Structural biologists face several challenges when trying to solve the structure of large and dynamic complexes. However, the combination of different techniques such as Mass Spectrometry and Cryo-EM, an approach known as integrative structural biology, is revolutionizing the understanding of protein structure, function, and dynamics.

**Program:**

9.30 am-10.00 am: **Check-in and light breakfast**

10.00 am-10.30 am: **Natalia de Val, Ph.D., Thermo Fisher**

"Introduction to Cryo-EM and its Integration with Mass Spectrometry, Application Results"

10.30 am-10.35 am: **Q&A**

10.35 am-11.05 am: **Rosa Viner, Ph.D., Thermo Fisher**

"Introduction to Mass Spectrometry and its Integration with Cryo-EM, Application Results"

11.05 am-11.10 am: **Q&A**

11.10 am-11.40 am: **Albert Konijnenberg, Ph.D., Thermo Fisher**

"Direct Single Molecule Imaging on a Modified QExactive UHMR with Electron Holography Capability"

11.40 am-11.45 am: **Q&A**

1.45 pm-2.45 pm: **Coffee Break**

2.45 pm-3.15 pm: **Kyle Anderson, Ph.D., NIST-IBBR**

"Advancing HDX-MS for Adoption in QC Programs and Better Comparability of Biosimilars"

3.15 pm-3.45 pm: **Matthew Metcalf, Ph.D., UM College Park-IBBR**

"Structural Characterization of an Engineered Soluble Form of the HCV E1E2 Heterodimer"

3.45 pm-4 pm: **Closing remarks** by IBBR leadership

4 pm-6 pm: **Reception** (provided by Thermo)