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Bringing light to discovery

ASMS 2025
Baltimore, Maryland • June 1–5

Contents

Greetings ASMS 2025 attendees

Learn about continued innovations in mass spectrometry technologies and solutions. From compounds to clinics, discover how scientists and researchers are transforming quantitation with mass spectrometry solutions, crossing boundaries to solve some of today's toughest analytical challenges.

Sunday annual users' meeting

Attend our users' meeting on Sunday at the Baltimore Marriott Waterfront to hear firsthand from renowned guest speakers on the following applications:

- **Proteomics**
- **Metabolomics**
- **BioPharma & pharma**
- **Clinical research**

Sunday customer hospitality event – PowerPlant Live!

After attending our users' meeting, join us for our customer hospitality event at PowerPlant Live! just a 13-minute walk from the hotel along the waterfront. You'll be able to unwind, network with the speakers and have some fun while enjoying great food and drinks.

Daily breakfast workshops

Attend our lineup of breakfast workshops from Monday through Thursday in the Hilton Baltimore Inner Harbor and Baltimore Convention Center. Use this guide to determine the location of your workshop. You'll learn more about the latest research solutions in mass spectrometry in small, focused groups.

Nightly hospitality suite

In the evenings, visit our hospitality suite in Key Ballroom 5 at the Hilton Baltimore Inner Harbor for refreshments and to see our latest technologies and solutions. You'll have the opportunity to network with scientists and experts and get answers to your technical questions.

Booth #301 – Baltimore Convention Center

Visit us throughout the week at Booth #301 in the Baltimore Convention Center to speak with experts and to learn about the most recent innovations in mass spectrometry.

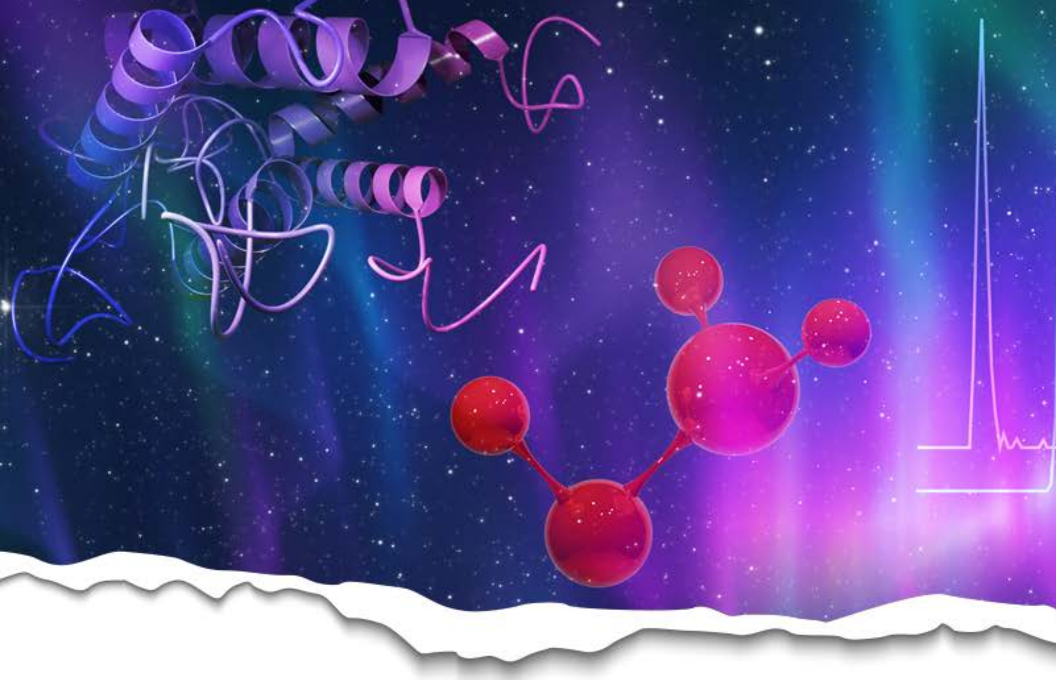
This guide features all the activities we're hosting at ASMS 2025. We hope you enjoy the perfect balance of science and networking during the 73rd Annual ASMS Conference.

Hospitality suite

Hilton Baltimore Inner Harbor, Key Ballroom 5

Join us throughout the day in our hospitality suite to delve into the future of mass spectrometry. Engage directly with our experts in Key Ballroom 5 at the Hilton Baltimore Inner Harbor and explore the latest breakthroughs that cover the full molecular spectrum. From precision quantitation in small molecules to advanced high-throughput proteomics and transformative digital solutions that enhance biological research—our suite serves as a showcase of the latest innovations in mass spectrometry.

As the day transitions into night, our hospitality suite transforms into a vibrant gathering spot. Relax and connect with your peers over refreshments, and experience firsthand our cutting-edge technologies and solutions. This casual, engaging atmosphere provides the perfect backdrop to network with industry leaders and experts who can answer all of your technical questions, ensuring that you leave with both valuable insights and new connections.



Coming soon

Discover new innovations

New systems and tools coming to ASMS 2025

Annual users' meeting
Sunday, June 1

Plenary session

New innovations in mass spectrometry

Baltimore Marriott Waterfront, 4th Floor - Harborside Ballroom A-C

7:00 - 8:00 am	Breakfast & registration
8:00 – 8:10 am	Gianluca Pettiti, *Executive Vice President, Thermo Fisher Scientific*
8:10 – 8:25 am	Iain Mylchreest, Ph.D. *Vice President Research and Development, Thermo Fisher Scientific*
8:25 – 8:40 am	Jesper Olsen, Ph.D. *Professor, University of Copenhagen*
8:40 – 8:55 am	Jennifer Geddes-McAlister, Ph.D. *Associate Professor, University of Guelph*
8:55 – 9:10 am	Jonathan Martin, Ph.D. *Professor, Stockholm University*
9:10 – 9:25 am	Melanie Bailey, Ph.D. *Professor, University of Surrey*
9:25 – 9:40 am	Jonathan Bones, Ph.D. *Principal Investigator and Director of CONCEPT, NIBRT*
9:40 – 9:55 am	Christian Hock, Ph.D. *Director R&D Instrument Development, Thermo Fisher Scientific*
9:55 – 10:00 am	Aaron Robitaille, Ph.D. *Director of Marketing, Mass Spectrometry, Thermo Fisher Scientific*
10:00 – 10:15 am	Coffee break

Proteomics: Peptides, proteins, PTMs, and proteoforms

Baltimore Marriott Waterfront, 4th Floor – Harborside Ballroom A-C

10:15 – 10:20 am	Tonya Pekar Hart *Senior Manager, Vertical Marketing, Thermo Fisher Scientific*
10:20 – 10:45 am	Erwin Schoof, Ph.D. *Associate Professor, Technical University Utrecht*
10:45 – 11:10 am	Gregory Potts, Ph.D. *Principal Research Scientist, AbbVie*
11:10 – 11:35 am	Amy Kessler, Ph.D. *Postdoctoral Researcher, Utrecht University*
11:35 – 12:00 pm	Dylan Mitchell, Ph.D. *Director, Head of Proteomics,, Flagship Pioneering*
12:00 pm	Tonya Pekar Hart *Senior Manager, Vertical Marketing, Thermo Fisher Scientific*

