CONFERENCE PROGRAM

Additional front matter information will be available with the Program Overview Booklet distributed at the conference.

This program was created on May 7, 2026 and is subject to change (e.g. presenter changes, oral presentation alternates, and more). The intention of this static document is as a resource for those who prefer not to use the Online Planner or Mobile App. The Online Planner and Mobile App will be “the” up-to-date source for detailed program information.

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SATURDAY

8:00 - 9:00 am	**Short Course Badge Printing,** Sails Pavilion (upper level), San Diego Convention Center
9:00 am - 5:00 pm	**Short Courses**, various rooms at the San Diego Convention Center. Pick up a map when you print your badge. **Badge Printing,** Sails Pavilion (upper level), San Diego Convention Center

SUNDAY

8:00 am - 9:00 pm	**Short Course Badge Printing,** Sails Pavilion (upper level), San Diego Convention Center
9:00 am - 5:00 pm	**Short Courses,** various rooms at the San Diego Convention Center. Pick up a map when you print your badge.
9:00 am - 8:00 pm	**Name Badge Printing & Information,** Sails Pavilion (upper level), San Diego Convention Center
4:00 – 4:45 pm	**What to See and Do at ASMS? For students and any interested first timers,** Halll D (ground level)
5:00 - 6:30 pm	**Tutorial Lectures,** Hall D (ground level)  5:00 pm **Lan Huang** University of California, Irvine  5:45 pm **Of Bits and Ions: How Computation Enabled Mass Spectrometry** **Michael MacCoss** University of Washington
6:45 - 7:45 pm	**Opening Plenary,** Hall D (ground level)  **Protein and Ligand Discovery on a Global Scale** **Benjamin Cravatt** The Scripps Research Institute
7:45 - 9:30 pm	**Welcome Reception,** Exhibit-Poster Hall (Hall ABC, ground level)

Consult online planner or mobile app for detailed program.

MONDAY

7:00 - 8:15 am	**Corporate Member Breakfast Seminars,** Convention Center and Marriott Marquis
8:30 - 10:30 am	**Oral Sessions** MOA am: Informatics: Multiomics Integration and Applications, Hall D (ground level) MOB am: Ion Mobility: Instrumentation & Method Development, Ballroom 20A (upper level) MOC am: Fundamentals: Ion Activation and Dissociation, Ballroom 20BC (upper level) MOD am: Chemoproteomics and Protein Probes, Ballroom 20D (upper level) MOE am: Clinical Analysis: Applications, Room 6A (upper level) MOF am: Posttranslational Modifications: Qualitative and Quantitative Analysis, Room 6B (upper level) MOG am: Environmental: Non-Target Analysis and Emerging Contaminants, Room 6CF (upper level) MOH am: Instrumentation: New Developments in Ionization and Sampling, Room 6DE (upper level)
10:30 am - 2:30 pm	**Poster Session and Exhibits,** Monday posters present 10:30 am - 12:00 pm AND 1:00 - 2:30 pm.
12:00 pm	**Deadline to purchase Closing Event Ticket.** Ticket sales close Monday June 1 at 12pm NOON or when tickets sell out. There is a capacity limit for this event, buy your ticket NOW if you wish to join us at the USS Midway.
12:00 - 1:00 pm	**Networking Session A, far-left corner in the Poster-Exhibit Hall** Celebrating Women Mass Spectrometrists
2:30 - 4:30 pm	**Oral Sessions** MOA pm: Informatics: Peptide and Protein Identification and Quantification, Hall D (ground level) MOB pm: Neuroscience and Neurological Disorders Research, Ballroom 20A (upper level) MOC pm: Instrumentation: High-Resolution Mass Spectrometry, Ballroom 20BC (upper level) MOD pm: Fundamentals: Native MS and Structures of Large Ions, Ballroom 20D (upper level) MOE pm: Exposomics, Toxicology and Health Outcomes, Room 6A (upper level) MOF pm: Imaging: Spatially Resolved Omics, Room 6B (upper level) MOG pm: Drug Metabolism and Pharmacokinetics, Room 6CF (upper level) MOH pm: Carbohydrates: From Mono to Poly, Room 6DE (upper level)
4:45 - 5:30 pm	**Award Session & Lecture,** Hall D  **John B. Fenn Distinguished Contribution in Mass Spectrometry** Preceded by the Al Yergey MS Scientist Awards presentations. **Albert J.R. Heck** Utrecht University
5:45 - 7:00 pm	**Evening Workshops** All workshop rooms are on the upper level. 01 DIA for PTMs: Ready for Primetime? (Bioinformatics MS Interest Group), Ballroom 20A 02 Art, Museums and Archaeology (Art, Museums, and Archaeology Interest Group), Ballroom 20BC 03 Mass Spectrometry Approaches for Characterizing Complex Biotherapeutics Modalities (Biotherapeutics Interest Group), Ballroom 20D 04 Entrepreneurship in Mass Spectrometry: Launching through Bootstrapping and Seed Stage Venture Capital (Independent), Room 6A 05 Prediction is Not Proof: Structural Mass Spectrometry in the AlphaFold Era (XL/CL/HDX Interest Group), Room 6B 06 Young Mass Spectrometrist Workshop: Graduate School Through Early Career Forum (Young Mass Spectrometrists Interest Group), Room 6CF 07 Beyond Accurate Mass: Mobility Separation and Ultrahigh-Resolution FTMS (FT-MS Interest Group), Room 6DE 08 Million-Dollar Instruments, Lean Times: How to Build a Sustainable Mass Spectrometry Service Portfolio (Analytical Lab Managers Interest Group), Room 1A 09 Basics and Beyond: Undergraduate Education, Training, and Mentorship in Mass Spectrometry (Undergraduate Research in MS Interest Group), Room 1B 10 Advancing DMPK and Bioanalytical Strategies for New Therapeutic Modalities Through Mass Spectrometry (DMPK Interest Group), Room 2 11 Bridging the External and Internal Exposome through Advanced Mass Spectrometry (Exposomics Interest Group), Room 3 12 The NIH and NSF Review and Funding Process (Independent), Room 4
8:00 - 11:00 pm	**Corporate Member Hospitality Suites at Marriott Marquis**

TUESDAY

7:00 - 8:15 am	**Corporate Breakfast Seminars,** Convention Center and Marriott Marquis
8:30 - 10:30 am	**Oral Sessions** TOA am: Quantitative Proteomics: Instrumentation and Applications, Hall D (ground level) TOB am: Metabolomics: New Technologies and Applications, Ballroom 20A (upper level) TOC am: Drug Discovery and Development: Qualitative and Quantitative, Ballroom 20BC (upper level) TOD am: Challenges in MS Analysis of Complex Mixtures, Ballroom 20D (upper level) TOE am: Biomarkers: Quantitative Analysis, Room 6A (upper level) TOF am: Instrumentation: Detection of High-Mass Analytes, Room 6B (upper level) TOG am: GC-MS Instrumentations Instrumentation and Application, Room 6CF (upper level) TOH am: Plants and Natural Products, Room 6DE (upper level)
10:30 am - 2:30 pm	**Poster Session and Exhibits,** Tuesday posters present 10:30 am - 12:00 pm **AND** 1:00 - 2:30 pm.
12:00 - 1:00 pm	**Networking Session A, far-left corner in the Poster-Exhibit Hall** Elevating South Asian Leadership in Mass Spectrometry and AI **Networking Session B, far-right corner in the Poster-Exhibit Hall** Career Opportunities for Chinese Students and Scholars
2:30 - 4:30 pm	**Oral Sessions** TOA pm: Biomarkers: Qualitative Analysis, Hall D (ground level) TOB pm: Fundamentals: Ionization Methods, Ballroom 20A (upper level) TOC pm: Artificial Intelligence in MS in Instrumentation and Applications, Ballroom 20BC (upper level) TOD pm: Biotherapeutics: Characterizations and Quantitation, Ballroom 20D (upper level) TOE pm: Lipidomics: New MS Technologies and Applications, Room 6A (upper level) TOF pm: Industry: Trace Analysis, Quality Control, and Automation, Room 6B (upper level) TOG pm: Instrumentation: New Hybrid and Multimodal Approaches, Room 6CF (upper level) TOH pm: Stable Isotope Labeling Applications, Room 6DE (upper level)
4:45 - 5:30 pm	**Award Session & Lecture,** Hall D  **Biemann Medal** Preceded by the Research Award and PUI Research Award Presentations **Nikolai Slavov** Northeastern University, Parallel Squared Research Institute
5:45 - 7:00 pm	**Evening Workshops** 01 Top-Down Proteomics: Emerging Advances and Future Directions (Top-Down Proteomics Interest Group), Ballroom 20A 02 Career Development (Career Development Interest Group), Ballroom 20BC 03 High Resolution Ion Mobility: Toward The Need for Standardized Data and Reporting (Ion Mobility MS Interest Group), Ballroom 20D 04 Mass Spectral Libraries: The Past, Present, and Future (Mass Spectral Libraries Interest Group), Room 6A 05 Chemoproteomics: Analytical Rigor, Biological Interpretation, and Translational Application (Independent), Room 6B 06 Real time Mass Spectrometry in Proteomics and Beyond (Independent), Room 6CF 07 Mass Spectrometry of Nucleic Acids: Emerging Challenges and New Opportunities (Oligonucleotides and Nucleic Acids Interest Group), Room 6DE 08 Software and Data Solutions: A Reivew of Current User-Created Platforms. (Lipids & Lipodomics Interest Group), Room 1A 10 JASMS: The Life of a Manuscript and Being a Superstar Reviewer (Independent), Room 1B 09 Celebrating 100 Years of Photoionization MS: Early Developments, Modern Applications, and Future Directions (Photoionization MS Interest Group), Room 2 11 Trapping the Future: The Commercial Resurgence of Ion Trap MS (Ion Trap MS Interest Group), Room 3 12 Advancements in Tools for Studying Materials-Based Catalytic Processes in Polymers and Energy (Polymeric Materials & Energy, Petroleum and Biofuels Interest Groups), Room 4 13 The peptide renaissance: emerging modalities and analytical challenges (Pharmaceuticals Interest Group), Room 7AB 14 Clinical Chemistry Workshop - Small Samples, Big Discussion (Clinical Chemistry Interest Group), Room 8
8:00 - 11:00 pm	**Corporate Member Hospitality Suites at Marriott Marquis**

WEDNESDAY

7:00 - 8:15 am	**Corporate Member Breakfast Seminars,** Convention Center and Marriott Marquis
8:30 - 10:30 am	**Oral Sessions** WOA am: Data-Independent Acquisition: Acquisition and Multiplexing, Hall D (ground level) WOB am: Lipodomics: Targeted and Untargeted, Ballroom 20A (upper level) WOC am: Informatics: Innovations, Ballroom 20BC (upper level) WOD am: Fundamentals: Unconventional Approaches in MS, Ballroom 20D (upper level) WOE am: Instrumentation: Innovative Separation Approaches Coupled to MS, Room 6A (upper level) WOF am: Imaging: Pharmaceuticals, Metabolites, Lipids, and Glycans, Room 6B (upper level) WOG am: Forensics, Innovations and Applications, Room 6CF (upper level) WOH am: Environmental: Innovative Approaches and Instrumentation, Room 6DE (upper level)
10:30 am - 2:30 pm	**Poster Session and Exhibits,** Wednesday posters present 10:30 am - 12:00 pm AND 1:00 - 2:30 pm.
12:00 - 1:00 pm	**Networking Session A, far-left corner in the Poster-Exhibit Hall** Hispanics and Latinx in MS
2:30 - 4:30 pm	**Oral Sessions** WOA pm: Biotherapeutics: Proteins, Antibodies, and Antibody Drug Conjugates, Hall D (ground level) WOB pm: Fundamentals: Chemistry of Gas-Phase Ions (Honoring Michael Bowers), Ballroom 20A (upper level) WOC pm: Protein-Ligand and Protein-Protein Interactions, Ballroom 20BC (upper level) WOD pm: Metabolomics Untargeted Approaches, Ballroom 20D (upper level) WOE pm: Instrumentation: Ambient Ionization and Applications, Room 6A (upper level) WOF pm: Microbes and the Microbiome, Room 6B (upper level) WOG pm: Nucleic Acids and Nucleotides, Room 6CF (upper level) WOH pm: Glycopeptides, Glycoproteins, Room 6DE (upper level)
4:45 - 5:30 pm	**ASMS Meeting**, Hall D Board reports, Awards, and drinks!
5:45 - 7:00 pm	**Evening Workshops** All workshop rooms are on the upper level. 01 Environmental Applications: You Are What You Eat and Breathe (Environmental Applications Interest Group), Ballroom 20A 02 When Gas Phase Biomolecular Structure Differs from Solution Phase (Fundamentals & Native Mass Spec Interest Groups), Ballroom 20BC 03 Advantages of Using Mass Spectrometry Assays (MSA) rather than Ligand Binding Assays (LBA) for the Quantitation of Protein & Peptide Biomarkers (Regulated Bioanalysis Interest Group), Ballroom 20D 04 Careers and Opportunities in Forensic Mass Spectrometry (Forensics & Homeland Security Interest Group), Room 6A 05 AI in Mass Spectrometry-based Metabolomics (Metabolomics Interest Group), Room 6B 06 MS Imaging: Multiplexing and Multimodal Integration for Deeper Insight (Imaging MS Interest Group), Room 6CF 07 Quantitative DIA Data Analysis (Data Independent Acquisition Interest Group), Room 6DE 08 De Novo Peptide Sequencing: ongoing opportunities and challenges (Independent), Room 1A 09 Best Practices for Non-Targeted Analysis - Toward Reproducible Workflows and Defensible Reporting (Independent), Room 1B 10 Analytical Selectivity in Ambient Ionization: From Ion Generation to Mass Analysis (Ambient Sampling & Ionization Interest Group), Room 2 11 Surfing the Next Wave of Metaproteomics: Quantification, Multi-omics and PUFs ! (Metaproteomics Interest Group), Room 3 12 Charge Detection Mass Spectrometry (Independent), Room 4 13 Flavor, Fragrance, and Foodstuff Discussion: Analyte Identifications and Sample Characterizations with GC& LC-MS and modeling tools (Food, Flavor, and Foodstuff Interest Group), Room 7AB
8:00 - 11:00 pm	**Corporate Member Hospitality Suites at Marriott Marquis**

THURSDAY

7:00 - 8:15 am	**Corporate Member Breakfast Seminars,** Convention Center
8:30 - 10:30 am	**Oral Sessions** ThOA am: Single Cell Omics, Hall D (ground level) ThOB am: Integration of Multi-omics Approaches, Ballroom 20A (upper level) ThOC am: Informatics: Metabolomics, Lipidomics and Glycomics, Ballroom 20BC (upper level) ThOD am: Cancer and Immunity, Ballroom 20D (upper level) ThOE am: Structural Biology, Room 6A (upper level) ThOF am: Fundamentals: Ion Structures, Energetics, and Reactions, Room 6B (upper level) ThOG am: Covalent Labeling and Chemical Crosslinking, Room 6CF (upper level) ThOH am: Food Chemistry & Safety: New Innovations, Room 6DE (upper level)
10:30 am - 2:30 pm	**Poster Session and Exhibits**, Thursday posters present 10:30 am - 12:00 pm **AND** 1:00 - 2:30 pm
2:30 - 4:30 pm	**Oral Sessions** ThOA pm: Top-Down Proteomic Analysis, Hall D (ground level) ThOB pm: Small Molecules: Structural Characterization and Quantitation, Ballroom 20A (upper level) ThOC pm: High Throughput MS and Automation, Ballroom 20BC (upper level) ThOD pm: Clinical Analysis: Innovations, Ballroom 20D (upper level) ThOE pm: Food Chemistry & Safety: Foodomics, Allergens, Bacteria, Foods and Supplements, Room 6A (upper level) ThOF pm: Imaging Instrumentation & Method Development, Room 6B (upper level) ThOG pm: Ion Mobility: Structure Determination & Applications, Room 6CF (upper level) ThOH pm: Synthetic Polymers and New Materials, Room 6DE (upper level)
4:45 - 5:30 pm	**Closing Plenary**, Hall D  **Science Integrity** **Elisabeth Bik** Elisabeth Bik, PhD is a microbiologist and independent scientific integrity expert based in the San Francisco Bay Area. With over 20 years of experience, she specializes in identifying problematic data and images in the scientific literature, contributing to more than 1,600 retractions and 1,200 corrections. She previously spent over a decade at Stanford University School of Medicine and now advises journals, publishers, and institutions on research integrity and publication ethics. Her work has been featured in Nature, Science, The New York Times, and The Wall Street Journal. She is the recipient of several international honors, including the John Maddox Prize and the Einstein Foundation Award.
6:30 – 10:00 pm	**Closing Event aboard the USS Midway - ADVANCE PURCHASE TICKET REQUIRED** Ticket sales close Monday June 1 at 12pm NOON or when tickets sell out. There is a capacity limit for this event, buy your ticket NOW if you wish to join us at the USS Midway. 

MOA am: Informatics: Multiomics Integration and Applications
Hall D

MOA am 08:30
Integrative Multiomic Analysis of Cell Signaling and Lipid Metabolism in Diet-Induced Obesity; Yukun Niu[1]; Amy Deik[2]; Clary Clish[2]; Norman J Kennedy[3]; Roger J Davis[3]; Tigist Y Tamir[1, 4, 5, 6]; *[1] Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill, Chapel Hill, NC; [2] Metabolomics Platform, The Broad Institute of MIT and Harvard, Cambridge, MA; [3] Program in Molecular Medicine, University of Massachusetts Chan Medical School, Worecester, MA; [4] Department of Nutrition, Gillings School of Global Public Health, University of North Carolina at Chapel Hill, Chapel Hill, NC, United States, Chapel Hill, NC; [5] Computational Medicine Program, School of Medicine, University of North Carolina at Chapel Hill, Chapel Hill, NC; [6] Lineberger Comprehensive Cancer Center, School of Medicine, University of North Carolina at Chapel Hill, Chapel Hill, NC*

MOA am 08:50
Predictive Multi-Omic Signatures of Immune Responsiveness in the Aging Immunome; Prasanna Vadhana Ashok Kumaar[1]; Kevin Schneider[1]; Jordon Burton[1]; Christina D. King[1]; Durai Sellegounder[1]; Benjamin Ambrose[1]; Birgit Schilling[1]; David Furman[1]; Eric Verdin[1]; *[1] Buck Institute for Research on Aging, Novato, CA*

MOA am 09:10
Probabilistic Modeling and Functional Clustering in Multi-Omics Data Integration; Chi Yen Tseng[1]; John R Tipton[1]; Emilio S Rivera[1]; Tara Harvey[1]; Joshua D. Breidenbach[1]; Brett R. Blackwell[1]; Salvator J. Palmisano[1]; Emilia Solomon[1]; Claire K. Sanders[1]; Grace M. Thornhill[1]; Kes Luchini[1]; Ethan M. Mcbride[1]; Jessica Salguero[1]; Francie E. Rodriguez[1]; Phillip M. Mach[1]; Trevor G. Glaros[1]; *[1] Los Alamos National Laboratory, Los Alamos, NM*

MOA am 09:30
Leveraging Large Language Models for Redundancy-Aware Pathway Analysis and Deep Biological Interpretation; Xiaotao Shen[1]; Yifei Ge[1]; Feifan Zhang[1]; Yijiang Liu[1]; Chuchu Wang[1]; Sai Zhang[2]; Chao Jiang[3]; Peng Gao[4]; Xin Zhou[5]; Nguan Soon Tan[1]; *[1] Nanyang Technological University, Singapore, Singapore; [2] Yale University, West Haven, CT; [3] Zhejiang University, Zhejiang, China; [4] Harvard University, Boston, MA; [5] Fudan University, Shanghai, China*

MOA am 09:50
Harnessing the Power of AI for the Integration and Interpretation of Multi-Omics Data Using a Generalized WGCNA Framework; Ivo Kwee[1]; Antonino Zito[1]; Xavier E Montagut[1]; Axel Martinelli[1]; Klidel F Rellin[2]; Michael Witting[2]; George Rosenberger[3]; Nikolas Kessler[4]; Murat Akhmedov[1]; *[1] BigOmics Analytics SA, Lugano, Switzerland; [2] Helmholtz Munich - Metabolomics and Proteomics Core, Neuherberg, Germany; [3] Bruker Switzerland AG, Fällanden, Switzerland; [4] Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

MOA am 10:10
MAPtoGO: extending gene ontology analysis to lipidomics-centered multiomics data; Dominik Kopczynski[1]; Cristina Coman[2]; Nils Hoffmann[2, 3]; Robert Ahrends[2]; *[1] Department of Analytical Chemistry, University of Vienna, Vienna, Austria; [2] University of Vienna, 1090 Vienna, Austria, Vienna, Austria; [3] Institute for Bio- and Geosciences (IBG-5), Forschungszentrum Jülich GmbH, Jülich, Germany*

MONDAY MORNING ORALS

MOB am: Ion Mobility: Instrumentation & Method Development
Ballroom 20A

MOB am 08:30
Increasing Sensitivity for Single-Residue HDX with Cyclic™ IMS Wideband Enhancement; Vanessa Duerr[1, 2]; Dale Cooper-Shepherd[2]; Owen Cornwell[2]; Jeff Brown[2]; Argyris Politis[1]; *[1]University of Manchester, Manchester, United Kingdom; [2]Waters Corporation, Wilmslow, United Kingdom*

MOB am 08:50
Strategies for Improving Ion Transmission, Mobility Resolution, and CCS Measurement Precision of Small Molecules in Trapped Ion Mobility Spectrometry; Siya Deng[1]; Jody C May[2]; Karly B. Serrano[2]; Erica M. Forsberg[3]; Matthew R. Lewis[4]; John A McLean[2]; *[1]Vanderbilt University, Nashville, TN; [2]Department of Chemistry, Vanderbilt University, Nashville, TN; [3]Bruker Daltonics, Billerica, MA; [4]Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

MOB am 09:10
High-Throughput, automated Collision Induced Unfolding Enabled by Multi-Nozzle Nano-electrospray Ionization; Michael R. Armbruster[1]; Daojing Wang[2]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI; [2]Newomics Inc, Berkeley, CA*

MOB am 09:30
Evaluation of Plasticizer Degradation Dependent on Irradiation Dose using Ultra-High Performance Liquid Chromatography-High Resolution Ion Mobility-Mass Spectrometry; Brooke Baumgarten[1]; Austin Anderson[1]; Chris E Freye[1]; Patricia L Huestis[1]; *[1]Los Alamos National Laboratory, Los Alamos, NM*

MOB am 09:50
MicroLC-HRdm-IMS-MS for sn-Position Resolved Lipidomics: Enhanced Sensitivity Analysis of Volume-Limited Biological Samples; Guillermo Viejo-Palenzuela[1, 2]; Jorge R. Álvarez-Buylla[1, 2]; Héctor González-Iglesias[1, 2]; Marcos Bouza Areces[1, 2]; *[1]Instituto de Productos Lácteos de Asturias (IPLA-CSIC), Oviedo, Spain; [2]Consejo Superior de Investigaciones Científicas (CSIC), Oviedo, Spain*

MOB am 10:10
PASEF-Melodies: Mobility-gated acquisition modes for multi-modal proteomics from single cells to PTMs; Christopher Below[1]; Claudia Martelli[2]; Diana Vitko[3]; Stephanie Kaspar-Schoenefeld[4]; Daniel Hornburg[5]; *[1]Biognosys AG, Schlieren, Switzerland; [2]Bruker Switzerland AG, Fällanden, Switzerland; [3]Bruker Scientific LLC, Billerica, MA; [4]Bruker Daltonics GmbH & Co.KG, Bremen, Germany; [5]Bruker Corporation, San Francisco, CA*

MOC am: Fundamentals: Ion Activation and Dissociation (Honoring Jon Amster) Ballroom 20BC

MOC am 08:30
Top-Down Electron Detachment Dissociation at 20-100 eV with High Space Charge Capacity Trapped Ion FT-ICR Cells at 9.4 tesla; Steven A DeFiglia[1, 2]; Nathan K Kaiser[1]; Greg T Blakney[1]; Marek Polak[1]; Kristina Hakansson[1, 2]; *[1]Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, Tallahassee, FL; [2]Department of Chemistry and Biochemistry, Florida State University, Tallahassee, FL*

MOC am 08:50
Thermometer ions for modern mass spectrometers: Increasing mass and decreasing bond strength for more accurate ion temperatures; Evan H Perez[1]; George Jijieshvili[1]; Christian Ieritano[2]; Scott Hopkins[2]; Brian H Clowers[3]; Peter B. Armentrout[1]; *[1]University of Utah, Salt Lake City, UT; [2]University of Waterloo, Ontario, ON; [3]Washington State University, Pullman, WA*

MOC am 09:10
Exploring the mechanisms of radical directed dissociation enabled by novel cupric lipid ion types; Zunaira Naeem[1]; Yingchan Guo[1]; Boone M. Prentice[2]; *[1]University of Florida, Gainesville, FL; [2]University of Florida, Department of Chemistry, Gainesville, FL*

MOC am 09:30
Investigation of Energy-& Time-resolved Collision Cross Section Changes in Crown Ether Complexes Using Fourier Transform Ion Cyclotron Resonance Mass Spectrometry; Sanaz Mohammadzadeh Koumleh[1]; Statton Sparks[1]; David V Dearden[1]; *[1]Brigham Young University, Provo, UT*

MOC am 09:50
Life beyond glycosaminoglycans: acidic plant polysaccharides as the next frontier for gas-phase sequencing by negative electron transfer dissociation (NETD); Franklin E. Leach III; *University of Georgia, Athens, GA*

MOC am 10:10
Annotating the Collision Induced Unfolding Pathways of Protein Ions Using Electron Capture Dissociation; Cheng-Hua Ma[1]; Michael R. Armbruster[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

MOD am: Chemoproteomics and Protein Probes
Ballroom 20D

MOD am 08:30
Expediting the Discovery of Potent and Selective Deubiquitinase Inhibitors by Activity Proteomics; Hannah B Jones[1]; Simeon D Draganov[1]; Sofia Schoenbauer[1]; Peter AC Wing[1]; Zhu Liang[1]; Emma Murphy[1]; Alice Beard[1]; Angela Chen[1]; Andrea Pierangelini[1]; Jack W Houghton[2]; Sarah Flannery[1]; Iolanda Vendrell[1]; Edward W Tate[2]; Paul R Elliott[1]; Darragh P O'Brien[1]; Eidarus Salah[1]; Andrew P Turnbull[3]; Christopher J Schofield[1]; Benedikt M Kessler[1]; Lennart Brewitz[1]; Adan Pinto-Fernandez[4]; *[1]University Of Oxford, Oxford, United Kingdom; [2]Imperial College London, London, United Kingdom; [3]Cancer Research Horizons, London, United Kingdom; [4]University of Oxford, Oxford, United Kingdom*

MOD am 08:50
Large-scale chemoproteomic profiling of the current clinical kinase inhibitor landscape; Amy L George[1]; Maria Reinecke[1]; Amirhossein Sakhteman[1, 2]; Stephan Eckert[1]; Felix Klingelhuber[1]; Bernhard Kuster[1, 2]; *[1]Chair of Proteomics and Bioanalytics, Technical University of Munich, Freising, Germany; [2]Bavarian Center for Biomolecular Mass Spectrometry (BayBioMS), Technical University of Munich, Freising, Germany*

MOD am 09:10
Discover covalent ligands for protein targets with Ptarmigan; William E Fondrie[1]; Lillian T. Tatka[1]; Sebastian J Paez[1]; Anastasiya V. Prymolenna[1]; Daniele Canzani[1]; Andrea Gutierrez[1]; Kyle Siebenthall[1]; Julia Robbins[1]; Evan E Hubbard[1]; Margaux McBirney[1]; Sydney Huff[1]; Brian McEllin[1]; Gaelle Mercenne[1]; Lindsay K Pino[1]; Alexander J Federation[1]; *[1]Talus Bioscience, Seattle, WA*

MOD am 09:30
CHIPP: An automated, plate-format and chaotrope-based denaturation for drug target identification; Dominik Steinbrunn[1]; Viktoria Fischer[1]; Alexander Betz[1]; Gözde Kibar[1]; Christin Zasada[1]; Götz-Norman Hagemann[1]; Stephan Sieber[2]; Hannes Hahne[1]; *[1]Momentum Biotechnologies, Freising, Germany; [2]Department of Bioscience, School of Natural Sciences, Technical University of Munich, Munich, Germany*

MOD am 09:50
Fast Photochemical Iodination and Capture by Suzuki Captures the State-dependent Proteome; Miranda Villanueva[1]; Elijah Biletch[1]; Andrew Becker[1]; Nikolas Burton[1]; Sho Takechi[1]; Joelle Darrouj[1]; Nithesh Perumal[1]; Lisa Boatner[1]; Ashley Julio[1]; Julian Whitelegge[1]; Keriann Backus[1]; *[1]UCLA, LOS ANGELES, CA*

MOD am 10:10
A Live-Cell Chemoproteomic Atlas of Stereoselective Ligand–Protein Interactions Reveals Site-Specific Engagement at Protein–Protein Interfaces; Geordon A. Frere[1]; Ka Yang[1]; Joao A. Paulo[1]; Edward L. Huttlin[1]; Steven P. Gygi[1]; *[1]Harvard Medical School, Boston, MA*

MOE am: Clinical Analysis: Applications
Room 6A

MOE am 08:30
Intraoperative Application of the MasSpec Pen for Rapid Molecular Detection and Subtyping ofBrain Tumors; Keziah E Liebenberg[1]; Charles A Wolfe[1]; Emily X Ma[1]; Sherise D Ferguson[2]; Sujit S Prabhu[2]; Chibawanye I Ene[2]; Frederick Lang[2]; Maria A Gubbiotti[2]; Jason T Huse[2]; Leomar Y Ballester[2]; Dima Suki[2]; Jeffrey Weinberg[2]; Livia S Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX; [2]MD Anderson Cancer Center, Houston, TX*

MOE am 08:50
Rapid Metabolite Profiling of Indeterminate Thyroid Fine-Needle Aspiration Biopsies Using Paper Spray Ionization Miniature Mass Spectrometry; Tzu-Yin Wan[1]; Laura Min Xuan Chai[1]; Jia-Ying Yu[1]; Yi-Hsin Chen[1]; Ting-Chun Kuo[1]; Ming-Hsun Wu[2]; Kuen-Yuan Chen[2, 3]; Cheng-Chih Hsu[1, 4]; *[1]National Taiwan University, Taipei, Taiwan; [2]National Taiwan University Hospital, Taipei, Taiwan; [3]National Taiwan University Cancer Center, Taipei, Taiwan; [4]Leeuwenhoek Laboratories Co. Ltd., Taipei, Taiwan*

MOE am 09:10
At the Speed of Quality - Application of a Novel Mass Spectrometer to Highly Multiplexed Urine Drug Analysis; Brian Rappold[1, 2]; Julia Yllanes[1]; Payton Ozburn[1]; Samuel Huggins[1]; Matthew Campbell[1]; Gregory Janis[1]; *[1]LabCorp, Raleigh, NC; [2]University of Iceland, Reykjavik, Iceland*

MOE am 09:30
High-Resolution Mass Spectrometry Testing of Monoclonal Proteins for Monoclonal Gammopathies; Ruben Luo[1]; Priscilla Yeung[1]; *[1]Stanford University, Palo Alto, CA*

MOE am 09:50
Speed Meets Precision: High-Throughput Plasma Analysis of Vitamins B3 and B5; Sylvain Letarte[1]; Serge Auger[2]; Mégane Moreau[2]; Pierre Picard[2]; Sarah Demers[2]; Jonathan Rochon[2]; Jean Lacoursiere[2]; *[1]Ingenio Sciences, Calgary, AB; [2]Phytronix Technologies, Inc., Quebec, QC*

MOE am 10:10
Integrative Blood Proteomics Reveals the HuBP Atlas of over 10,000 Proteins Informing Human Physiology and Disease; Zhenyu Sun[1]; T. Mamie Lih[1]; Yuanyu Huang[1]; Yingwei Hu[1]; Yuefan Wang[1]; Hui Zhang[1]; *[1]Johns hopkins university, baltimore, MD*

MOF am: Posttranslational Modifications: Qualitative and Quantitative Analysis
Room 6B

MOF am 08:30
Bent trap pre-accumulation enables fast EThcD-based site-specific analysis of thousands of labile PTMs on the Orbitrap Excedion Pro mass spectrometer; Sara C. Buch-Larsen[1]; Ivo A. Hendriks[1]; Peter Krüger[2]; Andreas Kühn[2]; Adnan Halim[3]; Hanno C. Resemann[2]; Alexander Harder[2]; Markus Kellmann[2]; Jesper V. Olsen[1]; *[1]NNF Center for Protein Research, University of Copenhagen, Denmark; [2]Thermo Fisher Scientific, Bremen, Germany; [3]Copenhagen Center for Glycocalyx Research, University of Copenhagen, Denmark*

MOF am 08:50
Performance of PTM Identification Strategies in Multi-Modification Search; Alec Michael Candib[1]; Adam Labadorf[1]; Joseph Zaia[1]; *[1]Boston University, Boston, MA*

MOF am 09:10
A global analysis of steady-state phosphorylation-dephosphorylation dynamics by stable isotope labelling; Juan M Valverde[1, 2]; Andrea Corno[1]; Lindsey A Allan[1]; Tobias Dürr-Mayer[3]; Sathish K.R. Padi[4, 5]; Wolfgang Peti[4]; Henning Jessen[3]; Tony Ly[1]; Adrian Saurin[1]; *[1]University of Dundee, Dundee, Scotland, United Kingdom; [2]Universidad de Costa Rica, San Jose, Costa Rica; [3]University of Freiburg, Freiburg, Germany; [4]University of Connecticut, Connecticut, CT; [5]University of Alabama, Birmingham, AL*

MOF am 09:30
Benchmarking and optimizing DIA workflows for robust post-translational modification analysis; Laura J Keller[1]; Christopher M Rose[1]; Hanna Budayeva[1]; Meena Choi[1]; *[1]Genentech, South San Francisco, CA*

MOF am 09:50
The mouse tissue PTM atlas; Benton J. Anderson[1, 2]; Annie Jen[1, 2]; Noah M. Lancaster[2, 3]; Ross W. Soens[1, 2, 4]; Katherine A. Overmyer[1, 2, 4]; Joshua J. Coon[1, 2, 3, 4]; *[1]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [2]National Center for Quantitative Biology of Complex Systems, Madison, WI; [3]Department of Chemistry, University of Wisconsin-Madison, Madison, WI, Madison, WI; [4]Morgridge Institute for Research, Madison, WI*

MOF am 10:10
STAMP-MS: High-Throughput Thermostability Mapping of HLA Class I/II Immunopeptidomes, including PTMs and Non-canonical Ligands; Mohammad Shahbazy[1]; Ruimin Wang[1]; Peter Kubiniok[2]; Isabelle Leo[1]; Valeria Azcoitia[1]; Etienne Caron[1, 3]; *[1]Department of Immunobiology, Yale School of Medicine, Yale University, New Haven, CT; [2]Quantivum Inc., montreal, QC; [3]Yale Center for Immuno-Oncology, Yale Center for Systems and Engineering Immunology, Yale Center for Infection and Immunity, Yale School of Medicine, New Haven, CT*

MOG am: Environmental: Non-Target Analysis and Emerging Contaminants
Room 6CF

MOG am 08:30
From Lab to Legislation: A Harmonized Experimental Approach to Drinking Water Treatment Assessments for Plant Protection Products; Michael Kubicki[1]; Patrick Olaf Helmer[2]; Thomas Boultwood[3]; Michael Swift[4]; David Pelzer[1]; Sonja Weishaupt[2]; Hannah Jakubovic[3]; *[1]Bayer AG, Monheim, Germany; [2]BASF SE, Limburgerhof, Germany; [3]Syngenta Ltd., Berkshire, United Kingdom; [4]Corteva Agriscience, Indianapolis, IN*

MOG am 08:50
Leveraging Ion Mobility for PFAS Non-Targeted Analysis using FluoroMatch IM 2.0 and a Collision Cross Section (CCS) Atlas; Sheher Mohsin[1, 2]; Jeremy Koelmel[2]; Parker Chang[2]; Yanan Chen[3]; Olivier P. Chevallier[4]; Erin S. Baker[5]; Kara M. Joseph[5]; Sarah M. Stow[4]; Rachel Smolinski[3]; Lauren Royer[6]; Emma E. Rennie[4]; Michael Kummer[7]; Paul Stelben[2]; Jacqueline Bangma[8]; Mark Strynar[8]; David Schiessel[2]; Carrie McDonough[3]; Krystal J. Godri Pollitt[2]; *[1]Beyond Spectral Peaks, Barrington, IL; [2]Yale University, New Haven, CT; [3]Carnegie Mellon University, PITTSBURGH, PA; [4]Agilent Technologies, Santa Clara, CA; [5]University of North Carolina at Chapel Hill, Chapel Hill, NC; [6]MOBILion Systems, Inc, Chadds Ford, PA; [7]Innovative Omics, Sarasota, FL; [8]Environmental Protection Agency, Research Triangle Park, NC*

MOG am 09:10
Improved non-targeted coverage of PFAS using mass defect informed data-dependent analysis; Christine Fisher[1]; Brian Ng[1]; Jeremy Koelmel[2, 3]; Susan Genualdi[1]; *[1]FDA, College Park, MD; [2]Department of Environmental Health Sciences, School of Public Health, Yale University, New Haven, CT; [3]Innovative Omics, Sarasota, FL*

MOG am 09:30
Azobenzene Disperse Dye Exposure Biomarkers: What Can Public-Repository GNPS Data Tell Us?; Kirsten E Overdahl[1]; Alan K. Jarmusch[2]; *[1]National Institute of Environmental Health Sciences, Research Triangle Park, NC; [2]National Institute of Environmental Health Sciences, National Institutes of Health, Research Triangle Park, NC*

MOG am 09:50
Spatial Detection of Polystyrene Plastics in Full-Body Murine Tissue with MALDI TIMS MSI; Karina A Vargas[1]; Elizabeth Neumann[1]; Amy Parkhurst[1]; Fawaz Haj[1]; *[1]University of California, Davis, Davis, CA*

MOG am 10:10
Uncovering PFAS bioaccumulation in seal livers: Insights from suspect screening and nontarget analysis using HPLC-IMS-QTOF-MS; Yanan Chen[1]; Leenia Mukhopadhyay[1]; Bernard Crimmins[2]; Carrie McDonough[1]; *[1]Carnegie Mellon University, Pittsburgh, PA; [2]Academic Environmental/Analytical Consulting Services (AEACS), LLC, New Kensington, PA*

MONDAY MORNING ORALS

MOH am: Instrumentation: New Developments in Ionization and Sampling
Room 6DE

MOH am 08:30
Helios2D: A Cell-Preserving Method for Mass Spectrometric Analysis of Living Cells under Near-Native Conditions; Timm Schaefle; *University of Tübingen, Tübingen, Germany*

MOH am 08:50
Peptide barcoding enables high-throughput enzyme screening with droplet-ESI-MS; Berk G. Kocar[1]; Denijel Y. Latifovic[1]; Tania M. Roberts[1]; Sven Panke[1]; *[1]ETH Zurich, Zurich, Switzerland*

MOH am 09:10
Scalable Native Mass Spectrometry Enabled by Online Tangential Flow Filtration; Gabrielle Blake[1]; Raihana Afroz[1]; Carter Asef[2]; Suraj Dhungana[2]; Mason Chilmonczyk[2]; Varun V Gadkari[1]; *[1]University of Minnesota, Minneapolis, MN; [2]Andson Biotech, Atlanta, GA*

MOH am 09:30
Reframing NanoESI Desolvation Limits through Decoupled Post-Emission Thermal Conditioning of Charged Droplets; Xiaokun Duan[1]; Charles C. Liu[1]; *[1]ASPEC Technologies Limited, Beijing, China*

MOH am 09:50
Trace metal analysis in the field: real-time detection of airborne particles by microwave induced plasma time-of-flight mass spectrometry (mipTOF); Alexander Gundlach-Graham[1]; Michael Groessl[1]; Abigail Koss[2]; Jay Slowik[3]; Andre Prevot[3]; Ed Fortner[4]; John Jayne[4]; Martin Tanner[1]; *[1]Tofwerk, Thun, Switzerland; [2]TOFWERK, Thun, Switzerland; [3]PSI Center for Energy and Environmental Sciences, Villigen, Switzerland; [4]Aerodyne Research, Billerica, MA*

MOH am 10:10
Ship Based- and Underwater-Photoionization Mass Spectrometry (MI-PIMS) for On-Line Detection of Dumped Ammunition and Leaking Bunker-Fuel from Ship Wrecks; Ralf Zimmermann[1, 2]; Thomas Kroeger-Badge[3]; Carolin Schwarz[3]; Sven Ehlert[4]; Ralf Prien[5]; Detlef Schulz-Bull[5]; Eric Achterberg[6]; Johannes Passig[3]; Thorsten Streibel[3]; Andreas Walte[4]; *[1]University of Rostock, Chair of Analytical Chemistry, Rostock, Germany; [2]University of Eastern Finland, Kuopio, Finland; [3]University of Rostock, Rostock, Germany; [4]Photonion GmbH, Schwerin, Germany; [5]Institut fuer Ostseeforschung, Warnemuende, Germany, Warnemuende, Germany; [6]Geomar, Kiel, Germany*

MOA pm: Informatics: Peptide and Protein Identification and Quantification
Hall D

MOA pm 02:30

Systematic Assessment of Entrapment Strategies for Accurate FDR Validation in DIA Proteomics; Monika Pepelnjak[1]; Oliver M. Bernhardt[1]; Tejas Gandhi[1]; [1]*Biognosys AG, Schlieren, Switzerland*

MOA pm: Informatics: Peptide and Protein Identification and Quantification
Hall D

MOA pm 02:50

Differential Proteoform Regulation Limits Accuracy of Protein Quantification in Bottom-up Proteomics; Justus L Grossmann[1]; Vadim Demichev[1]; [1]*Charité - University Medicine Berlin, Berlin, Germany*

MOA pm: Informatics: Peptide and Protein Identification and Quantification
Hall D

MOA pm 03:10

In-Source or In Vivo? Disentangling Immunopeptidome Identifications with RT-Predicted Fragment Flags; Hem R Gurung[1]; Kristin Leskoske[1]; Ana Marcu[1]; Christopher M Rose[1]; Susan Klaeger[1]; [1]*Genentech, South San Francisco, CA*

MOA pm: Informatics: Peptide and Protein Identification and Quantification
Hall D

MOA pm 03:30

Transcriptome-informed peptide search spaces redirect low-confidence identifications toward biologically supported peptides in DIA proteomics; Regina M Edgington[1]; Jacob W Smith[2]; Vladislav Belyy[1, 3]; Damien B Wilburn[1, 3]; [1]*The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH;* [2]*The Ohio State Biochemistry Program, Columbus, OH;* [3]*The Ohio State Center for RNA Biology, Columbus, OH*

MOA pm: Informatics: Peptide and Protein Identification and Quantification
Hall D

MOA pm 03:50

GDPilot: an integrative software solution to enable real-time multiplexed targeted proteomics on a modified Orbitrap Tribrid mass spectrometer; Qing Yu[1]; Fangyi Zhai[2]; Daniel Richards[2]; Shaoxian Li[2]; Zixuan Ye[2]; [1]*University of Massachusetts Chan Medical School, Worcester, MA;* [2]*UMass Chan Medical School, Worcester, MA*

MOA pm: Informatics: Peptide and Protein Identification and Quantification
Hall D

MOA pm 04:10

PAW Agent: AI Agent for Proteomics Automated Workflows; Nathaniel K Berney[1]; David J Foreman[2]; Gaurav Chopra[2]; [1]*Purdue University, West Lafayette, IN;* [2]*Purdue Univeristy, West Lafayette, IN*

MOB pm: Neuroscience and Neurological Disorders Research
Ballroom 20A

MOB pm 02:30
Pan-neurodegeneration proteomics reveals disease subtypes and molecular signatures; Him K Shrestha[1]; Huan Sun[1]; Jay M. Yarbo[1]; DongGeun Lee[1]; Danting Liu[1]; Erming Wang[2]; Meghan McReynolds[1]; Nan Zhang[1]; Boer Xie[1]; Shu Yang[1]; Kaiwen Yu[1]; Suresh Poudel[1]; Yuxin Li[1]; Zuo-Fei Yuan[1]; Dehui Kong[3]; Minghui Wang[2]; Zhen Wang[1]; Mingming Niu[1]; Hong Wang[1]; Masihuz Zaman[1]; Ju Wang[1]; David Vanderwall[1]; Yu Sun[1]; Zhiping Wu[1]; Ping-Chung Chen[1]; Bing Bai[1]; Anthony A. High[1]; Julia Faura[4]; Chunyu Liu[5]; David A. Bennett[6]; Erik C. B. Johnson[7]; Nicholas T. Seyfried[7]; Allan I. Levey[7]; Vahram Haroutunian[2]; Geidy E. Serrano[8]; Thomas G. Beach[8]; Michael DeTure[9]; Takahisa Kanekiyo[9]; Ronald C. Petersen[10]; Guojun Bu[9]; Pamela J. McLean[9]; Dennis W. Dickson[9]; Rosa Rademakers[4]; Gang Yu[11]; Xusheng Wang[3]; Bin Zhang[2]; Junmin Peng[1]; *[1]St. Jude Children's Research Hospital, Memphis, TN; [2]Icahn School of Medicine at Mount Sinai, Friedman Brain Institute, New York City, NY; [3]University of Tennessee Health Science Center, Memphis, TN; [4]University of Antwerp, Antwerpen, Belgium; [5]SUNY Upstate Medical University, Syracuse, NY; [6]Rush University Medical Center, Chicago, IL; [7]Emory University, Atlanta, GA; [8]Banner Sun Health Research Institute, Sun City, AZ; [9]Mayo Clinic, Jacksonville, FL; [10]Mayo Clinic, Rochester, MN; [11]University of Texas Southwestern Medical Center, Dallas, TX*

MOB pm 02:50
Quantitative Imaging and Characterization of Brain Ganglioside Phenotypes in Parkinson's Disease; Kim Ekroos[1]; Shadrack M Mutuku[2]; Reza Ranjbar Choubeh[3]; Nicolas Tomasiello[2]; Caine Smith[4]; Maria José Q Mantas[3]; Greg Sutherland[4]; Nathan G. Hatcher[5]; Nico Verbeeck[3]; Shane R Ellis[2]; *[1]Lipidomics Consulting Ltd, Esbo, Finland; [2]Molecular Horizons, School of Chemistry and Molecular Bioscience, University of Wollongong,, Wollongong, Australia; [3]Aspect Analytics, Genk, Belgium; [4]The University of Sydney, Sydney, NSW, Australia, Sydney, Australia; [5]Merck & Co., Inc., West Point, PA*

MOB pm 03:10
Integrating MALDI-MSI and Spatial Transcriptomics to Resolve Amyloid Plaque Heterogeneity in Alzheimer's disease; Alicja Szadziewska[1]; Maciej Dulewicz[1]; Sophia Weiner[1, 2]; Junyue Ge[1]; Sofia Johansson[1]; Henrik Zetterberg[1, 2, 3, 4, 5]; Martin Johansson[1]; Tammaryn Lashley[2]; Jorg Hanrieder[1, 2, 3]; *[1]Gothenburg university, gothenburg, Sweden; [2]University College London, London, United Kingdom; [3]Sahlgrenska University Hospital, Gothenburg, Sweden; [4]University of Wisconsin-Madison, Madison, WI; [5]Hong Kong Center for Neurodegenerative Diseases, Hong Kong, China*

MOB pm 03:30
Localized nanodialysis with capillary electrophoresis mass spectrometry to profile a neuromuscular junction model; Ashley E Lenhart[1, 2]; Christopher K Brenden[1, 2]; Hyegi Min[1]; Weihua Shi[1]; Keyin Li[1]; Woong Kim[1]; Jerry Xu[1]; Rashid Bashir[1, 2]; Yurii Vlasov[1, 2]; Jonathan V Sweedler[1, 2]; *[1]University of Illinois Urbana Champaign, Urbana, IL; [2]Biohub, Chicago, IL*

MOB pm 03:50
Single-cell proteomics in Alzheimer's disease to infer disease progression; Corinna Friedrich[1]; Peyton Stewart[1]; Jason Derks[1]; Megan Elcheikhali[1]; Theresa Connors Stewart[2]; Alexandra Melloni[2]; Derek Oakley[2]; Bradley T Hyman[2]; Mahlon Collins[1]; Nikolai Slavov[1, 3]; *[1]Parallel Squared Technology Institute, Watertown, MA; [2]Department of Neurology, Massachusetts Alzheimer's Disease Research Center, Massachusetts General Hospital, Harvard Medical School, Boston, MA; [3]Departments of Bioengineering, Biology, Chemistry, and Chemical Biology, Single Cell Proteomics Center, and Barnett Institute, Northeastern University, Boston, MA*

MOB pm 04:10
Using complementary discovery and targeted proteomic techniques on cerebrospinal fluid (CSF) provides unprecedented insight into Alzheimer's Disease (AD); Lauren Tang[1]; Evgeny Kanshin[1]; Dominique Leitner[1]; Tovia Jacobs[1]; Luisa F Figueredo[1]; Ricardo M Osorio Suarez[1]; Thomas Wisniewski[1]; Beatrix Ueberheide[1]; *[1]NYU Langone Health, New York, NY*

MOC pm: Instrumentation: High-Resolution Mass Spectrometry
Ballroom 20BC

MOC pm 02:30
Non-Fourier transform processing of ICR MS transients for improved and super-resolved spectra; Ulviyya ABDULKARIMOVA[1, 2]; Pierre COLLET[3]; Christian Rolando[4]; [1]*Azerbaijan State Oil and Industry University, Baku, Azerbaijan;* [2]*French-Azerbaijani University, Baku, Azerbaijan;* [3]*Universidad Andrés Bello, Viña del Mar, Chile;* [4]*Univ. de Lille, Sciences et Technologies, Villeneuve D'ascq, France*

MOC pm 02:50
Fundamental Understanding of the Role of LiPO2F2 as Additive in Lithium-Ion Electrolytes Elucidated by High-Resolution Mass Spectrometry ; Egon Kherchiche[1, 2, 3]; Théo Sombret[3, 4]; Julien Maillard[5]; Antonin Gajan[2]; Marie Hubert-Roux[3, 4]; Carlos Afonso[3, 4]; Pierre Giusti[3, 5]; [1]*University of Rouen (CARMeN), Rouen, France;* [2]*Saft, Corporate Research, 33074, Bordeaux, France;* [3]*International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France;* [4]*University of Rouen-CARMeN institut, Mont-Saint-Aignan, France;* [5]*TotalEnergies Research and Technology Gonfreville, Harfleur, France*

MOC pm 03:10
Untargeted HRMS Screening of Emerging Contaminants in Food Contact Materials: PFAS, Bisphenols, and NIAS; Marinella Vitulli[1]; Flavia Cozzolino[1]; Filippo Pratesi[1]; [1]*Food Contact Center s.r.l., Serravalle Pistoiese, Italy*

MOC pm 03:30
High Resolution Charge Detection Mass Spectrometry with Radially Segmented Ion Mirrors; David Reitenbach[1]; Martin F Jarrold[2]; [1]*Indiana University, Bloomington, IN;* [2]*Indiana University Bloomington, Bloomington, IN*

MOC pm 03:50
High-Order Velocity Focusing Enabled by a Single-Stage Reflectron TOF-MS: A Theoretical Study; Yi-Hong Cai[1]; Yi-Sheng Wang[1]; [1]*Genomics Research Centre (GRC) Academia Sinica, Taiwan, Taipei, Taiwan*

MOC pm 04:10
Unique Insights into FTMS Performance from an Orbitrap Eclipse-ICR Hybrid Instrument; Chad R. Weisbrod[1]; Nathan K. Kaiser[1]; Martha L Aguilera[1]; Ryan P. Rodgers[1]; Christopher L. Hendrickson[1]; Kristina Hakansson[1, 2]; [1]*National High Magnetic Field Laboratory, Tallahassee, FL;* [2]*Department of Chemistry and Biochemistry, Florida State University, Tallahassee, FL*

MOD pm: Fundamentals: Native MS and Structures of Large Ions
Ballroom 20D

MOD pm 02:30
Stability and Structural Connectivity of Genome-Loaded Adeno-Associated Virus Vectors Revealed by Advanced Mass Spectrometry; JAYOTI ROY[1]; Elizabeth Duselis[1]; Zhongping Liao[2]; Shannon Raab[2]; Zhirui Lian[2]; Vicki H. Wysocki[1, 3]; *[1]Georgia Institute of Technology School of Chemistry and Biochemistry, Atlanta, GA; [2]Eli Lilly & Company, Indianapolis, IN; [3]Native MS Guided Structural Biology Center, Georgia Institute of Technology, Atlanta, GA*

MOD pm 02:50
Investigating small heat shock protein structure using electrospray ion beam deposition and cryo-EM; Noor H Naseeb[1]; Laurence Seeley[2]; Lukas Eriksson[3]; Jingjin Fan[3]; Justin L.P. Benesch[3]; Lindsey Baker[2]; Stephan Rauschenbach[3]; *[1]University of Oxford, Oxford, United Kingdom; [2]Department of Biochemistry, University of Oxford, Oxford, United Kingdom; [3]Department of Chemistry, University of Oxford, Oxford, United Kingdom*

MOD pm 03:10
Decoding Membrane Protein Glycosylation and Its Structure-Function Roles Using PTR-Based Native Mass Spectrometry; Ning-En Chang[1]; Guan-Ting Lian[1, 2]; Weijing Liu[3]; Kay-Hooi Khoo[1]; Hsin-Yung Yen[1, 2]; *[1]Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan; [2]Institute of Biochemical Sciences, National Taiwan University, Taipei, Taiwan; [3]Thermo Fisher Scientific, San Jose, CA*

MOD pm 03:30
Integrated Collision-Induced Unfolding, Ion Mobility, and Electron Capture Dissociation Reveal Structural Effects of Metal Loss in Superoxide Dismutase 1; Lester S. Manly[1]; Ryan N. Coyle[2]; Yury V. Vasil’ev[3]; Joseph S. Beckman[4]; Blaine R. Roberts[1]; *[1]Emory University, Atlanta, GA; [2]Vanderbilt University, Nashville, TN; [3]Agilent Technologies Inc., Corvallis, OR; [4]Oregon State University, Corvallis, OR*

MOD pm 03:50
Using Native Electron Capture Charge Reduction Mass Spectrometry to Structurally Characterize Amyloidogenic Protein Oligomers; Eileen Jacqueline Olivares[1]; Rebecca A. Jenkins[1]; Melanie J. Olivares[2]; Zoe J. Heidersbach[1]; Jiahui Lu[1]; Emily Byrd[3]; Jeffrey Zhang[1]; David Boyer[1]; Roni Haj Hussein[1]; Liisa Lutter[1]; David S. Eisenberg[1]; Jose A. Rodriguez[1]; Rachel R. Ogorzalek Loo[1]; Joseph A. Loo[1]; *[1]University of California, Los Angeles, Los Angeles, CA; [2]University of Southern California, Los Angeles, CA; [3]University of Leeds, Leeds, United Kingdom*

MOD pm 04:10
Determining Thermochemical Barriers for Higher-Order Collision Induced Unfolding Transitions Across Commercial Instruments to Understand Gas-Phase Protein Structure; Austin W. Green[1]; Michael R. Armbruster[2]; Kenneth R. Newton[1]; Ruwan T. Kurulugama[3]; Brandon T. Ruotolo[2]; James S Prell[1]; *[1]University of Oregon, Eugene, OR; [2]University of Michigan, US, MI; [3]Agilent Technologies, Inc., Santa Clara, CA*

MONDAY AFTERNOON ORALS

MOE pm: Exposomics, Toxicology and Health Outcomes
Room 6A

MOE pm 02:30
Proteomic remodeling of human satellite III DNA as a marker of cellular response to environmental stress; Sahar Attar[1]; Conor P Herlihy[1]; Lidan Li[1]; Elijah Biletch[2]; Keriann M. Backus[2]; Brian J Beliveau[1]; Devin K Schweppe[1]; *[1]Department of Genome Sciences, University of Washington, Seattle, WA; [2]Department of Chemistry and Biochemistry, University of California Los Angeles, Los Angeles, CA*

MOE pm 02:50
Towards a safe and environmentally sustainable valorisation of post-consumer cotton and polycotton garments; Tim Roland Jan Åström[1]; Abhirami Manoj[1]; Jutta Hildenbrand[2]; Aji Mathew[1]; Ulrika Nilsson[1]; *[1]Stockholm University, Stockholm, Sweden; [2]Research institutes of Sweden, Göteborg, Sweden*

MOE pm 03:10
Multi-Omics Integration Reveals Metabolic Signatures Linking Air Pollution to Immune Dysregulation and Epigenetic Changes in Children; Xiangping Lin[1]; Xinyue Zhang[2]; Mary Margaret Johnson[3]; Maya M. Kasowski[4]; Kari Christine Nadeau[3]; Michael P. Snyder[2]; *[1]Stanford University, Stanford, CA; [2]Department of Genetics, Stanford University School of Medicine, Stanford, CA; [3]Department of Environmental Health, Harvard T.H. Chan School of Public Health, Boston, MS; [4]Department of Pathology, Stanford University School of Medicine, Stanford, CA*

MOE pm 03:30
Rapid, Sensitive Analysis of Nitrite Content in Pharmaceutical Products: Method Transfer to SIFT-MS; Leslie P Silva[1]; Mark J Perkins[2]; Vaughan S Langford[3]; *[1]Syft Technologies, Studio City, CA; [2]Da Vinci Laboratory Solutions UK & Ireland Limited, Cambridge, United Kingdom; [3]Syft Technologies Ltd, Christchurch, New Zealand*

MOE pm 03:50
Quantitative PFAS Determination by Flow-Chemistry–Constrained Chromatography Using the Blake–Schmidt Band-Spreading Framework; Mihira Kasun[1]; Leiver Campeon[1]; Pulasthi Ekanayake[1]; Harshani Bandara[1]; Lalin Theverapperuma[1]; *[1]EXPERT Intelligence, Santa Clara, CA*

MOE pm 04:10
Early Life Microplastic Exposure and its Impacts on Bile Acid Homeostasis; Emily C Vincent[1]; Benjamin Czapla[2]; Sadie M. Disselkoen[1]; Subharthe Samandra[3]; Brad O. Clarke[3]; Casey M. Theriot[4]; Lincon A. Stamp[2]; Marlene A. Hao[2]; Erin S. Baker[1]; *[1]UNC-Chapel Hill, Chapel Hill, NC; [2]Department of Anatomy and Physiology, University of Melbourne, Melbourne, Australia; [3]Australian Laboratory for Emerging Contaminants, University of Melbourne,, Melbourne, Australia; [4]Department of Population Health and Pathobiology, North Carolina State University, Raleigh, NC*

MOF pm: Imaging: Spatially Resolved Omics
Room 6B

MOF pm 02:30
Maximizing Molecular Yield From a Single Section Through an Optimized Sequential Spatial Multi-Omics Acquisition Strategy; Esther Sok Hwee Cheow[1]; Matthew Choo[1]; U-Ming Lim[1]; Aaron Zefrin Fernandis[1]; Asad Abu Bakar Ali[1]; *[1]MSD International GmbH (Singapore), Singapore, Singapore*

MOF pm 02:50
Tissue Expansion Mass Spectrometry Imaging oftheCrustacean Nervous System; Thao U Duong[1]; Kendra G Selby[2]; Vu Ngoc Huong Tran[3]; Hua Zhang[3]; Penghsuan Huang[2]; Lingjun Li[2, 3]; *[1]University of Wisconsin-Madison, Madison, WI; [2]UW-Madison Department of Chemistry, Madison, WI; [3]UW-Madison School of Pharmacy, Madison, WI*

MOF pm 03:10
Micron-scale spatial profiling of placental lipids and lipid mediators using complementary mass spectrometry workflows; Marija Velickovic[1]; Leena Kadam[2]; Rosalie K Chu[1]; Kent J Bloodsworth[1]; Kevin J. Zemaitis[1]; Thomas L Fillmore[1]; Priscila M Lalli[1]; Jennifer E Kyle[1]; Leslie Myatt[2]; Kristin E Burnum-Johnson[1]; *[1]Pacific Northwest National Laboratory (PNNL), Richland, WA; [2]Department of Obstetrics and Gynecology, Oregon Health & Science University, Portland, OR*

MOF pm 03:30
Spatially Resolved Omics by Nano-DESI MSI Reveals Dysregulation of C-Peptides and Lipids in Pancreatic Islets Across Multiple Diabetic Models; Mushfeqa Iqfath[1]; Frederick Nguele Meke[2]; Manxi Yang[1]; Xindi Tang[1]; Zhong-Yin Zhang[2]; Julia Laskin[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN; [2]Purdue University, west lafayette, IN*

MOF pm 03:50
Novel Photocleavable Mass-Tags for Multiplexed Immunohistochemical DESI-MS Imaging of Biomarkers in Tissues; Gargey B. Yagnik[1]; Zhi Wan[1]; Andrew Yatsuhashi[1]; Emmanuelle Claude[2]; Steven Pringle[2]; Joanne Ballantyne[2]; Kenneth J Rothschild[1, 3]; Mark J Lim[1]; *[1]AmberGen, Inc., Billerica, MA; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Department of Physics and Photonics Center, Boston University, Boston, MA*

MOF pm 04:10
A multimodal spatial atlas of lipid metabolism in the human intestine; Bobby Y.X. Ni[1]; Lukasz G Migas[2]; Jiaqi Liu[1]; Rachel Wu[1]; Seung Hyun Jin[1]; Ky Ariano[1]; Julio Margarall[1]; Madeline E Colley[3, 4]; Melissa A. Farrow[3, 4]; Raf Van De Plas[2, 3]; Jeffrey M Spraggins[3, 4, 5, 6]; John Hickey[1]; Angela R. S. Kruse[7, 8]; *[1]Department of Biomedical Engineering, Duke University, Durham, NC; [2]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [3]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [4]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [5]Department of Biochemistry, Vanderbilt University, Nashville, TN; [6]Department of Chemistry, Vanderbilt University, Nashville, TN; [7]Department of Microbial Infection and Immunity, The Ohio State University, Columbus, OH; [8]Comprehensive Cancer Center, The Ohio State University, Columbus, OH*

MOG pm: Drug Metabolism and Pharmacokinetics
Room 6CF

MOG pm 02:30
Implementation of microscale chromatography for high sensitivity & throughput quantification of peptide-based GLP-1 receptor agonists and oligonucleotide drugs in plasma; Robert S Plumb[1]; Mary Trudeau[2]; Neil Walsh[3]; *[1]Waters, Milford, MA; [2]Waters Corporation, Milford, MA; [3]Waters Corporation, Wilmslow, United Kingdom*

MOG pm 02:50
Targeted and untargeted bottom-up LC-FAIMS-HRMS workflows for biotherapeutic quantification in mouse tissues to support pharmacokinetic/pharmacodynamic (PK/PD) studies; Minh-Trang PHAN[1, 2]; Mathieu Dupré[1]; Vincent Gervat[1]; Valegh Hamde Faid[1]; Valérie Couturier[3]; Delphine Valente[3]; Fabienne Gallen[4]; Christine Mauriac[3]; François Becher[2]; *[1]LCMS Bioanalysis, Laboratory Sciences, Translational Medicine Unit, Sanofi R&D, Vitry-sur-Seine, France; [2]Université Paris Saclay, CEA, INRAE, Département Médicaments et Technologies pour La Santé (DMTS), Gif-sur-Yvette, France; [3]Quantitative Pharmacology, Translational Medicine Unit, Sanofi R&D, Vitry-sur-Seine, France; [4]In vivo Research Center, Research Platforms and Computational R&D, Sanofi R&D, Vitry-sur-Seine, France*

MOG pm 03:10
A Multiplexed Isotope-Dilution LC-MRM-MS Method for The Quantification of 14 Antibiotics in Human Plasma, Urine, and Breast Milk; Jiaxi Cai[1]; Kerri Bertrand[2]; Christina Chambers[2]; Shirley M. Tsunoda[3]; Jeremiah D Momper[3]; Raymond T Suhandynata[3, 4]; *[1]University of California, San Diego, La Jolla, CA; [2]Department of Pediatrics, School of Medicine, University of California San Diego, La Jolla, CA; [3]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [4]Department of Pathology, University of California San Diego, La Jolla, CA*

MOG pm 03:30
Accelerated CYP Profiling via Acoustic Ejection Mass Spectrometry to Generate Public ADMET Datasets of Unprecedented Scale ; Anastasia Lindahl[1]; Robert Warneford-Thomson[1]; Scott Simpkins[1]; Daniel Szczepankiewicz[1]; Sam Sabaat[1]; Lauren Orr[1]; Steven Edgar[1]; L Naomi Handly[1]; Sri Kosuri[1]; *[1]Octant Bio, Emeryville, CA*

MOG pm 03:50
High-Throughput Mass Spectrometry Assessment of Drug Metabolism and Drug-Drug Interactions: from Screening to Quantitation; Mousumi Saha[1]; Nari Talaty[2]; Nicolas M Morato[3]; Mahdiyeh Shahi[1]; Christopher J Welch[4]; Yunfei Feng[1]; Christina Ferreira[5]; David Wagner[2]; Andreas Kaerner[6]; Robert Graham Cooks[1]; *[1]Purdue University, Department of Chemistry, West Lafayette, IN; [2]AbbVie Inc., North Chicago, IL; [3]Purdue Institute for Cancer Research, West Lafayette, IN; [4]Indiana Consortium for Analytical Science and Engineering (ICASE), Indianapolis, IN; [5]Bindley Bioscience Center, Purdue University, West Lafayette, IN; [6]Eli Lilly & Co, Louisville, CO*

MOG pm 04:10
LC-HRMS and LC-MS/HRMS (CID & EAD) Characterization of GalNAc-L96 Metabolites in Liver S9, Hepatocytes and HepatoPac® In Vitro Systems; Apoorva S Metkari[1]; Alex (Hong) Zang[1]; Zamas Lam[1]; Ragu Ramanathan[2]; *[1]QPS, LLC, Newark, DE; [2]Quest Pharmaceutical Services, Newark, DE*

MOH pm: Carbohydrates: From Mono to Poly
Room 6DE

MOH pm 02:30
MALDI-TIMS-TOF-Mass Spectrometry Enables Ultra Rapid Human Milk Typing by Structural Distinction of Abundant Human Milk Oligosaccharides; Marko Mank[1]; Aliye Ozalp[1]; Bernd Stahl[1, 2]; *[1]Danone Global R&I Utrecht, Utrecht, Netherlands; [2]Department of Chemical Biology & Drug Discovery, Utrecht Institute for Pharmaceutical Sciences, Utrecht University,, Utrecht, Netherlands*

MOH pm 02:50
Development of Derivatization-enhanced EIEIO-driven oligosaccharide structural identification (DEED-OSI) strategy and its application to Human milk oligosaccharides profiling; Xin Zheng[1]; Cai Tie[2]; Xinge Cui[1]; *[1]Peking Union Medical College Hospital, Beijing, China; [2]China University of Mining and Technology-Beijing, Beijing, China*

MOH pm 03:10
EThcD enables distinction of Co^{2+}-adducted anomeric pentasaccharides within mixtures; Lyssa A. Garber[1]; Alexes N. Thurman[1]; Elyssia S. Gallagher[1]; *[1]Baylor University, Waco, TX*

MOH pm 03:30
Mass spectrometry–based glycomics uncovers microbial reconstruction of soybean carbohydrates during fermentation; JaeHui Song[1]; HyunJi Lee[1]; Eunhye Jo[2]; Jaeho Cha[2]; Carlito B. Lebrilla[3]; Hyeyoung Lee[1, 3]; *[1]Dong-eui University, Busan, South Korea; [2]Pusan National University, Busan, South Korea; [3]University of California, Davis, Davis, CA*

MOH pm 03:50
Using TIMS-MSI to uncover glycosaminoglycan sulphate pattern changes in Alzheimer’s disease; Dorcas Cheung[1]; Anthony J Devlin[1]; *[1]Rosalind Franklin Institute, Didcot, United Kingdom*

MOH pm 04:10
MS- and deep learning-based structure-specific N-glycoproteomics and applications; Zhixin Tian; *School of Chemical Science and Engineering, Tongji University, Shanghai, China*

TOA am: Quantitative Proteomics: Instrumentation and Applications
Hall D

TOA am 08:30

Laser focused on TMT: Improving multiplexed proteomics with novel instrumentation; Christopher D McGann[1]; Steven R Shuken[1]; Ka Yang[1]; Joao A Paulo[1]; Jonathan G Van Vranken[1]; Steven P Gygi[1]; *[1]Harvard Medical School, Boston, MA*

TOA am 08:50

Performance of targeted TMT assays using Adaptive Real-Time Library Search on a modified Orbitrap Tribrid mass spectrometer; William J Comstock[1]; Brett Larsen[1]; William Barshop[1]; Tonya Pekar Hart[1]; Rafael Melani[1]; Graeme McAlister[1]; Amirmansoor Hakimi[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

TOA am 09:10

Comparison of Linear Ion Trap and Orbitrap instruments for a FAIMS-PRM amol-sensitivity targeted clinical proteomics assay; Beom-Jun Kim[1]; Camille Lombard[1]; Lihe Zhang[1]; Yeoun Jin Kim[1]; Steve M Sweet[1]; *[1]AstraZeneca, Gaithersburg, MD*

TOA am 09:30

Generation of an in-depth tissue-resolved proteomics atlas of the non-human primate Macaca fascicularis on the timsUltra-AIP.; Sandra Schär[1]; Jan Muntel[2]; Polina Shichkova[1]; Alan Shomo[2]; Nicole Barlow[2]; Igor Sobanski[1]; Matevsz Stefancic[1]; Marco Tognetti[1]; Christopher Below[1]; Patrick Van Zalm[1]; Damiano Robbiani[1]; Eduardo Yago Vicent[1]; Yuehan Feng[1]; Tejas Gandhi[1]; Roland Bruderer[1]; Jakob Vowinckel[1]; *[1]Biognosys AG, Schlieren, Switzerland; [2]Biognosys Inc., Newton, MA*

TOA am 09:50

Independently validated 9-protein panel improves emergency department venous thromboembolism triage and imaging decisions beyond D-dimer; David Kotol[1]; Philip Smith[2]; Maria Farm[3, 4]; Maria Magnusson[3, 5]; Jovan Antovic[3, 4]; Lynn Butler[3, 4, 6, 7]; Mathias Uhlén[6]; Fredrik Edfors[6]; Maria Jesus Iglesias[6]; Jacob Odeberg[2, 5, 6, 7, 8]; *[1]ProteomEdge AB, Stockholm, Sweden; [2]Department of Medicine, Karolinska Institutet, Stockholm, Sweden; [3]Clinical Chemistry and Blood Coagulation Research, Department of Molecular Medicine and Surgery, Karolinska Institutet, Stockholm, Sweden; [4]Clinical Chemistry Karolinska University Laboratory, Karolinska University Hospital, Stockholm, Sweden; [5]Coagulation Unit, Department of Hematology, Karolinska University Hospital, Stockholm, Sweden; [6]Science for Life Laboratory, Department of Protein Science, CBH KTH Royal Institute of Technology, Stockholm, Sweden; [7]Department of Clinical Medicine, UiT The Arctic University of Norway, Tromsø, Norway; [8]Division of Internal Medicine, University Hospital of North Norway (UNN), Tromsø, Norway*

TOA am 10:10

Capturing Protein Turnover Dynamics in a Drosophila melanogaster Retinal Degeneration Model using Pulsed Stable Isotope Labeling; Miranda R Muhoberac[1]; Lucas Kramer[2]; Leah Pierce[2]; Radhika Bhaumik[3]; Seema Mattoo[2, 3]; Vikki M Weake[2]; Bryon S Drown[1]; *[1]James Tarpo Jr. and Margaret Tarpo Department of Chemistry, Purdue University, West Lafayette, IN; [2]Department of Biochemistry, Purdue University, West Lafayette, IN; [3]Department of Biological Sciences, Purdue University, West Lafayette, IN*

TOB am: Metabolomics: New Technologies and Applications
Ballroom 20A

TOB am 08:30
Metabolomic Responses linked to Chemical Exposures and Breast Cancer Phenotypes; Julia Füreder[1, 2]; Delia Castilla-Fernández[1]; Max Lennart Feuerstein[1, 3]; Giulia Guerra[4]; Claudia Agnoli[4]; Sabina Sieri[4]; Benedikt Warth[1, 3]; *[1]University of Vienna, Department of Food Chemistry and Toxicology, Vienna, Austria; [2]University of Vienna, Vienna Doctoral School in Chemistry (DoSChem), Vienna, Austria; [3]Exposome Austria, Research Infrastructure and National EIRENE Node, Vienna, Austria; [4]Fondazione IRCCS Istituto Nazionale dei Tumori, Epidemiology and Prevention Unit, Milan, Italy*

TOB am 08:50
Low-temperature HILIC provides enhanced separations and stability for LC-MS-based metabolomics; Yifan Liu[1]; Madison L. Jastrab[1]; Michael Xiao[1]; Miriam Lisci[2]; Taysir K. Bader[3]; Alexis A. Jourdain[2]; Thomas E. Wales[1]; Owen S. Skinner[1]; *[1]Northeastern University, Boston, MA; [2]University of Lausanne, Lausanne, Swaziland; [3]Waters Corporation, Milford, MA*

TOB am 09:10
Annotating compounds by helical resonator plasma accurate mass GC-MS (ecTOF) by predicting formulas, mass spectra and retention indices; Bala Subrahanyam Seetha[1]; Luis Valdivez[1]; Tong Shen[1]; Valerie Kuklovsky[2]; Giovanni Galizia[2]; Elina L Niño[1]; Eliska Ceznerova[3]; Sonja Klee[4]; Oliver Fiehn[1]; *[1]UC Davis, Davis, CA; [2]University of Konstanz, Konstanz, Germany; [3]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [4]Tofwerk, Thun, Switzerland*

TOB am 09:30
Metabolite Identification Using Combined-Spectrum Searching of the NIST26 Tandem Mass Spectral Library; Xiaoyu Yang[1]; Pedatsur Neta[1]; Yuxue Liang[1]; Yuri A. Mirokhin[1]; Dmitrii V. Tchekhovskoi[1]; Guanghui Wang[1]; Sergey Sheetlin[1]; Meghan Burke[1]; Yi Liu[1]; Yamil Simón-Manso[1]; Tytus D. Mak[1]; Brian T. Cooper[1]; Nirina Rabe Andriamaharavo[1]; Connie Remoroza[1]; Stephen E. Stein[1]; *[1]NIST, Gaithersburg, MD*

TOB am 09:50
Hospital-derived pooled plasma reference material for clinical metabolomics: expanded metabolite and xenobiotic coverage by applying enhanced dynamic range scan mode; Barbora Pisklakova[1]; Ales Kvasnicka[1]; Sander Johannes Thorbjørnsen Guttorm[1]; Michał Kaczmarek[2]; Helge Rootwelt[1]; Hanne Bendiksen Skogvold[1]; Elise Sandås Sand[1]; Susan S. Bird[3]; Katja Benedikte Prestø Elgstøen[1]; *[1]Section for Metabolomics and Lipidomics, Oslo University Hospital, Oslo, Norway; [2]Thermo Fisher Scientific, Bremen, Germany; [3]Thermo Fisher Scientific, San Jose, CA*

TOB am 10:10
Untargeted Multiple Reaction Monitoring (uMRM); Winnie Uritboonthai[1]; Aries Aisporna[1]; Linh Hoang[1]; Bill Webb[1]; Elizabeth M. Billings[1]; Corey Hoang[1]; Mirna Tobea[1]; Chelsea C. Cates-Gatto[1]; Amanda J. Roberts[1]; Tony Teav[2]; Rebecca Borreggine[2]; Ioanna Kyritsi@unil.ch[2]; Hector Gallart-Ayala[2]; Julijana Ivanisevic[2]; Anna Popova[1]; James R. Williamson[1]; Robert Plumb[3, 4]; Gary Siuzdak[1]; *[1]Scripps Research, La Jolla, CA; [2]University of Lausanne, Lausanne, Swaziland; [3]University of Liverpool, Liverpool, United Kingdom; [4]Waters Corporation, Milford, MA*

TOC am: Drug Discovery and Development: Qualitative and Quantitative
Ballroom 20BC

TOC am 08:30
Proteomic Profiling of Cullin-Ring Ligase Activity across 28 Human Cell Lines; Jeffrey J Liu[1]; Xiaorui Fan[2]; Robert G Guenette[2]; Seung Wook Yang[2]; M Amine Sadok[2]; Bo Zhou[1]; James A Wohlschlegel[1]; P Ryan Potts[3]; *[1]Discovery Proteomics, Amgen, Thousand Oaks, CA; [2]Induced Proximity Platform, Amgen, Thousand Oaks, CA; [3]DATA, Amgen, Thousand Oaks, CA*

TOC am 08:50
Standardizing Proteomics Frameworks in Fast-Tracking High-Quality Drug Discovery; Liang Xue; *Pfizer, Cambridge, MA*

TOC am 09:10
DIA-Based Phosphoproteomics Defines AP-1 Signaling Dynamics Driving Remodeling in Airway Epithelial Cells; Vanshika Patel[1]; Jianshi Yu[1]; Mehari Weldemariam[1]; Paul Shapiro[1]; Deepak Deshpande[2]; Maureen A Kane[1]; *[1]University of Maryland, School of Pharmacy, Department of Pharmaceutical Sciences, Baltimore, MD; [2]Center for Translational Medicine, Jane and Leonard Korman Lung Center, Thomas Jefferson University, Philadelphia, PA*

TOC am 09:30
Utilizing Theta-Tip Mixing to Observe Transient Protein-Ligand Interactions by Native Mass Spectrometry; Calvin T Baker[1]; Leon Li Cyun Chen[1]; Xin Yan[1]; *[1]Texas A&M University, College Station, TX*

TOC am 09:50
State-of-the-art MS ADC Pharmacokinetic Assays: Pre-clinical Translation to Clinical Deployment and Impact; Chao Gong[1]; John Kellie[1]; Craig Stovold[1]; *[1]AstraZeneca, Gaithersburg, MD*

TOC am 10:10
AI-guided screening rapidly discovers covalent modulators of STAT6 activity in cells; Andrea I Gutierrez[1]; Lillian T. Tatka[1]; Gaelle Mercenne[1]; Daniele Canzani[1]; Julia Robbins[1]; Evan E Hubbard[1]; Sebastian J Paez[1]; Anastasiya V. Prymolenna[1]; William E Fondrie[1]; Lindsay K Pino[1]; Alexander J Federation[1]; *[1]Talus Bioscience, Seattle, WA*

TOD am: Challenges in MS Analysis of Complex Mixtures
Ballroom 20D

TOD am 08:30
Library-Assisted Mass Defect Analysis (LAMDA): Application to Lipid A Structural Identification; Abanoub Mikhael[1, 2]; Gillian Leach[1]; Linda Nartey[1]; Helena Pětrošová[1, 2]; David Goodlett[1, 2]; *[1]University of Victoria, Victoria, BC; [2]UVic Genome BC Proteomics Centre, Victoria, BC*

TOD am 08:50
Improvements to ion pipelining and ion-ion reaction conditions to dig deeper into the glycoproteome; Haley M. Schramm[1]; Joshua D. Hinkle[2]; Jingjing Huang[2]; David Bergen[2]; Rafael D. Melani[2]; Graeme C. McAlister[2]; Christopher Mullen[2]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA; [2]Thermo Fisher Scientific, San Jose, CA*

TOD am 09:10
Comprehensive AAV Vector Assessment Using Charge Detection Mass Spectrometry Throughout Downstream Purification; Rebecca D'Esposito[1]; Brad Williams[1]; Anisha Haris[2]; Noah Miller-Medzon[3]; Tim Fenn[3]; Ying Qing Yu[1]; Michelle Chen[4]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Lexeo Therapeutics, New York City, NY; [4]Waters Corporation, Goleta, CA*

TOD am 09:30
Evaluating Metaproteomic Complex Mixture Analysis by Orbitrap Astral MS Using a Taxonomic Ground-Truth Microbial Community; Nicole Nightingale[1]; Jana Richter[2]; Nicolas Hartel[3]; Mak A. Saito[4]; Manuel Kleiner[5]; Timothy J Griffin[1]; Pratik D Jagtap[1]; *[1]University of Minnesota, Minneapolis, MN; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]Thermo Fisher Scientific, San Jose, CA; [4]Woods Hole Oceanographic Institution, Woods Hole, MA; [5]North Carolina State University, Raleigh, NC*

TOD am 09:50
Detection of siderophore-metal complexes in dissolved organic matter (DOM) by ultra-high resolution mass spectrometry (FTICR) and electron paramagnetic resonance (EPR); Ziad Mahmoud[1]; Marie Hubert-Roux[1]; Hervé Vezin[2]; Pierre Giusti[1, 3, 4]; Carlos Afonso[1, 3]; *[1]Université de Rouen Normandie, INSA Rouen Normandie, Université de Caen Normandie, ENSICAEN, CNRS, Institut CARMeN UMR 6064, F-76821 Mont-Saint-Aignan Cedex, France, Rouen, France; [2]Univ. Lille, CNRS, UMR 8516 – LASIRE - Laboratoire de Spectroscopie pour les Interactions, la Réactivité & l'Environnement F-59000 Lille, France, Lille, France; [3]International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France; [4]TotalEnergies One Tech, R&D, Downstream Processes & Polymers, TotalEnergies Research & Technology Gonfreville, BP 27, Harfleur, France*

TOD am 10:10
Revealing the Molecular Heterogeneity of Bio-Oils with Ultrasound-Assisted Sequential Extraction and LC-FT-ICR MS to Expose Renewable Biofuel Precursors; Olivia C Moss[1]; Carly J Hill[1, 2]; Martha L. Aguilera[1]; Ryan P. Rodgers[1]; David C Dayton[3]; *[1]National High Magnetic Field Laboratory, Tallahassee, FL; [2]Juniata College, Huntingdon, PA; [3]RTI International, Research Triangle Park, NC*

TOE am: Biomarkers: Quantitative Analysis
Room 6A

TOE am 08:30
A Mass Spectrometry Based Assay For Detection Of KEAP1 Target Engagement In Clinical Samples; Christie L Eissler[1]; Melissa Hoffman[1]; Gitte Bohm[2]; Egor Vorontsov[2]; Stephanie Ballweg[2]; Zachary Turman[1]; Sarah Jacinto[1]; Joseph McLaughlin[1]; Tine Wyseure[1]; Ian Pike[2]; Nil Roy[1]; Gabriel Simon[1]; *[1]Vividion Therapeutics Inc., San Diego, CA; [2]Proteome Sciences R&D GmbH & Co. KG, Frankfurt, Germany*

TOE am 08:50
Targeted phosphoproteomics of erythrocytes for the diagnosis and monitoring of synucleinopathies; Martin Acosta-Parra[1]; Ruiqi Jian[1]; Lihua Jiang[1]; Kathleen L Poston[1]; Michael P. Snyder[1]; *[1]Stanford University, Stanford, CA*

TOE am 09:10
Nano-flow SQUAD LC-HRAM enables ultrasensitive, multi-matrix bile acid quantitation and discovery; Robert Harlan[1]; Bashar Amer[1]; Cynthia Grim[1]; Rahul Deshpande[1]; Nichole Reisdorph[2]; Katrina Doenges[2]; Michael Armstrong[2]; Susan Bird[3]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]University of Colorado Anschutz, Aurora, CO; [3]Thermo Fisher Scientific, Lexington, MA*

TOE am 09:30
Enhancing Quantitative Plasma Proteomics by Nano-LC–MRM-MS to Increase Throughput and Reduce Cost in Large Clinical Cohorts; Margret Thorsteinsdottir[1]; Kari Arnarson[1]; Valborg Gudmundsdottir[1, 2]; Vilmundur G. Gudnason[1, 2]; Christoph H. Borchers[3, 4, 5, 6]; Finnur F. Eiriksson[7]; *[1]University of Iceland, Reykjavik, Iceland; [2]Icelandic Heart Association, Reykjavík, Iceland; [3]Segal Cancer Proteomics Centre, Lady Davis Institute for Medical Research, McGill University, Montreal, QC; [4]Gerald Bronfman Department of Oncology, Lady Davis Institute for Medical Research, Jewish General Hospital, Montreal, QC; [5]Division of Experimental Medicine, McGill University, Montreal, Montreal, QC; [6]Department of Pathology, McGill University, Montreal, QC; [7]Univeristy of Iceland, Reykjavik, Iceland*

TOE am 09:50
A Window of Opportunity: Liquid Biopsy Proteomics for Early Detection of Pancreatic Cancer; Jumana Yousef[1, 2]; Susanne I Wudy[1, 2]; Sukhdeep Spall[1, 2]; Belinda Lee[1, 2, 3, 4]; Samantha J Emery-Corbin[1, 2]; Ka Yee Fung[1, 2]; Peter Gibbs[1, 2, 5]; Tracy Putoczki[1, 2]; Laura F Dagley[1, 2]; *[1]Walter and Eliza Hall Institute for Medical Research, Parkville, Australia; [2]Department of Medical Biology, Faculty of Medicine, Dentistry & Health Sciences, The University of Melbourne, Parkville, Australia; [3]Peter MacCallum Cancer Centre, Parkville, Australia; [4]Northern Health, Melbourne, Australia; [5]Western Health, Melbourne, Australia*

TOE am 10:10
Differentiating Amyloid-β Polymorphs with the Covalent Protein Footprinting; Tom Casimir Bamberger[1]; Jolene K. Diedrich[1]; Titus Jung[1]; Jeffery B Lane[1]; Jan-Hannes Schaefer[1]; Gabriel C. Lander[1]; Douglas Galasko[2]; John R. Yates III[1]; *[1]Scripps Research Institute, La Jolla, CA; [2]University of California San Diego, San Diego, CA*

TOF am: Instrumentation: Detection of High-Mass Analytes
Room 6B

TOF am 08:30
Single Ion Detection with FT-ICR MS: Trapped ion kinetic energy correction for improved charge determination; Nathan K Kaiser[1]; Steven C. Beu[2]; Christopher L Hendrickson[1]; John P. Quinn[1]; Jared O Kafader[3]; Chad R. Weisbrod[1]; [1]*National High Magnetic Field Laboratory, Tallahassee, FL;* [2]*S.C. Beu Consulting, Austin,, TX;* [3]*Northwestern University, Evanston, IL*

TOF am 08:50
Charge Detection Mass Spectrometry Implemented on a Modified Orbitrap Tribrid Mass Spectrometer Enables Advanced Top-Down Protein and Oligonucleotide Characterization Capabilities; Kyle Patrick Bowen[1]; Graeme McAlister[2]; Christopher Mullen[2]; Weijing Liu[2]; Rafael D Melani[2]; Jesse D Canterbury[2]; David Bergen[2]; Joshua D Hinkle[2]; Michael P Goodwin[2]; Michael Senko[2]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*ThermoFisher Scientific, San Jose, CA*

TOF am 09:10
Extending timsOmni Capabilities for Multi-Level Native Analysis of the ~700 kDa 20S Proteasome; Gili Ben-Nissan[1]; Athanasios Smyrnakis[2]; Maria-Aggeliki Kosmopoulou[2]; Dimitris Papanastasiou[2]; Michal Sharon[1]; [1]*Weizmann Institute of Science, Rehovot, Israel;* [2]*Fasmatech Science and Technology, Athens, Greece*

TOF am 09:30
Study Gas-Phase Ion Temperature Using a Stacked Ring Ion Guide Interface for CD-MS; Minh Tram Ha[1]; David W. Reitenbach[1]; David E. Clemmer[1, 2]; Martin F. Jarrold[1, 2]; [1]*Indiana University - Bloomington, Bloomington, IN;* [2]*Megadalton Solutions, Bloomington, IN*

TOF am 09:50
CDMS analysis of adeno-associated viral vectors by Orbital Frequency Analyser; Aleksandr Rusinov[1]; Ryoji Nakatsuka[2]; Sergey Smirnov[1]; Patrick Knight[1]; Gordon Kearney[1]; [1]*Shimadzu Research Laboratory (Europe) Ltd., Manchester, United Kingdom;* [2]*Shimadzu Corporation, Kyoto, Japan*

TOF am 10:10
Single Molecule Native Proteomics Using a Nanoelectromechanical Systems Mass Spectrometry Device; Jeffrey J. Jones[1]; Atakan Ari[1]; Michael L Roukes[1]; [1]*Caltech, Pasadena, CA*

TOG am: GC-MS: Instrumentation and Applications
Room 6CF

TOG am 08:30
Applications of Flow-Modulated GCxGC-Quadrupole Mass Spectrometry at High Flow Rate; Kirk R Jensen; *JEOL USA, Inc., Peabody, MA*

TOG am 08:50
Automated High-Throughput Quantitation of 197 Pesticides in Durian Using GC-MS/MS with PAL3 Autosampler; Yufeng Zhang[1]; Feng Gu[1]; Lay Peng Tan[1]; [1]*Agilent Technologies Singapore (sales) Pte Ltd, Singapore, Singapore*

TOG am 09:10
Utilizing Solid Phase Incremental Capillary Extraction to Improve GCMS Headspace Analysis of Aromas, Fragrances, and Odors in Consumer Products; Daniel Cardin[1]; Victoria L Vogel[2]; Weier Hao[2]; Daniel J Cardin[2]; Tom Robinson[2]; [1]*Entech Instruments, Simi Valley, CA;* [2]*Entech Instruments, Simi Vally, CA*

TOG am 09:30
Ultra-Low Detection of Controversial Microdroplet Oxidation Products Observed by Cryogenic Focusing Gas Chromatography Mass Spectrometry; Paul R Tumminello[1]; Nathan R Bays[1]; David Schafer[1]; Samantha M Kruse[1]; Brynal Benally[1]; Jake Zenker[1]; Leonid Sheps[2]; Ryan D Davis[1]; [1]*Sandia National Laboratories, Albuquerque, NM;* [2]*Sandia National Laboratories, Livermore, CA*

TOG am 09:50
Tensor models are the new black: automated deconvolution, identification and quantification of untargeted GC-MS across complex sample sets; Beatriz Quintanilla-Casas[1]; Jesper L Hinrich[1]; Rasmus Bro[1]; [1]*University of Copenhagen, Copenhagen, Denmark*

TOG am 10:10
Cryogenic zone compression to enhance quadrupole MS sensitivity for trace PAHs in complex food and environmental matrices; Antonio Ferracane[1]; Alessia Arena[2]; Mariosimone Zoccali[3]; Luigi Mondello[1, 2]; [1]*Messina Institute of Technology c/o Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Messina, Italy;* [2]*Chromaleont s.r.l., c/o Department of Chemical, Biological, Pharmaceutical and Environmental Sciences, University of Messina, Viale G. Palatucci 13, 98168 – Messina, Italy, Messina, Italy;* [3]*Department of Mathematical and Computer Science, Physical Sciences and Earth Sciences, University of Messina, Viale F. Stagno d'Alcontres 31, 98166, Messina, Italy, Messina, Italy*

TOH am: Plants and Natural Products
Room 6DE

TOH am 08:30

Spatial Metabolic Signatures in Plant–Pathogen Interactions as revealed by High-Resolution MALDI Mass Spectrometry Imaging; Amelia Locatelli[1]; Davide Magrin[1]; Simone Stefano[1]; Luciana Galetto[2]; Cristina Marzachì[2]; Enrico Davoli[3]; Renzo Bagnati[1]; Alice Passoni[1]; *[1]Istituto di Ricerche Farmacologiche Mario Negri - IRCCS, Milan, Italy; [2]CNR-IPSP Istituto per la Protezione Sostenibile delle Piante, Turin, Italy; [3]Università degli Studi di Torino, Turin, Italy*

TOH am 08:50

plantMASST: a mass spectrometry tool for mining public datasets from plants; Helena Mannochio-Russo[1]; Xiaofeng Wang[2]; Wilhan D. Gonçalves Nunes[1]; Roland D. Kersten[2]; Pieter C. Dorrestein[1]; Paulo Wender Portal Gomes[3]; *[1]University of California, San Diego, San Diego, CA; [2]University of Michigan, US, MI; [3]Universidade Federal do Pará, Belém, Brazil*

TOH am 09:10

Structural Elucidation of Fructooligosaccharides and Raffinose Family Oligosaccharides: A New Workflow; Wun-Long Li[1]; Chi-Kung Ni[2, 3]; *[1]Institute of Atomic and Molecular Sciences, Academia Sinica, Taipei, Taiwan; [2]Institute of Atomic and Molecular Sciences, Academia Sinica, Taiwan, Taipei, Taiwan; [3]Department of Chemistry, National Tsing Hua University, Hsinchu, Taiwan*

TOH am 09:30

Metabolic pulse-label analysis of rapid systemic signaling in Arabidopsis; Ronald J Myers Jr[1]; Amith R Devireddy[1, 2]; Sara I Zandalinas[3]; Devasantosh Mohanty[1]; Richard A Ferrieri[1]; Lloyd W Sumner[1]; Ron Mittler[1, 4]; *[1]University of Missouri-Columbia, Columbia, MO; [2]Claflin University, Orangeburg, SC; [3]University Jaume I, Castelló de la Plana, Spain; [4]Tel-Hai University of Kiryat Shmona and the Galilee, Kiryat Shmona, Israel*

TOH am 09:50

Multi-omics mass spectrometry resolves cell-type and protein-defined mitochondrial subpopulations reflecting heat stress-response in Arabidopsis thaliana; Mario Waespy[1]; Chinmay Joshi[1]; Sara Jalili[1]; Magdalene Reinkensmeier[2]; Viola Jeck[2]; Aiko Barsch[2]; Verena Tellstroem[2]; Stephanie Kaspar-Schoenefeld[2]; Stefanie Wernisch[2]; Andreas Schmidt[2]; Markus Lubeck[2]; Matthew Lewis[2]; Rita Groß-Hardt[1]; *[1]University of Bremen, Bremen, Germany; [2]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany*

TOH am 10:10

Spatial Multiomic Insights into Sorghum–Colletotrichum Interactions and Bacteria-Mediated Biocontrol Mechanisms; Ljiljana Pasa-Tolic[1]; Kevin J. Zemaitis[1]; Pranav Dawar[1]; Dora Farago[2]; Audrey G. Thomas[3]; James M. Fulcher[1]; Theresa F. Law[3]; Janaka N. Edirisinghe[4]; Christopher S. Henry[4]; Louis K. Prom[5]; Jeffery L. Dangl[3]; Qun Liu[2]; *[1]Pacific Northwest Natl Lab, Richland, WA; [2]Brookhaven National Laboratory, Upton, NY; [3]University of North Carolina at Chapel Hill, Chapel Hill, NC; [4]Argonne National Laboratory, Argonne, IL; [5]USDA ARS, Southern Plains Agricultural Research Center, College Station, TX*

TOA pm: Biomarkers: Qualitative Analysis
Hall D

TOA pm 02:30

High-Throughput and Sensitive Proteomics Workflow for Biomarker Discovery from 1-µL Murine Cerebrospinal Fluid Samples; Weng Wong[1]; Erika Kelmer Sacramento[1]; Jose Imperio[1]; Meena Choi[1]; Chang Hoon Cho[1]; William J. Meilandt[1]; Nikhil Janak Pandya[1]; Ying Zhu[1]; *[1]Genentech Inc., South San Francisco, CA*

TOA pm 02:50

Spatially-Driven Lipid Biomarker Discovery at Cellular, Neighborhood, and Sub-FTU Scales in Human Kidney; Thai H Pham[1, 2]; Lukasz G Migas[1, 3]; Martin Dufresne[1, 4]; Madeline E Colley[1, 2]; Olof Isberg[1, 2]; Anna J Smith[1, 2]; Mark DeCaestacker[5]; Melissa A Farrow[1, 4]; Raf Van De Plas[1, 3, 4]; Jeffrey M Spraggins[1, 2, 4, 6, 7]; *[1]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [2]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [3]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [4]Department of Biochemistry, Vanderbilt University, Nashville, TN; [5]Division of Nephrology and Hypertension, Department of Medicine, Vanderbilt University Medical Center, Nashville, TN; [6]Department of Chemistry, Vanderbilt University, Nashville, TN; [7]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN*

TOA pm 03:10

Isobaric peptide probes for multiplexed detection of disease biomarkers using mass spectrometry-based immunoassay; Stephanee Joy B Zerrudo[1]; Santosh Raman Acharya[1]; Hianka J.C. De Carvalho[1]; Ayesha Seth[1]; Abraham Badu-Tawiah[1]; *[1]The Ohio State University, Columbus, OH*

TOA pm 03:30

Orthogonal LC–MS/MS Defines Inflammation-Driven Suppression of Microbiota-Derived Luminal Metabolites in a Mouse Model of Colitis; Brianna R. Swank[1]; Luisa Seguella[2]; Jacob J. Haffner[3]; Hani Habra[3, 4]; Ryutaro Einar Jacobson[5]; Patrick Huck[6]; Aurora Zilli[2]; Julia Jamka[2]; Brian Gulbransen[2]; Tian (Autumn) Qiu[5]; Maryam Goudarzi[3, 4]; *[1]Department of Chemistry, Michigan State University, East Lansing, MI; [2]Department of Physiology, Michigan State University, East Lansing, MI; [3]Mass Spectrometry and Metabolomics Core, Michigan State University, East Lansing, MI; [4]Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI; [5]Department of Chemistry, Michigan State Univeristy, East Lansing, MI; [6]Osteopathic Surgical Specialties, Michigan State University, East Lansing, MI*

TOA pm 03:50

Remote Microsamplers for the Collection, Preservation, and Proteomic Profiling of Dried Blood- and Urine-Derived Extracellular Vesicles; Yi-Kai Liu[1]; Nathaniel Miller[1]; Yuxin Zhuang[1]; Jyoti Singh[1]; Ana Maria Medina[1]; Julio Rivera-De Jesus[2]; Juan C. Mesa[2]; Ronald S. Boris[3]; Jacqueline C. Linnes[2]; Majid Kazemian[1, 4]; Anton Iliuk[1, 5]; W. Andy Tao[1, 4, 6]; *[1]Department of Biochemistry, Purdue University, West Lafayette, IN; [2]Weldon School of Biomedical Engineering, Purdue University, West Lafayette, IN; [3]Departments of Urology, Indiana University School of Medicine, Indianapolis, IN; [4]Purdue Institute for Cancer Research, West Lafayette, IN; [5]Tymora Analytical Operations, West Lafayette, IN; [6]James Tarpo Jr. and Margaret Tarpo Department of Chemistry, Purdue University, West Lafayette, IN*

TOA pm 04:10

Integrative regulome profiling of DNA damage responses to discover DNA repair-directed therapeutics in aging; Lindsay K Pino[1]; Julia Robbins[1]; Andrea Gutierrez[1]; Yan Ting Zhao[2]; Evan E Hubbard[1]; Daniele Canzani[1]; Kyle Siebenthall[1]; Sydney Huff[1]; Margaux McBirney[1]; Anastasiya V. Prymolenna[1]; Lillian T. Tatka[1]; Sebastian J Paez[1]; Brian McEllin[1]; Gaelle Mercenne[1]; William E Fondrie[1]; Alexander J Federation[1]; Benjamin Blue[2]; *[1]Talus Bioscience, Seattle, WA; [2]Ora Biomedical, Seattle, WA*

TOB pm: Fundamentals: Ionization Methods
Ballroom 20A

TOB pm 02:30
Negative Gaseous Ions in Positive-Voltage Electrospray Ionization Mass Spectrometry; Xing-Bo Wang[1]; Ochir Ochirov[1]; Bo-Cheng Ke[1]; Noor Hidayat Abu Bakar[1]; Chamarthi Maheswar Raju[1]; Ioan Marginean[2]; Pawel L. Urban[1]; *[1]National Tsing Hua University, Hsinchu City, Taiwan; [2]University of Baltimore, Baltimore, MD*

TOB pm 02:50
Direct Charge Measurement Identifies Electrospray Ionization Mode via Charge Information and Instantaneous Frequency of the Droplet; Mhar Ian Cua Estayan[1, 2]; Shao-Yu Liang[1]; Zheng-An Qiu[1]; Immanuel Joseph Tiu[1]; Wen-Ping Peng[1]; *[1]National Dong Hwa University, Shoufeng, Taiwan; [2]University of Santo Tomas, Manila, Philippines*

TOB pm 03:10
Molecular Insights into Ion and Solvent Dynamics within an ESI Capillary: Electrophoretic Formation of Highly Charged Droplets; Lars Konermann[1]; Mahsa Dolatkhah Ouch Bolagh[2]; *[1]Univ. of Western Ontario, London, ON; [2]The University of Western Ontario, London, ON*

TOB pm 03:30
Molecular Dynamics Simulations Reveal Competition between Bead Ejection and Charge Residue Models of Ionization for Multi-Domain Nucleic Acids; Michael S Cordes[1]; Elyssia S Gallagher[1]; *[1]Baylor University, Waco, TX*

TOB pm 03:50
Mg^{2+} Dependent Folding of the 10-23 DNAzyme Characterized by cVSSI-Ion Mobility Mass Spectrometry; Chandrima Banerjee[1]; Colin R Johnson[2]; Vikum K. Dewasurendra[1]; Sarah O'Keefe[2]; Thomas Hughart[1]; Matthew B. Johnson[1]; David E. Clemmer[3]; Stephen J. Valentine[4]; *[1]West Virginia University, Morgantown, WV; [2]Indiana University - Bloomington, Bloomington, IN; [3]Indiana University, Bloomington, IN; [4]University of Louisville, Louisville, KY*

TOB pm 04:10
Evaluation of sensitivity and in-source fragmentation of labile drug metabolites across Exploris and non-commercial Orbitrap platforms to improve metabolite identification; Alena N Joignant[1]; Reiko Kiyonami[2]; Min Du[3]; Richard D Burton[4]; Claire Dauly[5]; Gary Jenkins[4]; Sebastien Morin[6]; Nari Talaty[4]; *[1]AbbVie Inc., Chicago, IL; [2]ThermoFisher Scientific, Lexington, MA; [3]Thermo Fisher Scientific, Lexington, MA; [4]AbbVie Inc., North Chicago, IL; [5]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [6]Thermo Fisher Scientific, Mississauga, ON*

TOC pm: Artificial Intelligence in MS in Instrumentation and Applications
Ballroom 20BC

TOC pm 02:30
Model-Driven Metabolomics Acquisition Optimization by Predicting MS2 Identifiability Before Fragmentation Using Positive-Unlabeled Learning; Madina Bekbergenova[1, 2]; Tao Jiang[1]; Louis-Félix Nothias[1]; Wout Bittremieux[2]; *[1]Université Côte d'Azur, Nice, France; [2]University of Antwerp, Antwerpen, Belgium*

TOC pm 02:50
PeptDeepKontext: A Universal Model for Predicting Peptide Properties Across Instruments, Conditions, and Post-Translational Modifications Trained on a New Foundational Dataset; Georg Wallmann[1, 2]; Mohamed Kotb[1]; Mikhail Lebedev[1]; Johannes Bruno Müller-Reif[1]; Matthias Mann[1]; *[1]Max Planck Institute of Biochemistry, Planegg, Germany; [2]Aplusia GmbH, Munich, Germany*

TOC pm 03:10
De novo sequencing of chimeric spectra using Casanovo; Yuhui Hong[1]; Isha Gokhale[1]; Justin Sanders[1]; Gwenneth Straub[1]; Wout Bittremieux[2]; William S Noble[1]; *[1]University of Washington, Seattle, WA; [2]University of Antwerp, Antwerpen, Belgium*

TOC pm 03:30
Building An Omics-Agnostic Cross-Kingdom Foundation Model for Mass Spectrometry; Ashfiqur Rahman[1]; Yuqian Gao[1]; Christine Chang[1]; Ryan Danehy[1]; Jaelyn Litzinger[1]; Aivett Bilbao[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

TOC pm 03:50
Uncovering the dark fragmentome through an explainable de novo sequencing model; Joel Lapin[1]; Guillaume Médard[2]; Mathias Wilhelm[1, 3]; *[1]Technical University of Munich, Freising, Germany; [2]National and Kapodistrian University of Athens, Athens, Greece; [3]Munich Data Science Institute (MDSI), Technical University of Munich, Garching, Germany*

TOC pm 04:10
AutoProteo: A Local-First, Language-Driven Agentic AI System for Proteomics Data Analysis and Biological Interpretation; Chi-Hsuan Chu[1]; Ciao-Syuan Chen[2]; Yu-Ju Chen[2]; Kun-Pin Wu[1, 3]; *[1]Institute of Biomedical Informatics, National Yang Ming Chiao Tung University, Taipei, Taiwan; [2]Academia Sinica, institute of chemistry, Taipei, Taiwan; [3]Ph.D. Program of Interdisciplinary Medicine, National Yang Ming Chiao Tung University, Taipei, Taiwan*

TOD pm: Biotherapeutics: Characterizations and Quantitation
Ballroom 20D

TOD pm 02:30
Disassembly of AAV9 Capsids Studied by Variable Temperature ESI CD-MS: Mapping Intermediates and Genome Release; Akalanka Gunaratne[1]; Shannon Raab[2]; Zhirui Jerry Lian[2]; Martin F Jarrold[1, 3]; David E. Clemmer[1]; *[1]Indiana University, Bloomington, IN; [2]Eli Lilly and Company, Indianapolis, IN; [3]Megadalton Solutions, Bloomington, IN*

TOD pm 02:50
Targeted Quantitation of High-Risk Host Cell Proteins associated with Monoclonal Antibody Biotherapeutics utilizing the Stellar Mass Spectrometer; Josh Smith[1]; Jae H Choi[2]; Jenny Ho[3]; Alan Atkins[3]; Corentin Beaumal[1]; Wes Rogers[4]; Deanna L Plubell[4]; Bhavinkumar B Patel[2]; Scott M Peterman[4]; Sara Carillo[1]; Jonathan Bones[1, 5]; *[1]National Institute for Bioprocessing Research & Training, Dublin, Ireland; [2]Thermo Fisher Scientific, Rockford, IL; [3]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [4]Thermo Fisher Scientific, San Jose, CA; [5]School of Chemical and Bioprocess Engineering, University College Dublin, Dublin, Ireland*

TOD pm 03:10
In <40 minutes from sample to result: PRM-based absolute quantitation after rapid thermolysin digestion, exemplified by rituximab in human plasma; Xuehui Jiang[1]; Ying Lao[1]; Versha Banerji[2]; Rene Zahedi[1]; *[1]Manitoba Centre for Proteomics and Systems Biology, Winnipeg, MB; [2]University of Manitoba, Winnipeg, MB*

TOD pm 03:30
Assessing Serum Stability and Bioanalytical Strategy for Antibody-siRNA Conjugates; Yihan Li[1]; Radek Abarca[1]; Lu Wang[2]; Colin J Phipps[3]; Hetal Sarvaiya[1]; *[1]AbbVie Inc., South San Francisco, CA; [2]AbbVie Inc., Worcester, MA; [3]AbbVie Inc., North Chicago, IL*

TOD pm 03:50
HILIC-MS – Enabled Subunit Level MAM: Advancing the Future of Biotherapeutic Characterization; Benqian Wei[1]; Zhengqi Zhang[1]; Ekaterina G Deyanova[1]; *[1]Analytical Research and Development, MRL, Merck & Co., Inc., Rahway, NJ*

TOD pm 04:10
Assessing biotherapeutic stability through forced degradation using intact and subunit icIEF-UV/MS workflows; Jingwen Ding[1]; Haichuan Liu[1]; Zoe Zhang[1]; *[1]SCIEX, Redwood City, CA*

