

SUPPLEMENTAL MATERIALS

Site-specific proteomic analysis of lipoxidation adducts in cardiac mitochondria reveals chemical diversity of 2-alkenal adduction

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Figure S1-77: Mass spectral data for the peptides identified with 2-alkenal adductions.

Figure S78: Proposed structures of ARP-specific ions observed in the MS/MS spectra reported.

Figure S79: Biological network and pathway analysis of the carbonylated proteins identified in this study.

AT5F1_RAT: ATP synthase B chain

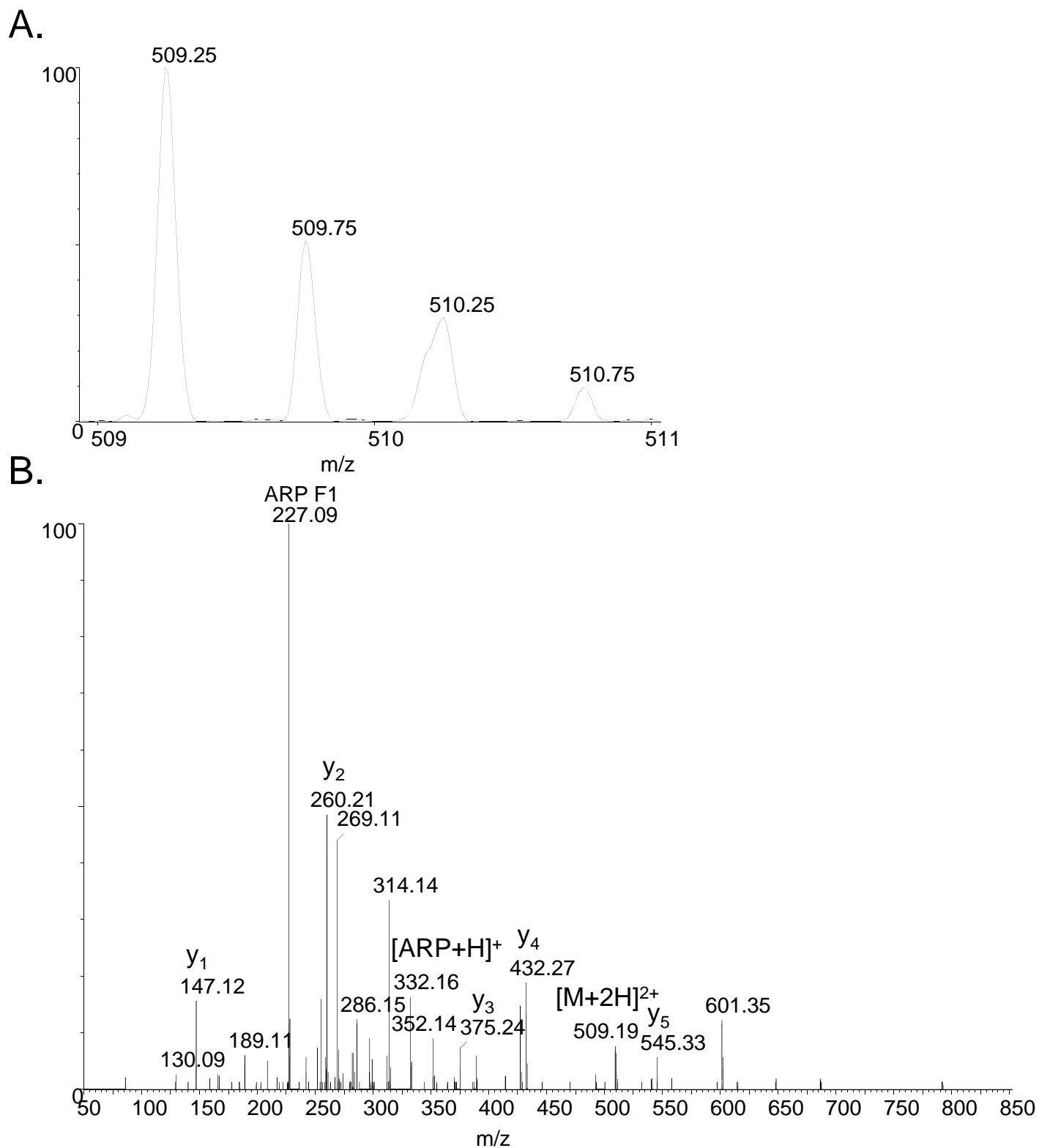
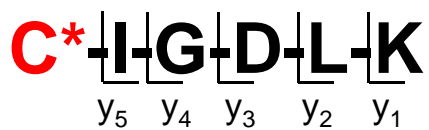


Figure S1. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide C*IGDLK; monoisotopic m/z_{calc} 509.25; accuracy $\Delta(m/z) = 0.00$ Da

AT5F1_RAT: ATP synthase B chain

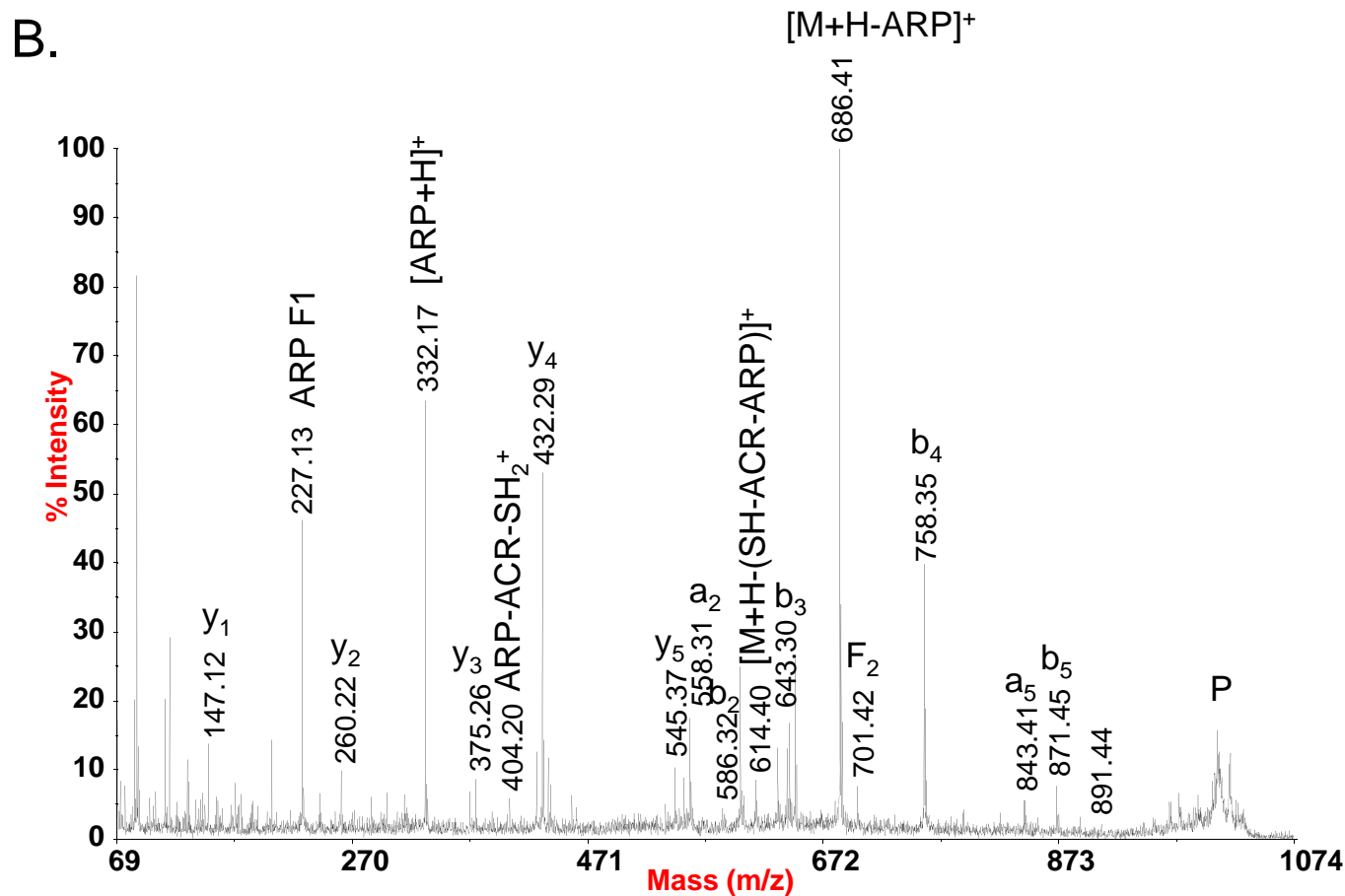
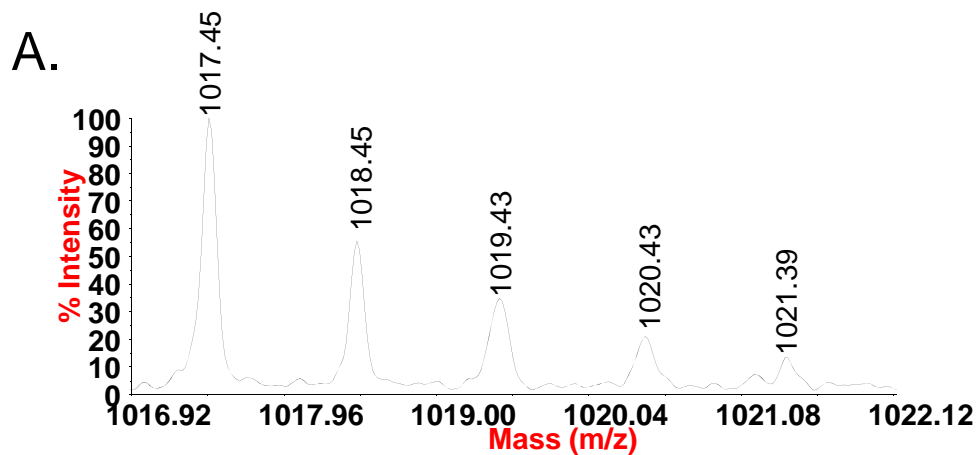
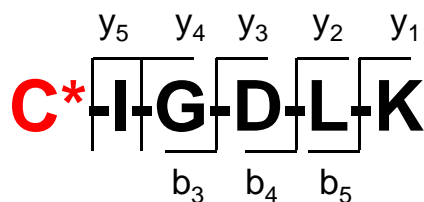
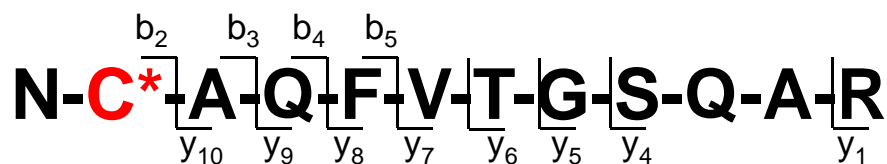
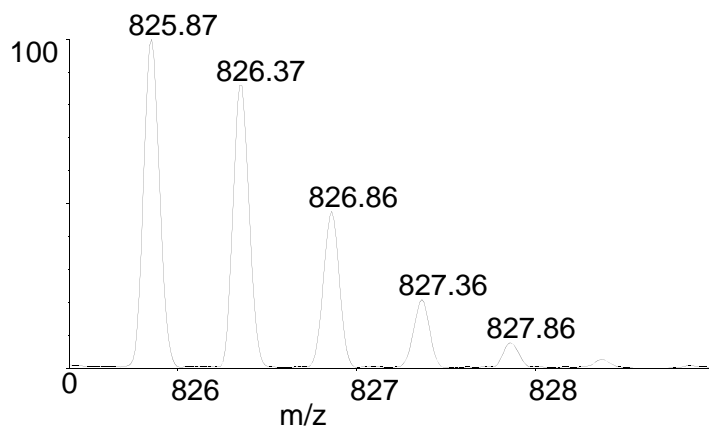


Figure S2. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide C*IGDLK; monoisotopic m/z_{calc} 1017.49; accuracy Δ(m/z) = -0.04 Da

ATP5H_RAT: ATP synthase D chain



A.



B.

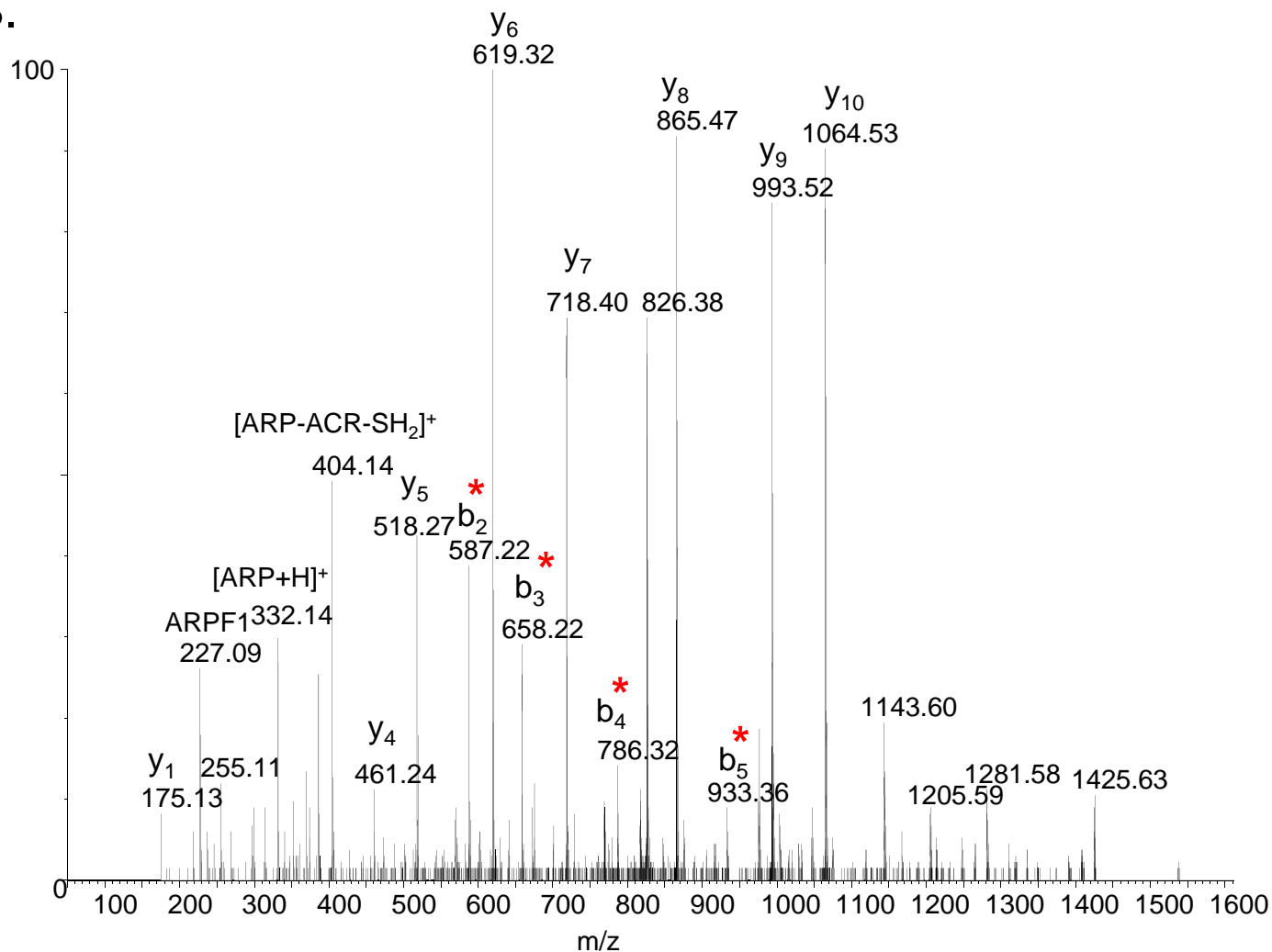


Figure S3. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide NC^{*}AQFVTGSQAR; monoisotopic m/z_{calc} 825.88; accuracy $\Delta(m/z) = -0.01$ Da

ATPA_RAT ATP synthase subunit alpha

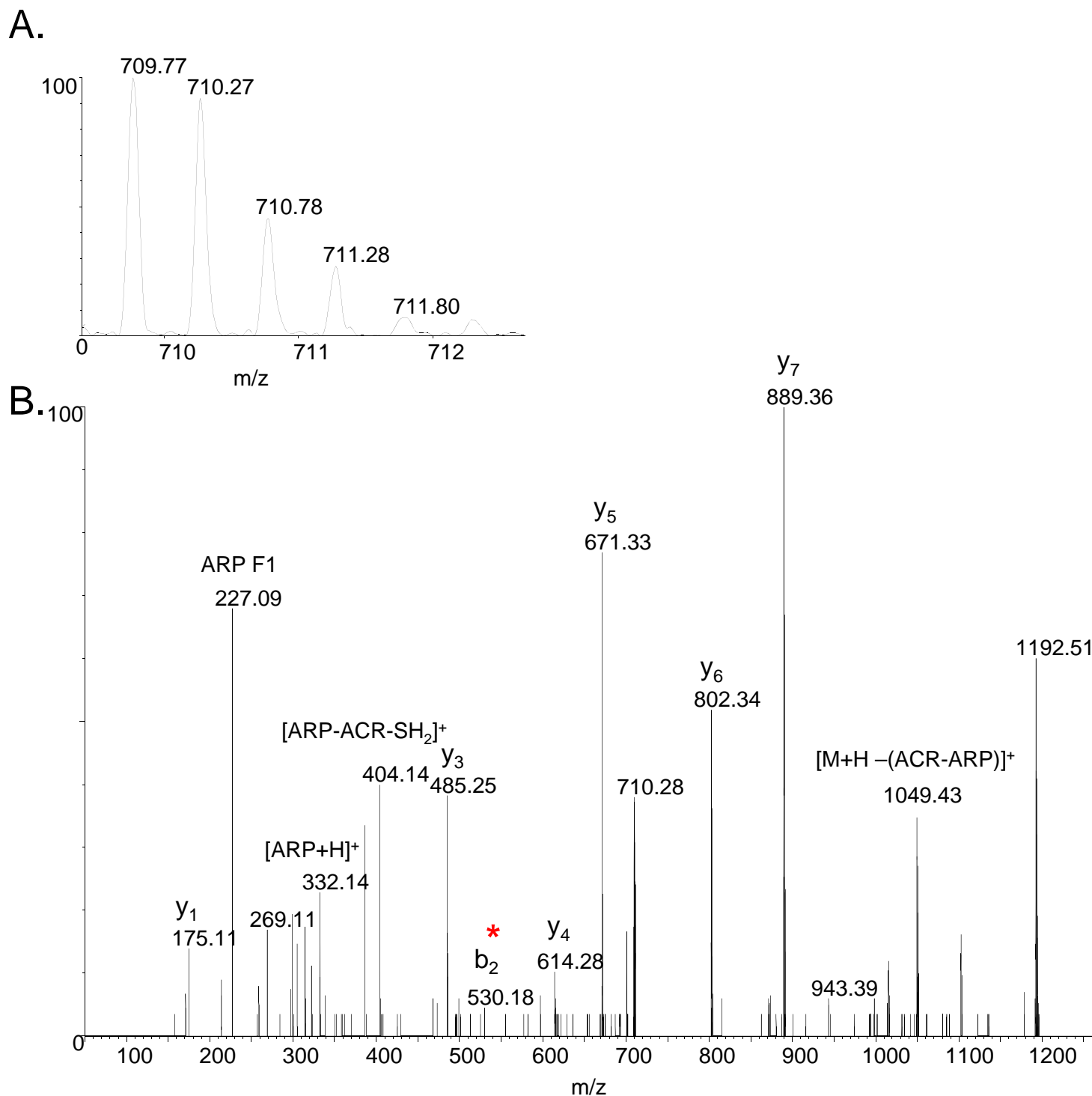
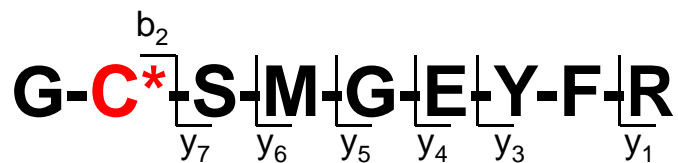


Figure S5. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the [M+2H]²⁺ ion of the ARP labeled, acrolein modified peptide GC*SMGEYFR; monoisotopic m/z_{calc} 709.79; accuracy Δ(m/z) = -0.02 Da

ATPA_RAT ATP synthase subunit alpha

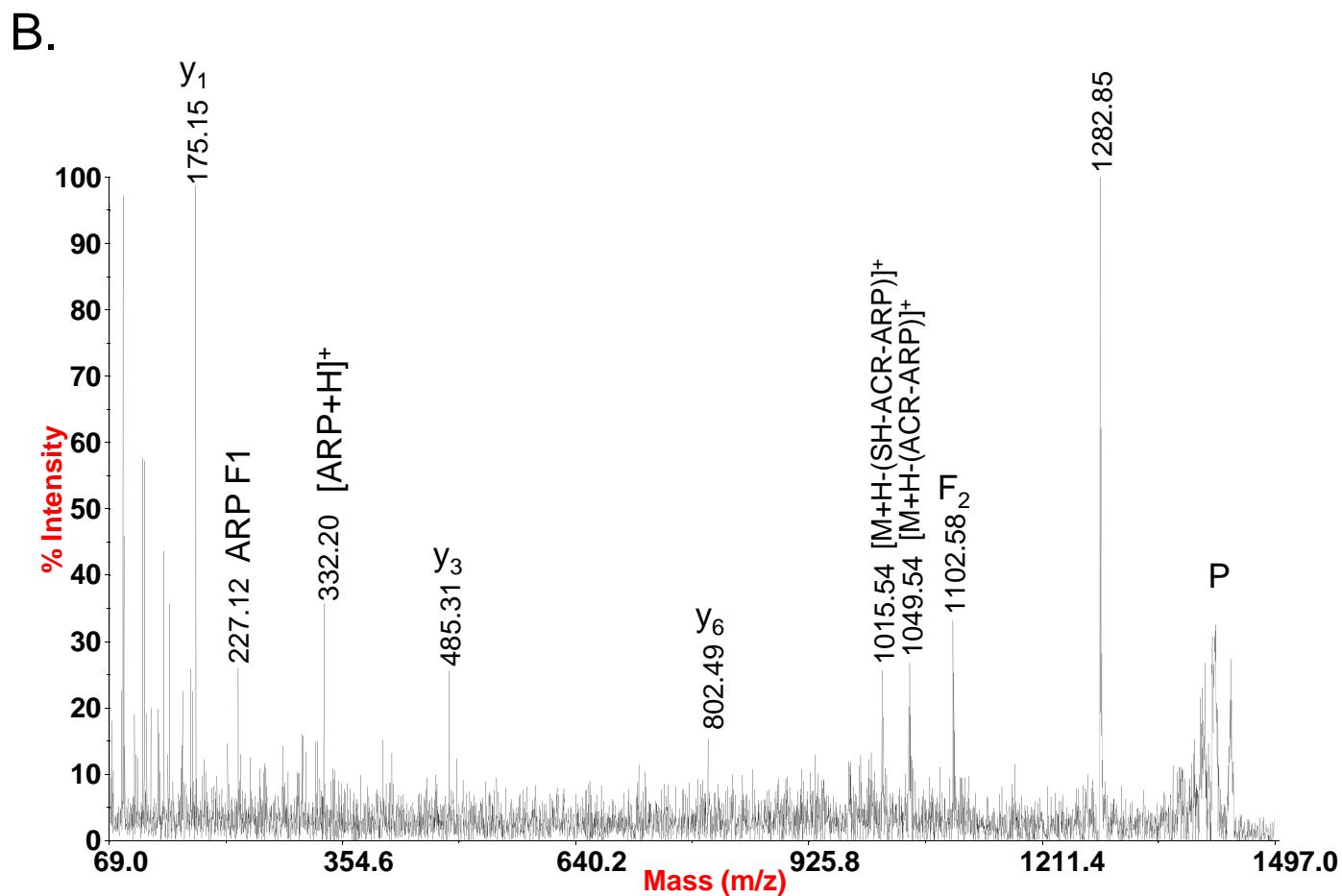
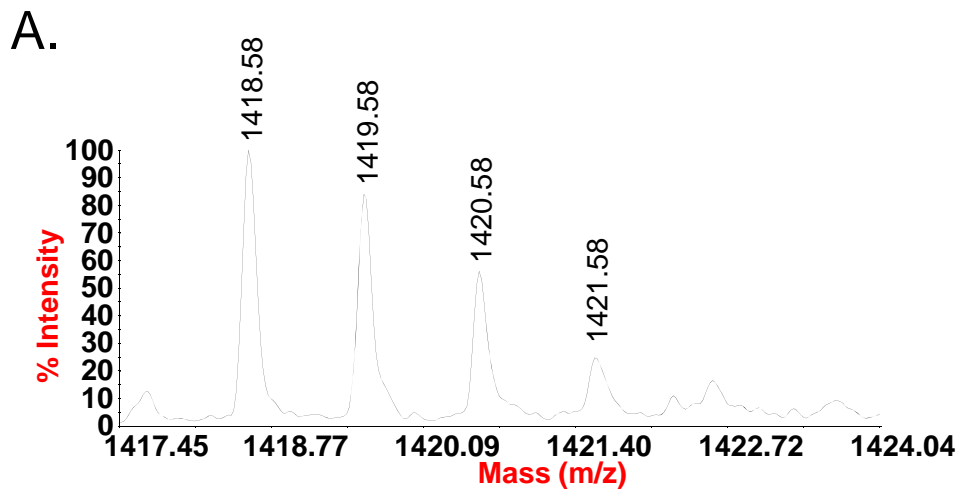
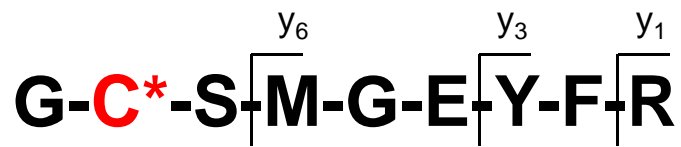


Figure S6. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide GC*SMGEYFR; monoisotopic m/z_{calc} 1418.57; accuracy $\Delta(m/z) = 0.01$ Da

ATPA_RAT ATP synthase subunit alpha

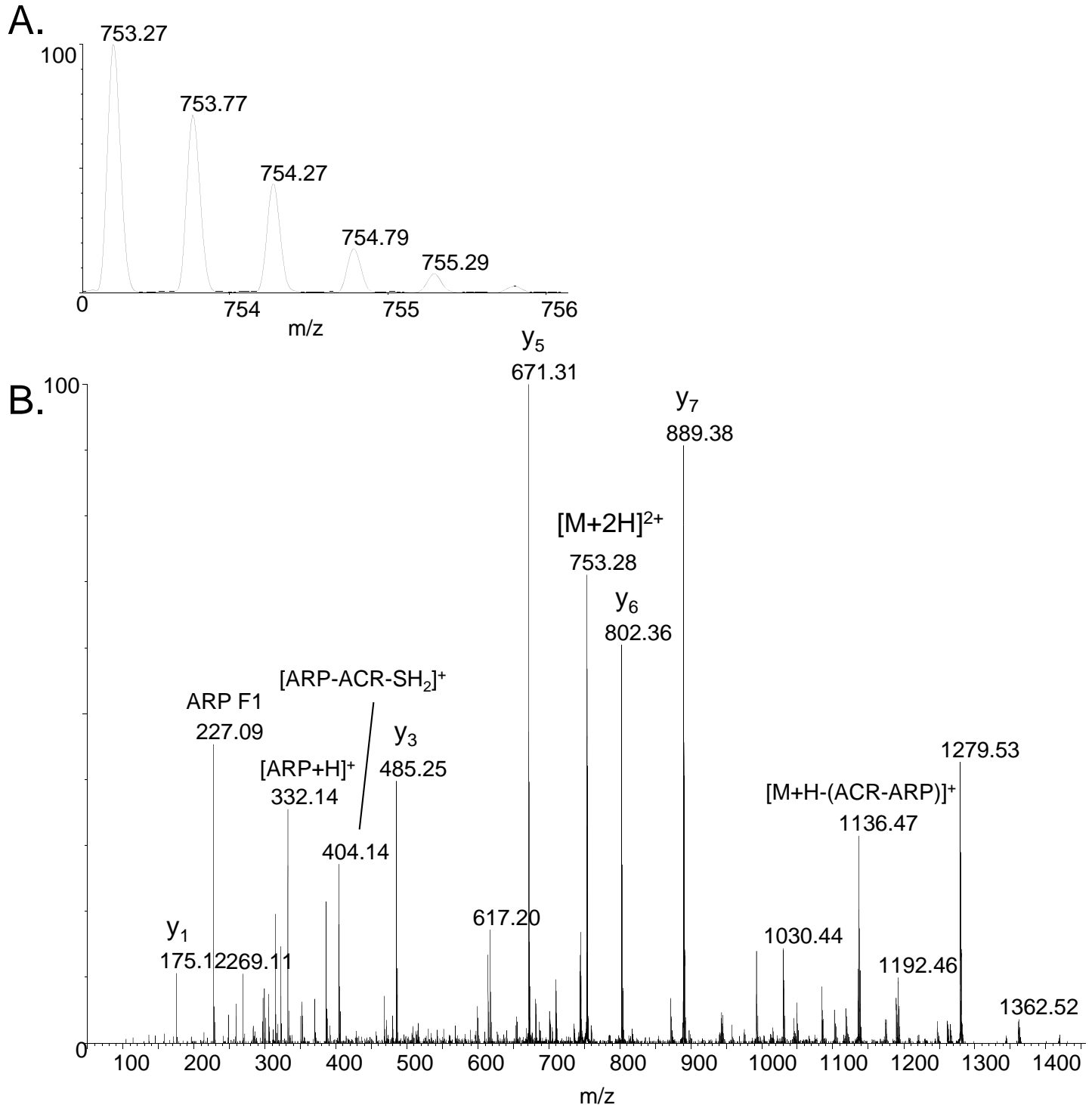
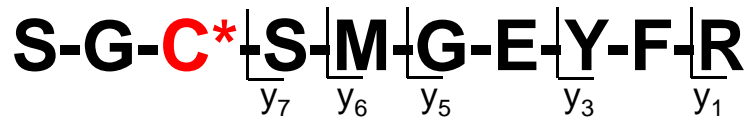


Figure S7. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide SGC*SMGEYFR; monoisotopic m/z_{calc} 753.30; accuracy $\Delta(m/z) = -0.03$ Da

ATPA_RAT ATP synthase subunit alpha

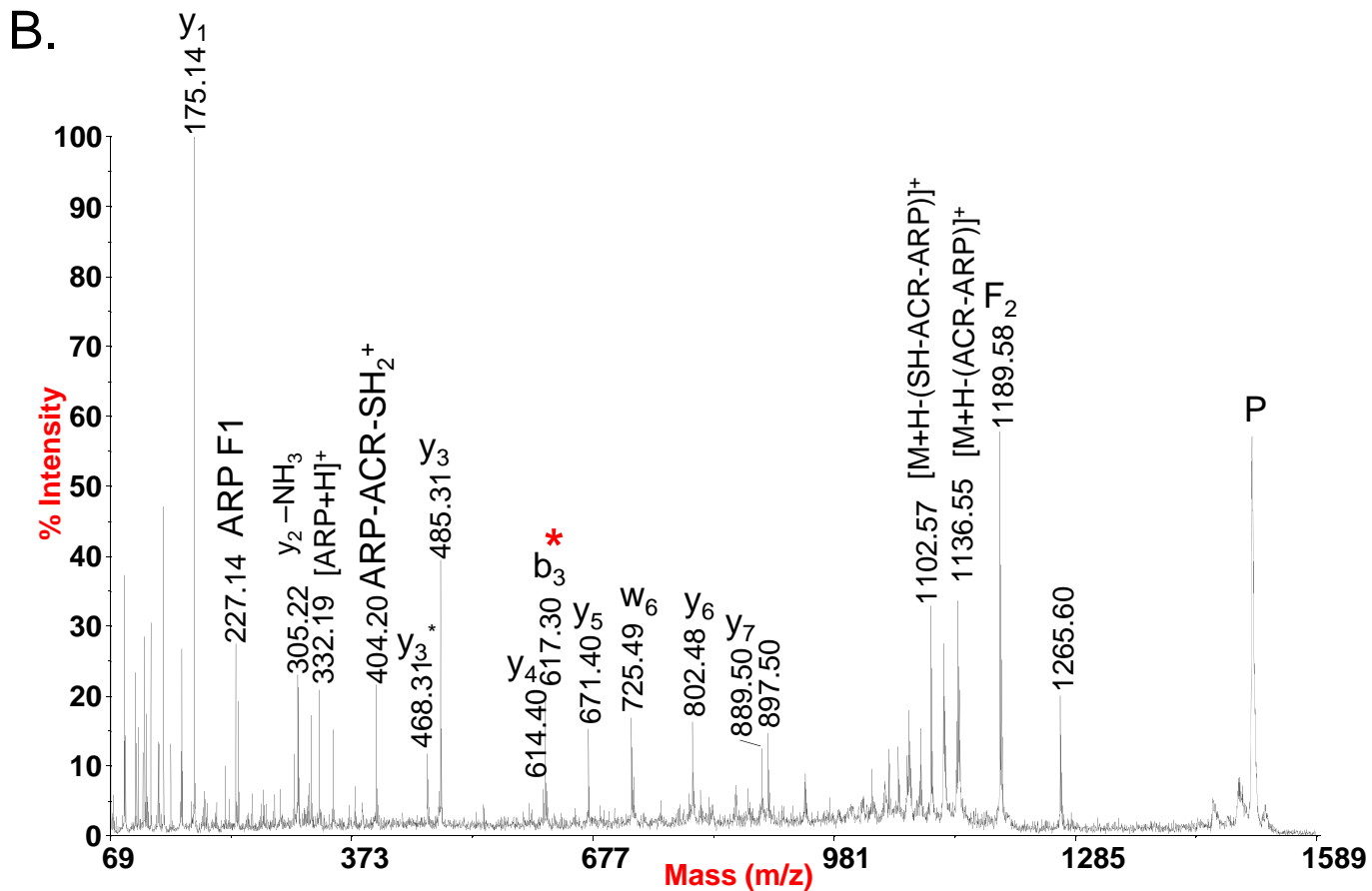
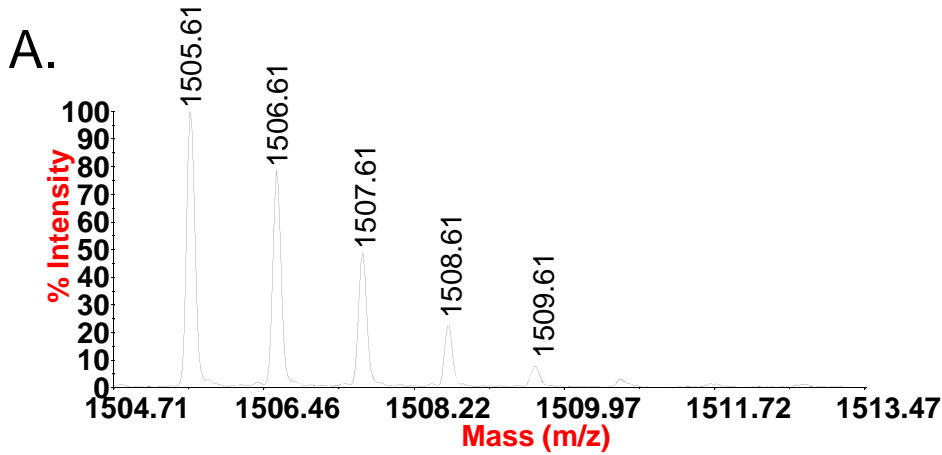
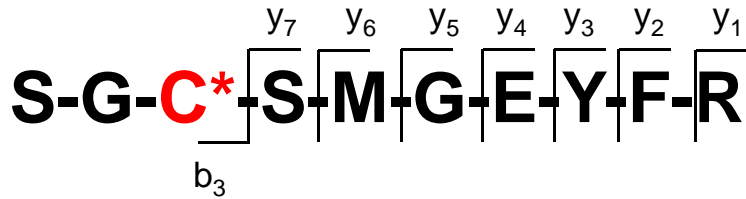


Figure S8. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide SGC*SMGEYFR; monoisotopic m/z_{calc} 1505.60; accuracy $\Delta(m/z) = 0.01$ Da

ATPA_RAT ATP synthase subunit alpha

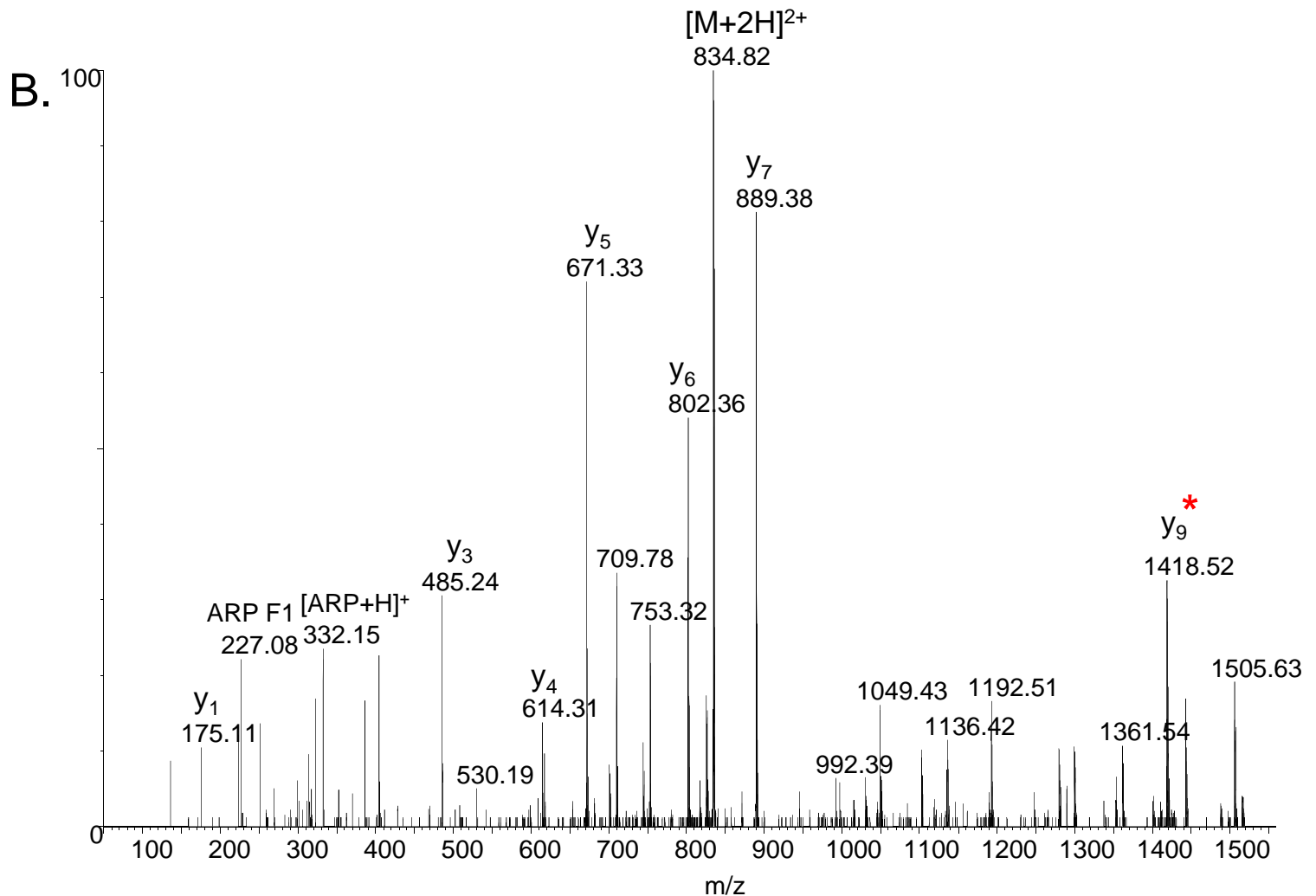
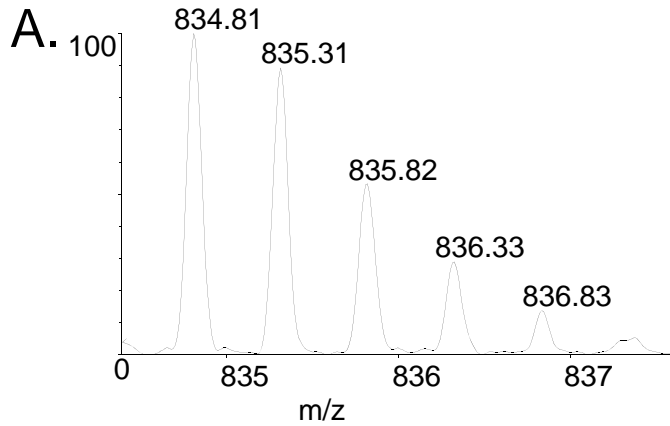
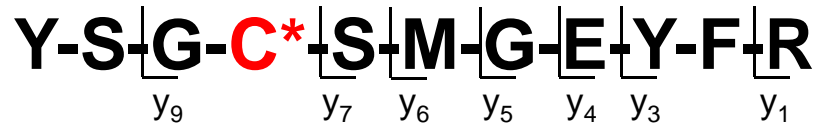


Figure S9. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide YSGC*SMGEYFR; monoisotopic m/z_{calc} 834.83; accuracy $\Delta(m/z) = -0.02$ Da

ATPA_RAT ATP synthase subunit alpha

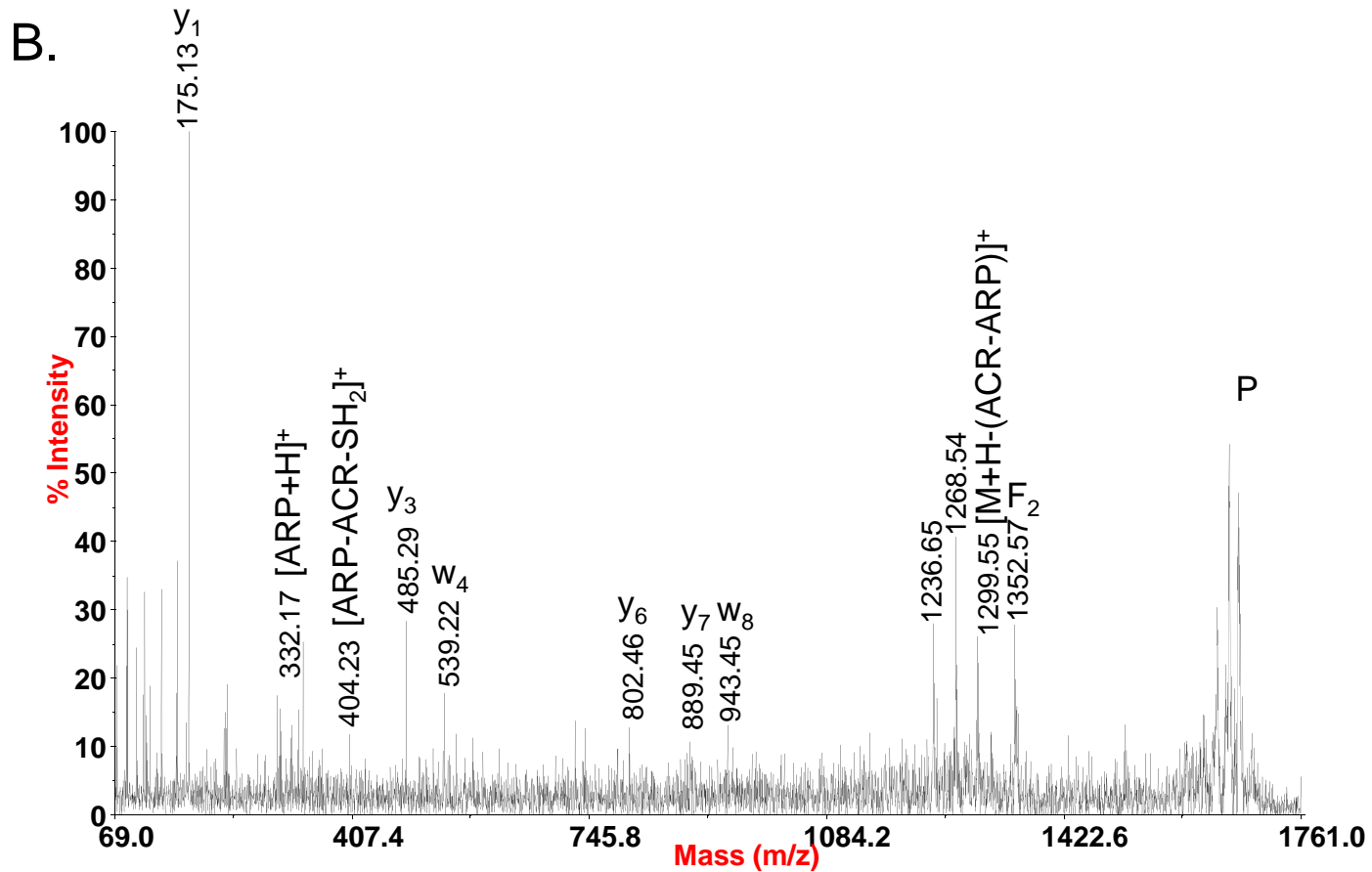
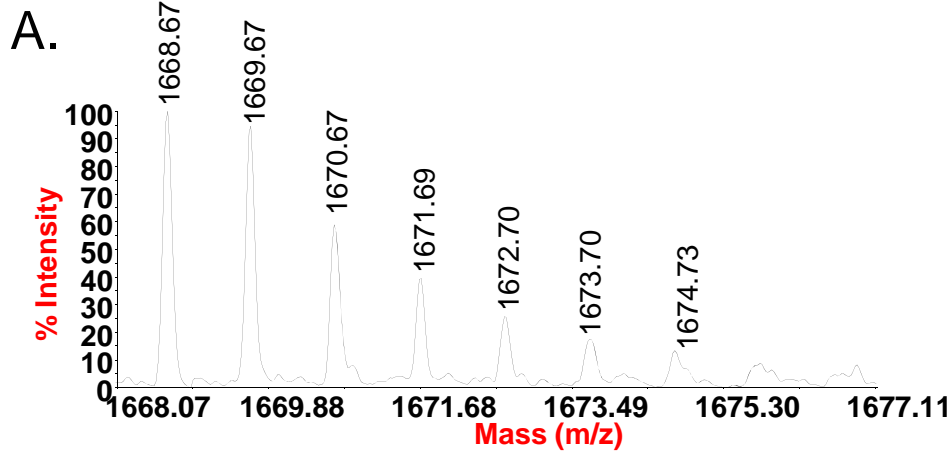
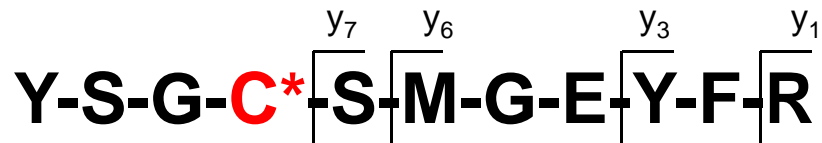


Figure S10. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide YSGC*SMGEYFR; monoisotopic m/z_{calc} 1668.66; accuracy Δ(m/z) = -0.01 Da

ATPA_RAT ATP synthase subunit alpha

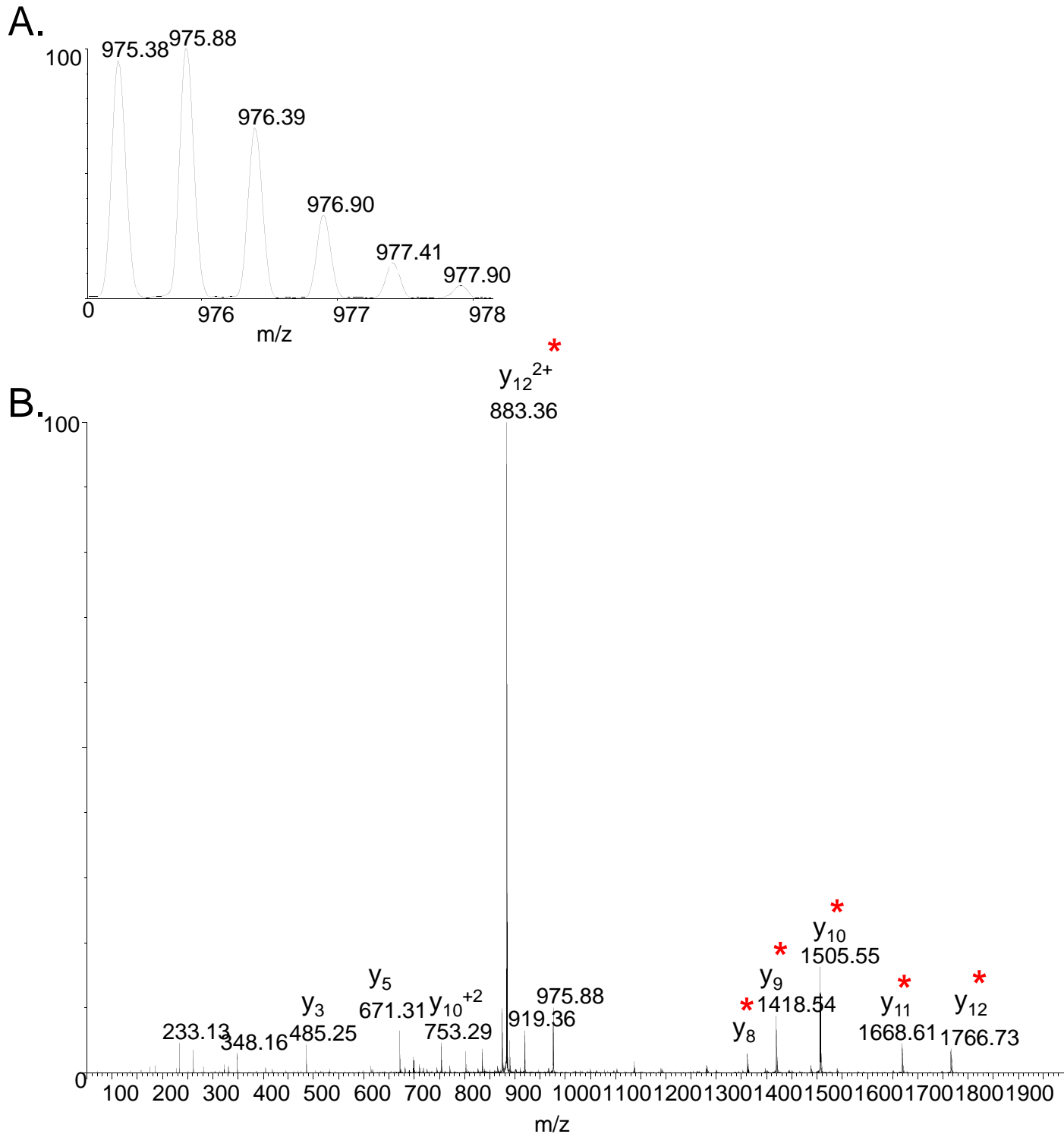
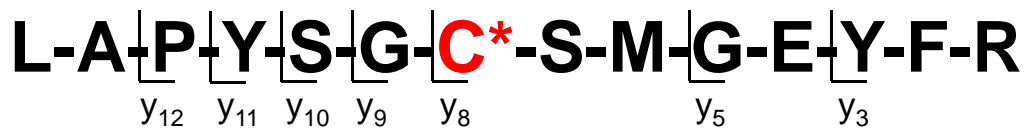


Figure S11. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide LAPYSGC*SMGEYFR; monoisotopic m/z_{calc} 975.42; accuracy $\Delta(m/z) = -0.04$ Da