Metabolomics: Metabolites, lipids, and multiomics methods

Baltimore Marriott Waterfront, 4th Floor – Harborside Ballroom E

10:15 – 10:20 am	Susan Bird, Ph.D. *Senior Manager, Vertical Marketing, Thermo Fisher Scientific*
10:20 – 10:45 am	Jennifer Campbell, Ph.D. *Chief Scientific Officer, Matterworks*
10:45 – 11:10 am	Katie Overmyer, Ph.D. *Associate Director, Lab for Biomolecular Mass Spectrometry*
11:10 – 11:35 am	Celia Berkers, Ph.D. *Professor, Utrecht University*
11:35 – 12:00 pm	Abigail Ellis *Mass Spectrometry Core Lab Manager, Van Andel Institute*
12:00 pm	Susan Bird, Ph.D. *Senior Manager, Vertical Marketing, Thermo Fisher Scientific*

Biopharma & pharma: Empowering discovery and development for large and small molecules

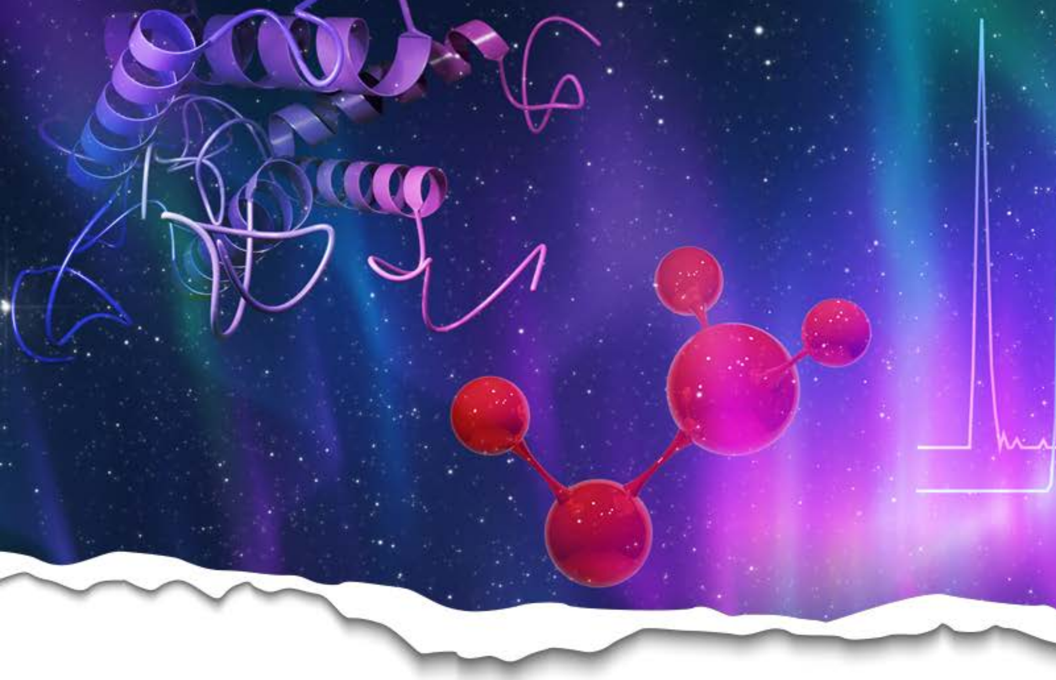
Baltimore Marriott Waterfront, 4th Floor – Harborside Ballroom D

10:15 – 10:20 am	Kelly Broster, Ph.D. *Senior Manager, Vertical Manager, Thermo Fisher Scientific*
10:20 – 10:45 am	Andrew Mahan, Ph.D. *Associate Director, Johnson & Johnson Innovative Medicine*
10:45 – 11:10 am	Mark Dickman, Ph.D. *Professor, University of Sheffield*
11:10 – 11:35 am	Ryan Shirey, Ph.D. *Scientist II, Avidity Biosciences*
11:35 – 12:00 pm	Katherine Wright *Senior Principal Scientist, Pfizer*
12:00 pm	Kelly Broster, Ph.D. *Senior Manager, Vertical Manager, Thermo Fisher Scientific*

Clinical research: Innovations in translational and clinical research

Baltimore Marriott Waterfront, 4th Floor – Laurel A-C

10:15 – 10:20 am	Kerry Hassell, Ph.D. *Manager, Vertical Marketing, Thermo Fisher Scientific*
10:20 – 10:45 am	Camille Lombard-Banek, Ph.D. *Associate Director, AstraZeneca*
10:45 – 11:10 am	Patrick Vanderboom, Ph.D. *Senior Associate Consultant, Mayo Clinic*
11:10 – 11:35 am	Jihyeon Lee, Ph.D. *Postdoctoral Scientist, Cedars-Sinai*
11:35 – 12:00 pm	Arran Dokal, Ph.D. *Chief Technology Officer, Kinomica*
12:00 pm	Kerry Hassell, Ph.D. *Manager, Vertical Marketing, Thermo Fisher Scientific*



Coming soon

Discover new innovations

New systems and tools coming to ASMS 2025

Breakfast workshops
Monday, June 2

Proteomics: Unrivalled productivity and performances for protein quantitation

Hilton Baltimore Inner Harbor, 2nd Floor – Key Ballroom 5

7:00 – 8:15 am

Discover new technologies that enable high-performance proteomics, benefiting a wide range of applications including chemoproteomics, targeted protein degradation, and narrow-window Data-Independent Acquisition (DIA) based Label-Free Quantitation (LFQ).

Tonya Pekar Hart
Senior Manager, Vertical Marketing, Thermo Fisher Scientific

Andreas Tebbe, Ph.D.
Vice President, Global Mass Spectrometry, Evotec International

Mukesh Kumar, Ph.D.
Principal Scientist, Cell Signaling Technology

Christopher Rose, Ph.D.
Senior Director & Distinguished Scientist, Genentech

Biopharma & pharma: Molecular insights through mass spectrometry-enabled analysis

Hilton Baltimore Inner Harbor, 2nd Floor – Key Ballroom 1-2

7:00 – 8:15 am

Learn more about new tools for the structural characterization of macromolecules, including native protein complexes, antibody-drug conjugates, and comprehensive antibody characterization.

Min Du, Ph.D.
Senior Manager, Product Applications, Thermo Fisher Scientific

Josh Hinkle, Ph.D.
Staff Scientist, Thermo Fisher Scientific

Jessica Hoskins, Ph.D.
Principal Research Scientist I, AbbVie

Yilong Zheng, Ph.D.
Research Scientist, PPD Clinical Research Services

Breakfast workshops
Tuesday, June 3

Metabolomics: Highly sensitive instrumentation for metabolite and lipid quantitation

Hilton Baltimore Inner Harbor, 2nd Floor – Key Ballroom 5

7:00 – 8:15 am

Explore new approaches in metabolomics applications including SQUAD (Simultaneous Quantitation and Discovery) exposomics and alternative fragmentation methods enhancing small molecule characterization.

