

Supporting information for

Efficient Separations of Intact Proteins Using Slip-Flow with Nano- Liquid Chromatography - Mass Spectrometry

Zhen Wu, Bingchuan Wei, Ximo Zhang, Mary J. Wirth*

Department of Chemistry, Purdue University, West Lafayette, IN 47907

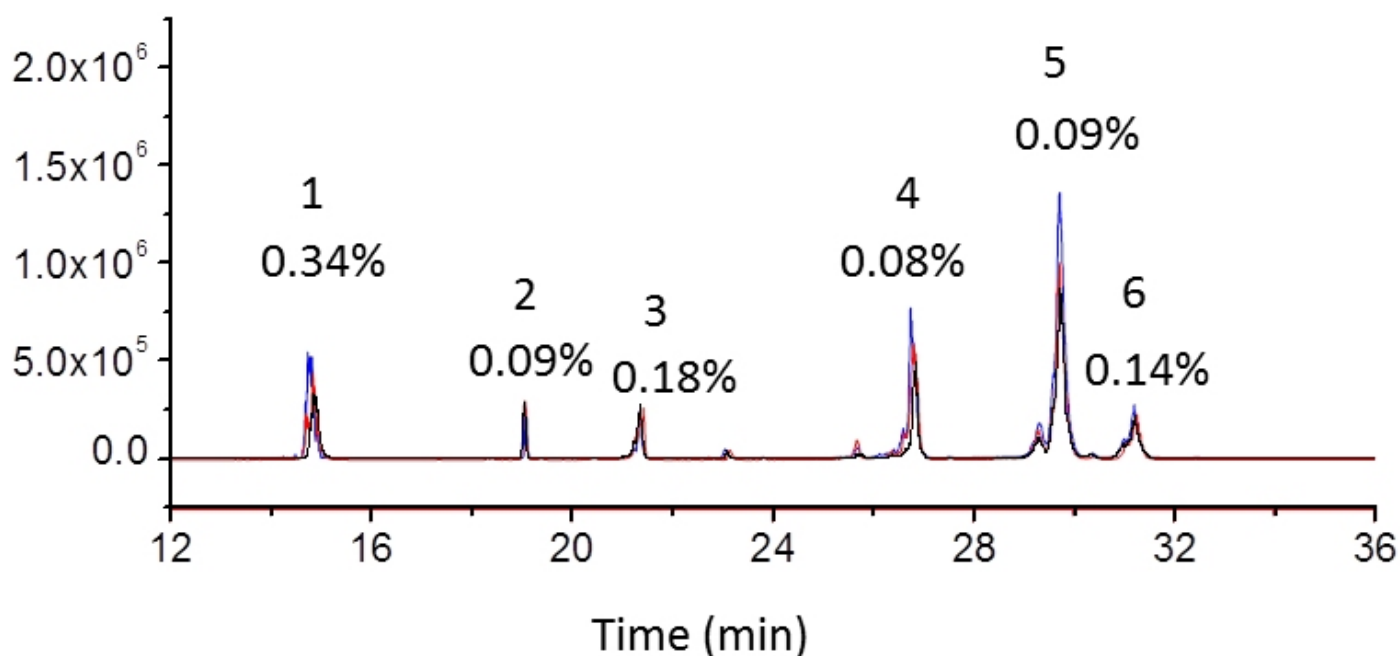


Figure S1. Three replicate chromatograms of the model protein mixture, superimposed in three different colors: black red and blue. The peaks are numbered in the same way as in Figure 2 of the paper. Above each peak is shown the relative standard deviation of its retention time, establishing high reproducibility. A much larger variation in the intensity axis is evident, which is typical of LCMS.

