



Proteome Discoverer Workshop

September 27-29, 2022

London 13:00 – 17:00

Berlin 14:00 – 18:00

You are being invited to join a virtual Proteome Discoverer Training Workshop delivered via Microsoft Teams.

The workshop is designed to get novice/intermediate users up to speed with Proteome Discoverer (PD) sw package. There are three interactive on-line sessions planned, featuring hands-on exercises, discussion of PD features, parameters, and optimized settings. To get the most out of the hands-on sessions having either of the following versions PD 2.4, 2.5 or 3.0 up and running is recommended.

The sessions should allow ample time for the participants to get their PD-related questions answered in real time. We will also review the new features in PD 3.0 (the version just released). For detailed agenda please refer to the next page.

Registration deadline is September 23, 2022. Links to individual training sessions and for downloading the training materials will be send out on September 26, 2022. The sessions will be recorded and recordings made available to all registered participants.

Please register using the link below.

[Registration link](#)

Learn more at thermofisher.com/proteomediscoverer
or email us at Pd.support@thermofisher.com

Agenda

Session 1 (~4 hours)

1. **Getting started**
 - Create a Study
 - FASTA file management
 - Default workflows
2. **Processing simple data files**
 - Workflow node settings
 - Specifics of different MS2 data types
 - Validation of peptide identifications
 - Protein grouping
3. **Reviewing results**
 - Results tables
 - Filtering results
 - Graphics
 - Result Summaries
 - Exporting data from PD
4. **Processing complex data files**
 - Processing Tribrid data
 - Multiconsensus report
 - Iterative searches
 - Chimeric spectra

Session 2 (~4 hours)

1. **Spectral libraries**
2. **INFERYS**
3. **CHIMERYs**
4. **Maximizing IDs**
 - Working with QC (human) dataset
5. **PTM analysis**
 - Modifications and Isoforms results tables
 - Review of phosphopeptide data set
6. **Annotations/Pathways**
 - Partial reprocessing
7. **Nodes overview**
 - Parameters of processing/consensus nodes discussed
 - Recommended parameter settings

Session 3 (~4 hours)

1. **Understanding quantification in PD**
 - Setting up an LFQ experiment
 - Nested x non-nested design
 - Study factors
 - Replicates
2. **Quantification experiment setup examples**
 - SILAC
 - TMT simple
 - TMT with study factor
3. **Validating ratios and statistics**
 - ANOVA
 - Background protein t-test
 - Volcano plots
 - PCA
4. **TMT experiment hands-on**
 - (only if time allows)