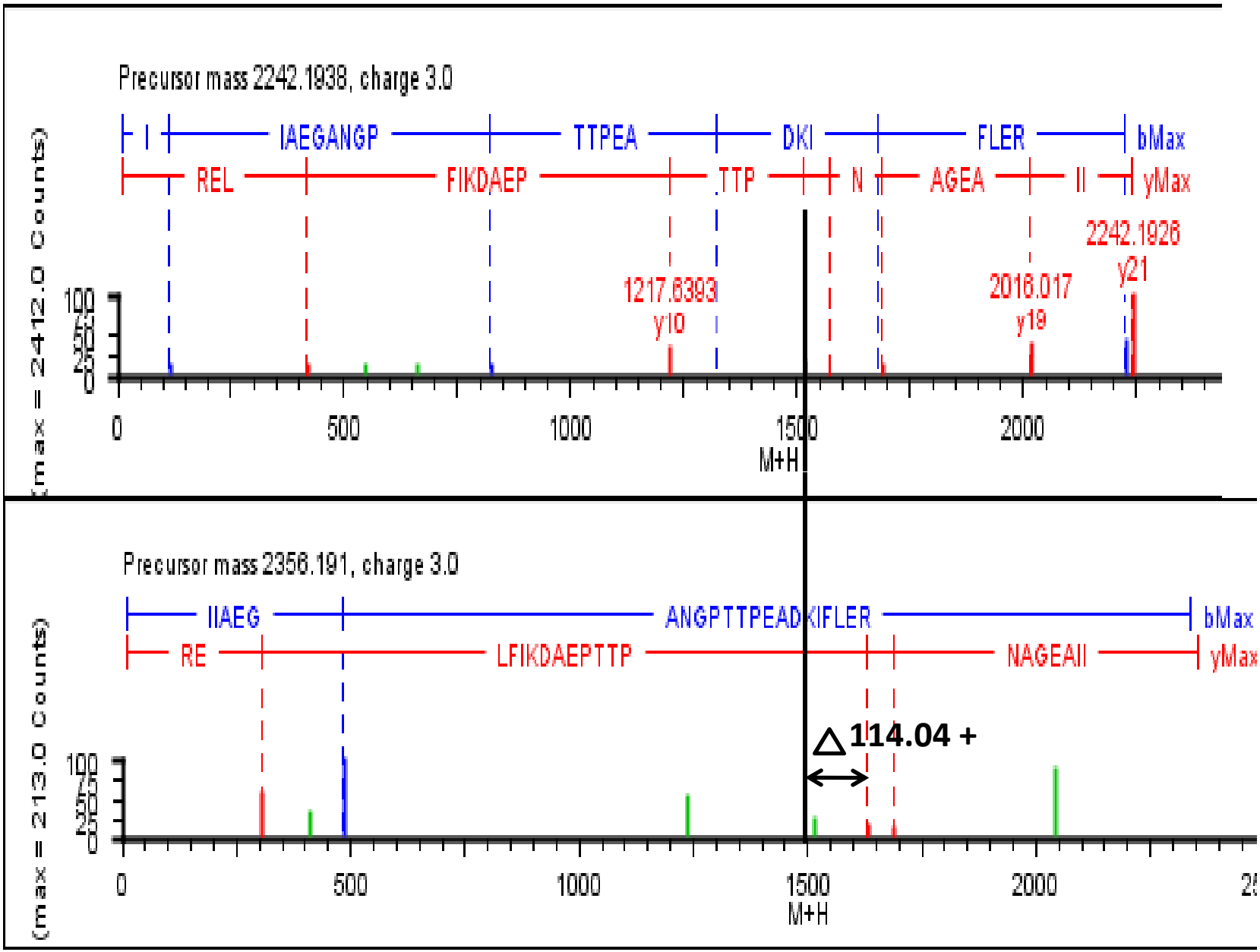
10-24 (K)YEPAAVSEHGDKK(AFGP)SK(Ubi)(K)



1-21

(-)MGKGVGRDKYEPAAVSEHGDK(Pyr)(K)

GDH

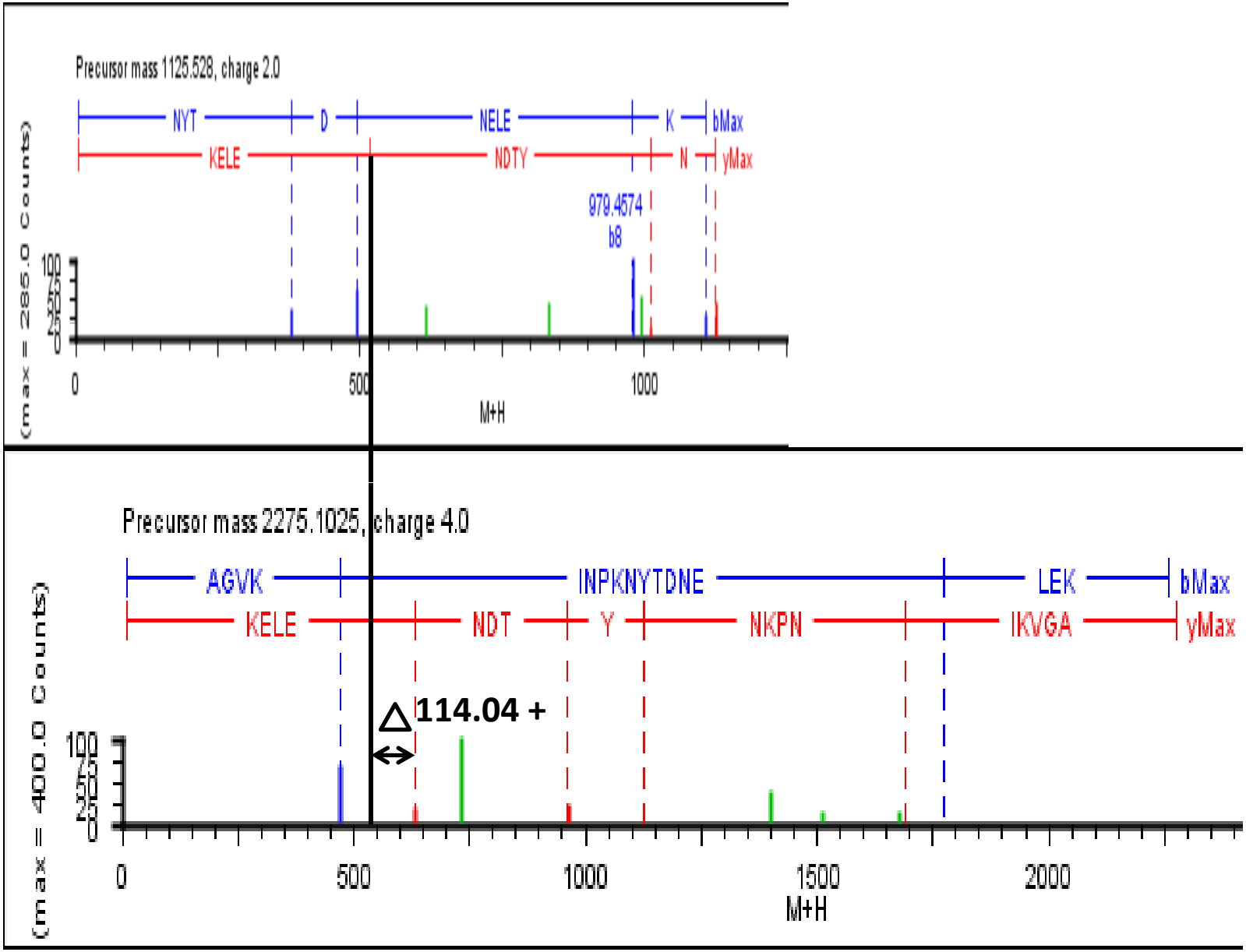


1516.8114

1630.8544: (1516.81+ 114.04)

400-420

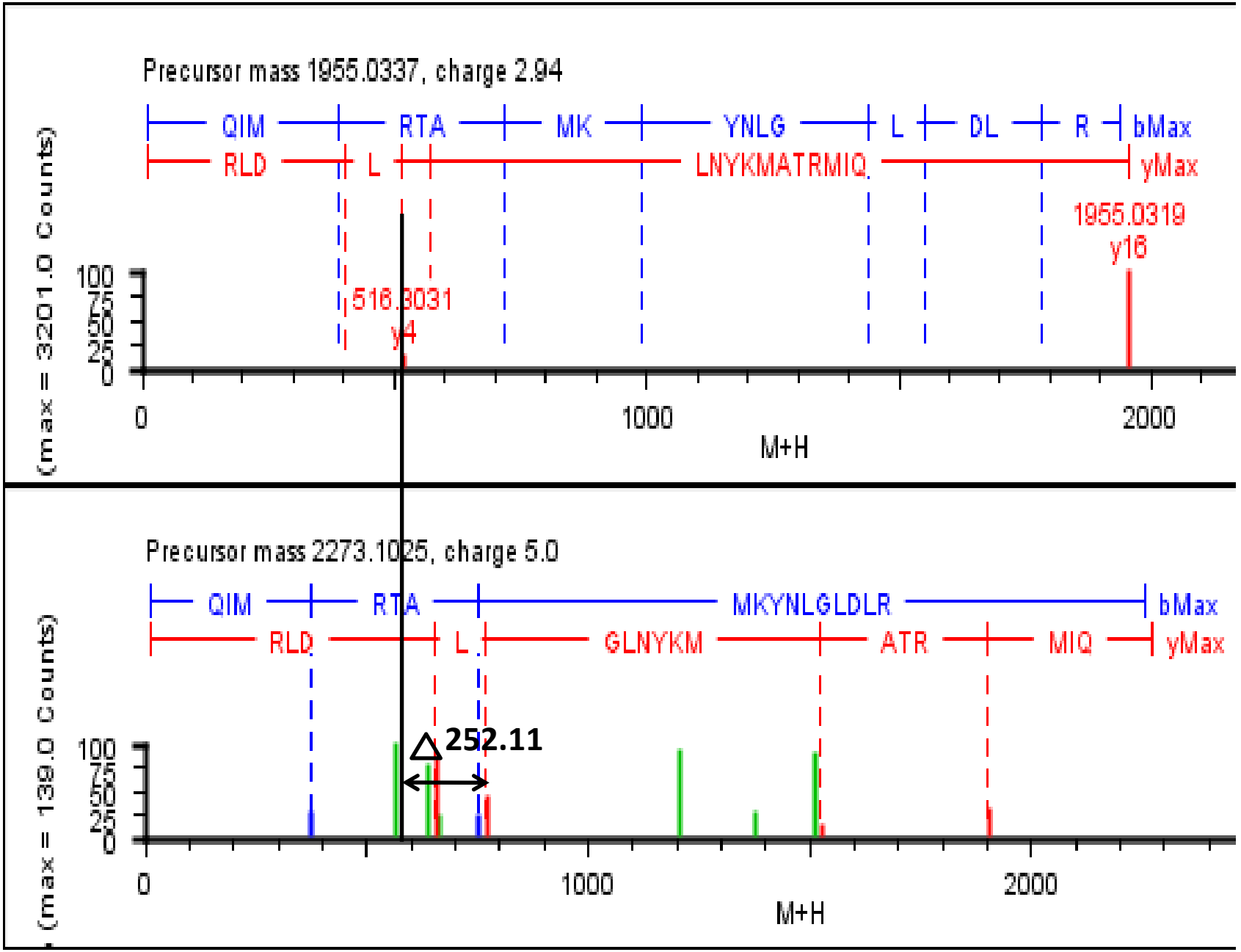
(K)IIAEGANGPTTPEADK(Ubi)IFLER(N)



518.2836

632.3735: (518.28+ 114.04)

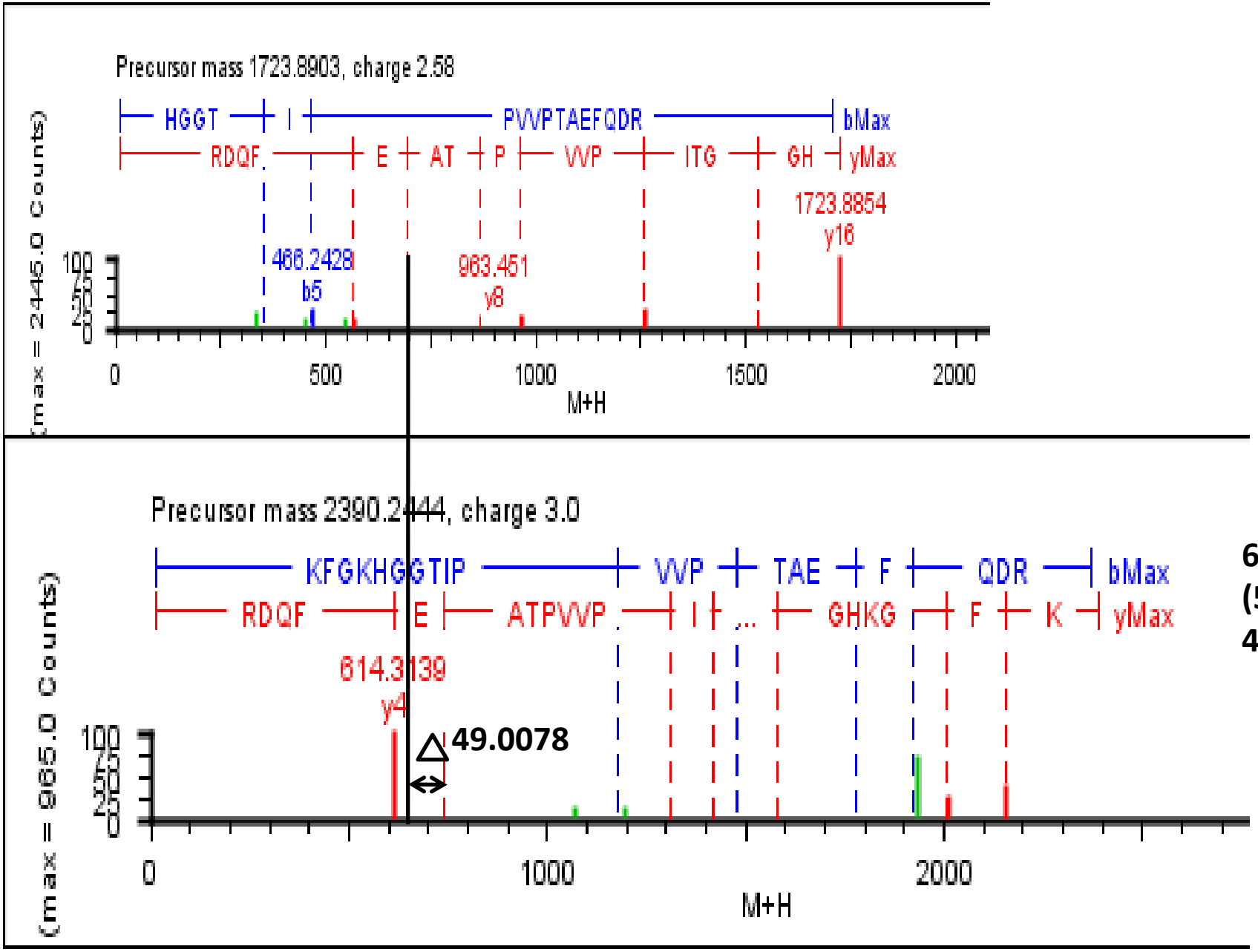
184-200 (K)AGVKINPKNYTDNELEK(Ubi)(I)



403.2613

655.3238: (403.26+ 252.11)

520-535 (R)QIMRTAMKYNLGLDLR(Crossline)(T)

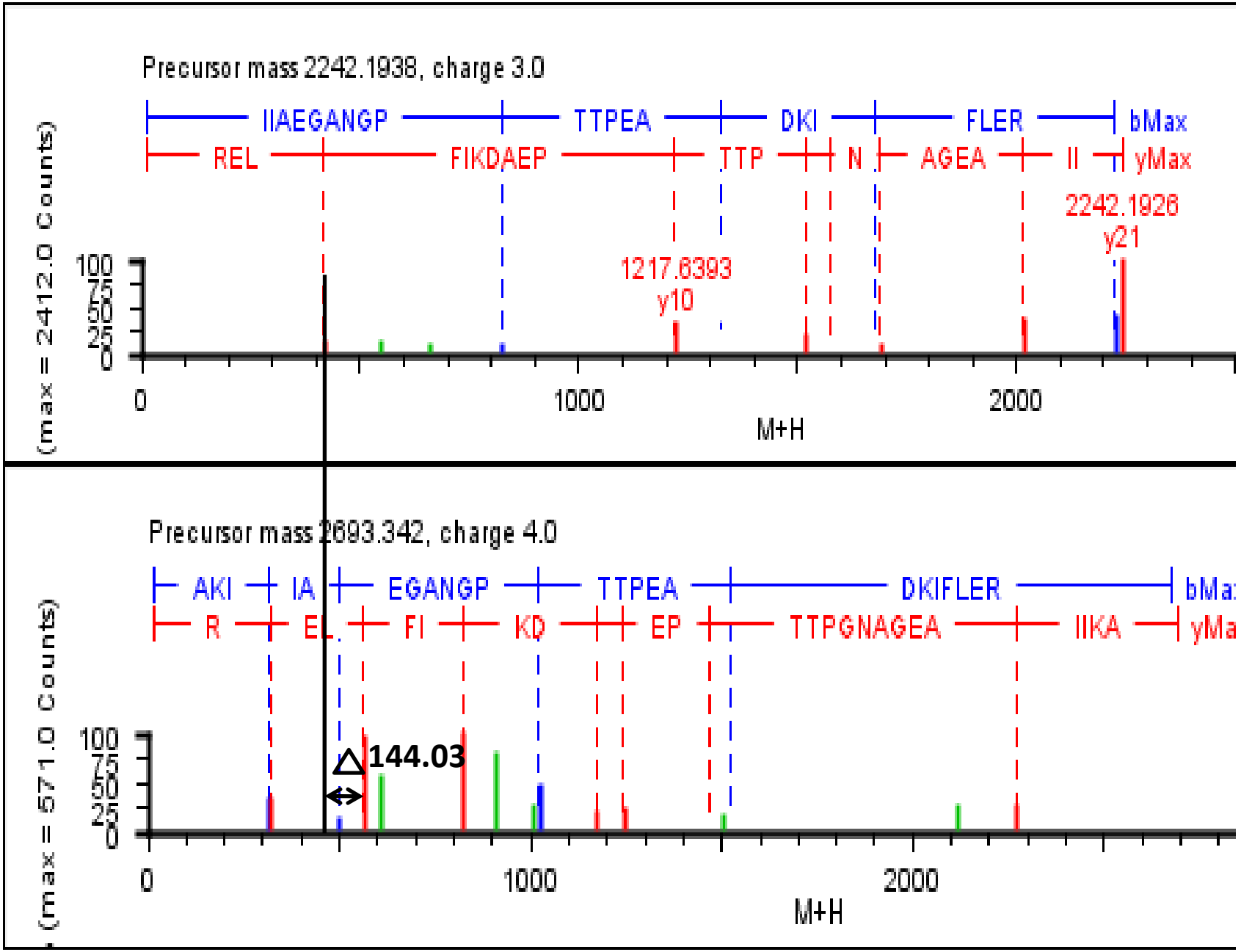


565.2727

614.3139: (565.27+ 49.00)

477-496

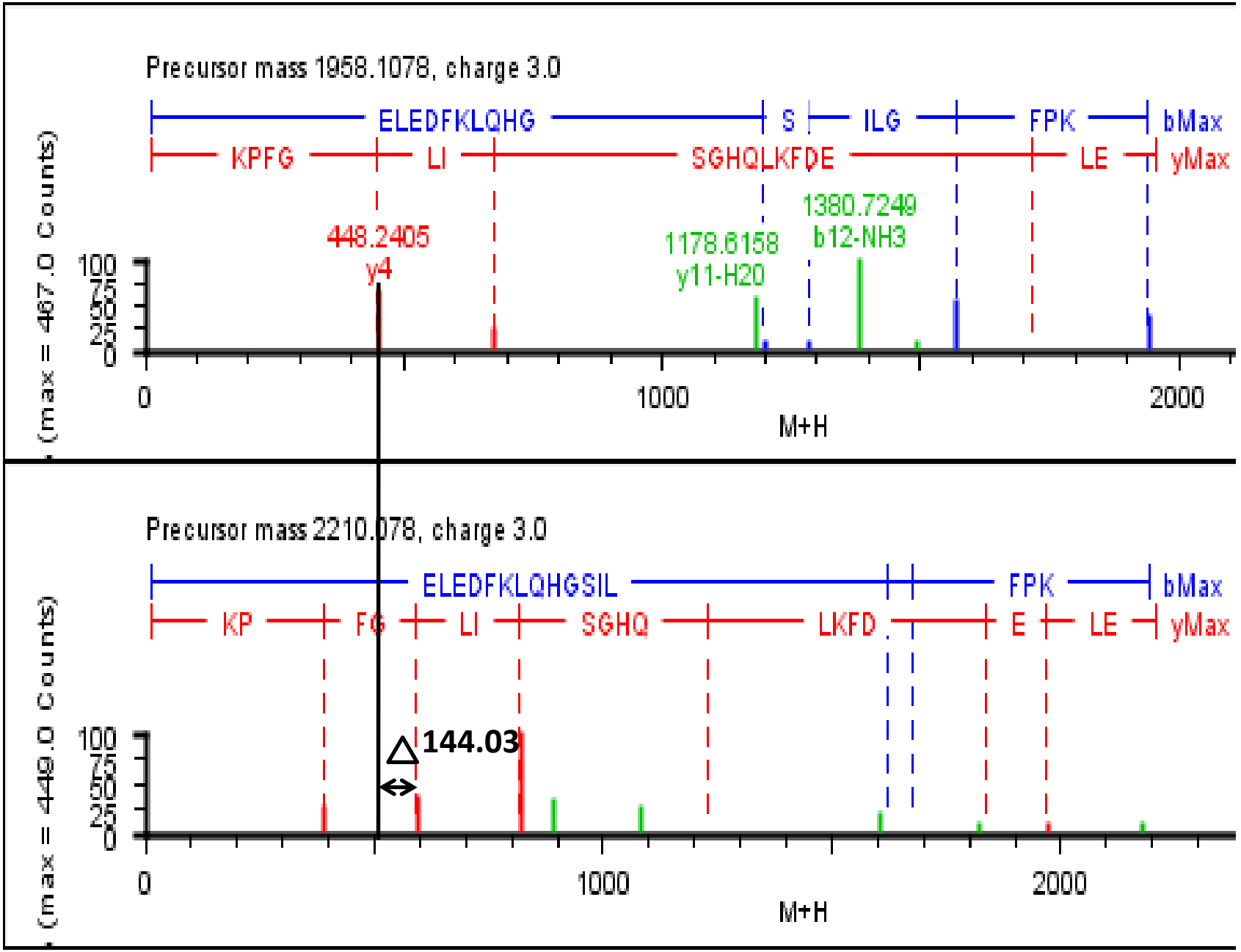
(R)KFGKHGGTIPVVPTAEFQDR(MOLD)(I)



