

# Supporting Information

## Sensitive and Unequivocal Determination of $pK_a$ Values of Individual Histidine Residues in Proteins Using Mass Spectrometry

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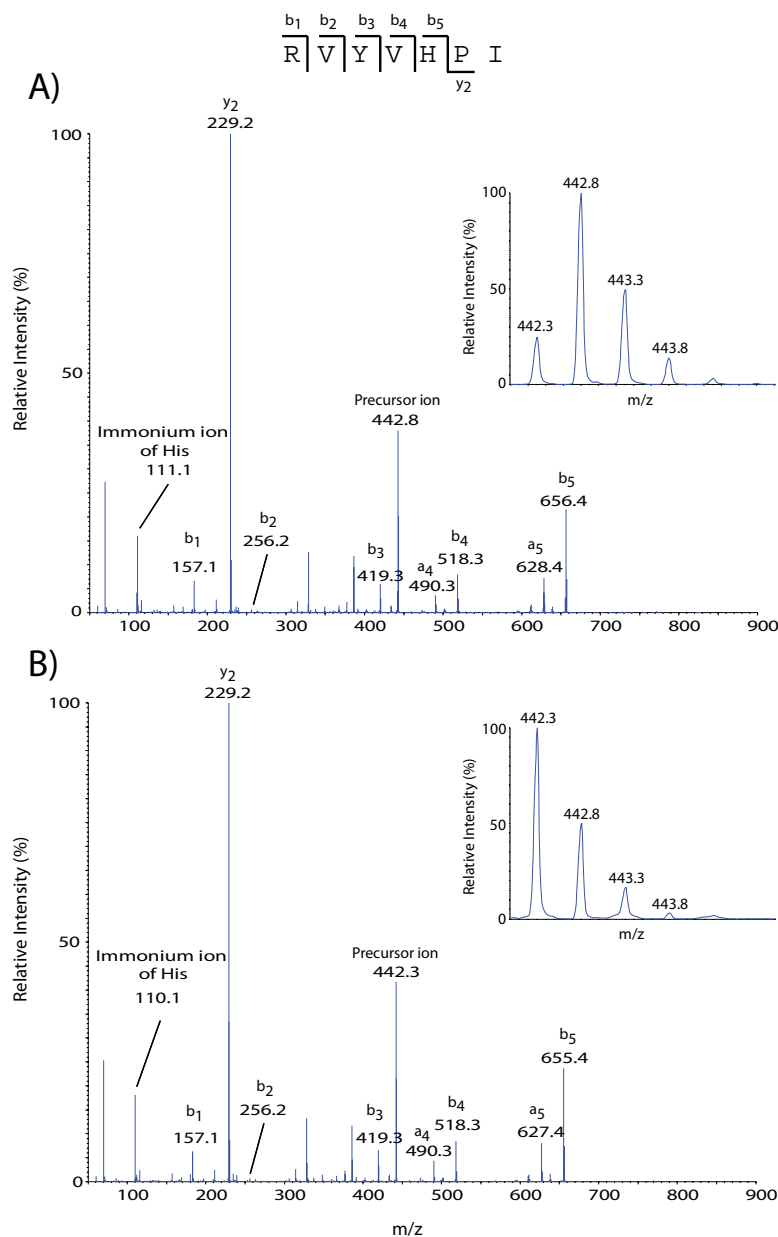
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### Supplemental Figures:

