

**Programme: Wednesday 15 December 2021, 15.45 – 18.15**

(15:45-18:15 BST, 10:45-13:15 EST, 07:45-10:15 PST)

<b>Welcome</b>	
15:45-15:55	Participants join
15:55-16:00	Welcome from the Chairs, <b>Julia Chamot-Rooke</b> , Institut Pasteur, Paris, France, <b>Albert Heck</b> , Utrecht University, Utrecht, The Netherlands

<b>Session 1</b>	<b>Chair: Julia Chamot-Rooke</b>
16:00-16:15	New Strategies in Top-down Proteomics for Precision Medicine <b>Ying Ge</b> , UW-Madison, USA
16:15-16:30	Bioinformatics challenges related to proteoform-centric data: the need for a standard notation and a common identifier system <b>Juan Antonio Vizcaino</b> , EMBL EBI, Hinxton, UK
16:30-16:45	Challenges in MS-based de novo sequencing of polyclonal antibodies <b>Sem Tamara</b> , Utrecht University, Utrecht, The Netherlands
16:45-17:00	Q&A with the 3 speakers, moderated by <b>Julia Chamot-Rooke</b>
17:00-17:15	Coffee break

<b>Session 2</b>	<b>Chair: Albert Heck</b>
17:15-17:30	Deciphering the tubulin code with top-down proteomics <b>Megan Gant</b> , Institut Pasteur, Paris, France
17:30-17:45	The expanding role of top-down mass spectrometry in the structural analysis of monoclonal antibodies <b>Yury Tsybin</b> , Spectroswiss, Lausanne, Switzerland
17:45-18:00	Criteria for selecting a top-down identification algorithm <b>David Tabb</b> , Institut Pasteur, Paris, France
18:00-18:15	Q&A with the 3 speakers, moderated by <b>Albert Heck</b>