417.234

561.2697: (417.23+ 144.03)

400-420 (K)IIAEGANGPTTPEADKIFLER(ImiA)(N)

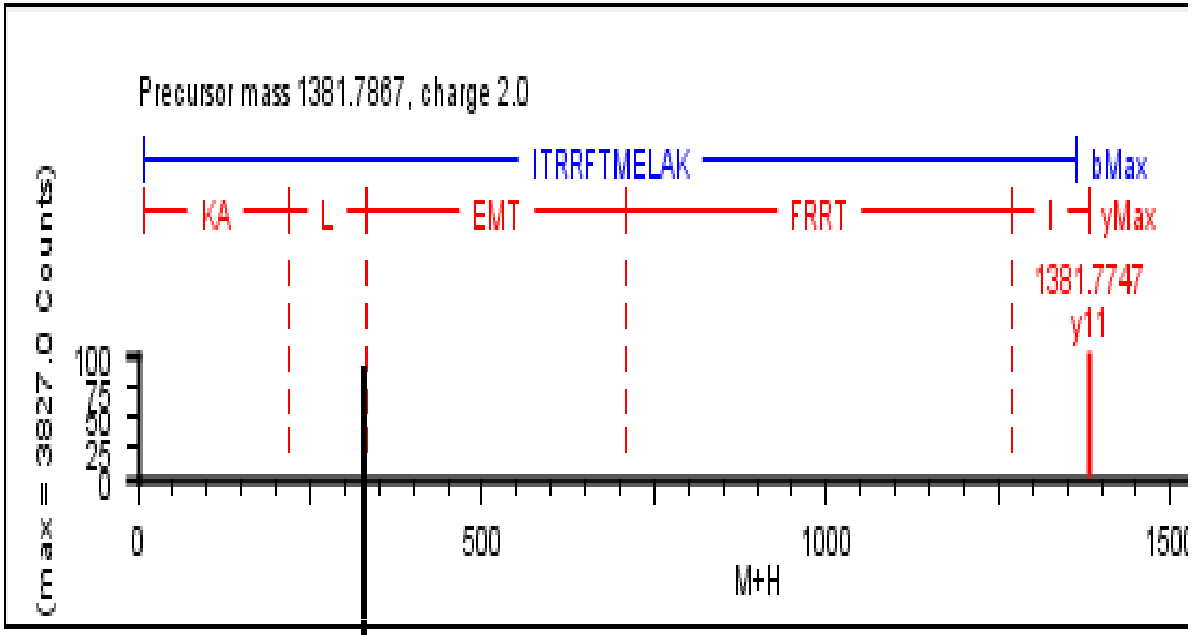


448.2405

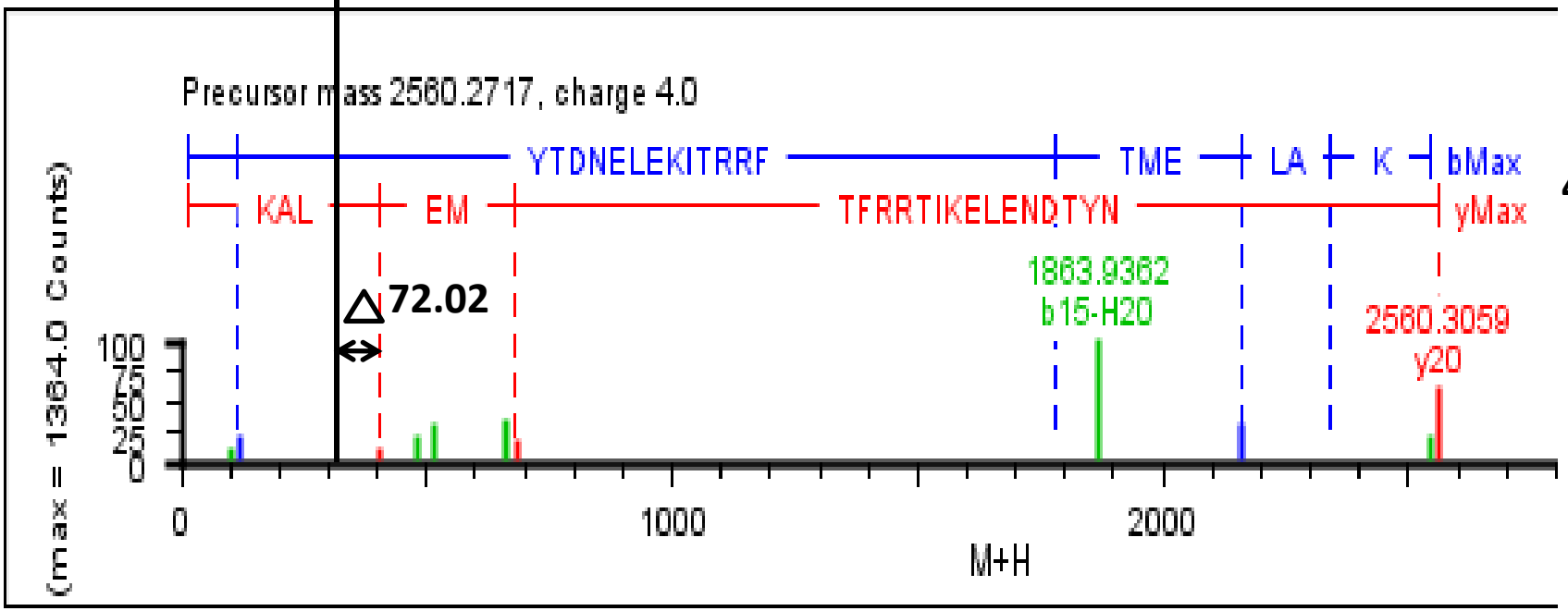
592.2623: (448.24+ 144.03)

(K)ELEDFKLQHGSILGFPK(ImiA)(A)

347-363



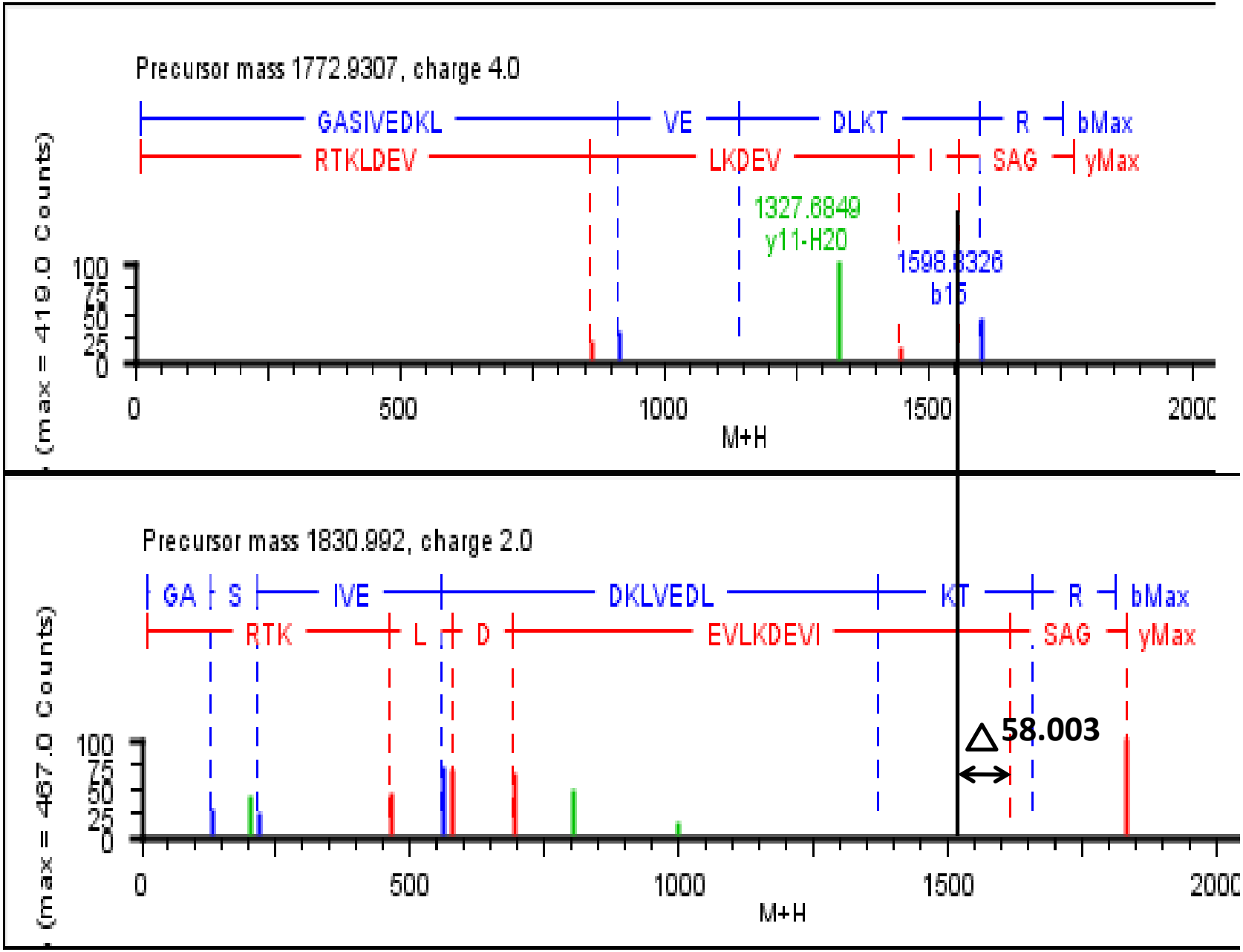
331.2295



403.2362

192-211

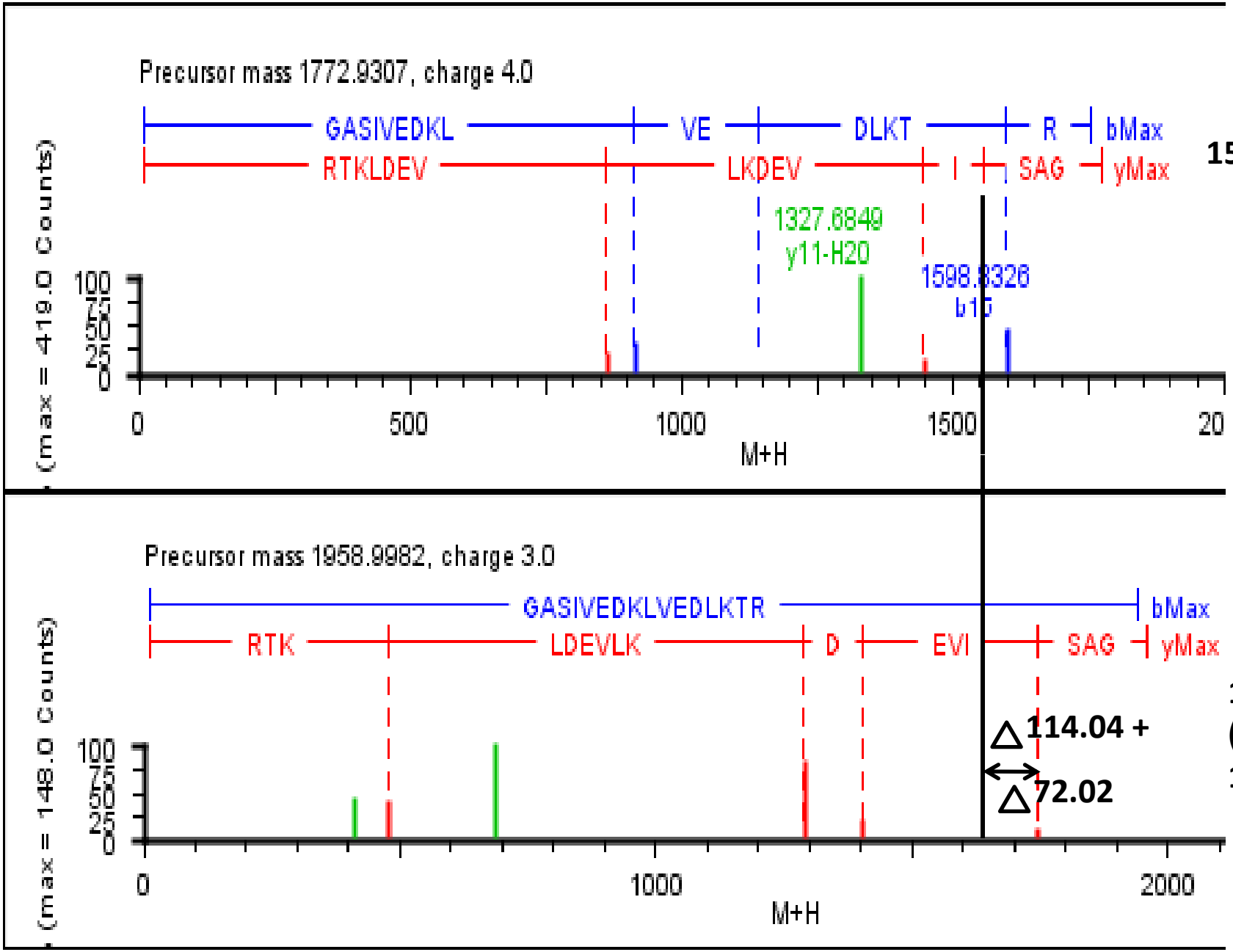
(K)NYTDNELEKITRRFTMELAK(CEL)(K)



1557.872

1615.7312: (1557.87+ 58.003)

77-92 (R)GASIVEDKLVEDLK(CML)TR(E)



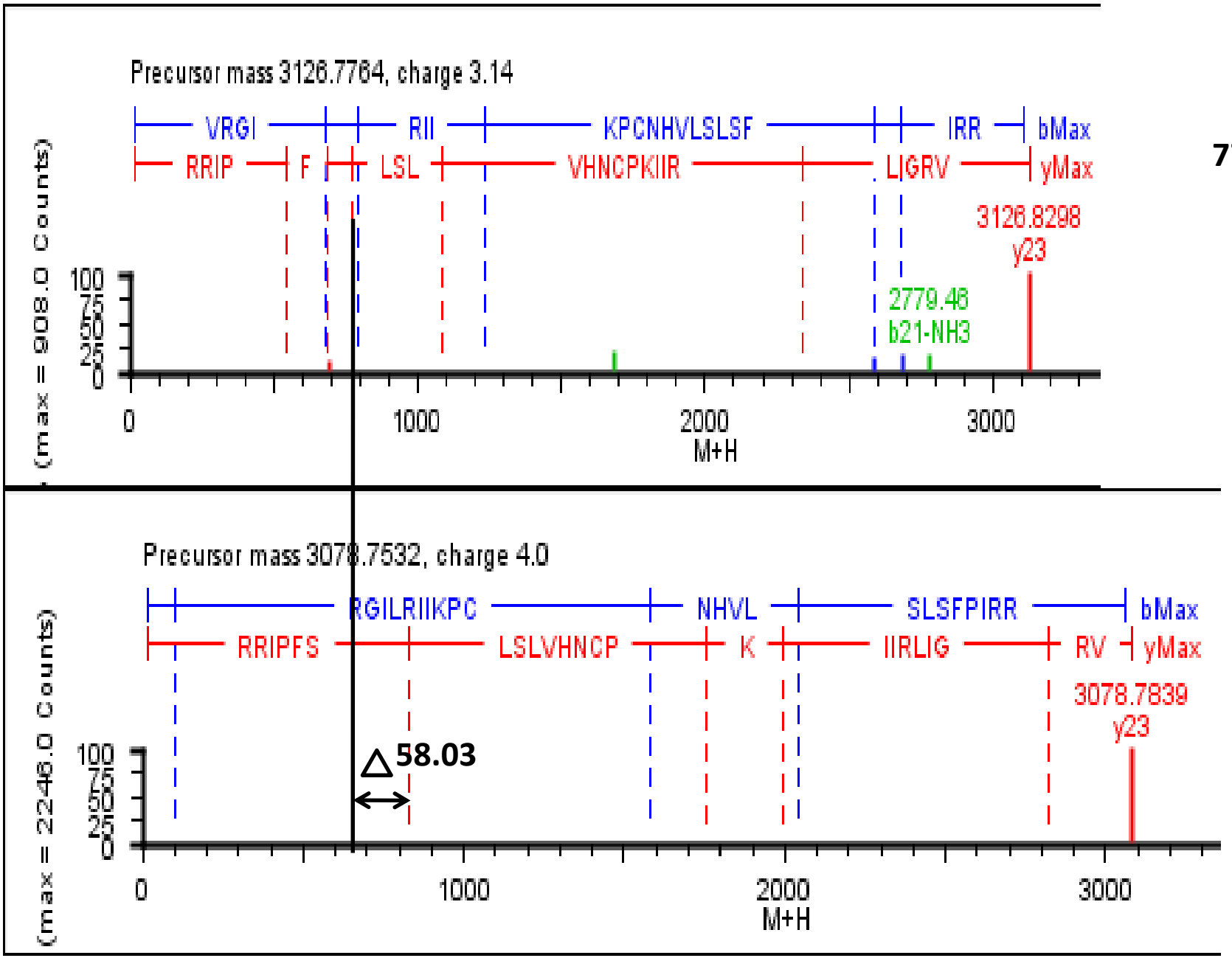
1557.8727

Δ114.04 +

Δ72.02

1744.0854:
(1557.8727+
144.04+
72.02)

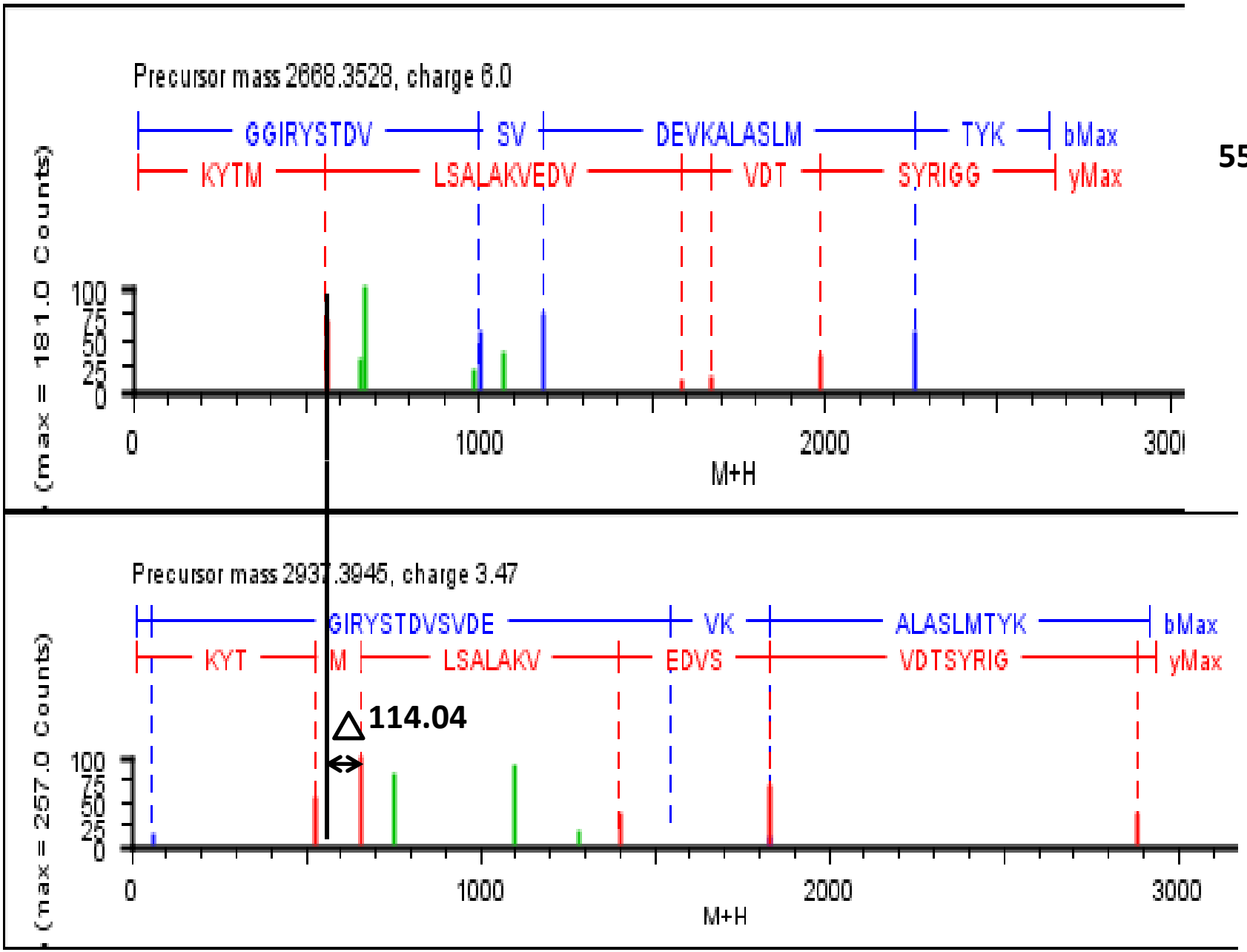
77-92 (R)GASIVEDK(Ubi)LVEDLK(CEL)TR(E)