TOE pm: Lipidomics: New MS Technologies and Applications
Room 6A

TOE pm 02:30
Harnessing Lipids from Extracellular Vesicles to Track Biological Responses to Wildfire Exposure; Haley C. Jostes[1]; Allison C. Spring[1]; Elise Hickman[1]; Jaclyn M. Goodrich[2]; Jefferey L. Burgess[3]; Melissa A. Furlong[3]; Shawn C. Beitel[3]; Julia E. Rager[1]; Erin S. Baker[1]; *[1]UNC-Chapel Hill, Chapel Hill, NC; [2]University of Michigan, Ann Arbor, MI; [3]University of Arizona, Tucson, AZ*

TOE pm 02:50
Structural lipidomics using OAD- and EAD MS/MS with MS-DIAL 5 environment; Hiroshi Tsugawa[1]; Kuniyoshi Shimidzu[2]; Fumika Mi-ichi[3]; Bujinlkham Buyantogtokh[2]; Hiroaki Takeda[4]; Hidenori Takahashi[5]; Mami Okamoto[5]; Yuki Matsuzawa[2]; Takeshi Harayama[6]; *[1]Tokyo University of Agriculture and Technology, Tokyo, Japan; [2]Tokyo University of Agriculture and Technology, Koganei, Japan; [3]Nagasaki University, Nagasaki, Japan; [4]National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan; [5]Shimadzu Co., Kyoto, Japan; [6]CNRS UMR7275, Valbonne, France*

TOE pm 03:10
Integrating Metabolic Glycan Labeling and Deep Profiling to Decipher the Dynamic Landscape of Ganglioside Metabolism in Breast Cancer Cell Lines; Yichun Wang[1]; Chengyang Lai[2]; Chen Xing[2]; Yu Xia[1]; *[1]Tsinghua University, Beijing, China; [2]Peking University, Beijing, China*

TOE pm 03:30
Near-complete structural identification of native cardiolipins using multi-tandem mass spectrometry coupled with collision-induced dissociation (CID) and electronically excited dissociation (EED); Ashish Pradhan[1]; Takashi Baba[1]; *[1]SCIEX, Concord, ON*

TOE pm 03:50
In-Depth Profiling of Subcellular Organellar Lipidomes with Nano-LC/MS; Zidan Wang[1]; Zihao Lin[1]; Souvik Roy[1]; Rahul Deshpande[2]; Susan S. Bird[2]; Yeongho Kim[1]; Kallol Gupta[1]; *[1]Yale University, New Haven, CT; [2]Thermo Fisher Scientific, San Jose, CA*

TOE pm 04:10
Dual-isotope labeling lipidomics and targeted oxy-lipidomics reveal di-arachidonoyl phospholipids underlying ferroptosis sensitivity in wild-type and ACSL4-KO cells; Noelle Reimers[1]; Libin Xu[1]; *[1]University of Washington, Seattle, WA*

TOF pm: Industry: Trace Analysis, Quality Control, and Automation
Room 6B

TOF pm 02:30
Dual Automated Workflows for Comprehensive PFAS Screening in Cosmetics Using Triple Quadrupole GC/MS and LC/MS Platforms; Aimei Zou[1]; Auni Wong[2]; Gwen Sin Yee Lim[3]; *[1]Agilent Technologies Singapore, Singapore, Singapore; [2]Agilent Technologies, Singapore, Singapore; [3]CTC Analytics AG, Zwingen, Switzerland*

TOF pm 02:50
Quantitative Native Speciation of Trace Metals in Semiconductor-Grade Solvents via BTC-ICP-MS: Identifying Species Transformations for Process Optimization; Ray Su[1, 2]; Will Leung[1]; Yin-Hung Lai[1]; *[1]National Yang Ming Chiao Tung University, Beitou Dist., Taiwan; [2]National United University, Miaoli, Taiwan*

TOF pm 03:10
Integrated MAM and NPD LC–MS Approach for Comprehensive Peptide Impurity Monitoring in GMP Release Testing; Pingli Wei[1]; Boyu Zhao[2]; Gordon Lambertus[2]; Chen-Chun Chen[2]; *[1]Eli Lilly and Company, Carmel, IN; [2]Eli Lilly & Company, Indianapolis, IN*

TOF pm 03:30
Accelerating Impurity Quantification Without Standards: Leveraging HPLC-ESI-MS and ICP-MS for Pharmaceutical Analysis; Kunyu Zheng[1]; Maximilian Wilfinger[1]; Holly VanMetre[1]; Kyle Kotecki[1]; Mitchell Gates[1]; *[1]AbbVie Inc., North Chicago, IL*

TOF pm 03:50
An Integrated Approach Combining Mass Spectrometry, NMR, and Chemometrics for Quality and Authenticity Assessment of Essential Oils; Mei Wang[1]; Jianping Zhao[2]; Ikhlas A. Khan[2]; *[1]USDA, ARS, NPURU, University, MS; [2]University of Mississippi, University, MS*

TOF pm 04:10
Direct highly-selective analysis of ethylene oxide and acetaldehyde from aqueous and injection-unfriendly matrices for food safety screening by MRR; Christopher J Thompson[1]; Alexander V. Mikhonin[2]; Voislav Blagojevic[2]; Justin L. Neill[2]; *[1]BrightSpec, Inc., Waltham, MA; [2]BrightSpec Inc., Charlottesville, VA*

TOG pm: Instrumentation: New Hybrid and Multimodal Approaches
Room 6CF

TOG pm 02:30
Advances in Compact Multi-Reflecting Time-of-Flight Mass Spectrometry; Jason L Wildgoose[1]; Matthew E Daly[1]; Lee A Gethings[1]; Johannes P C Vissers[1]; Richard I Lock[1]; James I Langridge[1]; [1]*Waters Corporation, Wilmslow, United Kingdom*

TOG pm 02:50
When Electrons Meet Photons: Multimodal Dissociation for Native Top-Down MS Analysis; Ezgi Gurler[1, 2]; Alan Kadek[1]; [1]*Czech Academy of Sciences Institute of Microbiology, Prague, Czech Republic;* [2]*Charles University, Prague, Czech Republic*

TOG pm 03:10
Next-Generation Tribrid Mass Spectrometry Driven by Improved Ion Operation Synchronization; Graeme C McAlister[1]; Jingjing Huang[1]; Lilian Heil[1]; William D Barshop[1]; Joshua D Hinkle[1]; Jesse D Canterbury[1]; Christopher Mullen[1]; Rafael D Melani[1]; [1]*Thermo Fisher Scientific, San Jose, CA*

TOG pm 03:30
High throughput screening of isomeric reaction products by droplet microfluidics coupled to cyclic ion mobility mass spectrometry; Laura I Penabad[1]; Roger C Diehl[1]; Aidan Olman[1]; Brandon T. Ruotolo[1]; Alison R.H. Narayan[1]; Robert T Kennedy[1]; [1]*University of Michigan-Ann Arbor, Ann Arbor, MI*

TOG pm 03:50
High resolution hybrid IMS MS technique for effective protein structure characterization; Kaiqun Wu[1]; Junhui Li[1]; Keqi Tang[1]; [1]*Ningbo University, Ningbo, China*

TOG pm 04:10
Evolving Hardware Architecture and Functionality of the timsOmni MS Platform; Dimitris Papanastasiou[1]; Athanasios Smyrnakis[1]; Maria-Aggeliki Kosmopoulou[1]; Anastasios Grigoriadis[1]; Ioanna Barla[1]; Ioannis Orfanopoulos[1]; Nikolaos Manolis[1]; Ilias Panagiotopoulos[1]; Rafail Gioves[1]; Florian Busch[2]; Jean-François Greisch[2]; Hongxia Bai[3]; Gad Armony[4]; Kristina Marx[5]; Konrad Winkels[6]; Stuart Pengelley[5]; Michael Krause[5]; Niels Goedecke[5]; Oliver Raether[6]; Eduardo Carrascosa[6]; [1]*Fasmatech Science and Technology, Athens, Greece;* [2]*Bruker Switzerland AG, Fällanden, Switzerland;* [3]*Bruker, Billerica, MA;* [4]*Bruker Nederland B.V., Leiderdorp, Netherlands;* [5]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [6]*Bruker Daltonics GmbH & Co KG, Bremen, Germany*

TOH pm: Stable Isotope Labeling Applications
Room 6DE

TOH pm 02:30
Non-canonical amino acid-protein incorporation via ribosomal translation in human cells; Joanna M Gongora[1]; Daniel Ramirez[1]; Zongtao Lin[2]; Benjamin Garcia[1]; [1]*Washington University School of Medicine in Saint Louis, Saint Louis, MO;* [2]*Rutgers, New Brunswick, NJ*

TOH pm 02:50
SILAC-STAMP reveals temporal-spatial regulation of protein synthesis and degradation as a key checkpoint of G0 transit; Rachel E Turn[1]; Mohammad Ovais Aziz-Zanjani[1]; Amin Mobedi[1]; Peter K. Jackson[1]; [1]*Stanford University, Stanford, CA*

TOH pm 03:10
Revealing the role of dietary monosaccharides in protein biosynthesis through stable isotope labeling with 13C-monosaccharides and high-resolution mass spectrometry; Michael Russelle S Alvarez[1]; Sheryl Joyce G Alvarez[1]; Adeola Adeyemi[1]; Carlito B. Lebrilla[1]; [1]*University of California Davis, Davis, CA*

TOH pm 03:30
18O-water labeling enables protein turnover measurements during embryogenesis.; Edward R Cruz[1, 2]; Argit Marishta[1, 2]; Gloria Bao[1, 2]; Alex Johnson[1, 2]; Felix C Keber[1, 2]; Michael Neinast[1, 2]; Joshua D. Rabinowitz[1, 2]; Eric F Wieschaus[1]; Martin Wühr[1, 2]; [1]*Princeton University, Princeton, NJ;* [2]*Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ*

TOH pm 03:50
High-Resolution LC-QTOF Mass Spectrometry for Dual ^{13}C and ^{15}N Stable Isotope Tracing in Metabolomics; Maleesha De Silva[1]; Yoannis Imbert-Fernandez[1]; Brian F. Clem[1]; Steven Lai[2]; Pawel Lorkiewicz[1]; [1]*University of Louisville, Louisville, KY;* [2]*Waters Corporation, Milford, MA*

TOH pm 04:10
High throughput stable isotope feature extraction for xenobiotic metabolite identification; Chris J Brown[1]; Yury O. Tsybin[2]; Konstantin O. Nagornov[2]; Matt Chase[3]; Jeff Gilbert[3]; Heiko Neuweger[4]; [1]*Corteva Agrisciences, Indianapolis, IN;* [2]*Spectroswiss, Lausanne, Switzerland;* [3]*Corteva Agriscience, Indianapolis, IN;* [4]*Bruker, Bremen, Germany*

WOA am: Data-Independent Acquisition: Acquisition and Multiplexing
Hall D

WOA am 08:30
DDA's Not Dead, yet: Evaluating its Merits in a World of nDIA High-Speed Mass Spectrometry; Naomi J O'Sullivan[1]; Florian Bayer[1]; Nicole Kabella[1]; Bernhard Kuster[1]; [1]*Technical University Munich, Freising, Germany*

WOA am 08:50
Direct On-Bead 18O Labeling with SP3 Sample Preparation (SP-18O) and DIA-MS Enables Robust Quantitative Proteomics; Shakhzodjon Uzokboev[1]; Yi-Kai Liu[2, 3]; Zheng Zhang[2]; Lucas Kramer[2]; Vikki Weake[2]; W. Andy Tao[1, 2, 4]; [1]*Purdue University Dept of Chemistry, West Lafayette, IN;* [2]*Department of Biochemistry, Purdue University, West Lafayette, IN;* [3]*Purdue University, west lafayette, IN;* [4]*Purdue Institute for Cancer Research, West Lafayette, IN*

WOA am 09:10
Enabling deep proteome coverage at ultra-high throughput using stepped-quadrupole DIA on a novel MRT benchtop MS; Matthew E Daly[1]; Lee A Gethings[1]; Richard Lock[1]; Johannes PC Vissers[1]; Jason L Wildgoose[1]; James Langridge[1]; [1]*Waters Wilmslow UK, Wilmslow, United Kingdom*

WOA am 09:30
A Foundational Benchmark for DIA Proteomics: Evaluating Data Analysis Strategies in the Presence of Biological Noise; Therese Dau[1]; Hem Gurung[1]; Jinyan Chan[1]; William J. Meilandt[1]; Susan Klaeger[1]; Corey Bakalarski[1]; Christopher M Rose[1]; Alessandro Ori[1]; Meena Choi[1]; [1]*Genentech Inc, South San Francisco, CA*

WOA am 09:50
ProteomeScout-HT: A High-Throughput DIA-Based Screening Platform for Proteome-Wide Analysis of Degraders and Molecular Glues; Johannes Krumm[1]; Barbara Schnitzer[1]; Theresa Keil[1]; Raffaela Berger[1]; Michael Zollo[1]; Viktoria Fischer[1]; Janine Sequeira[1]; Marius Seiche[1]; Christin Zasada[1]; Hannes Hahne[1]; [1]*Momentum Biotechnologies, Freising, Germany*

WOA am 10:10
ScreenPep2.0 - Enabling High-Throughput in-depth Proteome-Wide Drug Screening at 276 and 720 SPD; Isabella Straub[1]; Thomas Lanzinner[1]; Andreas Weiss[2]; Inaki Morao[3]; Barbara Kracher[1]; Oliver Kardell[1]; Patrick Allihn[1]; Florian Flenkenthaler[1]; Giada Marino[1]; Johannes Trefz[1]; Dezbah Turnblad-Phillips[1]; Nagarjuna Nagaraj[1]; Andreas Tebbe[1]; [1]*Evotec International GmbH, Munich, Germany;* [2]*Evotec SE, Hamburg, Germany;* [3]*Evotec UK Ltd, Abingdon, United Kingdom*

WOB am: Lipidomics: Targeted and Untargeted
Ballroom 20A

WOB am 08:30
Confirming a 3D cell model - senescence associated lipids in human skin and skin equivalents; Martina Marchetti-Deschmann[1, 2]; Samuele Zoratto[1, 2]; Christoph Kremslehner[2, 3]; Michaela Schirato[2, 3]; Gaelle Gendronneau[2, 4]; Agnès Tessier[2, 4]; Florian Gruber[2, 3]; *[1]TU Wien, Vienna, Austria; [2]Christian Doppler Laboratory for Multimodal Imaging of Aging and Senescence - SKINMAGINE, Vienna, Austria; [3]Medical University Vienna, Vienna, Austria; [4]Chanel PB, Pantin, France*

WOB am 08:50
Mechanism-guided Discovery of Phosphatidylcholine 38:4 as an Abcb4/Mdr2 Inhibition Biomarker in Rats Using Untargeted-to-targeted Lipidomics; Renmeng Liu[1]; Zachary Rabow[1]; Tingyuan Yang[2]; Xin Yan[2]; Yiding Hu[1]; Chenling Xiong[1]; Yurong Lai[1]; *[1]Gilead Sciences Inc., Foster City, CA; [2]Texas A&M University, College Station, TX*

WOB am 09:10
i2PB for multiplexed quantitation of fatty acids down to C=C Locations; Lipeng Qiao[1]; Jing Zhao[1]; Yu Xia[1]; *[1]Tsinghua university, Beijing, China*

WOB am 09:30
Isotopically Pure 7Li+ Enhances the Detection of Fluorinated Storage Lipids; Daniel Roeth[1]; Weidong Hu[1]; Patty Wong[1]; Jack Shively[1]; Markus Kalkum[1]; *[1]City of Hope, Duarte, CA*

WOB am 09:50
Automated Untargeted LC–MS/MS Discovery of Oxidized Triacylglycerols Links Lipid Droplet Chemistry to Microglial Phenotypes; Katherine A Walker[1]; Thomas G. Lubinsky[2]; Caitlin Randolph[2]; Gaurav Chopra[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, Department of Chemistry, West Lafayette, IN*

WOB am 10:10
Lipid CAT: An Open-Access Contaminant Annotation Tool to enhance MS-Based Lipidomics Workflows; Carlos R. Canez[1]; Bowen Yang[1]; Liang Li[1, 2]; *[1]Department of Chemistry, University of Alberta, Edmonton, AB; [2]The Metabolomics Innovation Centre, Edmonton, AB*

WEDNESDAY MORNING ORALS

WOC am: Informatics: Innovations
Ballroom 20BC

WOC am 08:30

ProteomeAtlas: a comprehensive protein expression profiling across 200+ human cell lines; Christin Zasada[1]; Johannes Krumm[1]; Johanna Wallner[1]; Raffaela Berger[1]; Hannes Hahne[1]; *[1]Momentum Biotechnologies, Freising, Germany*

WOC am 08:50

immunotype: Deep Learning-Based HLA Class I Typing Directly from Immunopeptidomics Data; Matteo Felipe Pilz[1, 2]; Jonas Scheid[1, 2, 3, 4, 5]; Alina Bauer[1]; Steffen Lemke[1, 2, 3, 4, 5]; Timo Sachsenberg[1, 2]; Jens Bauer[3, 4, 6]; Annika Nelde[3, 4]; Josua Stadelmeier[1, 2, 5]; Axel Walter[3, 4, 5]; Hans-Georg Rammensee[4, 6, 7]; Sven Nahnsen[1, 2, 5, 8]; Oliver Kohlbacher[1, 2, 9]; Juliane Sarah Walz[3, 4, 6, 10]; *[1]Department of Computer Science, University of Tübingen, Tübingen, Germany; [2]Institute for Bioinformatics and Medical Informatics (IBMI), University of Tübingen, Tübingen, Germany; [3]Department of Peptide-based Immunotherapy, Institute of Immunology, Univ. and Univ. Hospital Tübingen, Tübingen, Germany; [4]Cluster of Excellence iFIT (EXC2180) “Image-Guided and Functionally Instructed Tumor Therapies”, Tübingen, Germany; [5]Quantitative Biology Center (QBiC), Tübingen, Germany; [6]German Cancer Consortium (DKTK) and German Cancer Research Center (DKFZ), partner site Tübingen, Tübingen, Germany; [7]Institute of Immunology, University of Tübingen, Tübingen, Germany; [8]M3 Research Center, University Hospital of Tübingen, Tübingen, Germany; [9]Institute for Translational Bioinformatics, University Hospital Tübingen, Tübingen, Germany; [10]Clinical Collaboration Unit Translational Immunology, Department of Internal Medicine, University Hospital Tübingen, Tübingen, Germany*

WOC am 09:10

Statistical analysis of multi-tissue mass spectrometry imaging experiments enables reproducible comparison of complex spatial patterns between experimental groups; Ethan Rogers[1]; Olga Vitek[1]; *[1]Northeastern University, Boston, MA*

WOC am 09:30

Continuous Telemetry-Driven Quality Control for Proactive LC–MS Performance in Proteomics Core Facilities; Inigo Casanova[1]; Steve Binos[2, 3]; Luca Scotti[1]; Kiran Kamboj[1]; Maria Ortega[1]; Adolfo Fernandez-Gomez De Enteria[1]; Laura F Dagley[3, 4]; Daniel Lopez Ferrer[1]; *[1]Montara BioLabs, Las Rozas de Madrid, Spain; [2]Walter and Eliza Hall Institute for Medical Research, Parkville, Australia; [3]Department of Medical Biology, Faculty of Medicine, Dentistry & Health Sciences, The University of Melbourne, Parkville, Australia; [4]Walter and Eliza Hall Institute of Medical Research, Parkville, Australia*

WOC am 09:50

Radiant DIA™: A Fast, Sensitive, and Accurate DIA Proteomics Search Engine for Quantitative Proteomics; Seth Just[1]; Andrew Nichols[1]; Lee S Cantrell[1]; Jian Wang[1]; Janos Kis[1]; Iman Mohtashemi[1]; Theodore Platt[1]; Omid Farokhzad[1]; Serafim Batzoglou[1]; *[1]Seer, Inc, Redwood City, CA*

WOC am 10:10

MealTime-MS 2.0: A novel supervised learning approach for the real-time optimization of mass spectrometry data acquisition increases proteome coverage; Iryna Abramchuk[1]; Yun-En Chung[1]; Alona Petrova[1]; Jonathan St-Germain[2]; Jens Decker[3]; Brian Raught[2]; Jonathan Krieger[4]; Tharan Srikumar[4]; Mathieu Lavallée-Adam[1]; *[1]University of Ottawa, Ottawa, ON; [2]Princess Margaret Cancer Centre, Toronto, ON; [3]Bruker Daltonics GmbH & Co.KG, Bremen, Germany; [4]Bruker Ltd, Milton, Canada, Toronto, ON*

WEDNESDAY MORNING ORALS

WOD am: Fundamentals: Unconventional Approaches in MS
Ballroom 20D

WOD am 08:30
Unit Resolution, No Problem: Reimagining DIA on a Hybrid Quadrupole-Linear Ion Trap Mass Spectrometer; Lauren Fields[1]; Bo Wen[1]; Chris Hsu[1]; Deanna L Plubell[2]; Philip M. Remes[2]; Lilian Heil[2]; Michael J. MacCoss[1]; *[1]University of Washington, Seattle, WA; [2]Thermo Fisher Scientific, San Jose, CA*

WOD am 08:50
Multimass Three-Dimensional Velocity Map Imaging from Surfaces; Yifeng Jia[1]; Felicia M Green[2]; Kieran Chung[1]; Mark Brouard[1]; *[1]University of Oxford, Department of Chemistry, Oxford, United Kingdom; [2]Rosalind Franklin Institute, Didcot, United Kingdom*

WOD am 09:10
Parallel-Valet Ion Parking in Native Mass Spectrometry: Selective Escape of Products During an Ion/Ion Reaction Over an Axial Pseudopotential; Seth A Horn[1]; Boukar K. S. Faye[1]; Teresa Lee[1]; Scott A. McLuckey[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

WOD am 09:30
Maximizing ion utilization in time-of-flight MS using a novel T-shaped trap with ultrafast m/z-selective orthogonal ejection and parallel ion processing; Martin Breitenlechner[1]; Stephen Zanon[1]; Maozi Liu[1]; James Wallace[1]; Alex Mordehai[1]; James Bertsch[1]; *[1]Agilent Technologies, Santa Clara, CA*

WOD am 09:50
Study of Ion Cloud Interaction Effects on High-Resolution Gas-Phase Isomer Separation in Ion Traps; Liwen Liang[1]; Zhuofan Wang[1]; Shuai Li[1]; Xiaoyu Zhou[2]; Zheng Ouyang[1]; *[1]State Key Laboratory of Precision Measurement Technology and Instruments, Department of Precision Instrument, Tsinghua University, Beijing, China; [2]School of Biomedical Engineering, Hainan University, Hainan 572024, China, Haikou, China*

WOD am 10:10
A soft-landing instrument with tight ion focusing enables multi-sample deposition on a single cryoEM grid; Alexander Makarov[1]; Henning Wehrs[1]; Tim Esser[2]; Tobias P. Woerner[1]; Wenfei Song[2]; Eric Wapelhorst[1]; Kyle Fort[1]; Jan Fiala[2]; Silke Seedorf[1]; Robert Tapken[1]; Thomas Heise[1]; Wilko Balschun[1]; Deepak Kini[2]; Dmitry Grinfeld[1]; Rosa Viner[3]; Huaning Wang[4]; Thomas Wehkamp[1]; Idrees Khan[2]; Markéta Červinková[5]; Albert Konijnenberg[2]; Aurelien Botman[2]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]ThermoFisher Scientific, Eindhoven, Netherlands; [3]Thermo Fisher Scientific, San Jose, CA; [4]Thermo Fisher Scientific, Hillsboro, OR; [5]Thermo Fisher Scientific, Brno, Czech Republic*

WEDNESDAY MORNING ORALS

WOE am: Instrumentation: Innovative Separation Approaches Coupled to MS
Room 6A

WOE am 08:30
A modified 2D-LC system enables online mAb charge variant separation coupled with ultrafast microdroplet reaction technology; Madison Roeckel[1]; Hui Zhao[1]; Jim Lau[1]; Joel Praneeth[2]; Hao Chen[2]; Harsha P. Gunawardena[3]; *[1]Agilent Technologies, Wilmington, DE; [2]New Jersey Institute of Technology, Newark, NJ; [3]Johnson & Johnson Innovative Medicine, Spring House, PA*

WOE am 08:50
A Perfect Coupling: Integrating Asymmetrical Flow Field-Flow Fractionation (AF4) with Charge Detection Mass Spectrometry (CDMS) to Resolve Biopharmaceutical Heterogeneity; Chen Du[1]; Yingchan Guo[1]; Victoria C Cotham[1]; Shunhai Wang[1]; Ning Li[1]; *[1]Analytical and Biological Mass Spectrometry, Regeneron Pharmaceuticals Inc., Tarrytown, NY*

WOE am 09:10
Deep Proteoform Mapping in Human Heart Enabled by Top-Down Proteomics with Online Multidimensional Liquid Chromatography and Machine Learning; Matthew S Fischer[1]; Eli J Larson[1]; Thomas S Weir[1]; Ryan K Schroeder[1]; Holden T. Rogers[1]; Hsin-Ju Chan[1]; Zhan Gao[2]; Jiaqi Chen[3]; Heewon Choi[1]; Yang Lu[4]; Ying Ge[1, 2, 5]; *[1]Department of Chemistry, University of Wisconsin−Madison, Madison, WI; [2]Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI; [3]Department of Biochemistry, University of Wisconsin-Madison, Madison, WI; [4]Department of Biomedical Engineering, University of Wisconsin-Madison, Madison, WI; [5]Human Proteomics Program, School of Medicine and Public Health, University of Wisconsin-Madison, Madison, Wisconsin 53705, USA., Madison, WI*

WOE am 09:30
Trapping-Enrichment Multidimensional Liquid Chromatography-Mass Spectrometry for Characterization of Low-Level, Unstable Biotherapeutic Targets; Devin Makey[1]; Rodell Barrientos[1]; Zhengqi Zhang[1]; Eli Larson[1]; Sasidhar Nirudodhi[1]; Erik Regalado[1]; *[1]Merck & Co., Inc., Rahway, NJ*

WOE am 09:50
New Advances in Ultra-Low Flow Liquid Phase Separations for Enhanced MS Sensitivity in Proteomic and Multi-omic Analysis of Limited Samples; Michal Gregus[1]; Yunfan Gao[1]; Thao Tran[1]; Michael Krawitzky Krawitzky[2]; Anne-Lise Marie[1]; Alexander R. Ivanov[1]; *[1]Northeastern University, Boston, MA; [2]Bruker Scientific LLC, Billerica, MA*

WOE am 10:10
Online enrichment of phosphotyrosine peptides by affinity LC-MS; Lindsay Morrison[1]; Jeffrey C. Silva[2]; Ryan Sinapius[2]; Kevin Wyndham[1]; *[1]Waters Corporation, Milford, MA; [2]Cell Signaling Technology Inc, Danvers, MA*

WOF am: Imaging: Pharmaceuticals, Metabolites, Lipids, and Glycans
Room 6B

WOF am 08:30
MALDI-TIMS-MS Imaging Reveals Isomer-Specific Distribution of Perfluorooctane Sulfonate (PFOS) and Exposure-Induced Alteration in Spatial Lipid Profiles in Mouse Tissues; Aidan J Reynolds[1]; Jaide A Mickel[2]; Kira Baker[1]; Alexa Bajouwa[1]; Ryutaro Einar Jacobson[1]; Srijana Shrestha[3]; James G Wagner[4]; Rance Nault[2, 5]; Tian (Autumn) Qiu[1, 5]; *[1]Department of Chemistry, Michigan State University, East Lansing, MI; [2]Department of Pharmacology and Toxicology, Institute for Integrative Toxicology, Michigan State University, East Lansing, MI, United States, East Lansing, MI; [3]Genetics and Genome Sciences, Michigan State University, East Lansing, MI; [4]Pathobiology and Diagnostic Investigation, Michigan State University, East Lansing, MI; [5]Center for PFAS Research, Michigan State University, East Lansing, MI*

WOF am 08:50
Assessing multimodal DESI and MALDI strategies for lipid and peptide imaging in formalin-fixed paraffin-embedded and fresh-frozen human brain tissues; Tassia Venga Mendes[1]; Patrick R. Hof[2]; Merina T. Varghese[3]; Dan E. Meyer[4]; Demian Ifa[1]; Livia S. Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX; [2]Icahn School of Medicine at Mount Sinai, Nash Family Department of Neuroscience, New York, NY; [3]University of Rhode Island, George & Anne Ryan Institute for Neuroscience, Kingston, RI; [4]GE HealthCare Technology & Innovation Center, Niskayuna, NY*

WOF am 09:10
Mass Spectrometry Imaging of Pimonidazole as a Hypoxia Marker in 3D Cell Cultures to Evaluate Hypoxia-Activated Prodrug Metabolism; Andrew T Freeman[1]; Amanda B. Hummon[1, 2, 3]; *[1]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH; [2]Ohio State Biochemistry Program (OSBP), The Ohio State University, Columbus, OH; [3]The Ohio State University Comprehensive Cancer Center, Columbus, OH*

WOF am 09:30
Drug-Induced Metabolic Reprogramming at Single Cell Resolution Using MALDI MSI; Lauren E Hill[1]; Lyndsay E.A. Young[1]; James W. Dressman[1]; Muhammed F. Bayram[1]; Anand Mehta[1]; Richard R. Drake[1]; *[1]Medical University of South Carolina, Charleston, SC*

WOF am 09:50
Spatial metabolic gradients in the liver and small intestine; Laith Samarah[1]; Clover Zheng[1]; Xi Xing[1]; Won Dong Lee[1]; Amichay Afriat[1]; Uthsav Chitra[2]; Michael MacArthur[1]; Wenyun Lu[1]; Connor Jankowski[1]; Cong Ma[3]; Craig Hunter[1]; Michael Neinast[1]; Daniel Weilandt[1]; Lingfan Liang[1]; Benjamin Raphael[1]; Joshua D. Rabinowitz[1]; *[1]Princeton University, Princeton, NJ; [2]Broad Institute of MIT and Harvard, Cambridge, MA; [3]University of Michigan-Ann Arbor, Ann Arbor, MI*

WOF am 10:10
From Micro to Meso Imaging: Merging MALDI MSI and High Throughput Phenotypic Microscopy for Mapping Small Molecule Effects on Cells; Emily R. Sekera[1]; Fabio Stossi[1]; Steven J. Philips[1]; Ashraf Mohammed[1]; Taosheng Chen[1]; John J. Bowling[1]; Aseem Z. Ansari[1]; *[1]St. Jude Children's Research Hospital, Memphis, TN*

WEDNESDAY MORNING ORALS

WOG am: Forensics, Innovations and Applications
Room 6CF

WOG am 08:30
Hand-held Laser Sampling Probe with Flexible Transfer Line for Non-proximate Desorption Photoionization; G. Asher Newsome; *Smithsonian Museum Conservation Institute, Suitland, MD*

WOG am 08:50
Mass spectrometry imaging and spectroscopic detection of counterfeits and forgery; Veronika Tibljas[1]; Simona Francese[1]; Jennifer Clark[1]; Marjory Da Costa Abreu[1]; Ian Goodall[2]; Frazer Birch[3]; Robert Bradshaw[1]; *[1]Sheffield Hallam University, Sheffield, United Kingdom; [2]The Scotch Whisky Research Institute, The Robertson Trust Building, Research Avenue North, Edinburgh, United Kingdom; [3]Edrington, Great Western Road, Glasgow G15 6RW, Glasgow, United Kingdom*

WOG am 09:10
Answering burning questions: A comparative analysis and identification of cannabidiol and Δ9-tetrahydrocannabinol pyrolysis products; Niara A. Nichols[1]; A. John Dane[1]; Kirk Jensen[2]; Robert B Cody[2]; Rabi A. Musah[1]; *[1]Louisiana State University, Baton Rouge, LA; [2]JEOL USA, Inc., Peabody, MA*

WOG am 09:30
Accelerating Hair Drug Testing via LDTD–MS/MS Technology; Sarah Demers[1]; Serge Auger[2]; Mégane Moreau[2]; Pierre Picard[2]; Jonathan Rochon[2]; Jean Lacoursiere[2]; *[1]Phytronix Technologies, Quebec City, QC; [2]Phytronix Technologies, Inc., Quebec, QC*

WOG am 09:50
Detection and Quantification of Abused Drugs by Electrokinetic Stacking Paper Spray Method at Low Parts-Per-Trillion level in Plasma; Varadaraju Vadakekatte Dyavegowda[1]; Lahiru Wedasingha[1]; Jamison Riley Polley[1]; Nicholas E Manicke[1]; *[1]Indiana University Indianapolis, Indianapolis, IN*

WOG am: Forensics, Innovations and Applications
WOG am 10:10
Evidence of bone collagen cross-linking changes thought time by mass spectrometry; Fabrice Bray[1, 2]; Lisa Garrbe[2]; Stéphanie Flament[1, 2]; Isabelle Fabrizi[3]; Marc Haegelin[1]; Tarek Oueslati[4]; Patrick Auguste[5]; David Herisson[6, 7, 8]; Jean-luc Locht[9, 10]; Pierre Antoine[10]; Sophie Clement[6, 11]; Céline Coussot[10, 11]; Grégory Bayle[11]; Marie-Anne Julien[12]; Christian Rolando[13]; *[1]UAR 2638 IMEC CNRS, Villeneuve d'ascq, France; [2]US 41 - UAR 2014 - PLBS, Lille, France; [3]UMR 8576 - UGSF, Villeneuve d'ascq, France; [4]UMR 8164 – HALMA, Villeneuve d'ascq, France; [5]UMR 8198 - EEP, villeneuve d'ascq, France; [6]UMR 7041 - ARSCAN, Paris, France; [7]Univ. Paris 8, Paris, France; [8]Univ. Paris 1, Paris, France; [9]Inrap Hauts-de-France, Glisy, France; [10]UMR 8591 LGP, Paris, France; [11]Inrap Île-de-France, Paris, France; [12]GéoArchÉon, Paris, France; [13]UMR 6064 CARMEN, Rouen, France*

WOH am: Environmental: Innovative Approaches and Instrumentation
Room 6DE

WOH am 08:30

An Open-Source Mass Spectrometer for Atmospheric Sampling; Kevin A. Wokosin[1]; Timothy H. Bertram[1]; Shondiin Lawson[2]; Abigail LePinske[2]; Steven J Kregel[2]; [1]*University of Wisconsin-Madison, Madison, WI;* [2]*Bradley University, Peoria, IL*

WOH am 08:50

Molecular Insights into Ammonia–Diesel Dual-Fuel Marine Engine Emissions via Complementary Online and Offline High-Resolution Mass Spectrometry; Helly Johanna Hansen[1]; Christopher Paul Rüger[1]; Fabian Carl[1]; Hendryk Czech[1]; Kevin Schnepel[1]; Thorsten Streibel[1]; Uwe Etzien[1]; Felix Wenig[1]; Bert Buchholz[1]; Ralf Zimmermann[1]; [1]*University of Rostock, Rostock, Germany*

WOH am 09:10

Autofluorescence-guided analysis and imaging of environmental biofilms with nanospray desorption electrospray ionization mass spectrometry; Syeda Nazifa Wali[1]; Qiaorong Xie[1]; Julia Laskin[1]; [1]*Purdue University Dept of Chemistry, West Lafayette, IN*

WOH am 09:30

Differential Bioaccumulation of Individual PFAS Species in Zebrafish Visualized by DESI-MSI Combined with Single- and Multi-Pass IMS; Emmanuelle Claude[1]; Matthew J Smith[2]; Angélica Diaz Basabe[2, 3]; Joanne Ballantyne[1]; Craig E Wheelock[2]; [1]*Waters Corporation, Wilmslow, United Kingdom;* [2]*Unit of Integrative Metabolomics, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden;* [3]*Center for Molecular Medicine (CMM), Karolinska University Hospital, SE-171 64 Solna, Sweden*

WOH am 09:50

Isotopic Stability Plateau as a tool for High-Precision $\delta^{13}C$ Orbitrap IRMS in Complex Mixtures; Hugo Gontijo Machado[1]; Elliot P. Mueller[2, 3]; Júlio C. Ribeiro[1]; Giovanni Bevilaqua[1]; Gabriel Dos Santos[1]; Alexandre Andrade Ferreira[4]; Ygor Rocha[4]; Surjyendu Bhattacharjee[2, 5]; John M Eiler[2]; Boniek Gontijo[1]; [1]*UFG, Goiânia, Brazil;* [2]*California Institute of Technology, Pasadena, CA;* [3]*University of Colorado Boulder, Boulder, CO;* [4]*PETROBRAS, Rio de Janeiro, Brazil;* [5]*Yale University, West Haven, CT*

WOH am 10:10

Ion Mobility-Constrained Non-Targeted Screening of PFAS in Complex Matrices Using gTIMS Coupled to 18 T FTICR Mass Spectrometry; Meng Jiao[1]; Simon Ollivier[2, 3]; Marie Hubert-Roux[2, 3]; Mathilde Lauzent[2, 3]; Jean-Philippe Croué[1]; Carlos Afonso[2, 3]; [1]*Institute de Chimie des Milieux et des Matériaux de Poitiers (IC2MP), UMR 7285, CNRS, University of Poitiers, Poitiers, France;* [2]*CARMeN institute, UMR 6064, CNRS, University of Rouen Normandy, Rouen, France;* [3]*International Joint Laboratory for Complex Matrices Molecular Characterization (iC2MC), Harfleur, France*

WOA pm: Biotherapeutics: Proteins, Antibodies, and Antibody Drug Conjugates
Hall D

WOA pm 02:30
An Optimized Native Reverse-Phase LC-MS Method with Native Affinity Capture for Comprehensive Characterization of Antibody-Drug Conjugates in In-Vitro Biotransformation Studies; Xiaoyu Zhu[1]; Shuli Tang[1]; Wenjing Peng[1]; Yuetian Yan[1]; Shunhai Wang[1]; Ning Li[1]; [1]*Analytical and Biological Mass Spectrometry, Regeneron Pharmaceuticals, Inc., Tarrytown, NY*

WOA pm 02:50
High-throughput monitoring of isoaspartate in therapeutic antibodies via enzymatic labeling and direct infusion mass spectrometry; Marcel Morgenstern[1]; Mark Scalf[2]; Emily Johnson[2]; Craig D. Wenger[2]; John S. Chlystek[2]; Alexander S. Hebert[2]; Lloyd M. Smith[2, 3]; Joshua J. Coon[2, 3, 4]; [1]*Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*University of Wisconsin-Madison, Madison, WI;* [3]*CeleramAb Inc., Middleton, WI;* [4]*Morgridge Institute for Research, Madison, WI*

WOA pm 03:10
Rapid Determination of Drug-to-Antibody Ratios in Antibody–Drug Conjugates Using Ultrafast Microdroplet Digestion Technology; Yongqing Yang[1]; Juana Perez[1]; Thomas Walker[2]; Jim Lau[3]; Mike Knierman[3]; Hui Zhao[3]; Xi Qiu[3]; Karen Luo[3]; Harsha P. Gunawardena[4]; Munkhtsetseg Baatar[5]; Hao Chen[1]; [1]*New Jersey Institute of Technology, Newark, NJ;* [2]*Agilent Technologies, Lexington, MA;* [3]*Agilent Technologies, Wilmington, DE;* [4]*Johnson & Johnson Innovative Medicine, Spring House, PA;* [5]*National University of Mongolia, Ulaanbaatar, Mongolia*

WOA pm 03:30
Archaeal HTA-Proteases Facilitate One-Enzyme De Novo Protein Sequencing, Novel Biomarker Discovery, Rapid Clinical Proteomics and Markedly Accelerate Routine Proteomics Analyses; Simion Kreimer[1]; Allison M Narlock-Brand[2]; Jennifer E. Van Eyk[3, 4]; Albert J.R. Heck[5]; Steven M Yannone[2]; [1]*Cedars Sinai Medical Center, Los Angeles, CA;* [2]*CinderBio, San Leandro, CA;* [3]*Cedars-Sinai Medical Center, Smidt Heart Institute, Los Angeles, CA;* [4]*Cedars-Sinai Medical Center, LA;* [5]*Netherlands Proteomics Center, Utrecht, Netherlands*

WOA pm 03:50
Native Top-Down MSn characterization of Antibody-Oligonucleotide conjugates with support of PTCR and DMT on state-of-the-art Orbitrap Tribrid platforms; Thierry Besson[1]; Jonathan Dhenin[1]; Daniela Miranda[1]; Patrick Schindler[1]; [1]*Novartis pharma AG, basel, Switzerland*

WOA pm 04:10
Integrated Native MS Approaches for Characterizing Antibody Structural Stability under Stress; Eledon S Beyene[1]; Rowan Matney[1]; Sachin Tennakoon[2]; Lasini Amunugama[2]; Jared B Shaw[2]; Varun V Gadkari[1]; [1]*University of Minnesota-Twin Cities, Minneapolis, MN;* [2]*University of Nebraska-Lincoln, Lincoln, NE*

WOB pm: Fundamentals: Chemistry of Gas-Phase Ions (Honoring Michael Bowers) Ballroom 20A

WOB pm 02:30
Topology-Encoded Kinetic Barriers Stabilize Native-Like Protein Structures in the Gas Phase; Christian Bleiholder[1]; Fanny C Liu[1]; [1]*Florida State University, Tallahassee, FL*

WOB pm 02:50
Capturing Charge-State Dependent Protein Conformations across the Unfolding Landscape; Zhenyu Xi[1]; Robert Rider[1]; David H Russell[1]; [1]*Texas A&M Univesity, College Station, TX*

WOB pm 03:10
Sodium Cation Removal from Peptides via Gas-Phase Ion/Ion Reactions using Clusters of Weakly Coordinating Anions; Zachary T Kruger[1]; Alexander M. Koers[1]; Scott A. McLuckey[1]; [1]*Purdue University Dept of Chemistry, West Lafayette, IN*

WOB pm 03:30
The Structures and Dissociation Behavior of Protonated Guanosine Nucleoside Analogues Populated by Electrospray Ionization Depend on the Protonation Reagent Used; Mary T Rodgers[1]; Bijoy K. Roy[1]; Nicholas M. R. Frieler[1, 2]; Giel Berden[3]; [1]*Wayne State University, Detroit, MI;* [2]*University of Michigan-Ann Arbor, Ann Arbor, MI;* [3]*Radboud University, Nijmegen, Netherlands*

WOB pm 03:50
Using Fundamental Gas-Phase Ion Chemistry to Enable High-Confidence, Non-Targeted PFAS Identifications; Allison N Fry[1]; Christian Ieritano[2, 3]; Scott Hopkins[2, 3]; Peter B. Armentrout[4]; James N. Dodds[1]; Erin S. Baker[1]; [1]*Department of Chemistry, University of North Carolina at Chapel Hill, Chapel Hill, NC;* [2]*Department of Chemistry, University of Waterloo, Waterloo, ON;* [3]*WaterFEL, University of Waterloo, Waterloo, ON;* [4]*Department of Chemistry, University of Utah, Salt Lake City, UT*

WOB pm 04:10
Activation of Methane by Nb+ and Ta+ Studied by Infrared Multiple Photon Dissociation Spectroscopy and Quantum Chemistry; Abraham Tillquist[1]; Peter B. Armentrout[1]; [1]*University of Utah, Salt Lake City, UT*

WOC pm: Protein-Ligand and Protein-Protein Interactions
Ballroom 20BC

WOC pm 02:30

A Time-Resolved Native Mass Spectrometry Platform for Quantifying Protein-Protein and Protein-Ligand Kinetics; Virginia K James[1]; Lauren Stover[1]; Hanieh Bahramimoghaddam[1]; Tanishq Khandelwal[1]; Jing-Yuan Chang[1]; James Downing[1]; Elena Scott[1]; Kathleen Bailey[1]; David H Russell[1]; Lane A Baker[1]; Arthur Laganowsky[1]; *[1]Texas A&M University, College Station, TX*

WOC pm 02:50

targetDig: A TMT-based platform for discovering and validating protein-ligand interactions of a proteome-wide scale; Alex J Bott[1]; Christopher D McGann[1]; Joao A Paulo[1]; Steve P Gygi[1]; Jonathan G Van Vranken[1]; *[1]Harvard Medical School, Boston, MA*

WOC pm 03:10

Modular photocatalytic proximity labeling enables genetic-free mapping of protein, RNA, and DNA interactomes in fixed samples; Elijah Biletch[1, 2]; Conor P Herlihy[3]; Lidan Li[3]; Olivia Weissenfels[3]; Hanna G. Goldberg[1, 2]; Devin K Schweppe[3, 4, 5]; Brian J Beliveau[3, 4, 5]; Keriann M Backus[1, 2, 6, 7, 8, 9, 10]; *[1]Department of Chemistry and Biochemistry, University of California, Los Angeles, Los Angeles, Los Angeles, CA; [2]Biological Chemistry Department, David Geffen School of Medicine, University of California, Los Angeles, Los Angeles, CA; [3]Department of Genome Sciences, University of Washington, Seattle, WA; [4]Brotman Baty Institute for Precision Medicine, Seattle, WA; [5]Institute for Stem Cell & Regenerative Medicine, University of Washington, Seattle, WA; [6]Department of Human Genetics, David Geffen School of Medicine, University of California, Los Angeles, Los Angeles, CA; [7]Molecular Biology Institute, University of California, Los Angeles, Los Angeles, CA; [8]UCLA-DOE Institute for Genomics and Proteomics, University of California, Los Angeles, Los Angeles, CA; [9]Jonsson Comprehensive Cancer Center, University of California, Los Angeles, Los Angeles, CA; [10]Eli and Edythe Broad Center of Regenerative Medicine and Stem Cell Research, University of California, Los Angeles, Los Angeles, CA*

WOC pm 03:30

Elucidating structure-function interplays between GPCRs and phosphoinositides by native mass spectrometry; Guan-Ting Lian[1, 2, 3]; Rong Chen[1, 2]; Yi-Quan Wang[1]; Yi-An Chen[1]; Hsin-Yung Yen[1, 2]; *[1]Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan; [2]Institute of Biochemical Sciences, National Taiwan University, Taipei, Taiwan; [3]Taiwan International Graduate Program, Taipei, Taiwan*

WOC pm 03:50

Luminal surface proteome of the brain vasculature uncovers blood-brain barrier regulators; Namrata D. Udeshi[1]; Zijian Zhu[2]; Zuzhi Jiang[2]; Yupu Wang[2]; Khanh Nguyen[1]; Yuxiang Zhang[2]; Genxuan Lian[1]; D. R. Mani[1]; Steven A. Carr[1]; Jiefu Li[2]; *[1]Broad Institute, Cambridge, MA; [2]Janelia Research Campus, Howard Hughes Medical Institute, Ashburn, VA*

WOC pm 04:10

Mapping the subcellular interactome of ciliary GPR161 using structure prediction–coupled membrane AP-MS; Anushweta Asthana[1]; Rachel E Turn[2]; Mohammad Ovais Aziz-Zanjani[2]; Ananya D Ramkumar[2]; Roy Ng[2]; Haoqing Wang[1]; Peter K. Jackson[2]; *[1]Stanford University, Stanford, CA; [2]Stanford School of Medicine, Palo Alto, CA*

WOD pm: Metabolomics Untargeted Approaches
Ballroom 20D

WOD pm 02:30
Untargeted LC-MS/MS Metabolomics Uncovers Distinct Vascular and Erythropoietic Metabolic Axes in Hemoglobinopathies; Joy O Solomon[1]; Sherifdeen B Onigbinde[1]; Oluwatosin Daramola[1]; Abdulrahman Abdulmumin[1]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX*

WOD pm 02:50
Rapid Metabolomics in Blood Microsamples: Optimization and Biomarker Discovery Feasibility; Marlene N Thaitumu[1, 2]; Ana Sanchez Lorenzo[3]; Elizabeth Want[3]; Georgios Theodoridis[1, 4]; Helen Gika[1, 4]; *[1]Aristotle University of Thessaloniki, Thessaloniki, Greece; [2]Biomic AUTh, Center for Interdisciplinary Research and Innovation, Thessaloniki, Greece; [3]Imperial College London, London, United Kingdom; [4]BIOMIC_AUTH, Center for Interdisciplinary Research and Innovation, Thessaloniki, Greece*

WOD pm 03:10
Multi-omics Profiling of Autoimmune Conditions Reveals Novel Potential Biomarker Candidates; Michaël Méret[1]; Aglaia Kakoulidou[2]; Kirsten Kuhlbrodt[2]; Dennis Özcelik[2]; Olha Novokhatska[2]; Julien Peladan[1]; Pauline Sartre[1]; Stephanie Delmas[1]; Lucile Pacquet[1]; Pierre-Benoit Ancey[1]; Antje Hombach-Barrigah[2]; Antoine Berthemy[1]; Michael Rohe[2]; François Autelitano[1]; Elizabeth L. Van Der Kam[2]; *[1]Evotec SAS, Toulouse, France; [2]Evotec SE, Hamburg, Germany*

WOD pm 03:30
Comparing workflows for annotating unknown compounds via MS-FINDER, Feature Based Molecular Networking and Fuzzy Search within MassWiki; Meghna Srivastava[1]; Xukun Wang[1]; Fanzhou Kong[1]; Gert Wohlgemuth[1]; Oliver Fiehn[1]; *[1]UC Davis, Davis, CA*

WOD pm 03:50
From Manual Curation to Discovery: Development of an Automated Platform for Untargeted Chiral Metabolomics; Valeria Impedovo[1]; Ruggiero Gorgoglione[2]; Yujin Lee[1]; Alessia Lodi[1, 3]; Stefano Tiziani[1, 3, 4, 5]; *[1]Department of Nutritional Sciences, College of Natural Sciences, The University of Texas at Austin, Austin, TX; [2]Biosciences, Biotechnologies and Biopharmaceutics Department, The University of Bari Aldo Moro, Bari, Italy; [3]Department of Pediatrics, Dell Medical School, The University of Texas at Austin, Austin, TX; [4]Department of Oncology, Livestrong Cancer Institutes, Dell Medical School, The University of Texas at Austin, Austin, TX; [5]Center for Molecular Carcinogenesis and Toxicology, The University of Texas at Austin, Austin, TX*

WOD pm 04:10
From Hand-Drawn Pathways to GPS-Like Navigation: Repository-Scale Data Science Is Transforming Untargeted Metabolomics; Pieter Dorrestein; *University of California, San Diego, La Jolla, CA*

WOE pm: Instrumentation: Ambient Ionization and Applications
Room 6A

WOE pm 02:30
Development of a direct discharge ionization source for laser desorption mass spectrometry in a Mars-like atmosphere; Caroline E. R. Rowell[1, 2]; Marco E. Castillo[2, 3]; Joseph M. Pasterski[2, 4]; Desmond A. Kaplan[2, 5]; Benjamin J. Winkler[2, 6]; Friso H. W. Van Amerom[2, 7]; Xiang Li[2]; William B. Brinckerhoff[2]; Jacob D. Graham[2]; Andrej Grubisic[2]; *[1]NASA Postdoctoral Program / ORAU, Oak Ridge, TN; [2]NASA Goddard Space Flight Center, Greenbelt, MD; [3]Aerodyne Industries, LLC, Cape Canaveral, FL; [4]University of Maryland, College Park, MD; [5]Kapscience, LLC, Tewksbury, MA; [6]Danell Consulting, Inc., Winterville, NC; [7]Mini-Mass Consulting, Inc., Hyattsville, MD*

WOE pm 02:50
Multischeme Ambient Chemical Ionization Orbitrap Mass Spectrometry for Broad-Spectrum Pesticide Detection; Fariba Partovi[1, 2]; Joona Mikkilä[1]; Siddharth Iyer[2]; Jussi Kontro[1]; Suvi Ojanperä[3]; Aleksei Shcherbinin[1]; Netta Vinkvist[4]; Matti Rissanen[2, 4]; *[1]Karsa Ltd., Helsinki, Finland; [2]University of Tampere, Tampere, Finland; [3]Finnish Customs, Helsinki, Finland; [4]Helsinki University, Helsinki, Finland*

WOE pm 03:10
Advances on a Miniaturized 2D MS platform for Detection of Chemical Threats; Conor C Jenkins[1]; Paul S Demond[2, 3]; *[1]U.S. Army DEVCOM CBC, APG, MD; [2]DEVCOM Chemical Biological Center, Aberdeen Proving Ground, MD; [3]Precise Systems Inc., Lexington Park, MD*

WOE pm 03:30
Rapid Screening of Recycled and Bio-plastics via Ambient IR-ELDI Mass Spectrometry and Machine Learning Algorithms; Chun-Ting Liu[1]; Shao-Hsun Ho[1]; I-Chung Lu[1]; *[1]Department of Chemistry, National Chung Hsing University, Taichung City, Taiwan*

WOE pm 03:50
Solventless workflow for rapid screening of drugs of abuse using SPME–DART–MS; Marc Driezen[1]; Wei Zhou[1]; François Espourteille[2]; Janusz Pawliszyn[1]; *[1]University of Waterloo, Waterloo, ON; [2]Bruker Daltonics, Billerica, MA*

WOE pm 04:10
Evaluation Of the OptiSpray Ion Source And Cartridges With Integrated Replaceable Emitters For Proteomics Data Acquisition; Katherine Walker[1]; Joshua Silveira[1]; Robertas Zilinskas[2]; Agata Kocarian[2]; John Crellin[1]; Runsheng Zheng[3]; Alec Valenta[3]; Jeff Op De Beeck[4]; Vytautas Tamosiunas[2]; Romain Huguet[1]; Eloy Wouters[1]; Shanhua Lin[5]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Vilnius, Lithuania; [3]Thermo Fisher Scientific, Germering, Germany; [4]Thermo Fisher Scientific, Zwijnaarde, Belgium; [5]Thermo Fisher Scientific, Sunnyvale, CA*

WOF pm: Microbes and the Microbiome
Room 6B

WOF pm 02:30
Distinct patterns of co-occurring nutrient stresses on a Pacific Basin metaproteomics transect; Annaliese C.S. Meyer[1]; Matthew R. McIlvin[2]; Paloma Lopez[2]; Arianna Krinos[3]; Margaret Mars Brisbin[4]; Mak A. Saito[2]; *[1]Woods Hole Oceanographic Institution/Massachusetts Institute of Techonology, Woods Hole; [2]Woods Hole Oceanographic Institution, Woods Hole, MA; [3]Brown University, Providence, RI; [4]University of South Florida, Tampa, FL*

WOF pm 02:50
De novo proteomics of an 'unknown' species in a complex metaproteomic sample; Noelle Held[1]; Khiry L. Patterson[1]; Maxfield Palmer[1]; Nicolas Hartel[2]; *[1]University of Southern California, Los Angeles, CA; [2]Thermo Fisher Scientific, San Jose, CA*

WOF pm 03:10
Data-Independent Acquisition Analysis of Metaproteomics Data with MaxDIA Enables Accurate Identification, Quantification, and Efficient Resource Allocation; Jinqiu Xiao[1]; Walter Viegener[1]; Juergen Cox[1]; *[1]Max Planck Institute of Biochemistry, Martinsried, Germany*

WOF pm 03:30
Transfer of Maternal Antibiotics into Human Milk Alters the Infant Gut Microbiome and Metabolome; Kine Eide Kvitne[1]; Simone Zuffa[1]; Abubaker Patan[1]; Vincent Charron-Lamoureux[1]; Shipei Xing[1]; Victoria Deleray[1]; Yasin El Abiead[1]; Jiaxi Cai[2]; Jeremiah D Momper[1]; Raymond T Suhandynata[1, 3]; Kerri Bertrand[4]; Rob Knight[4]; Christina Chambers[4]; Pieter C. Dorrestein[1]; Shirley M. Tsunoda[1]; *[1]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [2]Shu Chien-Gene Lay Department of Bioengineering, University of California San Diego, La Jolla, CA; [3]Department of Pathology, University of California San Diego, La Jolla, CA; [4]Department of Pediatrics, University of California San Diego, La Jolla, CA*

WOF pm 03:50
Multidimensional LC–MS/MS Reveals the Deep Metabolome of the Gut–Microbiome–Brain Axis; Stilianos Papadopoulos Lambidis[1]; Carolin Wilhelm[1]; Dennis Jakob[1]; Claudia Miretta-Barone[1]; Daniel Petras[2]; Ruth E. Ley[1]; *[1]Max Planck Institute for Biology, Tuebingen, Germany; [2]UC RIVERSIDE, Riverside, CA*

WOF pm 04:10
Mapping Calprotectin-Mediated Molecular Adaptation in Staphylococcus aureus Biofilms; Alexis P. Pope[1, 2]; Jeffrey A. Freiberg[3, 4]; Lukasz G. Migas[5]; Raf Van De Plas[1, 5]; Walter J. Chazin[6, 7]; Eric P. Skaar[3, 8]; Jeffrey M. Spraggins[1, 2, 6, 7, 8, 9]; *[1]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [2]Chemical and Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [3]Vanderbilt Institute for Infection, Immunology, and Inflammation, Vanderbilt University Medical Center, Nashville, TN; [4]Division of Infectious Diseases, Department of Medicine, Vanderbilt University Medical Center, Nashville, TN; [5]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [6]Department of Chemistry, Vanderbilt University, Nashville, TN; [7]Department of Biochemistry, Vanderbilt University, Nashville, TN; [8]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN; [9]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN*

WOG pm: Nucleic Acids and Nucleotides
Room 6CF

WOG pm 02:30
OligoFragger: A Graph-Based Search Tool for Comprehensive Identification and Quantification of Modified RNA by Mass Spectrometry; Jiechen Shen[1]; Daniel Polasky[1]; Fengchao Yu[1]; Bojing Zhu[1]; Kristin S. Koutmou[1]; Alexey I. Nesvizhskii[1]; *[1]University of Michigan, Ann Arbor, MI*

WOG pm 02:50
Stable Isotope-Labeled Isobaric Tags for Sequencing of RNA Modifications by Liquid Chromatography-Tandem Mass Spectrometry (SIL-Seq); Nina Fitzgerald[1]; Max Sharin[1]; Kevin D. Clark[1]; *[1]Tufts University, Medford, MA*

WOG pm 03:10
Assessing backbone effects on oligonucleotide therapeutics fragmentation using multiple ion activation methods implemented on the timsOmni™ platform; Arjun Mani Mallika[1]; Frederic Rosu[1]; Dimitris Papanastasiou[2]; Valerie Gabelica[1]; *[1]University of Geneva, Geneva, Switzerland; [2]Fasmatech Science & Technology, Athens, Greece*

WOG pm 03:30
Characterization of Isomeric siRNA Metabolites Using LC-MS/HRMS (Data-Independent & -Dependent) in Combination with Similarity Index and Spectral Contrast Angle; Timothy Snow[1]; Andrew May[1]; Limin Deng[1]; Apoorva S Metkari[1]; Zamas Lam[1]; Ragu Ramanathan[2]; *[1]QPS, LLC, Newark, DE; [2]Quest Pharmaceutical Services, Newark, DE*

WOG pm 03:50
Universal and Multiplexed LC–MS Quantification of RNA Nanoparticles with Label-Free Spatial Imaging in Ocular Tissues; Mohammed S Hassan[1]; Bibek Hamal[1]; Alaa S Hassan[1]; Kevin S Li[1]; Patrick A. Limbach[1]; *[1]University of Cincinnati, Cincinnati, OH*

WOG pm 04:10
Orthogonal Algorithm-Driven Interpretation of Low-q CID LC–MS/MS mRNA Sequence Mapping Data Using Oligo Finder Software; Scott R. Kronewitter[1]; Joshua D. Hinkle[2]; Alexander A. Gudzovskiy[1]; John E. P. Syka[2]; James L. Stephenson Jr. [1]; Ismail Belmostefa[1]; Ilkka J. Borg[1]; Mikael P.O. Mäkelä[1]; Christopher Knowles[3]; Shweta Chhajed[2]; David A. Odelson[1]; Thomas C. Minshull[4]; Jessica S. Dale[4]; Mark Dickman[4]; Jean-Jacques Dunyach[2]; *[1]Thermo Fisher Scientific, Lexington, MA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Altrincham, United Kingdom; [4]University of Sheffield, Sheffield, United Kingdom*

WOH pm: Glycopeptides, Glycoproteins
Room 6DE

WOH pm 02:30
Sugar Matters: How Protein Glycosylation Shapes Ligand Binding; Jing Huang[1]; Samm Arnold[1]; Ling Han[1]; Duong T. Bui[1]; Lara K. Mahal[1]; John Klassen[1]; *[1]University of Alberta, Edmonton, AB*

WOH pm 02:50
A hydrogen-deuterium exchange mass spectrometry (HDX-MS) workflow for residue- and glycan-level analysis of glycoproteins to unveil glycans' motions; Valeria Calvaresi[1]; Dale Cooper-Shepherd[2]; Owen Cornwell[2]; Weston B Struwe[1]; *[1]University of Oxford, Department of Biochemistry, Oxford, United Kingdom; [2]Waters Wilmslow UK, Wilmslow, United Kingdom*

WOH pm 03:10
Glycopeptide Structural Elucidation Using Hybrid Collision- and Electron-Based Dissociation Strategies; Cristian D Gutierrez Reyes[1]; Sherifdeen Onigbinde[1]; Vishal Sandilya[1]; Anastasios Grigoriadis[2]; Ioanna Barla[2]; Hongxia Bai[3]; Kristina Marx[4]; Gadi Armony[5]; Florian Busch[6]; Athanasios Smyrnakis[2]; Dimitris Papanastasiou[2]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock,, TX; [2]Fasmatech Science and Technology, Athens, Greece; [3]Bruker Scientific LLC, Billerica, MA; [4]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [5]Bruker Nederland B.V., Leiderdorp, Netherlands; [6]Bruker Switzerland AG, Fällanden, Switzerland*

WOH pm 03:30
Direct Glycopeptide Identification from DIA Data Using MSFragger-DIA; Daniel Polasky[1]; Fengchao Yu[1]; Jiechen Shen[1]; Alexey I Nesvizhskii[1]; *[1]University of Michigan, Ann Arbor, MI*

WOH pm 03:50
Real-Time Library Searching for Structural Glycoproteomics; Kathryn Kothlow[1]; Bo Wen[1]; Anna G Duboff[1]; Jacob H Russell[1]; William S Noble[1]; Nicholas M Riley[1]; *[1]University of Washington, Seattle, WA*

WOH pm 04:10
Quantitative Glycomics and Glycoproteomics Link N-Glycan Processing to Metabolic Regulation Across Cell Types; Riya Gogte[1]; Michael Russelle S. Alvarez[2]; Sheryl Joyce G Alvarez[1]; Anirudh Yadlapati[1]; Carlito B. Lebrilla[1]; *[1]University of California, Davis, Davis, CA; [2]University of California Davis, Davis, CA*

ThOA am: Single Cell Omics
Hall D

ThOA am 08:30
Affinity reagent aided signal amplification for single-cell proteomics by mass spectrometry; Jakob Woessmann[1]; Judit Pina Agullet[1]; Anne Louise Blomberg[1]; Bo Torben Porse[2]; Steffen Goletz[1]; Erwin Schoof[1]; *[1]Technical University of Denmark, Kongens Lyngby, Denmark; [2]University of Copenhagen, Copenhagen, Denmark*

ThOA am 08:50
Direct Integration of Function and Proteoforms in Single Human Muscle Cells by Top-Down Proteomics; Mallory C Wilson[1, 2]; Zhan Gao[2]; Yanlong Zhu[3]; Ying Ge[2, 3]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI; [3]Human Proteomics Program, School of Medicine and Public Health, University of Wisconsin-Madison, Madison, Wisconsin 53705, USA., Madison, WI*

ThOA am 09:10
Mapping human brain development using single cell proteomics; Lihua Jiang[1]; Tianzhi Wu[2]; Ruiqi Jian[1]; Tiffany Trinh[1]; Michael P. Snyder[1]; Jingjing Li[2]; *[1]Stanford University School of Medicine, Palo Alto, CA; [2]University of California San Francisco, San Francisco, CA*

ThOA am 09:30
Single-Cell Proteomic Browser Reveals Accelerated Aging Signatures in Space-Flown Human Cortical Organoids; Aline M. A. Martins[1]; Reynaldo M Melo[2]; Chrystopher Glynn[2]; Kenneth Gee[2]; Blake Tsu[1]; Lucas Sales[3]; Marlon D. M. Santos[3, 4]; Juliana S. G. Fischer[1]; Joshua Cantlon[5]; Natalia C. S. Moreira[1]; Luisa B. V. Colelho[1]; Stephanie S Almeida[1]; Isabelle Luz[1]; John R. Yates III[2]; Alysson R. Muotri[1]; Paulo C Carvalho[1, 3]; *[1]UCSD, La Jolla, CA; [2]The Scripps Research Institute, La Jolla, CA; [3]Fiocruz, Curitiba, Brazil; [4]Institut Pasteur Montevideo, Montevideo, Uruguay; [5]Scienion, Seattle, WA*

ThOA am 09:50
Increased single cell lipidomics coverage and annotation confidence using a modified Orbitrap Hybrid mass spectrometer; Rahul Ravi Deshpande[1]; Katherine Walker[1]; Claire Dauly[2]; Susan S. Bird[1]; Bashar Amer[1]; Nicole Zehethofer[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

ThOA am 10:10
Expanding Surface Proteome Profiling to Single Cells for Immune Cell Antigen Discovery in Inflammatory Disease; Amanda Lorentzian[1]; Juliet Bartleson[1]; Zhichang Yang[1]; Meena Choi[1]; William T Yewdell[1]; Ying Zhu[1]; *[1]Genentech Inc., South San Francisco, CA*

THURSDAY MORNING ORALS

ThOB am: Integration of Multi-omics Approaches
Ballroom 20A

ThOB am 08:30
MOSAICS: An End-to-End Spatial Multiomics Approach for Analyzing a Single Tissue Section; Brittney Gorman[1]; Elizabeth Duong[2]; Erick Alvarado[2]; Jamie Verheyden[2]; Ravi Misra[3]; Gautam Bandyopadhyay[3]; Jeffrey Purkerson[3]; Heidi Vandyk[1]; Dusan Velickovic[1]; Heidie Huyck[3]; Lingyan Shi[2]; Gloria Pryhuber[3]; Geremy Clair[1]; Christopher Anderton[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]University of California, San Diego, La Jolla, CA; [3]The University of Rochester Medical Center, Rochester, NY*

ThOB am 08:50
From Separation to Synergy: Integration of parallel HRMS omics pipelines for Caenorhabditis eleganslongevity research; Klidel Fae Rellin[1, 2]; George Rosenberger[3]; Nikolas Kessler[4]; Aiko Barsch[4]; Ivo Kwee[5]; Murat Akhmedov[5]; Ann-Christine König[6]; Stefanie M. Hauck[1]; Matthew R. Lewis[7]; Michael Witting[1, 8]; *[1]Metabolomics and Proteomics Core, Helmholtz Zentrum München German Research Center for Environmental Health, Neuherberg, Germany; [2]School of Chemistry, Aristotle University of Thessaloniki, Thessaloniki, Greece; [3]Bruker Switzerland AG, Fällanden, Switzerland; [4]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [5]BigOmics Analytics, Via Serafino Balestra 12, Lugano, Switzerland; [6]PreOmics GmbH, Am Klopferspitz 19, 82152, Planegg, Germany; [7]Bruker UK Ltd., Coventry, United Kingdom; [8]Chair of Analytical Food Chemistry, TUM School of Life Sciences, Technical University of Munich, Maximus-von-Imhof-Forum 2, 85354, Freising-Weihenstephan, Germany*

ThOB am 09:10
Large-scale multi-omics reveals ancestry- and geography-dependent molecular aging networks in healthy humans; Shubham Gupta[1]; Nasim Bararpour[2]; Yue Wu[2]; John Z. Cao[3]; Sara Ahadi[2]; Robert L. Moritz[4]; Michael P. Snyder[2]; *[1]Stanford University, Palo Alto, CA; [2]Stanford University, Stanford, CA; [3]Stanford School of Medicine, Palo Alto, CA; [4]Institute For Systems Biology, Seattle, WA*

ThOB am 09:30
Targeted Nutrition: Metabolomic Drivers of Larval Honey Bee Development; Jonathan Nixon[1, 2]; Christopher J Brown[2]; Daniel D Hu[2]; Brock A Harpur[1]; *[1]Purdue University, West Lafayette, IN; [2]Corteva Agriscience, Indianapolis, IN*

ThOB am 09:50
Integrative Multi-omics Analysis of the Human Skeletal Muscle Response to Acute Endurance and Resistance Exercise: Findings from MoTrPAC; Hasmik Keshishian[1]; Gina M Many[2]; Natalie M Clark[1]; Gregory Smith[3]; Gayatri Iyer[4]; Patrick Hart[1]; Malene E Lindholm[5]; Samuel Montalvo[5]; Zidong Zang[3]; Christopher Jin[5]; James A Sanford[2]; Joshua N Adkins[2]; Scott Trappe[6]; William E Kraus[7]; Stuart C Sealfon[3]; Daniel H Katz[5]; Christopher B Newgard[7]; Charles F Burant[4]; Paul M Coen[8]; Bret H Goodpaster[8]; Steven A. Carr[1]; *[1]Broad Institute of MIT and Harvard, Cambridge, MA; [2]Pacific Northwest National Laboratory (PNNL), Richland, WA; [3]Icahn School of Medicine at Mount Sinai, Nash Family Department of Neuroscience, New York, NY; [4]University of Michigan, Ann Arbor, MI; [5]Stanford University School of Medicine, Palo Alto, CA; [6]Ball State University, Muncie, IN; [7]Duke University School of Medicine, Durham, NC; [8]AdventHealth Orlando, Translational Research Institute, Orlando, FL*

ThOB am 10:10
PRISM: A Network-Based, Proteomics-Driven Framework for Identifying Multi-Omic Cross-talk and Signal Recovery in Disease Pathology; Sandeep Acharya[1]; Ethan Stancliffe[1]; Douglas V. Guzior[1]; Monil Gandhi[1]; Ashima Mehta[1]; Adam Richardson[1]; Tom Cohen[1]; Gary J Patti[1, 2]; *[1]Panome Bio Inc, St Louis; [2]Washington University in St.Louis, St.Louis, MO*

ThOC am: Informatics: Metabolomics, Lipidomics and Glycomics
Ballroom 20BC

ThOC am 08:30
LIPID+: Cascaded Artificial Intelligence Drives Comprehensive Lipid Identification and Analysis Pipeline; Bowen Yang[1]; Carlos R Canez[1]; Rui Qin[2]; Jerrica Yang[1]; Fernanda Sousa Monteiro[1]; Zhan Cheng[2]; Liang Li[1, 2]; *[1]Department of Chemistry, University of Alberta, Edmonton, AB; [2]The Metabolomics Innovation Centre, Edmonton, AB*

ThOC am 08:50
Removing noise and merging mass spectra in MassWiki and LC-BinBase for high quality large scale databases in metabolomics and lipidomics; Oliver Fiehn[1]; Leon Fiehn[1]; Fanzhou Kong[1]; Ziyue Yang[1]; Uri Keshet[1]; Diego Pedrosa[1]; Daniel Rundle[1]; Xukun Wang[1]; Yuanyue Li[2]; Gert Wohlgemuth[1]; *[1]UC Davis, Davis, CA; [2]Zhejiang University, Zhejiang, China*

ThOC am 09:10
Improved spectrum clustering increases interpretability of large-scale molecular networks; Janne Heirman[1]; Yasin El Abiead[2]; Mingxun Wang[3]; Wout Bittremieux[1]; *[1]University of Antwerp, Antwerpen, Belgium; [2]UC San Diego, San Diego, CA; [3]UC RIVERSIDE, Riverside, CA*

ThOC am 09:30
Navigating the Pan-Repository Conjugated Metabolome Using Reverse Spectral Search at Billion-Spectrum Scale; Shipei Xing[1]; Abubaker Patan[1]; Julius Agongo[1]; Harsha Gouda[1]; Vincent Charron-Lamoureux[1]; Yasin El Abiead[2]; Zhewen Hu[1]; Haoqi Nina Zhao[3]; Ipsita Mohanty[4]; Jasmine Zemlin[1]; Wilhan D. Gonçalves Nunes[1]; Lindsey A. Burnett[1]; Mingxun Wang[5]; Dionicio Siegel[1]; Pieter C. Dorrestein[1]; *[1]University of California San Diego, La Jolla, CA; [2]University of Natural Resources and Life Sciences Vienna, Department of Chemistry, Institute of Analytical Chemistry, Muthgasse 18, 1190, Vienna, Austria, Vienna, Austria; [3]Stanford University, Stanford, CA; [4]Pennsylvania State University, University Park, PA; [5]University of California Riverside, Riverside, CA*

ThOC am 09:50
Dark Matter Annotation in LC-MS/MS Metabolomics: Density-Based Clustering of MetFrag Candidates in HMDB Space; Ahmad Mani-Varnosfaderani[1, 2]; Hailemariam Abrha Assress[1, 2]; Renny S. Lan[1, 2]; Colin Kay[1, 2]; Laxmi Yeruva[2, 3]; Brian D. Piccolo[1, 2]; *[1]University of Arkansas for Medical Sciences, Little Rock, AR; [2]Arkansas Children's Nutrition Center, Little Rock, AR; [3]USDA-ARS Microbiome and Metabolism Research Unit, Little Rock, AR*

ThOC am 10:10
Clinically anchored benchmarking of data processing methods for untargeted metabolomics; Jessica Kain[1]; Kevin Contrepois[1]; Casandra Trowbridge[1]; Basil Michael[1]; Frank Wong[1]; Denver Bradley[1]; Jonathan Bernstein[1]; Tina Cowan[1]; Michael Snyder[1]; *[1]Stanford University, Stanford, CA*

THURSDAY MORNING ORALS

ThOD am: Cancer and Immunity
Ballroom 20D

ThOD am 08:30

Catching Killer Immune Cells in the Act: Quantitative Mapping of Tumor–NK Immune Synapses by Proximity Labeling and SILAC-DIA Proteomics; Maria Cristina Trueba Sanchez[1, 2]; Christopher Zala[1, 2]; Maarten Altelaar[1, 2]; Kelly E Stecker[1, 2]; *[1]Utrecht University, Utrecht, Netherlands; [2]Netherlands Proteomics Center, Utrecht, Netherlands*

ThOD am 08:50

Unbiased In-depth Surfaceome Profiling of Acute Myeloid Leukemia Reveals Novel Immunotherapy Targets Beyond Canonical Surfaceome; Abhilash Barpanda[1]; Szu-Ying Chen[1]; Bonell Patiño Escobar[1]; Benson M. George[2]; Trenton Peters-Clarke[1]; Peiyuan Chai[3]; Audrey Kishishita[1]; Vipul Kumar[1]; Sujata Walunj[1]; Amit Prabhakar[1]; Sanjana Prudhvi[1]; Snehal Ganjave[1]; Rohit Bhadoria[1]; Darwin Kwok[1]; Marko A. Thai Wiita[1]; Rucha Deo[1]; Jeremiah Wong[1]; Nicole Lei[1]; Veronica Steri[1]; Huimin Geng[1]; Aaron C. Logan[1]; Kevin Leung[1]; Benjamin J. Huang[1]; Jonathan Ostrem[1]; Andrej Sali[1]; James A. Wells[1]; Ryan A. Flynn[2, 3]; Arun P. Wiita[1]; *[1]UCSF, San Francisco, CA; [2]Harvard Medical School, Boston, MA; [3]Boston children's hospital, Boston, MA*

ThOD am 09:10

Longitudinal deep proteomic profiling of plasma and neutrophils reveals pathological hallmarks of ICANS during CAR-T therapy; Min Ma[1]; Maosheng Wei[1]; Erfei Shang[1]; Ming Zhang[1]; Chao Xue[1]; Yingyi Lian[1]; Marco Davila[2]; Megan Herr[2]; Jun Qu[1]; *[1]University at Buffalo, Buffalo, NY; [2]Roswell Park Comprehensive Cancer Center, Buffalo, NY*

ThOD am 09:30

A Low-Cell-Input and Automated MHC-II-Associated Peptide Proteomics (MAPPs) Workflow for Immunogenicity Assessment of mAbs and AAVs; Shihan Huo[1]; Fanning Xia[1]; Song Nie[1]; Shunhai Wang[1]; Ning Li[1]; *[1]Analytical and Biological Mass Spectrometry, Regeneron Pharmaceuticals, Inc., Tarrytown, NY*

ThOD am 09:50

An atlas of intestinal MHC II self-peptides dynamically tracks gut tissue state; Vladyslav Holiar[1]; Vladislav Rudenko[1]; Sacha Lebon[1]; Marco Canella[1]; Petro Busko[1]; Aviya Habshush Menachem[1]; Moshe Biton[1]; *[1]Weizmann Institute of Science, Rehovot, Israel*

ThOD am 10:10

Deep learning extensions to the iPepGen and iMetaPep pipelines increases discovery of host neoantigens and microbial metapeptides in immunopeptidomics; Katherine T Do[1]; Subina Mehta[1]; Reid Wagner[2]; Fengchao Yu[3]; Alexey I Nesvizhskii[3, 4]; Timothy J Griffin[1, 5]; Pratik D Jagtap[1, 5]; *[1]Department of Biochemistry, Molecular Biology and Biophysics, University of Minnesota, Minneapolis, MN; [2]Minnesota Supercomputing Institute, University of Minnesota, Minneapolis, MN; [3]Department of Pathology, University of Michigan, Ann Arbor, MI; [4]Department of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI; [5]Masonic Cancer Center, University of Minnesota, Minneapolis, MN*

THURSDAY MORNING ORALS

ThOE am: Structural Biology
Room 6A

ThOE am 08:30
A Novel Mass Spectrometry-Based Chemical Footprinting Method for Probing Higher Order Structure of RNA; Sanjeev Kumar[1]; Hsin-Chieh (Natashia) Yang[1]; Don Rempel[1]; Henry Rohrs[1]; Leah Hanliu Wang[2]; Brian Gau[2]; Michael Gross[1]; *[1]Washington University in St.Louis, St.Louis, MO; [2]Pfizer, Chesterfield, MO*

ThOE am 08:50
An Integrated Native MS and Structural Bioinformatics Strategy to Assess the N297 Glycan's Contribution to IgG1 Fc Integrity; Yu Zhou[1]; Jakub Baudys[1]; Theodore Keppel[1]; Sarah Osman[1]; John Barr[1]; Dongxia Wang[1]; *[1]CDC, Atlanta, CA*

ThOE am 09:10
Characterizing Multi-State Ensembles in Ribosome Biogenesis by Crosslinking Mass Spectrometry, Integrative Modeling and Deep Neural Networks; Xingyu Chen[1]; Kai Steffen Stroh[2]; Riccardo Pellarin[2]; Jan Erzberger[3]; Florian Stengel[1]; *[1]University of Konstanz, Konstanz, Germany; [2]École Normale Supérieure de Lyon, Lyon, France; [3]UTSouthwestern Medical Center, Dallas, TX*

ThOE am 09:30
Next generation data processing for HDX-MS; Boosting functionality, flexibility and scalability; Iggy Kass[1]; Owen Cornwell[2]; Dale A Cooper-Shepherd[2]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom*

ThOE am 09:50
Hierarchical characterization of membrane protein proteoforms, structure, and interactions by integrated native mass spectrometry; Weijing Liu[1]; Graeme C McAlister[1]; Hariharan Parameswaran[2]; Lan Guan[2]; Thomas Moehring[3]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Texas Tech University, Lubbock, TX; [3]Thermo Fisher Scientific, Bremen, Germany*

ThOE am 10:10
Native architecture of membrane protein structure preserved at atomic resolution during gas-phase transfer; Jingjin Fan[1, 2]; Clare De'Ath[1, 3, 4]; Lukas Eriksson[1, 2]; Carl Von Hallerstein[1, 2]; Louise J. Persson[5]; Abraham O. Oluwole[1, 2]; Noor Naseeb[1, 2]; Aziz Qureshi[1, 2]; Susanne Mesoy[1, 2]; Laurence T. Seeley[1, 2, 3]; Simon B. Knoblauch[1, 2]; Neha Kalmankar[1, 2]; Erik G. Marklund[5]; Tim Esser[1]; Carol V. Robinson[1, 2]; Lindsay Baker[1, 3]; Stephan Rauschenbach[1, 2]; *[1]Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom; [2]Department of Chemistry, University of Oxford, Oxford, United Kingdom; [3]Department of Biochemistry, University of Oxford, Oxford, United Kingdom; [4]Sir William Dunn School of Pathology, University of Oxford, Oxford, United Kingdom; [5]Department of Chemistry for Life Sciences, Uppsala University;, Uppsala, Sweden*

ThOF am: Fundamentals: Ion Structures, Energetics, and Reactions
Room 6B

ThOF am 08:30
Visualizing the Ionization of Large Macromolecular Protein Complexes during Electrospray using Molecular Dynamics Simulations; Michael S Cordes[1]; Elyssia S. Gallagher[1]; [1] *Baylor University, Waco, TX*

ThOF am 08:50
Spectroscopic evaluation of MSn fragment ion structures predicted by computational fragmentation models; Lara Van Tetering[1, 2]; Lieke Bianchi[1, 2]; Anne Kramer[1, 2]; Teun Van Wieringen[1, 2]; Jonathan Martens[1, 2]; Giel Berden[1, 2]; Jos Oomens[1, 2]; [1] *HFML-FELIX, Nijmegen, Netherlands;* [2] *Radboud University, Nijmegen, Netherlands*

ThOF am 09:10
Proton Transfer Reagent Cations for Ion-Ion Charge State Manipulation of High Mass Negatively-charged Analytes in an Electrodynamic Ion Trap; Nicholas R. Ellin[1]; Boukar K.S. Faye[1]; Seth A. Horn[1]; Alexander M. Koers[1]; Scott A. McLuckey[1]; [1] *Purdue University Dept of Chemistry, West Lafayette, IN*

ThOF am 09:30
Mapping the Conformational Landscape of Protein Interactions and Unfolding with IM-MS; Robert L Rider[1]; Zhenyu Xi[1]; Kacie A. Evans[1]; Carter Lantz[1]; Elena Scott[1]; Arthur Laganowsky[1]; David H Russell[1]; [1] *Texas A&M Univesity, College Station, TX*

ThOF am 09:50
Sulfation and Sialylation Govern Lectin–Glycan Interactions and Gas-Phase Stability; Duong T. Bui[1, 2]; Xinrui Ji[1]; Jing Huang[1]; Ziyu Zhang[1]; Samm K. Arnold[1]; Ling Han[1]; Elena Kitova[1]; Lara K. Mahal[1]; John Klassen[1]; [1] *University of Alberta, Edmonton, AB;* [2] *University of Waterloo, Ontario, ON*

ThOF am 10:10
Linking Gas-Phase Ion Chemistry and MicroED for Chemically Consistent Small-Molecule Structure Elucidation; Aleyna Lumsden[1, 2]; Artemy Novokhrost[1]; Amar Rai[3]; Zhiyuan Ding[1]; Timea Palmai-Pallag[1]; Zoltan Takats[3, 4]; Angus Kirkland[1]; Marcus Gallagher-Jones[1]; Bela Paizs[1, 3, 4]; [1] *Rosalind Franklin Institute, Didcot, United Kingdom;* [2] *University Of Oxford, Oxford, United Kingdom;* [3] *Imperial College London, London, United Kingdom;* [4] *deShape ltd., London, UK., London, United Kingdom*

ThOG am: Covalent Labeling and Chemical Crosslinking
Room 6CF

ThOG am 08:30
Rapid, Zero-Order Tyrosine Crosslinking Defines Protein Interaction Landscapes; Trenton M Peters-Clarke[1]; Johnathan Maza[1]; Paul Burroughs[1]; Yifei Chen[1]; Kevin Leung[1]; Jim A. Wells[1]; [1]*University of California, San Francisco, San Francisco, CA*

ThOG am 08:50
Covalent labeling to study the binding site of membrane receptor LRP1 and Tau in vitro and on cells.; Vanessa L. Stahl[1]; Caiqin Wang[1]; Wen-Chuan Chou[1]; Jennifer N. Rauch[1]; Richard W. Vachet[1]; [1]*UMass Amherst, Amherst, MA*

ThOG am 09:10
Cysteine-enabled Cleavability to Advance Cross-linking Mass Spectrometry for Global Analysis of Endogenous Protein-Protein Interactions; Fenglong Jiao[1]; Merav Braitbard[2]; Clinton Yu[1]; Ben Shor[2]; Bjorn-Erik Wulff[3]; Dina Schneidman-Duhovny[2]; Lan Huang[1]; [1]*Department of Physiology and Biophysics, University of California Irvine, Irvine, CA;* [2]*The Rachel and Selim Benin School of Computer Science and Engineering, The Hebrew University of Jerusalem, Jerusalem, Israel;* [3]*Department of Biochemistry, Stanford University, Stanford, CA*

ThOG am 09:30
Development of photoactivatable and enrichable lysine reactive crosslinking reagents; Adam Cahill[1]; Keith Livingstone[1]; Martin Walko[1]; Megan Wright[1]; Nikil Kapur[1]; Antonio N. Calabrese[1]; [1]*University of Leeds, Leeds, United Kingdom*

ThOG am 09:50
Time-Resolved Covalent Footprinting Reveals Early Conformational Transitions during Full-Length Tau Aggregation; Jie Sun[1]; Claudia de Jesus Ramos[1]; [1]*University of Tennessee Knoxville, Knoxville, TN*

ThOG am 10:10
Photocatalytic Proximity Labeling and Explainable Proteoform Reasoning for Glycoform Resolved Analysis of Immune Checkpoint Proteins; David S. Roberts[1]; Vishnu R. Tejus[1]; Andrew H. Reiter[1]; Carolyn R. Bertozzi[1, 2]; [1]*Stanford University, Stanford, CA;* [2]*Howard Hughes Medical Institute, Chevy Chase, MD*

ThOH am: Food Chemistry & Safety: New Innovations
Room 6DE

ThOH am 08:30
Integrated GC-MS/MS and HPLC-QDA profiling of volatile and physicochemical components in Japanese and US sake; Rahul Sen[1]; Katie Hope[2]; Ben Bell[2]; Scott Lafontaine[1]; *[1]University of Arkansas - Fayetteville, AR, Fayetteville, AR; [2]Origami Sake, Hot springs, AR*

ThOH am 08:50
Making Pour Decisions: Extraction Method Optimization and Quantification of PFAS in Craft Beer; Ashlee T Falls[1]; Kara M Joseph[1]; Emily C Vincent[1]; Erin S Baker[1]; *[1]University of North Carolina - Chapel Hill, Chapel Hill, NC*

ThOH am 09:10
Towards smart food-processing in coffee roasting: A real-time prediction-model for coffee flavor and antioxidant-contend based on on-line photoionization-process mass spectrometry; Hendryk Czech[1]; Jan Heide[2]; Sven Ehlert[2]; Andreas Walte[2]; Thomas Koziorowsk[3]; Ralf Zimmermann[1, 4]; *[1]University of Rostock, Rostock, Germany; [2]Photonion GmbH, Schwerin, Germany; [3]Probat SE, Emmerich, Germany; [4]University of Eastern Finland, Kuopio, Finland*

ThOH am 09:30
Global Profiling of Rice Aroma Volatiles by HS-SPME-GC-MS/MS with Sensory-Anchored Interpretation; Heena Rani[1]; Rahul Sen[1]; Christian De Guzman[2]; Scott Lafontaine[1]; *[1]University of Arkansas - Fayetteville, AR, Fayetteville, AR; [2]Rice Research and Extension Center, University of Arkansas, Stuttgart, AR*

ThOH am 09:50
From Molecules to Decisions: Integrating High-Resolution Mass Spectrometry and Nanosensing via Hybrid Machine Learning for Rapid Quinoa Quality Assessment; Chuping Lee[1]; Leon Li Cyun Chen[2]; Guan-Sheng Ho[1]; *[1]Department of Chemistry, National Chung Hsing University, Taichung City, Taiwan; [2]Department of Chemistry, Texas A&M University, College Station, TX*

ThOH am 10:10
DIET-IF: dietary exposure inference from mixed meals using cross-over metabolomics; Debra KM Tacad[1]; Huaxu Yu[2]; Xuan He[3, 4]; John W Newman[2, 3, 5]; Sean H Adams[6, 7, 8]; Francene M Steinberg[3]; Brian J Bennett[3, 5]; Carolyn M Slupsky[3, 4]; Oliver Fiehn[2]; *[1]UC Davis, Davis, CA; [2]West Coast Metabolomics Center, University of California Davis, Davis, CA; [3]Department of Nutrition, University of California-Davis, Davis, CA; [4]Department of Food Science and Technology, University of California-Davis, Davis, CA; [5]Western Human Nutrition Research Center, Agricultural Research Service, United States Department of Agriculture, Davis, CA; [6]Department of Surgery, University of California Davis School of Medicine, Sacramento, CA; [7]Center for Alimentary and Metabolic Science, University of California Davis, Sacramento, CA; [8]Nutrition for Transformative Healthcare Program, University of California Davis, Sacramento, CA*

THURSDAY AFTERNOON ORALS

ThOA pm: Top-Down Proteomic Analysis
Hall D

ThOA pm 02:30
Resolving Co-Occurring PTMs on Intact GPCRs by Native Top-Down Mass Spectrometry; Frances I Butroid[1, 2]; Jack L Bennett[1, 2]; Carla Kirschbaum[1, 2]; Joshua Hinkle[3]; John E. P. Syka[3]; Christopher Mullen[4]; Tarick J El-Baba[1, 2]; Corinne A Lutomski[1, 2]; Carol V Robinson[1, 2]; *[1]Department of Chemistry, University of Oxford, Oxford, United Kingdom; [2]Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom; [3]Thermo Fisher Scientific, San Jose, CA; [4]ThermoFisher Scientific, San Jose, CA*

ThOA pm 02:50
Multi-omic analysis of brain regions from humanized 3xTg-AD mice using deep mass spectrometric profiling and tau proteoform analysis; Nicholas Devanney[1]; Samah Shah[1]; James Joly[2]; Christina D. King[1]; Joanna Bons[1]; Katie Winters[2]; Brittany Nortman[2]; Jamie Kuhar[2]; Andreas FR Huhmer[2]; Parag Mallick[2]; Lisa M Ellerby[1]; Birgit Schilling[1]; *[1]Buck Institute for Research on Aging, Novato, CA; [2]Nautilus Biotechnology, San Carlos, CA*

ThOA pm 03:10
Top-Down Proteomics is dominated by chimeric spectra; Kyowon Jeong[1]; Josefine Rost[2]; Philipp T Kaulich[2]; Tom D. Müller[1]; Oliver Kohlbacher[1, 3]; Andreas Tholey[2]; *[1]University of Tübingen, Tübingen, Germany; [2]Christian-Albrechts-Universität zu Kiel, Kiel, Germany; [3]University Hospital Tübingen, Tübingen, Germany*

ThOA pm 03:30
Optimized Top-Down Proteomic Methods for RAS Proteoform Characterization; Grace M. Scheidemantle[1]; Robert A. D'Ippolito[1]; Alexandria L. Sohn[1]; Matthew R. Drew[1]; Peter Frank[1]; Min Hong[1]; Jennifer Mehalko[1]; Simon Messing[1]; Shelly Perkins[1]; Kelly Snead[1]; Vanessa Wall[1]; Mackenzie Meyer[1]; Scott Eury[1]; Abigail Neish[1]; Katie Powell[1]; Kanika Sharma[1]; Nicole Fer[1]; Brian Smith[1]; Carissa Grose[1]; William Burgan[1]; William Gillette[1]; Anna E. Maciag[1]; Dominic Esposito[1]; Frank McCormick[1, 2]; Dwight V. Nissley[1]; Caroline DeHart[1]; *[1]Frederick National Laboratory for Cancer Research, Frederick, MD; [2]Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, CA*

ThOA pm 03:50
Analysis of Membrane Protein Mixtures under Near-Native Conditions Using Capillary Electrophoresis-Mass Spectrometry; Noah Gould[1]; Thao Tran[1]; Alexander R. Ivanov[1]; *[1]Barnett Institute of Chemical and Biological Analysis, Department of Chemistry and Chemical Biology, Northeastern University, Boston, MA*

ThOA pm 04:10
Revealing Hidden in vivo Biotransformations in Biotherapeutics with timsOmni Top-Down Mass Spectrometry; Lucile Kogey-Fuchs[1, 2, 3]; Athanasios Smyrnakis[4]; Anastasios Grigoriadis[4]; Mariangela Kosmopoulou[4]; Jonathan Dhenin[5]; Alain Krick[1]; Mathieu Dupré[1]; Christine Mauriac[1]; Jean-François Greisch[6]; Dimitris Papanastasiou[4, 6]; Julia Chamot-Rooke[2, 3]; *[1]Sanofi, Vitry-sur-Seine, France; [2]Institut Pasteur, Paris, France; [3]Université Paris Cité, Paris, France; [4]Fasmatech Science & Technology, Chalandri, Greece; [5]Novartis pharma AG, Basel, Switzerland; [6]Bruker Switzerland AG, Fällanden, Switzerland*

ThOB pm: Small Molecules: Structural Characterization and Quantitation
Ballroom 20A

ThOB pm 02:30
Structures and energetics of protonated bipyridine–cucurbituril complex isomers in the gas phase; Doui Kim[1]; Jongcheol Seo[1]; [1]*POSTECH, Pohang, South Korea*

ThOB pm 02:50
Conformational Effects of Monovalent Cations on PFCA Homodimers Investigated by IMS-MS/MS and Theoretical Calculations; Aurore Lisette Schneiders[1]; Johann Far[1]; Edwin De Pauw[1]; Lidia Belova[2]; Adrian Covaci[2]; Gauthier Eppe[1]; [1]*Mass Spectrometry Laboratory, Université of Liège, Liège, Belgium;* [2]*Toxicological Centre, University of Antwerp, Wilrijk, Belgium*

ThOB pm 03:10
Diagnostic CAD Reactions of Protonated N-Nitrosamines in MS2 and MS3 Experiments; Annika M Little[1]; Meghan A Cortez[1]; Hilkka I Kenttämaa[1]; [1]*Purdue University, Department of Chemistry, West Lafayette, IN*

ThOB pm 03:30
De novo structural identification of drug metabolites using integrated MS/MS, ion mobility, and computational fragmentation; Amar Rai[1, 2]; Daniel Simon[1, 3]; Yuchen Xiang[1, 3]; Andras Marton[4, 5]; Stefania Maneta-Stavrakaki[1]; Elizabeth Want[1]; Stephen Wilkinson[6]; Stephen W. Holman[7]; Andrew D. Ray[8]; Béla Paizs[1, 2, 9]; Zoltán Takáts[1, 2, 3, 9]; [1]*Faculty of Medicine, Department of Metabolism, Digestion and Reproduction, Imperial College London, W12 0NN, UK, London, United Kingdom;* [2]*The Rosalind Franklin Institute, Building R113 Rutherford Appleton Laboratory, Harwell Campus, Didcot, Oxfordshire, OX11 0QX, UK, Didcot, United Kingdom;* [3]*Institut für Funktionelle Genomik, University Regensburg, 9 Am Biopark, Regensburg 93053, Germany, Regensburg, Germany;* [4]*Department of Chemical and Environmental Process Engineering, Faculty of Chemical Technology and Biotechnology, Budapest University of Technology and Economics, Műegyetem rkp. 3., H-1111 Budapest, Hungary, Budapest, Hungary;* [5]*Ambimass Kft, Záhony u. 7, H-1031 Budapest, Hungary, Budapest, Hungary;* [6]*DMPK, Oncology, R&D, AstraZeneca, 1 Francis Crick Avenue, Cambridge CB2 0AA, United Kingdom, Cambridge, United Kingdom;* [7]*Chemical Development, Pharmaceutical Technology & Development, Operations, AstraZeneca, Macclesfield, UK, Macclesfield, United Kingdom;* [8]*Global Product Development, Pharmaceutical Technology & Development, Operations, AstraZeneca, Macclesfield, UK, Macclesfield, United Kingdom;* [9]*deShape ltd., London, UK., London, United Kingdom*

ThOB pm 03:50
Alkamines are an underappreciated widespread class of metabolites and represent an overlooked form of drug metabolism; Julius Agongo[1]; Subhaskar Reddy Panga[2]; Shipei Xing[2]; Vincent Lamoureux Charron[2]; Harsha Gouda[2]; Yasin El Abiead[2]; Megan Nelson[2]; Ipsita Mohanty[2]; Jeongin Seo[2]; Prajit Rajkumar[2]; Abubaker Patan[2]; Sadie Giddings[2]; Helena Russo Mannochio[2]; Jasmine Zemlin[2]; Victoria Deleray[2]; Zhewen Hu[2]; Andres Mauricio Rodriguez Caraballo[2]; Gary Perdew[3]; Mingxun Wang[4]; Dionicio Siegel[2]; Pieter C. Dorrestein[2]; [1]*University of California San Diego, San Diego, CA;* [2]*UC San Diego, San Diego, CA;* [3]*Pennsylvania State University, University Park, PA;* [4]*UC RIVERSIDE, Riverside, CA*

ThOB pm 04:10
Simultaneous quantitation and deep untargeted plasma metabolomics using a modified Orbitrap Hybrid mass spectrometer with extended dynamic range; Bashar Amer[1]; Alexander Harder[2]; Michal Kaczmarek[2]; Claire Dauly[2]; Rahul Deshpande[3]; Thomas Moehring[2]; Susan S. Bird[3]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany;* [3]*Thermo Fisher Scientfic, San Jose, CA*

ThOC pm: High Throughput MS and Automation
Ballroom 20BC

ThOC pm 02:30
Thermal Inkjet Printed Single-Cell Microarrays enable Absolute Quantification of Drugs, Peptides, Lipids, and Proteins in 100,000 individual cells per day; Stanislau Stanisheuski[1]; Sima Ziyaee[1]; Caroline Hernandez[1]; Hyo-Sang Jang[2]; Maude David[1]; Claudia Maier[1]; *[1]Oregon State University, Corvallis, OR; [2]HP Life Science Solutions, Corvallis, OR*

ThOC pm 02:50
Highly Multiplexed MS3-Supported DIA; Soroush Hajizadeh[1, 2, 3, 4]; Johannes Kreuzer[1, 3]; Wilhelm Haas[3, 5, 6]; *[1]MGH, Boston, MA; [2]Broad Institute of MIT and Harvard, Cambridge, MA; [3]Harvard Medical School, Boston, MA; [4]Universität Graz, Graz, Austria; [5]Harvard University, Boston, MA; [6]Mass General Brigham, Boston, MA*

ThOC pm 03:10
Towards Unmanned Proteomics Data Generation: A Fully Automated Sample-to-Data System for Proteomic Experiments; Dongxue Wang[1, 2]; Jing Yang[2]; L Tang[3]; Ruijun Tian[4]; Fuchu He[2]; *[1]Beijing Proteome Research Center, National Center for Protein Sciences, Beijing, China; [2]International Academy of Phronesis Medicine (Guangdong), Guangzhou, China; [3]National Center for Protein Sciences (Beijing), Beijing, China; [4]Southern University of Science and Technology, Shenzhen, China*

ThOC pm 03:30
Made for speed: high throughput proteomics with the Orbitrap Astral Zoom mass spectrometer and the Evosep Eno at 500 SPD; William Comstock[1]; Iulia Macavei[2]; Brett Larsen[1]; Eugen Damoc[3]; Nicolai Bache[2]; Dorte B. Bekker-Jensen[2]; Amirmansoor Hakimi[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Evosep Biosystems, Odense, Denmark; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

ThOC pm 03:50
Population-Scale Proteoform Profiling of Human Tissue Heterogeneity Using Single-Cell Arrays; Claudia Ctortecka[1]; Pei Su[1, 2]; Hannah Zhu[1]; Indira Pla[1]; Michael AR Hollas[1]; Jared O Kafader[1]; Neil L Kelleher[1]; *[1]Northwestern University, Evanston, IL; [2]University of California, Riverside, Riverside, CA*

ThOC pm 04:10
High-throughput intact protein analysis with acoustic ejection mass spectrometry; Xuejiao Yin[1]; Chiu Cheong Aw[1]; Han Wang[1]; Chang Liu[2]; *[1]SCIEX, Singapore, Singapore; [2]SCIEX, Concord, ON*

ThOD pm: Clinical Analysis: Innovations
Ballroom 20D

ThOD pm 02:30
Rapid Screening and Detection of Skin Cancer using the MasSpec Pen Technology; Ruth Costa[1]; Jacob I Mardick[1]; Brian J Armijo[1]; Sean Boutros[1]; Nathan Sanders[2]; Justin Wiseman[2]; Livia S. Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX; [2]MSPen Technologies, Houston, TX*

ThOD pm 02:50
Enhancing the early detection and diagnosis of cervical precancer and cancer through innovative metabolomics-based techniques; Duncan Roberts[1]; Apostolia Galani[1]; Stefania Maneta-Stavrakaki[1]; Laura Burney Ellis[1]; Amelia Fraser-Dale[1]; Daniel Simon[2]; Jinshi Zhao[1]; Burak Temelkuran[1]; Yuchen Xiang[1, 2]; Robert Murray[1]; Yu Wang[1]; Deirdre Lyons[3]; Zoltan Takats[1, 2]; Maria Kyrgiou[1]; Maria Paraskevaidi[1]; *[1]Imperial College London, London, United Kingdom; [2]University of Regensburg, Department of Immunomedicine, Regensburg, Germany; [3]Imperial College Healthcare NHS Foundation Trust, London, United Kingdom*

ThOD pm 03:10
Interlaboratory Comparison of a Glucagon & Oxyntomodulin Immuno-LC-MS/MS Assay: Implications for Diabetes Research; Annie Moradian[1]; Jessica O. Becker[2]; Lorenz A, Nierves[3]; Tai-Tu Lin[3]; Salvatore Sechi[4]; Michael J. MacCoss[2]; Wei-Jun Qian[3]; Jennifer E. Van Eyk[5]; Andrew N. Hoofnagle[2]; *[1]Precision Biomarker Laboratories / Cedars-Sinai, Los Angeles, CA; [2]University of Washington, Seattle, WA; [3]Pacific Northwest National Laboratory, Richland, WA; [4]National Institute of Health, NIDDK, Bethesda, MD; [5]Cedars-Sinai Medical Center, Smidt Heart Institute, Los Angeles, CA*

ThOD pm 03:30
Real-World Plasma Proteomics Distinguishes Acute Recurrent and Chronic Pancreatitis in Children: Robust Diagnostic Signatures Despite Pre-Analytical Variability; Dylan Nicholas Tabang[1, 2]; Zainab Wurie[1]; Clara Gewinner[1]; Xiaoyang Li[3]; Gretchen A. Cress[4]; Ying Yuan[5]; Bernhard Y. Renard[6, 7, 8]; Jami L. Saloman[9]; Liang Li[3]; Hanno Steen[1, 2]; Mark Lowe[10]; Aliye Uc[4]; *[1]Department of Pathology, Boston Children's Hospital, Boston, MA; [2]Harvard Medical School, Boston, MA; [3]Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Houston, TX; [4]University of Iowa, Stead Family Children's Hospital, Iowa City, IA; [5]The University of Texas, MD Anderson Cancer Center, Houston, TX; [6]Hasso Plattner Institute, Digital Engineering Faculty, University of Potsdam, Potsdam, Germany; [7]Hasso Plattner Institute for Digital Health at Mount Sinai, Icahn School of Medicine at Mount Sinai, New York, NY; [8]Windreich Department of Artificial Intelligence & Human Health, Icahn School of Medicine at Mount Sinai, New York, NY; [9]Center for Pain Research and Department of Neurobiology, University of Pittsburgh, Pittsburgh, PA; [10]Washington University in St Louis School of Medicine, St. Louis, MO*

ThOD pm 03:50
Intraoperative Mass Spectrometric Detection of Cortisol for Precision Anesthesia Management; Wenpeng Zhang[1]; Nan Zhang[2]; Xiao Chen[1]; Zheng Ouyang[1]; *[1]Tsinghua University, Beijing, China; [2]PURSPEC Technology (Beijing) Ltd., Beijing, China*

ThOD pm 04:10
A Single-Aliquot, Enrichment-Free Workflow for High-Throughput Plasma Proteome and N-Glycoproteome Profiling; Kun-Hao Chang[1, 2, 3]; Jared Deyarmin[4]; Tiara Pradita[1]; Yi-Ju Chen[1]; Stephanie N. Samra[4]; Gee-Chen Chang[5]; Chong-Jen Yu[6]; Yi-Shuang Chuang[1]; Tabiwang N. Arrey[7]; Hsiang-En Hsu[1]; Yue Xuan[7]; Pei-Rong Huang[1]; Kuen-Tyng Lin[1]; Ke-Hsin Yen[8]; Hsing-jui Tsai[1]; Daniel Hermanson[4]; YaHsuan Chang[9]; Sung-Liang Yu[10]; Pan-Chyr Yang[11]; Yu-Ju Chen[1]; *[1]Institute of Chemistry, Academia Sinica, Taipei, Taiwan; [2]Molecular Science and Technology Program, Taiwan International Graduate Program, Academia Sinica, Taipei, Taiwan; [3]Department of Chemistry, National Tsing Hua University, Hsinchu, Taiwan; [4]Thermo Fisher Scientific, San Jose, CA; [5]Department of Internal Medicine, Division of Pulmonary Medicine, Chung Shan Medical University Hospital, Taichung, Taiwan; [6]Department of Surgery, National Taiwan University Hospital, Taipei, Taiwan; [7]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [8]Institute of Statistical Science, Academia Sinica, Taipei, Taiwan; [9]Institute of Molecular and Genomic Medicine, National Health Research Institutes, Maioli, Taiwan; [10]Department of Clinical Laboratory Sciences and Medical Biotechnology, College of Medicine, National Taiwan University, Taipei, Taiwan; [11]Department of Surgery, National Taiwan University Hospital and National Taiwan University College of Medicine, Taipei, Taiwan*

ThOE pm: Food Chemistry & Safety: Foodomics, Allergens, Bacteria, Foods and Supplements
Room 6A

ThOE pm 02:30
Learning food-derived molecular fingerprints to decode dietary intake from untargeted metabolomics; Harsha Gouda[1]; Julius Agongo[1]; Patricia Kelly[2]; Marta Sala-Climent[3]; Wilhan Nunes[1]; Shipei Xing[1]; Victoria Deleray[1]; Crystal X Wang[1]; Vincent Charron-Lamoureux[1]; Haoqi Nina Zhao[1]; Mingxun Wang[4]; Nicholas J W Rattray[5]; Konstantinos Gerasimidis[2]; Monica Guma[3]; Pieter C. Dorrestein[1, 6, 7]; *[1]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [2]School of Medicine, Dentistry & Nursing, University of Glasgow, Glasgow, United Kingdom; [3]Department of Medicine, University of California,, San Diego, CA; [4]University of California, Riverside, Riverside, CA; [5]Strathclyde Institute of Pharmacy and Biomedical Science, Glasgow, United Kingdom; [6]Center for Microbiome Innovation, Jacobs School of Engineering, University of California San Diego, La Jolla, CA; [7]Collaborative Mass Spectrometry Innovation Center, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA*

ThOE pm 02:50
Improved analysis and characterization of brominated vegetable oil in multiple beverages using LC-MS/MS and LC-HRMS; Jessica P Rafson[1]; Christopher R. Beekman[1]; Katherine Carlos[1]; *[1]US Food and Drug Administration, College Park, MD*

ThOE pm 03:10
An HPLC-MS/MS Multi-Omics Platform for Profiling Undigested Glycans and Short-Chain Fatty Acids of a High-Arabinose Diet in the Human Gut; Bryan Martinez Hernandez[1]; Jada Kate Garcia[1]; Christopher Suarez[1]; Sophia Jiang[1]; Charlie Weng[1]; Orla Cagney[2]; Stephanie Wilson[2]; Danielle G. Lemay[2]; David A. Mills[3]; Jennifer T. Smilowitz[2]; Carlito B. Lebrilla[1]; *[1]Department of Chemistry, University of California, Davis, Davis, CA; [2]Department of Nutrition, University of California-Davis, Davis, CA; [3]Department of Food Science and Technology, University of California-Davis, Davis, CA*

ThOE pm 03:30
Development of a novel targeted MS method for detection and quantification of fermented gluten in beer and yogurt matrices; Sara K. Schlange[1]; Joseph L. Baumert[1]; Melanie L. Downs[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE*

ThOE pm 03:50
Current status of mass spectrometry-based analysis and database construction for functional components in Korean Agri-food resources; Heon-Woong Kim[1]; Ryeong Ha Kwon[1]; Ju Hyung Kim[1]; Jeong-Hyeon Ahn[1]; Seong-Jin Kim[1]; Eun-Suk Jung[1]; Sang Hoon Lee[1]; Kwang-Sik Lee[1]; Seon Mi Yoo[1]; Young-Hee Park[1]; *[1]National Institute of Crop and Food Science, Wanju-gun, South Korea*

ThOE pm 04:10
Multi-Laboratory Assessment Reveals Variable Ion Species Profiles in Electrospray Ionization Mass Spectrometry; Melanie Odenkirk[1]; Jacqueline Michelle Chaparro[1, 2]; Nathan Montgomery[2]; Katrina L Leaptrot[3]; Stacy D. Sherrod[3]; Jody C May[3]; Henriette Van Eekelen[4]; Bert Schipper[4]; Juliana Chaura[5]; Gabriel Esteban Velez[5]; Wimonphan Chathiran[6]; Cole R. Michel[7]; Katrina A Doenges[7]; Richard Reisdorph[7]; Mari Maeda-Yamamoto[8]; Luis Valdiviez[9]; Uri Keshet[9]; Jeremiah D Wells[9]; Scott Mackell[9]; David Bell[10]; Sebastian Tapia Leiva[10]; Simon Partridge[10]; Daniela Rago[11]; Linda Ahonen[11]; Yuki Ito[12]; Satoshi Yamaki[12]; Margaret L Read[1]; J. Christopher Evans[1]; Macy J Gruszczynski[1]; Leokadja Szalach[1]; Stephen C Boyko[1]; Steven Watkins[13]; Rodrigo Ledesma-Amaro[14]; Oliver Fiehn[9]; Nichole Reisdorph[7]; Warangkana Srichamnong[6]; Andres Jaramillo-Botero[5]; Ric C H De Vos[4]; Robert D Hall[4]; John A McLean[3]; Corey D Broeckling[2]; Jessica E Prenni[1]; *[1]Colorado State University, Fort Collins, CO; [2]Colorado State University, ARC-BIO, Fort Collins, CO; [3]Vanderbilt University, Nashville, TN; [4]Wageningen University & Research, Wageningen, Netherlands; [5]iÓMICAS Research Institute, Pontificia Universidad Javeriana, Cali, Colombia; [6]Institute of Nutrition, Mahidol University, NakhonPathom, Thailand; [7]Skaggs School of Pharmacy and Pharmaceutical Sciences, Aurora, CO; [8]Institute of Food Research, National Agriculture and Food Research Organization, Tsukuba Ibaraki, Japan; [9]West Coast Metabolomics Center, University of California Davis, Davis, CA; [10]Department of Infectious Diseases, Imperial College London, London, UK; [11]Novo Nordisk Foundation Center for Biosustainability, Danmarks Tekniske Universitet, Kongens Lyngby, Denmark; [12]Shimadzu Co., Kyoto, Japan; [13]Verso Biosciences, Davis, CA; [14]Imperial College London, London, UK*

ThOF pm: Imaging Instrumentation & Method Development
Room 6B

ThOF pm 02:30
Untargeted Molecular Imaging using LA-DBDI-MS/MS; Ciara Conway[1, 2]; Markus Weber[1, 2]; Christoph Haisch[2]; Jan-Christoph Wolf[1]; Thomas Wolf[1]; *[1]Plasmion, Augsburg, Germany; [2]Technical University of Munich, Freising, Germany*

ThOF pm 02:50
Metrology for ion suppression and quantitation in small molecule MALDI and DESI MSI; Felicia Wirtz[1]; Angeliki Christakopoulou[1]; Enya Murray[1]; Alex Dexter[1]; Shannen Leroi[2]; Johan Vande Voorde[2]; Josephine Bunch[1, 3]; Rory Thomas Steven[4]; *[1]National Physical Laboratory, Teddington, United Kingdom; [2]University of Glasgow, Glasgow, United Kingdom; [3]Imperial College London, London, United Kingdom; [4]National Physical Laboratory, London, United Kingdom*

ThOF pm 03:10
Portable Atmospheric Pressure MALDI-2 Imaging Mass Spectrometry for Automated Bacterial Identification; Nathan Grimes[1]; Krisztian Gabor Torma[1]; William Yang Terziyan[1]; *[1]BaySpec, San Jose, CA*

ThOF pm 03:30
On-Tissue Chemical Derivatization Using 1-Amino-4-Methylpiperazine for DESI-MSI of Neuroactive Steroids in an Opioid Use Disorder Rat Model; Adrian A Coello[1]; Wendy J Lynch[2]; Eleanor Blair Towers[2]; Xin Ma[1]; *[1]University of Virginia Department of Chemistry, Charlotesville, VA; [2]University of Virginia Department of Psychiatry and Neurobehavioral Sciences, Charlottesville, VA*

ThOF pm 03:50
Chemical Landscape of Alzheimer's Disease: Relative Quantification and Metabolic Insights from DESI-MSI; Lanaia Itala Maciel[1]; Jussara Roque[1]; Pâmela Yasmin Ferreira[1]; Jéssica Gardone Vitório[1]; Paulo César Ghedini[1]; Andrea Rodrigues Chaves[1]; Boniek Gontijo[1]; *[1]Federal University of Goiás, Goiânia, Brazil*

ThOF pm 04:10
A pixel level quantitative mass spectrometry imaging method of metabolites for diagnostic applications; Julia R Bonney[1]; Kaitlyn E Bootz[1]; Jaimie Lee[1, 2]; Sankha S Basu[1]; Nathalie Y.R. Agar[1]; *[1]Brigham and Women's Hospital/Harvard Medical School, Boston, MA; [2]Northeastern University, Boston, MA*

ThOG pm: Ion Mobility: Structure Determination & Applications
Room 6CF

ThOG pm 02:30
Conformational-Selective Antigen Binding in Multispecific Antibodies Revealed by Non-Ensemble Measurements in Tandem-Trapped Ion Mobility Spectrometry; Fanny Caroline Liu[1]; Thais Pedrete[1]; Mark E. Ridgeway[2]; Melvin A. Park[2]; Andrew H. Beaven[3]; Harsha P. Gunawardena[4]; Christian Bleiholder[1]; *[1]Florida State University, Tallahassee, FL; [2]Bruker Daltonics, Billerica, MA; [3]Johnson and Johnson, Malvern, PA; [4]Johnson & Johnson Innovative Medicine, Spring House, PA*

ThOG pm 02:50
Ligand Dependent Stoichiometry and Conformation Shifts in an ATPase Characterized by Native MS; Evan N Whitford[1, 2]; Charlie J Hitchman[3]; Hee-Won Park[3]; Vicki H. Wysocki[1, 2]; *[1]School of Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA; [2]Native MS Guided Structural Biology Center, Georgia Institute of Technology, Atlanta, GA; [3]Department of Biochemistry and Molecular Biology, Tulane University School of Medicine, New Orleans, LA*

ThOG pm 03:10
Investigating Protein Misfolding and Aggregation with Ion Mobility-Mass Spectrometry and Charge Detection Mass Spectrometry; Jared Hampton[1]; Robert Rider[2]; Carter Lantz[2]; David H Russell[2]; *[1]Texas A&M University, College Station, TX; [2]Texas A&M Univesity, College Station, TX*

ThOG pm 03:30
Towards the Prediction of Enzyme Evolvability using Collision Induced Unfolding Data; Sydney D. Neibert[1]; Maxwell J. Unger[1, 2]; Katie Jane Torma[1, 2]; Chang-Hwa Chiang[1, 2]; Cole C. Meyer[2]; Alison R.H. Narayan[1, 2]; Robert T. Kennedy[1, 3]; Brandon T. Ruotolo[1]; *[1]Department of Chemistry, University of Michigan, Ann Arbor, MI; [2]Life Sciences Institute, University of Michigan, Ann Arbor, MI; [3]Department of Pharmacology, University of Michigan, Ann Arbor, MI*

ThOG pm 03:50
Conformer-specific amylin oligomerisation interface mapping by native top-down tandem Ion mobility mass spectrometry and electron-capture dissociation; Zijie Dai[1]; Tianle Zhang[1]; Dale Cooper-Shepherd[2]; Anisha Haris[2]; Emma Marsden-Edwards[2]; Daniel Raleigh[1, 3]; Konstantinos Thalassinos[1]; *[1]Institute of Structural and Molecular Biology, Division of Biosciences, Darwin Building, University College London, London, United Kingdom; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Department of Chemistry, Stony Brook University, New York, NY*

ThOG pm 04:10
Following Temperature Induced Structural Changes by vT-nESI, HDX and TIMS-MS/MS; Marissa A Carter[1]; Kevin Jeanne Dit Fouque[1]; Tatiana Ramos-Del Campo[1]; Pablo R. B. Oliveira[1]; Fenfei Leng[1]; Francisco Fernandez Lima[1]; *[1]Florida International University, Miami, FL*

ThOH pm: Synthetic Polymers and New Materials
Room 6DE

ThOH pm 02:30

Electrospray Ionization-Ion mobility-qTOF Analysis of Low Molecular Weight Polyethyleneimine; Mark A Arnould; *Corning Inc, Painted Post, NY*

ThOH pm 02:50

Identification of Microplastics and Additives from the Lake Erie Watershed and the Cuyahoga River Using MALDI-MS and DART-MS; Luciana V Rivera Molina[1]; Robert Brand[2, 3]; Calum Bochenek[1]; Chrys Wesdemiotis[1]; *[1]University of Akron, Akron, OH; [2]Cuyahoga County Board of Health, Parma, OH; [3]University of the Free State, Bloemfontein, South Africa*

ThOH pm 03:10

Polymer Network Graph (PNG) Analysis Using Automated Kendrick Mass Defect (KMD) Cluster; Cole Stapleton[1]; Christopher J Shaffer[1]; *[1]3M, Maplewood, MN*

ThOH pm 03:30

Size, shape and surface: multidimensional analysis of synthetic nanomaterials using charge detection mass spectrometry; Veena S Avadhani[1]; Yuna Kwak[2]; Juyeon Yoo[2]; Jihyeon Choi[2]; Jared Huzar[1]; Conner Harper[1]; Jwa-Min Nam[2]; Grigory Tikhomirov[1]; Evan R. Williams[1]; *[1]University of California, Berkeley, Berkeley, CA; [2]Seoul National University, Seoul, South Korea*

ThOH pm 03:50

Trace Analysis of High Molecular Weight Polyvinyl Alcohol on a Triple Quadrupole Mass Spectrometer (SEC-MS/MS); James Keating[1]; Jason Winget[1]; Ping Sun[1]; Vincenzo Agostiniano[2]; Kevin Goodall[2]; Jason Price[1]; *[1]Procter and Gamble, Mason, OH; [2]Procter and Gamble, Brussels, Belgium*

ThOH pm 04:10

On the repeatability and quantitation of Polyethylene by pyrolysis GC-MS; Edward Erisman[1]; Yamil Simón-Manso[1]; William E. Wallace[1]; *[1]NIST, Gaithersburg, MD*

MONDAY POSTERS

Set-up for all posters
6:30 - 9:00 am

ALL POSTERS PRESENT
10:30 - 12:00 pm AND 1:00 - 2:30 pm

Remove all Monday posters
5:00 - 8:00 pm

Ambient Ionization: Fundamentals and Instrumentation	001-014
Biomarkers: Quantitative Analysis I	015-037
Disease Biomarkers	038-055
Education: Teaching MS	056-058
Elemental Analysis	059-065
Energy: Petroleum, Biofuels, and Algae	066-077
Environmental: General I	078-110
Exposomics	111-136
Fundamentals: Ion Activation/Dissociation	137-150
Fundamentals: Unconventional Approaches in MS	151-161
H/D Exchange: Hardware, Software and Methodology	162-174
High Throughput MS	175-210
Imaging MS: Pharmaceuticals, Metabolites, Lipids, and Glycans	211-247
Imaging: Spatially-Resolved Omics I	248-267
Informatics: Protein ID and Quantification	268-271
Informatics: Workflow and Data Management I	272-291
Instrumentation: Mini/Portable/Fieldable MS	292-301
Instrumentation: New Developments in Mass Analyzers and Ion Detection	302-322
Ion Mobility: Applications	323-357
Ion Mobility: FAIMS/DMS	358-361
Ion Mobility: General	362-369
LC/MS: Chromatography and Software	370-393
LC/MS: Sample Preparation I	394-415
Lipids: General	416-439
Metabolomics: Untargeted Metabolite Profiling I	440-463
Microorganisms and the Microbiome I	464-486
Neuroscience and Neurodegenerative Disease Research	487-511
Nucleic Acids and Oligonucleotides	512-537
Peptides: Targeted and Quantitative Analysis	538-566
Protein Therapeutics: Quantitative Analysis	567-584
Proteins: General and Membrane	585-595
Proteomics: New Approaches I	596-620
Proteomics: Tissue	621-639
Single Cell MS I	640-664
Small Molecules: Qualitative and Quantitative Analysis	665-703
Synthetic Polymers and New Materials	704-717
Toxicology	718-732

TUESDAY POSTERS

Set-up for all posters
6:30 - 9:00 am

ALL POSTERS PRESENT
10:30 - 12:00 pm AND 1:00 - 2:30 pm

Remove all Tuesday posters
5:00 - 8:00 pm

Antibodies & Antibody Drug Conjugates I	001-027
Biomarkers: Discovery I	028-051
Biomarkers: Quantitative Analysis II	052-074
Covalent Labeling and Chemical Crosslinking I	075-099
Environmental: General II	100-132
Food Safety: General	133-162
Forensics	163-195
Fundamentals: Ionic Clusters, Nanomaterials, and Catalysis	196-199
Fundamentals: Ionization	200-205
GC/MS: Instrumentation and Applications	206-236
High Mass Accuracy / High Performance MS: Applications, Automation, & Instrumentation	237-256
Imaging MS: Computational Methods, Software, and Analysis	257-265
Imaging MS: Disease Markers	266-269
Imaging: Spatially-Resolved Omics II	270-288
Informatics: General, SRM, and DIA	289-300
Informatics: Multiomics Integration	301-313
Informatics: Workflow and Data Management II	314-333
Instrumentation: New Concepts	334-346
Instrumentation: New Developments in Ionization and Sampling	347-367
Ion Mobility: Fundamentals	368-376
Ion Mobility: Structure	377-394
LC/MS: General	395-413
LC/MS: Sample Preparation II	414-432
Lipids: Targeted and Quantitative Analysis	433-462
MALDI: Applications	463-475
MALDI: Innovation in Instrumentation and Sample Preparation	476-480
Metabolomics: Targeted and Quantitative Analysis	481-510
Metabolomics: Untargeted Metabolite Profiling II	511-533
Microorganisms and the Microbiome II	534-555
Nanoscale / Microfluidic and Capillary Electrophoresis Separations and MS	556-564
Natural Products	565-583
Neuroscience and Neurodegenerative Disease Research II	584-608
Nucleic Acids and Oligonucleotides II	609-636
Proteins: PTMs	637-668
Proteomics: New Approaches II	669-691
Single Cell MS II	692-716
Systems Biology	717-729

Consult online planner or mobile app for detailed program.

