

**MONDAY, December 03**

**9:00**                    **Arrival and Registration**

**10:30**                    **Opening and Welcome – Local Organizer (Nico Jehmlich)**

**Session 1: New methods and trends in metaproteomics (Chair: Dörte Becher)**

**10:45**                    **Manuel Kleiner** (North Carolina State, USA)  
*Metaproteomics methods to determine biomass contributions and carbon sources of species in microbial communities*

**11:15**                    **Dirk Benndorf** (Otto-von-Guericke University Magdeburg, Germany)  
*Speedup of metaproteomics pipelines - from samples to microbial community data in less than 24 hours*

**11:45**                    **Pratik Jagtap** (University of Minnesota, USA)  
*metaQuantome: An integrated, quantitative metaproteomics approach reveal connections between taxa, function & protein expression in microbiomes*

**12:00**                    **Lunch**

**Session 2: Intestinal microbiome – Part I (Chair: Martin von Bergen)**

**13:30**                    **Daniel Figeys** (University of Ottawa, Canada)  
*Metaproteomics in Inflammatory Bowel Disease and drug screening*

**14:00**                    **Robert Heyer** (Otto-von-Guericke University Magdeburg, Germany)  
*Analysis of patients with inflammatory diseases of the human gut using LC-MS/MS based metaproteome analysis*

**14:15**                    **Martin von Bergen** (Helmholtz-Centre for Environmental Research – UFZ, Germany) - *Verrucomicrobia and Desulfovibrionaceae benefit from high fat diet as detected by in vivo metabolic labelling*

**14:45**                    **Alessandro Tanca** (Porto Conte Recherche, Alghero, Italy)  
*Caloric restriction promotes functional changes involving short-chain fatty acid biosynthesis in the rat gut microbiota*

**15:00**                    **Catherine Juste** (INRA, France)  
*ProteoCardis: an intestinal metaproteome-wide association study of coronary artery disease*

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15:15	<b>Coffee break</b>
15:30	<b>Poster-Pitch</b> - Presentation of the posters (2 min each presenter) <i>Vote for the best presentation on a sheet – the best three presentations get a prize from MDPI</i>
16:15	<b>Poster Session</b>
18:30	<b>End Day 1</b>
19:30	<b>Christmas Market Leipzig (free attendance)</b>

## TUESDAY, December 04

### Session 2: Intestinal microbiome – Part II (Chair: Robert Hettich)

10:00	<b>Robert Hettich</b> (Oak Ridge National Laboratory, USA) <i>Leveraging microbial metaproteomics to characterize the development of the gut microbiomes metabolic network in preterm human infants</i>
10:15	<b>Goor Sasson</b> (Ben-Gurion University of the Negev, Israel) <i>Bovine energy harvesting from feed is correlated with rumen metaproteome composition</i>
10:30	<b>Live Hagen</b> (Norwegian University of Life Science, Norway) <i>Elucidating the functional roles rumen microbes using (meta)genome-guided metaproteomics</i>
10:45	<b>Simon Deusch</b> (University of Hohenheim, Germany) <i>Impact of prebiotics on the active fraction of the HIV-associated Gut Microbiota</i>
11:00	<b>John Gaby</b> (Norwegian University of Life Science, Norway) <i>Dietary Mannan Selectively Enriches and Activates Microbes in the Cecum and Colon of Pigs</i>
11:15	<b>Coffee Break</b>

### Session 3: Environmental & biotechnology microbiome (Chair: Dirk Benndorf)

11:30	<b>Felipe Bastida</b> (CEBAS-CSIC, Spain) <i>Global biogeography of soil proteins: understanding the biotic and abiotic factors shaping soil microbial communities</i>
12:00	<b>Christian Büttner</b> (University of Applied Sciences Coburg, Germany) <i>Complex microbial interaction patterns during anaerobic degradation in 16 biogas plants discovered by network analyses of metaproteome data sets</i>
12:15	<b>Augustin Geron</b> (University of Stirling, United Kingdom) <i>Bioinformatic workflow in environmental metaproteomics: metagenome derived protein databases and their biological interpretation discrepancies</i>
12:30	<b>Daniela Zühlke</b> (University of Greifswald, Germany) <i>Microbial community structure and expression of antibiotic resistance determinants in urban wastewater treatment plants</i>
12:45	<b>Lunch</b>