775.4271

833.4669: (775.42+ 58.03)

102-124 (R)VRGILRIIKPCNHVLSLSFPIRR(Pento)(D)

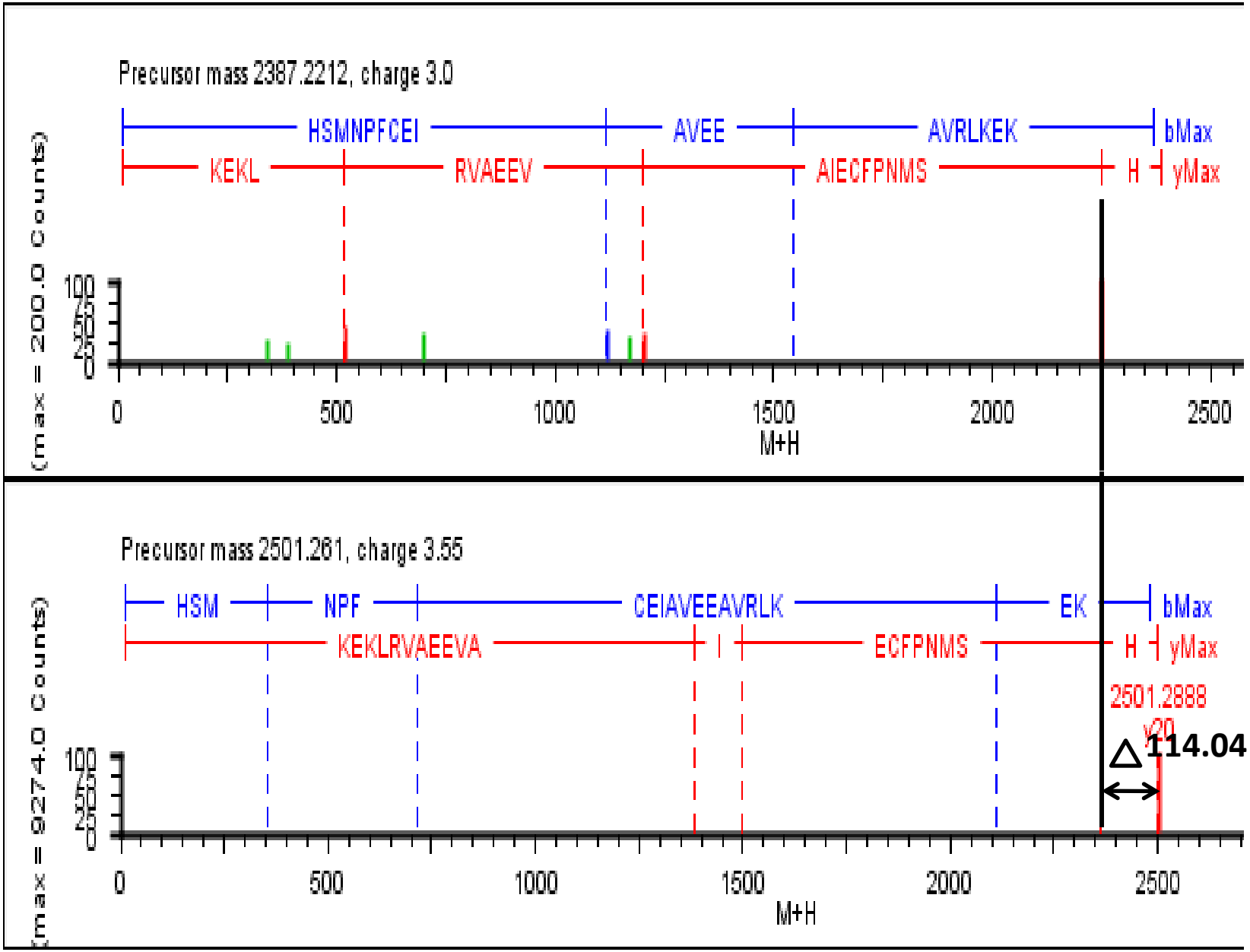


558.2449

656.3623: (558.24+ 114.04)

148-171 (K)GGIRYSTDVSVDEVKALASLMTYK(Ubi)(C)

eTFP



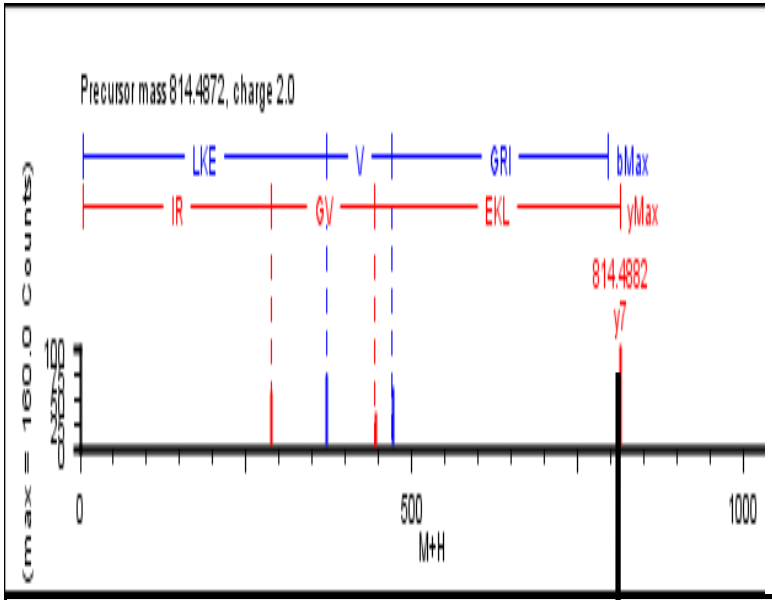
2250.1228

2364.1572: (2250.12+ 114.04)

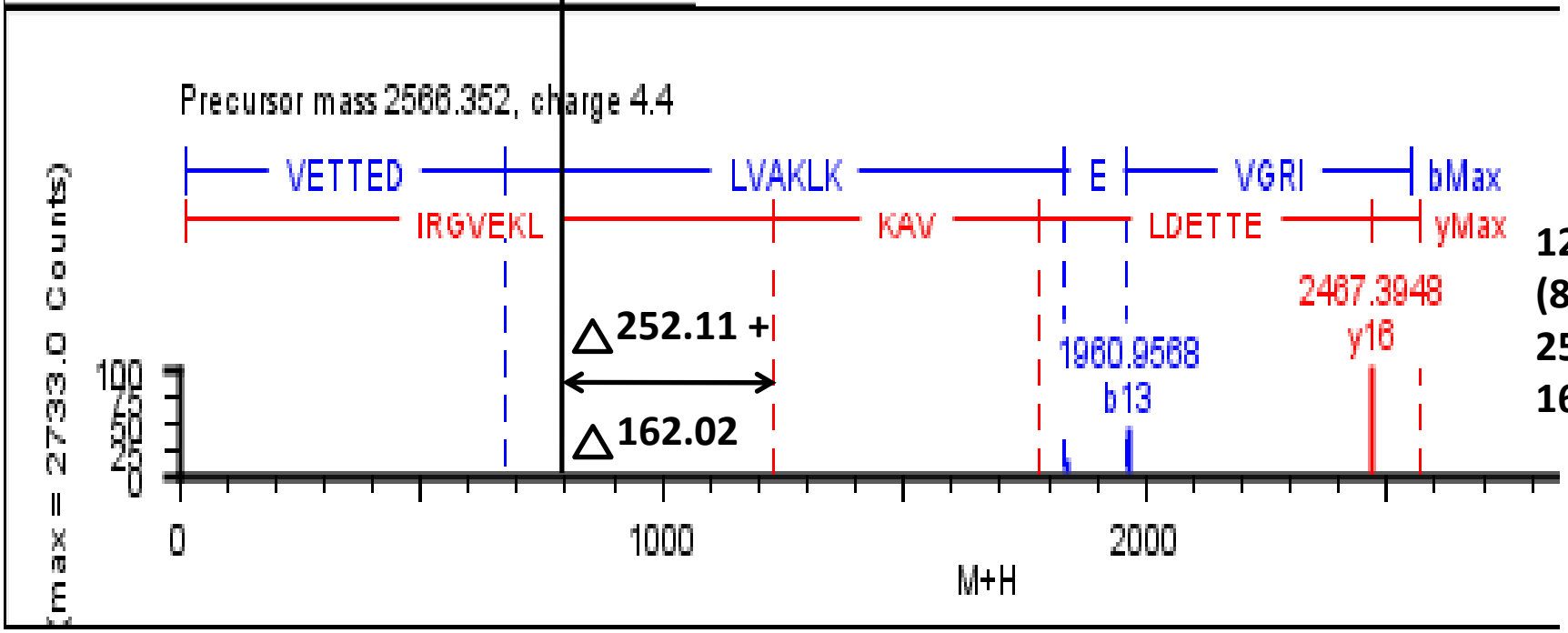
Δ 114.04 +

36-55

(K)HSMNPFCEIAVEEAVRLKEK(Ubi)(K)

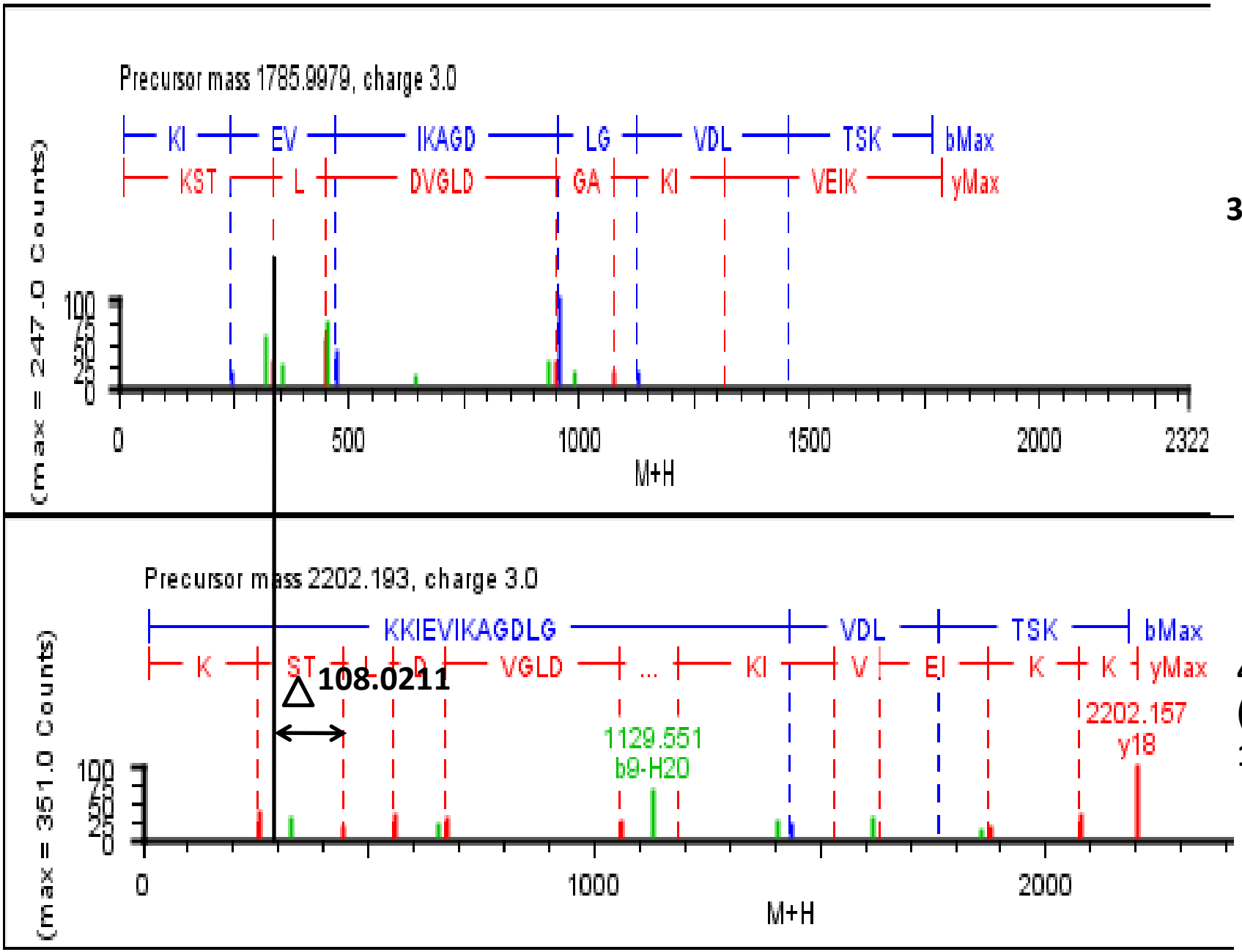


814.4882

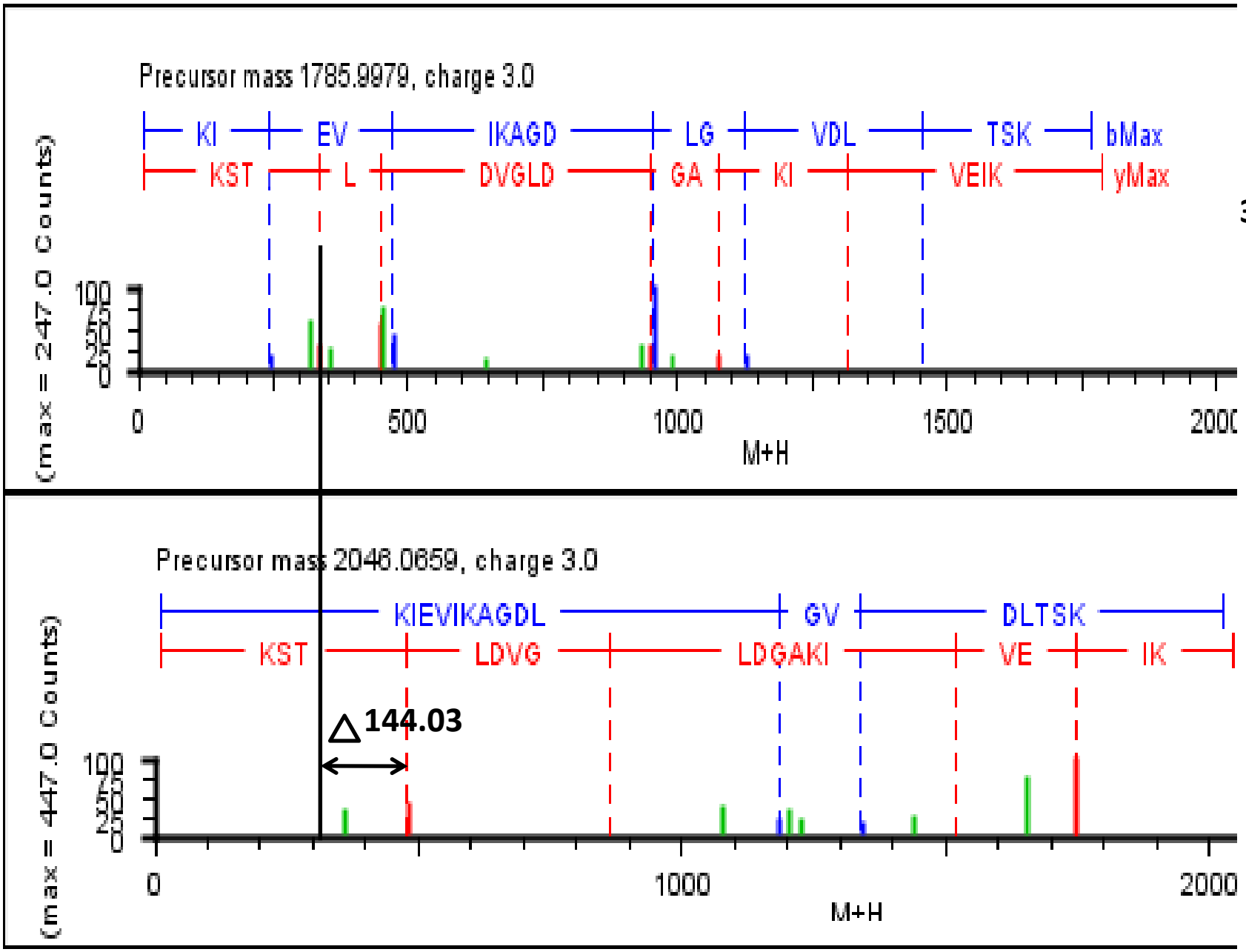


1228.5914: (814.48+ 252.11+ 162.02)

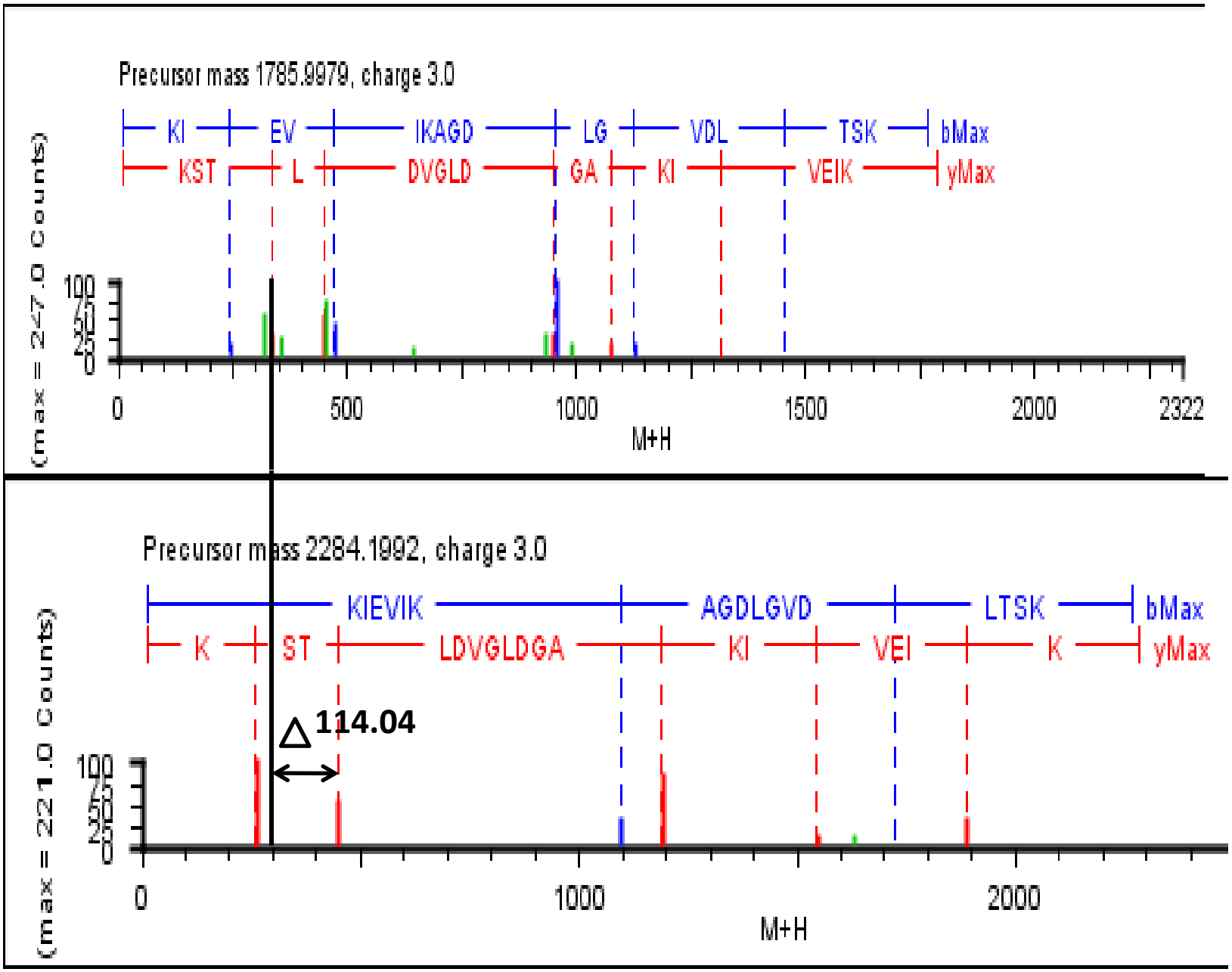
239-255 (K)VETTEDLVAKLK(Crossline)EVGR(Gly)I(-)



204-221 (K)KKIEVIKAGDLGVDLTSK(Pyr)(V)



