

Program overview

Tuesday, 28 June 2022

13:00-13:05

**Welcome – Loïc Dayon (Nestlé Research) & LS²
Proteomics Board**

13:05-15:05

Oral Session I

*Chairs: Oliver Rinner (Biognosys) & Manuel Tzouros
(Hoffmann-La Roche Basel)*

13:05-13:50

Keynote 1:

Prof. Jochen M. Schwenk (SciLifeLab, Sweden)
*"The dynamic architecture of the circulating
proteome"*

13:50-14:05

Oral presentation 1:

**Ulrich Auf Dem Keller (Technical University of
Denmark)**
*"High-throughput targeted proteomics monitoring of
biomarkers in wound exudates for clinical wound
management"*

14:05-14:20

Flash presentations 1-3:

Ino Karemaker (*Biognosys AG*)

"Investigation of proteomic signatures in healthy aging, mild cognitive impairment and Alzheimer's disease in a paired CSF and plasma study"

Izabela Noll (*SomaLogic*)

"Development and validation of a blood based protein only predictor of 5-year lung cancer risk in ever smokers"

Harini Lakshminarayanan (*University Hospital Zurich*)

"Liquid biopsy-based biomarkers as a tool for disease monitoring in clear cell renal cell carcinoma"

14:20-14:35

Oral presentation 2:

Minia Antelo (*University of Basel*)

"Exploring the potential of targeted proteomics in clinical settings"

14:35-15:00

Coffee Break

15:00-16:40

Oral Session II

Chairs: Bernd Wollscheid (ETH Zurich) & Loïc Dayon (Nestlé Research)

15:00-15:15

Oral presentation 3:

Lydia Liu (*University of Toronto*)

"Expanding the prostate cancer proteome: custom database to non-canonical ORFs"

15:15-15:30

Oral presentation 4:

Peter Doubleday (ETH Zurich)

"Unraveling mechanism-based inhibitor inactivation pathways with top-down and native proteomics for improved therapeutics in hepatocellular carcinoma"

15:30-15:45

Oral presentation 5

Xiaokang Li (CHUV)

"An automated microfluidics workflow enabling the HLA immunopeptidome discovery from low sample input by mass spectrometry"

15:45-16:00

Flash presentations 4-6:

Diego Chiappe (EPF Lausanne)

"Nanoparticle Corona proteome study for the detection of potential Melanoma biomarkers"

Emmanuelle Lezan (Hoffmann-La Roche)

*"Development and application of a new IP-MS strategy for the quantification of the dioxidized WT1 RMFPNAPYL HLA-A*02 associated peptide"*

Sebastian Müller (Biognosys AG)

"Multi-Site Plasma and Serum LC-MS Analysis to Assess Comparability Using Targeted Acquisition and Reference Peptides Covering More Than 500 Proteins"

16:00-16:10

Sponsor talk: PreOmics

PREOMICS

Quentin Enjalbert

"The time capsule: BeatBox & iST workflows enable evolutionary in-depth analysis of tissue & cell proteomes"

16:10-16:40

Coffee Break

16:40-18:00

Oral Session III

*Chairs: Maria Pavlou (EPF Lausanne)
& Paolo Nanni (Functional Genomics Center Zurich,
UZH/ETH Zurich)*

16:40-16:55

Oral presentation 6

Thierry Nordmann (*Max Planck Institute of
Biochemistry, Munich*)
*"Deep Visual Proteomics for single-cell type analysis
of severe cutaneous adverse drug reactions"*

16:55-17:15

Flash presentations 7-10

Nicolas Autret (*Covaris*)
*"A Robust LC-MS analysis of C. albicans - Differential
Protein Expression using AFA focused ultrasonication,
SP3 and TMT labelling"*

Axel Ducret (*Hoffmann-La Roche*)
*"Designing targeted mass spectrometry assays for
membrane proteins in complex matrices using a
peptide immuno-enrichment strategy"*

Charlotte Macron (*Nestlé Research*)
*"Proteomics of Human Milk: Definition of a Discovery
Workflow for Clinical Research Studies"*

Jonas Albinus (*ETH Zurich*)
*"Spatiotemporal surfaceome dynamics in human B
lymphocytes"*

17:15-17:30

Oral presentation 7

Jens Settelmeier (ETH Zurich)