- 13:30**      **Doreen Schultz** (University of Greifswald, Germany)  
*Establishment of a metaproteomics pipeline to unravel the mechanisms of polysaccharide degradation of particle-associated microbial communities*
- 13:45**      **Henning Schiebenhöfer** (Robert-Koch-Institute, Germany)  
*Prophane – Metaproteomic Data Analysis and Interpretation Made Simple*
- 14:00**      **Guillermina Hernandez Raquet** (LISBP – INRA)  
*Deciphering the temporal dynamics of lignocellulolytic enzymes in microbial consortia derived from cow rumen and termite gut throughout wheat straw degradation*
- 15:00**      **Coffee break**
- Contest: Multi-Omics study of microbiome samples**  
(Chair: Nico Jehmlich & Dirk Benndorf)
- 16:00**      **Open discussion**
- 17:30**      **Congress Dinner**  
Restaurant Patakan (Gondwanaland, Zoo Leipzig)

## WEDNESDAY, December 05

### Session 4: Integrative multi-OMICS & bioinformatics (Chair: Thilo Muth)

- 10:00**      **Timothy Griffin** (University of Minnesota, USA) **and Magnus Arntzen** (Norwegian University of Life Science, Norway)  
*Multi-omic informatics for characterizing microbiomes and their role in health disease and environment*
- 10:15**      **Pratik Jagtap** (University of Minnesota, USA)  
*Survey of metaproteomics software tools for functional microbiome analysis*
- 10:30**      **Praveen Kumar** (University of Minnesota, USA)  
*Slice and Splice: An accessible Galaxy-based metaproteomic database sectioning approach improves taxonomic and functional microbiome characterization*
- 10:45**      **Bart Mesuere** (University of Ghent, Belgium)  
*Unipept 4.0: functional analysis of metaproteome data*
- 11:00**      **Coffee break**

### Session 4: Integrative multi-OMICS & bioinformatics – Part II (Chair: Thilo Muth)

- 11:15**      **Johannes Werner** (Leibniz Institute of Baltic Sea, Germany)  
*mPies: a novel tool for generating reproducible annotated protein databases for metaproteomics*
- 11:30**      **Jinqiu Xiao** (Max Planck Institute of Psychiatry, Germany)  
*Metagenomic Taxonomy-Guided Database-Searching Strategy for Improving Metaproteomic Analysis*
- 11:45**      **Judson Hervey** (Naval Research Laboratory, USA)  
*Sipros Ensemble: a Robust Database Search Application for Complex Human and Environmental Metaproteomes*

- 12:00**      **Benoit Kunath** (LCSB Luxembourg)  
*Meta-omics integration generates a more comprehensive database and enhances proteins identification*
- 12:15**      **Olivier Pible** (CEA, DRF/Joliot/SPI/Li2D, France)  
*A large-scale quality assessment of taxonomy and assembly databases to select genomes and proteomes suitable for meta-omics*
- 12:30**      **Lunch**
- Session 5: Modelling and managing of microbial communities (Chair: Florian Centler)**
- 13:30**      **Florian Centler** (Helmholtz-Centre for Environmental Research -UFZ; Germany)  
*Flux Balance Analysis modeling going META*
- 13:45**      **Sabine Koch** (Max-Planck-Institute for Dynamics of Complex Technical Systems, Germany) - *The RedCom approach for metabolic modeling of microbial communities and its application for analyzing experimental datasets from anaerobic digestion*
- 14:00**      **Neeraj Kumar** (Technical University of Munich, Germany)  
*MIMIC- A new computational method for automated generation of minimal bacterial consortia based on functional metagenomic profiles*
- 14:15**      **Susann Müller** (Helmholtz-Centre for Environmental Research -UFZ; Germany)  
*Can microbial communities be controlled in managed systems?*
- 14:30**      **Final Discussion**
- 15:00**      **Closing Remarks**