



New and Advanced Proteomics Technologies



Monday 26 September:

19.00 Meet and Greet and Registration – Drinks and snacks provided at the VSpa conference centre lobby

Tuesday 27 September (45 min presentations + 15 min Q&A)

Time	Title	Speaker
08.00 – 08.20	Registration	
08.20 – 08.30	Introduction to the EPIC-XS workshop	Sergo Kasvandik & Kathryn Lilley
08.30 – 09.30	Native proteomics	Albert Heck , Utrecht University, The Netherlands
09.30 – 10.30	Cross-linking MS for structural analysis of protein and protein-RNA complexes	Alexander Leitner , ETH Zurich, Switzerland
10.30 – 11.00	Coffee break	
11.00 – 12.00	MS-based profiling of histone post-translational modifications in clinical samples	Tiziana Bonaldi , European Institute of Oncology, Italy
12.00 – 13.00	Lunch break (conference centre lobby)	
13.00 – 14.00	Utilizing the power of ZenoTOF 7600 system for proteomics and in biopharma characterization	Stephen Lock , Senior Marketing & Market Development Manager, Sciex, Leeds, UK
14.00 – 15.00	Enhancing data processing using AI	Bernard Delanghe , Thermo Fisher Scientific
15.00 – 15.30	Coffee break	
15.30 – 16.10	On standardizing high-throughput separation (30 min presentation +10 min Q&A)	Ole Vorm , Founder & Director, Evosep, Denmark
17.00 – 19.00	Guided tour at the Estonian National Museum	
17.00	Bus to the museum	
18.45	Bus to the restaurant	
19.00...	Dinner at Vilde & Vine restaurant	

Wednesday 28 September (45 min presentations + 15 min Q&A)

Time	Title	Speaker
9.00 – 10.00	Phosphoproteomics to analyze cell signaling networks	Jesper V. Olsen , University of Copenhagen
10.00 – 11.00	How to create a spatial map of the cell	Kathryn Lilley , UCAM, UK
11.00 – 11.15	Coffee break	
11.15 – 12.15	Adding a proteomic component to personalized oncology (+15 min Q&A)	Bernhard Küster , Technical University of Munich, Germany
12.15 – 13.15	N-terminal proteoforms in human disease (+15 min Q&A)	Kris Gevaert , VIB–UGent Center for Medical Biotechnology, Belgium
13.15 – 14.15	Lunch break (conference centre lobby)	
14.15 – 15.15	How proteomics public data is reused more and more in the community (+15 min Q&A)	Juan Antonio Vizcaíno , EMBL–EBI, UK
15.15 – 16.15	Top-down and intact analyses of proteins (+15 min Q&A)	Julia Chamot–Rooke , Institut Pasteur, Paris, France
16.15 – 16.30	Coffee Break	
16.30 – 17.30	Thermal stability, solubility and the secretome (+15 min Q&A)	Marcus Bantscheff , GlaxoSmithKline UK
17.30 – 17.40	Closing remarks	Sergo Kasvandik