Susan Bird, Ph.D.
Senior Manager, Vertical Marketing, Thermo Fisher Scientific

Tong Shen, Ph.D.
Project Scientist, West Coast Metabolomics Center, UC Davis

Justin Elliott
Graduate Student, Texas A&M University, Corpus Christi

Olivia Murtagh
Graduate Student, Department of Chemistry, University of Texas at Austin

Proteomics: Innovative solutions for expanded PTM and spatial analysis

Hilton Baltimore Inner Harbor, 2nd Floor – Key Ballroom 1-2

7:00 – 8:15 am

Listen as expert speakers highlight improved workflow solutions that benefit the study of post-translational modifications (PTMs), including phosphorylation and histone modifications, as well as advancements in spatial proteomics analysis using label-free quantitation strategies.

Brett Larsen
Senior Vertical Marketing Manager, Thermo Fisher Scientific

Benjamin Garcia, Ph.D.
Washington University School of Medicine

Emma Lundberg, Ph.D.,
Associate Professor, Stanford University

Joshua Coon, Ph.D.
Professor, University of Wisconsin - Madison

Breakfast workshops
Wednesday, June 4

Structural biology: Fresh solutions to elucidate the structure-function relationship of macromolecules

Hilton Baltimore Inner Harbor, 2nd Floor – Key Ballroom 5

7:00 – 8:15 am

Discover advancements in structural biology applications, including charge detection approaches such as Direct Mass technology mode, protein cross-linking, and hydrogen-deuterium exchange (HDX).

Weijing Liu, Ph.D.
Vertical Marketing Manager, Thermo Fisher Scientific

Fan Liu, Ph.D.
Professor, Leibniz-Forschungsinstitut für Molekulare Pharmakologie (FMP)

Varun Gadkari, Ph.D.
Assistant Professor, University of Minnesota

Malvina Papanastasiou
Group Leader, Broad Institute

Translational applications: Workflows to bridge the gap between discovery and clinical research

Hilton Baltimore Inner Harbor, 2nd Floor – Key Ballroom 1-2

7:00 – 8:15 am

Explore oncology research using high-throughput MS assays and plasma proteomics. Discover how these researchers identify non-BRCA predictive biomarkers for ovarian cancer and early lung cancer detection, promising significant improvements in patient diagnosis, stratification, and treatment outcomes.

Stephanie Samra
Senior Manager, Vertical Marketing, Thermo Fisher Scientific

Yu-Ju Chen, Ph.D.
Distinguished Research Fellow, Academia Sinica

Stefani Thomas, Ph.D.
Assistant Professor, University of Minnesota

Jessica Moore, Ph.D.
Senior Scientist, Discovery Life Sciences

Breakfast workshops
Thursday, June 5

Environmental & food safety: Comprehensive solutions for analytical testing in areas from food safety to water quality

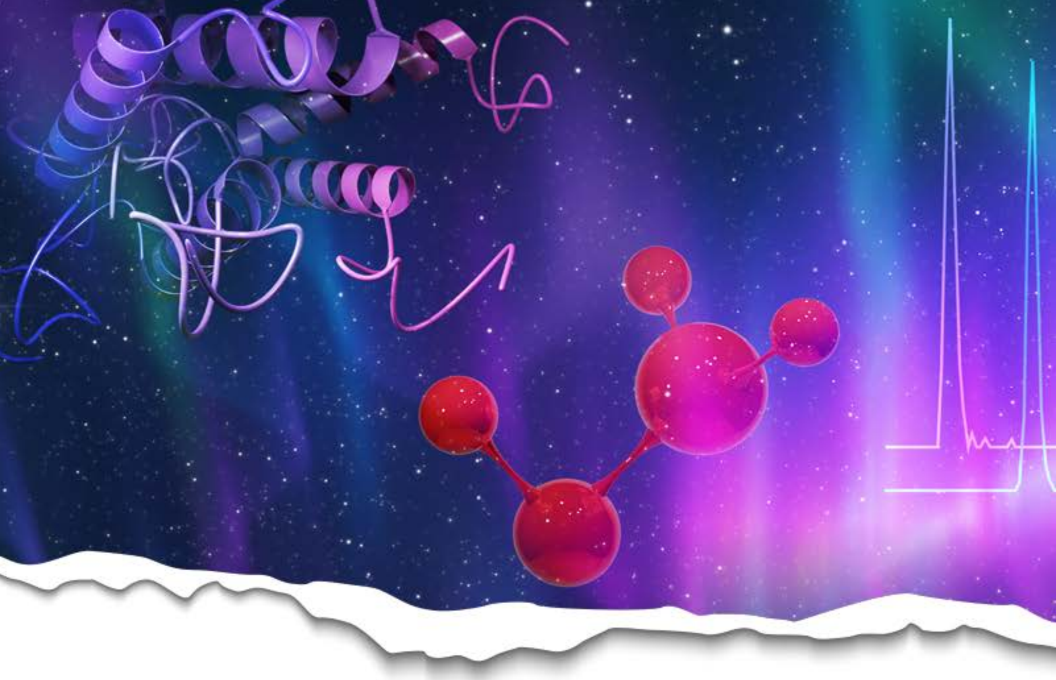
Baltimore Convention Center – Room 341/342

7:00 – 8:15 am	Learn about streamlined and validated workflows for the analysis of PFAS and other environmental contaminants. This session will also cover techniques for food authentication and safety monitoring. Ed George *Global EFS Regulatory Strategy and KOL Manager, Thermo Fisher Scientific* Kuanliang Shao, Ph.D. *Post Doctoral Fellow, Emory University* Sébastien Sauvé, Ph.D., MSRC/FRSC *Professor, University of Montreal*

Digital transformation of software: Innovation capabilities and connectivity to enhance productivity

Baltimore Convention Center – Room 343/344

7:00 – 8:15 am	Experience advancements in proteomics, small molecule analysis, and biopharmaceutical research with software that seamlessly connects data, applications, instruments, and scientists. Shannon Eliuk, Ph.D. *Director Software Product Management, Thermo Fisher Scientific* Reinaldo Almeida, Ph.D. *Director Proteomics, Monte Rosa Therapeutics* Josh Nicklay, Ph.D. *Principal Scientist, Bristol-Myers Squibb* Da Ren, Ph.D. *Founder & CEO, BioTherapeutics Solutions* Mark Sanders, Ph.D. *Director Partner Management, Thermo Fisher Scientific*



Coming soon

Discover new innovations

New systems and tools coming to ASMS 2025

Oral presentations
Monday, June 2

MOA 8:30 am	Modified Orbitrap Astral MS allows for higher scan rates without compromising spectral quality and sensitivity in proteomics
MOA 8:50 am	Ultra-sensitive quantitation and rapid method development for targeted immunopeptidomics using the Stellar mass spectrometer
MOG 10:10 am	Highly parallel metabolite profiling of yeast extracts using GC-MS/MS technology with automated method development and TBDMS derivatization
MOC 2:30 pm	AAV6 VP3-only capsids for standardization in ion-exchange chromatography, native mass spectrometry, and charge detection mass spectrometry
MOG 2:30 pm	Evaluation of a modified Orbitrap Astral mass spectrometer for quantitative proteomics – beyond identifications lists
MOB 2:30 pm	Stable isotope labeling applications
MOG 2:30 pm	Instrumentation: New hybrid and multimodal approaches
MOG 2:50 pm	Fully parallelized tandem MS on a 21 T FT-ICR/Orbitrap/quadrupole/ion trap hybrid mass spectrometer
MOC 3:30 pm	Amplify laboratory efficiency by Simultaneous Quantitation and Discovery: SQUAD can elevate high-resolution MS analysis of known and unknown nitrosamines
MOF 3:30 pm	High-throughput and highly selective quantitative lipidomics approach with the Stellar mass spectrometer – A novel hybrid nominal mass instrument
MOA 4:10 pm	Simultaneous Quantitation and Discovery (SQUAD) of fecal bile acids and conjugates in adults with autism spectrum disorder

Oral presentations
Tuesday, June 3

TOA 8:50 am	Comprehensive characterization of disulfide linkages in cysteine-engineered bispecific antibody using EThcD on a modified Orbitrap Hybrid mass spectrometer
TOA 9:30 am	Investigating the complexity of Fc fusion proteins using a modified hybrid Orbitrap mass spectrometer

Oral presentations
Tuesday, June 3 (cont.)

