

Be Selective Rise above the noise

2018 North America
Mass Spec Users' Meeting

New York, NY

October 24, 2018 Convene | 730 3rd Avenue

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| 8:00 AM | Continental Breakfast and Name Badge Pick-up | |
| 9:00 AM | Welcome and Introductions <i>Rich Klein, Thermo Fisher Scientific</i> | |
| 9:10 AM | Be Selective-Rise Above the Noise with Mass Spectrometry Advancements <i>Ken Miller, Thermo Fisher Scientific</i> | |
| 9:50 AM | Plenary Lecture: Deconstructing Assemblies of Membrane Proteins through Native Mass Spectrometry <i>Kallol Gupta, Ph.D., Yale School of Medicine</i> | |
| 10:30 AM | Coffee Break | Vendor Fair |
| 10:45 AM | The Whole Enchilada for Protein ID <i>Romain Huguet, Ph.D., Thermo Fisher Scientific</i> | |
| 11:15 AM | Improved Accuracy and Sensitivity for Multiplexed, Quantitative Proteomics using FAIMS <i>Devin Schweppe, Ph.D., Harvard Medical School</i> | |
| 11:45 AM | Integrative High-resolution Mass Spectrometry to Sequence the Human Exposome <i>Doug Walker, Ph.D., Mount Sinai</i> | |
| 12:15PM | Lunch | Meet with representatives and our trusted service and solutions providers to ask questions, provide valuable feedback and gain more knowledge at our Vendor Fair. |
| 1:00 PM | Raffle | |
| 1:15 PM | Thermo Scientific™ Orbitrap ID-X™ Tribrid™ Mass Spectrometer: Breaking the Bottleneck of Small Molecule Unknown Identification <i>Mark Sanders, Ph.D., Thermo Fisher Scientific</i> | |
| 1:55 PM | Comprehensive Tissue Analysis of Biotherapeutics and Targets with High Sensitivity <i>Jun Qu, Ph.D., SUNY Buffalo</i> | |
| 2:25 PM | Break | |
| 2:35 PM | Strategies for Analyzing Biomarkers Using Tag Triggers <i>Robert Salzler, M.S., Regeneron</i> | |
| 3:05 PM | Bayesian Confidence Intervals for Multiplexed Proteomics Integrate Ion-Statistics with Peptide Quantification Concordance <i>Martin Wuhr, Ph.D., Princeton University</i> | |
| 3:35 PM | Wrap-up and Final Raffle | |
| 4:00 PM | Adjourn | |

Register at thermofisher.com/MSUsersMeeting

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