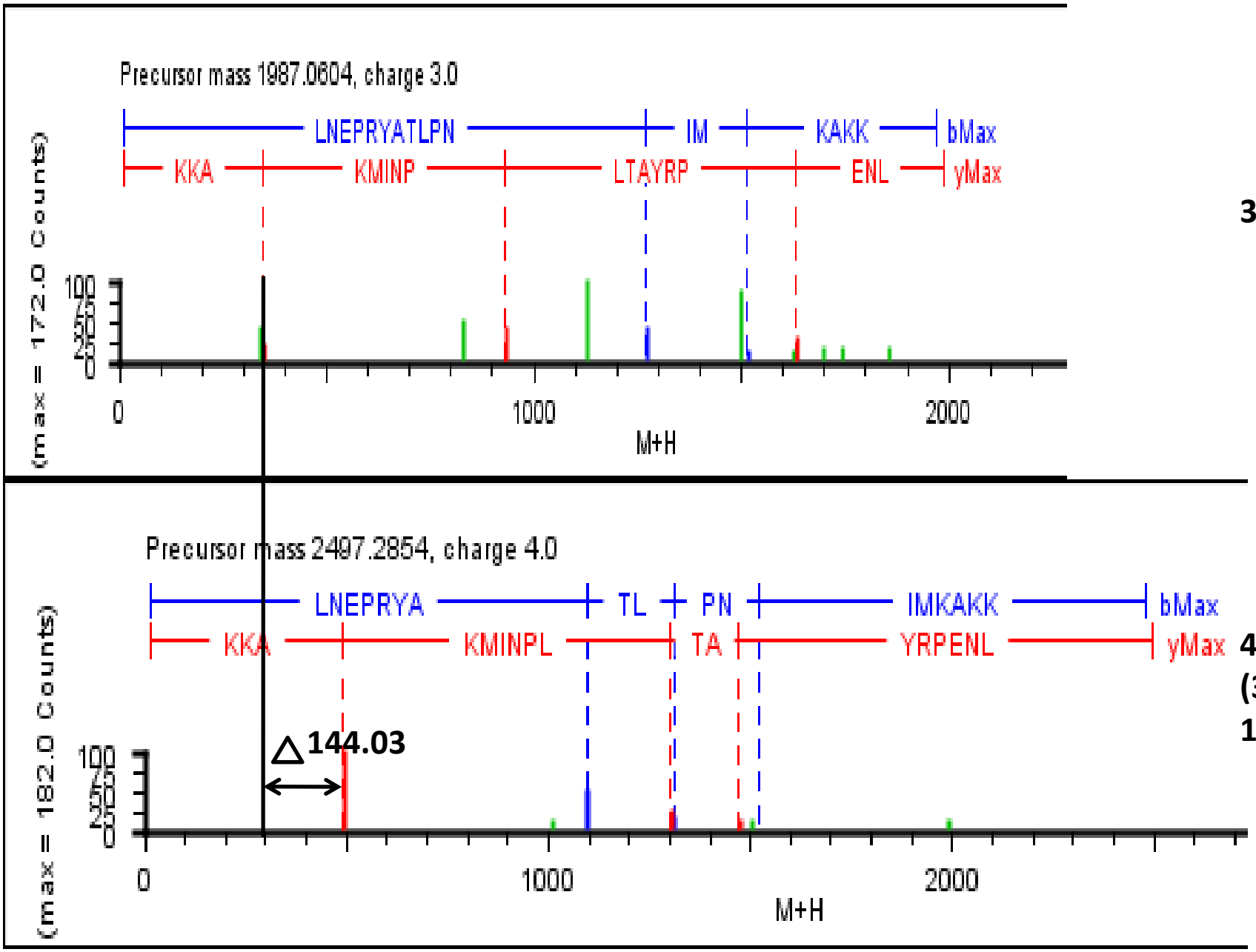
205-221 (K)KIEVIKAGDLGVDLTSK(ImiA)(V)



335.1796

449.1928: (3335.17+ 114.04)

205-221 (K)KIEVIKAGDLGVDLTSK(Ubi)(V)

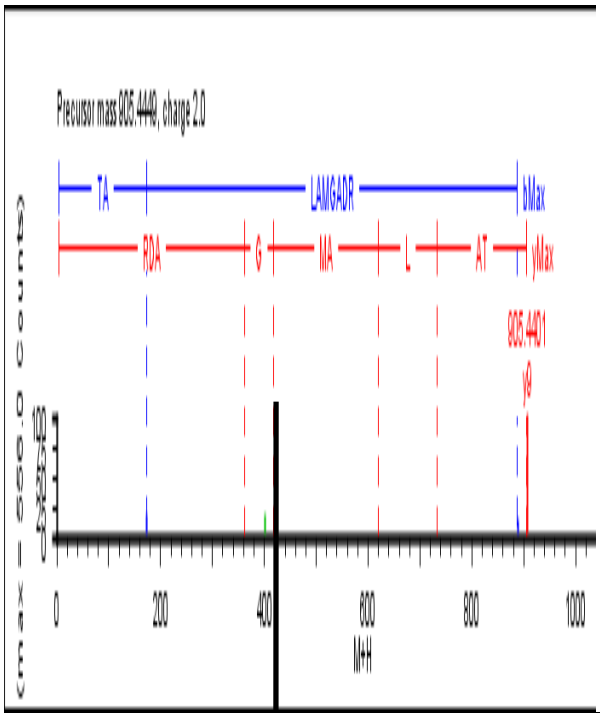


346.2521

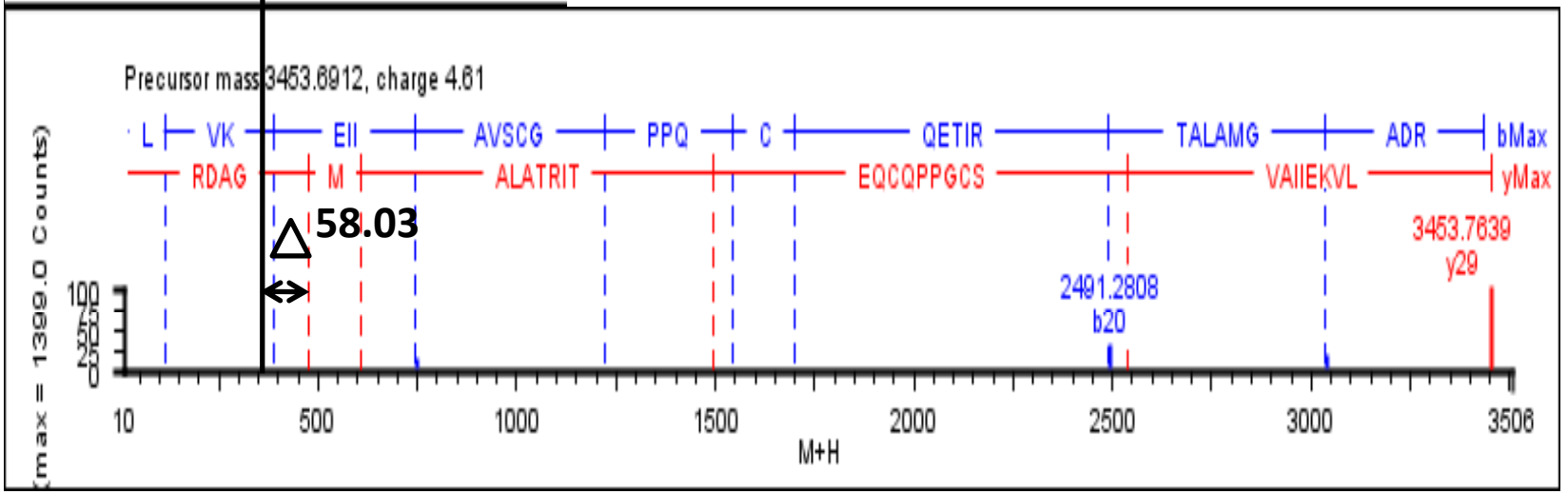
490.2319: (346.25+ 144.03)

187-203

(R)LNEPRYATLPNIMKAK(ImiA)K(K)

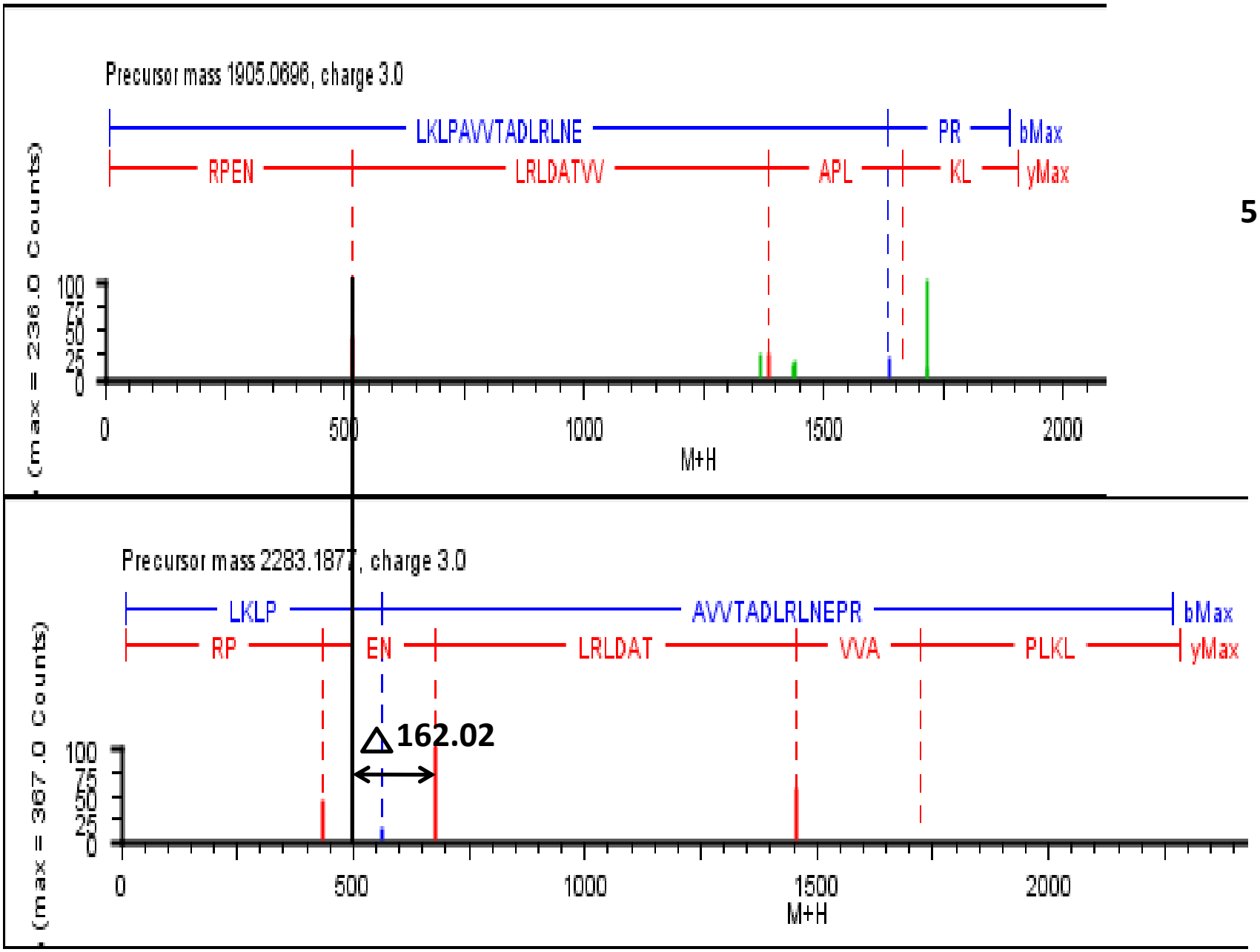


418.1695



476.2495: (418.16+ 58.03)

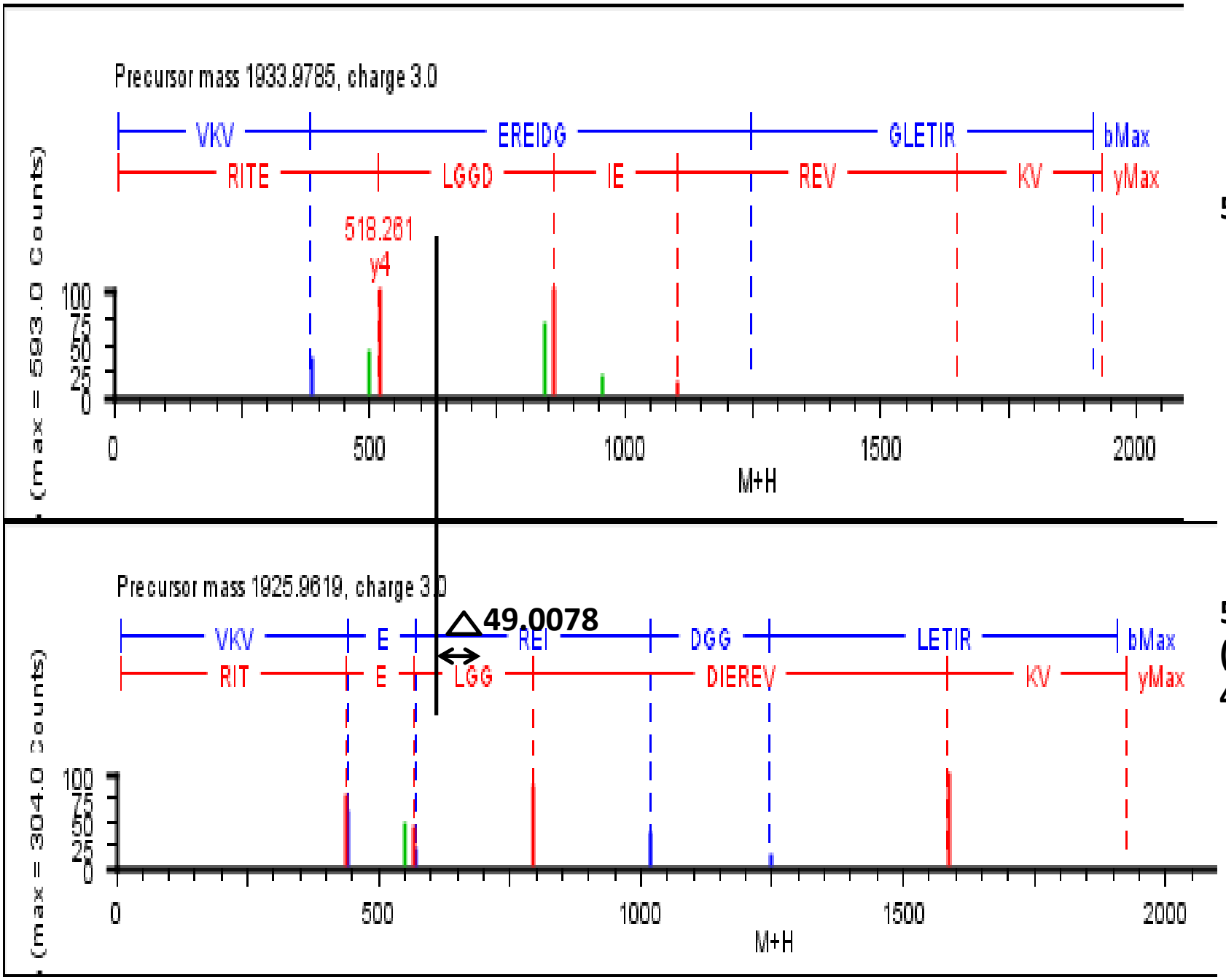
57-85 (K)LVKEIIAVSCGPPQCQETIRTALAMGADR(Pento)(G)



515.2375

677.3167: (515.23+ 162.02)

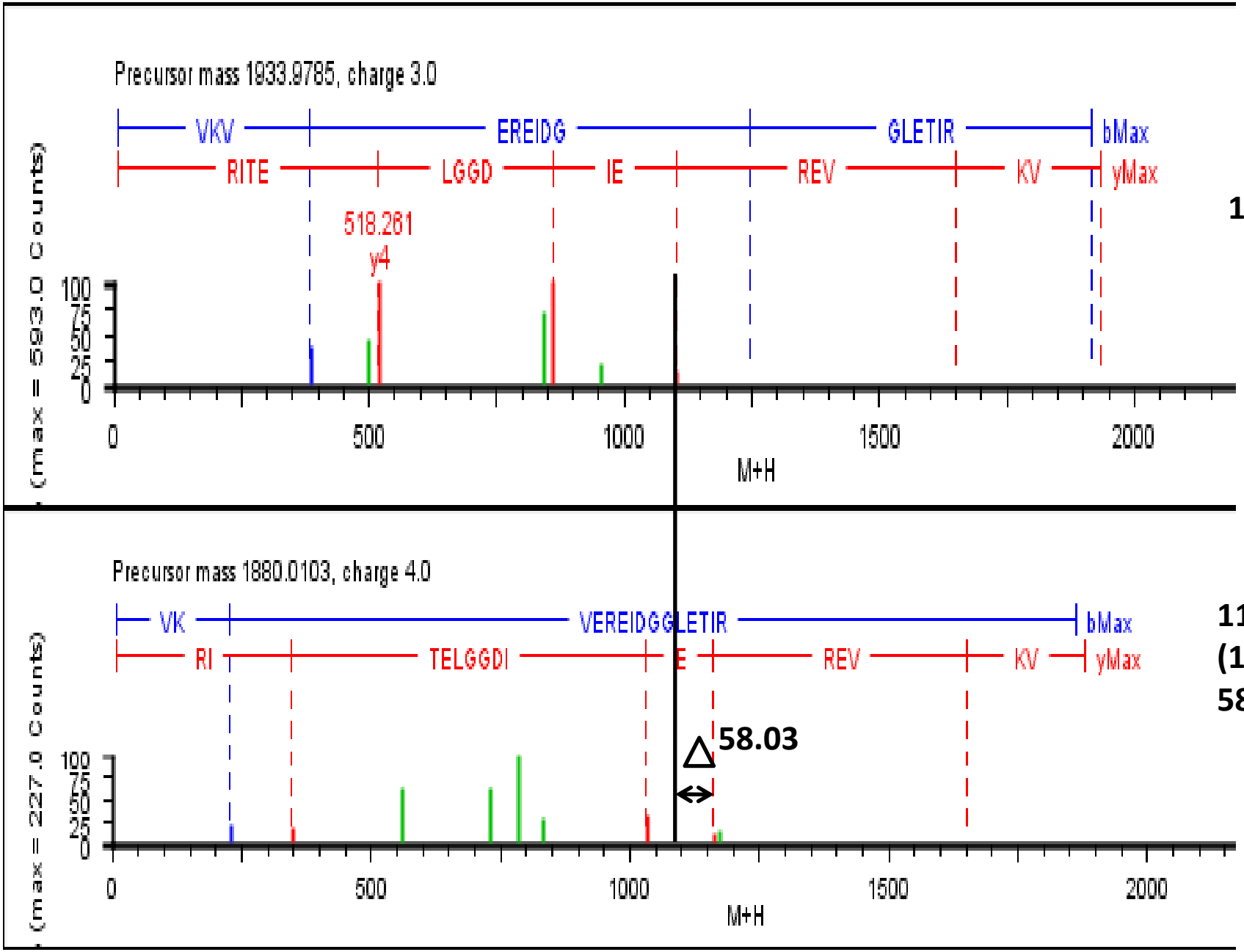
175-191 (R)LKLPAVVTADLRLNEPR(Gly)(Y)



518.261

567.3021: (518.26+ 49.00)

160-174 (K)VKVEREIDGGLETIR(MOLD)(L)

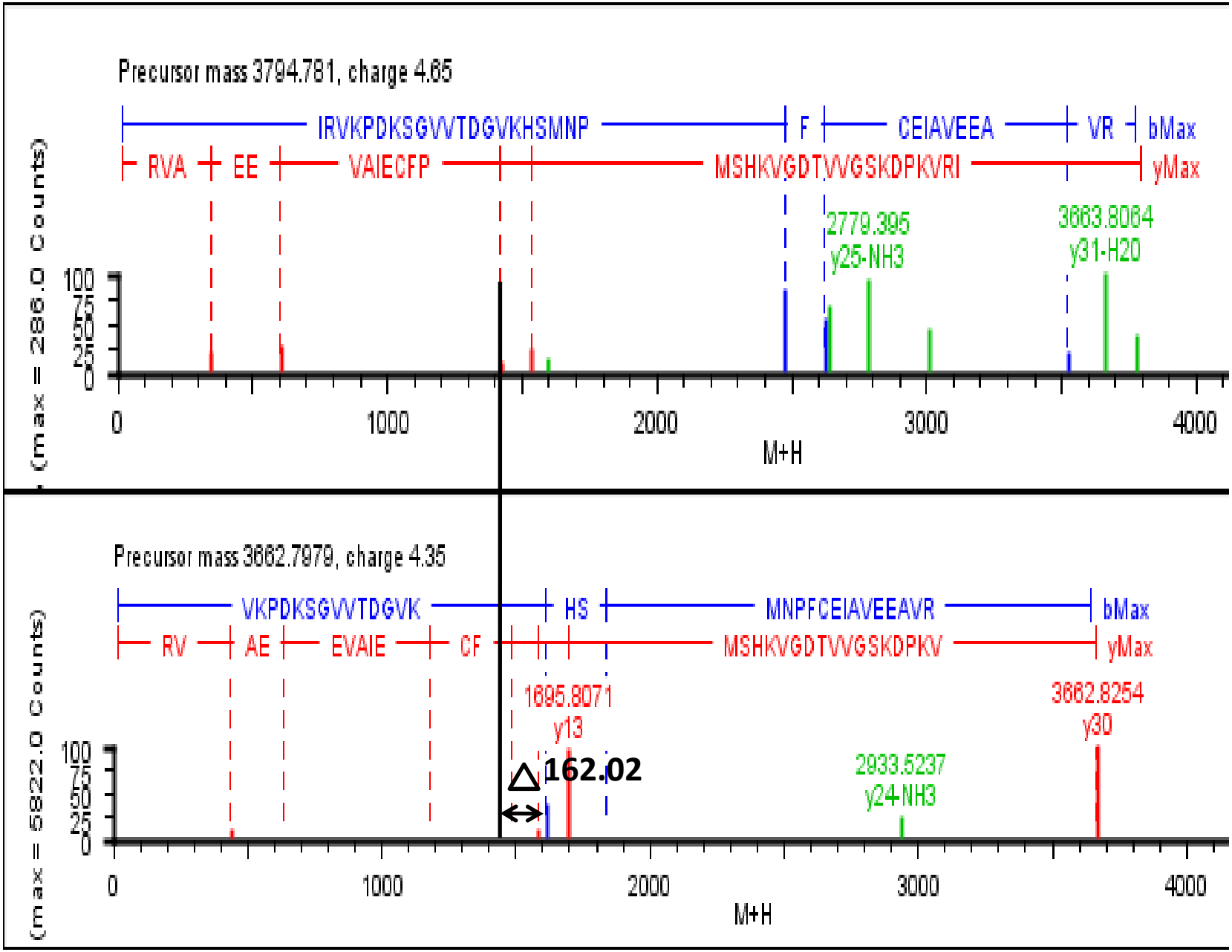


1102.5507

1160.5115: (1102.55+ 58.03)

