## An On-Line, High-Pressure Digestion System for Protein Characterization by Hydrogen Deuterium Exchange

Lisa M. Jones, Hao Zhang, Ilan Vidavsky, and Michael L. Gross

Department of Chemistry, Washington University, St. Louis, MO 63130

## Supplementary material

## **EXPERIMENTAL SECTION**

**Digestion Apparatus**. The apparatus was plumbed with silica tubing (O.D. 360  $\mu$ m, I.D. 150  $\mu$ m), and a 20  $\mu$ L sample loop was used for protein injection. For digestion, a constant flow of solvent A (99.9% H<sub>2</sub>O, 0.1% formic acid) was kept through the system. An 8 min gradient from 0-100% solvent B (99.9% acetonitrile, 0.1% formic acid) with a flow rate of 40  $\mu$ L/min was run prior to MS analysis.

**Back Exchange Correction**. To account for back exchange during analysis, the deuterium content was calculated from:

$$D_{\text{H} \to \text{D}} = \frac{m - m_{0\%}}{m_{100\%} - m_{0\%}} \times N$$

where, m,  $m_{0\%}$ , and  $m_{100\%}$  are the centroids for each peptide peak after a specified HDX period, zero-time control, and the 100% control. The 100% exchange control was the result for 48 hr exchange. The average back exchange for both the high and low pressure digestion was ~20%.