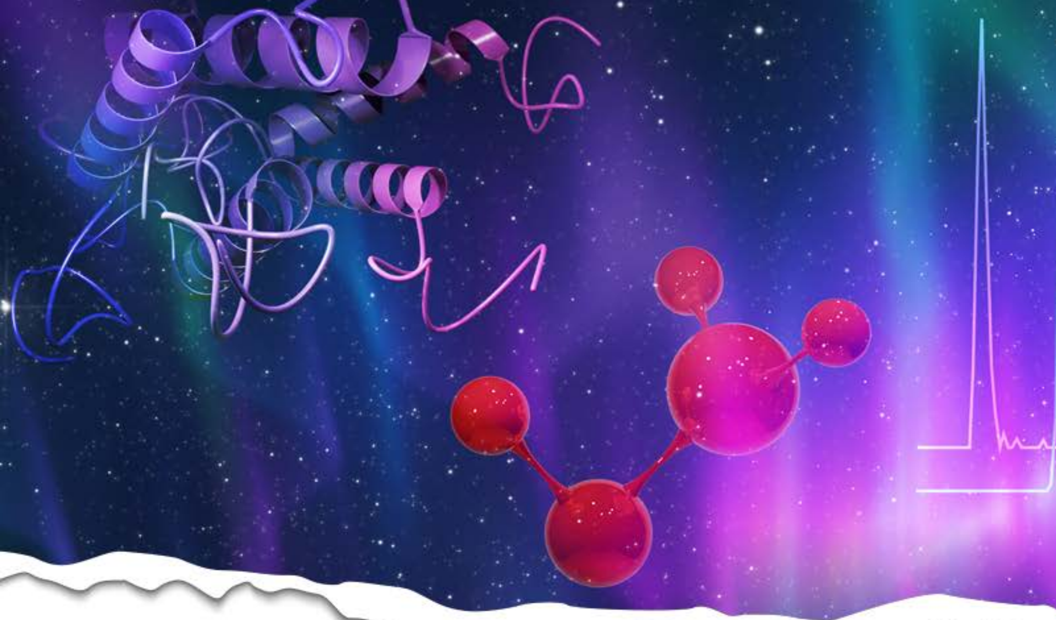
TOG 2:30 pm	Elucidation of the importance of hydrogren bonding of amines for the characterization of CRISPR RNA
TOA 2:50 pm	Accurate multiplexing on the Orbitrap Astral with TMTpro complementary ion quantification
TOG 2:50 pm	New oligonucleotide mode on Orbitrap Tribrid instruments enables optimized tandem MS analysis of oligonucleotide anions
TOA 3:30 pm	Closing the gap between targeted and untargeted measurements using intelligent data acquisition on Stellar MS
TOH 4:10 pm	Unbiased metabolite profiling of bladder cancer tissues using Orbitrap IQ-X mass spectrometry

Oral presentations
Wednesday, June 4

WOF 8:30 am	A novel high resolution multi-residue pesticide workflow for the chromatographer that is comprehensive, selective, productive, and designed for ease-of-use
WOE 8:30 am	Higher-throughput analysis with parallelized pre-accumulation
WOG 8:30 am	Refining structural surfaceomics to further characterize tumor specific surface protein conformations

Oral presentations
Thursday, June 5

ThOE 8:30 am	Next-generation multiplexed targeted pathway proteomics quantifies post-translational modifications with high target throughput in 3.4 minutes per sample
ThOD 9:10 am	Collisional cross section measurement via Orbitrap mass analysis: Figures of merit for high-throughput applications
ThOC 9:10 am	Expedient electron transfer dissociation for improved glycoproteome characterization
ThOE 4:10 pm	Twenty years of Orbitrap mass spectrometry as a mainstream technology for high-resolution accurate mass analysis



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New systems and tools coming to ASMS 2025

Poster presentations
Monday, June 2

Poster boards present 10:30 AM - 2:30 PM

MP 003	Improving charge variant analysis of complex monoclonal antibodies at intact level using DIA-PTCR
MP 016	Complete characterization of Kadcyla using a modified hybrid quadrupole-Orbitrap mass spectrometry with electron-transfer/higher-energy collision dissociation (EThcD) fragmentation
MP 023	Comprehensive characterization of monoclonal antibodies on a modified hybrid Orbitrap mass spectrometer
MP 072	Transforming cancer biomarker discovery through maximum ID and high-throughput plasma proteomics workflows
MP 078	Comprehensive and high-throughput plasma proteome profiling for biomarker discovery using a modified Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer
MP 093	In-depth plasma proteome profiling for high-throughput biomarker discovery using PreOmics sample preparation kits and Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer
MP 096	LC-MS workflows for diverse omics analysis of plasma samples in a mini cancer cohort using the Orbitrap Astral mass spectrometer
MP 116	Metabolic characterization of hepatocellular carcinoma cells using a novel enhanced dynamic range MS mode reveals potential key metabolic pathways
MP 124	Mass spectrometry-based proteomic investigation of patient-derived tumoroids using the Orbitrap Astral mass spectrometer informs precision oncology and drug discovery
MP 169	Innovative data-independent acquisition (DIA) workflows for protein–nucleic acid interaction
MP 189	MS-cleavable cross-linking analysis on modified Orbitrap Astral mass spectrometer
MP 203	Development of DIA workflow for multiplex hydroxyl radical protein footprinting
MP 204	High-throughput PROTAC compound screening workflow for targeted protein degradation on an Orbitrap Astral mass spectrometer with accurate label-free quantitation
MP 217	Leveraging Adaptive RT on Orbitrap Ascend MultiOmics Tribrid mass spectrometer for improved sensitivity and throughput in targeted and hybrid workflows

Poster presentations
Monday, June 2 (cont.)