WEDNESDAY POSTERS

Set-up for all posters
6:30 - 9:00 am

ALL POSTERS PRESENT
10:30 - 12:00 pm AND 1:00 - 2:30 pm

Remove all Wednesday posters
5:00 - 8:00 pm

Antibodies & Antibody Drug Conjugates II	001-028
Antidoping, Cannabis, and Opioid Detection	029-034
Art, Archaeology & Paleontology	035-041
Artificial Intelligence in MS Instrumentation and Applications I	042-068
Biomarkers: Discovery II	069-092
Cancer Research I	093-118
Clinical Analysis I	119-145
Covalent Labeling and Chemical Crosslinking II	146-169
Data-Independent Acquisition	170-197
Drug Discovery, DMPK, ADME	198-223
Drug Discovery: Qual / Quant Analysis I	224-250
Environmental: General III	251-283
Environmental: Pharmaceuticals and Pesticides	284-297
Epigenetic Modifications	298-302
Extractables & Leachables	303-321
Food Safety & Chemistry: Foodomics, Allergens, Bacteria, Foods, and Supplements I	322-340
Fundamentals: Ion Molecule, Ion/Ion, Ion/Electron Interactions	341-352
Fundamentals: Ion Spectroscopy	353-359
Fundamentals: Molecular Modeling / Quantum Mechanical Calculations	360-361
Fundamentals: Native MS	362-376
Glycoproteins I	377-397
H/D Exchange: Protein Structure/Function	398-410
Industry: Trace Analysis, Quality Control, and Automation	411-427
Informatics: Metabolomics, Lipidomics, and Glycomics	428-448
Informatics: Peptide ID and Quantification	449-479
Lipids: Profile Analysis	480-507
Metabolomics: General	508-540
Metabolomics: Untargeted Metabolite Profiling III	541-564
Nucleic Acids and Oligonucleotides III	565-591
Peptides: Identification and Fragmentation Mechanisms	592-608
Peptides: PTM Identification	609-626
Process Development MS	627-630
Proteins: Complexes/Non-covalent Interactions	631-655
Proteomics: Intact Proteins and Top Down Analysis I	656-682
Proteomics: Quantitative I	683-714
Viruses and Virus-Like Particles	715-722

THURSDAY POSTERS

Set-up for all posters
6:30 - 9:00 am

ALL POSTERS PRESENT
10:30 - 12:00 pm AND 1:00 - 2:30 pm

Remove all Thursday posters
2:30 - 3:00 pm

Ambient Ionization: Applications	001-025
Antibodies & Antibody Drug Conjugates III	026-054
Artificial Intelligence in MS Instrumentation and Applications II	055-078
Biomarkers: Discovery III	079-100
Cancer Research II	101-124
Carbohydrates	125-135
Clinical Analysis II	136-158
Drug Discovery: Qual / Quant Analysis II	159-186
Drug and Metabolite Analysis	187-214
Food Safety & Chemistry: Foodomics, Allergens, Bacteria, Foods, and Supplements II	215-235
Fundamentals: Ion Structure / Energetics / Reactions	236-258
Glycomics	259-266
Glycoproteins II	267-287
Lipids: ID and Structural Analysis	286-410
Imaging MS: Instrumentation	288-300
Imaging MS: Method Development	301-336
Informatics: Algorithms and Statistical Advances	337-363
Instrumentation: General	364-378
Isotope Labeling and Fluxomics Applications	379-385
Metabolomics: Clinical Applications	411-418
Metabolomics: Identification of Unknown Metabolites	419-437
Metabolomics: Sample Preparation	438-445
Peptidomics and Immunopeptidomics	446-470
Phosphopeptides and Phosphoproteins	471-487
Plant Biology and Biotechnology	488-492
Protein Therapeutics: Structural Characterization	493-520
Proteins: Conformation Analysis and Structural Biology	521-545
Proteomics: Chemoproteomics	546-581
Proteomics: Clinical Applications	582-611
Proteomics: Infectious Diseases	612-631
Proteomics: Intact Proteins and Top Down Analysis II	632-658
Proteomics: Quantitative II	659-690
Stable Isotope Labeling	691-706

MONDAY POSTERS

MP 001 **Development of an Electrokinetic Loading-Aided Paper Spray–Mass Spectrometry Device Coupled with Faradaic Ion Concentration Polarization**; Lahiru Wedasingha[1]; Varadaraju Vadakekatte Dyavegowda[1]; Jamison Riley Polley[1]; Nicholas E Manicke[1]; *[1]Indiana University Indianapolis, Indianapolis, IN*

MP 002 **Monolithic 3D-printed microfluidic nano-DESI probe enables robust, low-cost, high-throughput mass spectrometry**; Mohsen Latif[1]; Dalton Snyder[1]; Edwin Gonzalez[1]; Andy Eller[1]; Ann Donnelly[2]; Anna Leech[1]; Mitch Wells[1]; *[1]Teledyne FLIR Detection, WEST LAFAYETTE, IN; [2]Teledyne FLIR Detection, West Lafayette, IN*

MP 003 **Reduction of Organic Solvent to 5 µL per Sample by Coated Blade Spray–Mass Spectrometry (CBS-MS) with Self-Wettable Sorbent Material**; Wei Zhou[1, 2]; Janusz Pawliszyn[1, 2]; *[1]University of Waterloo, Waterloo, ON; [2]Sun Yat-sen University, Zhuhai, China*

MP 004 **Gold nanoparticle-mediated redox ionization of steroids using an ambient MALDESI source**; Paul Zerebinski[1]; Kyle Morgan[1]; Namodhi Wijerathne[1]; Ruwan T. Kurulugama[2]; Sarah M. Stow[2]; Richard A. Yost[1]; Timothy J Garrett[1, 3]; Wei David Wei[1]; Boone M. Prentice[1]; *[1]University of Florida, Department of Chemistry, Gainesville, FL; [2]Agilent Technologies, Santa Clara, CA; [3]University of Florida, College of Medicine, Department of Pathology, Immunology, and Laboratory Medicine, Gainesville, FL*

MP 005 **Development of fabric spray ionization – optimization and its applications**; Ramesha Dilhani Gaspe Ralalage[1]; Nelson R Vinueza Benitez[1]; *[1]North Carolina State University, Raleigh, NC*

MP 006 **Event-camera plume imaging, surface profiling, and correlative ambient mass spectrometry benchmarking of pulsed infrared laser ablation sources**; William J C Francis[1]; David F Blair[1]; Anna L Chauvet[1]; Lucy Noyes[1, 2]; Milena Micic[1]; Daniel Simon[3]; Zoltan Takats[2, 3]; Robert T Murray[1]; *[1]Department of Physics, Imperial College London, London, United Kingdom; [2]Department of Metabolism, Digestion and Reproduction, Imperial College London, London, United Kingdom; [3]Institute for Multimodal Imaging of Intercellular Communication, Universität Regensburg, Regensburg, Germany*

MP 007 **Imaging of the Corona Plasma Formed by a Nanoelectrode used in nAPCI**; Nicole C. Auvil[1]; Frederick Lanni[1]; Mark E. Bier[1]; *[1]Carnegie Mellon University, Pittsburgh, PA*

MP 008 **High-Throughput Automated 3D-Printed Cone Spray Ionization Mass Spectrometry Workflow for Rapid Analyte Detection in Complex Matrices**; Matthew J. Carlo[1]; Jamie P. Butalewicz[1]; Patrick W. Fedick[1]; *[1]Naval Air Warfare Center Weapons Division, China Lake, CA*

MP 009 **Ambient heating for desolvation of Electrosprayed Methanol and Micrometer-Sized Polystyrene Droplets**; Shao-Yu Liang[1]; Wei-Chun Chiu[2]; Shiu-Yao Yeh[2]; Avinash A. Patil[2]; Mhar Ian Cua Estayan[2, 3]; Wen-Ping Peng[2]; *[1]Department of Physics, Hualien, Taiwan; [2]National Dong Hwa University, Shoufeng, Taiwan; [3]University of Santo Tomas, Manila, Philippines*

MP 010 **Optimizing a mobile Rapid Evaporative Ionization Mass Spectrometry system for intraoperative surgical aerosol analysis during HNSCC surgery**; Gabriel Stefan Horkovics-Kovats[1]; István Pap[1]; Daniel Simon[1]; Nathalie Gumpert[2]; Luisa Symeou[2]; Julian Künzel[2]; Kathrin Renner[2]; Christopher Bohr[2]; Tamás Karancsi[3]; Zoltán Takáts[1]; *[1]University of Regensburg, Department of Immunomedicine, Regensburg, Germany; [2]University Hospital Regensburg, Department of Otorhinolaryngology, Regensburg, Germany; [3]Ambimass Kft, Záhony u. 7, H-1031 Budapest, Hungary, Budapest, Hungary*

MP 011 **MOF Spray Mass Spectrometry (MOF-SMS): Novel Substrates for Ambient Mass Spectrometry**; Leonardo Di Donna[1]; Ilaria Santoro[1]; Carmine Maletta[2]; Lucia Bartella[1]; Fabio Mazzotti[1]; Amira Nour[1]; Teresa Fina Mastropietro[1]; Pietro Magarò[2]; Donatella Armentano[1]; *[1]Università della Calabria, Dipartimento di Chimica e Tecnologie Chimiche, Rende, Italy; [2]Università della Calabria, Dipartimento di Ingegneria Meccanica, Energetica e Gestionale, Rende, Italy*

MP 012 **Development and Characterization of a Higher-Throughput Electrokinetic Preconcentration Device for the Screening of Illicit Drugs via Paper Spray Mass Spectrometry**; Jamison R Polley[1]; Lahiru Wedasingha[1]; Varadaraju Vadakekatte Dyavegowda[1]; Nicholas E Manicke[1]; *[1]Indiana University Indianapolis, Indianapolis, IN*

MP 013 **Corona Assisted ESI MS**; Drew Sauter; *Nanoliter, LLC, Henderson, NV*

MP 014 **Papers Spray Mass Spectromtery Triacylglycerol Profile Characterization for the Authentication of Extra Virgin Olive Oils**; Ilaria Santoro[1]; Lucia Bartella[1]; Fabio Mazzotti[1]; Leonardo Di Donna[1]; [1]*Università della Calabria, Dipartimento di Chimica e Tecnologie Chimiche, Rende, Italy*

MP 015 **Addition of Hyperthermal Acidic Protease Peptides to Tryptic Analysis Increases Identification of Proteins and Post-Translational Modifications**; Mario M Alba[1]; Lindsey Becker[2]; Ethan Canfield[3]; Jonathan Katz[3]; Jennifer E. Van Eyk[2]; Simion Kreimer[2]; [1]*Cedars-Sinai Medical Center, Karsh Division of Gastroenterology and Hepatology, LOS ANGELES, CA;* [2]*Cedars-Sinai Medical Center, Smidt Heart Institute, Los Angeles, CA;* [3]*Ellison Medical Institute, Los Angeles, CA*

MP 016 **Efficient Proteome-Scale Glycoproteomics: Combining Ultrafast Open Search and Machine Learning for Automated Biomarker Discovery**; Jake Yang[1]; Shenye Wen[1]; Yu Gao[1, 2]; Xinyu Miao[1]; Jianbo Deng[1, 2]; Chunyan Hou[3]; Junfeng Ma[3]; Junhong Jiang[4]; [1]*Shantou University Medical College, Shantou, China;* [2]*Soochow University, Suzhou, China;* [3]*The Georgetown University, Washington DC, DC;* [4]*The Fourth Affiliated Hospital of Soochow University, Suzhou, China*

MP 017 **LC-MS proteomics reveals a discordance between frataxin E levels and clinical phenotype in compound heterozygous Friedreich's ataxia**; Teerapat Rojsajjakul[1]; Clementina Mesaros[1]; David R. Lynch[2]; Ian Alexander Blair[1]; [1]*University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA;* [2]*Children's Hospital of Philadelphia, Philadelphia, PA*

MP 018 **Affordable and Comprehensive Absolute Quantification of the Human Proteome in a Tissue-specific Manner with SysQuan**; Timon Geib[1]; Elodie Logerot[1]; Peter Kubiniok[2]; Victor Spicer[3]; Stoyan Stoychev[4]; Robert Popp[5]; René P. Zahedi[3]; Dorte B. Bekker-Jensen[4]; Nicolai Bache[4]; Christoph H. Borchers[1, 6]; [1]*McGill University - Lady Davis Institute, Montreal, QC;* [2]*Quantivum Inc., montreal, QC;* [3]*Department of Biochemistry and Medical Genetics, University of Manitoba, Winnipeg, MB, Canada, winnipeg, MB;* [4]*Evosep Biosystems, Odense, Denmark;* [5]*MRM Proteomics Inc, Montreal, QC;* [6]*Department of Pathology, McGill University, Montreal, QC*

MP 019 **Next-Level Sensitivity: Polyamine Profiling in Human Serum Using LC/TQ**; Yulan Bian[1]; Daniel Cuthbertson[2]; Aveline Neo[1]; [1]*Agilent Technologies, Singapore, Singapore;* [2]*Agilent Technologies, Santa Clara, CA*

MP 020 **Proof-of-Concept Online Affinity Capture–MS Workflow for Automated, Selective, and Sensitive Insulin Detection**; Alex Kyranos[1]; Susan E. Abbatiello[1]; Nathan Canniff[1]; Yeliz Sarisozen[1]; Martin Gilar[1]; Beatrice Muriithi[1]; Kevin Wyndham[1]; [1]*Waters Corporation, Milford, MA*

MP 021 **Investigation of Therapeutic Options for Crohn's Disease Using Patient-Derived Enteroids via Targeted Mevalonate Pathway Metabolomics**; David Lewis[1]; Albert Vega[1]; Jason Matthews[2]; Connor Moore[3]; Sachith Munasinghe[2]; Jason Papin[3]; Subra Kugathasan[2]; Sana Syed[4]; Facundo M Fernández[1]; Anum Chotani[4]; Adam Greene[4]; Amber Kelly[2]; Jenascia Davis[2]; Tommy Doan[2]; Fortunata Michael[2]; Bernadette Martineau[2]; Samuel Fisher Rhoads[3]; Prerana Dubey[3]; Fatima Habib[3]; [1]*Georgia Institute of Technology School of Chemistry and Biochemistry, Atlanta, GA;* [2]*Emory University, Atlanta, GA;* [3]*University of Virginia, Charlottesville, VA;* [4]*Duke University, Durham, NC*

MP 022 **Ultrasensitive Dilute-and-Shoot HILIC–MS/MS Method for Quantifying Acetylcholine in Rat Brain Microdialysates**; Leslie Nguyen[1]; Ian Fraser[1]; Ryan Wyatt[1]; Weixuan Chen[2]; [1]*Johnson & Johnson, San Diego, CA;* [2]*Johnson and Johnson, San Diego, CA*

MP 023 **Identification of Novel Estradiol-Derived Hemoglobin Modifications and Quantification in Breast Cancer Patients using Nanoflow Liquid Chromatography High-Resolution Tandem Mass Spectrometry**; Hauh-Jyun Candy Chen[1]; Yan-Ling Liao[1]; Lee Ren-Jye[1]; Chi-Wen Tu[2]; [1]*National Chung Cheng Univ., Ming-Hsiung, Chia-Yi, Taiwan;* [2]*Ditmanson Medical Foundation Chia-Yi Christian Hospital, Chia-Yi city, Taiwan*

MP 024 **Simultaneous LC–MS/MS Quantification of Urinary DNA, Lipid, and Protein Oxidation Biomarkers**; Giacomo L Visconti[1]; Elisa Bassotti[1]; Elena Caponi[1]; Antonio Medugno[1]; Alessandro Baldi Talini[1]; [1]*Sentinel CH S.p.A., Milan, Italy*

MP 025 **Bacterial Flagellin as a Cost-Effective Internal Standard for Absolute Quantification and Glycopeptide Enrichment Assessment in LC-PRM-MS/MS**; Vishal Sandilya[1]; Sherifdeen B. Onigbinde[1]; Sarah Sahioun[1]; Abderrahmane Koraich[1]; Abiodun M. Adewolu[1]; Yehia Mechref[1]; [1]*Texas Tech University, Lubbock, TX*

MP 026 **Targeted Liquid Chromatography Multi-Reflecting Time of Flight Mass Spectrometry for Comprehensive Metabolic and Lipidomic Profiling**; Samantha Ferries[1]; Masoumeh Dorrani[2]; Jamie Humphries[2]; Richard Lock[1]; Rav Sheth[3]; Elizabeth O'Day[2]; Johannes PC Vissers[1]; John Vukovic[4]; [1]*Waters, Wilmslow, United Kingdom;* [2]*Olaris, Framingham, MA;* [3]*Waters Corporation, Milford, MA;* [4]*Waters Corporation, Wilmslow, United Kingdom*

MP 027 **Targeted Proteomics Enables Pathway-Level Functional Proteogenomics in Cancer Cells**; Khatereh Motamedchaboki[1]; Philip Remes[1]; Lilian Heil[1]; Katherine Walker[1]; Amirmansoor Hakimi[1]; Cristina Jacob[1]; Scott Peterman[1]; Romain Huguet[1]; [1]*Thermo Fisher Scientific, San Jose, CA*

MP 028 **Comparing Anti-Peptide Antibody Enrichment and SPE Workflows for Targeted MS Quantification of EGFR Peptides in FFPE Sections**; Lizhuo Ai[1]; Joseph M Eckenrode[1]; Jun Yan[2]; Kevin P Gillespie[2]; Carolina Cabral[2]; Michael E Lassman[2]; [1]*Merck & Co., Rahway, NJ;* [2]*Merck & Co, Rahway, NJ*

MP 029 **Efficient Transfer of Untargeted MS/MS Food Intake Biomarker Discovery to Targeted MS/MS Profiling**; Ahsan Hameed[1]; Isabel F Snodgrass[1]; Nuanyi Liang[1]; Huaxu YU[1]; Francene M Steinberg[2]; Sean H Adams[3, 4, 5]; Brian J Bennett[2, 6]; Carolyn M Slupsky[2, 7]; Oliver Fiehn[1]; John W Newman[1, 2, 6]; [1]*West Coast Metabolomics Center, University of California Davis, Davis, CA;* [2]*Department of Nutrition, University of California-Davis, Davis, CA;* [3]*Department of Surgery, University of California Davis School of Medicine, Sacramento, CA;* [4]*Center for Alimentary and Metabolic Science, University of California Davis, Sacramento, CA;* [5]*Nutrition for Transformative Healthcare Program, University of California Davis, Sacramento, CA;* [6]*Western Human Nutrition Research Center, Agricultural Research Service, United States Department of Agriculture, Davis, CA;* [7]*Department of Food Science and Technology, University of California-Davis, Davis, CA*

MP 030 **High-throughput LC-HRMS method for the quantitation of 20 Bile Acids in Human Serum and Urine**; Danialle Ronnow[1]; Chris Hardcastle[1]; Brandon Wilcock[1]; Alexander Schwartz[1]; Troy Voelker[1]; Scott Reuschel[1]; [1]*Aliri Bioanlaysis, Millcreek, UT*

MP 031 **Comprehensive Proteomic Analysis of Low-volume Mouse Serum Identifies Molecular Alterations Linked to Western Diet Exposure**; Nan Wang[1]; Wei Wu[1]; [1]*HHMI Janelia, Ashburn, VA*

MP 032 **Absolute Quantitation of the Whole-brain Proteome in Preclinical Alzheimer's Disease Mouse Models Utilizing the SysQuan Platform**; Elyssa N. Baker[1, 2]; Elodie Logerot[1]; Timon Geib[1]; Christoph H. Borchers[1, 2, 3, 4, 5]; [1]*Lady Davis Institute McGill University, Montréal, QC;* [2]*Division of Experimental Medicine, McGill University, Montreal, Montreal, QC;* [3]*Segal Cancer Proteomics Center, McGill University, Montreal, QC;* [4]*Gerald Bronfman Department of Oncology, Lady Davis Institute for Medical Research, Jewish General Hospital, Montreal, QC;* [5]*Department of Pathology, McGill University, Montreal, QC*

MP 033 **Development of a Quantitative Hybrid LC-MS/MS Method for Multiple High Abundant Protein Biomarkers in Human Heart Tissue**; Rathna J Veeramachaneni[1]; Taylor Dufield[1]; Ryan Darling[1]; Dawn R Dufield[1]; [1]*KCAS Bio, Olathe, KS*

MP 034 **Quantitative Serum Proteomics in BC Identifies Blood Coagulation Factors as Dysregulated**; Tochukwu Victor Njoku[1]; Sumona Mondal[2]; Thevasha Sathiyakumar[2]; Claudia Gaither[3, 4]; Adeline Shanker[3]; Robert Popp[3]; Christoph H. Borchers[5, 6, 7, 8]; Costel C. Darie[1]; [1]*Department of Chemistry and Biochemistry, Clarkson University, Potsdam,13699-5810, NY;* [2]*Department of Mathematics and Statistics, Clarkson University, Potsdam, 13699-5810, NY;* [3]*MRM Proteomics Inc., Montréal, QC;* [4]*Département de biomédecine vétérinaire, Faculté de médecine vétérinaire, Université de Montréal,* *Saint-Hyacinthe, J2S 2M2, QC; [5]Segal Cancer Proteomics Centre, Lady Davis Institute for Medical Research, McGill University, Montreal, QC; [6]Gerald Bronfman Department of Oncology, Lady Davis Institute for Medical Research, Jewish General Hospital, Montreal, QC; [7]Division of Experimental Medicine, McGill University, Montreal, QC; [8]Department of Pathology, McGill University, Montreal, QC*

MP 035 **Quantifying Cortisol and Other Steroids in Human Eccrine Sweat Using Direct Analysis in Real Time Mass Spectrometry**; J. Ray Runyon[1]; David W Tano[2]; Diezel Cochenour[2]; Rebecca Oddes[2]; *[1]University of Arizona Andrew Weil Center for Integrative Medicine, Tucson, AZ; [2]University of Arizona, Tucson, AZ*

MP 036 **A multimodal LC–MS and MALDI-MSI workflow for mapping methylation potential biomarkers (SAM/SAH) in preclinical melanoma models**; Weiyuan Hu[1]; Weiyi Peng[2]; Xinli Liu[1]; *[1]Department of Pharmacological and Pharmaceutical Sciences, University of Houston, Houston, TX; [2]Department of Biology and Biochemistry, University of Houston, Houston, TX*

MP 037 **Development of a Quantitative Assay for Peripheral PI3Kα Cys242 Target Engagement by RAS–PI3K Disruptors**; Melissa Hoffman[1]; Egor Vorontsov[2]; Stephanie Ballweg[3]; Sabrina Fuhrmann[3]; Zachary Turman[1]; Michael Bremang[4]; Stefan Selzer[3]; Antje Berfelde[3]; Marie Pariollaud[1]; Joseph Klebba[1]; Stephen McComish[1]; Marielena Mata[1]; Emma Maesteller[1]; Matthew Patricelli[1]; David Van Meter[3]; Ian Pike[3]; Gabriel Simon[1]; *[1]Vividion Therapeutics, San Diego, CA; [2]Thermo Fisher Scientific, Molndal, Sweden; [3]Proteome Sciences R&D GmbH & Co. KG, Frankfurt am Main, Germany; [4]Arcondis Corporation, Boston, MA*

MP 038 **Development of a Plasma IP-MS Assay for N-Secretase–Derived APP Fragments in Alzheimer's Disease**; Benjamin Panitz[1]; Dorota Tokmina-Roszyk[1]; Gregg Fields[1]; *[1]Florida Atlantic University, Jupiter, FL*

MP 039 **High-Depth Proteomics of Synovial Fluid Reveals Osteoarthritis Biomarkers**; Daniel Young[1]; Diego M Assis[2]; Cameron Ellis[3]; Matthew Willetts[2]; Antoine Dufour[1]; *[1]University of Calgary, Calgary, AB; [2]Bruker Daltonics, Billerica, MA; [3]PreOmics GmbH, Am Klopferspitz 19, 82152, Planegg, Germany*

MP 040 **Longitudinal Proteomic Profiling Defines a Two-Stage Remodeling Trajectory of Tauopathy in PS19 Mice**; Shuaixin Gao[1]; Huan Zhang[2]; Xinru Pang[1]; Jiangjiang Zhu[1]; *[1]The Ohio State University, Columbus, OH; [2]Dartmouth College, Hanover, NH*

MP 041 **Multi-Omics Integration of Proteomics and Metabolomics Reveals Donor Biofluid Signatures of Kidney Graft Viability**; Sadr Ul Shaheed[1]; Fenna E.M. Van De Leemkolk[2]; Corinna Snashall[3]; Chris W. Sutton[4]; Rutger J. Ploeg[3]; Jan H.N. Lindeman[2]; *[1]University of Oxford, Oxford, United Kingdom; [2]Leiden University Medical Center, Leiden, Netherlands; [3]University Of Oxford, Oxford, United Kingdom; [4]University of Bradford, Bradford, United Kingdom*

MP 042 **Proteomic reprogramming and immune remodeling drive endometrial cancer aggressiveness**; Jiyoung Yu[1]; Jung-Yoon Yoo[2]; Kwangseon Lee[3]; Sungryul Yu[4]; Kyunggon Kim[5]; *[1]Clinical Core Lab, Convergence Medicine Research Center, Asan Medical Center, Seoul, South Korea; [2]Department of Biomedical Laboratory Science, Yonsei University MIRAE Campus, Wonju, South Korea; [3]Asan Medical Center, Songpa-gu, South Korea; [4]Department of Clinical Laboratory Science, Semyung University, Jecheon, South Korea; [5]University of Ulsan College of Medicine, Asan Medical Center, Seoul, South Korea*

MP 043 **Systematic Assessment of Multiple Protein Biomarkers for Bladder Cancer: Bridging Verification and Clinical Application**; Yi-Ting Chen[1]; Yu-Ting Chen[2]; Chien-Lun Chen[2]; Hsiao-Wei Chen[1]; Shu-Hsuan Fu[1]; Wei-Shan Wei[1]; Yu Chang[1]; Chi Yang[1]; *[1]Chang Gung University, Taoyuan, Taiwan; [2]Department of Urology, Chang Gung Memorial Hospital, Taoyuan City, Taiwan*

MP 044 **Altered network roles of citrullination-linked serum proteins in rheumatoid arthritis**; Sora Mun[1]; Seungyeon Lee[2]; Yeeun Yun[3]; Jiyeong Lee[3, 4]; Hee-Gyoo Kang[1, 2, 3]; *[1]Department of Biomedical Laboratory Science, College of Health Sciences, Eulji University, Seongnam, South Korea; [2]Department of Senior Healthcare, Graduate School, Eulji University, Uijeongbu, South Korea; [3]Department of*

Biomedical Laboratory Science, Graduate School, Eulji University, Uijeongbu, South Korea; [4]Department of Biomedical Laboratory Science, College of Health Sciences, Eulji University, Uijeongbu, South Korea

MP 045 **Deep Proteomic Profiling of the Human Pancreas Reveals a Distinct Citrullination Signature in Type 1 Diabetes**; Hung-Yu (Eric) Chiang[1]; Bin Wang[2]; Zexin Zhu[2]; Daniel Tremmel[3]; Sara D Sackett[3]; Jon S Odorico[3]; Lingjun Li[1, 2, 4]; *[1]Biophysics Program, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Department of Surgery, University of Wisconsin-Madison, Madison, WI, Madison, WI; [4]Department of Chemistry, University of Wisconsin-Madison, Madison, WI, Madison, WI*

MP 046 **Quantitative Proteomic Profiling of Human Pancreatic Tissues in Type 1 and Type 2 Diabetes by DIA with PRM Validation**; Jingwei Zhang[1]; Haiyan Lu[2]; Feixuan Wu[2]; Connie S Chamberlain[3]; Jon S Odorico[3]; Lingjun Li[1, 2]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Department of Surgery, University of Wisconsin-Madison, Madison, WI, Madison, WI*

MP 047 **Plasma metabolomics differentiates cardiometabolic disease progression from endurance-associated lipid remodeling**; Pramod P Wangikar[1, 2]; Sneha Rana[1]; Nikita Savalsang[1]; Deepti Sahasrabuddhe[1]; Avinash Vellore Sunder[1]; Rakesh Sahay[3]; Manisha Sahay[3]; Renuka Munshi[4]; Milind Gurjar[1]; Venkatraman Pichumani[5]; Marcus Ranney[6]; *[1]Indian Institute of Technology Bombay, Mumbai, India; [2]Clarity Bio Systems India Pvt. Ltd., Pune, India; [3]osmania medical college, Hyderabad, India; [4]Topiwala National Medical College and Bai Yamunabai Laxman Nair Charitable Hospital, Mumbai, India; [5]You Too Can Run, Mumbai, India; [6]Human Edge Pvt. Ltd., Mumbai, India*

MP 048 **A Label-Free MultiOmics Analysis of Whole Blood Samples from Patients with Parkinson's Disease in Emirati Population**; Alexander Brzhozovskiy[1, 2]; Dia Advani[1]; Frederico Garcia Pinto[1]; Suzan Kayali[1]; Alexander Giddey[1]; Nasna Nassir[1, 3]; Mohammed Jashim Uddin[1]; Nelson Soares[1, 3]; *[1]Center for Applied and Translational Genomics (CATG), Mohammed Bin Rashid University of Medicine and Health Sciences (MBRU), Dubai Health, Dubai 19099, United Arab Emirates (UAE)., Dubai, United Arab Emirates; [2]Center for Bio- and Medical Technologies, Moscow, 121205, Russian Federation, Moscow, Russia; [3]College of Medicine-Mohammed Bin Rashid University of Medicine and Health Sciences (MBRU), Dubai Health, Dubai 19099, UAE., Dubai, United Arab Emirates*

MP 049 **MS-based proteomic characterization of SOD1- G93A mouse model**; Bo Yang[1]; Disha Sood[1]; Steven Rodriguez[1]; Hendrik Wesseling[1]; Bailin Zhang[1]; *[1]Sanofi, Cambridge, MA*

MP 050 **CSF Extracellular Vesicle Proteomics Reveals Disease-Associated Signatures in GAD65-IgG Associated Autoimmune Epilepsy**; Yun Tang[1]; Andrea Stabile[1]; Anuja Patil[1]; Patrick Vanderboom[1]; Surendra Dasari[1]; Brian Searle[1]; Divyanshu Dubey[1]; *[1]Mayo Clinic, Rochester, MN*

MP 051 **Multi-Omics Approach to Biomarker-Based Characterization of Canine Hepatocellular Carcinoma**; Esandi S Kurulugama[1]; Resmi Ravindran[1]; Yutong Ji[1]; William Culp[1]; Dongguang Wei[1]; Imran Khan[1]; *[1]UC Davis, Davis, CA*

MP 052 **Linearity and Metabolite Coverage Assessment for HILIC and Reversed Phase Metabolomics in Rare Genetic Diseases**; Christopher L. Souders[1]; M. Grace Thornhill[1]; Timothy J. Garrett[1]; *[1]University of Florida, College of Medicine, Department of Pathology, Immunology, and Laboratory Medicine, Gainesville, FL*

MP 053 **Potential Biomarker Identification from Cerumen and Sebum of Parkinson's Disease Patients**; Leilei Sun[1]; Katrina Mazinke[1]; Diego Diaz[1]; Paul Jones[1]; Alex Rajput[1, 2]; Eric Noyes[1, 2]; Haixia Zhang[1]; *[1]University of Saskatchewan, Saskatoon, SK; [2]Saskatchewan Health Agency, Saskatoon, SK*

MP 054 **Lipidomic profiling of Plasmodium vivax dormancy and relapse**; STEVE V. DJOVA[1]; Michele Spring[2, 3]; Rhoel R. Dinglasan[4]; Timothy J. Garrett[1]; *[1]University of Florida, Department of Pathology, Immunology and Laboratory Medicine, Gainesville, FL; [2]- State University of New York Upstate Medical University, Syracuse, NY; [3]Armed Forces Research Institute of Medical Sciences (AFRIMS), Bangkok, Thailand; [4]University of Florida, Department of Infectious Disease and Immunology, Gainesville, FL*

MP 055 **Systemic citrullination–associated serum protein signatures**; Yeeun Yun[1]; Sora Mun[2]; Seungyeon Lee[3]; Jiyeong Lee[1,4]; Hee-Gyoo Kang[1,2,3]; *[1]Department of Biomedical Laboratory Science, Graduate School, Eulji University, Uijeongbu, South Korea; [2]Department of Biomedical Laboratory Science, College of Health Sciences, Eulji University, Seongnam, South Korea; [3]Department of Senior Healthcare, Graduate School, Eulji University, Uijeongbu, South Korea; [4]Department of Biomedical Laboratory Science, College of Health Sciences, Eulji University, Uijeongbu, South Korea*

MP 056 **Toward Teaching Chemistry Concepts Across the Curriculum Using Mass Spectrometry: A Review of the Literature**; Amanda Patrick; *Mississippi State University, Mississippi State, MS*

MP 057 **Advancing Field-Based Detection: 3D-Printed Cone Spray Ionization and Portable Mass Spectrometry Training for Forensic Scientists**; Jamie P. Butalewicz[1]; Eleanor Castracane[1]; Christopher C. Mulligan[2]; Ryan M. Bain[3]; Patrick W. Fedick[1]; *[1]Naval Air Warfare Center Weapons Division, China Lake, CA; [2]Illinois state university, Normal, IL; [3]Bureau of Alcohol, Tobacco, Firearms and Explosives, Beltsville, MD*

MP 058 **Teaching Deployment-Ready Analytical Chemistry: Portable MS and Next-Generation Ambient Ionization Methods Vertically Integrated into Undergraduate Laboratory Curriculum**; Madelynn G. Anderson[1]; Jamie P. Butalewicz[2]; Eleanor Castracane[2]; Ebenezer H. Bondzie[1]; Kingsley C. Nwaiwu[1]; Patrick W. Fedick[2]; Christopher C. Mulligan[1]; *[1]Illinois state university, Normal, IL; [2]Naval Air Warfare Center Weapons Division, China Lake, CA*

MP 059 **Validated low-volume ICP-MS method for comprehensive analysis of essential and toxic elements in human milk**; Gaurav Pandey[1,2]; Mitra Hooshmand[1,2]; Lars Bode[1,2,3]; *[1]Human Milk Institute (HMI), Milk Analytics Core (MAC), University of California San Diego, La Jolla, CA; [2]Department of Pediatrics, School of Medicine, University of California San Diego, La Jolla, CA, United States, La Jolla, CA; [3]Larsson-Rosenquist Foundation Mother-Milk-Infant Center of Research Excellence (MOMI CORE), University of California San Diego, La Jolla, CA*

MP 060 **Method of Standard Addition for Improved Analysis of Trace Elements in Plutonium Metal Matrix**; Emilio S Rivera[1]; Michael Rearick[1]; Gabriel Infantino[1]; Desiree Martinez[1]; Kate McIntosh[1]; *[1]Actinide Analytical Chemistry Group (C-AAC), Chemistry Division, Los Alamos, NM*

MP 061 **ICP MS analysis of cellulose based dried biofluids using 10, 50, and 70 µL collection devices**; Donald H. Chace[1]; Charles Harper[1]; Nesta Bortey Sam[2]; Jerry Vockley[3]; *[1]miQro Lab Solutions, A capitainer company, East Providence, RI; [2]University of Pittsburgh, Pittsburgh, PA; [3]UPMC Children's Hospital of Pittsburgh, Pittsburgh, PA*

MP 062 **Quality Control of High-Purity Copper Using ICP-OES and ICP-MS for Ultra-Trace Metals Analysis**; Ana S Garcia Gonzalez[1]; Bert Woods[2]; *[1]Agilent Technologies, Wilmington,, DE; [2]Agilent Technologies, Wilmington, DE*

MP 063 **Ultra-trace analysis of surface impurities in polysilicon for photo-voltaic applications**; Thomas Paul K[1]; Vinay Jain[2]; Vivek Dhyani[3]; Mark Kelinske[4]; *[1]Agilent Technologies India Pvt. Ltd, Bangalore, India; [2]Agilent Technologies, Inc., Manesar, India; [3]Agilent Technologies Inc., Mumbai, India; [4]Agilent Technologies, Wilmington, DE*

MP 064 **Ultra-Trace Elemental Analysis of Undiluted Naphtha using Inductively Coupled Plasma Mass Spectrometry**; Venkata Chinna Sampath Pulletikurthi[1]; Anant Lohar[1]; *[1]Shimadzu Middle East and Africa FZE, Dubai, United Arab Emirates*

MP 065 **Characterization of Nickel and Vanadium Complexes in Different Asphaltene Samples Using Multiprong Mass Spectrometry and Spectroscopy Methods**; Sahil Makhani[1]; Bismark A Nyaaba[1]; Thanuja M Thilakarathna[1]; Patrick J Farmer[1]; Touradj Solouki[1]; *[1]Baylor University, Waco, TX*

MP 066 **Biofuel extraction from microalgal feedstock (III)**; Takashi Ted Nohmi; *HysafeNohmi, Setagaya-Ku, Japan*

MP 067 **Molecular Profiles of Interfacially Active Compounds in Lignocellulosic Pyrolysis Bio-Oils Revealed by Off-line LC and FT-ICR MS**; Aleksandra N Hilliard[1, 2]; Olivia C Moss[2]; Ryan P Rodgers[2]; Kristina Hakansson[1, 2]; Martha L Aguilera[2]; *[1]Department of Chemistry and Biochemistry, Florida State University, Tallahassee, FL; [2]Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, Tallahassee, FL*

MP 068 **Unburnt/Partially Burnt Fuel Increases Tugboat Particulate Emissions Upon Fuel Switching to Biodiesel by Two Orders of Magnitude**; Julia Zaks[1]; Atefeh Zarei[2]; Nishan Sapkota[2]; Cameron Varcoe[2]; Mang Guan[2]; Anand Kumar[2]; Jeremy Rochussen[2]; Naomi Zimmerman[2]; Patrick Kirchen[2]; Brett Smith[3]; Tim Sipkens[3]; Joel C. Corbin[3]; Steven N. Rogak[2]; Allan K. Bertram[1]; *[1]Department of Chemistry, University of British Columbia, Vancouver, BC; [2]Department of Mechanical Engineering, University of British Columbia, Vancouver, BC; [3]Metrology Research Centre, National Research Council Canada, Ottawa, ON*

MP 069 **Applying an LC–MS/MS lipidomics method to evaluate microalgal extracts obtained by liquefied ammonia extraction**; Kiyoshi Sakuragi[1]; Yuki Maeda[1]; Haruki Yoshino[2]; Takayuki Marutani[2]; *[1]Central research institute of electric power industry, Kanagawa, Japan; [2]Institute of Microalgal Technology, Hiroshima, Japan*

MP 070 **CHARACTERIZATION OF ENERGY-RELEVANT LIQUID PRODUCTS FROM VACUUM PYROLYSIS OF HDPE MICROPLASTIC BY HIGH-RESOLUTION MASS SPECTROMETRY**; Lays Rafalscky[1]; Hugo Fonseca Brandolini[2]; Marcelo Lopes Cocco[2]; Edilton Nunes da Silva[2]; Jamilson Silva Junior[2]; Amanda Eiriz Feu[3]; Lindamara Maria de Souza[3]; Robson Costa de Souza[2]; Wandersão Romão[2, 3]; *[1]UFES, vitória, Brazil; [2]Federal University of Espírito Santo, 29500-000, Alegre, ES, Brazil., alegre, Brazil; [3]Federal Institute of Espírito Santo, Vitória, Brazil*

MP 071 **Development of on-line coupling between supercritical fluid chromatography and 18 T FTICR MS for the molecular characterization of wood bio-oil**; Guillaume Limousin[1, 2]; Theo Imhoff[1, 2, 3]; Marie Hubert-Roux[1, 2]; Pierre Giusti[1, 2, 3]; Mélanie Mignot[1, 2]; Carlos Afonso[1, 2]; *[1]Université de Rouen Normandie, INSA Rouen Normandie, CNRS, Laboratoire CARMeN UMR 6064, INC3M FR 3038, Mont Saint Aignan, France; [2]International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France; [3]TotalEnergies One Tech, R&D, Downstream Processes & Polymers, TotalEnergies Research & Technology Gonfreville, BP 27, Harfleur, France*

MP 072 **Isomer-Level Description of Complex Bio-Oils Enabled by gTIMS Hyphenated to 18 T FTICR MS**; Pierre Giusti[1, 2, 3]; Theo Imhoff[2, 3, 4]; Simon Ollivier[2, 3]; Julien Maillard[2, 4]; Caroline Barrère-Mangote[2, 4]; Marie Hubert-Roux[2, 3]; Mélanie Mignot[2, 3]; Carlos Afonso[2, 3]; *[1]TotalEnergies, Harfleur, France; [2]International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France; [3]CARMeN institute, UMR 6064, CNRS, University of Rouen Normandy, Rouen, France; [4]TotalEnergies Research and Technology Gonfreville, Harfleur, France*

MP 073 **High-Resolution Characterization of Bio-Oils Using Reversed-Phase LC Coupled to an 18 T FT-ICR Mass Spectrometer**; Julien Maillard[1, 2]; Theo Imhoff[1, 2, 3]; Maxime SUEUR[1, 2, 3]; Marie Hubert-Roux[2, 3]; Guillaume Limousin[2, 3]; Mélanie Mignot[2, 3]; Caroline Barrère-Mangote[1, 2]; Carlos Afonso[2, 3]; Pierre Giusti[2, 3, 4]; *[1]TotalEnergies Research and Technology Gonfreville, Harfleur, France; [2]International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France; [3]CARMeN institute, UMR 6064, CNRS, University of Rouen Normandy, Rouen, France; [4]TotalEnergies, Harfleur, France*

MP 074 **Addressing Fulvic Acids Chemical diversity and structural complexity with High Resolution Trapped Ion Mobility, FT-ICR Mass Spectrometry, and Machine Learning**; Pablo R Batista Oliveira[1]; Bilal Shabbir[1]; Kevin Jeanne Dit Fouque[1]; Chad Weisbrod[2]; David Stranz[3]; Anton N. Kozhinov[4]; Konstantin Nagornov[4]; Yury O. Tsybin[4]; Fahad Saeed[1]; Francisco Fernandez-Lima[1]; *[1]Florida International University, Miami, FL; [2]National High Magnetic Field Laboratory Department of ICR, Tallahassee, FL; [3]Sierra Analytics, Inc., Modesto, CA; [4]Spectroswiss, Lausanne, Switzerland*

MP 075 **Characterization of Fulvic Acids using high resolution FT-ICR MS, HCD MS/MS, and Graph DOM**; Maria Lucia Masferrer Bertoli[1]; Pablo R. B. Oliveira[2, 3]; Bilal Shabbir[4]; Chad Weisbrod[5]; Fahad Saeed[3, 4]; Francisco Fernández-Lima[2]; *[1]Florida International University, Miami, FL; [2]Department of Chemistry and*

Biochemistry, Florida International University, Miami, FL; [3]Institute of Environment, Florida International University, Miami, FL; [4]School of Computing and Information Science, Florida International University, Miami, FL; [5]National High Magnetic Field Laboratory, Ion Cyclotron Resonance Facility, Florida State University, Tallahassee, FL

MP 076 **Class-Specific Chemical Tagging via Mass Deficient Derivatization and Automated Identification of Signal Repositing in Complex Mixtures**; Thanuja M. Thilakarathna[1]; Ayhaan Isaac Solouki[2]; Bismark A. Nyaaba[1]; Sahil Makhani[1]; Patrick J. Farmer[1]; Touradj Solouki[1]; *[1]Baylor University, Waco, TX; [2]Midway High School, Waco, TX*

MP 077 **Dramatically Improved Hydrocarbons Analysis Using GC-MS with Cold EI**; Aviv Amirav[1]; Benny Neumark[2]; Oneg Elkabets[2]; Alex Yakovchuk[2]; *[1]Tel-Aviv University, Tel-Aviv, Israel; [2]Tel Aviv University, Tel Aviv, Israel*

MP 078 **PFAS and DBP Worlds Collide: Discovery of New Fluorinated Disinfection By-product and Its Precursors in Chlorinated and Chloraminated Drinking Water**; Susan Richardson[1]; Jiafu Li[1]; *[1]University of South Carolina, Columbia, SC*

MP 079 **Targeted LC-MS/MS Method Development for PFAS in Cosmetic Products**; Anant Lohar[1]; Jessin Mathai[1]; Jenishia Menezes[1]; *[1]Shimadzu Middle East and Africa FZE, Dubai, United Arab Emirates*

MP 080 **Advancing PCB Congener Analysis: GC Triple Quadrupole with High Volume MMI and Dynamic MRM**; Tim Conjelko[1]; Amy Cuthbertson[2]; Alexis Willey[2]; Anastasia Andrianova[2]; Nick Harden[3]; *[1]Agilent Technlogies, Traverse City, MI; [2]Agilent Technologies, Wilmington, DE; [3]Agilent Technologies, Santa Clara, CA*

MP 081 **Optimizing SVOC Analysis using GC-MS/MS with Automated Pretreatment and High-Speed Analytical Methods**; Yoshiro Hiramatsu[1]; Courtney F Mayhew[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD*

MP 082 **Quantitation of Microcystins and Nodularin in Drinking Water Samples to Meet EPA Method 544 Requirements Using LC/MS/MS**; Autumn Payne[1]; Jacob Jalali[1]; Victor Cai[1]; *[1]Perkin Elmer, Downers Grove, IL*

MP 083 **Tracking background laboratory PFAS contamination in the EPA 1633 LC-MS workflow**; Nishaben Patel[1]; Atis Chakrabarti[1]; Stephanie Pollard[1]; Matt James[1, 2]; Gemma Lo[1, 2]; Helen Poole[1, 2]; *[1]Avantor, Bridgewater, NJ; [2]Avantor, Theale, United Kingdom*

MP 084 **Profiling of Monoterpene Metabolites Using LC–MS and Integrated Library-Guided Analysis**; Zhengzhi Xie[1]; Rachel J. Keith[1]; Daniel J. Conklin[1]; Jackie Gallagher[1]; Aruni Bhatnagar[1]; Pawel Lorkiewicz[1]; *[1]University of Louisville, Louisville, KY*

MP 085 **Development of an LC-MS/MS-Based Method for the Quantitation of 6PPD and its Transformation Products in Fish**; Paul D Kennedy[1]; Samantha K Goodwin[1]; Matthew J Kiewski[2]; Dilrukshika S.W. Palagama[1]; Miguel A Gijon[1]; *[1]Cayman Chemical Company, Ann Arbor, MI; [2]Cornell University, Ithaca, NY*

MP 086 **Implementation of complete mobile and stationary monitoring solutions for ambient and fenceline VOC measurements**; Tucker Kitchengs[1]; Leslie P Silva[2]; *[1]Syft Technologies, West Chester, PA; [2]Syft Technologies, Studio City, CA*

MP 087 **Trace aldehydes in alcohol and drinking water using on-fiber derivatization SPME Arrow and GC/TQ**; Amy Cuthbertson[1]; Erinn M O'Neill[1]; Matthew Curtis[2]; *[1]Agilent Technologies, Wilmington, DE; [2]Agilent, Santa Clara, CA*

MP 088 **Quantitation of Microcystins and Nodularin in Drinking Water Samples to Meet EPA Method 544 Requirements Using QSight LC/MS/MS**; Milan Mitich[1]; Jacob Jalali[1]; VICTOR CAI[1]; Autumn Payne[1]; *[1]PerkinElmer US, LLC, Shelton, CT*

MP 089 **High-Resolution Mass Spectrometric Determination of Siderophores Produced by Sonoran Desert-Adapted Bacteria**; Kimber Focke[1]; Avril Perez[1]; Malak Tfaily[1]; *[1]University of Arizona, Tucson, AZ*

MP 090 **Revealing hidden marine dissolved organic sulfur using optimized sequential SPE and chromatography coupled with high-resolution mass spectrometry**; Jacquelyn R Jones[1]; Bashar Amer[2]; Susan S. Bird[2]; Hussain Abdulla[1]; *[1]Texas A&M University- Corpus Christi, Corpus Christi, TX; [2]ThermoFisher Scientific, San Jose, CA*

MP 091 **Simplifying PFAS analyses in fish tissue with an improved dual bed solid-phase extraction workflow**; Alexis Shelow[1]; Jason Hoisington[1]; Diego A Lopez[1]; Elena Gairloch[1]; Ramkumar Dhandapani[1]; *[1]Restek Corporation, Bellefonte, PA*

MP 092 **PFAS analysis using a novel triple quadrupole mass spectrometer: EPA 533 and 1633A**; Craig Butt[1]; Holly Lee[2]; Phil Bassignani[3]; Nathan Sorelle[3]; *[1]SCIEX, Marlborough, MA; [2]SCIEX, Concord, ON; [3]Pace Analytical, Mansfield, MA*

MP 093 **Evaluating Data-Dependent Acquisition (DDA), Data-Independent Acquisition (DIA), and Intelligent Acquisition with AcquireX for High-Resolution Mass Spectrometry-Based Non-Targeted PFAS Analysis**; Siyu Li[1]; Cynthia Adebayo[2]; Jeremy Koelmel[3]; Katherine E. Manz[2]; *[1]Department of Chemistry, University of Michigan, Ann Arbor, MI; [2]Department of Environmental Health Sciences, University of Michigan School of Public Health, Ann Arbor, MI; [3]Department of Environmental Health Sciences, Yale School of Public Health, New Haven, CT*

MP 094 **Applying a Novel Breath Sampling Device to Evaluate Longitudinal Changes in Per- and Polyfluoroalkyl Substances (PFAS) from Human Alveolar Spaces**; Elijah A Bliss[1]; Peter Stambeck[2]; Jack Henion[3]; Kara M. Joseph[1]; James N Dodds[1]; Erin S. Baker[1]; *[1]Department of Chemistry, University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]Munkplast AB, Uppsala, Sweden; [3]Advion Interchim Scientific, Ithaca, NY*

MP 095 **Trace Quantitation of Multiple Polycyclic Aromatic Hydrocarbon Classes in Marine Sediment Using Gas Chromatography with Time-of-Flight Mass Spectrometry**; Emma L. Macturk[1]; David E. Alanso[1]; Joseph E Binkley[1]; Gregg Tomy[2]; Nipuni Vitharana[2]; Zhe Xia[2]; John M Hayes[1]; Katie Redinius[1]; *[1]LECO Corporation, Saint Joseph, MI; [2]Centre for Oil and Gas Research and Development, University of Manitoba, Winnipeg, MB*

MP 096 **PFAS Screening by Real-Time Tandem Mass Spectrometry**; Seyyedhadi Khatami[1]; Sarah Waller[1]; Jenna Covey[1]; Thilani Anthony[1]; Marlene Moskowitz[1]; Samuel Putnam[1]; Marc Chalom[1]; Jeffrey Zonderman[1]; Francois A. Espourteille[1]; *[1]Bruker Scientific LLC, Billerica, MA*

MP 097 **Solvent Extraction and Thermal Decomposition ICP-MS Data Combined with UV-Vis and EPR Spectroscopy Reveals Metal Speciation in Asphaltenes**; Bismark A Nyaaba[1]; Sahil Makhani[2]; Thanuja M Thilakarathna[2]; Patrick J Farmer[2]; Touradj Solouki[2]; *[1]Baylor university, Waco, TX; [2]Baylor University, Waco, TX*

MP 098 **Characterization and Differentiation of Linear and Branched Perfluorooctanoic acid (PFOA) Isomers using MALDI-MS Coupled with Trapped Ion Mobility Spectrometry (TIMS)**; Kira Baker[1]; Tian (Autumn) Qiu[1, 2]; *[1]Department of Chemistry, Michigan State Univeristy, East Lansing, MI; [2]Center for PFAS Research, Michigan State University, East Lansing, MI*

MP 099 **Identification of Novel Chlorine-Resistant Anabaenopeptins in Lake Erie using UHPLC-HRMS/MS: Implications for Drinking Water Safety**; Sharmila I Thenuwara[1]; Judy A Westrick[1]; Jeremy Kodanko[1]; Dragan Isailovic[2]; *[1]Wayne State University, Detroit, MI; [2]University of Toledo, Toledo, OH*

MP 100 **High School Student–Led LC–MS Method Development for Urban Waterway Analysis**; Alejandra Perez-Brizuela[1]; Francisco Castro[1]; Susana Galindo[1]; Gustavo Sanchez[1]; Danna Zavaleta[1]; Karen L. Lohnes[2]; Felix Grun[3]; *[1]Huntington Park Institute of Applied Medicine at Linda Marquez High School, Huntington Park, CA; [2]LAUSD/UCLA Extension, Los Angeles, CA; [3]UCI, Irvine, CA*

MONDAY POSTERS

MP 101 **Multiple Isotopologue and Charge State Reaction Monitoring Approach for High-throughput Quantification of Microcystin-LR in Water Using LC-MS/MS**; Yohan Chandika Yasanga Sudusingha[1]; Dragan Isailovic[1]; *[1]University of Toledo, Toledo, OH*

MP 102 **Non-Target Analysis of Runoff Waters from Urban Fires Using LC/QTOF-MS "Finding Nylon Degradation Products in a Drinking-Water Sources"**; Michael Thurman[1]; Imma Ferrer[2]; Elizabeth Almasi[3]; James Pyke[4]; *[1]University of Colorado, Boulder, CO; [2]University of Colorado Boulder, Boulder, CO; [3]Agilent Technologies, Santa Clara, CA; [4]Agilent Technologies, Inc., Santa Clara, CA*

MP 103 **Metabolomic Evidence of Per- and Polyfluoroalkyl substances-Induced Disruption in Mung Bean (Vigna radiata) Root TCA Cycle Bioenergetics**; Amrita Dhakal[1]; Samira Mahdi[1]; Adenike Adeyeye[1]; Niya Tu[1]; Ruipu Mu[2]; Qingbo Yang[1]; *[1]Lincoln University of Missouri, Jefferson City, MO; [2]University of Health Sciences and Pharmacy in St Louis, St Louis, MO*

MP 104 **Analysis of fluorescently derivatized anatoxins using LC-FLD-MS**; Buddhima N P Thelge[1]; Dragan Isailovic[1]; *[1]University of Toledo, Toledo, OH*

MP 105 **Planetary-scale metabolomics uncovers the widespread presence of xenobiotics in marine ecosystems**; Tilman Schramm[1]; Maxence Derbez-Morin[2]; Laura Carretero Santos[2]; Yourae Shin[1]; Abzer K Pakkir Mohamed Shah[2, 3]; Rithi Krishnaraj[2]; Mingxun Wang[2]; Jarmo-Charles Julian Kalinski[2, 4]; Daniel Petras[1]; *[1]University of California Riverside, Riverside, CA; [2]University of California, Riverside, Riverside, CA; [3]University of Tuebingen, Tuebingen, Germany; [4]Rhodes University, Grahamstown, South Africa*

MP 106 **Matrix-Dependent Photooxidative Transformation of Tire Wear Particle–Derived Additives**; Leah M Cogar[1]; Nigel Lascelles[1, 2, 3]; Justin Elliott[1]; Hussain Abdulla[1]; *[1]Texas A&M University-Corpus Christi, Corpus Christi, TX; [2]Harte Research Institute for Gulf of Mexico Studies, Corpus Christi, TX; [3]National Oceanic and Atmospheric Administration Center for Coastal and Marine Ecosystems, Charleston, SC*

MP 107 **Evaluating the potential of thermal evaporation for onsite retention of per- and polyfluoroalkyl substances (PFAS) in landfill leachate**; Alina S. Timshina[1]; Allison R Cerlanek[1]; Ashley M. Lin[1]; Timothy G. Townsend[1]; John A. Bowden[1]; *[1]University of Florida, Gainesville, FL*

MP 108 **Bridging Chemical Threat Preparedness and Public Health Biomonitoring: Advanced Analytical Capabilities of a CDC LRN-C Level 1 Laboratory**; Ruth Muchiri; *New Mexico State Department of Health, Albuquerque, NM*

MP 109 **Non-target profiling of the wastewater metabolome across diverse treatment plants using a suite of HRMS tools(GC-TOF/MS, RPLC-TOF/MS and HILIC-TripleTOF/MS)**; Damia Barcelo[1]; Montserrat Carrascal[2]; Joaquin Abian[2]; Ester Sanchez-jimenez[2]; Antoni Ginebreda[3]; *[1]UNIVERSITY OF ALMERIA, Almeria, Spain; [2]Biological and Environmental Proteomics, IIBB-CSIC/IDIBAPS, Barcelona, Spain; [3]Institute of Environmental Assessment and Water Studies, IDAEA-CSIC, Barcelona, Spain*

MP 110 **Targeted and Suspect Screening of PFAS Using LC-Q/TOF HRMS in a Snowmelt-Dominated River-Reservoir System**; Junhan Chen[1]; Jonah Riggs[1]; Carmen N. Maruri[1]; Zane J. Sandall[1]; Christopher M. Tracy[1]; Jaron C. Hansen[1]; *[1]Department of Chemistry and Biochemistry, Brigham Young University, Provo, UT*

MP 111 **Pan-European Airborne Chemical Exposomics in Indoor and Outdoor Air: Integrating Passive Sampling, Comprehensive HRMS Analysis and Toxicological Metadata**; Adrià Sunyer-Caldú[1]; Jean Froment[2]; Pawel Rostkowski[2]; Stefano Papazian[1, 3]; Jonathan W. Martin[1, 3]; *[1]Department of Environmental Science (ACES, Exposure & Effects), Science for Life Laboratory, Stockholm University, Stockholm, Sweden; [2]Department of Environmental Chemistry and Health Effects, NILU, Kjeller, Norway; [3]National Facility for Exposomics, Science for Life Laboratory, Solna 171 65, Sweden, Solna, Sweden*

MP 112 **Toward Perfluorome-Scale Screening: Development of a Workflow for Rapid PFAS Monitoring**; Aryan D. Patel[1]; Catherine E. Mullins[1]; Yiran Liu[1]; Douglas I. Walker[1]; *[1]Gangarosa Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, GA*

MP 113 **High-Throughput Quantitation of 57 Per- and Polyfluoroalkyl Substances in Human Serum via Magnetic Solid-Phase Extraction Coupled with LC-MS/MS**; Ziqing Kong[1]; Wei Jia[1]; Anxian Huang[1]; Xue Zhang[1]; Aiping Yu[1]; Pengyun Liu[1]; Huafen Liu[1]; [1]*CALIBRA Scientific, Inc, Hangzhou, China*

MP 114 **Exposomics Survey Reveals Community Trends in Non-Targeted Analysis Workflows in Lipidomics, Metabolomics, Proteomics, and Xenobiotics analysis**; Jeremy Koelmel[1]; Fanny Chu[2]; Randolph R. Singh[3]; Sophie Thuault-Restituito[3]; Abigail Melican[3]; Thomas O. Metz[2]; Krystal J. Godri Pollitt[1]; [1]*Yale University, New Haven, CT;* [2]*Pacific Northwest National Laboratory, Richland, WA;* [3]*Columbia University, New York, NY*

MP 115 **Qualitative and Quantitative Analysis on Human PFAS Exposure Profiles: A Comparison Across Global Cohorts**; Sheng Liu[1]; Jeremy Koelmel[1, 2]; Elizabeth Ziying Lin[1]; Krystal J. Godri Pollitt[1]; [1]*Yale University, New Haven, CT;* [2]*Innovative Omics, Sarasota, FL*

MP 116 **A Hybrid Analytical Workflow Using Automated Extraction for PFAS Quantitation and Exposomics Profiling**; Jihyun Kang[1]; Michaela Schwaiger-Haber[1]; Byoungsook Goh[1]; Gary Patti[1]; [1]*Washington University in St.Louis, St.Louis, MO*

MP 117 **Development of a High-Throughput Quantification Method for Occupational Benzene and Toluene Exposure Using Urinary Biomarkers by LDTD–MS/MS**; Serge Auger[1]; Mégane Moreau[1]; Pierre Picard[1]; Sarah Demers[1]; Jonathan Rochon[1]; Jean Lacoursière[1]; [1]*Phytronix Technologies, Quebec, QC*

MP 118 **How Can High-Resolution Mass Spectrometry Help Resolve Ongoing Controversies in MNP Measurement in Human Biospecimens?**; Kuanliang Shao[1]; Ronnie Smith[1]; Christian Freeman[1]; Parth Jariwala[1]; Mattie Braselton[1]; Nelly Saenen[2]; Amanda Durkin[3]; Runyu Zou[3]; YIngyue Ni[4]; Bethany Knox[5]; Mariona Bustamante[5]; Tim Nawrot[2]; Martine Vrijheid[5]; Roel Vermeulen[3]; Douglas I. Walker[1]; [1]*Emory University, Atlanta, GA;* [2]*Hasselt University, Hasselt, Belgium;* [3]*Utrecht University, Utrecht, Netherlands;* [4]*Boston University, Boston, MA;* [5]*Barcelona Institute of Global Health, Barcelona, Spain*

MP 119 **Characterizing the Placenta Exposome: High-Resolution Mapping of Maternal Chemical Exposures that Transfer to the Placental**; Tom Cohen[1]; Ashima Mehta[1]; Douglas V. Guzior[1]; Caitlin Kelly[1]; Sandeep Acharya[1]; Sharla Friend[1]; Kathleen Fisch[2]; Kevin Cho[1, 3]; Gary Patti[1, 3]; Adam Richardson[1]; Ethan Stancliffe[1]; Monil Gandhi[1]; [1]*Panome Bio, Saint Louis, MO;* [2]*UC San Diego, San Diego, CA;* [3]*Washington University in St.Louis, St.Louis, MO*

MP 120 **To DIA or not to DIA? Comparison of MS/MS acquisition and data-processing strategies for untargeted chemical exposomics**; Triston Groff[1]; Byoungsook Goh[2]; Jihyun Kang[2]; Michaela Schwaiger-Haber[2]; Kevin Cho[2]; Gary J Patti[2]; [1]*Washington University in St. Louis, St. Louis, MO;* [2]*Washington University in St.Louis, St.Louis, MO*

MP 121 **Assessment of Blood Plastic-Associated Exposomes by Mass Spectrometry Reveals an Association with Lung Cancer Mortality**; Ranran Wu[1]; Ehsan Irajizad[1]; Johannes Fahrmann[1]; Hamid Khoshfekr Rudsari[1]; Jennifer Dennison[1]; Edwin Ostrin[1]; Jaffer Ajani[1]; Sam Hanash[1]; [1]*MD Anderson, Houston, TX*

MP 122 **Ion mobility lipidomics reveals early lipid remodeling preceding cytotoxicity during low-level cadmium exposure**; Fernanda Sousa Monteiro[1, 2]; Tobias Wong[1]; Adriana Zardini Buzatto[1, 2, 3]; [1]*University of Calgary, Calgary, AB;* [2]*Calgary Metabolomics Research Facility (CMRF), Calgary, AB;* [3]*Alberta Centre for Advanced Diagnostics (ACAD), Calgary, AB*

MP 123 **Early lipid remodelling in human liver cells under exposure-relevant PFAS conditions**; Tobias Wong[1]; Fernanda Sousa Monteiro[1, 2]; Adriana Zardini Buzatto[1, 2, 3]; [1]*University of Calgary, Calgary, AB;* [2]*Calgary Metabolomics Research Facility (CMRF), Calgary, AB;* [3]*Alberta Centre for Advanced Diagnostics (ACAD), University of Calgary, Calgary, AB*

MP 124 **Capturing Consumer Product Chemical Profiles of Individualized Exposures: Real-world Exposomics as Large-capacity Modeling Source (REALMS)**; Kristin A Favela[1]; William Watson[1]; Jake Janssen[1]; Sarah Palmeri[1]; Christopher Gonzalez[1]; [1]*Southwest Research Institute, San Antonio, TX*

MP 125 **Multi-metric ICP-MS fingerprinting of Diwali firework metals in PM2.5 aerosols**; Radhey Shyam[1]; Ini Afia[2]; *[1]Agilent Technology India, Manesar, India; [2]Agilent Technologies, Inc., Santa Clara, CA*

MP 126 **Development of a Universal Chromatography MS System by Combining SFC and Dielectric Barrier Discharge Ionization**; Ciara Conway[1]; Jan-Christoph Wolf[1]; Christoph Haisch[2]; Jan Bucek[1]; *[1]Plasmion, Augsburg, Germany; [2]Technical University of Munich, Freising, Germany*

MP 127 **Target and Suspect Screening of Endogenous and Exogenous Chemicals in Silicone Wristbands**; Guomao Zheng; *Southern University of Science and Technology, Shenzhen, China*

MP 128 **Deciphering the Exposome by Unconventional Mass Spectrometric Approaches**; Benedikt Warth; *University of Vienna, Vienna, Austria*

MP 129 **Measuring Pesticides and Environmental Pollutants in Human Plasma Using GC-QQQ: Novel Extraction, Novel Injection, and Ultra-Sensitive GC/MS-QQQ**; Daniel D Smith[1]; Anastasia Andrianova[2]; Daniel J Cuthbertson[2]; Ipsita Chakraborty[3]; Jeffrey G McDonald[3]; *[1]UTSouthwestern Medical Center, Dallas, TX; [2]Agilent Technologies, Santa Clara, CA; [3]UT Southwestern Medical Center, Dallas, TX*

MP 130 **High-Sensitivity Drug and Microbial Metabolite Detection in Environmental Study Samples with Untargeted Fragment Ion and CCS Screening**; Beixi Wang[1]; Haoqi Nina Zhao[2, 3]; Birgitta Ryback[4]; Victoria Deleray[2]; Liling Fang[1]; Xuejun Peng[1]; Erica M Forsberg[1]; *[1]Bruker Scientific LLC, San Jose, CA; [2]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [3]Department of Civil and Environmental Engineering, Stanford University, Stanford, CA; [4]Bruker Scientific LLC, Billerica, MA*

MP 131 **Improving Annotation Confidence to Enable Quantitative LC–MS Analysis of Phase II Metabolites for Environmental Exposure Assessment**; Jin Y Chen[1]; Breandon Taylor[1]; Tatiana Krivokhizhina[1]; Zhengzhi Xie[1]; Pawel Lorkiewicz[1]; Sanjay Srivastava[1]; *[1]University of Louisville, Louisville, KY*

MP 132 **The Ongoing Development of a Mass Spectrometry Resource for the Untargeted Metabolomic Profiling of the Chemical Exposome**; Megan R Nelson[1]; Haoqi Nina Zhao[2]; Pieter C. Dorrestein[2]; *[1]University of California, San Diego, La Jolla, CA; [2]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA*

MP 133 **Evaluation of supramolecular solvent (SUPRAS)-based extraction as an alternative to solid phase extraction (SPE) for extended urinary exposome profiling**; Žan Rekar[1, 2]; Riccardo De Santo[3]; Stefanela Stevanović[4]; Helena Plešnik[1, 2]; Tarek Moufawad[5]; Jean-Philippe Antignac[5]; Baninia Habchi[6]; Sophie Ndaw[6]; Katrin Vorkamp[7]; Linyan Zhu[7]; Emilien L. Jamin[8]; Anna Laura Iamiceli[9]; Tina Kosjek[1, 2]; *[1]Department of Environmental Sciences, Jožef Stefan Institute, Ljubljana, Slovenia; [2]Jozef Stefan International Postgraduate School, Ljubljana, Slovenia; [3]Department of Chemistry, Sapienza University, Rome, Italy; [4]Faculty of Computer and Information Science, University of Ljubljana, Ljubljana, Slovenia; [5]Oniris, INRAE, LABERCA, Nantes, France; [6]Department of Toxicology and Biomonitoring, INRS, Vandoeuvre-Lés-Nancy, France; [7]Department of Environmental Science, Aarhus University, Roskilde, Denmark; [8]Toxalim, Université de Toulouse, INRAE, ENVT, EI-Purpan, Toulouse, France; [9]Department of Environment and Health, Italian National Institute for Health, Rome, Italy*

MP 134 **Real-Time Measurements of PFAS Emissions in Air from Consumer Chemical Products Using Chemical Ionization Mass Spectrometry**; Maya Abou-Ghanem[1]; Joel R. Kimmel[1]; Spiro Spiro Jorga[2]; Veronika Pospisilova[2]; Omar El Hajj[1]; Abigail Koss[1]; *[1]TOFWERK, Boulder, CO; [2]TOFWERK, Thun, Switzerland*

MP 135 **Structural similarity guided design of internal standards for exposure science enabling class based normalization in untargeted metabolomics studies**; Kruttika Dabke[1]; Jennifer Kyle[2]; Tao Liu[2]; Jiajun Lei[1]; Jerry S.H. Lee[1, 3, 4, 5, 6]; Jonathan E. Katz[1, 3, 5, 6]; *[1]Ellison Medical Institute, Los Angeles, CA; [2]Biological Sciences Division, Pacific Northwest National Laboratory, Richland, WA; [3]Murtha Cancer Center/Research Program, Uniformed Services University of the Health Sciences/Walter Reed National Military Medical Center, Bethesda, MD; [4]Department of Chemical Engineering and Material Sciences, Viterbi School of Engineering, University of Southern California, LOS ANGELES, CA; [5]Dornsife College* *of Letters, Arts and Sciences, University of Southern California, Los Angeles, CA; [6]Department of Medicine, Keck School of Medicine, University of Southern California, Los Angeles, CA*

MP 136 **A Streamline Skyline and R-Programming Data Analysis Pipeline for Quality Insurance and Quantitation of Microplastics in Biological Samples**; Christian D Freeman[1]; Kuanliang Shao[1]; Ronald Smith[1]; Parth Jariwala[1]; Douglas I. Walker[1]; *[1]Gangarosa Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, GA*

MP 137 **DNA length in a DNA:protein complex determines surface collision products**; Zihao Qi[1, 2]; Carter T. Wheat[3, 4]; Charles E. Bell[3, 4]; Vicki H. Wysocki[1, 2]; *[1]School of Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA; [2]Native MS Guided Structural Biology Center, Georgia Institute of Technology, Atlanta, GA; [3]Department of Biological Chemistry and Pharmacology, The Ohio State University, Columbus, OH; [4]Ohio State Biochemistry Program (OSBP), The Ohio State University, Columbus, OH*

MP 138 **Employing nature to do the dirty work: Amino acid chains for selective actinide binding**; Amanda R. Bubas[1]; Richard M Cox[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

MP 139 **Quantum Tunneling and Two-State Reactivity in Co^+–Acetic Acid Activation Probed by SPIDRR Molecular-Beam Mass Spectrometry**; Simon Udochukwu Okafor; *Baylor University, Waco, TX*

MP 140 **Systematic Evaluation of Gas Dynamics and Electrospray Emitter Position as Reagent-Free Supercharging Methods for Native Mass Spectrometry**; Haocheng Qian[1]; Addison E. Bergman[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

MP 141 **Bringing the heat: Infrared irradiation on a Orbitrap Tribrid Mass Spectrometer Expand the Toolkit for Biomolecule Characterization**; Josh Hinkle[1]; Graeme C. McAlister[1]; Kyle P. Bowen[1]; Lilian Heil[1]; Jingjing Huang[1]; David Bergen[1]; Rafael Melani[1]; Christopher Mullen[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

MP 142 **Determination and Implications of Transition State Thermodynamic Parameters for Lysophospholipid Dissociation Using Dipolar DC Kinetics**; Katherine J. Lee[1]; Samantha A. Mehnert[1]; Scott A. McLuckey[1]; *[1]Purdue University, Department of Chemistry, West Lafayette, IN*

MP 143 **Exploring the benefits of collision induced dissociation (CID) prior ultra-violet photodissociation (UVPD)**; Mircea Guna[1]; Anjali Chelur[1]; Yves Le Blanc[2]; *[1]SCIEX, Concord, ON; [2]SCIEX, Concord, On, ON*

MP 144 **Not All Subunits Are Equal: Context-Dependent Structural Stability Revealed by Tandem SID-CIU on a Cyclic Ion Mobility Platform**; Rowan Matney[1]; Varun V Gadkari[1]; *[1]University of Minnesota, Minneapolis, MN*

MP 145 **Structural assignment of [An, O, H]+ from inductively coupled plasma tandem mass spectrometry collision induced dissociation reactions**; Richard Cox[1]; Amanda R. Bubas[1]; Amanda D. French[1]; Wenjin Cao[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

MP 146 **The interplay of coordination sites and oxidation states in temperature-controlled N2 absorption through stepwise activation and reduction of Co3O(OAc)6·Py3+**; Fabian S Menges[1]; Madeeha Salik[1]; Gereon Niedner-Schatteburg[2]; Mark A. Johnson[1]; *[1]Yale University, New Haven, CT; [2]RPTU, Kaiserslautern, Germany*

MP 147 **Infrared Photon-Assisted Electron-Based Activation Enables Multi-level Intact and Subunit Analysis of Antibody Modalities**; Linda B Lieu[1]; Amy K Carfagno[1]; Cynthia Nagy[1]; Jingjing Huang[2]; Rafael Melani[2]; Luca Fornelli[1]; *[1]University of Oklahoma, Norman, OK; [2]Thermo Fisher Scientific, San Jose, CA*

MP 148 **Collision-Induced Dissociation of Heme from Electrosprayed Protein Ions**; Evelyn H MacKay-Barr[1]; Nyanasoundari Lourdsamy[1]; Lars Konermann[1]; *[1]University of Western Ontario, London, ON*

MP 149 **S-nitrosylation enables selective Radical-Directed Dissociation (RDD) and Radical initiated Photodissociation (RIPD) from intact proteins**; Aidan G Purcell[1]; Ryan R Julian[2]; *[1]University of California, Riverside, Riverside, CA; [2]University of California, Riverside, CA*

MP 150 **De novo Sequencing of Intact Proteins by Radical-Initiated Photodissociation**; Jessica T Lee[1]; Hill Harman[2]; Ryan R. Julian[2]; *[1]University of California Riverside, Riverside, CA; [2]University of California, Riverside, CA*

MP 151 **Variable-Depth Surface Composition Measurements of Microplastics Using Matrix Assisted Laser Desorption Ionization (MALDI) Mass Spectrometry Enabled by Machine Learning**; Samantha Kruse[1]; Corey Carlos[1]; Mohammad Shohel[1]; David Schafer[1]; Trinity Griffus[1]; Brynal Benally[1]; Steve Storch[1]; Jake Zenker[1]; Andres Sanchez[1]; Jessica Kustas[1]; Ryan D Davis[1]; *[1]Sandia National Laboratories, Albuquerque, NM*

MP 152 **De novo sequencing of multi-charged peptides in the new physical dimension enabled by the Orbitrap Astral MS**; Hamish Stewart[1]; Sophia Steigerwald[1]; James Zachary Tarrant[2]; Sunan Xu[3]; Marina Edelson-Averbukh[2]; Alexander A. Makarov[1]; Pavel Pevzner[4]; Vitali Averbukh[2]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Imperial College London, London, United Kingdom; [3]University of California San Diego, San Diego, CA; [4]University of California San Diego, La Jolla, CA*

MP 153 **Analyzing native and digested proteins in picolitre aerosol droplets using droplet-assisted ionization mass spectrometry**; Edward Neal[1]; Archie Ramsden[1]; Jim S Walker[1]; Bryan R Bzdek[1]; *[1]University of Bristol, Bristol, United Kingdom*

MP 154 **Thin Film Reaction Acceleration by Spin Coating**; Courtney Yelton[1]; Ryan Saltzman[1]; Patrick W. Fedick[1]; *[1]Naval Air Warfare Center Weapons Division, China Lake, CA*

MP 155 **Liquid chromatography and cyclic ion mobility to the rescue of mass spectrometry for investigating challenging photoswitching samples**; Thomas Robert[1]; Benjamin Tassignon[1]; Gwendal Henrard[1]; Quentin Duez[1]; Ali Syed[1]; Céline Bette[1]; Philippe Dugourd[2]; Julien De Winter[1]; Fabien Chirot[2]; Pascal Gerbaux[1]; *[1]University of Mons, Mons, Belgium; [2]University Claude Bernard Lyon 1, Lyon, France*

MP 156 **Suspension-based Sample Preparation for Laser-Induced Acoustic Desorption Increases Signal Intensity in Mass Spectrometry Experiments**; David S. Toba-Veloza[1]; Kawthar Z. Alzarieni[2]; Bright H. Adu[1]; Hendrik M. Ma[1]; Jaskiran Kaur[1]; Voislav Blagojevic[3]; Hilkka I. Kenttämaa[1]; *[1]James Tarpo Jr. and Margaret Tarpo Department of Chemistry, Purdue University, West Lafayette, IN; [2]Jordan University of Science & Technology, Department of Medicinal Chemistry and Pharmacognosy, Irbid, Jordan; [3]BrightSpec Inc., Charlottesville, VA*

MP 157 **Nanometer-scale carbon nanotube field-effect transistor mass analyzer**; Namita Narendra[1]; Christina Ferreira[2]; R. Graham Cooks[3]; Tillmann Kubis[1]; *[1]Elmore Family School of Electrical and Computer Engineering, Purdue University, West Lafayette, IN; [2]Bindley Bioscience Center, Purdue University, West Lafayette, IN; [3]Purdue University Dept of Chemistry, West Lafayette, IN*

MP 158 **Comparing the Energy Consumption of Different LC Single Quadrupole Mass Spectrometry Systems**; John Wright[1]; Sue D'Antonio[2]; Naomi Serillo[3]; *[1]Agilent, Troy, MI; [2]Agilent Technologies Inc., Santa Clara, CA; [3]Agilent Technologies, Wilmington, DE*

MP 159 **Laser Rehydration of Cryogenically Soft-Landed Particles Improves Structural Similarity to Native Proteins**; Dylan Forbes[1]; Colin A Hemme[1]; Drew Jordahl[1]; Mitchell D Probasco[1]; Mark Scalf[1]; Keaton L Mertz[1]; Austin Z Salome[1]; Kenneth W Lee[1]; Michael S Westphall[1]; Scott T Quarmby[1]; Timothy Grant[1]; Joshua J Coon[1]; *[1]University of Wisconsin-Madison, Madison, WI*

MP 160 **Thin-Films via Paperspray Ionization-Mass Spectrometry and Raman Spectroscopy of SERS Substrates: A Comparison in Reaction Monitoring**; Elise E. Tseng[1]; Patrick W. Fedick[1]; *[1]Naval Air Warfare Center Weapons Division, China Lake, CA*

MP 161 **From Local Descriptors to Mass Spectra: New Insights into the Chemoselective Synthesis and Reactivity of Schiff Base-Derived CNN-Pt Pincers**; Jorge Gabriel Ascencio Delgado[1]; Oracio Serrano Torres[1]; Katarzyna Dorota Wrobel[1]; Kazimierz Wrobel[1]; *[1]University of Guanajuato, Guanajuato, Mexico*

MP 162 **Assessing Water Vapor-Driven Deuterium Loss Across Different MS Platforms**; Julien Margaret A. Dagan[1]; Alesi R. Escobedo[1]; Anran Yu[1]; Miklos Guttman[1]; *[1]University of Washington, Seattle, WA*

MP 163 **Enabling Epitope Analysis of Glycoproteins via HDX-MS Using Antigens with Uniformed N-linked Glycans**; Ayako Kurimoto[1]; Ilker Sen[1]; *[1]Protein Metrics LLC, Boston, MA*

MP 164 **Site Specific Hydrogen Deuterium Exchange Mass Spectrometry Enables Deep Explorations of Dynamic Allosteric Networks in Protein-Drug Interactions**; Joseph Anacleto[1, 2]; Esther Wolf[3]; Suzanne Ackloo[3]; Cheryl Arrowsmith[3]; Yves LeBlanc[4]; Cristina Lento[2]; Derek Wilson[2]; *[1]Emeritus, Brampton, ON; [2]York University, Toronto, ON; [3]Structural Genomics Consortium, University of Toronto, Toronto, ON; [4]SCIEX, Concord, ON*

MP 165 **Effect of Quench Conditions on Deuterium Back-Exchange in Peptides and Protein in HDX-MS**; Sandeep Kumar[1]; Kyle W. Anderson[1, 2]; *[1]Institute for Bioscience and Biotechnology Research, National Institute of Standards and Technology, and the University of Maryland, College Park, Rockville, MD; [2]National Institute of Standards and Technology, Bioprocess Measurements Group, Biomolecular Measurement Division, Rockville, MD 20850, United States, Rockville, MD*

MP 166 **Optimized PNGase Rc In-line Deglycosylation Enables Robust HDX-MS of Glycoproteins: Applications to HIV-1 Envelope and Insulin Receptor Protein**; Shruti Nayak[1]; Theresa Buckley[1]; Sussane Walker[1]; Ioannis Manolaridis[1]; Paul Zuck[1]; David McLaren[1]; Haihong Zhou[1]; *[1]Merck & Co., Inc., Rahway, NJ*

MP 167 **Improving hydrogen/deuterium exchange efficiency in ESI-MS through a multi-method approach**; Jenna Lewis[1]; Young Jin Lee[1]; *[1]Iowa State University, Ames, IA*

MP 168 **HDXtend – Capturing Force-dependent conformations using a hybrid HDXMS workflow**; Ellie S Holden[1]; Justin Benesch[2, 3]; Dirk Aarts[2]; Lucia Parolini[2]; *[1]Ellison Institute of Technology, Oxford, United Kingdom; [2]University Of Oxford, Oxford, United Kingdom; [3]Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom*

MP 169 **Systematic Low-scrambling Calibrations for Single-Residue HDX-MS application on Thermo Scientific Orbitrap Tribrid Platforms**; Yuqi Shi[1]; Graeme McAlister[1]; Christopher Mullen[1]; Jia Tang[1]; Weijing Liu[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

MP 170 **Interleaved gentle/harsh targeted MS2 for negating the effects of hydrogen scrambling and achieving single amide HDX-MS**; Rebecca Skotheim[1]; Charlie Mundorff[1]; Lisa M Tuttle[1]; Peter Brzovic[1]; Rachel E Klevit[1]; Yuqi Shi[2]; Graeme C McAlister[2]; Miklos Guttman[1]; *[1]University of Washington, Seattle, WA; [2]Thermo Fisher Scientific, San Jose, CA*

MP 171 **Comprehensive study of trapped ion mobility implementation in HDX experiments: investigation of deuterium loss inside ion mobility**; Tomas Smrcka[1, 2]; Dmitry Loginov[1]; Alan Kadek[1]; Petr Man[1]; *[1]Institute of Microbiology CAS, Prague, Czech Republic; [2]Charles University, Prague, Czech Republic*

MP 172 **High-Throughput HX-MS^2 with Fragment-Based Validation in HDX Workbench**; Roberto Vera Alvarez[1]; Matthew Mann[2]; Timothy R. O'Leary[2]; Patrick R. Griffin[2]; Bruce Pascal[1]; *[1]Omics Informatics LLC, Honolulu, HI; [2]The Herbert Wertheim UF Scripps Institute for Biomedical Innovation & Technology, Jupiter, FL*

MP 173 **Internal Exchange Reporters as Tools for Verifying and Normalizing HDX-MS Experiments**; Clint Vorauer[1]; Miklos Guttman[1]; Taylor Murphree[1, 2]; *[1]University of Washington, Seattle, WA; [2]University of Manchester, Manchester, United Kingdom*

MP 174 **Fabrication of Silicon Electrospray Emitters with Embedded Microfluidic Mixers and Sheath Gas Lines for Microsecond Small Molecule H/D Exchange Analysis**; Neha Srikumar[1]; Seongsu Cho[1];

Vasant Iyer[1, 2]; Stephanie Yang[1]; David Issadore[1]; Benjamin Garcia[3]; *[1]University of Pennsylvania, Philadelphia, PA; [2]Northwestern University, Chicago, IL; [3]Washington University School of Medicine, St. Louis, MO*

MP 175 **Ultra-High throughput Microdroplet Digestion of Antibodies Enabled via RapidFire Mixing and Flow Injection Analysis**; Harsha Gunawardena[1]; Hao Chen[2]; Bhavin Patel[3]; Mike D. Knierman[4]; Peter T. Rye[5]; *[1]JOHNSON AND JOHNSON, Spring House, PA; [2]New Jersey Institute of Technology, Newark, NJ; [3]Johnson and Johnson, Malvern, PA; [4]Agilent Technologies, Santa Clara, CA; [5]Momentum Biotechnologies, Billerica, MA*

MP 176 **Enhancing speed and sensitivity: Integration of high-throughput acoustic ejection with next-generation QTOF MS**; Anuja Bhalkikar[1]; Han Wang[2]; John Gibbons[3]; Rahul Baghla[4]; *[1]Sciex, Framingham, MA; [2]SCIEX, Singapore, Singapore; [3]SCIEX, Concord, ON; [4]SCIEX, CA, CA*

MP 177 **Development of a miniaturized, automated, and high-throughput TMT workflow for C. elegans proteomics**; Valentine V Courouble[1]; Patricia K Dranchak[1]; Ravi Tharakan[1]; James Inglese[1]; Christopher A LeClair[1]; Dingyin Tao[1]; *[1]NIH/NCATS, Rockville, MD*

MP 178 **Ultra-high throughput proteomics at >500 samples/day using advanced Vanquish Neo UHPLC methods with Orbitrap Astral Zoom MS for screening applications**; Till Reinhardt[1]; Tabiwang N. Arrey[1]; Christopher Pynn[2]; Alec Valenta[2]; Andrius Žilionis[3]; Runsheng Zheng[2]; Eugen Damoc[1]; Martin Rendl[2]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientific, Germering, Germany; [3]Thermo Fisher Scientfic, Vilnius, Lithuania*

MP 179 **Enhancing AAV Analysis with Automated ELIT-CDMS Sample Delivery**; Rosie Upton[1]; Jakub Ujma[2]; Emily Christofi[2]; Anisha Haris[2]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Wilmslow UK, Wilmslow, United Kingdom*

MP 180 **High-Throughput MALDI-TOF-MS Analysis of Derivatized Triacetic Acid Lactone (TAL) from Random Mutagenesis ofR. toruloides**; Blake Mirman[1]; Quanhui Ye[1]; Andrew Crow[1]; Jonathan V Sweedler[1]; Yong-Su Jin[1]; *[1]University of Illinois Urbana Champaign, Urbana, IL*

MP 181 **The $10 proteome: low-cost, deep proteome profiling of limited samples using the Orbitrap Astral and timsTOF Ultra mass spectrometers**; Ryan Kelly[1]; Siqi Huang[1]; Chao Wang[1]; Hsien-Jung Lavender Lin[1]; *[1]Brigham Young University, Provo, UT*

MP 182 **Multicolumn LC System Enabling Single-Cell Proteomics at a Throughput of 288-500 Samples Per Day**; Chao Wang[1]; Hsien-Jung L Lin[1]; Thy Truong[2]; Siqi Huang[1]; Garrett D. Haynie[1]; Kenneth S. Triggs[1]; R. J. S. Miercort[1]; Jacob H. Clark[1]; Ella E. Norton[1]; YenJou Chang[1]; Xiaofeng Xie[2]; Ryan T. Kelly[1]; *[1]Brigham Young University, Provo, UT; [2]MicrOmics Technologies, Spanish Fork, UT*

MP 183 **Integrated Tools for Scripted Automation of Tuning, Review and Analysis Pipelines**; Philip M Remes[1]; Nicholas Shulman[2]; Cristina C. Jacob[1]; Courtney Patterson[1]; Qingling Li[1]; David Kotol[3]; Alan Atkins[1]; Wes Rodgers[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]University of Washington, Seattle, WA; [3]ProteomEdge, Stockholm, Sweden*

MP 184 **High-Throughput Mass Spectrometry Enables TDP2 Inhibitor Screening**; Yating Wang[1]; Emily Fu[1]; Stephen Mercer[1]; Brianne Dudiak[1]; Daniel Downes[2]; Darby Ball[2]; David Weis[2]; Jeffrey Tredup[2]; Susan Kiefer[2]; Liudmila Dzhekieva[2]; Deepa Rajasekaran[2]; Aparna Mukherjee[2]; Margarita Tararina[2]; YiTing Paung[2]; Jack Sloane[1]; Michelle Stewart[1]; Joanne Bronson[1]; Cheng-Yu Chen[1]; Travis Pemberton[1]; Zhigang Wang[1]; *[1]Bristol Myers Squibb, Cambridge, MA; [2]Bristol-Myers Squibb R&D, Princeton, NJ*

MP 185 **Developing a High-Throughput Methodology for Assessing Gross Nitrification Rates in Soil**; Jessica LaFond[1]; Dana Carper[1]; Stephen Zambrzycki[1]; Vilmos Kertesz[1]; John F. Cahill[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN*

MP 186 **Robust and High-Throughput Targeted Peptide Quantitation Using a Next-Generation Triple Quadrupole-Ion Source platform**; Qin Fu[1]; Katherine L. Walker[1]; Runsheng Zheng[2]; Neloni Wijeratne[3]; Charles E. Maxey[1]; Alec Valenta[4]; Huguet Romain[1]; Jennifer E. Van Eyk[5]; Kerry Hassell[1]; *[1]Thermo Fisher*

Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Germering, Germany; [3]Thermo Fisher Scientfic, San Jose, CA; [4]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [5]Cedars-Sinai Medical Center, LA

MP 187 **A High-Throughput Biocatalytic Platform for Screening Isomeric Kainoid Natural Products**; Robert A Shepherd[1]; Manasa Ramachandra[1]; Conrad Fihn[1]; Shaun McKinnie[1]; Laura Sanchez[1]; *[1]University of California, Santa Cruz, Santa Cruz, CA*

MP 188 **A Robust and Versatile Affinity Enrichment MS Platform Enabling 500 Interactomes Per Day for Systematic Protein Interaction Mapping**; Elisabeth Zollbrecht[1]; Louisa Grauvogel[1]; Tim Heymann[1]; André Clemens Michaelis[1]; Matthias Mann[1]; *[1]MPI of biochemistry, Planegg, Germany*

MP 189 **A Quantitative Comparison of Automated Desalting Methods for the High-Throughput Collision Induced Unfolding Analysis of Biotherapeutics Direct from Formulation**; Amanda Cicali[1]; Michael R. Armbruster[1]; Carter Asef[2]; Suraj Dhungana[2]; Mason Chilmonczyk[2]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI; [2]Andson Biotech, Atlanta, GA*

MP 190 **StageTip Automation Implementation on the MiniLab for High-throughput Proteomic Sample Preparation**; Gregory A Davidson[1]; Cheng Tse Huang[1]; Guotao Lu[1]; Xiaohui Zhang[1]; *[1]CDS Analytical LLC, Oxford, PA*

MP 191 **Accelerated Protein Engineering of Small Molecule Kinases using a High-Throughput Automated Ambient Mass Spectrometry Platform**; Nicolas M Morato[1]; Ahram Kim[2]; Prabir Saha[3]; Aqeel A Niyaz[3]; Rui Huang[3]; R. Graham Cooks[4]; Jared C Lewis[2]; *[1]Purdue University, West Lafayette, IN; [2]Indiana University, Bloomington, IN; [3]Indiana University, Bloomington; [4]Purdue University, West lafayette, IN*

MP 192 **High-Throughput Controlled Atmosphere Electrochemical Synthesis Enabled by Robotic Automation and Ambient-MS Screening**; Solita M. Wilson[1]; Elise E. Tseng[1]; Dana M. Pinson[1]; Benjamin G. Harvey[1]; Patrick W. Fedick[1]; *[1]Naval Air Warfare Center Weapons Division, China Lake, CA*

MP 193 **An integrated platform for high-throughput native mass spectrometry screening and thermodynamic profiling**; Hongyuan Yang[1]; Jiaxin Feng[1]; Raelyn Raygosa[1]; Xin Yan[1]; *[1]Texas A&M University, COLLEGE STATION, TX*

MP 194 **Multi-Level High Duty Cycle SLIM Board Design Enables Dual Path Ion Mobility Operation with Increased Dynamic Range and Throughput**; Mick Greer[1]; Liulin Deng[1]; Leonard C. Rorrer III[1]; Frederick Strathmann[1]; Daniel DeBord[1]; *[1]MOBILion Systems, Inc, Chadds Ford, PA*

MP 195 **Affinity Selection–Driven Hit Filtering Enhanced by Isotopic Envelope Shape Distance Scoring**; Chelsea Nikula[1]; Edward Waterman[2]; Edward Pallister[3]; Alexander Stolz[2]; Andrew Hayward[3]; Stephen Kok[4]; Reto Ossola[2]; Cameron Scott[5]; Juan Florez Weidinger[5]; Stephan Steigele[5]; John Huynh[4]; Matthew Green[3]; *[1]Genedata, Lexington, MA; [2]Genedata GmbH, Munich, Germany; [3]Genedata Ltd, Cambridge, United Kingdom; [4]Genedata Inc, San Francisco, CA; [5]Genedata AG, Basel, Switzerland*