ATPB_RAT: ATP synthase subunit beta

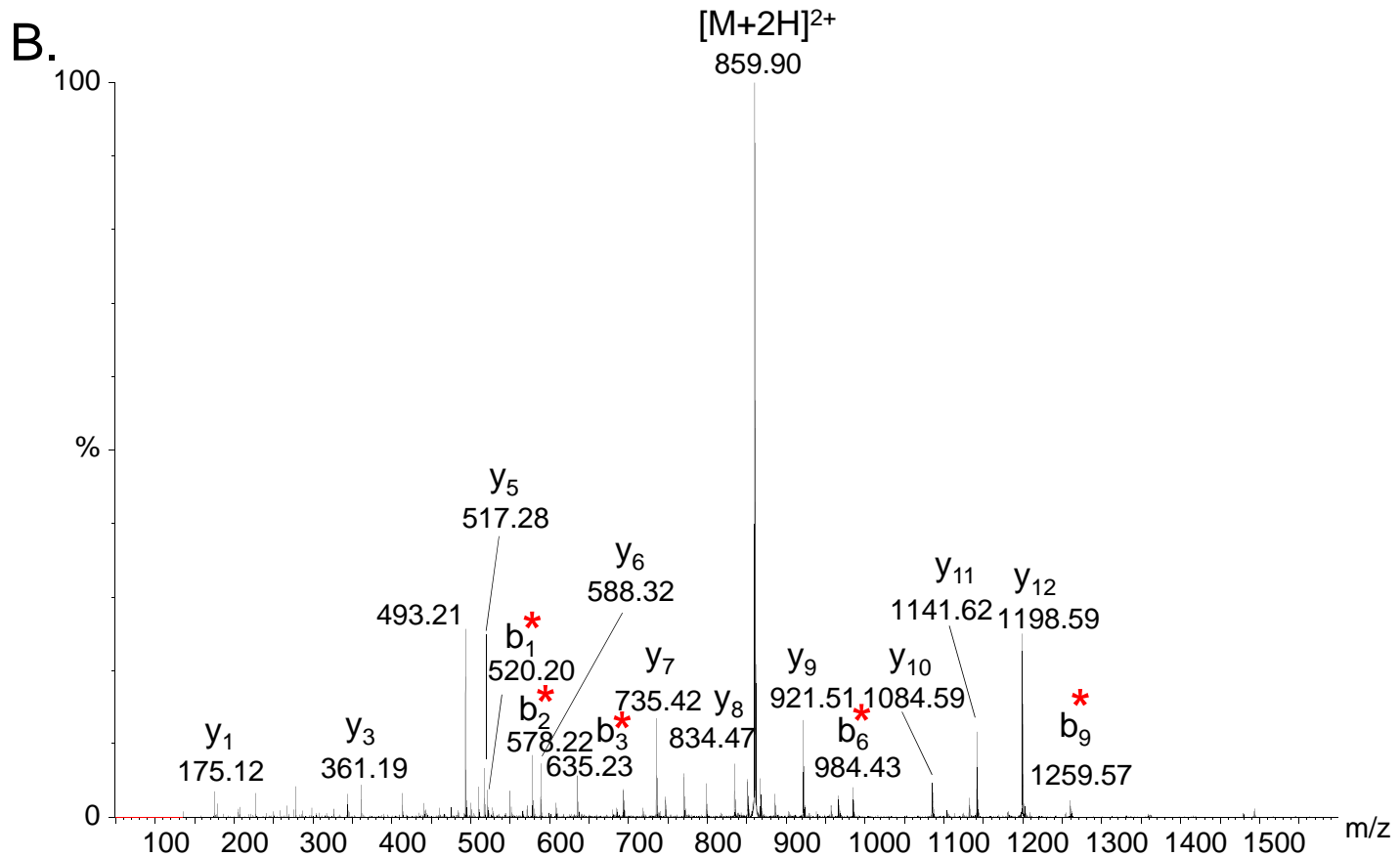
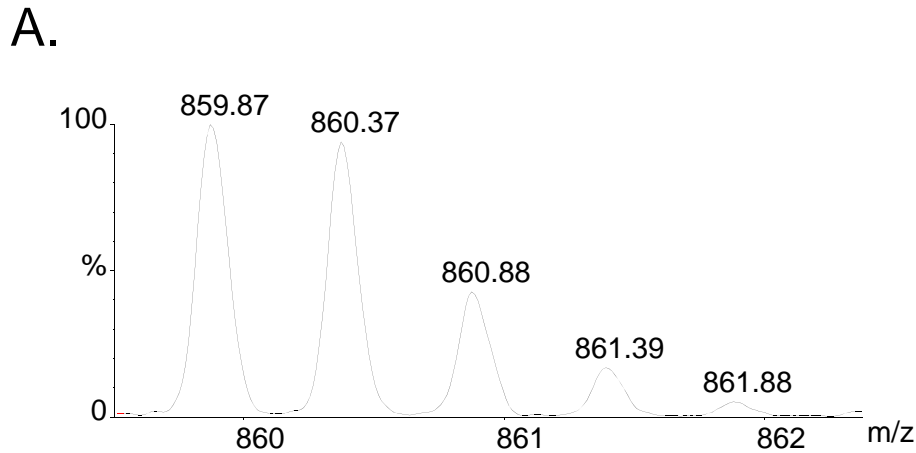
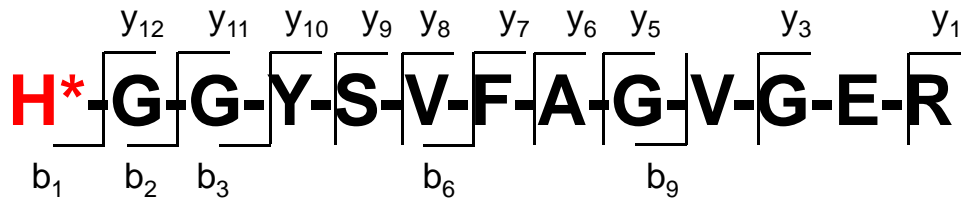


Figure S12. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, crotonaldehyde modified peptide H*GGYSVFAGVGER; monoisotopic m/z_{calc} 859.91; accuracy $\Delta(m/z) = -0.04$ Da

ATPB_RAT: ATP synthase subunit beta

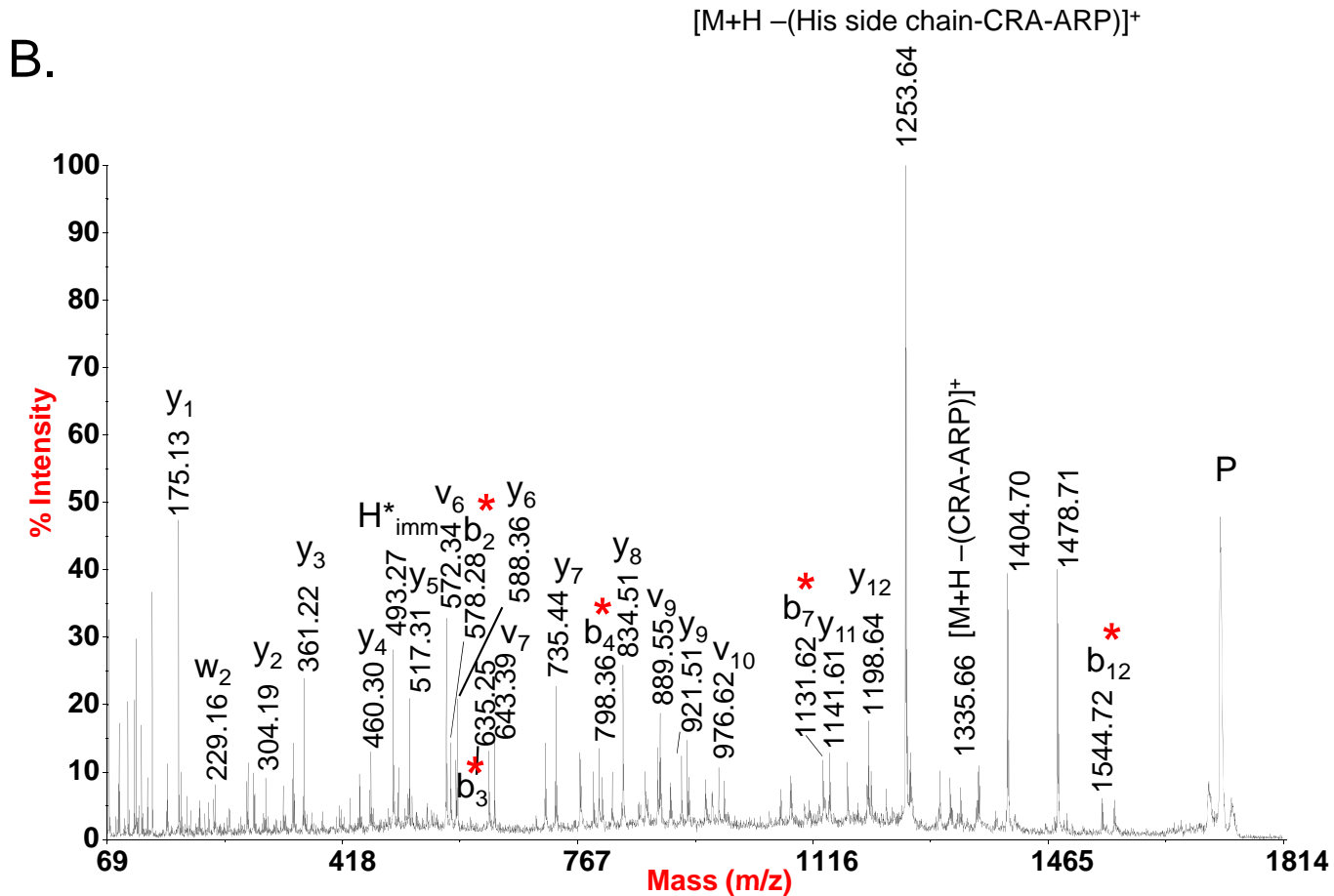
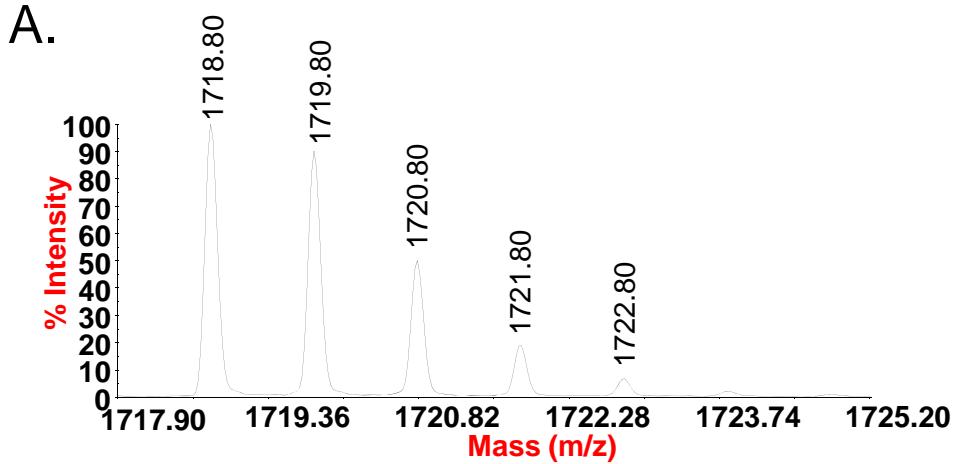
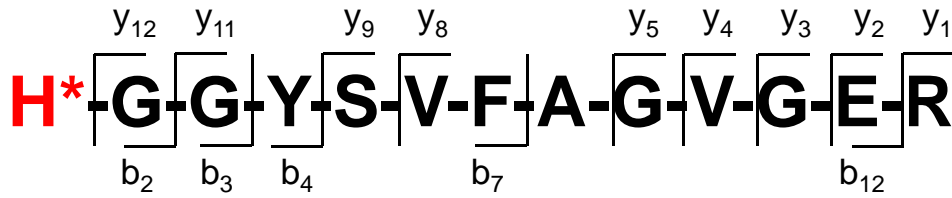


Figure S13. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, crotonaldehyde modified peptide H*GGYSVFAAGVGER; monoisotopic m/z_{calc} 1718.81; accuracy $\Delta(m/z) = -0.01$ Da

ATPG_RAT: ATP synthase gamma chain

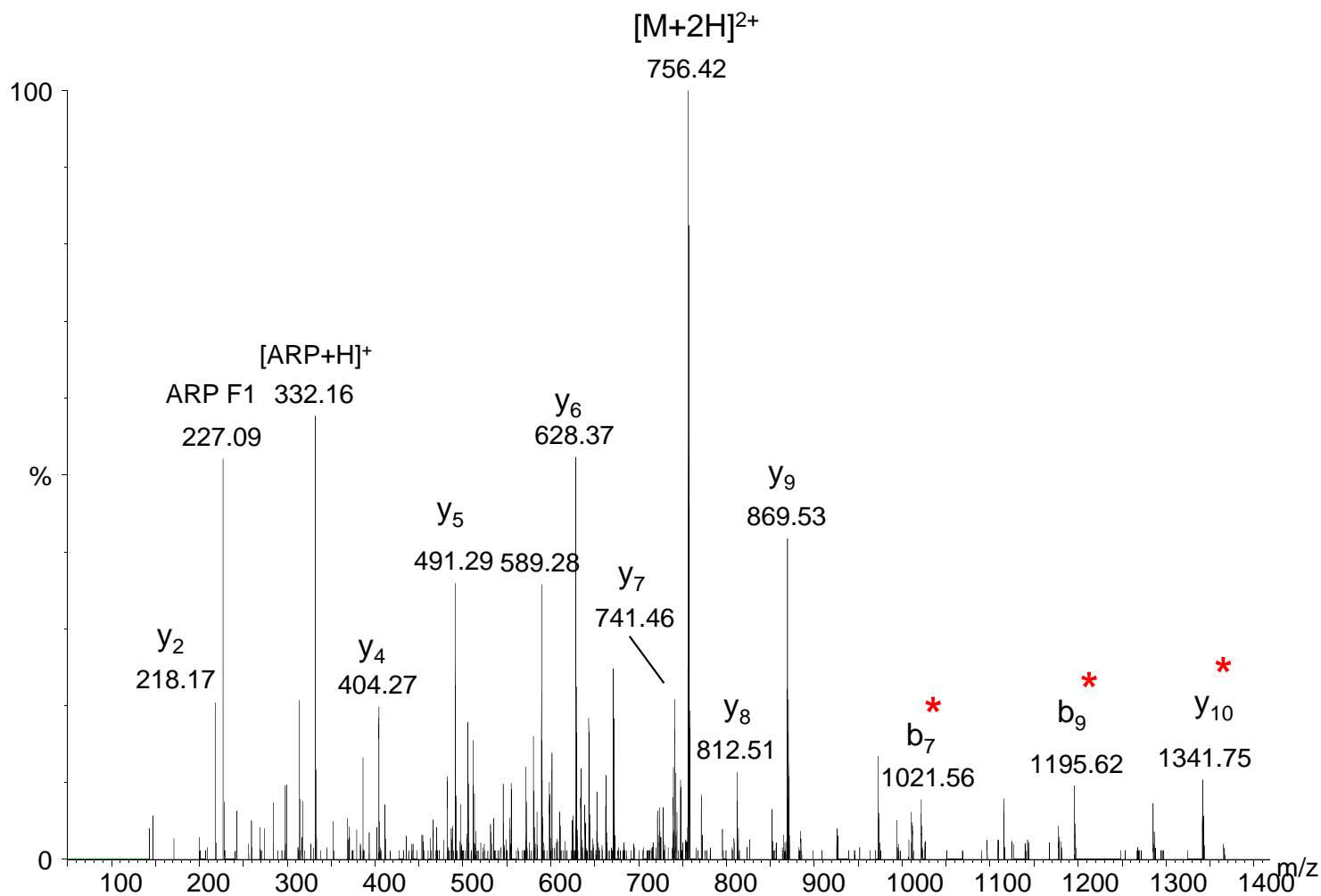
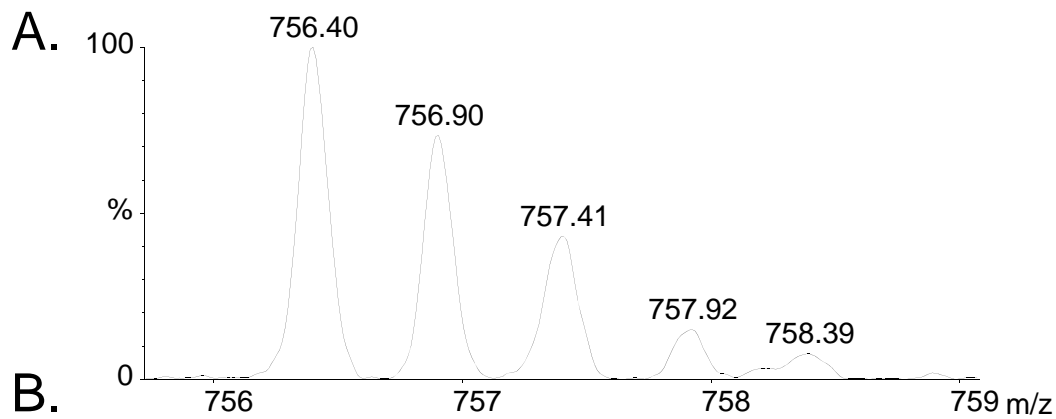
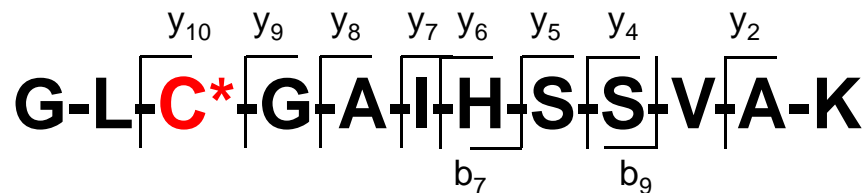


Figure S14. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide GLC*GAIHSSVAK; monoisotopic m/z_{calc} 756.38; accuracy $\Delta(m/z) = 0.02$ Da

ATPG_RAT: ATP synthase gamma chain

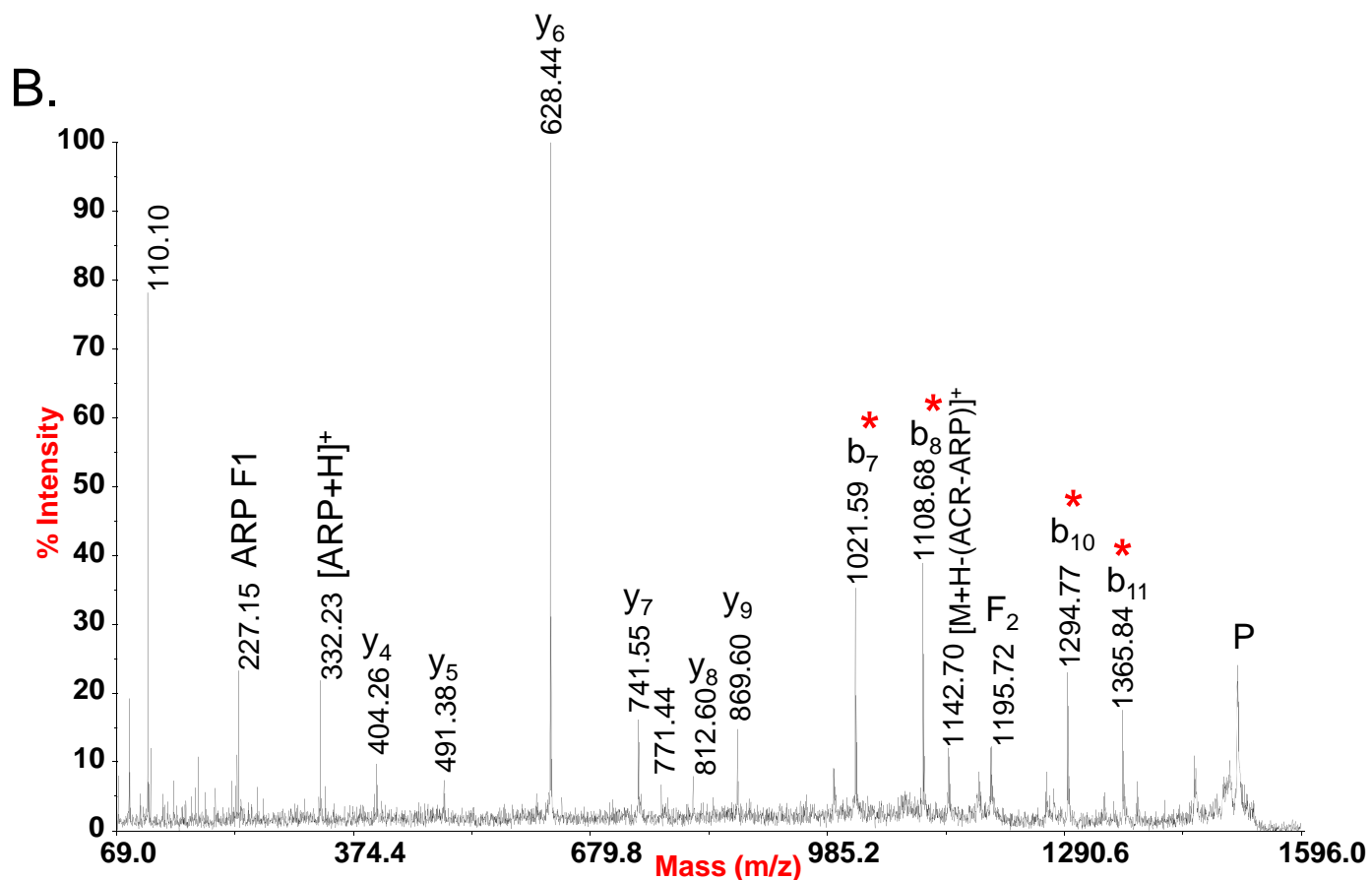
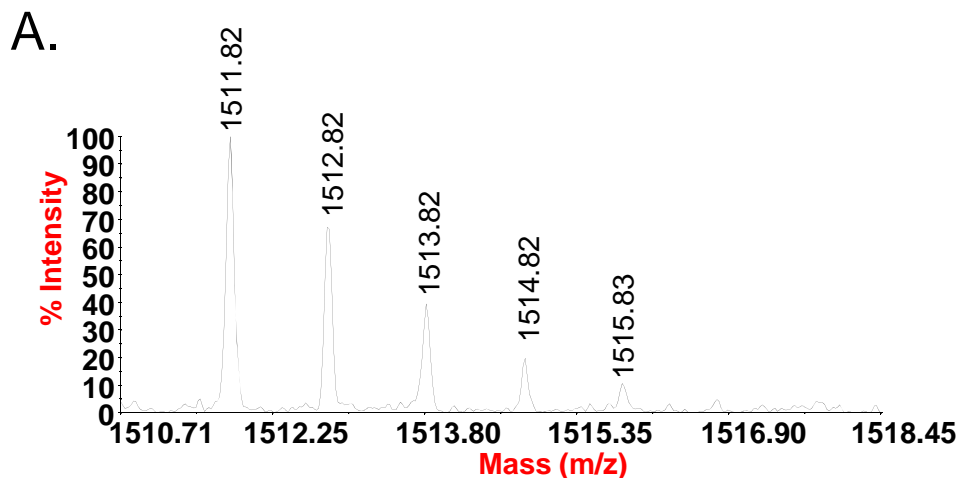
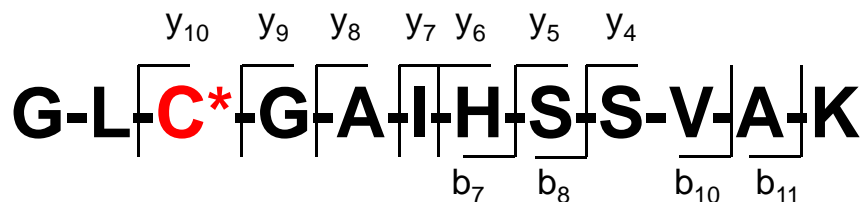
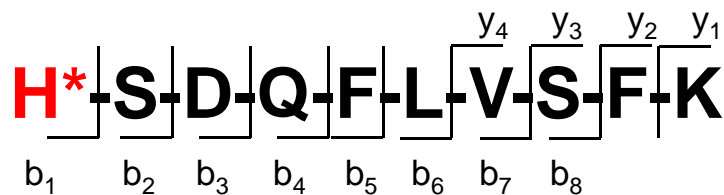
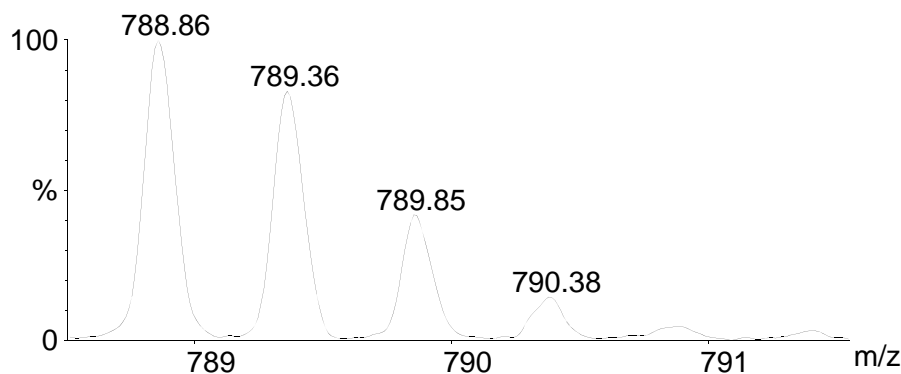


Figure S15. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide GLC*GAIHSSVAK; monoisotopic m/z_{calc} 1511.75; accuracy $\Delta(m/z) = 0.07$ Da

ATPG_RAT: ATP synthase gamma chain



A.



B.

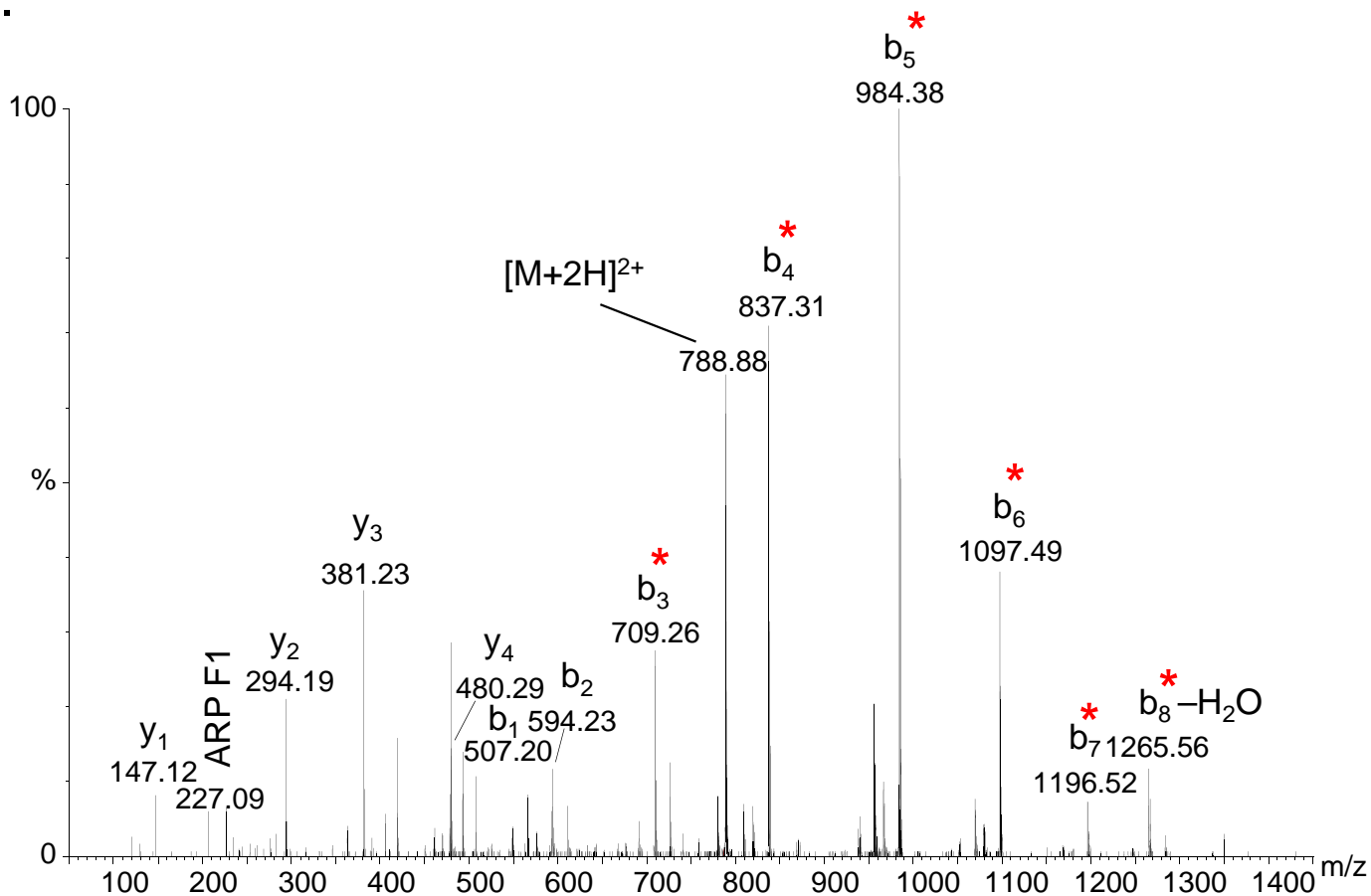
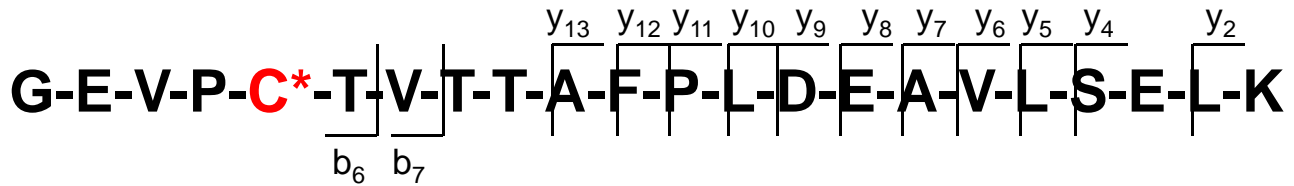
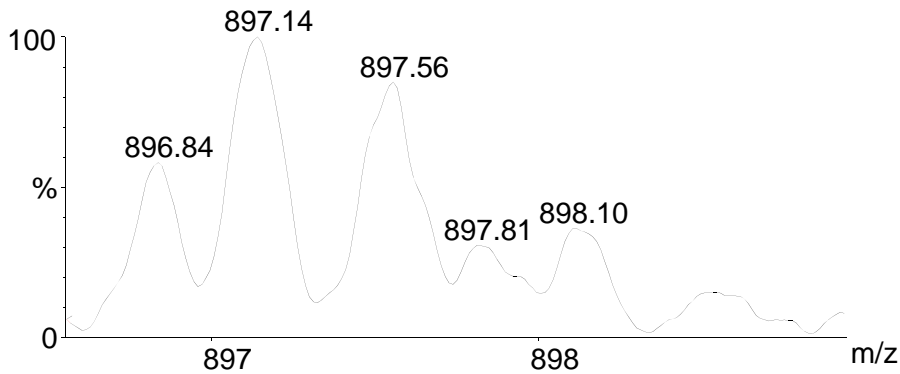


Figure S16. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide H*SDQFLVSFK; monoisotopic m/z_{calc} 788.88; accuracy $\Delta(m/z) = -0.02$ Da

ATPO_RAT: ATP synthase O subunit



A.



B.

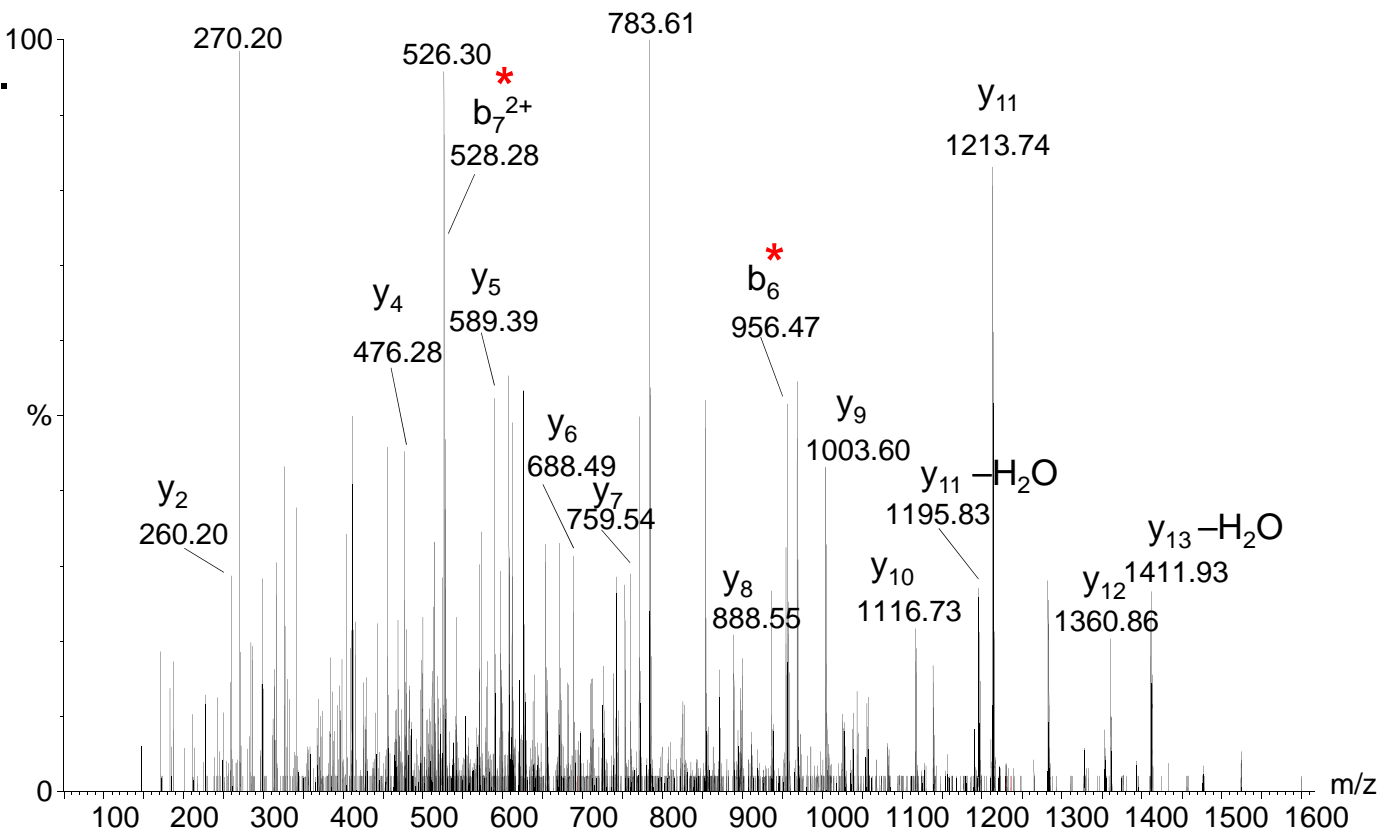
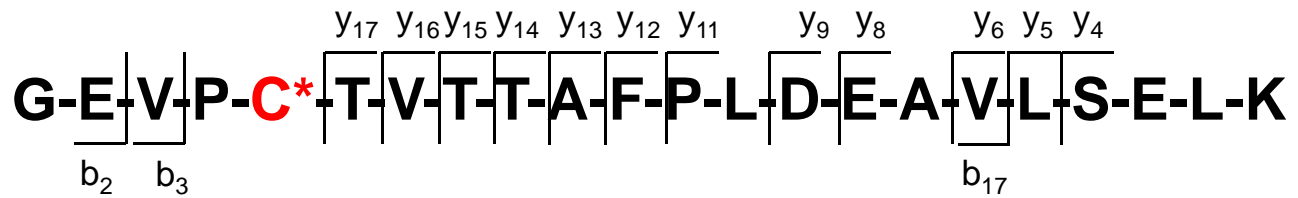
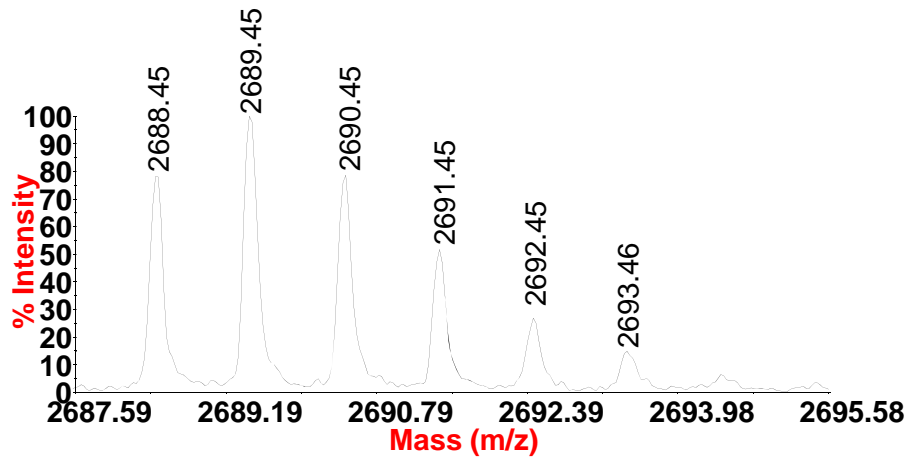


Figure S18. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+3H]^{3+}$ ion of the ARP labeled, acrolein modified peptide GEVPC*TVTTAFPLDEAVLSELK; monoisotopic m/z_{calc} 896.78; accuracy $\Delta(m/z) = 0.06$ Da

ATPO_RAT: ATP synthase O subunit



A.



B.

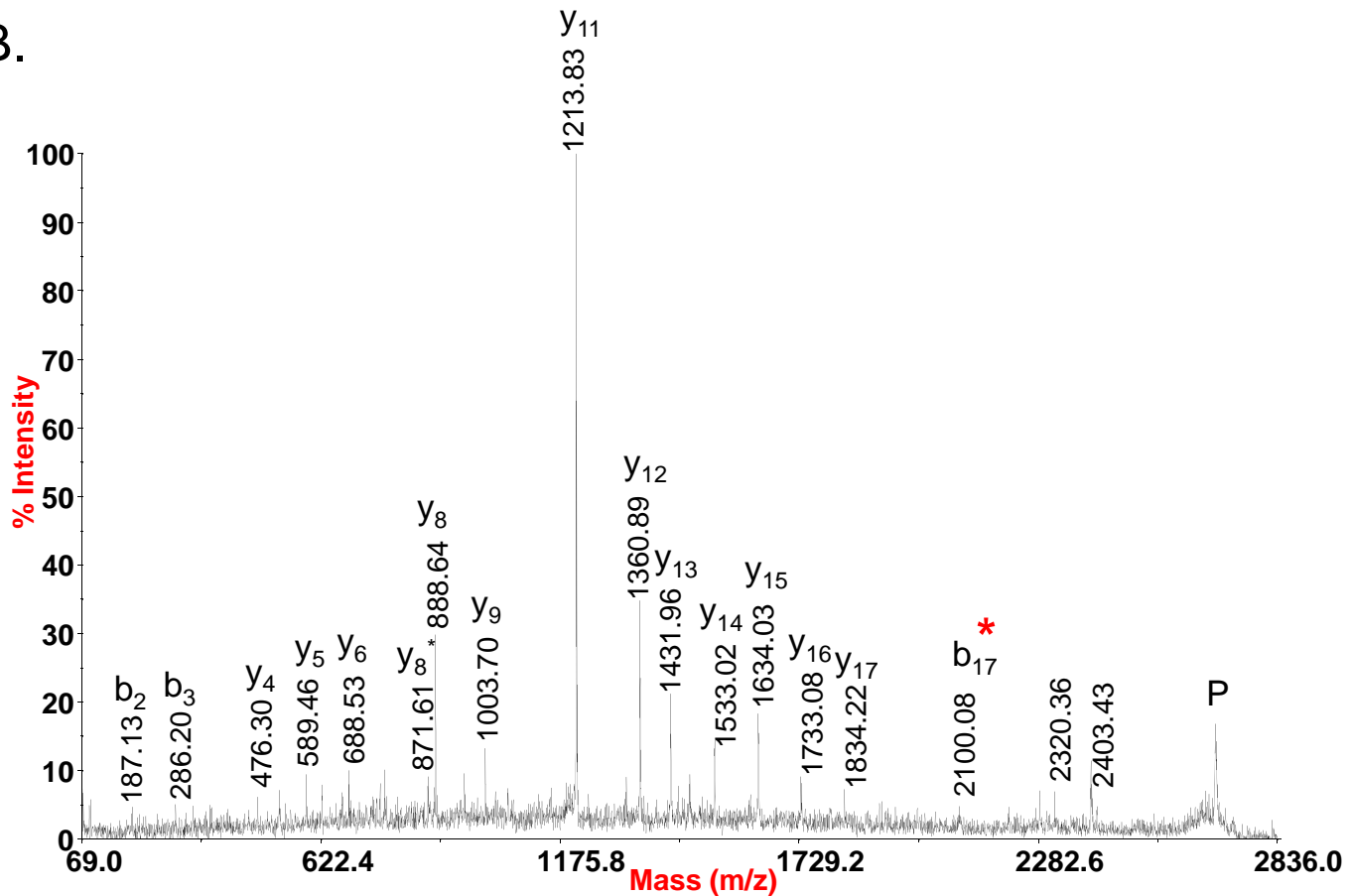
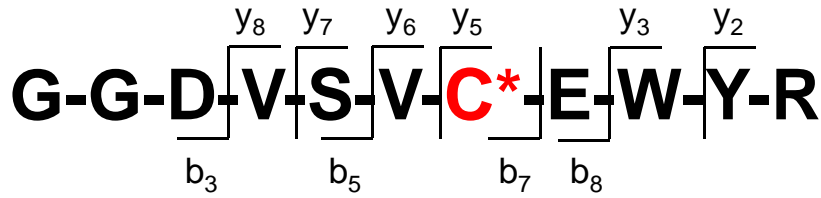
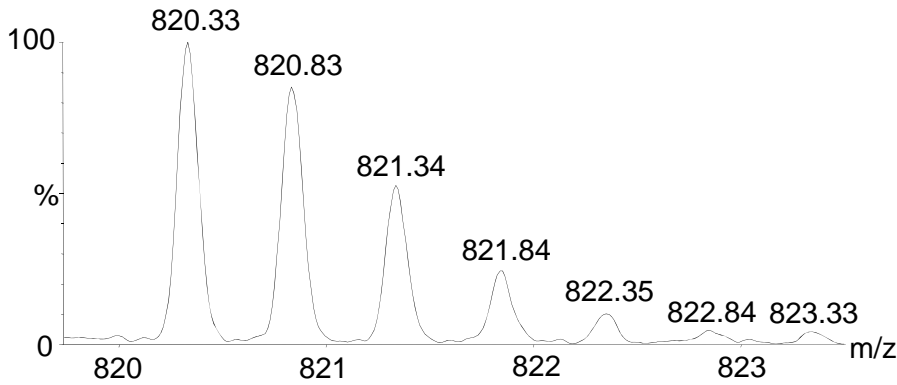


Figure S19. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide GEVPC*TVTTAFPLDEAVLSELK; monoisotopic m/z_{calc} 2688.33; accuracy $\Delta(m/z) = 0.12$ Da

CX6B1_MOUSE, Cytochrome c oxidase subunit VIb isoform



A.



B.

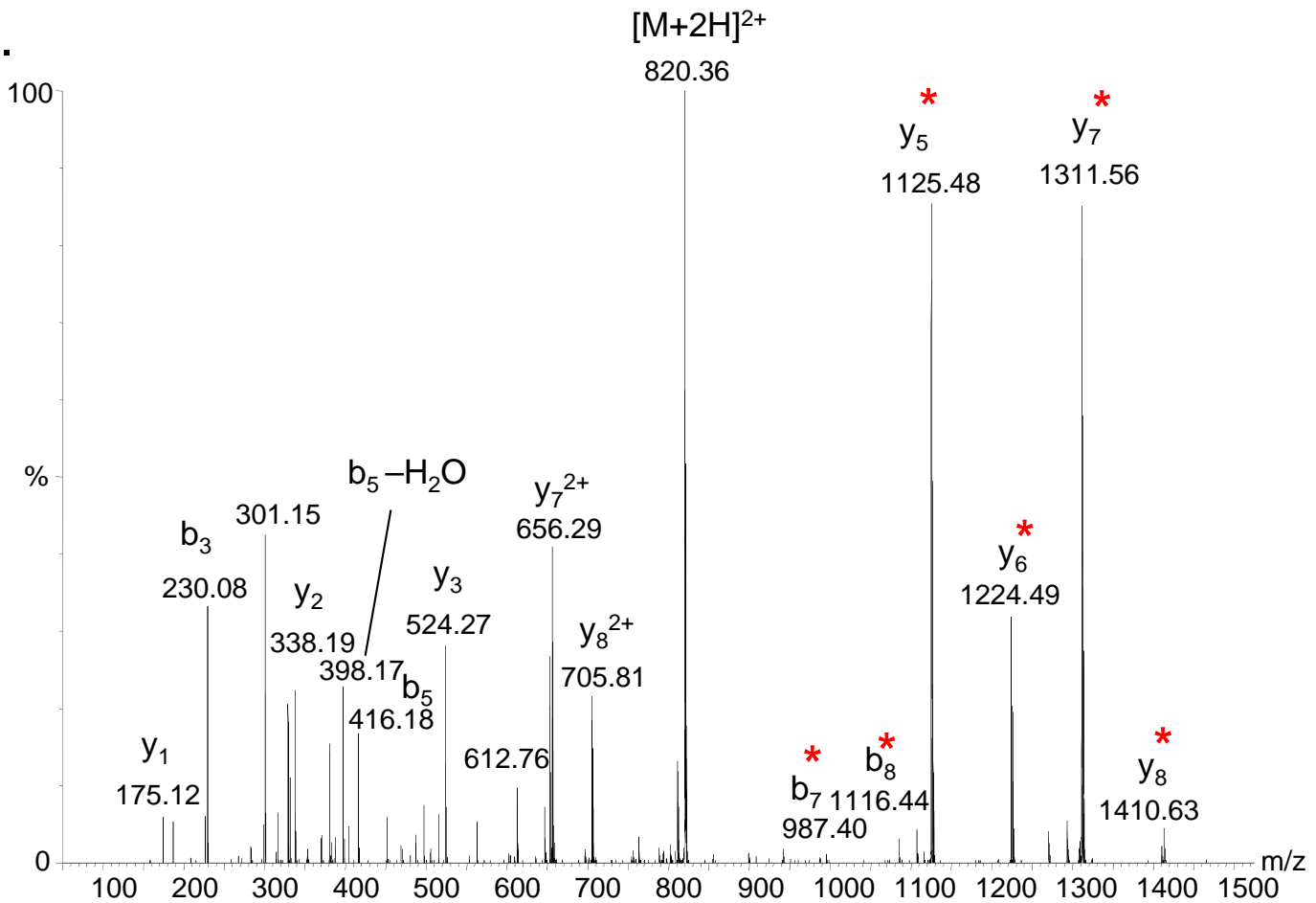


Figure S20. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide GGDVSV-C*EWYR; monoisotopic m/z_{calc} 820.35; accuracy $\Delta(m/z) = -0.02$ Da

NDUV1_MOUSE: NADH dehydrogenase [ubiquinone] flavoprotein 1

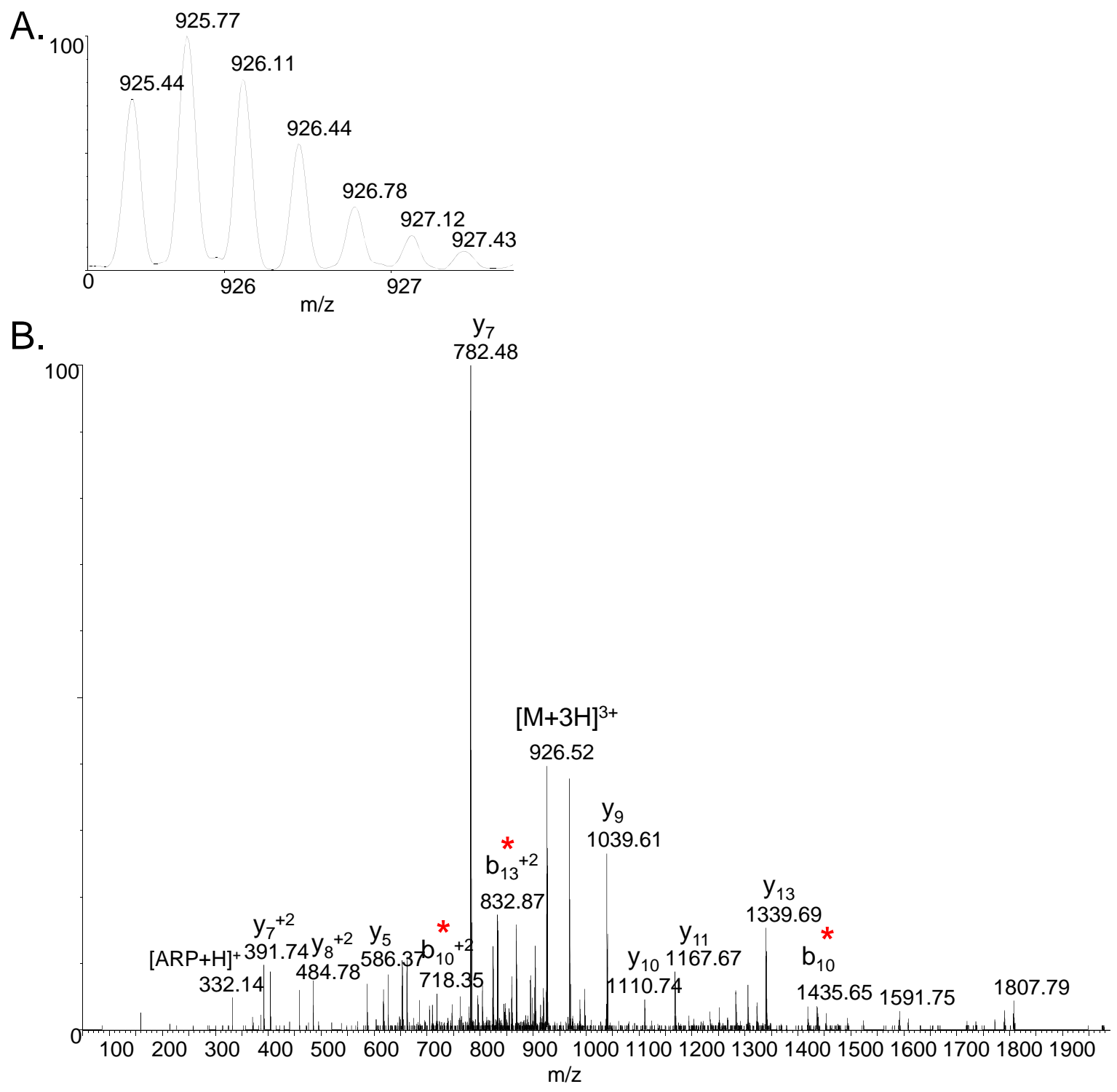
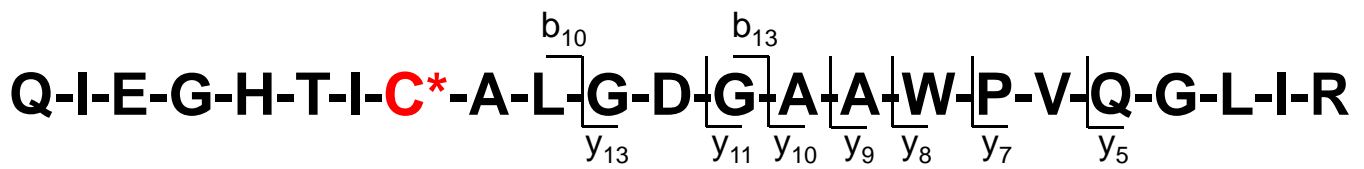


Figure S21. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the [M+3H]³⁺ ion of the ARP labeled, acrolein modified peptide QIEGHTIC*ALGDGAAWVPVQGLIR; monoisotopic m/z_{calc} 925.47; accuracy Δ(m/z) = -0.03 Da

