

Be Selective Rise above the noise

2018 North America
Mass Spec Users' Meeting

Burlingame, CA

September 19, 2018 San Francisco Airport Marriott Waterfront

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| 8:00 AM | Continental Breakfast and Name Badge Pick-up | | |
| 9:00 AM | Welcome and Introductions <i>Jack Cunniff, Ph.D.</i> , Thermo Fisher Scientific | | |
| 9:15 AM | Be Selective - Rise Above the Noise with Mass Spectrometry Advancements <i>Ken Miller</i> , Thermo Fisher Scientific | | |
| 9:45 AM | Plenary Lecture: Isotope Filtering Combined with Novel MSⁿ Data Acquisition for Metabolite Identification <i>Jeff Gilbert, Ph.D.</i> , Dow AgroSciences | | |
| 10:25 AM | Coffee Break | | |
| | Breakout Room 1 | Breakout Room 2 | Vendor Fair |
| | Metabolism, Food, and Small Molecule Quantitation and Characterization | Classical Proteomics, Metabolomics and Biopharma Characterization | |
| 10:45 AM | Enhanced Metabolite Identification using Thermo Scientific™ Orbitrap™ Tribrid™ Mass Spectrometer <i>Shuguang Ma, Ph.D.</i> , Genentech | In-depth Characterization of In Vivo Biotransformations for Intact Antibody-drug Conjugates by High-resolution Accurate-mass Mass Spectrometry <i>Jintang He, Ph.D.</i> , Genentech | |
| 11:15 AM | The Thermo Scientific™ Q Exactive™ MS in the Drug Metabolism Lab <i>Ron Aoyama, Ph.D.</i> , Gilead | Toward Assessing the Critical Quality Attributes of Biotherapeutics by HDX-MS <i>Jennifer Zhang, Ph.D.</i> , Genentech | |
| 11:45 AM | Developing Targeted NanoLC-MS/MS Methods to Monitor Growth Factors as Indicators of Prohibited Substance Abuse <i>Sophie Bromilow, Ph.D.</i> , UC Davis | Quantitative Map of Human Tissue Proteome <i>Lihua Jiang, Ph.D.</i> , Stanford University | |
| 12:15 PM | Lunch | | |
| 1:15 PM | Return to Breakouts | | Meet with representatives and our trusted service and solutions providers to ask questions, provide valuable feedback and gain more knowledge at our Vendor Fair. |
| 1:25 PM | Unknown Identification Has Never Had It So Good. Thermo Scientific™ Compound Discoverer™ Software Takes Unknown Analysis to a Whole New Level with Newly Integrated Annotation Tools <i>Ralf Tautenhahn, Ph.D.</i> , Thermo Fisher Scientific | Enhance your Mass Spec Sensitivity by 10X+ <i>Daojing Wang, Ph.D.</i> , Newomics Inc. | |
| 1:55 PM | A New Flavor for Flavonoid Analysis: A Class-based MS ⁿ Approach <i>Reiko Kiyonami, Ph.D.</i> , Thermo Fisher Scientific | Assessing Biosimilarity of an Intact Monoclonal Antibody Drug by Simultaneously Monitoring Charge Heterogeneity and Glycoform Profile using Thermo Scientific™ Orbitrap™ Native LC-MS <i>Aaron Bailey, Ph.D.</i> , Thermo Fisher Scientific | |
| 2:25 PM | Solutions for Small Molecule Structure Analysis and Impurity ID using the Latest Mass Spectrometry Tools and Data Analysis Software/Database <i>Kate Comstock</i> , Thermo Fisher Scientific | Advances in Thermo Scientific™ Orbitrap™ Instrumentation for Native Top-down Analysis of Non-covalent Protein Complexes <i>Rosa Viner, Ph.D.</i> , Thermo Fisher Scientific | |
| 2:55 PM | The Thermo Scientific™ VetDrugs Explorer Collection: A Comprehensive Multi-class Veterinary Drug Analytical Workflow for a Variety of Animal Matrices <i>Ed George</i> , Thermo Fisher Scientific | Wide and Deep: New Reagents and Workflows for Multiplexed Quantification of the Phospho Proteome and Plasma Proteome <i>Rosa Viner, Ph.D.</i> , Thermo Fisher Scientific | |
| 3:25 PM | Wrap Up | | |

Register at thermofisher.com/MSUsersMeeting

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