MP 196 **High-Throughput Cysteine Chemoproteomics Workflow Enables Rapid Screening of Electrophilic Fragments at Proteome Scale**; Violette Gautier[1]; Marion Tondeur[1]; Guillaume Vink[1]; Pierre-Olivier Maux[1]; Philippe Fabre[1]; Till Kindel[2]; Giada Marino[2]; Nagarjuna Nagaraj[2]; Andreas Tebbe[1]; Rudy Aussel[1]; Marie Guillemot[1]; Catherine Pech[1]; Francois Autelitano[1]; *[1]Evotec SE, Toulouse, France; [2]Evotec International GmbH, Munich, Germany*

MP 197 **From 384-Wells to Actionable Insights in One Week: A High-Throughput Proteomics Pipeline Accelerating In Vitro Drug Safety Assessment**; Colten Eberhard[1]; Claire Martin[1]; Konstantin Barylyuk[2]; Santosh Renuse[1]; Benjamin Pullman[1]; Stewart MacArthur[3]; Navratan Bagwan[4]; Beatriz Roson[5]; Shivaprasad Patil[5]; Kevin Moreau[3]; Bhavik Chouhan[2]; Prasad Kamble[2]; Marco Maugeri[2]; Mansi Ved[2]; Jorrit Homberg[2]; Daisy Yuill[3]; Jurre Kamphorst[1]; *[1]AstraZeneca, Gaithersburg, MD; [2]AstraZeneca, Gothenburg, Sweden; [3]Astrazeneca, Cambridge, United Kingdom; [4]AstraZeneca, Bangalore, India; [5]AstraZeneca, Barcelona, Spain*

MP 198 **Accelerating Microbial Proteomics with Short-Gradient LC-DIA for High-Throughput Phenotyping**; Yuqian Gao[1]; Carrie D Nicora[1]; Kwame Attah[1]; Thomas L Fillmore[1]; Kyle R Pomraning[1]; Shuang Deng[1]; Jeffrey J Czajka[1]; Joonhoon Kim[1]; Meagan C Burnet[1]; Ron J Moore[1]; Paul D Piehowski[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

MP 199 **Discovery and Characterization of RAS Ligands Using Affinity Selection and Native Mass Spectrometry**; Peter T Rye[1]; Jeremiah Bowers[1]; Jillian Hartka[1]; Zane Thistleford[1]; Patrick O'Loughlin[1]; Christina Thompson[1]; Kevin Uggowitzer[1]; Aaron Wolfe[2]; Sekar Ramachandran[2]; William LaMarr[1]; Can Ozbal[1]; *[1]Momentum Biotechnologies, Billerica, MA; [2]Ichor Life Sciences, Syracuse, NY*

MP 200 **Automated High-Throughput UPLC-MS Quality Control Pipeline for Small Molecules in Pediatric Cancer Research**; Tharindu Ranathunge[1]; Mary Ashley Rimmer[1]; Nathaniel Twarog[1]; Sharnise Mitchell[1]; Mariana Santana Smith[1]; Carolina Adura[1]; Anang Shelat[1]; Lei Yang[1]; *[1]St Jude Children's Research Hospital, Memphis, TN*

MP 201 **Adapting Intact Mass LC-MS Workflows for High-throughput Protein Production**; Edward J. Hsieh[1]; Ashley Yoon[1]; Aiden Geha-Hsu[1]; Daniela Tomazela[1]; *[1]Gilead Sciences, Foster city, CA*

MP 202 **High Throughput Sensitive Chemical Analysis Using the Open Port Sampling Interface Coupled to HPLC/MS**; Vilmos Kertesz[1]; Jessica LaFond[1]; John F. Cahill[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN*

MP 203 **Cost-effective proteomics sample prep with just a pipettor: the EcoTip™**; Alia Sagatova[1]; Sandra Wilson[1]; John Wilson[1]; *[1]ProtiFi LLC, Fairport, NY*

MP 204 **High-Throughput Screening of SARS-CoV-2 Main Protease using Acoustic Ejection Native Mass Spectrometry**; Patrick J. Rudewicz[1]; Kerri Grove[1]; Liliana Pedro[1]; Weiping Jia[1]; Thomas Botzanowski[1]; Johanna M. Jansen[1]; Charles Wartchow[1]; Thomas R. Covey[2]; Chang Liu[2]; *[1]Novartis Biomedical Research, Emeryville, CA; [2]SCIEX, Concord, ON*

MP 205 **Multi-Method Drug Analysis in Human Plasma Using Fault-Tolerant High-Throughput LC-MS/MS System**; Yuki Suzuki[1]; Eishi Imoto[2]; Logan Miller[1]; Shohei Sato[1]; Vikki Johnson[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Shimadzu Corporation, Kyoto, Japan*

MP 206 **Real-time targeted proteomics assays with sample multiplexing and infrared photoactivation reveal alterations in functional cysteines during macrophage polarization**; Fangyi Zhai[1]; Daniel Richards[2]; Zixuan Ye[2]; Shaoxian Li[2]; Roger Davis[2]; Qing Yu[2]; *[1]Umass Chan Medical School, Worcester, MA; [2]UMass Chan Medical School, Worcester, MA*

MP 207 **A ‘dilute-and-shoot’ method for high-throughput glucose quantitation in fermentation medium using the ECHO MS system**; Jonas Rombout[1, 2]; Vermeersch Liesolotte[1]; Samuel Hanon[1]; Rebekah Sayers[3]; Paul RS Baker[4]; Cool Lloyd[1]; Kevin J Verstrepen[1]; *[1]VIB Laboratory for Systems Biology, VIB-KU Leuven Center for Microbiology, Leuven, Belgium; [2]CMPG Laboratory of Genetics and Genomics, Department M2S, KU, Leuven, Belgium; [3]SCIEX, Alderley Park, United Kingdom; [4]SCIEX, Homewood, AL*

MP 208 **From Intact to Subunits in Real Time: A High-throughput Integrated Online mAb Characterization using a Modified Orbitrap Tribrid Mass Spectrometer**; Rafael D Melani[1]; David Bergen[1]; Jingjing Huang[1]; Shari M Wheeler[2]; Jared Drader[2]; Andrew Norris[3]; Ales Holfeld[3]; Christopher Mullen[1]; Graeme C McAlister[1]; Philip Compton[2]; Kristina Srzentic[3]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Integrated Protein Technologies, Carlsbad, CA; [3]Thermo Fisher Scientific, Reinach, Switzerland*

MP 209 **A Cost-Efficient, Fully Automated High-Throughput Sample Preparation Platform Enabling Large-Scale Discovery Proteomics**; Maurine Fucito[1]; Stoyan Stoychev[1]; Pia H. Jensen[1]; Veronica Macaluso[1]; Adrian Hody[1]; Nicolai Bache[1]; Dorte B. Bekker-Jensen[1]; *[1]Evosep, Odense, Denmark*

MP 210 **Reproducible and robust plasma proteomics on Orbitrap Astral MS using an OptiSpray Ion Source and a novel high-throughput cartridge column**; Martins Jansons[1]; Joshua Silveira[2]; Katherine Walker[2]; Runsheng Zheng[3]; Alec Valenta[2]; Jared Deyarmin[2]; Stephanie N. Samra[2]; Maowei Dou[2];

Amirmansoor Hakimi[2]; *[1]Thermo Fisher Scientific, Vilnius, Lithuania; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Germering, Germany*

MP 211 **Enhanced Spatial Analysis of Cholesterol and Steroid Hormones with MALDI-MSI via DMAB-Based On-Tissue Chemical Derivatization**; Sophia Melnyk[1, 2]; Kelly Lu[1]; Andrew Schneider[3, 4]; Luigi Puglielli[3, 4]; Lingjun Li[1, 2]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Department of Medicine, University of Wisconsin-Madison, Madison, WI; [4]Waisman Center, University of Wisconsin-Madison, Madison, WI*

MP 212 **Characterizing Age-Driven Differences in Neck Vascular Mechanics and Brain Biochemistry in Healthy Murine Controls**; Allison Jones[1]; Anna Colleen Crouch[2]; *[1]University of Tennessee, Knoxville; [2]University of Tennessee, Knoxville, TN*

MP 213 **Multimodal Mass Spectrometry ImagingReveals Region-Specific GangliosideDysregulation in Alzheimer's Disease Brain**; Emily M Hubecky[1]; Hua Zhang[2]; Angelique Steenhagen[3, 4]; Luigi Puglielli[3, 4]; Lingjun Li[1, 2]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Department of Medicine, University of Wisconsin-Madison, Madison, WI; [4]Waisman Center, University of Wisconsin-Madison, Madison, WI*

MP 214 **Tandem Quadrupole DESI Imaging To Visualize Spatial Distribution of Gefitinib and Related Metabolites in Rat liver**; Anthony J Midey[1]; Robert Plumb[1]; Nikunj Tanna[1]; Ian D. Wilson[2]; *[1]Waters, Milford, MA; [2]Imperial College London, London, United Kingdom*

MP 215 **Use of an endoglycoceramidase in mass spectrometry imaging to visualize the localization of glycosphingolipid glycans in Ascaris suum**; Julia Dreifus[1]; Vanessa Gregory[1]; Edwin Escobar[1]; Jeremy Foster[1]; *[1]New England Biolabs, Ipswich, MA*

MP 216 **MALDI-IHC Workflow Implementation on an Atmospheric-Pressure MALDI Mass Microscope for a Panel of Mouse Cancer Protein Biomarkers**; Katarzyna Walendzik[1]; Ei-ichi Matsuo[2]; Jeffrey Dahl[3]; Toshiya Matsubara[3]; Joselin Velasco[1]; Adriana Ventura[1]; Shinichi Yamaguchi[2]; Philipp E. Scherer[1]; Ruth Gordillo[1]; *[1]UTSouthwestern Medical Center, Dallas, TX; [2]Shimadzu Corporation, Kyoto, Japan; [3]Shimadzu Scientific Instruments, Columbia, MD*

MP 217 **Metabolic insights of new biofilm treatments using mass spectrometry imaging**; Min Qiu[1]; Sandra Wiedbrauk[2]; Kathryn Fairfull-Smith[2]; Nicole Strittmatter[1]; *[1]Department of Bioscience, School of Natural Sciences, Technical University of Munich, Munich, Germany; [2]School of Chemistry and Physics, Centre for Materials Science, Queensland University of Technology, Brisbane, Australia*

MP 218 **MALDI Imaging for Forensic Analysis of Drug-Contaminated Fingerprints using a ion mobility QToF mass spectrometer**; Rohith Krishna[1]; Emmanuelle Claude[2]; James Langridge[2]; Laura Cole[1]; Robert Bradshaw[1]; Simona Francese[1]; *[1]Sheffield Hallam University, Sheffield, United Kingdom; [2]Waters Corporation, Wilmslow, United Kingdom*

MP 219 **Visualizing Neurotransmitter Localization: TPP Derivatization for Tissue and Single-Cell Mass Spectrometry Imaging**; Chen H. Sirois[1]; Hsi-Chun Chao[1]; Andrew G. Hamilton[1]; Jonathan V. Sweedler[1]; Stanislav S. Rubakhin[1]; *[1]University of Illinois Urbana-Champaign, Urbana, IL*

MP 220 **Depth-resolved spatial profiling of mobility-separated losartan degradation product isomers using MALDI-timsTOF imaging of serial tablet sections**; Rekha Thomas[1, 2]; Karina A Vargas[2]; Zhenqi Shi[1]; Christopher M. Crittenden[1]; Elizabeth Neumann[1]; *[1]Genentech, South San Francisco, CA; [2]UC Davis, Davis, CA*

MP 221 **Lipid Assessment of mice treated with anti-retroviral therapies and diet modulation using MALDI MSI**; Alyssa Espley[1]; Cory White[2]; Kyle Vanderschoot[1]; Dionna Williams[2]; Elizabeth Neumann[1]; *[1]UC Davis, Davis, CA; [2]Emory University, Atlanta, GA*

MP 222 **Chemical and metabolic alterations following hepatic artery thermoembolization in a swine model**; Erik Cressman[1]; Susanne J. Lin[1]; Erin H. Seeley[1]; *[1]MD Anderson, Houston, TX*

MP 223 **Mapping Autophagy-Associated Lipid Remodeling at Single-Cell Resolution in C4 Maize Using Mass Spectrometry Imaging**; Emily M. Hubecky[1]; Elissa Shan[1]; Charlotte Steelheart Molina[2]; Marisa S. Otegui[2]; Lingjun Li[1, 3]; *[1]UW-Madison Department of Chemistry, Madison, WI; [2]UW-Madison Center for Quantitative Cell Imaging, Madison, WI; [3]UW-Madison School of Pharmacy, Madison, WI*

MP 224 **Developing an Innovative Sample Preparation Protocol for Spatial N-Glycomics on Formalin-Fixed Paraffin Embedded and Fresh Frozen Tissues**; Heidi L. Vandyk[1]; Marija Velickovic[1]; Kumar Sharma[2]; Christopher R. Anderton[1]; Dusan Velickovic[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]University of Texas Health Science Center at San Antonio, San Antonio, TX*

MP 225 **Metabolite Profiling of the Optic Nerve Regeneration and Degeneration with AP/MALDI Tandem Mass Spectrometry Imaging**; Nivedita Bhattacharya[1]; Sean Meehan[2]; Caleigh Rose O'Connor[1]; Konstantin Novoselov[1]; Eugene Moskovets[1]; Sanjoy K Bhattacharya[2]; *[1]MassTech, Columbia, MD; [2]Bascom Palmer Eye Institute, Miller School of Medicine, University of Miami, Miami, FL, USA, Miami, FL*

MP 226 **High Resolution Imaging Mass Spectrometry (10 µm) of Gastric Tissue from Mongolian Gerbils Experimentally Infected with Helicobacter pylori**; Michelle Reyzer[1]; Gabrielle E. Fortier[1]; Timothy L. Cover[1, 2]; Kevin L. Schey[1]; Jeffrey M Spraggins[1]; *[1]Vanderbilt University, Nashville, TN; [2]Veterans Affairs Tennessee Valley Healthcare System, Nashville, TN*

MP 227 **Imaging the Metabolomic Landscape of Uveal Melanoma to Determine Key Biomarkers**; Georgia M Millard[1]; Neil A Cross[1]; Jennifer Clark[1]; Helen Kalirai[2]; Karen Aughton[2]; Laura M Cole[1]; *[1]Sheffield Hallam University, Sheffield, United Kingdom; [2]University of Liverpool, Liverpool, United Kingdom*

MP 228 **Stepwise Phosphate Derivatization for Unified and Enhanced Phospholipid Detection in Positive-Mode MALDI Mass Spectrometry Imaging**; Kelly Lu[1]; Wei Wilson Li[2]; Andrew Schneider[3, 4]; Luigi Puglielli[3, 4]; Lingjun Li[1, 2]; *[1]University of Wisconsin-Madison Department of Chemistry, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]University of Wisconsin-Madison, Department of Medicine, Madison, WI; [4]Waisman Center, University of Wisconsin-Madison, Madison, WI*

MP 229 **A Multiplatform Imaging Workflow for Spatially Resolved Metabolism and Drug Distribution in Pseudomonas putida Biofilms**; Daniel Smaje[1]; Andreas Baumeister[2]; Corné Tak[3]; Howbeer Muhamadali[1]; *[1]University of Liverpool, Liverpool, United Kingdom; [2]Shimadzu Europa GmbH, Duisburg, Germany; [3]Shimadzu Benelux, 's-Hertogenbosch, Netherlands*

MP 230 **Mapping Spatial Lipid Dynamics in Mouse Skin Across Telogen and Anagen Hair Cycle Phases**; Katarzyna Walendzik[1]; Ei-ichi Matsuo[2]; Jeffrey Dahl[3]; Toshiya Matsubara[3]; Adriana Ventura[1]; Shinichi Yamaguchi[2]; Philipp E. Scherer[1]; Ruth Gordillo[1]; *[1]UTSouthwestern Medical Center, Dallas, TX; [2]Shimadzu Corporation, Kyoto, Japan; [3]Shimadzu Scientific Instruments, Columbia, MD*

MP 231 **Characterization of Sulfated N-Linked Glycans in β-Catenin-Driven Murine HCC and Human Tissues**; Lily J. Harshaw[1]; Muhammed F. Bayram[1]; Satdarshan P. Monga[2]; Peggi M. Angel[1]; Richard R. Drake[1]; Anand S. Mehta[1]; *[1]Medical University of South Carolina, Charleston, SC; [2]University of Pittsburgh, Pittsburgh, PA*

MP 232 **The roles of FXR in lipid biochemistry within hepatocellular carcinoma using MALDI MSI**; Kayle J Bender[1]; Chuo Ying Zhai[1]; Elizabeth Neumann[2]; *[1]University of California, Davis, Davis, CA; [2]University of California, Davis, CA*

MP 233 **Understanding Neuronal Excitability using Mass Spectrometry Imaging of SCN2A-deficient Organoid and Assembloid Systems**; Alyssa Moore[1]; Xiaoling Chen[2]; Yang Yang[2]; Julia Laskin[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, Lafayette, IN*

MP 234 **Short-Chain Fatty Acid Depletion Alters Lipid and Metabolite Profiles in a Cocaine-treated Mouse Model as Revealed by IR-MALDESI MS Imaging**; Alora R Dunnavant[1]; Marta Koperska[2]; Qianqian Shao[3]; Florine Collin[3]; TuKiet T Lam[3, 4]; Drew D Kiraly[2]; David C. Muddiman[1]; Mary F Wang[1]; *[1]Biological Imaging Laboratory for Disease and Exposure Research, Department of Chemistry, North Carolina State University, Raleigh, NC; [2]Wake Forest Center for Addiction Research, Wake Forest University School of*

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MP 235 **An integrative mass spectrometry strategy for interpreting spatial and structural diversity of monoterpenoid indole alkaloids in Catharanthus roseus**; Tetsuya Mori[1]; Noriko Takeda-Kamiya[1]; Keijiro Ohshimo[2]; Miyako Sakurai[1]; Reiki Yasukawa[2]; Mai Uzaki[1]; Kiminori Toyooka[1]; Masami Yokota Hirai[1, 3]; *[1]RIKEN CSRS, Yokohama, Japan; [2]Hokkaido University of Education, Sapporo, Japan; [3]Nagoya University, Nagoya, Japan*

MP 236 **Mass Spectrometry Imaging of Low-Abundance Sulfatides Using Nano-DESI MRM Mode**; Anthony H Choi[1]; Aiming Zheng[2]; Tommy Zhang[2]; Julia Laskin[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, Department of Chemistry, West Lafayette, IN*

MP 237 **Deciphering Metabolic Heterogeneity in Lung Cancer Cell Lines Using High-Resolution MALDI Mass Spectrometry Imaging**; Siavash Mansouri[1, 2]; Tanja Bien[3]; Janina Oetjen[3]; Corinna Henkel[3]; Andras Kiss[3]; Michael Easterling[4]; Marieke A. Boecker[1, 2]; Nadezhda Nikulina[1, 2]; Jens Hoehndorf[3]; Rajkumar Savai[1, 2]; *[1]Lung Microenvironmental Niche in Cancerogenesis, Institute for Lung Health (ILH), Justus Liebig University, 35392, Giessen, Germany, Giessen, Germany; [2]Max Planck Institute for Heart and Lung Research, Member of the German Center for Lung Research (DZL), Member of the Cardio-Pulmonary Institute (CPI), Bad Nauheim, 61231, Germany., Bad Nauheim, Germany; [3]Bruker Daltonics GmbH & Co.KG, Bremen, Germany; [4]Bruker Scientific LLC, Billerica, MA*

MP 238 **Analysis of neural human organoids via AP-SMALDI mass spectrometry imaging**; Julius Wollmann[1, 2]; Alina Schindler[1]; Wuji Cao[3]; Amena Saleh[4]; Esther B. E. Becker[4]; Barbara Treutlein[3]; Bernhard Spengler[1, 2]; *[1]Institute of Inorganic and Analytical Chemistry, Justus Liebig University, Giessen, Germany; [2]TransMIT GmbH, Giessen, Germany; [3]Department of Biosystems Science and Engineering, ETH Zurich, Zurich, Switzerland; [4]Nuffield Department of Clinical Neurosciences, University of Oxford, Oxford, United Kingdom*

MP 239 **Neutral Lipid Imaging of Human Alzheimer's Disease Brain Tissue using Salt-Enhanced MALDI-2 IMS**; Kameron Molloy[1, 2]; Cody R Marshall[2, 3]; Martin Dufresne[2, 4]; Lukasz G Migas[2, 5]; Melissa A. Farrow[2, 4]; Matthew Schrag[6, 7, 8]; Raf Van De Plas[2, 5, 9]; Jeffrey M Spraggins[1, 2, 4, 9, 10]; *[1]Department of Chemistry, Vanderbilt University, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Chemical and Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [4]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [5]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [6]Department of Neurology, Vanderbilt University School of Medicine, Nashville, TN; [7]Vanderbilt Brain Institute, Vanderbilt University, Nashville, TN; [8]Vanderbilt Memory and Alzheimer's Center, Vanderbilt University Medical, Nashville, TN; [9]Department of Biochemistry, Vanderbilt University, Nashville, TN; [10]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN*

MP 240 **MALDI and DESI mass spectrometry imaging of retinoid metabolism in a mouse heart failure (HF) model**; Temple Andrews[1]; Jianshi Yu[1]; Sogol Sedighi[2]; Brian Foster[2]; Maureen A Kane[1]; *[1]University of Maryland School of Pharmacy, Baltimore, MD; [2]Johns Hopkins University, Baltimore, MD*

MP 241 **MALDI imaging analysis of diabetes-induced disruptions in the spatial organization of kidney lipid metabolism in genetic mouse models**; Moshe Levi[1]; Dalton R. Brown[2]; Caitlin M. Tressler[2]; Avi Z. Rosenberg[3]; Xiaoxin Wang[1]; Komuraiah Myakala[1]; Kristine Glunde[2]; *[1]Department of Biochemistry and Molecular & Cellular Biology, Center for Biological and Biomedical Engineering, Georgetown University School of Medicine, Washington, DC; [2]Johns Hopkins Applied Imaging Mass Spectrometry (AIMS) Core, The Russell H. Morgan Department of Radiology and Radiological Science, Johns Hopkins University School of Medicine, Baltimore, MD; [3]Department of Pathology, Johns Hopkins University School of Medicine, Baltimore, MD*

MP 242 **Spatiomolecular characterization of a chronic pain murine model using multimodal MALDI imaging mass spectrometry**; Lauren G White[1, 2]; Rachel McKee[1, 3]; Lauren Emmerson[1, 2]; Thai H Pham[2, 4]; Benjamin Asbury[3]; Melissa A. Farrow[2, 4]; Jonathan Schoenecker[1, 3, 4]; Jeffrey M Spraggins[1, 2, 4, 5, 6, 7]; *[1]Chemical Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]vanderbilt Center for Bone*

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MP 243 **Imaging Duterated Lipids in Lung Injury Remodeling Zones Using Ion Mobility to Separate lipids Similar in Mass to Charge Space**; David M. G. Anderson[1]; Madeline E Colley[2]; Scott McCall[3]; Jeffrey M Spraggins[2]; *[1]Vanderbilt University, Department of Biochemistry, Nashville, TN; [2]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [3]divsion of allergy, pulmonary and critical care, department of medicine, vanderbilt medical center, Nashville, TN*

MP 244 **Determination of the Spatial Distribution of Benzalkonium Chlorides (BACs) and Differentially Expressed Lipids in Mouse Hearts Exposed to BACs**; Corrina K Cooper[1]; Marie Brzoska[1]; Ryan P. Seguin[1]; Vanessa Lopez[1]; Libin Xu[1]; *[1]University of Washington, Seattle, WA*

MP 245 **MALDI Mass Spectrometry Imaging of Verapamil Parent Drug Distribution Along a Rat Liver Sinusoid**; Rachel Parise[1]; Bingming Chen[1]; Christopher Gibson[2]; Mark T Cancilla[3]; Kenneth Korzekwa[4]; Swati V Nagar[4]; *[1]Merck & Co., Rahway, NJ; [2]Incyte, Wilmington, DE; [3]GSK, Philadelphia, PA; [4]Temple University, Philadelphia, PA*

MP 246 **Visualizing the Distribution of the Anti-TB Drug Q203 in Human-Like Necrotic Granulomas using High-Resolution MALDI Mass Spectrometry Imaging**; Leon Gröschel[1]; Christoph Hölscher[2]; Kerstin Walter[2]; Andreas Römpp[1]; *[1]Chair of Bioanalytical Sciences and Food Analysis, University Bayreuth, Bayreuth, Germany; [2]German Center for Infection Research, Thematic Translational Unit Tuberculosis, Borstel, Germany, Borstel, Germany*

MP 247 **DESI Imaging: small molecule metabolites on tissue using the Xevo™ Multi-Reflecting time-of-flight mass spectrometer**; Helen Yates[1]; Joel Keelor[2]; Emmanuelle Claude[1]; Joanne Ballantyne[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

MP 248 **Spatial Multi Omics Reveals Modulation of the Tumor Microenvironment in Ovarian Cancer**; Erin H Seeley[1]; Chun Wai Ng[1]; Basant Gamal[1]; Yadira Pacheco[1]; Christopher Pacheco[1]; Jared K. Burks[1]; Samuel Mok[1]; Sammy Ferri-Borgogno[1]; *[1]MD Anderson Cancer Center, Houston, TX*

MP 249 **Defining the Molecular Trajectory of Staphylococcus aureus Abscesses by Spatial Multi-omics**; Jacqueline M Van Ardenne[1, 2]; Anna J Smith[2, 3]; Thai H Pham[2, 3]; Lukasz G Migas[2, 4]; Roy Lardenoije[5]; Jeffrey A Freiberg[6, 7]; Katherine N Gibson-Corley[8]; Isaac Thomsen[9]; Andy Weiss[9]; Isis Kanevsky[9]; Melissa A Farrow[2, 3]; Joana P Goncalves[5]; Raf Van De Plas[2, 4, 10]; Eric P Skaar[7, 11, 12]; Jeffrey M Spraggins[1, 2, 3, 7, 10, 13]; *[1]Department of Chemistry, Vanderbilt University, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [4]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [5]Department of Intelligent Systems, Delft University of Technology, Delft, Netherlands; [6]Division of Infectious Diseases, Department of Medicine, Vanderbilt University Medical Center, Nashville, TN; [7]Vanderbilt Institute for Infection, Immunology, and Inflammation, Vanderbilt University Medical Center, Nashville, TN; [8]Division of Comparative Medicine, Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, TN; [9]Vaccine Research and Development, Pfizer Inc, Pearl River, NY; [10]Department of Biochemistry, Vanderbilt University, Nashville, TN; [11]Division of Molecular Pathogenesis, Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, TN; [12]Vanderbilt Institute for Chemical Biology, Vanderbilt University, Nashville, TN; [13]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN*

MP 250 **A modified tribrid mass spectrometer enables improvements in throughput and reproducibility of targeted multiplexed spatial proteomics**; Anna Bakhtina[1]; Anatalia Robles[1]; Kayley Hake[1]; Magdalena Preciado Lopez[1]; Fiona McAllister[1]; *[1]Calico Life Sciences LLC, South San Francisco, CA*

MP 251 **Mass spectrometry imaging for multi-omic spatial atlasing of pancreatic intraductal papillary mucinous neoplasm tissues**; Caroline Kittrell[1]; Abigail Weatherford[1]; Sarah Lowery[2]; Grace Grimsley[1]; David Bayadyan[1]; Kristin Clift[3]; Anand Mehta[1]; Stacy Malaker[2]; Yan Bi[3]; Peggi M. Angel[1]; Richard R.

Drake[1]; *[1]Medical University of South Carolina, Charleston, SC; [2]Yale University, New Haven, CT; [3]Mayo Clinic, Jacksonville, FL*

MP 252 **Spatial lipidomic analysis reveals age- and cataract-related lipid modifications in human lenses**; Zhen Wang[1]; Sergei Chetyrkin[1]; Kevin L. Schey[1]; *[1]Vanderbilt University, Nashville, TN*

MP 253 **Optimized Low-Flow DESI-MSI Enables High-Resolution Multiomic Imaging of Human Cancer Tissues with Spatial Transcriptomics**; Trevor M. Godfrey[1]; Rachel J. DeHoog[1]; Mark W. Towers[2]; Lisa A. Towers[2]; Emrys A. Jones[2]; Joanne B. Ballantyne[2]; James W. Suliburk[1]; Faith E. Jackobs[1]; Yaohong Wang[3]; Amalia R. Gonzalez[3]; Hop S. Tran Cao[3]; Livia S. Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX; [2]Waters Corporation, Wilmslow, United Kingdom; [3]MD Anderson, Houston, TX*

MP 254 **Integrated MALDI Imaging and Spatial Transcriptomics Define Spatiomolecular Phenotypes of Staphylococcus aureusOsteomyelitis**; Lauren Emmerson[1, 2]; Audra M Judd[2, 3]; Anna J Smith[2, 4]; Lukasz G Migas[2, 5]; Raf Van De Plas[2, 3, 5]; Joana P Goncalves[6]; James E Cassat[7, 8, 9, 10]; Jeffrey M Spraggins[1, 2, 3, 4, 7, 10, 11]; *[1]Chemical and Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Department of Biochemistry, Vanderbilt University, Nashville, TN; [4]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [5]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [6]Delft Department of Intelligent Systems, Delft University of Technology, Delft, Netherlands; [7]Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, Nashville, TN; [8]Department of Pediatrics, Vanderbilt University Medical Center, Nashville, TN; [9]Department of Biomedical Engineering, Vanderbilt University, Nashville, TN; [10]Vanderbilt Institute for Infection, Immunology, and Inflammation, Vanderbilt University Medical Center, Nashville, TN; [11]Department of Chemistry, Vanderbilt University, Nashville, TN*

MP 255 **An Improved Opto-Proteomics Approach with Enrichment Independent Positive Detection of Sub-Cellular Proteomes**; Benjamin L. Muselius[1]; Spencer C. Funk[1]; Christina L. Pan[1]; Pauline Douglas[1]; Bruno C. Amaral[1]; David C. Schriemer[1]; *[1]University of Calgary, Calgary, AB*

MP 256 **Quantitative Proteomics of Cell Fate Specification in the Early Drosophila Embryo**; Argit Marishta[1]; Edward Cruz[1, 2]; Graeme C McAlister[3]; Martin Wühr[1, 2]; Eric Wieschaus[1, 2]; *[1]Princeton University, Princeton, NJ; [2]Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ; [3]Thermo Fisher Scientific, San Jose, CA*

MP 257 **CFTR function and chronicity-associated Pseudomonas aeruginosastrain adaptations drive distinct spatial immunometabolic adaptations in a CF model**; Shanaliz Natta[1]; Tialfi Bergamin De Castro[1]; Janette Harro[1]; Robert K Ernst[1]; Alison Scott[2]; *[1]University of Maryland, Baltimore, Baltimore, MD; [2]University of Maryland, Baltimore, MD*

MP 258 **Spatial multiomics signatures reveal sexual dimorphism in atherosclerosis**; ROBIN JOSHI[1]; Soon Yew Tang[2]; Ujjalkumar Subhash Das[2]; Daniel J Boehmler[2]; Antonijo Mrčela[2]; E. James Petersson[2]; Aalim M. Weljie[2]; Garret A. FitzGerald[2]; *[1]University of Pennsylvania, Philadelphia, PA; [2]University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA*

MP 259 **Mapping Alzheimer's Brain Pathology Using MALDI and DESI Multi-Omic MSI**; Bandana Bera[1]; Sudipta Senapati[1]; David Beaver[1]; Jia Yi Liew[1]; Rakez Kayed[1]; Brendan Prideaux[1]; *[1]University of Texas Medical Branch, Galveston, TX*

MP 260 **Targeted Three-Dimensional Molecular Imaging of Human Glomeruli Using Integrated MALDI IMS and Microscopy**; Ellie L. Pingry[1, 2]; Allison B. Esselman-Lawrence[2, 3]; Martin Dufresne[2, 3]; Lukasz G. Migas[4]; Melissa A. Farrow[2, 3]; Raf Van De Plas[2, 4, 5]; Jeffrey M. Spraggins[2, 3, 5, 6, 7, 8]; *[1]Chemical Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [4]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [5]Department of Biochemistry, Vanderbilt University, Nashville, TN; [6]Chemical and Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [7]Department of Chemistry, Vanderbilt University, Nashville, TN; [8]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN*

MP 261 **Integrating imaging, proteomics, and transcriptomics to map nucleic acid molecular neighborhoods**; Conor P Herlihy[1]; Elijah Biletch[2, 3]; Lidan Li[1]; Olivia Weissenfels[1]; Keriann M. Backus[2, 3, 4, 5, 6, 7]; Brian J Beliveau[1, 8, 9]; Devin Schweppe[1, 8, 9]; *[1]Department of Genome Sciences, University of Washington, Seattle, WA; [2]Department of Chemistry and Biochemistry, University of California Los Angeles, Los Angeles, CA; [3]Biological Chemistry Department, David Geffen School of Medicine, University of California Los Angeles, Los Angeles, CA; [4]Department of Human Genetics, David Geffen School of Medicine, University of California, Los Angeles, Los Angeles, CA; [5]Molecular Biology Institute, University of California, Los Angeles, Los Angeles, CA; [6]UCLA-DOE Institute for Genomics and Proteomics, University of California, Los Angeles, Los Angeles, CA; [7]Eli and Edythe Broad Center of Regenerative Medicine and Stem Cell Research, University of California, Los Angeles, Los Angeles, CA; [8]Brotman Baty Institute for Precision Medicine, Seattle, WA; [9]Institute for Stem Cell & Regenerative Medicine, University of Washington, Seattle, WA*

MP 262 **Phos-MASP: a reproducible, sensitive spatial proteomics and phosphoproteomics mapping tool provides insights into Alzheimer's Disease**; Min Ma[1, 2]; Maosheng Wei[1]; Shihan Huo[1]; Ming Zhang[1, 2]; Erfei Shang[1]; Yingyi Lian[1]; Jun Qu[1, 2]; *[1]University at Buffalo, Buffalo, NY; [2]Center of Excellence in Bioinformatics and Life Sciences (CBLS), Buffalo, NY*

MP 263 **High-Resolution Whole-Body Mass Spectrometry Imaging for Spatial Lipidomics of Perinatal interscapular Brown Adipose Tissue (iBAT) Across Species**; Maiko Okamura[1]; Takashi Nirasawa[2]; Akio Hayashi[3]; Tadashi Nomura[4]; Masaya Ikegawa[1]; *[1]Doshisha University, Kyotanabe-city, Japan; [2]Bruker Japan K.K., Yokohama, Japan; [3]The University of Osaka, CENTER FOR INFECTIOUS DISEASE EDUCATION AND RESEARCH, Suita, Japan; [4]Kyoto institute of technology, School of Science and Technology, Kyoto, Japan*

MP 264 **Imaging isotope patterns from tissues with high mass spectral resolving power improves flux analysis**; Viktoriya S Anokhina[1]; Michaela Schwaiger-Haber[1]; Dhanalakshmi Anbukumar[1]; Gary J Patti[1]; *[1]Washington University in St.Louis, St.Louis, MO*

MP 265 **Integrated Submicron Spatial Omics in Single Neurons Enabled by Cryogenic Plasma/Water Gas Cluster Ion Beam SIMS**; Hua Tian[1]; Paul Blenkinsopp[2]; Valerian E. Kagan[1, 3]; Hülya Bayır[1]; *[1]Columbia University, New York, NY; [2]Ionoptika Ltd, Eastleigh, United Kingdom; [3]University of Pittsburgh, Pittsburgh, PA*

MP 266 **Evaluation of targeted and untargeted workflows by DESI MSI of novel photocleavable Mass-Tagged Antibodies to image biomarkers in tissues**; Emmanuelle Claude[1]; Gargey Yagnik[2]; Zhi Wan[2]; Andrew Yatsuhashi[2]; Steven Pringle[1]; Kenneth J Rothschild[2, 3]; Mark J Lim[2]; Joanne Ballantyne[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]AmberGen, Billerica, MA; [3]Department of Physics and Photonics Center, Boston University, Boston, MA*

MP 267 **Mapping the Lipidomic Landscape of Human Proximal Tubule Segments with Integrated MALDI IMS and CODEX**; Megan S. Ward[1, 2]; Thai Pham[1, 3]; Allison B. Esselman-Lawrence[1, 4]; Katerina V. Djambazova[1, 3]; Martin Dufresne[1, 3]; Madeline E. Colley[1, 3]; Lukasz G. Migas[1, 5]; Melissa A. Farrow[1, 3]; Raf Van De Plas[1, 5]; Jeffrey M. Spraggins[1, 2, 3, 4, 6, 7]; *[1]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [2]Chemical Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [3]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [4]Department of Chemistry, Vanderbilt University, Nashville, TN; [5]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [6]Department of Biochemistry, Vanderbilt University, Nashville, TN; [7]Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, Nashville, TN*

MP 268 **Informatics of top-down individual ion mass spectrometry enables rapid and deep proteoform characterization**; Michael A R Hollas[1]; Lily Miller[1]; Nickolas P Fisher[1]; Ryan T Fellers[2]; Kenneth R Durbin[2]; Jared O Kafader[1]; Neil L Kelleher[1]; *[1]Northwestern University, Evanston, IL; [2]Proteinaceous, Evanston, IL*

MP 269 **Mass Spectrometry-based Proteomics on iPSC-derived Motor Neurons shows Sex-based Differences in ALS Patients**; Niveda Sundararaman[1]; Kirstin Washington[2]; Ali Haghani[3]; Oliver Wang[3]; Rakhi Pandey[3]; Christopher Murray[3]; Jennifer E. Van Eyk[2]; *[1]Cedars-Sinai Medical Center, Los Angeles, CA; [2]Cedars Sinai Medical Center, Los Angeles, CA; [3]Cedars-Sinai Medical Center, LA*

MP 270 **De Novo Sequencing of Monoclonal Antibodies Using Multi-Enzyme, Antibody-Specific Transformer models**; Leiver Campeon[1]; Harshani Bandara[1]; Osanda Hemachandra[1]; Sanoj Silva[1]; Pulasthi Ekanayake[1]; Doreen Chrishanthy[1]; *[1] EXPERT Intelligence, Santa Clara, CA*

MP 271 **Development of unnatural proteins and LC-MS/MS sequencing for data storage and retrieval**; Cheuk Chi A. Ng[1]; Yin Zhou[1]; Chengxi Liu[1]; Wai Man Tam[2]; Francis C. M. Lau[2]; Zhongping Yao[1]; *[1] Department of Applied Biology and Chemical Technology, The Hong Kong Polytechnic University, Hong Kong, Hong Kong; [2] Department of Electrical and Electronic Engineering, The Hong Kong Polytechnic University, Hong Kong, Hong Kong*

MP 272 **Accelerating Molecular Network Construction and Spectral Library Search for Metabolomics at Scale with Hierarchical Graph Indexing**; Andrew M P Roberts[1]; Alexander Semenov[2]; Vladimir Boginski[3]; Alexander Aksenov[1]; *[1] University of Connecticutt, Storrs, CT; [2] University of South Florida, Tampa, FL; [3] University of Central Florida, Orlando, FL*

MP 273 **Experiment-Specific Spectral Libraries Unlock Additional Peptide Identifications from Public Orbitrap Astral DIA Data**; Peter Askovich[1, 2]; Bo Wen[3]; Kyla Teplitz[1]; Michael J. MacCoss[3]; *[1] EuropaDX, Inc., Redmond, WA; [2] SEATTLE BIOSOFTWARE, INC., Redmond, WA; [3] University of Washington, Seattle, WA*

MP 274 **Tesseract Interact: A Skyline Tool for Streamlined Interrogation of High Resolution Ion Mobility Mass Spectrometry Data**; Lauren C Royer[1]; Mark Jennings II[1]; Rachel A. Harris[1, 2]; Miriam Fico[1]; Frederick G. Strathmann[1]; Daniel DeBord[1]; *[1] MOBILion Systems Inc., Chadds Ford, PA; [2] Waters, Milford, MA*

MP 275 **Deep learning powered ion mobility feature extraction and demultiplexing for robust multidimensional metabolomics quantification**; Aviral Singh[1]; Deepti Sahasrabuddhe[2]; Pramod P Wangikar[1, 2]; *[1] Clarity Bio Systems India Pvt. Ltd., Pune, India; [2] Indian Institute of Technology Bombay, Mumbai, India*

MP 276 **Deep learning powered SWATH peak deconvolution and precursor-product association for robust fragment-based quantification**; Aviral Singh[1]; Deepti Sahasrabuddhe[2]; Pramod P Wangikar[1, 2]; *[1] Clarity Bio Systems India Pvt. Ltd., Pune, India; [2] Indian Institute of Technology Bombay, Mumbai, India*

MP 277 **If You Wrote It Down, Is It Useful? Creating a Database of Chemicals Identified in Consumer Products through Non-Targeted Analysis**; Anna K. Boatman[1]; Nathaniel Charest[1]; Troy M. Ferland[1]; Kristin K. Isaacs[1]; John F. Wambaugh[1]; Mark Wilson[2]; Heather D. Whitehead[1]; *[1] UL Research Institutes, Morrisville, NC; [2] UL Research Institutes, Marietta, GA*

MP 280 **Accelerating Astral nDIA Phosphoproteomics with Scalable Data Analysis Pipelines**; Marc Isaksson[1]; Emma Åhrman[1]; Valentina Siino[1]; Ignacio Arribas Diez[1]; Sofija Skoric[1]; Caroline Wigerup[1]; David Proia[2]; Joon Jung[2]; Magnus E Jakobsson[1]; Kristina Masson[2]; Peter Blume-Jensen[2]; *[1] Acrivon AB, Lund, Sweden; [2] Acrivon Therapeutics Inc, Watertown, MA*

MP 281 **An R-Based Platform for Proteomics Sample Tracking and Workflow Transparency Using Institutional Submission Systems**; Ludyanna Lebon; *Georgia Institute of Technology, Atlanta, GA*

MP 282 **Context is Key: Using multi-agent AI teams to bridge the translational gap in metabolomics**; James Campbell[1]; Will Thompson[2]; Scott Mellors[2]; J. Michael Ramsey[2]; *[1] Move Analytical, Cary, NC; [2] Move Analytical LLC, Carrboro, NC*

MP 283 **Refinements in Data Processing and Quality Control Metrics of In Vivo MasSpec Pen Data Collected Intraoperatively**; Faith E Jackobs[1]; Charles A. Wolfe[1]; Michael F Keating[1, 2]; Livia S. Eberlin[1]; *[1] Baylor College of Medicine, Houston, TX; [2] University of Texas at Austin, Austin, TX*

MP 284 **Streamlined Peptide Search Workflows in Skyline for DDA and DIA Proteomics**; Matthew C Chambers[1]; Michael J. MacCoss[2]; Brendan MacLean[2]; Nicholas Shulman[2]; *[1] University of Washington, Stamford, CT; [2] University of Washington, Seattle, WA*

MP 285 **MassIVE: enhancing sensitive data access security with rigorous federal standards compliance**; Jeremy Carver[1]; Nuno Bandeira[1]; *[1]UCSD, La Jolla, CA*

MP 286 **ProteoBrowser™: turning quantitative proteomics into translational decisions with interactive biomarker and pathway analytics**; Salvador Martínez-Bartolomé[1]; James T Sorrentino[1]; Mohamed Rdait[1]; Mahan Abbasian[1]; Christina Lamm[1]; Antonius Koller[1]; Afshin Mahmoudi[1]; Pilgrim Jackson[1]; *[1]Yatiri Bio, San Diego, CA*

MP 287 **Maximizing the value of spectral libraries with the SpectralLibrarian software package**; Yunwon Kang[1]; Triston Groff[1]; Gary J Patti[1]; *[1]Washington University in St. Louis, St. Louis, MO*

MP 288 **Automated LC–MS System Readiness Assessment for MAM Using Purpose-Designed Peptide Standards**; Mahsan Miladi[1]; Mike Knierman[2]; Tristan Chutka[1]; Melissa Sato[1]; Andrew McEachran[1]; *[1]Agilent Technologies, Santa Clara, CA; [2]Agilent Technologies Inc., Santa Clara, CA*

MP 289 **Enhanced System Suitability Plotting and Instrument Scheduling in Panorama and AutoQC**; Josh Eckels[1]; Ankur Juneja[1]; Vagisha Sharma[2]; Gennifer Merrihew[2]; Richard Johnson[2]; Michael J. MacCoss[2]; Brendan MacLean[2]; *[1]LabKey, San Diego, CA; [2]University of Washington, Seattle, WA*

MP 290 **Evaluation of New Peak Detection Performance in MAM Using a Controlled Peptide Spike-in Strategy**; Mahsan Miladi[1]; Gordon Slysz[1]; Tristan Chutka[1]; Lichen Xiu[1]; Melissa Sato[1]; Mike Knierman[1]; Andrew McEachran[1]; *[1]Agilent Technologies, Santa Clara, CA*

MP 291 **Improving accessibility and utility of open-source DDA workflows by leveraging Nextflow and Limelight for automation, visualization, and data sharing**; Michael Riffle[1]; Daniel Jaschob[1]; Alex Zelter[1]; Matthew C Chambers[1]; Jimmy K Eng[1]; Michael R Hoopmann[1]; Brendan X MacLean[1]; Nina Isoherranen[1]; Michael J MacCoss[1]; *[1]University of Washington, Seattle, WA*

MP 292 **Development of a Machine Learning Enhanced Miniature Mass Spectrometer with Dual Ionization Sources and Intelligent 2D MS/MS-DDA**; Dalton Snyder[1]; Megan Guetzloff[1]; Andrew Eller[1]; Alexander Gordon[1]; Alexander Huynh[1]; Conner Harper[1]; Diandra Hassan[1]; Edwin Gonzalez[1]; Patrick Cutler[2]; Derek Eidum[2]; Anna Leech[1]; Mitch Wells[1]; *[1]Teledyne FLIR, West Lafayette, IN; [2]Teledyne Scientific & Imaging, Durham, NC*

MP 293 **Miniature Multi-Reflecting TOF Mass Spectrometer**; Vadym Berkout[1]; Scott Ecelberger[1]; Stuart Collymore[1]; Max Cetta[1]; Lara Moore[1]; Wayne Bryden[1]; *[1]Zeteo Tech, Inc., Sykesville, MD*

MP 294 **Simplifying Agrochemical Residue Testing Through Miniaturized Ion Trap MS and Intuitive Detection and Analysis Software**; Scott J Campbell[1]; John H Moncur[1]; Caleigh O'Connor[2]; Vishal Mahale[2]; Madhuri Gupta[2]; Subodh Chawan[2]; Venkat Panchagnula[2]; *[1]SpectralWorks Ltd., Runcorn, United Kingdom; [2]MassTech Inc., Columbia, MD*

MP 295 **Miniature CE-LIT/LIT System for High-Efficiency Multiplexed Bioanalysis**; Zihao Liao[1]; Wen Li[2]; Wenpeng Zhang[2]; Zheng Ouyang[2]; *[1]Tsinghua University, BeiJing, China; [2]Tsinghua University, Beijing, China*

MP 296 **Field-Portable AFT-MS for Direct Vapor Detection of Drugs and Explosives with High Selectivity in Operational Environments**; Krisztian Gabor Torma[1]; Mike Chai[1]; William Yang Terziyan[1]; *[1]BaySpec Inc., San Jose, CA*

MP 297 **Vehicle-Based DART-MS/MS Using a Bruker EVOQ DART-TQ+ for Field-Deployable VOC Monitoring with Remote Connectivity**; Christian Vargas[1, 2]; Travis Vargas[1]; Martin Hubert[1]; Benjamin Katz[1]; Michael Boric[1]; *[1]Daltonian Flux, Costa Mesa, CA; [2]University of California Irvine, Irvine, CA*

MP 298 **SFC/MS Purification and Characterization of Natural Main Components with a Direct Sampling Atmospheric Pressure MS/MS**; Enrico Davoli[1]; Oscar Cabrices[2]; Konstantin Novoselov[2]; Alberto Asteggiano[3]; *[1]Università degli Studi di Torino, Torino, Italy; [2]MassTech Inc., Columbia, MD; [3]Università degli Studi di Torino, Turin, Italy*

MP 299 **Development of a Portable UPLC Mass Spectrometer and Its Applications**; Chung-Hsuan Chen[1, 2, 3, 4]; Ju Yao Chang[2]; Chun-Jen Hsiao[2]; Jung-Lee Lin[2, 4]; *[1]Genomic Research Center, Taipei,, Taiwan; [2]i Analyzer Inc., Taipei, Taiwan; [3]National Sun Yet-sen University, Kaohsiung, Taiwan; [4]Academia Sinica, Taipei, Taiwan*

MP 300 **A spaceflight dual-source capillary electrophoresis and gas chromatograph mass spectrometer for astrobiology missions to ocean worlds**; Desmond A. Kaplan[1, 2]; Maria Fernanda Mora[3]; Tomas Drevinskas[3]; Ryan Danell[2, 4]; Aaron Noell[3]; Andrej Grubisic[2]; Jacob Graham[2]; Mauro Ferreira Santos[3]; Peter Willis[3]; William Brinckerhoff[2]; *[1]Kapscience, LLC, Tewksbury, MA; [2]NASA GSFC, Greenbelt, MD; [3]NASA Jet Propulsion Lab, La Cañada Flintridge, CA; [4]Danell Consulting, Inc., Winterville, NC*

MP 301 **Turning the Volume Down – Controlling, Characterizing, and Conquering Intrinsic Contamination and Chemical Background Signals in the Dragonfly Mass Spectrometer**; Ryan M. Danell[1, 2]; Andrej Grubisic[1]; Joseph M. Pasterski[1, 3]; Jacob D. Graham[1]; Xiang Li[1]; Desmond A. Kaplan[1, 4]; Marco E. Castillo[1, 5]; William B. Brinckerhoff[1]; Melissa G. Trainer[1]; *[1]NASA Goddard Space Flight Center, Greenbelt, MD; [2]Danell Consulting, Inc., Winterville, NC; [3]CREST II, University of Maryland, College Park, MD; [4]Kapscience, LLC, Tewksbury, MA; [5]Aerodyne Industries, LLC, Cape Canaveral, FL*

MP 302 **Wide dynamic-range ion detectors combining discrete dynodes with an avalanche diode for quadrupole mass spectrometers**; Hiroshi Kobayashi[1]; Kotani Masahiro[1]; Kotaro Shimizu[1]; Hayato Inoue[1]; *[1]HAMAMATSU PHOTONICS K.K., Iwata, Japan*

MP 303 **Evaluation of Ion-Droplet Separation Performance in Conjugated Octupole–Quadrupole Ion Guide**; Motoki Date[1]; Masuyuki Sugiyama[1]; Hideki Hasegawa[1]; Yuichiro Hashimoto[2]; *[1]Hitachi, Ltd., Kokubunji-shi, Tokyo, Japan; [2]Hitachi High-Tech Corporation, Ibaraki, Japan, Ibaraki, Japan*

MP 304 **Exploration on the Function and Utility of a Dynamic State Nested Electrostatic Linear Ion Trap (NELIT)**; Jordan M Fritz[1]; Eric T Dziekonski[1]; Scott A. McLuckey[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

MP 305 **Performance Optimization and Comparison of Stepped-Electrode and Hyperbolic Linear Ion Traps**; Conner C Harper[1]; Mohsen Latif[1]; Dalton Snyder[1]; *[1]Teledyne FLIR, West Lafayette, IN*

MP 306 **Ion charge control in FT-ICR MS for automatic regulation and calibration of space charge effects**; Konstantin Aizikov[1]; Gregory Brabeck[2]; Alina Theisen[1]; Christopher Andrew Wootton[3]; *[1]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [2]Bruker Daltonics, Billerica, MA; [3]Bruker, Bremen, Germany*

MP 307 **Investigating Biomolecular Complexes using Charge Detection on an Orbital Frequency Analyser**; Frank Sobott[1]; Aleksandr Rusinov[2]; Dinesh Kumar Chinthapalli[1]; Tiago Moreira[1]; Sergey Smirnov[2]; Patrick Knight[2]; Gordon Kearney[2]; *[1]University of Leeds, Leeds, United Kingdom; [2]Shimadzu Research Laboratory (Europe) Ltd., Manchester, United Kingdom*

MP 308 **Fast gain switching in electron multipliers**; Antony N Jones[1]; Jay W. Archer[1]; Amruta Nawarange[1]; Keneth C. Wright[2]; Ian Lake[3]; *[1]IMI Adaptas, Clyde, Australia; [2]IMI Adaptas, Palmer, MA; [3]IMI Adaptas, Worthing, United Kingdom*

MP 309 **Utilizing discrete charge loss events on a minaturized dual sector CDMS analyser to determine charge state by frequency measurement alone**; John B Hoyes[1]; Raj Parikh[1]; Alexey Barkhanskiy[1]; Richard Chapman[1]; Gavin Wray[1]; *[1]TrueMass, Rowarth, United Kingdom*

MP 310 **Increased Throughput and Charge Measurements from a Miniaturized Dual Sector Design for Charge Detection Mass Spectrometry**; John B Hoyes[1]; Raj Parikh[1]; Alexey Barkhanskiy[1]; Richard Chapman[1]; Gavin Wray[1]; *[1]TrueMass, Rowarth, United Kingdom*

MP 311 **Sub-nanosecond High Dynamic Range Detector for TOF-MS**; Jonathan Garel[1]; Semyon Shofman[1]; Dmitry Zakgeim[1]; Amit Weingarten[1]; Aleksey Vorobyev[2]; Oleg Nikandrov[2]; Andrey Novikov[2]; Anatoly Verenchikov[2]; *[1]Exosens, Rehovot, Israel; [2]MSC, Bar, Montenegro*

MP 312 **Long-lifetime, wide dynamic range detectors for ion trap and Quadrupole mass spectrometers**; Amit Weingarten[1]; Semyon Shofman[1]; Jonathan Garel[1]; [1]*Exosens, Rehovot, Israel*

MP 313 **Improvement of Orbitrap-Based CDMS Data Via Removal of Time-Domain Pulses**; Michael P Goodwin[1]; David Bergen[2]; Graeme C. McAlister[2]; Michael Senko[2]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Thermo Fisher Scientfic, San Jose, CA*

MP 314 **Product isolation using a linear RF ion trap installed in a cylinder magnet in an Electron-Activated Dissociation device**; Takashi Baba[1]; Ashish Pradhan[1]; Pavel Ryumin[1]; [1]*SCIEX, Concord, ON*

MP 315 **Development of Collinear Resonance Ionisation Spectroscopy (CRIS) Instrumentation for Next Generation Ultra-High Abundance Sensitivity Detectors**; Giles Edwards[1, 2]; Kieran Flanagan[1, 2]; Matthew Duggan[1]; Holly Perrett[1]; Sam Smithies[2]; Chris Yates[2]; Alexandra Roberts[1]; Ethan Vale[1]; Charlie Agg[1]; [1]*The University of Manchester, Manchester, United Kingdom;* [2]*Artemis Analytical Ltd., Manchester, United Kingdom*

MP 316 **Performance Evaluation of Bipolar TOF Detectors Using Lead-Free ALD-Functionalized MCPs Compared to Standard MCPs**; Till Cremer[1]; Joe Czekner[1]; Paula Holmes[1]; Stephen M Ritzau[1]; Muhammed Sajjad[1]; [1]*Photonis Scientific, Sturbridge, MA*

MP 317 **A Novel High-Resolution CDMS Instrument Prototype**; Keith Richardson[1]; David Langridge[1]; Andy Jarrell[2]; Anisha Haris[1]; Wade Leveille[2]; Thomas Moore[1]; Duncan Leonard[1]; Jakub Ujma[1]; Jeffery Brown[1]; [1]*Waters Corporation, Wilmslow, United Kingdom;* [2]*Waters Corporation, Milford, MA*

MP 318 **RF Phase–Dependent Transfer Efficiency and Loss Mechanisms in a STorIT–CIT Coaxial Ion Trap**; Dallin C Tyger[1]; Daniel E. Austin[2]; Nicholas Taylor[3]; [1]*Brigham Young University, PROVO, UT;* [2]*Brigham Young Uniersity, Provo, UT;* [3]*Western Michigan University, Kalamazoo, MI*

MP 319 **Optimization of q Value for Ultra-Sensitive Detection of Nucleosides and Peptides by MS3**; Zheng Duan[1]; Yinsheng Wang[2]; Chen Wang[2]; [1]*University of California Riverside, Riverside, CA;* [2]*University of California, Riverside, Riverside, CA*

MP 320 **Towards 1 kDa Resolution Nanoelectromechanical Mass Sensors: Fabrication Innovations and Performance Benchmarking**; Atakan Ari[1]; Jeffrey J. Jones[1]; Michael L Roukes[1]; [1]*Caltech, Pasadena, CA*

MP 321 **Improving Sequence Coverage in Top-down Proteomics Through Charge Detection Mass Spectrometry on a modified Orbitrap Tribrid**; David Bergen[1]; Jingjing Huang[1]; Weijing Liu[1]; Christopher Mullen[1]; Kyle Patrick Bowen[1]; Graeme C McAlister[1]; Rafael D Melani[1]; [1]*Thermo Fisher Scientific, San Jose, CA*

MP 322 **Extended Mass Range CDMS and Dynamics of Water Droplet-Surface Interactions in Mass Spectrometer Inlets: Implications for Droplet Chemistry**; Matthew S. McPartlan[1]; Casey Chen[1]; Evan R. Williams[1]; [1]*University of California, Berkeley, Berkeley, CA*

MP 323 **Chemical Insights on the Structural Heterogeneity of Polysorbate Mixtures Uncovered Using High Resolution Ion Mobility-Mass Spectrometry Analysis**; Kyle E Lira[1]; Alexander D Goodness[1]; Jody C May[1]; John A McLean[1]; [1]*Vanderbilt University, Nashville, TN*

MP 324 **Why Neutrons Matter: Predicting the Effects of Isotopic Substitution in Ion Mobility Separations**; Noah D Roberts[1]; Gabe Nagy[1]; [1]*University of Utah, Salt Lake City, UT*

MP 325 **Human Exposure Biomonitoring Using LC-IMS-MS: A Pilot Analysis of Serum from Military Service Members and Scalable Workflow for Large Cohorts**; James N. Dodds[1]; Kara M. Joseph[1]; Sarah J. Rehm[1]; Haley C. Jostes[1]; Allison N. Fry[1]; Nikki Barlow[2]; Ivan Rusyn[2]; Erin S. Baker[1]; [1]*University of North Carolina at Chapel Hill, Chapel Hill, NC;* [2]*Texas A&M Univesity, College Station, TX*

MP 326 **Characterization of Pharmaceutical Degradants in the Environment using Ion Mobility-Tandem Mass Spectrometry (IM-MS/MS)**; Heidi Sabatini[1]; Wendy Cory[2]; Christopher Chouinard[1]; [1]*Clemson University, Clemson, SC;* [2]*College of Charleston, Charleston, SC*

MP 327 **Targeted Carbonyl Derivatization to Expand Ion Mobility-Mass Spectrometry Characterization of Ketosteroids**; Sabrina M Fernandez[1]; Bradley B Garrison[1]; Heidi Sabatini[1]; Christopher Chouinard[1]; [1]*Clemson University, Clemson, SC*

MP 328 **Cyclic Ion Mobility Separations of Oxidized Free Fatty Acids**; Eric Gier[1]; Facundo M. Fernández[1]; [1]*Georgia Institute of Technology, Atlanta, GA*

MP 329 **SLIM Ion Mobility–Mass Spectrometry as a High-Throughput Platform for Reaction Screening Stereochemical Assessment**; Meenakshi Goel[1]; Raymond Lieu[1]; Adam Childs[1]; Tao Chen[1]; Christopher M. Crittenden[1]; [1]*Genentech Inc., South San Francisco, CA*

MP 330 **High-Field Traveling Wave Conditions Change Collision Cross Sections**; Megan R Rooney[1]; Gabe Nagy[1]; [1]*University of Utah, Salt Lake City, UT*

MP 331 **Chromatography-Resolved SEC-CIU enablescorrelation between the higher order structure of bird hemoglobin homologues and their function.**; Turkan Nabiyeva[1, 2]; Léa Letissier[1, 2]; Maïly Kervella[1]; Stephane Hourdez[3]; Christine Schaeffer[1, 2]; François Criscuolo[1]; Fabrice Bertile[1, 2]; Sarah Cianferani[1, 2]; Oscar Hernandez Alba[1, 2]; [1]*Strasbourg University, Strasbourg, France;* [2]*Infrastructure Nationale de Protéomique (ProFI), Strasbourg, France;* [3]*Sorbonne University, Paris, France*

MP 332 **Elucidating the Fine Structure of Fructan Isomers in Agave using Cyclic Ion Mobility Mass Spectrometry**; Luis F Pérez-Vega[1]; Hernando Olivos[2]; Jose J Ordaz-Ortiz[1]; [1]*Center for Research and Advanced Studies of the National Polytechnic Institute (Cinvestav), Irapuato, Mexico;* [2]*Waters Corporation, Milford, MA*

MP 333 **Chiral Selectivity of Copper-Amino Acid Complexation for Ion Mobility Analysis of Small Molecule Enantiomers**; Nina A Metzger[1]; Benjamin K Blakley[2]; Jody C May[1]; John A McLean[1]; [1]*Department of Chemistry, Center for Innovative Technology, Institute of Chemical Biology, Institute for Integrative Biosystems Research, and Education, Nashville, TN;* [2]*Department of Chemistry, Center for Innovative Technology, Institute of Chemical Biology, Institute for Integrative Biosystems Research and Education, Nashville, TN*

MP 334 **Collision Induced Unfolding differentiates the Impact of Fab and Fc glycans in monoclonal antibody structure and stability**; Thomas o. Pereira[1]; Valentina Rangel-Angarita[1]; Addison E. Bergman[1]; Brandon T. Ruotolo[1]; [1]*University of Michigan, Ann Arbor, MI*

MP 335 **Assessing the Prebiotic Plausibility of Boron-Assisted Amino Acid Oligomerization by MS/MS and FAIMS**; Marcos N Eberlin[1]; Guilherme Obeid[2]; Welisson Valerindo Oliveira[1]; Thiago Carita Correra[2]; [1]*Mackenzie University, São Paulo, Brazil;* [2]*University of Sao Paulo, Sao Paulo, Brazil*

MP 336 **Direct Measurement of High-Field Effects in Traveling Wave Ion Mobility Separations Using Isotopologues and Comparison to Quantitative Simulations**; Paige E Robinson[1]; Wiljones Assonfack Djoutsop[2]; Noah D Roberts[1]; Carlos Larriba-Andaluz[2]; Gabe Nagy[1]; [1]*University of Utah, Salt Lake City, UT;* [2]*Purdue University, west lafayette, IN*

MP 337 **Separating Isomeric Monosaccharides via Optimized LC-MS/MS and Ion Mobility Mass Spectrometry**; Gavin Beauchamp[1]; Esabella R. Powers[1]; Elizabeth R Flammer[1]; Timothy J Garrett[1, 2]; [1]*University of Florida, Department of Chemistry, Gainesville, FL;* [2]*University of Florida, College of Medicine, Department of Pathology, Immunology, and Laboratory Medicine, Gainesville, FL*

MP 338 **Probing the interactions of proteins with macrocyclic hosts via collision-induced unfolding experiments in the gas phase**; Sudam Shivaji Mane[1]; David V Dearden[1]; Kenneth W Lee[1]; [1]*Brigham Young University, Provo, UT*

MP 339 **Leveraging Ion Mobility-Mass Spectrometry (IM-MS) and Collision-Induced Unfolding (CIU) to Investigate Anti-Amyloid Antibody Binding**; Saachi Kheterpal[1]; Valentina Rangel-Angarita[1]; Brandon T. Ruotolo[1]; [1]*University of Michigan, Ann Arbor, MI*

MP 340 **Decoding Photochemical Reactivity and Selectivity with Cyclic Ion Mobility–Mass Spectrometry**; Quentin Duez[1]; Catherine Johnson[2]; Ludovic Troian-Gautier[2]; Julien De Winter[1]; Pascal Gerbaux[1]; [1]*University of Mons, Mons, Belgium;* [2]*Catholic University of Louvain, Louvain-la-Neuve, Belgium*

MP 341 **Benchmarking Collision Cross Section Prediction Tools for Intact Proteins Using Drift Tube Ion Mobility Measurements**; JAHZIEL CHASE[1]; Aarthie Senathirajah[2]; Jared Auclair[1]; Mathieu Lavallée-Adam[2]; [1]*Northeastern University, Boston, MA;* [2]*University of Ottawa, Ottawa, ON*

MP 342 **Improved Analysis of Antibody Polymer Conjugates Using Collision Induced Unfolding**; Tiam Farajzadeh[1]; Brandon T. Ruotolo[1]; [1]*University of Michigan-Ann Arbor, Ann Arbor, MI*

MP 343 **Evaluating of IM-MS for Determining the Binding Efficiency of Alternative Histidine Affinity Tags to Zn and Ni Chelating Resins**; Mohammad Arar[1]; Ameryn A. Dixon[1]; Laurence A Angel[1]; [1]*East Texas A&M University, Commerce, TX*

MP 344 **Chiral LC and Ion Mobility Separation of Antibody Drug Conjugate Stereoisomers**; OROBOLA E. OLAJIDE[1]; Daniel Zewge[1]; Jiaxuan Yan[1]; David J. Schenk[1]; Frank Bernardoni[1]; Erica Schwalm[1]; [1]*Merck & Co, Rahway, NJ*

MP 345 **Resolving ADC Heterogeneity and Linker-Payload Stereochemistry Using UPLC-Cyclic Ion Mobility-Mass Spectrometry**; Hee-Jin Yoo[1, 2]; Abhik Mojumdar[1, 3]; Minsun Kim[1]; Sunhee Choi[1]; Yeowoon Koo[1, 3]; Eunji Jeon[1]; Sunho Yun[1]; Kun Cho[1, 3]; [1]*Korea Basic Science Institute, Ochang, Cheongju, South Korea;* [2]*Sogang University, Seoul, South Korea;* [3]*University of Science and Technology, Daejeon, South Korea*

MP 346 **Rapid Structural Elucidation of Thermally Degraded α-NPD in OLED Films by Cyclic Ion Mobility Mass Spectrometry**; Xi Li[1]; Fumiaki Kato[1]; Hikaru Takano[1]; Hiroshi Fujimoto[2]; Shinya Kitagawa[3]; [1]*Toray Research Center, Inc., Otsu, Japan;* [2]*Fukuoka Industry, Science & Technology Foundation, Fukuoka, Japan;* [3]*Nagoya Institute of Technology, Nagoya, Japan*

MP 347 **Precursor and Product Ion Mobility and Collision Cross Section Determination by Travelling Wave Cyclic Ion Mobility–Mass Spectrometry**; Michael McCullagh[1]; Stephen Wong[2]; Lance Nicolaysen[3]; Johannes Vissers[1]; [1]*Waters Corporation, Wilmslow, United Kingdom;* [2]*Waters Pacific Pte. Ltd., Singapore 117528, Singapore, Singapore;* [3]*Waters, Milford, MA*

MP 348 **Trapped Ion Mobility Spectrometry Enables Selective Analysis of Sugar Phosphates and Acyl-CoA Metabolites**; Erica Marie Forsberg[1]; Prasanna Vadhana Ashok Kumaar[2]; Beixi Wang[3]; Birgitta Ryback[4]; Birgit Schilling[2]; Eric Verdin[2]; [1]*Bruker Daltonics, San Jose, CA;* [2]*Buck Institute for Research on Aging, Novato, CA;* [3]*Bruker Scientific LLC, San Jose, CA;* [4]*Bruker Scientific LLC, Billerica, MA*

MP 349 **Fast and ultra-sensitive screening of PFAS in surface waters using a novel TIMS-QTOF MS and large volume injection**; Carsten Baessmann[1]; Birgit Schneider[1]; Ilona Nordhorn[1]; Karin Wendt[1]; Yann Hebert[2]; [1]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [2]*Bruker France SAS, Wissembourg, France*

MP 350 **IMoS 2.0 Simulations Reveal Negligible Relaxation Effects and Quantify High Field Transport in Traveling Wave Ion Mobility Systems**; Wiljones A Djoutsop[1]; Carlos Larriba-Andaluz[1]; [1]*Purdue University, West lafayette, IN*

MP 351 **Collision-Induced Unfolding of Native-Like Proteins using Structures for Lossless Ion Manipulation High-Resolution Ion Mobility**; Walker N Hodges[1]; Jody C May[1]; John A McLean[1]; [1]*Vanderbilt University, Nashville, TN*

MP 352 **A MALDI-TIMS-TOF Method Tailored for Low-Mass and High-Ion-Mobility Ions Enables the Molecular Characterization of Passivation Layers in Lithium-Ion Batteries**; Théo Sombret[1, 2, 3, 4];

Egon Kherchiche[2, 3, 4, 5]; Marie Hubert Roux[2, 5]; Antonin Gajan[4]; Julien Maillard[2, 3]; Simon Ollivier[2, 5]; Carlos Afonso[2, 5]; Pierre Giusti[2, 3, 5]; *[1]University of Rouen-CARMeN institut, Mont-Saint-Aignan, France; [2]International Joint Laboratory for Complex Matrices Molecular Characterization (iC2MC), Harfleur, France; [3]TotalEnergies Research and Technology Gonfreville, Harfleur, France; [4]Saft, Corporate Research, 33074, Bordeaux, France; [5]CARMeN institute, UMR 6064, CNRS, University of Rouen Normandy, Rouen, France*

MP 353 **Non-Targeted Cyclic IMS Analysis of Fungi-Induced Per- and Polyfluoroalkyl Substances (PFAS) Degradation**; Rachel A Harris[1]; Nan Qiu[1]; Hilary Wyner[2]; Areen Banerjee[2]; Julia Balog[1]; *[1]Waters Corporation, Milford, MA; [2]Allonia, Boston, MA*

MP 354 **Whole-Omics Analysis of Foodborne Pathogens using High-Resolution Ion Mobility Mass Spectrometry and Innovative Machine Learning Algorithms**; Adebowale Oyerinde[1]; Kimberly Y. Kartowikromo[1]; Jessica S Pizzo[1]; Iffat Jerin[1]; Michael Zirpoli[1]; Md Naymor Rahaman[1]; Viraj D Gandhi[1]; Kristen Marshall[1]; Jingyi Zheng[1]; Ahmed Mohamed Hamid[2]; *[1]AUBURN UNIVERSITY, Auburn, AL; [2]Auburn University, Auburn, AL*

MP 355 **Improving Detection and Selectivity of PFAS Molecules Using Cyclic Ion Mobility Wideband Enhancement**; Michael McCullagh[1]; Yuriy Yuriy Pyatkivskyy[2]; Bryan McCullough[1]; Darren Hewitt[1]; Zoltan Laszlow[1]; Chris Hughes[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

MP 356 **Coupling variable-temperature electrospray with trapped ion mobility mass spectrometry can support the structure-driven discovery of new selective antiviral drugs**; Michael Addo[1]; Daniele Fabris[2]; *[1]University of Connecticut, Storrs, CT; [2]University of Connecticut, Connecticut, CT*

MP 357 **Assessing Relative Response of Four European-Regulated PFAS in Human Serum Using Cyclic Ion Mobility MS**; Pennante Bruce-Vanderpuije[1]; Kabre Heck[2]; Sara Beverley[3]; Kwadwo Ansong Asante Ansong Asante[1]; David Megson[4]; Stuart Adams[3]; Michael McCullagh[3]; *[1]CSIR-Water Research Institute, Accra, Ghana; [2]Waters Corporation, Milford, MA; [3]Waters Corporation, Wilmslow, United Kingdom; [4]Manchester Metropolitan University, Manchester, United Kingdom*

MP 358 **Fractionation of Protein Conformers, Oligomers, and Mixtures by Enhanced Divergent Field Ion Mobility Focusing (DIFIMOF) with High-Resolution MS**; Adetayo S. Afolayan[1]; Hayden A. Thurman[1]; Alexandre A. Shvartsburg[1]; *[1]Wichita State University, Wichita, KS*

MP 359 **Structural Characterization of Organic Compounds via Comprehensive Isotopic Shift Matrices from Ion Mobility Separations with Ultrahigh Resolution FT-ICR Mass Spectrometry**; Steven A. DeFiglia[1, 2]; Hayden A. Thurman[3]; Nathan K. Kaiser[2]; Chad R. Weisbrod[2]; Greg T. Blakney[2]; John P. Quinn[2]; Kristina Hakansson[1, 2]; Alexandre A. Shvartsburg[3]; *[1]Florida State University, Tallahassee, FL; [2]National High Magnetic Field Laboratory, Tallahassee, FL; [3]Wichita State University, Wichita, KS*

MP 360 **Modulating ion transmission with FAIMS by changing electrode temperature improves coverage in complex biological samples**; Michael Belford[1]; Lilian Heil[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

MP 361 **The benefit of differential mobility separation (DMS) for the analysis of phosoporylated peptides**; Yves Le Blanc[1]; Yang Kang[2]; Harikrishnan Sukumar[2]; Bradley B Schneider[2]; *[1]SCIEX, Concord, On, ON; [2]SCIEX, Concord, ON*

MP 362 **SLIM IMS meets PTR-TOF-MS: Characterization and Applications of an Advanced Prototype for Real-Time Isomer Separation and Quantification at pptv Levels**; Jacob Jordan[1]; Alfons Jordan[1]; Christian Lindinger[1]; Gernot Hanel[1]; Tobias Fügenschuh[1]; Martin K. Beyer[2]; Philipp Sulzer[1]; *[1]IONICON Analytik GmbH., Innsbruck, Austria; [2]Depart-ment of Ion Physics and Applied Physics; University of Innsbruck, Innsbruck, Austria*

MP 363 **High-Resolution Ion Mobility Aids in Separation of Irganox from its Degradation Products with Overlapping Retention Times and Isotopic Distributions**; Austin R Anderson[1]; Chris E Freye[1]; Amanda L. Duque[1]; *[1]Los Alamos National Laboratory, Los Alamos, NM*

MP 364 **Development of a Multidimensional Library for Persistent Organic Pollutants using Gas Chromatography-Ion Mobility Spectrometry-Mass Spectrometry (GC-IMS-MS)**; Hayley F. O'Harrah[1]; Kara M. Joseph[1]; James N. Dodds[1]; Erin S. Baker[1]; [1]*University of North Carolina at Chapel Hill, Chapel Hill, NC*

MP 365 **Bis-MPA Dendrimers as Cross-Platform Ion Mobility Calibrants Validated by DMA-MS, and First-Principles Modeling**; Leyan Hua[1]; Md Mahmudul Hasan[1]; Carlos Larriba-Andaluz[1]; [1]*Purdue University, Indianapolis, IN*

MP 366 **Evaluation of TIMS-Derived Peptide Mobility Measurements: Calibration Strategy and MS1/MS2 Discrepancies**; Anh Tran[1]; Tytus Mak[1]; Meghan C. Burke[1]; William E. Wallace[1]; [1]*NIST, Gaithersburg, MD*

MP 367 **Optimization of funnel-SLIM injection interface for higher ion transmission with preserved mobility resolution**; Viraj D Gandhi[1]; Kimberly Y Kartowikromo[1]; Gordon A. Anderson[2]; Aneesh Prabhakaran[3]; Ahmed M Hamid[1]; [1]*AUBURN UNIVERSITY, Auburn, AL;* [2]*GAA Custom Electronics, Kennewick, WA;* [3]*Bruker Daltonics GmbH & Co.KG, Bremen, Germany*

MP 368 **A mobility zoom scanning mode for increased resolution using Waters SELECT Series cyclic IMS-MS**; Colin R Johnson[1]; Sarah M. O'Keefe[1]; David E. Clemmer[1]; [1]*Indiana University - Bloomington, Bloomington, IN*

MP 369 **CCSBase2: A Unified Benchmark Dataset and Machine Learning Framework for Accurate and Generalizable CCS Prediction**; Amogh Bantwal[1]; Reuben Santoso[1]; Ryan Nguyen[1]; Griffin Rangel[1]; Libin Xu[1]; [1]*University of Washington, Seattle, WA*

MP 370 **Systematic LC Method Development: A Case Study on Mupirocin**; Jenny C Lewis[1]; Crystal Holt[1]; [1]*Phenomenex Inc., Torrance, CA*

MP 371 **Gradient UHPLC–MS/MS PFAS Analysis for Standards and Cosmetics Using Shodex C18U 2B with an ODP-50 4B Delay Column**; Tanya Napolitano[1]; Hiroki Takenaka[2]; [1]*Shodex, New York, NY;* [2]*Shodex Service Center, Resonac Corporation, Kawasaki, Japan*

MP 372 **Integrator: Enabling fast and consistent peak integration in multi-batch targeted metabolomics**; Karel Kalecký[1]; Teodoro Bottiglieri[1]; [1]*Baylor Scott & White Research Institute, Dallas, TX*

MP 373 **LC-MS/MS-based screening for novel glycolipid biosurfactants by feature-based and ion identity molecular networking**; Philipp Otzen[1]; Marie Dielentheis-Frenken[2, 3]; Kerstin Schipper[4, 5]; Ansgar Korf[6]; Till Tiso[3]; Lars M. Blank[2]; Heiko Hayen[1]; [1]*Institute of Inorganic and Analytical Chemistry, University of Münster, Münster, Germany;* [2]*iAMB - Institute of Applied Microbiology, ABBt - Aachen Biology and Biotechnology, RWTH Aachen University, Aachen, Germany;* [3]*Systems Biotechnology, Faculty of Technology, Bielefeld University, Bielefeld, Germany;* [4]*Institute of Microbiology, Heinrich-Heine University Düsseldorf, Düsseldorf, Germany;* [5]*Bioeconomy Science Center (BioSC), C/O Forschungszentrum Jülich, Jülich, Germany;* [6]*mzio GmbH, Bremen, Germany*

MP 374 **Advanced 2D LC-MS workflow for enhanced resolution of protein components in Indian Cobra venom using HIC-RP chromatography**; KUNAL KRISHNA[1]; Sunil Kumar[2]; [1]*IIT Delhi, Delhi, India;* [2]*The University of Pavia, PV, Italy*

MP 375 **Single-shot Multi-omic Analysis with an Intelligent Ion Source and Micropillar Array Columns**; Li-Yu Chen[1, 2]; Benjamin Chadwick[3]; Salma I. Abouelhassan[2, 4]; Scott T. Quarmby[2, 4]; Katherine L. Walker[5]; Graeme C. McAlister[5]; Katherine A. Overmyer[2, 3, 4]; Joshua J. Coon[1, 2, 3, 4]; [1]*Department of Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI;* [3]*Morgridge Institute for Research, Madison, WI;* [4]*National Center for Quantitative Biology of Complex Systems, Madison, WI;* [5]*Thermo Fisher Scientific, San Jose, CA*

MP 376 **Simple and Robust NanoLC system for High Throughput Proteomics**; Shi-Yuan Michael Su[1]; Xiaofeng Xie[2]; Thy Truong[2]; Michael Williams[2]; [1]*Brigham Young Uniersity, Provo, UT;* [2]*MicrOmics Technologies, Spanish Fork, UT*

MP 377 **Performance, carry-over and robustness evaluation of a newly available LC-MS/MS setup for proteomics profiling**; Kevin Pacios[1]; Mario Mirabelli[2]; Sebastian Mueller[1]; Roland Bruderer[1]; *[1]Biognosys AG, Schlieren, Switzerland; [2]Bruker Switzerland AG, Fällanden, Switzerland*

MP 378 **Systemic Evaluation of Nano-LC Column Configurations for High-Throughput Mass Limited Proteomics**; Mai A. Atallah[1]; Zhitao Zhao[1]; Samin Anjum[1]; Anju Teresa Sunny[1]; Si Wu[1]; *[1]University of Alabama, Tuscaloosa, AL*

MP 379 **iFAMS 1-Click: Accurate and Fully Automatic Gábor-Transform-Based Deconvolution for Multi-Analyte and Top-Down Analysis of Biomolecules**; Kayd L Meldrum[1]; James S Prell[1]; *[1]University of Oregon, Eugene, OR*

MP 380 **Dereplicating LC-TIMS-MS Data Through Deep Learning Molecular Networking in mzmine's Compound Dashboard**; Robin Schmid[1]; Ansgar Korf[1]; Steffen Heuckeroth[1]; Tomáš Pluskal[2]; Nikolas Kessler[3]; Aiko Barsch[3]; Sven Meyer[3]; Claudia Martelli[3]; Heiko Neuweger[3]; Matthew R. Lewis[3]; *[1]mzio GmbH, Bremen, Germany; [2]IOCB of the CAS, Prague, Czech Republic; [3]Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

MP 381 **Load-Dependent Flow Rate Optimization For Balancing Sensitivity And Throughput In High-Throughput Proteomics**; Jeff Op De Beeck[1]; Frederic Fontaine[2]; Pedro Magalhães[3]; Bart Ghesquiere[3]; Marcel Bühler[4]; Emin Araftpoor[4]; Kris Gevaert[4]; Natalie Van Landuyt[1]; Paul Jacobs[1]; *[1]Thermo Fisher Scientific, Gent, Belgium; [2]Thermo Fisher Scientific, Courtaboeuf, France; [3]KU Leuven Laboratory of Applied Mass Spectrometry, Leuven, Belgium; [4]UGent Gevaert Lab, Gent, Belgium*

MP 382 **High-performing PepSep Advanced columns enable deep profiling of P2-enriched plasma samples on an Orbitrap Astral**; Bettina Streckenbach[1]; Christopher Below[1]; Sandra Schaer[1]; Sebastian Mueller[1]; Leander S. Runtsch[2]; Martin Schirmer[3]; Nils A Kulak[2]; Roland Bruderer[1]; *[1]Biognosys AG, Zurich, Switzerland; [2]PreOmics GmbH, Martinsried, Germany; [3]Bruker Daltonics GmbH & Co.KG, Bremen, Germany*

MP 383 **High-Performance Biphenyl HPLC Columns with Enhanced pH Stability**; Chris Collins[1]; Gabrielle Zabala[2]; Bonnie Alden[2]; Cheryl Boissel[2]; Weiqiang Gu[2]; Thomas H Walter[2]; Daniel P Walsh[2]; Jim Cook[2]; Kenneth Berthelette[2]; Melissa Aiello[2]; *[1]Waters Corporation, Wake Forest, NC; [2]Waters Corporation, Milford, MA*

MP 384 **Chromatography Comparison of Ultra-Short-Chain PFAS in Complex Food Matrix Extracts**; Chenchen He[1]; Limian Zhao[1]; *[1]Agilent Technologies, Wilmington, DE*

MP 385 **Guard-Column-Protected Dual-Column Single-Emitter LC–MS Enables Uninterrupted High-Throughput Clinical Proteomics**; Michele Puglia[1]; Paola Pisano[1]; Victor Castañeda-Monsalve[1]; Estrella Silva-Pavez[1]; Runsheng Zheng[2]; Alec Valenta[2]; Michael Wierer[1]; *[1]University of Copenhagen, Copenhagen, Denmark; [2]Thermo Fisher Scientific, Germering, Germany*

MP 386 **Solving Analytical Challenges in PFAS Testing: Robust Calibration Data, Low Mass Confirmation and Isomer Quantification**; David Gould[1]; Narendra Meruva[2]; Dimple Shah[2]; *[1]Waters, Wilmslow, United Kingdom; [2]Waters Wilmslow UK, Wilmslow, United Kingdom*

MP 387 **A User-Friendly, Regulatory-Compliant Multi-Attribute Method Workflow for Monitoring Critical Quality Attributes and Enabling Method Transfer**; Lichen Xiu[1]; Mike Knierman[1]; Mahsan Malidi[1]; Melissa Sato[1]; Robert Barkovich[1]; Julie Horner-Buxton[1]; *[1]Agilent Technologies, Santa Clara, CA*

MP 388 **Stability and Impurity Monitoring of GLP-1 Therapeutic Peptide Retatrutide Using a 2D-LC/TOF MS Platform**; Li Gu[1]; Elizabeth Almasi[1]; Linfeng Wu[1]; Guannan Li[1]; *[1]Agilent Technologies, Santa Clara, CA*

MP 389 **Customizable Intelligent Reflex Workflows: Embedding User-Defined Reaction Logic in Automatic High Throughput LC/MS Analysis**; Disha M Shah[1]; Amol Waware[2]; Lee J Bertram[1]; Emma E Rennie[1]; Yu Zhu[1]; *[1]Agilent Technologies, Inc., Santa Clara, CA; [2]Persistent Systems Ltd., Pune, India*

MP 390 **A simplified workflow using MassHunter Explorer 2.0 with Sirius to evaluate Dalbavancin impurities**; Xiuhong Sun[1]; Jia Tu[1]; [1]*Agilent Technologies (China) Co.,Ltd, Shanghai, China*

MP 391 **Oligonucleotide Analysis with new tools: Pluses and Minuses**; St John Skilton[1]; Ignat Shilov[2]; Steven Broome[2]; Gary Wilson[2]; Stephen Kurzyniec[3]; [1]*Protein Metrics, Inc., Boston, MA;* [2]*Protein Metrics, Boston, MA;* [3]*Shimadzu Scientific Instruments, Inc, Columbia, MD*

MP 392 **Reducing the Interpretation Bottleneck in Untargeted Lipidomics Using HRMS Decision Support**; Osanda Hemachandra[1]; Harshani Bandara[1]; Sanoj Silva[1]; Rukshan Wijesinghe[1]; Lalin Theverapperuma[1]; [1]*EXPERT Intelligence, Santa Clara, CA*

MP 393 **Overcoming amide rotamer–induced peak splitting through mobile-phase optimization in high-performance LC-MS quantification**; Chang Liu[1]; Pei Wang[1]; Christopher Ciptadjaya[1]; Jie Ding[1]; [1]*Thermofisher Scientific, Middleton, WI*

MP 394 **Quantifying PFAS in Archived Formalin-Fixed and Paraffin-Embedded Tissues Using LC–MS/MS for Retrospective Biomonitoring**; Kushal Biswas[1]; Jennifer J. Schlezinger[2]; Anila Bello[1]; Dhimiter Bello[1]; [1]*University of Massachusetts Lowell, Lowell, MA;* [2]*Boston University, Boston, MA*

MP 395 **Sample Miniaturization for Plasma Proteomics Using Nanotrap PEAK**; Natalie L Smith[1]; Anurag Patnaik[1]; Ben Lepene[1]; [1]*Ceres Nanosciences, Manassas, VA*

MP 396 **$10 Plasma Proteome: A Streamlined Two-Track Preparation Workflow for High-Throughput, Low-Cost Plasma Proteomics**; Raphaela M. De Oliveira[1]; Michael Krawitzky[2]; Chao Wang[1]; Ken Triggs[1]; Garrett Haynie[1]; Ryan T. Kelly[1]; [1]*Brigham Young University, Provo, UT;* [2]*Bruker Scientific LLC, San Jose, CA*

MP 397 **Drug Driving: Optimised Sample Preparation for Drugs of Abuse Extraction from Oral Fluid prior to UHPLC-MS/MS Analysis**; Lucy Richards[1]; Lee Williams[1]; Russell Parry[1]; Helen Lodder[1]; Adam Senior[1]; Zainab Khan[1]; Charlotte Hayes[1]; Geoff Davies[1]; Claire Desbrow[1]; [1]*Biotage GB Limited, Cardiff, United Kingdom*

MP 398 **ELAEXIA Ca+Re: Highly Specific Exosome Capture and Controlled Release for Mass Spectrometry Proteomics**; Evelyn Hammer[1]; Rudolf Napieralski[1]; Antonio Piras[1]; Catharina Strube[1]; Sabrina Richter[1]; Christoph Krisp[2, 3]; Gary Kruppa[2]; Gabriele Schricker[1]; Bastian Hoechst[4]; Valter Bergant[5, 6]; Andreas Pichlmair[5]; Olaf G. Wilhelm[1]; Percy A. Knolle[4]; [1]*therawis diagnostics GmbH, Munich, Germany;* [2]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [3]*MDC-Bruker Center of Excellence for Single Cell Omics, Max Delbrück Center for Moleculare Medicine in the Helmholtz-association, Berlin, Germany;* [4]*Institute of Molecular Immunology, TUM University Hospital, TUM, Munich, Germany;* [5]*Institute of Virology, TUM, Munich, Germany;* [6]*National Institute of Chemistry, Ljubljana, Slovenia*

MP 399 **Subcellular Proteomic Enrichment of Human Cortical Tissue by Biochemical Fractionation**; Alek H. Grady[1]; Susan Erickson[1]; Robert A. Sweet[1]; Matthew L. MacDonald[1]; [1]*University of Pittsburgh, Pittsburgh, PA*

MP 400 **Evaluation of Various Sample Preparation Techniques for the Extraction of GLP-1 Analogues from Plasma Prior to UHPLC-MS/MS Analysis**; Helen Lodder[1]; Charlotte Hayes[1]; Russell Parry[1]; Lee Williams[1]; Lucy Richards[1]; Geoff Davies[1]; Adam Senior[1]; Zainab Khan[1]; Claire Desbrow[1]; Esraa AboJasser[2]; [1]*Biotage GB Limited, Cardiff, United Kingdom;* [2]*Biotage, Charlotte, NC*

MP 401 **Mag-NetTM HP provides a simple and robust workflow for deeper plasma proteome profiling using hyper-porous magnetic bead technology**; Amy Van Graan[1, 2]; Melissa Vorster[1]; Isak Gerber[1]; Justin Jordaan[1, 2]; Previn Naicker[1]; [1]*ReSyn Biosciences, Pretoria, South Africa;* [2]*Rhodes University, Grahamstown, South Africa*

MP 402 **Evaluation and comparison of C18 Tips performance for peptide and phosphopeptide desalting in MS-based proteomics workflows**; Brett Phinney[1]; Seamus R. Morrone[2]; Robert L. Moritz[2]; Mana Shafaei[3]; Kaynoush Naraghi[4]; [1]*University of California, Davis, CA;* [2]*Institute For Systems Biology, Seattle, WA;* [3]*AFFINISEP USA, Miami, FL;* [4]*AFFINISEP, Le Houlme, France*

MP 403 **Extraction of anti-miR-17 oligonucleotide RGLS4326 by Biotage® Oligo SPE from human plasma prior to LC-MS/MS Analysis**; Sohel Rana[1]; Jacob Slizel[2]; Esraa AboJasser[1]; Lee Williams[3]; Farah Mavandadi[4]; [1]*Biotage LLC, Charlotte, NC;* [2]*Biotage, Charlotte, NC;* [3]*Biotage GB Limited, Cardiff, United Kingdom;* [4]*Biotage, San Jose, CA*

MP 404 **Overcoming Salt-Induced Disruption: Methanol Enhancement of Protein Aggregate Capture**; Dana L Carper[1]; Paul Abraham[1]; Richard Giannone[1]; [1]*Oak Ridge National Laboratory, Oak Ridge, TN*

MP 405 **A comparison of EV isolation techniques using human saliva**; Bruce Mousseau[1, 2]; Gavin Li[2]; Sean W Harshman[2]; Rhonda Pitsch[2]; [1]*AV Inc, Beavercreek, OH;* [2]*Air Force Research Laboratory, Dayton, OH*

MP 406 **A Novel Lysine-specific Protease with Superior Digestion Efficiency**; Philip J Widdowson[1]; John Turman[2]; Magdalena Widgren-Sandberg[1]; Andreas Nägeli[1]; John Lindsay[2]; [1]*Genovis AB, Kävlinge, Sweden;* [2]*Genovis Inc., Cambridge, MA*

MP 407 **On-line Affinity-LC-MS Detection of Amyloid-Beta Proteoforms from Complex Sample Matrices**; Susan E. Abbatiello[1]; Jeffrey C. Silva[2]; Ryan Sinapius[2]; Kevin Wyndham[1]; [1]*Waters Corporation, Milford, MA;* [2]*Cell Signaling Technology Inc, Danvers, MA*

MP 408 **An Optimized Workflow for the Proteomic Analysis of Exosomes**; Michael Rosenblatt[1]; Lindsey Johnson[1]; Kevin Mayer[1]; Zach Van Den Heuvel[2]; Marjeta Urh[1]; [1]*Promega, Madison, WI;* [2]*Agilent Technologies, Santa Clara, CA*

MP 409 **Breaking the Sample Prep Barrier in LC-MS Quantification of Biotherapeutics in Preclinical In Vivo Studies**; Gwendolyne Adjamgba[1]; Joséphine Cherrière[1]; Valérie Lafont[1]; Mathieu Dupré[1]; [1]*LCMS Bioanalysis, Laboratory Sciences, Translational Medicine Unit, Sanofi R&D, France, Vitry-sur-Seine, France*

MP 410 **Fully-Automated Magnetic Bead based Approaches for Mass Spec Sample Preparation**; Michael Rosenblatt[1]; Zach Van Den Heuvel[2]; Lindsey Johnson[1]; Chris Hosfield[1]; Ellen Crummy[1]; Zhiyang Zeng[1]; Wenhui Zhou[1]; Marjeta Urh[1]; [1]*Promega Corporation, Madison, WI;* [2]*Agilent Technologies, Inc., Santa Clara, CA*

MP 411 **Benchmarking Bead-Based Workflows for Automated Peptide Desalting to Enable Robust LC–MS/MS Proteomics**; Melissa Vorster[1]; Amy Van Graan[1, 2]; Isak Gerber[1]; Justin Jordaan[1, 2]; Previn Naicker[1]; [1]*ReSyn Biosciences, Pretoria, South Africa;* [2]*Rhodes University, Grahamstown, South Africa*

MP 412 **Benchmarking Extracellular Vesicle Enrichment and Protein Precipitation Workflows for Urinary Proteomic Profiling**; Jennifer Roof[1]; Hossein Fazelinia[1, 2]; Luca Musante[3]; Erik Nash[1]; Elizabeth M Brown[1]; Michael Krawitzky[4]; Lynn A Spruce[1]; [1]*Proteomics Core Facility, Children's Hospital of Philadelphia, Philadelphia, PA;* [2]*Department of Biomedical and Health Informatics, Children's Hospital of Philadelphia, Philadelphia, PA;* [3]*Extracellular Vesicle Core Facility, University of Pennsylvania School of Veterinary Medicine, Philadelphia, PA;* [4]*Bruker Scientific LLC, Billerica, MA*

MP 413 **Improved Mammalian Tissue Processing for Multi-Omic Mass Spectrometry**; Xiaomeng Liang[1]; Mark Sartain[2]; Genevieve C. Van De Bittner[2]; Karen Yannell[2]; Donghui Yi[2]; Manorama Tummala[2]; Ritin Sharma[3, 4]; Stephen Mok[1]; Xinran Qi[1]; Katarzyna Dabrowska[3]; Khyatiben V. Pathak[4]; Roger Moore[3]; Sameer Vasantgadkar[5]; Fang Xie[5]; Debadeep Bhattacharyya[5]; Patrick Pirrotte[3, 4]; Jennifer Karmouch[1]; Robert R. Jenq[1]; Philip L. Lorenzi[1]; [1]*Department of Hematology and Hematopoietic Cell Transplantation, City of Hope National Medical Center, Duarte, CA;* [2]*Agilent Technologies, Santa Clara, CA;* [3]*Integrated Mass Spectrometry Shared Resource Facility, City of Hope National Medical Center, Duarte, CA;* [4]*Early Detection and Prevention Division, Translational Genomics Research Institute, Phoenix, AZ;* [5]*Covaris LLC, Woburn, MA*

MP 414 **From Discovery to Application: A Fully Automated and High-Throughput Workflow for large-Scale Targeted Plasma Proteomics**; Iulia Macavei[1]; Stoyan Stoychev[1]; Pia H Jensen[1]; Veronica Macaluso[1]; Adrian H Bache[1]; Nicolai Bache[1]; Dorte B. Bekker-Jensen[1]; [1]*Evosep Biosystems, Odense, Denmark*

MP 415 **Enzymatic Digestion-Coupled LC-MS/MS: A Novel Strategy for PROTACsQuantification in Disease-State Human Plasma Overcoming Protein Binding Challenges**; Kasie Fang[1]; Hermes Licea-Perez[1]; Timothy Sikorski[1]; *[1]GSK, Collegeville, PA*

MP 416 **Multidimensional Analysis of Oxylipin Profiles in Ischemic and Non-ischemic Cardiomyopathy Patients**; Amie M. Solosky[1]; Jonah P. Parker[1]; Kyu Shik Kim[2]; Rebekah L. Gundry[2]; Erin S. Baker[1]; *[1]University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]University of Nebraska Medical Center, Omaha, NE*

MP 417 **Nano Flow Lipidomics: Sensitivity, Reliability, and Practical Implementation**; Ciara J. Sallowicz[1]; Thiago Mattos[1]; Rahul R. Deshpande[1]; Bashar Amer[1]; Susan S. Bird[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

MP 418 **Cyclic Ion Mobility–Mass Spectrometry Reveals Saccharide-Driven Reactivity in IPBA Suzuki Functionalization of Glycosphingolipids**; Chao Pang[1]; Kenneth W. Lee[2]; *[1]Brigham Young University, Provo, UT; [2]Brigham Young Uniersity, Provo, UT*

MP 419 **IM-QTOF LCMS for Untargeted Lipidomic research on human Extracellular vesicles derived from subcutaneous and omental adipose stem cells**; Qin (Shirley) Xu[1]; Theresa Evans-Nguyen[1]; Brianna Jones[1, 2]; Niketa Patel[1, 2]; Laurent Calcul[1]; *[1]University of South Florida, Tampa, FL; [2]James A. Haley Veterans Hospital, Tampa, FL*

MP 420 **Spatial patterns of lipid perturbation in leafcutter ant fungal gardens exposed to a pathogenic fungus**; Lea Jean-Francois[1]; Marija Velickovic[2]; Jennifer Kyle[2]; Erin S. Baker[3]; Kristin Burnum-Johnson[2]; *[1]UNC Chapel Hill, CHAPEL HILL, NC; [2]PNNL, Richland, WA; [3]UNC- Chapel Hill, Chapel Hill, NC*

MP 421 **Lipidomic Analysis of Bone Tissue Reveals Genotype and 25-Hydroxycholesterol-related Perturbations in an Alzheimer's Disease Mouse Model**; Sarah G Clark[1]; Charles A Schurman[2]; Lisa M Ellerby[2]; Birgit Schilling[2]; Erin S. Baker[1]; *[1]University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]Buck Institute for Research on Aging, Novato, CA*

MP 422 **Evaluation of Retention Time Prediction Methods for Non-targeted Lipidomics Using Liquid Chromatography, Ion Mobility Spectrometry and Mass Spectrometry**; Quentin M DuVal-Smith[1]; Amie M. Solosky[2]; James N Dodds[2]; Erin S. Baker[2]; *[1]University of North Carolina at Chapel Hill Chemistry Department, Chapel Hill, NC; [2]University of North Carolina at Chapel Hill, Chapel Hill, NC*

MP 423 **Pharmacological Inhibition of Ficolin via Drug Repurposing Alters Brain Lipid Profiles and Related Biological Pathways Revealed by LC-MS/MS**; Tanjina Akter Suma[1]; Reham M. Fayed[2]; Abderrahmane Koraich[1]; Odunayo Oluokun[1]; Oluwatosin Daramola[1]; Vishal Sandilya[1]; Hisham A. Nematalla[2, 3]; Ihab Talat Abdel-Raheem[2]; Ahmed F. El-Yazbi[3, 4]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Damanhour University,, Damanhour, Egypt; [3]Alamein International University, Alamein, Egypt; [4]Alexandria University, Alexandria, Egypt*

MP 424 **Using Analysis of Variance - Simultaneous Component Analysis (ASCA) to Quantify Variability in Two Lipidomic Datasets**; Aleesa E Chua[1]; Eden P Go[1]; Heather Desaire[1]; *[1]University of Kansas, Lawrence, KS*

MP 425 **Determination of Double Bond Positions in Unsaturated Fatty Acids UsingPermanganate Oxidation and Tandem Mass Spectrometry of CuIICl+ Adducted Ions**; Tak-Wah Dominic Chan[1]; Dong Zhang[1]; Danna Hu[1]; *[1]The Chinese Univ. of Hong Kong, Hong Kong Sar, China*

MP 426 **High-fat Diet Modulates the Cardiac Lipidomics Response to Traumatic Brain Injury in Mice**; Abderrahmane Koraich[1]; Oluwatosin Daramola[1]; Akeem Sanni[1]; Odunayo O. Oluokun[1]; Tanjina Akter Suma[1]; Abiodun M. Adewolu[1]; Esther O. Oji[1]; Judith Nwaiwu[1]; Stanley Ibeh[2]; Sarin Mekhjian[3]; Firas H. Kobaissy[4]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Dalhousie University, Halifax, NS; [3]American University of Beirut, Beirut, Lebanon; [4]Center for Neurotrauma, Multiomics & Biomarkers (CNMB) Morehouse School of Medicine, Atlanta, GA*

MP 427 **LC-MS/MS Lipidomics Reveals Obesity-Stage–Specific Lipidome Remodeling and Its Effects on Inflammation and Mitochondrial Function**; Shafia Shafiq Nishe[1]; Judith Nwaiwu[1]; Cristian D Gutierrez-Reyes[1]; Oluwatosin Daramola[1]; Tuli Bhattacharjee[1]; Sergio Guzman-Rodriguez[2]; Bruno A Marichal-Cancino[2]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Center of Basic Sciences, Department of Physiology and Pharmacology, Universidad Autónoma de Aguascalientes, Aguascalientes, Mexico*

MP 428 **Direct Measurement of Lipoprotein Particle Heterogeneity Using CDMS**; Brad Williams[1]; Rebecca D'Esposito[1]; Joanne Agus[2]; Ying Qing Yu[1]; Michelle Chen[3]; Angela M. Zivkovic[2]; *[1]Waters Corporation, Milford, MA; [2]University of California, Davis, Davis, CA; [3]Waters Corporation, Goleta, CA*

MP 429 **Characterizing Lipid Nanoparticle Vaccines Using CDMS and FFF-MALS: A Multi-Dimensional Approach**; Rebecca D'Esposito[1]; Martin Kurnik[2]; Sophia Kenrick[2]; Ying Qing Yu[1]; Michelle Chen[2]; Erin McAllister[1]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Goleta, CA*

MP 430 **MS2-Driven Lipid Identity Verification – Building Robust Targeted MRM Methods from Discovery Lipidomics**; Charles M. Nichols[1]; Moises Zapata[1]; Yu Han[1]; Kim Ekroos[2]; Rachel Culp-Hill[1]; Shannon Kilkenny[1]; James R. White[3]; Enkhtuya Radnaa[1]; Brendan M. Giles[1]; Maria Wong[1]; Mattie Goldberg[1]; Vuna S. Fa[1]; Cory Bystrom[1]; Abigail McElhinny[1]; *[1]AOA Dx, Denver, CO; [2]Lipidomics Consulting Ltd, Esbo, Finland; [3]Resphera Biosciences, Baltimore, MD*

MP 431 **Isolation and Analytical Choices Define the Observable Lipidome of Small Extracellular Vesicles**; Danielle Maundy[1]; Fernanda Sousa Monteiro[1,2]; Adriana Zardini Buzatto[1,2,3]; *[1]University of Calgary, Calgary, AB; [2]Calgary Metabolomics Research Facility (CMRF), Calgary, AB; [3]Alberta Centre for Advanced Diagnostics (ACAD), Calgary, AB*

MP 432 **Lipidomics Analysis Reveals Synergistic Effects of High-Fat Diet and Traumatic Brain Injury on Liver Metabolism**; Md Faizur Rahman[1]; Favour M. Chukwubueze[1]; Akeem Sanni[1]; Tuli Bhattacharjee[1]; Shafia Shafiq Nishe[1]; Tanjina Akter Suma[1]; Judith Ijeoma Nwaiwu[1]; Oluwatosin Daramola[1]; Stanley Ibeh[2]; Sarin Mekhjian[3]; Firas H. Kobeissy[3,4]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Dalhousie University, Halifax, NS; [3]American University of Beirut, Beirut, Lebanon; [4]Center for Neurotrauma, Multiomics & Biomarkers (CNMB) Morehouse School of Medicine, Atlanta, GA*

MP 433 **Parallel Orbitrap–21T FT-ICR LC–MS/MS Acquisition for Confident Lipid Annotation in Complex Marine Matrices**; Martha L Aguilera[1]; Robert Horn[2]; Blaženka Gašparović[2]; Jelena Godrijan[2]; Chad R. Weisbrod[1]; Lissa C Anderson[1,3]; Huan Chen[1]; Kristina Hakansson[1,3]; *[1]National High Magnetic Field Laboratory, Tallahassee, FL; [2]Division for Marine and Environmental Research, Ruđer Bošković Institute, Zagreb, Croatia; [3]Florida State University - Department of Chemistry & Biochemistry, Tallahassee, FL*

MP 434 **Whole Cell and Organelle Resolved Lipidomic Analyses for Human T Cells**; Jonah P Parker[1]; Amie M. Solosky[1]; Andrew S Kennedy[2]; Jessica E Thaxton[1,2]; Erin S. Baker[1]; *[1]University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]Lineberger Comprehensive Cancer Center, Chapel Hill, NC*

MP 435 **Alteration of Lipid Profile in Patients with Narcolepsy Type 1**; Akeem Sanni[1]; Abiodun M Adewolu[1]; Waziha Tasnim Purba[1]; Md Mostofa Al Amin Bhuiyan[1]; Md Abdul Hakim[1]; Farid Talih[2]; Giuseppe Lanza[3,4]; Firas H. Kobeissy[5,6]; Giuseppe Plazzi[7,8]; Fabio Pizza[7]; Raffaele Ferri[4]; Yehia Mechref[1]; *[1]Department of Chemistry and Biochemistry, Texas Tech University, Lubbock, TX; [2]Department of Psychiatry, Faculty of Medicine, American University of Beirut, Beirut, Lebanon; [3]Department of Surgery and Medical-Surgical Specialties, University of Catania, Catania, Italy; [4]Sleep Research Centre, Department of Neurology IC, Oasi Research Institute- IRCCS, Troina, Italy; [5]Department of Biochemistry and Molecular Genetics, American University of Beirut, Beirut, Lebanon; [6]Department of Neurobiology, Center for Neurotrauma, Multiomics & Biomarkers, Neuroscience Institute, Morehouse School of Medicine (MSM), Atlanta, GA; [7]IRCCS, Istituto delle Scienze Neurologiche di Bologna, Bologna, Italy; [8]Department of Biomedical, Metabolic and Neural Sciences, University of Modena and Reggio Emilia, Modena, Italy*

MP 436 **Fluoroalcohol-Induced Aqueous Multiphase Extraction Coupled with Offline HILIC×RPLC and High-Resolution LC–MS for Advanced Lipidomics**; Md Al Amin[1]; Morteza Khaledi[2]; *[1]The University of Texas at Arlington, ARLINGTON, TX; [2]The University of Texas at Arlington, Arlington, TX*

MP 437 **Quantifying Omega-6/Omega-3 Ratios in Stool and Blood via Lipidomics to Assess the Impact of High Fish Intake**; Chani Sahabandu Hewa Sahabanduge[1]; Suresh Bhandari[1]; Gokalp Kagan Kurtoglu[1]; Remy Burcelin[2]; Kelsey M Mangano[1]; Dhimiter Bello[1]; Pengyuan Liu[1]; *[1]University of Massachusetts Lowell, Lowell, MA; [2]Aviwell SAS, Toulouse, France*

MP 438 **Tandem neutral loss isobaric tag enables accurate lipid identification and quantification with complete isomer resolution**; Jiaxin Feng[1]; Hongyuan Yang[1]; Gopal Reddy Ramidi[1]; Xin Yan[1]; *[1]Texas A&M University, College Station, TX*

MP 439 **Targeted LC-MS/MS Strategy for Sterol Profiling via Multi-dimensional Characterization and Identification**; Wonjae Lee[1, 2]; Jae-Seung Lee[1, 2]; Jungeun Kim[1, 2]; Hye-Jung Kim[3]; Joo-Youn Cho[1, 2]; *[1]Department of Biomedical Sciences, Seoul National University College of Medicine,, Seoul, South Korea; [2]Department of Clinical Pharmacology and Therapeutics, Seoul National University College of Medicine and Hospital, Seoul, South Korea; [3]Gyeongsang National University College of Medicine, Jinju, South Korea*

MP 440 **Impact of aerosol particulate matter on the Scindapsus(Epipremnum aureum) metabolites: High-resolution mass spectrometry based untargeted approach**; Seungwoo Son[1]; Sunghwan Kim[1, 2]; *[1]Mass spectrometry convergence research institute, Kyungpook National University, Daegu, South Korea; [2]Department of Chemistry, Kyungpook National University, Daegu, South Korea*

MP 441 **Metabolomic Characterization of Human Saliva for Identification of Biomarkers of Physical Performance**; Hannah L Whitacre[1]; Elizabeth C. Evin[1]; Chi Yen Tseng[1]; Jessica A. Salguero[1]; Kes A. Luchini[1]; Grace M. Thornhill[1]; Ethan M. McBride[1]; Phillip M. Mach[1]; Trevor G. Glaros[1]; Brett R. Blackwell[1]; *[1]Los Alamos National Laboratory, Los Alamos, NM*

MP 442 **Siderophore-mediated iron sequestration reshapes fungal-bacterial community dynamics by inhibiting specialized metabolism**; Huong Thi Pham[1]; Wonyong Kim[2]; Jeongeun Jang[1]; Ji Seon Kim[3]; Young Woon Lim[3]; Ákos T. Kovács[4]; Kyo Bin Kang[1]; *[1]Sookmyung Women's University, Seoul, South Korea; [2]Department of Applied Biology, College of Agriculture and Life Sciences, Chonnam National University, Gwangju 61186, South Korea; [3]School of Biological Sciences and Institute of Biodiversity, Seoul National University, Seoul 08826, South Korea; [4]Institute of Biology, Leiden University, Leiden 2333BE, Netherlands*

MP 443 **Transparent Reconstruction and Quality Assessment of AIF-Derived MS/MS Spectra for Confident Metabolite Annotation**; Qingqing Mao[1]; Haotian Deng[1]; Xiaoyang Su[1]; *[1]Rutgers, New Brunswick, NJ*

MP 444 **Discovering drug metabolism by mining public metabolomics repositories with a large-scale drug library**; Victoria Deleray[1]; Haoqi Nina Zhao[1]; Jeongin Seo[1]; Shipei Xing[1]; Julius Agongo[1]; Mingxun Wang[2]; Pieter C. Dorrestein[1]; *[1]University of California, San Diego, La Jolla, CA; [2]University of California, Riverside, Riverside, CA*

MP 445 **Nontargeted UHPLC-TIMS-TOF-MS Analyses Identify Bioactive Compounds in American Elderflowers (Sambucus nigra subsp. canadensis)**; Zhentian Lei[1]; Khanh-Van Ho[1]; Sydney Moore[1]; Caleb O'Neal[1]; Matthew Huchteman[1]; Andrew Thomas[1]; Lloyd W Sumner[1]; *[1]University of Missouri-Columbia, Columbia, MO*

MP 446 **Untargeted metabolomics profiling in rodent models of chronic alcohol exposure**; Deirdre A Thornton[1]; Elisha Scott[1]; Charles Levy[1]; Armando Salinas[1]; Hyung W Nam[1]; *[1]LSUHS Shreveport, Shreveport, LA*

MP 447 **Serum metabolite signatures of cognitive resilience in human aging revealed by untargeted metabolomics**; Jeong In Seo[1]; Toon A.W. Scheurink[2]; Lurian Caetano David[3]; Crystal X Wang[1]; Deyvis Solis[4]; Jasmine Zemlin[1]; Jaclyn Bergstrom[1]; Pieter C. Dorrestein[1]; Ipsita Mohanty[5]; Anthony Molina[1]; *[1]University of California San Diego, La Jolla, CA; [2]Center for Clinical Neuroscience and Cognition, University Medical Centre Groningen (UMCG), University of Groningen (RUG), Groningen, Netherlands; [3]Laboratório de Métodos de Extração e Separação (LAMES), Instituto de Química (IQ), Universidade*

Federal de Goiás (UFG), Campus II – Samambaia, Goiânia, Brazil; [4]National University of Santa, Nuevo Chimbote, Peru; [5]Pennsylvania State University, University Park, PA

MP 448 **Improved fecal metabolomics discovery using MS/MS spectral libraries**; Brianna Hunt[1]; Katrina A Doenges[1]; Cole R. Michel[1]; Richard Reisdorph[1]; Kevin Deane[2]; Marie Feser[2]; Catherine Lozupone[2]; Nichole Reisdorph[1]; *[1]Department of Pharmaceutical Sciences, University of Colorado Anschutz Medical Campus, Aurora, CO; [2]Department of Medicine, University of Colorado Anschutz Medical Campus, Aurora, CO*

MP 449 **Expanding plasma metabolome coverage with enhanced dynamic range and iterative MS/MS acquisition on a modified Orbitrap Hybrid mass spectrometer**; Michał Kaczmarek[1]; Bashar Amer[2]; Rahul Deshpande[3]; Maciej Bromirski[1]; Susan S. Bird[2]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientfic, San Jose, CA; [3]Thermo Fisher Scientific, San Jose, CA*

MP 450 **Developing Black Planaria (Dugesia dorotocephala) as Model Organisms for Nutri-Omics Studies**; Rachel Valentine[1]; Vladimir Shulaev[1]; *[1]University of North Texas, Denton, TX*

MP 451 **A non-targeted metabolomics analysis of SARS-CoV-2 and influenza infection in children**; Emily G Armitage[1]; Parthena Savvidou[2]; Olga Begou[3]; Alan Barnes[1]; Elias Iosifidis[2]; Helen Gika[3]; Neil J. Loftus[1]; Emmanuel Roilides[2]; Charalampos Antachopoulos[2]; *[1]Shimadzu Corporation, Manchester, United Kingdom; [2]Infectious Disease Unit, 3rd Department of Pediatrics, Aristotle University School of Medicine, Hippokration General Hospital, Thessaloniki, Greece; [3]Biomic AUTh, Center for Interdisciplinary Research and Innovation, Thessaloniki, Greece*

MP 452 **Metabolomics-Integrated Sleep Architecture Profiling Reveals Gut–Brain Tryptophan Disruption in D-Galactose–Induced Accelerated Aging**; Jae Eun Lee[1]; Khoa Nguyen Tran[2]; Yeasmin Akter Munni[2]; In-Jun Yang[2]; Jeeyoun Jung[1]; *[1]Korea Institute of Oriental Medicine, Daejeon, South Korea; [2]Dongguk University, Gyeongju, South Korea*

MP 453 **Hemispheric Metabolic Alterations and Immune–Inflammatory Pathway Modulation in Hemorrhagic Traumatic Brain Injury**; Tuli Bhattacharjee[1]; Oluwatosin Daramola[1]; Favour Chukwubueze[1]; Waziha Purba[1]; Md. Mostofa Al Amin Bhuiyan[1]; Shafia Shafiq Nishe[1]; Sherifdeen Onigbinde[1]; Marawan Sayed[2]; Fletcher A. White[2, 3]; Makram Obeid[2, 3]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Indiana University School of Medicine, Indianapolis, IN; [3]Stark Neurosciences Research Institute, Indianapolis, IN*

MP 454 **Optimization of workflow for HILIC separations in LC-MS-based metabolomics**; Debasish Ghosh[1]; Chris Beecher[2]; Marcel L Prokai[1]; Rachel Valentine[1]; Ron Benson[3]; Alex Schrum[3]; Tanya Napolitano[3]; Felice De Jong[2]; Vladimir Shulaev[1]; *[1]University of North Texas, Denton, TX; [2]IROA Technologies, Chapel Hill, NC; [3]Shodex, New York, NY*

MP 455 **High throughput metabolic phenotyping for biotechnology applications using the RapidFire 400**; Nathalie Munoz[1]; Daniel J Orton[1]; Jeffrey J Czajka[1]; Jesse Trejo[1]; Andrea Harrison[1]; Sarah M. Stow[2]; Ryan Clark[2]; Aivett Bilbao[1]; Alex Beliaev[1]; Paul Piehowski[1]; *[1]Pacific Northwest National Lab, Richland, WA; [2]Agilent Technologies Inc., Corvallis, OR*

MP 456 **Ultrahigh-throughput metabolomics for large-scale studies using MALDI-MS**; Daisuke Miura[1]; Takeshi Bamba[2]; *[1]Nat'l Inst. of Advanced Industrial Science & Technology, Ibaraki, Japan; [2]Kyushu University, Fukuoka, Japan*

MP 457 **Age-Associated Skin Metabolites of Bacterial Origin**; Jhordan Ojeda González[1]; Hector Alexis Angel Arce[1]; Aldo Moreno Ulloa[1]; *[1]CICESE, Ensenada, Mexico*

MP 458 **Harnessing in vivo deuterium labeling for identification of new resistance biomarkers in bacteria during antibiotic exposure**; Vy T Tat[1]; Paul Lueth[1]; Bryan Bellaire[1]; Young Jin Lee[1]; *[1]Iowa State University, Ames, IA*

MP 459 **Comprehensive Untargeted Metabolomic Analysis from Five Stages of Blueberry Development by High Resolution Accurate Mass Spectrometry**; Sarah A Monti[1]; Valeria Zerda-Pinto[2]; Ahmed G.