160-174

(K)VKVEREIDGGLETIR(Pento)(L)

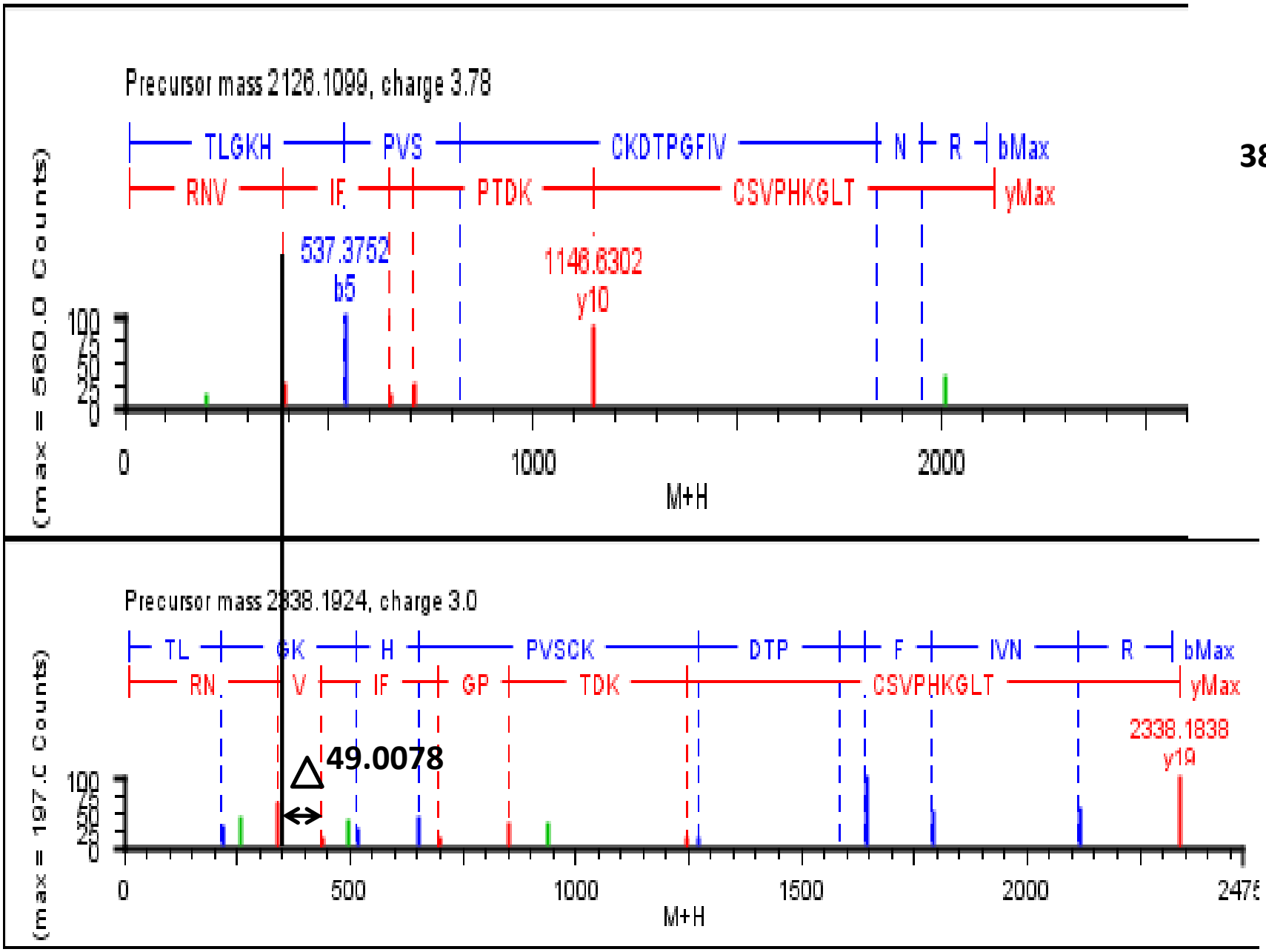


1419.7747

1581.7728: (1419.77+ 162.02)

22-51 (R)VKPDKSGVVTDGVKHSMNPFCEIAVEEAVR(Gly)(L)

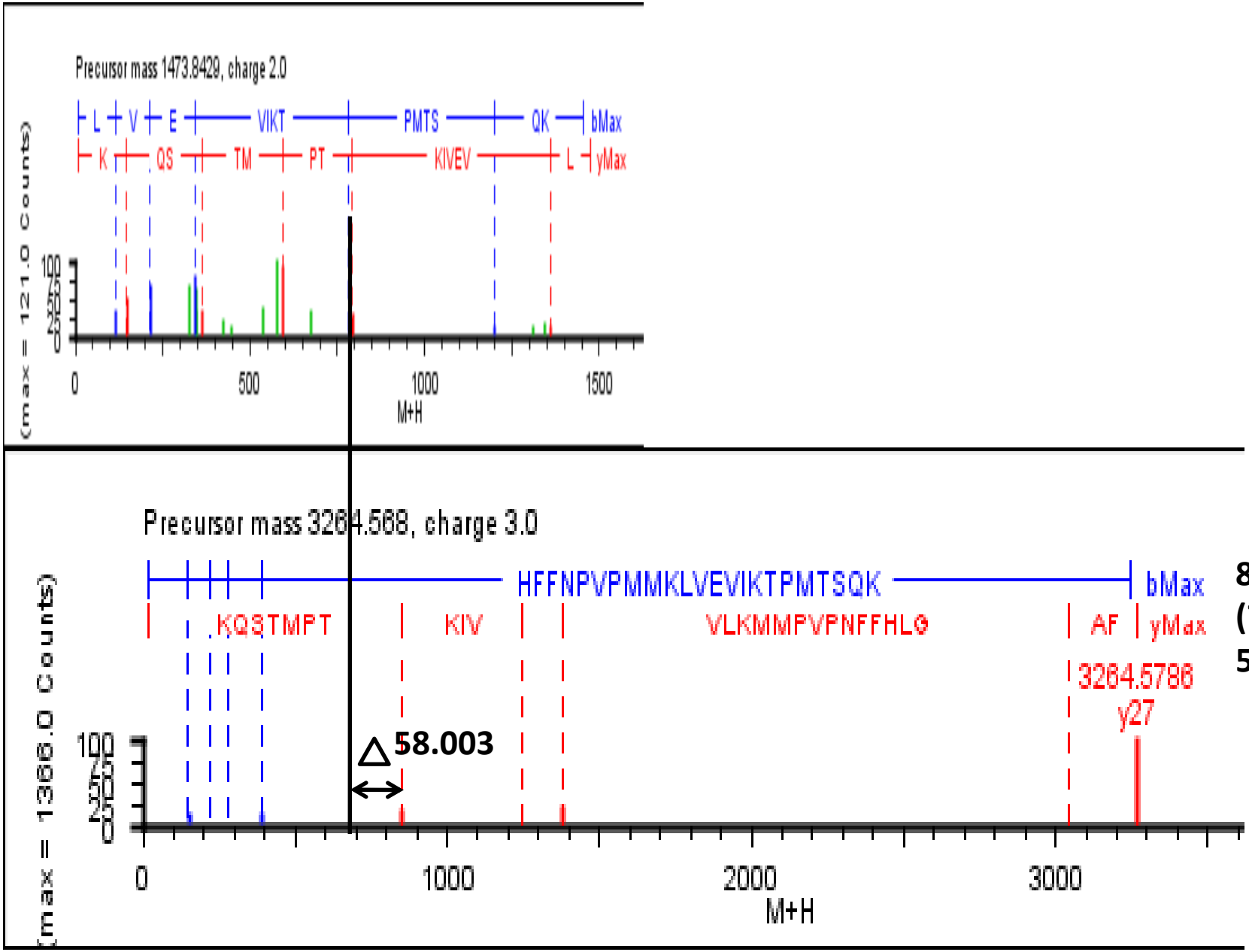
Hydroxy Acyl Co A



388.2265

437.2614: (388.22+ 49.00)

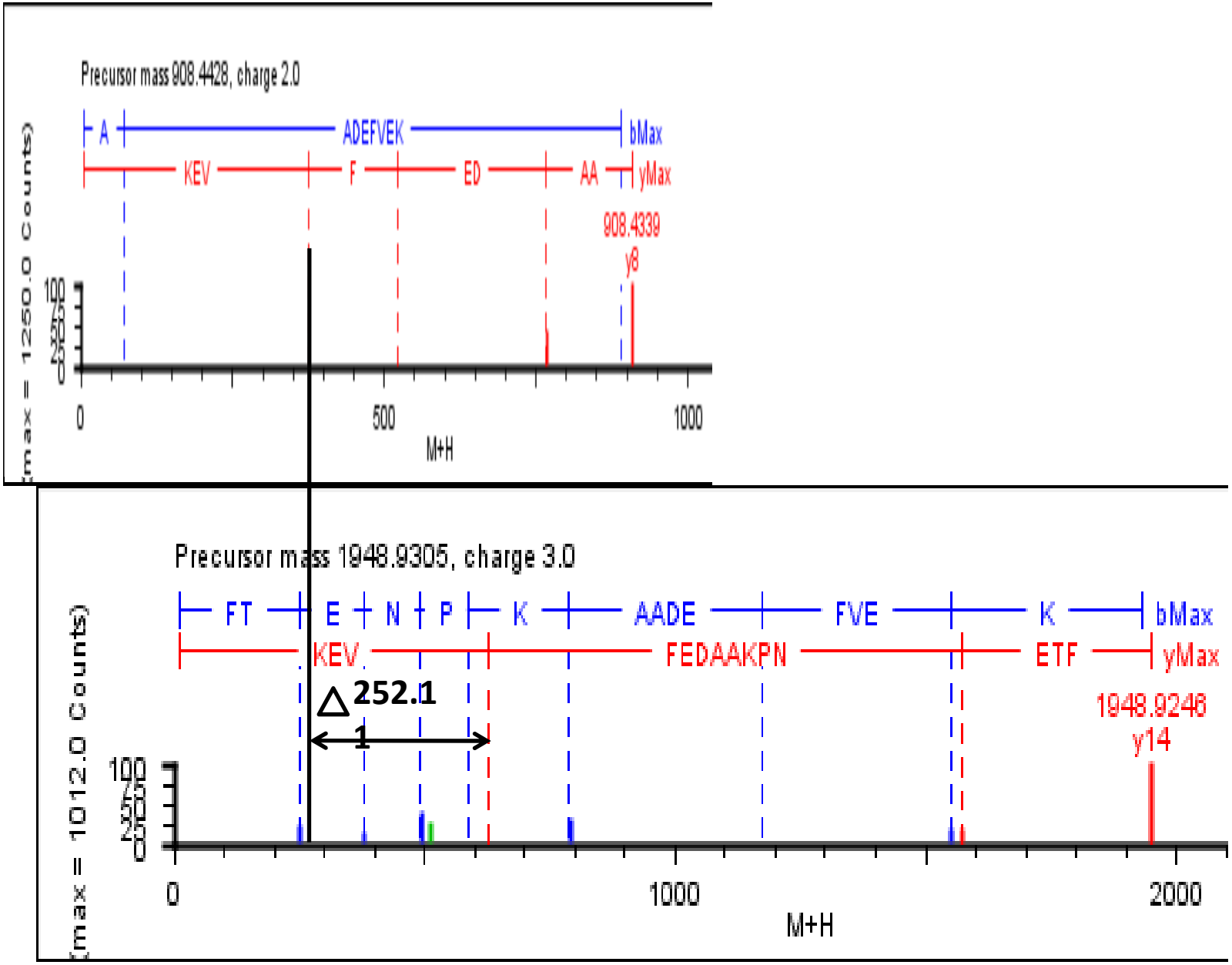
203-221 (K)TLGKHPVSCKDTPGFIVNR(MOLD)(L)



792.4211

850.4138: (792.42+ 58.003)

166-192 (R)FAGLHFFNPVPMMKLVEVIKTPMTSQK(CML)(T)

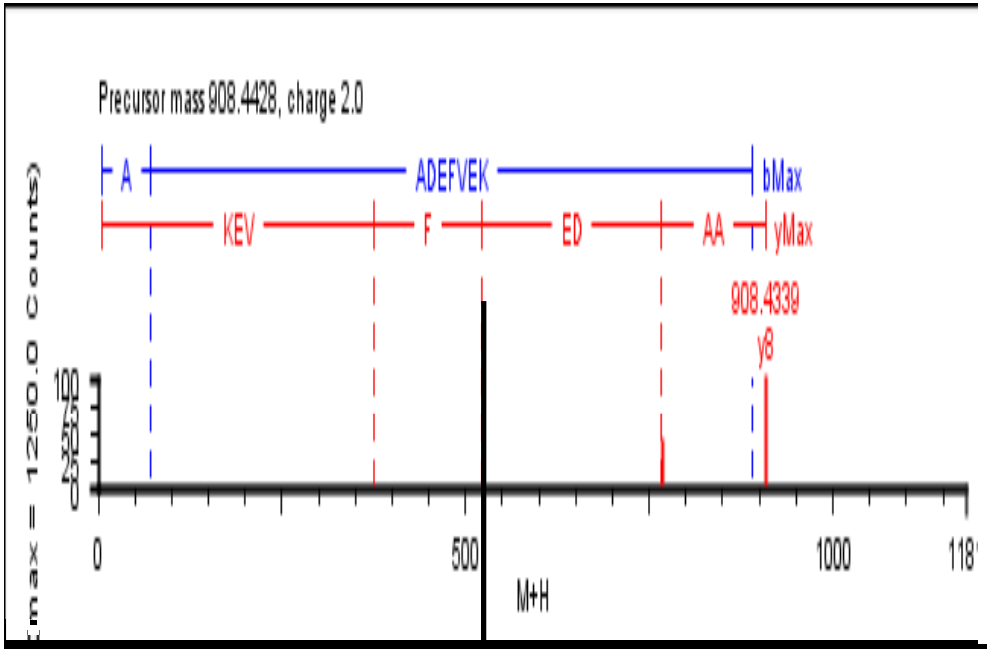


375.2369

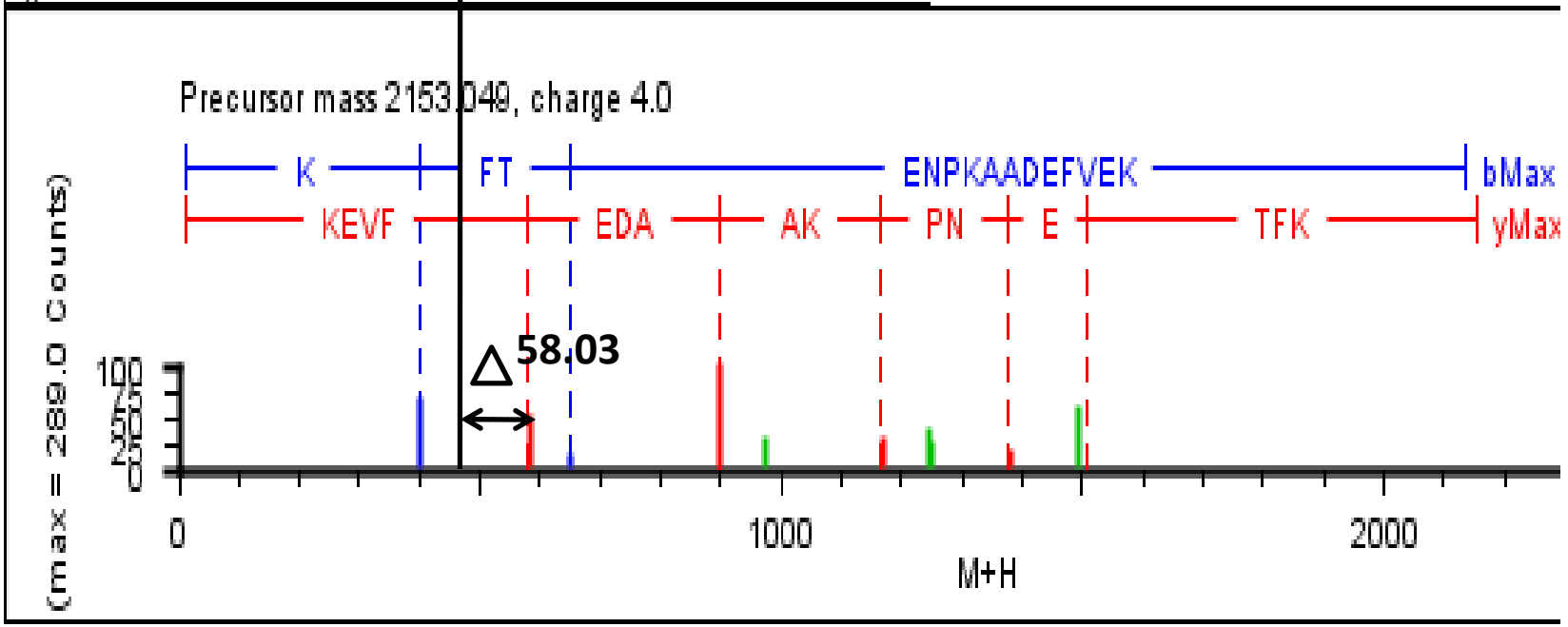
627.3756: (375.23+ 252.1)

82-95

(K)FTENPKAADEFVEK(Crossline)(T)

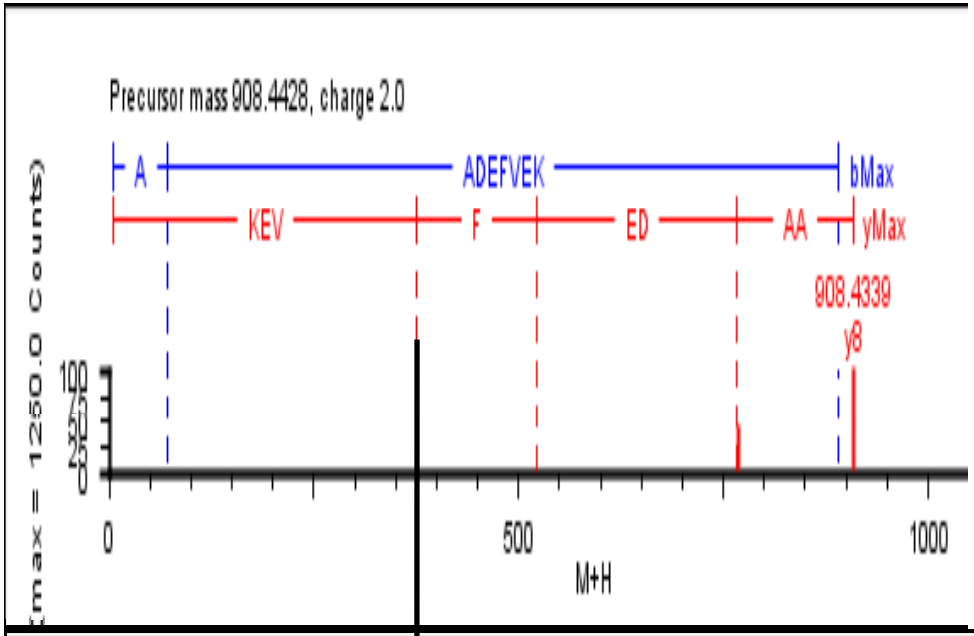


522.3075

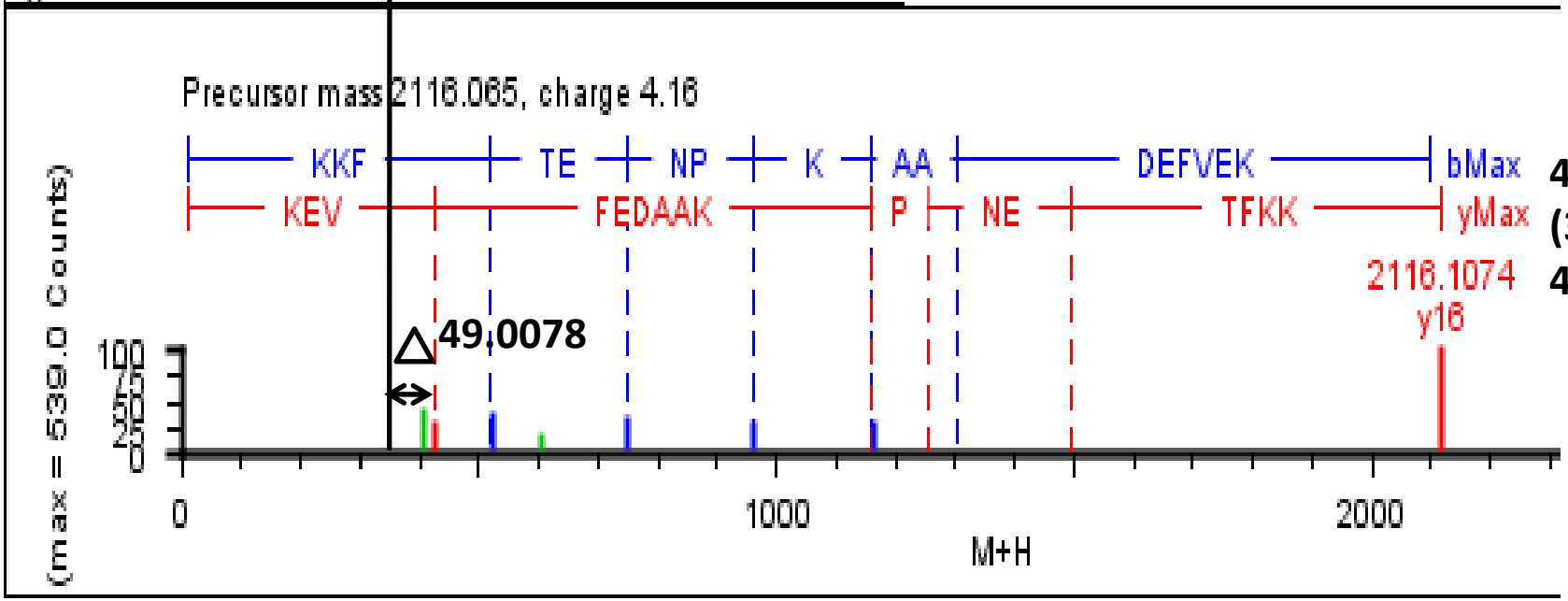


580.2976: (522.30+ 58.03)

