

Thermo Fisher Scientific at ASMS 2021

Our scientific experts and collaboration partners are as excited as you are to attend ASMS in person this year. Join us during our technical workshops, attend our oral sessions, and check out our scientific posters. We hope you find this guide useful in planning your schedule.

Daily LC-MS software demos (Nov 1-4) in Booth 201 from 10:30 a.m. - 1:30 p.m. EST.

- BioPharma Finder™
- Proteome Discoverer™
- Compound Discoverer™

Workshops	Food safety
Biopharma	Metabolomics and lipidomics
Pharma	Proteomics and structural biology
Clinical research and forensic toxicology	Technology hardware
Environmental testing	Ornament giveaway

Visit us at the booth **#201**

Workshops

Breakfast Workshops

7-8:15 a.m. Room 118 AB
Seating is limited due to social distancing protocols.

Monday, November 1

Go beyond searching with artificial intelligence driven peptide identification

See how the newest version of Thermo Scientific Proteome Discoverer software redefines proteomics data analysis by leveraging artificial intelligence for deeper mining of proteomics data. This innovative approach substantially increases the identification rate and the number of unique peptide identifications, improves protein coverage and quantification capabilities, facilitates more efficient data acquisition schemes, and enables scientists to generate more biological insights from their existing and newly acquired data.

Speakers:

David Horn, Product Manager, Thermo Fisher Scientific
Martin Fresno, Co-founder and CEO, MSAID GmbH

Tuesday, November 2

Achieve in-depth small molecule characterization utilizing Orbitrap-based intelligent data acquisition

In this workshop, our expert speakers will lay out strategies that combine next generation technologies in mass spectrometry hardware and software innovations to achieve increased confidence for small molecule unknown analysis using a Thermo Scientific Orbitrap LX Tribrid mass spectrometers. Hear from expert users on the identification of botanical plant extracts, which present unique analytical challenges due to the abundance of isomers and analogs. Full characterization of botanical extracts is often required to determine authenticity and identify suspected toxicants. Learn about how the application of Real-Time Library Searching greatly increases efficiency and maximizes the likelihood that each scan provides vital, relevant information. This strategy decreases the need for additional runs and sample re-preparation, which is particularly valuable when sample and time are limited. This example highlights a broad method capable of increasing confidence using intelligent data acquisition to capture more low-abundance analytes for structure elucidation and on-the-fly identification of small molecules.

Speakers:

Brandon Ellis, Product Manager, Thermo Fisher Scientific
Vincent Sica, Senior Scientist, Procter & Gamble

Wednesday, November 3

Bringing Multi-Attribute Method (MAM) to the next level

The multi-attribute method (MAM) offers the potential to reduce the number of traditional LC-MS/MS assays and accelerate the rate of bringing high quality biopharmaceuticals to market. However, the implementation of MAM is hindered by the lack of comprehensive and fit-for-purpose solutions. Join us to learn a holistic, compliance-ready MAM platform that enables deployment of MAM across all stages of biopharmaceutical development and manufacturing with seamless knowledge sharing at global scale.

Speakers:

Yi Zhang, Ph.D, Vertical Marketing Manager, Pharma & BioPharma, Thermo Fisher Scientific
Hao Yang, Ph.D, Senior Product Applications Specialist, Pharma & BioPharma, Thermo Fisher Scientific

Thursday, November 4

Overcoming the challenges of the targeted quantitative landscape

(All live attendees will be given a Thermo Scientific TSQ Altis Plus MS building blocks giveaway)

Excel in productivity using Thermo Scientific TSQ Plus mass spectrometers

Rapidly changing regulatory and clinical research requirements demand adaptive targeted quantitative workflow solutions to maintain productivity. The innovative hardware and software advancements incorporated into the TSQ Plus mass spectrometers are ideally suited to address throughput, sensitivity, and robustness while simplifying the operation. This workshop will demonstrate how the new features combine with the existing platform enabling users to excel in quantitative productivity in a range of market applications.

Detection of Intra-Articular Corticosteroids

The financial impact of equine lameness is a significant influence for determining the use of clinical medication choices in horse racing. The equine regulatory environment requires strict control for the use of potent anti-inflammatory medications. The University of Kentucky – Equine Analytical Chemistry Laboratory has selected the Thermo Scientific™ TSQ Altis Triple Quadrupole Mass Spectrometer to detect this group of compounds at very low concentrations in biological matrices. Using this platform, we can detect the analytical drug targets, with the validated confirmatory analysis. This provides a state-of-the-art multi-functional instrument for anti-doping control.