Darwish[3]; Ahmed Abobakr[4]; Ethan R Hain[2]; Lihini Mendis[2]; Aron Jaffe[2]; Landon A Wiest[2]; Dominika Gruzsecka[2]; Jacob Smith[5]; Allie Ferranti[5]; Stephen Kurzyniec[5]; Christopher Gilles[2]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Shimadzu Scientific Instruments, Inc, Columbia, MD; [3]Texas A&M University, College Station, TX; [4]Texas A&M Univesity, College Station, TX; [5]Shimadzu Scientific Instruments, Carlsbad, CA*

MP 460 **Metabolomic investigation of specialized phytochemical variation in Eriodictyon californicum extracts produced from different parts of the same plants**; Carolina Nicole Saucedo Cervantes[1]; Robyn Johanna Araiza[1, 2]; Alli J. Adams[1]; Lisa Cumper[3]; Richard Lee Bugbee[4]; Mei Wang[5]; Pamela Maher[6]; Clinton C. Shock[7]; C. Benjamin Naman[1]; *[1]San Diego Botanic Garden, Encinitas, CA; [2]California State University, San Marcos, San Marcos, CA; [3]Tribal Historic Preservation Office, Jamul Indian Village of California, Jamul, CA; [4]Kumeyaay Community College, El Cajon, CA; [5]USDA, ARS, NPURU, University, MS; [6]Cellular Neurobiology Laboratory, The Salk Institute for Biological Studies, La Jolla, CA; [7]Scientific Ecological Services, Inc., Ontario, OR*

MP 461 **Analysis of metabolic variation in Artemisia californica plants grown under differentially controlled horticultural conditions**; Robyn Johanna Araiza[1, 2]; Ashleigh Fischer[1]; Emma Cheves[2]; Lisa Cumper[3]; Richard Lee Bugbee[4]; Todd Micheal[2]; Ari Novy[2]; C. Benjamin Naman[2]; *[1]CSUSM, San Marcos, CA; [2]San Diego Botanic Garden, Encinitas, CA; [3]Tribal Historic Preservation Office, Jamul Indian Village of California, Jamul, CA; [4]Kumeyaay Community College, El Cajon, CA*

MP 462 **To derivatize, or not to derivatize? Comparison of old and new derivatization methods to improve sensitivity in (un)targeted LC-MS metabolomics**; Abraham Raskind[1]; Charles Evans[1]; *[1]U of Michigan, Ann Arbor, MI*

MP 463 **Metabolomic profiling of lactic acid fermented nuts**; Megan Danielewicz[1]; Juliet Tran[1]; Tim Richards[2]; Ryan D. Leib[1]; *[1]Stanford University, Stanford, CA; [2]Philosopher Foods, Inc., Santa Rosa, CA*

MP 464 **Lipidomic Profiling of Prominent Gut Symbionts Reveals Species-specific Evolutionary Strategies and Co-adaptation with Mammalian Host**; Sungwhan F Oh[1, 2]; Kyoo Heo[1]; Ji-Sun Yoo[1]; *[1]Brigham and Women's Hospital, Boston, MA; [2]Harvard Medical School, Boston, MA*

MP 465 **Decoding personalized glycemic responses to whole wheat bread: Integrated metabolomics and microbiome analyses reveals gut microbiome-specific metabolic networks**; Chao Guo[1]; Huan Zhang[1, 2]; Li Chen[1]; Shiqi Zhang[1]; Shuaixin Gao[1]; Jiangjiang Zhu[1]; *[1]The Ohio State University, Columbus, OH; [2]Dartmouth College, Hanover, NH*

MP 466 **MS-based Multi-omics Profiling of Host-Candida Interactions Reveals High-Mannose N-glycan Alterations Correlated with Pathogenicity**; Sheryl Joyce G Alvarez[1]; Michael Russelle S. Alvarez[1]; Luiz Eduardo Lacerda[2]; Ricardo Wagner Portela[2]; Carlito B. Lebrilla[1]; *[1]University of California Davis, Davis, CA; [2]Universidade Federal da Bahia, Salvador, Brazil*

MP 467 **Impact of environmentally relevant PFAS concentrations on secondary metabolism of soil bacteria Pseudomonas protegens Pf5**; Amanda May[1]; Nimat Ajide-Bamigboye[1]; *[1]University of Tennessee, Knoxville, TN*

MP 468 **Snapshot of the Bronchoalveolar Metaproteome of Mice Infected with Mycobacterium tuberculosis**; Gustavo Diaz[1]; Andres Obregon-Henao[2]; Corey D Broeckling[1]; *[1]Analytical Resources Core: Bioanalysis and Omics, Colorado State University, Fort Collins, CO, Fort Collins, CO; [2]NTM Center, Mycobacteria Research Laboratory, Department of Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA., Fort Collins, CO*

MP 469 **GutMICS with Quantitative LC–MS Multi-Omics Defines C. difficile Pathogenesis and Probiotic Barrier Protection at the Gut Interface**; Sung-Hyun Jo[1]; Seo-Young Kwon[1]; Joonha Park[2]; Jessie S. Jeon[2]; Yun-Gon Kim[1]; *[1]Soongsil University, Seoul, South Korea; [2]Korea Advanced Institute of Science and Technology, Daejeon, South Korea*

MP 470 **IsoPairFinder: A tool for deciphering microbial pathway intermediates with stable isotope tracing metabolomics**; Zhiwei Zhou[1]; Yuanyuan Liu[1]; Mingxun Wang[2]; Dylan Dodd[1]; *[1]Stanford University, Palo Alto, CA; [2]University of California Riverside, Riverside, CA*

MP 471 **Development of rapid screening of methicillin-resistant Staphylococcus aureus using MALDI-TOF MS with machine learning**; Jong-Min Park; *Major in Materials Science and Engineering, Hallym University, Chuncheon, South Korea*

MP 472 **Characterization of Cleavage Specificity of Novel Proteases in Environmental Microbes**; Fadime Renée Stemmer[1, 2, 3]; Matthew R. McIlvin[2]; Mak A. Saito[2]; *[1]MIT/WHOI Joint Program in Applied Ocean Science and Engineering, Cambridge, MA; [2]Woods Hole Oceanographic Institution, Woods Hole, MA; [3]Massachusetts Institute of Technology, Cambridge, MA*

MP 473 **Metabolomics Analysis Reveals Fatty Acid Auxotrophy and Host Lipid Incorporation in Female Urogenital Lactobacilli**; HRISHIKESH H DALVI[1]; Michael L Neugent[1]; Ceejay N Saenz[1]; Jessica Gauch[1]; Nikki S Koonjbearry[1]; Nicole J. De Nisco[1, 2]; *[1]The University of Texas at Dallas, Richardson, TX; [2]The University of Texas southwestern Medical center, Department of Urology, Dallas, TX*

MP 474 **Metaproteomics as a tool to map prebiotic action**; Kristian Jensen Pedersen[1]; Marlene Jara Portocarrero[1]; Jason Oneill[2]; Chloé Moritz[3]; Renata Blatnik[4]; Schmit Pierre-Olivier[5]; Morten Danielsen[1]; *[1]CMbio, Copenhagen, Denmark; [2]Bruker Daltonics, Billerica, MA; [3]PreOmics GmbH, Martinsried, Germany; [4]Bruker Daltonics GmbH & Co KG, Bremen, Germany; [5]Bruker Daltonique S.A., Wissembourg, France*

MP 475 **Nanomachines in the Human Gut: Elucidating Cellulosome Localization and Componentry in Ruminococcus callidus**; Matthew Kensil[1, 2]; Robert P. Gunsalus[2, 3, 4]; Christine M. Minor[1, 2]; Allen Takayesu[1, 2]; Michael R. Sawaya[1, 2, 4]; Lucasz Salwinski[2, 4]; Robert T. Clubb[1, 2, 4]; Matteo Pellegrini[2, 5]; Rachel R. Ogorzalek Loo[1, 2, 4]; Joseph A Loo[1, 2, 4]; *[1]Department of Chemistry and Biochemistry, University of California, Los Angeles, Los Angeles, Los Angeles, CA; [2]UCLA-DOE Institute for Genomics and Proteomics, University of California, Los Angeles, Los Angeles, CA; [3]Department of Microbiology, Immunology and Molecular Genetics, University of California, Los Angeles, Los Angeles, CA, USA., LOS ANGELES, CA; [4]Molecular Biology Institute, University of California, Los Angeles, Los Angeles, CA; [5]Department of Molecular, Cell, and Developmental Biology, University of California, Los Angeles, Los Angeles, CA*

MP 476 **Lipase-mediated alteration of the S. aureus lipidome and its antibiotic susceptibility**; David T Brewer[1]; Kelly M Hines[1]; *[1]University of Georgia, Athens, GA*

MP 477 **Proteome remodeling during fungal depolymerization of PBAT microplastics**; Olga Rusiecka[1]; Rafal Szewczyk[2, 3]; Przemyslaw Bernat[1]; *[1]University of Lodz, Faculty of Biology and Environmental Protection, Department of Industrial Microbiology and Biotechnology, Lodz, Poland; [2]LabExperts sp z o.o., Gdansk, Poland; [3]Bioanalytic sp. z o.o., Gdansk, Poland*

MP 478 **Nontargeted analysis of harmful algal blooms using liquid chromatography with a multi-reflecting high resolution mass spectrometer**; Aubrey Trapp[1]; Raphe Kudela[1]; Andrew Baker[2]; *[1]University of California, Santa Cruz, Santa Cruz, CA; [2]Waters, Inc., Pleasanton, CA*

MP 479 **Nano-DESI Mass Spectrometry for Early-Stage Detection of Environmental Microbial Contaminants**; RENKAI DONG[1]; Bartek Rajwa[2]; Brianna Corman[2]; Syeda Nazifa Wali[1]; Julia Laskin[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN; [2]Purdue University, west lafayette, IN*

MP 480 **Metaproteomic SIP to Quantify Gut Microbial Activity and Protein Turnover**; Yi Xiong[1]; Ryan S. Mueller[2]; Shichao Feng[3]; Bailu Zhang[3]; Xuan Guo[3]; Chongle Pan[1]; *[1]University of Oklahoma, Norman, OK; [2]Oregon State University, Corvallis, OR; [3]University of North Texas, Denton, TX*

MP 481 **Artificial Intelligence-Driven Phenotyping Reveals the Spatiotemporal Mechanics of Antifungal Interactions in Microbial Communities**; Edanur Oksuz[1, 2]; Emily Smith[1, 2]; Annand Seethepalli[1]; Larry York[1]; Tomás Rush[1]; Joshua Michener[1]; Mirko Pavicic Venegas[1]; John Lagergren[1]; Paul Abraham[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN; [2]University of Tennessee, Knoxville, TN*

MP 482 **The Dicamba Dilemma: Pollinator Gut Metabologenomics Reveals Metabolite and Microbial Perturbation in Apis mellifera, Bombus impatiens, and Polistes dominula**; Luke M. Collier[1]; Katherine L. Lev[1]; Yaxuan Guo[1]; Sean Newmister[1]; Chase Arkins[1]; Isabelle Lamug[1]; Sinit Habtemariam[1]; Bahumitha Govindaraj[1]; Regina Baucom[1]; Elizabeth Tibbetts[1]; David H. Sherman[1]; *[1]University of Michigan, Ann Arbor, MI*

MP 483 **Decoding emerging microbial lipids and proteins in diet-liver-gut crosstalks**; Ifrat Tamanna[1]; Abdul Qadeer[1]; Helena Mannochio Russo[2]; Abhijit Paul[1]; Mirva Pääkkönen[1]; Matilda Kråkström[1]; Axel Kornerup Hansen[3]; Xiaorui Zhao[4]; Otto Kauko[1]; Hanne Christine Bertram[4]; Santosh Lamichhane[1, 5]; *[1]University of Turku, TURKU, Finland; [2]University of California San Diego, San Diego, CA; [3]University of Copenhagen, Copenhagen, Denmark; [4]Aarhus University, Aarhus, Denmark; [5]Turku Clinical Microbiome Bank, Clinical Microbiology, Turku University Hospital,, Turku, Finland*

MP 484 **Expanded characterization of community composition and associated protein functions in soil microbial synthetic communities (SynComs) using DIA metaproteomics**; Jonghyun Kim[1]; Delaney G. Beals[1]; Dale A. Pelletier[1]; Mitchel J. Doktycz[1]; Robert L. Hettich[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN*

MP 485 **Investigating the involvement of lipids in surface adhesion of Pantoea using liquid microjunction-surface sampling probe mass spectrometry**; Emily A. Kurfman[1]; Charini Maladeniya[1]; Spenser R. Brown[1]; Zhefei Yang[1]; Amber N. Bible[1]; Yue Yuan[1]; Vilmos Kertesz[1]; Jennifer L. Morrell-Falvey[1]; John F. Cahill[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN*

MP 486 **Using the dynamic microbiome proteome as a biological microsensor: predicting harmful algal blooms with time-resolved quantitative DIA peptide measurements**; Miranda C Mudge[1]; Brook Nunn[1]; Michael Riffle[1]; Gabriella Chebli[2]; Deanna L Plubell[1]; Tatiana Rynearson[3]; William S Noble[1]; Emma Timmins-Schiffman[1]; *[1]University of Washington, Seattle, WA; [2]Georgia Institute of Technology School of Chemistry and Biochemistry, Atlanta, GA; [3]University of Rhode Island, Graduate School of Oceanography, Kingston, RI*

MP 487 **Quantitative Peptidomics Reveals Neurochemical Changes in the Spinal Cord Induced by Disease-Modifying Osteoarthritis Drugs (DMOADs)**; Vu Ngoc Huong Tran[1]; Marilyn Frézier[2]; Gaoyuan Lu[1]; Colombe Otis[2]; Kendra Selby[3]; Bertrand Lussier[2]; Guillaume Saint-Jean[2, 4]; Hélène Beaudry[2]; Eric Troncy[2]; Lingjun Li[1, 3]; *[1]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [2]Groupe de Recherche en Pharmacologie Animale du Québec (GREPAQ), Université de Montréal, Saint-Hyacinthe, QC; [3]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [4]Department of Pathology and Microbiology, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC*

MP 488 **Global & Spatial Mass Spectrometry Analysis reveals disease-specific post-translational modifications in Alzheimer's Disease Brain Tissue**; Joseph T Nigro[1]; Margaret Dpwns[1]; Amber Grewal[1]; Simran Raikundalia[1]; Isha Chauhan[1]; Shriya Jain[1]; Alec Candib[1, 2]; Jonathan S. Vogelgsang[3, 4]; Torsten Klengel[3, 4]; Sabina Berretta[3, 4]; Joseph Zaia[1, 2]; Manveen K Sethi[1]; *[1]Department of Biochemistry & Cell Biology, Boston University Chobanian and Avedisian School of Medicine, Boston, MA; [2]Boston University Bioinformatics Program, Boston University, Boston, MA; [3]Department of Psychiatry, Harvard Medical School, Boston, MA; [4]Translational Neuroscience Laboratory, McLean Hospital,, Belmont, MA*

MP 489 **A Sequential Affinity Proteomics Approach Reveals Potential Glycation and Succinylation Crosstalk of Key Proteins in Alzheimer's Disease**; Qin Fu[1]; Elizabeth T. Anderson[1]; Andy Lui[1]; Gary E. Gibson[2]; Sarah A. Flowers[3]; Hening Lin[4]; Sheng Zhang[1]; *[1]Cornell University, Ithaca, NY; [2]Weill Cornell Medicine, New York, NY; [3]University of Virginia, Charlottesville, VA; [4]University of Chicago, Chicago, IL*

MP 490 **Multiomics Mapping of Environmental Exposures to Pathway Perturbation in Alzheimer's Disease**; Cassandra G Kempf[1]; Ethan Stancliffe[2]; Monil Gandhi[2]; Sandeep Acharya[2]; Douglas V. Guzior[2]; Ashima Mehta[2]; Caitlin Kelly[2]; Sharla Friend[2]; Adam Richardson[2]; Tom Cohen[2]; Kevin Cho[1]; Gary J Patti[1]; *[1]Washington University in St. Louis, St. Louis, MO; [2]Panome Bio, Saint Louis, MO*

MP 491 **ALS-associated hSOD1H46R and Engineered hSOD1H46R/H48Q Exhibit Partial and Full Demetallation Alongside Intramolecular Disulfide Bond Reduction in Transgenic Mouse Models**;

Cameron Baines[1]; Oliver J. Hale[1]; Toshiyuki Akari[2]; Marcelo R. Vargas[3]; Helen J. Cooper[1]; *[1]University of Birmingham, Birmingham, United Kingdom; [2]National Center of Neurology and Psychiatry, Kodaira, Japan; [3]University of Wisconsin-Madison, Madison, WI*

MP 492 **Monitoring Amyloid β1–42 Aggregation by Mass Spectrometry–Based Benzoyl Fluoride Footprinting**; Xinzhu Li[1]; Don Rempel[1]; Michael Gross[1]; *[1]Washington University in St.Louis, St.Louis, MO*

MP 493 **Cell type-resolved proteomics reveals intra- and intercellular signaling in Alzheimer's disease**; Xue Zhang[1]; Kaiwen Yu[2]; Him K. Shrestha[2]; Ying Zhou[3]; Jiyuan Yang[2]; Zhen Wang[2]; Xiaokang Ren[2]; Ping-Chung Chen[2]; Huan Sun[2]; Danting Liu[2]; Yun Jiao[2]; Jay M. Yarbro[4]; Ju Wang[2]; Zhiping Wu[2]; Kiara Harper[4]; Liusheng He[2]; Zuo-Fei Yuan[2]; Xusheng Wang[5]; Anthony A. High[2]; Gang Yu[6]; Jiyang Yu[2]; Zhexing Wen[3]; Junmin Peng[2]; *[1]St Jude Children's Research Hospital, Memphis, TN; [2]St. Jude Children's Research Hospital, Memphis, TN; [3]Emory University, Atlanta, GA; [4]St.Jude Children Research Hospital, Memphis, TN; [5]University of Tennessee Health Science Center, Memphis, TN; [6]University of Texas Southwestern Medical Center, Dallas, TX*

MP 494 **Deep proteomic profiling of the subgenual anterior cingulate cortex in bipolar disorder identifies coordinated dysregulation of the nucleosome and myelination**; Akayla Lewin[1]; Alek Grady[1]; Jordan Gilardi[1]; Margaret Stapleton[2]; Yevgenia Kozorovitskiy[2]; Lambertus Klei[1]; Bernie Devlin[1]; David Lewis[1]; Panos Roussos[3]; Matthew MacDonald[1]; *[1]University of Pittsburgh, Pittsburgh, PA; [2]Northwestern University, Evanston, IL; [3]Icahn School of Medicine at Mount Sinai, Friedman Brain Institute, New York City, NY*

MP 495 **Sex Differences in the Proteome of Major Depressive Disorder**; Kelly Barko[1, 2]; Shelby Ruiz[3]; Lambertus Klei[4, 5]; Bernie Devlin[4, 5]; Akayla Lewin[4]; Alek Grady[4]; Marianne Seney[2, 5]; Matthew MacDonald[2, 5]; *[1]University of Pittsburgh, Pittsburgh, PA; [2]Center for Neuroscience at University of Pittsburgh, Pittsburgh, PA; [3]University of Pittsburgh, Pittsburgh, Pittsburgh, PA; [4]UPMC, Pittsburgh, PA; [5]Department of Psychiatry, University of Pittsburgh School of Medicine, Pittsburgh, PA*

MP 496 **LC-MS/MS reveals proteomic changes following calcium channel gating modifier GV-58 treatment in an Amyotrophic Lateral Sclerosis (ALS) mouse model**; Alexandra J Gilsrud[1]; Yomna Badawi[1]; Xuemei Zheng[1]; Thomas Karikari[1]; *[1]University of Pittsburgh, Pittsburgh, PA*

MP 497 **Convergent Metabolic and Neuroendocrine Dysregulation Underlying Synaptic Dysfunction in the Prefrontal Cortex of Parkinson's Disease Brains**; Moyinoluwa Adeniyi[1]; Mojibola Fowowe[1]; Odunayo Oluokun[1]; Sarah Sahioun[1]; Oluwatosin Daramola[1]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX*

MP 498 **Solid Drug Nanoparticle Embedded Thermosensitive Hydrogel Eye Drop for Enhanced Glaucoma Management**; Lei Xu[1]; Tzu-Chen Wang[2]; Shichu Chang[3]; Lin Qi[2]; Vimalin Jeyalatha Mani[2]; Bohong Zhang[1]; Ned Kronenberg[3]; Jie Huang[1]; Yang Hu[4]; Xiaorong Liu[3]; Hu Yang[2]; *[1]Missouri University of Science and Technology, Rolla, MO; [2]Marquette University and Medical College of Wisconsin, Milwaukee, WI; [3]University of Virginia, Charlottesville, VA; [4]Stanford University School of Medicine, Palo Alto, CA*

MP 499 **Metabolomics-driven plasma biomarker discovery in Parkinson's disease**; FUYUE WANG[1]; Hong YAN[2]; Zongwei CAI[3]; *[1]Hong Kong Baptist University, Hong Kong, China; [2]Hong Kong Baptist University, Kowloon City, Hong Kong; [3]Hong Kong Baptist University, Kowloon Tong City, Hong Kong*

MP 500 **Targeted proteomics panel enables absolute quantification of complement pathway proteins in neurodegenerative studies utilizing stable-isotope-standard protein epitope signature tags (SIS-PrESTs)**; Mahmud Hossain[1]; Georgia Ntermentzaki[1]; Fabrizio Pontarelli[1]; Timothy Hammond[1]; Hendrik Wesseling[1]; Bailin Zhang[1]; *[1]Sanofi, Cambridge, MA*

MP 501 **Spaceflight suppresses NOTCH signaling and remodels synaptic proteomic networks in Alzheimer's iPSC-derived cortical organoids**; Natalia Chermont Dos Santos Moreira[1]; Luisa Bulcao Vieira Coelho[1]; Juliana de S. da G. Fischer[1]; Blake Tsu[1]; Paulo C Carvalho[1, 2]; Stephanie Almeida[1];

Alysson R. Muotri[1]; Aline Martins[1]; *[1]UCSD, San Diego, CA; [2]FIOCRUZ, Carlos Chagas Institute, Curitiba, Brazil*

MP 502 **LC-HRIM-MS–Based Structural and Quantitative Analysis of Brain Ganglioside Alterations in a Transgenic Mouse Model of Tauopathy**; Jack P. Ryan[1]; David L. Williamson[2]; Yao Lihang[1]; Nathan G. Hatcher[1]; Kim Ekroos[3]; Komal D. Kedia[1]; *[1]Merck & Co., Inc., West Point, PA; [2]Merck & Co, Rahway, NJ; [3]Lipidomics Consulting Ltd, Esbo, Finland*

MP 503 **Biochemical Characterization of Diet-Induced Hippocampal Metabolic and Synaptic Rewiring**; Zohaib Khan; *Weill Cornell Medicine, New York, NY*

MP 504 **Spatial proteomic landscape of Alzheimer's Disease and Progressive Supranuclear Palsy across brain regions**; Ivan C Mounteer[1]; Jared Deyarmin[2]; Yusheng Qian[1]; Haven G Tillmon[1]; Casey C Abbo[2]; Sam Pardo[1]; Simran Sood[2]; Fei Gao[1]; Louis Perez[1]; Susan T Weintraub[1]; Stephanie N. Samra[2]; Juan Pablo Palavicini[1]; Kevin Bieniek[1]; Oleg Klykov[1]; *[1]UT Health San Antonio, San Antonio, TX; [2]ThermoFisher Scientific, San Jose, CA*

MP 505 **Neuroproteomic Analysis of the Relationship between Tau Pathogenesis and Impaired Proteostasis**; Emily X Dexter[1]; Jeffrey N Savas[1]; *[1]Northwestern University Feinberg School of Medicine, Chicago, IL*

MP 506 **Molecular Dysregulation of Glycosylation in SH-SY5Y Models of Alzheimer's Aβ and Tau Pathology**; Sarah A. Sahioun[1]; Isabel Castro[2]; Sherifdeen B. Onigbinde[1]; Mojibola O. Fowowe[1]; Abderrahmane Koraich[1]; Joy O. Solomon[1]; Odunayo O. Oluokun[1]; Yehia Mechref[1]; *[1]Department of Chemistry and Biochemistry, Texas Tech University, Lubbock, TX; [2]Center for Biotechnology and Genomics, Texas Tech University, Lubbock, TX*

MP 507 **Silver ion (Ag+) interaction with Amyloid-β peptide studied by mass spectrometry**; Vairamani Mariappanadar[1, 2]; Kameswararao Mula[3]; Tarang M Jadav[3]; Michael Gross[3]; *[1]Washington University in St.Louis, Saint Louis, MO; [2]SRM Institute of Science and Technology, Kattankulathur, TN, India; [3]Washington University in St.Louis, St.Louis, MO*

MP 508 **One PACS2 point-mutation signature, two MS generations: patient-aligned Pacs2(E209K) knock-in mouse multi-tissue DIA from Or**; Dominik Cysewski[1, 2]; Tomasz Kowalczyk[1]; Arkadiusz Zbikowski[1]; Gabriela Zynel[1]; Malgorzata Mackiewicz[1]; Justyna Klimaszewska[1]; Kacper Lukasiewicz[3]; Anna Pryczynicz[1]; Katarzyna Guzińska-Ustymowicz[1]; Marlena Tynecka[1]; Piotr Kosla[2]; Malgorzata Kosla[2]; *[1]Medical University of Bialystok, Bialystok, Poland; [2]PACS2 Research Foundation, Warsaw, Poland; [3]VIZJA University, Warsaw, Poland*

MP 509 **Qualitative Analysis and Deep Sequencing of Tau Proteoforms by Integrated Top-Down LC–MS, Individual Ion MS, and PTCR**; Nhat Le[1]; Ben James Des Soye[1]; Aniel Sanchez[1]; Sophia Leng[1]; Joshua B Rubin[1]; Michael Caldwell[1]; Steven M. Patrie[1]; Robert J. Vassar[2]; Rudy Castellani[2]; Tamar Devora Gefen[2]; Neil L Kelleher[3, 4]; *[1]Northwestern University, Evanston, IL; [2]Northwestern University Feinberg School of Medicine, Chicago, IL; [3]Northwestern University, Chicago, IL; [4]Northwestern University, Feinberg School of Medicine, Chicago, IL*

MP 510 **Psychedelics Driven Modulation of Neuronal Plasticity in the Medial Prefrontal Cortex - By a Proteomics Approach**; Kuldeep Giri; *Princeton University, Princeton, NJ*

MP 511 **Gut Metabolite Shifts in a Pretangle Tau Model of Alzheimer's Disease**; Onyedikachi Belolise[1]; Qi Yuan[1]; Shyamchand Mayengbam[1]; *[1]Memorial University of Newfoundland, St. John's, NL*

MP 512 **Quantitative Bioanalysis of Therapeutic RNA in Biological Matrices**; Thanh Nguyen[1]; Mohamed G. Gadallah[1, 2]; Nick McHugh[3]; Ken Yamada[3]; Dimas Echeverria[3]; Anastasia Khvorova[3]; Jennifer S. Brodbelt[1]; *[1]Department of Chemistry, University of Texas at Austin, Austin, TX, Austin, TX; [2]Department of Pharmaceutical Analytical Chemistry, Faculty of Pharmacy, Assiut University, Assiut 71526, Egypt, Assiut, Egypt; [3]RNA Therapeutics Institute, University of Massachusetts Chan Medical School, Worcester, MA 01605, USA, Worcester, MA*

MP 513 **Strategies for Integrating Strong Anion Exchange Chromatography with Mass Spectrometry for Oligonucleotide Structural Analysis**; Mirandia Szramowski[1]; Zabrina Malto[2]; Jace W. Jones[2]; *[1]University of Maryland Baltimore, Baltimore, MD; [2]University of Maryland, Baltimore, Baltimore, MD*

MP 514 **Characterizing the Poly(A) tail in mRNA using Ion-Pairing Reversed-Phase LC/MS (IPRP-LC/MS) and Deconvolution Tools**; Stephen Sciuto[1]; Mike Knierman[2]; Thomas Walker[3]; Brian Rivera[1]; *[1]Agilent Technologies, Santa Clara, CA; [2]Agilent Technologies, Gary, IN; [3]Agilent Technologies, Lexington, MA*

MP 515 **Cyclic™ Ion Mobility Separation as a tool in gRNA impurity profiling**; Pavel Aronov[1]; Dale A Cooper-Shepherd[2]; Michael Ruehl[3]; Christopher Gawlig[3]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Biospring AG, Frankfurt am Main, Germany*

MP 516 **Fully Automated mRNA Mapping for Robust MS/MS-Based Product Quality Attribute Analysis**; Abigail E. McShane[1]; Cece Cui[1]; Michelle English[1]; Amy Claydon[2]; *[1]Genedata Inc, Boston, MA; [2]Genedata Ltd, Cambridge, United Kingdom*

MP 517 **Characterizing Nucleic Acid Payloads in Lipid Nanoparticles and Viral Vectors via Charge Detection Mass Spectrometry**; Rebecca D'Esposito[1]; Alexandre F Gomes[1]; Emily Christofi[2]; Ying Qing Yu[1]; Michelle Chen[3]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Waters Corporation, Goleta, CA*

MP 518 **Impact of HFIP Vendor Variability on MS Sensitivity in IP-RP LC–MS Oligonucleotide Analysis**; Toshi Ono[1]; Makoto Ozaki[2]; Tomomi Kuwayama[2]; Motoshi Shimotsuma[2]; Junji Kawakami[3]; Tsunehisa Hirose[2]; *[1]Nacalai USA, San Diego, CA; [2]Nacalai Tesque, Inc., Kyoto, Japan; [3]FIRST, Konan University, Kobe, Japan*

MP 519 **A New HILIC-MS Method and the Use of Performance Verification and Resolution Mix in Oligonucleotide Analysis**; Arun Babu Kumar[1]; Sarah Aijaz[1]; Uma Sreenivasan[1]; Patrik Appelblad[2]; *[1]MilliporeSigma, Round Rock, TX; [2]Merck Life Science AS, Oslo, Norway*

MP 520 **GreatCAT: An Automated Fragment Annotation and Quantification Software for Fast Photochemical Oxidation of Nucleic Acids**; Evgeniya Biryukova[1, 2]; Marek Polak[3]; Daniel Kavan[3]; Petr Novak[3]; *[1]Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Republic; [2]Charles University, Prague, Czech Republic; [3]Institute of Microbiology CAS, Prague, Czech Republic*

MP 521 **A streamlined MALDI-DIT-MS workflow for molecular-weight, sequence, and terminal-modification analyses of oligonucleotide therapeutics**; Yuko Fukuyama[1]; Sadanori Sekiya[1]; Koichi Tanaka[1]; *[1]Shimadzu Corporation, Kyoto, Japan*

MP 522 **Analysis of DNA oligonucleotide impurities on a new Hybrid Orbitrap instrument**; Cong Wang[1]; Fiona Rupprecht[2]; Patrick Pankert[3]; Ulrik Hvid Mistarz[4]; Yang Hao[5]; Min Du[6]; Claire Dauly[1]; *[1]Thermo Fisher Scientific, Bremen, Germany; [2]Thermo Fisher Scientific, Dreieich, Germany; [3]Thermo Fisher Scientific, Germering, Germany; [4]Thermo Fisher Scientific, Copenhagen NV, Denmark; [5]ThermoFisher Scientific, San Jose, CA; [6]Thermo Fisher Scientific, Lexington*

MP 523 **Integrated Immobilized RNase Reactors for Comprehensive LC–MS Characterization of Therapeutic Oligonucleotides**; Katarina Molnarova[1]; Evgeniya Biryukova[2, 3]; Petr Pompach[1]; Michael Volny[2]; Petr Novak[2]; *[1]AffiPro s.r.o., Vestec, Czech Republic; [2]Institute of Microbiology of the Czech Academy of Sciences, Vestec, Czech Republic; [3]Faculty of Science, Charles University, Prague, Czech Republic*

MP 524 **Optimizing native electron detachment dissociation on the timsOmni platform to reveal structural footprints along RNA sequences**; Rim Chiba[1]; Ceyuan Zheng[1]; Frédéric Rosu[1]; Valerie Gabelica[1]; *[1]University of Geneva, Geneva, Switzerland*

MP 525 **Native Ion Mobility-Mass Spectrometry Reveals the Impact of Lipid Nanoparticle Formulations on the Structures and Stabilities of Ribonucleic Acid Therapeutics**; Caela Fedraw[1]; Courteney R Dufrene[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

MP 526 **Development of a Mass Spectrometry Based Assay to Detect Viral RNA Polymerase Activity and Inhibition**; Agbo-oma A Uwakweh[1]; Rinky D Parakra[1]; Juliet O Obi[1]; Daniel J Deredge[1]; *[1]University of Maryland, School of Pharmacy, Department of Pharmaceutical Sciences, Baltimore, MD*

MP 527 **Development and Qualification of In-Process and Release IPRP LC-HRMS Methods for Analyzing the Purity of Synthetic sgRNA**; Amy M Kuzminov[1]; Scott A McPhee[1]; Ian Marshall[1]; Timothy Ramseyer[1]; Jasmin Casillas[1]; *[1]TriLink Biotechnologies, San Diego, CA*

MP 528 **Improved Oligonucleotide LC–MS Performance through Inert Column Hardware and Alternative Separation Strategies**; Andrew Coffey[1]; Anne Blackwell[2]; Jordy Hsiao[3]; *[1]Agilent Technlogies, Church Stretton, United Kingdom; [2]Agilent Technologies, Wilmington, DE; [3]Agilent Technologies, Santa Clara, CA*

MP 529 **Analysis of modified nucleosides from Aplysia californica neurons with a UHPLC-TIMS-TOF Instrument**; Gabriella Floro[1]; Kevin D Clark[1]; *[1]Tufts University, Medford, MA*

MP 530 **Trapped ion mobility mass spectrometry enables mapping and quantification of sub-stoichiometric ribosomal RNA modifications from low abundance samples**; Max Sharin[1]; Aryasai Radhakrishnan[1]; Kevin D Clark[1]; *[1]Tufts University, Medford, MA*

MP 531 **siRNA phosphorothioate diastereomer profiling by nuclease P1 digestion and LC-MS for stereochemical comparability assessment**; Haeri Seol[1]; Ming Huang[1]; Haibo Qiu[1]; Ning Li[1]; *[1]Regeneron, Tarrytown, NY*

MP 532 **Software Tools for Automated LC-MS Analysis of Critical Quality Attributes of mRNA Molecules**; Catalin E Doneanu[1]; Alexandre F Gomes[1]; Jo-Anne Riley[2]; Tatiana Johnston[1]; Chris Preston[2]; Matt Gorton[2]; Balasubrahmanyam Addepalli[1]; Ying Qing Yu[1]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom*

MP 533 **From Duplex to Detail: HILIC–MS/MS Analysis of Highly Modified and Conjugated siRNA Therapeutics**; Mohamed Ibrahim Gadallah[1, 2]; Noha M El Zahar[3]; Thanh Nguyen[1]; Kailyn L. Nonhof[1]; Nick McHugh[4]; Ken Yamada[4]; Dimas Echeverria[4]; Anastasia Khvorova[4]; Jennifer S. Brodbelt[1]; *[1]Department of Chemistry, The University of Texas at Austin, Austin, TX, 78712, USA, Austin, TX; [2]Department of Pharmaceutical Analytical Chemistry, Faculty of Pharmacy, Assiut University, Assiut 71526, Egypt, Assiut, Egypt; [3]Department of Pharmaceutical Analytical Chemistry, Faculty of Pharmacy, Ain Shams University, Cairo, Egypt; [4]RNA Therapeutics Institute, University of Massachusetts Chan Medical School, Worcester, MA 01605, USA, Worcester, MA*

MP 534 **Practical LC–MS Workflows for siRNA and sgRNA Characterization Using a Single-Quadrupole Mass Spectrometer**; Vikki Johnson[1]; Risa Suzuki[2, 3]; Toyama Atsuhiko[2, 3]; Jeffrey Dahl[2]; Kosuke Uchiyama[3]; Toshiya Matsubara[2]; *[1]Shimadzu Scientific Instruments, Carlsbad, CA; [2]Shimadzu Scientific Instruments, Columbia, MD; [3]Shimadzu Co., Kyoto, Japan*

MP 535 **Intact mass characterization of siRNA without ion pairing agents**; Elina Ly; *KBI Biopharma, Louisville, CO*

MP 536 **Comprehensive characterization of oligonucleotides and related impurities using advanced LC/QTOF analytical workflows**; Preeti Bharatiya[1]; Ashish Pargaonkar[2]; Vivek Dhyani[3]; Saikat Banerjee[2]; *[1]Agilent technologies, Bangalore, India; [2]Agilent Technologies, Hyderabad, India; [3]Agilent Technologies Inc., Mumbai, India*

MP 537 **LC-MS Oligonucleotide Mapping and Intact-Mass Characterization of Endogenous tRNA in CHO Cell Lines**; Mona Goli[1]; Robert L Ross[2]; Elsa Gorre[1]; Beth Sorichillo[1]; Min Du[2]; Hirsh Nanda[1]; Partha Chowdhury[1]; Andrew D Mahan[1]; *[1]Johnson & Johnson Innovative Medicine, Spring House, PA; [2]ThermoFisher Scientific, Lexington, MA*

MP 538 **Multiplexed Thiol-Reactive Isobaric Tagging for Quantitative Chemoproteomic Profiling of Dehydroalanine in Tau Proteoforms**; Alexander Nassar[1]; Lingjun Li[1]; *[1]University of Wisconsin-Madison, Madison, WI*

MP 539 **15N-Semaglutide Enables Robust, Regulatory-Aligned LC-MS Bioanalysis of Peptide Drugs**; Jung-Eun Lee; *PEPGENE INC, Gyeonggi-do, South Korea*

MP 540 **Label- Free Quantification Of Cumulative Cytosolic Peptides Concentration Using Mass Spectrometry**; Mona Sharar[1]; Heather Pascual[1]; Guoyun Bai[1]; Zhicai Shi[2]; *[1]Johnson and Johnson, San Diego, CA; [2]JOHNSON AND JOHNSON, Spring House, PA*

MP 541 **Overcoming Non-specific Binding Challenges in LC-MS/MS Quantification of a Therapeutic Peptide**; Yan-Ping Lin[1]; Shuyu Hou[1]; Tian-Sheng Lu[1]; *[1]Medpace, Cincinnati, OH*

MP 542 **Resolving TB-4 / TB-500 Mislabeling in the RUO Peptide Market Using Triple-Quadrupole LC-MS/MS**; Jason Snitker[1]; Earl L White[1]; *[1]MDx Bioanalytical, College Station, TX*

MP 543 **Development and Optimization of a Targeted Mass Spectrometry Method for Quantitative Monitoring of DNA Replication and DNA Damage Checkpoint Machinery**; Ziyi Wang[1]; Yunjing Zhang[1]; Jiaxi Cai[1]; Weihua Mao[1]; Huilin Zhou[1]; Raymond T Suhandynata[1]; *[1]University of California San Diego, San Diego, CA*

MP 544 **Sensitive Detection of Collagen-Triggered DDR1 and DDR2 Phosphorylation via Targeted LC-MS/MS Workflow**; Ahmed Moghieb[1]; Stephen P. O'Brien[1]; Leonid Gaidukov[1]; Yunhao Tan[1]; Yram A. Foli[1]; Christyne Kane[1]; Cedric Hubeau[1]; Mario Richter[1]; Gary Jenkins[1]; Qin C Ji[1]; *[1]AbbVie, Inc., North Chicago, IL*

MP 545 **High throughput targeted proteomic workflows with Adaptive Retention Time on the Orbitrap Astral Zoom**; Sophia Steigerwald[1]; Kyle Le Huray[1]; Max Hoek[1]; Michael Baggio Lorenz[2]; Tabiwang N. Arrey[1]; Anna Pashkova[1]; Benjamin Kluwe[3]; Philip M. Remes[4]; Hamish Stewart[1]; Matthias Mann[2]; Christian Hock[1]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Max Planck Institute of Biochemistry, Munich, Germany; [3]Thermo Fisher Scientific, Brno, Czech Republic; [4]Thermo Fisher Scientific, San Jose, CA*

MP 546 **Understanding Endoplasmic Reticulum (ER) Pre-Emptive Quality Control (preQC) by Proximity Labeling and Parallel Reaction Monitoring (PRM) Approach**; Swechha Rimal[1]; Jasmine P. Castellanos[1]; Qiqi Lin[1]; Lyna T. Huynh[1]; Wei Q. Shi[2]; Joseph C. Genereux[1]; *[1]University of California, Riverside, CA; [2]Ball State University, Muncie, IN*

MP 547 **A sensitive LC-MS/MS method for quantifying residual Endo S2 enzyme in one step antibody–drug conjugate preparation**; Shasha Li[1]; Yarong Qu[1]; Wei Lu[1]; ZhengQuan Zhang[1]; Mao Yin[1]; Ling Xu[1]; *[1]PrimeLink Therapeutics, Suzhou, JIangsu Province, MA*

MP 548 **LLOQ Enhancement: A Case Study of LC-MS/MS Quantification for a Peptide in Dog Plasma**; Ting Zhang[1]; Meijuan He[1]; Haiyan Li[1]; Xinxin Wen[1]; Cheng Chen[2]; Minqiang Zhu[2]; Xiaotong Li[1]; Zhiyu Li[1]; Lili Xing[1]; Yi Tao[1]; Liang Shen[1]; *[1]WuXi AppTec, Pudong, Shanghai, China; [2]WuXi AppTec (Nanjing) Co., Ltd., Nanjing, China*

MP 549 **Quantitative FAIMS-PRM targeted phosphoproteomics assay for microgram-scale FFPE clinical samples: implementation enabling precise biomarker measurement and translational insights**; Lihe Zhang[1]; Mary Melkie[1]; Miaomiao Chen[1]; Camille Lombard-Banek[1]; Stephanie Zalesak-Kravec[1]; David J Clark[1]; Yeoun Jin Kim[1]; Steve Sweet[1]; *[1]AstraZeneca, Gaithersburg, MD*

MP 550 **Robust Quantitation of GLP-1 Analogs in Human Plasma: Advancing Anti-Obesity Drug Development**; Hao Yang[1]; Neloni Wijeratne[1]; Min Du[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Lexington, MA*

MP 551 **Microflow LC–MS Bioanalysis of GLP-1 Receptor Agonists in Human Plasma**; Hao Yang[1]; Ke Ma[2]; Claire Dauly[3]; Min Du[4]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Sunnyvale, CA; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [4]Thermo Fisher Scientific, Lexington, MA*

MP 552 **Improved quantitation in data-independent acquisition proteomics via retention time boundary imputation**; Lincoln J Harris[1]; Michael Riffle[1]; Nicholas Shulman[1]; William E Fondrie[2]; Christine C Wu[1]; Michael J. MacCoss[1]; William S Noble[1]; *[1]University of Washington, Seattle, WA; [2]Talus Bioscience, Seattle, WA*

MP 553 **Transforming quantitative sensitivity for synthetic peptide analysis using a high-resolution workflow**; Jonghae Youn[1]; Sujata Rajan[2]; Sashank Pillai[2]; Eshani Galermo[1]; Rahul Baghla[1]; *[1]SCIEX, Redwood City, CA; [2]SCIEX, Bangalore, India*

MP 554 **Normalization and Batch Correction in Skyline 26.2**; Nicholas Shulman[1]; Brendan MacLean[1]; Michael J. MacCoss[1]; *[1]University of Washington, Seattle, WA*

MP 555 **Comparison of Net Contents Determination of Natural and Synthetic Peptides by HPLC/UV-VIS and Electrospray Mass Spectrometry Detection**; Earl L. White[1]; Jason Snitker[1]; Ellis Z. Echols[2]; *[1]MDx BioAnalytical Laboratory, Inc., College Station, TX; [2]MDx Bioanalytical, College Station, TX*

MP 556 **A Rugged LC-SPS MS3 Method for Reliable Bioanalysis of GLP-1 Peptides**; Hao Yang[1]; Cristina C. Jacob[1]; Scott M Peterman[1]; Min Du[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Lexington, MA*

MP 557 **Supercritical Fluid Chromatography MS/MS Method Development for the Analysis of GLP-1 Analogues**; Jonathan Ferguson[1]; Kathleen Luo[1]; Brian Domanski[1]; Risa Suzuki[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD*

MP 558 **Integration of Real-Time Library Search with Adaptive Retention Time Scheduling Enables High-Density Multiplexed Targeted Proteomics**; Ryan Lumpkin[1]; Amanda M Tallon[1]; Nicole Hinkle[1]; Dylan C Mitchell[1]; *[1]Expedition Medicines, Cambridge, MA*

MP 559 **Development and validation of LC-MS/MS method for quantifying dynorphin B in mouse cerebrospinal fluid**; Eman M Mohamed[1]; David J Anderson[1]; Michael D Hammonds[1]; Tony L Sahley[1]; *[1]Cleveland State university, Cleveland, OH*

MP 560 **Enhanced LCMSMS Platform to Address the Workflow Challenges for Quantitative Bioanalysis of Modern Peptide and Oligonucleotide Therapeutics**; Allison Ferranti[1]; Stephen Kurzyniec[2]; Elizabeth Bloch[2]; Vikki Johnson[2]; Mark Lazari[2]; Jacob Smith[2]; Ethan R Hain[2]; *[1]Shimadzu Scientific Instruments, Inc., Columbia, MD; [2]Shimadzu Scientific Instruments, Inc, Columbia, MD*

MP 561 **Quantitative comparison of therapeutic peptides on Sciex ZenoTOF and QQQ platforms**; Christopher Good[1]; Yue-Ting Wang[1]; Julie Liu[1]; Gary Jenkins[1]; Estelle Maes[1]; Nari Talaty[1]; *[1]AbbVie, North Chicago, IL*

MP 562 **Glycine Addition to TFA Mobile Phases Provides >10× Sensitivity Improvement in ESI-MS for Peptide Mapping Without Compromising LC Chromatography**; Andrew Kleinberg[1]; Yuan Mao[1]; *[1]Regeneron, Tarrytown, NY*

MP 563 **Adaptive Real-Time Library Search: Advanced Targeted TMT Method Support**; William D Barshop[1]; Jesse D Canterbury[1]; Philip M. Remes[1]; Peter Mowlds[1]; Rafael Melani[1]; Graeme McAlister[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

MP 564 **Technical Considerations for Targeted Neuropeptidomic Analysis and Quantification**; Angel E. Ibarra[1]; Lingjun Li[1, 2]; *[1]University of Wisconsin-Madison Department of Chemistry, Madison, WI; [2]University of Wisconsin-Madison School of Pharmacy, Madison, WI*

MP 565 **Quantitative LC-MS profiling of critical HCP clearance and optimization of antibody depletion–based HCP enrichment workflows**; Jae Choi[1]; Nikki Jarrett[1]; Alan Atkins[2]; Dominic Hoch[3]; Terry Hicks[4]; Matthew R. Daniels[4]; Kay Opperman[1]; Bhavin Patel[1]; *[1]Thermo Fisher Scientific, Rockford, IL; [2]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [3]Thermo Fisher Scientific, Reinach, Switzerland; [4]Thermo Fisher Scientific, St. Louis, MO*

MP 566 **Enhancing quantitative sensitivity for analysis of amylin analogs using a triple quadrupole LC-MS/MS workflow**; Mahbod Hajivandi[1]; Lakshmanan Deenadayalan[2]; Sujata Rajan[2]; Sashank Pillai[2]; Eshani Galermo[3]; Rahul Baghla[3]; *[1]SCIEX, Marlborough, MA; [2]SCIEX, Bangalore, India; [3]SCIEX, Redwood City, CA*

MP 567 **Evaluation and Standardization of Reducing Conditions in LC–MS Peptide Mapping for Antibody Multi-Attribute Methods**; Thao Bich Nguyen[1]; Mami Gomibuchi[1]; Ryota Tomioka[2]; Miho Ogasawara[3]; Naoki Kawase[3]; Masaaki Senda[4]; Shinji Katsura[5]; Hikari Yamada[6]; Maki Yoshida[7]; Atsushi Oda[8]; Kohsaku Kawakami[9]; *[1]Eisai Co., Ltd., Tokyo, Japan; [2]Shionogi & Co., Ltd., Osaka, Japan; [3]Astellas Pharma Inc., Tokyo, Japan; [4]Sawai Pharmaceutical Co., Ltd., Osaka, Japan; [5]Taiho Pharmaceutical Co., Ltd., Tokyo, Japan; [6]Daiichi Sankyo Co., Ltd., Tokyo, Japan; [7]Chugai Pharmaceutical Co., Tokyo, Japan; [8]Ono Pharmaceutical Co., Ltd, Osaka, Japan; [9]National Institute for Materials Science, Tsukuba, Japan*

MP 568 **Monitoring N-Glycan Occupancy by Peptide MAM Supporting Clone Selection and Biosimilar Comparability**; Gus H M F Souza[1]; Koen Van Der Drift[1]; Michael J. Nold[1]; *[1]KBI Biopharma Inc., Durham, NC*

MP 569 **Impact of an Extra Cysteine Residue on IgG1 Stability**; Rishabh Kaushik[1]; Stella Y. Ren[2]; Carl Kolvenbach[3]; Da Ren[3]; *[1]Newbury Park High School, Newbury Park, CA; [2]Oaks Christian School, Westlake Village, CA; [3]BioTherapeutics Solutions, Westlake Village, CA*

MP 570 **Standardizing Digestion Protocols for Multi-Attribute Method (MAM) to Improve Reproducibility in Therapeutic Antibody Quality Control**; Ryota Tomioka[1]; Miho Ogasawara[2]; Naoki Kawase[2]; Nguyen Bich Thao[3]; Masaaki Senda[4]; Shinji Katsura[5]; Hikari Yamada[6]; Maki Yoshida[7]; Atsushi Oda[8]; Kohsaku Kawakami[9]; *[1]Shionogi & Co., Ltd., Toyonaka, Japan; [2]Astellas Pharma Inc., Tokyo, Japan; [3]Eisai Co.,Ltd., Tsukuba-shi, Japan; [4]Sawai Pharmaceutical Co., Ltd., Osaka, Japan; [5]Taiho Pharmaceutical Co., Ltd., Tokyo, Japan; [6]Daiichi Sankyo Co., Ltd., Tokyo, Japan; [7]Chugai Pharmaceutical Co., Tokyo, Japan; [8]Ono Pharmaceutical Co., Ltd, Osaka, Japan; [9]National Institute for Materials Science, Tsukuba, Japan*

MP 571 **Interlaboratory Reproducibility Study and Comprehensive Method Optimization in Multi-Attribute Method (MAM) for Antibody Therapeutics**; Miho Ogasawara[1]; Naoki Kawase[1]; Ryota Tomioka[2]; Nguyen Bich Thao[3]; Masaaki Senda[4]; Shinji Katsura[5]; Hikari Yamada[6]; Maki Yoshida[7]; Atsushi Oda[8]; Kohsaku Kawakami[9]; *[1]Astellas Pharma Inc., Tokyo, Japan; [2]Shionogi & Co., Ltd., Osaka, Japan; [3]Eisai Co., Ltd., Tokyo, Japan; [4]Sawai Pharmaceutical Co., Ltd., Osaka, Japan; [5]Taiho Pharmaceutical Co., Ltd., Tokyo, Japan; [6]Daiichi Sankyo Co., Ltd., Tokyo, Japan; [7]Chugai Pharmaceutical Co., Ltd., Tokyo, Japan; [8]Ono Pharmaceutical Co., Ltd, Osaka, Japan; [9]National Institute for Materials Science, Tsukuba, Japan*

MP 572 **Analytical Repeatability and Precision of the XevoTM CDMS System for AAV Capsid Characterization**; Emily Christofi[1]; Rebecca D'Esposito[2]; Erin Panczyk[2]; Stephen McDonald[2]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

MP 573 **Hybrid DIA and PRM Acquisition Enables In-Depth Host Cell Protein Profiling with Relative Quantitation of Problematic Targets**; Christopher Sauer[1]; Abby Chiang[2]; Elsa Gorre[1]; Jae Choi[3]; Nikki Jarrett[3]; Bhavin Patel[3]; Min Du[4]; Andrew Mahan[1]; Hirsh Nanda[1]; *[1]Johnson & Johnson Innovative Medicine, Spring House, PA; [2]Protein Metrics, LLC, Boston, MA; [3]Thermo Fisher Scientific, Rockford, IL; [4]Thermo Fisher Scientific, San Jose, CA*

MP 574 **High Throughput Peptide Mapping of Therapeutic Proteins by Rapid UHPLC coupled to Orbitrap Astral**; Andrew Dykstra[1]; Mikayla Shanafelt[2]; Zoltan Szabo[2]; Nicolas Hartel[2]; Prashant N. Jethva[1]; Daniel W Woodall[1]; Jason Richardson[1]; Zhongqi Zhang[1]; Dominique Figueroa[2]; Pavel V. Bondarenko[1]; *[1]Amgen, Inc., Thousand Oaks, CA; [2]Thermo Fisher Scientific, San Jose, CA*

MP 575 **Source-Aware Capillary Microflow LC–MS for Peptide and Intact-Protein Quantification with Controlled Charge-State and High-m/z Performance**; Greg Ward[1]; Xiaoli Dong[2]; Matthew Morse[1]; Sam Foster[1]; Patrick Batoon[2]; *[1]Axcend, Provo, UT; [2]Agilent Technologies, Santa Clara, CA*

MP 576 **Optimized Hi3 Label-Free Mass Spectrometry for Stepwise Host Cell Protein Clearance in Biopharmaceutical Process Development**; Sungyoon Moon[1]; Kahyun Kim[1]; Cheol-woo Noh[1]; Byoungju Lee[1]; *[1]Analytical Characterization Team, R&D QM Unit, GC BioPharma, Yongin-si, Gyeonggi-do, South Korea*

MP 577 **Progressive Deconvolution for Comprehensive Analysis of the Highly Deglycosylated Therapeutic Protein Erythropoietin**; Krisztina Radi[1]; Gary Wilson[2]; Lucy Fernandes[1]; Ignat Shilov[2]; Andreas Nägeli[3]; Helen Nyhlén[3]; *[1]Protein Metrics, Bishops Strotford, United Kingdom; [2]Protein Metrics, Boston, MA; [3]Genovis AB, Kävlinge, Sweden*

MP 578 **Sensitive and robust quantification of high-risk host cell protein by mass spectrometry using stable isotope-labeled synthetic AQUA peptides**; Eric Huang[1]; Jae H Choi[2]; Bhavin Patel[2]; Rosalynn Molden[1]; *[1]Just Evotec, Redmond, WA; [2]Thermo Fisher Scientific, Bannockburn, IL*

MP 579 **Mass spectrometry and chemiluminescent quantification and characterization of an adhesive protein adsorbed on polypropylene surfaces**; Maede Yosefii[1]; Neda Feizi[1]; Sarah Jalli[1]; Touradj Solouki[1]; *[1]Baylor University, Waco, TX*

MP 580 **Mass Spec Software Formula One to Aid Data Interpretation at the Speed of Biotherapeutics Development**; Andrew D Mahan[1]; St John Skilton[2]; Michael Poltash[3]; Gary Wilson[2]; Krisztina Radi[2]; Luis Fernandes-Ruiz[2]; Paul DiGregorio[2]; Jing Li[2]; Hirsh Nanda[3]; Yong Kil[2]; *[1]Johnson and Johnson Innovative Medicine, Spring House, PA; [2]Protein Metrics, Boston, MA; [3]Johnson & Johnson Innovative Medicine, Spring House, PA*

MP 581 **Comprehensive Assessment of Pharmacokinetics and In-Vivo Drug-to-Antibody Ratio Shift of ADCs Using LC-HRMS and LC-MS/MS Monitoring Techniques**; Ines C Santos[1]; Joshua Powers[1]; Jian Chen[1]; Nicholas Colletti[1]; Lai Yeung[1]; Dara Hawthorne[1]; Madhan Masilamani[1]; Yongjun Xue[1]; Jim X Shen[1]; *[1]Bristol Myers Squibb, Princeton, NJ*

MP 582 **Real skin, real insights: Evaluating cell-free amniotic fluid biodistribution and wound healing with an ex vivo viable human skin model**; Gary A Schultz[1, 2, 3]; Aaron D Strickland[2]; Oleksa Vatamaniuk[2]; John Gamble[4]; Roger Ilagan[4]; *[1]Emeritus, Ithaca, NY; [2]iFyber LLC, Ithaca, NY; [3]Munson Technology, LLC, Ithaca, NY; [4]Merakris Therapeutics, Durham, NC*

MP 583 **Optimizing Parameters of Data Analysis to Improve Inter-Laboratory Precision of Multi Attribute Monitoring（MAM）in therapeutic mAbs**; Hikari Yamada[1]; Miho Ogasawara[2]; Naoki Kawase[2]; Nguyen Bich Thao[3]; Masaaki Senda[4]; Shinji Katsura[5]; Ryota Tomioka[6]; Maki Yoshida[7]; Atsushi Oda[8]; Kohsaku Kawakami[9]; *[1]Daiichi Sankyo Co.,Ltd., Kanagawa, Japan; [2]Astellas Pharma Inc., Tokyo, Japan; [3]Eisai Co., Ltd., Tokyo, Japan; [4]Sawai Pharmaceutical Co., Ltd., Osaka, Japan; [5]Taiho Pharmaceutical Co., Ltd., Tokyo, Japan; [6]Shionogi & Co., Ltd., Osaka, Japan; [7]Chugai Pharmaceutical Co., Ltd., Tokyo, Japan; [8]Ono Pharmaceutical Co., Ltd, Osaka, Japan; [9]National Institute for Materials Science, Tsukuba, Japan*

MP 584 **Cross Lab comparison of a Routine HCP Characterization Method Using a High Resolution MultiReflecting time-of-flight MS Platform**; Jonathan E Fox[1]; Scott Berger[2]; *[1]Waters, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

MP 585 **Mapping Rare Misreading Errors in Human Mitochondrial Translation**; Rhythm Bharti[1]; Kärt Denks[1]; Ingo Wohlgemuth[1]; Henning Urlaub[1]; Marina Rodnina[1]; *[1]Max Planck Institute for Multidisciplinary Sciences, Goettingen, Germany*

MP 586 **Exploring Membrane Interactions of α-Synuclein with Nanodiscs**; Olivia E Dioli[1]; Estevan Cleveland[1]; Robert W Newberry[1]; Michael T Marty[1]; Jennifer S. Brodbelt[1]; *[1]University of Texas at Austin, Austin, TX*

MP 587 **Investigation of detergents and mixed micelles for the detection, identification and imaging of proteins and protein complexes directly from tissue**; Sarah Vickers[1]; Oliver J. Hale[1]; Leonhard H. Urner[2]; Helen J. Cooper[1]; *[1]University of Birmingham, Birmingham, United Kingdom; [2]Technical University Dortmund, Dortmund, Germany*

MP 588 **Detecting heterogeneous multimembrane protein assemblies from tunable liposomes using nativeCDMS: Elucidating mechanisms of rare neurological disorders**; Samantha O Shepherd[1]; Dipayan Bose[1]; Weijing Liu[2]; Shyam Krishnakumar[1]; Kallol Gupta[1]; Kyle P. Bowen[2]; *[1]Yale University, New Haven, CT; [2]Thermo Fisher Scientfic, San Jose, CA*

MP 589 **Integrated IR Activation and Direct Mass Technology for Native Analysis of Membrane Vesicles**; Corinne Lutomski[1]; Frances I Butroid[2]; Jack L Bennett[2]; Tarick J El-Baba[2]; Joshua D Hinkle[3]; Kyle Patrick Bowen[3]; Rafael D Melani[3]; John E. P. Syka[3]; Christopher Mullen[3]; Carol V Robinson[2]; *[1]University of Oxford, Oxford, United Kingdom; [2]University of Oxford, Department of Chemistry, Oxford, United Kingdom; [3]Thermo Fisher Scientific, San Jose, CA*

MP 590 **Peak Pooling to Couple Reversed Phase Liquid Chromatography with Charge Detection-Mass Spectrometry**; Brian H. Tran[1]; Tian Tian[2]; Iain D. G. Campuzano[2]; Elizabeth Hecht[2]; Michael Thomas Marty[1]; *[1]University of Texas at Austin, Austin, TX; [2]Amgen, Thousand Oaks, CA*

MP 591 **Delineating Transmembrane Proteomics and N-Glycomics of Large versus Small Extracellular Vesicles**; Leilei Zhang[1]; Thaddeus Tripp[2]; Aarti Patel[2]; Lyndsay E.A. Young[3]; Grace Grimsley[3]; Rupak Mukherjee[4]; Jeffery Jones[4, 5]; Anand S. Mehta[3]; Jean Marie Ruddy[1, 5]; Richard R. Drake[3]; Peggi M. Angel[3]; Mijin Kim[6]; Colin Hisey[2]; Cassandra L Clift[1]; *[1]Division of Vascular Surgery, Medical University of South Carolina, Charleston, SC; [2]Department of Biomedical Engineering, Northwestern University, Evanston, IL; [3]Department of Pharmacology and Immunology, Medical University of South Carolina, Charleston, SC; [4]Department of Cardiothoracic Surgery, Medical University of South Carolina, Charleston, SC; [5]Ralph H. Johnson Veterans Administration Health Care System, Charleston, SC; [6]Department of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA*

MP 592 **Rapid Microdroplet Assisted Digestion for Identification of Membrane Proteins**; Timothy Yaroshuk[1]; Hannia Silvestre[1]; Baatar Munkhtsetseg[2]; Harsha P. Gunawardena[3]; Qinghai Zhang[4]; Bin Xu[5]; Hui Zhao[6]; Xi Qiu[6]; Jim Lau[6]; Mike Knierman[6]; Hao Chen[1]; *[1]New Jersey Institute of Technology, Newark, NJ; [2]National University of Mongolia, Ulaanbaatar, Mongolia; [3]Johnson & Johnson Innovative Medicine, Spring House, PA; [4]Scripps Research Institute, La Jolla, CA; [5]Columbia University, New York, NY; [6]Agilent Technologies, Wilmington, DE*

MP 593 **Breaking barriers: defining the molecular architecture of the abalone egg coat**; Stella M Lai[1, 2]; Regina M Edgington[1]; Alexander S Ristau[1]; Damien B Wilburn[1, 2]; *[1]Department of Chemistry and Biochemistry, The Ohio State University, Columbus, OH; [2]Ohio State Biochemistry Program, The Ohio State University, Columbus, OH*

MP 594 **Compartmental Lipid Interaction of Cannabinoid Receptor 1 Revealed by Native Mass Spectrometry**; Rong Chen[1, 2]; Guan-Ting Lian[1, 2, 3]; Yi-An Chen[1]; Sophie de Giorgio[4]; Sarah L. Rouse[4]; George T Hedger[4]; Hsin-Yung Yen[1, 2]; *[1]Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan; [2]Institute of Biochemical Sciences, National Taiwan University, Taipei, Taiwan; [3]Taiwan International Graduate Program, Academia Sinica, Taipei, Taiwan; [4]Department of Life Sciences, Sir Ernst Chain Building, Imperial College London, London, United Kingdom*

MP 595 **Mapping the Cell-Surface Interactome via Photocatalytic Proximity Labeling**; Ellen Spaeth[1]; Tess Branon[2]; Alessandro Ori[2]; Heinrich Jasper[2]; *[1]Genentech Inc., South San Francisco, CA; [2]Genentech Inc, South San Francisco, CA*

MP 596 **Multi-faceted technical evaluation of Illumina, Olink, and Seer+Orbitrap Astral Zoom for plasma proteomics**; William F. Beimers[1]; Hilary A. Kenny[2]; Emmajay Sutherland[3]; Jacob H. Russell[3]; Nicholas M. Riley[3]; Ernst Lengyel[2]; Katherine A. Overmyer[1, 4, 5]; Joshua J. Coon[1, 4, 5, 6]; *[1]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Obstetrics and Gynecology/Section of Gynecologic Oncology, The University of Chicago, Chicago, IL; [3]Department of Chemistry, University of Washington, Seattle, WA; [4]Morgridge Institute for Research, Madison, WI; [5]National Center for Quantitative Biology of Complex Systems, Madison, WI; [6]Department of Chemistry, University of Wisconsin-Madison, Madison, WI*

MP 597 **Performance Evaluation of OptiSpray Technology and the Orbitrap Astral Zoom MS for high-throughput LFQ Proteomics Applications**; Tabiwang N. Arrey[1]; Till Reinhardt[1]; Anna Pashkova[1];

Katherine Walker[2]; Joshua Silveira[2]; Runsheng Zheng[3]; Alec Valenta[3]; Jeff Op de Beeck[4]; Romain Huguet[2]; Eloy Wouters[2]; Eugen Damoc[1]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Germering, Germany; [4]Thermo Fisher Scientific, Zwijnaarde, Belgium*

MP 598 **Improved MS/MS Quality and Higher ID Rates Through ChargeTailored Collision Energies in dda-PASEF**; Ulrike Schweiger-Hufnagel[1]; Jens Decker[1]; Stephanie Kaspar-Schoenefeld[1]; Dennis Trede[1]; Jonathan Krieger[2]; *[1]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [2]Bruker Ltd, Milton, Canada, Toronto, ON*

MP 599 **Quinoa Bioester Treatment Shifts Human Skin Proteome Toward Younger Molecular Signatures Using Support Vector Regression**; Amanda Caroline Camillo De Andrade[1]; Lucas A Sales[1]; Carolina M. Catarino[2]; Bruna Bosquetti[2]; Camila F. S Oliveira[2]; Patricia H. Szuchman[3]; Andrezza D. P. M. Canavez[2]; Ana Raquel I. Firmino[2]; Rodrigo C. Romanhole[3]; Gustavo Dieamant[3]; Desiree C Shuck[2]; Rosario Duran[4]; Juliana de S. da G. Fischer[1]; Marlon Dias Mariano Dos Santos[1]; Paulo C Carvalho[1, 5]; *[1]Instituto Carlos Chagas, Fiocruz - PR, Curitiba, Brazil; [2]Product Performance Department, Grupo Boticário, Curitiba, PR, Brazil, Curitiba, Brazil; [3]Research and Development Department, Grupo Boticário, Curitiba, PR, Brazil, Curitiba, Brazil; [4]Institut Pasteur de Montevideo, Montevideo, Uruguay; [5]University of California San Diego, San Diego, CA*

MP 600 **Spatial Single-Cell Proteomics Defines Functional and Morphological Diversity of Microglia in Alzheimer's Disease**; Youngshik Choe[1]; Jaemyung Jang[2]; Seungeun Yeo[1]; *[1]Korea Brain Research Institute, Daegu, South Korea; [2]Korea Research Institute of Bioscience and Biotechnology, Daejeon, South Korea*

MP 601 **Bioluminescence-powered photocatalysis enables a novel and highly specific proximity labeling platform**; Mark Klein[1]; Ellen Crummy[1]; Christopher M Hosfield[1]; Alex Fister[2]; Michael M Rosenblatt[1]; Marjeta Urh[1]; Thomas Machleidt[1]; Rachel Friedman Ohana[1]; *[1]Promega Corporation, Madison, WI; [2]University of Wisconsin-Madison, Madison, WI*

MP 602 **Reproducible Low-Input Yeast Proteomics using Femtosecond Laser Desorption with Inline Imaging**; Aosheng Gu[1]; Athanasios Litsios[2]; Khaled Madhoun[1]; Stephen Vanderburgt[3]; Brenda Andrews[2, 4]; R. J. Dwayne Miller[1, 3]; *[1]Department of Physics, University of Toronto, Toronto, ON; [2]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON; [3]Department of Chemistry, University of Toronto, Toronto, ON; [4]Department of Molecular Genetics, University of Toronto, Toronto, ON*

MP 603 **An Automated Magnetic Bead–Based Proteomics Workflow Featuring a Magnetically Confined Immobilized Enzyme Reactor**; Quanqing Zhang[1]; Jenny Zhang[2]; Jingran Zhang[2]; Qunjie Wang[2]; *[1]UC RIVERSIDE, Riverside, CA; [2]Unified Separation Technologies Inc., North Whales, PA*

MP 604 **Adaptive focused acoustics technology integrated with proteome profiling of macrophages exclusively detects low abundance immune-associated proteins**; Jennifer Geddes-McAlister[1]; Jason A McAlister[1]; Michael J P Woods[1]; Lia Abarzua[2]; Sameer Vasantgadkar[2]; Debadeep Bhattacharyya[2]; *[1]University of Guelph, GUELPH, ON; [2]Covaris LLC, Woburn, MA*

MP 605 **500 SPD Plasma Proteomics Enabled by Proteonano HT Assay with Built-in Data Calibration & Standardization**; Shao Huan Samuel Weng[1]; Zilu Ye[2]; Le Shen[3]; Hao Wu[1]; *[1]Nanomics Biotechnology Co., Ltd., Hangzhou, China; [2]State Key Laboratory of Common Mechanism Research for Major Diseases, Suzhou Institute of Systems Medicine, Chinese Academy of Medical Sciences & Peking Union Medical College, Suzhou, China; [3]The University of Chicago, Chicago, IL*

MP 606 **Microwave-enhanced Trypsin Digestion for Bottom-Up Proteomics Mapping**; Matthew N. Machelor[1]; Brynn Nelson[1]; Zara Braimah[1]; Troy D Wood[1]; *[1]University at Buffalo, Buffalo, NY*

MP 607 **Improving the Quantitative Performance of Isobaric Tags with IRMPD**; Zhimin Ma[1]; Peng-Kai Liu[1]; Daniel J. Nesbitt[1]; Noah M. Lancaster[1]; Li-Yu Chen[1]; Katherine A. Overmyer[2, 3]; Matthew T. Flowers[1]; Scott T. Quarmby[1, 3]; Joshua D. Hinkle[4]; Graeme C. McAlister[4]; Dawn B. Davis[1]; Lingjun Li[1]; Joshua J Coon[1, 2, 3]; *[1]University of Wisconsin, Madison, Madison, WI; [2]Morgridge Institute for Research, Madison,* *WI; [3]National Center for Quantitative Biology of Complex Systems, Madison, WI; [4]Thermo Fisher Scientific, San Jose, CA*

MP 608 **Nanoflow RPLC-CZE-MS/MS optimization for top-down proteomics of histones in metastatic and nonmetastatic colorectal cancer cells**; Lance M Thorp[1]; Liangliang Sun[1]; Fei Fang[1]; Yifan Yue[1]; *[1]Michigan State University, Department of Chemistry, East Lansing, MI*

MP 609 **Uncovering Biological Biases in Sample Preparation Methods for Plasma Proteomics: A Comparative Evaluation of P2-iST, SPEED, and MagNET**; Juan Pablo Galindo[1]; Casey Powers[1]; Garvey McKenzie[1]; Fang Liu[1]; Ryan Leib[1]; *[1]Stanford University Mass Spectrometry, Palo Alto, CA*

MP 610 **Cross-Laboratory Evaluation of Medium- and Low-Load Proteome Quantitation Using OptiSpray Technology on the Orbitrap Astral MS**; Nicolas Hartel[1]; Roxana Pinna-Martinez[2]; Sonja Radau[2]; Martins Jansons[3]; Katherine Walker[1]; Runsheng Zheng[4]; Joshua Silveira[1]; Alec Valenta[4]; Romain Huguet[1]; Eloy Wouters[1]; Amirmansoor Hakimi[1]; Glenn Damkroeger[2]; Joshua P. Kline[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Dreieich, Germany; [3]Thermo Fisher Scientific, Vilnius, Lithuania; [4]Thermo Fisher Scientific, Germering, Germany*

MP 611 **Development of a 151-plex Pan-cancer Panel forLow-Input Spatial Proteomics: Bridging High-Resolution Discovery and Precise Targeted Quantification**; Dongyoon Shin[1, 2]; Yeongshin Kim[2]; Sumin Lee[3]; Amos Chungwon Lee[3]; Han Suk Ryu[4]; Junho Park[1, 2]; Youngsoo Kim[1, 2]; *[1]AI Omics Research Center, CHA Research Institute, Bundang CHA Hospital, Seongnam, South Korea; [2]Department of Medical Science, CHA University School of Medicine, Seongnam, South Korea; [3]Meteor Biotech, Seoul, South Korea; [4]Seoul National University Hospital, Seoul, South Korea*

MP 612 **Leveraging high-resolution clinical proteomics strategies to address food safety and security against rising incidences and severity of fungal disease**; Jennifer Geddes-McAlister[1]; Seyedehsanaz Ramezanpour[2, 3]; Nasim Alijanimamaghani[4]; Jason A McAlister[2]; Jared Deyarmin[5]; Stephanie N. Samra[5]; David Hooker[4]; *[1]University of Guelph, GUELPH, ON; [2]University of Guelph, Guelph, ON; [3]Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran; [4]University of Guelph - Ridgetown, Ridgetown, ON; [5]Thermo Fisher Scientific, San Jose, CA*

MP 613 **Assessment of strategies to detect small open reading frames (smORFs) in mouse plasma**; Ole Østergaard[1, 2]; Ana Belén Alonso Aguado[3]; Alba Concepción[3]; Guadalupe Sabio[3]; Jesper Velgaard Olsen[1, 2]; *[1]NNF CENTER FOR PROTEIN RESEARCH, Copenhagen, Denmark; [2]Copenhagen Center for Glycocalyx Research, Department of Cellular and Molecular Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark; [3]Organ crosstalk in metabolic diseases, Centro Nacional de Investigaciones Oncológicas, Madrid, Spain*

MP 614 **Integration of High-Sensitivity timsUltra AIP and SISPROT Technology for High-Spatial-Resolution Proteomics**; Xiaoxian Du[1]; Qian Kong[2]; Xianming Liu[1]; Ruijun Tian[2]; *[1]Bruker, Shanghai, China; [2]Department of Chemistry and Research Center for Chemical Biology and Omics Analysis, College of Science, Southern University of Science and Technology, Shenzhen, China*

MP 615 **Optimized nanoparticle-based enrichment workflow for high- throughput detection of low-abundant proteins for plasma proteomics**; Amarjeet Flora[1]; Jared Deyarmin[2]; Qingling Li[2]; Stephanie N. Samra[2]; Bhavin Patel[1]; *[1]Thermo Fisher Scientific, Rockford, IL; [2]ThermoFisher Scientific, San Jose, CA*

MP 616 **Nanotrap PEAK enrichment enables deep proteomic analysis of plasma from several species and synovial fluid**; Gabriela Grigorean[1]; Lauren Y Dixon[2]; Brett Phinney[2]; *[1]University of CA Davis, Davis, CA; [2]University of California, Davis, CA*

MP 617 **Building an Atlas of Protein Turnover in Cynomolgus Monkeys**; Ghazaleh Yassaghi[1]; Liang Xue[2]; Robert J Seward[1]; Yasi Jami[1]; Vahid Farrokhi[1]; Hendrik Neubert[1]; *[1]Pfizer Inc., Andover, MA; [2]Pfizer, Cambridge, MA*

MP 618 **Evaluating Commercial Protease Specificity via De novo Analysis with PEAKS software**; Mynaja Ferguson[1]; Jason J. Evans[1]; *[1]Univeristy of Massachusetts Boston, Boston, MA*

MP 619 **DegDig, Digging the fate of proteins under degrader control by multiplexed Target-Guided Proteomics in a 384 well format**; Uthpala I Seneviratne; *AstraZeneca, Waltham, MA*

MP 620 **A semi-automated 384-well global and targeted proteomics workflow for high-throughput hit-to-lead optimization**; Juan Wang; *AstraZeneca, Waltham, MA*

MP 621 **Multi-omics analysis reveals mechanisms of secondary mitochondrial dysfunction in lysosomal storage disease Niemann-Pick type C**; Roshan Javanshad[1]; Stephanie Cologna[1]; *[1]University of Illinois Chicago, Chicago, IL*

MP 622 **Optimized FAIMS-DIA LC-MS/MS Workflow for Deep Proteomic Profiling of Aqueous Humor**; Suk-Joon Hyung[1]; Ali Basirattalab[1]; Ola M Saad[1]; *[1]Genentech Inc., South San Francisco, CA*

MP 623 **An optimized method for fixed tissue-based proteomics analysis by mass spectrometry**; Hiroyuki Katayama[1]; Jody Vykoukal[1]; Candace Garrett[1]; Wenling He[1]; Yining Cai[1]; Fu Chung Hsiao[1]; Ehsan Irajizad[2]; Johannes Fahrmann[1]; Jennifer Dennison[1]; Sam Hanash[1]; *[1]The University of Texas, MD Anderson, Department of Clinical Cancer Prevention, Houston, TX; [2]The University of Texas, MD Anderson, Department of Biostatistics, Houston, TX*

MP 624 **Towards the systematic building of high-throughput proteomics platforms to uncover novel biology in inflammatory bowel disease**; Jose Navarrete-Perea[1]; Jiaming Li[1]; Wendy Kang[1]; Ryan Gerkman[1]; Marc Alexander Sze[1]; An Chi[1]; *[1]Merck & Co., Inc., Cambridge, MA*

MP 625 **Investigating the Crystallin Eye Lens Proteins of the Vermillion Rockfish by Bottom-Up Proteomics**; Karen S Campos[1]; Linye Zhou[2]; Elizabeth Wingen[2]; Jeremy Serr[2]; Rachel W. Martin[2]; *[1]University of California Irvine, Irvine, CA; [2]University of California, Irvine, Irvine, CA*

MP 626 **Harnessing biological fractionation allows for deep proteome analysis to determine the role of HMG-CoA reductase in skeletal muscle physiology**; Emma K Luhmann[1]; Kevin P Campbell[1]; *[1]University of Iowa Department of Molecular Physiology and Biophysics, Iowa City, IA*

MP 627 **Untargeted Bottom-Up Proteomics of Digestive Proteins in the Carnivorous Plant Drosera capensis**; Linye Zhou[1]; Zane Long[1]; Karen Sofia Campos[1]; Rachel W. Martin[2]; *[1]University of California, Irvine, Irvine, CA; [2]University of California Irvine, Irvine, CA*

MP 628 **Proteomics Profiling of Mouse Liver Reveals Diet Dependent Responses to Traumatic Brain Injury**; Favour M. Chukwubueze[1]; Mojibola Fowowe[1]; Tuli Bhattacharjee[1]; Esther O. Oji[1]; Abderrahmane Koraich[1]; Judith Nwaiwu[1]; Stanley Ibeh[2]; Sarin Mekhjian[3]; Firas H. Kobeissy[3, 4]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Dalhousie University, Halifax, NS; [3]American University of Beirut, Beirut, Lebanon; [4]Center for Neurotrauma, Multiomics & Biomarkers (CNMB) Morehouse School of Medicine, Atlanta, GA*

MP 629 **Hypothalamic Proteomic Signatures Underlying Susceptibility and Resistance to Diet-Induced Weight Gain**; Judith Ijeoma Nwaiwu[1]; Sergio Guzman-Rodriguez[2]; Cristian D Gutierrez Reyes[1]; Ricardo Romero-Guevara[2]; Jesús Chávez-Reyes[2]; Favour M. Chukwubueze[1]; Oluwatosin Daramola[1]; Tuli Bhattacharjee[1]; Bruno A Marichal-Cancino[2]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock,, TX; [2]Departamento de Fisiología y Farmacología, Centro de Ciencias Básicas, Universidad Autónoma de Aguascalientes, Ciudad Universitaria, 20131 Aguascalientes, Ags., México, Aguascalientes, Mexico*

MP 630 **Catalyst-aided mass spectrometry-based sample preparation increases proteome coverage in FFPE tissues for spatial proteomics**; Andikan Jones Nwosu[1]; Liang Chen[1]; Yu Mi Kwon[1]; Rashmi Kumar[1]; Shaun Goodyear[2]; Adel Kardosh[2]; James M. Fulcher[1]; Ljiljana Pasa-Tolic[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]Oregon Health & Science University, Portland, OR*

MP 631 **Spatially Resolved Proteomic Profiling Reveals Differential Tubulointerstitial and Glomerular Alterations in Chronic Renal Failure**; Hong-Beom Park[1, 2, 3]; Gyuri Park[2, 3, 4]; Eunseo Kim[1, 2, 3]; Jin Lee[1, 2, 3]; Yerin Kim[2, 3, 4]; Minhyeok Kang[2, 3, 4]; Jiyeon Choi[2, 3]; Yiseo Rho[2, 3, 4]; Woosol Chris Hong[2, 3]; Jiho Lee[2, 3]; Seung-Hee Yang[5]; Dohyun Han[2, 3]; *[1]Department of Biomedical Science, College of Medicine, Seoul National University, Seoul, South Korea; [2]Department of transdisciplinary medicine, Seoul National*

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MP 632 **Spatial proteomics identifies FXYD6 as a dual-site protein of neuromuscular junction in the diaphragm**; Nitin George Eapen[1]; Luisa Schmidt[2]; Michael Saynisch[1]; Jan Wilm Lackmann[1]; Christian Hoegsbjerg[3]; Abigail L. Mackey[3]; Manuel Koch[4]; Bent Brachvogel[4]; Philipp Antczak[5]; Marcus Krüger[1]; *[1]CECAD, University of Cologne, Köln, Germany; [2]Novo Nordisk Foundation Center for Protein Research, Department of Cellular and Molecular Medicine, Copenhagen, Denmark; [3]University of Copenhagen, Copenhagen, Denmark; [4]University of Cologne, Cologne, Germany; [5]CMMC, University of Cologne, Cologne, Germany*

MP 633 **Beyond the Pattern: Spatial Proteomics Signatures in Lung Adenocarcinoma**; Denise Jansen[1, 2, 3]; Benedikt Niedermaier[2, 4]; Lisa Strotmann[2, 3, 5, 6]; Martin Bernd Schneider[1]; Dario Frey[1]; Barbara Helm[7]; Marc André Schneider[2, 5]; Hauke Winter[2, 4]; Dominic Helm[1, 7]; *[1]Proteomics Core Facility, German Cancer Research Center (DKFZ), Heidelberg, Germany; [2]Translational Lung Research Center Heidelberg (TLRC), Member of the German Center for Lung Research (DZL), Heidelberg, Germany; [3]Heidelberg University, Faculty of Biosciences, Heidelberg, Germany; [4]Department of Thoracic Surgery, Thoraxklinik at the University of Heidelberg, Heidelberg, Germany; [5]Translational Research Unit, Thoraxklinik at Heidelberg University Hospital, Heidelberg, Germany; [6]Division Systems Biology of Signal Transduction, German Cancer Research Center (DKFZ), Heidelberg, Germany; [7]Proteomics Core Facility, The University of Texas, MD Anderson Cancer Center, Houston, TX*

MP 634 **Deep-Visual LC-MS Proteomics of Charcot-Leyden-like Crystallopathy in Fra2 Mice**; Hendrik Wesseling[1]; Ingeborg Langohr[1]; Hong Ma[1]; Colleen Maloney[1]; Caroline Morel[1]; Peter Piepenhagen[1]; Keith Graver[1]; Dinesh Bangari[1]; Bailin Zhang[1]; *[1]Sanofi, Cambridge, MA*

MP 635 **Proteomic and Lipidomic Insights into PGRN-Linked Neurodegeneration in Frontotemporal Dementia**; Yohannes Ambaw[1]; Hui Liu[2]; Zhuoning Li[2]; Alissa L. Nana[3]; William W. Seeley[3]; Mara Monetti[2]; Robert V. Farese Jr[1]; Tobias C. Walther[1, 4]; *[1]Cell Biology Program, Sloan Kettering Institute, MSKCC, New York, NY; [2]Proteomics Innovation Laboratory and Proteomics and Metabolomics Core, Sloan Kettering Institute, MSKCC, New York, NY; [3]Department of Neurology, Memory and Aging Center, University of California, San Francisco, CA; [4]Howard Hughes Medical Institute, New York, NY*

MP 636 **Development of a Robust and High-Throughput Proteomics Preparation Workflow for Bottom-Up Biomarker Analysis in Human Heart Tissue**; Andrew Bergdorf[1]; Ryan Darling[1]; Dawn Dufield[1]; Rathna Veeramachaneni[1]; *[1]KCAS Bio, Olathe, KS*

MP 637 **MALDI MSI Detection of TMT Labeled Peptides: Towards Unifying Proteomic Imaging and LC Platforms**; Harrison Taylor[1]; Mi-hye Lee[1]; Charles A Schurman[2]; Richard R. Drake[1]; Anand Mehta[1]; Kurt Prins[1]; Lauren Ball[1]; Birgit Schilling[2]; Peggi Angel[1]; *[1]Medical University of South Carolina, Charleston, SC; [2]Buck Institute for Research on Aging, Novato, CA*

MP 638 **Simple and Highly Efficient One- or Two-step Proteomic Preparation for FF and FFPE Tissues Evaluates Preservation-Dependent Proteome Bias**; Chuping Wei; *Southern University of Science and Technology, Guangzhou, China*

MP 639 **The Hunt for Placental Opioid-Enhancing Factor (POEF): Bottom-up proteomics mapping of rat amniotic fluid, placenta, and liver**; Brynn Nelson[1]; Mark B Kristal[1]; Alexis C Thompson[1]; Jean M DiPirro[2]; Troy D Wood[1]; *[1]University at Buffalo, Amherst, NY; [2]Buffalo State University, Buffalo, NY*

MP 640 **High-Throughput Single-Cell Organic Mass Cytometry for Rapid and Robust Screening of Rare Cells**; Murong Du; *Tsinghua University, Beijing, China*

MP 641 **Deep Single-Cell Proteome Profiling of Cardiomyocytes Using Advanced Ion Processing Coupled with Trapped Ion Mobility**; Johannes Janssens[1]; Lizhuo Ai[2]; Diego Assis[3]; Madelyn Arzt[1]; Matthew Willetts[3]; Michael Krawitzky Krawitzky[3]; Ajay Bharadwaj[1]; Aleksandr Stotland[1]; Arun Sharma[1]; Daniel

Hornburg[4]; Aleksandra Binek[1]; Jennifer E. Van Eyk[1]; [1]*Cedars-Sinai Medical Center, Smidt Heart Institute, Los Angeles, CA;* [2]*Merck & Co, Rahway, NJ;* [3]*Bruker Daltonics, Billerica, MA;* [4]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

MP 642 **Single-Cell Proteomic Landscape of Biological Heterogeneity in Oocyte Aging Models**; Da-Yeon Lee[1]; Seung A Oh[1, 2]; Hyun-Seung Lee[1, 2]; Dongyoon Shin[3, 4]; Youngsoo Kim[3]; Jae Ho Lee[1, 2]; Junho Park[3, 4]; [1]*Department of Biomedical Science, CHA University, Seongnam, South Korea;* [2]*CHA Fertility Center, Seoul Station, Seoul, South Korea;* [3]*Artificial Intelligence Omics Research Center, CHA Research Institute, Bundang CHA Hospital, Seongnam, South Korea;* [4]*Department of Medical Science, CHA University School of Medicine, Seongnam, South Korea*

MP 643 **Single-cell proteome atlas of the mouse spleen**; Selin Ulukaya[1, 2]; Aline Konrad[3, 4]; Syed Azmal Ali[1]; Rienk Offringa[3, 4]; Jeroen Krijgsveld[1, 2]; [1]*German Cancer Research Center (DKFZ), Division of Proteomics of Stem Cells and Cancer, Heidelberg, Germany;* [2]*Heidelberg University, Medical Faculty, Heidelberg, Germany;* [3]*German Cancer Research Center (DKFZ), Division of Molecular Oncology of Gastrointestinal Tumors, Heidelberg, Germany;* [4]*University Hospital Heidelberg (UKHD), Department of General, Visceral and Transplantation Surgery, Heidelberg, Germany*

MP 644 **Profiling the metabolic modulation of human CD4+ T cells with high-throughput single-cell metabolomics**; Luisa Abreu[1, 2, 3]; Theodore Alexandrov[1, 2, 4, 5]; [1]*Department of Pharmacology, University of California San Diego, La Jolla, CA;* [2]*Molecular Systems Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany;* [3]*Collaboration for joint PhD degree between EMBL and Heidelberg University, Faculty of Biosciences, Heidelberg, Germany;* [4]*Department of Bioengineering, University of California San Diego, La Jolla, CA;* [5]*DeepCyte Inc., San Diego, CA*

MP 645 **Spatial and low input proteomics at scale with the timsUltra AIP**; Christoph Krisp[1, 2]; Melissa Klingeberg[2, 3, 4]; Leandro Santiago[2, 3]; Anjali Seth[5]; Dorte B. Bekker-Jensen[6]; Nicolai Bache[6]; Pierre-Oliver Schmit[7]; Stefan Kempa[2, 3]; Fabian Coscia[2, 3]; Daniel Hornburg[8]; [1]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [2]*MDC-Bruker Center of Excellence for Single Cell Omics, Max Delbrück Center for Moleculare Medicine in the Helmholtz-association, Berlin, Germany;* [3]*Max-Delbrück-Center for Molecular Medicine in the Helmholtz Association (MDC), Berlin, Germany;* [4]*Humboldt University Berlin, Berlin, Germany;* [5]*Cellenion SASU, Lyon, France;* [6]*Evosep, Odense, Denmark;* [7]*Bruker France SAS, Wissembourg, France;* [8]*Bruker Scientific LLC, Billerica, MA*

MP 646 **Evaluation of prioritized peptide acquisition using automated retention time alignment for multiplexed single-cell proteomics on an Orbitrap Astral Zoom MS**; Bernard Delanghe[1]; Martin Zeller[1]; Tabiwang N. Arrey[1]; Jeff Op De Beeck[2]; Anjali Seth[3]; Julia Kraegenbring[1]; Jana Richter[1]; Tonya Pekar Hart[4]; Thomas Moehring[5]; [1]*Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany;* [2]*Thermo Fisher Scientific, Zwijnaarde, Belgium;* [3]*Cellenion SASU, Lyon, France;* [4]*Thermo Fisher Scientific, San Jose, CA;* [5]*Thermo Fisher Scientfic, San Jose, CA*

MP 647 **Single-cell High resolution MALDI imaging of human primary macrophages**; Paula Martinez Oca[1]; Quentin Vanbellingen[2]; Lyna Sellami[3]; Giovanna Roberta Meloni[4]; Carmen Buchrieser[1]; Pedro Escoll[1]; Sandrine Aros[2]; [1]*Institut Pasteur, Biology of Intracellular Bacteria Unit, Paris, France;* [2]*Institut Pasteur, Metabolomics Core Facility, Paris, France;* [3]*Shimadzu Europa GmbH, Duisburg, Germany;* [4]*Shimadzu Italy, Milano, Italy*

MP 648 **Orbitrap™ Astral™ with FAIMS enables deep and high dynamic range proteomic profiling of low input human FFPE tissue-derived samples**; Yunyun ZHU[1]; Jeff Martin[2]; Amanda Guise[2]; Brendan Gallagher[2]; [1]*Thermo Fisher Scientific, Lexington, MA;* [2]*Biogen, Cambridge, MA*

MP 649 **Minimizing Protein and Peptide Absorption Loss in Single-Cell Proteomics Using a Chemically Inert Polymer**; Cameron B Braswell[1]; Shelby Ruiz[1]; Ben Orsburn[1]; [1]*University of Pittsburgh, Pittsburgh, PA*

MP 650 **Deep Single-Cell Proteomic Analysis of Isogenic APP and PSEN2 Mutant Neurons Reveals Distinct Molecular Signatures in Alzheimer's Disease Pathogenesis**; Reynaldo Melo[1]; Natalia C Dos Santos[2]; Blake Tsu[2]; Juliana de S. da G. Fischer[2, 3]; Paulo Costa Carvalho[2, 3]; Joshua Cantlon[4]; Alysson R. Muotri[2]; Aline Martins[2]; John R. Yates III[2]; [1]*The Scripps Research Institute, la jolla, CA;* [2]*Integrated*

Space Stem Cell Orbital Research Center, La Jolla, CA; [3]Carlos Chagas Institute, Fiocruz, Curitiba, Brazil; [4]Scienion, Seattle, WA

MP 651 **Robust identification of 7,300 proteins from single-HeLa cells and 4,100 proteins from single-PBMCs using the Orbitrap Astral Zoom mass spectrometer**; Ivo A. Hendriks[1]; Sara C. Buch-Larsen[1]; Martin Rykar[1]; Maico Y. Lechner[1]; Anders H. Kverneland[1]; Tabiwang N. Arrey[2]; Daniel Hermanson[2]; Eugen Damoc[2]; Jesper V. Olsen[1]; *[1]NNF Center for Protein Research, Department of Cellular and Molecular Medicine, University of Copenhagen, Copenhagen, Denmark; [2]Thermo Fisher Scientific, Bremen, Germany*

MP 652 **High-Throughput SCP: Rapid Separations coupled with Orbitrap Astral enables the analysis of >2000 nPOP-prepared TMT-labeled single cells per day**; Sachini N Moratuwage[1]; Hannah Harens[2]; Orhun Kok[2]; Chao Wang[3]; Seth M Kelly[3]; Clayton B Tacker[3]; Brandon M Gassaway[3]; Nikolai Slavov[2, 4]; Ryan T. Kelly[3]; *[1]Brigham Young University, Provo, UT; [2]Northeastern University, Boston, MA; [3]Brigham Young Uniersity, Provo, UT; [4]Parallel Squared Technology Institute, Watertown, MA*

MP 653 **Metabolomics, Lipidomics, and Mass Spectrometry Imaging of Tumor Cell Heterogeneity in Multiple Myeloma Drug Resistance**; Min Liu[1]; Dario Magaletti[1]; Esabella R. Powers[2]; Carolina Cruz Cepeda[1]; Mark Meads[1]; Timothy J Garrett[3]; Kenneth Shain[1]; John M. Koomen[1]; *[1]Moffitt Cancer Center, Tampa, FL; [2]University of Florida, Department of Chemistry, Gainesville, FL; [3]University of Florida, GAINESVILLE, FL*

MP 654 **High-Throughput Single-Cell Proteomics Enabled with Hyperplexing Barcoding of Peptides**; Giulia Barotti[1]; Ronald Cutler[1]; Simone Sidoli[1]; *[1]Albert Einstein College of Medicine, Bronx, NY*

MP 655 **Single-Cell Proteomic Profiling of Chemotherapy-Resistant Ovarian Cancer Cells**; Zongkai Peng[1]; Deepti Bhusal[1]; Nagib Ahsan[2]; Zhibo Yang[1]; *[1]University of oklahoma HSC, Oklahoma city, OK; [2]University of Oklahoma, Norman, OK*

MP 656 **Phenotyping of Single Neurons In Tissue by Patch-Clamp CE–MS Proteomics**; Cole C Johnson[1]; Sam B Choi[1]; Juan A Zegers Delgado[1]; Alexandre Kisner[2]; Ricardo C Araneda[1]; Abigail M Polter[2]; Peter Nemes[1]; *[1]University of Maryland, College Park, MD; [2]George Washington University, Washington DC, DC*

MP 657 **Bulk and single-cell dimorphic protein profiling of human neutrophils in resting and activation states**; Isabelle S. Luz[1]; Reynaldo M. Melo[2]; Joshua Cantlon[3]; Alysson R. Muotri[1]; Wagner Fontes[4]; Aline M.A. Martins[1]; *[1]Integrated Space Stem Cell Orbital Research (ISSCOR) Center,, San Diego, CA; [2]Scripps Research Institute, La Jolla, CA; [3]Scienion, Seattle, WA; [4]Laboratory of Biochemistry of Protein Chemistry, University of Brasilia, Brasília, Brazil*

MP 658 **Quantitative Top-Down Proteomics Analysis from 1–50 Human Cells Using Spray-Capillary CE-MS**; Samin Anjum[1]; Zhitao Zhao[1]; Kellye A. Cupp-Sutton[1]; Si Wu[1]; *[1]The University of Alabama, Tuscaloosa, AL*

MP 659 **Cross-Platform Single-Cell Metabolomics: Comparing Nanoflow Sheath-Liquid Interfaces for CE-NanoESI-MS**; Shuangshuang Chen[1]; Chen Huang[1]; Satirtha Saha Protya[1]; Yash Nelavelli[1]; Stanislav S Rubakhin[1]; Hsi-Chun Chao[1]; Michael Knierman[2]; Jonathan V Sweedler[1]; *[1]University of Illinois Urbana Champaign, Urbana, IL; [2]Agilent Technologies, Santa Clara, CA*

MP 660 **An End-to-End Workflow for Sensitive Single Cell Proteomics at 95 SPD**; Nicolas Hartel[1]; Mikayla Shanafelt[1]; Dylan Multari[2]; Chris Xu[2]; Michelle Cielesh[3]; Angela Connolly[3]; Sudipa Maity[1]; Ben Crossett[3]; Stuart Cordwell[3]; Ralf Schittenhelm[2]; Daniel Hermanson[1]; Mark Larance[3]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Monash University, Melbourne, Australia; [3]The University of Sydney, Camperdown, Australia*

MP 661 **Doubling Protein Identification from Limited Samples with Porous Layer Open-Tubular LC-MS**; Michal Gregus[1]; Noah Gould[1]; Ziyu Zhang[1]; Thao Tran[1]; Virginie Sjoelund[1]; Alexander R. Ivanov[1]; *[1]Northeastern University, Boston, MA*

MP 662 **Integrating single-cell transcriptomics, histone PTM profiling, and proteomics to quantify mutation-driven regulatory network destabilization**; Ronald Cutler[1]; Johanna Heid[1]; Moonsook Lee[1]; Jennifer Aguilan[1]; Jan Vijg[1]; Simone Sidoli[1]; [1]*Albert Einstein College of Medicine, Bronx, NY*

MP 663 **MALDI-MSI Detection of Mitochondria-Targeted Compounds in Single Cells**; Sima Ziyaee[1]; Stanislau Stanisheuski[1]; Hyo Sang Jang[2]; Claudia Maier[1]; [1]*Oregon State University, Corvallis, OR;* [2]*HP Life Science Solutions, Corvallis, OR*

MP 664 **Exploring hepatocyte diversity with single cell proteomics**; Shelby Ruiz[1]; Cameron B Braswell[1]; Daniela Gil[1]; Sean Farris[1]; Mahboubeh Varmazyad[1]; Mark T Miedel[1]; Ben Orsburn[1]; [1]*University of Pittsburgh, Pittsburgh, PA*

MP 665 **A Robust and High-throughput Method for Quantification of Metformin in Human Plasma Using HILIC-UPLC-MS/MS**; Yan Luo[1]; Andy (Hongfang) Xue[1]; Xiuling Liu[1]; Aihua Liu[1]; [1]*Resolian, Malvern, PA*

