

Organized by the Core Unit Proteomics of the Interdisciplinary Center for Clinical Research Münster Prof. Simone König & Dr. Rita Naskar and SERVA Electrophoresis GmbH Günter Theßeling

Preface

The Münster Conference on Biomolecule Analysis 2017 focused on mass spectrometry-based imaging. In a special workshop organized by the group of Klaus Dreisewerd at the Institute of Hygiene, attendees were able to watch experiments and see instruments in action. The keynote lecture was given by Ron Heeren, the scientific director of the Maastricht MultiModal Molecular Imaging Institute.

High-ranking speakers from the protein analysis field reported about their exciting research. The conference also provided a platform for companies to showcase their products and interact with customers in workshops. The international event successfully met the increasing interest in proteomic and imaging technologies and provided a valuable information source in particular for Ph.D. students.

Since 2004, the Core Unit Proteomics (CUP) of the Interdisciplinary Center for Clinical Research Münster has organized the event as an annual series of bioanalytical conferences. Resulting from the award of the Transfer Prize 2014 of the University of Münster to CUP and SERVA Electrophoresis GmbH, the company had joined the organizing team.

Münster, Dec. 7, 2017 Simone König

Program

Chairs: Simone König, Günter Theßeling, Klaus Dreisewerd

NOVEMBER 29, 2017

WORKSHOP I

Stefan Scory, PALL FortéBio

Biolayer Interferometry (BLI) – a label-free, biosensor-based technology to monitor molecular interactions and signal transduction in living cells

WORKSHOP II

Michael Batey, Waters Corp.
Molecular imaging by mass spectrometry: Applications in biomedical research and drug discovery
Klaus Dreisewerd, Institute of Hygiene
Brief introduction to MALDI-MS imaging and MALDI-2-MS imaging
LAB TOUR
Demonstration of experiments and data evaluation strategies via Team Viewer
1. Simeon Vens-Cappell, Institute of Hygiene Enhanced MALDI-MSI analysis of glycolipids
2. Jens Soltwisch, Eike U. Brockmann, Institute of Hygiene MALDI-2-MSI analysis of bacterial metabolites with a Synapt G2-S
3. Dennis Trede, SCiLS Conceptual strategies for visualisation and analysis of mass spectrometry imaging data

NOVEMBER 30, 2017

Keynote Lecture: Ron Heeren, Maastricht *Translational molecular imaging: diagnosing the structure in disease*

Matthias Wilm, Dublin

Conditio sine qua non - Ensuring reproducibility in proteomic mass spectrometric analysis: A tale of innovation and implementation

Ilka Wittig, Frankfurt am Main *Methods to study assembly and dynamics of protein complexes*

Iris Finkemeier, Münster Mass spectrometry-based profiling of lysine acetylation and HDAC activity in plants

Julia Bandow, Bochum Identification of targets and mechanisms of metalloantibiotics

Peter James, Lund

Modern technologies and their application to the diagnosis, prognosis and treatment of breast cancer

WORKSHOPS III

Arndt Asperger, Bruker

Complementary MALDI imaging solutions based on latest MALDI-TOF and -FTICR MS technology

Marc Kipping, Waters Corp.

An overview of past, present and future of data independent acquisition strategies **Gottfried Pohlentz**, Münster Efficient analysis of proteolytic peptides and glycopeptides using ion mobility separations (IMS) and subsequent low energy collision-in duced dissociation

Günter Theßeling, Reiner Westermeier, Serva Electrophoresis

Protein electrophoresis for professionals