Speakers:

Neloni Wijeratne, Product Manager, Thermo Fisher Scientific
Abigail Burrows, Ph.D, Post-Doctoral Scholar, University of Kentucky-Gluck Equine Research Center

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Biopharma

Oral presentations

2:50-3:10 p.m., Nov 1, Ballroom B Streamlined workflow for complete characterization of synthetic oligonucleotides, impurities and their degradation products by IPRP-LC-HRAM MS/M

3:50-4:10 p.m., Nov 1, Ballroom B Leveraging Mass Spectrometry for the Characterization of Multispecific Antibody Aggregation

Posters

MP-282 Adeno-associated virus host cell protein profiling using microflow separation on a UHPLC-HRAM MS platform

TP-283 Characterization of Adeno-Associated Viral assemblies on an Ultra-High Mass Range Hybrid Quadrupole-Orbitrap Mass Spectrometer

TP-278 Multiple ion activations and proton transfer charge reduction facilitate the characterization of capsid proteoforms of recombinant adeno-associated virus 6 (AAV6)

WP-335 Developing a method for investigating metal content in single Chinese Hamster Ovary cells using ICP-MS

TP-277 Demonstrate method robustness and seamless method transfer, a step towards enabling high resolution accurate mass multi-attribute method for biopharmaceutical quality control

FP-574 High throughput analysis of synthetic DNA using a compliant LC-MS based workflow

THP-249 Characterization of mRNA therapeutics using a novel LC-MS based workflow

FP-023 At-line monoclonal antibody analysis using affinity-chromatography with mass spectrometry detection and fully compliant data acquisition and processing

FP-024 Multi-Attribute Method for batch-to-batch comparison of Etanercept fusion protein

FP-021 In depth characterization of mAb charge variants by ICIEF fractionation followed by peptide mapping analysis

FP-020 Comprehensive Characterization of Cysteine-conjugated Antibody Drug Conjugate (ADC) on a Hybrid Quadrupole-Orbitrap Mass Spectrometer

MP-147 Software development for improved sensitivity of mass spectrometry-based thermal shift assays (MS-TSA) for target engagement and drug discovery

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Pharma

Oral presentations

2:30-2:50 p.m., Nov 2, Room 114 Extractable Analysis of Rubber Stoppers for Pharmaceutical Applications using Orbitrap Exploris 120 MS and Vanquish UHPLC and Comprehensive Data Mining Tool

Posters

TP-345 High Resolution MS and Advanced Structure Analysis Software for Confident Impurity Structure Profiling

MP-023 Drug-Target Identification Using Improved Mass-Spectrometry-based Acquisition Approaches for Thermal Stability Assays

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Clinical research and forensic toxicology

Oral presentations

8:30-8:50 a.m., Nov 1, 201 ABC Breaking Down the Barrier to Rapid Anti-bacterial Drug Levels with Paper Spray-Mass Spectrometry: Simultaneous Quantitation of Five beta-lactams from Plasma

10:10-10:30 a.m., Nov 3, 113 ABC Paper Spray Mass Spectrometry as a Rapid Quantitative Drug Checking Technology for Opioid Misuse Harm Reduction and Illicit Drug Surveillance

Posters

TP-353 Screening and Semi-Quantitation of 212 Fentanyl Analog Compounds by Orbitrap Exploris 120™ mass spectrometer

TP-074 Automated Dried Spot Analysis for Rapid Quantitation of Tramadol and Metabolites

THP-084 Automated and High-throughput Urine Drug Screening using Paper Spray Mass Spectrometry

MP-043 Analysis of Intact Resistance Markers for Metallo-beta-Lactamases in Bacterial Chromatons

TP-124 Quantitative Analysis of Testosterone from Human Serum using High-Flow Liquid Chromatography and FAIMS on a Triple Quadrupole Mass Spectrometer

FP-748 High-Flow LC/MS Analysis of Immunosuppressant Drugs in Human Blood Using FAIMS Technology

THP-272 Developing a quick and robust mass spectrometry-based method for the detection of SARS-CoV-2

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Environmental testing

Oral presentations

10:10-10:30 a.m., Nov 2, Room 114 Fieldable, Dual-Technique Assay for the Analysis of Organophosphorus Compounds for Environmental and Chemical Defense Applications

Posters

MP-164 Enhanced performance of a Triple Stage Quadrupole Mass Spectrometer with a novel Axial Field Collision Cell

