

*Exploring the metrology of hydrogen exchange-mass spectrometry (David Weis)*

Hydrogen exchange-mass spectrometry (HX-MS) is widely-used analytical tool to probe the structure and dynamics of proteins with applications in the pharmaceutical industry and fundamental studies of protein biophysics. Improving the precision of the technology requires a fundamental understanding of the major sources of experimental variation. The goal of this project is to understand how mass spectrometry contributes to the measurement error. The isotopically labeled proteins will be used to construct a series of model systems of known and constant isotopic enrichment that can be used to define the mass measurement capabilities of the mass spectrometer. In this project, the student will learn to express and purify isotopically labeled recombinant proteins and how to characterize these proteins using liquid chromatography and mass spectrometry.