MP 223	Simultaneous Quantitation and Discovery (SQUAD) workflow using multiple fragmentation techniques for quantitation and characterization of trace level nitrosamines in medicines
MP 245	Trace metals analysis in baby food using triple quadrupole inductively coupled plasma mass spectrometry (TQ-ICP-MS)
MP 248	Performance evaluation of GC-MS/MS for dioxin analysis with amendments to EU Regulations 644/2017 and 771/2017 for food and feed
MP 275	Using the new Stellar mass spectrometer to confirm and quantify 31 drugs of abuse, including THC, in oral fluid
MP 329	Evaluating a next generation ion source for proteomics
MP 343	An automated approach for the analysis of VOCs in drinking and surface water by using a VOC sample prep station
MP 344	Streamlined untargeted workflow for priority and unknown pollutant identification in industrial stack particulate by GC-Orbitrap high resolution mass spectrometry
MP 345	Non-targeted analysis of whisky using SPME Arrow and Orbitrap Exploris GC 240 mass spectrometer
MP 354	Unveiling VOC complexity: High-resolution quantitation with GC-EI-Orbitrap MS
MP 402	On-the-fly retention time adjustment on a modified Orbitrap hybrid mass spectrometer enabling targeted and discovery workflows with high efficiency
MP 404	Metabolite and lipid analysis (MLA) profiling using mass spectrometry with data visualization and a chemometrics workflow
MP 408	Non-targeted LC-Orbitrap collision cross section measurements to enhance lipid annotation
MP 409	Simultaneous Quantitation and Discovery (SQUAD): An intelligent combination of targeted and untargeted workflows using a modified Orbitrap Astral mass spectrometer
MP 420	Combining AP-SMALDI with data independent analysis to enable localization and improved identification of compounds in MALDI MS imaging
MP 443	Hybrid-DIA and SureQuant on a modified Orbitrap Astral MS
MP 446	A scalable approach to assess statistical confidence of peptides in targeted proteomics assays

Poster presentations
Monday, June 2 (cont.)

MP 447	Comprehensive multiomics data integration: Bridging proteomics and genomics
MP 476	SQUAD analysis of plasma using modified Orbitrap Hybrid MS for enhanced dynamic range, reduced unintentional MS1 fragmentation, and improved sensitivity
MP 490	State-of-the-art rapid stepped collision energy in a modified Orbitrap Astral MS
MP 504	Orbitrap Exploris MS without downtime between LIFDI and ESI spectra acquisitions
MP 542	Analyzing the HYE species mix: A comprehensive reference standard for mass spectrometry quality control and method development
MP 563	A next generation ion source for robust, low-flow LC-MS workflows enables sensitive and precise peptide quantitation and global proteomics analysis
MP 566	Evaluating a tandem LC workflow for eliminating mass spectrometer idle time
MP 570	Extended lifespan of innovative column assemblies in low-flow ion sources
MP 572	Targeted MS3 approach for quantifying triacylglycerols with resolved fatty acid composition in breast milk using Stellar mass spectrometer
MP 584	Improving selectivity and sensitivity of lipid mediator analyses by coupling nano-flow chromatography with the Stellar mass spectrometer
MP 605	LAP-MALDI – an alternative ionization technique on commercial instrumentation
MP 621	Combining targeted MS2 and MS3 approaches for the quantitation of bile acids in biological specimens using the Stellar mass spectrometer
MP 622	Broad profiling, quantitative metabolomics using the MxP® Quant 500 XL kit on TSQ Altis series mass spectrometers
MP 692	High select Fe-NTA magnetic beads for phosphopeptide enrichment
MP 695	Improved phosphoproteome coverage using CHIMERYS and LPGF protein validation
MP 699	Proteomics and phosphoproteomics of salt-induced C3 to CAM transition in *Mesembryanthemum crystallinum*

Poster presentations
Monday, June 2 (cont.)

MP 728	Enabling spatial top-down proteomics of the human cell using gas-phase fractionation and ion-ion reactions
MP 740	Sensitive and accurate proteome profiling of embryogenesis using Real-Time Search and TMTproC quantification
MP 742	Characterizing 32-plex TMTpro reagents for high-throughput quantitative proteomics on Orbitrap platforms
MP 746	Improved accuracy and identification in label-free quantitative proteomics with a novel ion source and separation cartridge with integrated replaceable emitters
MP 747	Deeper proteome profiling with higher throughput via optimized ion processing on a modified Orbitrap Astral mass spectrometer
MP 748	Enhancing the resolving power on a novel Orbitrap Astral instrument for TMT35plex applications

Poster presentations
Tuesday, June 3

TP 017	A novel multidimensional liquid chromatography workflow with in-loop enzymatic digests of multiple heart-cuts for fast & flexible characterization of biotherapeutic protein variants
TP 028	Rapid monitoring of mAb aggregates during the purification process development of therapeutic mAbs using a modified Orbitrap hybrid MS
TP 032	High-sensitivity host cell protein (HCP) analysis on a modified hybrid quadrupole-Orbitrap mass spectrometer with optimized sample preparation
TP 036	Analysis of bispecific and multispecific antibody therapeutics using native mass spectrometry on a modified hybrid Orbitrap mass spectrometer
TP 038	Multi-attribute analysis of cysteine-linked ADC under native conditions by using a flexible online multiple heart-cutting 2D-LC-HRAM mass spectrometry
TP 061	Unleash the power of hybrid-DIA data analysis with AI-driven software for biomarker discovery and validation in translational research
TP 065	Enhanced identity spectrum search with AI/ML confidence scoring for HRAM data

Poster presentations
Tuesday, June 3 (cont.)

TP 175	Enhanced ocean metaproteomic profiling with Orbitrap Astral MS in data independent acquisition
TP 180	DIA analysis on the Orbitrap Astral MS combined with PTMScan enrichment provides an expanded global view of protein post translational modifications
TP 182	Redefining targeted activity-based protein profiling (ABPP) depth by Stellar mass spectrometer
TP 193	DIA for the masses: Strategies for implementation in unit resolution
TP 248	High-throughput data-independent acquisition mass spectrometry workflow for in-depth identification of protein ubiquitination using an Orbitrap Astral mass spectrometer
TP 249	High-throughput PROTAC compound screening workflow for targeted protein degradation on an Orbitrap Astral mass spectrometer with accurate label-free quantitation
TP 264	Comprehensive non-targeted analysis of perfluoroalkyl substances in complex AFFF formulations and AFFF-impacted soils
TP 316	Simultaneous targeted, non-targeted PFAS screening as part of extractables screening for pharmaceutical packaging, manufacturing components, and medical device by LC-HRAM-MS
TP 346	Native charge detection mass spectrometry enables accurate mass and structural measurements of messenger RNA and ribosomal particles
TP 368	Atlas of N-linked protein glycosylation in the mouse
TP 384	Proton transfer charge reduction enhances glycoproteoform resolution in online and offline mass spectrometry
TP 432	High-resolution imaging of plant tissue sections and 3D surfaces using AP-SMALDI Orbitrap MSI
TP 479	Modified cosine similarity for real-time library search
TP 488	Reducing false annotations in lipidomics using Compound Discoverer 3.4 software
TP 512	Correction of retention time shifts between deuterated and non-deuterated fragment series for TMTpro 32plex and 35plex datasets
TP 539	Comprehensive data acquisition workflow on a modified Orbitrap Astral MS to achieve deep lipidome coverage with high confidence annotations
TP 560	Building biologically relevant libraries: How comprehensive libraries and deep MS/MS coverage enable intelligent library growth

Poster presentations
Tuesday, June 3 (cont.)

