



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

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

TUESDAY, December 04

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

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

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

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

- 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 Plack 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

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- 12:00** **Tim van den Bossche** (VIB – Ghent Center for Medical Biotechnology, Belgium)
Prediction-based reduction of the search space leads to increased identifications in metaproteomics without impacting sensitivity
- 12:15** **Benoit Kunath** (LCSB Luxembourg)
Meta-omics integration generates a more comprehensive database and enhances proteins identification
- 12:30** **Olivier Pible** (CEA, DRF/Joliot/SPI/Li2D)
A large-scale quality assessment of taxonomy and assembly databases to select genomes and proteomes suitable for meta-omics
- 12:45** **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**