QCR1_RAT: Ubiquinol-cytochrome-c reductase complex core protein 1

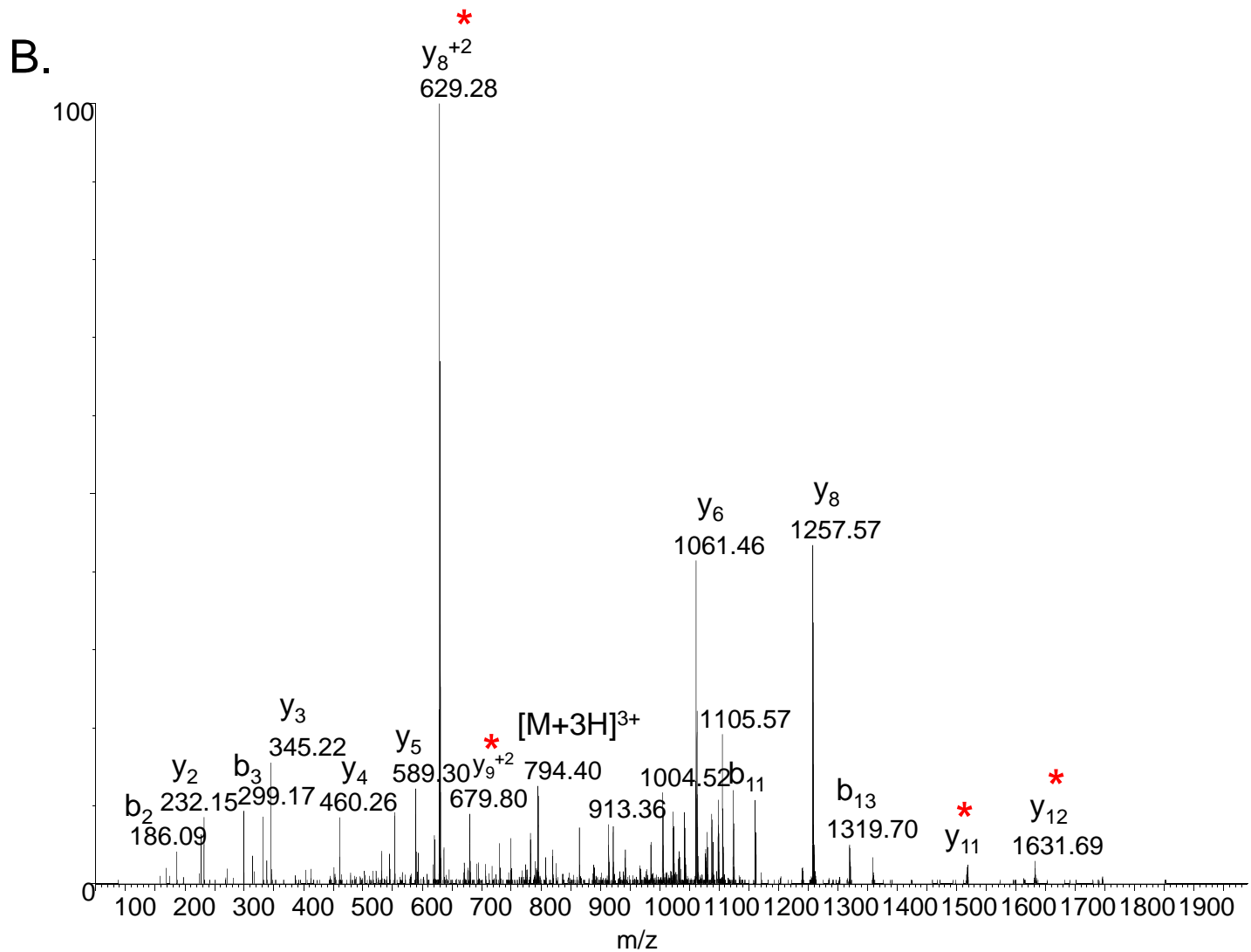
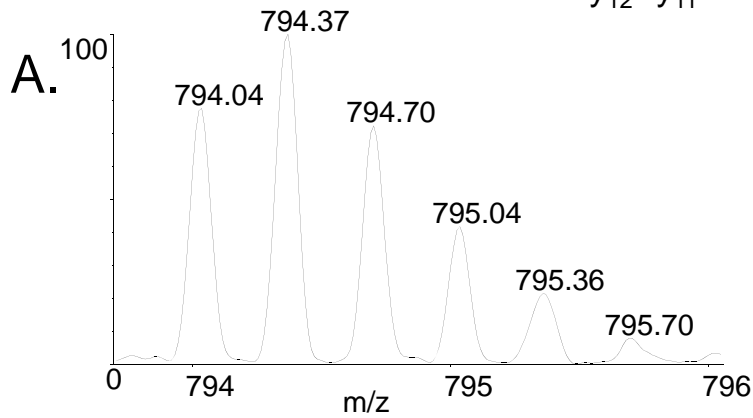
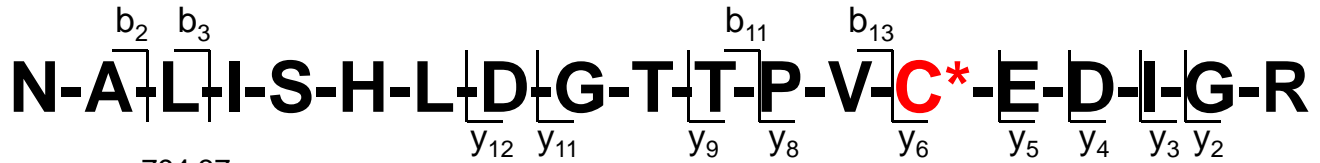


Figure S22. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+3H]^{3+}$ ion of the ARP labeled, acrolein modified peptide NALISHLDGTT $\overline{PVC^*}$ EDIGR; monoisotopic m/z_{calc} 794.05; accuracy $\Delta(m/z) = -0.01$ Da

QCR1_RAT: Ubiquinol-cytochrome-c reductase complex core protein 1

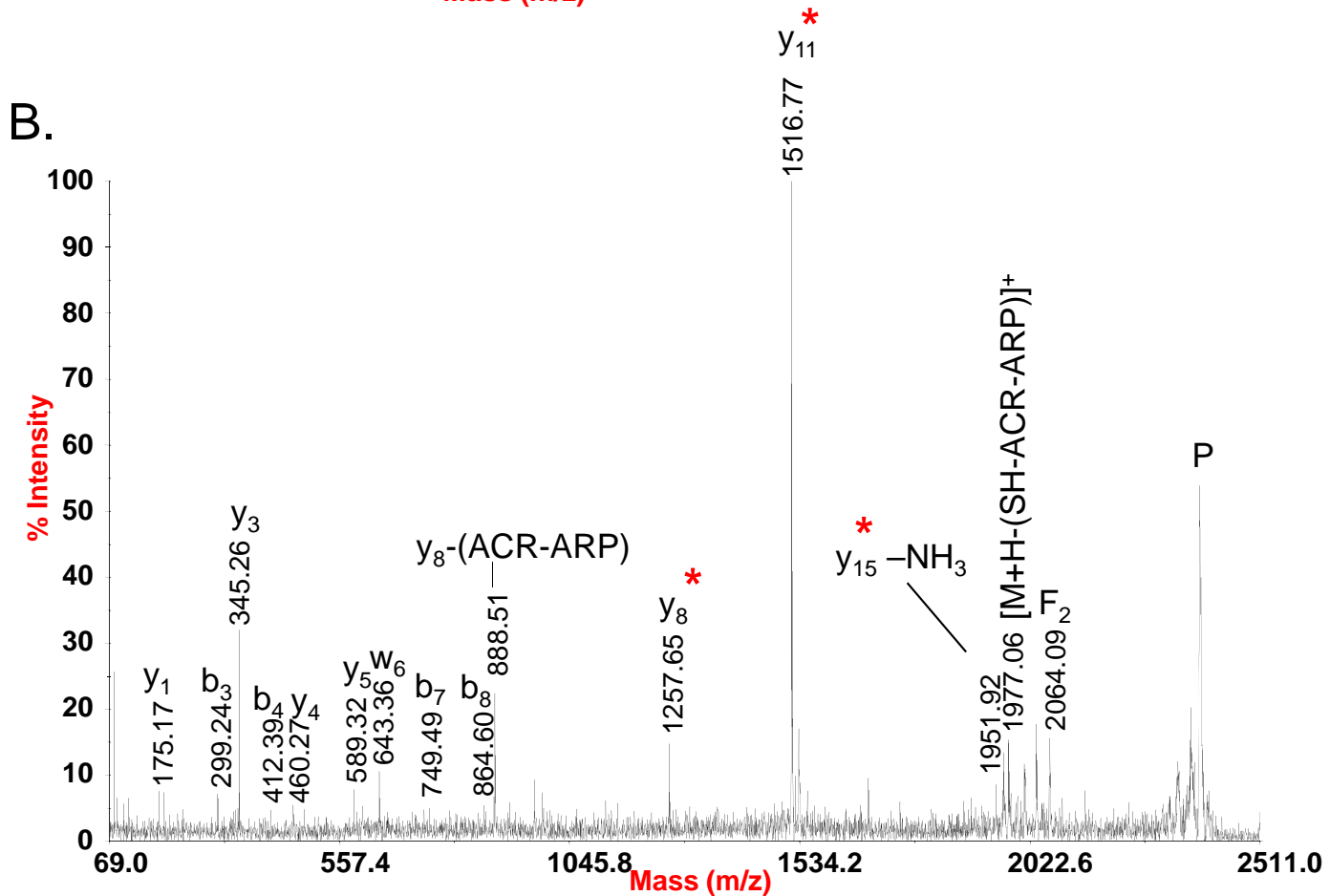
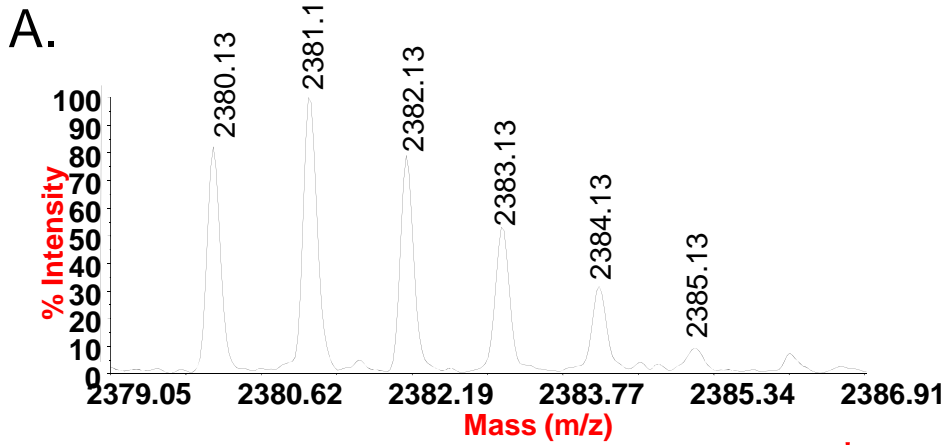
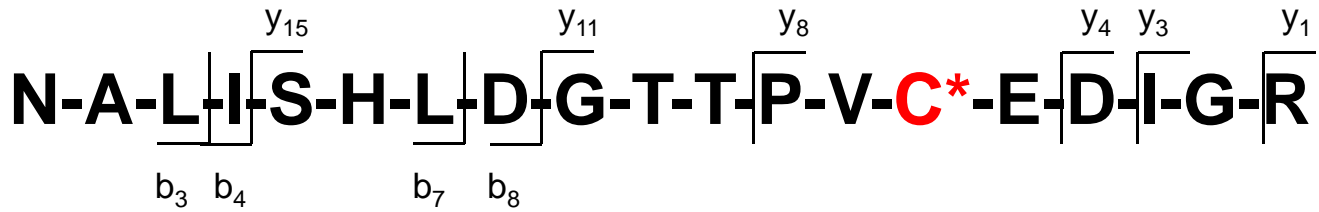
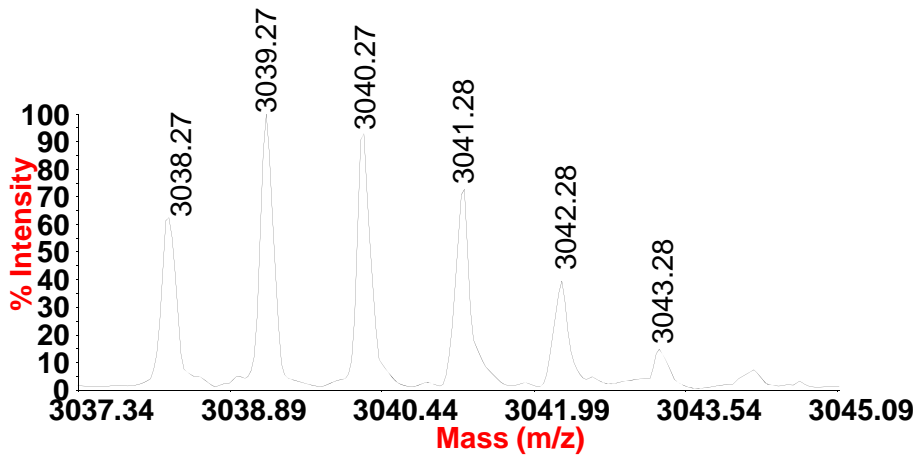


Figure S23. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide NALISHLDGTTTPVC*EDIGR; monoisotopic m/z_{calc} 2380.14; accuracy $\Delta(m/z) = -0.01$ Da

QCR1_RAT: Ubiquinol-cytochrome-c reductase complex core protein 1



A.



B.

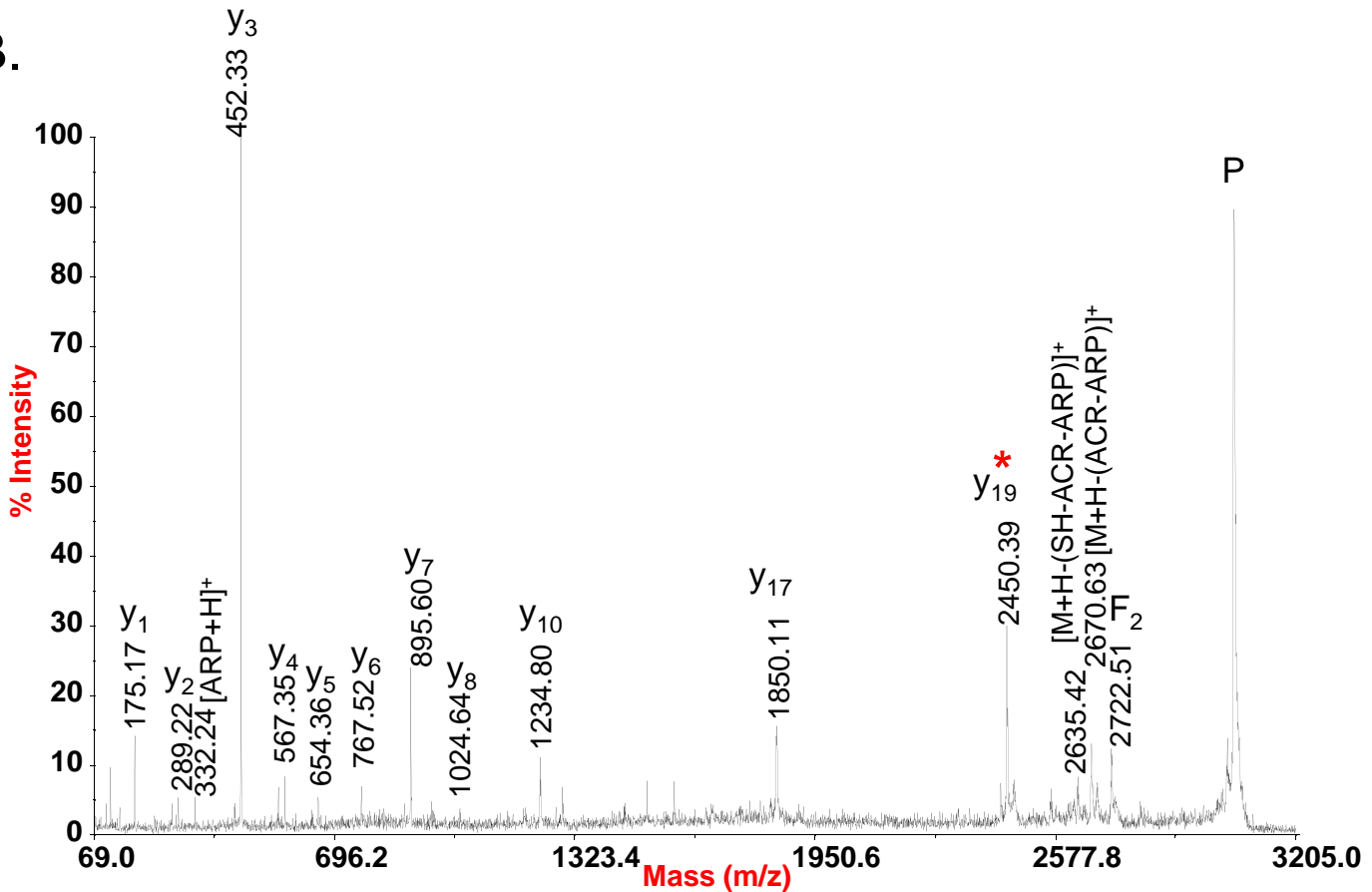


Figure S24. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide YFYDQC*PAVAGYGP...; monoisotopic m/z_{calc} 3038.34; accuracy $\Delta(m/z) = -0.07$ Da

QCR2_RAT: Ubiquinol-cytochrome-c reductase complex core protein 2

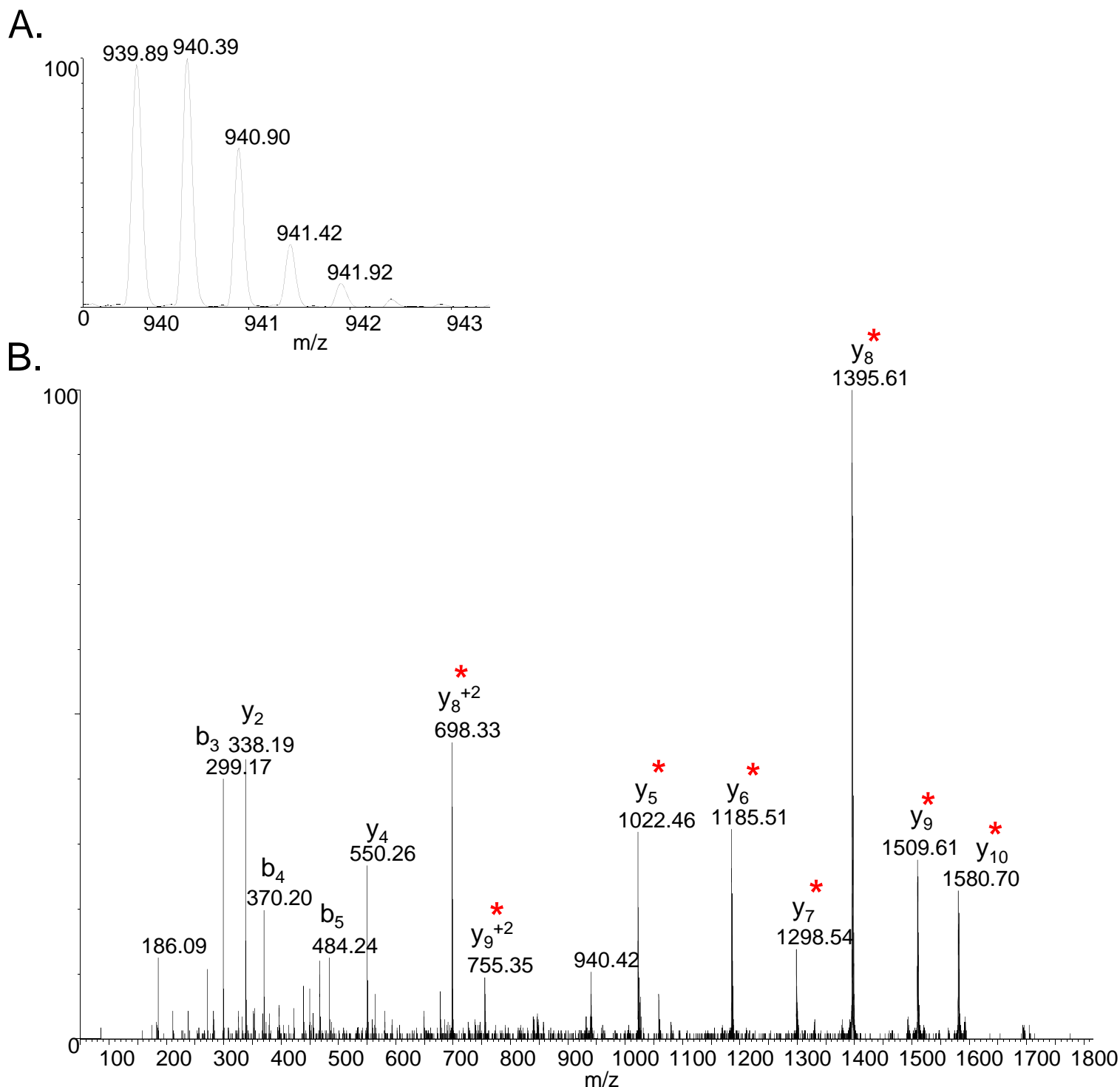
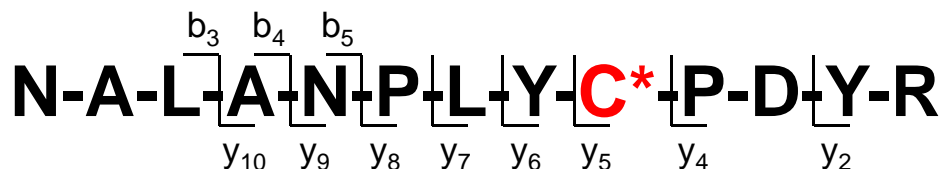


Figure S25. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide NALANPLYC*PDYR; monoisotopic m/z_{calc} 939.93; accuracy $\Delta(m/z) = -0.04$ Da

QCR2_RAT: Ubiquinol-cytochrome-c reductase complex core protein 2

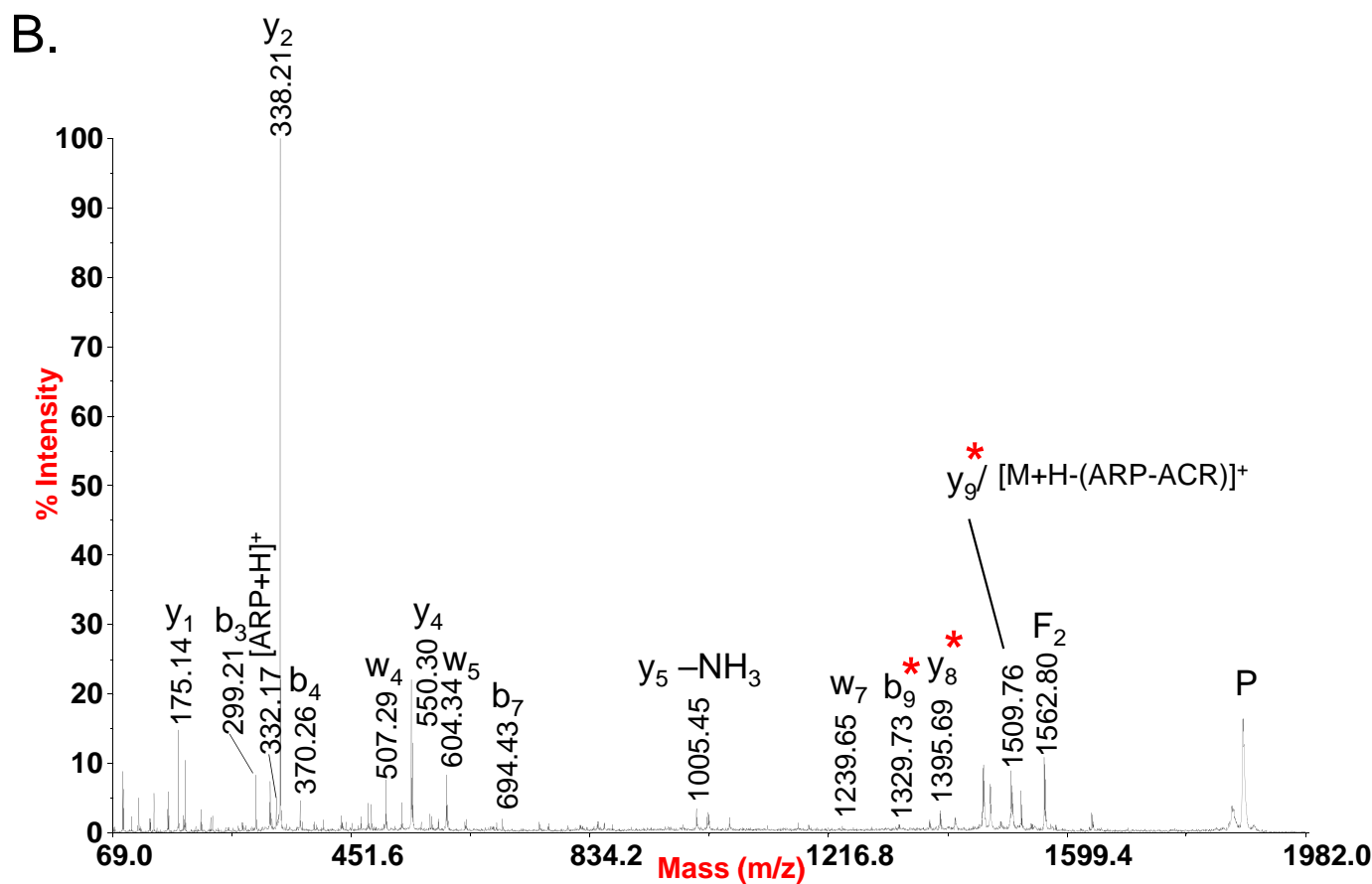
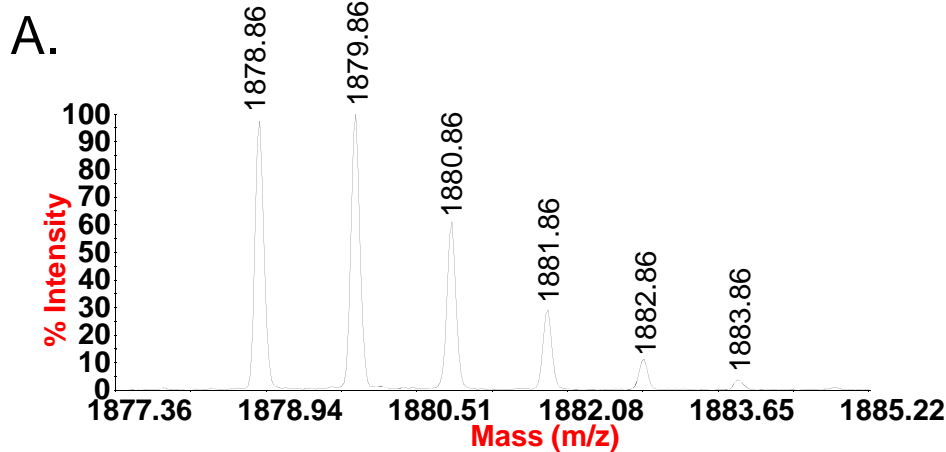
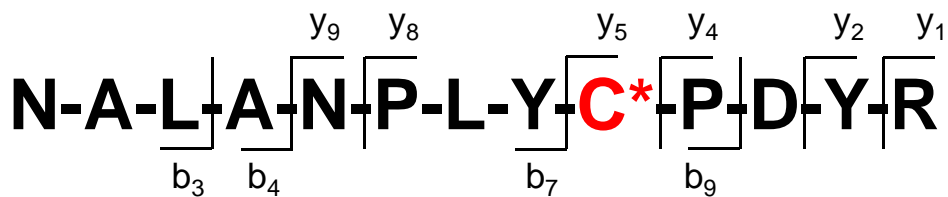


Figure S26. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide NALANPLYC*PDYR; monoisotopic m/z_{calc} 1878.86; accuracy $\Delta(m/z) = 0.00$ Da

QCR2_RAT: Ubiquinol-cytochrome-c reductase complex core protein 2

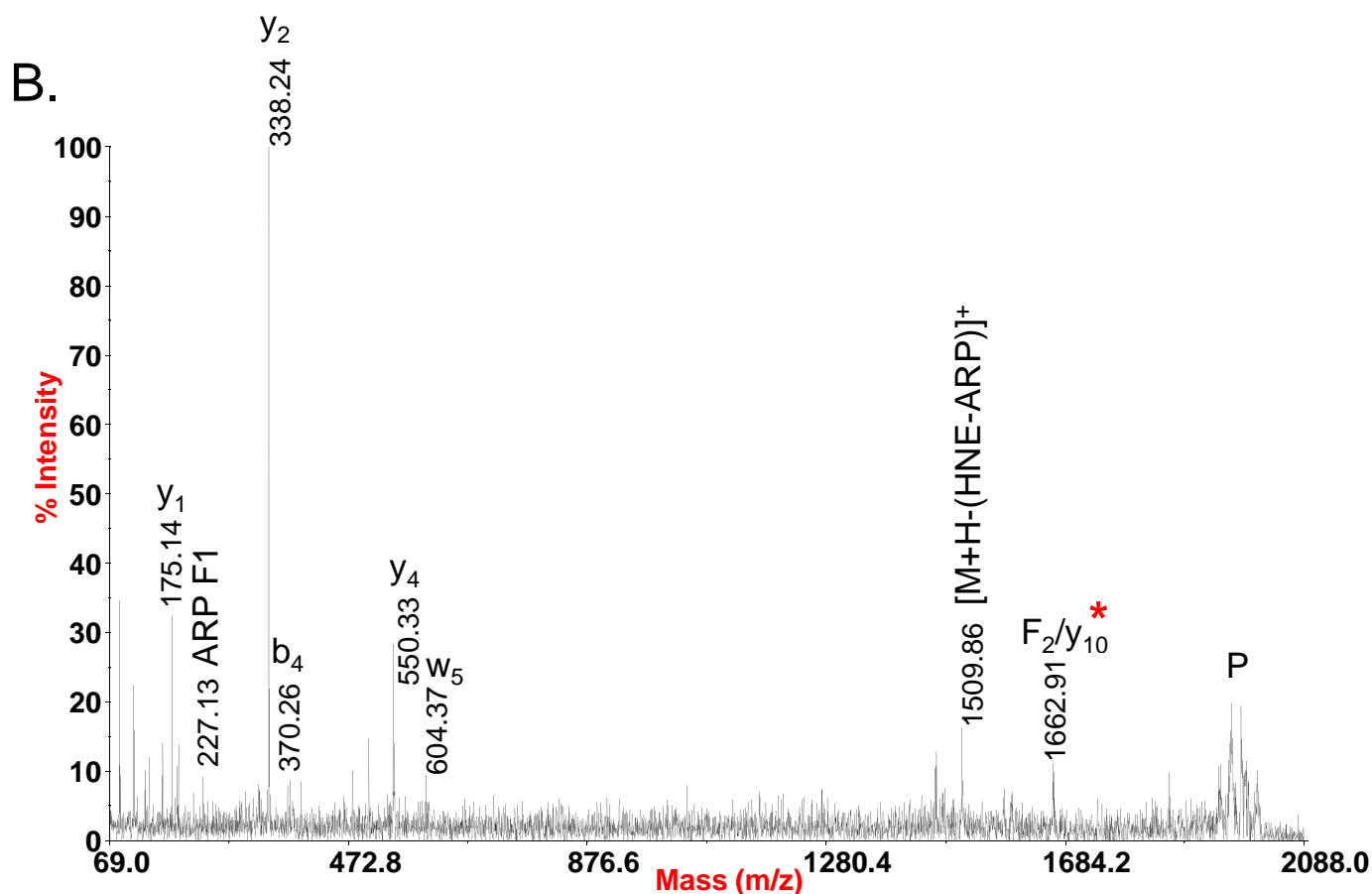
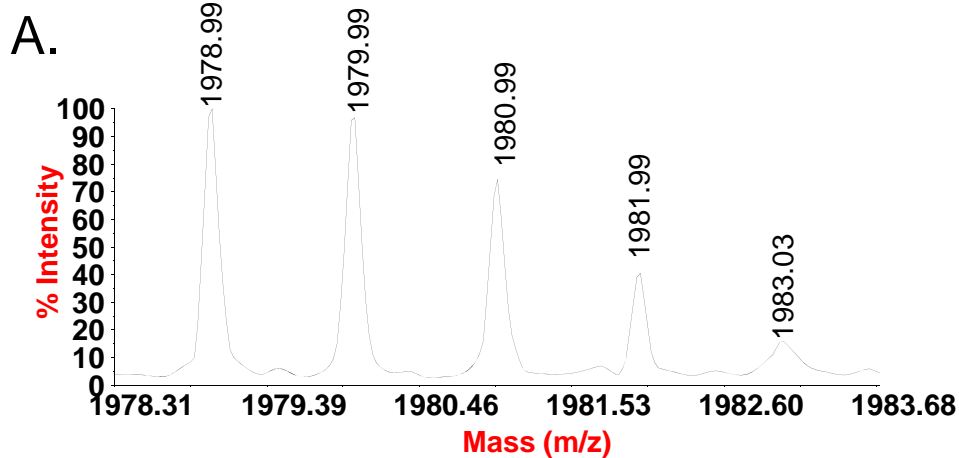
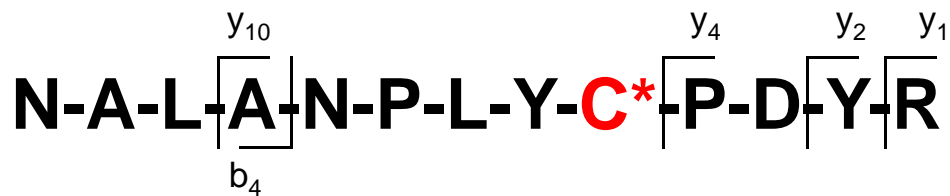


Figure S27. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, HNE modified peptide NALANPLYC*PDYR; monoisotopic m/z_{calc} 1978.95; accuracy $\Delta(m/z) = 0.04$ Da

QCR2_RAT: Ubiquinol-cytochrome-c reductase complex core protein 2

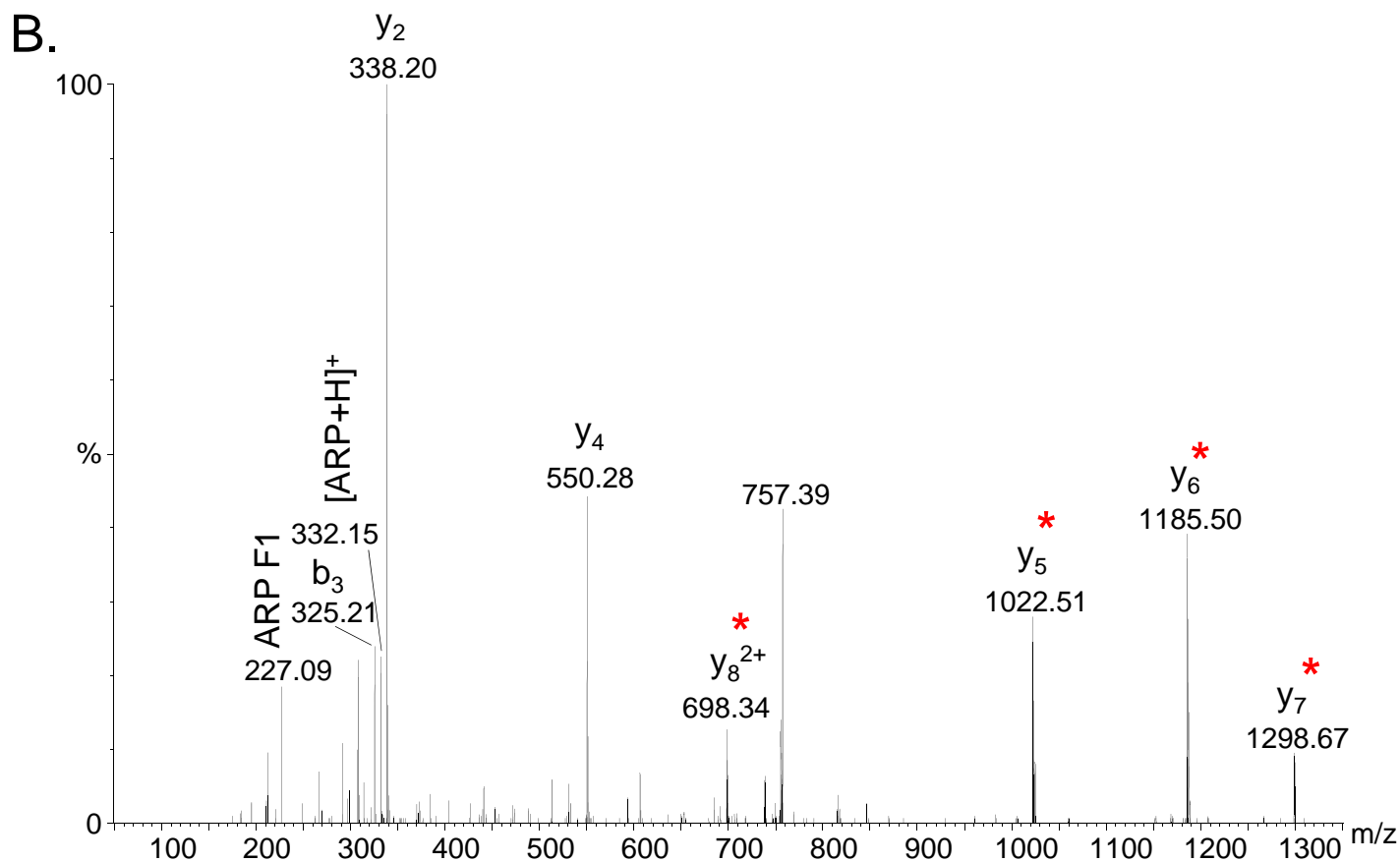
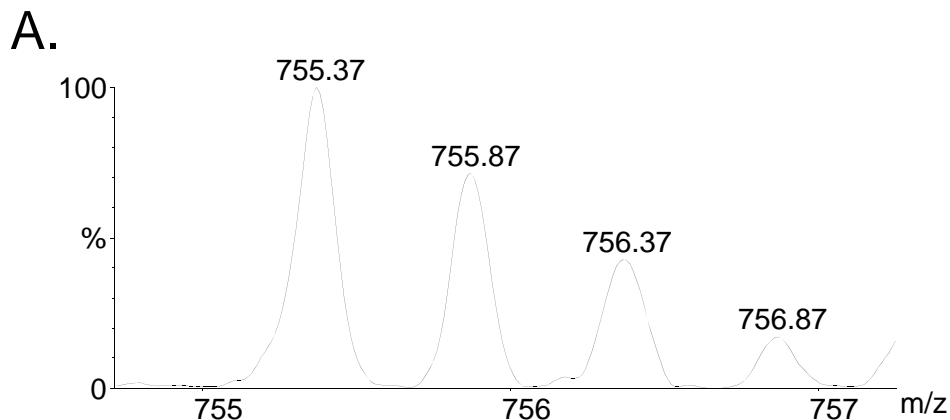
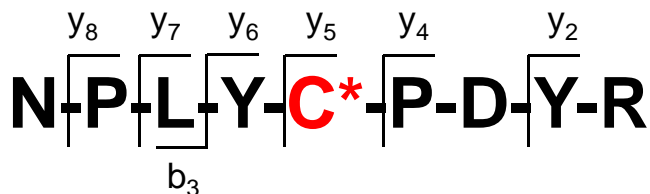


Figure S28. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide NPLYC*PDYR; monoisotopic m/z_{calc} 755.33; accuracy $\Delta(m/z) = 0.04$ Da

DHSA_RAT: Succinate dehydrogenase [ubiquinone] flavoprotein subunit

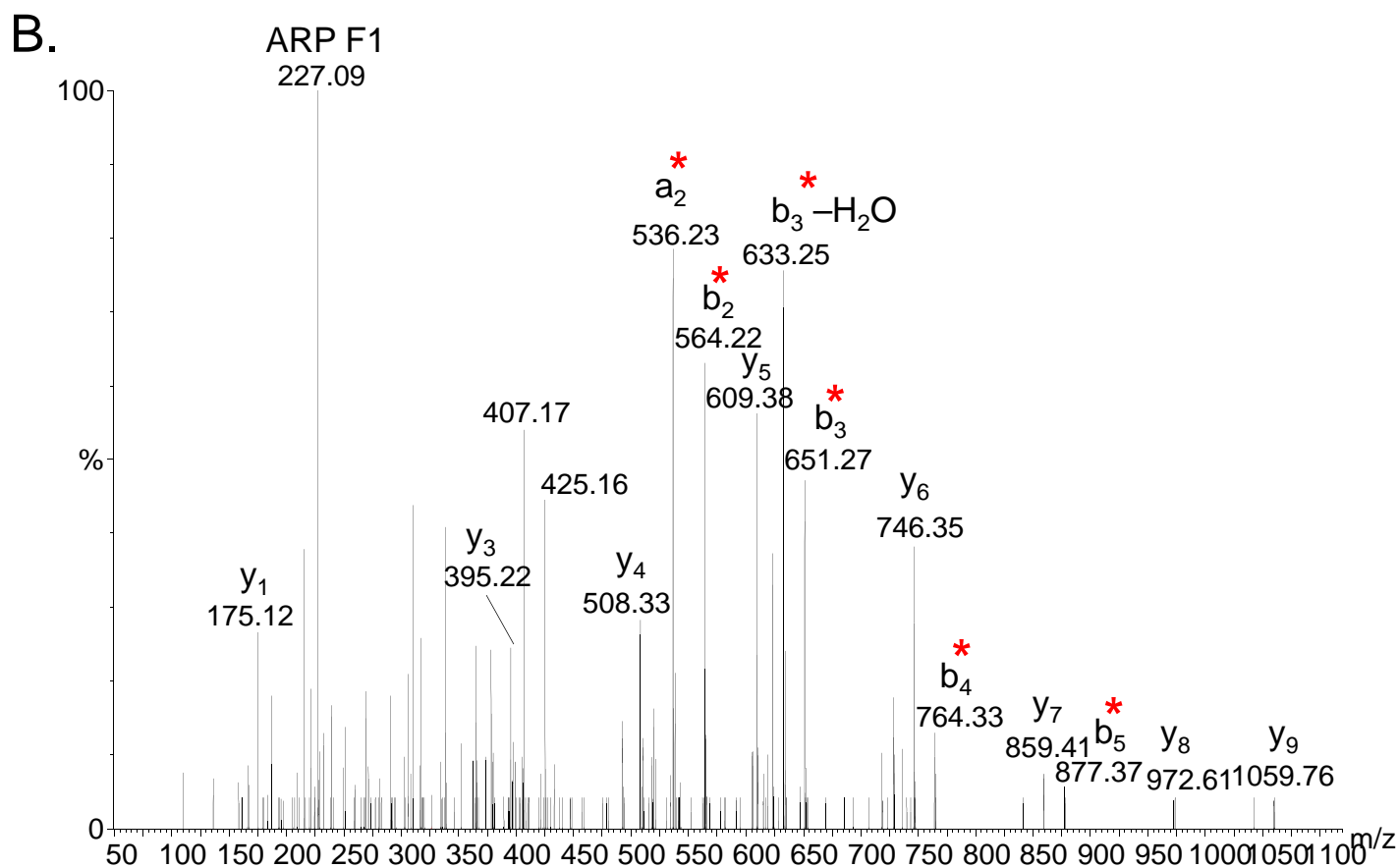
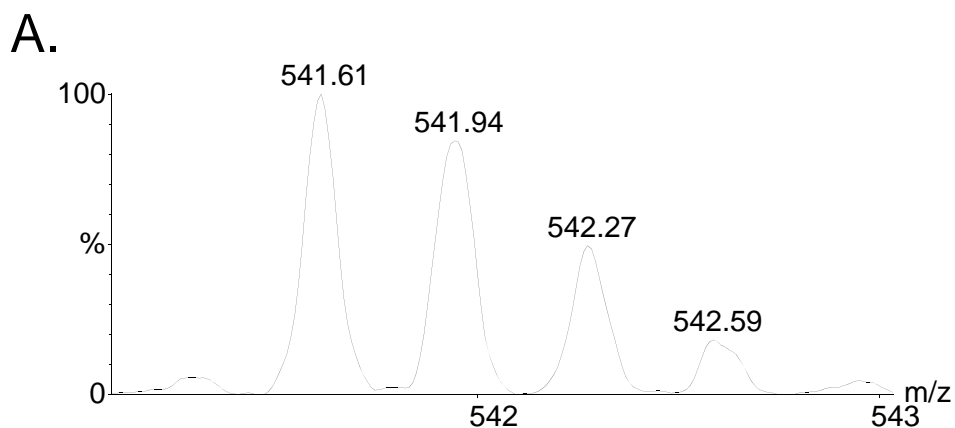
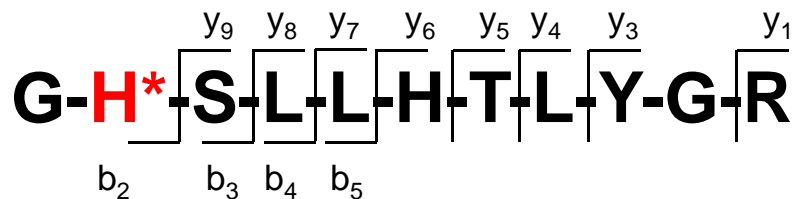


Figure S29. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+3H]^{3+}$ ion of the ARP labeled, acrolein modified peptide GH***S**LLHTLYGR; monoisotopic m/z_{calc} 541.61; accuracy $\Delta(m/z) = 0.00$ Da

DHSA_RAT: Succinate dehydrogenase [ubiquinone] flavoprotein subunit

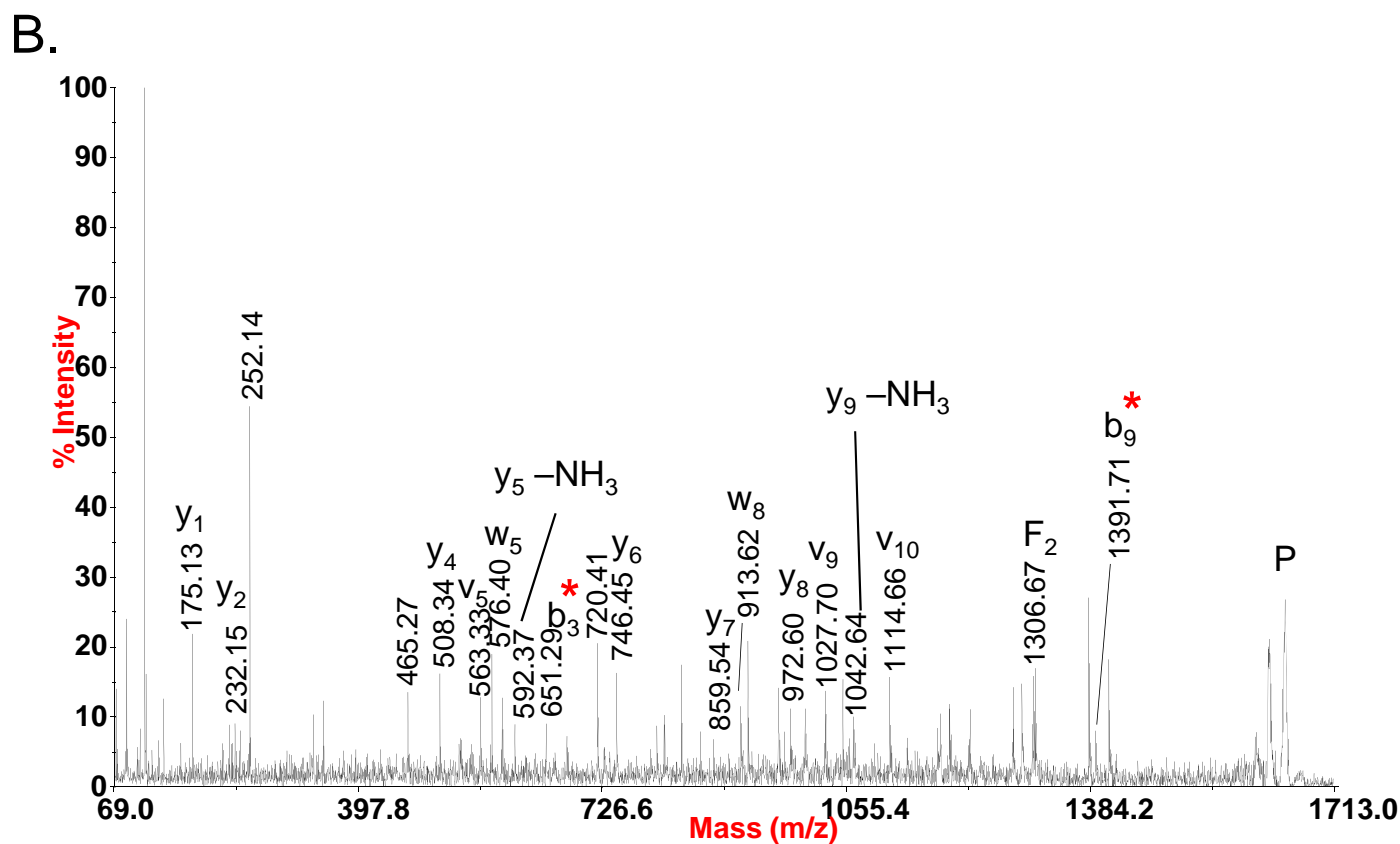
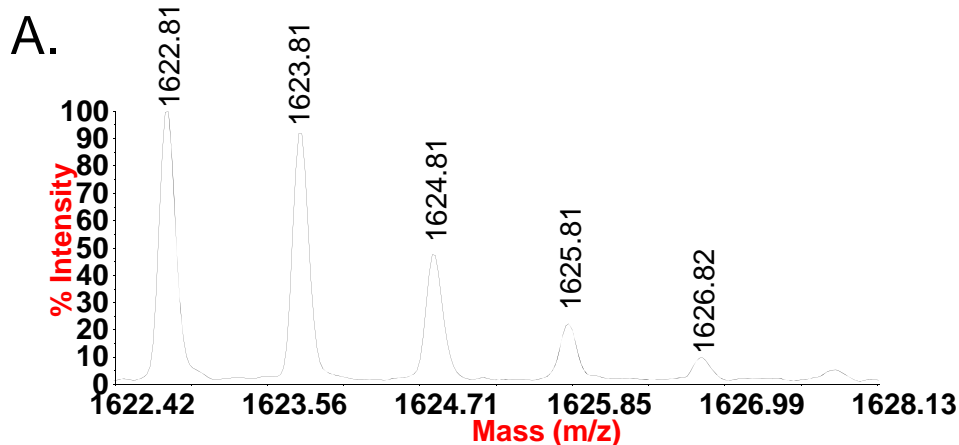
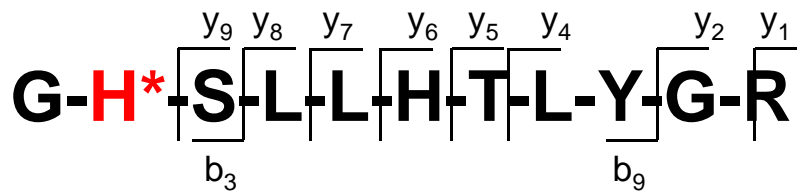


Figure S30. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide GH***S**LLHTLYGR; monoisotopic m/z_{calc} 1622.82; accuracy $\Delta(m/z) = -0.01$ Da

Q6IRH6_RAT: Slc25a3 protein

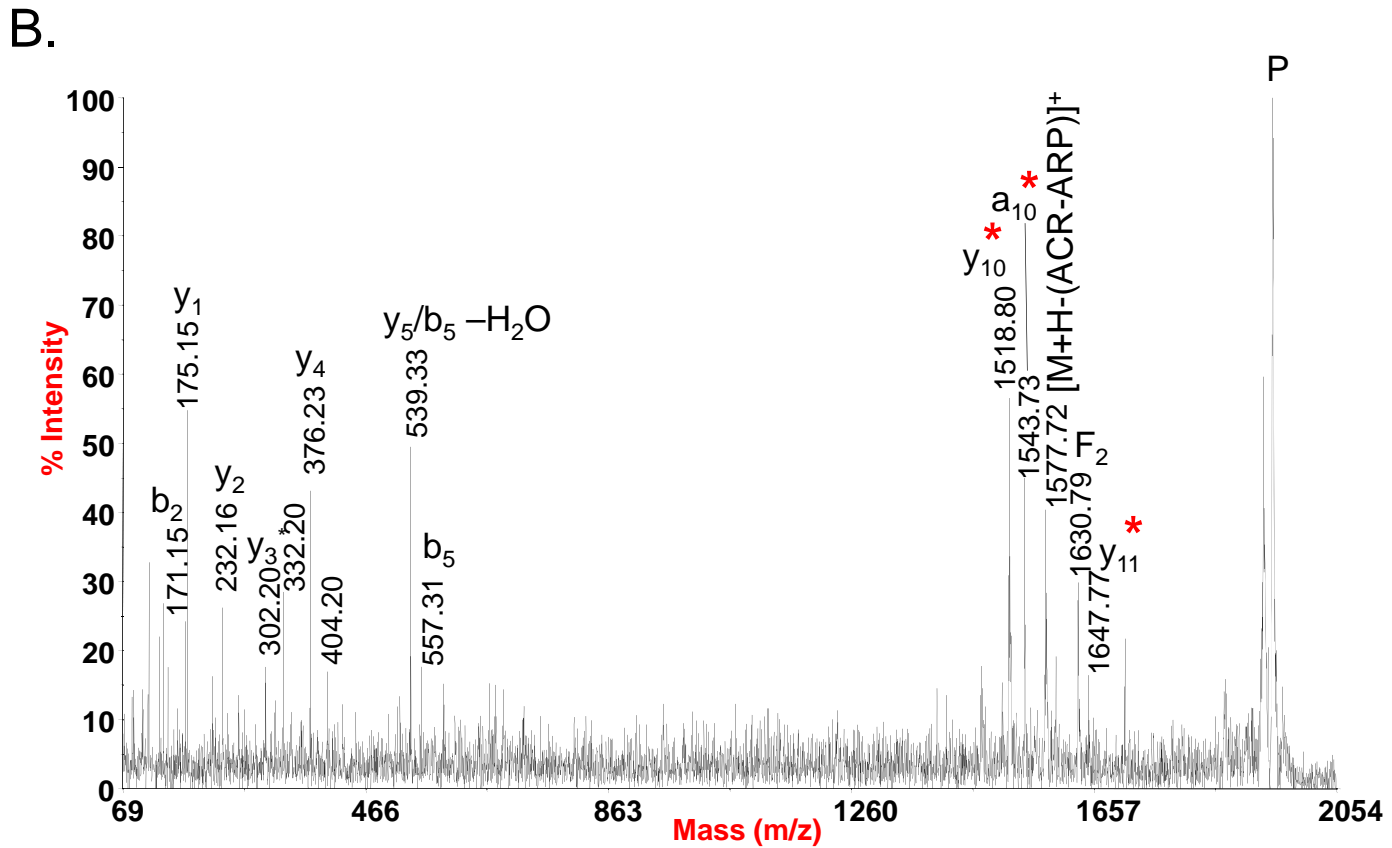
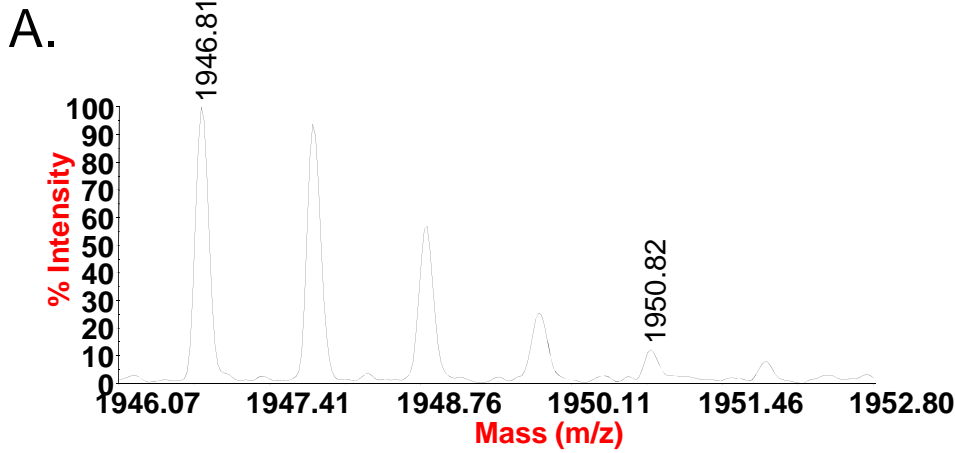
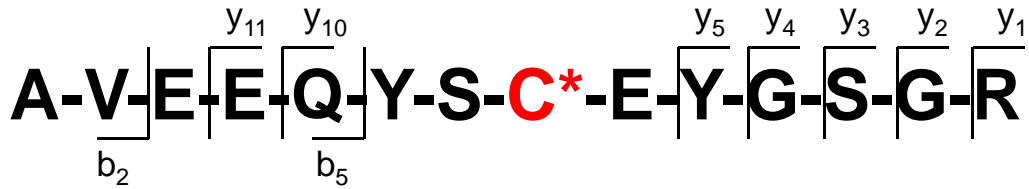
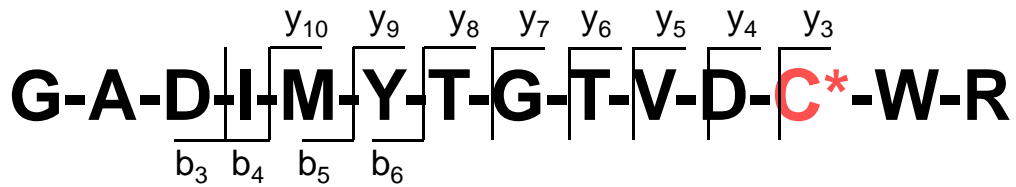
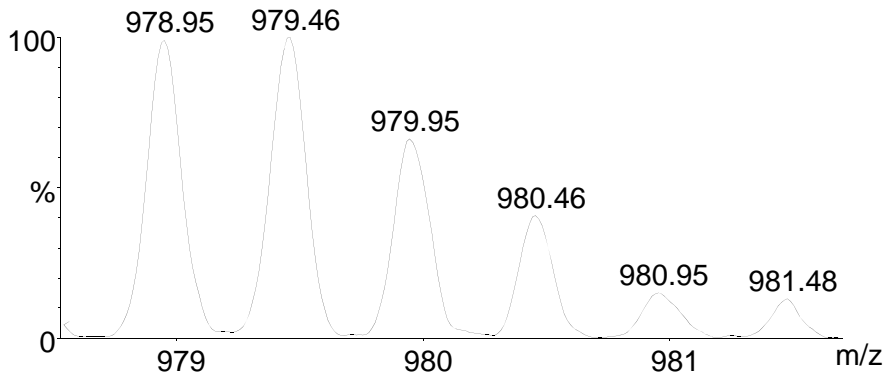


Figure S31. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide AVEEQYSC*EYGSGR; monoisotopic m/z_{calc} 1946.80; accuracy $\Delta(m/z) = 0.01$ Da

ADT1_RAT: ADP/ATP translocase 1



A.