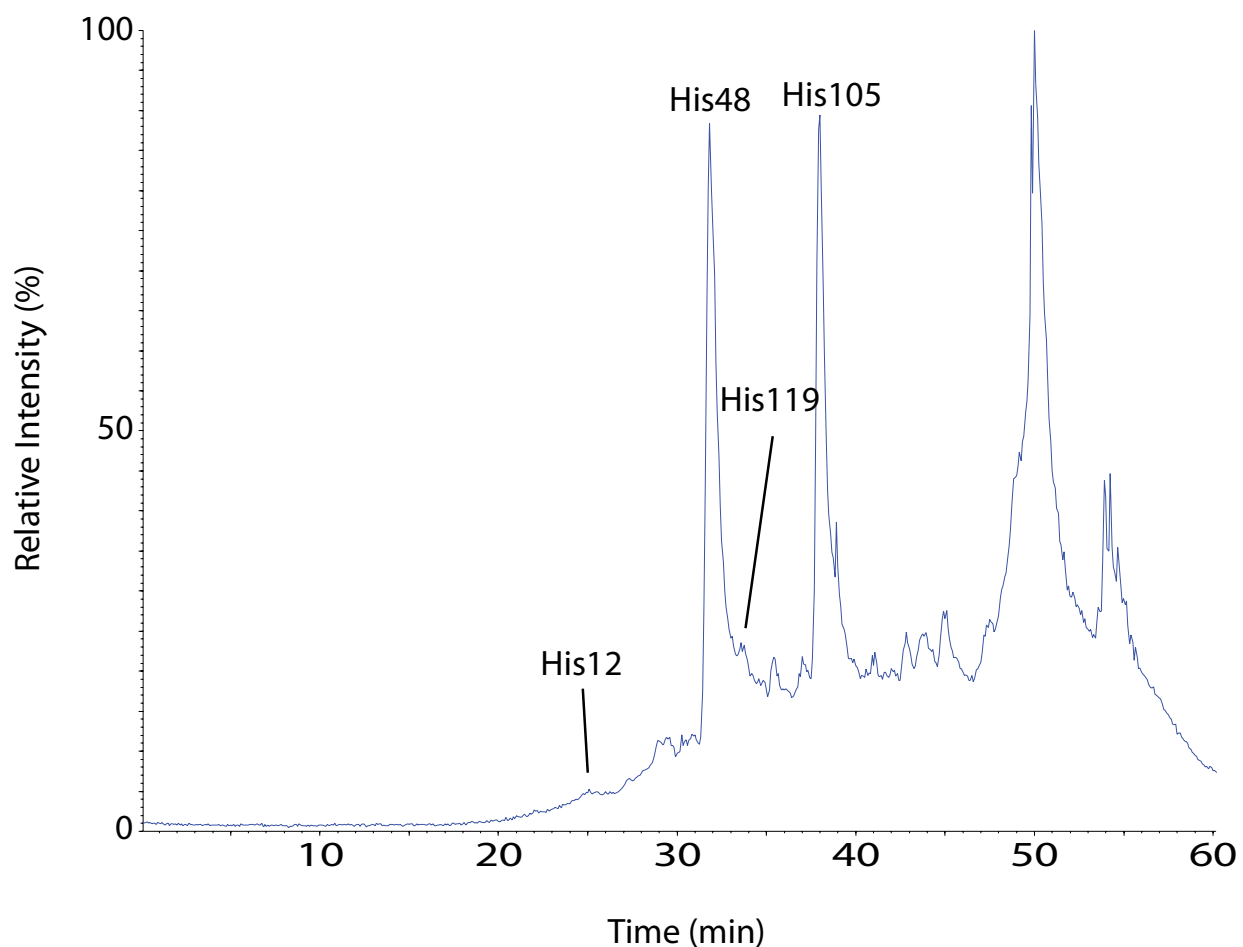
**Figure S-1.** Tandem mass spectrum of deuterated angiotensin III.