MP 666 **EAD Fragmentation as a Tool for Structural Elucidation of Unknown Pharmaceutical Impurities**; Roma Perłowska[1]; Rafał Szewczyk[1, 2]; Katarzyna Krupczyńska-Stopa[1, 2]; Maciej Stopa[1, 2]; [1]*LabExperts sp z o.o., Gdansk, Poland;* [2]*Bioanalytic sp. z o.o., Gdansk, Poland*

MP 667 **Quantitative analysis of Sumatriptan-NDSRI at Ultra-trace level in Sumatriptan while interference is resolved using LC/TQ**; Vikrant Goel[1]; Saikat Banerjee[2]; Vivek Dhyani[3]; [1]*Agilent Technologies, Gurgaon, India;* [2]*Agilent Technologies, Hyderabad, India;* [3]*Vivek Dhyani, Mumbai, India*

MP 668 **Accelerated characterization of cyclic peptides enabled by a new customizable workflow for unnatural amino acids**; Jiaxuan Yan[1]; Cece Cui[2]; Aude Tartiere[2]; Wendy Zhong[1]; Hillary A Schuessler[1]; [1]*Merck & Co., Rahway, NJ;* [2]*Genedata Inc, Boston, MA*

MP 669 **Optimized LC-HRMS for Trace Detection of Penicillin β-Lactam Contamination in Pharmaceuticals**; Fernando Gonzalez; *US FDA, San Juan, Puerto Rico*

MP 670 **Identification of isomeric bifunctional compounds in mixtures by using gas-phase ion chemistry**; Razieh Zamani[1]; Hilkka I. Kenttämaa[2]; [1]*Purdue University, West Lafayette, IN;* [2]*Purdue University, west lafayette, IN*

MP 671 **Ion Mobility-Mass Spectrometry Maps Early Purine Nucleoside Oligomerization and EGCG-Driven Perturbation of Oligomer Populations**; Happy Abena Safoah[1]; Damilola S. Oluwatoba[1]; Thanh D. Do[1]; [1]*University of Tennessee, Knoxville, Knoxville, TN*

MP 672 **Structure Elucidation of a Stable Phosphate-Containing Impurity in the Process Development of BMS-986465**; Ziyu Wang[1]; Junhe Ma[1]; Qinggang Wang[1]; Benjamin J. Hritzko[1]; Michael B. Peddicord[1]; [1]*Bristol Myers Squibb, New Brunswick, NJ*

MP 673 **Unraveling the unknown: Investigation of palladium catalyst poisoning by LC-MS during drug substance manufacturing reveals unexpected free-thiol poisons**; Justin Mak[1]; Bifan Chen[1]; [1]*Genentech Inc., South San Francisco, CA*

MP 674 **Profiling of polyphenols and glucosinolates in fruit and vegetable extracts by HPLC-MS/MS**; Wen Lu[1]; Cameron M. McCarthy[1]; Ana P. S. Siqueira[1]; Laura L. Sarabia[1]; Wesley W. Grace[1]; Rami S. Najjar[1]; Rafaela G. Feresin[1]; Siming Wang[1]; [1]*Georgia State University, Atlanta, GA*

MP 675 **Absolute Quantitation of Native Amino Acids and Biological Modifications in Serum − Monitoring Subject-Specific Protein Digestion in Large Feeding Trials**; Jada Kate Garcia[1]; Shawn Ehlers-Cheang[1]; Michael Gunning[2]; Alaa Al Dulaimi[1]; Angel Susantin[1]; Mariana Barboza[3]; Keith Baar[4]; Justin Siegel[1]; Carlito Lebrilla[1]; [1]*Department of Chemistry, University of California, Davis, Davis, CA;* [2]*Computer Science, University of California, Davis, Davis, CA;* [3]*Innovation Institute for Food and Health, University of California, Davis, Davis, CA;* [4]*College of Biological Sciences, University of California, Davis, Davis, CA*

MP 676 **Targeted and Nontargeted PFAS Analysis in Cosmetics Using APGC-MS/MS, UPLC-MS/MS, and LC-QTOF MS**; Shu-Hua Tsai[1]; Chia-Yang Chen[2]; *[1]Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei City, Taiwan; [2]National Taiwan University, Taipei City, Taiwan*

MP 677 **An R-based expert data analysis tool for fast annotation of flavonoids in food**; Jianghao Sun[1]; Mengliang Zhang[2]; Pei Chen[1]; *[1]USDA-ARS, Beltsivlle, MD; [2]Ohio University, Athens, OH*

MP 678 **Development of an LC-MS/MS method for an extended set of mutagenic small molecule nitrosamines in metformin drug substance**; Matt James[1]; Atis Chakrabarti[2]; Nishaben Patel[2]; Gemma Lo[1]; Helen Poole[1]; *[1]Avantor, Theale, United Kingdom; [2]Avantor, Bridgewater, NJ*

MP 679 **Comprehensive extractables and leachables characterization through an integrated single injection Quan/Qual analysis using a benchtop MRT MS**; Rachel J Sanig[1]; Lee A. Gethings[1]; Jayne Kirk[1]; Shashank Jain[2]; Richard Lock[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

MP 680 **Identification and sensitive quantitation of N-Nitrosotrientine and Di-N-Nitrosotrientine in Trientine API**; Ferran Sanchez[1]; Lakshmanan Deenadayalan[2]; Sashank Pillai[2]; Eshani Galermo[3]; *[1]SCIEX, Barcelona, Spain; [2]SCIEX, Bangalore, India; [3]SCIEX, Redwood City, CA*

MP 681 **Development and Validation of an LC-MS/MS Method for Quantification of Protein-Unbound Doravirine in Human Plasma using Rapid Equilibrium Dialysis**; Amanda P Schauer[1]; Craig Sykes[1]; Angela DM Kashuba[1]; *[1]University of North Carolina, Chapel Hill, NC*

MP 682 **Automated Fast Screening Workflow for Novel Psychoactive Substances by High Resolution Mass Spectrometry**; Cate Simmermaker[1]; Jennifer C Hitchcock[1]; Olivier P. Chevallier[1]; *[1]Agilent Technologies, Santa Clara, CA*

MP 683 **Fully Enantioselective Separation and Quantitative Determination 3,4-Methylenedioxy-methamphetamine (MDMA) and Its Phase-1 Metabolites in Human Plasma by HPLC-MS/MS Methods**; Jingguo Hou[1]; Xiaodong Zhu[1]; Steven Hoehen[1]; Alicia Bian[1]; Jason Hamilton[1]; *[1]Worldwide Clinical Trials, Austin, TX*

MP 684 **Quantitation of N-nitroso sitagliptin impurity (NTTP) in sitagliptin API**; Eshani Galermo[1]; Ebru Selen[1]; John Gibbons[2]; Craig Butt[3]; Rahul Baghla[1]; *[1]SCIEX, Redwood City, CA; [2]SCIEX, Concord, ON; [3]SCIEX, Marlborough, MA*

MP 685 **Sensitive, high-coverage plasma metabolomics in diet-induced obesity enabled by parallel SQUAD acquisition on a modified Orbitrap Tribrid MS**; Bashar Amer[1]; Daniel Hermanson[2]; Brandon Bills[2]; Sunandini Yedla[2]; Rahul Deshpande[2]; Rafael D Melani[2]; Thomas Moehring[3]; Susan S. Bird[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientfic, San Jose, CA; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

MP 686 **Development of a comprehensive LC–MS/MS Workflow for PFAS Quantitation in Cosmetic Matrices Containing Anionic Surfactants**; Mingyun Kim[1]; Bohyon Sung[1]; *[1]Kolmar Korea, Seoul, South Korea*

MP 687 **Development and validation of an LC-MS/MS assay for the quantification of a novel VEGFR kinase inhibitor in ocular tissues**; Mathias Salger[1]; Stefan Blech[1]; *[1]Boehringer Ingelheim Pharma GmbH & Co. KG, Biberach, Germany*

MP 688 **mzmine unifies untargeted LC-MS and auxiliary detector analysis**; Steffen Heuckeroth[1]; Philipp Otzen[2]; Heiko Hayen[2]; Ansgar Korf[1]; Robin Schmid[1]; *[1]mzio GmbH, Bremen, Germany; [2]University of Münster, Münster, Germany*

MP 689 **MS2/MS3 Electron Activation to locate chlorination at benzylic vs. aromatic positions, positioning of labile substituents and structure of aromatic heterocycles**; Gustaf Hulthe[1]; Athanasios Smyrnakis[2]; Maria-Aggeliki Kosmopoulou[2]; Dimitris Papanastasiou[2]; Christian Albers[3]; Michael Greig[4];

[1]AstraZeneca, Pharmaceutical Technology and Development, Gothenburg, Sweden; [2]Fasmatech Science & Technology, Athens, Greece; [3]Bruker Daltonik GmbH, Bremen, Germany; [4]Bruker, Carlsbad, CA

MP 690 **Quantitation of Psychedelics used to Treat Mental Illness from Human Saliva Using HPLC-MS/MS and HPLC-HRMS/MS**; Aidan O Dusho[1]; Chad Christianson[1]; Jennifer S Zimmer[1]; Leslie F Hvozda[1]; *[1]Alturas Analytics, Moscow, ID*

MP 691 **Unambiguous structural identification without reference standards using MRR**; Justin L Neill[1]; Steven T. Shipman[2]; Reilly E. Sonstrom[2]; Alexander V. Mikhonin[2]; Christopher J. Thompson[3]; *[1]BrightSpec, Inc., Charlottesville, VA; [2]BrightSpec Inc., Charlottesville, VA; [3]BrightSpec, Inc., Waltham, MA*

MP 692 **Fast-Track Quantitative Analysis of Anti-Arrhythmic Drugs Using a Laser Diode Thermal Desorption (LDTD) coupled to a Mass Spectrometer**; Anastasiia Shyian[1]; Anna Lenartowicz[2]; Maciej Stopa[1]; Katarzyna Krupczyńska-Stopa[2]; Serge Auger[3]; *[1]Bioanalytic sp. z o.o., Gdansk, Poland; [2]LabExperts sp z o.o., Lodz, Poland; [3]Phytronix Technologies, Inc., Quebec, QC*

MP 693 **Development of a targeted and sensitive UPLC-MS/MS method for sterol glucosides quantification in bio-oils destined for biofuel production**; Taous ABAR[1]; Tuyet Le[2]; Sophie Sambou[2]; Mathilde Lauzent[1]; Marie Hubert-Roux[1]; *[1]Université de Rouen Normandie, INSA Rouen Normandie, Université de Caen Normandie, ENSICAEN, CNRS, Institut CARMeN UMR 6064, Rouen, France; [2]Saipol, Rouen, France*

MP 694 **Down in the Weeds: Automated Fast Screening Workflow for Cannabinoids in Whole Blood Using High Resolution Mass Spectrometry**; Cate Simmermaker[1]; Jennifer Cottine Hitchcock[1]; Peter Stone[1]; *[1]Agilent Technologies, Santa Clara, CA*

MP 695 **Coupling Boronic Acid Click-Chemistry with Nano-electrospray Ionization Mass Spectrometry Enables Isomeric Characterization and Quantitation of NADH**; Huiying Guo[1]; Xinjie Wang[1]; Jiang Chang[1]; Xin Yan[1]; *[1]Texas A&M University, College Station, TX*

MP 696 **Aspartame quantification in beverages and sweetener solutions by MALDI MS/MS ion trap approach**; Muhammad Ali[1]; Emmanuel Chang[1, 2]; *[1]CUNY Graduate Center, New York, NY; [2]CUNY York College, New York City, NY*

MP 697 **Production and Characterization of Protonated Small Water Clusters**; Yixin Zhu[1]; Kai Tang[1]; *[1]Hangzhou Shanshangshui Technology Co., LTD, Hangzhou, China*

MP 698 **Practical LC-MS Analysis of NDSRIs Using Biphenyl Selectivity**; Vikram Shenoy[1]; Sean Orlowicz[1]; Jeremy Primack[1]; Pankaj Partani[2]; Rahul Baghla[3]; *[1]Phenomenex Inc., Torrance, CA; [2]SCIEX, Bangalore, India; [3]SCIEX India Private limited, Bangalore, India*

MP 699 **A Nano-LC Orbitrap Astral SQUAD Workflow Enables Multi-Tissue Bile Acid Profiling in Mice**; Philip L Lorenzi[1]; Xiaomeng Liang[1]; Bashar Amer[2]; Wai Kin Chan[3]; Yun Xiong[3]; Iqbal Mahmud[3]; Lin Tan[4]; Jibin Ding[3]; Bao Tran[3]; Stephen Mok[1]; Xinran Qi[1]; Sameer Vasantgadkar[5]; Fang Xie[5]; Debadeep Bhattacharyya[5]; Patrick Pirrotte[6, 7]; Jennifer Karmouch[1]; Robert R Jenq[1]; Susan S. Bird[8]; *[1]City of Hope National Medical Center, Duarte, CA; [2]Thermo Fisher Scientific, San Jose, CA; [3]The University of Texas, MD Anderson Cancer Center, Houston, TX; [4]The University of Texas MD Anderson Cancer Center, Houston, TX; [5]Covaris LLC, Woburn, MA; [6]Integrated Mass Spectrometry Shared Resource Facility, City of Hope National Medical Center, Duarte, CA; [7]Early Detection and Prevention Division, Translational Genomics Research Institute, Phoenix, AZ; [8]ThermoFisher Scientific, San Jose, CA*

MP 700 **An Ultra-Sensitive, High-Throughput, and Robust Assay to Quantify Carboplatin in Human Plasma Using HPLC-MS/MS**; Mary (Yuehui) Ma[1]; Shu Li[2]; Lauren D'Orazio[2]; Elese Christ[2]; Yan Luo[2]; Aihua Liu[3]; *[1]Resolian Inc, Malvern, PA; [2]Resolian, Malvern, PA; [3]Resolian (Formally Alliance Pharma), Malvern, PA*

MP 701 **LC–MS/MS Method Development for Isomeric Sugar Phosphate Analysis Using Anion-Exchange and Derivatization Strategies**; Kun Wang[1]; Yijin Xiao[1]; Song Zhao[1]; Xiaonan Tang[1]; [1]*Frontage Laboratories, Exton, PA*

MP 702 **Exploratory Bile Acid Profiling in Women with Fibromyalgia Using SQUAD Optimized Orbitrap Mass Spectrometry**; Annukka Willstedt Justel[1]; Jose A. Horcajadas[2]; Bashar Amer[3]; Susan S. Bird[3]; Hussain Abdulla[4]; [1]*Texas A&M Corpus Christi, Corpus Christi, TX;* [2]*SINAE S.L., Seville, Spain;* [3]*ThermoFisher Scientific, San Jose, CA;* [4]*Texas A&M University- Corpus Christi, Corpus Christi, TX*

MP 703 **Automated Elucidation of Hydrolytic Soft-Spot Cyclic-Peptide Isobars Using High-Resolution ESI-MS-MS/MS Data and MASSPEC Soft-Spot Structure Elucidation Software with Structural Constraints**; Marshall M. Siegel[1]; Gary E. Walker[1]; Serhiy Hnatyshyn[2]; [1]*MS Mass Spec Consultants, Fair Lawn, NJ;* [2]*Bristol Myers Squibb, Princeton, NJ*

MP 704 **On the way to Self-Assembled Monolayers of azobenzene derivatives : photo and back isomerization reaction**; Emma Piplart[1]; Gwendal Henrard[1]; Julien De Winter[1]; Jérôme Cornil[1]; Marc Frère[1]; Pascal Gerbaux[1]; [1]*University of Mons, Mons, Belgium*

MP 705 **A Symbol-based System for Specification of Polymer Composition and Topology**; David Stranz[1]; Scott Campbell[1]; [1]*Sierra Analytics, Inc., Modesto, CA*

MP 706 **Characterization of Sustainable Plastics via Multidimenstional Mass Spectrometry Analysis**; Justin Dyer[1]; Dimitrios Bikiaris[2]; Chrys Wesdemiotis[1]; [1]*University of Akron, Akron, OH;* [2]*The Aristotle University of Thessaloniki, Thessaloniki, Greece*

MP 707 **A Novel and Efficient LC-MS/MS Method for Quantitation of Polysarcosine in Mouse Plasma**; Minqiang Zhu[1]; Meijuan He[2]; Cheng Chen[2]; Ting Zhang[2]; Haiyan Li[2]; Xiaotong Li[2]; Zhiyu Li[2]; Lili Xing[2]; Yi Tao[2]; Liang Shen[2]; [1]*WuXi AppTec (Nanjing) Co., Ltd., Nanjing, China;* [2]*WuXi AppTec, Pudong, Shanghai, China*

MP 708 **Fluorescent TPA–Cellulose Markers Identified by Py-GC/MS for Polymer Recycling**; Gyounglyul Jo[1]; Hyeon Ho Park[1]; Hye Kyeong Sung[1]; Kyoung-Mun Kim[1]; [1]*Korea Testing & Research Institute, Gwacheon, South Korea*

MP 709 **Functionality, Molecular Weight, and Architectural Analysis of Water-Soluble Polymers by Multidimensional Mass Spectrometry**; Calum Bochenek[1]; Jack Edwards[1]; Luciana V Rivera Molina[1]; Zhibo Liu[1]; Christina Mastromatteo[2]; Chrys Wesdemiotis[1]; [1]*The University of Akron, Akron, OH;* [2]*The Lubrizol Corporation, Cleveland, OH*

MP 710 **A Kendrick analysis to deconvolute complex polymer mass spectra and graphically assess the functionalization of poly(ether imine) oligomers**; Thierry Nicolas Jean Fouquet[1]; Sébastien Issa[2]; Trang N. T. Phan[2]; Didier Gigmes[2]; Laurence Charles[2]; [1]*Bausch + Lomb, Rochester, NY;* [2]*Aix Marseille Univ, CNRS, Institut de Chimie Radicalaire, UMR 7273-Campus Scientifique St Jérôme, Service 542, Marseille, France*

MP 711 **Structural Motifs in Crosslinked Polyester Networks Unveiled by Thermal Desorption/Pyrolysis Interfaced with Direct Analysis in Real Time Mass Spectrometry (TDPy-DART-MS)**; Calum Bochenek[1]; Jack Edwards[1]; Kayla Williams-Pavlantos[1]; Arsalaan Pathan[1]; James M Eagan[1]; Chrys Wesdemiotis[1]; [1]*The University of Akron, Akron, OH*

MP 712 **Thermo-oxidative degradation in cellulose-nanofiber–reinforced polypropylene revealed by high-resolution TG-TOFMS integrating non-negative matrix factorization (NMF) and Kendrick mass defect (KMD) analysis**; Taiki Ozawa[1]; Akihiro Oishi[1]; Yoshiko Takenaka[1]; Ryota Watanabe[1]; [1]*National Institute of Advanced Industrial Science and Technology, Tsukuba, Japan*

MP 713 **Insight into interfacial structures of polymer blends using evolved gas analysis with time-of-flight mass spectrometry under field ionization**; Ryota Watanabe[1]; Taiki Ozawa[1]; Mayumi Kishi[1]; Sayaka Nakamura[1]; [1]*National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan*

MP 714 **Comprehensive visualization of pyrolysis products in polyolefin blends using Chromatogram-Kendrick mass (CKM) plot**; Sayaka Nakamura[1]; Taiki Ozawa[2]; Hirohmi Watanabe[3]; Ryota Watanabe[1]; *[1]National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan; [2]National Institute of Advanced Industrial Science and Technology, Tsukuba, Japan; [3]National Institute of Advanced Industrial Science and Technology (AIST), Higashihirosyima, Japan*

MP 715 **Assuring Safety and Sustainability of Industrial Adhesive Products Using Comprehensive Mass Spectrometry**; Dayong Sun; *Henkel, Bridgewater, NJ*

MP 716 **Multiplatform Mass Spectrometric Characterization of Polyphosphate Structure and Interactions with Client Proteins**; Yi Du[1]; Evgenii B Serebriakov[1]; Igor A. Kaltashov[1]; *[1]University of Massachusetts Amherst, Amherst, MA*

MP 717 **Chemical characterization of polyethylene terephthalate (PET) synthetic and environmental micro- and nano-plastics by depolymerization and high resolution MS**; Bayan ALMASRI[1]; Christian Rolando[2]; *[1]University of Lille, UAR CNRS 2014, US Inserm 41, PLBS, Plateformes Lilloises en Biologie & Santé, Villeneuve d'Ascq, France; [2]Shrieking Sixties, 1-3 Allée Lavoisier, Villeneuve-d'Ascq, France*

MP 718 **Evaluation of Usnic Acid Hepatotoxicity Using a Liver-on-a-Chip Platform Combined with Mass Spectrometry-Based Proteomics**; Stephen Swatkoski[1]; Kirsten Eckstrum[1]; Matthew Miele[1]; Kyra Headrick[1]; Ann Knolhoff[1]; *[1]U.S. Food and Drug Administration, College Park, MD*

MP 719 **Rapid Urinary Screening of Polar Illicit Drugs via LDTD-MS/MS**; Joëlle DeBlois[1]; Mégane Moreau[1]; Serge Auger[1]; Pierre Picard[1]; Sarah Demers[1]; Jonathan Rochon[1]; Jean Lacoursiere[1]; *[1]Phytronix Technologies, Inc., Quebec, QC*

MP 720 **Development of an LC–MS/MS Method for Quantifying Methylglyoxal-Induced DNA–Protein Crosslinks in Human Cells**; Reinner O Omondi[1]; Luke Erber[1]; *[1]University of Kansas, Lawrence, KS*

MP 721 **Automated GC–MS Screening Annotation Using Large-Scale Toxicology Data and Rule-Based Prioritization**; Armann Andaya[1, 2]; Samuel Stump[1, 2]; Rebecca Shepard[1, 2]; James Langston[1, 2]; *[1]California Animal Health and Food Safety Laboratory System, Davis, CA; [2]UC Davis, Davis, CA*

MP 722 **Unveiling the Unseen: A Novel Automated Strategy to Identify Undescribed Metabolites of Emerging Drugs**; Bessem Brahim[1]; Constance Almeida[2]; Florence Gauthard[1]; Antoine Romen[3]; Vincent Revel[1]; Antoine Petitcollin[2]; Alban Huteau[1]; *[1]Shimadzu France, Noisiel, France; [2]Laboratoire de Pharmaco-toxicologie Biologique et Médico-Légale, CH Tarbes-Lourdes, Tarbes, France; [3]Service de Réanimation Médicale, CH de Pau, Pau, France*

MP 723 **Automated Magnetic Bead–Based Sample Preparation for Drugs of Abuse Analysis by LC–MS/MS**; Pengyun Liu[1]; Zhouyang Kang[1]; Weijia Wu[2]; Huafen Liu[1]; *[1]Calibra Scientific Inc, HANGZHOU, China; [2]3P BioSolutions, Woodbridge, VA*

MP 724 **Assessment of Environmental Oxidative Stress by Mass Spectrometry-Based Proteomics Using Hyalella azteca as an Aquatic Model Organism**; Marcel L Prokai[1]; Repala West[1]; Saharsh Tavva[1]; Prathyum Bada[1]; Carter DePoy[1]; Vladimir Shulaev[1]; *[1]University of North Texas, Denton, TX*

MP 725 **Screening to Confirmation: Complete Workflow for Comprehensive Forensic Toxicology Analysis Using a Single Software Platform**; Yoshiro Hiramatsu[1]; Cristina Matos Mejias[2]; Sarah Monti[2]; *[1]Shimadzu Scientific Instrument, Columbia, MD; [2]Shimadzu Scientific Instruments, Inc., Columbia, MD*

MP 726 **A new analytical method for the quantification of the neurotoxin tetrodotoxin and non-targeted LC-QTOF profiling of tetrodotoxin analogs in newts**; Casey S. Philbin[1, 2]; Catherine Simmermaker[3]; Ryan Murphy[4]; Jose Meza[3]; Christopher Feldman[2, 4]; Christopher S. Jeffrey[1, 2]; *[1]University of Nevada Reno Department of Chemistry, RENO, NV; [2]Hitchcock Center for Chemical Ecology, Reno, NV; [3]Agilent Technologies, Inc., Santa Clara, CA; [4]University of Nevada Reno Department of Biology, Reno, NV*

MP 727 **Proteomics Complementation of the Rat Uterotrophic Biossay for Estrogenic Endocrine Disruption**; Laszlo Prokai[1]; Khadiza Zaman[1]; Vien Nguyen[1]; Katalin Prokai-Tatrai[1]; *[1]University of North Texas Health Science Center, Fort Worth, TX*

MP 728 **Whole-body burden assessment revealed new insights into toxicokinetics of PFAS in a marine apex predator: The bonnethead shark (Sphyrna tiburo)**; Qaim Mehdi[1]; Cadance M Swearingen[1]; Adriana L Iorfida[1]; Christiana B Kirsch[1]; Jenna A Grison[1]; Jeremy P. Koelmel[2]; Krystal J. Godri Pollitt[2]; Gareth J Fraser[1]; Douglas H Adams[3]; John A. Bowden[1]; *[1]University of Florida, Gainesville, FL; [2]Yale University, New Haven, CT; [3]Florida Fish and Wildlife Conservation Commission, Tallahassee, FL*

MP 729 **Analysis of lead leaching from tampons and menstrual discs using Inductively Coupled Plasma – Mass Spectrometry (ICP–MS)**; Morgan A Montano[1]; Aubrey K Mckellips[1]; Faith M Mann[1]; Timothy W Pearce[1]; Callie Cole[1]; *[1]Fort Lewis College, Durango, CO*

MP 730 **A Ready-to-Run Workflow for Quantitating 80 Drugs of Abuse in Whole Blood with the TSQ Certis Triple Quadrupole MS**; Courtney Patterson[1]; Jingshu Guo[1]; Kerry Hassell[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

MP 731 **Your clues are in the proteins: enhancing toxicology insights with proteomics**; Socheata Lao[1]; Xin Liu[1]; Fan Fan[1]; *[1]Johnson & Johnson, San Diego, CA*

MP 732 **In Vitro Off-Target Degradation Profiling of Thalidomide and IMiDs Using dia-PASEF Proteomics for Preclinical Toxicity Risk Assessment**; Ryotaro Ban[1]; Yusaku Matsushita[1]; Atsuya Morita[1]; Daichi Onozato[1]; Takafumi Komori[1]; *[1]Eisai Co.,Ltd., Tsukuba-shi, Japan*

TUESDAY POSTERS

TP 001 **Unlocking Epitope Mapping of Patient-Derived HLA Antibodies using High sensitive low-flow HDX-MS**; Yuqi Shi[1]; Tri TM Vu[2]; Rui Pei[2]; David Lowe[3]; Weijing Liu[4]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Thermo Fisher Scientific, West hills, CA;* [3]*Thermo Fisher Scientific, Hemel Hempstead, United Kingdom;* [4]*Thermo Fisher Scientfic, San Jose, CA*

TP 002 **Impact of Lysis Context on IP-MS Validation of Plasma Membrane Antibodies**; HAIYING LI[1]; Marcus Sandaire[1]; Deborah Moshinsky[1]; [1]*Institute for Protein Innovation -, Boston, MA*

TP 003 **Integrating Electrochemical Flow-Cell with LC-MS Platform to Monitor Potential Critical Quality Attributes in Monoclonal Antibodies**; Lushuang Huang[1]; Yunlong Zhao[1]; Yuan Mao[1]; Ning Li[1]; [1]*Regeneron Pharmaceuticals, Inc., Tarrytown, NY*

TP 004 **Bioanalytical Challenges of Small Molecule ADC Payload: A Simple, Sensitive, and Robust Assay for Quantifying Total Payload in Serum**; Mariel Grace Mendoza[1]; Hermes Licea-Perez[1]; Timothy Sikorski[1]; [1]*GSK, Collegeville, PA*

TP 005 **Hybridization Extraction: Enabling LC-MS Quantitative Bioanalysis of Antibody–ASO Conjugates**; Guilherme J Guimaraes[1]; Ting Jiang[1]; Bekim Bajrami[1]; Long Yuan[1]; [1]*Biogen, Cambridge, MA*

TP 006 **Denaturing SEC-MS for the comprehensive characterization of low-molecular-weight variants in therapeutic mAbs**; Xin Wang[1]; Timothy N. Tiambeng[1]; Yuetian Yan[1]; Shunhai Wang[1]; Ning Li[1]; [1]*Regeneron Pharmaceuticals, Inc., Tarrytown, NY*

TP 007 **Integrating Automated Forced Degradation, Peptide Mapping, and in silico Model Generation to Accelerate Early PTM Liability Evaluation of Biologics**; John Patrick[1]; Richard Huang[1]; Steven Jacobs[1]; [1]*Johnson & Johnson Innovative Medicine, Spring House, PA*

TP 008 **Comprehensive Characterization of Lysine- and Cysteine-Linked ADCs using a New Multi-Reflecting-TOF Mass Spectrometer**; S Vara Prasad Chandrabatla[1]; Ci Xu[1]; Catherine Tremblay[2]; Rise Matsunami[2]; Jason Wang[1]; [1]*Veranova, Devens, MA;* [2]*Waters Corporation, Milford, MA*

TP 009 **Accelerating development and characterization of nanobodies using the integrated high-throughput Rapid Automated Binder Identification Technology (RABIT) and ultrasensitive nHDX-MS**; Shaunak Raval[1]; Daniel Rosen[1]; Jaechan Lee[1]; Nir Hacohen[1]; Steven A. Carr[1]; Malvina Papanastasiou[1]; [1]*The Broad Institute of MIT and Harvard, Cambridge, MA*

TP 010 **From Polyclonal to Recombinant: A Proteomics Workflow for Anti-Idiotype Antibody Development**; Dominic Narang[1]; Teresa Nunez De Villavicencio Diaz[1]; Chelsea Reitzel[1]; Thierry Le Bihan[1]; Bin Ma[1]; Kyle Suttill[1]; Marko Jovic[1]; Rosalin Dubois[1]; Sydney Tippelt; [1]*Rapid Novor, Kitchener, ON*

TP 011 **Real-time electron capture dissociation characterization of antibody subunits via microdroplet reactions**; Thomas E Walker[1]; Mike Knierman[2]; Hao Chen[3]; Harsha P. Gunawardena[4]; [1]*Agilent Technologies, Lexington, MA;* [2]*Agilent Technologies, Inc., Santa Clara, CA;* [3]*New Jersey Institute of Technology, Newark, NJ;* [4]*Johnson & Johnson Innovative Medicine, Spring House, PA*

TP 012 **Investigating mispairing heterogeneity in bispecific antibodies by ultra-high resolution icIEF-UV/MS**; Tian Xu[1]; Jingwen Ding[2]; Ning Wang[1]; Haichuan Liu[2]; [1]*Eli Lilly and Company, Indianapolis, IN;* [2]*SCIEX, Redwood City, CA*

TP 013 **Automated LC–MS Characterization of Disulfide Bonds in Biotherapeutics Using Positive Controls and MS1 Isotope Envelope Confidence**; Vahid Golghalyani[1]; Anna Galea[2]; Marziyeh Komeili[3]; Daniel Ayoub[2]; [1]*ProteinMetrics LLC, Boston, MA;* [2]*Fresenius Kabi Biopharma, Eysins, Switzerland;* [3]*EPFL, Lausanne, Switzerland*

TP 014 **Exploring Interdependencies Between Aggregation and Oxidation of Biopharmaceuticals using a Modified Tribrid Orbitrap MS Instrument**; Corentin Beaumal[1]; Sara Carillo[1]; Amy K Carfagno[2]; Linda Lieu[2]; Kristina Srzentic[3]; Jingjing Huang[4]; Rafael Melani[4]; Kelly Broster[5]; Luca Fornelli[2]; Jona; [1]*National*

Institute for Bioprocessing Research & Training, Dublin, Ireland; [2]University of Oklahoma, Norman, OK; [3]Thermo Fisher Scientific, Basel, Switzerland; [4]Thermo Fisher Scientific, San Jose, CA; [5</su]

TP 015 **Comprehensive Structural Characterization of a Next-Generation Tetravalent EGFR×HER3 Bispecific Antibody and Its DAR-8 ADC Derivative by Native and Middle-Down MS**; Corentin Beaumal1; Sara Carillo[1]; Kristina Srzentic[2]; Rafael D Melani[3]; Jonathan Bones[1, 4]; *[1]NIBRT, Dublin, Ireland; [2]Thermo Fisher Scientific, Reinach, Switzerland; [3]Thermo Fisher Scientific, San Jose, CA; [4]School of Chemical and Bioprocess Engineering, University College Dublin, Dublin, Ireland*

TP 016 **A Simple Glu-C Digestion Schema for Consistent Sequence Coverage of IgG1 Antibodies**; Jesse W Wilson[1]; Jason Gilmore[1]; *[1]Just-Evotec, Seattle, WA*

TP 017 **Elevating Protein Purification Efficiency: Transitioning from Manual Techniques to Automated Platforms**; Chris Suh[1]; Shadie Nimri[1]; Lee Hoang[1]; *[1]Biotage, San Jose, CA*

TP 018 **Decapping Sample Preparation Enables Mass Spectrometric Characterization of Engineered Cysteine Bi/Multispecific Antibodies for Bioconjugation**; Olivia Huffman[1]; Grace Chao[1]; Natalia Reixhach[1]; Kevin Hsu[1]; Xiaomin Yang[1]; Joomi Ahn[1]; *[1]Eli Lilly & Co, San Diego, CA*

TP 019 **Discovery of malaria neutralization antibodies through Mass Spectrometry–Based de novo Sequencing**; Weiwei Peng[1]; Jeffrey Marchioni[1]; Allison Seeger[1]; George Georgiou[1]; Eveline M. Bunnik[2]; Jason Lavinder[1]; *[1]The University of Texas at Austin, Austin,, TX; [2]University of Texas at San Antonio Health Science Center, San Antonio, TX*

TP 020 **Bringing Sequence Liability Assessment to the Next Level by Peptide Mapping Data Analysis using GeneData Expressionist Software**; Koyuki Takenaka[1]; Aaron Cazy[2]; Shayan Akhavan[3]; Angela Lee[1]; Olivia Huffman[1]; Joomi Ahn[1]; *[1]Lilly Biotechnology Center, San Diego, CA; [2]Eli Lilly & Company, Indianapolis, IN; [3]BCForward, San Diego, CA*

TP 021 **Stability Assessment of Therapeutic mAbs and ADCs in Biological Matrices by Aptamer-Enabled Native Immunoprecipitation Coupled to Native LC-MS**; Shuli Tang[1]; Wenjing Peng[1]; Yuetian Yan[1]; Shunhai Wang[1]; Ning Li[1]; *[1]Analytical and Biological Mass Spectrometry, Regeneron Pharmaceuticals Inc., Tarrytown, NY*

TP 022 **Multimodal Characterization of Targeted Lipid Nanoparticles Using Charge Detection MS and Orthogonal Separation Techniques**; Rebecca D'Esposito[1]; Esther Lewis[1]; Matthew Lauber[1]; Mateusz Imiolek[1]; Stephan M. Koza[1]; Balasubrahmanyam Addepalli[1]; Martin Kurnik[2]; Sophia Kenrick[2]; Michelle; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Goleta, CA*

TP 023 **Innovative Mass Spectrometry Approaches for Developing and Characterizing Non-Natural Amino Acid Antibodies**; Elsa Gorre[1]; Christopher Sauer[1]; Abby Chiang[2]; Annabel Torres[1]; Matthew J Amaral[1]; Soroosh Soltani[3]; Alexander Barnakov[1]; Andrew D Mahan[1]; Hirsh Nanda[1</su;] *[1]Johnson & Johnson Innovative Medicine, Spring House, PA; [2]Protein Metrics LLC, Boston, MA; [3]Johnson & Johnson Innovative Medicine, Malvern, PA*

TP 024 **A native MS study of large immune complexes formed by a bivalent antigen and scFv-based constructs**; Ruolan Cheng[1]; Yi Du[1]; Micheal D Levin[2]; Bogdan Olenyuk[2]; Igor A. Kaltashov[1]; *[1]University of Massachusetts Amherst, Amherst, MA; [2]Proteogenomics Research Institute for Systems Medicine, La Jolla, CA*

TP 025 **GRIFFIN: A Combined Bottom-Up and Middle-Down Mass Spectrometry-Based Method for Polyclonal Antibody Sequencing Directly from Protein**; Richard H Carson[1]; Stefano Bonisonne[1]; Natalie Castellana[1]; Thiago Lima[1]; Miin Lin[1]; Brinley Moorman[1]; *[1]Abterra Biosciences, San Diego, CA*

TP 027 **Unravelling Immunoglobulin A Structural Complexity from Top-Down and Bottom-Up Using a Modified Thermo Scientific Orbitrap Tribrid Mass Spectrometer**; Kristina Srzentic[1]; Jingjing Huang[2]; Jonathan Dhenin[3]; Thierry Besson[3]; Edwige Beng-Louka[3]; Mariavittoria Iazeolla[3]; Patrick Schindler[3]; Christopher Mullen[4]; Gr; *[1]Thermo Fisher Scientific, Basel, Switzerland; [2]ThermoFisher Scientific, San Jose, CA; [3]Novartis pharma AG, basel, Switzerland; [4]Thermo Fisher Scientific, San Jose, CA*

TP 028 **The functionally molecular characteristic of invasive progression in papillary thyroid microcarcinoma is unveiled by spatial proteomics**; Jun Luo[1, 2]; Wenchao LI[3]; Guixue Hou[2]; Jin Zi[2]; Kunpeng Hu[3]; Siqi Liu[1, 2]; [1]*College of Life Sciences, University of Chinese Academy of Sciences, Beijing, China;* [2]*HIM-BGI Omics Center, Zhejiang Cancer Hospital, Hangzhou Institute of Medicine (HIM), Chinese Academy of Sciences (CAS), Hangzhou, China;* [3</]

TP 029 **Antibody-Guided MALDI-MSI Reveals Spatiotemporal Tau Pathology in the hTau Alzheimer's Disease Model**; Sudipta Senapati1; Bandana Bera[1]; Dhvani Pansuriya[1]; Jia Yi Liew[1]; Brendan Prideaux[1]; Rakez Kayed[1]; [1]*University of Texas Medical Branch, Galveston, TX*

TP 030 **RAMP: Rapid Automated Metabolomics Platform for the accurate quantification of metabolites in human plasma for improved cancer treatment**; Annegret Ulke-Lemee[1]; Nicholas I. Brodie[1]; Dominique Bihan[1]; Saif Sikdar[1]; Mario E. Valdez-Tresanco[1]; Mario S. Valdez-Tresanco[2]; Meriem Messaoudene[3]; Bertrand Routy[3<;] [1]*University of Calgary, Calgary, AB;* [2]*University of Medellin, Medellin, Colombia;* [3]*Université de Montréal, Montréal, QC;* [4]*Western University, London, ON*

TP 031 **A Robust Platform for proteomics analysis of neuron derived extracellular vesicles in large-cohort plasma**; Minhyeok Kang[1, 2, 3]; Hong-beom Park[2, 3, 4]; Eunseo Kim[2, 3, 4]; Yerin Kim[1, 2, 3]; Jin Lee[2, 3, 4]; Gyuri Park[1, 2, 3]; Jiyeon Choi[2, 3]; Yiseo Rho[1, 2, 3]; Woosol C; [1]*Molecular Medicine and Biopharmaceutical Sciences, WCU Graduate School of Convergence Science and Technology Seoul National University, Seoul, South Korea;* [2]*Department of transdisciplinary medicine, Seoul National University Hospita*

TP 032 **Pharmacodynamic Biomarkers to Assess Dystrophin-Restoring Therapies in Duchenne Muscular Dystrophy**; Ahmed Naveed[1]; Bukola K Ojo[1]; Emily H Canessa[1]; Rita Spathis[1]; James S Novak[2]; Kanneboyina Nagaraju[1]; Yetrib Hathout[1]; [1]*Binghamton University, Binghamton, NY;* [2]*Children's Research Institute, Children's National Hospital., Washington DC, DC*

TP 033 **Deep Plasma Proteomics and Functional Genomics Reveal Drivers of Parkinson's Progression and Levodopa Response**; Ji-sun Kim[1]; Chanhee Jeong[2]; Seohyun Kim[3]; Hyeyeon Kim[1]; Stefanie N Kairs[4]; Blake L Tsu[4, 5]; Ki-Jun Yoon[3]; Dae-Kyum Kim[1, 6]; Han-Joon Kim[2]; Christopher A; [1]*McGill University, Montreal, QC;* [2]*Seoul National University Hospital, Seoul, South Korea;* [3]*Korea Advanced Institute of Science and Technology, Daejeon, South Korea;* [4]*NGeneBioAI, San Diego, CA;* [5]*Yatir*

TP 034 **Identification of 16 new Hepatocellular Carcinoma (HCC) biomarkers by enzymatic digestion and by Matrix-Assisted Laser Desorption/Ionization Imaging Mass Spectrometry (MALDI-IMS)**; Stephane E. Grauzam[1]; Mengjun Wang[1]; Hongyan Liang[1]; Peggi M. Angel[1]; Richard R. Drake[1]; Lauren Ball[1]; Anand S. Mehta[1]; [1]*Medical University of South Carolina, Charleston, SC*

TP 035 **From Speed to Depth: Scalable High-Precision DIA Plasma Proteomics using OptiSpray on the Orbitrap Excedion Pro Mass Spectrometer**; Jared Deyarmin[1]; Casey Abbo[1]; Mikayla Shanafelt[2]; Simran Sood[3]; Qingling Li[1]; Katherine Walker[2]; Stephanie N. Samra[2]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Thermo Fisher Scientfic, San Jose, CA;* [3]*ThermoFisher Scientific, San Jose, CA*

TP 036 **A Sensitive Glycoproteomics Pipeline for Protein A: S-Trap Processing, HILIC Enrichment, DIA Identification, PRM Quantitation**; Jongmin Woo[1]; Mehari Weldemariam[1]; Djordje Atanackovic[2]; Aerielle Matsangos[2]; Maureen A. Kane[1]; [1]*School of Pharmacy, University of Maryland Baltimore, Baltimore, MD;* [2]*School of Medicine, University of Maryland Baltimore, Baltimore, MD*

TP 037 **Integrating Deep-Coverage Workflows for Multi-fluid Proteomic Profiling Across Diverse Biological Matrices in Clinical Development: Saliva, Plasma, Urine, and CSF**; Zeinab Mokhtari[1]; Mike Baratta[1]; [1]*Takeda, Cambridge, MA*

TP 038 **Unveil plasma proteomics with cutting-edge hybrid-DIA methods utilizing two strategies on the Orbitrap Astral Zoom MS**; Qingling Li[1]; Jared Deyarmin[1]; Stephanie N. Samra[1]; [1]*Thermo Fisher Scientific, San Jose, CA*

TP 039 **Deep Plasma Proteomics Reveals Network-Level Signatures of Astrocyte Reactivity in Default Mode Network Hubs**; Ruyu Shi[1]; Xuemei Zeng[1]; Wasiu G. Balogun[1]; Marissa F. Farinas[1]; Brian J.

Lopresti[1]; Milos Ikonomovic[1]; Howard Aizenstein[1]; Victor L. Villemagne[1]; Ann D. Cohen<; [1]*University of Pittsburgh, Pittsburgh, PA*

TP 040 **High-throughput flow-injection mass spectrometry enables genome-wide association of lipids and metabolites with genomic variants**; Duncan Holbrook-Smith[1]; Julia Kozlitina[2]; Jonathan Cohen[2]; Edward Driggers[1]; [1]*General Metabolics, Cambridge, MA;* [2]*University of Texas Southwestern Medical Center, Dallas, TX*

TP 041 **Proteomics Analysis of TransfectedHEK293 Cellswith DifferentMitochondrial Membrane Potential**; Zahra ForoozanJahromi[1]; Seongkyu Yoon[1]; Pengyuan Liu[1]; [1]*University of Massachusetts Lowell, Lowell, MA*

TP 042 **Rapid Identification of Bacteria in Mixtures using LC-IM-MS/MS with Machine Learning Algorithms**; Adebowale S Oyerinde[1]; Iffat Jerin[2]; Md Naymor Rahaman[2]; Kristen Marshall[2]; Ahmed Mohamed Hamid[2]; [1]*Auburn University, Auburn, AL;* [2]*AUBURN UNIVERSITY, Auburn, AL*

TP 043 **High Resolution Metabolomic Profiling of Urine-Derived Extracellular Vesicles Identifies Potential Biomarkers for Early Bladder Cancer Detection**; Habiba Sultana[1]; Ebenezer Owusu[1]; Marcio Almeida[1]; Joanne E. Curran[1]; Sarah Williams Blangero[1]; John Blangero[1]; Anton Iliuk[2]; Auwal A. Bala[1]; Jacob A. Galan<sup; [1]*Department of Human Genetics, University of Texas Rio Grande Valley, Brownsville, TX;* [2]*Tymora Analytical Operations, West Lafayette, IN*

TP 044 **Headspace analysis of viral cell culture and odor transfer to polymer-based canine training aids for biological detection**; Samantha Hagerty[1]; Michelle Aono[1]; Adam Rivers[2]; Melissa Singletary[1, 3]; [1]*Auburn University, Department of Anatomy, Physiology, and Pharmacology, Auburn, AL;* [2]*United States Department of Agriculture, Agriculture Research Service, Gainesville, FL;* [3]*Auburn University, Canine Performance Sciences,*

TP 045 **Proteomic Signatures of Acquired PARP Inhibitor Resistance in High-Grade Serous Ovarian Cancer Cells**; Trudy J Philips[1]; Stefani N Thomas[2]; [1]*University of Minnesota, Twin Cities, Minneapolis, MN;* [2]*University of Minnesota - Twin Cities, Minneapolis, MN*

TP 046 **Metabolome Profiling of Half-Marathon Runners Identifies Recovery Dynamics and Biomarkers Linked to Performance and Experience**; Nikita Vijaykumar Savalsang[1]; Renu Pandey[1]; Avinash Vellore Sunder[1]; Deepti Sahasrabuddhe[1]; Venkatraman Pichumani[2]; Marcus Ranney[3]; Pramod P Wangikar[1, 4]; [1]*Indian Institute of Technology Bombay, Mumbai, India;* [2]*You Too Can Run, Mumbai, India;* [3]*Human Edge Pvt. Ltd., Mumbai, India;* [4]*Clarity Bio Systems India Pvt. Ltd., Pune, India*

TP 047 **Insights into COVID-19 Vaccine-Induced Immune Mechanisms in Immunocompromised Individuals Using Untargeted Proteomics and Post-Translational Modification Analysis**; Pallaprolu Nikhil[1]; Aishwarya Dande[1]; Ramalingam Peraman[1]; [1]*National Institute of Pharmaceutical Education and Research Hajipur, Hajipur, India*

TP 048 **Protein Biomarkers for Non-canonical ACE Activity**; Neethu G Issac[1]; Catalina Avenedo[1]; Daniel Röth[1]; Kenneth E Bernstein[2]; Markus Kalkum[1]; [1]*City of Hope, Duarte, CA;* [2]*Cedars Sinai Medical Center, Los Angeles, CA*

TP 049 **SQUAD bile acid profiling reveals cannabis-driven remodeling of the gut microbiome**; Nichole Reisdorph[1]; Bashar Amer[2]; Katrina A Doenges[1]; Nathan Anderson[3]; Winona Booher[1]; Susan S. Bird[4]; [1]*University of Colorado Anschutz Medical Campus, Aurora, CO;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*University of Colorado Boulder, Boulder, CO;* [4]*ThermoFisher Scientific, San Jose, CA*

TP 050 **Using a Standardized Metabolomics Pipeline Applied to the MiniMED trial to Unlock Dietary Insights for Healthier Lives**; Nichole Reisdorph[1]; Richard Reisdorph[1]; Adelle Price[1]; Brianna Hunt[1]; Chi-Ming Chien[2]; Katrina A Doenges[1]; Cole R. Michel[1]; Emily Hill[1]; Nancy Krebs[1]; [1]*University of Colorado Anschutz Medical Campus, Aurora, CO;* [2]*Verso Biosciences, Davis, CA;* [3]*University of Colorado Anschutz, Aurora, CO;* [4]*Purdue Univeristy, West Lafayette, IN*

TP 051 **Unlocking the Plasma Proteome: A Multi-Method Comparative Study**; Hieu T Nguyen[1]; Ghazaleh Yassaghi[1]; Kari Martyniak[1]; Yasi Jami[1]; Hendrik Neubert[1]; [1]*Pfizer, Andover, MA*

TP 052 **Retention Time Down-sampling Improves Sensitivity and Lower Limits of Quantification of prm-PASEF**; Simonas Savickas[1]; Veronique Laforte[1]; Sebastian Mueller[1]; Tejas Gandhi[1]; Roland Bruderer[1]; [1]*Biognosys AG, Schlieren, Switzerland*

TP 053 **Accurate In Vivo BTK Occupancy Measurement by Immunocapture-LC-MS/MS as a Pharmacodynamic (PD) Biomarker to Support a First-In-Human Dose Escalation Study**; Naiyu Zheng[1]; Gus Hui[2]; Ramakrishna Boyanapalli[1]; Jie Li[1]; Christine Nguyen[2]; Alban Allentoff[1]; Marc Gleichmann[1]; Yongjun Xue[1]; Jim X Shen[1]; [1]*Bristol Myers Squibb, Princeton, NJ;* [2]*PPD, part of Thermo Fisher Scientific, Henrico, VA*

TP 054 **Ultra-sensitive assessment of PD biomarkers using an automated targeted 2D-LC-MS/MS approach**; Jintang He[1]; Lingyao Meng[1]; Zhen Shi[1]; Aiying Yu[1]; Keyang Xu[1]; [1]*Genentech Inc., South San Francisco, CA*

TP 055 **A Multipathway Phosphopeptide Assay Development using StellarTM Mass Spectrometer with Adaptive RT for Rapid Phosphoproteomics**; Qingling Li[1]; Jared Deyarmin[1]; Stephanie N. Samra[1]; [1]*Thermo Fisher Scientific, San Jose, CA*

TP 056 **Discovery and targeted validation of erythrocyte proteomic biomarkers of recombinant human erythropoietin (rhEPO) misuse and hypoxic exposure at high altitude**; Vincent Richard[1]; Peter Kubiniok[2, 3]; Timon Geib[2]; Laleh Ebrahimi[2, 4]; Foroughsadat Absar[2]; Eileen Tudorica[2]; Constantinos Blidjios[2]; Thomas Bonne[5]; Jacob Bejde; [1]*McGill University - Lady Davis Institute, Montréal, QC;* [2]*Segal Cancer Proteomics Centre, Lady Davis Institute for Medical Research, McGill University, Montreal, QC;* [3]*Quantivum Inc., montreal, QC;* [4]*Division of E*

TP 057 **Robust and sensitive quantitation of 18 steroids in human samples using Thermo Scientific™ TSQ Certis™ Triple Quadrupole mass spectrometer**; Jingshu Guo[1]; Courtney Patterson[1]; Charles Maxey[1]; Neloni Wijeratne[1]; Kerry Hassell[1]; [1]*Thermo Fisher Scientific, San Jose, CA*

TP 058 **Rapid LC/MS/MS quantitation of urinary calystegine A3 as a marker for potato consumption**; Anna M. Caldwell[1]; Anya Klarner[1]; Wendy Hall[1]; Sarah Berry[1]; Ana Rodriguez-Mateos[1]; John M Halket[1]; [1]*King's College London, London, United Kingdom*

TP 059 **Develop a Hybrid LC-MS/MS Assay for Quantitation of INHBE protein biomarker in Human Serum**; Changjian Zhao[1]; Yue Ren[2]; Tao Yin[2]; Yuxin Li[2]; Laixin Wang[1]; Yuhuan Ji[1]; [1]*Resolian, Chongqing, China;* [2]*Acrobiosystems, beijing, China*

TP 060 **Determination of Total Androsterone and Etiocholanolone in Human Urine Using Liquid Chromatography - Tandem Mass Spectrometry (LC-MS/MS)**; Nicole Boone[1]; Emily A. Epure[1]; Shuyu Hou[1]; Tian-Sheng Lu[1]; [1]*Medpace, Cincinnati, OH*

TP 061 **A Robust and Specific LC-MS/MS Method for the Quantitation of 4β-Hydroxycholesterol in Human K2EDTA plasma**; Qiwei Hu[1]; Aiping Zhu[1]; Shuyu Hou[1]; Tian-Sheng Lu[1]; [1]*Medpace, Cincinnati, OH*

TP 062 **UPLC-MS/MS Method Development for the Quantitative Analysis of 5'-Deoxyadenosylcobalamin in Murine Models of Methylmalonic Acidemia**; Asvelt Nduwumwami[1]; Amy Wang[1]; Erik Wagner[1]; Eun-Young Choi[1]; Charles Venditti[1]; Xin Xu[1]; [1]*NIH, Bethesda, MD*

TP 063 **Optimizing Surrogate Matrix Selection for Endogenous Biomarker LC-MS/MS Quantitation Assays**; Nicole Gonzalez Salguero[1]; Benjamin Begley[1]; Simon Johnson[1]; John Begley[1]; Shane Karnik[1]; Davonne Auguste[1]; Theron Chung[1]; [1]*Aliri Bioanalysis, Colorado Springs, CO*

TP 064 **Comparison of common plasma proteomics workflows reveals distinct pre-analytical biases by sample preparation and nanoparticle enrichment**; Franziska Voellmy[1]; Stephan Eckert[1]; Prashant Kaushik[2]; Christoph Paschen[1]; Shahrzad Tavalaei[1]; Justine Fidelin[1]; Stefan Weiser[2]; Marcus

Bantscheff[1]; *[1]F. Hoffmann-La Roche Ltd, Basel, Switzerland; [2]F.Hoffmann-La Roche Ltd., Penzberg, Germany*

TP 065 **Comprehensive semaglutide metabolites characterization in plasma using a Modified Orbitrap hybrid mass spectrometer**; Aaron Lopes[1, 2, 3, 4]; Reiko Kiyonami[5]; Zhaohui Sunny Zhou[2]; Carlo Giovanni Traverso[1, 3, 4]; Claire Dauly[6]; Ismael Zamora Rico[7]; Sebastien Morin[8]; Min Du[5]; *[1]Massachusetts Institute of Technology, Cambridge, MA; [2]Northeastern University, Boston, MA; [3]Broad Institute, Cambridge, MA; [4]Mass General Brigham, Boston, MA; [5]Thermo Fisher Scientific, Lexington, M*

TP 066 **Translating Targeted Proteomics to IHC Positivity for CCNE1 in Ovarian Cancer FFPE Samples Using a Bayesian Framework**; William E Hackett[1]; Beom-Jun Kim[1]; Stephanie Zalesak-Kravec[1]; Shichen Shen[1]; Sophie Willis[2]; Andrea Storti[3]; Lenka Oplustil O'Connor[2]; Mari Heininen-Brown[3]; Dav; *[1]AstraZeneca, Gaithersburg, MD; [2]Astrazeneca, Cambridge, United Kingdom; [3]AstraZeneca, Munich, Germany*

TP 067 **A robust triple-stage quadrupole mass spectrometer for high-throughput clinical LC–MS/MS**; Jingshu Guo[1]; Courtney Patterson[1]; Qin Fu[1]; Charles Maxey[1]; Neloni Wijeratne[1]; Kerry Hassell[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

TP 068 **A Plug-and-Play Ion Source with an Integrated Separation Column and Replaceable Emitters Enables Ultra-High-Throughput Multiplexed PRM**; Tanis R Correa[1]; Qin Fu[2]; Katherine Walker[2]; Philip M. Remes[2]; Runsheng Zheng[3]; Lilian Heil[2]; Cristina C. Jacob[2]; Romain Huguet[2]; Jennifer E. Van Eyk[4</sup;] *[1]ThermoFisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Germering, Germany; [4]Cedars-Sinai Medical Center, Los Angeles, CA*

TP 069 **Performance assessment of absolute protein quantitation by LC/MRM-MS in 20 commercially available human plasma samples using novel SysQuan technology**; Claudia Gaither[1, 2]; Robert Popp[1]; Ruhi Jaiswal[1]; Pradyumn Maheshwari[1]; Timon Geib[3]; René P Zahedi[4]; Christoph H Borchers[3, 5, 6, 7]; *[1]MRM Proteomics Inc, Montreal, QC; [2]Département des Sciences Cliniques, Faculté de Médecine Vétérinaire, Université de Montréal, Saint-Hyacinthe, QC; [3]Segal Cancer Proteomics Centre, Lady Davis Institute for Medical Resear*

TP 070 **Development and Validation of a Parallel Reaction Monitoring Assay to Measure HDL-associated Plasma Lipoproteins in FPLC Fractions**; Carly Al Twigg[1]; Suad Ali[1]; Samantha Roemhild[1]; Danni Li[1]; Stefani N Thomas[1]; *[1]University of Minnesota, Minneapolis, MN*

TP 071 **Ultra-Sensitive LC–MS/MS Quantification of NAD^+ and NADHin Mouse MII Oocytes**; Dan Su[1]; Michelle Watson[1]; Rodger De Miranda[1]; Hui Qi[1]; Chunying Song[1]; *[1]WuXi AppTec, SAN DIEGO, CA*

TP 072 **Serum-derived small extracellular vesicles' proteome reflects the renal status in chronic kidney disease**; Daniel Fochtman[1]; Daria Kania[2]; Justyna Gołębiewska[3]; Monika Pietrowska[2]; Łukasz Marczak[1]; Anna Wojakowska[1]; *[1]Institute of Bioorganic Chemistry Polish Academy of Sciences, Poznan, Poland; [2]Center for Translational Research and Molecular Biology of Cancer, Maria Skłodowska-Curie National Research Center and Institute of Oncology Gliwice Bran*

TP 073 **Direct-Digestion LC-MS/MS Quantification of Endogenous Rat Alpha-1 Antitrypsin to Support a Pharmacodynamic Endpoint**; Irina Laczkovich[1]; Linlin Dong[1]; Kristy Szretter[1]; Mark Qian[1]; *[1]Takeda Pharmaceutical, Cambridge, MA*

TP 074 **A Multiplex Platform for Quantitation of Complement Biomarkers in Serum, Plasma, Cerebrospinal Fluid, and Brain Homogenate Using LC-MRM-MS**; Cong Wu[1]; Jianhui Zhu[2]; Tiffany Wong[1]; Racquel Corpuz[1]; Tiffany Wu[1]; William J. Meilandt[1]; Anne Biever[1]; Norbert LeClair[1]; Kelly Loyet[1]; Jesse Hanson[1<;] *[1]Genentech Inc, South San Francisco, CA; [2]NovaBioAssays, Woburn, MA*

TP 075 **Combination of Cross-Linking MS (XL-MS) and Structural Modeling approach for dynamic proteins structure elucidation**; Zheng Ser[1]; Wint Wint Phoo[2]; Jan Marzinek[1]; Kitti Wing Ki Chan[2]; Peter Bond[1]; Luo Dahai[3]; Subhash Vasudevan[2]; Radoslaw Sobota[1]; *[1]A*STAR, Singapore, Singapore; [2]Duke-NUS, Singapore, Singapore; [3]NTU Institute of Structural Biology, Nanyang Technological University, Singapore, Singapore*

TP 076 **DEPC covalent-labeling mass spectrometry reveals proteoform-dependent structural differences in histone h3**; Kaitlyn N Walls[1]; Kymeri Davis[1]; Ian Webb[1]; [1]*Indiana University Indianapolis, Indianapolis, IN*

TP 077 **Characterizing Interactions between Annular Lipids and Protein Transmembrane Domain via in situ Photo-Tagging and Mass Spectrometry**; Wei Wan[1]; Jing Zhao[1]; Yu Xia[1]; [1]*Tsinghua university, Beijing, China*

TP 078 **The Effects of Dietary Monosaccharides on Protein-Protein Interactions in the Cell Membrane Through Quantitative Cross-Linking Mass Spectrometry**; Kayla M Pakulski[1]; Michael Russelle S. Alvarez[2]; Riya Gogte[2]; Yixuan Xie[2]; Siyu Chen[2]; Carlito B. Lebrilla[2]; [1]*University of California Davis, Davis, CA;* [2]*University of California, Davis, Davis, CA*

TP 079 **Towards the 24-hour Human Interactome: timsUltra AIP Enables Proteome-Wide Crosslinking-MS with Unprecedented Speed and Depth**; Clement Potel[1]; Christoph Krisp[2, 3]; Ying Zhu[1]; Ke Pu[4]; Pengzhi Mao[5, 6]; Daniel Hornburg[7]; Fan Liu[4, 8]; Philip Loessl[1]; [1]*Absea BIotechnology GmbH, Berlin, Germany;* [2]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [3]*MDC-Bruker Center of Excellence for Single Cell Omics, Max Delbrück Center for Moleculare Medicine in the Helmholtz-association*

TP 080 **High-Throughput Epitope and Paratope Mapping of PCSK9-Evolocumab Biosimilar Interactions Using the AutoFox System with Agilent's 6545XT Q-TOF**; Emily Chea[1]; Thomas Walker[2]; Charles Mobley[1]; Scot R Weinberger[1]; Mike Knierman[2]; [1]*GenNext Technologies, Half Moon Bay, CA;* [2]*Agilent Technologies, Lexington, MA*

TP 081 **Increasing sensitivity of covalent protein painting with a plexDIA approach**; Sarah N Sipe[1]; Joshua J Abbott[1]; Corinna Friedrich[1]; Nikolai Slavov[1, 2]; [1]*Parallel Squared Technology Institute, Watertown, MA;* [2]*Northeastern University, Boston, MA*

TP 082 **Investigation of In Vitro Aggregation of Amyloid Beta 1-42 Utilizing Mass Spec-based Footprinting, Orthogonal ThT Fluorescence, and Kinetic Modeling**; Cole Hediger[1]; Michael Gross[2]; Don Rempel[2]; [1]*Washington University, St. Louis, MO;* [2]*Washington University in St.Louis, St.Louis, MO*

TP 083 **Optimized quantitative XL-MS analysison a modified Orbitrap Tribrid mass spectrometer**; Yi He[1]; Graeme C McAlister[1]; Rafael Melani[1]; Weijing Liu[2]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*ThermoFisher Scientific, San Jose, CA*

TP 084 **Searching MS2 Data from a MS-Cleavable Trivalent Crosslinker**; Peter R. Baker[1]; Clinton Yu[2]; Michael J. Trnka[1]; Lan Huang[2]; Robert Chalkley[1]; [1]*UCSF, San Francisco, CA;* [2]*UC Irvine, Irvine*

TP 085 **Automating Benchtop Hydroxyl Radical Protein Footprinting to Probe Protein Surfaces, Ligands, and Complex interfaces in a High-Throughput Manner**; Tyler C Cropley[1]; Beatrix M Ueberheide[1]; [1]*NYU Langone Medical Center, New york, NY*

TP 086 **Quantitative Mapping of Protein Complex Reorganization Under Oxidative Stress Enabled by Multiplexed Co-Fractionation Cross-Linking Mass Spectrometry**; Sean Tang[1]; Yi He[2]; Clinton Yu[3]; Xiaorong Wang[3]; Lan Huang[3]; [1]*university of california, Irvine, IRVINE, CA;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*University of California Irvine, Irvine, CA*

TP 087 **Development of A Targeted Proteomics Quantitation Approach for Fast Photochemical Oxidation of Proteins (FPOP) Using a Thermo Scientific Stellar MS**; Steve Silletti[1]; Deanna L Plubell[2]; Wes Rogers[2]; Lisa M Jones[1]; [1]*University of California San Diego, La Jolla, CA;* [2]*ThermoFisher Scientific, San Jose, CA*

TP 088 **TPOP: A peroxide free laser-based approach for microseconds hydroxyl radical protein footprinting in water**; Tarang M Jadav[1]; Don Rempel[1]; Weikai Li[2]; Michael L. Gross[1]; [1]*Washington University in St.Louis, St.Louis, MO;* [2]*Washington University School of Medicine, St. Louis, MO*

TP 089 **Development of Novel Photocaged Quinone Methide Chemistries for High-Resolution Optoproteomics**; Spencer Funk[1]; Benjamin L. Muselius[1]; Bruno C. Amaral[1]; Christina L. Pan[1]; Pauline Douglas[1]; David C. Schriemer[1]; *[1]University of Calgary, Calgary, AB*

TP 090 **Development of a novel sulfoxide-containing MS-cleavable heterobifunctional lysine-cysteine cross-linker to define protein interaction landscapes**; Kasandra Khiev[1]; Fenglong Jiao[1]; Bryant Lim[1]; Scott Rychnovsky[1]; Lan Huang[1]; *[1]University of California-Irvine, IRVINE, CA*

TP 091 **Structural Proteomics Enabled by Residue-Specific Covalent Labeling, Crosslinking, and AI Analysis**; Saiful M Chowdhury[1]; Akash Talukder[1]; Sepideh K. Firooz[1]; William Lafon[1]; *[1]University of Texas At Arlington, Arlington, TX*

TP 092 **Surfaceome Snapshots: In-cell DSBSO XL-MS with Glyco-enrichment to Map Membrane Protein Networks**; Clinton Yu[1]; Xiaorong Wang[1]; Yi He[2]; Audrey Kishishita[3]; Rosa Viner[2]; John Elizarraras[4]; Bing Zhang[4]; Arun P. Wiita[3]; Lan Huang[1]; *[1]University of California, Irvine, Irvine, CA; [2]Thermo Fisher Scientific, San Jose, CA; [3]University of California San Francisco, San Francisco, CA; [4]Baylor College of Medicine, Houston, TX*

TP 093 **Multivalent Binding Mode of Full-Length NCOA4 to Ferritin Revealed by Crosslinking Mass Spectrometry and Structural Modeling with AlphaCross-XL for PPIs**; Audrey Kishishita[1]; Ayush Srivastava[2]; Genki Terashi[2]; Rosa Viner[3]; Arun P. Wiita[1]; Anitha Rajendran[2]; Yeonni Zoo[4]; Georgia Papaefthymiou[4]; Daisuke Kihara[5;] *[1]UCSF, San Francisco, CA; [2]State University of New York at Potsdam, Potsdam, NY; [3]Thermo Fisher Scientific, San Jose, CA; [4]Villanova University, Villanova, PA; [5]Purdue University, Indianapolis, IN*

TP 094 **Cross-Technique Workflow Evolution in Structural Mass Spectrometry: Covalent Labeling, Crosslinking, and HDX**; SUMAN CHOUDHARY; *Independent Researcher, Karnal, India*

TP 095 **AI-Based Protein Language Models Predict Arginine Reactivity in Inflammatory Macrophages via Chemical Proteomics**; Sepideh K. Firooz[1]; Saiful M Chowdhury[1]; *[1]University of Texas At Arlington, Arlington, TX*

TP 096 **Chemical Crosslinking Reveals Structural Insights within F420-dependent glucose-6-phosphate dehydrogenase in Cryptosporangium arvum**; William LaFon[1]; Alaa Aziz[2]; Kayunta L. Johnson-Winters[2]; Saiful M Chowdhury[2]; *[1]University of Texas at Arlington, Arlington, TX; [2]University of Texas At Arlington, Arlington, TX*

TP 097 **Characterizing Transient Mitochondrial Protein Complexes by Native and Crosslinking Mass Spectrometry**; Suzanne E Enos[1]; Julia A Nguyen[1]; Lisa M Jones[1]; Rosa Viner[2]; Mark A Herzik[1]; *[1]University of California San Diego, La Jolla, CA; [2]ThermoFisher Scientific, San Jose, CA*

TP 098 **Complementary Footprinting and Modeling Characterization of a Bispecific Antigen-Binding Biotherapeutic (BABB)**; Weidong Cui[1]; Jake Pawlowski[1]; Pierre Havugimana[1]; Toby Goldner[1]; Michael Lanzillotti[1]; Ahmed Elbaradei[1]; Zoey Zheng[1]; Sabrina Benchaar[1]; Marisa Joubert[1</;] *[1]Amgen, Inc, Thousand Oaks, CA*

TP 099 **Conformational Biomarker Discovery by Radical Protein Footprinting in Mammalian Biofluids**; Mingming Zhao[1]; James A Stewart Jr. [1]; Brenton Laing[1]; Lisa M Jones[2]; Joshua S Sharp[1]; *[1]University of Mississippi, University, MS; [2]University of California San Diego, San Diego, CA*

TP 100 **Solid-Phase Extraction of Polycyclic Aromatic Hydrocarbons from Groundwater: Using Reduced Sample Volume and Non-Chlorinated Solvents**; Arielle Cocozza[1]; Bethany Magrann[1]; *[1]UCT, Bristol, PA*

TP 101 **Metabolomics and metallomic studies of intracellular metabolites of mammalian cells exposed to persistent organic pollutants**; Sam Li; *National University of Singapore, Singapore, Singapore*

TP 102 **Targeted and Non-Targeted Analyses of Per- and Polyfluoroalkyl Substances (PFAS) in Dogs with Gallbladder Mucoceles**; Sarah J. Rehm[1]; Kara M. Joseph[1]; Jody L. Gookin[2]; Erin S. Baker[1];

[1]Department of Chemistry, University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]Department of Clinical Sciences, College of Veterinary Medicine, North Carolina State University, Raleigh, NC

TP 103 **Assessing the impact of High-Performance Liquid Chromatography Conditions on structure resolved LC-MS/MS Analysis of Dissolved Organic Matter**; Tilman Schramm[1]; Christian Geibel[2]; Jarmo-Charles J. Kalinski[3]; Maxence Derbez-Morin[1]; Daniel Petras[1]; *[1]University of California, Riverside, Riverside, CA; [2]University of Tübingen, Tübingen, Germany; [3]Rhodes University, Grahamstown, South Africa*

TP 104 **Initial Reactions of Rice Straw and Polystyrene upon Fast Co-pyrolysis Explored Using Pyroprobe Integrated With an Ion Trap Mass Spectrometer**; Tanya Sharma[1]; Kumari Anshu[2, 3]; Sonal Thengane[3]; Hilkka I. Kenttämaa[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, west lafayette, IN; [3]Indian Institute of Technology Roorkee, Uttarakhand, India*

TP 105 **Multidimensional Characterization of Short Chain Chlorinated Paraffins (SCCPs) with GC-APCI and Cyclic Ion Mobility**; Sarah Dowd[1]; Lindsay Hatch[2]; Douglas Stevens[2]; Frank Dorman[2, 3]; *[1]Waters Corporation, Milford, MA; [2]Waters, Milford, MA; [3]Dartmouth College, Hanover, NH*

TP 106 **Automated Extraction and LC-MS/MS Analysis of PFAS from Sludge Matrices**; Chelsea Plummer[1]; Simone Marangoni[2]; Xavier Rodriguez[3]; Valentina Iacuzzi[4]; Tiziano Bonato[2]; *[1]Waters Corporation, Milford, MA; [2]S.E.S.A. SpA Laboratorio, Monselice, Italy; [3]Waters Corporation, Barcelona, Spain; [4]Waters Corporation, Sesto San Giovanni, Milan, Italy*

TP 107 **Comprehensive PFAS Screening in Food Contact Materials Using Combustion Ion Chromatography and High-Resolution Mass Spectrometry**; Jingli Hu; *Thermo Fisher Scientific, Sunnyvale, CA*

TP 108 **Improvements to the Analysis of PBDEs in Environmental Matrices: Transitioning from EI Magnetic Sector to GC-APCI TQ MS/MS**; Douglas M Stevens[1]; Daniel Furlong[2]; Stephanie Crombie[2]; Peter Hancock[3]; Narendra Meruva[1]; *[1]Waters Corporation, Milford, MA; [2]Environment and Climate Change Canada, Montreal, QC; [3]Waters Corporation, Wilmslow, United Kingdom*

TP 109 **Mass Spectrometric Workflow for Monitoring Polymer Biodegradation: Bridging Abiotic and Biotic Degradation of Polyhydroxybutyrate (PHB) via FIA-HRMS and MALDI-TOF**; Christian-Sebastiano Toppi[1, 2]; Arnaud Martel[2]; Samia Boudah[1]; Guillaume Cottin[1]; Alâa Bensetra[1]; Elsa Paiva[1]; Xavier Schultze[1]; Fabienne Lagarde[2]; Pascal Panda; *[1]L'Oréal R&I, Aulnay-sous-Bois, France; [2]Institut des Molécules et Matériaux du Mans (IMMM) - UMR 6283, Le Mans, France*

TP 110 **Non-Targeted Analysis of Air Pollutants Using Thermal Desorption GC-HRTOFMS with Machine Learning Structural Analysis**; Masahiro Hashimoto[1]; Chihiro Ueno[2]; Ryotaro Suzuki[2]; Katsuhito Yoshida[2]; Atsuyuki Sorimachi[2]; Masaaki Ubukata[1]; *[1]JEOL Ltd., Akishima, Japan; [2]Toyo University, Kawagoe, Japan*

TP 111 **Screening Analysis of PFAS in Textiles in Accordance with EN 17681-1/2 Using LC-MS/MS and GC-MS/MS**; Yui Higashi[1]; Masataka Furuta[1]; Riki Kitano[1]; Yoshiro Hiramatsu[2]; Kenichi Obayashi[1]; *[1]Shimadzu Co., Kyoto, Japan; [2]Shimadzu Scientific Instruments, Columbia, MD*

TP 112 **Inhibition of Gross Nitrification Rates Found Across PopulusGenotypes via a High Throughput Phenotyping by I.DOT/OPSI-MS.**; John F. Cahill[1]; Jessica LaFond[1]; Dana Carper[1]; Stephen Zambrzycki[1]; Mengjun Shu[1]; Brandon Sloan[1]; John Field[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN*

TP 113 **Identification of Novel Per-and-polyfluoroalkyl substance (PFAS) Isoform in Textile Using a Multi-Reflecting Time-of-Flight Mass Spectrometer Technology**; Hania Khoury-Hollins[1]; Sara Beverley[1]; Martin Palmer[1]; Jayne Kirk[1]; Richard Lock[1]; Sean Wu[2]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

TP 114 **Enhanced sensitivity and dynamic range for PFAS and emerging contaminant analysis using a modified hybrid Orbitrap mass spectrometer**; Lee Ferguson[1]; Christian Klaas[2]; Marzieh Shojaei[1];

Claire Dauly[2]; Stevan Horning[2]; Michal Kaczmarek[2]; Maciej Bromirski[2]; Alexander Harder[2]; Ed George[3</sup;] *[1]Duke University, Durham, NC; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]Thermo Fisher Scientific, San Jose, CA*

TP 115 **Putting the (Atmospheric) Pressure on Forever Chemicals: A Targeted Analysis of GC Amenable PFAS using APGC–MS/MS**; Kari Organtini[1]; Narendra Meruva[1]; Frank Dorman[1]; Ken Rosnack[1]; Kevin Stup[1]; *[1]Waters Corporation, Milford, MA*

TP 116 **LC-MS Analysis of Motorsport Contribution to 6PPD-Q Pollution in Proximal Water Systems**; Nevannah B Harlan[1]; Melissa Lenczewski[2]; Kevin R. Tucker[1]; *[1]Southern Illinois University Edwardsville, Edwardsville, IL; [2]Northern illinois University, DEKALB, IL*

TP 117 **Ultrafast Flame Ionization Mass Spectrometry Enables Direct Detection and Quantification of Microplastics and Nanoplastics in Complex Matrices**; Mengyuan Xiao[1]; Yongqing Yang[1]; Hanin Alahmadi[1]; Allison Harbolic[1]; Gina M. Moreno[2]; Terry Yu[1]; Jerry Liu[1]; Alex Guo[1]; Genoa R. Warner[1]; Phoebe Stapleton<su; *[1]New Jersey Institute of Technology, Newark, NJ; [2]Rutgers, New Brunswick, NJ*

TP 118 **Identifying Hundreds of PFAS in Dust Using Multimodal Mass Spectrometry Approaches: An Understudied Matrix with Potential Human Health Impact**; Parker Chang[1]; Jeremy P. Koelmel[1]; Cairo Ortiz[2]; Sheng Liu[1]; Joseph M. Braun[3]; Katherine E. Manz[4]; Aimin Chen[5]; Bruce P. Lanphear[6]; Kimberly Yolton[7];; *[1]Department of Environmental Health Sciences, Yale School of Public Health, New Haven, CT; [2]Innovative Omics, Sarasota, FL; [3]Department of Epidemiology, Brown University School of Public Health, Providence, RI; [4</sup]*

TP 119 **Targeted and Non-Targeted Screening of POP's (Persistant Organic Pollutants) in groundwater and trade effluent wastewater using a benchtop mass spectrometer**; Chris Henry1; Vendela Spalango[2]; *[1]Waters Corportaion, Cheshire, United Kingdom; [2]Waters Corporation, Milford, MA*

TP 120 **Integrated LC-MS/MS Workflow for Simultaneous PFAS and Cyanotoxin Analysis: Evaluating Mobile Phase Acid Effects to Improve Accuracy and Robustness**; Kate (Xiaomeng) Xia[1]; Om Shrestha[1]; Evelyn Wang[1]; Toshiya Matsubara[1]; Ruth Marfilvega[2]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Shimadzu Corporation, Kyoto, Japan*

TP 121 **Enhanced Quantification of Emerging UV Filter Contaminants in Drinking Water Using Optimized LC-MS/MS Technique**; Pingbo Zhang[1]; Om Shrestha[1]; Kathleen Luo[1]; Kate (Xiaomeng) Xia[1]; Andy Sandy[1]; Evelyn Wang[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD*

TP 122 **Online SPE with post-plasma chemical ionization MS for sensitive and rapid PFAS sum parameter quantitation in surface water samples**; Fabian Simon[1]; Kaveh Jorabchi[1]; *[1]Georgetown University, Washington Dc, DC*

TP 123 **A Multicomponent MAE–SPE–HPLC–MS/MS Workflow for the Analysis of Contaminants in Sediments and Microplastics**; Janina Heim[1]; Juliane Kramer[1]; Volker Schaible[2]; Mareike Prüfer[1]; Susanne Huhmann[1]; Karin Abraham[1]; Carsten Losch[1]; *[1]KNAUER Wissenschaftliche Geräte GmbH, Berlin, Germany; [2]CEM GmbH, Kamp-Lintfort, Germany*

TP 124 **Streamlined Measurement of Ultra-Short Chain PFAS in Landfill Groundwater via Altura Column Chemistry and LC-MS/MS**; Emily Parry[1]; Ivan Huang[2]; Mike Chang[2]; *[1]Agilent Technologies, Wilmington, DE; [2]Agilent Technologies, Santa Clara, CA*

TP 125 **High-Throughput Ultra-Short-Chain PFAS Analysis in Drinking Water using LC-MS/MS with Automated Sample Preparation**; Om k Shrestha[1]; Risa Suzuki[1]; Tiffany Liden[1]; Logan Miller[1]; Todd Anderson[2]; Evelyn Wang[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]ePrep PTY LTD, walnut creek, CA*

TP 126 **Spatial Profiling of Environmental Films Using Nanospray Desorption Electrospray Ionization Mass Spectrometry Imaging**; Govindi Soba Rashmiraji Walimuni Dewage[1]; Syeda Nazifa Wali[1]; Qiaorong Xie[1]; Julia Laskin[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

TP 127 **Resolving the Single-Particle Chemical Composition of Wildfire Aerosols in Real Time**; Johannes Passig[1]; Ellen Iva Rosewig[1]; Haseeb Hakkim[1]; Mika Ihalainen[2]; Anni Hartikainen[2]; Markus Somero[2]; Pasi Yli-Pirilä[2]; Olli Sippulä[2]; Saara Peltokorpi[;] *[1]University of Rostock, Rostock, Germany; [2]University of Eastern Finland, Kuopio, Finland; [3]Finnish Meteorological Institute, Helsinki, Finland; [4]Photonion GmbH, Schwerin, Germany*

TP 128 **Heat, Halogens, and Holobionts: LC-MS/MS Insights into Seasonal Metabolite Dynamics in Asparagopsis taxiformis**; Omri Nahor[1, 2]; Hadar Winckler-Aharoni[1]; Nataly Barger[1]; Maya Lalzar[3]; Michael Dubovis[1, 4]; Ivan Plyushchenko[1]; Álvaro Israel[1, 2]; Tal Luzzatto Knaan[1, 4]; *[1]Department of Marine Biology, The Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel; [2]Israel Oceanographic & Limnological Research, Tel Shikmona, Haifa, Israel; [3]University of Haifa Bioinformat*

TP 129 **Detection of trace metals in aerosols in the atmosphere of the Indian Ocean**; Aleksandrs Kalamašņikovs[1]; Ko-Keng Chang[1]; Haseeb Hakkim[1]; Marco Schmidt[1]; Robert Irsig[2]; Sven Ehlert[2]; Andreas Walte[2]; Eric Achterberg[3]; Johannes Passig[1<;] *[1]University of Rostock, Rostock, Germany; [2]Photonion GmbH, Schwerin, Germany; [3]Geomar, Kiel, Germany*

TP 130 **Comprehensive Non-Target Screening of Alpine Snow and Surface Waters by Complementary LC-HRMS and GC-MS**; Monika Adanyi[1]; Manuel Andino-Enriquez[2]; Masho Hilawie Belay[1]; Alessia Fabbris[1]; Arianna Ghignone[1]; Paola Calza[2]; Emilio Marengo[1]; Elisa Robotti[1]; *[1]University of Piemonte Orientale, Alessandria, Italy; [2]University of Turin, Torino, Italy*

TP 131 **Detection of SVOCs by Agilent 7010D GC/MS/MS Using Hydrogen Carrier Gas**; Erinn M O'Neill[1]; Alexis Willey[1]; Amy Cuthbertson[1]; Anastasia Andrianova[1]; *[1]Agilent Technologies, Wilmington, DE*

TP 132 **Development of an Integrated Data Infrastructure and Review Tool for Non-Targeted Analysis**; Heather D. Whitehead[1]; Anna K. Boatman[1]; Nathaniel Charest[1]; Mark Wilson[2]; Troy M. Ferland[1]; *[1]UL Research Institutes, Morrisville, NC; [2]UL Research Institutes, Marietta, GA*

TP 133 **Putative Identification of Potato Glycoalkaloids in Commercially Processed Foods by High-Resolution Mass Spectrometry**; Benjamin Katz; *UC Irvine, Irvine*

TP 134 **Quantitation of Aminoglycosides group of veterinary drugs in milk samples using LC-MS/MS without ion pairing agents in the mobile phase**; Prasanth Joseph[1]; Vinayak Azhakaprakalam[1]; Saikat Banerjee[1]; Vivek Dhyani[1]; *[1]Agilent Technologies, Bangalore, India*

TP 135 **Matrix Extension for a Quantitative LC-MS/MS Method for Regulating Diarrhetic Shellfish Toxins in the United States**; Christopher R. Beekman[1]; Brigid Carr[2]; Tyler Spillane[3]; Craig Burnell[2]; Stephen Archer[2]; Daniel Chavez[4]; Shelley Lankford[4]; Jonathan Deeds[1]; *[1]U.S. Food and Drug Administration, College Park, MD; [2]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME; [3]Department of Marine Resources, West Boothbay Harbor, ME; [4]Washington State Department of Health,*

TP 136 **LC-MS/MS Analysis of Ultra-short Chain PFAS in Tomatoes Using a Luna Polar Pesticides HPLC Column**; Mihir Thakar[1]; Francesco Romaniello, PhD[2]; Consolato Schiavone, PhD[2]; Chiara Portesi, PhD[2]; Maryam Sayeed[1]; Luigi Margarucci, PhD[3]; *[1]Phenomenex Inc., Torrance, CA; [2]Istituto Nazionale di Ricerca Metrologica, Torino, Italy; [3]Phenomenex Inc., Bologna, Italy*

TP 137 **Ambient mass spectra and fluorine status in fluorinated grease-proofers and fiber packaging**; Luke K Ackerman[1]; Clark Ridge[1]; Jennifer Janovick[1, 2]; Elsie Peprah[1]; Peter F. Scholl[1, 3]; *[1]FDA Human Foods Program, Office of Chem & Tox, College Park, MD; [2]Joint Institute For Food Safety & Applied Nutrition (JIFSAN), University of Maryland, College Park, MD; [3]Retired, Baltimore, MD*

TP 138 **Dioxin determination in food by isotope dilution gas chromatography coupled with triple quadrupole mass spectrometry**; Diego A Grassi[1]; Agustina Manassero[2]; Rosario Sandrini[2]; Lucas Agustín Pérez[1]; Ivan Cabanillas[2]; *[1]Analytical Technologies, Buenos Aires, Argentina; [2]JLA, General Cabrera. Córdoba, Argentina*

TP 139 **Flow-injection mass spectrometry combined with machine learning for rapid and green authentication of plant-based milk alternatives**; Grace Tseng[1]; Tianqi Li[1]; Yaxi Hu[1]; *[1]Carleton University, Ottawa, ON*

TP 140 **A Novel Separations Approach for Pyrrolizidine Alkaloid Isomers to Advance Food Safety**; Maria Aparicio Muriana[1]; Michela Pacchione[1]; Miriam Fico[2]; Kelly Moser[2]; Frederick Strathmann[2]; Christopher Elliott[1]; Nick Birse[1]; *[1]Queen's University Belfast, Belfast, Ireland; [2]MOBILion Systems, Chadds Ford, PA*

TP 141 **Improved detection capabilities for polychlorinated dibenzo-p-dioxins/furans (PCDD/Fs) using GC Orbitrap MS**; Xin Zheng[1]; Jason Cole[1]; Dominic Roberts[2]; Nicholas Warner[3]; Daniel Kutscher[3]; Kerstin Kratschmer[4]; *[1]Thermo Fisher Scientific, Austin, TX; [2]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [4]Wageningen Food Safety research, Wageningen, Netherla*

TP 142 **Triple Quad, Zero Panic: Detecting Ciguatoxins Without Comprehensive Standards**; Marco Marotta[1]; Kirk Gaston[1]; *[1]Food and Drug Administration, Dauphin Island, AL*

TP 143 **Is Your Next Sip Safe? A Simple, Rapid Method for Measuring volatile PFAS in Juices**; Andy Sandy[1]; Dominika Gruzsecka[1]; Evelyn Wang[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD*

TP 144 **Simultaneous Analysis of Eight Bisphenols in Food Storage Containers Using Liquid Chromatography-Triple Quadrupole Mass Spectrometry**; MAHO TANAKA[1]; Natsuki Iwata[2]; Manami Kobayashi[1]; Dominika Gruzsecka[3]; Samantha Olendorff[3]; *[1]Shimadzu corporation, Kawasaki, Japan; [2]Shimadzu Co., Kyoto, Japan; [3]Shimadzu Scientific Instruments, Columbia, MD*

TP 145 **Retail Survey of Grease-proof Coatings Containing 6:2 Fluorotelomer Alcohol in the US Food Contact Market from 2017-2025**; Victoria M Anderson[1]; Katherine Carlos[1]; Iris Yourick[1, 2]; Jordan Escavage[1]; Luke K Ackerman[1]; *[1]FDA, College Park, MD; [2]Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN*

TP 146 **Revealing Hidden Isomers: High-Resolution Separation of Regulated PFAS in Infant Formula**; Mark Jennings II[1]; Miriam Fico[1]; Frederick Strathmann[1]; Xanthippe Theurillat[2]; *[1]MOBILion Systems Inc., Chadds Ford, PA; [2]Nestlé Research, Lausanne, Switzerland*

TP 147 **Development of a new tailor-made solid-phase extraction column optimized for PFAS analysis in agricultural soil and the crops**; Mengmin Terashima[1]; Reika Takahara[1]; Manabu Takayanagi[1]; Shigenori Ota[1]; Shota Miyazaki[1]; Kenichi Suzuki[1]; Heesoo Eun[2]; *[1]GL Sciences. Inc, Tokyo, Japan; [2]National Agricultural Research Organization, Ibaraki, Japan*

TP 148 **Unmatched Method Robustness – StayClean™ QSight LC-MS/MS for Analysis of PFAS in Animal Tissues Based on EPA Method 1633**; Sheng-Suan (Victor) Cai[1]; Jacob Jalali[1]; *[1]PerkinElmer US, LLC, Shelton, CT*

TP 149 **Aptamer-Assisted Hollow Fiber Liquid Phase Microextraction Coupled with MALDI-MS for Rapid Mycotoxin Detection in Food Samples**; Jhih-Shan He[1]; He-Hsuan Hsiao[1]; *[1]National Chung Hsing University, Taichung, Taiwan*

TP 150 **Development of a Targeted LC-MS/MS Method for the Determination of Pyrrolizidine and Tropane Alkaloids in Food**; Weili Xiong; *U.S. FDA, College Park, MD*

TP 151 **Accelerating large scale pesticide screening programs with HR LC–MS/MS using automated non-targeted analysis software**; Simon Ashton[1]; Alan Barnes[1]; Emily G. Armitage[1]; Neil J. Loftus[1]; Steve Williams[2]; *[1]Shimadzu Corporation, Manchester, United Kingdom; [2]SGS Cambridge Limited, Cambridge, United Kingdom*

TP 152 **Development and Validation of an Orbitrap Tribrid Mass Spectrometric Method for Multi-Mycotoxin Analysis in Wheat, Barley, and Oats Grains**; Srinivas Sura[1]; Carlson Jules[1]; Avanthi Wijesinghe[1]; Maria Antonia Henriquez[1]; Xiben Wang[1]; *[1]Agriculture and Agri-Food Canada, Morden Research and Development Centre, Morden, MB*

TP 153 **Method Development and Validation of Catechol in Coffee Products by LC-MS/MS**; Fadwa Al-Taher[1]; Boris Nemzer[1, 2]; *[1]VDF FutureCeuticals Inc., Momence, IL; [2]University of Illinois Urbana-Champaign, Urbana, IL*

TP 154 **Evaluating Heavy Metals in Spices for Food Safety Compliance Using ICP-MS and ICP-OES**; Ana S Garcia Gonzalez[1]; Bert Woods[2]; *[1]Agilent Technologies, Wilmington,, DE; [2]AGILENT TECHNOLOGIES, Inc, Wilmington, DE*

TP 155 **Quantification of Poly Aromatic Hydrocarbons (PAHs) in Olive oil by GC-MS/MS**; Jessin Mathai[1]; Anant Lohar[2]; Jenishia Menezes[2]; *[1]Shimadzu, Dubai, United Arab Emirates; [2]Shimadzu Middle East and Africa FZE, Dubai, United Arab Emirates*

TP 156 **Ultra-fast MRM acquisition for large-panel contaminant analysis in food using a new generation triple quadrupole mass spectrometer**; Jianru Stahl-Zeng[1]; Michael Deng[2]; Ian Moore[2]; Lidija Kenjeric[3]; *[1]SCIEX, Darmstadt, Germany; [2]SCIEX, Concord, ON; [3]IFA Tulln, Tulln, Austria*

TP 157 **High-sensitivity LC-MS/MS for over 100 pesticides in food using micro flow rate analysis**; Wakana IWASAKI[1]; Eishi IMOTO[1]; Satoshi YAMAKI[1]; Tsuyoshi NAKANISHI[1]; *[1]Shimadzu Co., Kyoto, Japan*

TP 158 **Trace Level estimation of Glyphosate and Glufosinate in Red Chilli Pepper using FMOC-derivatization**; Vikrant Goel[1]; Abhishek Dave[2]; Saikat Banerjee[2]; Vivek Dhyani[2]; *[1]Agilent Technologies, Gurgaon, India; [2]Agilent Technologies India Pvt. Ltd, Bangalore, India*

TP 159 **Investigation into the presence of alkaloids in Areca catechu based single use food-contact articles (FCA)**; Brad Mangrum; *FDA, College Park, MD*

TP 160 **Metabolomic Profiling Reveals Enhanced Bioactive Compound Accumulation in Elderberry (Sambucus nigra) Cultivated under Good Agricultural Practices**; Samira Mahdi[1]; Xavier Jones[1]; Nadia Navarrete-Tindall[1]; Niya Tu[1]; Dipsana K.C. [1]; Ruipu Mu[2]; Qingbo Yang[1]; *[1]Lincoln University of Missouri, Jefferson City, MO; [2]University of Health Sciences and Pharmacy in St Louis, St Louis, MO*

TP 161 **UHPLC-MS/MS Metabolomic Assessment of Sochan and Hydroponic Collards Reveals Nutritional and Sustainable Potential of Underutilized Greens**; Dipsana KC[1]; Samira Mahdi[1]; Adenike Adeyeye[1]; Niya Tu[1]; Nadia Navarrete-Tindall[1]; Ruipu Mu[2]; Qingbo Yang[1]; *[1]Lincoln University of Missouri, Jefferson City, MO; [2]University of Health Sciences and Pharmacy in St Louis, St Louis, MO*

TP 162 **Nitrosamine-forming potential of meats cured with synthetic versus natural sources of nitrite**; Brittany Allison[1]; Leslie P. Silva[2]; Eli Tenefrancia[1]; Crystal McCaughey[1]; Sarah Reines[1]; *[1]CSUN, Northridge, CA; [2]Syft Technologies, Studio City, CA*

TP 163 **Redefining GC-MS for Explosives Analysis with Cold EI**; Benny Neumark[1]; Aviv Amirav[1]; *[1]Tel Aviv University, Tel Aviv, Israel*

TP 164 **Analysis of saxitoxin and analogues by reverse-phase LC-MS after derivatisation with ethyl chloroformate**; Karina Vignati[1]; George Kaklamanos[1]; Adriaan Marais[1]; Daniel Noort[1]; Prabhakar Sripadi[1]; Yue Wang[1]; Nathan McGill[1]; *[1]OPCW, Nootdorp, Netherlands*

TP 165 **Rapid derivatisation of novichok precursor amidines for improved detection by GC-MS and LC-MS**; Nathan McGill[1]; Courtney Mitchell[2]; Jayde Samuels[2]; Alysha Lee[2]; Patrick Mornane[2]; Lois Bright[3]; George Kaklamanos[1]; Simon Ovenden[2]; *[1]OPCW, Nootdorp, Netherlands; [2]Defence Science and Technology Group, Melbourne, Australia; [3]Defense Science and Technology Laboratory, Porton Down, United Kingdom*

TP 166 **Detection of Toxin Simulants Using Ambient Ionization Mass Spectrometry**; Lauren H Phan[1]; Leo Zhu[1]; Nicholas Manicke[1]; *[1]Indiana University Indianapolis, Indianapolis, IN*

TP 167 **Innovative BTC-ICP-MS method for quantitative native speciation of nanoparticles: insights into particle formation & adhesion mechanisms on silicon wafers**; Ray Su[1, 2]; Yin-Hung Lai[1]; Will Leung[1];

[1]National Yang Ming Chiao Tung University, Beitou Dist., Taiwan; [2]National United University, Miaoli, Taiwan

TP 168 **Using a Direct Insertion Probe Coupled to a High-Resolution Time-of-Flight Mass Spectrometer for Rapid Analysis of Pharmaceuticals**; Scott Pugh[1]; David E. Alonso[1]; Joe Binkley[1]; Viatcheslav Artaev[1]; *[1]LECO Corporation, St. Joseph, MI*

TP 169 **Streamlining Chemical Attribution Signature Profiling of Illicit Substances via Automated Mass Spectrometry-based Chemoinformatics**; Noah A. Lepinsky[1, 2]; Sarah E. Burry[1, 2]; Christian A. Rosales[2]; Jocelyn A. Menard[1, 2]; Karl V. Wasslen[1, 2]; Jeffrey C. Smith[1, 2]; *[1]Carleton University, Ottawa, ON; [2]Carleton Mass Spectrometry Centre, Ottawa, ON*

TP 170 **Chemical Communications: Discovery and Elucidation of Carrion Insect Cues that Prompt Carcass Colonization Behavior by DART-HRMS and TD/GC-MS**; Alexa Figueroa[1]; A. John Dane[2]; Jennifer Y. Rosati[3]; Rabi A. Musah[1]; *[1]Louisiana State University, Baton Rouge, LA; [2]Louisiana State University, Baton Rouge, Louisiana, LA; [3]John Jay College of Criminal Justice, New York, NY*

TP 171 **Development of Machine Learning assisted Fingermark Imaging Software (iFIS)**; Simona Francese[1]; Elias Jensen[2]; Sara Tortorella[3]; Chloe Spencer[1, 4]; Giuseppe Arturi[5]; Simon Cross[6]; Hassan Ugail[2]; *[1]Sheffield Hallam University, Sheffield, United Kingdom; [2]University of Bradford, Bradford, United Kingdom; [3]Mass Analytica, Sant Cugat del Valles, Spain; [4]University of Nottingham, Nottingham, United Kingdom; <*

TP 172 **Comprehensive Post-Blast Smokeless Powder Analysis: LC-MS detection of nitroguanidine and other smokeless powder additives from residues**; Matthew J Keller[1, 2]; Colby E Ott[1]; *[1]Federal Bureau of Investigation, Quantico, VA; [2]Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN*

TP 173 **Advanced canine detection: development of DART-TOF-MS and SPME/GC-MS identification methods of VOC's and odorants emitting from electronic storage devices**; Remi S. Acord[1, 2]; Riley P. McCullough[1, 2]; Christopher A. Tipple[1]; Colby E. Ott[1]; *[1]FBI, Quantico, VA; [2]Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN*

TP 174 **Optimization of drug extraction methods for DUID cases using LC-QTOF-MS**; Riley McCullough[1, 2]; Remi Acord[1, 2]; Christopher Tipple[2]; Colby E Ott[2]; *[1]Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN; [2]FBI, Quantico, VA*

TP 175 **Real-Time Detection of Narcotics and Explosives using Single-Particle Mass Spectrometry**; Haseeb Hakkim[1]; Ko-Keng Chang[1]; Johannes Passig[1]; Aleksandrs Kalamašņikovs[1]; Marco Schmidt[1]; Petra Hehet[2]; Michael Pütz[3]; Guangzhong Wang[4]; Heinrich Ruser[4];; *[1]University of Rostock, Rostock, Germany; [2]Federal Criminal Police Office, Munich, Germany; [3]Federal Criminal Police Office, Wiesbaden, Germany; [4]University of the Bundeswehr, Munich, Germany; [5]ParteQ*

TP 176 **Development and Validation of a Simple Microextraction Protocol for the Detection of Doping Agents in Blood Matrices**; Lia Visintin[1, 2]; Laurie De Wilde[1]; Koen Deventer[1]; Monica Mazzarino[1]; Kris Roles[1]; Peter Van Eenoo[1]; *[1]Doping Control Laboratory, Department of Diagnostic Sciences, Ghent University, Ghent, Belgium; [2]Drug Quality and Registration, Department of Pharmaceutical Analysis, Ghent University, Ghent, Belgium*

TP 177 **Utilizing Direct Analysis in Real Time-Triple Quadrupole-Mass Spectrometry (DART-TQ-MS) for the Identification of Challenging Novel Psychoactive Substances (NPS)**; Nicholas Khorozov[1]; Joshua DeBord[1]; Alex Krotulski[1]; Barry Logan[1, 2]; *[1]CFSRE, Horsham, PA; [2]NMS Labs, Horsham, PA*

TP 178 **A multidimensional approach to forensic investigations using mass spectrometry methods developed for food analysis**; Radoslaw Zbytniewski[1]; Jakub Czarny[1]; Pawel Cyplik[2]; Agnieszka Piotrowska-Cyplik[2]; Emilia Michalowska-Sobkowska[1]; Renata Stachewicz[1]; Jolanta Powierska-Czarny[1]; Magdalena; *[1]Institute of Forensic Genetics, Bydgoszcz, Poland; [2]University of Life Science, Poznan, Poland*

TP 179 **Identification of Genetically Variant Peptides in Human Hair by timsTOF Mass Spectrometry**; Zheng Zhang[1]; Guanghui Wang[1]; Anh Q. Tran[1]; Meghan C. Burke[1]; William E. Wallace[1]; *[1]NIST, Gaithersburg, MD*

TP 180 **Accelerating drug screening in forensic hair analysis by applying high-speed polarity switching in HR LC-MS/MS**; Nishi Rochelle[1]; Alan Barnes[2]; Emily G. Armitage[2]; Benjamin Barrett[3]; Ethan Webster[3]; Neil J. Loftus[2]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Shimadzu Corporation, Manchester, United Kingdom; [3]AttoLife, Norwich, United Kingdom*

TP 181 **Rapid Oral Fluid Screening of Gabapentin for Roadside Testing by LDTD-MS/MS**; Jean Lacoursiere[1]; Mégane Moreau[1]; Serge Auger[1]; Pierre Picard[1]; Sarah Demers[1]; Jonathan Rochon[1]; *[1]Phytronix Technologies, Inc., Quebec, QC*

TP 182 **Multi-Analyte Drug Panel Validation Impacted By Internal Standard Suppression from Unexpected Drug Interferences**; Victor E. Vandell; *Quest Diagnostics, Valencia, CA*

TP 183 **Developing a Fieldable Mass Spectrometry-Based Method for Onsite Processing of Fingernail Scraping Evidence for Exogenous Chemical Screening**; Madelynn G. Anderson[1]; Blaise R. Jones[1]; Bryse Boester[1]; Riley Means[1]; Christopher C. Mulligan[1]; *[1]Illinois state university, Normal, IL*

TP 184 **Rapid Screening of Drug Paraphernalia by DART-HRMS Using the Seized Drug Suite**; Juergen Kempf[1]; Ilona Nordhorn[2]; Carsten Baessmann[2]; Eva Niehaus[3]; Artem Filipenko[4]; *[1]Institute of Forensic Medicine, Medical Center - University of Freiburg, Freiburg, Germany; [2]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [3]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; <sup*

TP 185 **Development of a mass spectrometry-based approach for human identification and profiling using fingermark microbiome analysis**; George M Ward[1]; Alex Shenfield[1]; Simona Francese[1]; Tim Nichol[1]; *[1]Sheffield Hallam University, Sheffield, United Kingdom*

TP 186 **Multidimensional Scaling of Hybrid Similarity Search Match Factors for Fentanyl Analogs and Amphetamines**; Melinda A Kleczynski[1, 2]; Arun S Moorthy[3]; Anthony J Kearsley[1]; *[1]National Institute of Standards and Technology, Gaithersburg, MD; [2]Georgetown University, Washington, DC; [3]Trent University, Peterborough, ON*

TP 187 **Analysis of Fingerprints on Paper Substrates using Visible MALDESI**; Kenyon Evans-Nguyen[1]; Julia X Morelli[1]; *[1]The University of Tampa, Tampa, FL*

TP 188 **Tandem MS Analysis of Biotherapeutic GLP-1 Peptides Using ESI on a Compact 3D Ion Trap Platform**; Caleigh R O'Connor[1]; Vishal Mahale[1]; Madhuri Gupta[1]; Subodh Chawan[1]; Oscar Cabrices[1]; Venkat Panchagnula[1]; *[1]MassTech Inc., Columbia, MD*

TP 189 **Rapid On-Site Forensic Identification of Narcotic and Psychotropic Substances Using a Field-Deployable Ion Trap Mass Analyzer**; Vishal Mahale[1]; Madhuri Gupta[1]; Subodh Chawan[1]; Oscar Cabrices[1]; Caleigh R O'Connor[1]; Venkat Panchagnula[1]; *[1]MassTech Inc., Columbia, MD*

TP 190 **Machine Learning–Enabled Fingerprint Lipidomics for Noninvasive Diabetes Screening in Forensic and Clinical Applications**; Daphne R Patten[1]; Trevor T. Forsman[1]; Raven L. Buckman Johnson[1]; Yumi Imai[2]; Young Jin Lee[1]; *[1]Iowa State University, Ames, IA; [2]University of Iowa Department of Internal Medicine, Iowa City, IA*

TP 191 **Development and Validation of a UHPLC-MS Method for Quantitative Analysis of Neutral and Acidic Cannabinoids in Medicinal Cannabis Products**; Nayara Araujo Dos Santos[1]; Julie Massi Magalhães Figueiredo[1]; João Victor Macedo De Almeida[2]; Anny Rodrigues De Souza[1]; Alan Reinke Pereira[2]; Nathália dos Santos Conceição[2]; Eclair V; *[1]Federal Institute of Education, Science and Technology of Espírito Santo, Vila Velha, Brazil; [2]Federal University of Espírito Santo, Vitória, Brazil*

TP 192 **Library-Facilitated Drug Evidence Identification Using 3D-Printed Cone Spray Ionization (3D-PCSI-MS): A Decision-Support Approach for Forensic Operations**; Blaise R. Jones[1]; Madelynn G.