B.

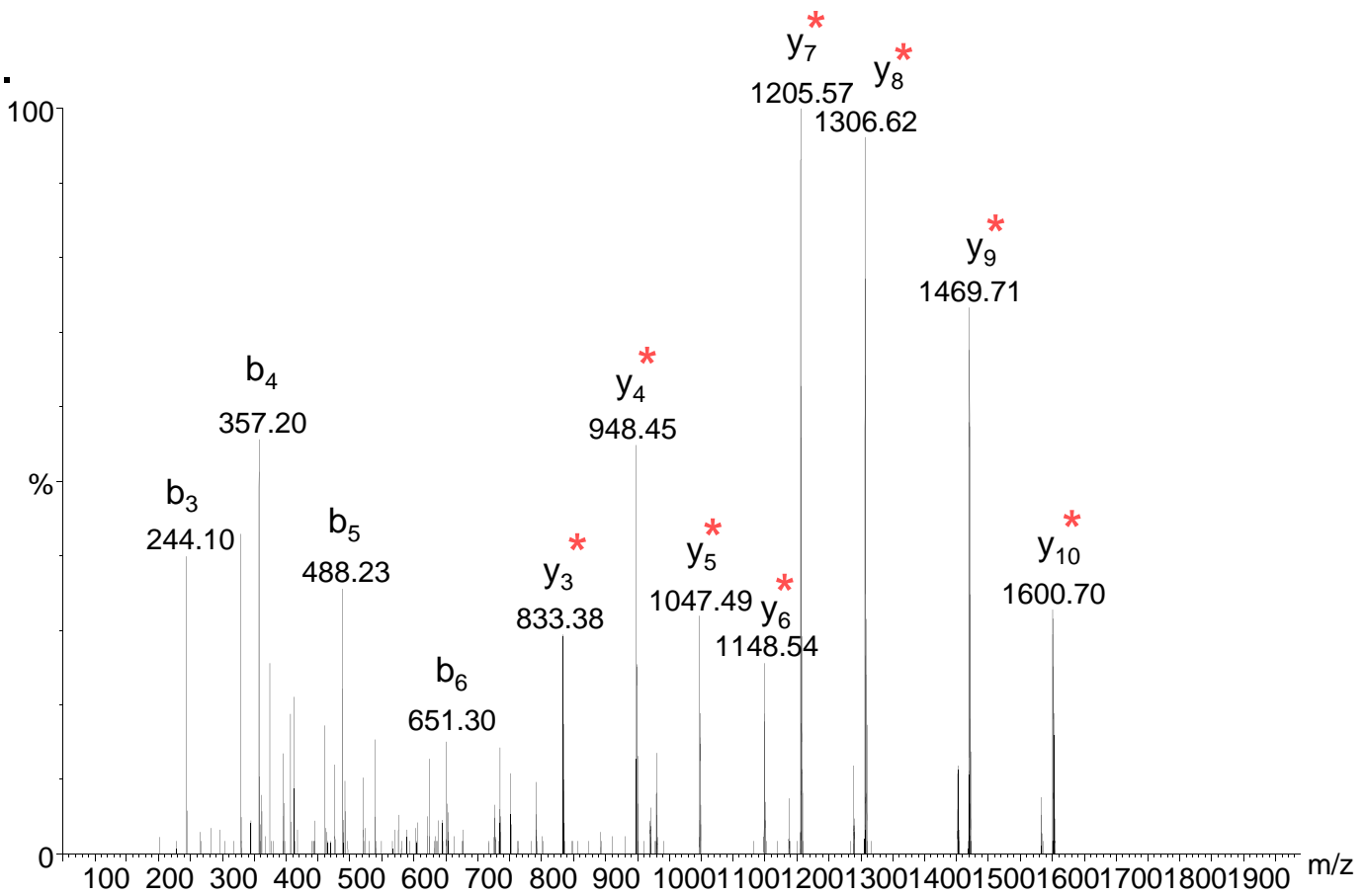


Figure S32. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide GADIMYTGTVD-C*WR; monoisotopic m/z_{calc} 978.92; accuracy $\Delta(m/z) = 0.03$ Da

ADT1_RAT: ADP/ATP translocase 1

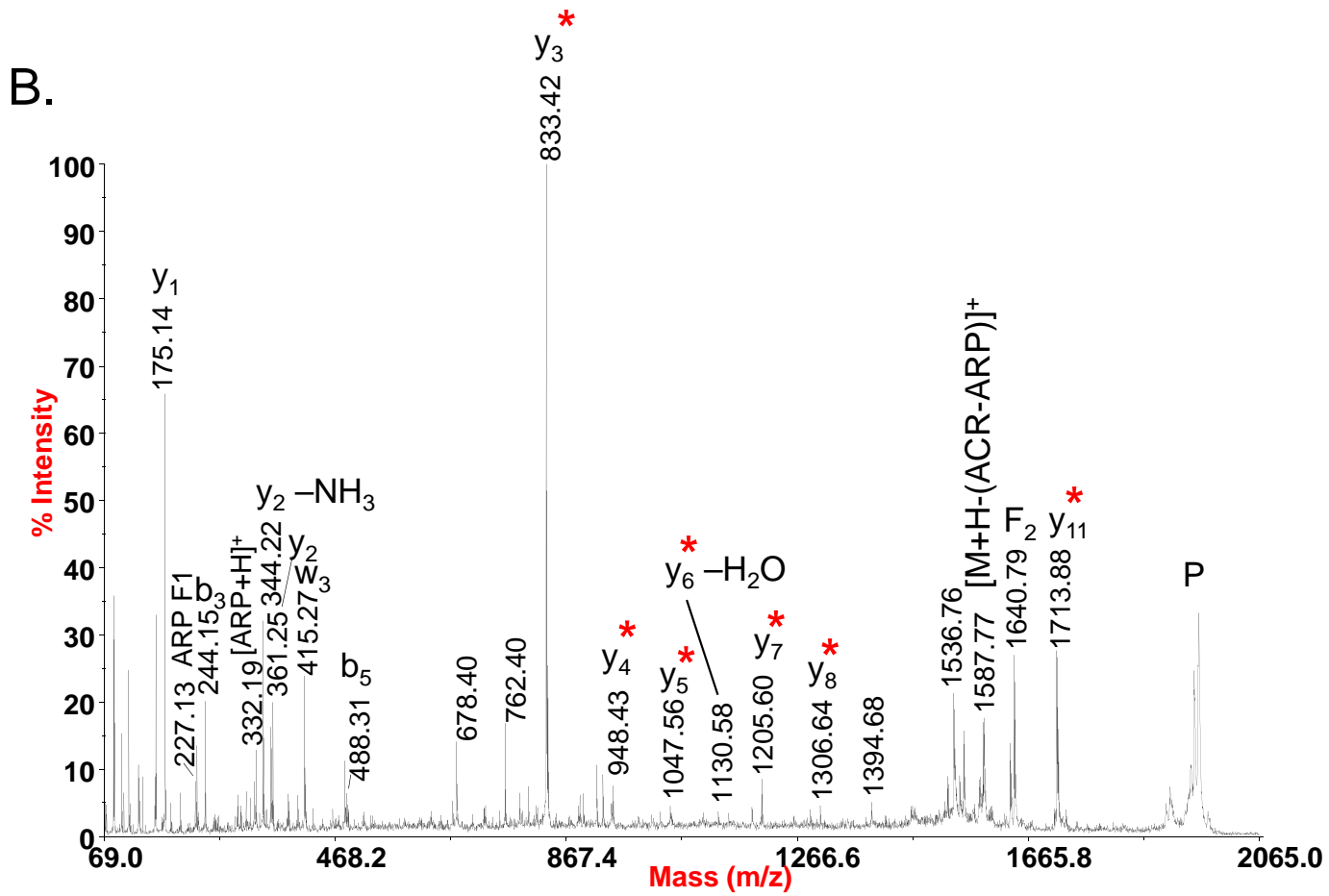
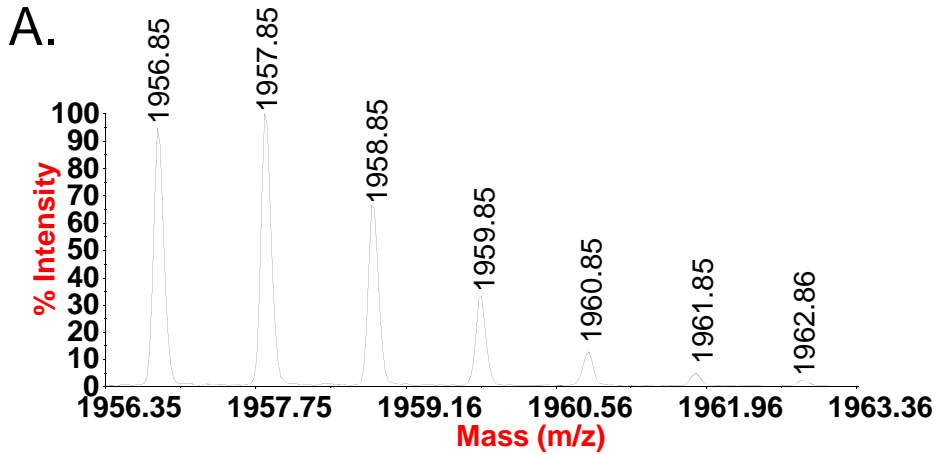
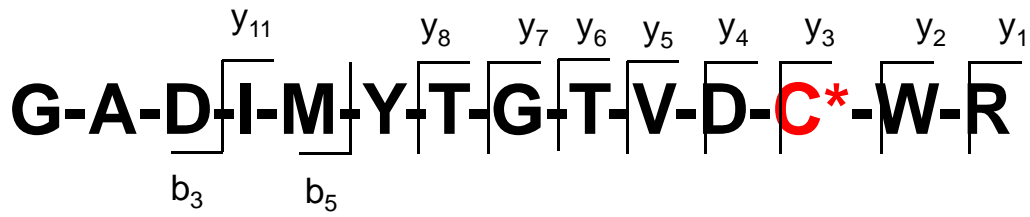


Figure S33. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide GADIMYTGTVDC*WR; monoisotopic m/z_{calc} 1956.84; accuracy $\Delta(m/z) = 0.01$ Da

ADT1_RAT: ADP/ATP translocase 1

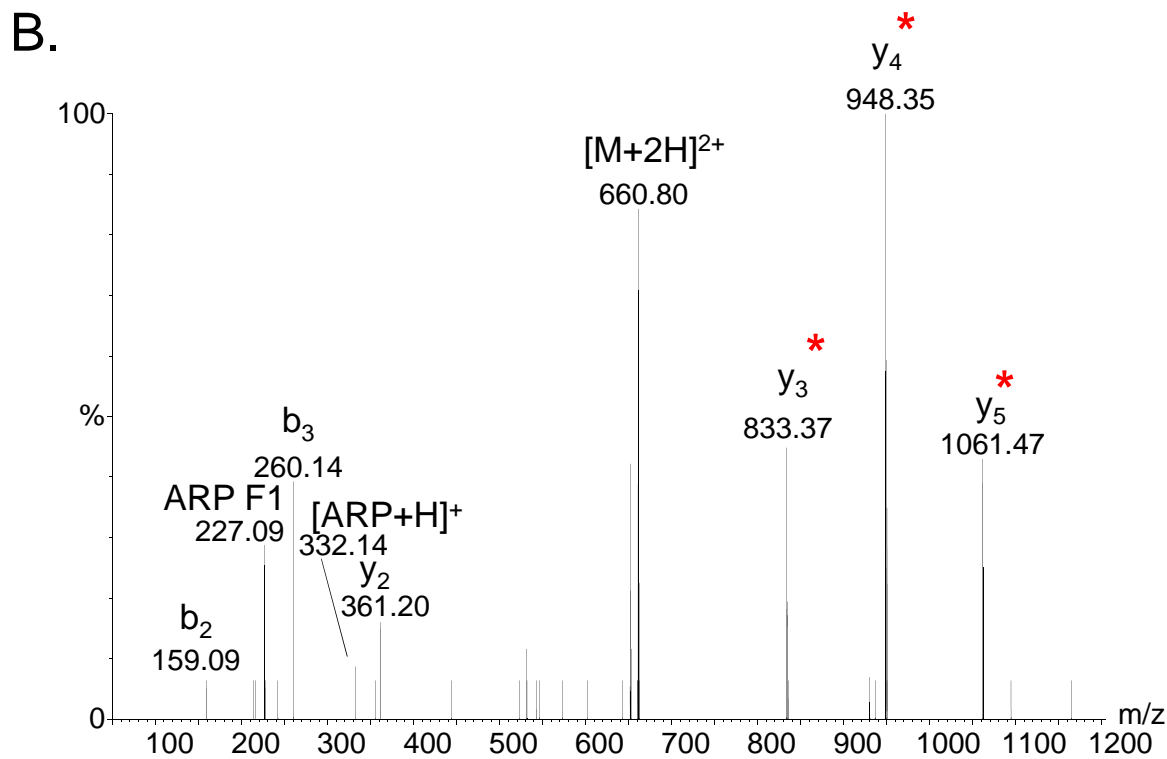
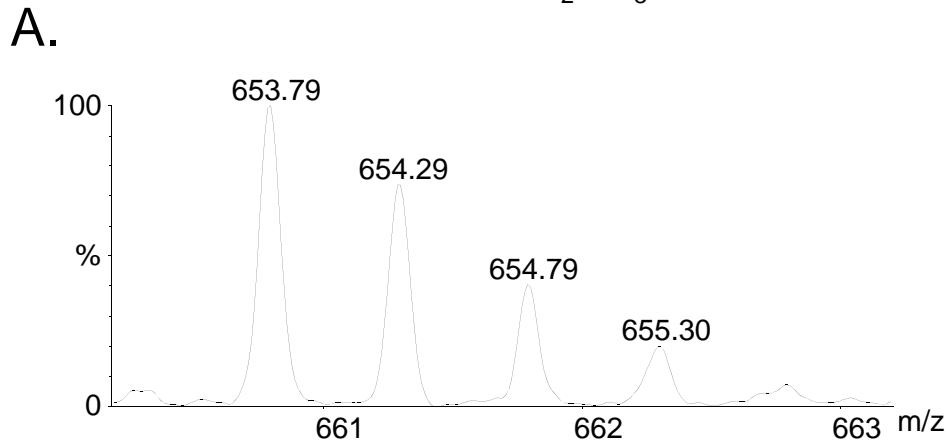
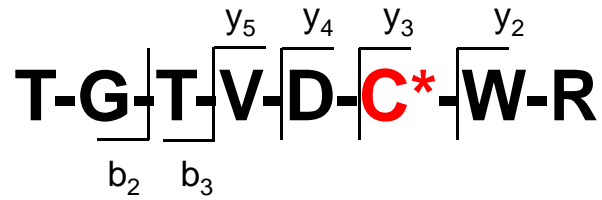


Figure S34. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide TGTVD C^* WR; monoisotopic m/z_{calc} 653.79; accuracy $\Delta(m/z) = 0.00$ Da

ADT1_RAT: ADP/ATP translocase 1

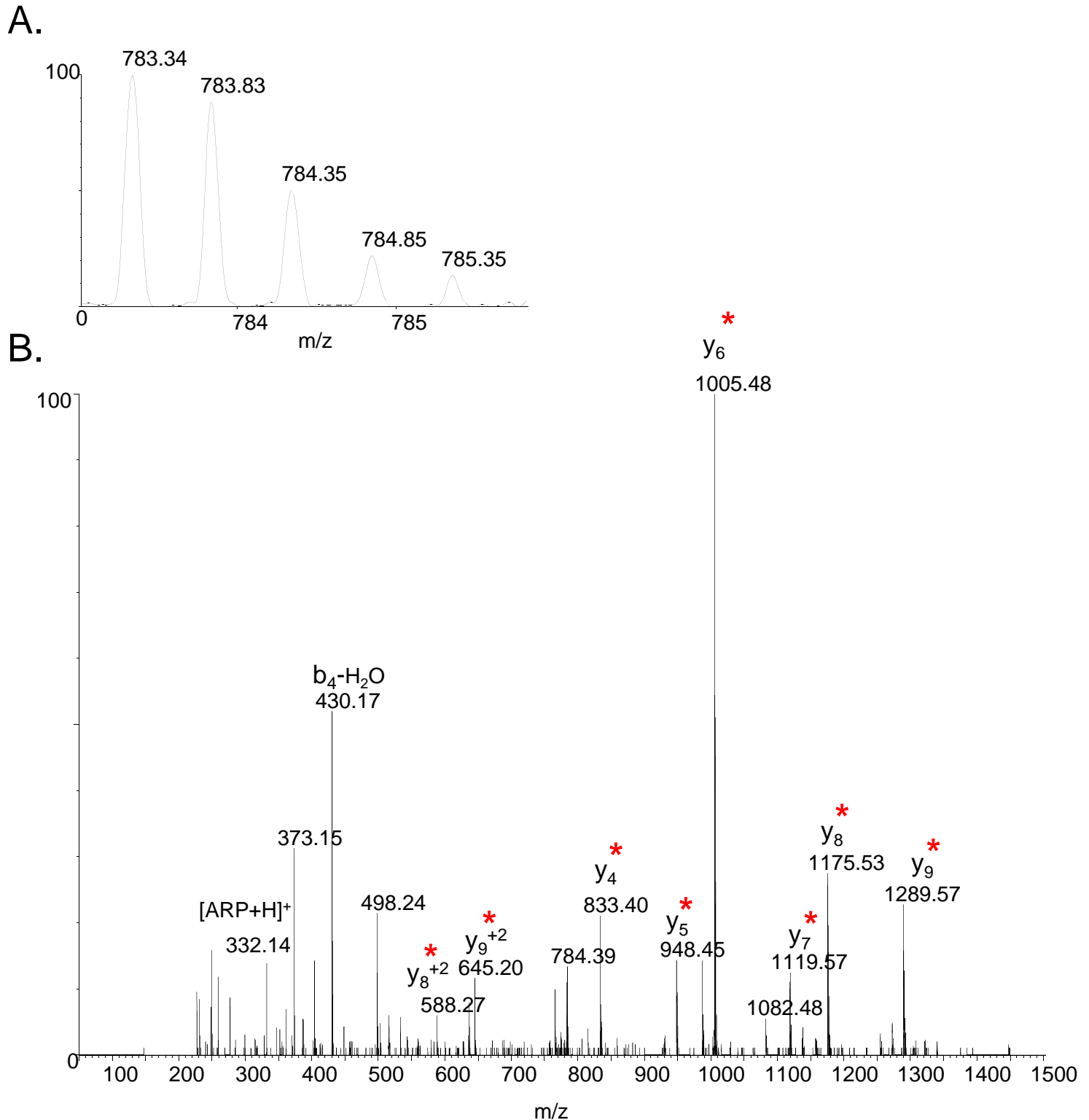
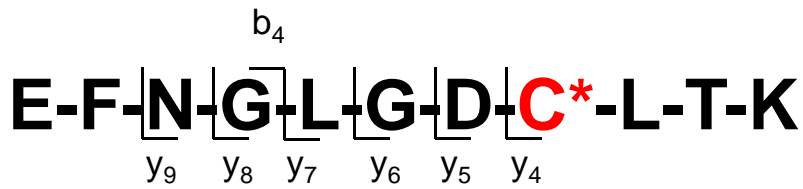


Figure S35. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide EFNGLGDC*LTK; monoisotopic m/z_{calc} 783.36; accuracy $\Delta(m/z) = -0.02$ Da

ADT1_RAT: ADP/ATP translocase 1

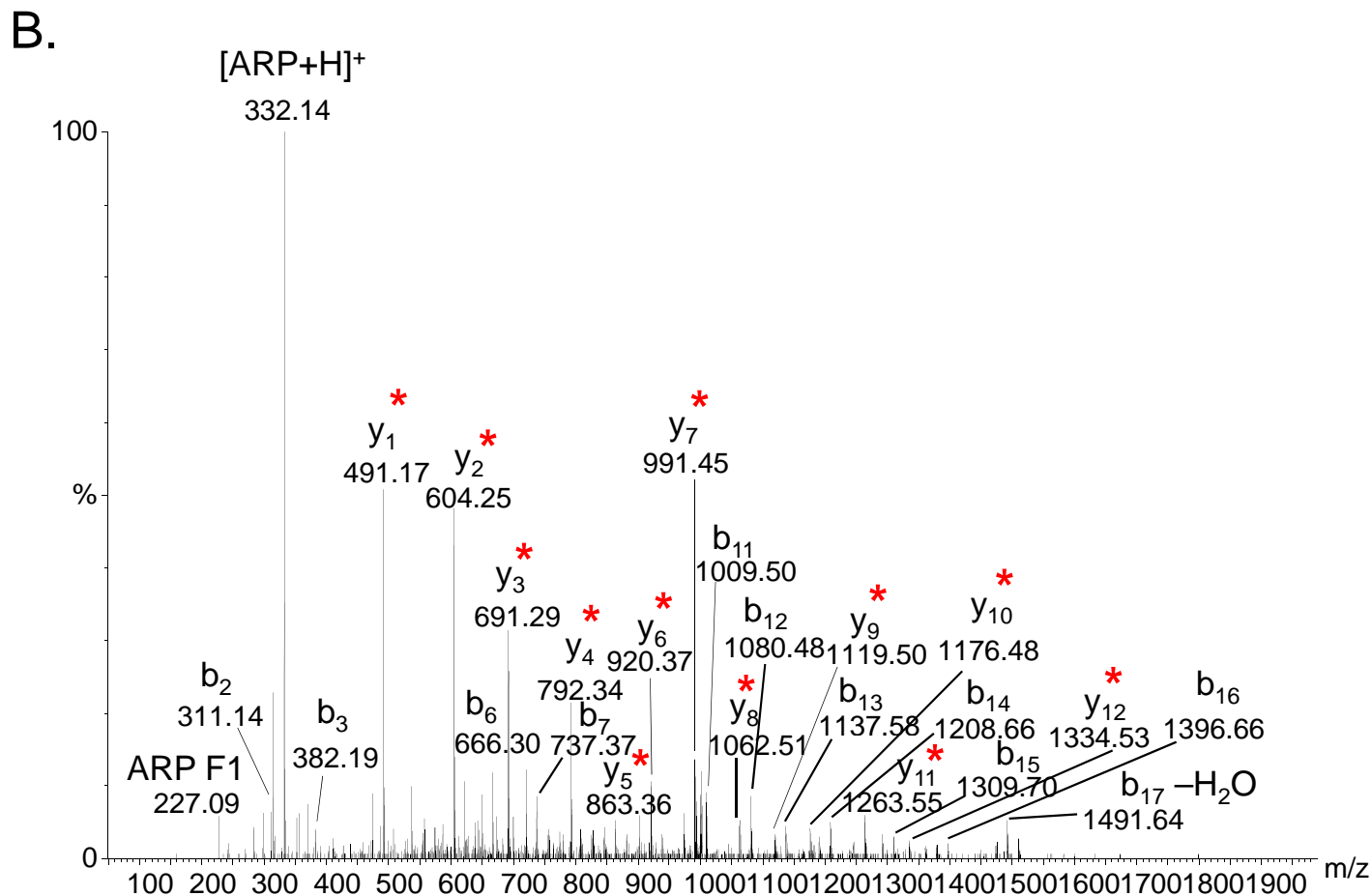
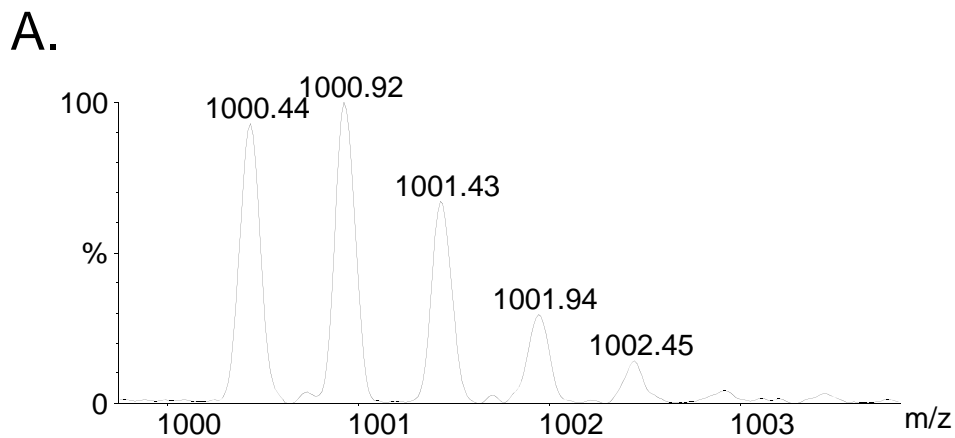
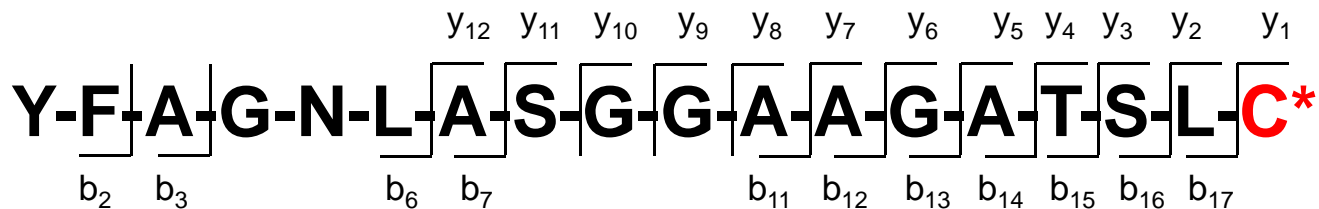
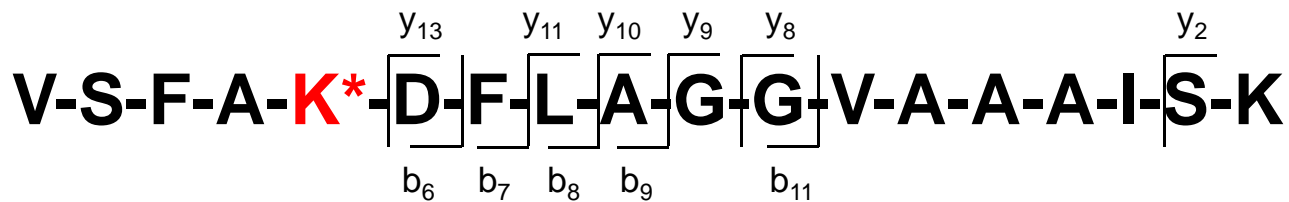
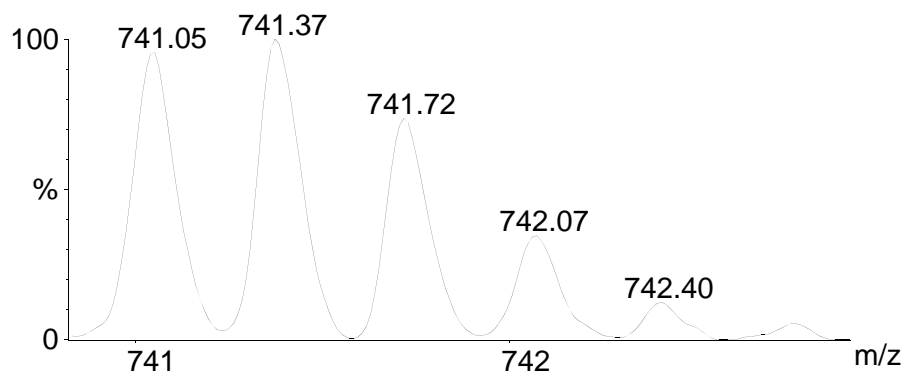


Figure S36. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide YFAGNLSGGAAGATSLC*; monoisotopic m/z_{calc} 1000.45; accuracy $\Delta(m/z) = -0.01$ Da

ADT2_RAT: ADP/ATP translocase 2



A.



B.

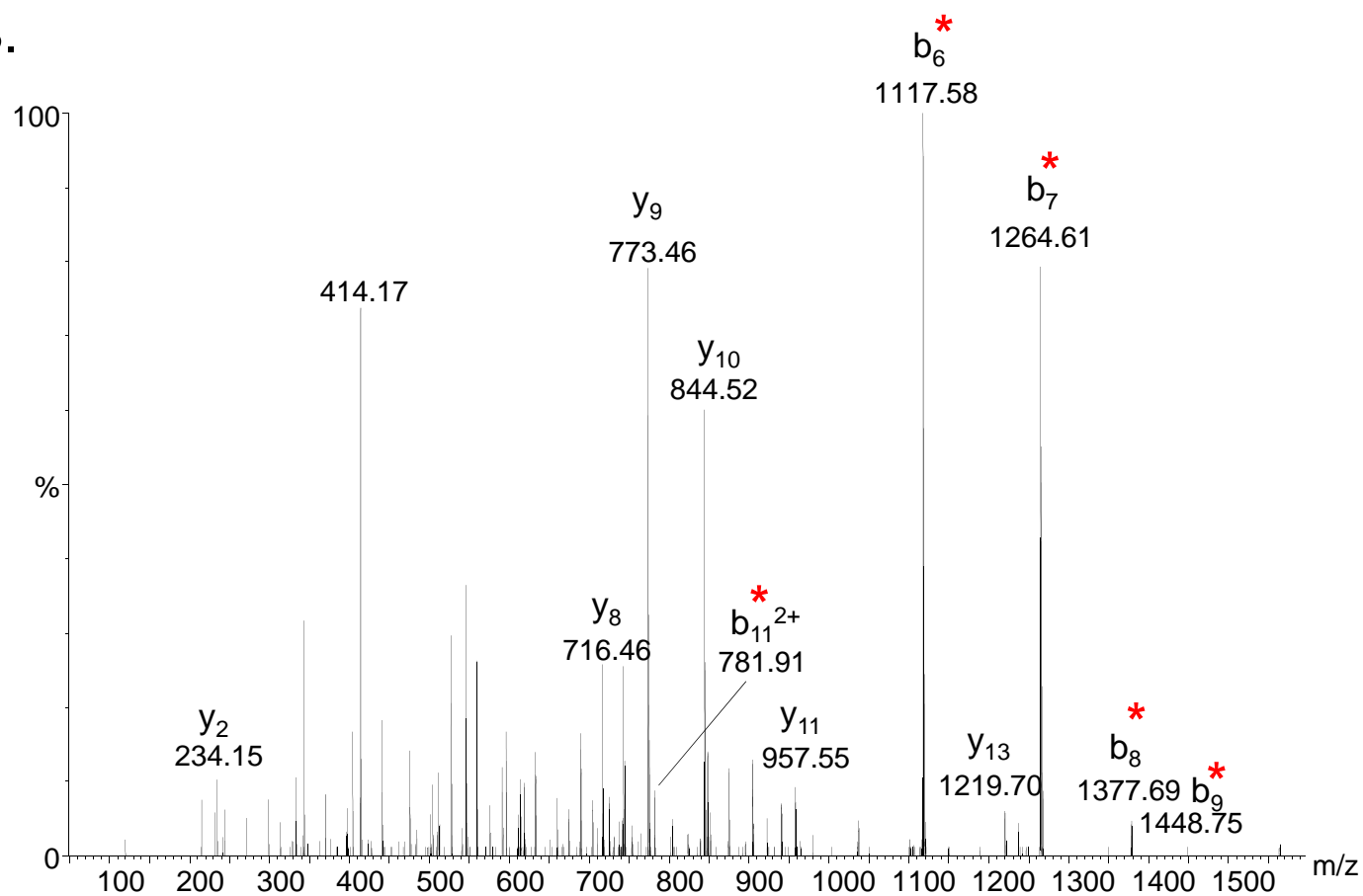


Figure S37. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+3H]^{3+}$ ion of the ARP labeled, HNE modified peptide V-S-F-A-K*DFLAGGVA-A-I-S-K; monoisotopic m/z_{calc} 741.07; accuracy $\Delta(m/z) = -0.02$ Da

ADT1_RAT: ADP/ATP translocase 1

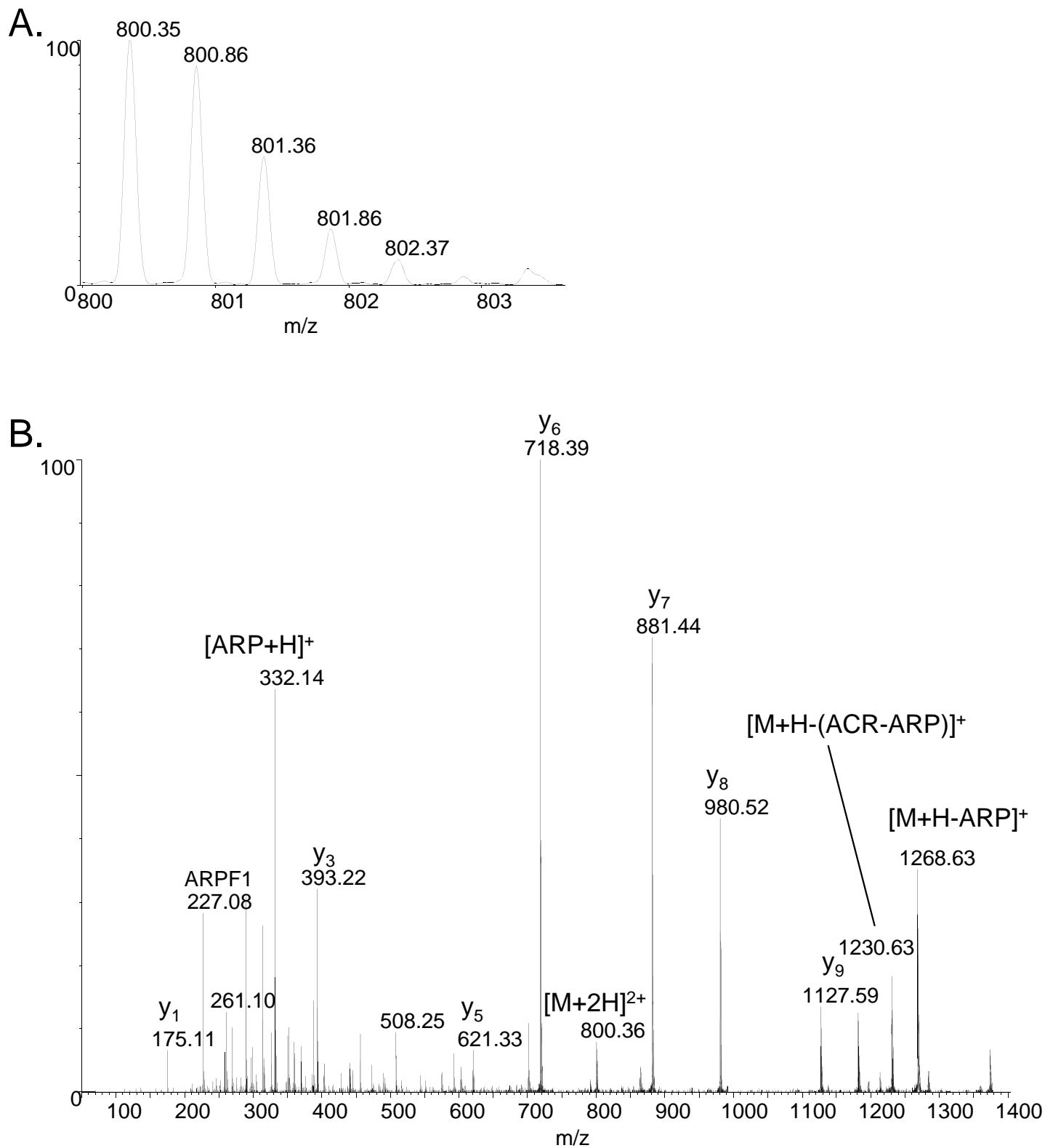
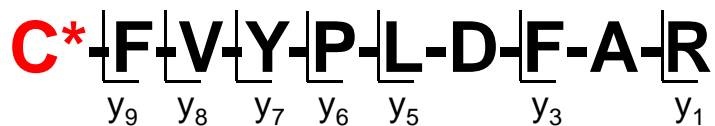


Figure S38. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide C*FVYPLDFAR; monoisotopic m/z_{calc} 800.38; accuracy $\Delta(m/z) = -0.03$ Da

ADT1_RAT: ADP/ATP translocase 1

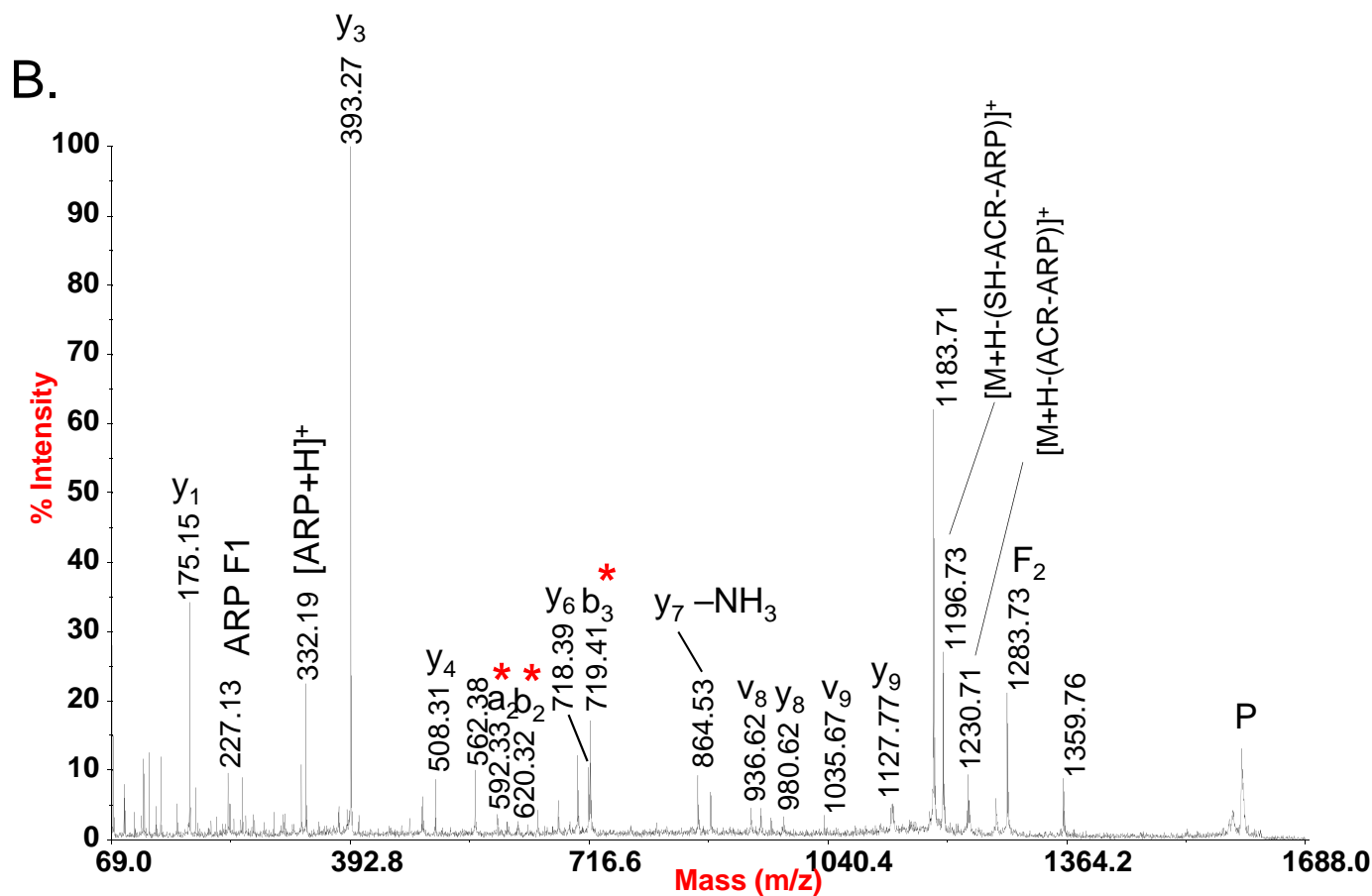
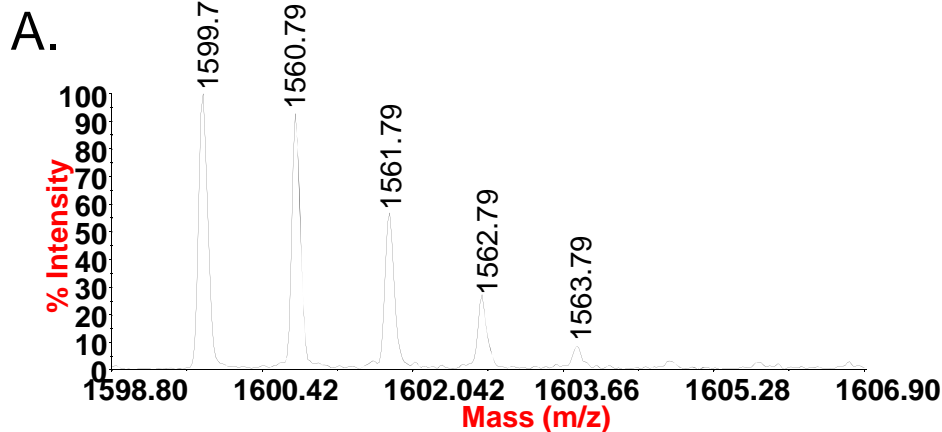
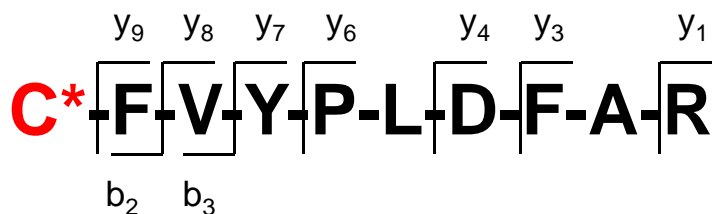
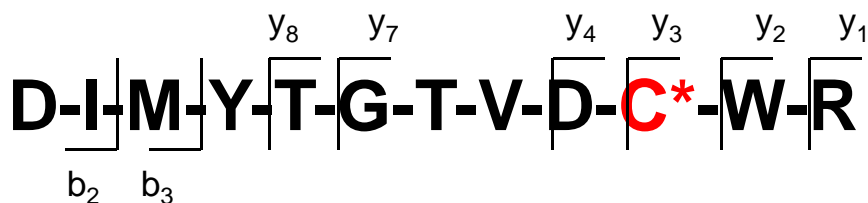
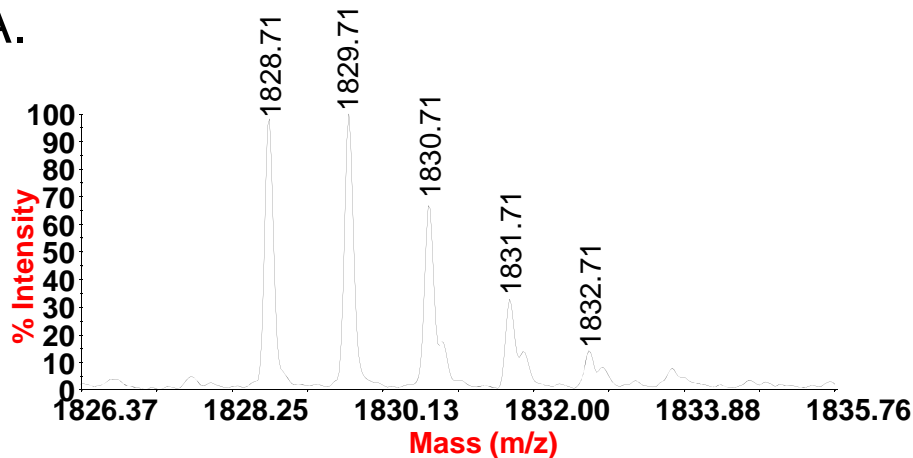


Figure S39. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide C*FVYPLDFAR; monoisotopic m/z_{calc} 1599.74; accuracy $\Delta(m/z) = 0.05$ Da

ADT1_RAT: ADP/ATP translocase 1



A.



B.

