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Member of
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LS2
Life Sciences Switzerland

23-24 May 2019, Eurotel Montreux

Annual Swiss Proteomics Meeting

MEETING BOOKLET

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Akademie der Naturwissenschaften
Accademia di scienze naturali
Académie des sciences naturelles

EuPA
EUROPEAN PROTEOMICS ASSOCIATION

This meeting booklet belongs to:

(please find space for your notes at the end of this booklet)

LS²
Life Sciences Switzerland
Proteomics

Table of Contents

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Program Overview

Thursday, 23th May 2019

12:30-12:40 **Welcome:**
Bernd Wollscheid (ETH Zurich) **& LS2 Proteomics Board**

12:40-16:00 **Oral Session I**
Chairs: Loïc Dayon (Nestlé Institute of Health Sciences, NIHS) *& Lydie Lane* (Swiss Institute of Bioinformatics)

12:40-13:30 **Keynote 1**
Mikhail SAVITSKI (EMBL, Heidelberg, DE)
"Protein Stability in Drug Discovery and Molecular Biology"

13:30-13:40 **Oral presentation 1**
Patrick Pedrioli (ETH Zurich)
"Characterization of Methylmalonic Acidemia patient cohort: emerging computational challenges and opportunities in the proteomics analysis of large patient cohorts"

13:40-13:55 **Flash presentations 1-5**
Christian Doerig (ETH Zurich)
"A structural systems biology approach to identify protein complex interfaces on a proteome-wide scale"

Fabian Frommelt (ETH Zurich)
"AP-SEC-SWATH: resolving protein complexes by profiling size fractionated affinity purifications"

Mikhail Gorshkov (INEPCP RAS, RU)
"5 min proteome"

Yury Tsybin (Spectroswiss Sàrl)
"Enhanced glycoprotein structural analysis using advanced FTMS data acquisition and processing approaches"

Peter Blattmann (ETH Zurich)
"Phosphoproteomic profiling of signaling pathways in patient- derived colorectal cancer organoids"

13:55-14:10 **Oral presentation 2**
Jianwen Zhou (University of Fribourg)
"Mass spectrometry-based study on the relationship between ubiquitination and autophagy"

14:10-14:25 **Flash presentations 6-10**
Marco Faini (ETH Zurich)
"Quantitative structural biology of endogenous protein complexes"

Sandra Goetze (ETH Zurich)
"Defining the relationship between high density lipoprotein (HDL) particle composition and clinical signaling capacity"

Martin Mehnert (ETH Zurich)
"Multilayered proteomics identifies cancer mutations that affect the composition and function of kinase complexes"

Gabriela Kultová (University of Hradec Králové, CZ)
"Plasma membrane proteins as new biomarkers of irradiation in humans"

Thomas Schneider (Philip Morris International)
"A proteomics approach for selective screening of nicotinic acetylcholine receptor subunit expression in experimental model systems"

14:25-14:35 **Gold Sponsor Talk**
Russel Golson (PreOmics GmbH & HSE GmbH)
"PreON: An automated protein sample processing platform for enhanced reproducibility and minimal hands-on time for increased laboratory efficiency"

14:35-14:50 **Oral presentation 3**
Erwin Schoof (DTU Copenhagen, DK)
"A quantitative single-cell proteomics approach to characterizing an acute myeloid leukemia hierarchy"

14:50-15:05 **Oral presentation 4**
Antonio Núñez Galindo (NIHS)
"Plasma and CSF proteomics in brain aging research"

15:05-16:00 ***Coffee Break***

16:00-18:15 **Oral Session II**
Chairs: Paola Picotti (ETH Zurich) *&*
Alexander Schmidt (University of Basel)

16:00-16:15 **Oral presentation 5**
George Rosenberger (Columbia University, US)
"SECAT: Network-centric analysis of size-exclusion chromatography protein complex profiles"

16:15-16:30 **Flash presentations 11-15**
Ivana Karlovska (Biognosys)
"An optimized single shot DIA workflow to quantify more than 1'000 proteins in depleted human plasma"

Christian Ahrens (Agroscope)
"An integrative proteogenomics strategy to identify unannotated small proteins in prokaryotic genomes"

Maik Müller (ETH Zurich)
"Shining light on cellular surfaceome organisation using LUX-MS"

Stephanie Lüthi (University of Zurich)
"A proteomics approach to identifying the ADP-ribosylome in serum"

Tatjana Sajic (ETH Zurich)
"A new class of protein biomarkers based on subcellular distribution: application to a mouse liver cancer model"

