

Conference on Biomolecule Analysis Registration & Accommodation

REGISTRATION

Please register online under https://campus.uni-muenster.de/cu-proteomics/konferenz-2017/

Registration fee:

Regular: 25 € / Students: 10 €

On-site:

Regular: 30 € / Students: 12 €

VENUES

Biomedical Mass Spectrometry Institute of Hygiene Robert-Koch-Straße 51 48149 Münster

Max-Planck-Institute for Molecular Biomedicine Röntgenstraße 20 48149 Münster





ACCOMODATION

Münster Tourist Information Tel: +49 (0) 251 / 492 2710 Fax: +49 (0) 251 / 492 7743

http://www.muenster.de/tourismus

CONFERENCE OFFICE & ORGANISATION

IZKF Scientific Office

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The Münster Conference on Biomolecule Analysis will be held from 29 - 30 November 2017 at the Institute of Hygiene and Max-Planck Institute for Molecular Biomedicine in Münster. The conference will be hosted by the Interdisciplinary Centre for Clinical Research (IZKF) Münster.

This year's conference will focus on imaging using MALDI mass spectrometry. An entire afternoon (Nov 29) will be dedicated to showcase such experiments in a workshop organized by Prof. Klaus Dreisewerd's team and Waters Corporation at the Institute of Hygiene.

The keynote lecture will be delivered by Prof. Dr. Ron Heeren, Maastricht MultiModal Molecular Imaging Institute (M4I). In addition, eminent speakers including Professors Matthias Wilm, University College Dublin and Peter James, Lund University, and other experts who have influenced proteomics research on many fronts will hold talks. Other leading manufacturers in the field of MALDI imaging instrumentation and protein analysis -Bruker, PALL FortéBio, SCiLS and SERVA Electrophoresis will further illustrate the current state-of-the-art in talks and hands-on-workshops.

We look forward to welcoming you in Münster to two days of stimulating discussions with fellow academicians and industrial partners.

This conference is sponsored by Bruker, FortéBio, Waters GmbH, and SERVA Electrophoresis.

Wednesday, 29 November		Thursday, 30 November	
	WORKSHOP I		CONFERENCE Venue: MPI for Molecular Biomedicine
40:20	Venue: Seminar Room Core Unit Proteomics Workshop Registration	08:30	Registration
10:30 11:00 - 12:00	Stefan Scory PALL FortéBio	09:00	Simone König, Günter Thesseling Welcome address
	Biolayer Interferometry (BLI) — a label-free, biosensor-based technology to monitor molecular interactions and signal transduction in living cells	09:05	Ron Heeren, Maastricht - Key Note Lecture Translational molecular imaging: diagnosing the structure in disease
12:00	LUNCH BREAK	09:50	Matthias Wilm, Dublin
13:00	WORKSHOP II Venue: Laboratories at the Institute of Hygiene Workshop Registration		Conditio sine qua non - Ensuring reproducibility in proteomic mass spectrometric analysis: A tale of innovation and implementation
13:15	Klaus Dreisewerd, Simone König	10:20	COFFEE BREAK
13:20	Welcome address Michael Batey	10:45	Ilka Wittig, Frankfurt am Main Methods to study assembly and dynamics of protein complexes
	Waters Corporation Molecular imaging by mass spectrometry: Applications in biomedical research and drug discovery	11:10	Iris Finkemeier, Münster Mass spectrometry-based profiling of lysine acetylation and HDAC activity in plants
14:20	Klaus Dreisewerd Institute of Hygiene Brief introduction to MALDI-MS imaging and MALDI-2-MS imaging	11:35	Julia Bandow, Bochum Identification of targets and mechanisms of metalloantibiotics
		12:00 Peter James, Lund	
15:00	COFFEE BREAK AND LAB TOUR IN SMALL GROUPS		Modern technologies and their application to the diagnosis, prognosis and treatment of breast cancer
16:15 - 18:00	Demonstration of Experiments and data evaluation strategies via Team Viewer	12:30	LUNCH WORKSHOP III
	1. Simeon Vens-Cappell Institute of Hygiene Enhanced MALDI-MSI analysis of glycolipids 2. Jens Soltwisch, Eike U. Brockmann	13:30	Arndt Asperger, Bruker Complementary MALDI imaging solutions based on latest MALDI-TOF and -FTICR MS technology
	Institute of Hygiene MALDI-2-MSI analysis of bacterial metabolites with a Synapt G2-S	14:00	Marc Kipping, Waters Corporation An overview of past, present and future of data independent acquisition strategies
	3. Dennis Trede SCILS Conceptual strategies for visualisation and analysis of mass spectrometry imaging data	15:00	Gottfried Pohlentz, Münster Efficient analysis of proteolytic peptides and glycopeptides using ion mobility separations (IMS) and subsequent low energy collision-induced

15:30

dissociation

SERVA Electrophoresis

Günter Thesseling, Reiner Westermeier,

Protein electrophoresis for professionals