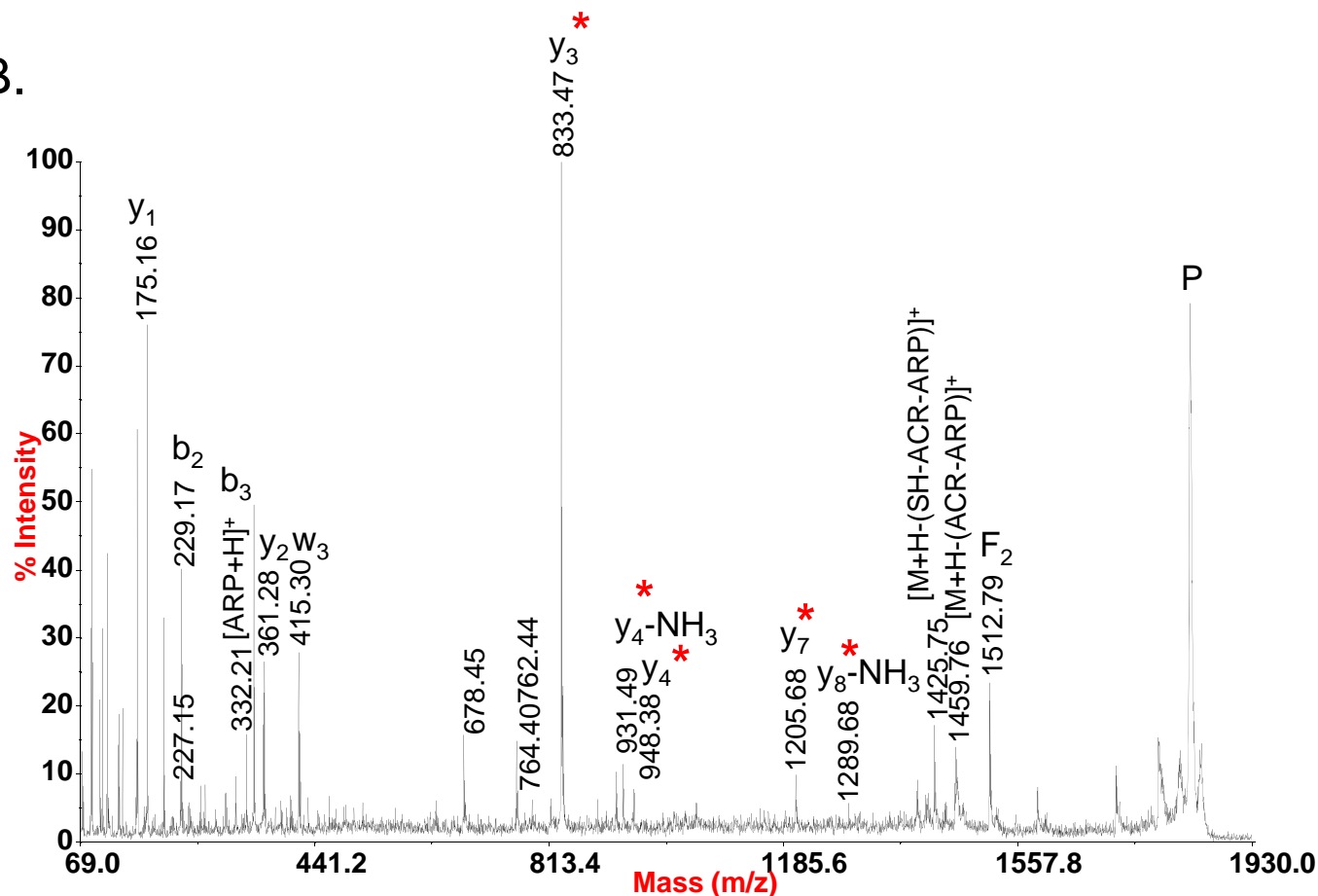


Figure S40. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide DIMYTGTVDC*WR; monoisotopic m/z_{calc} 1828.78; accuracy $\Delta(m/z) = -0.07$ Da

ADT1_RAT: ADP/ATP translocase 1

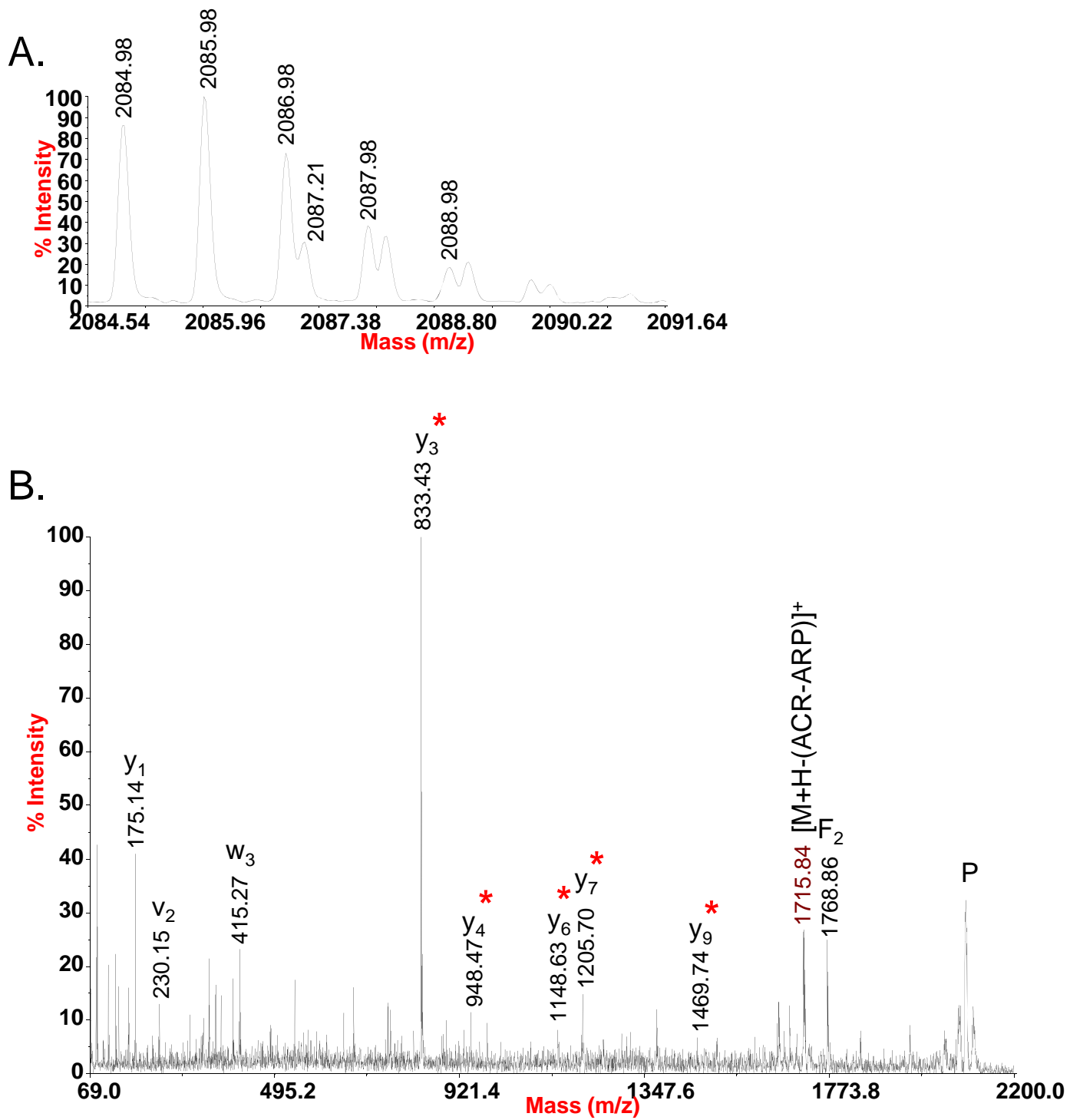
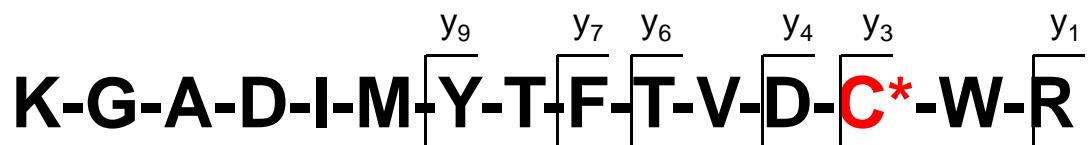


Figure S41. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide KGADIMYTGTVDC*WR; monoisotopic m/z_{calc} 2084.94; accuracy $\Delta(m/z) = 0.04$ Da

ADT2_RAT: ADP/ATP translocase 2

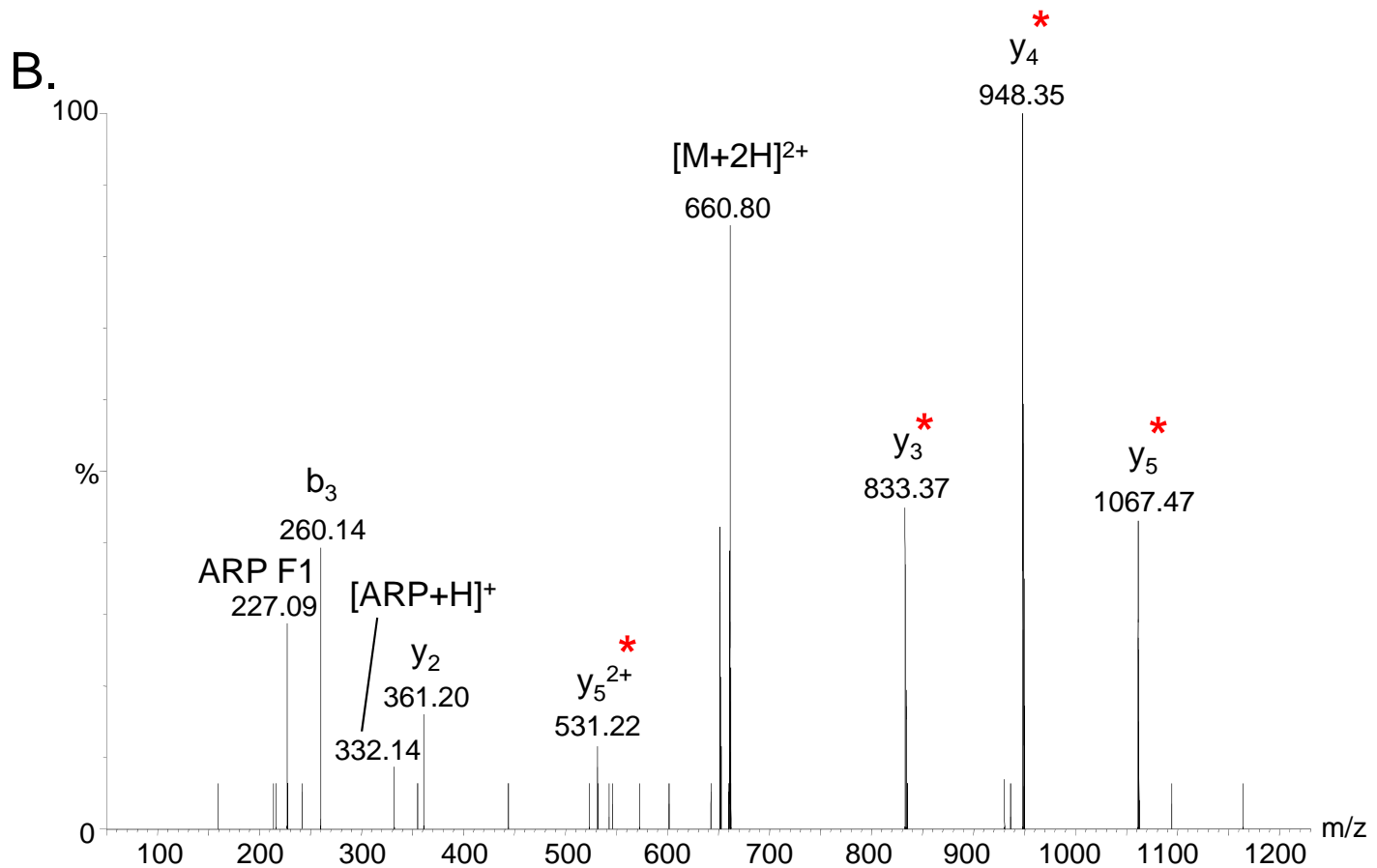
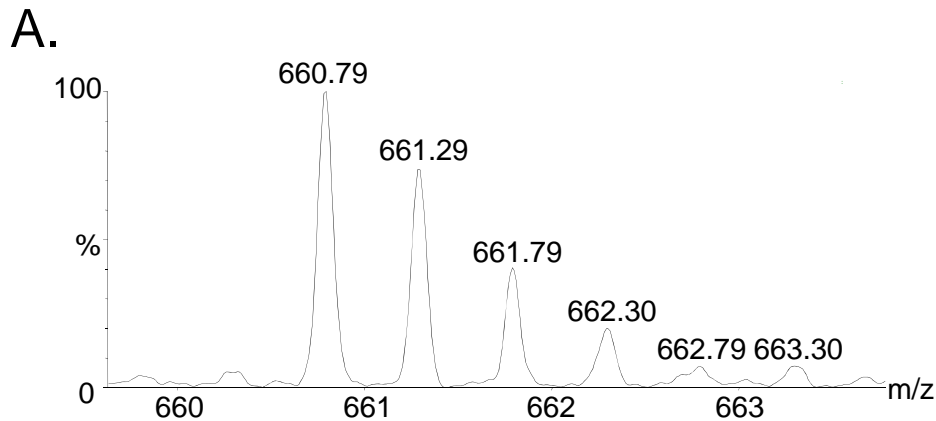
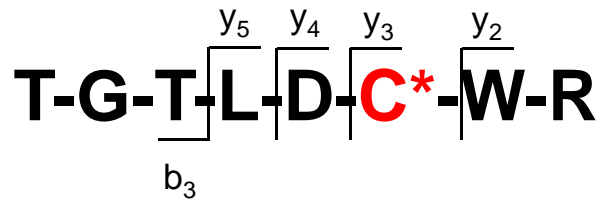


Figure S42. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide TGTLD C^* WR; monoisotopic m/z_{calc} 660.79; accuracy $\Delta(m/z) = 0.00$ Da

VDAC1_RAT: Voltage-dependent anion-selective channel protein 1

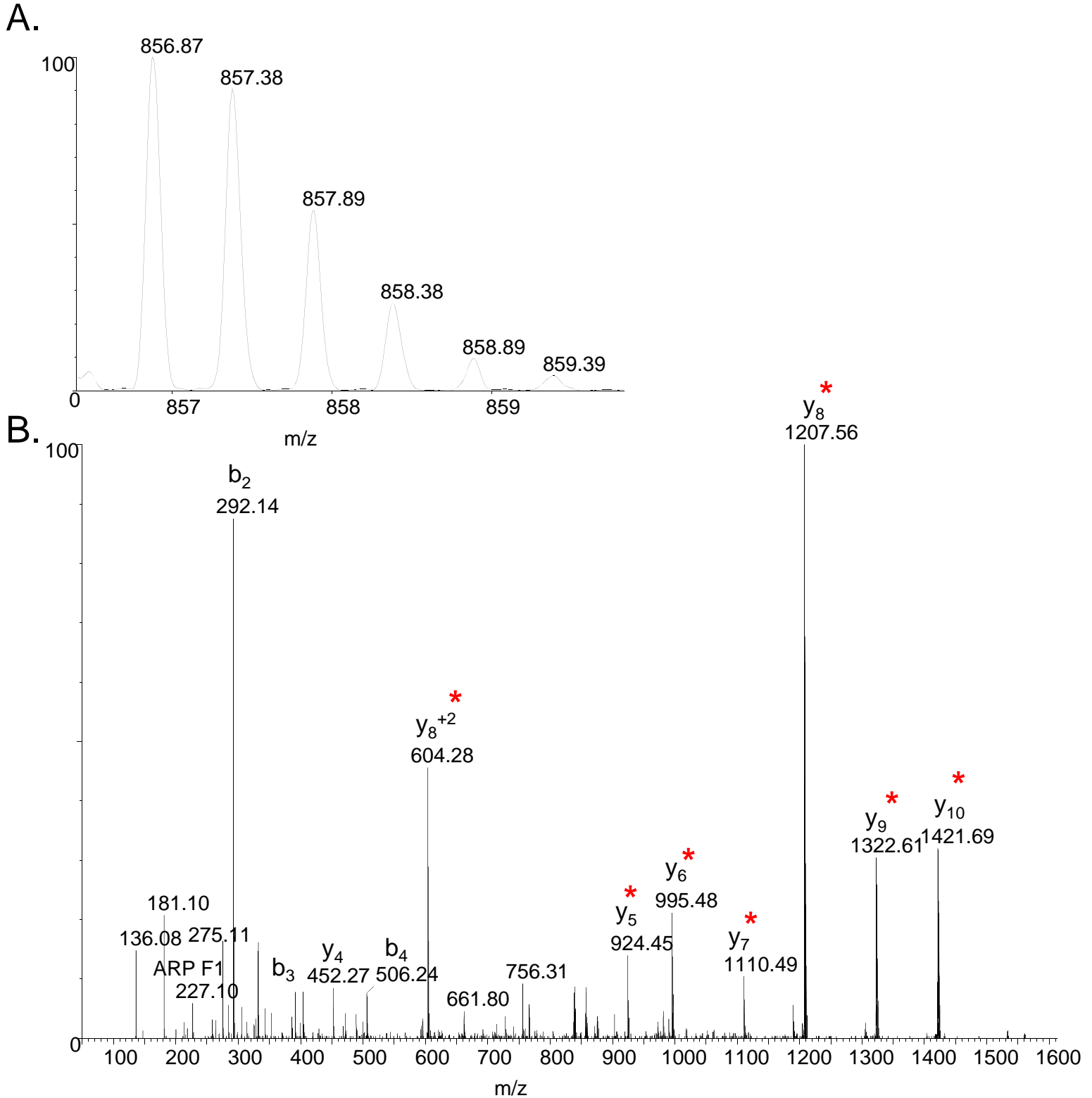
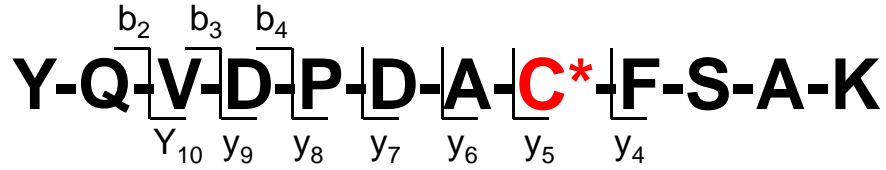


Figure S43. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide YQVDPDAC*FSAK; monoisotopic m/z_{calc} 856.87; accuracy $\Delta(m/z) = 0.00$ Da

VDAC1_RAT: Voltage-dependent anion-selective channel protein 1

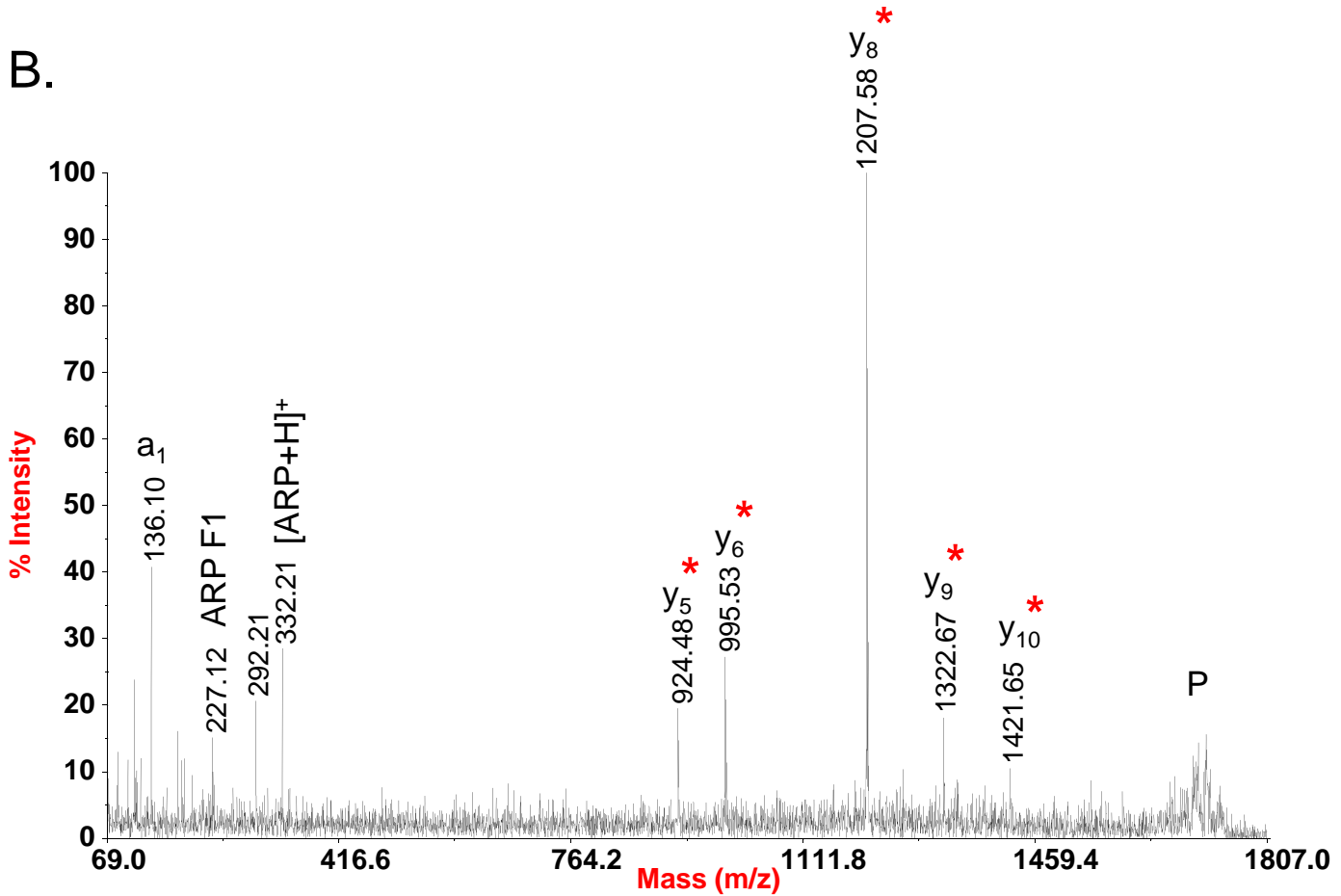
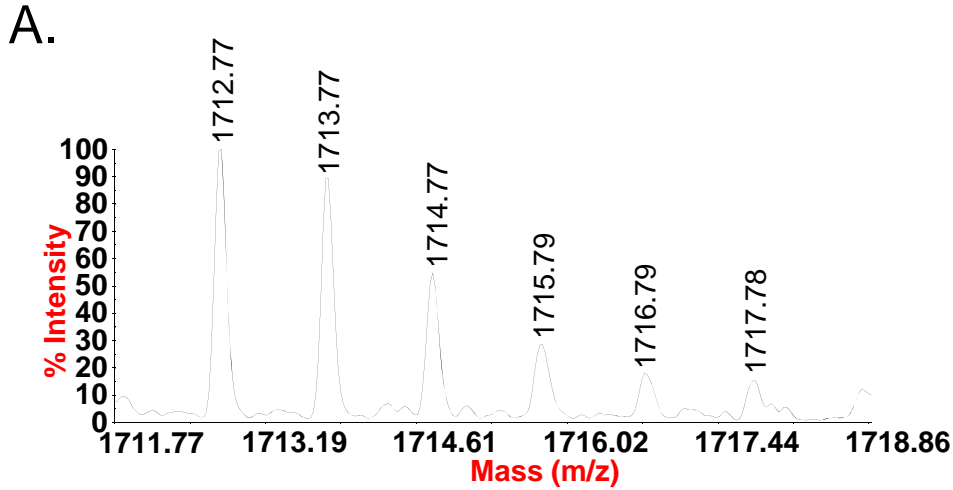
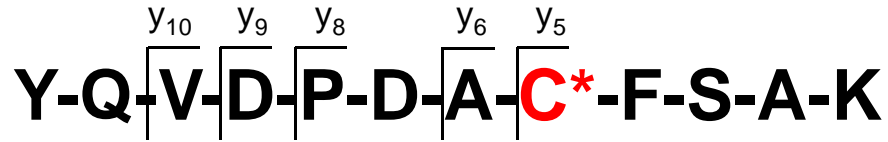


Figure S44. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide YQVDPDAC*FSAK; monoisotopic m/z_{calc} 1712.74; accuracy Δ(m/z) = 0.03 Da

VDAC3_RAT: Voltage-dependent anion-selective channel protein 3

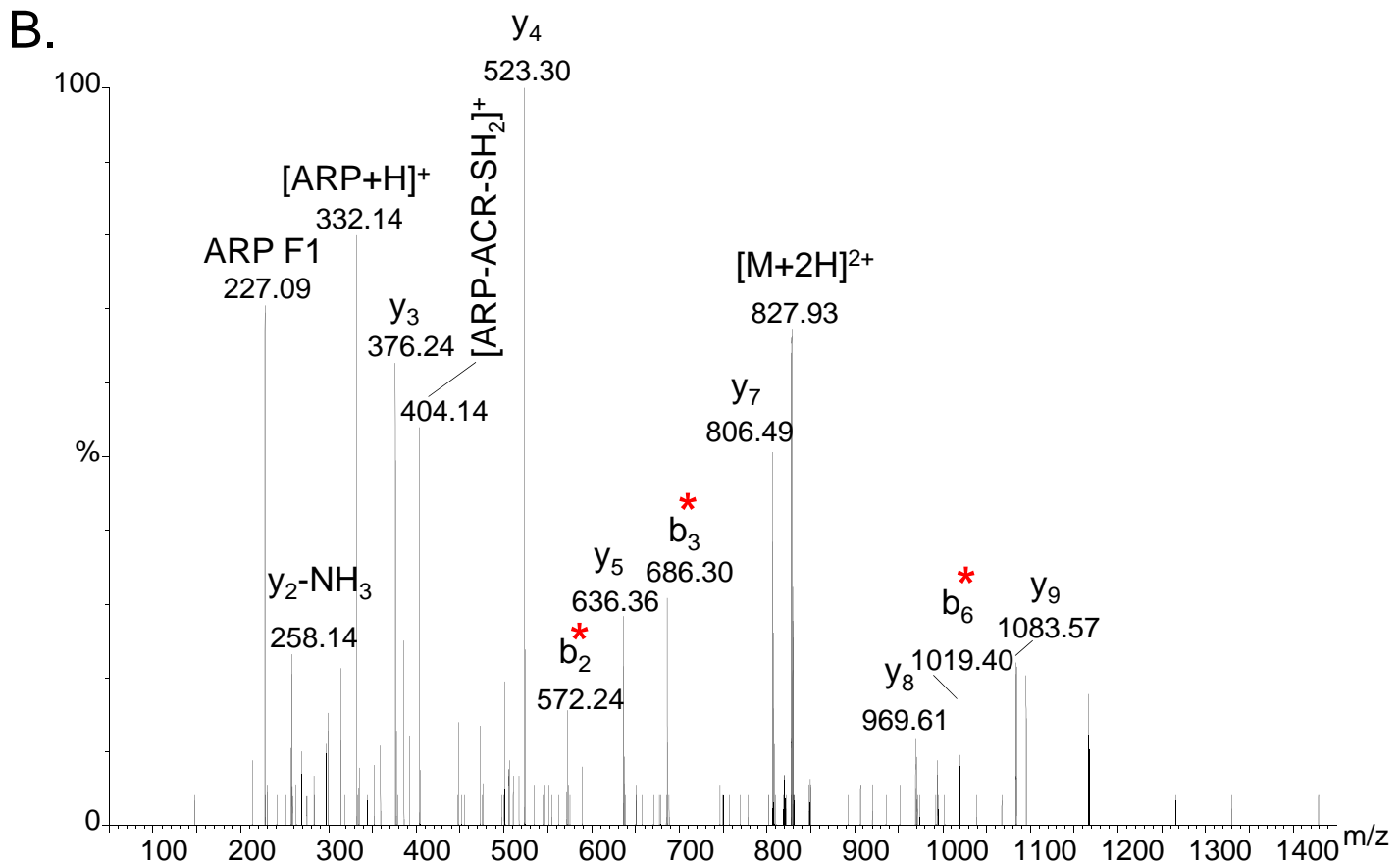
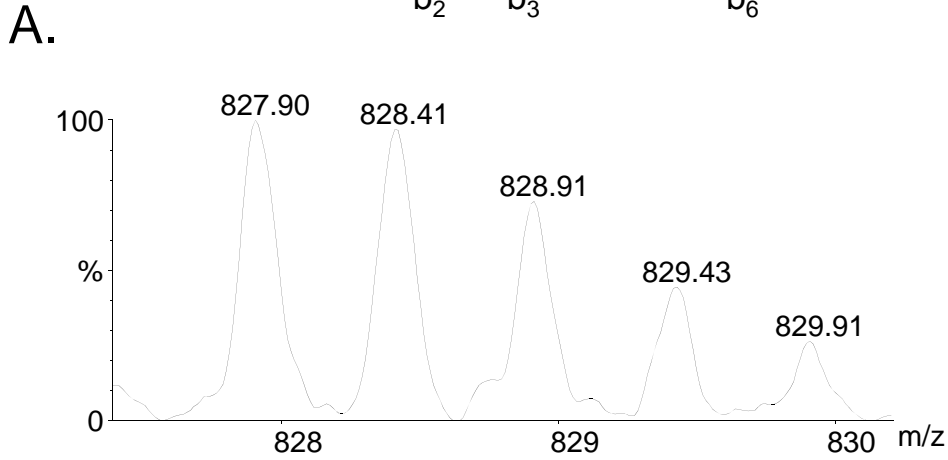
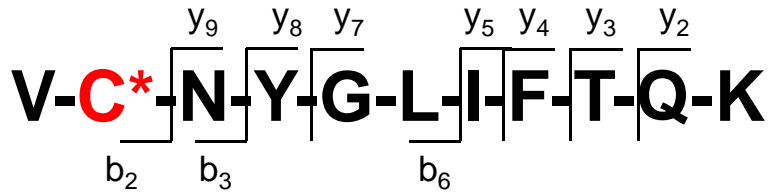


Figure S45. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide VC*NYGLIFTQK; monoisotopic m/z_{calc} 827.91; accuracy $\Delta(m/z) = -0.01$ Da

ACON_RAT:Aconitate hydratase

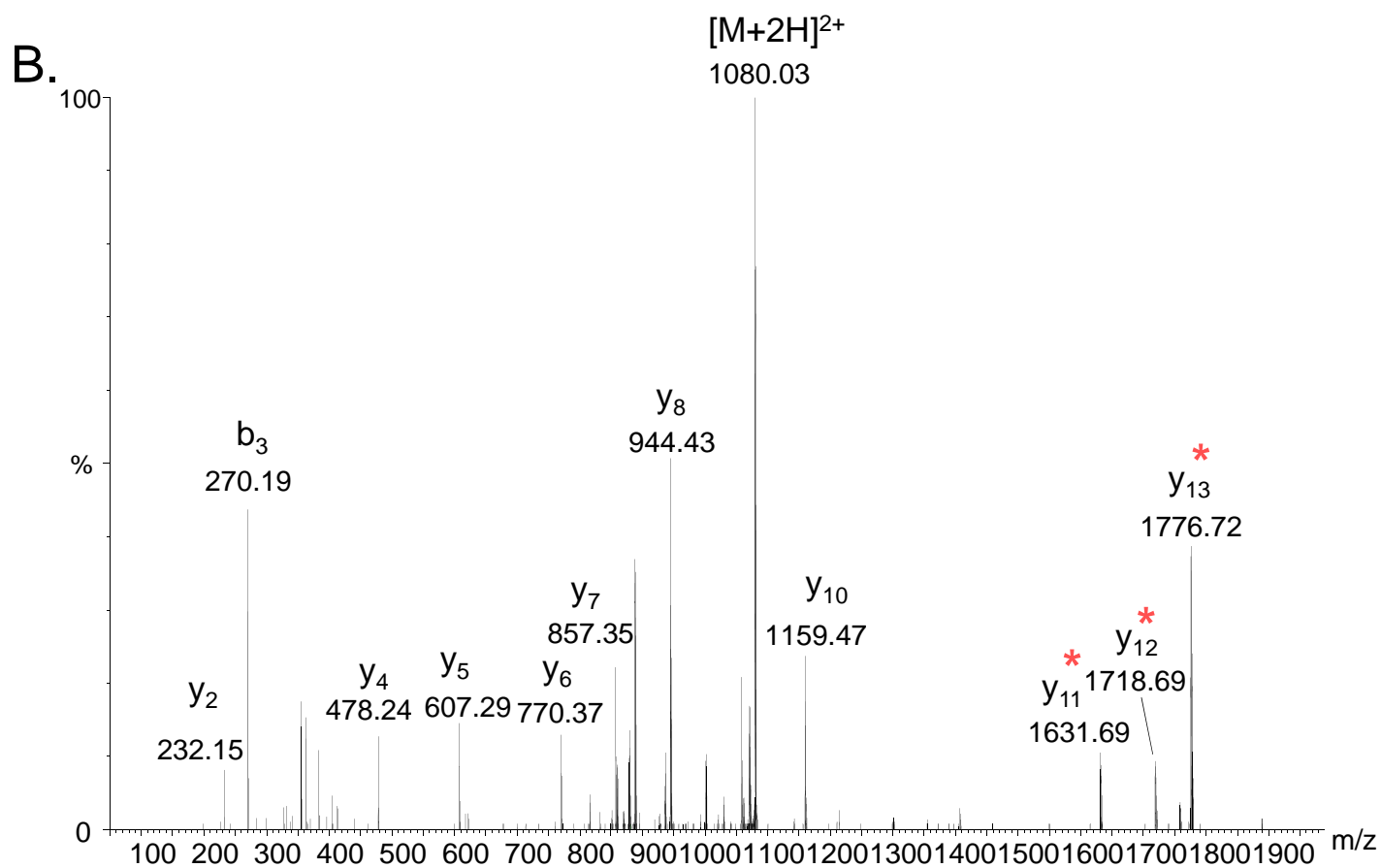
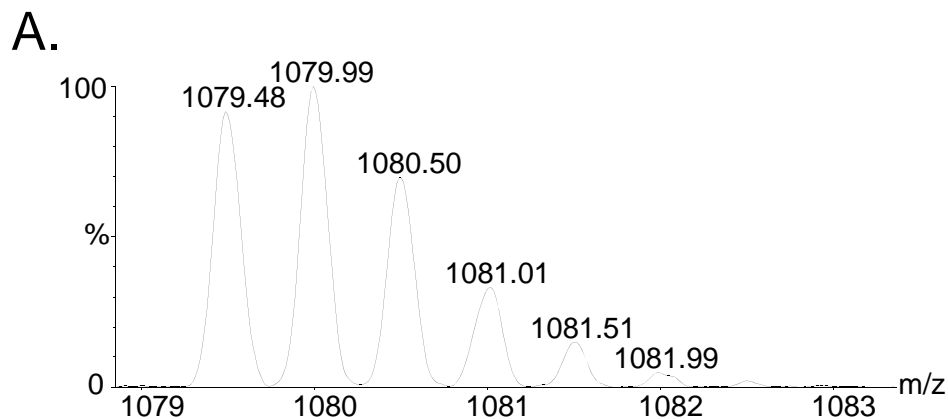
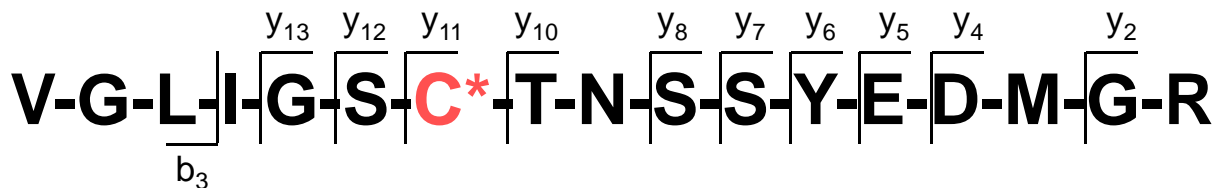


Figure S46. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide VGLIGSC*TNSSYEDMGR; monoisotopic m/z_{calc} 1079.47; accuracy $\Delta(m/z) = 0.01$ Da

ACON_RAT:Aconitate hydratase

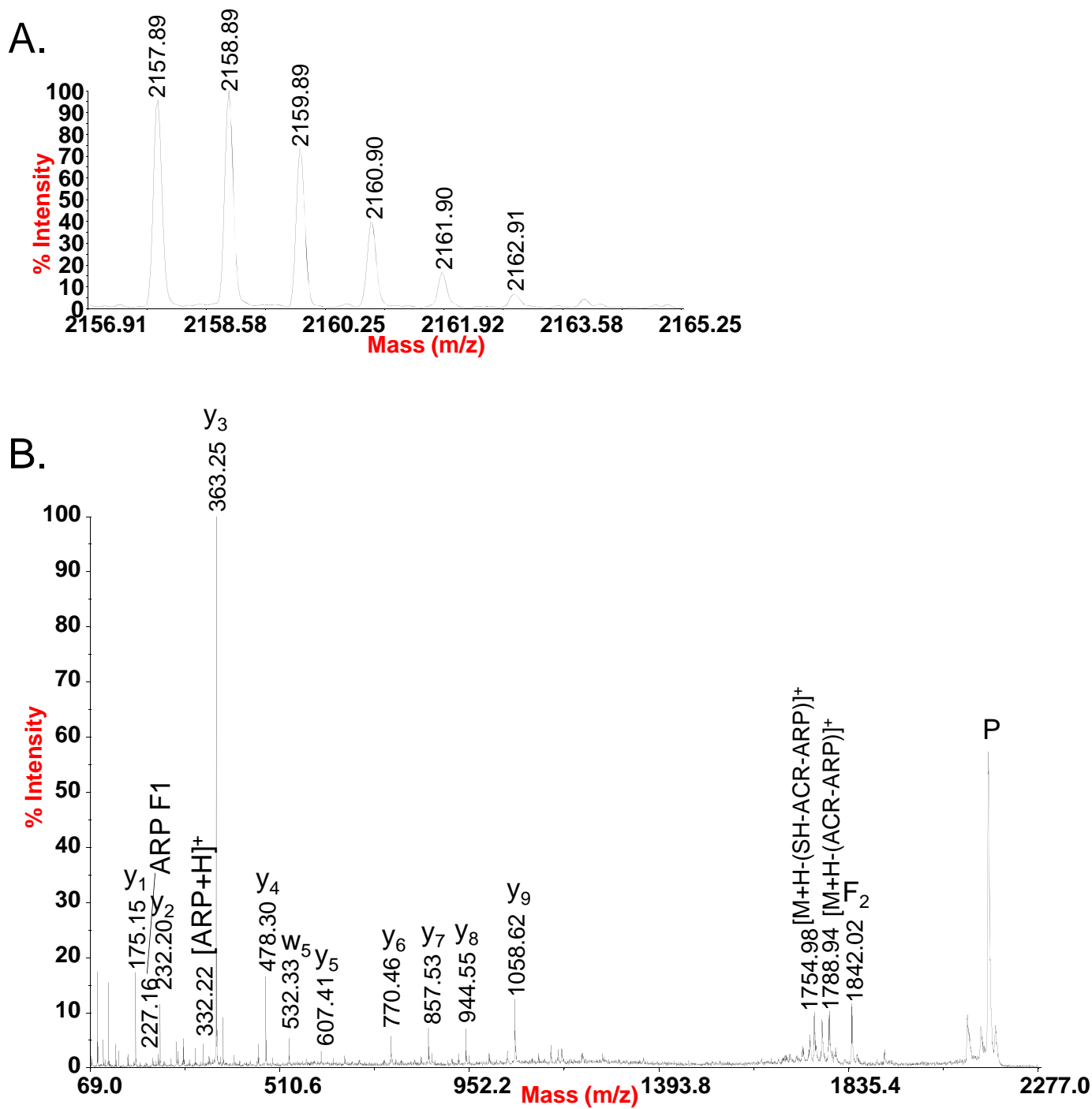
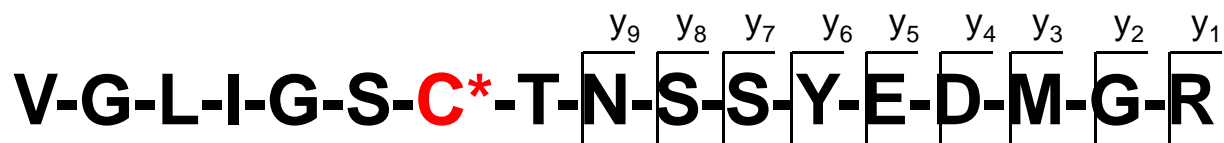


Figure S47. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide VGLIGSC*TNSSYEDMGR; monoisotopic m/z_{calc} 2157.94; accuracy $\Delta(m/z) = -0.05$ Da

ACON_RAT:Aconitate hydratase

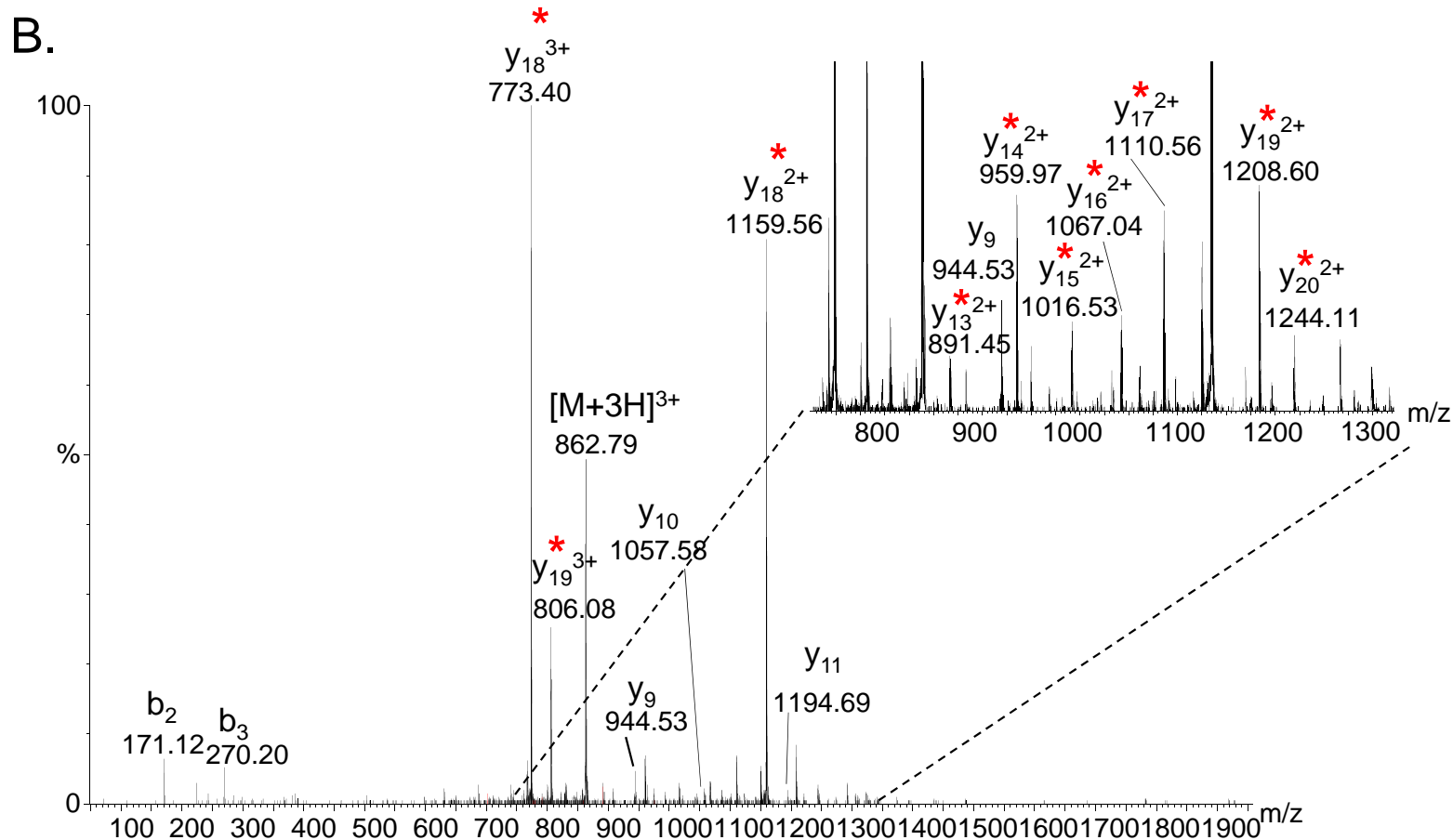
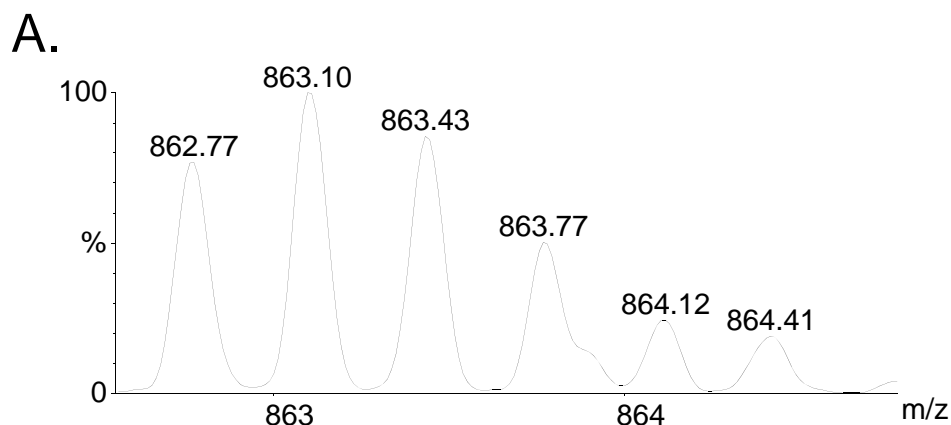
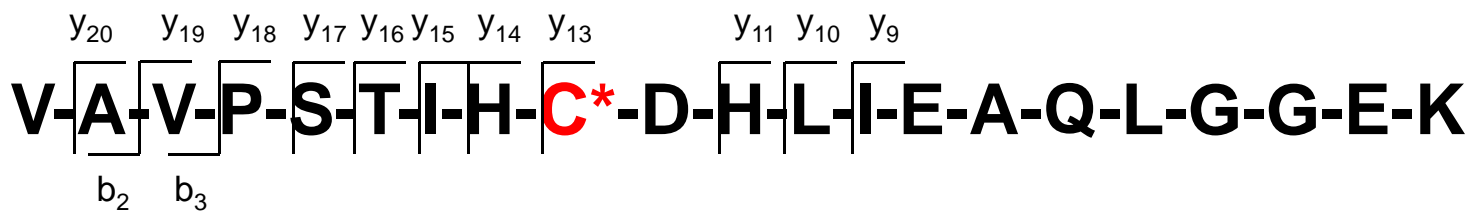


Figure S48. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+3H]^{3+}$ ion of the ARP labeled, acrolein modified peptide VAVPSTIHC*DHLIEAQLGGEK; monoisotopic m/z_{calc} 862.77; accuracy $\Delta(m/z) = 0.00$ Da

IDHP_RAT: Isocitrate dehydrogenase [NADP]

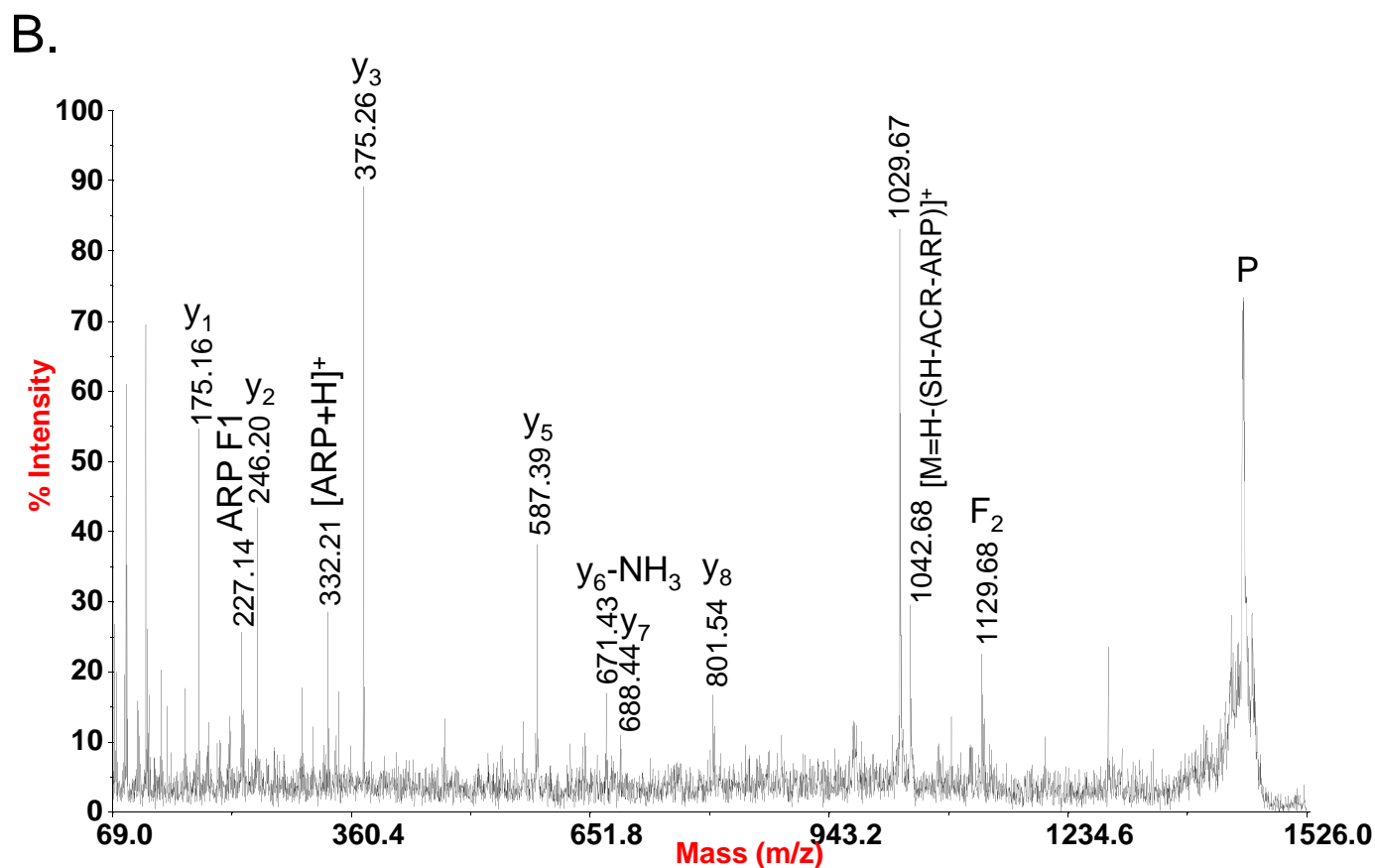
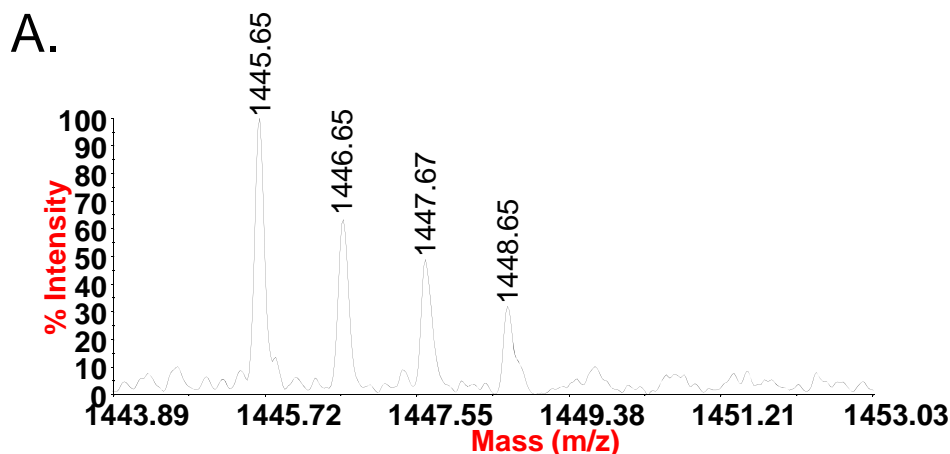
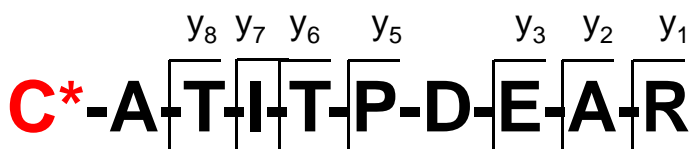


Figure S49. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide C*ATITPDEAR; monoisotopic m/z_{calc} 1445.65; accuracy Δ(m/z) = 0.00 Da

IDHP_RAT: Isocitrate dehydrogenase [NADP]