16:30-16:40 **Gold Sponsor Talk**
Christoph Mitterer (PharmaFluidics)
"Maximize the output of routine proteome analyses by using micro pillar array column technology"

16:40-16:55 **Flash presentations 16-20**
Federico Uliana (ETH Zurich)
"Dissection of YAP1 proteoforms and interactions"

Valentina Cappelletti (ETH Zurich)
"From genotype to phenotype: exploring the effect of genetic variation on protein structure and function"

Zehan Hu (University of Fribourg)
"*Multilayered control of protein turnover by ATG1 and TORC1"*

Jana Rykl (Shimadzu Schweiz GmbH)
"Quality control of two peptides forming water soluble alpha-helical barrels via LC-MS/MS and denovo structure elucidation"

Nicolas Autret (Covaris)
"Universal Sample Processing Of Multiple Sample Types For Reproducible Proteomic Sample Preparation"

16:55-17:10 **Oral presentation 6**
Marija Buljan (ETH Zurich)
"Protein quantitative relationships as reporters of disease-associated alterations in protein complex states"

17:10-17:25 **Flash presentations 21-25**
Liliana Malinovska (ETH Zurich)
"Probing the structural landscape of alpha synuclein in cells and tissues using LiP-MS"

Tatjana Vujic (ETH Zurich)
"DIA-MS approach used to understand the effect of paraquat on human brain microvascular endothelial cells"

Matej Vizovisek (ETH Zurich)
"High-throughput profiling of blood cascade proteases reveals thrombin-like and trypsin-like specificities"

Stoyan Stoychev (CSIR South Africa)
"Development of fully automated pipeline for phosphoproteome profiling"

Ales Holfeld (ETH Zurich)
"Proteome-wide elucidation of protein-protein interaction networks by limited proteolysis-coupled mass spectrometry"

17:25-17:40 **Oral presentation 7**
Michal Bassani-Sternberg (CHUV)
"Immunopeptidomics: Accelerating the development of personalized cancer immunotherapy"

17:40-17:55 **Flash presentations 26-30**
Ilaria Piazza (ETH Zurich)
"Shedding light on a new cellular interactomics: studying protein-small molecule interactions in biology and medicine"

Andrea Fossati (ETH Zurich)
"Systemati assessment of nuclear protein complexes dynamics upon mammalian dosage compensation"

Claudius Marondedze (CEA Grenoble, FR)
"Molecular mechanism of LEAFY activation upon UFO interaction"

Joe Weber (University of Zurich)
"Proteomic analyses of Drosophila spermatogenesis: large-scale testes isolation for increased sensitivity"

Lukas von Ziegler (ETH Zurich)
"The phosphoproteome of acute stress in the mouse hippocampus"

17:55-18:00 **Silver Sponsor Talk**
Scarlet Koch (Bruker Daltonik GmbH)
"High throughput body fluid analysis with a TIMS equipped QTOF and 4D feature alignment"

19:00-20:00 **Apéro, sponsored by Biognosys AG**

20:00-22:30 ***Dinner in Conference Hotel***

Friday, 24th May 2019

09:00-12:00 **Oral Session III**
Chairs: Deborah Bonenfant (Novartis Institutes for BioMedical Research) *& Marc Moniatte* (EPFL)

09:00-09:45 **Keynote 2**
Alexey NESVIZHSKII (Univ. of Michigan Medical School, US)
"Applications of Ultrafast Database Searching in Proteomics"

09:45-10:00 **Oral presentation 9**
Lukas Reiter (Biognosys)
"In Silico Libraries outperform resource libraries in the targeted extraction of DIA"

10:00-10:15 **Flash presentations 31-35**
Fabian Wendt (ETH Zurich)
"Exploring extracellular proteotype changes upon vaccinia virus infection to uncover cellular signalling at the infection site"

Mahmoud Hallal (University of Bern)
"Characterization of kinase activities inferred by phosphoproteomics in myeloid cell lines treated with targeting compounds for the identification of driving and bypassing oncogenic signaling pathways"

Marie-Therese Mackmull (ETH Zurich)
"Linking altered protein structures to Parkinson's Disease subtypes"

Jan Muntel (Biognosys)
"How to find the best protein quantification strategy in data-independent acquisition (DIA) experiments using controlled datasets"

Jelena Čuklina (ETH Zurich)
"Batch effect in proteomics and beyond"

10:15-10:20 **Silver Sponsor Talk**
Daniel Grenno (Thermo Fisher Scientific)
"Gaining advantages with the new FAIMS Pro™"

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10:20-11:00 ***Coffee Break***

11:00-11:15 **Flash presentations 36-40**
Charlotte Macron (NIHS)
"The proteome of human cerebrospinal fluid and the identification of missing proteins"