Anderson[1]; Jamie R. Wieland[1]; Patrick W. Fedick[2]; Christopher C. Mulligan[1]; *[1]Illinois state university, Normal, IL; [2]Naval Air Warfare Center Weapons Division, China Lake, CA*

TP 193 **Method Development for SIM Mode GCMS and LCMS Forensic Analysis of Amino Acid Ratios in Human Hair**; Lawren R. Paris[1]; Alyssa L. M. Marsico[1]; Robert Powers[1]; Marisia Fikiet[1]; *[1]University of New Haven, West Haven, CT*

TP 194 **Fentanyl Degradation by Oxidative Reactions: Is It Gas Phase or Solution-Based Reactions**; Mehdi Moini[1]; Brian Eckenrode[2]; Edward Bentil[2]; *[1]Picolytics, McLean, VA; [2]George Mason University, Manassas, VA*

TP 195 **Workflow for Detecting Counterfeit and Unapproved COVID-19 Treatment Products**; Christopher S Poulos[1]; Travis M Falconer[2]; Michael D Thatcher[2]; Adam Lanzarotta[2]; Martin Kimani[2]; *[1]Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN; [2]US Food & Drug Administration, Cincinnati, OH*

TP 196 **Plasmonic Bowl Array as an Ultrasensitive SALDI-MS Substrate for Detection of Small-Molecule Pollutants**; Jingtong Zhai[1]; Chunning Chen[1]; Jiaxin Lu[1]; Hongkun Zhao[1]; Nan Lyu[1]; *[1]Jilin University, Changchun, China*

TP 197 **Nature-Inspired Tandem Catalysts for CO2 Reduction**; Helen J Zeng[1]; Joel W Ager[1, 2]; *[1]Lawrence Berkeley National Laboratory, Berkeley, CA; [2]University of California, Berkeley, Berkeley, CA*

TP 198 **SIX2 (Simultaneous Isotope eXchange of two elements): A Novel Multiplex Tool to Probe Structure and Stability of Inorganic Materials**; Chanbopha Tho[1]; Daniil G. Ivanov[1]; Igor A. Kaltashov[1]; *[1]University of Massachusetts Amherst, Amherst, MA*

TP 199 **Controlling Reactivity of Ligated Metal Chalcogenide Clusters in the Gas Phase and on Surfaces by Combining Mono- and Bidentate Ligands**; Bethany Phillips[1]; Iliyas Iznat[2]; Xilai Li[2]; Julia Laskin[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, West lafayette, IN*

TP 200 **Online Chemical Analysis of Flowing Hydrocarbon Fuel Surrogates in a Pyrolysis Reactor by Optical Spectroscopy and Molecular Beam Mass Spectrometry**; Matthew C Rohan[1, 2]; Cole J VanDyke[1, 2]; Michael S Hanchak[1, 2]; Elizabeth M Craft[1, 2]; Elizabeth S Kurian[2]; Alexander D Tucker[2]; William K Lewis[2]; Andrew DeBlase[1, 2<;] *[1]University of Dayton Research Institute, Dayton, OH; [2]Air Force Research Laboratory, Dayton, OH*

TP 201 **Energy Shuttle Ionization in GC–MS: Collision-Assisted Energy Relay by Ethylene in Nitrogen Restores EI Sensitivity**; Yasuro Fuse[1]; Xue Chu[1]; *[1]Kyoto institute of technology, Kyoto, Japan*

TP 202 **Probing the effectiveness of supercharging in positive-ion and negative-ion electrospray ionization mass spectrometry**; Yiqi Yin[1]; Rachel R. Ogorzalek Loo[1]; Joseph A Loo[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

TP 203 **Gas Phase Ion Formation for Tryptic Peptides under LC/MS Conditions: Insights from MD Simulations of Acetonitrile/Water Droplets**; Noah F Ruscica[1]; Lars Konermann[1]; *[1]The University of Western Ontario, London, ON*

TP 204 **Peptide digestion via rapid-mixing using theta emitter nanoelectrospray ionization mass spectrometry**; Sebastian Ortiz Blanco[1]; Scott A. McLuckey[1]; *[1]Purdue University, Department of Chemistry, West Lafayette, IN*

TP 205 **One Hundred Years of Photoionization: A Historical Perspective**; Jack A. Syage[1]; G. Asher Newsome[2]; *[1]ZymagenX, Newport Beach, CA; [2]Smithsonian Museum Conservation Institute, Suitland, MD*

TP 206 **Catalyst-Free Gas-Phase Synthesis of Pyrones via Thermally Induced Aldol Condensation of Acetoacetate Derivatives Using GC–MS**; Isaac Agyekum[1]; Fernando Garcia[1]; *[1]University of North Georgia - Gainesville, Oakwood, GA*

TP 207 **Confident Identification of the Human Breath Matrix**; Eric Miller[1]; Samanthi Wickramasekara[1]; Mark Annunziato[1]; Chathurika Rathnayake[1]; Jamie Kim[1]; Krishna Patel[1]; [1]*Food and Drug Administration, Silver Spring*

TP 208 **Streamlined Sample Preparation for PAH Analysis in Edible Oils Using Polymeric Phase SPE Cartridge and GC-MS**; Joshua J Fera[1]; Kristen Schultz[1]; Olga Shimelis[1]; [1]*MilliporeSigma, Bellefonte, PA*

TP 209 **Optimizing Preconcentration of Volatile PFAS Precursors: A Comparative Study of SPME Arrow and Fiber Geometries**; Madison L. Williams[1]; Hagen M. Gegner[2]; Tiantian Li[2]; Stefan Cretnik[2]; Lucas Lüthy[2]; Tom Flug[2]; Michael Stebler[2]; Emanuela Gionfriddo[1]; [1]*University at Buffalo, Amherst, NY;* [2]*CTC Analytics AG, Zwingen, Switzerland*

TP 210 **Wake up and smell the coffee! AI-assisted structure determination of unknown molecules in coffee aroma volatiles**; Robert B Cody; *JEOL USA, Inc., Peabody, MA*

TP 211 **Cold EI as a Transformative Improvement to GC–MSSignal-to-Noise Ratios and Limits of Detection**; Alex Yakovchuk[1]; Aviv Amirav[1]; [1]*Tel Aviv University, Tel Aviv, Israel*

TP 212 **Molecular Ion Formation in GC-PCI-TOFMS Is Moiety Dependent: A Functional Group Limited Observation**; Craig Fowler[1]; Slava Artaev[1]; Albert T Lebedev[2]; [1]*LECO, St. Joseph, MI;* [2]*Shenzhen MSU-BIT University, Shenzhen, China*

TP 213 **Advancements in GC for picogram level analysis for semivolatiles and pesticides by GCMS/MS**; Ramkumar Dhandapani[1]; Jennifer Lindner[1]; [1]*Restek, Bellefonte, PA, PA*

TP 214 **Improved Baseline Stability and Sensitivity in GC–MS Using a Novel Column with an Uncoated Interface Section**; Ramkumar Dhandapani[1]; Javier Arrebola[2]; [1]*Restek, Bellefonte, PA, PA;* [2]*University of Almeria, Almeria, Spain*

TP 215 **Advancements in GC Column Deactivation for Robust Multi-Class Semivolatile Analysis**; Ramkumar Dhandapani[1]; Jennifer Lindner[1]; [1]*Restek, Bellefonte, PA, PA*

TP 216 **Instrumentation for Real-Time VOC Monitoring Using a Preconcentrator with Fast GC Coupled to a Miniaturized Multi-turn Time-of-Flight Mass Spectrometer**; Ping Chen[1, 2]; Yosuke Kawai[1]; Toshinobu Hondo[1]; Chia-Jung Lu[2]; Michisato Toyoda[1]; [1]*The University of Osaka, Osaka, Japan;* [2]*National Taiwan Normal University, Taipei, Taiwan*

TP 217 **Beyond Helium: Integrated Hydrogen and Air Infrastructure for Modern GC and GC-MS Laboratories**; Reuven Mery; *M. Snir Ltd, K. Ata, Israel*

TP 218 **Untargeted Analysis of Volatile PFAS in Indoor Air by Thermal Desorption GC High-Resolution Orbitrap Mass Spectrometry**; Dominic Roberts[1]; Priya Vaitheesvaran[2]; Terry Jeffers[2]; Xin Zheng[3]; Jason Cole[3]; Nicholas Warner[4]; Daniel Kutscher[4]; Monica Driscoll[2]; [1]*Thermo Fisher Scientific, Runcorn, United Kingdom;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*Thermo Fisher Scientific, Austin, TX;* [4]*Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

TP 219 **Structure Analysis Tools for Metabolite Identification by Combining Machine Learning and Artificial Intelligence with Gas Chromatography High-Resolution Time-of-Flight Mass Spectrometry**; Bryan Katzenmeyer[1]; Ayumi Kubo[2]; Masaaki Ubukata[2]; Azusa Kubota[2]; [1]*JEOL USA, Inc., Peabody, MA;* [2]*JEOL Ltd., Akishima, Japan*

TP 220 **Evaluation of Automated Derivatization and AI-Driven Data Interpretation for High-Throughput GC-MS Analysis**; Erwin Kupczyk[1]; Hagen Magnus Gegner[2]; Philipp Miro Pflüger[3]; Adelina-Elisa Olbrich[3]; Gernot Poschet[1]; [1]*Heidelberg University, Heidelberg, Germany;* [2]*CTC Analytics AG, Zwingen, Switzerland;* [3]*ChemInnovation GmbH, Köln, Germany*

TP 221 **Detection of Organic Acids using Agilent 7000E GC/TQ with PAL3 Series II RTC Autosampler**; Erinn M O'Neill[1]; Alexis Willey[1]; Saurabh U. Patel[1]; [1]*Agilent Technologies, Wilmington, DE*

TP 222 **Impact of Soil Matrix on Microplastics Analysis by Py-GC/MS**; Cristina Matos Mejias[1]; Yoshiro Hiramatsu[2]; *[1]Shimadzu, Columbia, MD; [2]Shimadzu Scientific Instruments, Columbia, MD*

TP 223 **Characterization of High-Performance Polymers Using Thermal Desorption/Pyrolysis and High-Resolution Mass Spectrometry**; David E Alonso[1]; Joseph E Binkley[2]; *[1]Leco Corporation, St. Joseph, MI; [2]LECO Corporation, St. Joseph, MI*

TP 224 **Extended dynamic range and long-life detector for GCMS quadrupole systems**; Ge Yu[1]; Elias Feresenbet[1]; Luis Cuadra-Rodriguez[1]; Alexander Mordehai[1]; Brooke Reaser[1]; Kai Chen[1]; *[1]Agilent Technologies, Santa Clara, CA*

TP 225 **Enhanced Sensitivity for the Quantitative Analysis of Pesticides Using an GC Orbitrap MS**; Dominic Roberts[1]; Giulia Riccardino[2]; Xin Zheng[3]; Jason Cole[4]; Daniel Kutscher[5]; *[1]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [2]Thermo Fisher Scientific, Milan, Italy; [3]Thermo Fisher Scientific, Austin, TX; [4]Thermo Fisher Scientific, Ausitn, TX; [5]Thermo Fisher Scient*

TP 226 **Benchmarking Machine Learning-Assisted Structure Elucidation for Database-Invisible Metabolite Standards using GC-HRTOFMS**; Azusa Kubota[1]; Ayumi Kubo[1]; Masaaki Ubukata[1]; *[1]JEOL, Ltd., Tokyo, Japan*

TP 227 **Analysis of aromatic amines in textile samples by GCMS using Hydrogen carrier gas**; Praveen Arya[1]; Vivek Dhyani[1]; *[1]Agilent Technologies Inc., Manesar, India*

TP 228 **Dual-Layer Solvent Vent Injection as a Strategy to Overcome Sensitivity Limitations in Hydrogen-Based GC-MS/MS**; Jose Antonio Martínez[1]; Jose Luis Oller[1]; Amadeo R. Fernández-Alba[1]; Anastasia Andrianova[2]; *[1]European Union Reference Laboratory for Pesticide Residues in Fruits & Vegetables, Almería, Spain; [2]Agilent Technologies, Wilmington, DE*

TP 229 **Detection of per- and polyfluoroalkylated substances by ASTM 8591-24 using Agilent thermal desorption tubes on a TD-GC-MS/MS**; Samuel Haddad[1]; Eric Park[1]; *[1]Agilent Technologies, Wilmington, DE*

TP 230 **Expanding a Comprehensive Electron Ionization Mass Spectral Library by 37,000 New High-Quality Spectra Including 15,000 Derivatized Compounds**; Weihua Ji[1]; James Little[1]; Kirill V. Tretyakov[1]; Nino G. Todua[1]; Nirina Rabe Andriamaharavo[1]; Yufang Zheng[1]; Quan-Long Pu[1]; Edward P. Erisman[1]; Dmitrii V. Tchek; *[1]NIST, Gaithersburg, MD*

TP 231 **Revealing the Full PFAS Picture with VASE–TD–GC-MS: Quantitative Per- and Polyfluoroalkyl Substance Analysis in Water, Soil, and Food**; VICTORIA VOGEL[1]; Jeff Schroeder[1]; Weier Hao[1]; Daniel J. Cardin[1]; Daniel B. Cardin[1]; *[1]Entech Instruments, Simi Valley, CA*

TP 232 **Analysis of Per- and Polyfluoroalkyl Substances (PFAS) in Consumer Products Using Flash Vacuum Assisted Sorbent Extraction**; Daniel J Cardin[1]; Weier Hao[1]; VICTORIA VOGEL[1]; Daniel B Cardin[1]; *[1]Entech Instruments, Simi Vally, CA*

TP 233 **Improvement in GC/MS Fast Scanning Acquisition**; Luis Cuadra-Rodriguez[1]; Ge Yu[1]; Siyuan Chen[1]; Elias Feresenbet[1]; Alex Mordehai[1]; Brooke Reaser[1]; Kai Chen[1]; *[1]Agilent Technologies, Santa Clara, CA*

TP 234 **Analysis of Per- and Polyfluoroalkyl Substances (PFAS) in Indoor Air Using Active Sampling**; Weier Hao[1]; Victoria Vogel[1]; Daniel B Cardin[1]; Daniel J Cardin[1]; *[1]Entech Instruments, Simi Valley, CA*

TP 235 **Assessing the Limits of Unknown Compound Identification Using Commercially Available EI MS and Local CI MS Libraries**; Grace Greene[1]; Bridger Johnston[1]; Hilkka I. Kenttämaa[1]; *[1]Purdue University, Department of Chemistry, West Lafayette, IN*

TP 236 **Trace-Level Analysis of Nitrosamine Impurities in Non-ionic Iodinated Contrast Agent and Formulations**; Soma Dasgupta; *Agilent Technologies India Pvt. Ltd, Bangalore, India*

TP 237 **Accelerating intact biotherapeutics analysis using Acoustic Ejection Mass Spectrometry**; Matthew D Stone[1]; DilipKumar Reddy[2]; Anuja Bhalkikar[1]; Jacob McCabe[2]; Han Wang[3]; Seo Bee Hong[3]; Matthew Green[4]; *[1]Sciex, Framingham, MA; [2]SCIEX, Marlborough, MA; [3]SCIEX, Singapore, Singapore; [4]Genedata, United Kingdom, United Kingdom*

TP 238 **Automated non-target screening approach using FTICR-MS for identifying radiological organoiodine compounds in natural organic matter**; Albert Vega-Herrera[1]; Caroline O. Granger[2]; Stephanie N. Gamble[2]; Joseph M. Mannion[2]; Facundo M. Fernández[1]; *[1]Georgia Institute of Technology, Atlanta, GA; [2]Savannah River National Laboratory, Jackson, SC*

TP 239 **Coupling trapped ion mobility with two-dimensional mass spectrometry to analyze complex organic matter on the new 18 T timsMRMS**; Maria Van Agthoven[1, 2]; Julien Maillard[2, 3]; Maxime SUEUR[1, 2, 3]; Simon Ollivier[1, 2]; Christopher A. Wootton[4]; Marc-André Delsuc[5]; Pierre Giusti[1, 2, 3]; Carlos Afonso; *[1]University of Rouen Normandy, Mont Saint-Aignan, France; [2]International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France; [3]TotalEnergies Research and Technology Gonfreville, Harfleur,*

TP 240 **Unlocking the Archived Proteome: Deep and Rapid FFPE Analysis Using a Novel Automated Ion Source and the Orbitrap Astral Mass-Spectrometer**; Sudipa Maity[1]; Amarjeet Flora[2]; Bhavin Patel[2]; William Comstock[3]; Katherine Walker[3]; Amirmansoor Hakimi[3]; Tonya Pekar Hart[3]; Ellen Casavant[3]; *[1]Thermo Fisher Scientfic, San Jose, CA; [2]Thermo Fisher Scientific, Rockford, IL; [3]Thermo Fisher Scientific, San Jose, CA*

TP 241 **A Robust Strategy for High-Throughput and Deep Proteomics by Combining Narrow-Window Data-Independent Acquisition and Isobaric Mass Tagging**; Chaewon Kang[1]; Jiwon HONG[1]; Hokeun Kim[1]; JeongSu Jo[1]; Sang-Won Lee[1, 2, 3]; *[1]Korea University, Seoul, South Korea; [2]TargetX Inc., Seoul, South Korea; [3]National Research Laboratory for Convergence Degradation Biology, Seoul, South Korea*

TP 242 **A.M.P.L.I.F.Y.: Automated Multi-Omics Pipeline Leveraging Integrated Front-End Robotics and Yield-Driven Analytics**; Raquel Shortt-Jackson[1, 2]; Jana Carpenter[2]; Conor Jenkins[2]; Gabrielle Rizzo[2]; *[1]Precise Systems Inc., Lexington Park, MD; [2]Chemical Biological Center, U.S. ARMY, Gunpowder, MD*

TP 243 **High-Throughput Gut Phenotyping: DoE-Optimized Dual UHPLC-HRMS for Integrated Fecal Metabolomics and Lipidomics**; Tiffany De Troyer[1]; Kimberly De Windt[1]; Vera Plekhova[1]; Beata Pomian[1]; Ellen De Paepe[1]; Lynn Vanhaecke[1, 2]; *[1]Ghent University, Ghent, Belgium; [2]Queen's University Belfast, Belfast, United Kingdom*

TP 244 **Comparing the Repeatability of Automated and Manual Peptide Mapping Sample Preparations**; Jackson J Scheppers; *KBI Biopharma, Louisville, CO*

TP 245 **How many Significant Figures after the Decimal? High Mass Accuracy and Precision using Low Resolving Power RPLC-MS Instrumentation**; Iain D. G. Campuzano[1]; Santino Valiulis[1]; Aniruddha Sahasrabuddhe[1]; Dylan Riggs[2]; Ramakrishnan Natesan[2]; Elizabeth Hecht[3]; John Robinson[1]; Danyang Gong[1]; Kevin; *[1]Amgen Inc., Thousand Oaks, CA; [2]Amgen Inc., Cambridge, MA; [3]Amgen Inc., South San Francisco, CA*

TP 246 **Identification of impurities in dimethyl carbonate by GC-HRTOFMS**; Christina N Kelly[1]; Joseph E Binkley[1]; John M Hayes[1]; Jean-François Borny[2]; David E Alonso[1]; *[1]LECO Corporation, Saint Joseph, MI; [2]Lummus Technology, Pasadena, TX*

TP 247 **Streamlining Regular Liquid Chromatography with MALDI-TOF MS and NMR Spectroscopy Using Automatic Full-Contact Splitless Spotting Interface and Flash-Tap Fractioning Collection**; Yung-Cheng Jair[1]; Chi-Minh Truong[2]; Yi-Hsin Liu[3]; Pin-Chuan Chen[4]; Pai-Shan Chen[5]; *[1]National Taiwan University, Taipei, Taiwan; [2]University of Auckland, Auckland, New Zealand; [3]National Taiwan Normal University, Taipei, Taiwan; [4]National Taiwan University of Science and Technology, Taipei City*

TP 248 **timsMRMS: A Gated TIMS FT-ICR MS instrument to decipher isomeric content of complex organic mixtures**; Alina Theisen[1]; Jochen Friedrich[2]; Gregory Brabeck[3]; J. Paul Speir[3]; Christopher A. Wootton[4];

[1]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [2]Bruker Daltonik, Bremen, Germany; [3]Bruker Scientific LLC, Billerica, MA; [4]Bruker, Bremen, Germany

TP 249 **UHPLC-Q-TOF MS-Based Profiling of Cell Culture Medium and Post-Culture SupernatantCombined with a Retention Time-Integrated Database**; Ming-Hui Sun; *Agilent, YANTAI, China*

TP 250 **A fully integrated Qual/Quan solution from a single injection using standardised sample preparation and chromatography with a benchtop MRT MS**; Matthew E Daly[1]; Brittney Racioppo[2]; Lee A Gethings[1]; Martin Palmer[1]; Richard Lock[1]; Rowan Moore[1]; James I Langridge[1]; *[1]Waters Wilmslow UK, Wilmslow, United Kingdom; [2]Waters, Milford, MA*

TP 251 **Implementation of a Precision Model Combined with Graph Theory and Calibration without Calibrants Transforms High-resolution MS Data Processing and Informatics**; Ryan P Rodgers[1, 2, 3]; Teja Potu[1, 4]; Lydia C. Babcock-Adams[1, 2]; Christopher L. Hendrickson[1, 2]; Martha L. Aguilera[1, 2]; Alvaro J. Tello-Rodriguez[1, 4]; Christopher Rüger[2, 5</s;] *[1]Nat'l High Magnetic Field Lab, Tallahassee, FL; [2]International Joint Laboratory for Complex Matrices Molecular Characterization (iC2MC), Harfleur, France; [3]Université de Pau et des Pays de l'Adour, IPREM UMR-CNRS, Pau, Py*

TP 252 **Automating Expert Intuition: A Multi-Agent LLM Framework for Real-Time Forensic Validation of Complex Chemical Space Revealed by FT-ICR MS**; Teja Potu[1, 2]; Germain Salvato Vallverdu[3, 4]; Lydia C Babcock-Adams[2, 4]; Ryan P Rodgers[2, 3, 4]; Gary Tyson[1]; *[1]Florida State University, Tallahassee, FL; [2]Nat'l High Magnetic Field Lab, Tallahassee, FL; [3]Université de Pau et des Pays de l'Adour, IPREM UMR-CNRS, Pau, Pyrénées-Atlantiques, France, France; [4]International J*

TP 253 **Rapid Broadband Automatic Phase Correction for FT-ICR MS Data Based Upon Linear Regression Analysis**; Greg T Blakney[1]; Steven C. Beu[2]; Christopher L Hendrickson[1]; Lydia C. Babcock-Adams[1]; Chad R. Weisbrod[1]; *[1]National High Magnetic Field Laboratory Department of ICR, Tallahassee, FL; [2]S.C. Beu Consulting, Austin, TX*

TP 254 **Tensor Train Compression for High-Resolution Mass Spectrometry Data With Linear Processing in Compressed Form**; Julius Jessen Terp[1]; Hayden Dean Gemeinhardt[2]; Paul-Albert Anselm Schneide[1]; Pedro Martinez Noguera[1]; Michael Kastoryano[2]; Rasmus Bro[1]; *[1]University of Copenhagen, Frederiksberg, Denmark; [2]University of Copenhagen, Copenhagen, Denmark*

TP 255 **Natural Products and Next-Gen MS: can 'Better' turn into 'Different'?**; Mostafa Hagar[1]; Roger Linington[1]; *[1]Simon Fraser University, Burnaby, BC*

TP 256 **Applications of high-throughput DIA-based Proteomics for targeted protein degradation drug discovery**; Lincoln Howarth[1]; Chris Browne[1]; Rujuta Kshirsagar[1]; Min Yuan[1]; Sara Martell[1]; Annissa Huhn[1]; Wendy Li[1]; Guang Liu[1]; Immanuel Utomo[1]; Dirk Walther<su; *[1]Kymera Therapeutics, Watertown, MA*

TP 257 **An LLM-Powered Agent for Streamlined Mass Spectrometry Imaging Data Mining**; Xindi Tang[1]; Xingpeng Sun[1]; Emerson Hernly[1]; Julia Laskin[1]; *[1]Purdue University, West Lafayette, IN*

TP 258 **Mathematical Framework for Quantifying Delocalization in MALDI-MSI via a Composite Scoring Approach**; Amin Jarrahi[1]; Allison Jones[1]; Weisheng Tang[1]; Hairong Qi[1]; Anna Colleen Crouch[1]; *[1]University of Tennessee, Knoxville, TN*

TP 259 **LA-ICP-MS and MALDI-MS image fusion for identifying hidden molecular features of therapeutic nanocarriers**; Gnana Venkata Sai Chaitanya Kumar Ponguru[1]; Monika Mahmud[1]; Teerapong Max Jantarat[1]; Jeerapat Doungchawee[1]; Richard W. Vachet[1]; *[1]University of Massachusetts Amherst, Amherst, MA*

TP 260 **A Computational Workflow for Marker-Free Plaque Segmentation and Region-Specific Lipid Profiling from Mass Spectrometry Imaging Across Alzheimer's Disease Progression**; Tzu-Yang Tseng[1, 2]; Timothy J Trinklein[2, 3]; Stanislav S Rubakhin[2, 3]; Sabitha K Rajesh[4]; Orly Lazarov[4]; Jonathan V Sweedler[1, 2, 3]; Fan Lam[1, 2]; *[1]Department of Bioengineering, University of Illinois Urbana-Champaign,* *Urbana, IL; [2]Beckman Institute for Advanced Science and Technology, University of Illinois Urbana Champaign, Urbana, IL; [3]Department of Chemistry, Uni*

TP 261 **Robust mass recalibration standardizes MALDI Imaging and enhances interpretability across large datasets**; Bram Heijs[1]; Harrison Taylor[2]; Andra Pascale-Henke[3]; Kai Zoellner[3]; Joe Ippolito[4]; Christopher Clark[5]; Richard R. Drake[2]; Tobias Boskamp[3]; Peggi M. Angel[2<;] *[1]Bruker Nederland B.V., Leiderdorp, Netherlands; [2]Medical University of South Carolina, Charleston, SC; [3]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [4]Washington University in St.Louis, St.Louis, MO; [5<]*

TP 262 **PeakMarkR: Unbiased Spatial Metabolomics via De Novo Formula Prediction and Zonal Isotope Validation in (Un)labeled MALDI-MSI**; Maciej Dulewicz1; Junyue Ge[1]; Alicja Szadziewska[1]; Henrik Zetterberg[1, 2, 3]; Jorg Hanrieder[1, 4]; *[1]University of Gothenburg, Gothenburg, Sweden; [2]University of Wisconsin-Madison, Madison, WI; [3]Hong Kong Center for Neurodegenerative Diseases, Hong Kong, China; [4]University College London, London, United Kingdo*

TP 263 **Probabilistic Alignment of Spatial Transcriptomics Experiments for MALDI Imaging Serial Section Alignment**; Daniel Castro; *Bruker Scientific LLC, Billerica, MA*

TP 264 **Evaluating methods and metrics for monitoring instrument performance and data quality in mass spectrometry imaging: results from a longitudinal study**; Alexander Reeve[1]; Ariadna Gonzalez[1]; Janella De Jesus[1]; Alex Dexter[1]; Martin Metodiev[1]; Caroline Pollard[1]; Lucy M Johns[1]; Spencer A Thomas[1]; Rory T Steven[1;] *[1]National Physical Laboratory, Teddington, United Kingdom; [2]Imperial College London, London, United Kingdom*

TP 265 **Spatial Mapping of Lipid Dysregulation in Mouse Lungs Following Silver Nanoparticle Exposure Using DESI-MSI**; Matheus Neves De Araujo[1, 2]; Nicolas Hunter Medel[1]; Weiwei Zhang[3]; Jenna Nicole Swihart[1]; Marcelo Zaiat[2]; Christina Ferreira[3]; Jonathan Henry Shannahan[1]; *[1]School of Health Sciences, Purdue University, West Lafayette, IN; [2]São Carlos School of Engineering, University of São Paulo, São Carlos, Brazil; [3]Bindley Bioscience Center, Purdue University, West Lafayette, IN*

TP 266 **Spatially targeted metabolic phenotyping of MTAP-deficient cancers reveals tumor-localized MTA accumulation and lipid remodeling**; Meredith Spradlin[1]; Jianfeng Chen[2]; Jianjun Gao[2]; Livia S. Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX; [2]MD Anderson Cancer Center, Houston, TX*

TP 267 **Spatial metabolomics reveals cholinergic and methylation pathway disruptions in primate models of Parkinson's disease and L-DOPA-induced dyskinesia**; Elva Fridjonsdottir[1]; Theodosia Vallianatou[1]; Ioannis Mantas[2]; Yea Rin Lee[1]; Jordan T Aerts[1]; Ibrahim Kaya[1]; Anna Nilsson[1]; Reza Shariatgorji[1]; Erik T Jansson[1</s;] *[1]Uppsala University, Uppsala, Sweden; [2]Karolinska Institute, Stockholm, Sweden; [3]Université de Bordeaux, Bordeaux, France*

TP 268 **Targeted DESI-MS Imaging for Spatial Mapping of Inflammatory Mediators and Metabolites of Pulmonary Tuberculosis**; David Beaver[1]; PREM SHANKAR[1]; Nikolas Shurgaia[2]; Mari Buziashvili2[2]; Sergo Vashakidze2[2]; Jeff Collins[3]; Russell Kempker3[3]; Brendan Prideaux[1, 4]; *[1]Department of Neurobiology, University of Texas Medical Branch, Galveston, TX; [2]The National Centre for Tuberculosis and Lung Diseases, Tbilisi, Georgia; [3]Department of Medicine, Division of Infectious Disease, School of*

TP 269 **Spatial N-Glycan MALDI-MSI with Machine Learning Maps Externally Validated HCC Margins and Reveals MGAT5-Linked Tetraantennary Branching in GS/Wnt-Active Tumors**; Muhammed F Bayram[1]; Jade K. Macdonald[1]; Andrew DelaCourt[1]; Peggi M. Angel[1]; Richard R. Drake[1]; Satdarshan P. Monga[2]; Amit Singal[3]; Anand Mehta[1]; *[1]Medical University of South Carolina, Charleston, SC; [2]University of Pittsburgh, Pittsburgh, PA; [3]University of Texas Southwestern Medical Center, Dallas, TX*

TP 270 **Unbiased Spatial Proteomics with Transcriptome-Directed Regional Targeting**; Ashley Tai[1]; Junxiang Xu[1]; Shaotai Hu[1]; Joakin Mori[1]; Christopher Heaphy[1]; Naomi Ko[1]; Ruben Dries[1]; Joseph Zaia[1]; *[1]Boston University, Boston, MA*

TP 271 **Integrated Spatial Multi-Omics Mapping Identifies Inflammatory Dysregulation and Fibrotic Signaling in Pulmonary Fibrosis**; U-Ming Lim[1]; Esther Cheow[1]; Matthew Choo[1]; Nikhil Tulsian[1]; Aaron Zefrin Fernandis[1]; Asad Abu Bakar Ali[1]; *[1]MSD International GmBH, Singapore, Singapore*

TP 272 **Extracellular Matrix, N-Glycan and Immune Cell Remodeling Define Dysplastic Microenvironments in Early-Onset Colorectal Precancer**; Jade K. Macdonald[1, 2]; Thai H Pham[1, 2]; Lukasz G Migas[2, 3]; Harsimran Kaur[1]; Frank Revetta[4]; Madeline E Colley[1, 2]; Seung Woo Kang[1]; Martin Dufresne[1, 2]; Audra; *[1]Vanderbilt University, Department of Cell and Developmental Biology, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Delft Center for Systems and Control, Delft University of Tech*

TP 273 **Isotope-Resolved Multimodal Mass Spectrometry Imaging Delineates Amyloid-β Plaque Associated Lipid Co-Aggregation Dynamics**; Lydia Fenson[1]; Junyue Ge[1]; Maciej Dulewicz[1]; Jeffrey Savas[2]; Jorg Hanrieder[1, 3]; *[1]University of Gothenburg, Gothenburg, Sweden; [2]Northwestern University, Evanston, IL; [3]University College London, London, United Kingdom*

TP 274 **Benchmarking High-Throughput Multiomic Imaging Mass Spectrometry for Spatial Proteomics of Cardiac Remodeling**; Deepika Rai[1]; Aleksandra Binek[1]; Pavithra Nedumaran[2]; Ajay Bharadwaj[1]; Jennifer E. Van Eyk[1]; Sarah J. Parker[1]; *[1]Cedars-Sinai Medical Center, Smidt Heart Institute, Los Angeles, CA; [2]Cedars-Sinai Medical Center, Biomedical Sciences, LOS ANGELES, CA*

TP 275 **Automated Tissue-Barcoding Platform for Spatial Proteomics and Phosphoproteomics**; Yuanwei Xu[1]; Hyeon-Cheol Park[2]; Jason Li[3]; Yuehan Liu[2]; Cheng-Yu Lee[2]; T. Mamie Lih[2]; Xingde Li[2]; Hui Zhang[2]; *[1]Johns Hopkins University, Baltimore, MD; [2]Johns hopkins university, baltimore, MD; [3]Automated Precision, Inc., Rockville, MD*

TP 276 **Development of Robust Spatial Multi-Plexed Proteomic and Peptidomic Techniques for Tissue Microarrays by Mass Spectrometry Imaging**; Jessica K Lukowski[1]; Young Ah Goo[1]; *[1]Washington University School of Medicine, St Louis, MO*

TP 277 **Distinct lipid profiles of hippocampal subregions and plaque microenvironments in an Alzheimer's Disease mouse model revealed by high-spatial resolution MALDI-imaging**; Nico Verbeeck[1]; Marko Zecevic[1]; Jayden C McKinnon[2]; Aimee Cox[3]; Manita Shakya[4]; Tialfi Bergamin De Castro[4]; Alice Ly[1]; Alison J Scott[4]; Shane R Ellis[2</sup;] *[1]Aspect Analytics, Genk, Belgium; [2]Molecular Horizons, School of Chemistry and Molecular Bioscience, University of Wollongong, Wollongong, Australia; [3]Molecular Horizons, School of Chemistry and Molecular Bioscience, Unive*

TP 278 **Agarose as an encasing medium for a microscale sampling LC-MS method for spatial multi-omics**; Ali Salam Waheed[1]; Vi Thanh Tran[1]; Caley Campkin[1]; Liang Li[1, 2]; *[1]University of Alberta, Edmonton, AB; [2]The Metabolomics Innovation Centre (TMIC), Edmonton, AB*

TP 279 **MALDI-TIMS Imaging and Spatial-pattern–guided iprm-PASEF Enable Confident Lipid Annotation and Spatial Multi-omics in p53 Mosaic Lung Tumors**; Shuo Qian[1, 2]; Ilze Olivi Gomes[1, 3]; Wenxue Li[1, 2]; Duo Zhang[1, 2]; Mandar Deepak Muzumdar[1, 3, 4, 5]; Yansheng Liu[1, 2, 4, 6]; *[1]Cancer Biology Institute, Yale University School of Medicine, Yale University, West Haven, CT; [2]Department of Pharmacology, Yale University School of Medicine, Yale University, New Haven, CT; [3]Department of Genetics, Yale*

TP 280 **Evaluation of Single Section Multimodal Spatial Omics: MALDI – Mass Spectrometry Imaging Lipidomics Combined with Spatial Transcriptomics**; Jaclyn B Dunne[1]; Khoi Chu[1]; Jessie Huang[1]; Nandita Joshi[1]; Elizabeth Bayne[2]; Alexey Makarov[2]; Marta Sans Escofet[1]; Alex Tamburino[1]; Iya Khalil[1]; Vane; *[1]Data, A.I., & Genome Sciences, MRL, Merck & Co., Inc., Cambridge, MA; [2]Discovery Analytical Research, Analytical R&D, MRL, Merck & Co., Inc., Boston, MA*

TP 281 **Ultrasensitive Spatial Phosphoproteomics of FFPE Tissue Enables Illumination of Early Recurrence–associated Signaling States in Lung Cancer**; Chang-Hong Jhong[1, 2]; Kwan Lee[1, 2]; Hsiang-En Hsu[2]; Jin-Yao Lai[3]; Min-Shu Hsieh[3]; Yu-Ju Chen[1, 2]; *[1]Department of Chemistry, National Taiwan University, Taipei, Taiwan; [2]Institute of Chemistry, Academia Sinica, Taipei, Taiwan; [3]Department of Pathology, National Taiwan University Hospital, Taipei, Taiwan*

TP 282 **Increased Sensitivity MALDI-IHC for Imaging High Value Low Abundance Targets Including the PD-L1 Immune Checkpoint Axis and Antibody-Drug Conjugates**; Andrew Yatsuhashi[1]; Gargey Yagnik[1]; Philip Carvalho[1]; Ziying Liu[1]; Leonardo G Dettori[1]; Weiyuan Hu[2]; Letao Ma[2]; Xinli Liu[2]; Kenneth J Rothschild[1, 3];; *[1]AmberGen, Billerica, MA; [2]Deptartment of Pharmacological and Pharmaceutical*

Sciences, University of Houston College of Pharmacy, Houston, TX; [3]Department of Physics and Photonics Center, Boston University, Boston, MA

TP 284 **Dietary Micro-Nanoplastics Exposure: A Multi-Omics Analysis of Murine Liver Homeostasis Powered by MALDI IMS**; Kes A Luchini[1]; Milad Mazloumi-Bakhshayesh[1]; Marcus A Garcia[1]; Ting Jiang[1]; Huayu Zheng[1]; Emilio S Rivera[2]; Changjian Feng[1]; Matthew J Campen[1]; *[1]University of New Mexico, Albuquerque, NM; [2]Los Alamos National Laboratory, Los Alamos, NM*

TP 285 **Construction of Spatial Proteomics Images (CSPI) with High Resolution Using Deep Learnin**; Gao Li[1, 2, 3]; Fan Linyuan[2, 3, 4]; Zhou Haichao[2, 3, 4]; Hou Guixue[3]; Liu Siqi[2, 3, 4]; *[1]School of Artificial Intelligence, University of Chinese Academy of Sciences, Beijing 100049, China., Beijing, China; [2]HIM-BGI Omics Center, Zhejiang Cancer Hospital, Hangzhou Institute of Medicine (HIM), Chinese Academy of Sciences*

TP 286 **Evaluating the utility of axial TOF MALDI Imaging–based multiplex MALDI-IHC in CNS tumor analysis**; Stefan Schmidt[1]; Rouzbeh Banan[2, 3]; Janina Oetjen[4]; Lars Gruber[1]; Corinna Henkel[4]; Nannan Tao[5]; Thomas Enzlein[1]; Henri Bogumil[2, 3]; Stefania-Alexandra Iakab<sup; *[1]CeMOS Research and Transfer Center, Mass Spectrometry and Optical Spectroscopy, Technische Hochschule Mannheim, Mannheim, Germany; [2]Department of Neuropathology, Institute of Pathology, University Hospital Heidelberg, Heidelberg, Ge*

TP 287 **Fully Automated High-Throughput Spatial Proteomics Integrated with AI-Guided Segmentation Reveal Pancreatic Tumor Heterogeneity**; Ruijun Tian; *Southern University of Science and Technology, Shenzhen, China*

TP 288 **Muti-modal Imaging: Utilizing high-resolution DESI followed by MALDI-IHC to Analyze Clear Cell Renal Cell Carcinoma Biopsies**; Mark Towers[1]; Greice M Zickuhr[2]; Joanne Ballantyne[1]; Hwa Um[2]; Lisa Towers[1]; David J Harrison[2]; Nicholas Ellor[3]; Alison Dickson[2]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]University of St Andrews, St Andrews, United Kingdom; [3]Waters Corporation, Milford, MA*

TP 289 **Method development kit for the Orbitrap Astral MS family**; Max Hoek[1]; Arne Kreutzmann[1]; Kyle Le Huray[1]; Sophia Steigerwald[1]; Hamish Stewart[1]; Johannes Petzoldt[1]; Eugen Damoc[1]; Christian Hock[1]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

TP 290 **Automated Integration of a Metabolomics Repository into Mass++ for Data Retrieval and Visualization**; Satoshi Tanaka[1, 2]; Masaki Murase[2]; Masaki Kato[2, 3, 4]; Hiroyuki Yamamoto[2, 5]; Masaaki Matsubara[2]; Yushi Takahashi[2, 6]; Tsuyoshi Tabata[2, 7]; Maiko Kusano[2, 8]; S; *[1]Trans-IT Co., Ltd., Mibu-machi, Tochigi Pref., Japan; [2]Mass++ Users Group, Kyoto, Japan; [3]Data Knowledge Organization Unit, RIKEN Information R&D and Strategy Headquarters, RIKEN, Wako, Japan; [4]Medical Research*

TP 291 **IMFrag: A Tool to Recognize In-Source Fragmentation in Ion Mobility-Enabled Data-Independent Acquisition Workflows**; Ryan Nguyen[1]; Anvitaa Anandkumar[1]; Jennifer Liem[1]; Yvonne S. Lin[1]; Libin Xu[1]; *[1]University of Washington, Seattle, WA*

TP 292 **proteoDA version 2.0: a reproducible R framework for quantitative proteomics with integrated data preprocessing, statistical analysis, visualization, and automated reporting**; Zuo-Fei Yuan[1]; Yingxue Fu[1]; Long Wu[1]; Vishwajeeth Pagala[1]; Anthony A. High[1]; Stephanie Byrum[1]; *[1]St Jude Children's Research Hospital, Memphis, TN*

TP 293 **Implementation of the DIA-NN Workflow in Proteome Discoverer for large cohort DIA proteomics analysis**; David Horn[1]; Philip Loziuk[1]; Hans Grensemann[2]; Pedro Navarro[2]; Kai Fritzemeier[2]; Carmen Paschke[2]; Christoph Henrich[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

TP 294 **Octopus: Web Application for Sample Plate Design in Mass Spectrometry Workflows**; Vagisha Sharma[1]; Gennifer Merrihew[1]; Christine Wu[1]; Michael Riffle[1]; Michael J. MacCoss[1]; *[1]University of Washington, Seattle, WA*

TP 295 **Agentic data science: AI-based, natural-language analysis of proteomics results**; Markus Schneider[1]; Daniel P Zolg[1]; Michelle Berger[1]; Alexander Hogrebe[2]; Siegfried Gessulat[2]; Tobias Schmidt[1]; Martin Frejno[1]; *[1]MSAID, Garching b.Muenchen, Germany; [2]MSAID, Berlin, Germany*

TP 296 **TagDB: a platform for large-scale analysis of candidate mass tags for peptide identification and proteomics multiplexing**; Mark Adamo[1]; Michael Agius[1]; David Barnes-Seeman[2]; Daniel Honeycutt[1]; Sarah Sipe[1]; Joshua Abbott[1]; Harrison Specht[1]; Nikolai Slavov[1, 3]; *[1]Parallel Squared Technology Institute, Watertown, MA; [2]CreaGen Biosciences, Woburn, MA; [3]Northeastern University, Boston, MA*

TP 297 **A Comprehensive Software Ecosystem for End-to-End Monoclonal Antibody and Antibody–Drug Conjugate Data Acquisition, Analysis, and Reporting**; Ruoji Luo[1]; Lichen Xiu[1]; Guannan Li[1]; Jordy Hsiao[1]; Linfeng Wu[1]; David Wong[1]; *[1]Agilent Technologies, Inc., Santa Clara, CA*

TP 298 **Pro-visualize: A Unified Platform for Longitudinal QC, Targeted Assay Validation, and Interactive Cohort Visualization**; Ajay Bharadwaj[1]; Niveda Sundararaman[1]; Jihyeon Lee[1]; Manasa Vegesna[1]; Qin Fu[1]; Christopher Murray[1]; Jennifer E. Van Eyk[1]; *[1]Cedars-Sinai Medical Center, Smidt Heart Institute, Los Angeles, CA*

TP 299 **Automated Data-Driven Optimization of MRM Transitions and Collision Energies in LC–MS/MS**; Behrooz Zekavat[1]; HUY BUI[1]; PETER WEIDNER[1]; *[1]Agilent Technologies, Santa Clara, CA*

TP 300 **rtmsEcho: An R Toolkit for Extracting, Analyzing, and Visualizing Acoustic Ejection Mass Spectrometry Data**; Mary Ashley Rimmer[1]; Nathaniel Twarog[2]; Tharindu Ranathunge[2]; Jingheng Wang[2]; Yong Li[2]; Taosheng Chen[2]; Anang Shelat[2]; Lei Yang[2]; *[1]St. Jude Children's Research Hospital, Memphis, TN; [2]St Jude Children's Research Hospital, Memphis, TN*

TP 301 **Single Dried Blood Spot Optimization for LC-MS/MS Multiomics**; Esabella R. Powers[1]; Lancia N.F. Darville-Bowleg[2]; John M. Koomen[3]; Timothy J. Garrett[1, 4]; *[1]Department of Chemistry, University of Florida, Gainesville, FL; [2]Moffitt Cancer Center, Tampa, FL; [3]Proteomics and Metabolomics Core, Moffitt Cancer Center, Tampa, FL; [4]Department of Pathology, Immunology and*

TP 302 **Leveraging Publicly Accessible Databases to Enhance Proteogenomic Variant Discovery**; Nithesh Perumal[1]; Neaam Dawood[2]; Heta Desai[2]; Flowreen Shikwana[3]; Alexandra C Turmon[2]; Keriann M. Backus[2]; *[1]University of California Los Angeles, Los Angeles, CA; [2]UCLA, Los Angeles, CA; [3]UCLA, LOS ANGELES, CA*

TP 303 **Biomarker Discovery via Integrative Multi-omics for Children exposed to Humidifier Disinfectant**; Hyunsoo Kim[1]; Jaeho Ji[1]; Ahrum Son[2]; Soo-Jong Hong[3]; *[1]Chungnam National University, Daejeon, South Korea; [2]University of Ulsan, Ulsan, South Korea; [3]National Medical Center, Seoul, South Korea*

TP 304 **PG-DIA: An end-to-end proteogenomic framework enabling sensitive and reproducible novel peptide discovery using data-independent acquisition**; Wenrong Chen[1, 2]; Matthew S. Glover[3]; Shreya Ahuja[3]; Shannon Marshall[3]; Matthew V. Holt[1]; Wen Yu[4]; Jixin Wang[5]; Wenyan Zhong[6]; Bing Zhang[1, 2]; *[1]Lester and Sue Smith Breast Center, Baylor College of Medicine, Houston, TX; [2]Department of Molecular and Human Genetics, Baylor College of Medicine, Houston, TX; [3]Discovery Sciences, BioPharmaceuticals R&D, AstraZeneca,*

TP 305 **From Proteins to PTMs: Unified Proteomics Analysis with Mass Dynamics 3.0**; Anna Quaglieri[1]; Aaron Triantafyllidis[1]; Andrew Ian Webb[1]; Giuseppe Infusini[1]; *[1]Mass Dynamics, Melbourne, Australia*

TP 306 **Employing a multi-omics approach to characterize cold-temperature adaptations in a methylotrophic yeast, Pichia (Komagataella phaffii)**; Trenton J. Winters[1]; Regina M Edgington[1]; Damien B Wilburn[1, 2]; *[1]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH; [2]The Ohio State Center for RNA Biology, Columbus, OH*

TP 307 **Variant-Resolved Long-Read Proteogenomics for Isoform and Mutation Detection**; Gautam Ghosh[1]; Yoon Jae-Guen[2]; Ariana Shannon[1]; Hwahyung Lee[2]; Parvinder Hothi[2]; Charles Cobbs[2]; Brian Searle[1]; *[1]Mayo Clinic, Rochester, MN; [2]Swedish Neuroscience Institute, Seattle, WA*

TP 308 **PineBioML: A Pipeline-Oriented Machine Learning Platform for Multi-Omics Data Analysis**; Kuang-Yi Chang[1]; Shuo-Fu Chen[2]; I-Chun Chi[1]; Hui-Yin Chang[1]; [1]*National Central University, Taoyuan City, Taiwan;* [2]*Department of Heavy Particles & Radiation Oncology, Taipei Veterans General Hospital, Taipei, Taiwan*

TP 309 **Multi-omics Rank-Based Learning (MORBL): An efficient high-throughput machine learning algorithm for multi-omics data with small sample sizes and missing information**; Lulu Song[1, 2]; Hamid Khoshfekr Rudsari[2]; Johannes Fahrmann[2]; Hiroyuki Katayama[2]; Yining Cai[2]; Ranran Wu[2]; James P. Long[2]; Kim-Anh Do[2]; Sam Hanash[2]; E; [1]*University of Texas Health Science Center at Houston, Houston, TX;* [2]*MD Anderson Cancer Center, Houston, TX*

TP 310 **From Big Data to Biology: Integrative Multiomics Analysis**; Khatereh Motamedchaboki[1]; Dave Abramowitz Abramowitz[2]; Mark R Ressler[1]; Eric M. Wilson M Wilson[1]; Brad Larson[1]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*ThermoFisher Scientific, San Jose, CA*

TP 311 **Multiomic Analysis of FFPE Tissue Reveals Concurrent Metabolic, Transcriptomic, and Proteomic Shifts in Colorectal Cancer**; Caitlin Kelly[1]; Ashima Mehta[1]; Ethan Stancliffe[1]; Sharla Friend[1]; Douglas V. Guzior[1]; Monil Gandhi[1]; Sandeep Acharya[1]; Adam Richardson[1]; Tom Cohen[1];; [1]*Panome Bio, Saint Louis, MO;* [2]*Washington University in St. Louis, Saint Louis, MO*

TP 312 **A Multimodal AI Workflow for Automated KEGG Pathway Analysis and Interpretation of Large-Scale Omics Data**; Manhoi Hur[1]; Wilhelmina Van De Ven[1]; Katayoon Dehesh[1]; [1]*The University of California, Riverside, Riverside, CA*

TP 313 **SimpliFi: intuitive multi-omics understanding of complex data series using mutual information**; Jim Palmeri[1]; John Wilson[1]; [1]*ProtiFi LLC, Fairport, NY*

TP 314 **SysQuan: Towards System-Wide Absolute Protein Quantification through a Multi-Tissue Targeted Assay Database**; Peter Kubiniok[1]; Timon Geib[2]; Vincent R. Richard[2]; Yassene Mohammed[3]; Elodie Longerot[2]; Eileen Tudorica[2]; Victor Spicer[4]; Robert Popp[5]; René P. Zahedi[4</su;] [1]*Quantivum Inc., montreal, QC;* [2]*Lady Davis Institute, Montreal, QC;* [3]*Leiden University Medical Center, Leiden, Netherlands;* [4]*Department of Biochemistry and Medical Genetics, University of Manitoba, Winnipeg, MB,*

TP 315 **PROTEOBASE: a free, sustainable public proteomics repository enabling flexible metadata capture and data reuse**; Kyla Teplitz[1]; Yevhen Panko[1]; Dmitry Sergeev[1]; Nikolay Galanov[1]; Brian Connolly[2]; Michael J. MacCoss[2]; Peter Askovich[1]; [1]*Europa Dx, Redmond, WA;* [2]*University of Washington, Seattle, WA*

TP 316 **PyC2MC: A Workflow-Driven Framework for FTMS Data Processing and Molecular Formula Attribution**; Maxime SUEUR[1, 2, 3]; Germain Salvato Vallverdu[2, 4]; Julien F. Maillard[2, 3]; Christopher Rüger[2, 5]; Alvarez J. Tello-Rodriguez[2, 6]; Ryan P. Rodgers[2, 7]; Martha L. Aguilera[2, 7</s;] [1]*Normandie Univ, UNIROUEN, INSA Rouen, CNRS, CARMeN, Mont Saint Aignan, France;* [2]*International Joint Laboratory, iC2MC: Complex Matrices Molecular Characterization, Harfleur, France;* [3]*TotalEnergies Research and Technology*

TP 317 **Transfer Learned Spectral Libraries Improve DIA Searches in FragPipe**; Kevin L Yang[1]; Kai Li[1]; Fengchao Yu[1]; Alexey I Nesvizhskii[1]; [1]*University of Michigan, Ann Arbor, MI*

TP 318 **MRMGlycoInsightR: Automated Signal Noise Separation, Quantification, and Clinical Risk Scoring for MRM Glycosylation via Biologically Informed Machine Learning**; San-Yuan Wang[1, 2, 3]; I-Lin Tsai[1, 2, 4, 5, 6, 7, 8]; [1]*Master Program in Clinical Genomics and Proteomics, Taipei Medical University, Taipei, Taiwan;* [2]*Department of Pharmaceutical Sciences, Taipei Medical University, Taipei, Taiwan;* [3]*Ph.D. Program in Drug Discovery and Develo*

TP 319 **mztabm2cytoscape: Pathway Mapping and Visualization of Metabolomics Data**; Kozo Nishida[1, 2]; Takaki Oka[2]; Mikiko Takahashi[3]; Yuki Matsuzawa[2]; Hiroshi Tsugawa[4]; [1]*RIKEN Center for Biosystems Dynamics Research (BDR), Kobe, Japan;* [2]*Tokyo University of Agriculture and Technology, Koganei, Japan;* [3]*RIKEN Center for Sustainable Resource Science, Yokohama-shi, Kanagawa, Japan;* [4</sup]

TP 320 **Optimized RUV-III-C-based Workflow for Reliable Batch Effect Correction in Complex Proteomics Datasets**; Shichen Shen[1]; Anqi Tu[1]; Yeoun Jin Kim[1]; Andrew Chambers[1]; [1]*AstraZeneca, Gaithersburg, MD*

TP 321 **JUMPdia: an automated workflow for DIA-MS data processing**; Zuo-Fei Yuan[1]; Ya Huang[1]; Jay M. Yarbro[1]; Yingxue Fu[1]; Vishwajeeth Pagala[1]; Zhen Wang[1]; Long Wu[1]; Xusheng Wang[2]; Anthony A. High[1]; Junmin Peng[1<]; [1]*St. Jude Children's Research Hospital, Memphis, TN;* [2]*University of Tennessee Health Science Center, Memphis, TN*

TP 322 **Ionization efficiency prediction for atmospheric pressure chemical ionization coupling with gas chromatography and high-resolution mass spectrometry for environmental analysis**; Wei-Chieh Wang[1]; Iris Hättestrand[1]; Xiaodi Shi[2]; Anneli Kruve[1, 2]; [1]*Department of Chemistry, Stockholm University, Stockholm, Sweden;* [2]*Department of Environmental Science, Stockholm University, Stockholm, Sweden*

TP 323 **mzPeak: An extensible open format for raw data storage**; Samuel P Wein[1, 2]; James Shofstahl[3]; Ralf Gabriels[4, 5]; Tim Van Den Bossche[5]; Joshua Charkow[6, 7]; Hannes Röst[6, 7]; Timo Sachsenberg[2, 8, 9]; Oliver Kohlbacher[2, 8, 9,]; [1]*University of Tübingen, Tübingen, Germany;* [2]*OpenMS Inc, Erie, PA;* [3]*Thermo Fisher Scientific, San Jose, CA;* [4]*VIB - UGent Center for Medical Biotechnology, Gent, Belgium;* [5]*Department of Biomolecular Me*

TP 324 **Perseus 3.0: a flexible and re-executable computational platform enabling advanced visualization for comprehensive (prote)omics data analysis**; Helen Hohenthanner[1]; Walter Viegener[1]; Pelagia Kyriakidou[1]; Juergen Cox[1]; Jinqiu Xiao[1]; [1]*Max Planck Institute of Biochemistry, Martinsried, Germany*

TP 325 **Punc'data: Open-Source Software for Ion Formula Assignment and Interactive Visualization of Complex Mass spectra**; Théo Voellinger[1]; Sébastien Schramm[1]; Pierre Pacholski[1]; Nathan Traullé[1]; Frédéric Aubriet[1]; [1]*Université de Lorraine, LCP-A2MC, METZ, France*

TP 326 **Enabling In Silico MS/MS Fragmentation Through a Scalable Web Platform**; Richard Lee[1]; Austin Blue[1]; Ryan Andrews[1]; Anne Marie Smith[1]; Sofya Chudova[1]; Artyom Petrovskiy[1]; Vitaly Lashin[1]; Rostislav Pol[1]; [1]*ACD/Labs, Toronto, ON*

TP 327 **An integrated platform for mass spectrometry data utilization in AI-guided drug discovery**; Anastasiya V. Prymolenna[1]; Sebastian J Paez[1]; Lillian T. Tatka[1]; Kyle Siebenthall[1]; Andrea Gutierrez[1]; Daniele Canzani[1]; Julia Robbins[1]; Evan E. Hubbard[1]; Marga; [1]*Talus Bioscience, Seattle, WA*

TP 328 **A High-Throughput Semiautomated Workflow for the Construction of In-House LC-MS Standard Libraries**; Samyukta Sah[1]; Mila Kocic[1]; Michelle Bramlett[1]; Maria Cardelino[1]; Jared Bailey[1]; Ronald Smith[1]; Douglas I. Walker[1]; [1]*Emory University, Atlanta, GA*

TP 329 **MSPMS: Mass Spectrometer Performance Monitoring System**; Steven C Pomerantz[1]; Roland M. Miller[1]; [1]*JOHNSON AND JOHNSON, Spring House, PA*

TP 330 **DE-LIMP a sophisticated and functional AI integrated proteomics platform vibe coded in 1 week by 1 person**; Brett Phinney; *Univeristy of CA, Davis, Davis, CA*

TP 331 **Expanding MSstatsShiny to Support Large Scale Processing of Proteomic and Chemoproteomic Experiments**; Anthony Wu[1]; Rudhik Shah[1]; Sarah Szvetecz[1]; Devon Kohler[1]; Olga Vitek[1]; [1]*Northeastern University, Boston, MA*

TP 332 **KPOP: Korea ProteOme rePository for Accelerating Proteomics Data Sharing**; Seungjin Na[1]; Jingi Bae[2]; Shinyeong Ju[3]; Heeyoun Hwang[1]; Hokeun Kim[2]; Cheolju Lee[4]; Jin Young Kim[1]; Sang-Won Lee[2]; Eunok Paek[5]; [1]*Korea Basic Science Institute, Cheongju, South Korea;* [2]*Korea University, Seoul, South Korea;* [3]*Korea Institute of Science and Technology, Seoul, South Korea;* [4]*Korea Institute of Science and Technology (KIST), Se*

TP 333 **Towards mzTab-M 2.1 - Evolving the HUPO-PSI standard format and ecosystem for reporting of small molecule mass spectrometry results**; Nils Hoffmann[1]; Philippine Louail[2]; Bo Burla[3]; Yasin El Abiead[4]; Eoin Fahy[5]; Franck Giacomoni[6]; Nicolas Guilhot[6]; Jürgen Hartler[7]; Steffen Heuckeroth[8</sup;] [1]*Forschungszentrum Jülich GmbH, Bielefeld, Germany;* [2]*Institute for Biomedicine, Eurac Research,*

Bolzano, Italy, Bolzano, Italy; [3]Singapore Lipidomics Incubator, Life Sciences Institute, National University of Singapore, Si

TP 334 **Integer property of ion detection and its implication for quantitative mass spectrometry analysis**; Haoyue Zheng[1]; Xiao Chen[1]; Xinwei Liu[1]; Jiexun Bu[2]; Xiaoyu Zhou[1]; Wenpeng Zhang[1]; Zheng Ouyang[1]; *[1]Tsinghua University, Beijing, China; [2]PURSPEC Technology (Beijing) Ltd., Beijing, China*

TP 335 **A Robust, User-Friendly Ion Source and Cartridge Workflow for Consistent, High-Quality LC–MS Data in Shared Facilities**; Casey A. Powers[1]; Fang Liu[1]; Katherine Walker[2]; Daniel Jackson[2]; Ellen Casavant[2]; Garvey McKenzie[1]; Ryan D. Leib[1]; *[1]Stanford University Mass Spectrometry, Palo Alto, CA; [2]Thermo Fisher Scientific, San Jose, CA*

TP 336 **Differentiation of Isomeric Anilines and Pyridines by Targeted Molecular Rotational Resonance Spectroscopy and Mass Spectrometry**; Hendrik M. Ma[1]; David S. Toba-Veloza[1]; Grace Greene[1]; Ruhaan Bajpai[1]; Kawthar Z. Alzarieni[2]; Voislav Blagojevic[3]; Justin L. Neill[3]; Hilkka I. Kenttämaa[1]; *[1]Purdue University, Department of Chemistry, West Lafayette, IN; [2]Jordan University of Science and Technology, Irbid, Jordan; [3]BrightSpec Inc., Charlottesville, VA*

TP 337 **Hybrid FPGA–GPU Architecture for Real-Time Pulse Processing in High-Speed Mass Spectrometry**; Måns Persson[1]; Jan-Erik Eklund[1]; Joe Sharp[1]; *[1]Teledyne Signal Processing Devices Sweden AB, Linkoping, Sweden*

TP 338 **High-resolution cryoEM structure determination of soluble proteins after soft-landing ESIBD**; Lukas Eriksson[1, 2]; Tim K Esser[1, 3]; Jingjin Fan[1, 2]; Justin L.P. Benesch[1, 2]; Carol V Robinson[1, 2]; Jani R Bolla[1, 4]; Lindsey Baker[1, 5]; Stephan Rauschenbach[1, 2</su;] *[1]Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom; [2]Department of Chemistry, University of Oxford, Oxford, United Kingdom; [3]ThermoFisher Scientific, Eindhoven, Netherlands; [4</su]*

TP 339 **Optimizing Access to Higher-Order Mathieu Space Stability Zones on a Digitally Driven QQQ**; Elizabeth Groetsema[1]; Gordon A. Anderson[2]; Shane Tichy[3]; Adam P Huntley[1]; Peter T.A. Reilly[1]; Brian H Clowers[1]; *[1]Washington State University, Pullman, WA; [2]GAA Custom Electronics, Kennewick, WA; [3]Agilent Technologies, Santa Clara, CA*

TP 340 **High-Accuracy Field and Trajectory Calculations in SIMION Using Bicubic Interpolation with Fractional Surface Constraints**; Robert Jackson; *Jackson Scientific Design Services,LLC, Wilton, NH*

TP 341 **Mass Starkometry: a new tool to separate and detect isomers and conformers of polar molecules**; Jibin Sudha Sobhanakumar[1]; Citlaly Landin-Bermudez[2]; Liam Duffy[2]; *[1]University of North Caroina at Greensboro, Greensboro, NC; [2]University of North Carolina Greensboro, Greensboro, NC*

TP 342 **Introduction of cryogenic infrared ion spectroscopy (CIRIS) into a commercial time-of-flight mass spectrometer**; Stephan Warnke[1]; Ahmed Ben Faleh[1]; Ali Abikhodr[1]; Thomas R. Rizzo[1, 2]; Shane Tichy[3]; *[1]Isospec Analytics SA, Renens, Switzerland; [2]EPFL, Lausanne, Switzerland; [3]Agilent Technologies, Santa Clara, CA*

TP 343 **Tandem rotating wall mass analyzer (tRWMA) for mass selection of ultrahigh-m/zions**; Masudur R Rahat[1]; Michael F Espenship[1]; Julia Laskin[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

TP 344 **High-Performance Data Acquisition Architecture for Modern Mass Spectrometry**; Jan-Erik Eklund[1]; Måns Persson[1]; Joe Sharp[1]; *[1]Teledyne Signal Processing Devices Sweden AB, Linkoping, Sweden*

TP 345 **High-Resolution Excitation of Trapped Ions for Enhanced Isobaric and Isomeric Analysis**; Shuai Li[1]; Zhuofan Wang[1]; Liwen Liang[1]; Xiaoyu Zhou[2]; Zheng Ouyang[1]; *[1]State Key Laboratory of Precision Measurement Technology and Instruments, Department of Precision Instrument, Tsinghua University, Beijing, China; [2]School of Biomedical Engineering, Hainan University, Hainan 572024, China, Haikou, C*

TP 346 **Parameter optimization for high-efficiency ion extraction in a quadrupole time-of-flight mass spectrometer**; Kang Guo[1]; Xiaoqiang Zhang[1]; Jiankui Liu[1]; Xinfeng Zhou[1]; Wenjian Sun[1]; *[1]Shimadzu Research Laboratory (Shanghai) Co.Ltd., Shanghai, China*

TP 347 **Nanobubbles with Desorption Electrospray Ionization Mass Spectrometry**; George Joseph[1]; Bincy Binny[1]; Andre R. Venter[1]; [1]*Western Michigan University, Kalamazoo, MI*

TP 348 **30 nm Diameter Nanopipette nESI Emitters Significantly Enhances Desalting and Sensitivity for Native Mass Spectrometry of Large Proteins**; Emily J Byrd[1, 2]; Zoe J Heidersbach[3]; Eileen Jacqueline Olivares[3]; Luchen Wuyang[3]; Matthew Kensil[3]; Paolo Actis[1]; Frank Sobott[1]; Antonio N Calabrese[1]; Rachel R; [1]*University of Leeds, Leeds, United Kingdom;* [2]*UCLA, Los Angeles, CA;* [3]*UCLA, LOS ANGELES, CA*

TP 349 **Next-generation Triboelectric Nanogenerator-Powered Laser Ablation Nanoelectrospray Ionization (TENG-LAESI) Mass Spectrometry Imaging Ion Source**; Joseph Corstvet[1]; David Lewis[1]; Dmitry Leontyev[2]; Xin Ma[3]; Rebecca Arnold[4]; John A. Petros[4]; Facundo M. Fernandez[1]; [1]*Georgia Institute of Technology, Atlanta, GA;* [2]*AbbVie Inc., Worcester, MA;* [3]*University of Virginia, Charlottesville, VA;* [4]*Emory University, Atlanta, GA*

TP 350 **Comprehensive Thermal Analysis with Ion Mobility Spectrometry and High-Resolution Mass Spectrometry for Polymer and Microplastic Characterization**; Christopher Paul Rüger[1, 2]; Fabian Etscheidt[1]; Philip Jürß[1]; Helly Johanna Hansen[1]; Sven Ehlert[3]; Carlos Afonso[2, 4]; Pierre Giusti[2, 5]; Arnd Ingendoh[6]; Yann Heb; [1]*University of Rostock, Rostock, Germany;* [2]*International Joint Laboratory for Complex Matrices Molecular Characterization (iC2MC), Harfleur, France;* [3]*Photonion GmbH, Schwerin, Germany;* [4]*University of Rouen Norma*

TP 351 **Integration of an LDTD Ion Source to a QTOF instrument inlet: geometry, gas and ion simulations and results**; Jonathan Rochon[1]; Pierre Picard[1]; Serge Auger[1]; Sarah Demers[1]; Jean Lacoursiere[1]; Atsuhiko Toyama[2]; [1]*Phytronix Technologies Inc., Québec, QC;* [2]*Shimadzu R&D Center Boston, Newton, MA*

TP 352 **Investigation of the fluid dynamics in nanospray desorption electrospray ionisation (nano-DESI) sampling probes**; Jack R Roberts[1]; Helen J Cooper[1, 2]; [1]*Rosalind Franklin Institute, Didcot, United Kingdom;* [2]*University of Birmingham, Birmingham, United Kingdom*

TP 353 **Photoionization Mass Spectrometry for Real-Time Process Control Enabled by Multi-Source Ionization, Hyper-Fast GC, and VUV F_2-Laser SPI**; Sven Ehlert[1]; Jan Heide[1]; Kevin Schnepel[2]; Fabian Carl[2]; Hendryk Czech[2]; Andreas Walte[1]; Ralf Zimmermann[2]; [1]*Photonion GmbH, Schwerin, Germany;* [2]*University of Rostock, Rostock, Germany*

TP 354 **Indirect Gas Analysis-Desorption Electrospray Ionization Mass Spectrometry for Simultaneous Detection of Trace Volatile Compounds in Sealed Systems**; Nathan Robert Bays[1]; David Schafer[1]; Shohel Mohammad[1]; Trinity Griffus[1, 2]; Brendan Nation[1]; Ryan Davis[1]; [1]*Sandia National Laboratories, Albuquerque, NM;* [2]*University of New Mexico, Albuquerque, NM*

TP 355 **Automated Electrospray Emitter Positioning Improves Ion Transmission and Quantitative Performance**; Brian Hood[1]; Katherine Walker[2]; Ellen Casavant[2]; Joshua Silveira[2]; Eloy Wouters[2]; Alec Valenta[2]; Runsheng Zheng[2]; Romain Huguet[2]; Kelly Conrads[1]; Nic; [1]*Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc., Bethesda, MD;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*Joint Pathology Center, Silver Spring, MD;* [4]*Uniformed Services University, Bet*

TP 356 **A low-power and accessible plasma reactor with chemical ionization for rapid quantitation of fluorochemicals**; Frenio A Redeker[1]; Fabian Simon[1]; Kaveh Jorabchi[1]; [1]*Georgetown University, Washington, DC*

TP 357 **Active Aspiration nano-DESI Mass Spectrometry for Low-Volume Direct Sampling of Biological Samples**; Jorge A Salazar[1]; James F. Davies[1]; Pei Su[1]; [1]*University of California, Riverside, Riverside, CA*

TP 358 **Spatially Resolved Phytochemical Mass Spectrometry via Ambient Infrared Laser Ablation Solvent Extraction**; Alexis Waite[1]; Liam M. McEvoy[1]; Jiahao Wan[1]; Hans Bechtel[1]; Evan R. Williams[1, 2]; Hoi-Ying Holman[1]; [1]*Lawrence Berkeley National Laboratory, Berkeley, CA;* [2]*University of California, Berkeley, Berkeley, CA*

TP 359 **Comparing External and Internal Capillary Flow Through DBD Ionization**; Jan-Christoph Wolf[1]; Atsuhiko Toyama[2]; Ciara Conway[1, 3]; *[1]Plasmion GmbH, Augsburg, Germany; [2]Shimadzu R&D Center Boston, Newton, MA; [3]Technical University of Munich, Freising, Germany*

TP 360 **Thermal Jet Desorption DBDI-MS for Fast and Flexible Whole Object Ambient Analysis**; Ciara Conway[1, 2]; Markus Weber[1, 3]; Jan-Christoph Wolf[1]; Thomas Wolf[1]; *[1]Plasmion, Augsburg, Germany; [2]Technical Universitiy of Munich, Freising, Germany; [3]Technical University of Munich, Freising, Germany*

TP 361 **Recovery and Characterization of Recombinant Proteins by DESI-MS with Magnetic Ni-NTA Beads**; Christopher Taylor[1]; Andre R. Venter[1]; *[1]Western Michigan University, Kalamazoo, MI*

TP 362 **Aroma-Resolved Fingerprint Screening Enabled by SPME–SICRIT Mass Spectrometry**; Zhenxing Li[1]; Wenhao Yu[1]; Bin Li[2]; Yachang Xu[1]; Xiaokun Duan[3]; Shujie Zou[3]; Echo W. Jia[3]; Weimin Ouyang[2]; Charles C. Liu[3]; Yu-An Sun[1]; *[1]Zhengzhou University of Light Industry, Zhengzhou, China; [2]Beijing Lumiere Tech Ltd, Beijing, China; [3]ASPEC Technologies Limited, Beijing, China*

TP 363 **Enhancing intact proteoform imaging in tissues using high-throughput multisegmented capillary electrophoresis**; Tommy Zhang[1]; Zhitao Zhao[2]; Si Wu[2]; Julia Laskin[1]; *[1]Purdue Univeristy, West Lafayette, IN; [2]University of Alabama, Tuscaloosa, AL*

TP 364 **Autonomous Benzene Cation VUV Chemical Ionization for Economical Atmospheric Trace Gas Monitoring using an RGA-based Mass Spectrometer**; Kevin A. Wokosin[1]; Abigail LePinske[2]; Shondiin Lawson[2]; Steven J. Kregel[2]; Timothy H. Bertram[1]; *[1]UW-Madison Department of Chemistry, Madison, WI; [2]Bradley University, Peoria, IL*

TP 365 **Targeted Qualitative Screening of Small Molecules Using DESI–Triple Quadrupole MRM Mass Spectrometry**; Aideen Hession[1]; Alexandra Beard[1]; *[1]Corteva Agriscience, Johnston, IA*

TP 366 **Coupling Ionization via Desorption by Impulsive Vibrational Excitation (i-DIVE) with an Orbitrap Ascend Mass Spectrometer for Native Top-Down Proteomic Analyses**; Semah Keissieh[1]; Khaled Madhoun[1, 2]; Pei Su[1]; *[1]University of California, Riverside, Riverside, CA; [2]University of Toronto, Toronto, ON*

TP 367 **Direct Analysis of Human-Exhaled Gas Phase Ions: Investigating Respiratory Transport and Loss of Ionized E-Cigarette Emissions via Mass Spectrometry**; Nicole C Auvil[1]; Mark E Bier[1]; *[1]Carnegie Mellon University, Pittsburgh, PA*

TP 368 **PFAS Effects on Serum Albumin Structure and Stability Measured Via Collision-Induced Unfolding**; EBUNOLUWA O KUKOYI[1]; Kenneth W Lee[2]; *[1]BRIGHAM YOUNG UNIVERSITY, PROVO, UT; [2]Brigham Young University, Provo, UT*

TP 369 **Modulation of drift gas composition for higher ion capacity in a U-shaped Mobility Analyzer**; Yiming Wang[1]; Yongkai Cai[1]; Yuanlong Wang[1]; Yuanyuan Huang[1]; Xiaoqiang Zhang[1]; Wenjian Sun[1]; *[1]Shimadzu Research Laboratory (Shanghai) Co.Ltd., Shanghai, China*

TP 370 **Assessing the Trapping Capacity of an Enlarged SLIM Ion Trap Design Expanding SLIM Trap Capacity for Improved Performance**; Leonard C Rorrer, III[1]; Daniel DeBord[1]; Liulin Deng[1]; *[1]MOBILion Systems, Chadds Ford, PA*

TP 371 **Diffusion Autocorrecting Waveforms in SLIM Provide Order-of-Magnitude Resolution Gains Predicted by Analytical Transport Modeling**; Xi Chen[1]; Mohsen Latif[2]; Wiljones Assonfack Djoutsop[3]; Farah Mubas-Sirah[3]; Carlos Larriba-Andaluz[3]; *[1]Johnson Controls, New Freedom, PA; [2]Teledyne FLIR Detection, West Lafayette, IN; [3]Purdue University, west lafayette, IN*

TP 372 **IMoS 2: General Boltzmann Solver for Arbitrary-Field Ion Mobility, Velocity Distributions, and Energy transfer in Gas Mixtures**; Carlos Larriba Andaluz; *Purdue University, Indianapolis, IN*

TP 373 **Quantifying Ion Heating Under RF Fields Using IMoS 2.0: Separating RF and High-Field thermal energy Contributions**; Wiljones A Djoutsop[1]; Trinav Singh[1]; Brian Herbert Clowers[2]; Carlos Larriba-Andaluz[1]; *[1]Purdue University, West lafayette, IN; [2]Washington State University, Pullman, WA*

TP 374 **Development of a Modular SLIM Platform for Extendable Path Lengths and Agile IMSn**; Nathaniel Morgan[1]; Brian H Clowers[1]; *[1]Washington State University, Pullman, WA*

TP 375 **SimIonSPA: Collision-Resolved Modeling of Protein Ion Temperatures in a SLIM model system**; Ken Newton[1]; Austin W Green[1]; Matthew F Bush[2]; James S. Prell[1]; *[1]University of Oregon, Eugene, OR; [2]University of Washington, Seattle, Seattle, WA*

TP 376 **Using Protonation Isomer Distributions to Elucidate Solvent and Source Effects on Electrospray Ionization**; Easton Cox[1]; Kenneth W. Lee[2]; *[1]Brigham Young University, Provo, UT; [2]Brigham Young Uniersity, Provo, UT*

TP 377 **COMPARATIVE EVALUATION OF MASON-SCHAMP COLLISION CROSS SECTIONS (CCS) OF ION MOBILITY SPECTROMETRY (IMS) WITH QUANTUM MECHANICAL DENSITY FUNCTIONAL THEORY**; Glenn E. Spangler; *Technispan LLC, Lutherville, MD*

TP 378 **Collision Induced Unfolding Differentiates Biosimilars Based on Sialic Acid Content**; Addison E. Bergman[1]; Nicole Rivera Fuentes[1]; Trey Theobald[1]; Valentina Rangel-Angarita[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

TP 379 **Enhancing Gas-Phase Chiral Recognition in Ion Mobility: Towards a Broad Chemical Understanding of Effective Chiral Reference Ligands**; Benjamin K Blakley[1]; Jody C. May[2]; Nina A. Metzger[2]; John A. McLean[2]; *[1]Department of Chemistry, Center for Innovative Technology, Institute of Chemical Biology, Institute for Integrative Biosystems Research, and Education, Nashville, TN; [2]Department of Chemistry, Center for Innovative Technology, Insti*

TP 380 **Robust Assessment of Directional Macromolecular Cross Sections by Upgraded Low-Field Differential IMS with Near-Perfect Flexible Rectangular Waveforms**; Egor Gusachenko[1]; Hayden A. Thurman[1]; Gordon A. Anderson[2]; Alexandre A. Shvartsburg[1]; *[1]Wichita State University, Wichita, KS; [2]GAA Custom Electronics, Kennewick, WA*

TP 381 **A refined domain-correlated collision induced unfolding mechanism for gas-phase antibody ions**; Valentina Rangel-Angarita[1]; Addison E. Bergman[1]; Michael R. Armbruster[1]; Nicole Rivera Fuentes[1]; Thomas o. Pereira[1]; Tiam Farajzadeh[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

TP 382 **High-Resolution and Tandem Ion Mobility Measurements to Understand Ambiguity in Fentanyl Fragmentation Pathways**; Bradley B Garrison[1]; Hernando Olivos[2]; Julia Januszewski[1]; Drew B. Whitman[1]; Christopher D. Chouinard[1]; *[1]Clemson University, Clemson, SC; [2]Waters, Milford, MA*

TP 383 **Increasing throughput in collision-induced unfolding studies: Enhancing sensitivity and streamlining set-up**; Noelle Elliott[1]; Dale A Cooper-Shepherd[2]; Bryan McCullough[2]; Emma Marsden-Edwards[2]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom*

TP 384 **Development of a modified Cyclic IMS platform for Enhanced Biomolecule Characterization**; Bryan McCullough[1]; Dale A Cooper-Shepherd[1]; Darren Hewitt[1]; Emma Marsden-Edwards[1]; David Harker[1]; *[1]Waters Corporation, Wilmslow, United Kingdom*

TP 385 **Force-Induced Collapse of Gas-Phase Polymer Ions Revealed by DMA-MS/MS and Molecular Dynamics**; Leyan Hua[1]; Carlos Larriba-Andaluz[1]; *[1]Purdue University, Indianapolis, IN*

TP 386 **Ganglioside isomer differentiation by trapped ion mobility spectrometry combined with anion-electron reactions**; Emily E. Hughes[1, 2]; Steven A. DeFiglia[1, 2]; Christopher A. Wootton[3]; Kristina Hakansson[1, 2]; *[1]Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, Tallahassee, FL; [2]Department of Chemistry & Biochemistry, Florida State University, Tallahassee, FL; [3]Bruker Daltonics GmbH & Co KG, Bremen, German*

TP 387 **On-Board, Conformer-Specific Fragmentation in High-Resolution SLIM**; Daniel Wu[1]; Brian H Clowers[1]; [1]*Washington State University, Pullman, WA*

TP 388 **Studying protein and peptide non-covalent complexes with ion mobility and electron capture dissociation mass spectrometry**; Yury V. Vasilev[1]; Rachel Franklin[1]; [1]*Agilent Technologies, CORVALLIS, OR*

TP 389 **To what extent do biopolymer structures observed by ion mobility spectrometry MS retain "memory" of their original solution counterparts?**; Michael Addo[1]; Jihyeon Lee[2]; Alexander Jr. D. MacKerell[2]; Daniele Fabris[3]; [1]*University of Connecticutt, Storrs, CT;* [2]*Dept. of Pharmaceutical Science, School of Pharmacy, University of Maryland Baltimore, Baltimore, MD;* [3]*University of Connecticut, Storrs, CT*

TP 390 **On the perils of parallel accumulation for native proteomics**; Addison E Roush[1]; Matthew F Bush[1]; [1]*University of Washington, Seattle, WA*

TP 391 **Ion Mobility–Mass Spectrometry and Hydrogen–Deuterium Exchange Reactions Reveal Alkali Metal–Dependent Peptide Stability**; Maede Yosefii[1]; Yilin Liu[1]; Touradj Solouki[1]; [1]*Baylor University, Waco, TX*

TP 392 **Exploring the Combination of Liquid- and Gas-phase Mobility Separation for Structural Peptide Analysis**; Freek Hollander[1]; David Alvarez Rodriguez[1]; Daniël Weissmann[1]; Anouk Rijs[1, 2]; Kevin Jooß[1, 2]; [1]*Vrije Universiteit Amsterdam, Amsterdam, Netherlands;* [2]*Centre for Analytical Sciences Amsterdam (CASA), Amsterdam, Netherlands*

TP 393 **Structural Characterization of protein – DNA complexes using nESI-TIMS-UVPD FT-ICR MS/MS**; Miguel Santos[1]; Fenfei Leng[1]; Kevin Jeanne Dit Fouque[1]; Francisco Fernandez-Lima[1]; [1]*Florida International University, Miami, FL*

TP 394 **Separation of PFAS Structural Isomers and Analysis of Stability by Multidimensional Cyclic Ion Mobility and Collision Induced Dissociation**; Meagan Gadzuk-Shea[1]; Raihana Afroz[2]; Varun V Gadkari[2]; Zijie Xia[1]; [1]*Claros Technologies, Minneapolis, MN;* [2]*University of Minnesota, Minneapolis, MN*

TP 395 **Capillary Microflow LC-QTOF Workflow for Robust Peptide Quantification with Reduced Energy and Solvent Consumption**; Greg Ward[1]; Matthew Morse[1]; Morlan Lunsford[1]; Sam Foster[1]; Warren Samms[1]; [1]*Axcend, Provo, UT*

TP 396 **Toward Improved Analytical Characterization of Imidazolium Cations with Small or Polar Substituents: PFPP Stationary Phase UHPLC and Class-Based In-Source CID**; Shuvro Chakraborty[1]; Hannah Lawson[1]; Taofiq Abdulraheem[1]; Amanda Patrick[1]; [1]*Mississippi State University, Mississippi State, MS*

TP 397 **Building a Mouse Lipidome Atlas with Cartridge-Based Nano-ESI and µPAC Separations**; Salma Ibrahim Abouelhassan[1, 2]; Li-Yu Chen[2, 3]; Katherine Walker[4]; Graeme McAlister[4]; Scott T Quarmby[1, 2]; Katherine A. Overmyer[1, 2, 5]; Joshua J. Coon[1, 2, 5, 6]; [1]*Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*National Center for Quantitative Biology of Complex Systems, Madison, WI;* [3]*Department of Chemistry, University of Wisconsin-Madison, Mad*

TP 398 **Evaluation of Inert Chemical Vapor Deposition Coatings on Column Hardware for Liquid Chromatography-Mass Spectrometry Applications**; Brady W. Drennan[1]; Jason A. Anspach[1]; [1]*Phenomenex Inc., Torrance, CA*

TP 399 **Identifying Tear Fluid Proteins Poorly Captured by Bottom-Up Mass Spectrometry**; Saleh Ahmed[1]; Victoria Cliffton[1]; Steven Safille[1]; Kumkum Kar[1]; Tae Jin Lee[1]; Shruti Sharma[1, 2]; Ashok Sharma[1, 2]; [1]*Center for Biotechnology and Genomic Medicine, Medical College of Georgia, Augusta University, Augusta, GA;* [2]*Department of Ophthalmology, Medical College of Georgia, Augusta University, Augusta, GA*

TP 400 **Cyclical High-Organic Wash strategies minimise carry-over between LC-MS samples**; Greta Briedyte[1]; Daniela-Lee Smith[1]; Palika Abayakoon[1]; Haley Oller[1]; Jarrod John Sandow[1]; *[1]IonOpticks, Melbourne, Australia*

TP 401 **Optimising Trap Column Design for High-Throughput UHPLC–MS Proteomics**; Liang Chen[1]; Todd Blackburn[1]; Daniela-Lee Smith[1]; Greta Briedyte[1]; Veronica Cashin[1]; Haley Oller[1]; Jarrod John Sandow[1]; *[1]IonOpticks, Melbourne, Australia*

TP 402 **Quantitation of N-Nitroso Duloxetine Nitrosamine Drug Substance Related Impurities (NDSRI) in drug substance and drug products**; Saravanan Thangavel; *Dr, Bangalore, India*

TP 403 **Effect of Emitter, Particle and Heater Design on the Performance of Integrated-Column for LC-MS-Based Proteomics**; Nathaniel B Axtell[1]; Xiaofeng Xie[2]; Thy Truong[2]; *[1]Micromics, Spanish Fork, UT; [2]MicrOmics Technologies, Spanish Fork, UT*

TP 404 **Effect of Column Bore and Length for Capillary Flow High Throughput Proteomics**; Thy Truong[1]; Xiaofeng Xie[1]; Nathaniel Axtell[1]; *[1]MicrOmics Technologies, Spanish Fork, UT*

TP 405 **Target Analyte n-Dimensional Liquid Chromatography**; Hanghui Liu[1]; Guy Servant[1]; Joseph Fotsing[1]; Rama Manam[1]; Purnendu K. Dasgupta[2]; *[1]dsm-firmenich, San Diego, CA; [2]The University of Texas at Arlington, Arlington, TX*

TP 406 **Mass-Based Fraction Collection (MBFC) for Scalable Purification in Pharma and Biopharma Applications**; Ronald Guilliet; *Agilent, Middelburg, Netherlands*

TP 407 **Integrated LC/UV and LC/MS Workflows for Impurity and Degradation Characterization of GLP-1 Agonists**; David Wong[1]; Suresh Babu Cugati Vishweshwaraiah[2]; *[1]Agilent Technologies, Santa Clara, CA; [2]Agilent Technologies Singapore (sales) Pte Ltd, Singapore, Singapore*

TP 408 **Expanding Biocatalysis Chemical Space through SFC and Mass Spectrometry**; Madeline Weber; *Novartis Institute for Biomedical Research, Cambridge, MA*

TP 409 **A High-Sensitivity Multiresidue Method for the Quantification of Pesticides Using Novel Fully Hybrid Silica Column in LC-MS/MS**; Anar Byambadorj[1]; Takumi Kunieda[1]; Mengmin Terashima[1]; Kenichi Suzuki[1]; Shota Miyazaki[1]; *[1]GL Sciences Inc., Fukushima City, Japan*

TP 410 **LC-MS/MS Characterization of AAV Structure-Function Relationships through Post-Translational Modification Profiling in Degradative Pathway Studies**; Jill Bradley-Graham[1]; Mohammad Safari[2]; Ning Pan[2]; Roberto Fernandez[2]; Long Zhang[2]; Monica Lane[2]; Alexgerard Mamaril[2]; Chrisopher Renzi[2]; Deblina Biswas[2</;] *[1]Sanofi Genzyme, Waltham, MA; [2]Sanofi, Waltham, MA*

TP 411 **High-Throughput HIC for ADC DAR Profiling Under LC–MS-Compatible Conditions**; Yinan Zhang[1]; Linting Li[1]; Xuyang Zhang[1]; Xingrong Zhu[1]; Ke Yang[1]; *[1]Sepax Technologies, Inc., Newark, DE*

TP 412 **Fast and Targeted Analysis of Cell Culture Media Components using QSight LC/MS/MS**; Jacob Jalali[1]; VICTOR CAI[1]; Autumn Payne[1]; *[1]PerkinElmer US, LLC, Shelton, CT*

TP 413 **Automated Electrostatic Attraction/Repulsion Hydrophilic Interaction Liquid Chromatography Screening for Polar and Charged Analytes in Complex Matrices**; Eli Larson; *Merck & Co., Rahway, NJ*

TP 414 **Automated Extraction, Clean-up, and Determination of Mycotoxins in Food using a Robotic Autosampler and LC-MS/MS**; Fred Foster[1]; Frederik Wuppermann[2]; *[1]Gerstel, Inc., Linthicum, MD; [2]LCTech GmbH, Obertaufkirchen, Germany*

TP 415 **Rapid sample preparation for SPE-UPLC-MS/MS analysis of EPA Priority 40 PFAS**; Deepak Timalsina[1]; David Alburty[2]; Michael Zhuo Wang[1, 3]; *[1]Department of Chemistry, University of Kansas, Lawrence, KS; [2]InnovaPrep LLC, Drexel, MO; [3]Department of Pharmaceutical Chemistry, University of Kansas, Lawrence, KS*

TP 416 **A “DMSO-keeper” partial-evaporation strategy minimizes semi-volatile loss and improves RPLC LC–MS plasma bioanalysis**; Hanghui Liu[1]; Yi Ren[1]; *[1]dsm-firmenich, San Diego, CA*

TP 417 **Feed Injection Enables the Use of High Organic Sample Solvents with Reversed-Phase HPLC**; David Borts[1]; Laura Burns[1]; Dwayne Schrunk[1]; Thomas Olsen[1]; *[1]Iowa State University, Ames, IA*

TP 418 **Ultra low-cost proteomic sample preparation and analysis of any sample**; Ximena Sanchez-Avila[1]; Ken S. Triggs[1]; Siqi Huang[1]; Ella E. Norton[1]; Jacob H. Clark[1]; R. J. S. Miercort[1]; Tyler Hunter[1]; Hyo-Sang Jang[2]; Ryan T. Kelly[1</su;] *[1]Brigham Young University, Provo, UT; [2]HP Life Science Solutions, Corvallis, OR*

TP 419 **From Rare Cells to Deep Proteomes: An Optimized Proteomics Workflow for Deep Profiling of Flow-Sorted Immune Cell Populations**; Shreya Ahuja[1]; Nicholas Battaglia[1]; Mohamed Moustafa[1]; Emanuel Salazar-Cavazos[1]; Benjamin Pullman[1]; Nikki Heller[1]; Matthew S. Glover[1]; Sonja Hess[1]; *[1]AstraZeneca, Gaithersburg, MD*

TP 420 **Comparison of SP3 and in-gel sample preparation workflows for mass spectrometry based proteomics**; Luisa Schwarzmüller[1, 2]; Dario Frey[2]; Piotr Zadora[2]; Stefan Wiemann[1]; Dominic Helm[2, 3]; *[1]Division of Molecular Genome Analysis, German Cancer Research Center (DKFZ), Heidelberg, Germany; [2]Proteomics Core Facility, German Cancer Research Center (DKFZ), Heidelberg, Germany; [3]Proteomics Core Facility, The Univer*

TP 421 **Weighing the Risk: Tirzepatide (Zepbound) Below Detection in Human Milk**; HANIN DIAB[1]; Krista Savage[2]; Lauren Covey[2]; Emma E Schmidt[2]; Herrick Schannon[2]; Teresa Baker[2]; Jonathan Thompson[1]; Palika Datta[2]; Kaytlin Krutsch[2]; *[1]Texas Tech University, Amarillo, TX; [2]Texas Tech University Health Sciences Center, Amarillo, TX*

TP 422 **Novel Nano-Magnetic Solid Phase Materials Enabling Efficient Automated, and Greener Sample Preparation**; Huafen Liu[1]; Pengyun Liu[2]; Qunjie Wang[3]; *[1]Calibra Diagnostics, San Jose, CA; [2]Calibra Scientific, Hangzhou, China; [3]Agile Bio, Suzhou, JIangsu Province, China*

TP 423 **Optimization of extraction methods for LC-MS-basedanalysis of per- and polyfluoroalkyl substances (PFAS) inedible fish**; Huyen TT Doan[1, 2]; Marti Z. Hua[1, 3]; Garnet McRae[3]; Joshua Marleau-Gillette[3]; Enea Pagliano[3]; Yaxi Hu[1, 2]; *[1]Department of Chemistry, Carleton University, Ottawa, ON; [2]Institute of Biochemistry, Carleton University, Ottawa, ON; [3]NRC Metrology, National Research Council Canada, Ottawa, ON*

TP 424 **Pressure-Driven Merging for User-Friendly 12-Hour Acoustic Levitation-Based Container-Free Chemistry and LC–MS Analysis**; Xueming Dong; *Nanyang Technological University, Singapore, Singapore*

TP 425 **Optimized FFPE Tissue Processing: Complete workflow for in-depth proteome analysis of multiple FFPE formats**; Kara West[1]; Measho H Abreha[1]; Zehan Hu[2]; Karin Yeoh[2]; Silvia Wuertenberger Wuertenberger[2]; Katrin Hartinger[2]; Nils A Kulak[2]; *[1]PreOmics Inc., Billerica, MA; [2]PreOmics GmbH, Martinsried, Germany*

TP 426 **Boosting Sample Preparation at Low Protein Input: A Workflow Engineered for Optimal Recovery and High Throughput**; Measho Abreha[1]; Ina Aretz[2]; Sandra Schaer[3]; Mayur V Bakshi[3]; Silvia Wuertenberger[2]; Zehan Hu[2]; Christina Antulic[2]; Roland Bruderer[3]; Garwin Pichler[2];; *[1]Preomics Inc, Billerica, MA; [2]PreOmics GmbH, Martinsried, Germany; [3]Biognosys AG, Schlieren, Switzerland*

TP 427 **Overcoming Challenges Associated with Oligonucleotide Extraction from Tissue Samples Prior to UHPLC-MS/MS Analysis**; Zainab Khan[1]; Lee Williams[1]; Stephen Plant[1]; Kyle Bevan[1]; Helen Lodder[1]; Charlotte Hayes[1]; Geoff Davies[1]; Lucy Richards[1]; Adam Senior[1]; Russell Parry; *[1]Biotage GB Limited, Cardiff, United Kingdom*

TP 428 **SEC-CDMS Enables Online Buffer Exchange and Characterization of Protein-Based Therapeutics**; Emily Christofi[1]; Jakub Ujma[1]; Lohra Miller Young[2]; Benjamin Draper[2]; Lavelay Kizekai[3]; Bala Addepalli[3];

Matthew Lauber[3]; Michelle Chen[4]; Martin Jarrold[2]; <; [1]*Waters Corporation, Wilmslow, United Kingdom;* [2]*Megadalton Solutions, Bloomington, IN;* [3]*Waters Corporation, Milford, MA;* [4]*Waters, Inc., Goleta, CA*

TP 429 **A Systematic Evaluation of Biotage Reversed-Phase Sorbents for Peptide Desalting Prior to Mass Spectrometry Analysis**; Jacob W Silzel[1]; Esraa AboJasser[1]; Sohel Rana[1]; Lee Williams[2]; [1]*Biotage, Charlotte, NC;* [2]*Biotage GB Limited, Cardiff, United Kingdom*

TP 430 **Using Adaptive Focused Acoustics for Sample Preparation for DIA Proteomics Workflow**; Anastasiia Lisovska[1]; Mynaja Ferguson[1]; Jason Evans[1]; Kai Zou[1]; [1]*University of Massachusetts Boston, Dorchester, MA*

TP 431 **A comparative evaluation of plasma sample preparation workflows for proteome analysis**; Yeongshin Kim[1]; Dongyoon Shin[1, 2]; Junho Park[1, 2]; Youngsoo Kim[1, 2]; [1]*Department of Medical Science, School of Medicine, CHA University, Gyeonggi-do, South Korea;* [2]*Artificial Intelligence Omics Research Center, CHA Research Institute, Bundang CHA Hospital, Gyeonggi-do, South Korea*

TP 432 **Technological Assessment onto Immunohistochemistry-based Spatial Proteomics on Tissue Slides of Formalin-Fixed Paraffin-Embedded**; Yuefei Zhang[1, 2, 3]; Guixue Hou[2]; Siqi Liu[1, 2, 3]; [1]*College of Life Sciences, University of Chinese Academy of Sciences, Beijing, China;* [2]*BGI-Shenzhen, Shenzhen, China;* [3]*Zhejiang Cancer Hospital, Hangzhou Institute of Medicine, Chinese Academy of Sciences, Hangzhou, China*

TP 433 **From Signal to Concentration: Challenges in Absolute Quantification by Reversed Phase LC-MS Lipidomics**; Dingyu Deng[1]; Carlos R. Canez[1]; Jerrica Yang[1]; Liang Li[1]; [1]*University of Alberta, Edmonton, AB*

TP 434 **Direct infusion acoustic droplet ejection mass spectrometry (diADE-MS): enabling high-throughput shotgun lipidomics**; Yu Zhang[1]; Amy Harms[2]; Lucas Jurado-Fasoli[3]; Jonatan R. Ruiz[3]; Nicolas Drouin[2]; Thomas Hankemeier[2]; [1]*Leiden university, Leiden, Netherlands;* [2]*Leiden University, Leiden, Netherlands;* [3]*University of Granada, Granada, Spain*

TP 435 **Untargeted Metabolomics and Absolute Quantitation of Lipids from Complex Matrix on Thermo Scientific™ Orbitrap Astral Zoom™ and Stellar™ MS Platforms**; Guohui Li[1]; Devanand M. Pinto[2, 3]; Daniel Hermanson[1]; Joshua P. Kline[1]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Pathology Department, Dalhousie University, Halifax, NS;* [3]*National Research Council, Halifax, NS*

TP 436 **High-Throughput Relative Quantitation of Phosphatidylcholines via 4-plex Isobaric DiLeuEN Labeling**; Yajing Lu[1]; Zicong Wang[1]; Shuling Xu[1]; Peng-Kai Liu[1]; Lingjun Li[1]; [1]*UW-Madison, Madison, WI*

TP 437 **Nuclear function of IRG1 drives innate-driven prostaglandin synthesis in inflammatory macrophages**; Katie A Acken[1]; Anthony M Cannon[1]; Luke A Bourner[1]; Linda A Chung[1]; Jordan Yokubonus[2]; Andrew Grigdesby[3]; Mackenzie J Pearson[1]; Kenneth D Roth[1]; [1]*Eli Lilly & Company, Indianapolis, IN;* [2]*ATL, Indianapolis, IN;* [3]*Cogent Scientific, Indianapolis, IN*

TP 438 **Application of a High-Throughput MS-Based Lipid Extraction and Quantitation Assay with DILI-Associated Clinical Samples**; Yuhong Fang[1]; Yi-Han Lin[1]; Yanyan Qu[1]; Mark J. Henderson[1]; Minjun Chen[2]; Christopher A LeClair[1]; Dingyin Tao[1]; [1]*National Institute of Health, NCATS, Rockville, MD;* [2]*FDA, National Center for Toxicological Research, Jefferson, AR*

TP 439 **Re-evaluation of the sulfo-phospho-vanillin reaction mechanism using mass spectrometry: Towards more accurate pre-quantitation for untargeted lipidomics normalization**; Laura S Bailey[1]; Fabian Kume[1]; Katie Heiden[1]; Kari B Basso[1]; [1]*University of Florida, Department of Chemistry, Gainesville, FL*

TP 440 **Accurate Quantification of Lipid Regioisomers by SCIEX ZenoTOF 8600 System using EAD-MRMHR**; Haihong Zha[1]; Chenchun Zhong[2]; Zhimin Long[2]; Bingjie Liu[3]; [1]*sciex, shanghai, China;* [2]*SCIEX, Shanghai, China;* [3]*SCIEX, Beijing, China*

TP 441 **Time-Dependent Non-Enzymatic Oxidation of Glycerophospholipids in a Controlled Liposomal Environment**; Sazia Arefin Kachi; *University of Maryland, Baltimore, Baltimore, MD*

TP 442 **Harmonizing Routine Oxylipin Profiling: A Multisite Evaluation of Inter-Laboratory Reproducibility**; Fernando (Ralph) Tobias[1]; Dominique Baldwin[2]; Cate Simmermaker[3]; Karen Yannell[3]; Judith A. Simcox[4]; *[1]Agilent Technologies, Chicago, IL; [2]University of Wisconsin-Madison, Madison, WI; [3]Agilent Technologies, Santa Clara, CA; [4]University of Wisconsin Madison, Madison, WI*

TP 443 **Targeted Oxylipin Lipidomics Reveals Prostaglandin Remodeling Associated with Functional Aging in C2C12 Myoblasts**; Chen Yu Chang; *Chang Gung University, Taoyuan City, Taiwan*

TP 444 **Pathway Analysis of PUFA synthesis intermediates in In-Process Fermentation Samples Using Targeted LC-MS Approach**; Durga Devi Khanal[1]; Bokkyoo Jun[1]; Yao Lu[1]; *[1]DSM-Firmenich, Company, Columbia, MD*

TP 445 **Enhanced Omega-3 Oils Differentiation by Triacylglycerol (TAG) Profiling Comparison Using LC–HRMS**; Bokkyoo Jun[1]; Durga Devi Khanal[1]; Yao Lu[1]; *[1]DSM-Firmenich, Company, Columbia, MD*

TP 446 **High-Throughput Multiplexed Quantification of Phospholipids in Human Diabetic Pancreas Using Diazobutanone-Enabled 18-Plex Isobaric SUGAR Labeling**; Wei Wilson Li[1]; Kelly H. Lu[2]; Zicong Wang[1]; Peng-Kai Liu[3]; Connie S. Chamberlain[4]; Jon S. Odorico[4]; Lingjun Li[1, 2, 3]; *[1]School of Pharmacy, University of Wisconsin-Madison, Madison, WI, Madison, WI; [2]Department of Chemistry, University of Wisconsin-Madison, Madison, WI, Madison, WI; [3]Biophysics Graduate Program, University of Wisconsin-Mad*

TP 447 **High-Throughput Bioinert UHPSFC/MS for Comprehensive Lipidomic Quantitation in Large Clinical Cohorts**; Michal Holcapek[1]; Ondrej Peterka[1]; Petra Peroutková[1]; Veronika Šubrtová[1]; Zuzana Lásko[1]; Robert Jirasko[1]; *[1]University of Pardubice, Faculty of Chemical Technology, Department of Analytical Chemistry, Pardubice, Czech Republic*

TP 448 **Chromatographic Separation of Phosphatidylinositol Phosphate Isomers Using Trimethylsilyldiazomethane Derivatization and Chiral Column Liquid Chromatography-Mass Spectrometry**; Steph Collins[1]; Lilu Guo[1]; Bailin Zhang[1]; *[1]Sanofi, Cambridge, MA*

TP 449 **Yoda1-Mediated Piezo1 Activation Modulates Arachidonic Acid (AA)-Derived Lipid Mediators in Mice**; Xiaohui Yu[1]; Yanqiong Jiang[1]; Dante Dikeman[1]; Xiangyu Chu[1]; Young-Kwon Hong[2]; Stan Louie[1]; *[1]University of Southern California, Los Angeles, CA; [2]Harvard Medical School, Boston, MA*

TP 450 **Quantitation of oleic acid incorporation in Staphylococcus aureus membrane lipids using the Sulfo-Phospho-Vanillin Assay and Targeted Mass Spectrometry**; Bridgette N Allen[1]; Kelly M Hines[1]; *[1]University of Georgia, Athens, GA*

TP 451 **LC-MS Redox Lipidomics Resolves the Lethal Phospholipid Species in Ferroptosis**; Sviatlana N. Samovich[1]; Alexander A. Kapralov[2, 3]; Louis J. Sparvero[2, 3]; Brian A. Kleiboeker[2, 3]; Mert Akdogan[2, 3]; Andrew A. Amoscato[2, 3]; Yulia Y. Tyurina[2, 3]; Sally E.; *[1]Department of Pediatrics, Division of Critical Care, Hospital and Palliative Medicine, Redox Health Center, Vagelos College of Physicians and Surgeons, Columbia University Irving Medical Center, New York, NY 10032, USA, New York, NY; [2</s]*

TP 452 **Comprehensive targeted lipidomics without compromise: A rapid, high-precision plasma lipidomic assay**; Brittany Lee[1]; Jia Wang[1]; Jiao Yang[2]; Judith Ngere[3]; Alan Atkins[3]; Cristina C. Jacob[4]; Khatereh Motamedchaboki[1]; Philip M. Remes[4]; Rahul Deshpande[4];; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Bannockburn, IL; [3]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [4]ThermoFisher Scientific, San Jose, CA*

TP 453 **LCMS-MRM Measurement of Sphingolipid and Individual Ceramide Species Levels in Human Lung Epithelial Cells Infected with Influenza A Virus**; Barbara W. Sumner[1]; Savannah McKenna[2]; Kwang Il Jung[2]; Jennifer J. Wolf[2]; Lloyd W. Sumner[1]; Bumsuk Hahm[2]; *[1]Metabolomics Center, University of Missouri, Columbia, MO; [2]Departments of Surgery and Molecular Microbiology & Immunology, University of Missouri, Columbia, MO*

TP 454 **Surpassing conventional coverage limits in lipidomics through ultrafast MS/MS acquisition**; Nicholas S Ly[1]; J. Rafael Montenegro-Burke[1]; Andrew T. Quaile[1]; *[1]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON*

TP 455 **Lipidomic and Genomic Characterization of Omega-3 Fatty Acids in Farm-Raised Eastern Oysters (Crassostrea virginica)**; Nathan B Stauber[1]; Chris Hollenbeck[1]; Joseph Matt[1]; Bashar Amer[2]; Hussain Abdulla[1]; Susan S. Bird[2]; *[1]Texas A&M University- Corpus Christi, Corpus Christi, TX; [2]ThermoFisher Scientific, San Jose, CA*

TP 456 **Developing Extraction and Mass Spectrometry Methods for Quantification of Oxylipins in Human Plasma and Erythrocytes**; Kyle Nguyen[1]; Brandie M. Ehrmann[1]; Anne E. Sanders[1]; *[1]University of North Carolina at Chapel Hill, Chapel Hill, NC*

TP 457 **Lipidomic Analysis of Dolphin Blubber Using a Simultaneous Quantitation–Discovery Workflow Across an Estuarine Gradient**; Makayla Guinn[1]; Dara Orbach[1]; Bashar Amer[2]; Susan S. Bird[2]; Hussain Abdulla[1]; *[1]Texas A&M University - Corpus Christi, Corpus Christi, TX; [2]ThermoFisher Scientific, San Jose, CA*

TP 458 **Oxylipin Profiling Reveals Distinct Inflammatory Signatures in HFpEF Pulmonary Remodeling Phenotypes**; Dominique A Baldwin[1]; John Shuster[1]; Jericha Mill[1]; Farhan Raza[1]; Judith A. Simcox[1, 2]; *[1]University of Wisconsin-Madison, Madison, WI; [2]Howard Hughes Medical Institute, Chevy Chase, MD*

TP 459 **Minimization and correction of solvent- and labware-derived contamination in high-resolution LC-MS analysis of C6-C33 fatty acids**; Xun Bao[1]; Yuanyuan Jiang[1]; Jing Li[1]; *[1]Karmanos Cancer Institute, Wayne State University, Detroit, MI*

TP 460 **A High-Throughput SLE-LC-MS/MS Workflow for Comprehensive Endocrine Profiling in Wild Songbirds**; Marissa A Mandell; *University of the Pacific, Stockton, CA*

TP 461 **Improved sensitivity in quantitative profiling of inflammatory and pro-resolving lipid mediators in tissue samples using nanoflow chromatography**; Rahul Ravi Deshpande[1]; Vasundhara Kain[2]; Ciara J. Sallowicz[1]; Thiago Mattos[1]; Susan S. Bird[1]; Ganesh Halade[2]; *[1]ThermoFisher Scientific, San Jose, CA; [2]College of Medicine Internal Medicine, USF, Tampa, FL*

TP 462 **Quantitative and qualitative analysis of oxylipins using high-resolution mass spectrometry with CID- and EAD-based fragmentation**; Paul RS Baker[1]; Paul Norris[2]; Thomas D Horvath[3, 4]; *[1]SCIEX, Seattle, WA; [2]SCIEX, Marlborough, MA; [3]Department of Pathology, Texas Children's Hospital, Houston, TX; [4]Department of Pathology and Immunology, Baylor College of Medicine, Houston, TX*

TP 463 **MALDI-TOF Analysis of Lipid Profiles in Mouse Brain Tissues at Varying Stages of Neuroinflammation in Positive Ionization Mode**; Mackenzy L McCormack[1]; Krista Berlin[1]; Mary Jo Valencia Morales[1]; Thomas Forsthuber[1]; Stephan Bach[1]; *[1]University of Texas San Antonio, San Antonio, TX*

TP 464 **Porous PtCu Alloys Decode Plasma Metabolic Fingerprints for the Recognition of Severe Community-Acquired**; Kexin Meng[1]; Kun Qian[1]; *[1]Shanghai Jiao Tong University, Shanghai, China*

TP 465 **Albumin Quantification Strategy Using MALDI-TOF MS**; Ji In Baek[1, 2]; Ji Yeong Song[1, 3]; Hae-Min Park[2]; Sohee Yoon[1, 3]; *[1]Korea research institute of standards and science, Daejeon, South Korea; [2]Chungnam National University, Daejeon, South Korea; [3]University of Science and Technology, Daejeon, South Korea*

TP 466 **MALDI MS and imaging of fatty acids, neurotransmitters, and cholesterol using the nitro functional group containing matrix 4-hydroxy-3-nitrobenzonitrile**; Jiyeong Song[1, 2]; Ji In Baek[1, 3]; Sohee Yoon[1, 2]; *[1]Korea research institute of standards and science, Daejeon, South Korea; [2]University of Science and Technology, Daejeon, South Korea; [3]Chungnam National University, Daejeon, South Korea*

TP 467 **On-Tissue Chemical Derivatization with Isotopically-Encoded Reagents Enables Confident Detection of Previously Undetectable Metabolites in MALDI-MS Imaging**; Monika Mahmud[1]; Jeerapat Doungchawee[1]; Fiona McEvoy[1]; Richard W. Vachet[1]; *[1]University of Massachusetts Amherst, Amherst, MA*

TP 468 **Matrix-Dependent Ionization Pathways for Phytoplankton Biomarkers Using Ultra-High-Resolution MALDI Mass Spectrometry**; Daniela Díaz-Pinzón[1]; Luis M Díaz-Sánchez[2]; Martha L Aguilera[3]; David Stranz[4]; Scott Campbell[4]; Cristian Blanco-Tirado[1]; Marianny Y Combariza[1]; *[1]UNIVERSIDAD INDUSTRIAL DE SANTANDER, Bucaramanga, Colombia; [2]Universidad de Pamplona, Pamplona, Colombia; [3]National High Magnetic Field Laboratory Department of ICR, Tallahassee, FL; [4]Sierra Analytics, Inc., Mo*

TP 469 **Unlocking the discriminative potential of MALDI-TOF profiling data with an AI-enabled software solution for biomarker discovery, classification and typing**; Luis Mancera[1]; Jesús Jiménez[1]; Manuel Arroyo[1]; Arndt Asperger[2]; *[1]Clover Bioanalytical Software, S.L., Granada, Spain; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

TP 470 **Quantification of HIV antiretroviral drugs in human plasma on a benchtop linear MALDI-TOF mass spectrometer**; Simona Salivo[1]; Tom K. Abban[1]; Matthew E. Openshaw[1]; Keith Worrall[1]; *[1]Shimadzu, Manchester, United Kingdom*

TP 471 **Rapid-Turnaround Top-Down Sequence Verification and Characterization of Modified Proteins and Oligonucleotides Using a Benchtop MALDI-TOF/TOF Instrument**; Sinduri Vuppala[1]; Savannah Snyder[1]; Arndt Asperger[2]; *[1]Bruker Scientific LLC, Billerica, MA; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