**Figure S-2.** LC/MS analysis of deuterated RNase A.

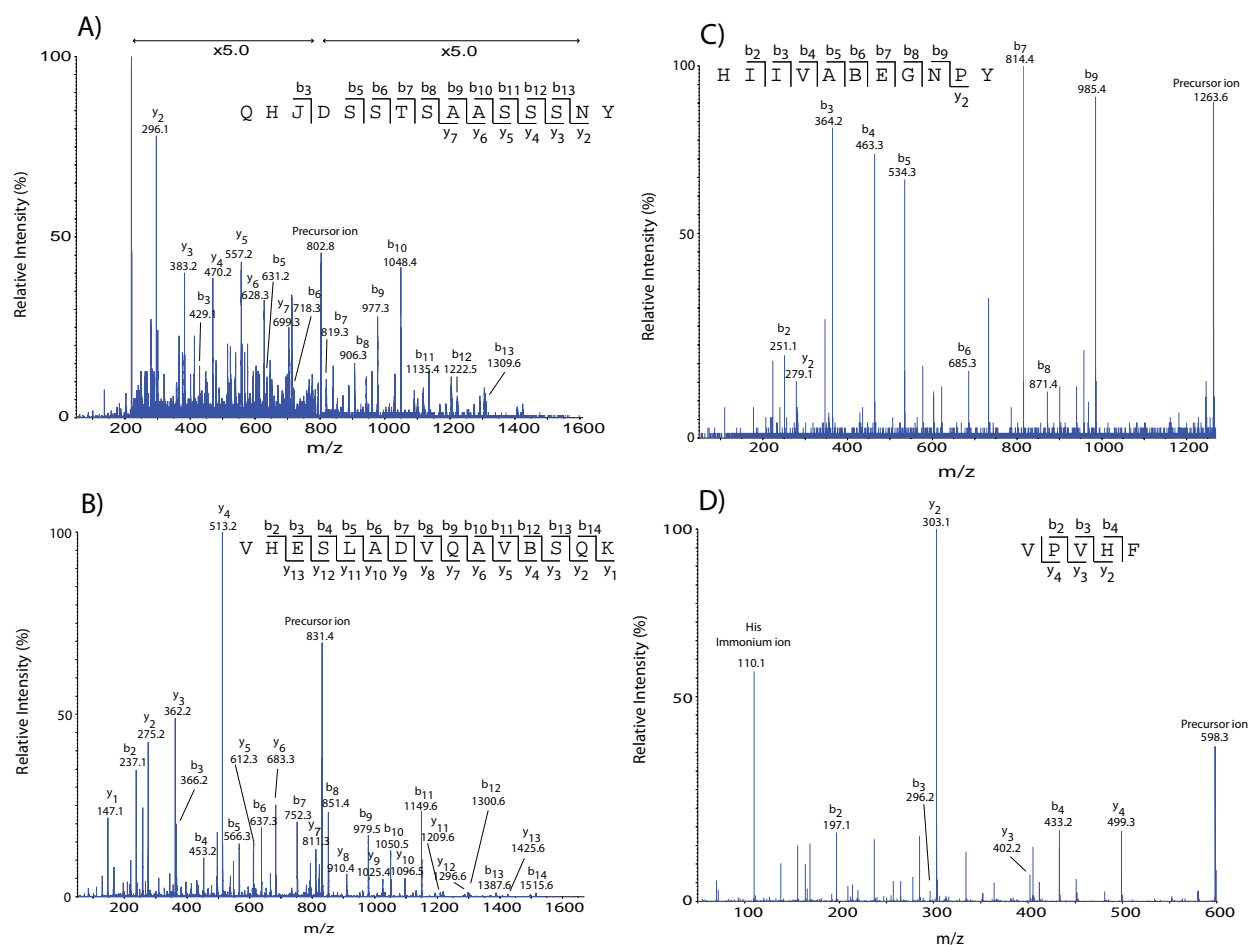
**Figure S-3.** Tandem mass spectra of His12- (A), His48- (B), His105- (C) and His119-peptide (D).



**Figure S-1.** Tandem mass spectrum of deuterated angiotensin III. Angiotensin III was incubated in D<sub>2</sub>O buffered with MES (pH 7.0) at 37 °C for 7 days, and the resulting peptide were analyzed by tandem mass spectrometry. Tandem mass spectra of A) deuterated- (precursor ion: m/z 442.8) and B) nondeuterated (precursor ion: m/z 442.3) angiotensin III are shown with their precursor ion spectra (inserted spectra). Deuterated angiotensin III gave 1 Da higher m/z values for the product ions that contain the histidine residue (a<sub>5</sub>, b<sub>5</sub> and immonium ion of histidine residue) than those ions produced from nondeuterated angiotensin III, while the same m/z values for the product ions that do not contain the histidine residue (b<sub>1</sub>, b<sub>2</sub>, b<sub>3</sub>, a<sub>4</sub>, b<sub>4</sub> and y<sub>2</sub>) were given from deuterated and nondeuterated angiotensin III. The result strongly suggest that the histidine residue in angiotensin III is the site of deuterium incorporation.



**Figure S-2.** LC/MS analysis of deuterated RNase A. A typical total ion current chromatogram is shown. the peptide mixture (5 mL, ca. 12.5 pmol) was injected directly into a reverse-phase analytical column (75 mm x 15 cm, Dionex, Sunnyvale, CA) washed with 2% acetonitrile/0.1% formic acid (v/v) in water for 15 min at a flow rate of 350 nL/min. The peptides were then eluted with a 40 min linear gradient of 2% acetonitrile/0.1% formic acid (v/v) in water to 22% acetonitrile/0.1% formic acid (v/v) in water at a flow rate of 350 nL/min. The column effluent was directed on-line to the nano-electrospray ion source. The total ion current was obtained in the mass range of  $m/z$  400-2000 in the positive ion mode with the acquisition time of 5 s for each scan.



**Figure S-3.** Tandem mass spectra of His12- (A), His48- (B), His105- (C) and His119-peptide (D). J and B in the amino acid sequences denote methionine sulfone and cysteic acid, respectively. Precursor ions were  $m/z$  802.8 ( $z = 2$ ), 831.4 ( $z = 2$ ), 1263.5 ( $z = 1$ ) and 598.3 ( $z = 1$ ) for His12-, His48-, His105- and His119-peptide, respectively. Only b and y series product ions are labeled.