TP 565	Simultaneous Quantitation and Discovery (SQUAD) analysis of flavonoid conjugates in blood, urine and food using high flow and nanoflow LC-MS/MS
TP 566	SQUAD metabolomics: Uniting targeted precision and untargeted discovery for in-depth fecal metabolite profiling on Orbitrap Astral MS
TP 570	High-resolution untargeted metabolomics of tea using a modified Orbitrap Astral mass spectrometer
TP 573	Enhancing SQUAD innovations: Comparative assessment of simultaneous quantitation and discovery workflow for organic acids analysis using multiple chromatographic techniques
TP 609	Detailed study into ASO impurity analysis, lessons learned, and myths dispelled while creating compliant platform methods
TP 617	In-depth peptide mapping of biopharmaceuticals using an electron-transfer/higher-energy collision dissociation (EThcD) implemented on a modified Orbitrap hybrid MS
TP 635	Confident and sensitive identification of semaglutide degradation products using liquid chromatography-high resolution accurate mass (HRAM) mass spectrometry
TP 645	DOE-based comparative analysis of MAM on Thermo Scientific Q Exactive HF MS and Orbitrap Exploris 240 MS for therapeutic antibodies
TP 664	Multi-dimensional high-throughput molecular glue screening via gas phase affinity selection native mass spectrometry and cryo-EM analysis
TP 720	Evaluation of a modified Orbitrap Astral mass spectrometer for label-free quantitation of proteomic samples
TP 728	High-throughput proteomics using narrow window DIA on a modified Orbitrap Astral mass spectrometer
TP 730	Expanding targeted instrumentation to discovery proteomics: Complement reporter ion quantification with an ion trap
TP 736	Impact of isolation window width and dynamic range of differential expression on quantitative FDR in DIA experiments

Poster presentations
Tuesday, June 3 (cont.)

TP 739	Evaluation of a novel ion source using a large-scale targeted liquid chromatography mass spectrometry (LC-MS) assay for translational proteomics research
TP 745	Determination of empty/full capsid ratio for adeno-associated viruses: A comparison between Q Exactive UHMR mass spectrometer and analytical ultracentrifugation
TP 746	The size the limit: STORI-method Orbitrap charge detection mass spectrometry of species greater than 10 MDa
TP 749	Characterization of Qβ virus-like particles using Orbitrap-based charge detection mass spectrometry (CDMS)

Poster presentations
Wednesday, June 4

WP 033	Characterization and quantification of human IgG light chain in biological samples by high-resolution mass spectrometer
WP 049	Revolutionizing translational research: Large-scale targeted PRM proteomics assays enabled by Stellar mass spectrometer (MS)
WP 050	Highly multiplex targeted proteomics assays in plasma using Stellar mass spectrometer with Adaptive RT
WP 051	Large-scale targeted biomarker analysis of volatile organic compounds in breath by TD-GS-Orbitrap MS
WP 052	Sensitive and selective quantitation of bile acids in children with autism spectrum disorder using targeted MS2/MS3 on the Stellar MS
WP 057	Development and evaluation of a multiplexed health surveillance panel using ultra-high throughput PRM-MS in an inflammatory bowel disease cohort
WP 093	Fast and sensitive metabolite profiling of the antisense oligonucleotide tofersen in liver homogenates using UHPLC-HRAM mass spectrometry
WP 138	Simplified PFAS in wastewater analysis through automation, retention time confirmation, and high resolution full scan data
WP 178	Unraveling the intricate behaviors of megadalton-sized ions during Orbitrap mass analysis

Poster presentations
Wednesday, June 4 (cont.)

WP 237	AP-SMALDI high-throughput screening at an Orbitrap Exploris MX mass detector
WP 238	High-throughput plasma proteomics pipeline enhanced biomarker discovery in early detection of non-smoking lung cancer
WP 245	Scalable high-throughput workflow for simultaneous targeted and discovery proteomics by hybrid DIA MS
WP 256	MS imaging with >100 pixels/sec and HRAM: TransMIT AP-SMALDI5AF ion source and Thermo Scientific Orbitrap Astral analyzer
WP 312	Interference of adjacent ion signals in CDMS: The effect on charge accuracy and potential correction algorithm
WP 316	Application of concepts from Adaptive Retention Time improves the robustness of LC peak integration in targeted MSn experiments
WP 338	Implementation of electron-transfer dissociation (ETD) and electron-transfer/higher-energy collision dissociation (EThcD) on a modified Orbitrap hybrid MS
WP 346	Triple quadrupole mass spectrometer performance: A novel ion guide design for increased robustness
WP 376	Investigating cellular metabolism on a modified Orbitrap hybrid mass spectrometer by the simultaneous use of differently labeled elemental isotope substrates
WP 383	Fully automated implementation of EPA Method 1633 for LC-MS/MS analysis of PFAS in environmental samples using a customized robotic autosampler
WP 450	The remaining discovery potential of untargeted metabolomics
WP 452	A workflow for the rigorous and automated identification of IROA peaks
WP 454	Moving beyond basic ddMS2: Improving annotation confidence in untargeted metabolomics using higher resolution MS and parallel ion trap experiments
WP 458	Enhancing untargeted metabolomics with a modified hybrid Orbitrap and IROA Kit for improved metabolites annotation and normalization

Poster presentations
Wednesday, June 4 (cont.)

WP 491	Sheath liquids and mobile phase additives for enhanced LC-MS analysis of oligonucleotide therapeutics
WP 493	Absolute quantification of epitranscriptomic modifications in *S. cerevisiae* using a microbore LC-MS/MS platform
WP 500	Highly sensitive quantification of therapeutic oligonucleotide in human plasma using a modified Orbitrap hybrid mass spectrometer
WP 508	Comprehensive evaluation of MS and LC-MS/MS based workflows for the characterization of double stranded small interfering RNA-based (siRNA) therapeutics
WP 513	LC-MS analysis of oligonucleotides on the Orbitrap Astral MS: Exploring sensitivity limits and comparison of stability in mouse tissue lysosomes
WP 522	Increased EThcD efficiency on a modified Orbitrap hybrid MS instrument boosts the identification depth and sequence coverage of HLA peptides
WP 526	Immunopeptide analysis with a modified Orbitrap Astral mass spectrometer maximizes peptide detection and quantitation in protein degrader applications
WP 529	Evolution of mass spectrometers driving deeper and sensitive immunopeptide analysis
WP 530	Optimized enrichment and analysis of MHC-I peptides for comprehensive immunopeptidome profiling
WP 543	High-sensitivity immunopeptidomics: Scalable MHC I and II profiling from limited samples reveals dynamic antigen presentation
WP 544	Leveraging advanced mass spectrometry technology for in-depth immunopeptidome profiling
WP 553	Accelerating ETD for global phosphoproteomics
WP 557	Optimizing plant phosphoproteomic data independent acquisition: Micro-pillar array columns and traditional packed bed technology
WP 563	Shining light into the daily growing cycles of *Arabidopsis* with proteomics
WP 581	Impurity profiling of approved and candidate GLP-1 therapeutic peptides using a modified hybrid Orbitrap mass spectrometer

Poster presentations
Wednesday, June 4 (cont.)