81-95 (K)KFTENPKAADEFVEK(Pento)(T)

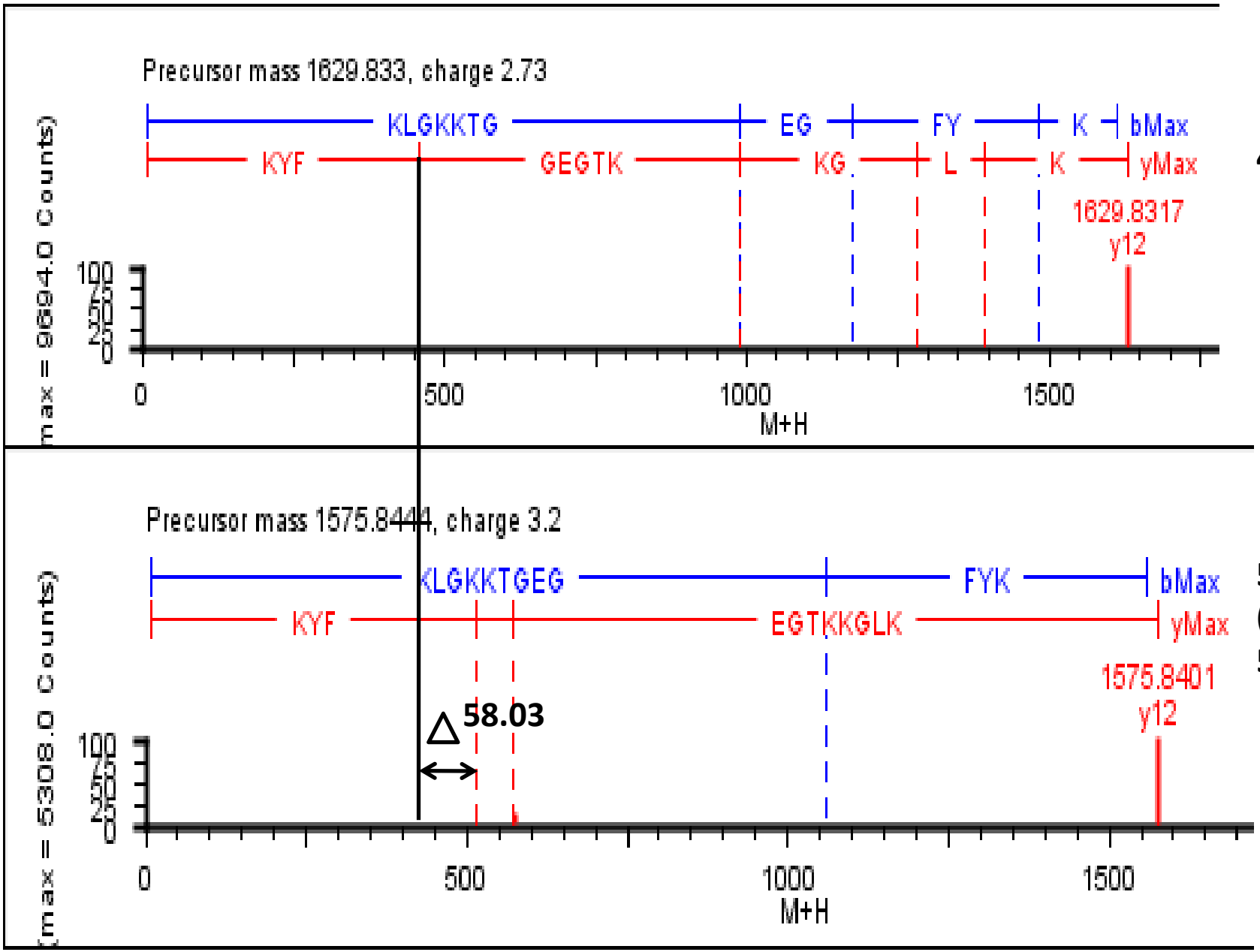


375.2369



424.2409: (375.23+ 49.00)

80-95 (K)KKFTENPKAADEFVEK(MOLD)(T)

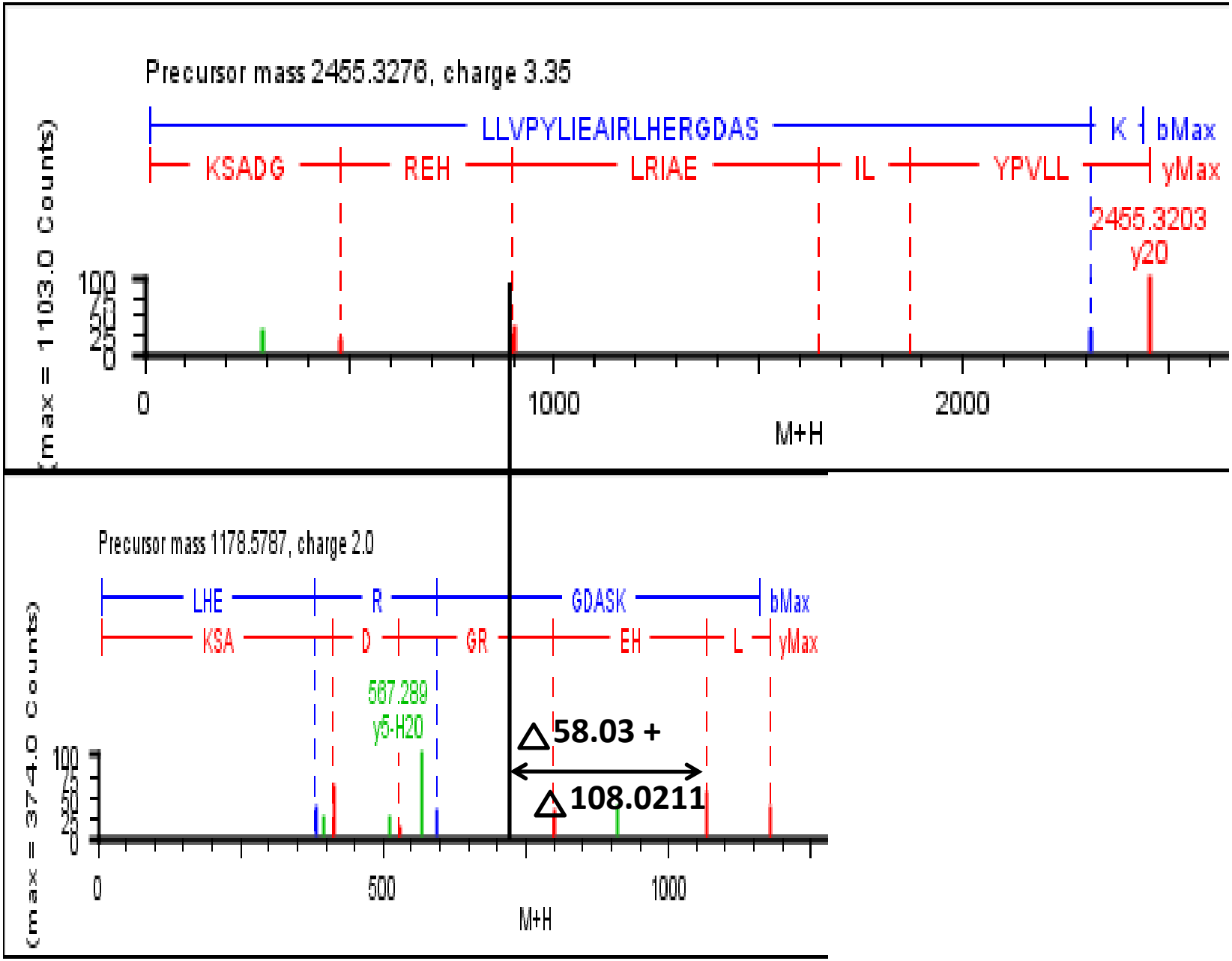


457.2186

515.2686: (457.21+ 58.03)

301-312

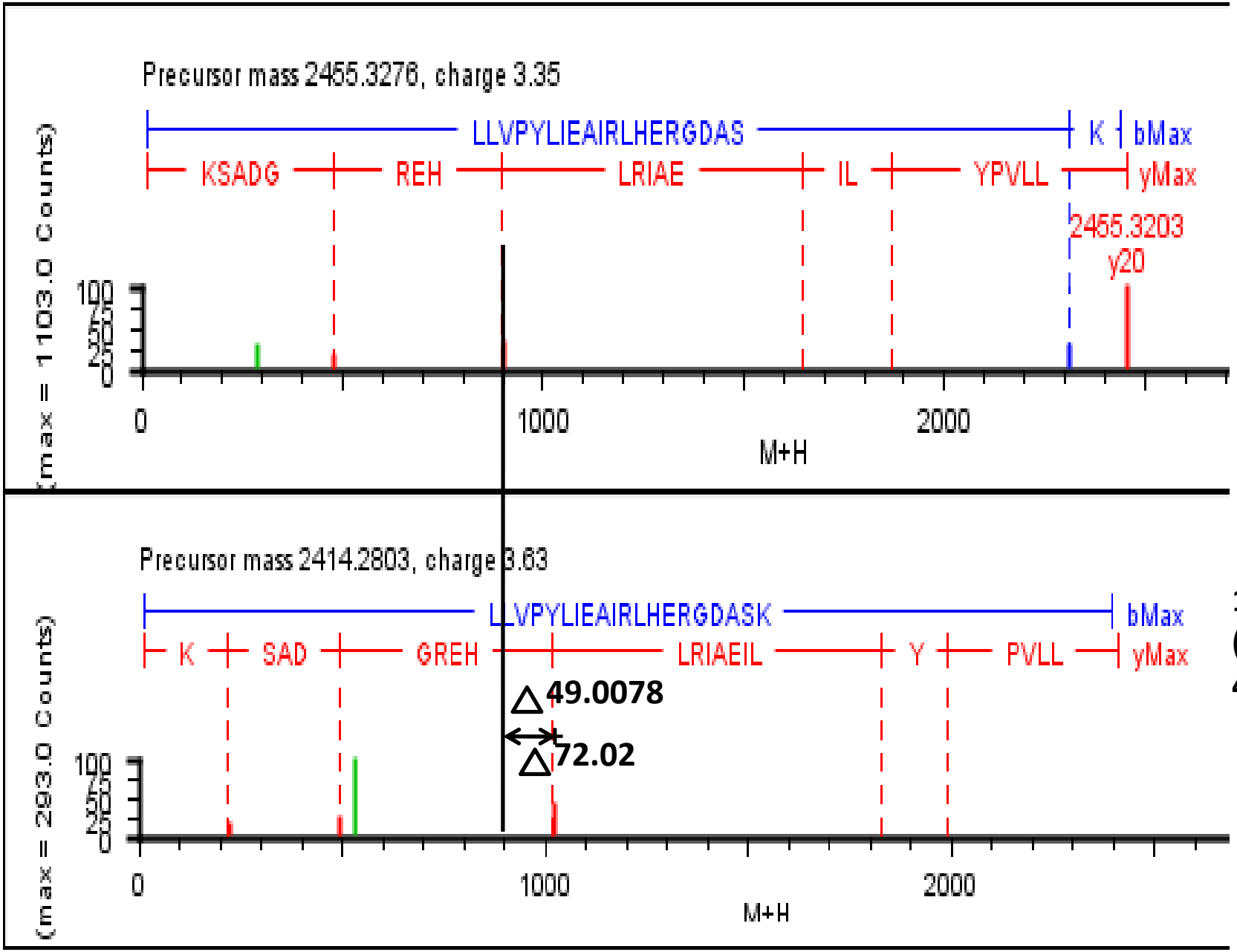
(K)KLGKKTGEGFYK(Pento)(Y)



899.45

1065: (899.45-58.03+ 108.0211)

233-241 (R)LHER(Pento)GDASK(Pyr)(E)

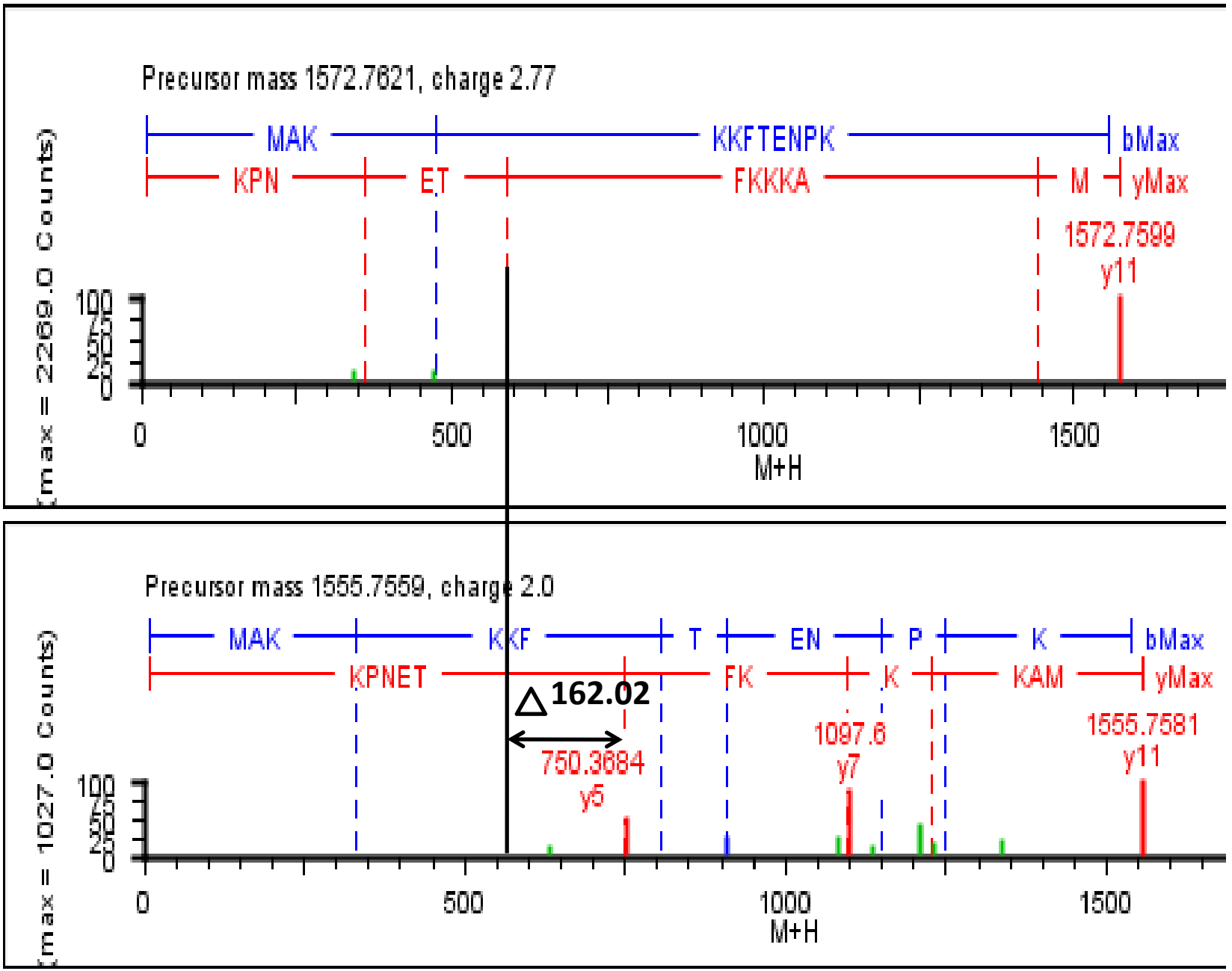


899.45

1020.5551: (899.45+ 49.00+ 72.02)

222-241

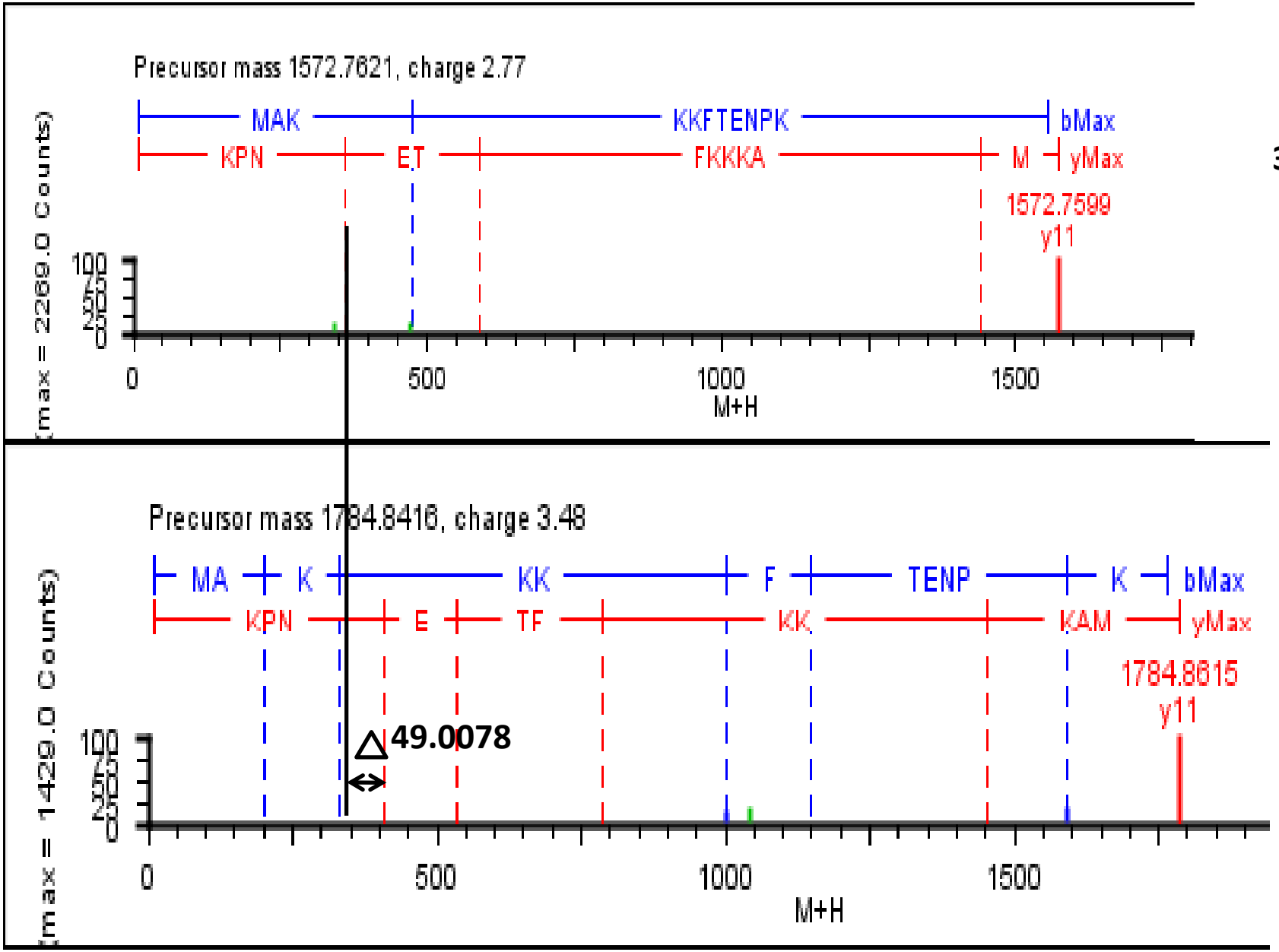
(R)LLVPYLIEAIRLHER(MOLD)GDASK(CEL)(E)



588.3188

750.3684: (588.32+ 162.02)

