

Be Selective

Rise above the noise

2018 North America
Mass Spec Users' Meeting

Bethesda, MD

October 4, 2018 Bethesda North Marriott Hotel & Conference Center | 5701 Marinelli Road | Rockville

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 <i>Joe Zaia, Ph.D., University of Boston</i>		
10:00 AM	Be Selective - Rise Above the Noise with Mass Spectrometry Advancements <i>Iain Mylchreest, Ph.D., Thermo Fisher Scientific</i>		
10:35 AM	Coffee Break		
	Breakout Room 1	Breakout Room 2	Vendor Fair
	Proteomics	Metabolomics and Small Molecule Analysis	
11:00 AM	Deconstructing Assemblies of Membrane Proteins through Native Mass Spectrometry <i>Kallol Gupta, Ph.D., Yale School of Medicine</i>	Re-inventing the Metabolomics Untargeted Workflow with the Thermo Scientific™ Orbitrap ID-X™ Tribrid™ MS <i>Ioanna Ntai, Ph.D., Thermo Fisher Scientific</i>	
11:30 AM	FAIMS Ion Magic – Now You See Me <i>Pierre Thibault, Ph.D., Université de Montréal</i>	Systems Biology Profiling for Identification of Biomarkers from Exposure to Carfentanil <i>Elizabeth Dhummakupt, Ph.D., US Army</i>	
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 <i>Christa Feasley, Ph.D., Thermo Fisher Scientific</i>	Discovery Workflows for Metabolism and Metabolomics with Thermo Scientific™ Compound Discoverer™ Software <i>Daniel Hermanson, Ph.D., Thermo Fisher Scientific</i>	
	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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