

Proteomics in Cell Biology and Disease Mechanisms
30 March – 1 April 2020

Wellcome Genome Campus
Hinxton, Cambridge

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 I: 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**
- 15:30-17:00 **Session I 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 I (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: Organelle**
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 Kraemer
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

16:00-17:00

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 **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 Epiroteomes
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

13:30

Coaches depart for Stansted and Heathrow Airport

13:45

Coaches depart for Cambridge Train Station and City Centre