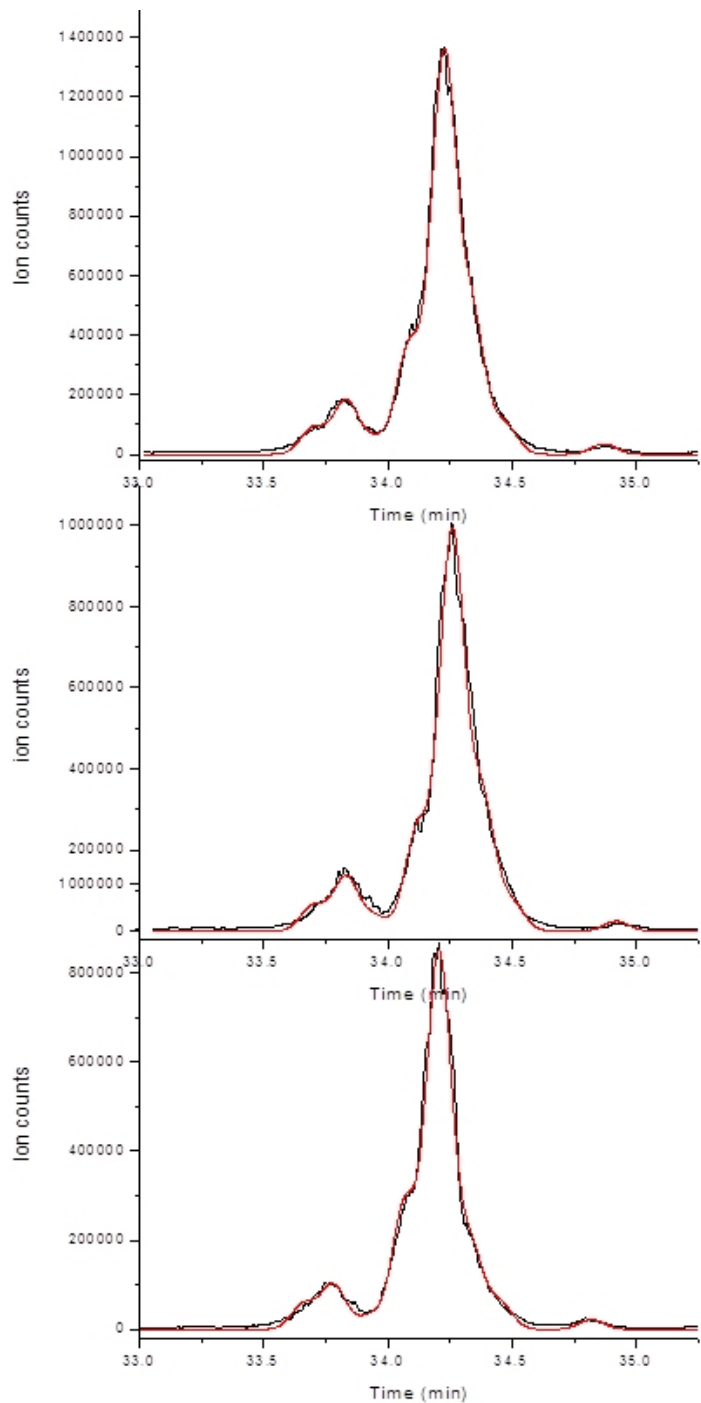


Figure S2. Expanded view of the replicate chromatograms, showing just the peak for carbonic anhydrase. These are plotted individually to show the data (—) and fit to multiple Gaussians (—). The same five Gaussians are fit to the three peaks, showing the fine structure is reproducible.

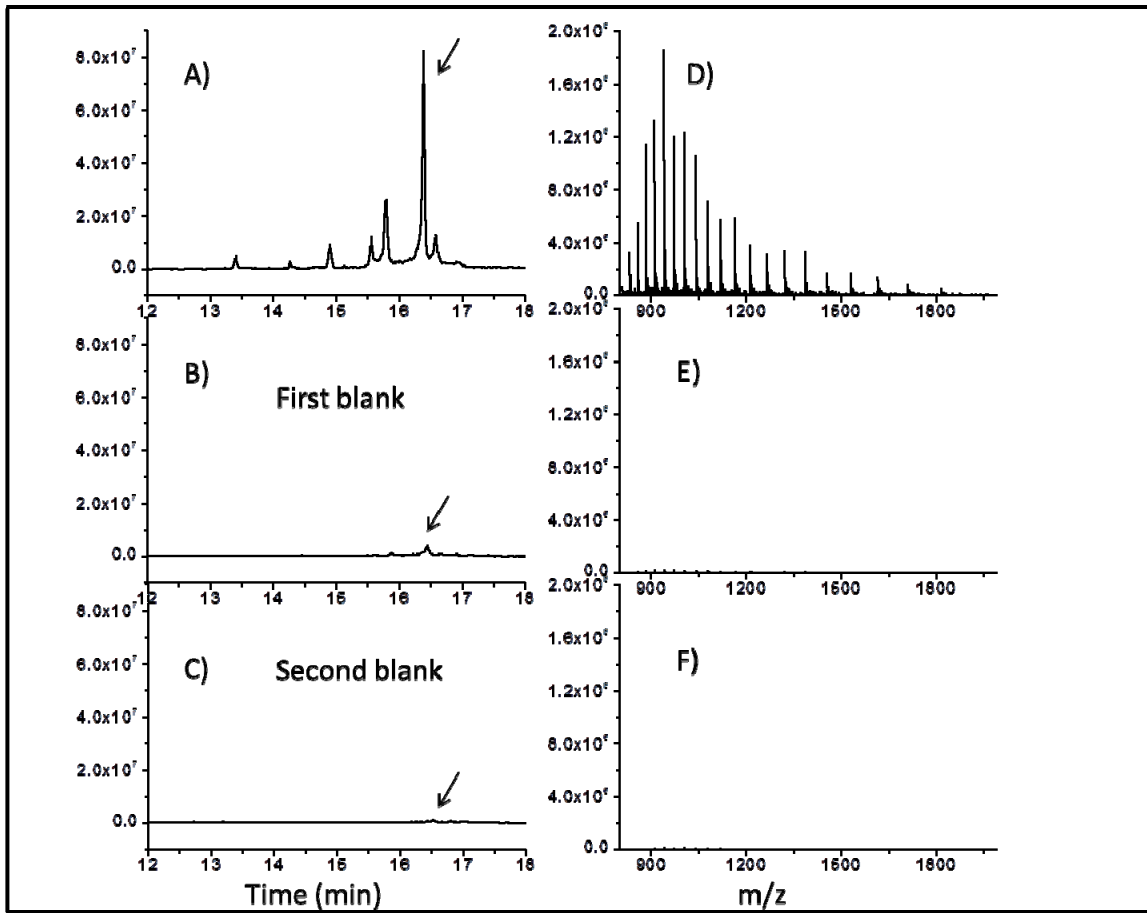


Figure S3: Carry-over study of the C18-bonded capillary. A) chromatogram of model protein mixture separation. B) First blank run after model protein separation. C) Second blank run after model protein separation. D-F) Mass spectra of corresponding peaks, indicated by arrows.