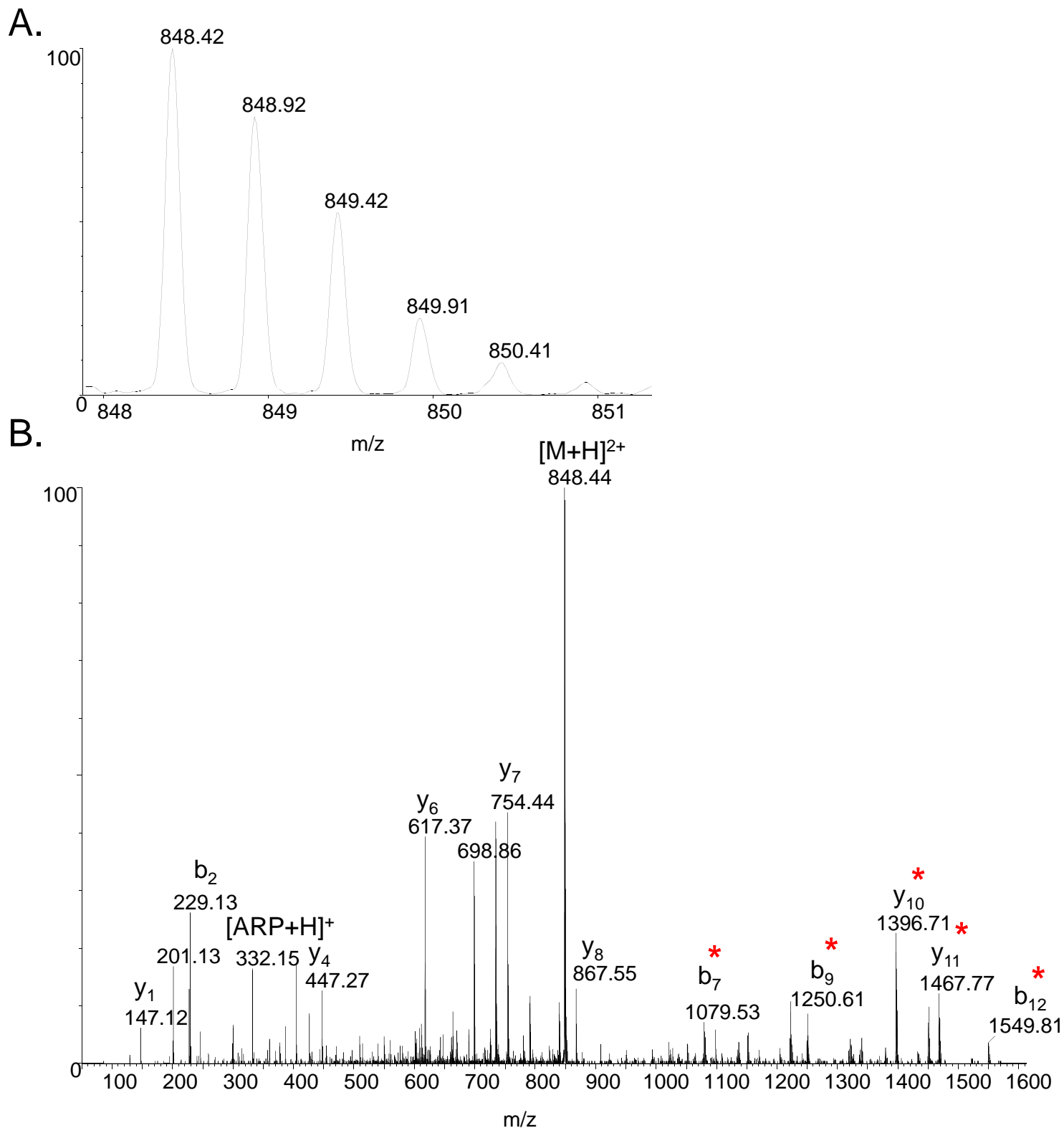
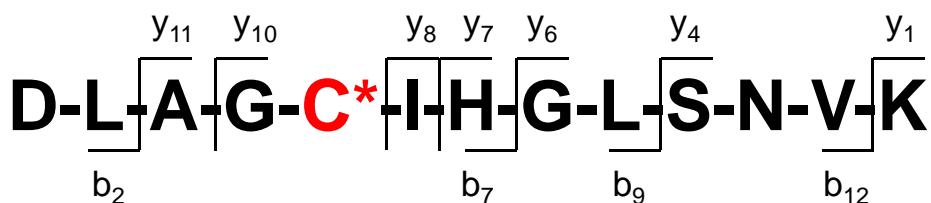


Figure S50. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide DLAGC*IHGLSNVK; monoisotopic m/z_{calc} 848.42; accuracy $\Delta(m/z) = 0.00$ Da

MDHM_RAT: Malate dehydrogenase

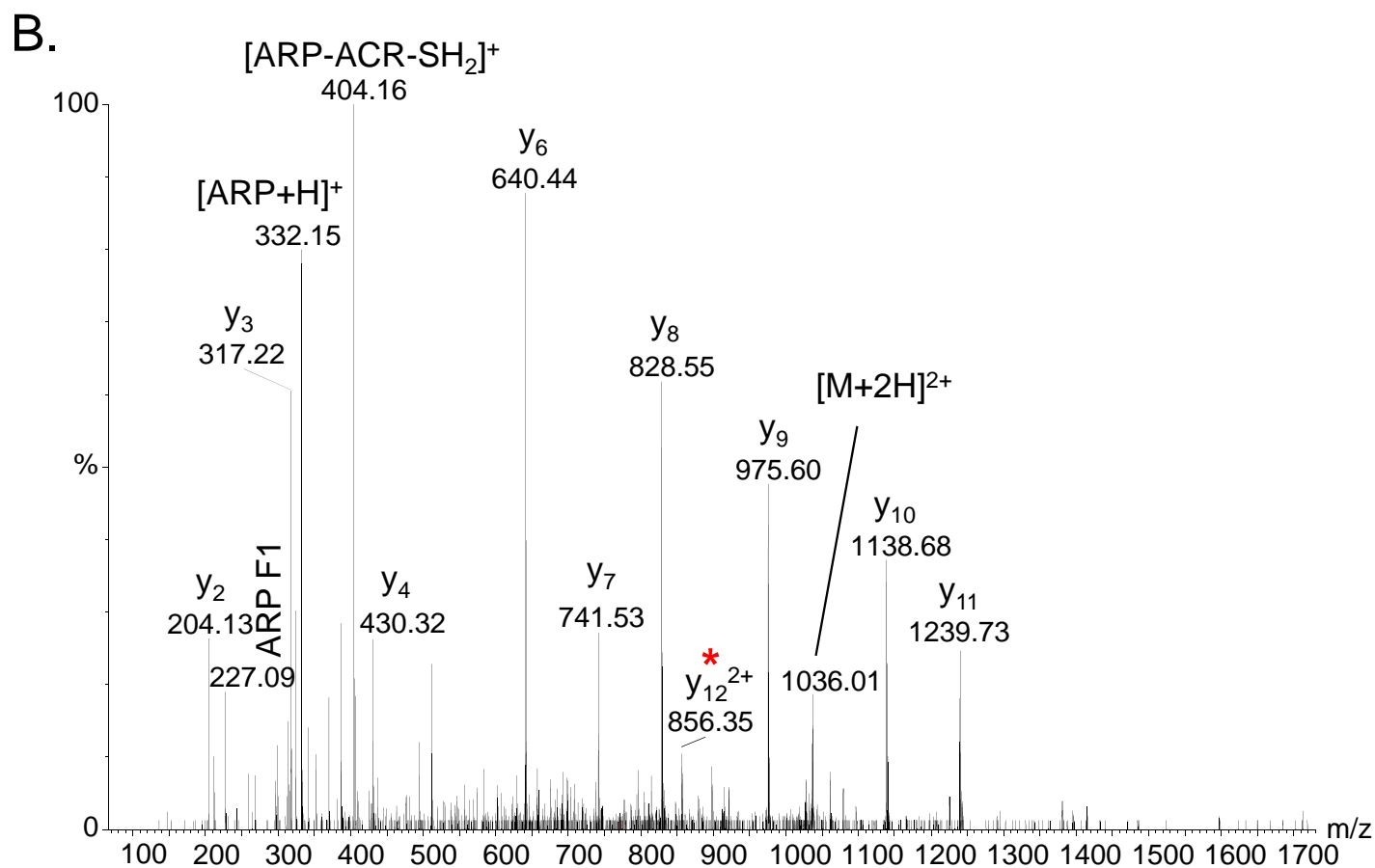
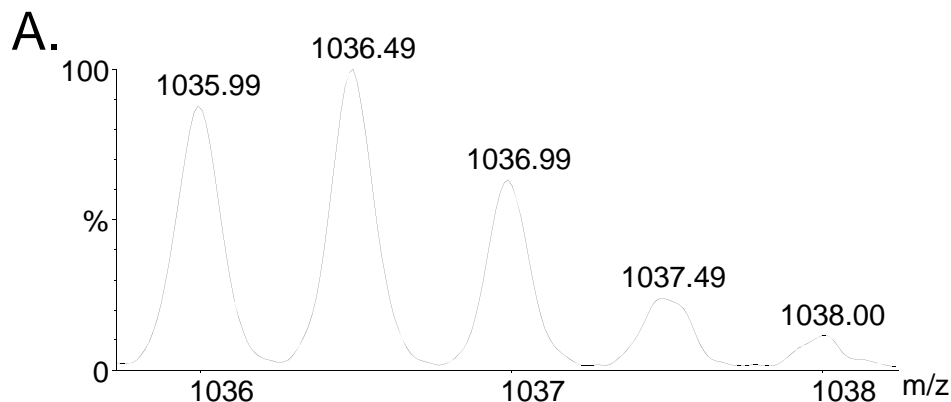
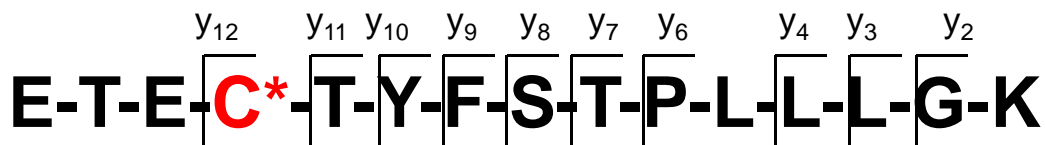


Figure S51. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the [M+2H]²⁺ ion of the ARP labeled, acrolein modified peptide ETEC*TYFSTPLLLGK; monoisotopic m/z_{calc} 1036.00; accuracy Δ(m/z) = -0.01 Da

MDHM_RAT: Malate dehydrogenase

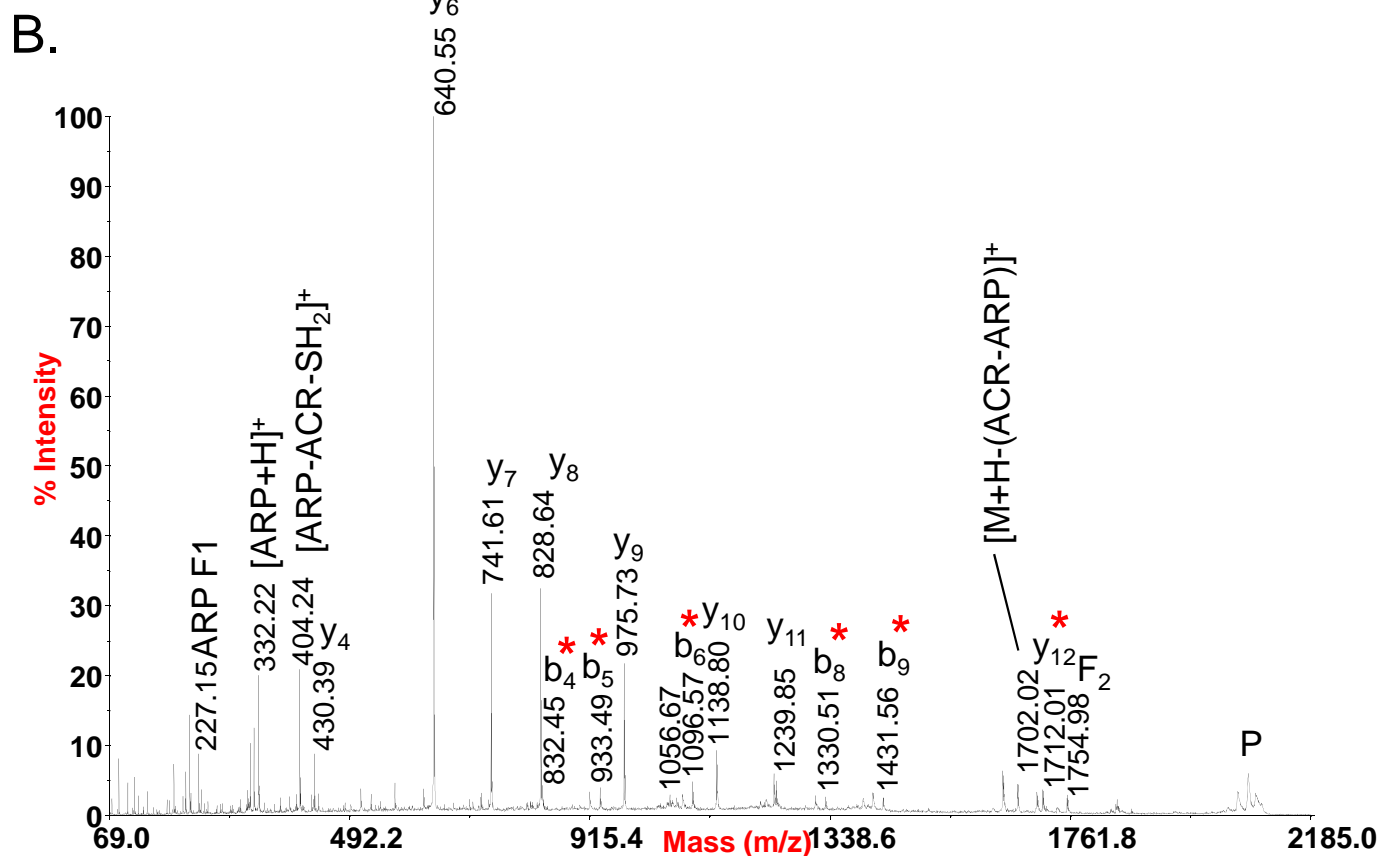
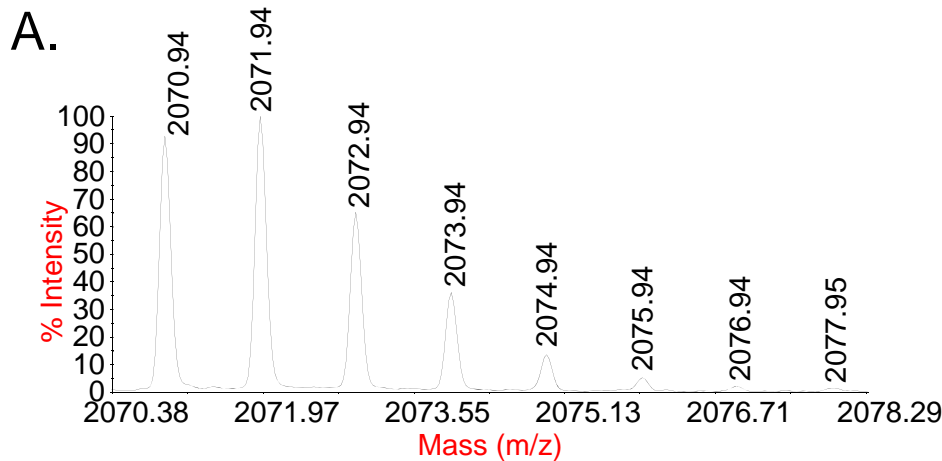
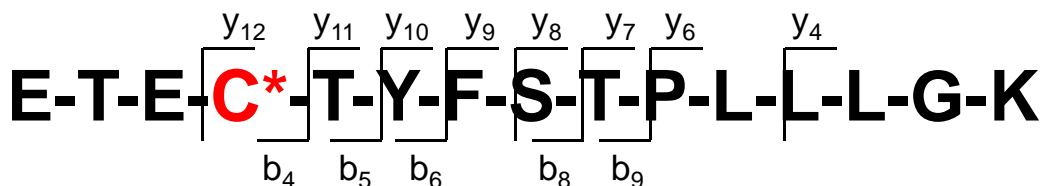


Figure S52. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide ETEC*TYFSTPLLLGK; monoisotopic m/z_{calc} 2070.99; accuracy Δ(m/z) = -0.05 Da

MDHM_RAT: Malate dehydrogenase

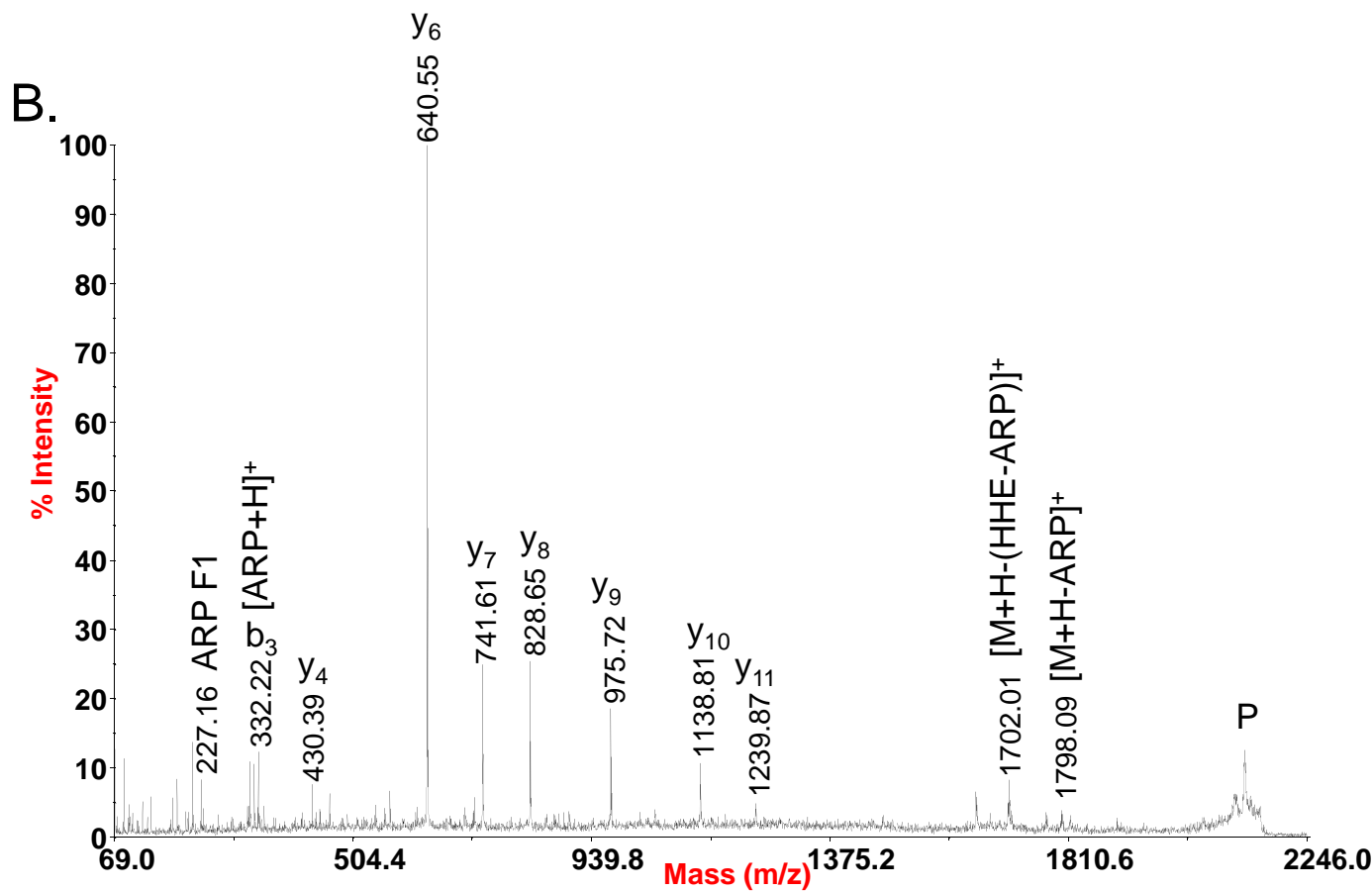
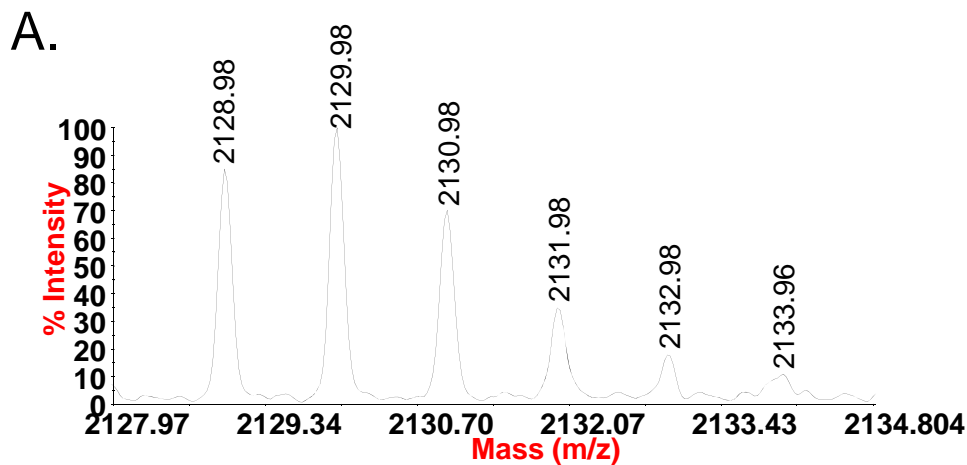
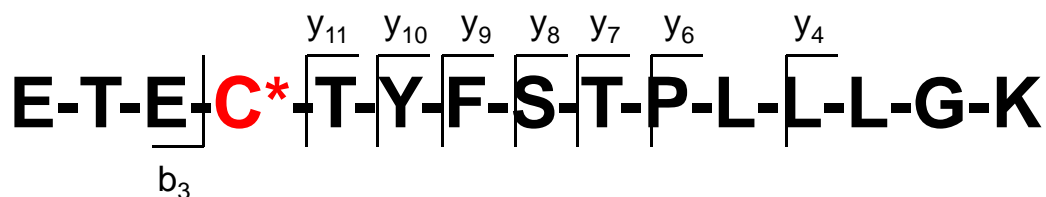
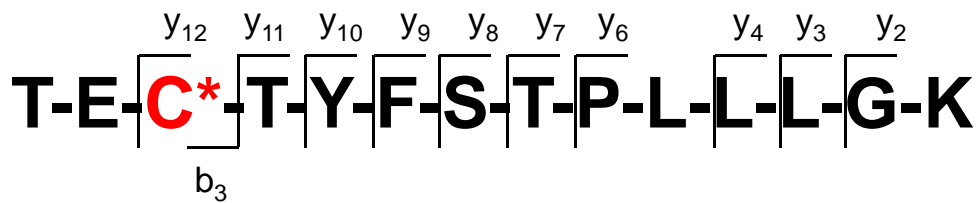
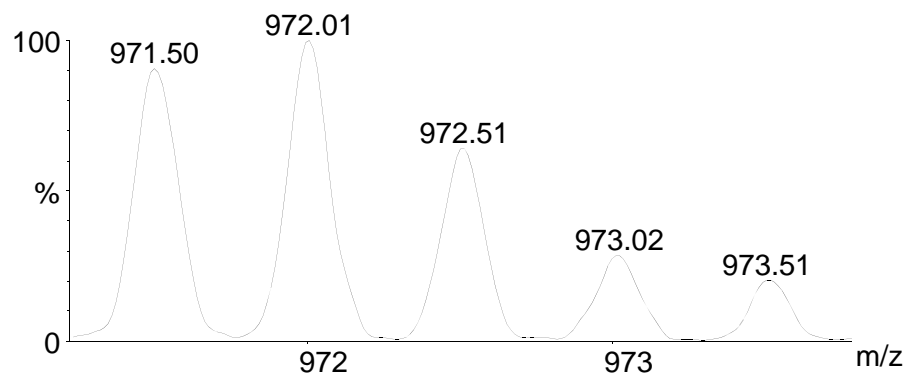


Figure S53. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, HHE modified peptide ETEC*TYFSTPLLLGK; monoisotopic m/z_{calc} 2129.03; accuracy $\Delta(m/z) = -0.05$ Da

MDHM_RAT: Malate dehydrogenase



A.



B.

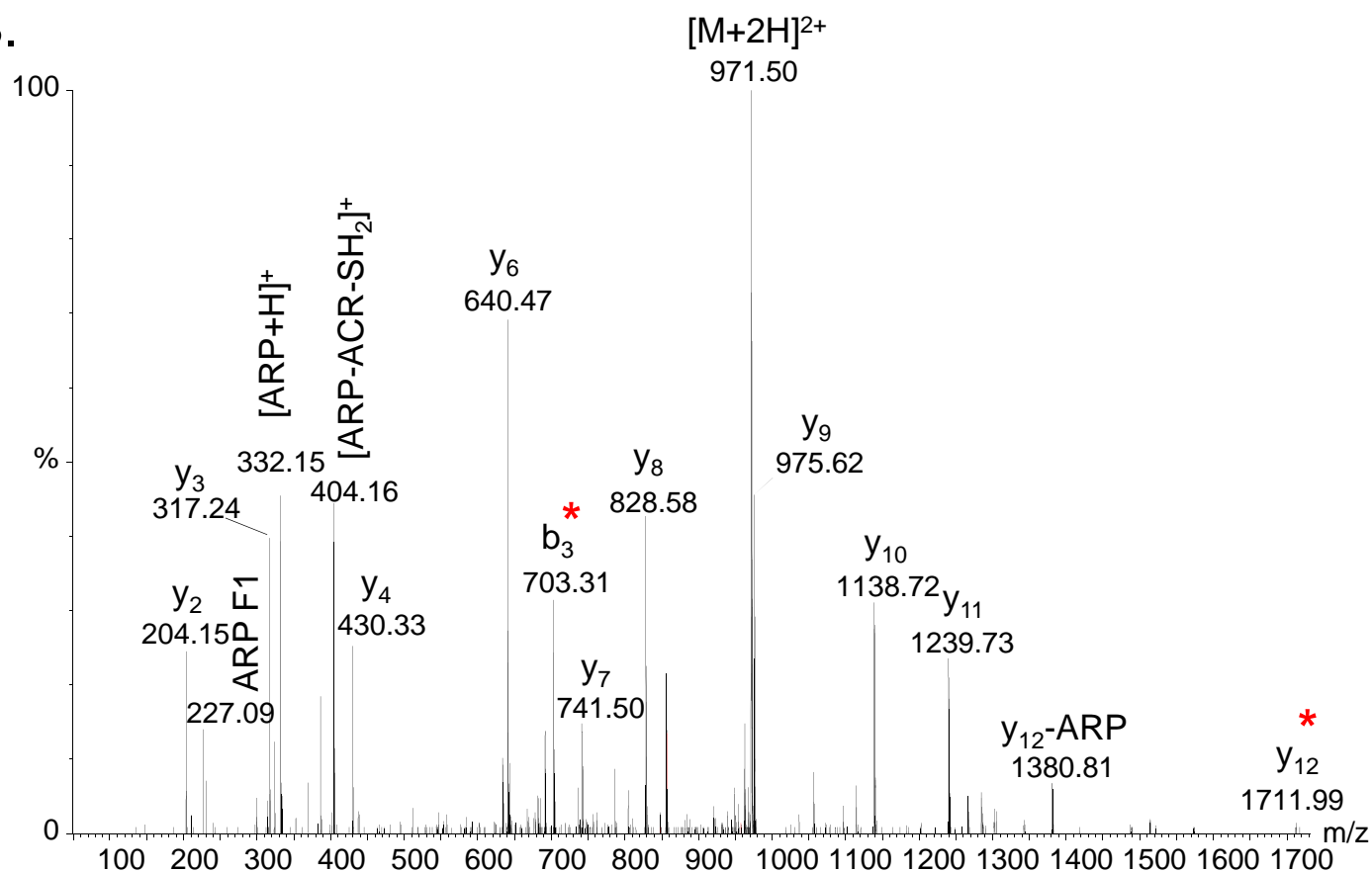


Figure S54. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide TEC*TYFSTPLLLGK; monoisotopic m/z_{calc} 971.48; accuracy $\Delta(m/z) = 0.02$ Da

MDHM_RAT: Malate dehydrogenase

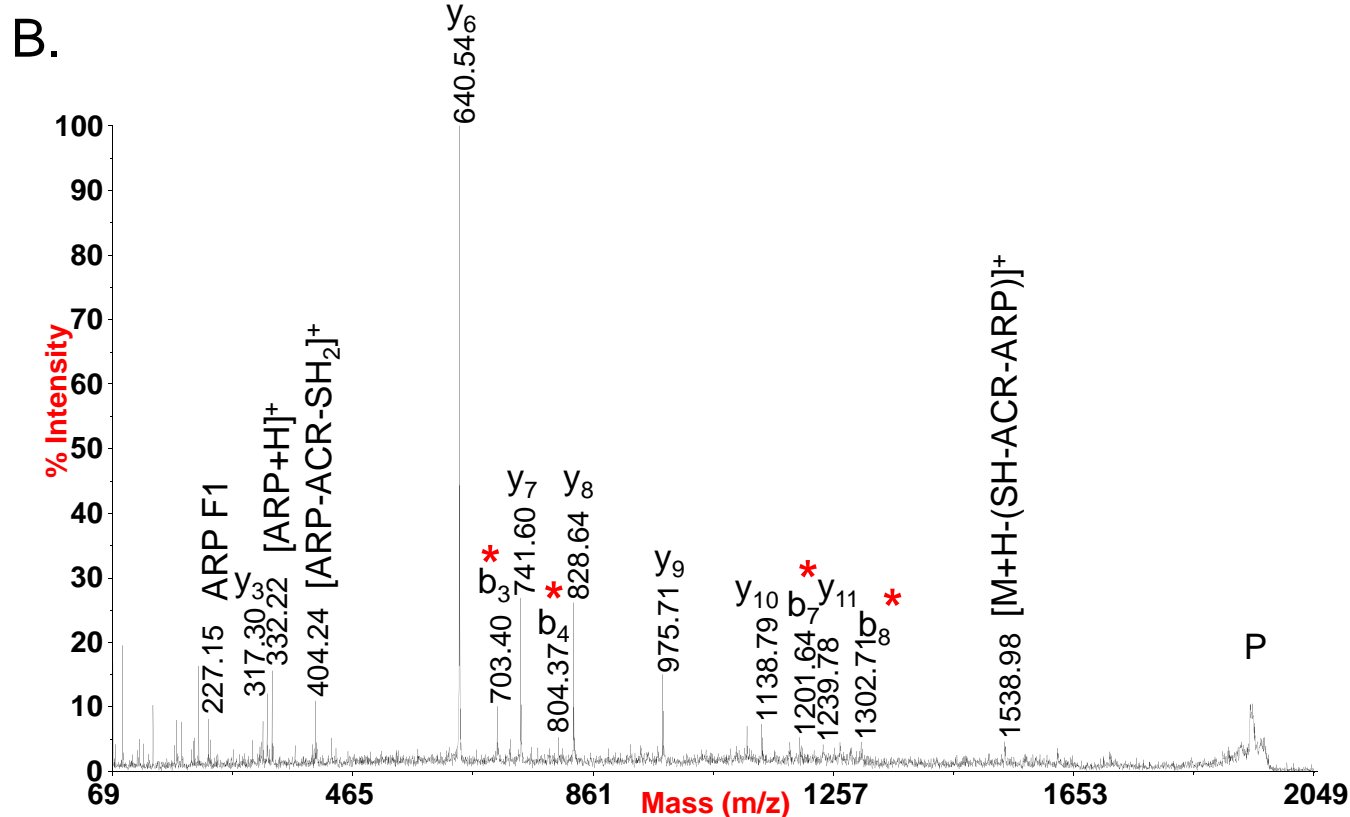
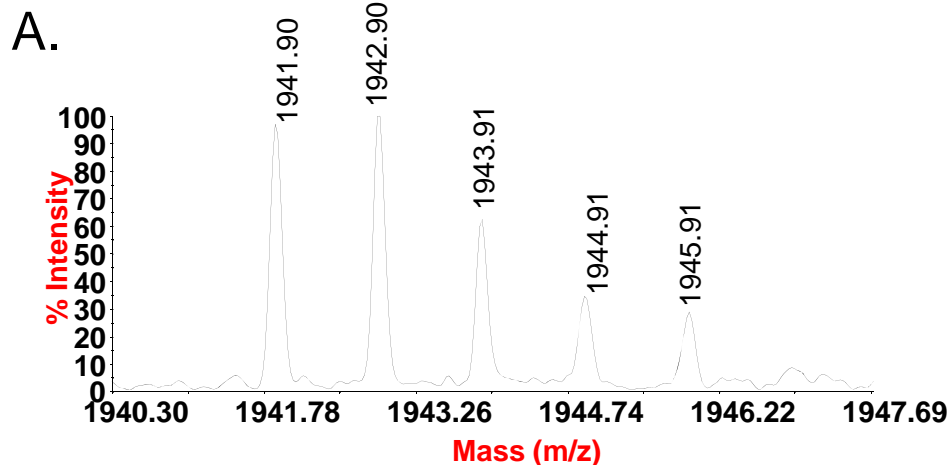
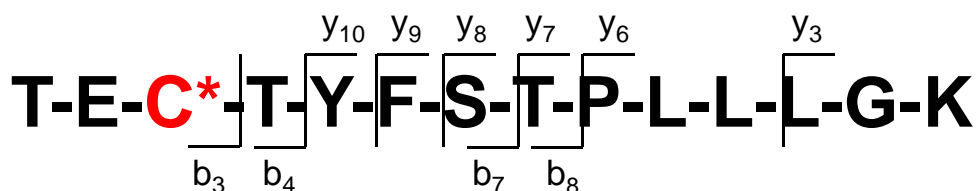


Figure S55. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide TEC*TYFSTPLLLGK; monoisotopic m/z_{calc} 1941.94; accuracy $\Delta(m/z) = -0.04$ Da

MDHM_RAT: Malate dehydrogenase

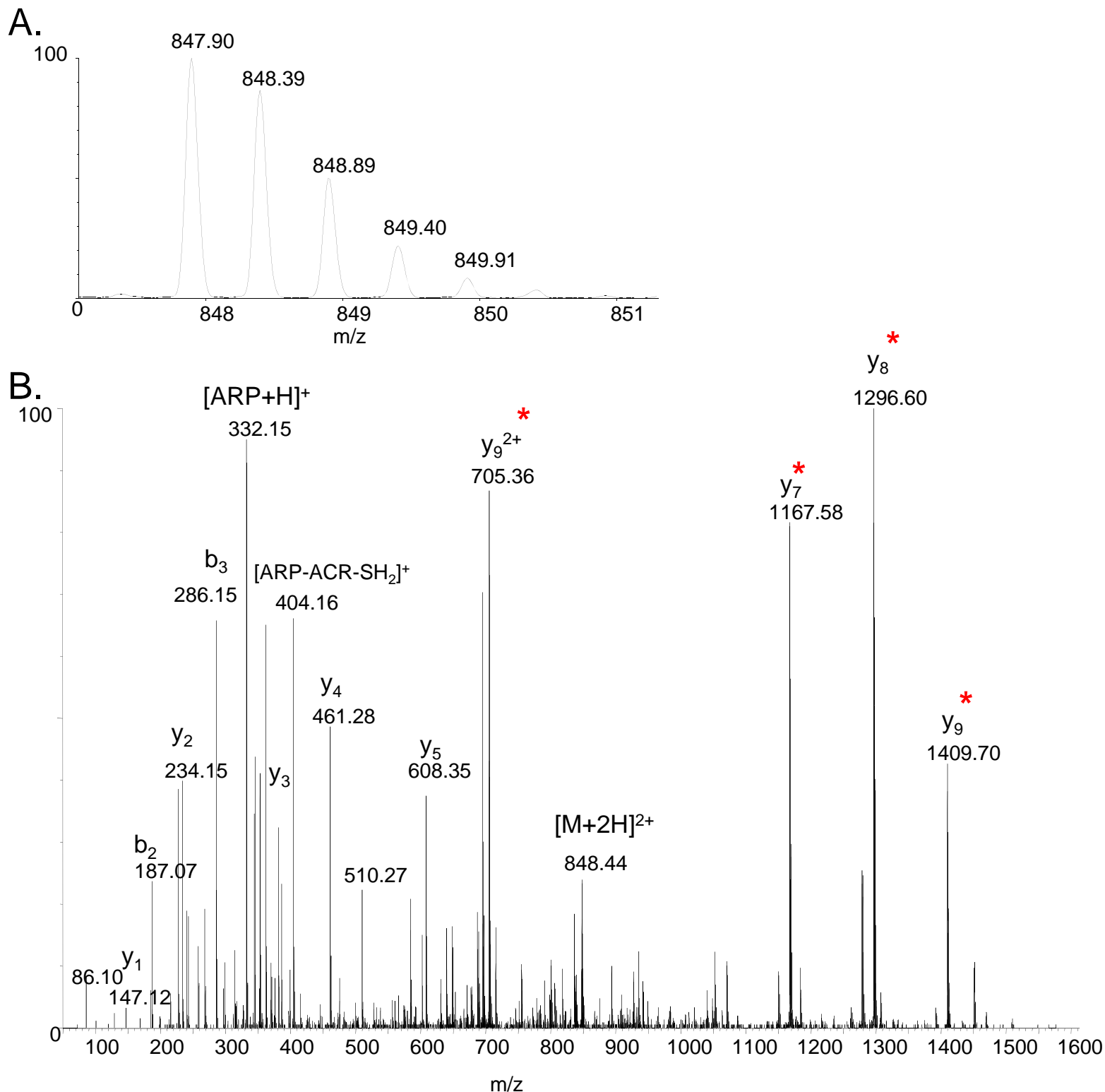
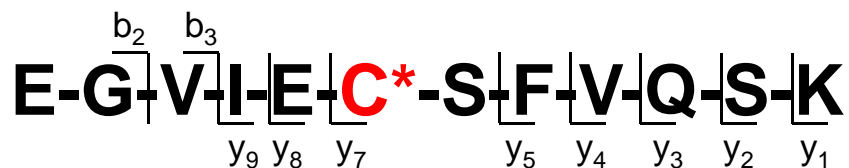


Figure S56. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide EGVIEC*SFVQSK; monoisotopic m/z_{calc} 847.90; accuracy $\Delta(m/z) = 0.00$ Da

MDHM_RAT: Malate dehydrogenase

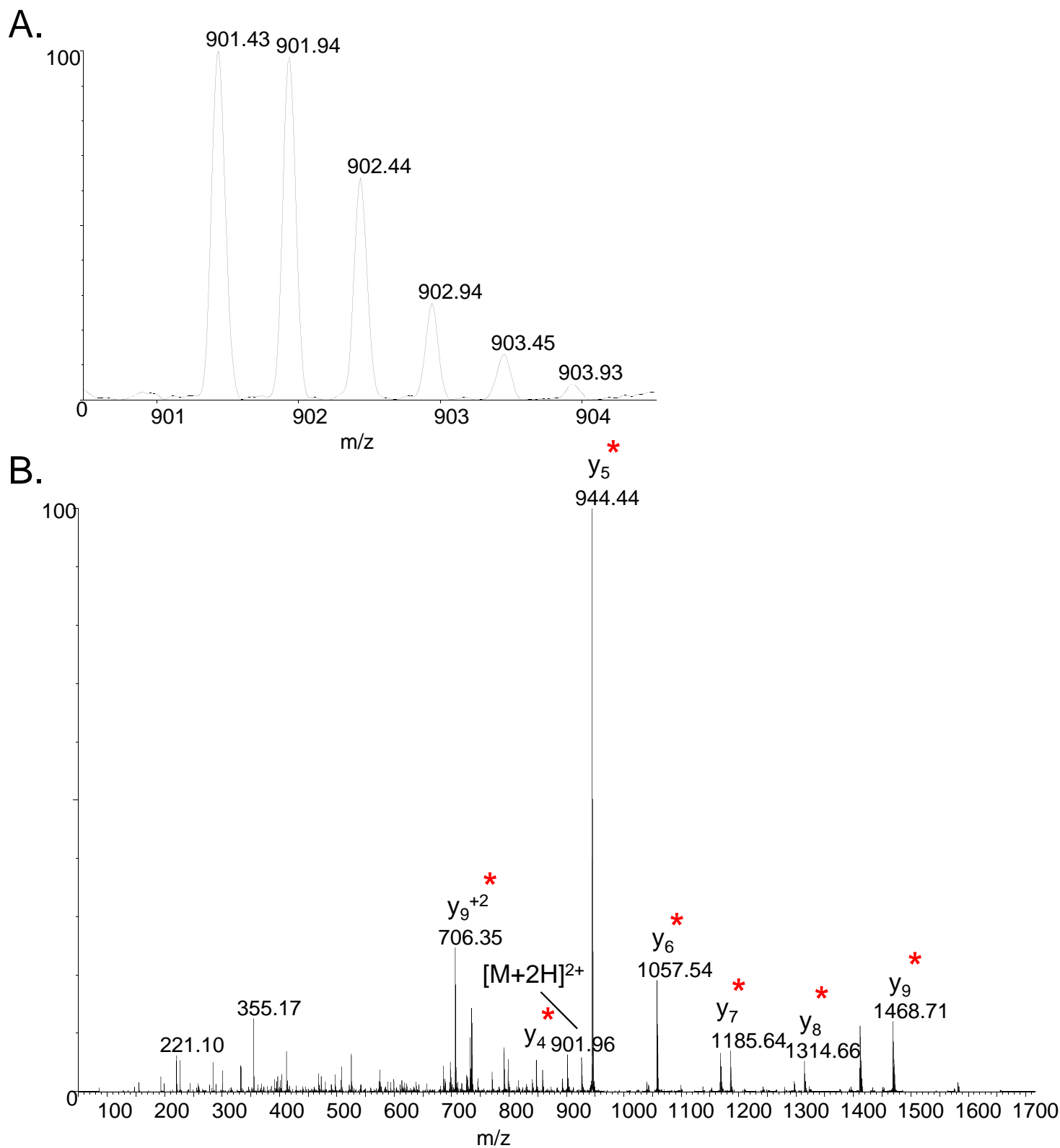
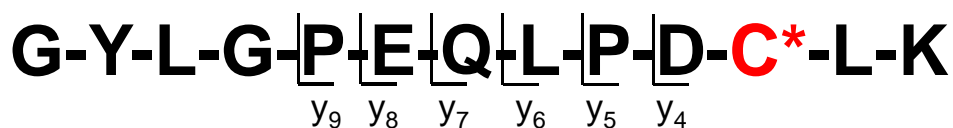


Figure S57. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the [M+2H]²⁺ ion of the ARP labeled, acrolein modified peptide GYLGP-EQLPDC*-LK; monoisotopic m/z_{calc} 901.43; accuracy $\Delta(m/z) = 0.00$ Da

MDHM_RAT: Malate dehydrogenase

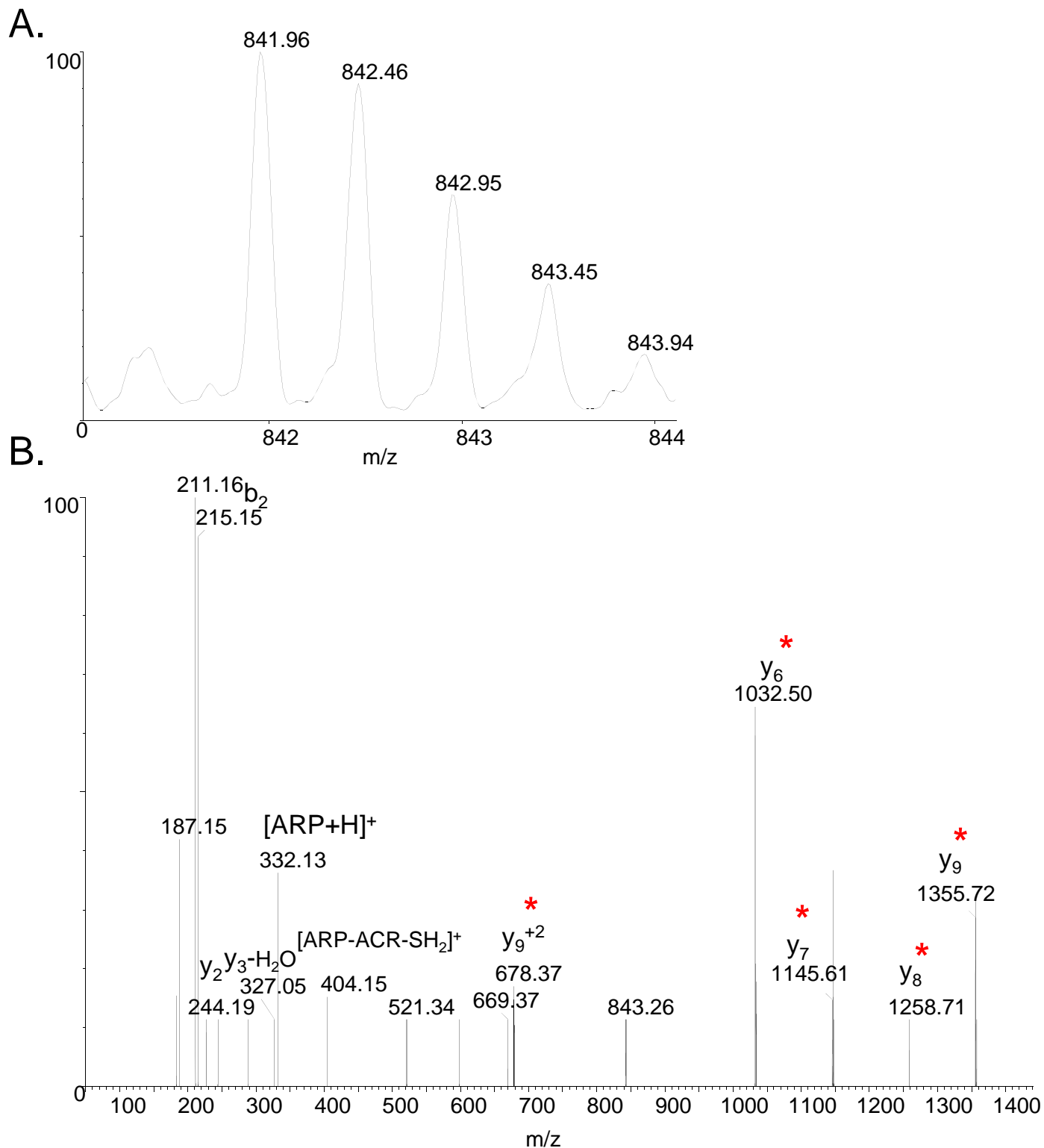
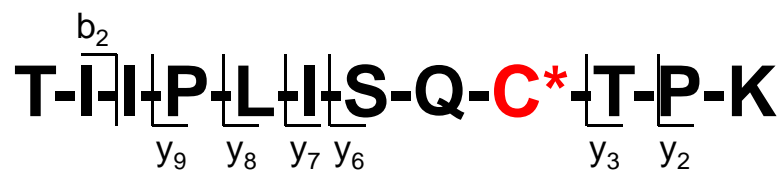


Figure S58. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide TIIP LISQC*TPK; monoisotopic m/z_{calc} 841.95; accuracy $\Delta(m/z) = 0.01$ Da

MDHM_RAT: Malate dehydrogenase

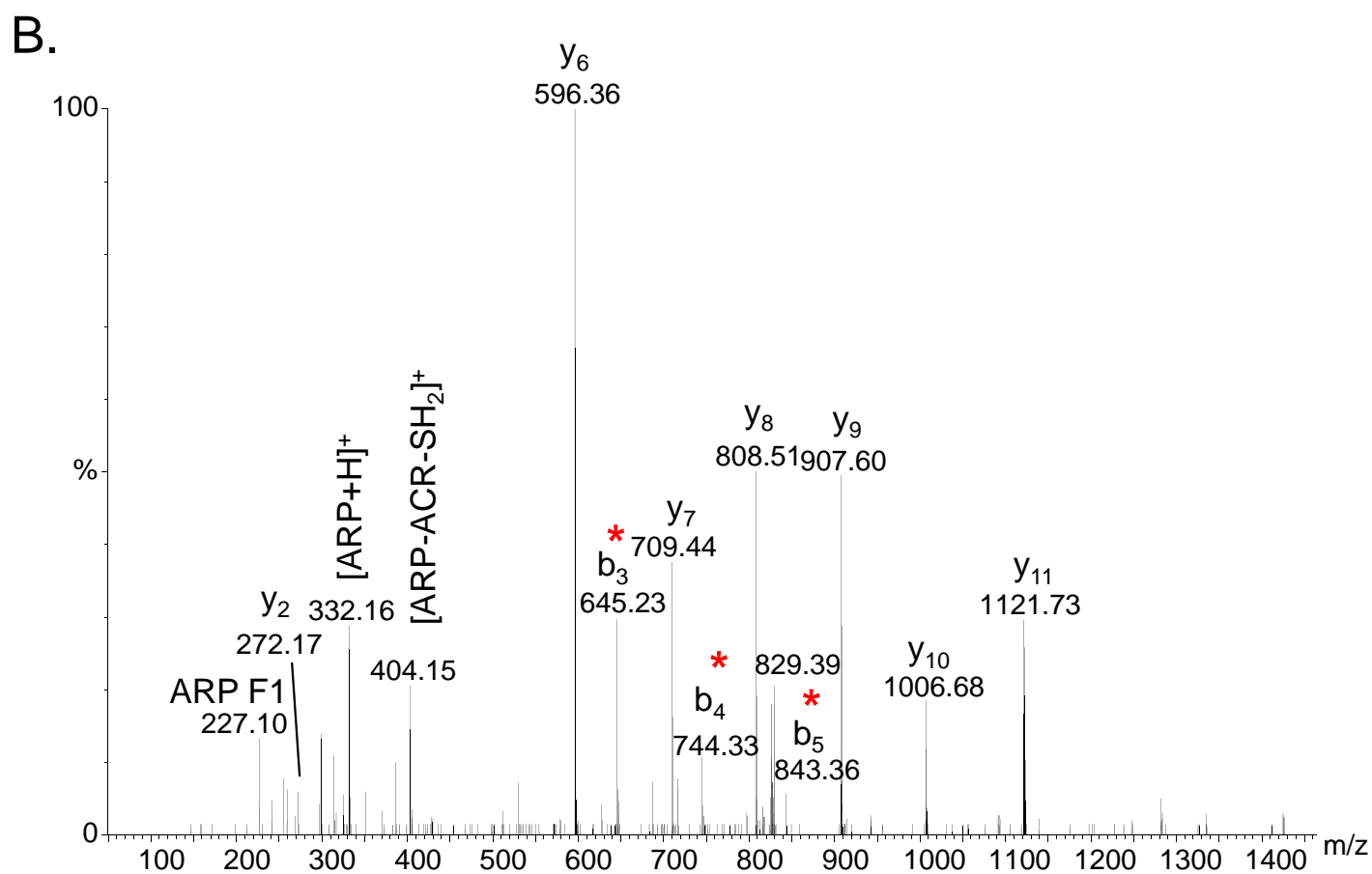
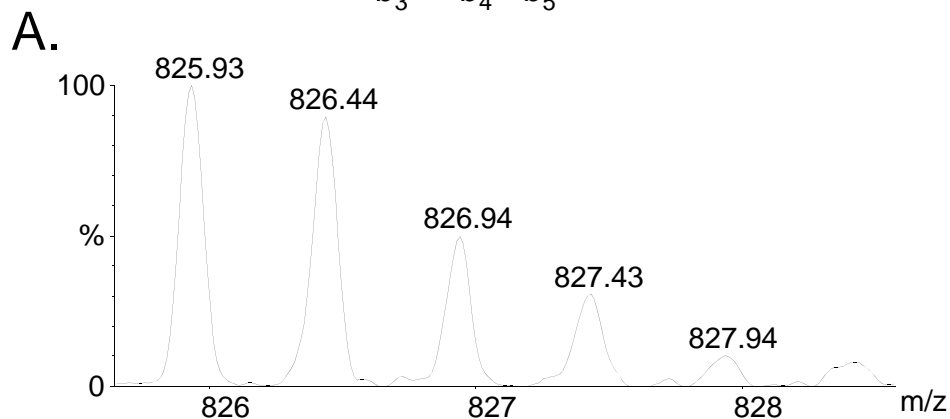
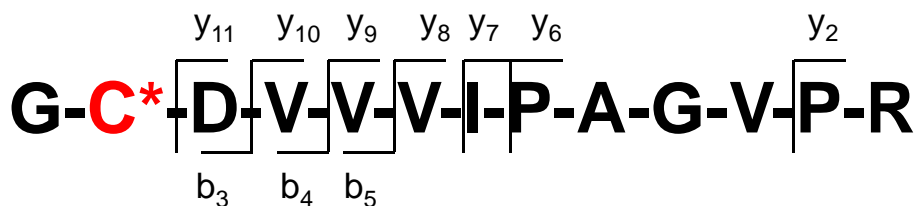


Figure S59. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide GC*DVVVIPAGVPR; monoisotopic m/z_{calc} 825.93; accuracy $\Delta(m/z) = 0.00$ Da

