

DAY 1 - AM - Plenary session 1 (Chair: Kris Gevaert)

Room:

- 08:30 - 09:05** Registration & coffee
- 09:05 - 09:15** Welcome by Kris Gevaert

PLENARY SESSION I: SINGLE CELL AND SPATIAL PROTEOMICS - PART I

Chair: Kris Gevaert

JAN VAN EYCK ROOM

- 09:15 - 09:50** The Human Protein Atlas – spatial proteomics for single cell analysis
Cecilia Lindskog Bergström, Uppsala University, SE
- 09:50 - 10:15** Single-Cell Spatial Phenotyping: Setting the pace of Discovery Biology
Virginie Goubert, Applications & Market Development Lead - EU, Akoya Biosciences, FR
- 10:15 - 10:50** Spatial patterns in tissue – what can we see and what can we measure?
Carolina Wählby, Department of Information Technology, Uppsala University and SciLifeLab, SE
- 10:50 - 11:20** Coffee break
- 11:20 - 11:45** Identification of novel tumor markers using high content imaging
Christoph Herbel, Group Lead CAR T cells for Solid Cancer Molecular Technologies & Stem Cell Therapy, Miltenyi Biotec, DE
- 11:45 - 12:20** Recent advances in single-cell and spatial proteomics
Ryan Kelly, Associate Professor, Department of Chemistry and Biochemistry, Brigham Young University, US
- 12:20 - 12:35** Mapping the composition of lysosomes in different cell types of the brain
Selected talk - Poster nr. 21
Alessandro Ori, Leibniz Institute on Aging – Fritz Lipmann Institute, DE
- 12:35 - 12:50** Alternative Protein, broadening the vision of the protein landscape
Selected talk - Poster nr. 8
Tristan Cardon INSERM U1192 Protéomique, Réponse Inflammatoire et Spectrométrie de Masse (PRISM), FR

DAY 1 - PM - Parallel session 1

- 12:50 - 13:45** Lunch
- 13:45 - 14:30** Poster session 1 (All odd numbers can present)

PARALLEL SESSION I: SINGLE CELL AND SPATIAL PROTEOMICS - PART 2

Chair: Charlotte Stadler

JAN VAN EYCK ROOM

- 14:30 - 15:05** Constructing a practical proteogenomic atlas of the liver
Martin Guillems, VIB-UGent Center for Inflammation Research, BE
- 15:05 - 15:30** From whole transcriptome tissue mapping down to the secret life of a single cell: spatial biology made easy at any scale
Tony Zucca, Technical Sales Specialist Manager EMEA/PAC, NanoString Technologies, UK
- 15:30 - 16:05** Proximity-dependent sensors for signaling
Anne-Claude Gingras, The Lunenfeld-Tanenbaum Research Institute, CA and University of Toronto, CA
- 16:05 - 16:30** cellenONE©, a platform for unmatched single cell proteomics sample preparation
Anjali Set, Head of Single Cell Proteomics, Cellenion, FR
- 16:30 - 17:00** Coffee break

PARALLEL SESSION 2: COMPUTATIONAL PROTEOMICS

Chair: Lieven Clement

HUGO VANDERGOES ROOM

- 14:30 - 15:05** Multilevel statistical modeling accounts for diverse sources of variation in proteomic experiments with complex designs
Olga Vitek, *Khoury College of Computer Sciences, Northeastern University, US*
- 15:05 - 15:30** Unlocking the untapped potential in mass spectrometry data using AI
Lukas Reiter, *CTO, Biognosys AG, CH*
- 15:30 - 16:05** The proteome, but not as we know it – a proteome-wide view on modifications
Lennart Martens, *VIB-UGent Center for Medical Biotechnology, BE*
- 16:05 - 16:40** Describing mismatches or challenging targets? Overcoming a two-decade-old statu quo about the role of decoy sequences
Thomas Burger, *Université Grenoble Alpes, INSERM, CEA, FR*
- 16:40 - 17:00** Coffee break

PLENARY SESSION 2: CLOSING DAY I

Chair: Lieven Clement

JAN VAN EYCK ROOM

- 17:00 - 17:35** Single-cell proteomics: a computational biologist's view on the current challenges, needs and opportunities
Laurent Gatto, *De Duve Institute – UC Louvain, BE*
- 17:35 - 18:10** Exploring functional protein covariation across single cells
Nikolai Salvov, *Northeastern University, US*
- 18:10 - 19:10** Reception
- 19:00 - 22:00** Guided walk + conference dinner (*Additional fee*)

