

LC-MS group-of-interest Meeting

Wednesday, 13.3.2024; 14:00 – 17:00; Lecture Hall 16

Schedule:

14:00 – 14:15

- 1. Introduction of the candidates running for the role of the speaker of the LC-MS interest group**
- 2. Election of the future speaker**

Talks:

14:15

Hartmut Schlüter, University Medical Center Hamburg-Eppendorf

Where are the future challenges in LC-MS?

14:27

Anna Shevchenko, Max Planck Institute, Dresden

Absolute quantification of fluorescently-labelled proteins by mass spectrometry.

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14:39

Michael Desor, Waters GmbH, Eschborn,

Data independent analysis evolution exploring the use of high resolving power multi-reflecting time-of-flight mass spectrometry selectivity for metabolite identification

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14:51

Tobias Kipura, Institute of Biochemistry, University of Innsbruck:

Absolute quantification of amino acids and tryptophan metabolites from human serum and plasma.

15:03

Thomas Letzel, Analytisches Institut für Non-Target Screening:

Mass Spectrometric Non-Target Screening – Interdisciplinary Solutions and Data Handling

15:15 – 15:35

Coffee Break

15:35

Marcel Kwiatkowski, Institute of Biochemistry, University of Innsbruck:

Proteo-Metabo-Flux: Determination of histone acetylation reaction rates by LC-MS.

15:47

Ali Biabani: University Medical Center Hamburg-Eppendorf

Sample Displacement Batch Chromatography of Proteoforms

15:59

Michael B. Richter, Bundeswehr Institute of Pharmacology and Toxicology, Munich

Identification of disulfide-adducts of small molecule thiols in human plasma resulting from exposure to malodorants.

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16:11

Andreas Zellner, Technical University of Munich, Mass Spectrometry in Systems
Neurosciences, Freising.

Advancing clinical peptidome profiling in plasma with a robust high-throughput workflow.

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16:23

Florian Martin Richter, Hochschule Mannheim, CeMOS Institut für Analytische Chemie,
Mannheim.

Site-specific structural changes in long-term stressed monoclonal antibody revealed with DEPC covalent-labeling and quantitative mass spectrometry.

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16:35

Karin Yeoh, PreOmics GmbH, Planegg, Germany

Innovative high-throughput ENRICH-iST workflow facilitates fast and deep plasma and serum proteome profiling.

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16:47

Stefan Loroach, Medizinisches Proteom-Center Ruhr-Universität Bochum

Towards LC-MS-based Proteomics to Solutions for Crime Scene Investigations