

Mass Spectrometric Characterization of 2-Amino-1-
methyl-6-phenylimidazo[4,5-*b*]pyridine *N*-Oxidized
Metabolites Bound at Cys³⁴ of Human Serum Albumin

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FIGURE LEGENDS

Figure S-1. Product ion mass spectra of A) HS-PhIP, B) H[³⁴S]-PhIP and C) HS-[²H₅]-PhIP.

Figure S-2. Reconstructed ion chromatograms of C*PF (C-desamino-PhIP), C*P (C-desamino-PhIP) and C-desamino-PhIP produced by pronase E digestion of NO₂-PhIP-modified human SA (left panel) and corresponding product ion mass spectra (right panel).

Figure S-3. Full scan mass spectrum of the acid hydrolysis products of the synthetic LQQC*PF (C-[S=O]-PhIP) sulfinamide. The protonated PhIP is observed at *m/z* 225.2 and the singly charged LQQC(SO₂H)PF is observed at *m/z* 767.4.

Figure S-4. Product ion mass spectrum of C*PF (C-[S=O]-PhIP).

Figure S-5. Comparison of trypsin/chymotrypsin digestion of NO-PhIP-modified human SA using different denaturing agents. The digestion efficiency was assessed through the measurement of the LQQC*PF (C-[S=O]-PhIP) sulfinamide adduct by LC-ESI/MS/MS. The NO-PhIP-modified SA was preincubated with denaturing reagents for 1 h at 37 °C prior to enzymatic digestion. The SA samples in the CH₃CN/NH₄HCO₃ solvent mixtures were digested without dilution, whereas the SA samples in 6 M urea or 50% trifluoroethanol were diluted by 10-fold prior to enzyme digestion. Each bar graph represents the average and standard deviation of 3 experiments.

