EPIC-XS Annual Meeting 2022

September 28 – 30, 2022, Tartu, Estonia

Programme overview
Location of all talks: Seminar Room Sweden (VSpa)

Wednesday, 28 September

18:00 – 18:30	Registration *Location: Conference Centre lobby (VSpa)*
18:30 – 18:45	Opening comments, **Jesper Olsen**, UCPH, and **Sergo Kasvandik,** UT
18:45 – 19:45	**Keynote Lectures** *Introduction – Jesper Olsen, UCPH* **Nurhan Özlü**, Koç University, Istanbul Phosphorylation Dynamics of Keratin Filaments in Dividing Mammalian Cells **Ruedi Aebersold**, Professor emeritus ETH, Zurich MultiOmics or MultiPROTEOmics?
20:00	Dinner *Location: Conference Centre Lobby*

Thursday, 29 September

08:40 – 09:00	Consortium access activities – **Kris Gevaert**, VIB
09:00 – 11:00	**User Sessions** *(15 min presentations + 5min Q&A)* *Chair: Christina Ludwig*
09:00 – 09:40	**User Session 1**
9:00 – 9:20	*Towards understanding the aggregation behaviour of immunoglobulin light chains* – **Alexander K. Buell,** Technical University of Denmark
9:20 – 9:40	*A proteomic approach to untangle the molecular bases underlying the complex network of plant-microbe interaction* - **Silvia Proietti**, University of Tuscia, Italy
09:40 – 10:00	Coffee break
10:00 – 11.00	**User Session 2** *(15 min presentations + 5min Q&A)*
10:00 – 10:20	*Histone post-translational dynamics in response to metabolic changes* - **Ferdinand von Meyenn**, ETH Zurich, Switzerland

10:20 – 10:40	*p53 as a regulator of metabolic flexibility in cancer and obesity* – **Andreas Prokesch,** Medical University of Graz, Austria
10:40 – 11:00	*Repurposing of a known antipsychotic drug to target arthritogenic synovial fibroblasts and scaffold-based design of novel small molecule therapeutics* – **Filippos Charalampous**, BSRC, Alexander Flemming, Greece

11:00 – 12:00   **Industrial Platform Session** *(15 min presentations + 5min Q&A)*
Chair: Michael L. Nielsen

11:00 – 11:20	CRISPR perturbation screens for the discovery of new targets – **Marcus Bantscheff**, Cellzome, GSK, Germany
11:20 – 11:40	*Advantages of the Unreduced Data in FTMS for Bottom-Up and Top-Down Proteomics* – **Yury Tsybin**, Spectroswiss, Switzerland
11:40 – 12:00	*Simplifying Separation for Clinical Proteomics* – **Ole Vorm,** Evosep, Denmark

12:00 – 13:30	Group photo followed by lunch
Location: Conference Centre Lobby

13:30 – 15:00   **JRA2: Future and Emerging Proteomics Technologies**
Chair: Ole Vorm

Overview of JRA2 – **Julia Chamot-Rooke**, IP
How do we measure success for a top-down proteome experiment – **David Tabb**, IP
The use of linear ion traps in data-independent acquisition methods for low-input proteomics – **Eduard Sabido**, CRG
Systems-wide and site-specific characterization of ADP-ribosylation using quantitative mass spectrometry – **Michael Lund Nielsen**, UCPH

15:00 – 15:30	Coffee break

15:30 – 16:30   **JRA4: Proteome Organization: Structural & Spatial Proteomics**
Chair: Mariette Matondo

Overview JRA4 – **Alexander Leitner,** ETH
Computational workflows for spatial proteomics, **Lisa Breckels,** UCAM
Fast photo-chemical oxidation of proteins for structural characterization of protein complexes, **Dmitry Loginov**, IMIC
Global in situ analysis of osmolyte mechanisms with LiP-MS, **Monika Pepelnjak**, ETH
Uncovering the basement membrane landscape through XLMS, **Katherine Stevens**, UU

17:00 – 18:45   **Social activity – Guided tour of Tartu Old Town**

19:00	Dinner - *Location: Joyce Restaurant VSpa Hotel, 1st floor*

Friday, 30 September

08:15 – 08:35   Consortium Objectives Review & Partner Roles – **Martina O'Flaherty,** UU

08:35 – 10:05   **JRA3: Translational proteomics**

Chair: Richard Scheltema
Overview JRA3 – **Maarten Altelaar (UU)**

Histone PTM and variant analysis from low-abundance clinical samples – **Roberta Noberini**, IEO

Tumour profiling of HER2+ breast cancer biopsies identifies signatures predictive of treatment response - **Maarten Altelaar,** UU

Re-assessment of extracellular vesicle cargo with protein correlation profiling - **Javier Munoz**, CNIO
Proteomics workflow to identify tissue leakage proteins in liquid biopsies, **Esperanza Fernandez,** VIB

10:05 – 10:20   Coffee break

10:20 – 11:50   **JRA1: Bioinformatics to support proteomics**

Chair: Javier Muñoz
Overview JRA1 – **Juan Antonio,** EMBL-EBI
Inferring functional association networks from proteomics data – **Sven Degroeve,** VIB
Prosit and ProteomicsDB in the context of EPIC-XS - **Wassim Gabriel**, TUM
Intelligent data acquisition for top-down proteomics via ultra-fast mass deconvolution – **Kyowon Jeong,** EKUT
Ongoing development of open data analysis pipelines for cloud infrastructures – **Juan Antonio,** EMBL-EBI

11:50 – 12:05   Closing comments **Jesper Olsen,** UCPH, and **Sergo Kasvandik**, UT

Lunch
Location: Conference Centre Lobby
Packed lunches for people taking the shuttle bus

12:45 – 15:00   **Shuttle bus from VSpa to Tallinn airport**