ODPA_RAT: Pyruvate dehydrogenase E1 component alpha subunit

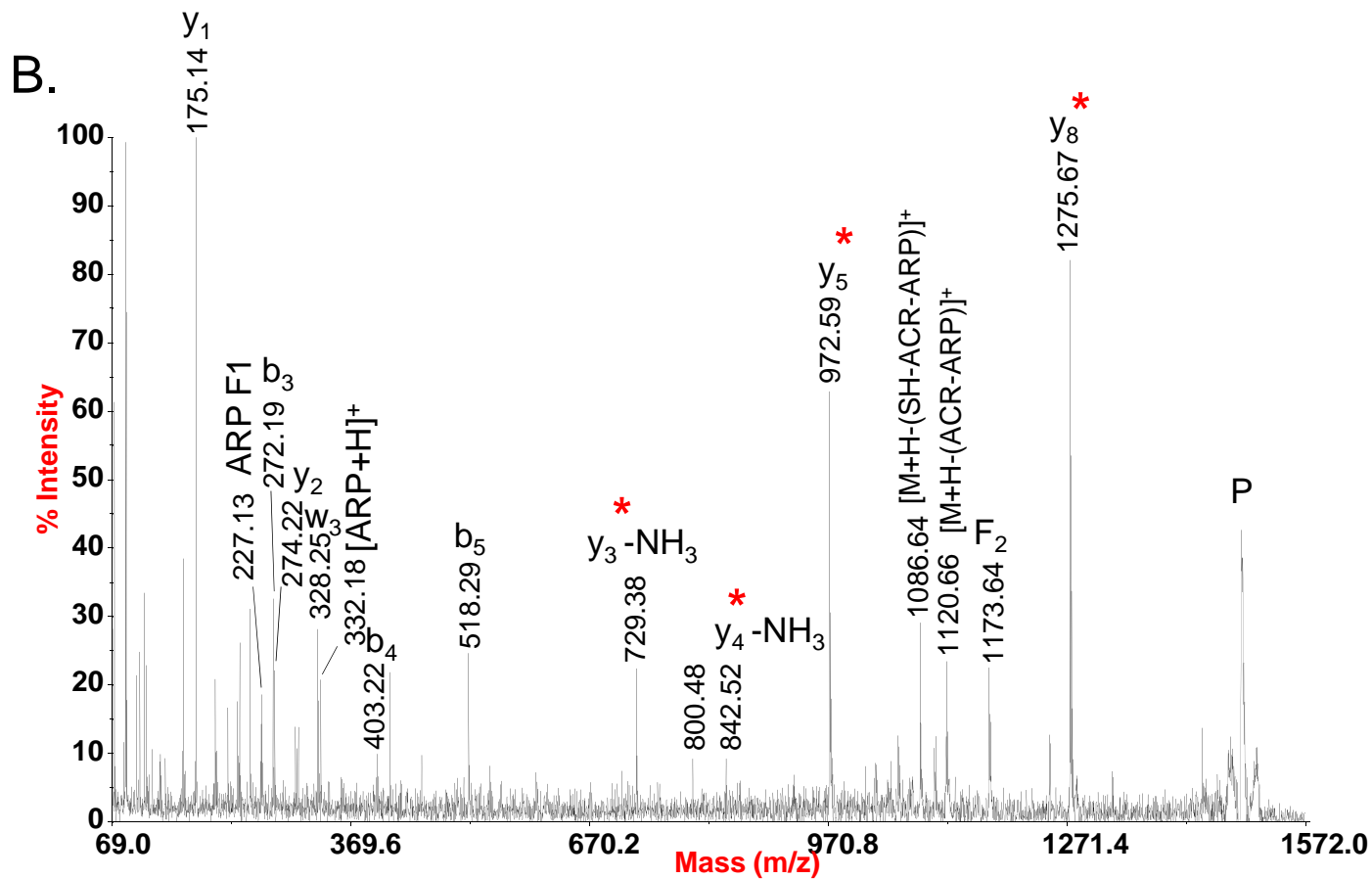
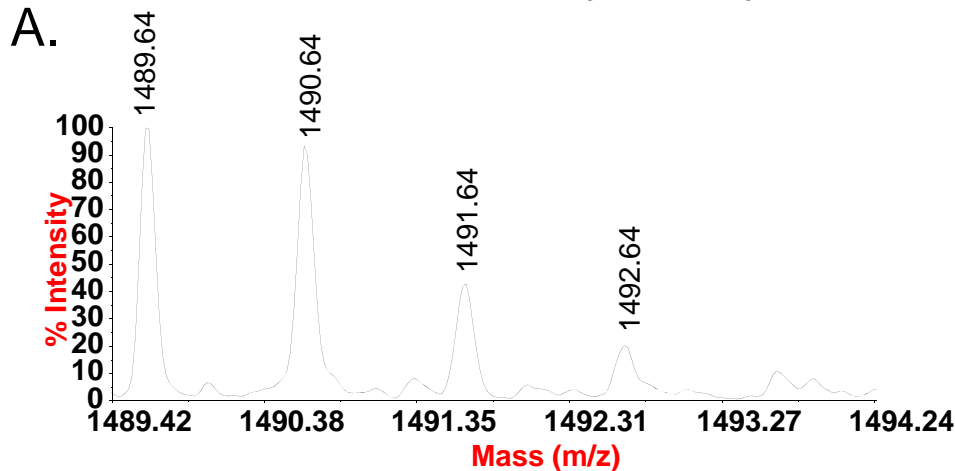
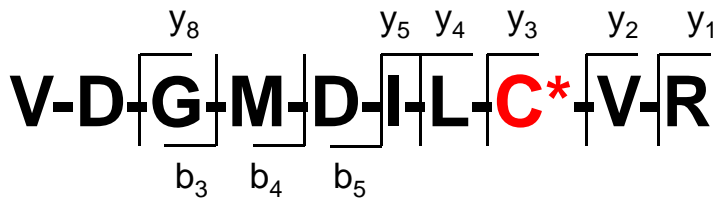


Figure S60. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide VDGMDILC*VR; monoisotopic m/z_{calc} 1489.70; accuracy $\Delta(m/z) = -0.06$ Da

ODPA_RAT: Pyruvate dehydrogenase E1 component alpha subunit

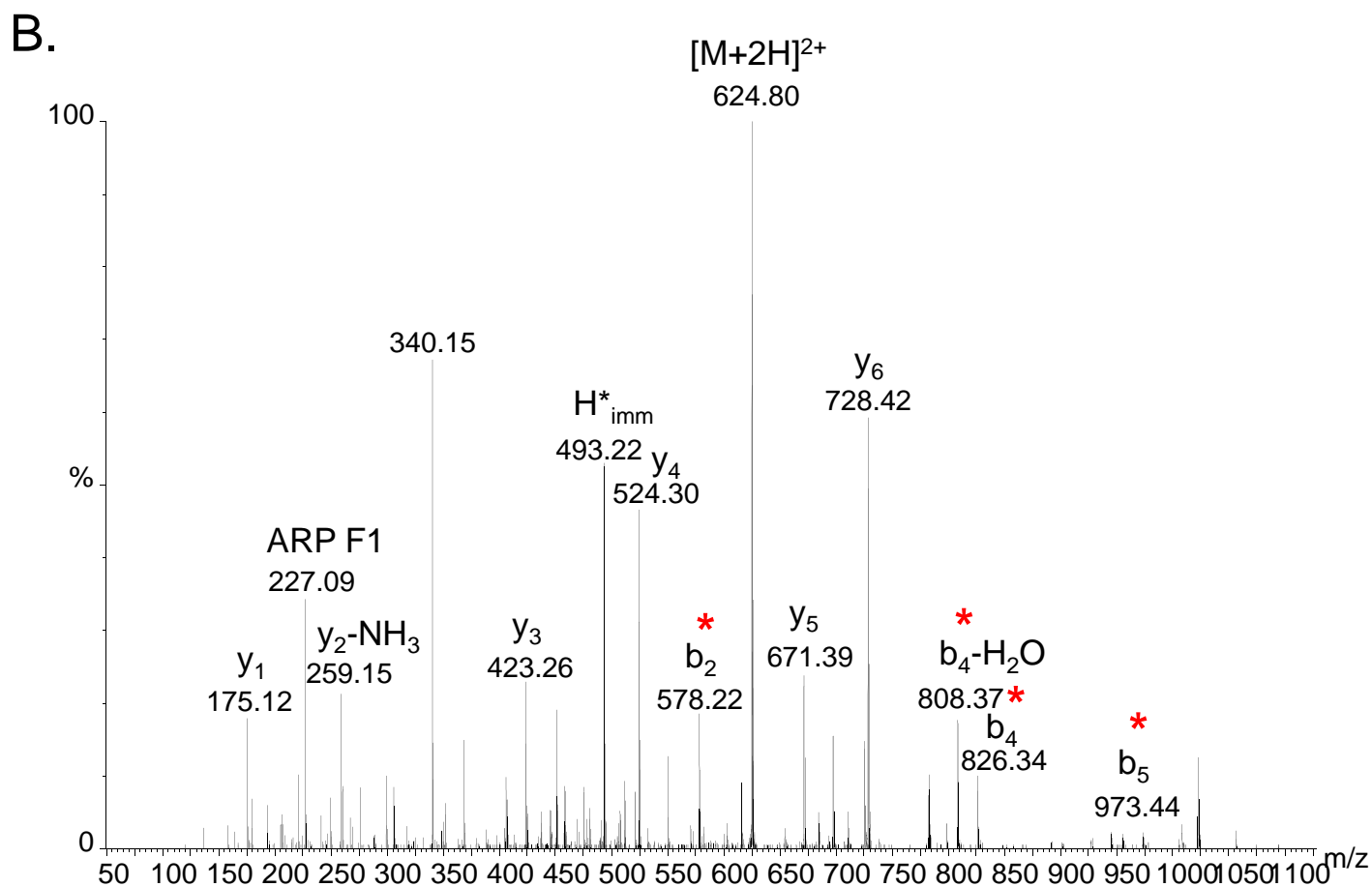
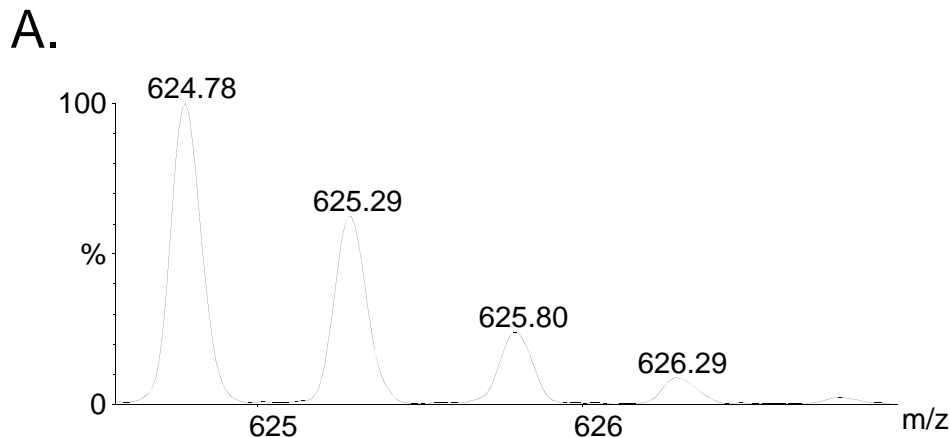
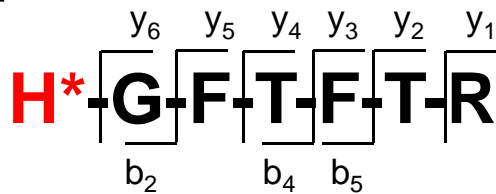


Figure S61. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, crotonaldehyde modified peptide $H^*GFTFTR$; monoisotopic m/z_{calc} 624.80; accuracy $\Delta(m/z) = -0.02$ Da

ODPB_RAT: Pyruvate dehydrogenase E1 component beta subunit

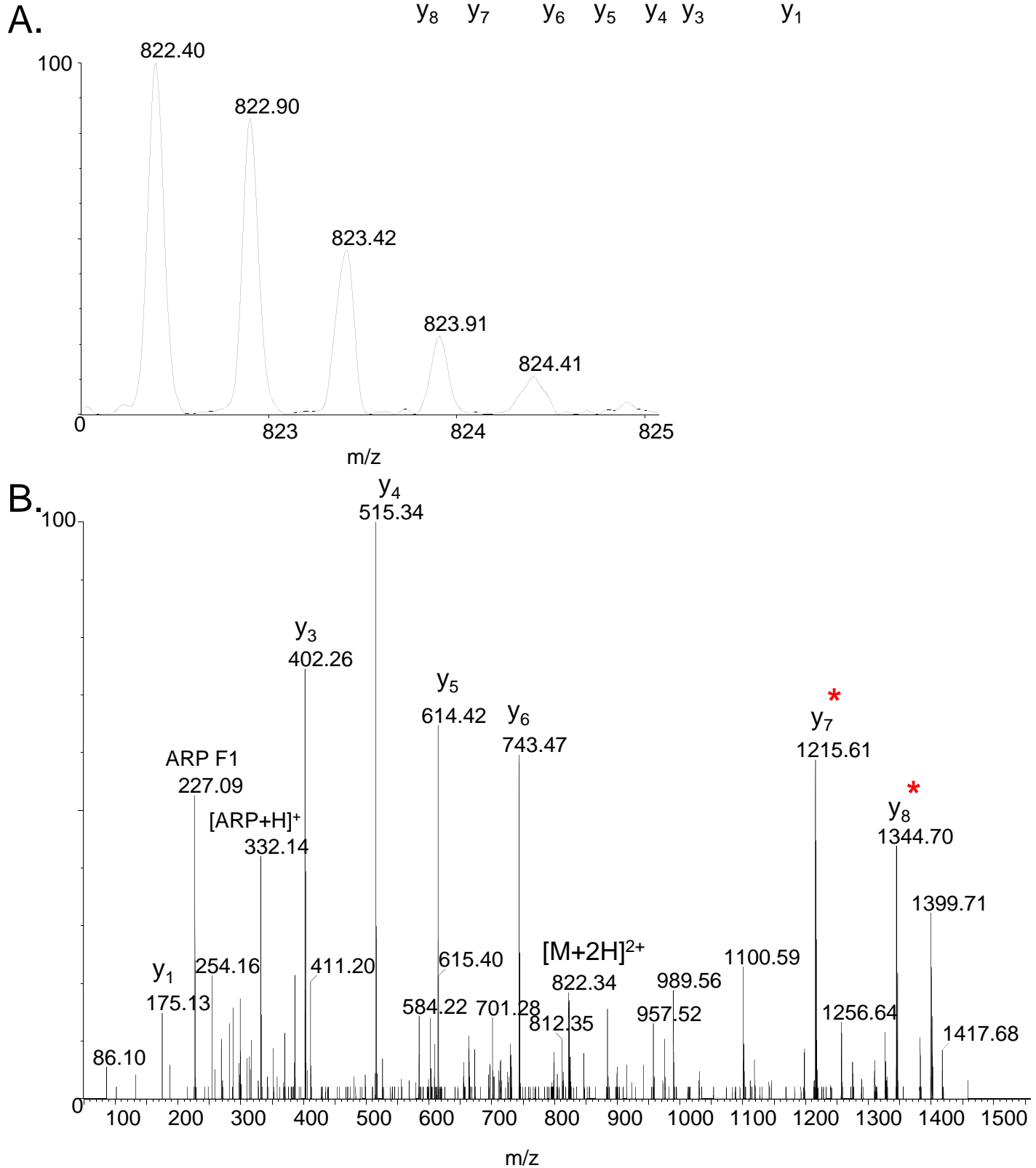
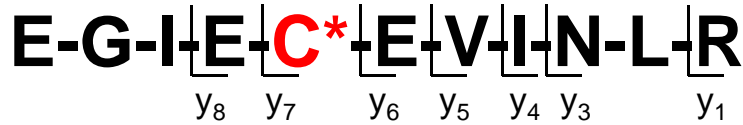


Figure S62. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide EGIEC*EVINLR; monoisotopic m/z_{calc} 822.40; accuracy $\Delta(m/z) = 0.00$ Da

ETFD_RAT: Electron transfer flavoprotein-ubiquinone oxidoreductase

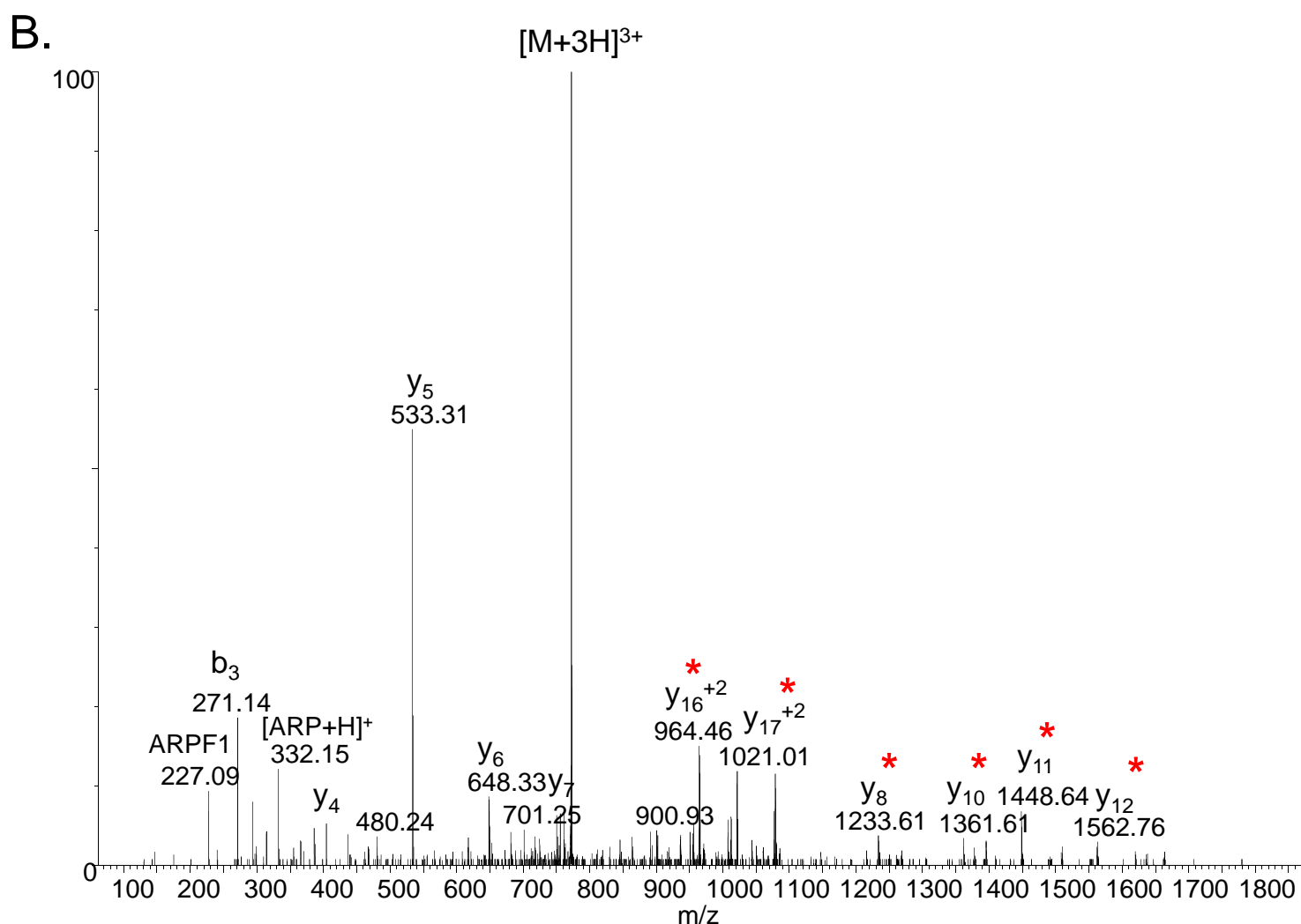
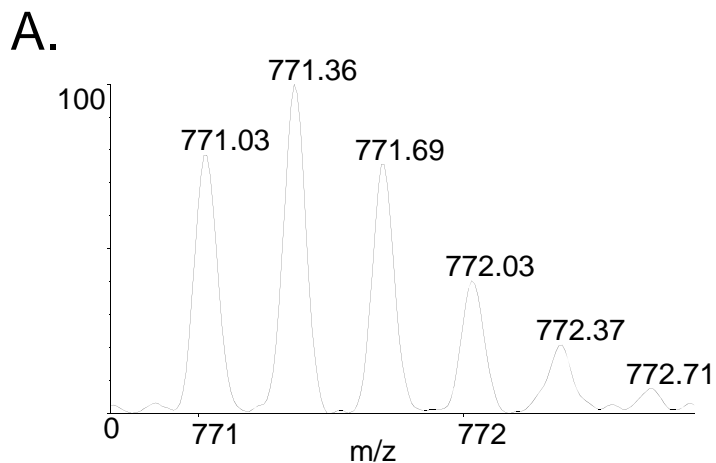
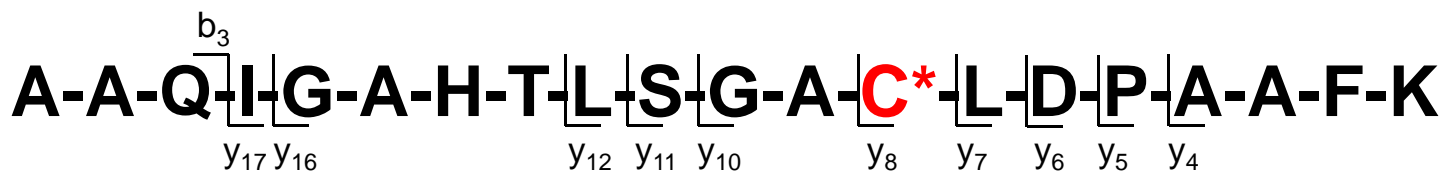
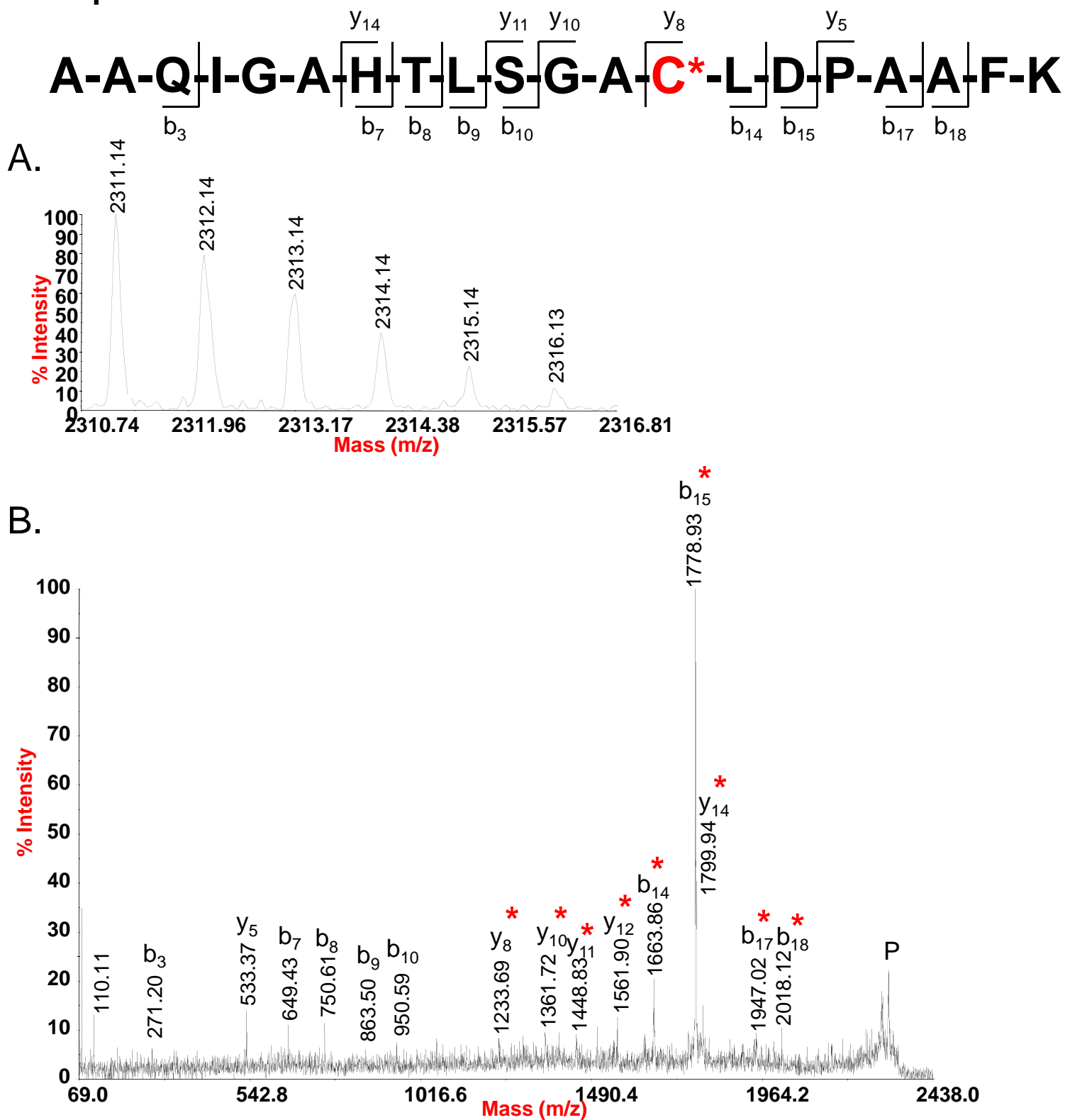
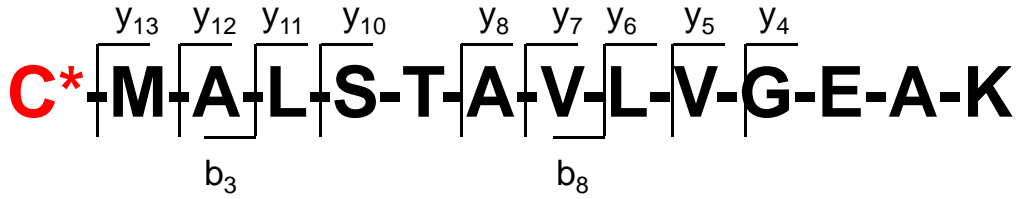


Figure S63. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+3H]^{3+}$ ion of the ARP labeled, acrolein modified peptide AAQIGAHTLSGAC*LDPAAFK; monoisotopic m/z_{calc} 771.05; accuracy $\Delta(m/z) = -0.02$ Da

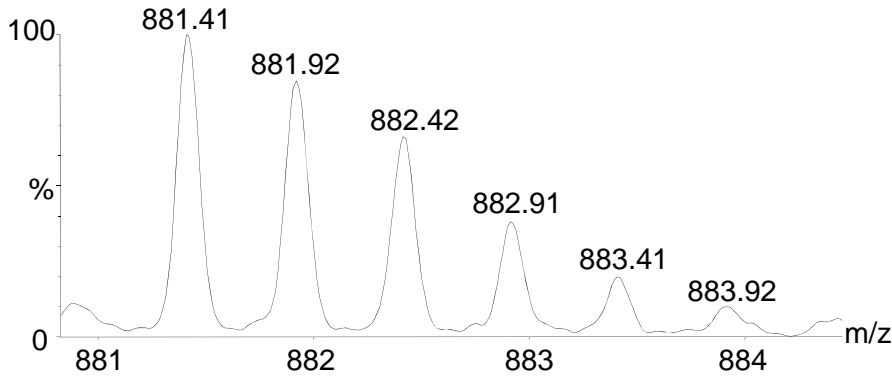
ETFD_RAT: Electron transfer flavoprotein-ubiquinone oxidoreductase



MMSA_RAT: Methylmalonate-semialdehyde dehydrogenase



A.



B.

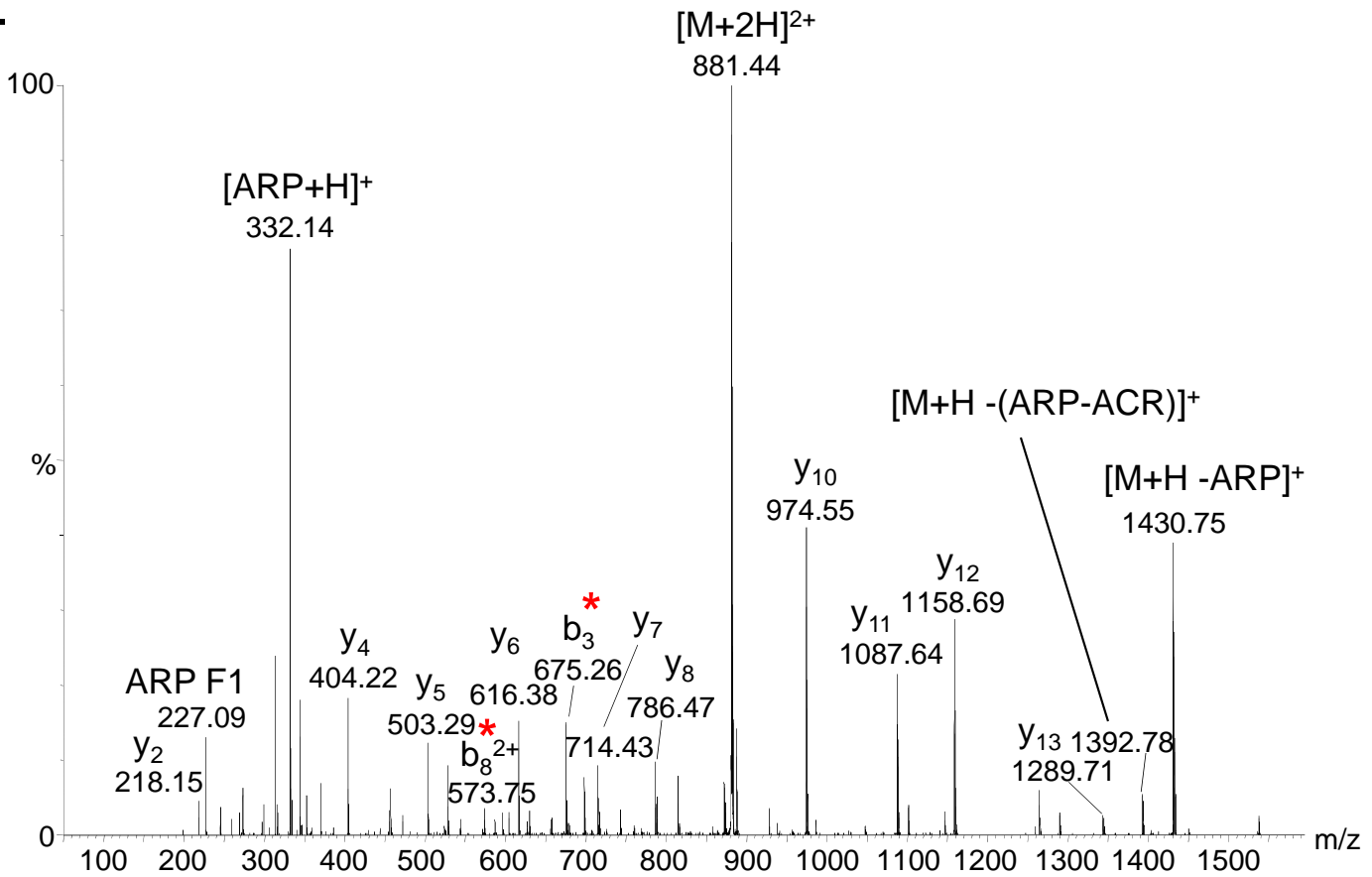


Figure S65. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide C^* MALSTAVLVGEAK; monoisotopic m/z_{calc} 881.44; accuracy $\Delta(m/z) = -0.03$ Da

MMSA_RAT: Methylmalonate-semialdehyde dehydrogenase

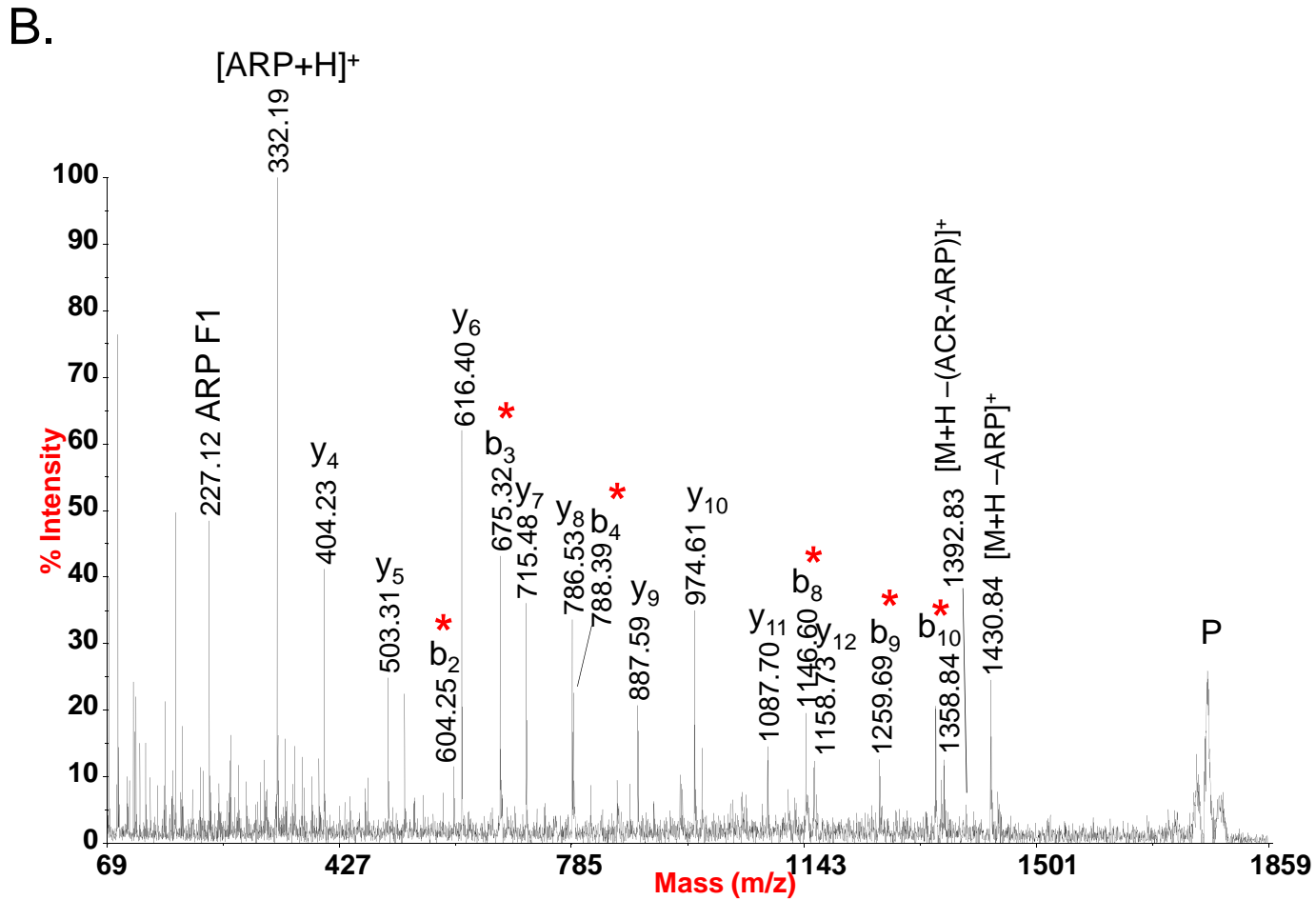
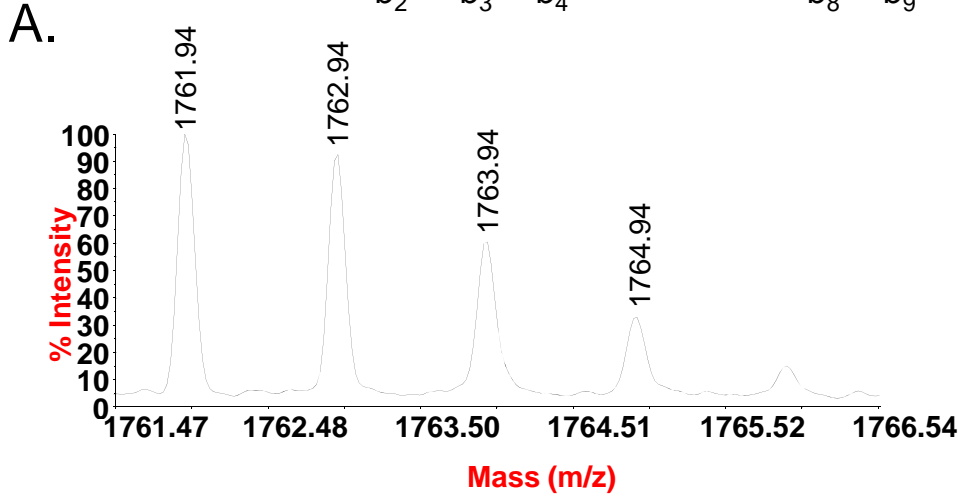
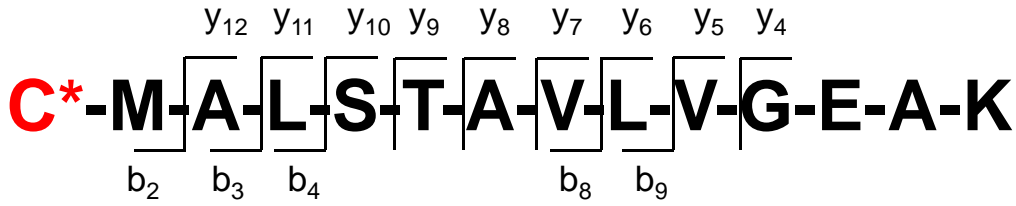


Figure S66. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide C*MALSTAVLVGEAK; monoisotopic m/z_{calc} 1761.87; accuracy $\Delta(m/z) = 0.07$ Da

NNTM_MOUSE: NAD(P) transhydrogenase

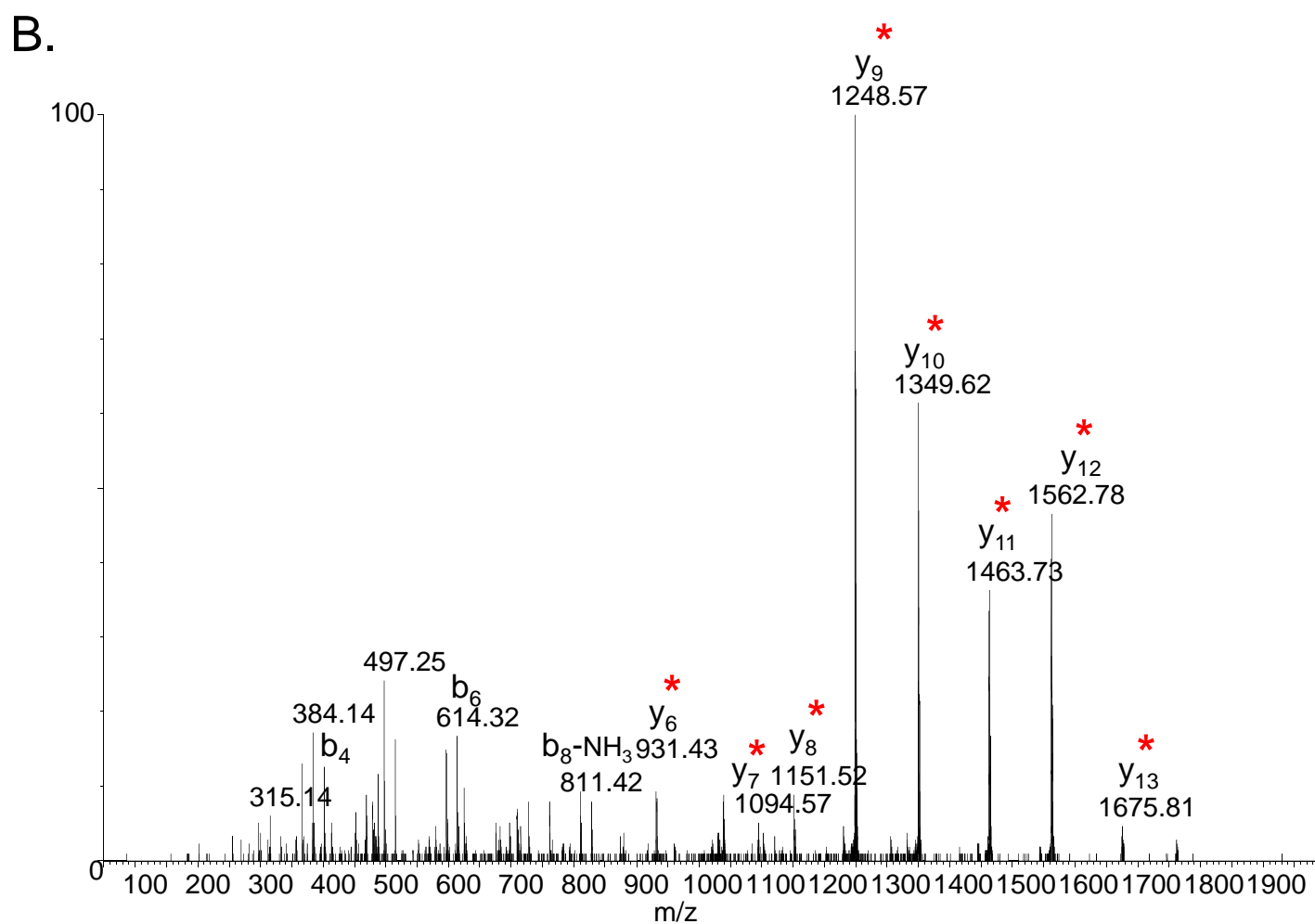
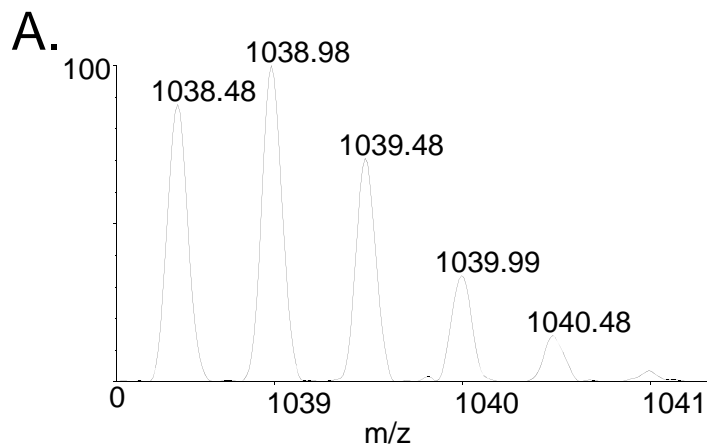
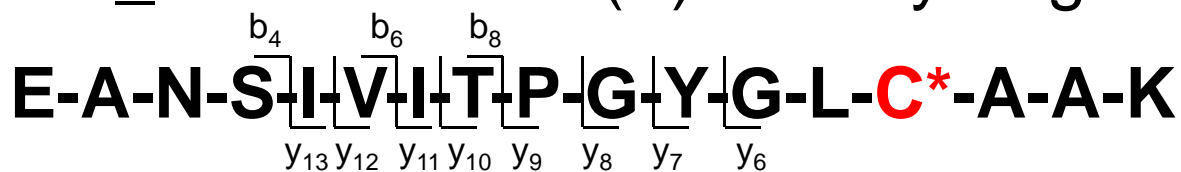


Figure S67. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide EANSIVITPGYGLC*AAK; monoisotopic m/z_{calc} 1038.52; accuracy $\Delta(m/z) = -0.04$ Da

NNTM_MOUSE: NAD(P) transhydrogenase

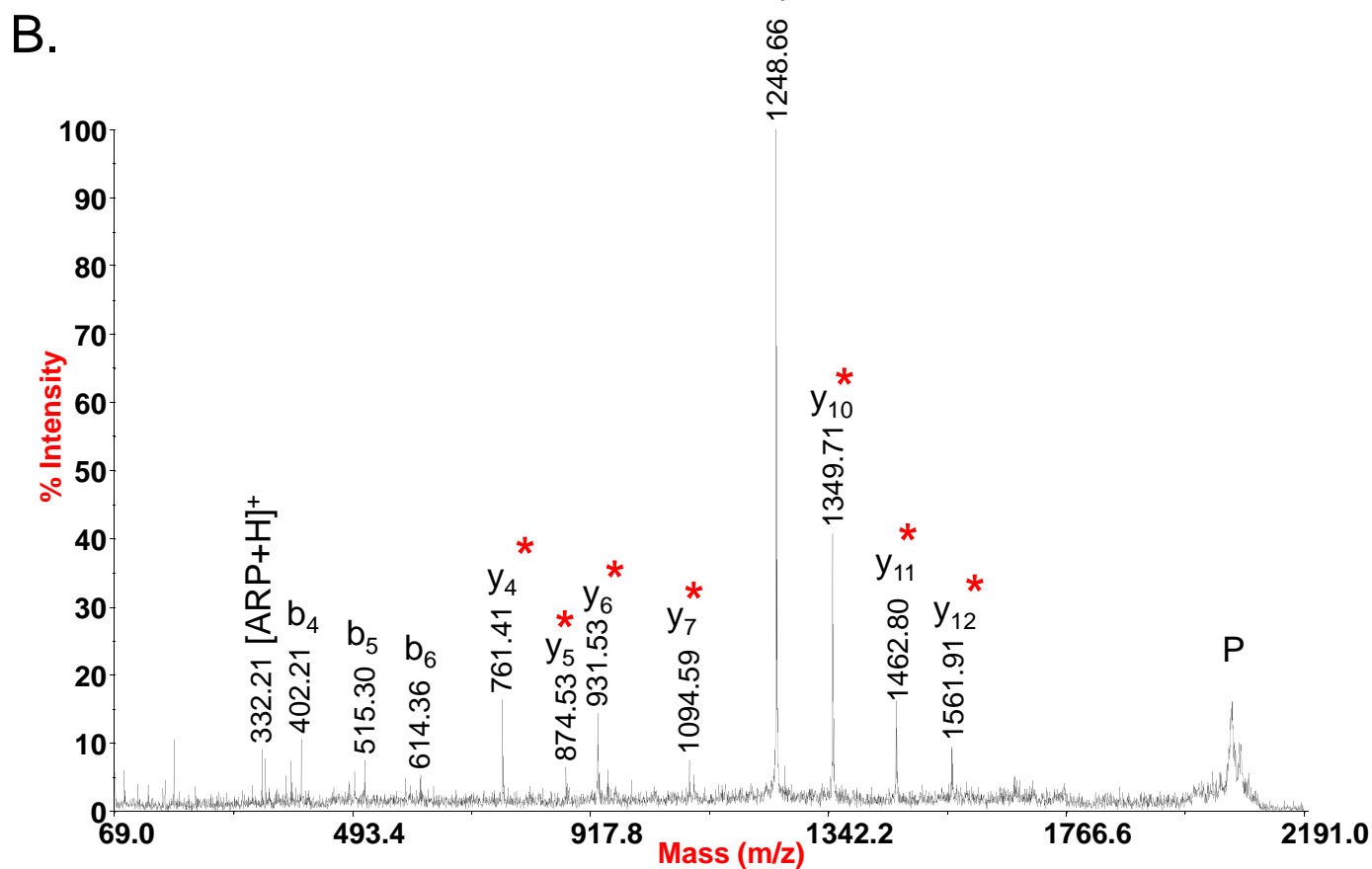
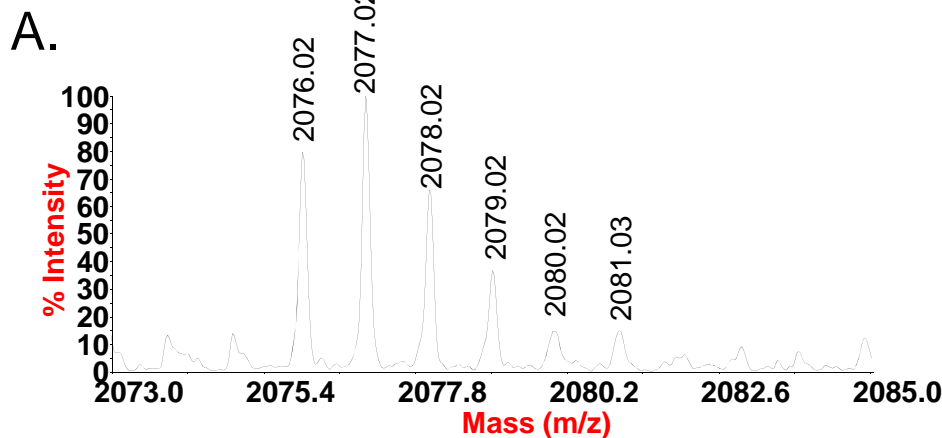
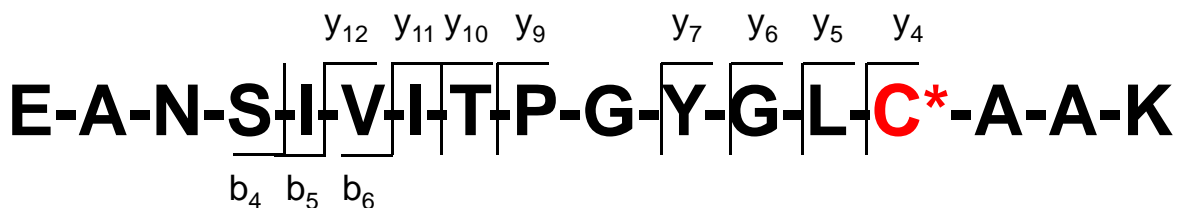


Figure S68. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, acrolein modified peptide EANSIVITPGYGLC*AAK; monoisotopic m/z_{calc} 2076.03; accuracy $\Delta(m/z) = -0.01$ Da

