Scope of Session: Hydrogen/deuterium exchange mass spectrometry (HDX-MS) is an increasingly popular protein characterization method. This session covers both the application and new method development of HDX-MS. The application of HDX-MS includes higher order structure analysis, protein-ligand interaction, and protein-protein interaction, particularly epitope mapping. Method development includes opportunities for higher resolution analysis using ETD fragmentation, data generation automation, and data extracting software.

Keywords: Hydrogen/deuterium exchange, Higher order structure, Protein-ligand interaction, Protein-protein interaction, Epitope mapping, ETD fragmentation, Automation, Software