WP 584	Characterization of recombinant cystine knot family proteins as raw materials in cell therapy manufacture using a modified hybrid Orbitrap MS
WP 587	Charge detection mass spectrometry and Glu-C/Lys-C digestion based data dependent approach confirm mono-PEGylation of beta epoetin
WP 592	Higher order structure characterization of ADCs using hydrogen-deuterium exchange mass spectrometry (HDX-MS)
WP 598	Multi-attribute characterization of a bispecific molecule leveraging fast EThcD and enhanced native MS on a modified Orbitrap Hybrid MS
WP 602	Alternative fragmentation is not enough for top-down MS and intact protein characterization
WP 639	The secret life of proteins and drugs through the lens of proteome thermal stability
WP 652	Orbitrap Astral MS provides deep coverage of cerebrospinal fluid (CSF) derived small extracellular vesicle (SEV) proteome for clinical insights
WP 704	Multi-draw: Revolutionizing lyophilization-free LC-MS proteomics with large volume injections
WP 717	Experimental characterization of automated emitter position optimization strategies for a new low-flow ion source and cartridge
WP 718	Accelerating the verification of predictive biomarkers of PARP inhibitor resistance in ovarian cancer using highly multiplexed PRM assays
WP 722	Comparison of static-nanospray- and liquid chromatography-mass spectrometry for single-cell metabolomics applied to infectious diseases, utilizing a modified hybrid Orbitrap MS
WP 723	Balancing sensitivity and throughput in single-cell proteomics using low-nanoflow LC-MS
WP 724	Improving the limit of quantification for single-cell proteomics by novel acquisition strategies on a modified Orbitrap Astral mass spectrometer
WP 727	Differential ion mobility single-cell proteomics provides new insights into thymic epithelial cell maturation and differentiation

Poster presentations

Wednesday, June 4 (cont.)

WP 733	Probing DNA damage response at the single-cell level using the Orbitrap Astral mass spectrometer
WP 744	Evaluation of prioritized peptide acquisition for multiplexed single-cell proteomics on a modified Orbitrap Astral mass spectrometer
WP 746	Robust identification of up to 6,600 proteins from a single HeLa cell using a modified Orbitrap Astral mass spectrometer
WP 752	Wide-isolation window PRM for stable isotope tracing metabolomics

Poster presentations

Thursday, June 5

ThP 015	Development and qualification of an LC-MS/MS method for quantification of MUC5AC and MUC5B mucins in spontaneous sputum
ThP 016	Selective and sensitive quantitation of 18 steroids in human serum using Thermo Scientific™ Stellar™ mass spectrometer
ThP 049	Capture scheduled retention time window shift in large scale of peptide quantitation using a modified Orbitrap hybrid mass spectrometer
ThP 060	Qualitative and quantitative analysis of structural isomer flavonoids using UPLC-Orbitrap MS
ThP 061	Method development and validation of pesticides by UPLC-MS/MS
ThP 062	Method development for PFAS analysis in drinking water using UPLC-MS/MS
ThP 129	Higher-throughput chemical exposomics in human serum with phospholipid removal and LC – Orbitrap HRMS analysis
ThP 141	Negative electron transfer dissociation on an Orbitrap Tribrid mass spectrometer to characterize glycosaminoglycans, peptides, and glycopeptides
ThP 155	Optimization of electron transfer dissociation (ETD) MS/MS spectral generation rates on a Tribrid mass spectrometer for peptide-based workflows
ThP 158	Electron capture charge reduction enables recording long transients in Orbitrap-based CDMS for low mass analytes

Poster presentations
Thursday, June 5 (cont.)

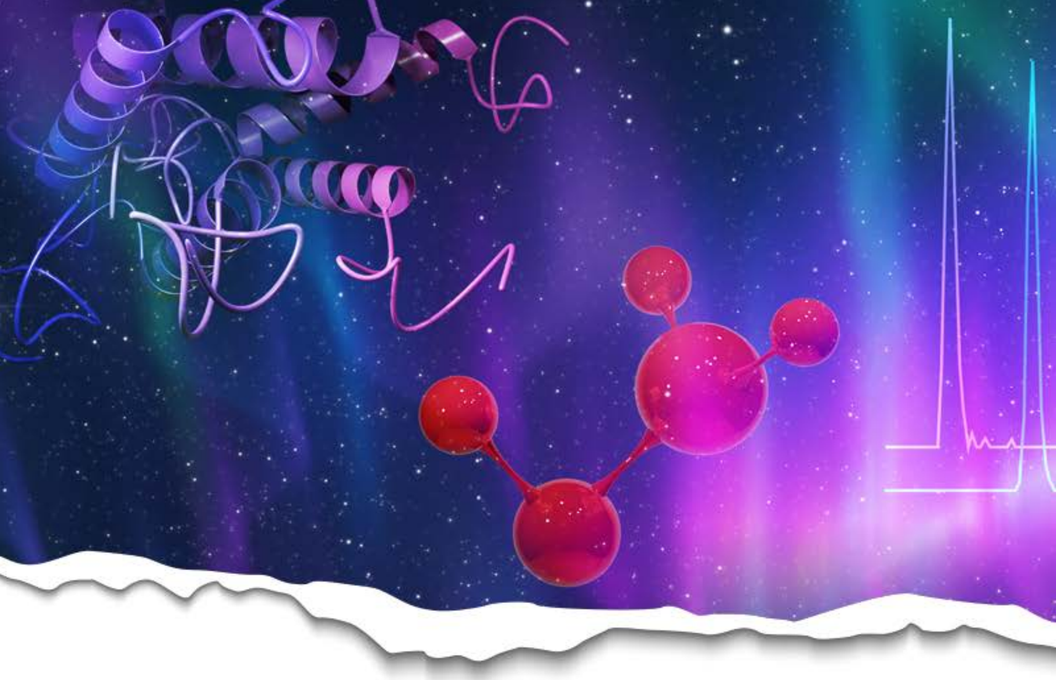
ThP 170	Evaluation of H/D scrambling propensities of various proteins and peptides
ThP 184	Assessment of amide H/D scrambling with UVPD
ThP 193	Efficient tandem capillary flow LC-MS with short µPAC columns and a single ionization source
ThP 202	Ultra high throughput chemoproteomics screening on the Stellar mass spectrometer
ThP 281	Use of real-time data for analytical quality control
ThP 320	Next generation Orbitrap Astral mass spectrometer accelerates discovery via enhanced speed, sensitivity, resolving power and dynamic range
ThP 321	Enabling up to 270 Hz acquisition speed on a modified Orbitrap Astral MS
ThP 324	The universal Orbitrap instrument - from metabolomics over targeted proteomics to native analyses
ThP 325	A dual conversion dynode ion detection system designed for ultimate polarity switching speed
ThP 327	Enhanced resolution multi-pass mode for a modified Orbitrap Astral analyzer
ThP 329	Improving Tribrid MS reliability through a new ion trap electron multiplier with a longer lifetime
ThP 330	TMT HR mode on a modified Orbitrap Astral mass spectrometer enables TMTproD 35plex analysis
ThP 377	Automatic detection and grouping of MS1 fragmentation in LC-MS data
ThP 380	A novel cation-exchange chromatography-MS/MS method for the analysis of basic metabolites and metal ions in biological samples
ThP 386	At the intersection between chromatographic performance, ESI efficiency and instrument productivity: Nano to capillary flow LC-MS on long µPAC columns
ThP 425	Simultaneous Quantitation and Discovery (SQUAD) analysis of lipids in commercial vegetable oils using LC-HRAM-Tribrid platforms
ThP 432	A modified Orbitrap hybrid mass spectrometer for improved sensitivity and reduced false annotations in lipidomic applications

Poster presentations
Thursday, June 5 (cont.)