"preDIATOR - pre-identification of Data Independent Acquisition measurements to detect targets of relevance for open searches and improve patient stratification"

17:30-17:50

Flash presentations 11-14

Witold Wolski (University of Zurich/ETH Zurich)

"prolfqua - An R-package for Proteomics Differential Expression Analysis"

Mihaela Diana Zanoaga / Ornella Cominetti (Nestlé Research)

"Assessing normalization methods in mass spectrometry-based proteome profiling of clinical samples"

Romain Hamelin (EPF Lausanne)

"Deciphering bioremediation energy metabolism in Firmicutes using quantitative proteomics"

Julia Boshart (ETH Zurich)

"Towards deciphering the surfaceome architecture on the single-cell level"

17:50-18:00

Sponsor talk: Bruker

Torsten Müller

"dia-PASEF® combined with TIMScore™ and TIMS DIA-NN for proteome depth at scale"



18:20-18:30 **Group picture**

18:30-19:30 *Apéro, sponsored by
Biognosys (upon
registration only!)*



19:30-22:00 *Dinner in the conference hotel (upon registration
only!)*

Wednesday, 29 June 2022

09:00-11:50 **Oral Session IV**
*Chairs: Alexander Leitner (ETH Zurich) & Alexander
Schmidt (University of Basel)*

09:00-09:15 **Oral presentation 8**
Sebastian Steiner (ETH Zurich)
*"Decoding the dynamic cell surface signaling
interactome"*

09:15-09:30 **Oral presentation 9**
Yibo Wu (University of Geneva)
*"Multilayered omics Reveal Sex- and Depot-
Dependent Adipose Progenitor Cell Heterogeneity"*

09:30-09:50 **Flash presentations 15-18**
Jacqueline Hammer (ETH Zurich)
*"Identification of surfaceome proteotypes using LUX-
CSC"*

Ane Laura Fineid Pedersen (Nestlé Research)
*"Structural investigation of the human milk proteome
using cross-linking mass spectrometry"*

Matthieu Porchet (*Philip Morris International*)
"Toxicoproteomics reveals an effect of clozapine on autophagy in human liver spheroids"

Heidi Funke (*ETH Zurich*)
"Decoding the extracellular interactome using nanobody-based LUX-MS"

09:50-10:00

Sponsor talk: Sciex



Petra Blankenstein
"The Sciex ZenoTOF 7600 – maximum sensitivity for qual and quant using ZenoSWATH"

10:00-10:30

Coffee Break

10:30-10:45

Oral presentation 10

Klemens Fröhlich (*University of Basel*)
"Benchmarking of Analysis Strategies for Data-Independent Acquisition Proteomics Using a Large-Scale Dataset Comprising Inter-Patient Heterogeneity"

10:45-10:50

Sponsor flash talk: ThermoFisher

Dominic G. Hoch
"What's New? – Innovative Tools & Technologies in Bottom-up Proteomics"



10:50-11:00

Flash presentations 19-20

Melanie Brunner (*University of Fribourg*)
"Phosphoproteomic characterization of GSK-3 targets in autophagy"

Alexandre Leytens (*University of Fribourg*)
"A targeted proteomics assay to monitor autophagy"

11:00-11:45

Keynote 2/Closing Lecture:

Prof. Markus Ralser (*Charité Universitätsmedizin
Berlin, Germany*)
"The metabolic and proteomic landscape of genome-
scale genetic perturbation"

12:00-12:15

Awards and closing remarks

*Chairs: Maria Pavlou (EPF Lausanne), Paolo Nanni
(Functional Genomics Center Zurich, UZH/ETH Zurich),
Alexander Schmidt (University of Basel), Bernd
Wollscheid (ETH Zurich), Loïc Dayon (Nestlé Research)
& Thomas Howe (Hamilton Bonaduz AG)*

12:00-12:10

**Best oral presentation prize (sponsored by
Hamilton Bonaduz AG) & best flash talk prize
(sponsored by LS² Section Proteomics)**

12:10-12:15

**Closing remarks – Loïc Dayon (Nestlé Research) & LS²
Proteomics Board**

12:30-14:00

Farewell Lunch (upon registration only!)

14:00-15:00

LS² Proteomics Board Meeting (if needed)