Proteome Discoverer 3.2 training workshop November 19-21, 2024

London 13:00-16:00/Berlin 14:00-17:00

You are invited to join a virtual Thermo Scientific™ **Proteome Discoverer™ software** workshop series delivered via Microsoft® Teams. The workshop is designed to update the user of Proteome Discoverer (PD) software on the newly added features in PD 3.2 version.

Session 1 is an overview of **PD 3.2 features** and will cater predominantly for novice users: it should help users get familiar with basic tasks, such as study creation, default workflows, processing simple data sets and reviewing the results with graphical outputs.

Session 2 will explain how quantitation is performed in PD, demonstrate a study setup for different quantitation approaches and conclude by introducing **TMTpro 32/35 plex.**

Session 3 is dedicated to **CHIMERYS™** intelligent algorithm for identification and **DIA-based quantitation.** We will also discuss individual nodes and parameter settings, concluding with practical tips to help you become a proficient Proteome Discoverer software user.

Participating with the most recent PD 3.2 version (demo license sufficient) is recommended. Demo access to CHIMERYS cloud service can also be obtained. Details will be provided shortly after the registration deadline, together with the links to the training session and download of the training materials.

Registration link

Registration deadline November 14, 2024. Sessions will be recorded and made available to all registered participants.

Agenda

Session 1 (~3.0 hours)

1. **What's new in PD 3.2**
2. **Getting started**
   - Create a Study
   - FASTA file management
   - Default workflows
3. **Processing simple data files**
   - Workflow node settings
   - Specifics of different MS2 data types
   - Validation of peptide identifications
   - Protein grouping
   - Reviewing results
4. **Processing complex data files**
   - Processing Tribrid data
   - Multiconsensus report
   - Iterative searches

Session 2 (~3.0 hours)

1. **Understanding quantification in PD**
   - Experimental design, study factors, replicates
   - Protein abundance and ratio calculations
2. **Validating ratios and statistics**
   - t-test (background based) method
   - Volcano plot
3. **Quan experiment setup**
   - Label-free quantitation
   - SILAC
   - TMT
4. **Introducing TMTpro 32/35 plex**

Session 3 (~3.0 hours)

1. **Introducing CHIMERYS intelligent algorithm**
   - Spectrum-centric deconvolution of chimeric spectra
   - The CHIMERYS workflow
   - Contribution-based quantification in MS2
   - Exemplary results for DDA, PRM and DIA data
2. **Identifications with CHIMERYS**
   - CHIMERYS node in PD
   - Discussion of parameters
   - Search space considerations
   - Processing time considerations
3. **Quantitation with CHIMERYS**
   - Match-between-runs
   - CHIMERYS inclusion file
4. **Nodes overview**
5. **Tips & Tricks**

About the presenters:

Martin Frejno In his role as Chief Executive Officer, Martin is responsible for the long-term strategy of MSAID. He is based in Cologne, Germany.

Daniel Zolg In his role as Chief Operating Officer, Daniel oversees the operations at MSAID. He is based in Garching, Germany.

Michaela Scigelova provides customer support to Proteome Discoverer users. She has been working at Thermo Fisher Scientific at various roles since 2000. She is based in Bremen, Germany.

Learn more at **thermofisher.com/proteomediscoverer**

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