ThP 439	Increasing plant metabolome coverage using Enhanced Dynamic Range (eDR) scan mode on a modified Orbitrap hybrid mass spectrometer
ThP 452	Communicating compound annotation confidence: Implementation of confidence levels using Compound Discoverer software’s Scripting Node
ThP 492	Improving spatial and temporal proteome mapping of fungal infection dynamics to reveal novel druggable targets
ThP 493	Advancing temporal resolution of fungal proteome modulation for personalized signature detection
ThP 546	Key RNA-binding domains in the La protein establish tRNA modification levels in *Trypanosoma brucei*
ThP 561	OligoFinder: A research software tool for automated oligonucleotide MS/MS spectral annotation and LC-MS/MS sequence mapping
ThP 566	The physics of ion trap-type resonant collision induced dissociation enables maximization of the yield of sequence ions from oligonucleotide anions
ThP 573	Comprehensive quantitation of the mitochondrial proteome with targeted mass spectrometry and real-time retention alignment on Orbitrap Eclipse and Stellar mass spectrometers
ThP 574	Enhanced HCP quantitation LC-MS/MS workflow solution using a magnetic MS sample prep method and heavy-peptide mixture
ThP 575	Synchronous precursor selection of light/heavy peptides on the MS-level using the Stellar MS platform
ThP 576	Detection and quantification of GLP-1 analogs in human plasma: A comprehensive analytical approach
ThP 577	Intelligent targeted MS acquisition achieves seven-order dynamic range in oocyte analysis
ThP 580	Development of a highly multiplexed PRM method on the Stellar MS to reduce instrument time and broaden CSF proteome coverage
ThP 591	Regulated bioanalysis for endogenous glucagon-like peptide-1 (GLP-1) and synthetic analog therapeutic peptide quantitation in biomatrix by LC–MS/MS
ThP 592	Enhanced proteomics quantitation with Stellar mass spectrometry for high-throughput applications

Poster presentations
Thursday, June 5 (cont.)

ThP 622	The adventure of hunting for a membrane protein standard expressed in mammalian cells for cryo-EM
ThP 629	Evaluation of a novel, automated ion source and column assemblies with integrated replaceable emitters for proteomics data acquisition
ThP 646	Advances in next generation ion sources: Enhancing rigor, reproducibility, and robustness within the shared resource environment
ThP 647	A hybrid-DIA approach for simultaneous targeted and untargeted analysis using an Orbitrap Tribrid system
ThP 680	Advancing low flow LC-MS for single cell proteomics with variable flow and 50 cm microfabricated pillar array columns
ThP 698	Enhanced sensitivity of a modified Orbitrap Astral mass spectrometer for deeper proteome coverage in single-cell proteomics applications
ThP 704	Quantitative measurement of ipratropium in human plasma using column switching and tandem mass spectrometry
ThP 705	Optimizing the SQUAD method execution on Orbitrap Tribrid MS to improve acquisition speed while maintaining mass accuracy
ThP 740	Automated tool for optimal quantitative analysis conditions using mzCloud spectral library



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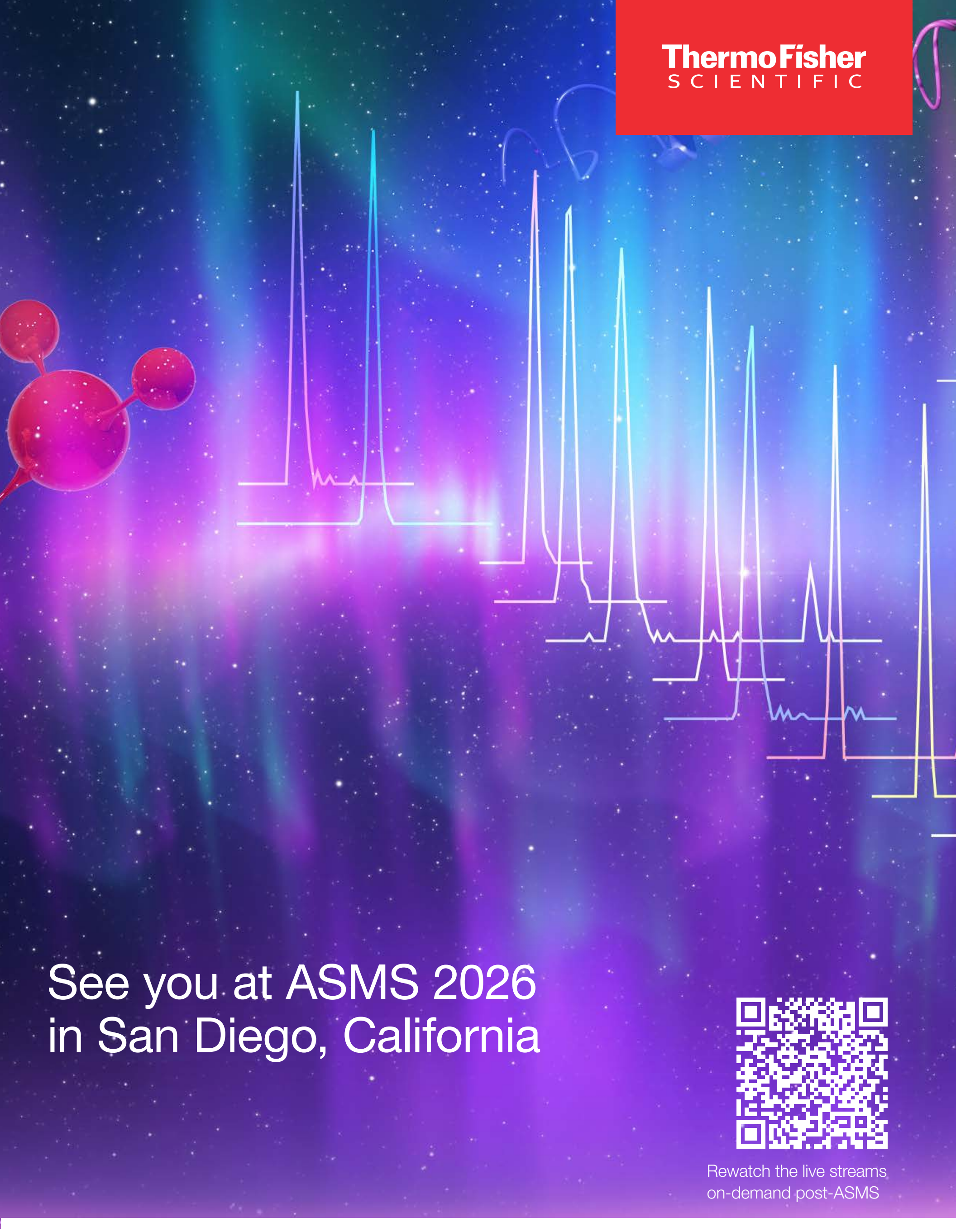

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