CH60_RAT: 60kDa heat shock protein

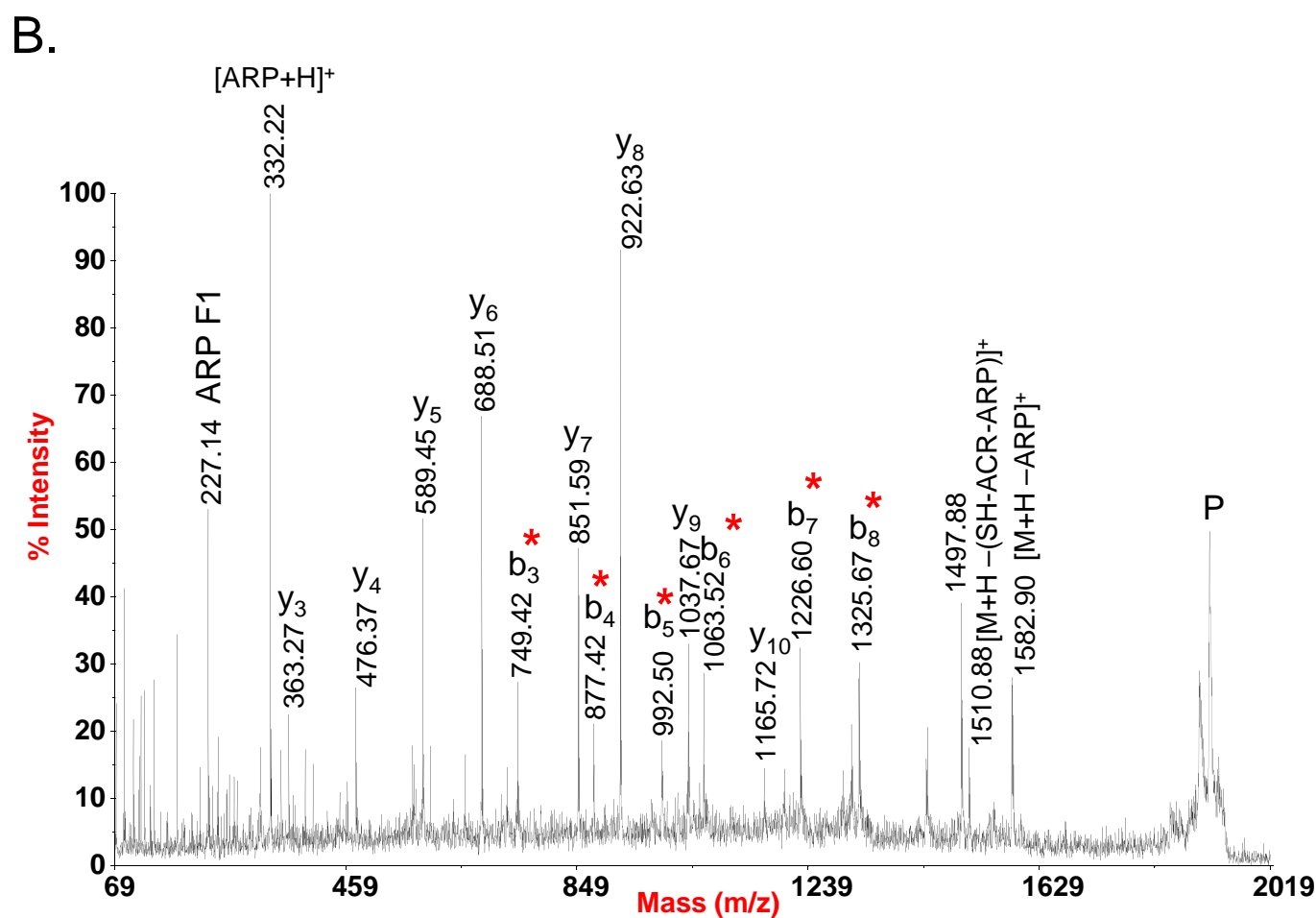
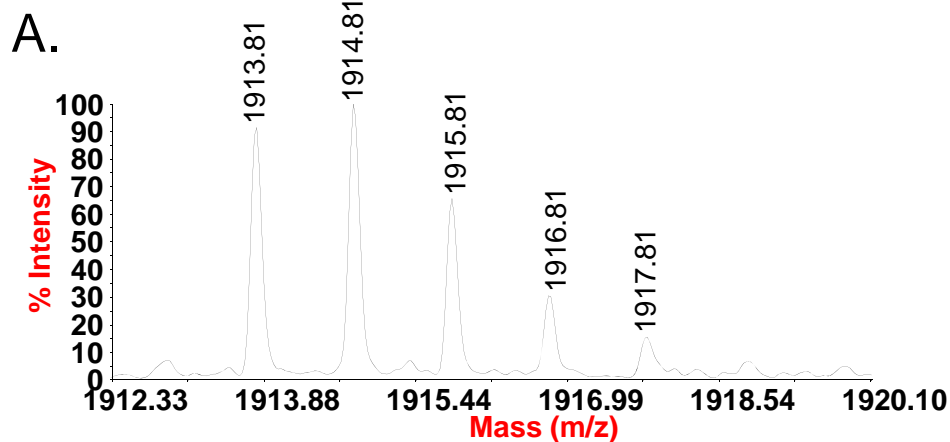
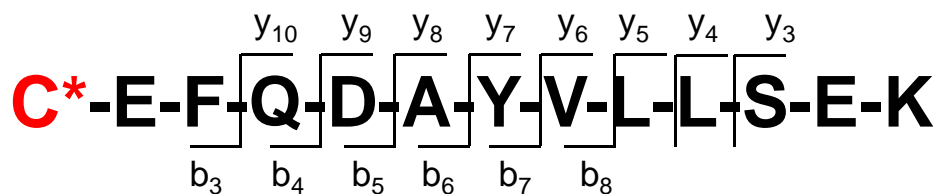


Figure S69. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide C*EFQDAYVLLSEK; monoisotopic m/z_{calc} 1913.88; accuracy $\Delta(m/z) = -0.07$ Da

ACADL_RAT: Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor

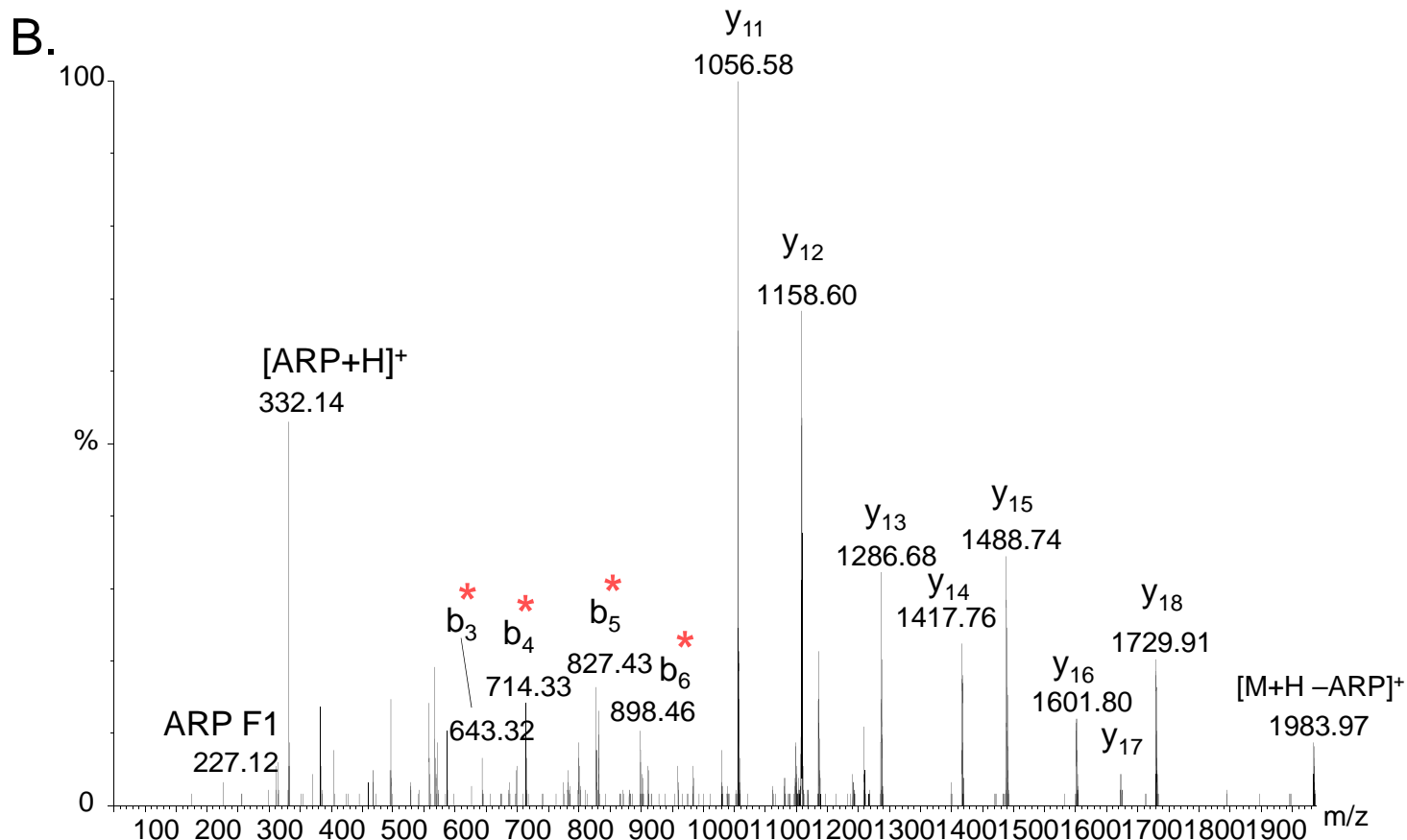
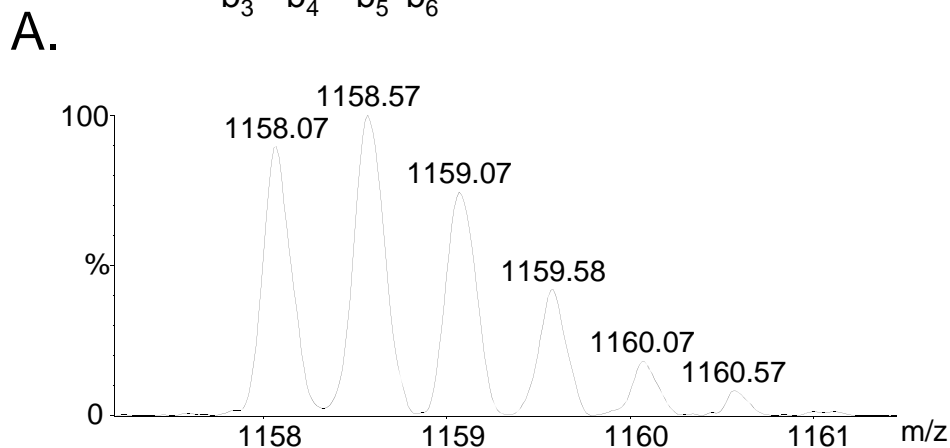
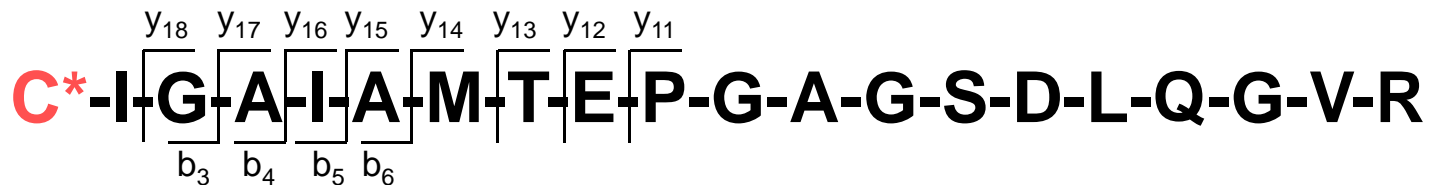


Figure S70. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide C*IGAIAMTEPGAGSDLQGV R; monoisotopic m/z_{calc} 1158.05; accuracy $\Delta(m/z) = 0.02$ Da

ACADL_RAT: Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor

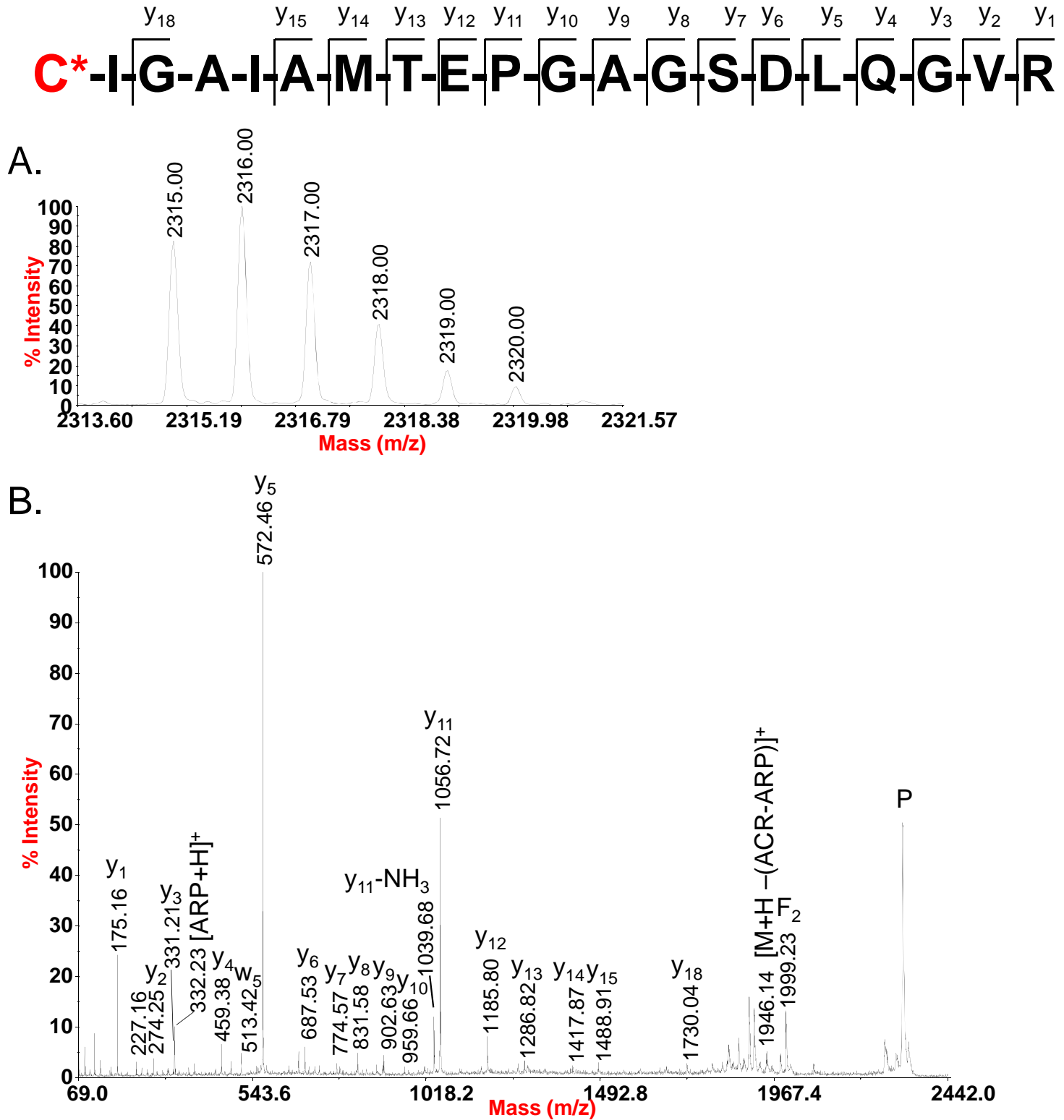


Figure S71. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, acrolein modified peptide C*IGAIAMTEPGAGSDLQGV-R; monoisotopic m/z_{calc} 2315.09; accuracy $\Delta(m/z) = 0.01$ Da

ACADL_RAT: Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor

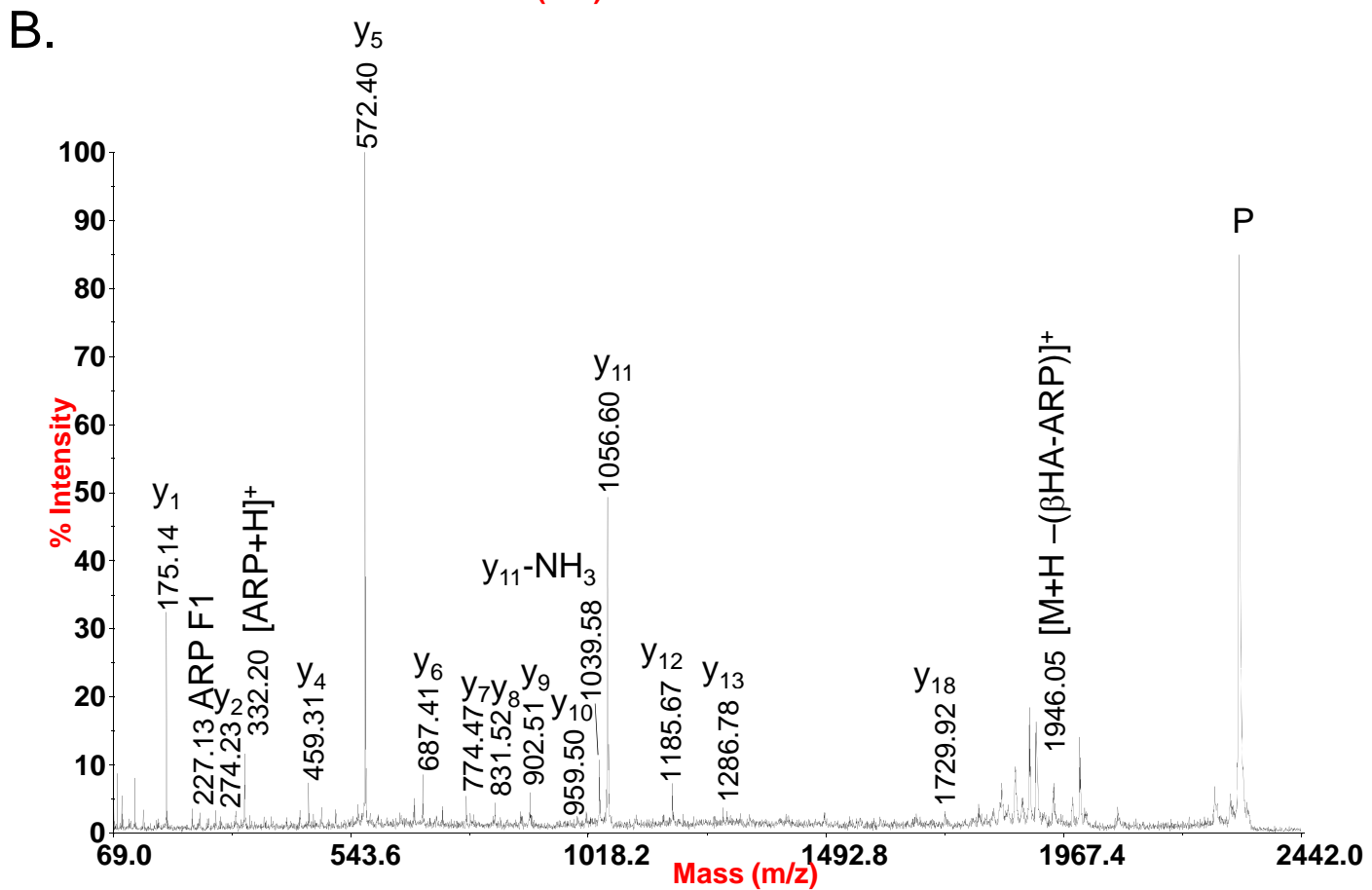
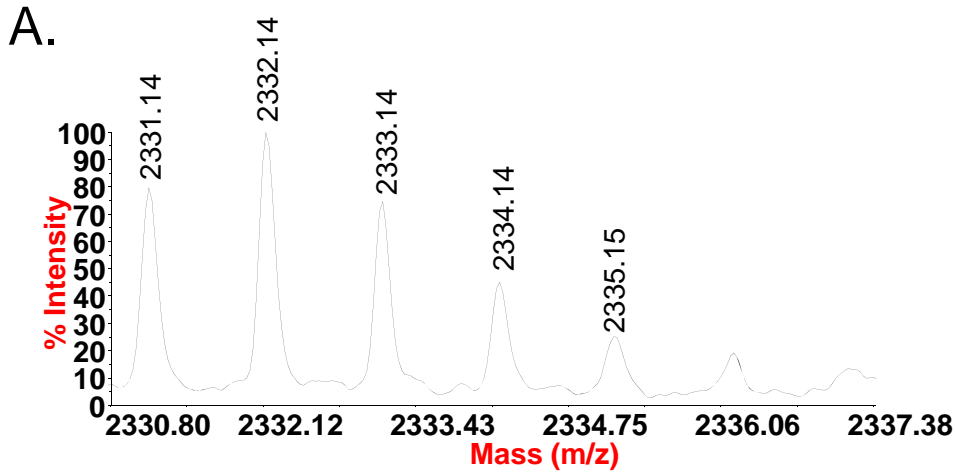
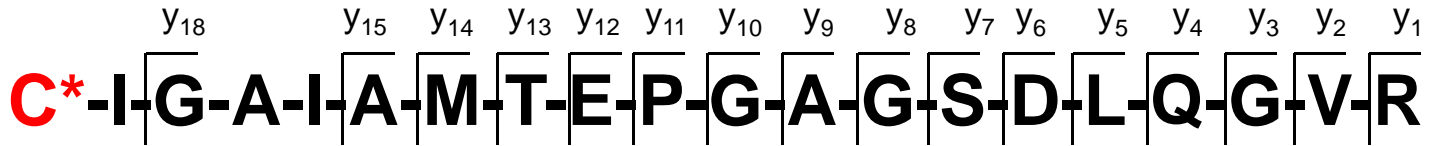


Figure S72. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the [M+H]⁺ ion of the ARP labeled, beta-hydroxyacrolein modified peptide C*IGAIAMTEPGAGSDLQGV-R; monoisotopic m/z_{calc} 2331.09; accuracy Δ(m/z) = 0.05 Da

ACADL_RAT: Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor

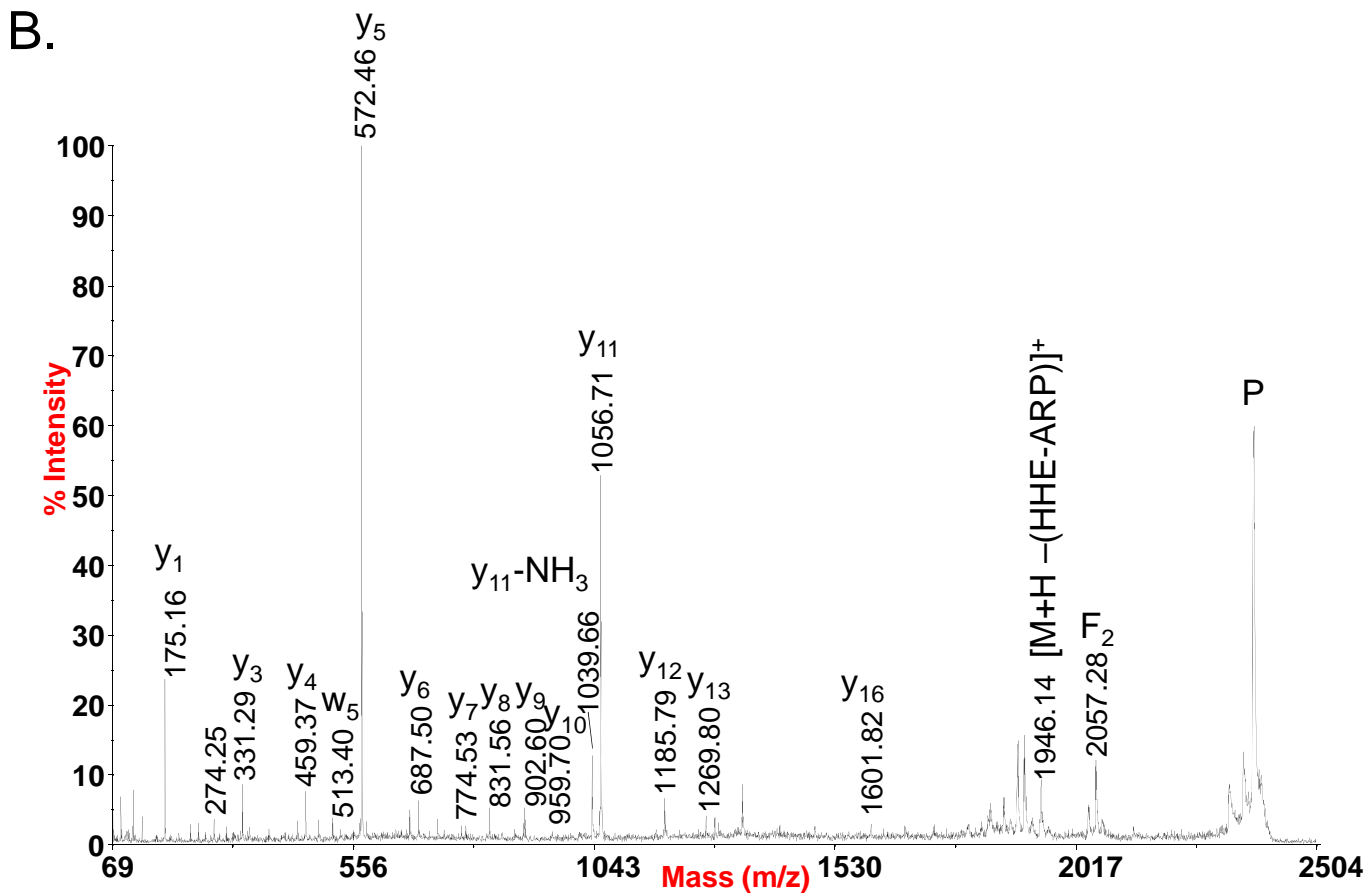
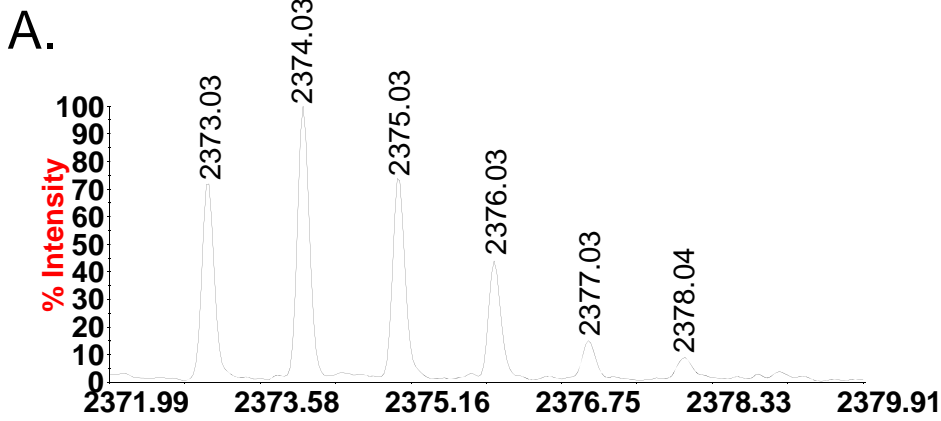
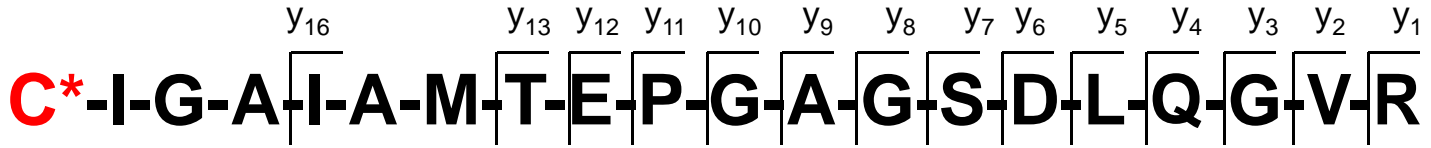


Figure S73. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, HHE modified peptide C*IGAIAMTEPGAGSDLQGV-R; monoisotopic m/z_{calc} 2373.14; accuracy $\Delta(m/z) = -0.11$ Da

ACADL_RAT: Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor

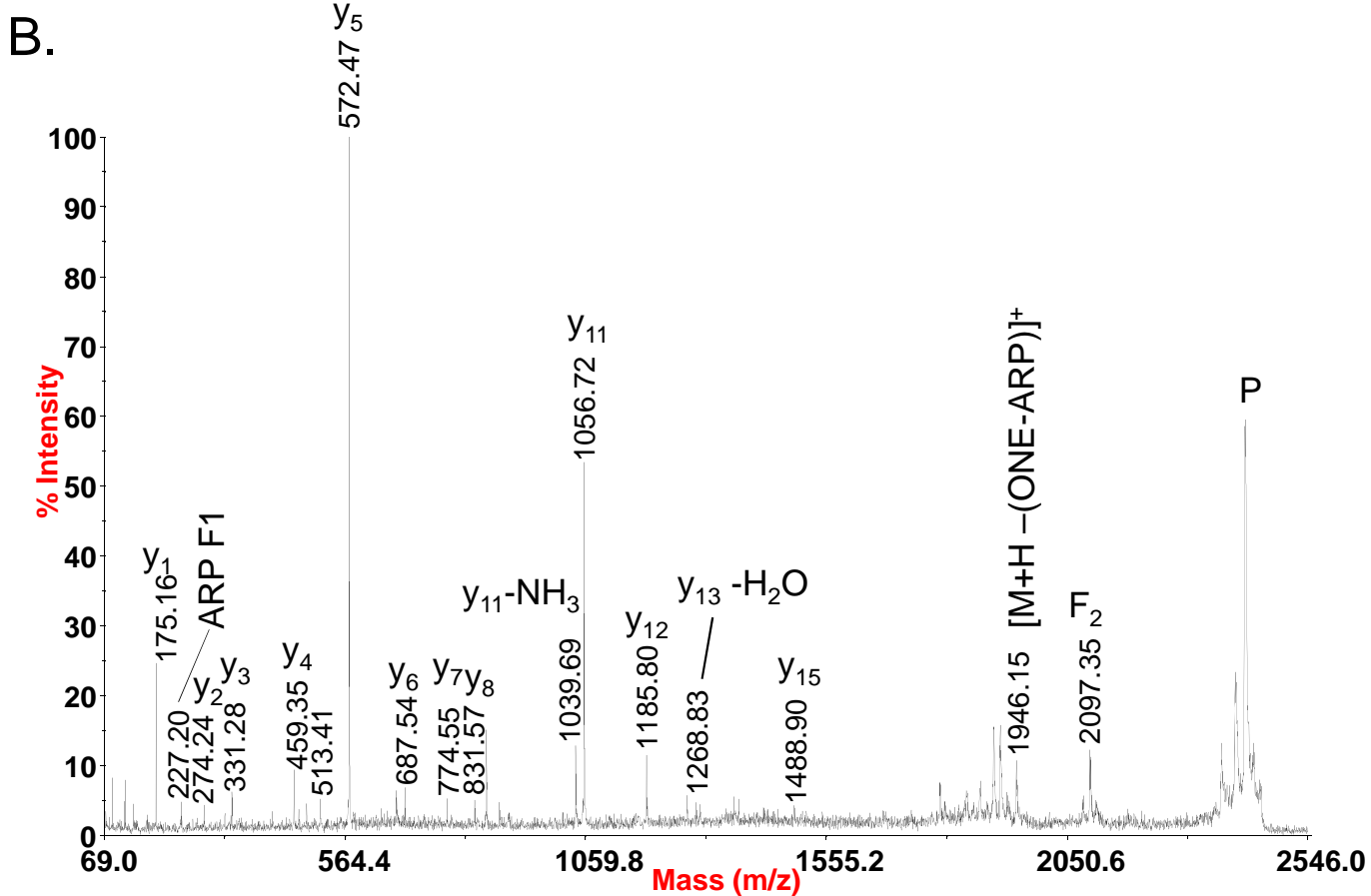
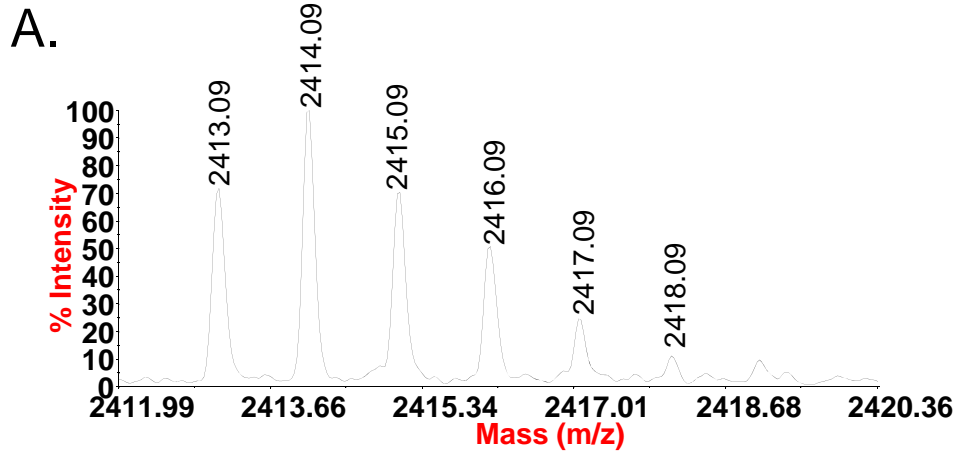
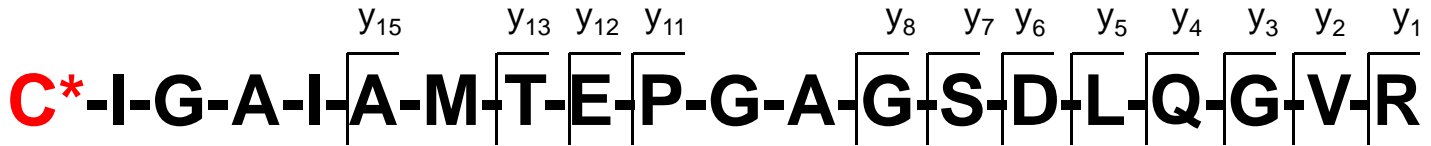


Figure S74. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, ONE modified peptide C*IGAIAMTEPGAGSDLQGV R; monoisotopic m/z_{calc} 2413.17; accuracy $\Delta(m/z) = -0.08$ Da

ACADL_RAT: Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor

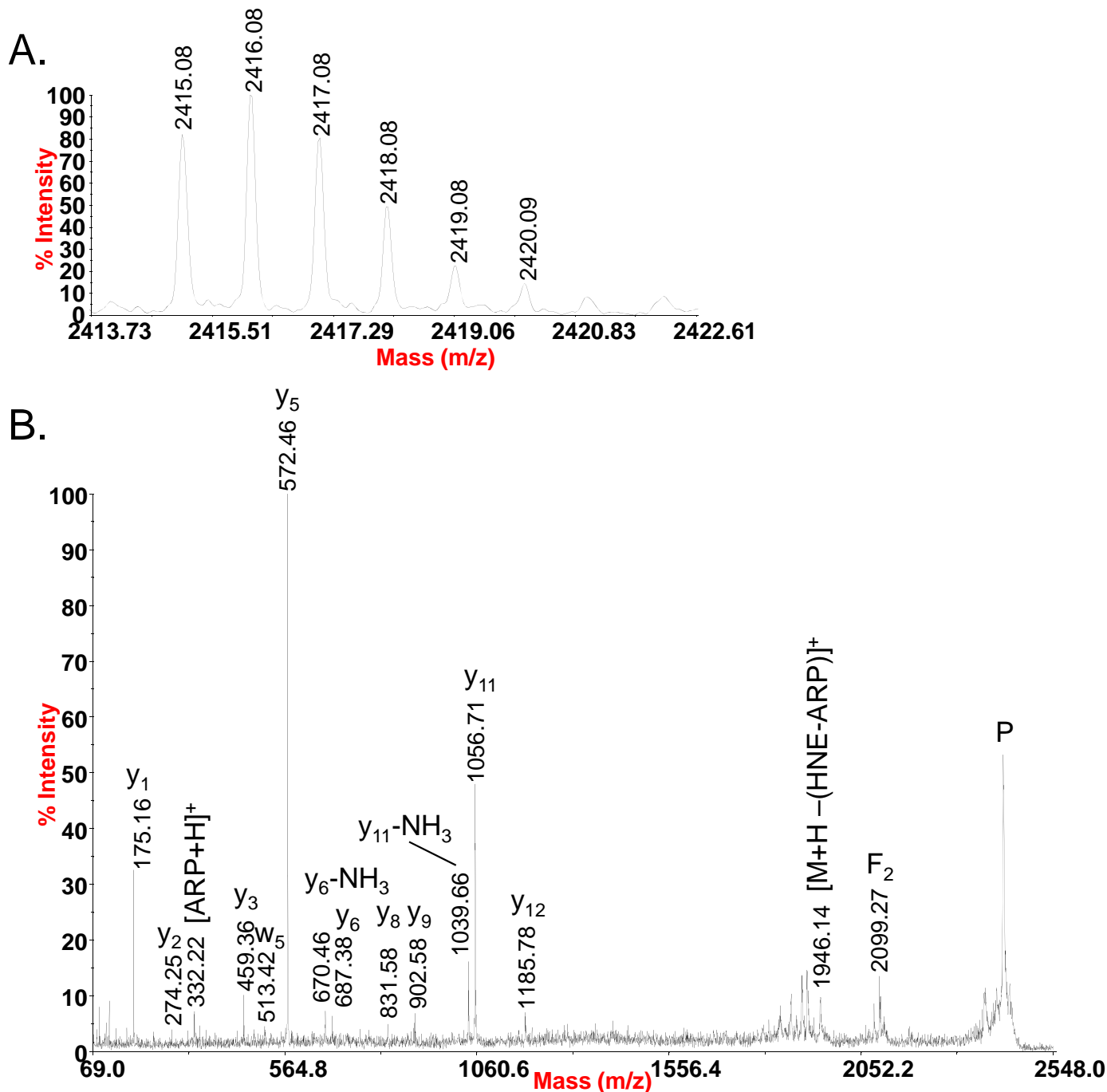
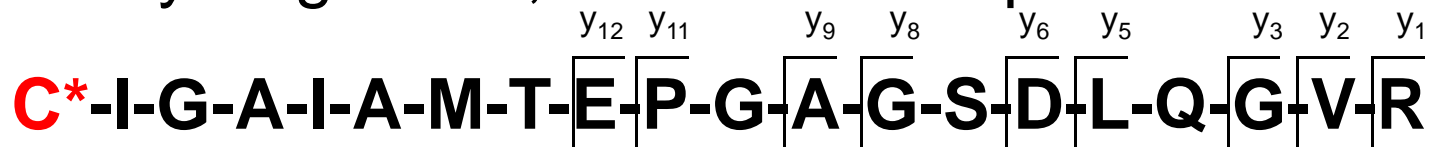


Figure S75. (A) Full mass spectrum and (B) MS/MS spectrum acquired by MALDI-TOF/TOF of the $[M+H]^+$ ion of the ARP labeled, HNE modified peptide C*IGAIAMTEPGAGSDLQGV R; monoisotopic m/z_{calc} 2415.18; accuracy $\Delta(m/z) = -0.10$ Da

KCRB_RAT: Creatine kinase B-type

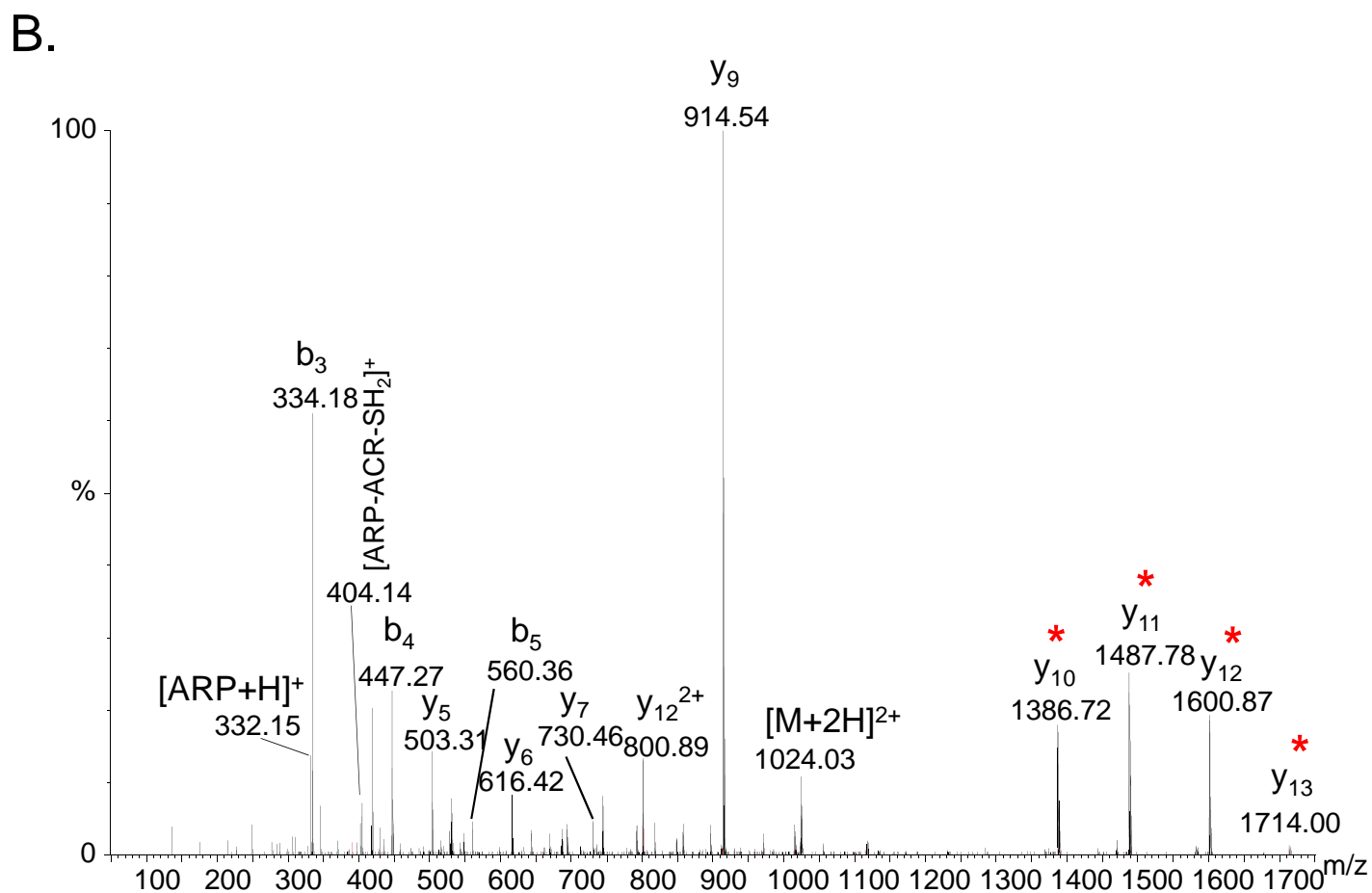
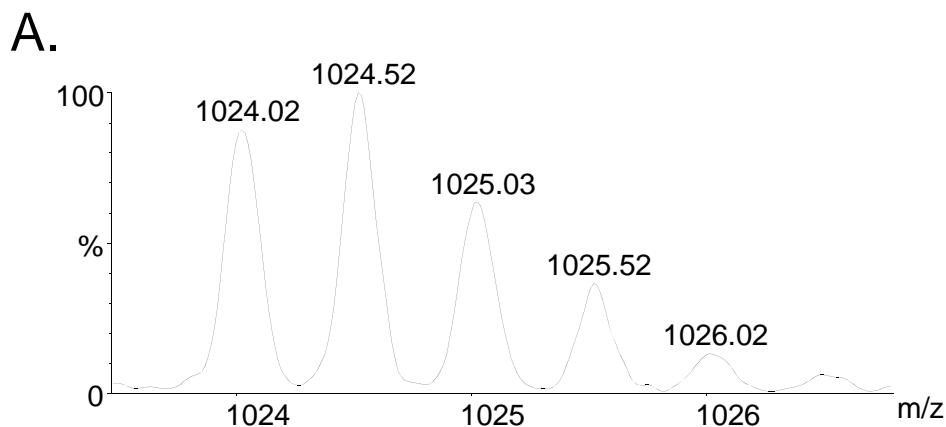
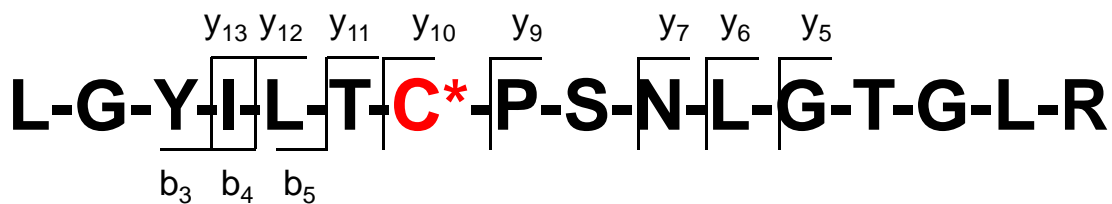
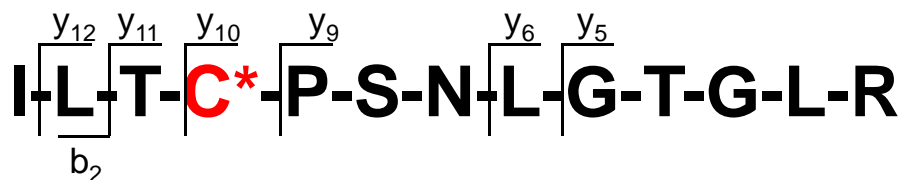
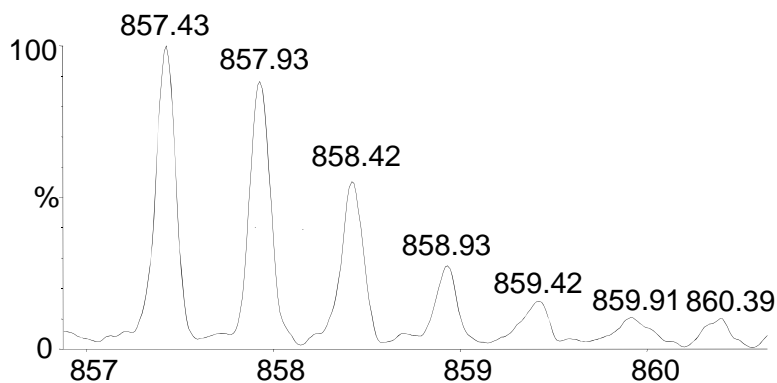


Figure S76. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the [M+2H]²⁺ ion of the ARP labeled, acrolein modified peptide LGYILTC*PSNLGTGLR; monoisotopic m/z_{calc} 1024.03; accuracy $\Delta(m/z) = -0.01$ Da

KCRB_RAT: Creatine kinase B-type



A.



B.

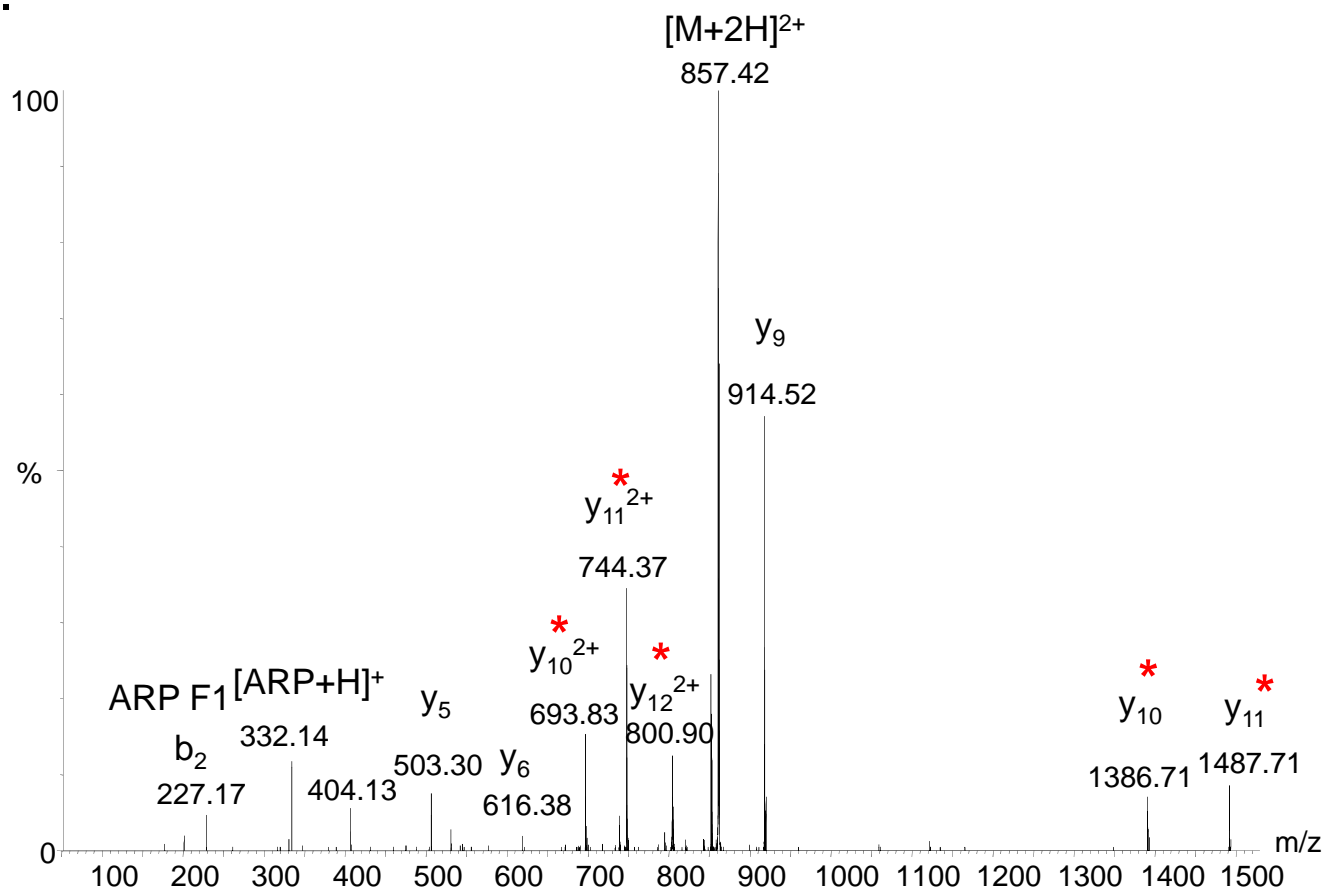
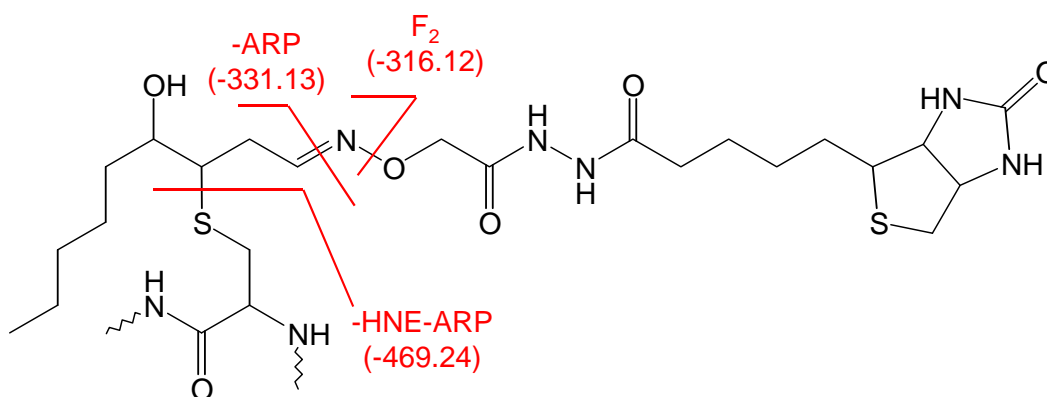


Figure S77. (A) Full mass spectrum and (B) MS/MS spectrum acquired by ESI-Q-TOF of the $[M+2H]^{2+}$ ion of the ARP labeled, acrolein modified peptide ILTC*PSNLGTGLR; monoisotopic m/z_{calc} 857.44; accuracy $\Delta(m/z) = -0.01$ Da

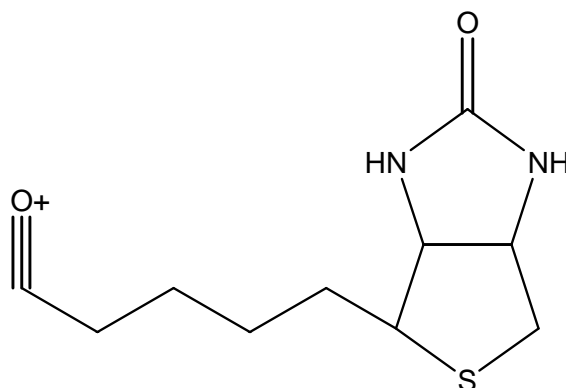
Observed ARP related neutral losses

ARP-HNE modified Cys



Observed ARP related fragment ions

ARP F1 (227.09 Da)



[ARP+H]⁺ (332.14 Da)

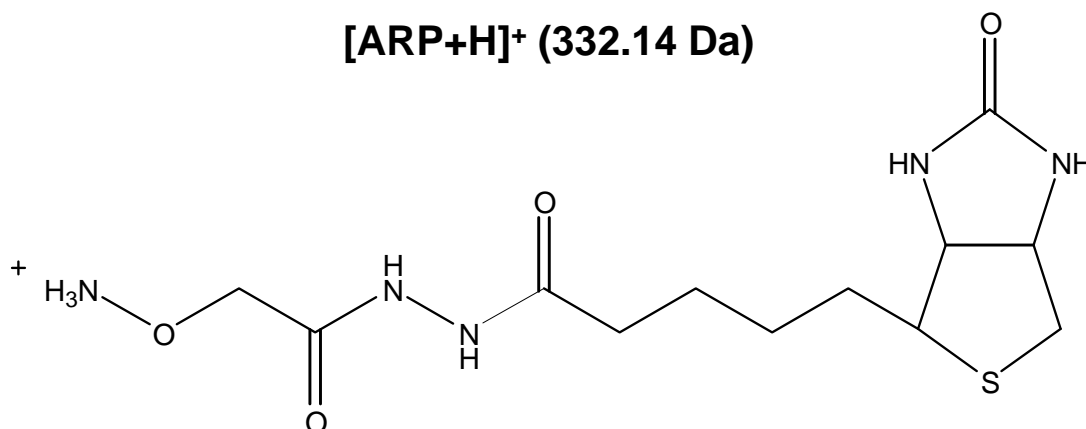


Figure S78. (A) Structure of ARP-HNE modified Cys, indicating the various neutral losses observed in CID MS/MS experiments. (B) Fragment ions generated by the ARP tag in CID MS/MS experiments