Devanarayana Siva Sankar (University of Fribourg)
"Identification of putative regulators of ULK1 and its phosphorylation substrates regulating autophagy"

Mattheus Wildschut (ETH Zurich)
"The Consequence of CALR Mutations on Proteostasis in Myeloproliferative Neoplasms"

Verena Waller (University of Zurich)
"Exploring the interactome of ADAM17 in the tumor microenvironment and its role for radiation"

Kathrin Frey (ETH Zurich)
"Associating HDL proteotype with clinical HDL particle signaling capacity"

11:15-12:00 **Special Keynote**
Ruedi AEBERSOLD (ETH Zurich)
"Technology drives biology - but in which direction?"

12:00-12:30 **Awards and Closing Remarks**
Chairs: Manuel Tzouros (Hoffmann-La Roche Basel) *& Oliver Rinner* (Biognosys)

12:00-12:20 **Best oral presentation prize & best flash talk prize**

12:20-12:30 **Closing remarks – Bernd Wollscheid & LS2 Proteomics Board**

12:30-13:30 ***Farewell Lunch***

13:30-14:30 **LS2 Proteomics Board Meeting**
Upon invitation only

LS² Life Sciences Switzerland Proteomics

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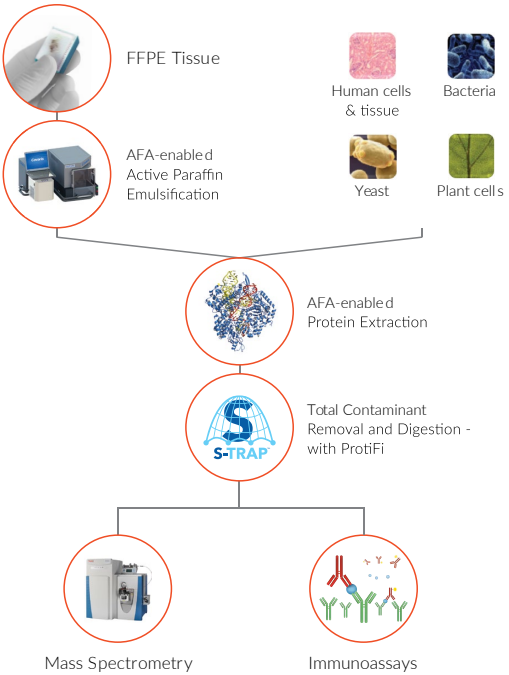

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Keynote Lectures

Keynote lecture 1: Thursday, 23.5.2019 12:40-13:30

Mikhail Savitski
(EMBL, Heidelberg, DE)

"Protein Stability in Drug Discovery and Molecular Biology"

Keynote lecture 2: Friday, 24.5.2019 09:00-09:45

Alexey Nesvizhskii
(University of Michigan Medical School, US)

"Applications of Ultrafast Database Searching in Proteomics"

Special keynote: Friday, 24.5.2019 11:15-12:00

Ruedi Aebersold
(ETH Zurich)

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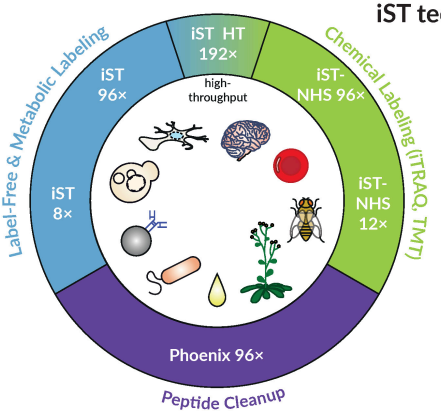

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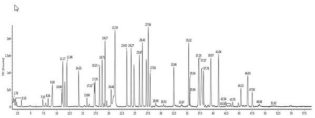
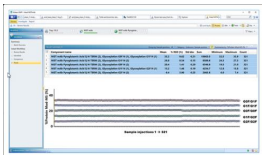


APPLICATION SPECIFIC CONSUMABLES

UNIFI

Streamline workflows from sample to result



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Sponsor talks & abstracts

Gold sponsor talks:

"PreON: An automated protein sample processing platform for enhanced reproducibility and minimal hands-on time for increased laboratory efficiency"

Russell Golson, Head of Sales and Marketing PreOmics GmbH
golson@preomics.com

[1]Sebastian Steiner, [2]Doris Jansen, [1]Jonas Albinus, [1]Sandra Goetze, [3]Harald Quintel, [3]Konstantin Lutze, [1]Bernd Wollscheid, [2]Russel Golson, [2]Fabian Hosp, [2]Nils Kulak

