Workshop 2   Monday, 17th September, 17:15-19:15 (Room D)

Hydrogen/Deuterium Exchange Mass Spectrometry
Organizers: Yoshitomo Hamuro (ExSAR, USA), Rachel A. Garlish (UCB, UK)

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

HDX-MS Workshop

Monday, September 17, 2012

5:15 – 5:20 **Introduction**
Rachel Garlish (UCB)

5:20 – 5:40 **HDX-MS: Overview and Application to Drug Discovery and Development**
Yoshitomo Hamuro (ExSAR Corporation)

5:40 – 6:00 **Dynamics of Protein-Ligand Interactions by HDX-MS:**
Applications for Fragment-Based Drug Discovery and Biological Therapeutics
Ganesh Anand (National University of Singapore)

6:00 – 6:20 **Coupling ETD to Bottom-up HDX-MS: Practical Considerations**
Kasper Rand (University of South Denmark)

6:20 – 6:40 **Automated HDX Methods for Screening Protein Ligand Interactions**
Mike Chalmers (Scripps Florida)

6:40 – 7:00 **Automated Analysis of HDX-MS Data: Increasing Trust in Computed Results**
Jeff Morrow (Sierra Analytics)

7:00 – 7:15 **Panel Discussion**
All speakers