**OVERVIEW**

**Motivation:**
There is considerable interest in the effects of macromolecular crowding on intracellular protein structure and function.

**Approach:**
HD exchange mass spectrometry is a valuable tool for probing protein structure and dynamics in crowded samples.

**Challenge:**
Crowding agents significantly interfere with LC-MS analysis of proteins of interest.

**Solution:**
We have developed a dual online extraction method using strong cation exchange and reverse phase to remove interference from crowding agents.

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**METHODS**

**H/D EXCHANGE**

- Three valves
- Temperature controlled
- Customizable experiments
- Fully automated

**LEAP HDX PAL**

- SCX Wash Restores Peptide Signals
- Myoglobin Peptides

**CUSTOMIZED CLEAN-UP METHOD**

- Ficoll exchange will be probed using IR spectroscopy.
- Slightly higher levels of back-exchange due to washup (max. 60% deuteration).
- Ficoll exchange will be probed using IR spectroscopy.

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**REFERENCES**