[1]ETH Zürich, Institute of Molecular Systems Biology, 8093 Zurich, Switzerland
[2]PreOmics GmbH, 82152 Martinsried, Germany
[3]HSE AG, 8634 Hombrechtikon, Switzerland

Sample preparation is an often overlooked yet very important component of the overall mass spectrometry-based proteomics workflow and remains to be a limiting factor for reproducible high-throughput analyses. One method to increase the throughput is sample multiplexing using chemical labeling approaches such as iTRAQ or TMT. Here, we present a fully automated end-to-end solution for standardized sample processing of cells and liquid biopsies, including cell lysis, digestion, TMT labeling and peptide cleanup with only 5 minutes hands-on time.
In order to minimize sample loss, improve reproducibility and efficiency, we sought to completely automate TMT sample processing from cell lysis to ready-to-measure labeled peptides. To facilitate this, we aimed to combine the NHS adaption of the iST technology (Kulak et al., 2014) with a newly developed automation platform called PreON (HSE AG).
The workflow described here integrates robotic handling with chemical labeling of peptides in the very same reaction device used for cell lysis, protein denaturation, reduction, alkylation, digestion as well as the peptide cleanup. This solution increases the sample reproducibility, minimizes variability as well as sample loss and dramatically reduces hands-on time compared to manual processing. The PreON platform features a built-in centrifuge, ultrasound liquid detection, deck load check and a drag-and-drop method selection for easy, fast and a convenient menu-driven guidance.

We demonstrate successful labeling of cancer cell lines using 11-plex TMT achieving >98% labeling efficiency and a reproducibility of R = 0.97 for biological replicates (CVs <20%). Furthermore, we present data on more complex samples such as yeast, or human plasma and tissue samples.
This hands-off workflow enables sample processing and TMT-labeling of up to 11 samples in parallel in a fully automated fashion and in less than 4 hours, scaling from 1-100 µg of protein input material. Additional workflows for processing of tissue samples combined with chemical labeling are to be implemented soon.

"Maximize the output of routine proteome analyses by using micro pillar array column technology"

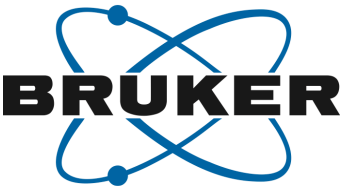
Christof Mitterer, Senior Key Account Manager PharmaFluidics
christof.mitterer@pharmafluidics.com

Christof Mitterer, Geert Van Raemdonck, Jeff Op de Beeck, Kurt Van Mol, Bo Claerebout, Natalie Van Landuyt, Wim De Malsche, Gert Desmet, Paul Jacobs

As an alternative to the conventional packed bed nano LC columns that are frequently used in bottom-up proteomics research, PharmaFluidics offers micromachined nano LC chip columns known as micro pillar array columns (µPAC™). The inherent high permeability and low 'on-column' dispersion obtained by the perfect order of the separation bed makes µPAC™ based chromatography unique in its kind. The peak dispersion originating from heterogeneous flow paths in the separation bed is eliminated (no A-term contributions) and therefore components remain much more concentrated during separation resulting in unprecedented separation performance. The freestanding nature of the pillars also leads to much lower backpressure allowing a high operational flow rate flexibility with exceptional peak capacities.
Complementary to its landmark 200cm long column, which is ideally suited to perform comprehensive proteome research, a 50cm long µPAC™ column is now available which can be used in a more routine research setting. With an internal volume of 3µL, this column is perfectly suited to perform high throughput analyses with shorter gradient solvent times (30, 60 and 90 minute gradients) and it can be used over a wide range of flow rates, between 100 and 2000 nL/min. Recently performed experiments with 500ng of HeLa cell digest indicate that an increase in protein identifications up to 50% and a gain of 70% in peptide identifications can be achieved when comparing the

50cm µPAC™ column to the current state-of-the-art in packed bed columns. The conventional packed bed columns (2 different vendors) used for this benchmarking experiment were 15cm in length and were packed with sub 2µm porous silica particles. LC pump pressures needed to operate these classical columns at a flow rate of 300 nL/min range between 200 and 300 bar, whereas only 40 bar was needed to operate the 50cm µPAC™ column at the same conditions.

