Practical TMT Workshop – Labelling, Data Acquisition, Data Processing
September 22-23, 2022

Berlin　　　**15:00 – 18:00**
London　　**14:00 – 17:00**

You are being invited to join a Practical TMT Workshop delivered via Microsoft Teams.

Thermo Fisher Scientific experts will cover the areas of the labelling chemistry, data acquisition methods, and data processing. There are two interactive on-line sessions planned, featuring presentations, discussion of questions, parameters, and optimized settings, as well as hands-on data processing in Proteome Discoverer. Having either of the following versions PD 2.4, 2.5 or 3.0 installed and licensed is recommended for the hands-on data processing session.
For detailed agenda please refer to the next page.

Registration deadline is September 16, 2022. Links to individual training sessions and for downloading the training materials will be send out on September 19, 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**

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Agenda

Session 1 (~3 hours)

Adapting EasyPep MS sample preparation and TMT labeling reagents for higher throughput platforms

Amarjeet Flora

1. Simplified, standardized, and scalable chemistry for reproducible proteomic sample preparation
2. Overview of TMT and TMTpro mass tag chemistry for multiplex quantitation
3. Sample preparation workflow tools to increase the depth of coverage and improve protein quantitation
4. Sample prep automation and reagent formats for higher throughput

LC-MS acquisition strategies for the analysis of TMT samples using the Orbitrap Tribrid and Exploris platforms

Jenny Ho

1. nanoLC gradient recommendations
2. MS2 acquisition using Orbitrap Exploris MS platforms
3. SPS MS3 and SPS MS3 with Real-Time Search acquisition strategies using Orbitrap Tribrid MS platforms

Session 2 (~3 hours)

TMT data processing in Proteome Discoverer

Michaela Scigelova

1. Workflows and parameter settings
2. Ratio calculation and statistics
3. TMT-labelled phosphopeptides
4. IodoTMT

5. Practical session
   a. TMT 10plex sample
   b. Editing quan methods
   c. Downloading FASTA file
   d. Study setup
   e. Study factors
   f. Workflow settings
   g. Sample groups, ratios
   h. Reviewing the results

6. Multiplexed TMT experiments
   a. Thresholds in Reporter Ions Quantifier node
   b. Normalization across multiple sets

7. Practical session
   Multiplexed TMT
   Multiplexed TMT with biological replicates, "pool" sample, and fractions

Amarjeet Flora is a research scientist at Thermo Fisher Scientific part of a mass spectrometry reagent development group with expertise in proteomic sample preparation based in Rockford, IL, USA.

Jenny Ho is a senior proteomics applications specialist at Thermo Fisher Scientific based in the Life Science Mass Spectrometry demonstration facility, in the UK.

Michaela Scigelova provides customer support to Proteome Discoverer users at Thermo Fisher Scientific in Bremen, Germany.

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