



Proteome Discoverer Workshop

March 8-11, 2022 10:00-13:00 CET (GMT+1)

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

The workshop is designed to get novice to intermediate users up to speed with PD 2.5. The workshop is planned as four interactive on-line sessions, focusing on hands-on exercises as well as the discussion of PD features, parameters, and optimized settings. That should also allow ample time for the participants to get their PD-related questions answered in real time.

Please refer to the agenda on the second page and registration link below.

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<https://forms.office.com/r/EihzHwb9WX>

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

thermo scientific

Agenda

Session 1 (~3 hours)

Agenda

- 1. Getting started**
 - Study
 - Default workflows
- 2. Processing data - basics**
 - Identification
 - Different MS2 types
 - Hands-on** working with simple LC-MS/MS data sets
- 3. Reviewing results – Hands-on**
 - Results tables
 - Filtering results
 - Graphics
 - Result Summaries
 - Exporting data from PD

Session 3 (~3 hours)

Agenda

- 1. PTM analysis**
 - ptmRS
 - Modifications and Isoforms results tables
 - Review of phosphopeptide data set - **Hands-on**
- 2. Partial Reprocessing Hands-on**
 - Adding protein annotation/pathways
- 3. Understanding quantification in PD**
 - Study factors
 - Handling replicates
 - Calculating ratios
- 4. Quantification experiment setup Hands-on**
 - Label-free quan (LFQ)
 - SILAC
 - TMT/iTRAQ
- 5. Validating ratios and statistics**
 - ANOVA
 - Background protein t-test
 - Volcano plots
 - PCA

Session 2 (~3 hours)

Agenda

- 1. Processing more complex data files**
 - Hands-on**
 - Processing tribrid data
 - Multiconsensus report
 - Iterative searches
 - Spectral library/Chimeric spectra
- 2. Maximizing IDs**
 - Hands-on** working with HeLa dataset
- 3. Nodes overview**
 - Parameters of processing/consensus nodes discussed
 - Recommended parameter settings

Session 4 (~3 hours)

Agenda

- 1. Considerations related to TMT quan**
 - Sample complexity
 - Multiplexing
 - Instrument acquisition methods
 - Data processing
- 2. Reporter ion quantitation Hands-on**
 - Create/edit quan method
 - Study setup, study factor definition
 - Study variable selection, ratios
- 3. Processing TMT 10plex data**
 - Hands-on** working with TKO TMT 10plex data set
 - Reporter Ions Quantifier node parameters explained
 - Comments on processing SPS MS3 data
 - Comments on processing TMT-labeled phosphopeptides