Pro–Met–
Proteomics and Metabolomics Facility

www.cemm.at

June 25th/26th, 2018

Translational Proteomics

Minisymposium and Workshops

An interesting mix of scientific lectures and practical workshops in the field of translational and applied MS-based proteomics.

June 25th, 2018, 12:30-17:00

Practical Hands-on Workshops

on Tips & Tricks to maximize Q Exactive performance, Proteome Discoverer data analysis and Data-Independent Acquisition (DIA) on Orbitrap platforms.

June 26th, 2018, 9:00-16:30

Going Applied and Translational

with a full day of highly interesting scientific talks from world leaders which will reach out to both technologist and biologist!

Snacks and drinks on the CeMM terrace will top off the event.

Hosts André C. Müller (CeMM), Viktoria Dorfer (FHOÖ) & Klaus Kratochwill (MUW)

Venue Pro-Met-Facility, Research Center for Molecular Medicine of the Austrian Academy of Sciences, Lazarettgasse 14, AKH BT 25.3, Seminar Rooms Level 8, 1090 Vienna, Austria

For further information and registration, please visit cemm.at/promet

Ce–M–M–
Research Center for Molecular Medicine
of the Austrian Academy of Sciences

ÖAW
AUSTRIAN ACADEMY OF SCIENCES

UNIVERSITY OF APPLIED SCIENCES UPPER AUSTRIA

MEDIZINISCHE UNIVERSITÄT WIEN

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Translational Proteomics
Program: Minisymposium and Workshops

Monday June 25th
Practical Hands-on Workshops

12:30 Registration
13:00 Workshops
13:00 **Tips and tricks to make the most of your Q Exactive mass spectrometers**
Lars Kristensen, Thermo Fisher Scientific
13:30 **Proteome Discoverer Part 1: Overview and new features**
Bernard Delanghe, Thermo Fisher Scientific
14:30 Coffee break
15:00 **Proteome Discoverer Part 2: Label-Free-Quant and TMT quantitation**
Bernard Delanghe, Thermo Fisher Scientific
16:00 **Achieving the utmost DIA performance by using Orbitrap mass spectrometry platforms and Spectronaut Pulsar software**
Claire Dauly, Thermo Fisher Scientific and Florian Marty, Biognosys
17:00 End

Tuesday June 26th
Going Applied and Translational

09:00 Welcome coffee
09:30 Introduction – André Mueller

Session 1 – Technology Advancement

09:45 **Keynote 1: Deep proteome and phosphoproteome analysis on the Q Exactive HF-X**
Jesper Velgaard Olsen,
University of Copenhagen, Denmark
10:30 **High throughput signaling pathway monitoring based on fast LC-PRM analyses**
Sébastien Gallien,
Thermo Fisher Scientific, France
11:00 Coffee break
11:15 **Identifying and validating chimeric spectra using CharmeRT**
Viktoria Dorfer, FH OÖ Hagenberg, Austria
11:45 **DpD – a new DIA workflow combining the depth of resource spectral libraries with iRT-precision of project-specific spectral libraries**
Florian Marty, Biognosys, Switzerland
12:15 Lunch break

Session 2 – Translational Aspects

13:30 **Systematic assessment of the functional status of mitochondria: can it improve the prediction of cellular responses to drug effects?**
Christopher Gerner,
University of Vienna, Austria
14:00 **Keynote 2: Neo-epitope peptide identification supporting cancer vaccine generation**
Christopher Rose, Genentech, USA
14:45 Coffee break
15:00 **Keynote 3: Connecting genotype and molecular phenotype by proteogenomics**
Janne Lehtiö, Karolinska Institut, Sweden
15:45 **Keynote 4: Peptide level turnover measurements enable the study of proteoform dynamics**
Bernhard Küster,
Technical University Munich, Germany
16:30 Concluding words
16:35 Drinks & snacks on the CeMM terrace
19:00 End