Silver sponsor talks:



"High throughput body fluid analysis with a TIMS equipped QTOF and 4D feature alignment"

Scarlet Koch, Bruker Daltonik GmbH
scarlet.koch@bruker.com

Thomas Kosinski 1, Raphael Heilig 2, Scarlet Koch 1; Nicolai Bache 3, Ole Bjeld Hørning 3, Roman Fischer 2, Heiner Koch 1;
1 Bruker Daltonik GmbH, Bremen, Germany; 2 Target Discovery Institute, Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom.
3 Evosep Biosystems, Odense, Denmark

Body fluids are the most commonly used samples for diagnostic analyses in the clinic due to their accessibility; they are routinely collected from patients with minimal or no invasiveness and can also be obtained through biobanks from thousands of clinical studies. The gold standard in routine clinical diagnostics is quantitative analysis by immunoassays, but here only a limited number of proteins can be measured simultaneously. Mass spectrometry (MS)-based proteomics is an attractive alternative to immunoassays but often lacks sufficient throughput to measure large sample cohorts. We have used a TIMS equipped QTOF coupled to short gradient run times to achieve a throughput of >50 LC-MS/MS runs per day, which provides clear benefits for biomarker discovery in large sample cohorts.
Methods
We have measured samples from human blood plasma on a TIMS equipped QTOF (timsTOF Pro, Bruker) coupled to an Evosep One LC (Evosep) to achieve high turnover rates. Peptides were delivered into the TIMS device where ions

are accumulated, separated and released based on their size-to-charge ratio. The quadrupole switches mass positions within 1.6ms allowing a sequencing speed at around 100Hz at a high MS1 sampling rate for accurate quantification on short gradient measurements. Post processing was performed with PEAKS studio (Bioinformatic Solutions) and search results were corrected to 1% FDR and identifications were transferred between runs using a 4D feature alignment.

Preliminary Data

We have combined the speed and sensitivity of a TIMS equipped QTOF with the high throughput LC-separation to analyze low sample amounts of body fluids (100- 200ng on short 21min runs). We have performed sample pre-fractionation of 25µg plasma for subsequent analysis on LC MS/MS to characterize the proteome depth that can be achieved. To evaluate the stability of the LC-MS/MS performance we have measured 50 blood plasma samples and found high quantitative reproducibility across the study (R2>0.97, median CV 10.2%) and no systematic drift in peptide and protein identification. Label-free quantification was applied with a novel 4D alignment approach (mobility, m/z, retention time and intensity). This approach reduces false positive identifications at matching of MS1 features between runs and improves the ID rate at a low number of missing values. By doing that, we could improve the number of quantified proteins groups per run. We have generated a matching library from the pre fractionated blood plasma samples and could boost the number of quantified proteins in a single 21min LC-MS/MS run from 200 to 479 protein groups. We found several proteins of lower abundance like tissue leakage proteins (TBP-2, PSA), demonstrating that this workflow can facilitate biomarker discovery in this abundance region. It is also in the range of expectation that a plasma proteome sample in a very large cohort with hundreds or thousands of samples would gain a lot in the number of quantified proteins if a 4D match between runs is applied. Taken together, we provide a robust and high throughput LC-MS/MS solution with sufficient depth that has potential for unbiased discovery of new biomarkers in body fluid samples.

"Gaining advantages with the new FAIMS Pro™"

Daniel Grenno, Area Sales Manager Thermo Fisher Scientific
daniel.grenno@thermofisher.com

Space for notes

Space for notes

Space for notes

Organizers

The executive committee of the LS² section Proteomics

- Bernd Wollscheid, President (ETH Zurich)
- Lydie Lane (Swiss Institute of Bioinformatics, Lausanne)
- Paola Picotti (ETH Zurich)
- Alexander Schmidt (Biozentrum Basel)
- Loïc Dayon (Nestlé Institute of Health Sciences)
- Manuel Tzouros (Roche Pharmaceuticals, Basel)
- Oliver Rinner (Biognosys AG)
- Debora Bonenfant (Novartis Institutes for BioMedical Research, Basel)
- Marc Moniatte (EPF Lausanne)

https://www.ls2.ch/sections/proteomics

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- Elena Cardenal & Carolin von Schoultz (Scientific Officers)
- Jacqueline Oberholzer (Executive Secretary)
- Dagmar Bocakova (design, bocakova@gmail.com)
- Dominique Ritter (administration)
- Michael Vögeli (IT)

Upcoming Proteomics events

- **HUPO**
  - 2019: 15 Sep 2019 - 19 Sep 2019, Adelaide, Australia
  - 2020: 18 Oct 2020 - 22 Oct 2020, Stockholm, Sweden
- **ASMS**
  - 2019: 3 June 2019 - 6 June 2019, Atlanta, US
  - 2020: 31 May 2020 - 4 June 2020, Houston, US

Thank you all for your participation!

Feedback to:
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