Figure S-1

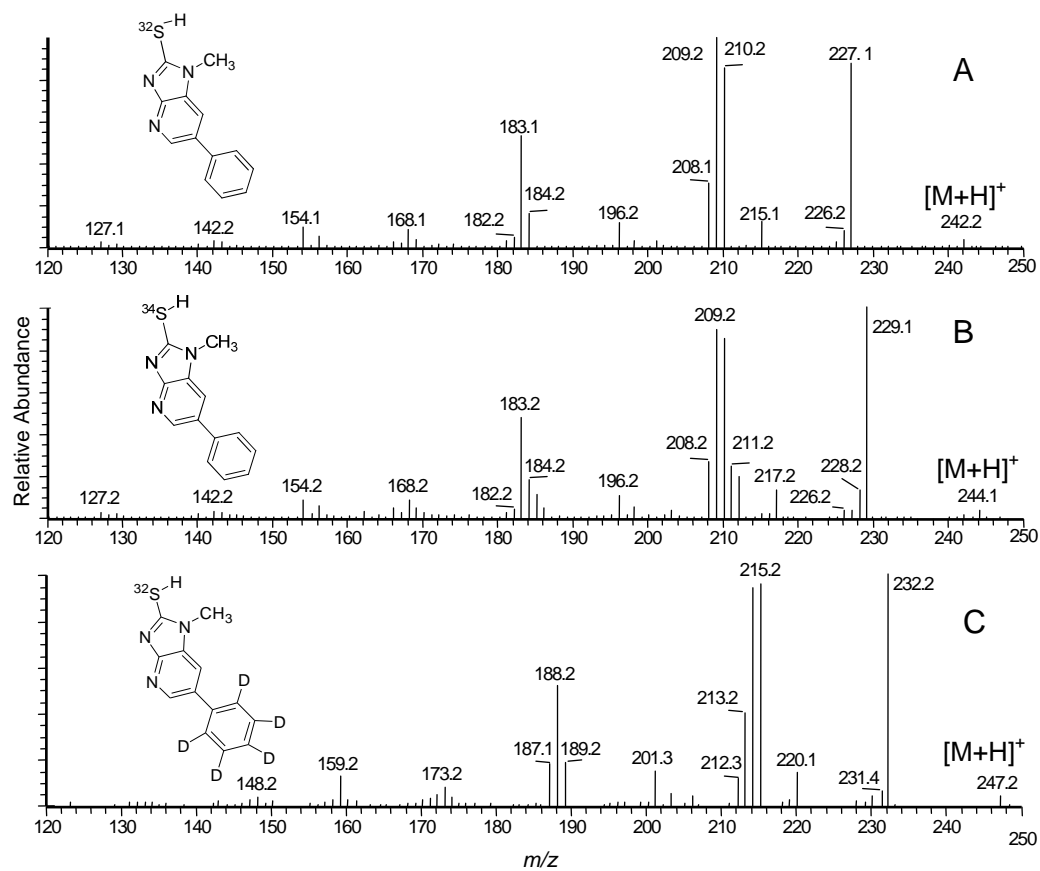


Figure S-2

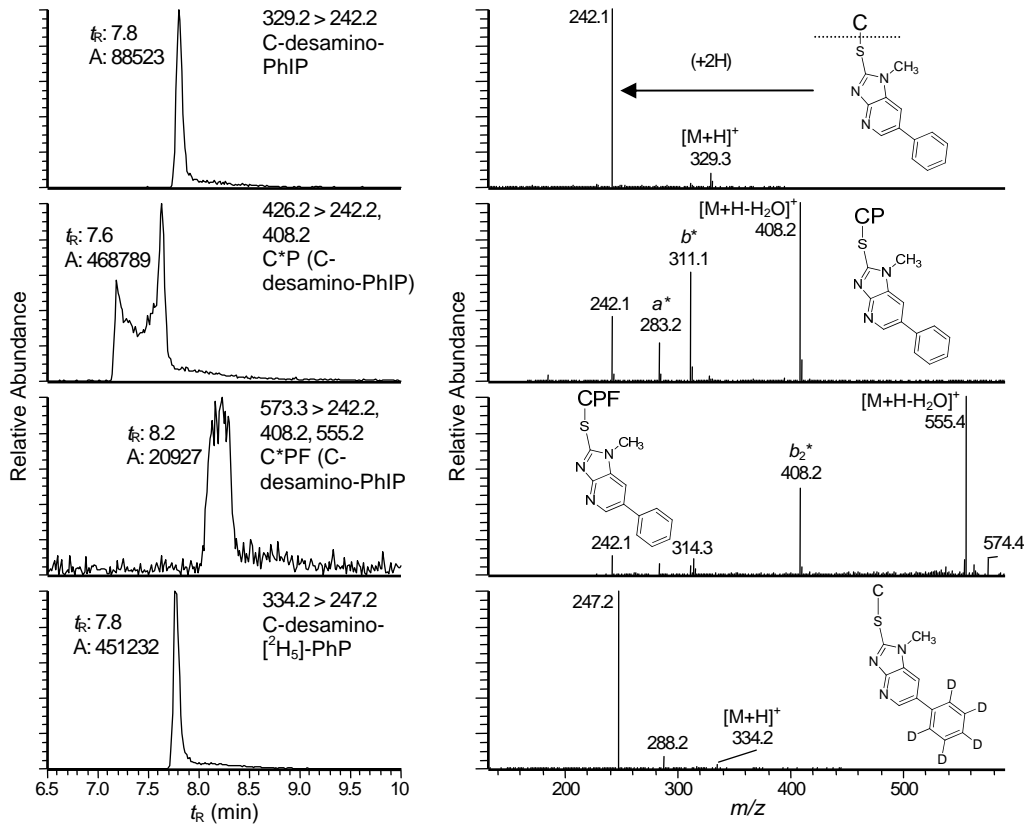


Figure S-3

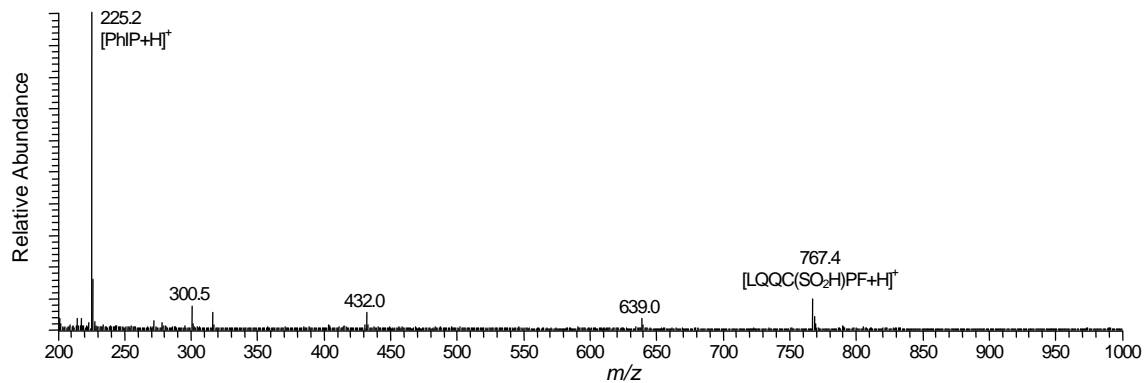


Figure S-4

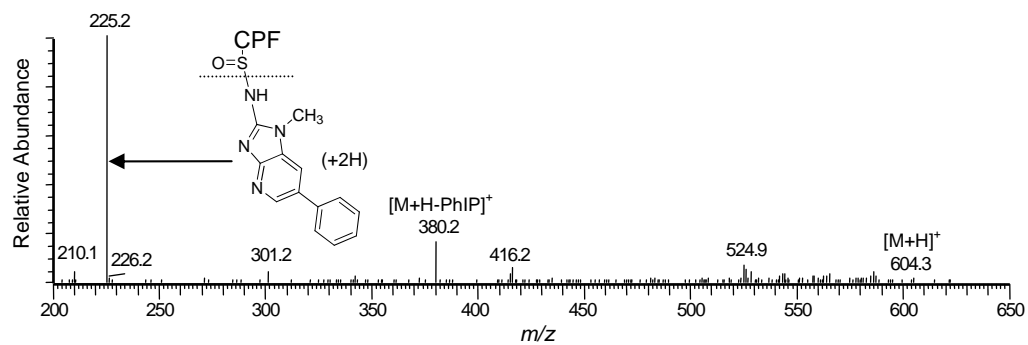


Figure S-5

