

**Please note that this program is preliminary and it may be subjected to update**

**The "2nd International Metaproteomics Symposium: what can we learn about microbial communities and their functions?"**

**Alghero (Italy) - June 14-16, 2017  
Porto Conte Ricerche**

**Wednesday, June 14**

**afternoon**      **Arrival and Registration**

**Opening and Welcome address**

**Session 1: New methods and trends in metaproteomics**

Chair: **Paul Wilmes** - *University of Luxembourg, Luxembourg*

**Robert Hettich**, *Oak Ridge National Lab, Oak Ridge, TN, USA*

**Alessandro Tanca**, *Porto Conte Ricerche, Alghero, Italy*

Up to **3 short talks** from selected participants

**Discussion - Q&A**

**Coffee and tea break**

**evening**      **Workshop 1: metaproteome biodiversity analysis with Unipept**

Coordinator: **Bart Mesuere** - *Ghent University, Belgium*

Description:

The Unipept workshop will give an overview of the different functionalities of the Unipept application; from exploring the biodiversity of a single sample to setting up a high-throughput data-analysis pipeline.

**Q&A and hors d'oeuvres**

**Thursday, June 15**

**morning**

**Session 2: Metaproteomics in health and disease**

Chair: **Sergio Uzzau** - *Porto Conte Ricerche, Alghero, Italy*

**Dennis Wolan** , *The Scripps Research Institute, La Jolla, CA, USA*

**Paul Wilmes**, *Luxembourg Centre for Systems Biomedicine, University of Luxembourg*

Up to **3 short talks** from selected participants

**Discussion - Q&A**

**Coffee and tea break**

**Session 3: Metaproteomics in environmental biotechnology and animal science**

Chair: **Dirk Benndorf** - *Otto von Guericke University, Germany*

**Jana Seifert** - *Universität Hohenheim, Stuttgart, Germany*

**Speaker TBA**

Up to **3 short talks** from selected participants

**Discussion - Q&A**

**Lunch break**

**evening**

**Workshop 2: Quantitative mass spectrometry and its potential for metaproteomics**

Coordinator: **Daniela Pagnozzi** - *Porto Conte Ricerche, Alghero, Italy*

Guests: **Lars Kristensen**- *Thermo Fisher Scientific*

**Robert Hettich** - *Oak Ridge National Lab, Oak Ridge, TN, USA*

Description:

The workshop will give an overview on quantitative mass spectrometry-based applications covering untargeted relative quantification methods for discovery studies and targeted methods for validation studies as well as label free and label based approaches. Specifically the following applications will be covered: Label free quantification by data dependent acquisition (DDA), Label free quantification by Data independent acquisition (DIA), Multiplexed quantification by isobaric tandem mass tag (TMT) labeling reagents, Multiplexed quantification by dimethyl labeling, targeted quantification by parallel reaction monitoring (PRM), and targeted quantification by selected ion monitoring (SIM).

Case studies will also be presented.

**Q&A and hors d'oeuvres**

**Friday, June 16**

**morning**

**Session 4: Bioinformatics for metaproteomics**

Chair: Lennart Martens - *Ghent University, Ghent, Belgium*

**Pratik Jagtap** - *University of Minnesota, Minneapolis, MN, USA*

**Haixu Tang** - *Indiana University, Bloomington, IN, USA*

Up to **3 short talks** from selected participants

**Discussion - Q&A**

**Coffee and tea break**

**Workshop 3: The MetaProteome Analyzer software - part I**

Coordinator: **Dirk Benndorf** - *Otto von Guericke University, Germany*

Description:

The MetaProteomeAnalyzer (MPA) is a software pipeline to analyze and visualize metaproteomics data. The new version 2.0 will be hosted soon, as a webservice of the German Network for Bioinformatics Infrastructure – de.NBI.

The workshop demonstrates the use of the MPA software as follows:

- Using multiple database search engines
- Grouping of protein identifications to metaproteins
- Metagenome annotation by BLAST
- Taxonomic and functional data analysis
- Comparison of multiple datasets

**Lunch break**

**evening**

**Workshop 3: The MetaProteome Analyzer software - part II**

Coordinator: **Dirk Benndorf** - *Otto von Guericke University, Germany*

Description:

Up to ten registered users can process own data within the MPA workshop using their own computers. The accounts for the MPA web service will be also available after symposium and offer full access to the software. Please register ([mpa@ovgu.de](mailto:mpa@ovgu.de)) and send us your spectrum files (MGF format) via file transfer until **May 15, 2016** (limited file size 1 GB, a link will be provided upon request).

**Q&A and hors d'oeuvres**