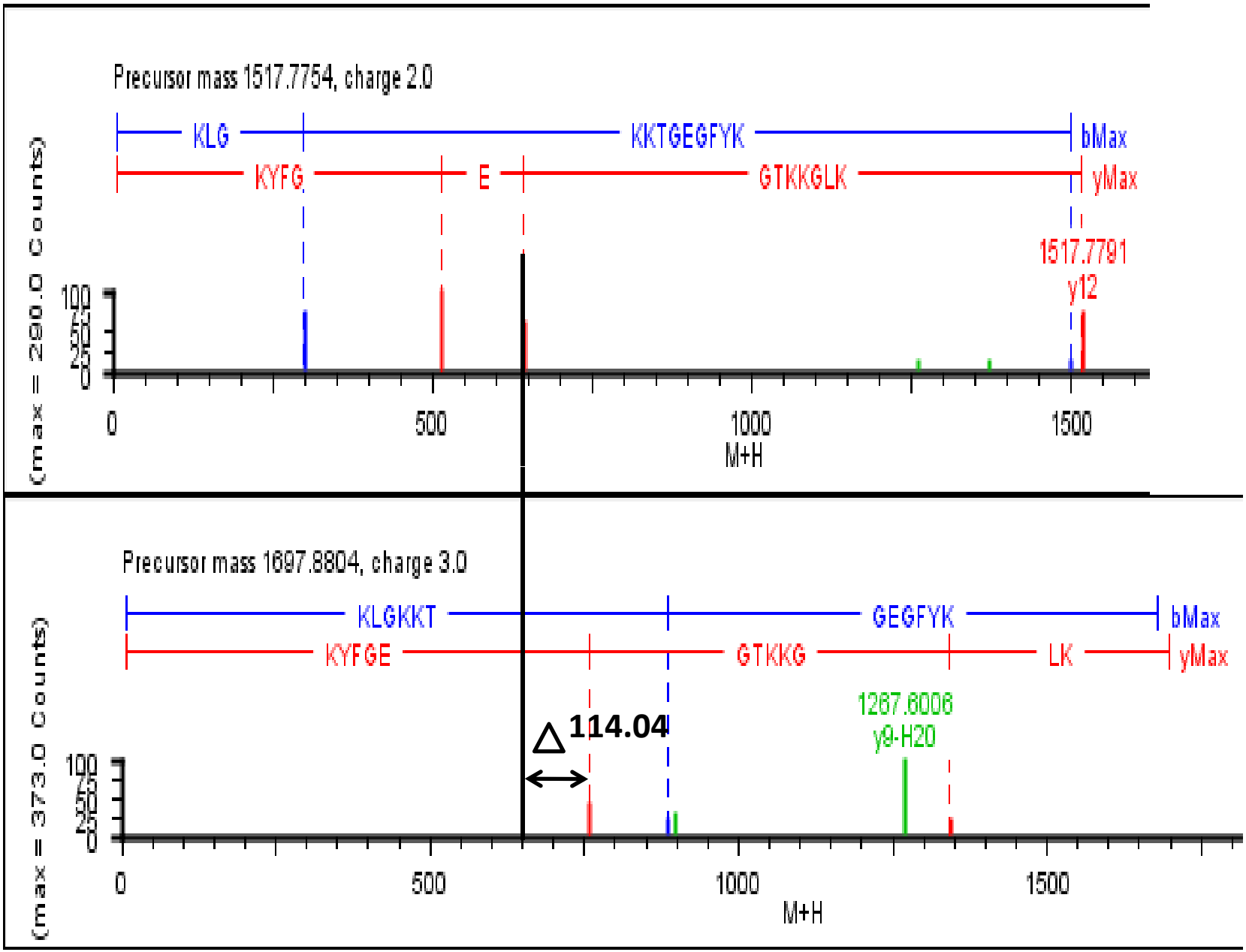
77-87 (R)MAKKKFTENPK(Gly)(A)



358.1869

407.1937: (358.18+ 49.00)

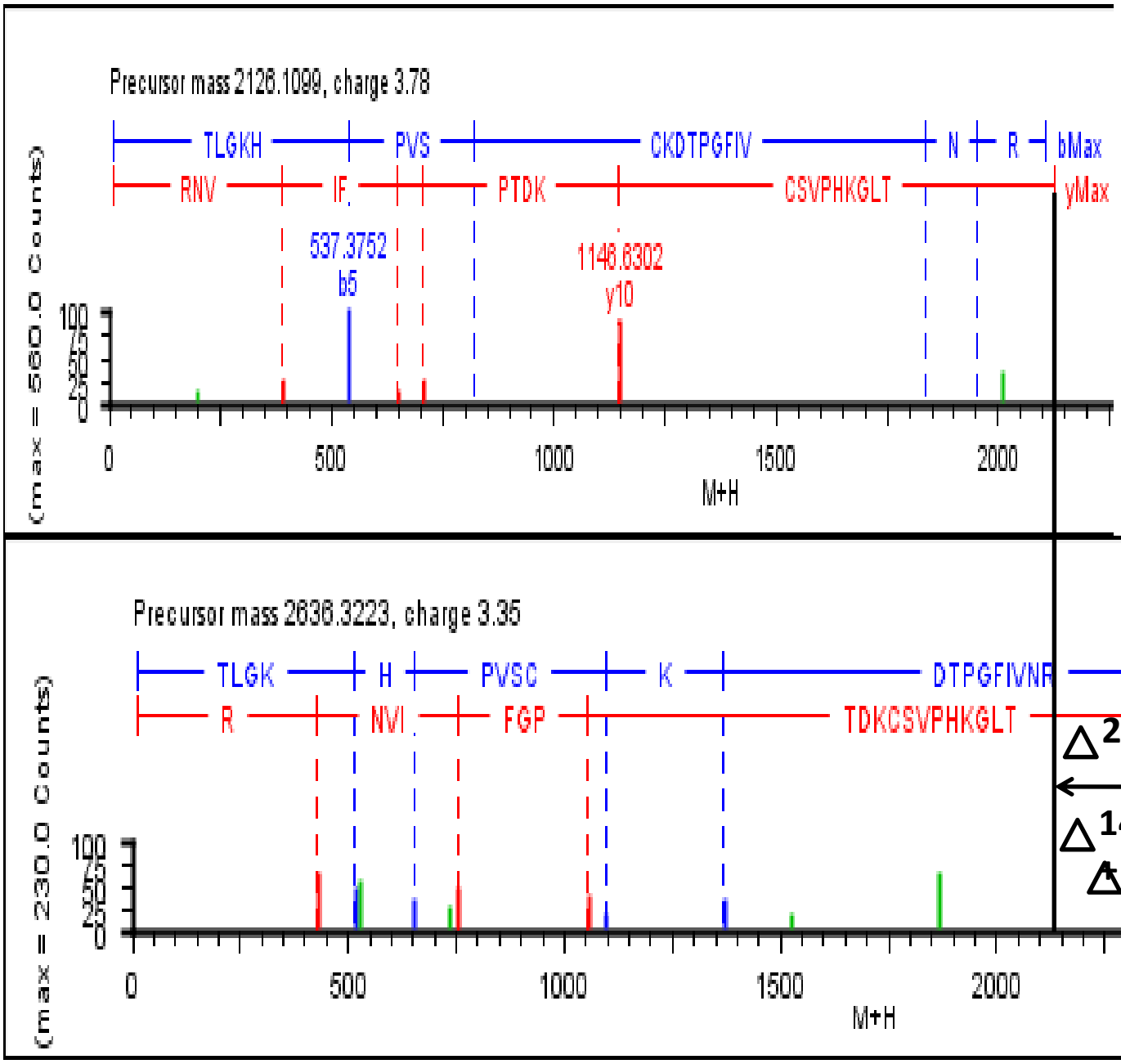
77-87 (R)MAKKKFTENPK(MOLD)(A)



643.2806

757.4102: (643.2806+ 114.04)

301-312 (K)KLGKKTGEGFYK(Ubi)(Y)

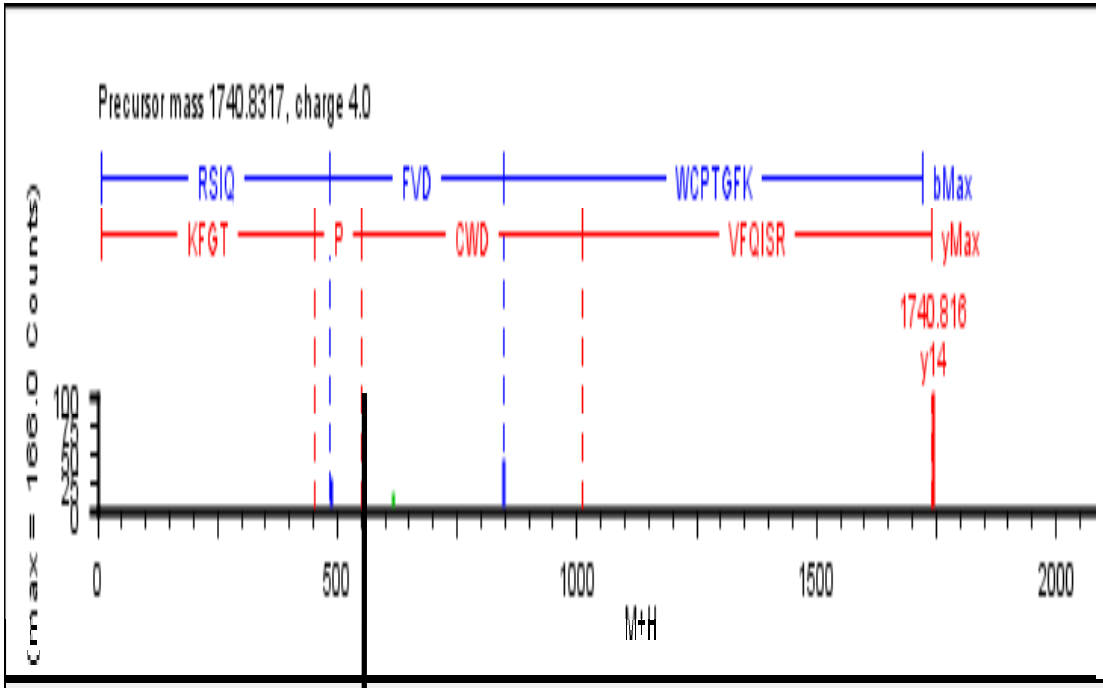


2126.1099

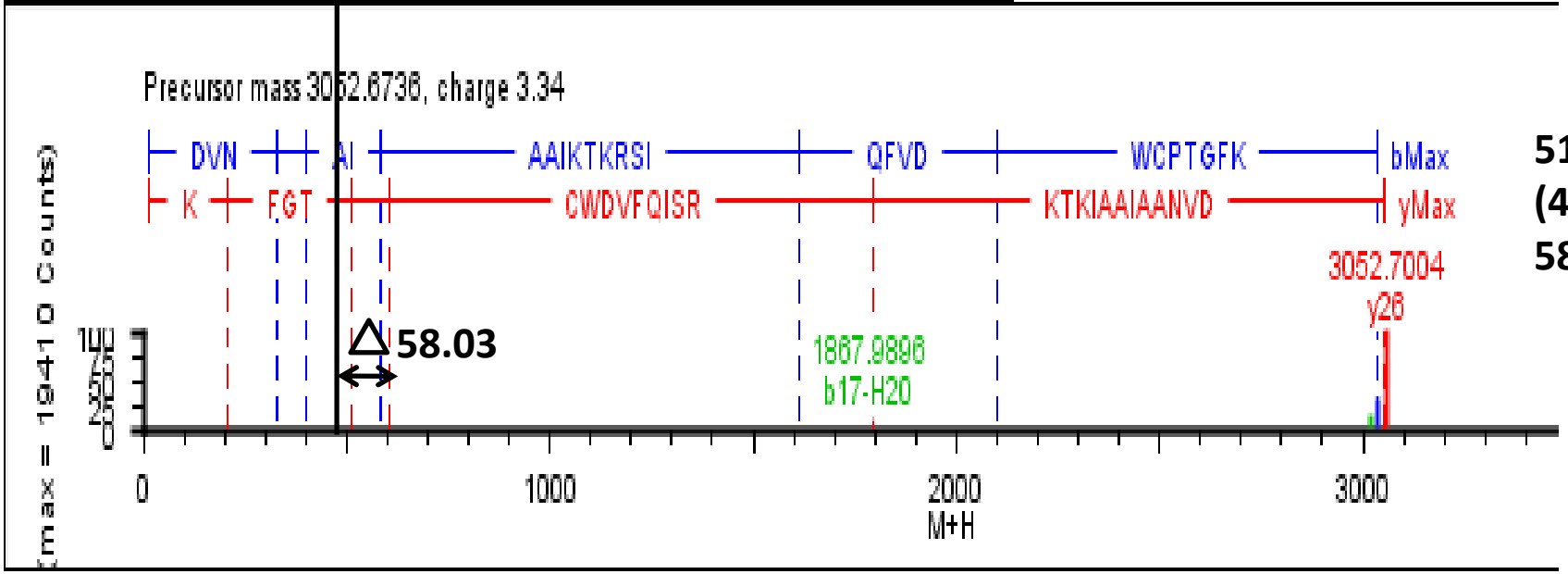
2636.3223: (2126.10+ 114.04+ 144.03+ 252.11)

203-221 (K)TLGK(Ubi)HPVSCK(ImiA)DTPGFIVNR(Crossline)(L)

Tubulin



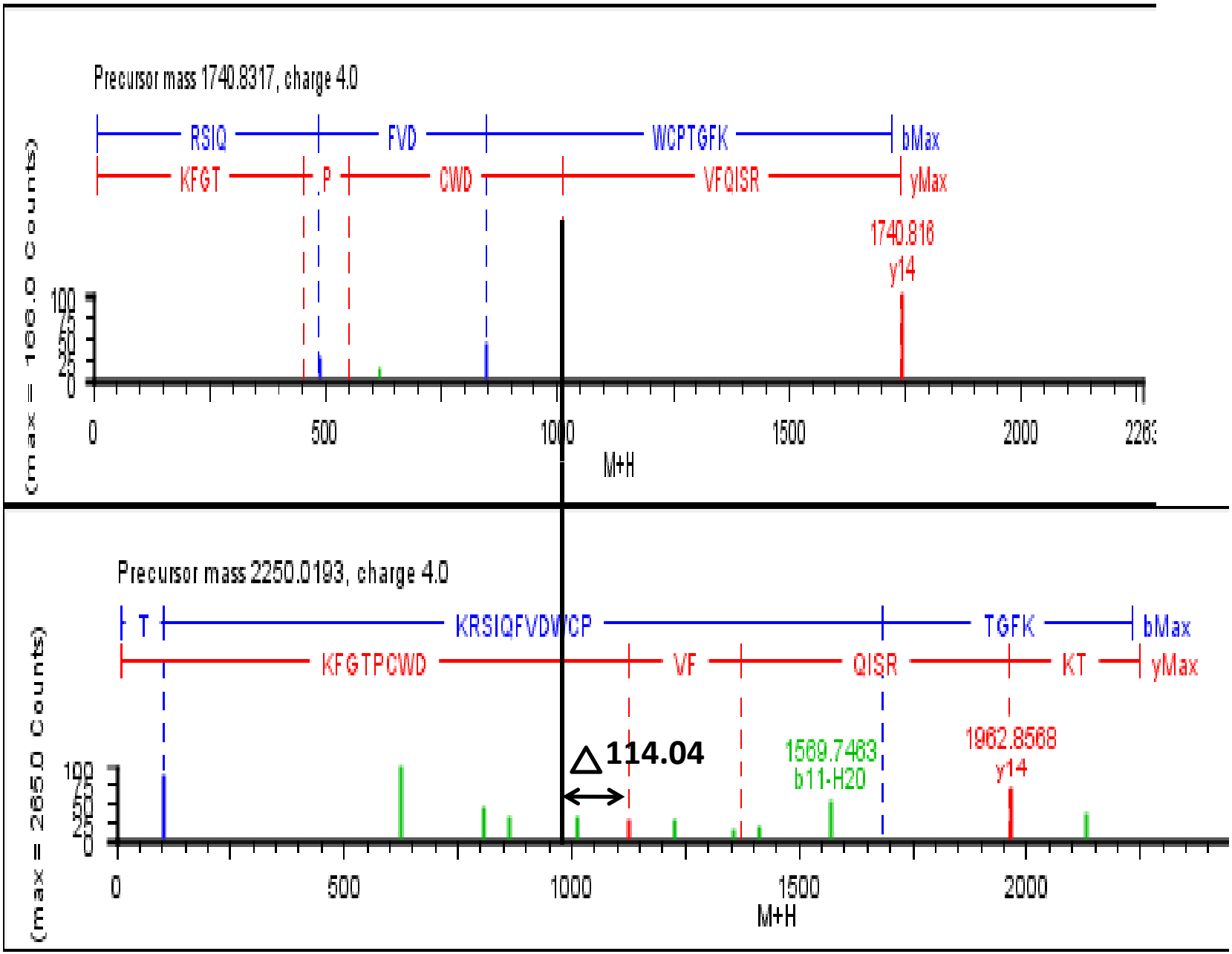
452.2536



510.3215: (452.25+ 58.03)

327-352

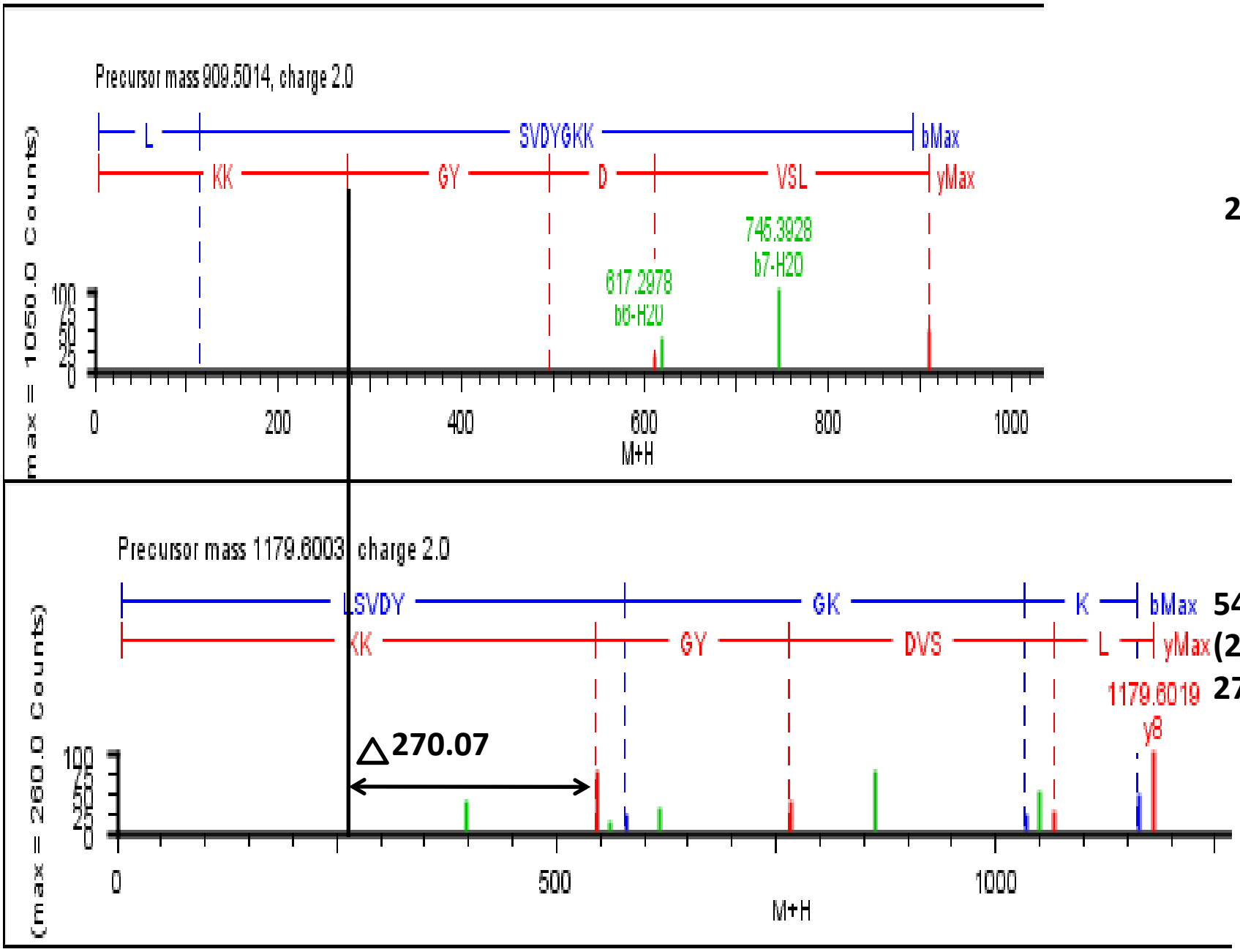
(K)DVNAAIAAIKTKRSIQFVDWCPTGFK(Pento)(V)



1010.3488

1124.4255: (1010.34+ 114.04)

