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 Richerche, 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
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/SP/2D)  
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