- 08:30 - 09:00** Registration & coffee

PLENARY SESSION 1: CLINICAL PROTEOMICS

Chair: Francis Impens

JAN VAN EYCK ROOM

- 09:00 - 09:35** The metabolic and proteomic landscape of genome-scale genetic perturbation
Markus Ralser, *The Francis Crick Institute, UK*
- 09:35 - 10:00** MosaicNeedles: A Platform for Large-scale Proteomics with High Sensitivity, High Multiplex and Large Dynamic Range
Qimin Quan, *CSO, NanoMosaic, US*
- 10:00 - 10:35** Antigen discovery for development of personalized cancer immunotherapy
Michal Bassani-Sternberg, *Ludwig Institute for Cancer Research Lausanne, CH*
- 10:35 - 11:05** Coffee break
- 11:05 - 11:30** Proteograph Analysis Suite: A cloud-scalable software suite for proteogenomics data analysis and visualization.
Daniel Hornburg, *Senior Director, Seer (Multi-Omics Mass Spec Technologies & Bioinformatics), US*
- 11:30 - 12:05** Precision phenotyping with the circulating proteome
Jochen Schwenk, *Science for Life Laboratory, KTH Royal Institute of Technology, SE*
- 12:05 - 12:20** Exploring cross-reactivity of SARS-CoV-2 antibodies to the human proteome
Anna Månberg, *KTH Royal Institute of Technology, SciLifeLab Stockholm, SE*
Selected talk
Poster nr. 24
- 12:20 - 12:35** Single-Molecule Protein Identification Using FRET X
Mike Filius, *Delft University of Technology, NL*
Selected talk
Poster nr. 17
- 12:35 - 12:40** Measuring biomarkers at lowest levels than ever before
Eva Ramos, *Field Application Scientist, Quanterix, DK*
Sponsored talk
- 12:40 - 13:20** Lunch
- 13:20 - 14:05** Poster session 2 (All even numbers can present)

DAY 2 - PM - Parallel Session 1 & 2

PARALLEL SESSION 1: SINGLE-MOLECULE PEPTIDE ANALYSIS

Chair: Michiel Bontinck

JAN VAN EYCK ROOM

- 14:05 - 14:40** Nanopore-Based Protein Fingerprinting
Abdelghani Oukhaled, *CY Cergy Paris University, FR*
- 14:40 - 15:05** Real-time dynamic single-molecule protein sequencing on the Quantum-Si platform
Brian Reed, *Head of Research, Quantum-Si, US*
- 15:05 - 15:30** Development of a Novel Single-Molecule Proteomics Analysis Platform based upon Protein Identification by Short epitope Mapping
Parag Mallick, *Founder, Nautilus Biotechnology, US*
- 15:30 - 15:55** Revealing the Proteome with the Power of DNA — Leveraging Genomic Principles to Create a Universal Approach to Proteomic Sequencing
Nigel Beard - *CTO, Encodia, USA*
- 15:55 - 16:30** Coffee break

PARALLEL SESSION 2: BIOPHYSICAL CHARACTERIZATION

Chair: Yu-Chun Wang

HUGO VANDERGOES ROOM

- 14:05 - 14:30** Protein-protein interactions in amyloidogenic growth as a new therapeutic avenue at Aelin Therapeutics.
Rodrigo Gallardo, *Senior Scientist, Aelin Therapeutics, BE*
- 14:30 - 14:55** Tracking Drug Action at the Cell Surface and in the Secreted Proteome
Markus Bantscheff, *Senior Scientific Director, Cellzome (a GSK company), DE*
- 14:55 - 15:30** Revealing protein dynamics with single-molecule tools
Sander Tans, *AMOLF institute, NL*
- 15:30 - 15:55** Fida: A New Biophysics Methodology Linking Protein Structure and Function
Henrik Jensen - *CSO of Fida Biosystems, DK*
- 15:55 - 16:30** Coffee break

PLENARY SESSION: CLOSING DAY 2

Chair: Yu-Chun Wang

JAN VAN EYCK ROOM

- 16:30 - 17:05** Highly multiplexed imaging of tissues with subcellular resolution by imaging mass cytometry
Bernd Bodenmiller, *University of Zurich, CH*
- 17:05 - 17:40** Using Mass Spectrometry to Size and Count Single Molecules and Probe Antibody Repertoires
Albert Heck, *Utrecht University, NL*
- 17:40 - 17:50** Closing words by Francis Impens