

## Supplementary Material

### Analysis of Overlapped and Noisy Hydrogen/Deuterium Exchange Mass Spectra

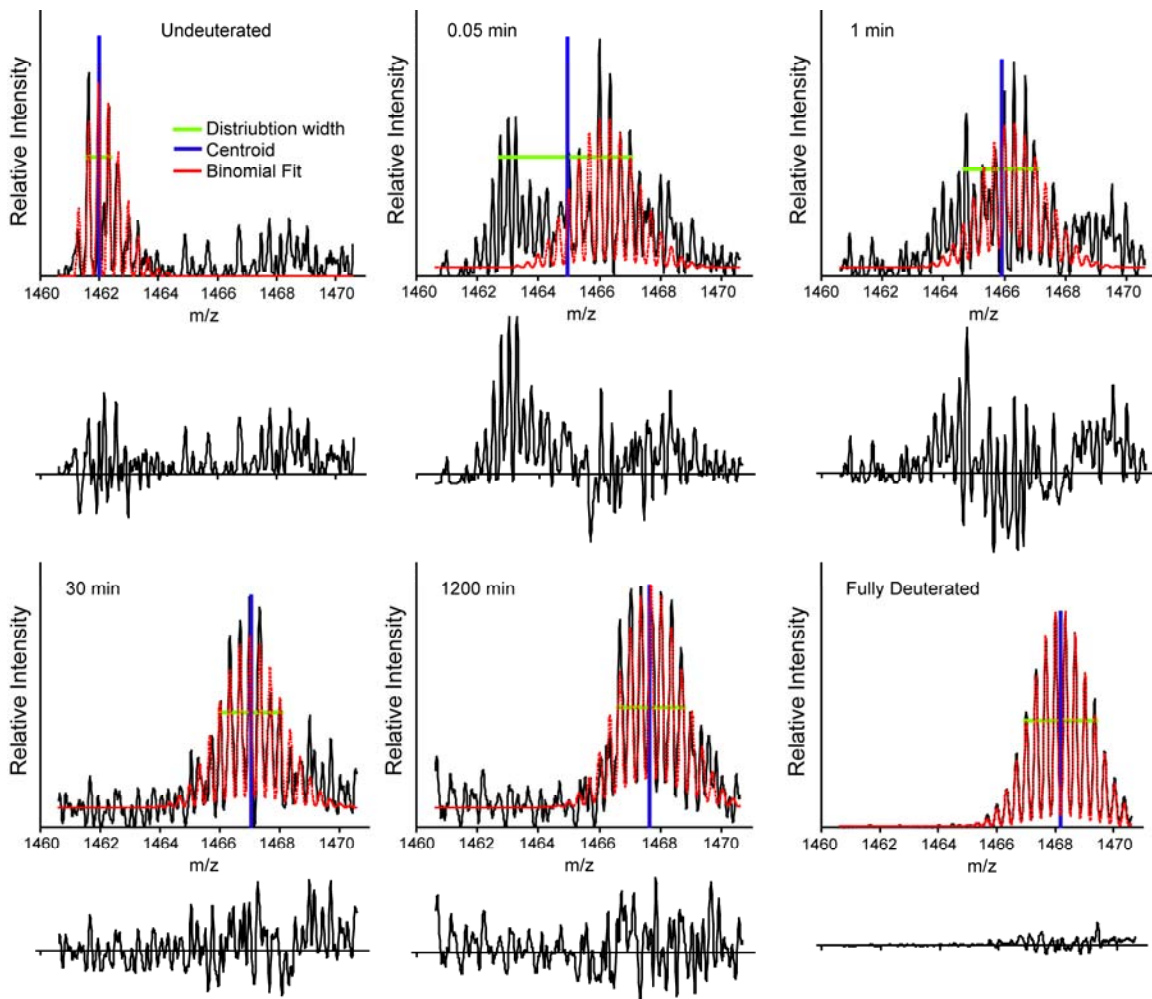
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Supplementary Figure 1: Raw spectral fitting to calculate the deuterium uptake of a glycopeptide with relatively weak signal to noise. The modeled binomial distribution (red) is overlaid with the raw spectral data (black). The 0.05 min and 1 min time points contain some signal at slightly lower m/z from a higher charge state of a different peptide that was not resolved by chromatography. Residuals are shown under each time point. Peak centers and widths from centroid analysis are shown with blue and green lines.