FP-251 A consolidated approach for routine analysis of soil contaminants using GC-Orbitrap mass spectrometry

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Food safety

Posters

WP-057 Combining superior interference removal and speed for elemental analysis using ICP-MS

FP-436 Quantitative analysis of sulfonamides in meat muscle matrix with a field asymmetric ion mobility interface on an Orbitrap™ Mass spectrometer

FP-213 Multi-class Veterinary Drugs Analyses of QueChERS Extracts using an Automated Online µSPE Clean-up Coupled to LC-MS/MS

FP-214 A comparison of IC-MS/MS and LC-MS/MS techniques for the multi-residue analysis of polar pesticides and metabolites in food

FP-197 Applying High-Resolution GC-Orbitrap Mass Spectrometry for Quantitation of Pesticides and PCB's in food samples

FP-254 Non-Targeted Approach for Authentication of Spices and Herbs using GC-Orbitrap MS technology

FP-211 Fast analysis of multi-class pesticides panel in garlic and cummin extracts using a Single Run LC-High Resolution Mass Spectrometry

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Metabolomics and lipidomics

Posters

THP-211 Robust lipidomic profiling to routinely quantitate ceramides and confidently identify unknown lipids

TP-199 Application of the FAIMS Pro Duo interface for selective detection of lower abundance lipid classes at analytical flow rates

FP-531 Identification of Small Molecules via Real-Time Library Search on an Orbitrap Tribrid Mass Spectrometer

MP-072 The Craze for the Haze: How Dry Hopping Influences the Metabolomics of Beer

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Proteomics and structural biology

Posters

WP-204 Routine single-shot identification of >9K proteins and >100K peptides with the next-generation low-flow UHPLC coupled to HRAM MS

MP-333 A TMTpro 18plex Proteomics Standard for Assessing Protein Measurement Accuracy and Precision

FP-661 Rapid and reproducible phosphoenrichment using Fe-NTA Magnetic beads

FP-688 Boosting Proteome Coverage by a Combination of the Next Generation UHPLC and a Novel Search Node in Proteome Discoverer

MP-039 Rapid proteome analysis using DIA and super-resolution Orbitrap mass spectrometry

FP-398 A Fully Automated High-Throughput, Deep-Scale Quantitative Plasma Proteomics Workflow Enables Quantitatively Profile More Than 1000 Proteins Per Sample.

WP-112 CHIMERYs: an AI-driven leap forward in peptide identification

MP-291 Identifying antibiotic resistance through direct detection of intact enzymes from bacterial lysates using LC-MS/MS: exploring MRSA and carbapenem resistance

WP-321 Benchmarking of Micro-flow Chromatography for Robust Proteomics Analysis

TP-125 Implementing Comet search engine into Proteome Discoverer to improve TMT Real-Time Search data processing

MP-254 SureQuant targeted mass spectrometry standards and assay panel for quantitative analysis of phosphorylated proteins from multiple signaling pathways

MP-092 Infrared activation enables using a Next-Down MS Analysis of Membrane Proteins and Protein Complexes

FP-197 Deep Metaproteome Analysis Using a Next Generation UHPLC System Coupled to an Orbitrap Eclipse Tribrid with FAIMS Pro Interface

FP-084 Elucidating the complexities of the human milk glycome with ion chromatography-proteomics (IC-MS)

FP-398 Combining the data-driven and hypothesis-driven approaches in one go via a novel intelligent data acquisition Hybrid-DIA mass spectrometry strategy

FP-720 Leveraging Bottom-Up Search Results to Build Sample Specific Top-Down Databases

WP-329 Beyond TurboTMT: Phi-SDM Super-resolution Methods for Next-generation Highly-multiplexed Quantitative Ultrasensitive and Single-Cell Proteomics via TMT Pro Complement Ion Deconvolution.

MP-176 Inference of Collisional Cross-Sections of peptides in an Orbitrap Mass Analyzer

THP-265 Novel hybrid-DIA acquisition strategy combines targeted and discovery proteomics to enable simultaneous quantification of global proteomes and predefined mutated peptides

TP-268 Notch3 epitope mapping using integrated structural proteomics techniques

MP-298 Development of mass spectrometry-screening methods for quality assessment of Cryo-EM standard

FP-399 An intelligent Hybrid-DIA data acquisition strategy for cracking the clinical sample complexity challenge in translational proteotyping

MP-069 A Journey into the Hazy Beer Proteome: How Does Dry Hopping Alter the Proteomic Landscape of Beer?

