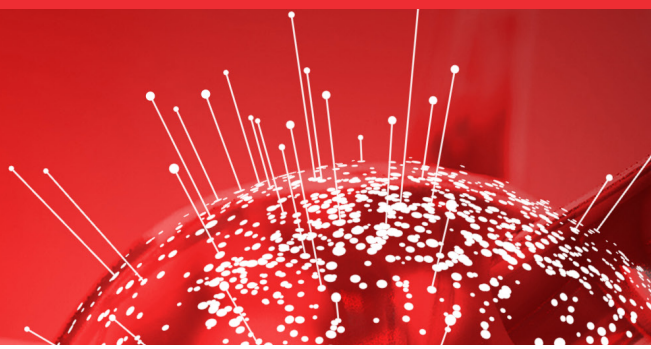
thermoscientific

# Be Selective
## Rise above the noise

**2018 North America Mass Spec Users' Meeting**



## Philadelphia, PA

October 2, 2018 Philadelphia Marriott West | 111 Crawford Avenue | West Conshohocken

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|---|---|---|---|
| 8:00 AM | **Continental Breakfast and Name Badge Pick-up** | | |
| 9:00 AM | **Welcome and Introductions** | | |
| 9:15 AM | **Plenary Lecture: Glycomics and Glycoproteomics using a Thermo Scientific™ Q Exactive™ HF MS and GlyReSoft**<br>*Joe Zaia, Ph.D.*, University of Boston | | |
| 10:00 AM | **Be Selective - Rise Above the Noise with Mass Spectrometry Advancements**<br>*Iain Mylchreest, Ph.D.*, Thermo Fisher Scientific | | |
| 10:35 AM | **Coffee Break** | | |
| | **Breakout Room 1** | **Breakout Room 2** | **Vendor Fair** |
| | **Proteomics and BioPharma** | **Metabolomics and Small Molecule Analysis** | |
| 11:00 AM | Deconstructing Assemblies of Membrane Proteins through Native Mass Spectrometry<br>*Kallol Gupta, Ph.D.,* Yale School of Medicine | Profiling Sphingolipid Metabolism: Tracer Metabolomics and Pharmacologic Inhibition<br>*Erik Allman, Ph.D.,* Janssen Research and Development, Patterson Lab, Penn State | |
| 11:30 AM | Assessing Biosimilarity of an Intact Monoclonal Antibody Drug by Simultaneously Monitoring Charge Heterogeneity and Glycoform Profile using Thermo Scientific™ Orbitrap™ Native LC-MS<br>*Fred Zinnel, Ph.D.*, Thermo Fisher Scientific | Novel $MS^n$ Data Acquisition Approaches for Metabolite Identification<br>*Jeffrey Gilbert, Ph.D.*, Dow AgroSciences | |
| 12:00 PM | **Lunch** | | |
| | **Software Workshop** | | |
| 1:00 PM | **Thermo Scientific™ Proteome Discoverer™ Software: A Deep Dive into Label Free Quantitation Including DDA+ and Tandem Mass Tags (TMT) Workflows**<br>*Christa Feasley, Ph.D.,* Thermo Fisher Scientific | **Discovery Workflows for Metabolism and Metabolomics with Thermo Scientific™ Compound Discoverer™ Software**<br>*Daniel Hermanson, Ph.D.,* Thermo Fisher Scientific | **Meet with representatives and our trusted service and solutions providers to ask questions, provide valuable feedback and gain more knowledge at our Vendor Fair.** |
| | Exploring the proteome without the right tools and knowing how to use them to their fullest can be frustrating and unproductive. In this workshop, you will learn how to optimize two workflows in the Proteome Discoverer software, one of the most powerful tools for proteomics research: Using an example dataset from the Thermo Scientific™ Q Exactive™ HF-X MS, the Label Free Quantitation (LFQ) section will cover data dependent acquisition plus, available templates, and how to optimize parameters in the processing and consensus workflows. The Tandem Mass Tags (TMT) session will cover data collection on a Thermo Scientific™ Orbitrap Fusion™ Lumos™ Tribrid™ MS with synchronous precursor selection (SPS). Other tools, such as quality control and data visualization, will also be addressed. No computer needed. | Embark on a journey into some of the most useful tools in Compound Discoverer 3.0 software. We will explore workflow nodes for drug metabolism and metabolomics, followed by data processing, visualization, and result filtering. Learn how to annotate compounds using the tools built into Compound Discoverer software, including mzCloud™, mzLogic, and FISh scoring. No analysis is complete without data export so we will discuss options to build Inclusion/Exclusion lists, use of Thermo Scientific™ TraceFinder™ software databases, and create custom reports. No computer needed. | |
| 2:45 PM | **Coffee Break** | | |
| 3:15 PM | **Return to Workshop** | | |
| 4:00 PM | **Wrap Up** | | |

Register at **thermofisher.com/MSUsersMeeting**



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