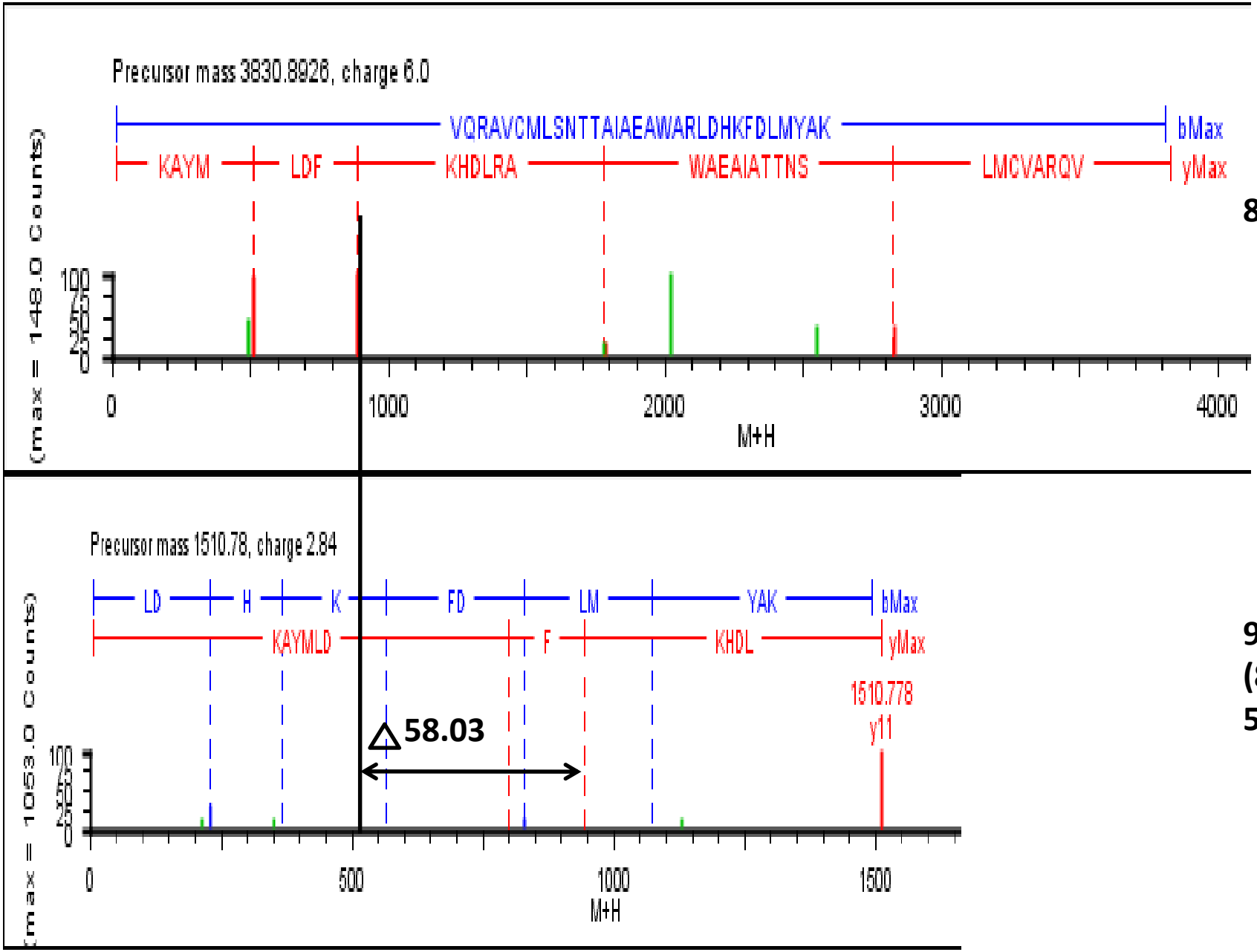
337-352 (K)TKRSIQFVDWCPTGFK(Ubi)(V)



275.2047

545.2849: (275.20+ 270.07)

157-164 (R)LSVDYGK(AFGP)K(S)

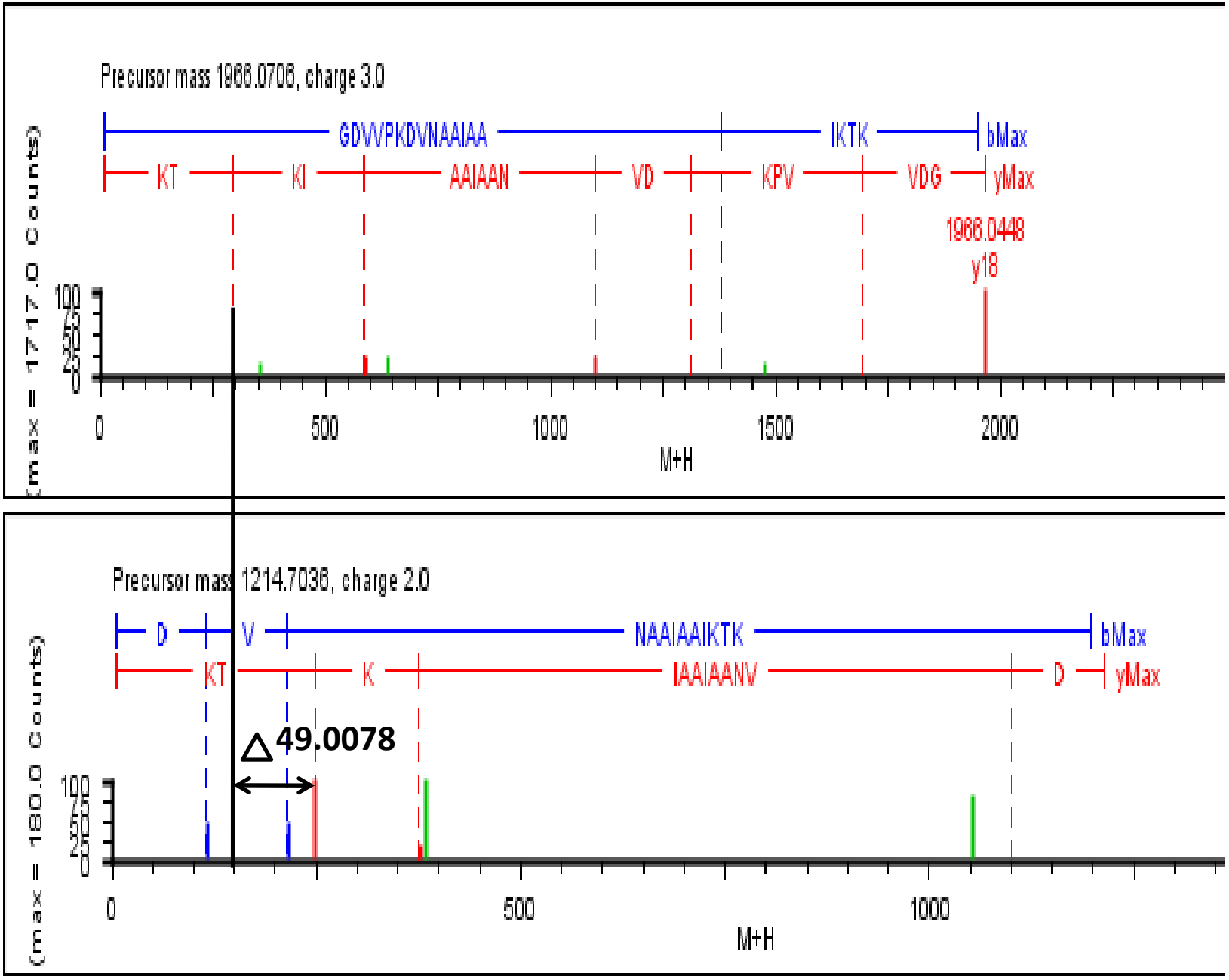


887.3968

945.47: (887.39+ 58.03)

391-401

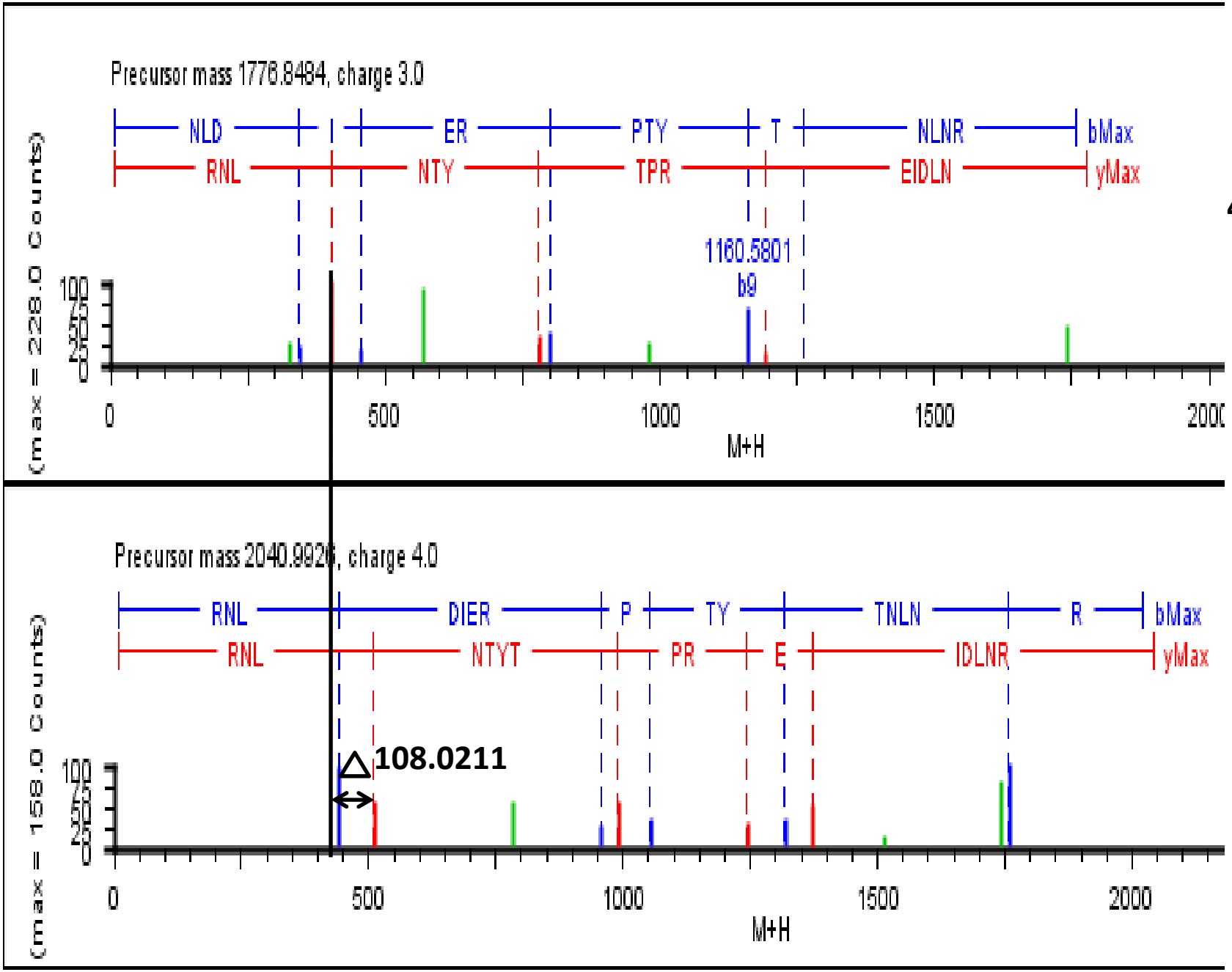
(R)LDHKFDLMYAK(Pento)(R)



248.1516

297.1633: (248.15+ 49.00)

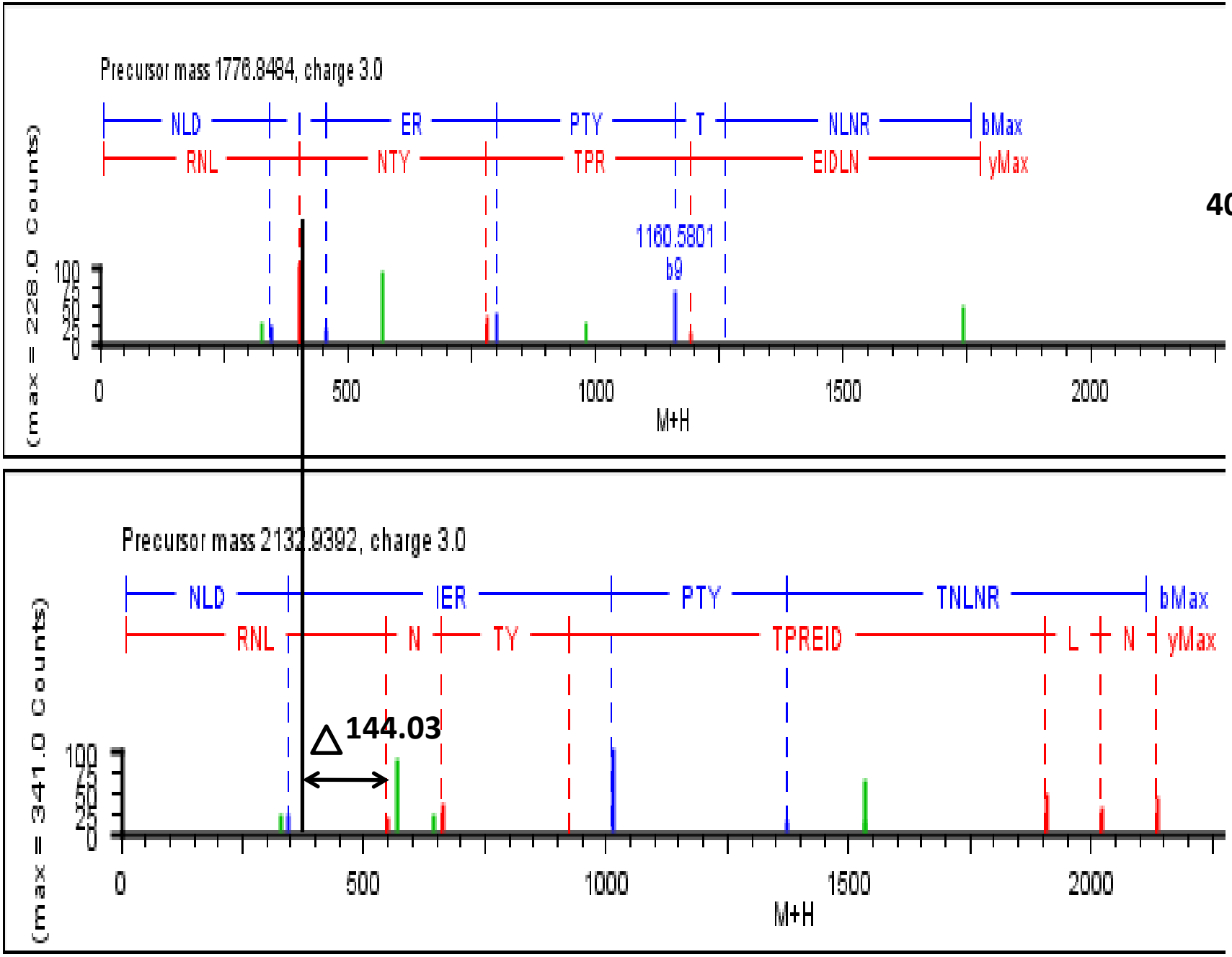
321-338 (R)GDVVPKDVNAAIAAIKTK(MOLD)(R)



402.2711

510.2541: (402.27+ 108.02)

215-229 (R)RNLDIERPTYTNLNR(Pyr)(L)

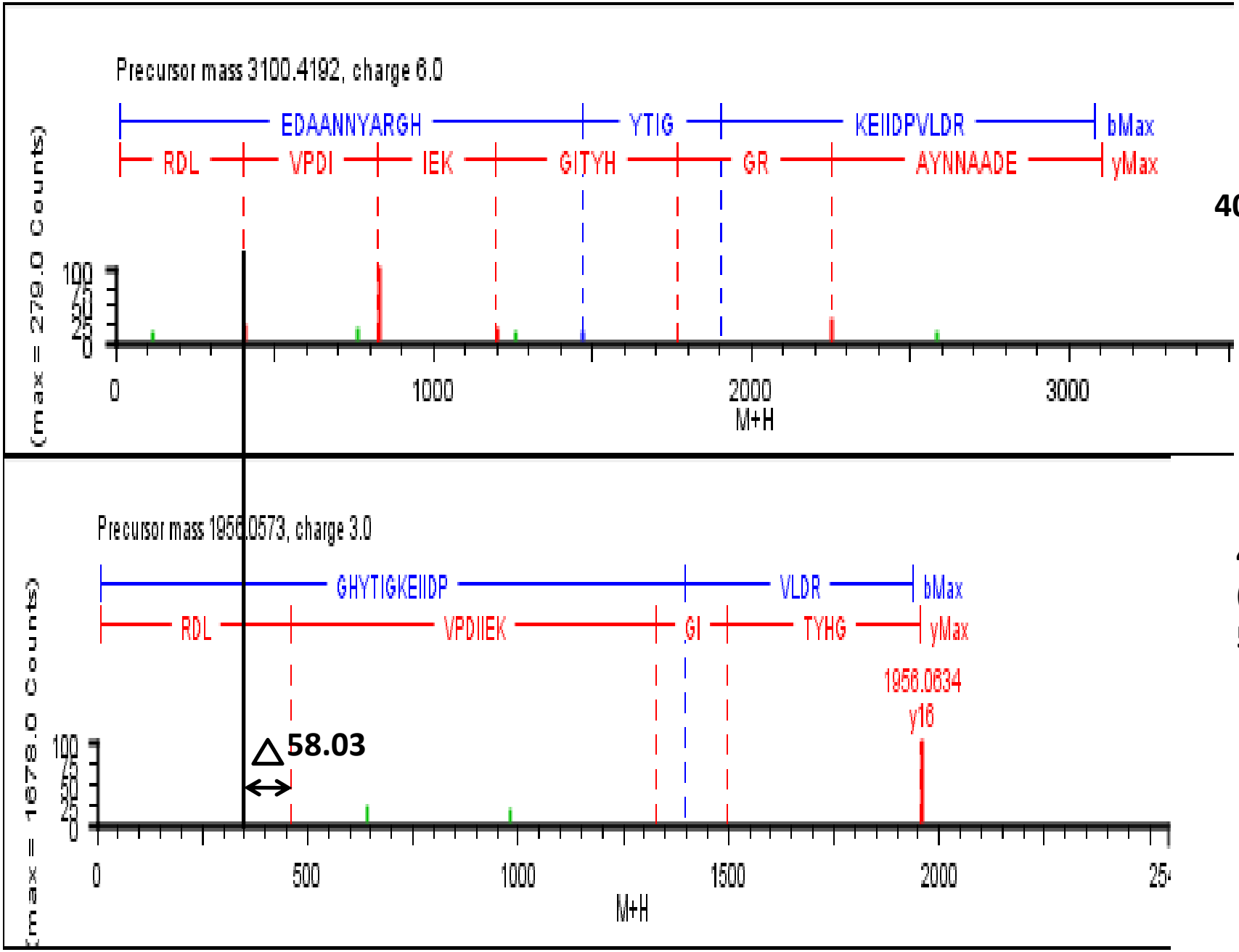


402.2711

546.2747: (402.27+ 144.03)

216-229

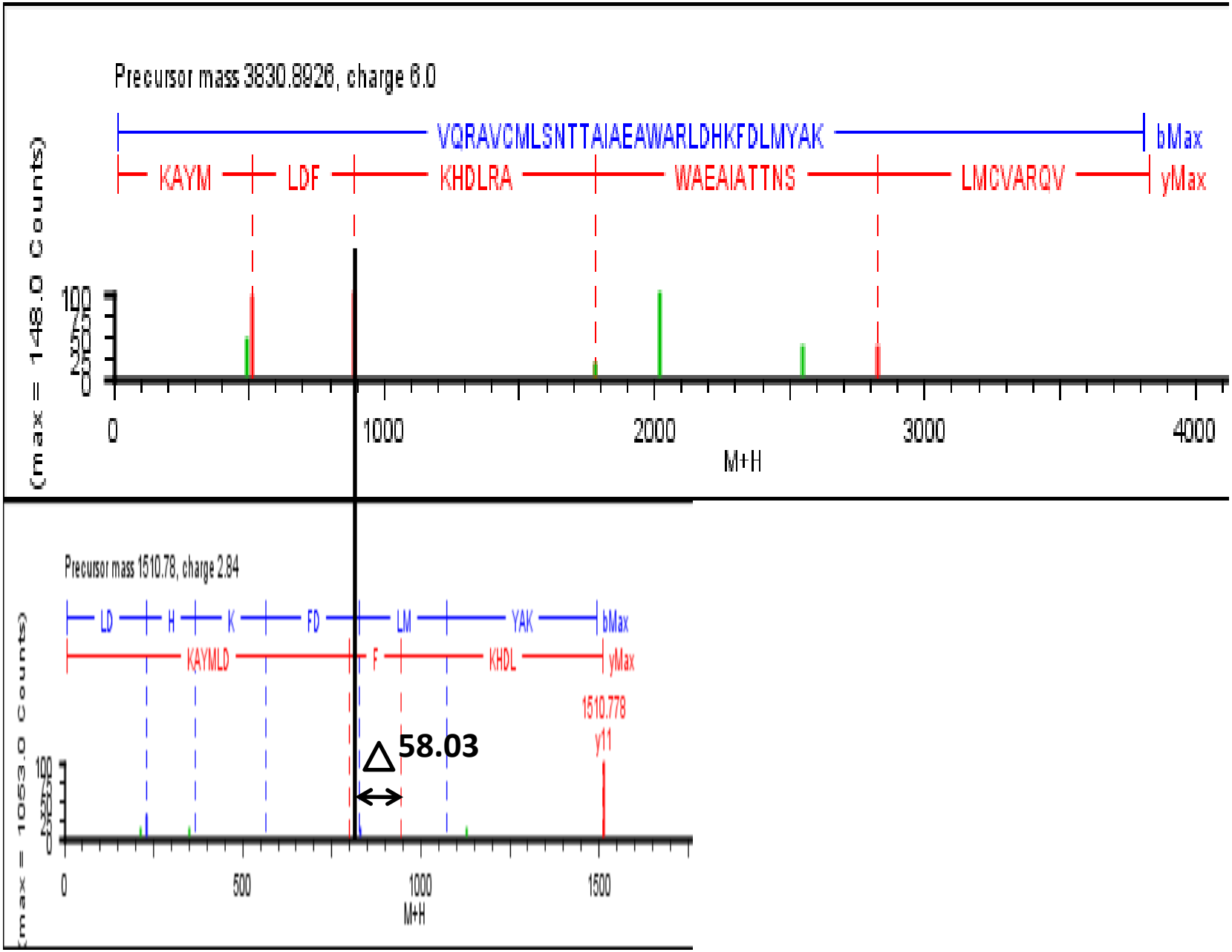
(R)NLDIERPTYTNLNR(ImiA)(L)



403.2225

461.29: (403.22+ 58.03)

106-121 (R)GHYTIGKEIIDPVLDR(Pento)(I)



887.3968

945.47: (887.39+ 58.03)

391-401 (R)LDHKFDLMYAK(Pento)(R)