



# EuBIC Winter School 2019

15th – 18th January 2019, Hotel Mercure Kasprowy, Zakopane, Poland



**Programme**



<https://www.proteomics-academy.org/eubic-winter-school-2019>

# Day 1 – 15. January 2019

## Educational Day

Time	Title		
09:30 - 10:00	Welcome coffee & Registration		
10:00 - 10:30	Opening Session		
10:30 - 12:00	Introduction to computational mass spectrometry using OpenMS, Part I	Computational introduction into DIA	Label-free quantification: concepts and algorithms
12:00 - 13:00	Lunch Break		
13:00 - 14:30	Introduction to computational mass spectrometry using OpenMS, Part I (continued)	Computational introduction into DIA (continued)	Quantitative proteomics: statistics, clustering and complexes
14:30 - 14:45	Coffee Break		
14:45 - 16:15	Introduction to computational mass spectrometry using OpenMS, Part II	Computational introduction into DIA (continued)	Quantitative proteomics: statistics, clustering and complexes (continued)
16:15 - 16:30	Coffee Break		
16:30 - 18:00	Introduction to computational mass spectrometry using OpenMS, Part II (continued)	Computational introduction into DIA (continued)	Discussion about best practices and common pitfalls

For further information on the workshops, please see the electronic version of the programme or the winter school's webpage.

## Day 2 – 16. January 2019

### DIA and Standards

Time	Title	Speaker(s)
08:35 - 08:40	Morning Welcome and Announcements	
08:40 - 09:25	XCorDIA: a new database search engine to detect geentic variants from DIA data	Brian Searle
09:25 - 10:10	Developing the tools for the personalized medicine revolution: Using mass spectrometry for longitudinal molecular profiling	Hannes Röst
10:10 - 10:30	Coffee Break	
10:30 - 11:15	Label-free Quantification of Complex Proteomes using Ion-Mobility-based DIA	Stefan Tenzer
11:15 - 12:00	Bioinformatics for Proteomics - any open questions?	Martin Eisenacher
12:00 - 13:00	Lunch Break	
13:00 - 13:50	Poster flash talks	
13:50 - 14:20	Sponsor talk	SVA
14:20 - 18:20	Workshop Session (Coffee break at 15:30-15:50)	see workshop descriptions
18:20 - open end	Poster Session & Come Together	

### Parallel Workshops

<b>Stefan Tenzer</b>	Quality Control and Benchmarking of Label-Free Quantification Workflows with LFQBench
<b>Martin Eisenacher</b>	The essentials before and after spectrum identification: Selecting the appropriate database and inference strategy
<b>ProFI</b>	Discovering the open-source Proline software suite, a new efficient and user friendly solution for label-free quantification
<b>Thermo</b>	Proteome Discoverer 2.3 Workshop

## Day 3 – 17. January 2019

### Result Interpretation

Time	Title	Speaker(s)
08:35 - 08:40	Morning Welcome and Announcements	
08:40 - 09:25	STRING – Large-scale integration of data and text	Lars Juhl Jensen
09:25 - 10:10	Prosit: Proteome-wide prediction of peptide tandem mass spectra by deep learning	Mathias Wilhelm
10:10 - 10:30	Coffee Break	
10:30 - 11:15	Using phosphoproteomics data to study context-specific signalling	Evangelia Petsalaki
11:15 - 12:00	Insights into the multi-functioning proteome	Kathryn Lilley
12:00 - 13:00	Lunch Break	
13:00 - 13:30	Sponsor Talk: Novel DIA Data Analysis Workflow: Integration of De Novo Sequencing and Database Search	BSI
13:30 - 17:30	Workshop Session (Coffee break at 15:30-15:50)	see workshop descriptions
17:30 - 18:00	EuBIC Meeting	All new members are welcome
19:00 - open end	Social Event	

### Parallel Workshops

<b>Lars Juhl Jensen</b>	Network visualization with Cytoscape and stringApp
<b>Evangelia Petsalaki</b> (13:30 - 15:30)	SELPHI: using data-driven approaches for analysis of phosphoproteomics datasets
<b>Florian Meier</b> (15:50 - 17:30)	Advanced data acquisition methods with MaxQuant.Live
<b>BSI</b>	PEAKS X: A Complete Solution for Discovery Proteomics with DDA and DIA Support
<b>Matthias Wilhelm</b>	Validation of peptide identifications

## Day 4 – 18. January 2019

### Innovative methods

Time	Title	Speaker(s)
09:00 - 09:05	Morning Welcome and Announcements	
09:05 - 09:50	Ionbot: a novel, fully data-driven search engine for open modification and mutation searches	Sven Degroeve
09:50 - 10:20	YPIC - Young Proteomics Investigators Club	
10:20 - 10:50	Coffee Break	
10:50 - 11:35	Trapped ion mobility spectrometry: a new dimension for mass spectrometry-based proteomics	Florian Meier
11:35 - 12:00	Announcement: Best Flash Talk, Best Poster Award, Closing Remarks	
12:00 - 12:45	Lunch	
13:00	Shuttle Buses leaving	

### Organizers

Dominik Kopczynski Leibniz-Institut für Analytische Wissenschaften – ISAS – e.V. dominik.kopczynski@isas.de	Julian Uszkoreit Ruhr University Bochum julian.uszkoreit@rub.de
Wout Bittremieux University of Antwerp wout.bittremieux@uantwerpen.be	David Bouyssie Institute of Pharmacology and Structural Biology (CNRS) bouyssie@ipbs.fr
Viktoria Dorfer University of Applied Sciences Upper Austria viktoria.dorfer@fh-hagenberg.at	Marie Locard-Paulet Institute of Pharmacology and Structural Biology (CNRS) marie.locard@ipbs.fr
Veit Schwämmle University of Southern Denmark veits@bmb.sdu.dk	Alessio Soggiu Universita Delgi Studi di Milano alessio.soggiu@unimi.it
Sander Willems Ghent University sander.willems@ugent.be	

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