Proteomics in Cell Biology and Disease Mechanisms

30 March – 1 April 2020

Wellcome Genome Campus,
Hinxton, Cambridge, UK

Conference Programme

Monday 30 March 2020

11:30-13:00 Registration

13:00-13:30 Welcome and introductions
Matthias Mann
Max Planck Institute of Biochemistry, Germany

13:30-14:30 Session 1: Computational Approaches
Chair: Angus Lamond, University of Dundee, UK

13:30 Infrastructure for Big Data at the EMBL-EBI
Johanna McEntyre
EMBL-EBI, UK

14:00 PRIDE and ProteomeXchange: Supporting “big data” approaches in proteomics
Juan Antonio Vizcaino
EMBL-EBI, UK

14:30 Next-gen proteomics: how machine learning opens up the epi-proteome
Lennart Martens
VIB – Ghent University, Belgium

15:00-15:30 Afternoon Tea

15:30-17:30 Session 1 continued: Computational Approaches

15:30 Deep learning to assist the identification of neoantigens
Matthias Wilhelm
TU Munich, Germany

16:00 Bayesian Analysis of Label-free Proteomics Data
Lukas Käll
KTH, Sweden
16:30  A Graph-centric framework for translational clinical proteomics
Ana Rita Colaco
NNF Center for Protein Research, Denmark

16:45  AlphaPept, a modern and ultrafast framework for the analysis of
MS-based proteomics
Maximilian Strauss
Max Planck Institute of Biochemistry, Germany

17:00-17:35  Lightning talks
Chair: Angus Lamond, University of Dundee, UK

17:35-18:35  Poster session 1 (odd numbers) with drinks reception

18:40 prompt  Buffet dinner

18:50  Cash bar

Tuesday 31 March 2020

09:00-10:30  Session 2: Structural Proteomics
Chair: Emma Lundberg, Science for Life Laboratory (KTH), Sweden

09:00  The modular proteome and its clinical significance
Ruedi Aebersold
ETH Zurich, Switzerland

09:30  The molecular architecture of human fibrin clots structurally
resolved by cross-linking mass spectrometry
Richard Scheltema
Utrecht University, The Netherlands

10.00  Complex-centric proteome profiling by SEC-SWATH-MS
Isabell Bludau
ETH Zürich, Switzerland

10.15  Probing Conformation-dependent Protein-Protein Interactions in
Complex Proteomes using LiP-MS
Ales Holfeld
ETH Zürich, Switzerland

10:30-11:00  Morning coffee

11:00-12:30  Session 3: Organella
Chair: Juan Antonio Vizcaino, EMBL-EBI, UK

11:00  Spatial organization of the transcriptome and proteome
Kathryn Lilley
University of Cambridge, UK
11:30  Organellar proteomics and phospho-proteomics reveal subcellular reorganization in diet-induced hepatic steatosis and intermittent fasting  
Natalie Krahmer  
Helmholtz Centre, Germany

12:00  Organellar dynamics during early human neuronal differentiation  
Julia Schessner  
Max-Planck-Institute of Biochemistry, Germany

12:15  Identification of a biomarker panel for clear cell Renal Cell Carcinoma by quantitative proteomics analysis  
Aydanur Senturk  
Koc University, Turkey

12:30-14:00  Lunch

14:00-15:30  Session 4: Spatial Proteomics  
Chair: Matthias Mann, Max Planck Institute of Biochemistry, Germany

14:00  Subcellular partitioning of proteins in time and space  
Emma Lundberg  
Science of Life Laboratory (KTH), Sweden

14:30  Highly multiplexed imaging of tissues with subcellular resolution by imaging mass cytometry  
Bernd Bodenmiller  
University of Zurich, Switzerland

15:00  Spatiotemporal proteomics and transcriptomics of the human cell cycle  
Anthony Cesnik  
Stanford University, USA

15:15  Age-associated changes in the human midbrain dopamine cell transcriptome and proteome  
Rahul Bharadwaj  
Lieber Institute for Brain Development, USA

15:30-16:00  Afternoon tea

16:00-17:30  Session 5: Protein – protein interactions  
Chair: Juan Antonio Vizcaino, EMBL-EBI, UK

16:00  Proximity-dependent sensors for the control of growth regulation  
Anne Claude Gingras  
Lunenfeld-Tanenbaum Research Institute, Canada

16:30  Functional proteome analysis of resistant p53 deficient cells to chemotherapeutic treatment  
Theocharis Efthymiopoulos  
EMBL, Germany
16:45 The Yeast Complexome - The Complex Portal rising to the challenge
   Birgit Meldal
   EMBL-EBI, UK

17:00-17:35 Lightning talks
   Chair: Juan Antonio Vizcaino, EMBL-EBI, UK

17:35-18:35 Poster session 2 (even numbers) with drinks reception

18:40 prompt Silver service conference dinner

18:50 Cash Bar

Wednesday 1 April 2020

09:00-10:30 Session 6: Post-translational Modifications
   Chair: Emma Lundberg, Science of Life Laboratory (KTH), Sweden

   09:00 Applying proteomics to understand circadian biology
      Maria Robles
      LMU Munich, Germany

   09:30 Identification of ligand-dependent GPCR protein interaction
      networks with temporal and spatial resolution
      Ruth Huettenhain
      UCSF, USA

   10:00 Targeted Proteomic Analysis Reveals Enrichment of Atypical
      Ubiquitin Chains in Contractile Tissues
      Tiaan Heunis
      Newcastle University, UK

   10:15 MS-based epi-proteomic mapping of clinical samples for biomarker
      discovery and cancer patient stratification
      Tiziana Bonaldi
      European Institute of Oncology, Italy

10:30-11:00 Morning coffee

11:00-12:45 Session 7: Technology
   Chair: Matthias Mann, Max Planck Institute of Biochemistry, Germany

   11:00 Personalized proteome diversity studied by hybrid mass
      spectrometry approaches
      Albert Heck
      Utrecht University, The Netherlands

   11:30 Enrichment-free O-glycoproteome based on Trapped Ion Mobility
      Q-TOF
      Catherine Wong
      Peking University, China
12:00  Proteomic analysis of cell state transitions using PRIMMUS
Tony Ly
University of Edinburgh, UK

12:15  Multi-omic Dissection of Oncogenically Active Epiproteomes
       Identifies Drivers of Proliferative and Invasive Breast Tumors
Xian Chen
University of North Carolina at Chapel Hill, USA

12:30 -12:45  Closing remarks
Angus Lamond, University of Dundee, UK

12:45 -13:30  Lunch

Coaches depart to Cambridge City Centre and Train Station,
Heathrow Airport via Stansted Airport