

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

[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.

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