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Technology hardware

Oral presentations

9:10-9:30 a.m., Nov 4, Ballroom A Extending the mass limit of collision cross sections of proteins in Orbitrap analyzers through kinetic energy and fragmentation behavior analysis

Posters

WP-200 Development of a Simplified User Interface for SRM Method Creation

FP-400 A method for the structural analysis and time resolved imaging of bio-macromolecular assemblies in mass spectrometry using Timepix detector

FP-390 Expanded Instrument Control using the Orbitrap Tribrid IAPl

WP-024 Novel Real-Time Library Search driven data acquisition strategy for identification and characterization of metabolites

FP-388 New high voltage power supplies for triple quadrupole MS polarity switching in under 5 ms

FP-437 Compensation Voltage Determination on a LC Time Scale

THP-127 Resonance-Enhanced Multiphoton Ionization inside the C-trap of an Orbitrap Mass Spectrometer

FP-389 Extending the interval between full-range mass calibrations on Orbitrap Exploris mass spectrometers

FP-702 Multi-site assessment of precision and reproducibility of high-throughput capillary-flow LC-MS proteome profiling with novel ultra-high-pressure LC coupled to HRAM MS

WP-195 Beyond the boundaries of LC-MS sensitivity and throughput with the next generation all-in-one nano-, capillary- and micro-flow UHPLC system

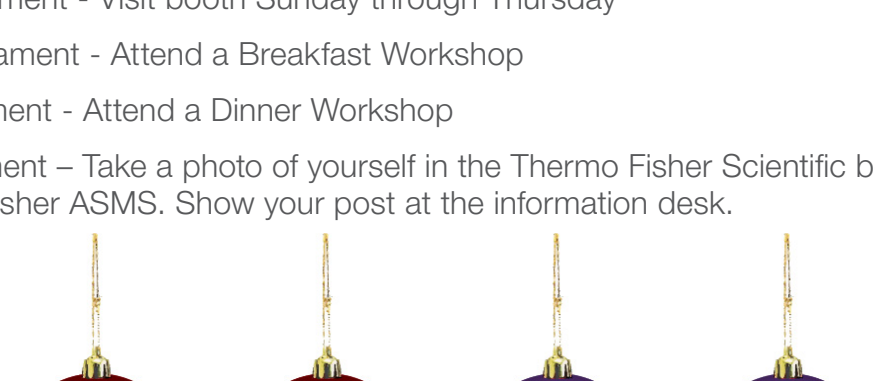
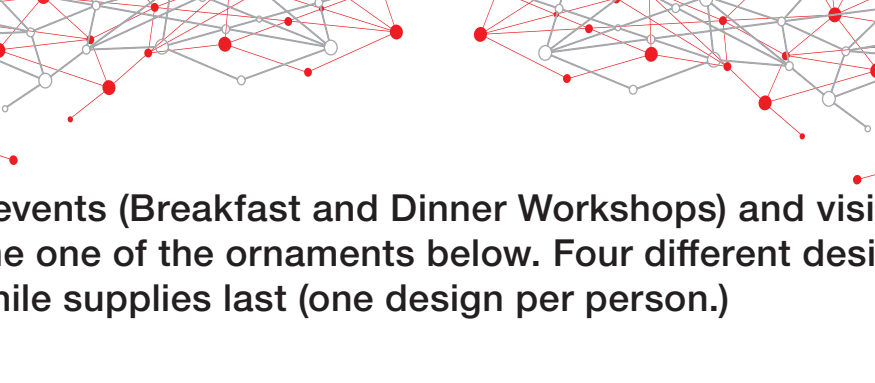
FP-263 Breakthrough analytical performance of a novel Gas Chromatography – Orbitrap Mass Spectrometry for routine and research applications

FP-447 Concepts for Elongated Spiral and Helical Ion Guides

Ornament giveaway

Attend our events (Breakfast and Dinner Workshops) and visit our booth to take home one of the ornaments below. Four different designs will be available while supplies last (one design per person.)

1. Black Ornament - Visit booth Sunday through Thursday
2. Purple Ornament - Attend a Breakfast Workshop
3. Blue Ornament - Attend a Dinner Workshop
4. Red Ornament - Take a photo of yourself in the Thermo Fisher Scientific booth. Post at #ThermoFisherASMS. Show your post at the information desk.



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Ornament giveaway