TP 472 **Feasibility for a PFAS screening protocol by Matrix Assisted Laser Desorption Ionisation – Time of Flight Mass Spectrometry (MALDI-TOF MSI)**; Caroline Jones[1]; Tom K. Abban[1]; Simona Salivo[1]; Keith Worrall[1]; Matthew E. Openshaw[1]; *[1]Shimadzu, Manchester, United Kingdom*

TP 473 **TIMS-enhanced MALDI spot analysis for high-throughput bacterial profiling and precise characterization of antibiotic-induced metabolic responses**; Edward Rudt[1]; Arndt Asperger[1]; Sofie Weinkouff[1]; Nikolas Kessler[1]; Phuong Y Mai[2]; Cédric Thépenier[2]; Sandrine Aros[2]; Ivo Gomperts Boneca[2]; Heiko Neuweger[1<;] *[1]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [2]Institut Pasteur, Paris, France; [3]Bruker UK Ltd., Coventry, United Kingdom*

TP 474 **Uptake and Translocation of Perfluoroalkyl Substances in Plants Assessed with MALDI-Mass Spectrometry Imaging: Implications for Food Security and Phytoremediation**; Tong Zhou[1]; Varuni Abhayaratne[1]; Joseph Akor[1]; Honglan Shi[1]; John Yang[2]; Paul Nam[1]; Joel Burken[1]; *[1]Missouri University of Science and Technology, Rolla, MO; [2]Lincoln University of Missouri, Jefferson City, MO*

TP 475 **Integrating Gold Nanoparticles with MALDI-TOF-MS for Membrane Protein Analysis**; Reihaneh Safavisohi[1]; Nichole Donofrio[1]; *[1]Seton Hall University, South Orange, NJ*

TP 476 **MXene-Assisted SALDI-TOF MS Platform for Detection of Small-Molecule New Pollutants**; Zifang Peng[1]; YANHAO ZHANG[2]; *[1]College of Public Health, Zhengzhou, China; [2]Hong Kong Baptist University, Hong Kong, Hong Kong*

TP 477 **Graphite as a Matrix for Characterization of Low Molecular Weight Analytes with MALDI-MS**; Carson E. Ward[1]; Alicia K. Friedman[1]; *[1]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH*

TP 478 **Matrix-Free Soft Ionization using Graphitized Mesoporous Nanocomposites for Multi-Class Drug Screening**; Yi-Hsin Liu[1]; Hong-Po Chen[1]; Yung-Cheng Jair[2]; Pin-Chuan Chen[3]; Pai-Shan Chen[4]; *[1]National Taiwan Normal University, Taipei, Taiwan; [2]National Taiwan Univeristy, Taipei, Taiwan; [3]National Taiwan University of Science and Technology, Taipei City, Taiwan; [4]Institute of Toxicology, School of Me*

TP 479 **Inlet Temperature and Accelerating Field Optimization in AP MALDI Source Coupled to High-Resolution Mass Spectrometer**; Eugene Moskovets[1]; Konstantin Novoselov[2]; Vladimir Doroshenko[2]; *[1]MassTech Inc, Columbia, MD; [2]MassTech Inc., Columbia, MD*

TP 480 **Enhancement of Sodiated Lipid Ions in Matrix-Assisted Laser Desorption/Ionization (MALDI) Mass Spectrometry by Rapidly Freeze-Dried Droplet (RFDD) Method**; HSIN-JUNG LIN[1]; Shih-Yang Hung[1]; I-Chung Lu[1]; *[1]Department of Chemistry, National Chung Hsing University, Taichung City, Taiwan*

TP 481 **Development of an LC MS MS Method for Quantitation of Endocrine Active Steroids in Aquatic Toxicology Studies**; Blessing Chisom Egbejiogu[1]; Jinlan Dong[1]; *[1]Corteva Agriscience, Newark, DE*

TP 482 **High-throughput Quantification of Carbonyl-containing Metabolites by 18-Plex Isobaric SUGAR Tag**; Kelly Lu[1]; Wei Wilson Li[2]; Zicong Wang[2]; Shashank Ramesh[1]; Connie S Chamberlain[3]; Jon S Odorico[3]; Lingjun Li[1, 2]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI, Madison, WI; [3]Department of Surgery, University of Wisconsin-Madison,*

TP 483 **Development of an LC-MS method for quantifying total levels and carbon-13 labeling of Coenzyme A from cells and tissues**; Amelia Taylor[1]; Nathaniel Snyder[2]; Caroline Bartman[1]; *[1]University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA; [2]Temple University, Philadelphia, PA*

TP 484 **Moving untargeted metabolomics forward: quantitative reporting and discovery in a natural products assay**; Jeremiah D Wells[1]; Uri Keshet[1]; Oliver Fiehn[1]; *[1]University of California, Davis, Davis, CA*

TP 485 **Accelerated analytical method development for quantifying putrescine in cell culture supernatant**; Francesca Ferlenghi[1]; Nicole Bradshaw[1]; Maria Sani[1]; James Graham[1]; *[1]Lonza, Slough, United Kingdom*

TP 486 **Standardized large-panel quantitative metabolomics and lipidomics using the MxP® Quant 1000 kit validated on the SCIEX Triple Quad 7500 system**; Stephen Dearth[1]; Markus Langsdorf[1]; Hai Pham-Tuan[1]; Gordian Adam[1]; Esther Wortmann[1]; Teodoro Bottiglieri[2]; Paula Ashcraft[2]; Aaron Gebert[2]; Karel Kalecký[2</;] *[1]Biocrates Life Sciences GmbH, Innsbruck, Austria; [2]Baylor Scott & White Research Institute, Dallas, TX*

TP 487 **Measurement of vitamin B12 vitamers in human blood: the technical challenges and a new LC-MRM/MS assay method**; Jun Han[1, 2]; Jessica Ngo[1]; Jason Bi[1]; Malia Lampard[1]; Jasmine Benoit[1]; Juncong Yang[1]; David R. Goodlett[1, 3]; *[1]Genome BC Proteomics Centre, University of Victoria, Victoria, BC; [2]Division of Medical Sciences, University of Victoria, Victoria, BC; [3]Department of Biochemistry and Microbiology, University of Victoria, Victoria, BC*

TP 488 **Derivatization-free single-run hydrophilic RP-UPLC targeted metabolomics assay of human plasma samples**; Adeline Shanker[1]; Evgeniy V. Petrotchenko[1]; Karen Yannell[2]; Jean-Francois Roy[2]; Christoph H. Borchers[1, 3]; *[1]Lady Davis Institute for Medical Research, Montreal, QC; [2]Agilent Technologies, Mississauga, ON; [3]Gerald Bronfman Department of Oncology, Jewish General Hospital, Department of Pathology, Division of Experimental Medicine*

TP 489 **Targeted UHPLC-HRMS Metabolomic Analysis of Steroid Alkaloids in Diverse Tomato Cultivars in Korea**; Chaeyeon Cho[1]; Min Kwak[1]; Donghyuk Baek[2]; Sang Hee Shim[2]; Heejung Yang[1]; *[1]Kangwon National University, Chun Cheon, South Korea; [2]Seoul National University College of Medicine, Seoul 08826, South Korea*

TP 490 **Challenges of Catecholamines and Metanephrines: Achieving Sensitivity for Trauma Research**; Ingvi K. Jonsson[1]; Finnur F. Eiriksson[2]; Margret Thorsteinsdottir[1, 2]; Baldur B. Sigurdsson[3]; Ottar Rolfsson[1]; *[1]University of Iceland, Reykjavik, Iceland; [2]ArcticMass, Reykjavík, Iceland; [3]Landspitali University-Hospital, Reykjavik, Iceland*

TP 491 **Single-analytical targeted metabolomics platform covering over 1,000 metabolites from highly polar to nonpolar**; Minsik Kang[1, 2]; Minkyu Lee[1, 3]; Jihyun Lee[1, 2]; Han Bin Oh[2]; Sangkyu Lee[4]; Geum-

Sook Hwang[5]; Jaeick Lee*[1]; *[1]Korea Institute of Science and Technology (KIST), Seoul, South Korea; [2]Sogang University, Seoul, South Korea; [3]Dongguk University, Seoul, South Korea; [4]Sungkyunkwan University, Suwon, South Korea; [5]K*

TP 492 **A High-Resolution Next generation Metabolomics Approach for PRMT Activity and Precision Patient Stratification**; Ashima Mehta[1]; Ethan Stancliffe[1]; Adam Richardson[1]; Sandeep Acharya[1]; Kevin Cho[2]; Monil Gandhi[1]; Douglas V. Guzior[1]; Caitlin Kelly[1]; Tom Cohen[1]; Shar; *[1]Panome Bio, Saint Louis, MO; [2]Washington University in St.Louis, St.Louis, MO*

TP 493 **Parallel Metabolome-Wide Quantification of Metabolites with 15N-Labeled Mouse Specimens through Mass Spectral Accuracy**; Christoph W. Turck[1]; Wenyun Lu[2]; Joshua D. Rabinowitz[2]; Yongdong Wang[3]; *[1]Silantes GmbH, Munich, Germany; [2]Princeton University, Princeton, NJ; [3]Cerno Bioscience, Las Vegas, NV*

TP 494 **High Resolution PRM Assays Enable Targeted Phenolic acid and Flavonoids Analysis of Grape and Sorghum Plants**; Fang Chen[1]; Sarah Metwally[1]; Yinping Jiao[2]; Thayne Montague[3]; *[1]Center for Biotechnology & Genomics, Texas Tech University,, Lubbock, TX; [2]Institute of Genomics for Crop Abiotic Stress Tolerance, Texas Tech University, Lubbock, TX; [3]Department of Plant and Soil Science, Texas Tech Uni*

TP 495 **Integrated multi-omics reveals opposing effects of exercise and rapamycin in aging skeletal muscle**; Jericha Mill[1]; Matthew Bruss[2]; Ryan Marshall[3]; Christian Elliehausen[2]; Michaela Trautman[2]; Aditya Ailiani[2]; Troy Hornberger[4]; Dudley Lamming[3]; Judith A. Simcox<; *[1]Department of Biochemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Medicine, Division of Geriatrics and Gerontology, University of Wisconsin-Madison, Madison, WI; [3]Department of Medicine, Division of*

TP 496 **The effects of nicotinamide mononucleotide on Thoroughbred training horses**; Takuya Yamane; *Osaka University, Suita, Japan*

TP 497 **Analytical strategies for the preservation and quantification of reduced folates: A systematic evaluation using high-resolution tandem mass spectrometry**; Keisuke Nakata[1]; Masatomo Takahashi[1]; Sho Tabata[1]; Yuri Imado[1]; Takeshi Bamba[1]; Yoshihiro Izumi[1, 2]; *[1]Kyushu University, Fukuoka, Japan; [2]The University of Osaka, Toyonaka, Japan*

TP 498 **Multi-platform and multi-laboratory evaluation of a quantitative metabolomics assay targeting over 1,200 metabolites using AI-driven peak picking**; Markus Langsdorf[1]; Stephen Dearth[1]; Tuan Hai Pham[1]; Ulf Sommer[1]; Agnes Scharrer[1]; Doreen Kirchberg[1]; Gordian Adam[1]; Esther Wortmann[1]; *[1]Biocrates Life Sciences GmbH, Innsbruck, Austria*

TP 499 **Broad profiling, quantitative metabolomics using the MxP® Quant 1000 kit optimized for the Bruker EVOQ® DART-TQ+ mass spectrometer**; Markus Langsdorf[1]; Tuan Hai Pham[1]; Ulf Sommer[1]; Agnes Scharrer[1]; Doreen Kirchberg[1]; Gordian Adam[1]; Esther Wortmann[1]; Jennifer Richardson[1]; *[1]Biocrates Life Sciences GmbH, Innsbruck, Austria*

TP 500 **Quant 500 XL targeted metabolomic analysis using a plasma spot collection device**; Teodoro Bottiglieri[1]; Paula Ashcraft[1]; Karel Kalecký[1]; *[1]Baylor Scott & White Research Institute, Dallas, TX*

TP 501 **Simultaneous Quantitation and Discovery of 1,500 Metabolites Using Complementary Chromatographic Platforms**; Hussain Abdulla[1]; Abigail Martinez[1]; Kylli Widas[1]; Paige Hart[1]; Bashar Amer[2]; Susan S. Bird[2]; *[1]Texas A&M University- Corpus Christi, Corpus Christi, TX; [2]Thermo Fisher Scientific, San Jose, CA*

TP 502 **Thermodynamics-based interpretation of untargeted metabolomics results using paired concentration measurements**; Luke S Ferro[1]; Tomo Oga[1]; Michelle Yu[1]; Craig Knisley[1]; Devesh Shah[1]; Ana S. H. Costa[1]; Sophia C. Carroll[1]; Jennifer S. Campbell[1]; Amy A Caudy[1]; *[1]Matterworks Inc, Sommerville, MA*

TP 503 **High-Throughput Emma-OPSI-MS Analysis of Energy Metabolism**; Stephan Siebel[1]; John Janiszewski[2]; Rebecca Cardone[1]; Richard Kibbey[1]; Erik Miller[3]; David Manura[3]; Chang Liu[4]; Thomas

Covey[4]; [1]*Yale University, New Haven, CT;* [2]*J2.Bioanalytical, Westerly, RI;* [3]*Adaptas Solutions, Palmer, MA;* [4]*SCIEX, Corncord, ON*

TP 504 **From untargeted metabolomics to quantitative assessment of xenobiotics in ocean water**; Maxence Derbez-Morin[1]; Tilman Schramm[1]; Daniel Petras[1]; [1]*Department of Biochemistry, University of California, Riverside, Riverside, CA*

TP 505 **Analysis of large cohorts of dried blood spot samples using the RAMP workflow**; Nicholas Brodie[1]; Mario E. Valdés-Tresanco[1]; Mario S. Valdés-Tresanco[1]; Ryan A Groves[1]; Raied Aburashed[1]; Ian Lewis[1]; [1]*University of Calgary, Calgary, AB*

TP 506 **Identification and Accurate Concentration Determination of Metabolites from a Single Injection**; Michelle Yu[1]; Tomo Oga[1]; Craig Knisley[1]; Luke S. Ferro[1]; Devesh Shah[1]; Ana S. H. Costa[1]; Sophia Carroll[1]; Jennifer M. Campbell[1]; Amy A. Caudy[1]; [1]*Matterworks Inc, Somerville, MA*

TP 507 **Comparative Analysis of Expanded Biocrates Q1000 Targeted-Discovery Metabolomics Assay on Standardized Reference Matrices Versus Previous Generation Q500 Assay**; Sophia Guerrero[1]; Greg Waitt[1]; Lucas Li[1]; [1]*Duke University, Durham, NC*

TP 508 **Cross-platform best practices towards standardization of a comprehensive quantitative metabolomic profiling kit**; Francis Briere[1]; Lun Zhang[2]; Jiamin Zheng[2]; Claudia Carpentier[1]; Jacques Corbeil[1]; [1]*Linearis Labs, Québec, QC;* [2]*TMIC Wishart Node, University of Alberta, Edmonton, AB*

TP 509 **Sensitive and robust quantitation of serum bile acids using a novel quantitative kit on Stellar MS to study Crohn's disease**; Cynthia M Grim[1]; Bashar Amer[1]; Will Thompson[2]; Philip M. Remes[1]; Scott Mellors[2]; James Campbell[2]; Andrew J. Percy[3]; Cristina C. Jacob[1]; Scott M Peterman[1</;] [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Move Analytical LLC, Carrboro, NC;* [3]*Cambridge Isotope Laboratories, Inc., Tewksbury, MA*

TP 510 **Metabolomics for the discovery of endogenous protein-metabolite interactions using equilibrium screening and lysate capture**; Fouad Choueiry[1, 2]; Serim Yang[2]; Roberto Zoncu[1, 2]; Julia Schaletzky[1, 2]; [1]*Molecular Therapeutics Initiative, University of California, Berkeley, CA;* [2]*Department of Molecular and Cellular Biology, University of California, Berkeley, CA*

TP 511 **Evaluating the Effects of Extracellular Matrix Microstructure on the Hepatic Metabolome via Time-of-Flight Mass Spectrometry**; Meagan Bauer[1]; Chengpeng Chen[1]; [1]*University of Maryland Baltimore County, Baltimore, MD*

TP 512 **FBMN-STATS-GUIde: An AI-integrated Web Application for Statistical Analysis of Feature-Based Molecular Networking Results**; Rithi Krishnaraj[1]; Abzer Shah[2]; Michael Strobel[1]; Axel Walter[2]; Jarmo-Charles J. Kalinski[1]; Mingxun Wang[1]; Daniel Petras[1, 2]; [1]*University of California, Riverside, Riverside, CA;* [2]*University of Tübingen, Tübingen, Germany*

TP 513 **Spatial Metabolic Mapping of Avian Influenza**; Caitlyn E Middleton[1]; Dikshya Regmi[2]; Flavio Cargnin Cargnin Faccin[3]; Lindsey Claire Gay[3]; Juliana Calilbrondani[3]; Teresa Mejias[3]; Garret Cribbs[3]; Lisa J. Stabler[3</s;] [1]*San Diego State University, San Diego, CA;* [2]*Department of Population Health, College of Veterinary Medicine, University of Georgia, Athens, GA, United States, Athens, GA;* [3]*Department of Population Health, College of Veter*

TP 514 **Application of Zeno SWATH DIA in multi-tissue metabolomic profiling**; Qing Zhao[1, 2]; Guo Shou Teo[1, 2]; Chenyuan Huang[2]; Jiong-Wei Wang[2]; Thusitha WASANTHA THILAKA Rupasinghe[3]; Paul R Baker[4]; Markus R Wenk[1, 2, 5]; Hyungwon Choi[1, 2]; [1]*Singapore Lipidomics Incubator (SLING), Life Sciences Institute, National University of Singapore, Singapore, Singapore, Singapore;* [2]*Yong Loo Lin School of Medicine, National University of Singapore, Singapore, Singapore, Singapore;*

TP 515 **Comparative Metabolomics Uncovers PKS–NRPS–Derived Signals Modulating Nematode Development**; Kevin Mai[1]; Chisu Yoon[1]; Dilip Prajapati[1]; Yuelan Li[1]; Rongrong Yu[1]; Hanh Witte[2]; Subradeep Bhar[1]; Likui Feng[1]; Abraham Elijah[1]; Matthew Gordon[1;] [1]*University of Florida, GAINESVILLE, FL;* [2]*Max Planck Institute for Biology, Tuebingen, Germany*

TP 516 **Metabolic Genome Wide Association Study Using DIA-Based Metabolomics Data from a Human Heart Failure Cohort**; Susanne Nguyen[1, 2]; Fabian Schmitt[1, 2]; Mathias Hagen[1, 2]; Robin Martens[1, 3]; Julia Weinmann-Menke[1, 4]; Konstantin Strauch[1, 5]; Philipp Lurz[1, 3]; Katharina Geschke[1,]; *[1]University Medical Center, Mainz, Mainz, Germany; [2]Institute of Immunology, Mainz, Germany; [3]Preventive Cardiology and Preventive Medicine, Department of Cardiology, Mainz, Germany; [4]Research Center for Immunot*

TP 518 **Comprehensive Metabolomics and Spatial Tumor Tissue Metabolic Profiling of Murine Colorectal Cancer in Obese, Insulin-Resistant Mice Induced by High-Fat Diet**; Vi Thanh Tran[1]; Yueyi Huang[2]; Amir Reza Hematyar Naghneh[2]; Sue Tsai[2]; Liang Li[1]; *[1]Department of Chemistry, University of Alberta, Edmonton, AB; [2]Department of Medical Microbiology and Immunology, University of Alberta, Edmonton, AB*

TP 519 **Confident 4D Annotation of Polar Metabolites Using Standardized Retention Times Combined with TIMS-HRMS Acquisition**; Aiko Barsch[1]; Cristian De Gobba[2]; Hai Pham-Tuan[3]; Sebastian Gottfried[3]; Matthew R. Lewis[4]; Ondřej Hodek[5]; Matthias Anagho-Mattanovich[6]; Thomas Moritz[7, 8]; *[1]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [2]Bruker Nordic Denmark, Filial of Bruker Nordic AB, Copenhagen, Denmark; [3]Biocrates Life Sciences GmbH, Innsbruck, Austria; [4]Bruker UK Ltd., Coventry, United Kin*

TP 520 **Stratum corneum metabolomic signatures distinguish lesional and non-lesional skin in atopic dermatitis**; Mira Choi[1, 2]; Se Kyoo Jeong[3]; Jung U Shin[4]; Kyoung-Soon Jang[1, 2]; *[1]University of Science and Technology, Daejeon, South Korea; [2]Korea Basic Science Institute, Cheongju, South Korea; [3]Incospharm Corp, Daejeon, South Korea; [4]CHA Bundang Medical Center, Seongnam, South Korea*

TP 521 **Small-scale Highly Accurate and Reproducible Platform for Analyzing Plant Seed Tissue**; Kaitlyn M Melo[1]; Daoquan Xiang[2]; Xian Luo[1]; Liang Li[1]; *[1]The Metabolomics Innovation Centre, University of Alberta, Edmonton, AB; [2]National Research Council, Saskatoon, SK*

TP 522 **A Unified LC–MS Workflow with Ion Mobility and Retention Index Standardization for Natural Product and Exposome Profiling**; Tong Shen[1]; Jeremiah Wells[1]; Samantha Duncan[1]; Jazlyn Dias[1]; Oliver Fiehn[1]; *[1]UC Davis, Davis, CA*

TP 523 **NeoMe-Finder: Decoding the Modified Metabolome via Transfer Learning**; Jae-Yoon Jo[1]; Chang-Mo Yoo[2]; Hyun-Woo Rhee[2]; Jong-Seo Kim[1]; *[1]School of Biological Sciences, Seoul National University, Seoul, South Korea; [2]Department of Chemistry, Seoul National University, Seoul, South Korea*

TP 524 **Decoding Dietary Signatures in Human Fecal Metabolomes Using a Novel timsTOF Platform**; Michael Witting[1, 2]; Klidel Fae Rellin[1]; Theano Rizou[3]; Christina Virgiliou[3]; Georgios Theodoridis[3]; Aiko Barsch[4]; Matthew R. Lewis[4]; *[1]Helmholtz Munich - Metabolomics and Proteomics Core, Neuherberg, Germany; [2]Technical University of Munich, Freising, Germany; [3]Aristotle University of Thessaloniki, Thessaloniki, Greece; [4]Bruker Daltonics GmbH*

TP 525 **Untargeted Metabolomics of Tropical Raw Milk Highlights Seasonal Variation in Milk Composition**; Wimonphan Chathiran[1]; Jaruwan Chimasangkanan[1]; Worakrit Saiyasombat[1]; Pattaraporn Morasin[1]; Warangkana Srichamnong[1]; *[1]Institute of Nutrition, Mahidol University, NakhonPathom, Thailand*

TP 526 **High-Confidence Annotation Workflow for 4D-Metabolomics in Biological Samples**; Alena Langová[1]; Robert Jirásko[1]; Aiko Barsch[2]; Edward Rudt[2]; Matthew R. Lewis[2]; Michal Holčapek[1]; *[1]University of Pardubice, Faculty of Chemical Technology, Department of Analytical Chemistry, Pardubice, Czech Republic; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

TP 527 **Evaluation of Qualitative and Quantitative Workflows for CHO Cell Culture Metabolomics in Bioprocessing**; Yudong Sun[1]; Mohamed Hemida[1]; Jack Howland[2]; Amy A Caudy[2]; Baljit K Ubhi[2]; Rodell Barrientos[1]; Erik Regalado[1]; Meiping Chang[3]; Xuanwen Li[1]; *[1]Analytical Research and Development, MRL, Merck & Co., Inc., Rahway, NJ; [2]Matterworks Inc, Sommerville, MA; [3]Merck & Co, Rahway, NJ*

TP 528 **Differential Metabolomic and Lipidomic Dysregulation in Chronic and Acute Organophosphate Exposure**; Waziha Tasnim Purba[1]; Md Mostofa Al Amin Bhuiyan[1]; Hira Tasqeen[1]; Dina Elgameel[2];

Mojibola Fowowe[1]; Oluwatosin Daramola[1]; Judith Nwaiwu[1]; Junyao Wang[1]; Noha A.; [1]*Texas Tech University, Lubbock, TX;* [2]*Alexandria University, Alexandria, Egypt;* [3]*Center of Excellence for Toxicological Testing, Giza, Egypt;* [4]*Alamein International University, Alamein, Egypt*

TP 529 **Using a Large Serum Cohort Analyzed by Chemical Isotope Labeling LC–MS to Validate Metabolite Biomarkers for Rheumatoid Arthritis**; Xiaohang Wang[1]; Liang Li[2]; Walter P. Maksymowych[3]; [1]*The Metabolomics Innovation Centre (TMIC), Edmonton, AB;* [2]*Department of Chemistry, University of Alberta, Edmonton, AB;* [3]*CARE Arthritis Limited, Edmonton, AB*

TP 530 **Metabolomic Profiling of Phytochemical Biotransformation by Human Skin Bacteria**; Kyungha Lee[1]; Yeji Kim[2]; Kyo Bin Kang[2]; [1]*College of Pharmacy, Sookmyung Women's University, Seoul, South Korea;* [2]*Sookmyung Women's University, Seoul, South Korea*

TP 531 **Untargeted LC-MS/MS Profiling of Halide-Supplemented Marine-Derived Fungi**; Yukyung Choi[1]; Kyo Bin Kang[1]; [1]*College of Pharmacy, Sookmyung Women's University, Seoul, South Korea*

TP 532 **Deciphering the Impact of Fasting on Biological Pathways through LC-MS/MS Profiling of Serum Metabolites**; MD MOSTOFA AL AMIN BHUIYAN[1]; Waziha Tasnim Purba[1]; Oluwatosin Daramola[1]; Haneen S. Dwaib[2]; Ahmed Elyazbi[1, 3, 4]; Yehia Mechref[1]; [1]*Department of Chemistry and Biochemistry, Texas Tech University, Lubbock, TX;* [2]*Clinical Nutrition Department, Palestine Ahliya University, Bethlehem, Palestine;* [3]*Department of Pharmacology and Toxicology, Faculty of Pharm*

TP 533 **MassID as a complete metabolomics software platform with identification probabilities**; Ethan Stancliffe[1]; Monil Gandhi[1]; Ashima Mehta[1]; Douglas V. Guzior[1]; Kevin Cho[2]; Sandeep Acharya[1]; Adam Richardson[1]; Tom Cohen[1]; Gary Patti[1, 2]; [1]*Panome Bio, Saint Louis, MO;* [2]*Washington University in St. Louis, St. Louis, MO*

TP 534 **Statistically Informed Molecular Networking Reveals Species-Specific Metabolites in a Synthetic Cystic Fibrosis Microbial Community**; Emily C. Giedraitis[1]; Daniel J. Breiner[1]; Vanessa V. Phelan[1]; [1]*University of Colorado Anschutz, Aurora, CO*

TP 535 **Quantitative Gut Metabolomics at Population Scale: Disconnect Between Dietary Fiber and Microbial Short-Chain Fatty Acids Revealed in 200 Adults**; Alexey V. Melnik[1]; Alexander A. Aksenov[1, 2]; Dana Moradi[2]; Ali Lotfi[2]; [1]*AROME SCIENCE, Farmington, CT;* [2]*University of Connecticut, Storrs, CT*

TP 536 **Per-and polyfluoroalkyl substances (PFAS) driven reorganization of brain metabolism is impacted by the gut microbes**; Xiayan Ye[1]; Amy C. Burrows[1]; Anthony J. Horak III[1]; J. Mark Brown[1]; [1]*Cleveland Clinic, Cleveland, OH*

TP 537 **A Multi-Organ Murine Metabolomics Atlas Reveals Molecular Dysregulations in Alzheimer's Disease**; Simone Zuffa[1]; Celeste Allaband[1]; Vincent Charron-Lamoureux[1]; Andres M. Caraballo-Rodriguez[1]; Abubaker Patan[1]; Ipsita Mohanty[1]; Julius Agongo[1]; John W. Bostick[2]; [1]*UC San Diego, La Jolla, CA;* [2]*University of Florida, Gainesville, FL;* [3]*Indiana University, Indianapolis, IN;* [4]*California Institute of Technology, Pasadena, CA;* [5]*Baylor Scott & White Research Institute*

TP 538 **Exploring Fecal Bile Acid Profiles Related to Acute Gastrointestinal Graft-versus-Host Disease to Evaluate Possible Microbial Associations with Disease Outcomes**; Sadie Disselkoen[1]; Emily C. Vincent[1]; Tessa M. Andermann[2]; Erin S. Baker[1]; [1]*Department of Chemistry, University of North Carolina at Chapel Hill, Chapel Hill, NC;* [2]*Division of Infectious Diseases, School of Medicine, University of North Carolina at Chapel Hill, Chapel Hill, NC*

TP 539 **Creating and Searching a Metadata Network Graph for Microbiome Metabolomics**; Vincent Charron-Lamoureux[1]; Shipei Xing[2]; Abubaker Patan[2]; Haoqi Nina Zhao[2]; Kine Eide Kvite[2]; Simone Zuffa[2]; Mingxun Wang[3]; Karsten Zengler[2]; Pieter C. Dorrest; [1]*University of California San Diego, La Jolla, CA;* [2]*University of California San Diego, San Diego, CA;* [3]*University of California Riverside, Riverside, CA*

TP 540 **Fitness compensation reshapes growth-phase membrane lipid remodelling in ceftriaxone-resistant Neisseria gonorrhoeae**; Julia W Adug[1]; Stephanie L. Bishop[2]; Ian A. Lewis[1, 3, 4]; Adriana

Zardini Buzatto[1, 3, 4]; *[1]University of Calgary, Calgary, AB; [2]Western University, London, ON; [3]Alberta Centre for Advanced Diagnostics (ACAD), University of Calgary, Calgary, AB; [4]Calgary Metabolomics Research Facility (CMRF), Calgary,*

TP 541 **Mass spectrometry reveals metabolic rewiring in Bacillus subtilis following loss of surfactin and plipastatin**; Nataly Barger[1]; Ivan Plyushchenko[1]; Shai M. Zaid[1]; Bat-hen Eylon[1, 2]; Tal Luzzatto-Knaan[1, 2]; *[1]Department of Marine Biology, The Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel; [2]The Interdisciplinary Center for Metabolomics, University of Haifa, Haifa, Israel*

TP 542 **Multi-Omic Extraction Method for Bacterial Identification with Flow Injection-Ion Mobility–Mass Spectrometry**; Alexis V Torrence[1]; Kelly M Hines[1]; *[1]University of Georgia, Athens, GA*

TP 543 **Deep Metaproteomic Profiling of a Mock Ocean Microbial Community Using the Orbitrap Astral Zoom Mass Spectrometer**; Khiry L. Patterson[1]; Noelle Held[1]; Maxfield Palmer[1]; Nicolas Hartel[2]; *[1]University of Southern California, Los Angeles, CA; [2]Thermo Fisher Scientfic, San Jose, CA*

TP 544 **The Ghent Metaproteomics Toolbox for Improving Metaproteomics Data Analysis**; Tim Van Den Bossche[1]; Pieter Verschaffelt[1]; Xuxa Malliet[1]; Tanja Holstein[1]; Tibo Vande Moortele[2]; Simon Van De Vyver[2]; Lennart Martens[2]; Bart Mesuere[2]; *[1]VIB - UGent Center for Medical Biotechnology, Gent, Belgium; [2]Ghent University, Ghent, Belgium*

TP 545 **Multi-OMICS analyses of fecal extracts to explore the microbiome of rats following administration of an agonist for the GPR40 receptor**; Lee A Gethings[1]; Adam King[1]; James Hallam[1]; Roy Martin[2]; Robert S Plumb[1]; Ian D Wilson[3]; *[1]Waters, Wilmslow, United Kingdom; [2]Waters, Milford, MA; [3]Imperial College London, London, United Kingdom*

TP 546 **Enhancing Differentiation of Taxonomic Relatedness in a Synthetic Microbial Community with an Orbitrap Astral Mass Spectrometer**; Sarah Garcia[1, 2]; Richard Giannone[2]; Robert L. Hettich[2]; *[1]University of Tennessee, Knoxville, TN; [2]Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN*

TP 547 **Elucidating the Inhibitor of Burkholderia cenocepacia H111 Produced by Pseudomonas aeruginosa PAO1**; Matthew A Mondragon[1]; Vanessa V. Phelan[2]; *[1]Department of Immunology & Microbiology, School of Medicine, University of Colorado-Anschutz Medical Campus, Aurora, CO; [2]Department of Pharmaceutical Sciences, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of Co*

TP 548 **Using DIA de novo tools to optimize sample-matched metaproteomic databases, revealing diversity in the largest Antarctic sea ice metaproteome study**; Emma Timmins-Schiffman[1]; Brook L. Nunn[1]; Karen Junge[1]; Katarina Abrahamsson[2]; *[1]University of Washington, Seattle, WA; [2]University of Gothenburg, Gothenburg, Sweden*

TP 549 **MiCId_GUI: a MS-based Workflow for Fast and Accurate Pathogen Identification, Antibiotic Resistance Protein Identification, Biological Function Assignment, and Biomass Estimation**; Aleksey Y Ogurtsov[1]; Gelio Alves[1]; Yi-Kuo Yu[1]; *[1]Division of Intramural Research, National Library of Medicine, National Institutes of Health, Bethesda, MD*

TP 550 **Antiretroviral screening via LC-MS/MS to assess microbiota and drug interactions**; Charlotte R Hemmila[1]; Christopher M Basting[2]; Timothy J Griffin[1]; Nichole R Klatt[2]; Candace R Guerrero[1, 2]; *[1]University of Minnesota, Center for Metabolomics and Proteomics, Department of Biochemistry, Molecular Biology, and Biophysics, Minneapolis, MN; [2]University of Minnesota, Department of Surgery, Division of Surgical Outcomes and Prec*

TP 551 **Machine Learning Augmented MALDI-TOF Microbial Dereplication**; Michael Strobel[1]; Nyssa K Krull[2]; Robert A Shepherd[3]; Laura M Sanchez[3]; Brian T Murphy[2]; Mingxun Wang[1]; *[1]University of California, Riverside, Riverside, CA; [2]University of Illinois, Chicago, IL; [3]University of California, Santa Cruz, Santa Cruz, CA*

TP 552 **Molecular Signatures of Pyomelanin Production in MDR Acinetobacter baumannii: A Proteomic Perspective**; Lipsa Panda[1]; Ankit Halder[2]; Santosh Kumar Singh[3]; Minakshi Gupta[4]; Sheela Devi C[5]; Shashikala P[5]; Abhilash Barpanda[6]; Prashanth K[1]; *[1]Pondicherry University, Puducherry, India; [2]Indian Institute of Technology Bombay, Mumbai, India; [3]Arka Jain University, Jharkhand, India; [4]Manipal Tata Medical College, Jharkhand, India; [5]Pondicherr*

TP 553 **Plasmid and lysogenic prophage proteins produced by Shiga toxin E. coli (STEC) identified by MALDI-TOF-TOF and targeted top-down analysis**; Clifton K Fagerquist[1]; Yanlin Shi[1]; Mahesh Koirala[1,2]; *[1]USDA, Albany, CA; [2]Research Participation Program administered by the Oak Ridge Institute for Science and Education, U.S. Department of Energy., Oak Ridge, TN*

TP 554 **Sebum-associated shifts in facial skin metabolome and microbiome reveal markers of sebaceous balance**; Britta De Pessemier[1,2]; Alexey V. Melnik[3,4]; Yorick Minnebo[2]; Alexander Aksenov[3,4,5]; Simone Zuffa[3,6]; Jasmine Zemlin[3,6]; Yang Chen[1]; Tyler Myers[7,8]; Aki; *[1]Department of Pediatrics, School of Medicine, University of California San Diego, La Jolla, CA; [2]Center for Microbial Ecology and Technology, Ghent University, Ghent, Belgium; [3]Collaborative Mass Spectrometry Innovation C*

TP 555 **AI-based MALDI-MS microbial identifications**; Yoshihiro Yamada[1]; Tatsuki Okubo[1]; Kanae Teramoto[1]; Shinichi Iwamoto[1]; Koichi Tanaka[1]; *[1]Shimadzu Corporation, Kyoto, Japan*

TP 556 **Orthogonal separations by near-native capillary zone electrophoresis–mass spectrometry (CZE-MS) and size-exclusion chromatography–mass spectrometry (SEC-MS) reveal PTM-dependent Proteoform-resolved Plasminogen**; Christian Neusüß[1]; Hadi Lioe[2]; Toby Dite[2]; Sawyen Ow[2]; Matthias Pelzing[2]; *[1]Aalen University, Aalen, Germany; [2]CSL, Melbourne, Australia*

TP 557 **Decades of dreams coming true: capillary zone electrophoresis-mass spectrometry for reproducible multi-level proteomics**; Guijie Zhu[1]; Yifan Yue[1]; Jorge A Colón Rosado[1]; Guangyao Gao[1]; Xiaowen Liu[2]; Liangliang Sun[1]; *[1]Michigan State University, East Lansing, MI; [2]Tulane University, New Orleans, LA*

TP 558 **Mechanistic insights decode laser desorption/ionization effect of self-assembled TiO_2/Au nanoarray**; Yanyan Li; *shanghai jiaotong university, shanghai, China*

TP 559 **Fractionation of Bispecific Antibody Charge Variants by MauriceFlex™ and their Aggregate Characterization by Mass Photometry**; Srinivasa Rao[1]; Brenda Watt[2]; Francisco Ramirez[1]; Chris Heger[1]; *[1]Bio-techne, San Jose, CA; [2]Refeyn Inc, Waltham, MA*

TP 560 **Enhanced CESI8000 Performance on High-Sensitivity ToF Instruments Using a Newly Enclosed Source with Precision Emitter Positioning**; Stanislav Beloborodov[1]; Bradley B. Schneider[2]; Susan Darling[3]; *[1]SCIEX, Corncord, ON; [2]SCIEX, Concord, ON; [3]SCIEX, Redwood City, CA*

TP 561 **Under Pressure - Extending accessible metabolite coverage for microchip CE-MS through novel methods of operation**; J. Scott Mellors[1]; Will Thompson[1]; James Campbell[1]; J. Michael Ramsey[1]; *[1]Move Analytical LLC, Carrboro, NC*

TP 562 **Non-Targeted Analysis of Per- and Polyfluoroalkyl Substances in Environmental Extracts by Microflow LC-QToF Coupled with Multi-spray ESI**; Kathleen K Luo[1]; Jonathan Ferguson[1]; Tiffany Liden[1]; Om K Shrestha[1]; Risa Suzuki[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD*

TP 563 **Online Disulfide-Bond Reduction Integrated into Capillary Isoelectric Focusing Mass Spectrometry (cIEF-MS) for Antibody Structural Characterization**; Stanislav Beloborodov[1]; Pavel Ryumin[2]; *[1]SCIEX, Corncord, ON; [2]SCIEX, Concord, ON*

TP 564 **Deciphering the Blob: Coupled Native Capillary Electrophoresis and Trapped Ion Mobility Increases Peak Capacity on E. coli Lysate**; Nicolas J Pizzala[1,2]; Yun-Jung Hsu[1,2]; William Moeller[1,2,3]; Zihao Qi[1,2,3]; Martha Ortega Zepeda[2,3]; Guangyao Gao[4]; Fei Fang[4]; Guijie Zhu[4]; Liangliang Su; *[1]Georgia Institute of Technology School of Chemistry and Biochemistry, Atlanta, GA; [2]Native MS Guided Structural Biology Center, Georgia Institute of Technology, Atlanta, GA; [3]Department of Chemistry and Biochemistry, The*

TP 565 **Accurate UHPLC-MS/MS Method for Simultaneous Quantification of Kavalactones and Flavokawains from Kava Extract in Primary Human Hepatocyte Medium**; Estatira Sepehr[1]; Yang Zhao[1]; Cory Vaught[1]; Kyra Headrick[1]; Megan Culbreth[1]; Jeffrey Yourick[1]; Kirsten Eckstrum[1]; [1]*Office of Chemistry and Toxicology, Office of Laboratory Operations and Applied Science, Human Foods Program, U.S. Food and Drug Administration, laurel, MD*

TP 566 **Metabolic plasticity of Oxyria digyna as a platform for sustainable production of phenolic bioactives**; Mira Choi[1, 2]; Moonkyo Kim[3]; Hyemi Jang[1]; Yoo Kyung Lee[3]; Kyoung-Soon Jang[1, 2]; [1]*Korea Basic Science Institute, Cheongju, South Korea;* [2]*University of Science and Technology, Daejeon, South Korea;* [3]*Korea Polar Research Institute, Incheon, South Korea*

TP 567 **An expert data analysis tool for analysis of proanthocyanidins (PACs) in cranberries using UHPLC-HRAM MS data**; Pei Chen[1]; Mengliang Zhang[2]; Ping Geng[3]; [1]*USDA-ARS, Beltsville, MD;* [2]*Ohio University, Athens, OH;* [3]*USDA-ARS, Beltsivlle, MD*

TP 568 **Validated LC-MS/MS Method for Total Aflatoxins in Herbal Medicines**; Juhyup Lee[1]; Hyunyoung Park[1, 2]; Gaeun Choi[1]; Inyeong Hwang[1]; Jinhee Hwang[1]; [1]*National Institute of Food and Drug Safety Evaluation, cheong ju, South Korea;* [2]*College of Pharmacy, Chungbuk National University, cheong ju, South Korea*

TP 569 **Searching for new antimicrobial agents by elicitor screening in a Kitasatospora isolate deficient in producing an annotated antimicrobial**; Frank M.L. Peeters[1]; Celina Anders[1]; Mortoza Ashraf[1]; Leonie Sagurna[1]; Julia E. Bandow[1]; [1]*Ruhr Universität Bochum, Bochum, Germany*

TP 570 **Closing the Volatile Gap: Complementing High Resolution LC-MS/MS with SPME and GC-TOF MS for Comprehensive Characterization of Natural Products**; Uri Keshet[1]; Luis Valdivez[1]; Jeremiah D Wells[1]; Oliver Fiehn[1]; [1]*UC Davis, Davis, CA*

TP 571 **Avoiding Misidentification of Hydroxylated Cannabidiol Metabolites: The Critical Role of Standards and MS/MS Fragmentation**; Giovanna Baron[1]; Sara Casati[1]; Larissa Della Vedova[1]; Alessandra Altomare[1]; Gabriella Roda[1]; Giulio Vistoli[1]; Benedetta Bassetti[2]; Alessandro Palmieri[2]; Lolita; [1]*University of Milan, Milan, Italy;* [2]*University of Camerino, ChIP Research Center, Camerino, Italy;* [3]*Indena S.p.A., Milan, Italy*

TP 572 **Mapping Fungal Metabolites to Lipoxygenase Inhibition Using MS/MS and Bioassays**; Eunah Jeong[1]; Kyo Bin Kang[1]; [1]*College of Pharmacy, Sookmyung Women's University, Seoul, South Korea*

TP 573 **Elucidating Zostera marina and Oryza sativa metabolic profiles by using computational mass spectrometry techniques**; Yoshimasa Todoroki[1]; Yuki Matsuzawa[1]; Shohei Nakamukai[2]; Wei He[3]; Hiroki Takezawa[4]; Makoto Fujita[4]; Hiroyuki Kasahara[2, 5]; Naoko Ohkama-Ohtsu[5]; Yu Umezawa[5]; [1]*Tokyo University of Agriculture and Technology, Koganei-shi, Tokyo, Japan;* [2]*RIKEN Center for Sustainable Resource Science, Yokohama-shi, Kanagawa, Japan;* [3]*Institute for Molecular Science, Okazaki-shi, Aichi, Japan;* [4]

TP 574 **Structural characterization of novel pyrrolizidine alkaloids in lamb's lettuce using liquid chromatography-coupled infrared ion spectroscopy**; Teun Van Wieringen[1, 2]; Leonie V. Straub[3, 4]; Patrick P. J. Mulder[3]; Dieuwertje E. Streefkerk[4]; Lara Van Tetering[1, 2]; Hidde Elferink[1, 2]; Giel Berden[1, 2]; Josipa Grzetic; [1]*HFML-FELIX, Nijmegen, Netherlands;* [2]*Radboud University, Nijmegen, Netherlands;* [3]*Wageningen Food Safety research, Wageningen, Netherlands;* [4]*Wageningen University & Research, Wageningen, Netherlands*

TP 575 **Quantification of Cyanogenic Glycoside in American Elderberry Cultivars**; Ronald J Myers[1]; Sydney D Moore[1]; Elizabeth Prenger[1]; Andrew L Thomas[2]; Lloyd W. Sumner[3]; [1]*University of Missouri-Columbia, Columbia, MO;* [2]*Southwest Research, Extension, and Education Center, University of Missouri, Mount Vernon, MO, Mt. Vernon, MO;* [3]*The University of Missouri at Columbia, Columbia, MO*

TP 576 **Funtctional Genomic Analyisis and UHPLC-HRMS Reveal the Molecular Basis for Caminic Acid Biosynthesis**; Hector Rogelio Najera-Gonzalez[1]; Luis Herrera-Estrella[2]; Gerardo Alejo-Jacuinde[2]; Nestor Daniel Ramos-Camacho[3]; [1]*Texas Tech University, Lubbock, TX;* [2]*Texas Tech University, Lubbock,, TX;* [3]*Centro de Investigacion y Estudios Avanzados, CINVESTAV, Irapuato, Mexico*

TP 577 **Discovery of a new fungal anthelmintic with a candidate halogenating PKS gene cluster via metabologenomics and nematode-focused bioactivity screening**; Raveena Gupta[1]; J.B. Collins[2]; Jin Woo Bok[3]; Harrison Estes[3]; Gini Besant[1]; Maanasa Narayanamoorthy[1]; Christos D. Malliakas[1]; Fatma A. Butun[1]; Nancy P. Keller<s; *[1]Northwestern University, Evanston, IL; [2]Johns Hopkins University, Baltimore, MD; [3]University of Wisconsin - Madison, Madison, WI*

TP 578 **Probing Non-Covalent Natural Product–Lipid Binding Using TIMS-MS/MS**; Kevin Jeanne Dit Fouque[1]; Ryan E Moreira[2]; Wilfred Van Der Donk[2]; Francisco Fernandez Lima[1]; *[1]Florida International University, Miami, FL; [2]University of Illinois at Urbana-Champaign, Urbana-Champaign, IL*

TP 579 **Profiling metabolomes of South African Landrace Cannabis Inflorescence**; Jarmo-Charles Julian Kalinski[1]; Ntobeko Songcata[1]; Aphiwe Mfuku[1]; Ronen Fogel[1]; Janice Limson[1]; *[1]Rhodes University, Grahamstown, South Africa*

TP 580 **Metabolic and Immunomodulatory Effects of a 2-Carbon Folate**; Cloe R Zimmerman[1, 2]; Daniel Röth[1]; Pradnya Patil[1]; Belinda Shen[1]; Xiancai Zhong[1]; Zuoming Sun[1, 2]; Markus Kalkum[1, 2]; *[1]City of Hope, Duarte, CA; [2]Iirell and manella graduate school of biological sciences, Duarte, CA*

TP 581 **LC/GC-MS fingerprinting in a Southern African wild Sesame plant: Phytochemical Studies and Biotechnological Application**; A O Adeeyo[1]; D Thabang[2]; R Makungo[2]; Hlengilizwe Nyoni[3]; Thabo T.I. Nkambule[1]; Titus A.M. Msagati[4]; *[1]Institute for Nanotechnology and Water Sustainability (iNanoWS), College of Science, Engineering and Technology (CSET), UNISA, South Africa, Johannesburg, South Africa; [2]Department of Earth Science, Faculty of Science, Engineering a*

TP 582 **LC–MS/MS-Based Metabolomic Profiling of Solvent-Polarity-Fractionated Akebia quinata Seed Extracts Linked to Bioactivity**; In Jin Ha[1, 2]; Mibae Jeong[2, 3]; Min Young Lee[1]; Jamoo Chun[3, 4]; Kwang Seok Ahn[2]; *[1]Korean Medicine Clinical Trial Center (K-CTC), Korean Medicine Hospital, Kyung Hee University, Seoul 02447, Republic of Korea, Seoul, South Korea, Seoul, South Korea; [2]Department of Science in Korean Medicine, College of Korean Medi*

TP 583 **Rapid source authentication and marker discovery of musk in traditional Chinese medicine using ambient SICRIT-QTOF**; Shujie Zou[1]; Echo W. Jia[1]; Xiaokun Duan[1]; Shuangshuang Zou[2]; Bin Liang[3, 4]; Charles C. Liu[1]; *[1]ASPEC Technologies Limited, Beijing, China; [2]Macau University of Science and Technology, Macau, China; [3]Tianjin University, Tianjin, China; [4]Guangdong University of Technology, Guangzhou, China*

TP 584 **Identifying novel biomarkers of neurocognitive impairment in people with HIV using untargeted fecal metabolomics data**; Crystal X Wang[1]; Helena Mannochio-Russo[1]; Megan R. Nelson[1]; Harsha Gouda[1]; Jasmine Zemlin[1]; Victoria Deleray[1]; Jennifer E. Iudicello[1]; Donald Franklin[1]; Robert; *[1]UC San Diego, San Diego, CA*

TP 585 **Multidimensional Ion Mobility Mass Spectrometry for Structural Characterization of Alzheimer's Disease Biomarkers**; Kimberly Y Kartowikromo[1]; Michael Zirpoli[1]; Jingyi Zheng[1]; Ahmed M Hamid[1]; *[1]AUBURN UNIVERSITY, Auburn, AL*

TP 586 **MALDI Mass Spectrometry Imaging of Lipids in Neurological Development and Degeneration**; Arya I Lall[1]; Elizabeth Reynolds[1]; Siyu Lin[1]; Aijun Wang[1]; Elizabeth Neumann[1]; *[1]University of California, Davis, Davis, CA*

TP 587 **Sequence-dependent ionization of antibody-siRNA conjugates: enabling intact multi-attribute method (iMAM) for comprehensive characterization and identification**; Hao Liu[1]; Jamie Veltri[1]; Clayton Gough[1]; Sean Crowe[2]; Elizabathe Davis[2]; Matt Whitaker[2]; Ciaran Buckley[2, 3]; Zhirui Lian[2]; *[1]Eli Lilly and Company, Indianapolis, IN; [2]Eli Lilly & Company, Indianapolis, IN; [3]Eli Lilly Kinsale Limited, Dunderrow, Ireland*

TP 588 **Protein interactome mapping in human excitatory neurons reveals novel risk genes and pathways in Alzheimer's disease**; Xiaomu Wei[1]; Katie Munechika[2, 3]; Yu Sun[1, 2]; Yuansong Wan[4]; Tianyu Xia[1, 2]; Yuan Hou[5]; Wenqiang Song[5]; Kumar Yugandhar[2]; Yiwen Wang[1, 2]; Se-In Lee<s; *[1]Department of*

Computational Biology, Cornell University, Ithaca, NY; [2]Weill Institute for Cellular and Molecular Biology, Cornell University, Ithaca, NY; [3]Meinig School of Biomedical Engineering, Cornell University, Ithac

TP 589 **Optimizing nESI-MS for Small Amyloid Protein Oligomers Elucidates Early-Stage Aggregation Pathways and Inhibition by Homologous Proteins**; Zoe J Heidersbach[1]; Eileen Jacqueline Olivares[1]; Emily J Byrd[1, 2]; Rachel R Ogorzalek Loo[1]; Joseph A Loo[1]; *[1]University of California, Los Angeles, Los Angeles, CA; [2]University of Leeds, Leeds, United Kingdom*

TP 590 **Dissecting the Tangled Web of Tau Protein: A Stepping-Stone Approach**; Marissa Bullard[1]; Robert Rider[1]; Zhenyu Xi[1]; Jared Hampton[1]; Carter Lantz[1]; David H Russell[1]; *[1]Texas A&M Univesity, College Station, TX*

TP 591 **Quantitative Glycoproteomics Reveals Aberrant Sialylation of Brain Proteins and Their Association with Depressive Behaviors in Mice**; Hee Young Jo[1, 2]; Myung Jin Oh[1, 2]; Bomi Chang[3]; Minji Son[3]; Boyoung Lee[3]; Hyun Joo An[1, 2]; *[1]Asia-Pacific Glycomics Reference Site, Chungnam National University, Daejeon, South Korea; [2]Graduate School of Analytical Science and Technology, Chungnam National University, Daejeon, South Korea; [3]Center for Cognition a*

TP 592 **Postmortem interval drives degradation and phosphorylation at specific protein domains in the brain**; Kimia Ghafari[1, 2]; Shelby Ruiz[1, 2]; Lambertus Klei[1]; Bernie Devlin[1]; Robert Sweet[1, 2]; Matthew MacDonald[1, 2]; *[1]Department of Psychiatry, University of Pittsburgh School of Medicine, Pittsburgh, PA; [2]Center for Neuroscience at University of Pittsburgh, Pittsburgh, PA*

TP 593 **Investigating the Reversibility of LMNB1 Overexpression in an ADLD Mouse Model Using Unbiased Mass-spectrometry-based Proteomics**; Alexandra M Izydorczak[1]; Xuemei Zeng[2]; Nathan Herdman[1]; Quasar S Padiath[1]; Thomas K. Karikari[1]; *[1]University of Pittsburgh, Pittsburgh, PA; [2]UPMC, Pittsburgh, PA*

TP 594 **Identification of Extremely Long-Lived Nucleolar Proteins in Mouse Brain**; SangEun Yeom[1]; Anika Wilen[1]; Jeffrey Savas[1]; *[1]Northwestern University, Chicago, IL*

TP 595 **Time-Resolved pSILAC-DIA proteomics reveals protein synthesis and degradation modulation during Tau seeding in Alzheimer's disease**; YUE DOU[1]; Sameek Singh[1]; Shuo Yuan[1]; Lulu Jiang[1]; Tian Zhang[1]; *[1]University of Virginia, Charlottesville, VA*

TP 596 **Mapping the proteomic landscape of human neurodegeneration over time with iNeurons**; Megan Hong[1, 2]; Vijaya Pandey[3]; Aria Mehrpour[2]; Saiya Shah[1]; James A Wohlschlegel[3, 4]; Avi Samelson[1]; Joseph A Loo[2, 3]; Gal Bitan[1]; *[1]Department of Neurology, David Geffen School of Medicine, UCLA, LOS ANGELES, CA; [2]Department of Biochemistry, UCLA, LOS ANGELES, CA; [3]Department of Biological Chemistry, David Geffen School of Medicine, LOS ANGELES, CA; <*

TP 597 **Utilization of a Novel Nanoflow LC-MS Platform to Detect and Quantitate AETA Fragments in Human Cerebrospinal Fluid**; Justyna A Dobrowolska Zakaria[1]; Helena Svobodova[2]; Gary Valaskovic[2]; Amanda Berg[2]; Robert J. Vassar[1]; *[1]Northwestern University Feinberg School of Medicine, Chicago, IL; [2]New Objective, Inc., Littleton, MA*

TP 598 **Dysregulated response to Epstein Barr virus lytic reactivation drives MS specific B cell perturbations**; Danielle M Caefer[1, 2]; Ethan Goodman[1]; Alena Zhirova[1]; Devin King[1, 2]; Kyle Downer[1]; Shrishti Saxena[1]; Tanuja Chitnis[1, 2]; *[1]Brigham and Women's Hospital, Boston, MA; [2]Harvard Medical School, Boston, MA*

TP 599 **Integrated multi-omic interrogation of Alzheimer's disease links known and novel disease pathologies**; Douglas V Guzior[1]; Ethan Stancliffe[1]; Monil Gandhi[1]; Sandeep Acharya[1]; Ashima Mehta[1]; Caitlin Kelly[1]; Sharla Friend[1]; Adam Richardson[1]; Tom Cohen[1]; C; *[1]Panome Bio, Saint Louis, MO; [2]Washington University in St. Louis, Saint Louis, MO*

TP 600 **Combining Direct Mass Technologies, Native MS, AP-MS, and Proteomics on a Modified Orbitrap Ascend to Define Brain-Isolated Neurotransmitter Receptor Organizations**; Tarick El-Baba[1]; Sophie Lawrence[2]; Frances I Butroid[2]; Jack L Bennett[2]; Olivia Ramsay[2]; Titas Radzevicius[2]; Corinne A

Lutomski[2]; Kenny Chan[3]; Cameron Fairweathe; *[1]University of Oxford, Oxford, United Kingdom; [2]Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom; [3]Icahn School of Medicine at Mount Sinai, Friedman Brain Institute, New York City, NY*

TP 601 **Advancing lipid identification and untargeted lipidomics of brain in Alzheimer's Disease by high-energy collisional dissociation and electron-activated dissociation mass spectrometry**; Cheuk Woon Lui[1]; Xuewei Ye[2, 3]; Elizabeth T, Anderson[2]; Robert Proos[4]; Santosh Gorti[4]; Qin Fu[2]; Gary E. Gibson[5]; Sheng Zhang[2]; *[1]Cornell University, Ithaca, NY; [2]Proteomics and Metabolomics Facility, Cornell University, Ithaca, NY; [3]Key Laboratory of Artificial Organs and Computational Medicine of Zhejiang Province, Shulan International Medical Col*

TP 602 **Defining the Impact of Amyloid Pathology on Synaptic Homeostasis Across the Sleep–Wake Cycle**; Ivan G Santiago Marrero[1]; Christopher J Olker[2]; Eun-Joo Song[2]; Martha H Vitaterna[2]; Jeffrey N Savas[3]; *[1]Northwestern University Fienberg School of Medicine, Chicago, IL; [2]Northwestern University, Evanston, IL; [3]Northwestern University Feinberg School of Medicine, Chicago, IL*

TP 603 **Impact of Space Exposome on Immunocompetent Cortical Organoids**; Luisa B.V. Coelho[1]; Natalia C.S. Moreira[2]; Juliana de S. da G. Fischer[2]; Blake Tsu[2]; Paulo Costa Carvalho[2, 3]; Alysson R. Muotri[2]; Aline Martins[2]; *[1]University of California San Diego, San Diego; [2]Integrated Space Stem Cell Orbital Research, San Diego, CA; [3]Carlos Chagas Institute, Fiocruz Paraná, Curitiba, Brazil*

TP 604 **Beyond Plaques and Tangles: Spatial Proteomic Imaging of Brain Subanatomical Regions in Alzheimer's Disease**; Peggi Angel[1]; Jessica Lord[1]; Anand Mehta[1]; Richard R. Drake[1]; Sean Bendall[2]; Stefan Prokop[3]; Ramon Sun[3]; Harrison B. Taylor[1]; *[1]Medical University of South Carolina, Charleston, SC; [2]Stanford School of Medicine, Palo Alto, CA; [3]University of Florida, Gainesville, FL*

TP 605 **High-Resolution MALDI-HiPLEX-IHC Reveals Plaque-Associated Remodeling of Gangliosides in Relation to AD-Associated Proteins in Alzheimer's Disease Brain**; Yumiko Toyama[1]; Takashi Nirasawa[2]; Maiko Okamura[3]; Kohei Yuyama[4]; Hui Sun[4]; Kazuhiro Irie[3]; Mark J. Lim[5]; Kenneth J Rothschild[5]; Gargey B. Yagnik[5]; Victor S; *[1]Doshisha University, Kyotanabe-city, Japan; [2]Bruker Japan K.K., Yokohama, Japan; [3]Doshisha University, Kyotanabe City, Japan; [4]Hokkaido University, Sapporo, Japan, Japan; [5]AmberGen, Inc., Billerica,*

TP 606 **Spatial-Omic Profiling of the Fmr1KO Mouse Brain Using Multi-faceted Mass Spectrometry**; Julia L Hoffman[1]; Thao Duong[1]; Hung-Yu Chiang[2]; Hua Zhang[3]; Hannah Miles[3]; Elliot Patrenets[4]; Ashley Phetsanthad[1]; Pamela R. Westmark[5]; Cara J. Westmark[5,;] *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Biophysics Program, University of Wisconsin-Madison, Madison, WI; [3]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [4]Depa*

TP 607 **Proteomics of Alzheimer's Disease Kinase-Specific Tau441 by Integrated Top-Down CZE–MS and Bottom-Up LC/CZE–MS/MS Reveals Distinct Phosphosignatures**; Reyhane Tabatabaeian Nimavard[1]; Jorge A Colón Rosado[1]; Seyed Amirhossein Sadeghi[1]; Yifan Yue[1]; Fei Fang[1]; Guijie Zhu[1]; Guangyao Gao[1]; Lance Thorp[1]; Liangliang; *[1]Michigan State University, East Lansing, MI*

TP 608 **Quantitative proteomic analysis of differentially expressed protein signatures in IRF5-knockout primary murine microglia**; Lipi Das[1]; Valeria Vasciaveo[2]; Cristina D'Abramo[2]; David S. Johnson[1]; Luca Giliberto[2]; Lewis M. Brown[1]; *[1]Department of Biological Sciences, Quantitative Proteomics and Metabolomics Center, Columbia University, New York City, NY; [2]Litwin-Zucker Center for the Study of Alzheimer's Disease, Northwell Health System, New York City, NY*

TP 609 **Overcoming Sensitivity and Recovery Challenges in Quantitation of Conjugated Oligonucleotide Therapeutics Using Clarity™ OTX Pro SPE Kits**; Tran N Pham[1]; Roxana Eggleston-Rangel[1]; Namrata Saxena[1]; Lucia Geis Asteggiante[1]; *[1]Phenomenex, Inc. - Torrance, CA, Torrance, CA*

TP 610 **Bioanalysis of oligonucleotide therapeutics across diverse lengths and chemistries using Enhanced Protein Precipitation followed by LCMS**; Afrand Kamali[1]; Juili D Shelke[1]; Michael M Hayashi[1]; Natthamon Chaisakhon[1]; Jianzhong Chen[1]; Guangnong Zhang[1]; *[1]Novo Nordisk, Lexington, MA*

TP 611 **A LC-MS Ready Size Exclusion Chromatographic Platform Method for Oligonucleotide and mRNA Identification**; Crystal Holt[1]; Shilin Cheung[1]; *[1]Phenomenex, Torrance, CA*

TP 612 **HFIP and amine ion pair free reversed-phase LC-MS platform for automated characterization of therapeutic oligonucleotides**; Ulrik Hvid Mistarz[1]; Silvia Millán-Martín[2]; Sara Carillo[2]; Ken Cook[3]; Jonathan Bones[2, 4]; *[1]Thermo Fisher Scientific, Copenhagen NV, Denmark; [2]National Institute for Bioprocessing Research and Training, Dublin, Ireland; [3]Thermo Fisher Scientific, Morpeth, United Kingdom; [4]School of Chemical and Biopro*

TP 613 **Enhancing DNA Triplex Stability: Native Mass Spectrometry and Chemical Modification Strategies**; Sarveenah R G Chandrasegaran[1]; Tara Pukala[1]; *[1]Adelaide University, Adelaide, Australia*

TP 614 **Structural Characterization of Ligand-bound RNA Hairpins on an Orbitrap Tribrid Mass Spectrometer**; Rosa Viner[1]; Joshua Hinkle[1]; Scott R. Kronewitter[2]; Robert Ross[2]; Kyle P Bowen[1]; Tobias P. Woerner[3]; Chris Vonnegut[4]; John C. Rogers[4]; Alexander A. Makarov; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Lexington, MA; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [4]Thermo Fisher Scientific, Eugene, OR*

TP 615 **Purification and Fractionation of Placental tRNA for Comprehensive LC-MS/MS Modification Analysis**; Hina Zain[1]; Bibek Hamal[1]; Patrick A. Limbach[1]; *[1]University of Cincinnati, Cincinnati, OH*

TP 616 **Characterization of poly(A) and poly(T) tail lengths in plasmid DNA by LC-HRMS**; Nour AL-TURIHI[1]; Anpu WANG[1, 2]; Delphine Allouche[1]; Maelle Queré[1]; Mathieu Sculler[1]; Samantha Nicolau[2]; Kaiyue Wu[2]; Xiaobo Gu[2]; Yanhua Yan[2]; Isabell; *[1]Sanofi, MARCY-L'ÉTOILE, France; [2]Sanofi, Waltham, MA*

TP 617 **Concerted strategies for the de novo sequence characterization of heavily modified gapmer antisense oligonucleotide biotherapeutics**; Sarah Mutchek[1]; Thomas Kenderdine[1]; Aubrie Soucy Verran[2]; Timothy Yu[2]; Dan Fabris[1, 3]; *[1]University of Connecticut, Storrs, CT; [2]Boston children's hospital, Boston, MA; [3]RiboDynamics, Manchester, CT*

TP 618 **Probing the Effect of Sequence Modifications on Ribonucleic Acid Stability by Collision Induced Unfolding**; Courteney R Dufrene[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

TP 619 **Metabolic Characterization of Dual-Lipid Conjugated siRNAs: Sequence Effects, Species Differences, and In Vitro-In Vivo Correlation**; Liping Deng; *Novartis GDC, San Diego, CA*

TP 620 **A Pipeline for the Epitranscriptomic Analysis of MicroRNAs by Liquid Chromatography/Mass Spectrometry**; Burke Niego[1]; Nicholas E. Bollis[1]; Claire E. Boos[1]; Mark Scalf[1]; Michael R. Shortreed[1]; Lloyd M. Smith[1]; *[1]University of Wisconsin-Madison, Madison, WI*

TP 621 **Magnetic-Solid Phase Extraction for LC-MS/MS Analysis of GalNAc-Conjugated Oligonucleotides in Plasma and Urine**; Yan Song[1]; Jin Xie[1]; Peiyun An[1]; Jinlian Lu[1]; Zhiyu Li[1]; Lili Xing[1]; Yi Tao[1]; Liang Shen[1]; Zhiren Yu[1]; *[1]WuXi AppTec, Pudong, Shanghai, China*

TP 622 **Higher-Energy Collisional Dissociation Fragmentation of siRNA Utilizing Nano Liquid Chromatography Tandem Mass Spectrometry to Characterize Unknown Synthetic Modifications**; Alan J. Zimmerman[1]; Tyler Chickering[1]; Patrick Miller[1]; Kaitlyn Pifer[1]; Juan Salinas[1]; Daniel Donnelly[1]; Mark Schlegel[1]; Punit Seth[1]; *[1]Alnylam Pharmaceuticals, Cambridge, MA*

TP 623 **Rapid standard-free determination of site-specific deamination rates in therapeutic antisense oligonucleotides by tandem mass spectrometry**; Zifan Li[1]; Haorong Li[1]; Tai Nguyen[1]; Jiabao Zhang[1]; Xuan Zhou[1]; George Bou-Assaf[1]; *[1]Biogen, Cambridge, MA*

TP 624 **Adducts of Oligonucleotides Formed with Background Chemical Impurities Upon Ion Pair-Reversed Phase (IP-RP) LCMS ESI Analysis**; Stilianos G. Roussis[1]; Claus Rentel[1]; *[1]Ionis Pharmaceuticals, Inc., Carlsbad, CA*

TP 625 **Size Exclusion Coupled with Mass Spectrometry (SEC-MS) for Early OAR Characterization of Antibody–Oligonucleotide Conjugates (AOCs)**; Tran N Pham[1]; Jeremy Primack[1]; Roxana Eggleston-

Rangel[1]; Lucia Geis Asteggiante[2]; Sujatha Chilakala[1]; *[1]Phenomenex, Inc. - Torrance, CA, Torrance, CA; [2]Phenomenex, Torrance, CA*

TP 626 **Characterizations of G-quadruplex RNA-Protein Interactions in Living Cells**; Xiaochen Liang[1]; Feng Tang[2]; Yinsheng Wang[3]; *[1]University of California Riverside, Riverside, CA; [2]Department of Chemistry, University of Florida, Gainesville, FL; [3]University of California, Riverside, Riverside, CA*

TP 627 **Integrative Mass Spectrometry Analyses Revealed the Mechanism underlying HMGB3's Functions in Minor-Groove DNA Alkylation Lesion Repair**; Ting Zhao[1]; Xiaochen Liang[1]; Xiaomei He[1]; Yinsheng Wang[1]; *[1]University of California, Riverside, CA*

TP 628 **Charge Detection Mass Spectrometry for Intact mRNA and Lipid Nanoparticle Characterization in RNA Therapeutics**; Lohra Miller[1]; Benjamin E Draper[1]; Mark Chipley[2]; Martin F Jarrold[1, 3]; *[1]Megadalton Solutions, Bloomington, IN; [2]Pfizer, Chesterfield, MO; [3]Indiana University Bloomington, Bloomington, IN*

TP 629 **Uncovering Manufacturing-Driven Variability in Phosphorothioate Oligonucleotide Isomer Profiles with cyclic Ion mobility MS**; Jonathan E Fox; *Waters, Wilmslow, United Kingdom*

TP 630 **A streamlined LC-MS workflow for intact oligonucleotide analysis with enhanced MS sensitivity**; Zoe Zhang[1]; Haichuan Liu[2]; Jingwen Ding[2]; *[1]Sciex, Redwood City, CA; [2]SCIEX, Redwood City, CA*

TP 631 **Enhancing transfer RNA (tRNA) modification mapping by LC-MS/MS through FPLC fractionation**; Aastha Gyawali[1]; Patrick A. Limbach[1]; *[1]University of Cincinnati, Cincinnati, OH*

TP 632 **Cation exchange chromatography directly coupled to high resolution mass spectrometry for the analytical characterization of phosphorodiamidate morpholino oligomers**; Ken Cook[1]; Silvia Millán-Martín[2]; Sara Carillo[3]; Ulrik Hvid Mistarz[4]; Jonathan Bones[3]; *[1]Thermo Fisher Scientific, Morpeth, United Kingdom; [2]National Institute for Bioprocessing Research and Training, Dublin, Ireland; [3]National Institute for Bioprocessing Research & Training, Dublin, Ireland; [4]Ther*

TP 633 **Optimizing low-energy CID fragmentation for maximizing sequence coverage of oligonucleotide therapeutics**; Zabrina Malto[1]; Sage Hoffman[2]; Mirandia Szramowski[1]; Jace W. Jones[1]; *[1]University of Maryland, School of Pharmacy, Department of Pharmaceutical Sciences, Baltimore, MD; [2]University of Maryland, College Park, MD*

TP 634 **Pairing multiple enzymes with a Universal Mass Exclusion List (UMEL) to map tRNA Modifications using LC-MS/MS**; Bibek Hamal[1]; Patrick A. Limbach[1]; *[1]University of Cincinnati, Cincinnati, OH*

TP 635 **Forced degradation studies of small oligonucleotide therapeutics: IPRP-HRAMS as a stability-indicating analytical method to decipher high complexity samples**; Silvia Millan Martin[1]; Felipe Guapo[1]; Corentin Beaumal[1]; Sara Carillo[1]; Ulrik Hvid Mistarz[2]; Ken Cook[3]; Jonathan Bones[1, 4]; *[1]NIBRT, Dublin, Ireland; [2]Thermo Fisher Scientific, Copenhagen NV, Denmark; [3]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom; [4]School of Chemical and Bioprocess Engineering, University College Dublin,*

TP 636 **High-Resolution Mass Spectrometry for Accelerated Stability Modeling and Shelf-Life Prediction of Lipid-Modified Oligonucleotides**; Laura Corveleyn[1]; Kevin Roeleveld[1]; Birger Zutterman[1]; Geert Van Raemdonck[1]; *[1]AnaBioTec, Evergem, Belgium*

TP 637 **Tandem Collision-Induced Unfolding and Molecular Dynamics Reveal How Post-Translational Succination Reshapes SUMO1 Unfolding Pathways**; Louis E Groignet[1]; Thomas Robert[1]; Quentin Duez[1]; Jehan Claessens[2]; Patrick Brocorens[1]; Mathieu Surin[1]; Pascal Gerbaux[1]; Julien De Winter[1]; *[1]University of Mons, Mons, Belgium; [2]UCB BioPharma SRL, Braine-l'Alleud, Belgium*

TP 638 **Polypeptide Size Affects Tyrosine-O-Sulfation Retention in Electron-Based Dissociation**; Kuan-Lu Wu[1, 2]; Sean D Dunham[1]; Julissa Bonilla[1, 2]; Neven N Mikawy[1, 2]; Lissa C Anderson[1, 2]; Kristina Håkansson[1, 2]; *[1]Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, Tallahassee, FL; [2]Florida State University, Tallahassee, FL*

TP 639 **Rapid Histone Post-Translational Modification Analysis Using Alternative Proteases and Tandem Mass Tags**; Natalie P Turner[1]; Sabyasachi Baboo[1]; Patrick T. Garrett[1]; Jolene K. Diedrich[1]; Michal Bajo[1]; Marisa Roberto[1]; John R. Yates III[1]; *[1]The Scripps Research Institute, La Jolla, CA*

TP 640 **Integrating Glass Fiber Frits into PTM Enrichment Tips for Robust Plant Phosphoproteome and N-Glycoproteome Profiling**; Ting-An Chen[1]; Chin-Wen Chen[1]; Pei-Yi Lin[1]; Chuan-Chih Hsu[1]; *[1]Academia Sinica, Taipei, Taiwan*

TP 641 **Electron Transfer Dissociation Reveals Sites of Autocatalytic Tyrosine Sulfation in Mammalian Tyrosylprotein Sulfotransferases**; Menatallah M Youssef[1, 2]; Ahmed M Mostafa[1, 2]; Kristina Hakansson[2, 3]; *[1]Faculty of Pharmacy, Ain Shams University, Cairo, Egypt; [2]University of Michigan, Ann Arbor, MI; [3]NHMFL/Florida State University, Tallahassee, FL*

TP 642 **Spatial PTM Proteomics as a High-Confidence Framework for Understanding Stress Granule Dynamics**; Minsang Hwang[1, 2]; Jong-Seo Kim[1, 2]; *[1]School of Biological Sciences, Seoul National University, Seoul, South Korea; [2]Center for RNA Research, Institute of Basic Science (IBS), Seoul, South Korea*

TP 643 **RNA Editing Rewires the Post-Translational Modification Landscape**; Jack M Moen; *University of California San Francisco, San Francisco, CA*

TP 644 **Triplex ATE1-based Arginylation Profiling (ABAP3) of the Cell Proteome**; Tom Lin[1]; Changfeng Deng[1]; Mingyang Jiang[1]; Sambavi Elangovan[1]; *[1]Rutgers University, Piscataway, NJ*

TP 645 **Proteome-wide ubiquitinome profiling reveals substrate-specific dynamics within the Ubiquitin-specific protease 7 (USP7) network**; Jeroen AA Demmers[1, 2]; Joyce Wolf - Van Der Meer[2]; Jan A Van Der Knaap[2]; Ayestha Sijm[2]; Karel Bezstarosti[2]; Dick HW Dekkers[2]; Wouter AS Doff[2]; Peter Verrijzer[2]; *[1]Leiden University, Leiden, Netherlands; [2]Erasmus MC, Rotterdam, Netherlands*

TP 646 **Proton transfer reactions and parallel ion parking for improved top-down MS/MS analysis of labile post-translational modifications**; Sean D Dunham[1]; Chad Weisbrod[1]; Lissa C Anderson[1, 2]; Kristina Hakansson[1, 2]; *[1]National High Magnetic Field Laboratory Department of ICR, Tallahassee, FL; [2]Florida State University, Tallahassee, FL*

TP 647 **SPEC as a universal platform for specific PTM enrichment: ubiquityl and glycoproteomics at microgram scale**; Lukas T Henneberg[1]; Tim Heymann[1]; Denys Oliinyk[1]; Matthias Mann[1]; *[1]Max Planck Institute of Biochemistry, Planegg, Germany*

TP 648 **Discovery of QPCT-mediated pyroglutamylation reveals proteome-wide substrates**; Le Sun; *the Scripps Research Institute, San Diego, CA*

TP 649 **Decoding isozyme-specific substrate recognition in protein arginine deiminases by proteome-wide citrullination mapping**; Sophia Laposchan[1]; Yi-Fang Yang[2]; Kai-Han Chan[2]; Rebecca Meelker Gonzalez[1]; Wassim Gabriel[1]; Mathias Wilhelm[1]; Hui-Chih Hung[2]; Chien-Yun Lee[1]; *[1]Technical University of Munich, Freising, Germany; [2]National Chung Hsing University, Taichung, Taiwan*

TP 650 **Efficient Arg0/Arg10 ATE1 arginylome profiling on Orbitrap™Astral™ mass spectrometer**; Kushani Attanayake[1]; Yunyun ZHU[2]; Joel Bucci[2]; Giorgis Isaac[2]; Changfeng Deng[3]; Tom Lin[3]; *[1]Thermo Fisher Scientific, Lexington, MA; [2]Thermo Fisher Scientific, Lexington; [3]Rutgers University, Piscataway, NJ*

TP 651 **DDM-Assisted Resolubilization and Multi-Protease Digestion Reveal Novel Targets in Early Immune Signaling**; Hyojung Kim[1, 2]; Jiraphorn Issara-Amphorn[2, 3]; Sung Hwan Yoon[2, 3]; Aleksandra Nita-Lazar[2, 3]; Anirban Banerjee[1, 2]; *[1]National Institute of Child Health and Human Development, Bethesda, MD; [2]National Institutes of Health, Bethesda, MD; [3]National Institute of Allergy and Infectious Diseases, Bethesda, MD*

TP 652 **Global profiling of protein arginine methylation in prmt-1 and prmt-5 knockout C. elegans**; Ali Basirattalab[1]; Dylan Wallis[2]; Nicolas Hartel[3]; Melina Jalalifarahani[4]; Carolyn Phillips[2]; Nick Graham[1];

[1]Mork Family Department of Chemical Engineering and Materials Science, University of Southern California, LOS ANGELES, CA; [2]Department of Biological Sciences, University of Southern California, LOS ANGELES, CA; [3]1Mork Fami

TP 653 **Ubi-SCAPE enables deep exploration of the poly-ubiquitylome**; Harvey E. Johnston[1, 2]; Andrew Frey[3, 4]; Guarav Barve[2]; Sam Carling[2]; Matthias Trost[3, 5]; Rahul S Samant[2]; *[1]Cambridge Institute for Medical Research, Cambridge, United Kingdom; [2]Babraham Institute, Cambridge, United Kingdom; [3]Biosciences Institute, Newcastle University, Newcastle-upon-Tyne, United Kingdom; [4]Translati*

TP 654 **Systematic phosphoproteomics of an analog-sensitive kinase library defines context-specific signaling networks**; Ryan J Separovich[1]; Julian Van Gerwen[1]; David Pincus[2]; Pedro Beltrao[1]; *[1]Institute of Molecular Systems Biology, ETH Zurich, Zurich, Switzerland; [2]Biological Sciences Division, University of Chicago, Chicago, IL*

TP 655 **Comparative Glycan Profiling of Patient-Derived Organoid Models for Preclinical Model Characterization and Quality Assessment**; Sumin Jung[1, 2]; Ji Eun Park[1, 2]; Myung Jin Oh[1, 2]; Wookyeom Yang[3]; Hyun Joo An[1, 2]; *[1]Graduate School of Analytical Science and Technology, Chungnam National University, Daejeon, South Korea; [2]Asia-Pacific Glycomics Reference Site, Daejeon, South Korea; [3]R&D Institute, Organoidsciences Ltd., Seongnam, Sout*

TP 656 **An Accelerated and Universal Peptide Mapping Method for High-Fidelity Analysis of Deamidation in Multiple AAV Serotypes**; Shailin Patel[1]; Victoria Cotham[1]; Shunhai Wang[1]; Ning Li[1]; *[1]Analytical and Biological Mass Spectrometry, Regeneron Pharmaceuticals Inc., Tarrytown, NY*

TP 657 **Map-Kinase, Pathway-Based Visualization for Phosphoproteomic Datasets**; Clayton B Tacker[1]; Brandon M Gassaway[1]; *[1]Brigham Young University, Provo, UT*

TP 658 **Evaluating the True Lability of Post-Translational Modifications in Top-Down Mass Spectrometry**; Chahat Sehgal[1]; Jared B Shaw[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE*

TP 659 **Radical Initiated Photodissociation (RIPD) enables top-down identification and characterization of unidentified fractionated object (UFO) proteoforms through residue-specific backbone fragmentations**; Lin He[1]; Haley M Schramm[2]; Nicholas M. Riley[2]; Ryan R. Julian[3]; *[1]University of California, Riverside, Riverside, CA; [2]Department of Chemistry, University of Washington, Seattle, WA; [3]University of California Riverside, Riverside, CA*

TP 660 **Conditionally proteinogenic homoarginine generates a site-resolved “shadow proteome” in human cells**; Daniel H Ramirez[1]; Max R. Garcia[1]; Joanna M Gongora[1]; Dominic Scopelliti[1]; Zongtao Lin[2]; Benjamin Garcia[1]; *[1]Washington University School of Medicine, St. Louis, MO; [2]Rutgers University, Piscataway, NJ*

TP 661 **Fragment-ion based acetylation turnover with 2H2O-metabolic labeling and high resolution mass spectrometry**; Andrea Arias-Alvarado[1]; Spencer Parrish[2]; Mirjavid Aghayev[2]; Serguei Ilchenko[2]; Takhar Kasumov[2]; *[1]NEOMED, Rootstown, OH; [2]Northeast Ohio Medical University, Rootstown, OH*

TP 662 **Leveraging ribosomal proteins for the unbiased detection of functional non-canonical post-translational chemical modifications**; Kavita R Matange[1]; Maria C Panepinto[1]; Paolo Cifani[1]; *[1]Cold Spring Harbor Laboratory, Cold Spring Harbor, NY*

TP 663 **Identification of protein SUMOylation sites with a novel anti-QQQTGG antibody and crosslinking mass spectrometry**; Timothy R O'Leary[1]; Mi Ra Chang[1]; Patrick R. Griffin[1]; *[1]UF Scripps, Florida, Jupiter, FL*

TP 664 **Development of a Non-canonical Arginine Analog for Click-Chemistry Based Enrichment and Detection of Arginylated Proteins**; Dominic Scopelliti[1]; Bibhuti Bhusana Palai[1]; Zongtao Lin[2]; Benjamin Garcia[1]; *[1]Washington University School of Medicine in Saint Louis, Saint Louis, MO; [2]Rutgers University, Piscataway, NJ*

TP 665 **High efficiency NTCB- mediated chemical digestion extends Mass-Spectrometry-based proteomics interrogations**; Christopher Glynn[1]; Mario De Leon[1]; Reynaldo Magalhães Melo[1]; Tom Casimir Bamberger[1]; Kenneth Hee[1]; Jolene K. Diedrich[1]; Natalie P Turner[1]; Claire Delahunty[1]; P; *[1]The Scripps Research Institute, La Jolla, CA*

TP 666 **Identification of TDP-43 kinases using fluorescence complementation mass spectrometry (FCMS)**; Amirhesam Mashaollahi[1, 2]; Zhuojun Luo[1]; Yanyan Du[1]; W. Andy Tao[1, 2, 3, 4]; *[1]Department of Biochemistry, Purdue University, West Lafayette, IN; [2]Purdue Institute for Cancer Research, West Lafayette, IN; [3]Tymora Analytical Operations, West Lafayette, IN; [4]Purdue University, Department of*

TP 667 **Protein Nitration in Early-Onset Gastric Cancer: Evidence for MPO-Independent Activation and Metastatic Potential**; Jaewon Oh[1]; Kwang Pyo Kim[1]; *[1]Kyung hee university, Suwon, South Korea*

TP 668 **Quantitative Subcellular Proteomics Reveals α-N-Methylation as a Regulator of Ran-Dependent Nucleocytoplasmic Transport**; Quanqing Zhang[1]; Yinsheng Wang[2]; *[1]UC Riverside, Riversdie, CA; [2]University of California, Riverside, Riverside, CA*

TP 669 **Automatic Blood Protein Enrichment by Magnetic-COFs Polymers**; Yuanyu Huang[1]; T.Mamie Lih[1]; Zhenyu Sun[2]; Liyuan Jiao[2]; Lijun Chen[2]; Hui Zhang[2]; *[1]Johns Hopkins University, Baltimore, MD; [2]Johns hopkins university, baltimore, MD*

TP 670 **Sequence-Based Enrichment of Structural and Dynamical Protein Representations for Large-Scale Proteomics**; Gabriel Bianchin De Oliveira[1]; Fahad Saeed[1]; *[1]Knight Foundation School of Computing and Information Sciences, Florida International University, Miami, FL*

TP 671 **Deep mass spectrometry profiling of 10,000+ proteins in FFPE tissue reveals novel functional biology**; Jeramie Watrous[1]; Carla Nieser[1]; Joseph Capri[1]; Sejun Park[1]; Tao Long[1]; Jessica Weant[1]; Mo Jain[1]; *[1]Sapient, San Diego, CA*

TP 672 **VAMS-enabled blood cell proteomics reveals coordinated nuclear and cytoskeletal failure: cancer-relevant mechanisms in heavy metal-exposed birds**; Zeshan Ali[1]; Max Mclennan-Gillings[1]; Riccardo Ton[2]; Janet Chik[1]; Simon Griffith[1]; Paul A. Haynes[1]; *[1]School of Natural Sciences, Macquarie University, North Ryde, Australia; [2]Cavanilles Institute of Biodiversity, University of Valencia, Valencia, Spain*

TP 673 **Unlocking the Cell Surface Proteome at Nanoscale Resolution Using Image-Guided Photo-Biotinylation and Orbitrap Astral & Oribtrap Astral Zoom Mass Spectrometry**; Po-Chao Chan[1]; Sudipa Maity[2]; Elate Huang[1]; Tina Chong[1]; Tonya Pekar Hart[2]; Ellen Casavant[2]; Michelli Faria de Oliveira[3]; Daniel Dlugolenski[3]; Jung Chi Liao<sup; *[1]Syncell Inc, Taipei, Taiwan; [2]Thermo Fisher Scientific, San Jose, CA; [3]Syncell Inc, Livermore, CA*

TP 674 **Extending Dynamic Range in Complex Mixture Analysis Using Modified DIA on the Orbitrap Astral**; Leila Afjehi[1]; Carlos Antonio Perez Rizquez[1]; *[1]University of Vienna, Research Support Facilities, Mass Spectrometry Unit, Vienna, Austria*

TP 675 **Automation of P2 Nanoparticle-Based Plasma Enrichment on the Opentrons Flex Enables Scalable, Reproducible Plasma Proteomics**; Maura Grey[1]; Alessandro Brambilla[2]; Zehan Hu[2]; Silvia Wuertenberger[2]; Katharina Limm[2]; Kinnari Watson[3]; Boren Lin[3]; *[1]PreOmics Inc., Billerica, MA; [2]PreOmics GmbH, Martinsried, Germany; [3]Opentrons Labworks Inc., Long Island City, NY*

TP 676 **Using sample and gas phase fractionation to improve proteomic coverage without optimizing new methods**; Tyler Kurtz[1]; Chao Wang[2]; Hsien-jung Lavender Lin[2]; Ryan T. Kelly[2]; *[1]Brigham Young University, Provo, UT; [2]Brigham Young Uniersity, Provo, UT*

TP 677 **Mass Spectrometry for Cell Signaling: A Metabolic STAMP Approach to Decipher GPCR-Regulated Insulin Secretion in Pancreatic β Cells**; Mohammad Ovais Aziz-Zanjani[1]; Rachel E. Turn[1]; Yan Hang[1]; Anushweta Asthana[1]; Leilani Elizabeth LaBrie[1]; Mohammadamin Mobedi[1]; Lucy Artemis Xu[1]; Michael Krawitzky[2</s;] *[1]Stanford University, Stanford, CA; [2]Bruker Scientific LLC, San Jose, CA*

TP 678 **Exploration of Semiconductor Chip-Based Single-Molecule Protein Sequencing for Identification of Hemoglobin Variants**; Ruben Y. Luo[1, 2]; Mathivanan Chinnaraj[3]; Kristin Blacklock[3]; Douglas Pike[3]; Ilya Chorny[3]; John Vieceli[3]; Carolyn V. Wong[2]; *[1]Stanford University, Stanford, CA; [2]Stanford Heath Care, Palo Alto, CA; [3]Quantum-Si, Branford, CT*

TP 679 **AUA-HOTPOTS – Robotic sample-agnostic AUtomAted High-thrOughpuT PrOTeomics in big pharma research**; Andreas David Brunner[1]; Benedikt Lukas Kuhs[2]; Simon Seebacher[1]; Christian Ziegler[1]; Andreas Harald Luippold[1]; Besnik Bajrami[1]; Michael Haas[1]; Tom Bretschneider[1]; *[1]Boehringer Ingelheim Pharma GmbH & Co. KG, Biberach, Germany; [2]University of Copenhagen, Copenhagen, Denmark*

TP 680 **Deep and Reproducible Plasma Proteomics Enabled by Single-Particle Enrichment and DIA-MS for Colorectal Cancer Biomarker Discovery**; Cameron Ellis[1]; Zehan Hu[2]; Katharina Limm[2]; Sandra Schär[3]; Jared Deyarmin[4]; Stephanie N. Samra[4]; *[1]PreOmics, Phoenix, AZ; [2]PreOmics GmbH, Martinsried, Germany; [3]Biognosys AG, Schlieren, Switzerland; [4]Thermo Fisher Scientific, San Jose, CA*

TP 681 **Automating N-glycan Labeling of Cell Surface Proteins to Enable Scalable Profiling of the Surfaceome**; Amanda Damon[1]; Namrata D Udeshi[1]; Brian Boyle[1]; Keith D Rivera[1]; Steve A Carr[1]; *[1]Broad Institute, Cambridge, MA*

TP 682 **Next-generation small molecules enable deep plasma proteome profiling using single nanoparticle enrichment on the Orbitrap Astral Zoom mass spectrometer**; Bahareh Ghaffari[1]; Behzad Mehrdad[2]; Han Liuchenxin[3]; Amir Ata Saei[2, 3]; Babak Borhan[1, 2]; Morteza Mahmoudi[1, 2]; *[1]Michigan State University, East Lansing, MI; [2]XProteome Inc., East Lansing, MI; [3]Karolinska Institute, Stockholm, Sweden*

TP 683 **Plasma proteomic profiling reveals biological insights and a signature of progression in multiple myeloma**; D. R. Mani[1]; Elizabeth D Lightbody[2]; Hasmik Keshishian[1]; Nayda Bidikian[2]; Michael A Gillette[1]; Steven A. Carr[1]; Irene M Ghobrial[2]; *[1]Broad Institute of MIT and Harvard, Cambridge, MA; [2]Dana-Farber Cancer Institute, Boston, MA*

TP 684 **Development of an Automated Metaproteomic Extraction Pipeline and Application to North Atlantic Ocean Environments**; Paloma Zaria Lopez[1]; Annie Stefanides[1]; Matthew R. McIlvin[1]; Fadime R. Stemmer[2]; Daniella Asturias[1]; Mak A. Saito[1]; *[1]Woods Hole Oceanographic Institution, Woods Hole, MA; [2]Woods Hole Oceanographic Institution/Massachusetts Institute of Techonology, Woods Hole*

TP 685 **Incorporation of fragment-ion indexing into real-time search for Tribrid instruments**; Jesse D. Canterbury[1]; William D Barshop[2]; Christopher D McGann[3]; Michael R Hoopmann[4]; Graeme McAlister[2]; Jimmy K. Eng[4]; Devin K Schweppe[4]; *[1]Thermo Scientific, San Jose, CA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Harvard Medical School, Boston, MA; [4]University of Washington, Seattle, WA*

TP 686 **Top-down and bottom-up proteomics characterization of rapid ultracentrifugation-based ribosome isolation**; Salina Mali[1]; Jared B Shaw[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE*

TP 687 **Dramatically increased compound throughput for activity-based protein profiling experiments with barcode-enabled massively parallel activity profiling (BarMAP)**; Kyle Brandt[1]; Katrina H Andrews[2]; Alexey I Nesvizhskii[3]; Brian J Beliveau[1]; Keriann Backus[2]; Devin Schweppe[1]; *[1]University of Washington, Seattle, WA; [2]University of California, Los Angeles, Los Angeles, CA; [3]University of Michigan, US, MI*

TP 688 **Seamless OptiSpray μPAC Neo Performance: Matching House-Packed Accucore in FAIMS-Optimized TMT and Label-Free Proteomics**; Joshua Silveira[1]; Katherine Walker[2]; Runsheng Zheng[3]; Eloy Wouters[2]; Steven P Gygi[4]; Joao A Paulo[4]; *[1]Thermo Fisher Scientfic, San Jose, CA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Germering, Germany; [4]Harvard Medical School, Boston, MA*

TP 689 **Making the most of a little: deep plasma proteomics on less than 50 μL of sample**; Jessica Moore[1]; Jaison Arivalagan[1]; Yukta Bhurke[1]; Lena Seyfarth[1]; Averie Covin[1]; Tiffany Louie[1]; Kyra Richardson[1]; Alejandra Cobos[1]; Don Skifter[1]; D; *[1]Discovery Life Sciences, Huntsville, AL*

TP 690 **High-Sensitivity Proteomics by NanoHILIC/MS/MS Using Direct Injection of the Entire Microvolume Eluate from a Reversed-Phase StageTip**; Koshin Akamatsu[1]; Eisuke Kanao[1, 2]; Yasushi Ishihama[1, 2]; [1]*Graduate School of Pharmaceutical Sciences Kyoto University, Kyoto, Japan;* [2]*National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan*

TP 691 **Evaluating a next generation ion source for DIA-based quantitative proteomics**; Dong-Gi Mun[1]; Benjamin J Madden[1]; Raghavendra Rao Pasupuleti[1]; Dowoon Nam[1]; Steven Draper[1]; Joshua Silveira[2]; Daniel Jackson[2]; Ellen Casavant[2]; Katherine Walker[2<;] [1]*Mayo Clinic, Rochester, MN;* [2]*ThermoFisher Scientific, San Jose, CA*

TP 692 **Single-cell lipidomic profiling of migratory leader-follower phenotypes and circulating tumor cells using live single-cell mass spectrometry**; Xiaoyue Huang[1]; Eiso Hiyama[2]; Sylvia E. Le Dévédec[3]; Ahmed Ali[1]; Thomas Hankemeier[1]; [1]*Metabolomics and Analytics Centre, Leiden Academic Centre for Drug Research, Leiden University, Leiden, Netherlands;* [2]*Natural Science Center for Basic Research and Development, Hiroshima University, Hiroshima, Japan;* [3]*Div*

TP 693 **A Journey into Single-Cell Proteomics in a Core Facility**; Hila Levy[1]; Corine Katina[1]; Yishai Levin[1]; [1]*Weizmann Institute of Science, Rehovot, Israel*

TP 694 **Single-plaque proteomics reveals conserved and dynamic amyloid microenvironments in Alzheimer's disease**; Ju Wang[1]; Mengqi Chu[1]; Jay M. Yarbo[1]; Ping-Chung Chen[1]; Him K. Shrestha[1]; Huan Sun[1]; Mingming Liu[1]; Zhen Wang[1]; Sarah Harvey[1]; Zhiping Wu[1]; [1]*St. Jude Children's Research Hospital, Memphis, TN;* [2]*University of Tennessee Health Science Center, Memphis, TN;* [3]*Banner Sun Health Research Institute, Sun City, AZ;* [4]*University of Texas Southwestern Medical Ce*

TP 695 **Single-cell lipidomic analysis with online μSFE-SFC-MS**; Jinlei Yang[1]; Sichun Zhang[2]; Xinrong Zhang[2]; [1]*Tsinghua University, Beijing, China;* [2]*Tsinghua university, Beijing, China*

TP 696 **Analysis of 50,000 Single Mammalian Mitochondria via MALDI-2 Mass Spectrometry**; Siheun Lee[1]; Seth J Croslow[1]; Timothy J Trinklein[1]; Stanislav S Rubakhin[1]; Jonathan V Sweedler[1]; [1]*University of Illinois Urbana-Champaign, Urbana, IL*

TP 697 **Balancing Speed and Depth: Doubling Throughput in Single-Cell Proteomics Using Orbitrap Astral Zoom MS**; Tabiwang N. Arrey[1]; Min Huang[2]; Till Reinhardt[1]; Anna Pashkova[1]; Eugen Damoc[1]; [1]*Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany;* [2]*ThermoFisher Scientific, Shanghai, China*

TP 698 **Using Single-Cell Proteomics to Analyse DNA Damage Response in Cells Using the Thermo Orbitrap Astral Zoom**; Georgina H Charlton[1]; Riccardo Chiozzi Zenezini[1]; Jonathan Ditcham[1]; Kish Adoni[1]; Silvia La Penna[1]; Konstantinos Thalassinos[1]; [1]*University College London, London, United Kingdom*

TP 699 **Unraveling proteome dynamics in adult hematopoietic stem and progenitor differentiation**; Valdemaras Petrosius[1]; Nil Üresin[1]; Jakob Woessmann[1]; Pedro Aragon-Fernandez[1]; Mafalda Araujo Pereira[2]; Benjamin Furtwängler[1]; Katherine L. Walker[3]; Romain Huguet[4</s;] [1]*Technical University of Denmark, Kongens Lyngby, Denmark;* [2]*Biotech Research and Innovation Centre, Copenhagen, Denmark;* [3]*Thermo Fisher Scientific, San Jose, CA;* [4]*Thermo Fisher Scientfic, San Jose, CA;* [5</s]

TP 700 **Low-resolution FAIMS for increased peptide coverage in low-load and single-cell proteomics**; Dominic Hoch[1]; Michael Belford[2]; Lilian Heil[3]; Karl Mechtler[4, 5, 6]; Manuel Matzinger[6]; [1]*Thermo Fisher Scientific, Reinach, Switzerland;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*Thermo Fisher Scientfic, San Jose, CA;* [4]*Research Institute of Molecular Pathology (IMP), Vienna Biocenter (VBC), Vienna,*

TP 701 **High-throughput Single-cell Proteomics Enabled by an Integrated Hyperplexing and Automatic Labelling Approach without Fractionation**; Yun Yang[1]; Hui Zhang[2]; Qing Zeng[1]; [1]*International Academy of Phronesis Medicine (Guang Dong), Guangzhou, China;* [2]*Southern University of Science and Technology, Shenzhen, China*

TP 702 **Optimizing end-to-end workflows for Shotgun Lipidomics with improved sample prep, Cyclic Ion Mobility and LipidXplorer**; Nyasha C Munjoma[1]; Emma Marsden-Edwards[1]; Ballal Hossen[2]; Dominik Schwudke[2]; Johannes PC Vissers[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Division of Bioanalytical Chemistry, Research Center Borstel - Leibniz Lung Center, Borstel, Germany*

TP 703 **Paired Single-Cell Proteomics and Lipidomics Uncover Sex Dimorphism in Astrocyte Responses to HCoV-229E**; Shuxin Chi[1]; Armando Alcazar[1]; Jason Rogalski[1]; Huan Zhong[1]; Leonard J Foster[1]; *[1]University of British Columbia, Vancouver, BC*

TP 704 **Comparative analysis of nerves and individual nerve fibers using MALDI-MSI**; Stanislav Rubakhin[1]; Jonathan V Sweewdler[1, 2]; *[1]Beckman Institute, UIUC, Urbana, IL; [2]Department of Chemistry, University of Illinois Urbana-Champaign, Urbana, IL*

TP 705 **Solid-Phase Extraction Capture (SPEC) sample preparation in ultra-small volumes enables robust and broadly applicable single-cell proteomics**; Nils Eikmeier[1]; Lukas Henneberg[1]; Tim Heymann[1]; Marvin Thielert[1]; Matthias Mann[1]; *[1]Max Planck Institute of Biochemistry, Martinsried, Germany*

TP 706 **Towards an Automated Platform for Single-Cell Metabolomics**; Felix Friedrich[1]; Sk Ramiz Islam[1]; Varun Sharma[1]; Ingela Lanekoff[1]; *[1]Uppsala University, Uppsala, Sweden*

TP 707 **Phenotype-Driven Single-Cell Proteomics for Deciphering CAR-T Cell Heterogeneity**; Keren ZHANG[1]; Bin Yao[2]; Henry Lam[1]; Ruijun Tian[2]; *[1]HKUST, Hong Kong, China; [2]SUSTech, Shenzhen, China*

TP 708 **Click chemistry combined with single-cell proteomics reveals disrupted ribosome stoichiometry and translation efficiency in aging mouse liver**; Maxwell Horton[1]; Ronald Cutler[1]; Derek Huffman[1]; Jeffrey Pessin[1]; Simone Sidoli[1]; *[1]Albert Einstein College of Medicine, Bronx, NY*

TP 709 **Combining single-cell metabolomics and protein imaging in T cells**; Sharath Krishnakumar Menon[1]; Theodore Alexandrov[2, 3]; *[1]University of California, San Diego, San Diego, CA; [2]University of California San Diego, San Diego, CA; [3]DeepCyte Inc., San Diego, CA*

TP 710 **Sheathless Capillary Electrophoresis–Mass Spectrometry for High-Sensitivity Metabolomic Analysis of Limited-volume Cellular Samples**; Akiyoshi Hirayama[1]; Yushi Kamei[1]; *[1]Keio University, Tsuruoka, Japan*

TP 711 **Improved label-free proteomics from low-input samples on Orbitrap Astral MS using the µPAC Plus 50 cm and µPAC trap column**; Martins Jansons[1]; William Comstock[2]; Jeff Op de Beeck[3]; Fernanda Salvato[4]; Runsheng Zheng[5]; Stephanie Koczur[6]; Alec Valenta[2]; Amirmansoor Hakimi[2]; *[1]Thermo Fisher Scientific, Vilnius, Lithuania; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Zwijnaarde, Belgium; [4]Thermo Fisher Scientfic, San Jose, CA; [5]Thermo Fisher Scientifi*

TP 712 **DIA-MS feature-based cell discrimination for high-throughput single-cell proteomics**; Tan Bao Nguyen[1]; Geul Bang[2]; Seungjin Na[2]; Jin Young Kim[2, 3]; *[1]Center for Target-to-Therapeutics Research, Korea Basic Science Institue, Cheongju, South Korea; [2]Center for Target-to-Therapeutics Research, Korea Basic Science Institute, Cheongju, South Korea; [3]Critical Diseases Diagno*

TP 713 **The CellOmix System: An Integrated Chip Platform for Deep and Efficient Single-Cell Proteome Profiling**; Renjun Zhang[1]; Liu Zhu[2]; Jin Jin[1]; Weixiang Yan[3]; Qian Yang[4]; Yani Gu[1]; Xueying Yang[5, 6]; Siyuan Wang[1]; Catherine CL Wong[1]; *[1]State Key Laboratory for Complex, Severe and Rare Diseases, Clinical Research Institute, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China; [2]Jingjie PTM BioLab*

TP 714 **High throughput multi-OMIC analyses at the single cell level using analytical scale chromatography with a multi-reflecting high resolution mass spectrometer**; QianYing Xu[1]; Scarlet Ferrinho[1]; Lee A Gethings[2]; Robert S Plumb[3]; David Heywood[4]; Matthew Spick[1]; Clare Mills[1]; *[1]University of Surrey, Guildford, United Kingdom; [2]Waters, Wilmslow, United Kingdom; [3]Waters Corporation, Milford, MA; [4]Waters Wilmslow UK, Wilmslow, United Kingdom*

TP 715 **Rapid Single-Cell Metabolomics Using Untargeted Tandem Mass Spectrometry Combined with Single-Cell Mass Cytometry for the Comprehensive Analysis of Cellular Subpopulations**; Patrick Mueller[1]; Martin Schaier[1]; Dina Baier-Romfeld[1]; Gunda Koellensperger[1]; *[1]University of Vienna, Vienna, Austria*

TP 716 **Optimizing single-cell proteomics workflow for organoid proteomics: A pilot study in Glioblastoma Multiforme**; Romell Gletten[1]; Samantha O'Connor[1]; Ritin Sharma[1, 2]; Nanyun Tang[1]; Michael Krawitzky[3]; Yue Hao[1]; Floris Barthel[1]; Anna Lasorella[4]; Antonio Iavarone[4]</sup; *[1]Translational Genomics Research Institute, Phoenix, AZ; [2]Integrated Mass Spectrometry Shared Resource Facility, City of Hope National Medical Center, Duarte, CA; [3]Bruker Daltonics, Billerica, MA; [4]Sylvester Com*

TP 717 **Developing Metabolite-protein Covariation Architecture Using Deep Metabolomics Data**; Bingsen Zhang[1, 2]; Edward T. Chouchani[1, 2, 3]; *[1]Department of Cancer Biology, Dana-Farber Cancer Institute, Boston, MA; [2]Department of Cell Biology, Harvard Medical School, Boston, MA; [3]Howard Hughes Medical Institute, Chevy Chase, MD*

TP 718 **Compartment-Resolved Proteomic and Phosphoproteomic Analysis Reveals Non-Linear Regulatory Remodeling in Aging Liver**; Mario M Alba[1, 2]; Ajay Bharadwaj[2, 3]; Brent Beadell[1]; Jihyeon Lee[3, 4]; Ielyzaveta Slarve[5]; Qi Tang[5]; Prince Anand[6]; Tanyalak Parimon[6]; Simion Kreimer[3, 4]</; *[1]Cedars-Sinai Medical Center, Karsh Division of Gastroenterology and Hepatology, LOS ANGELES, CA; [2]Advanced Clinical BioSystems Research Institute, Cedars-Sinai Medical Center, Los Angeles, CA; [3]Cedars-Sinai Medical Center*

TP 719 **PARIC: In Situ Mapping of the PAR Interactome and PAR-Binding Regions**; Sanghyuk Lee[1, 2]; Seonmin Ju[1, 2]; Jong-Seo Kim[1, 2]; *[1]School of Biological Sciences, Seoul National University, Seoul, South Korea; [2]Center for RNA Research, Institute of Basic Science (IBS), Seoul, South Korea*

TP 720 **Towards rational media design for chicken cell cultivation using spent media analysis and metabolic modeling**; Avinash Vellore Sunder[1]; Abhi Manjunath Dasari[2]; Ankita Srivastav[3]; Sandip Shinde[1]; Pranav Adhyapak[2]; Dimple Lalchandani[2]; Deepti Sahasrabuddhe[1]; Shubhankar Takle[3]</s; *[1]Indian Institute of Technology Bombay, Mumbai, India; [2]Clarity Bio Systems India Pvt. Ltd., Pune, India; [3]MyoWorks Pvt. Ltd., Mumbai, India*

TP 721 **Quantitative Proteomics Reveals Complement Cascade Activation Following Nuclear RNA Surveillance Disruption by Mtr4 Depletion**; Karl A. T. Makepeace[1, 2]; Pavel A. Vlasov[1]; James L. Manley[1]; Lewis M. Brown[1, 2]; *[1]Department of Biological Sciences, Columbia University, New York, NY; [2]Quantitative Proteomics and Metabolomics Center, Columbia University, New York, NY*

TP 722 **Proteome-wideQTL mapping enables gene-protein network construction in a genetically diverse MASLD mouse model**; Margaret L Robinson[1]; Giorgia Benegiamo[2]; Wenyu Liu[2]; Gordon Smith[3]; Miller Williams[1]; Katherine A. Overmyer[1, 4, 5]; Samuel Klein[3]; Johan Auwerx[2]; Joshua J Coon; *[1]University of Wisconsin-Madison, Madison, WI; [2]Laboratory of Integrative Systems Physiology, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland; [3]Washington University School of Medicine, St. Louis, MO;*

TP 723 **A covariation-based framework to model proteome network dynamics and phenotypic heterogeneity in Candida albicans**; Luise C. Nagel1; Austin Mottola[1]; Savvas Kourtis[2]; Ziyue Wang[1]; Ludwig R. Sinn[1]; Andrea Lehmann[1]; Daniela Ludwig[1]; Michal Nadler-Holly[3]; Yue Xuan[3]; M; *[1]Institute of Biochemistry, Charité - Universitätsmedizin Berlin, Berlin, Germany; [2]Centre for Cell Biology University of Edinburgh, Edinburgh, United Kingdom; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

TP 724 **Phosphoproteomic Investigation of Tonic Signaling Driving Reduced Specificity in 'AND'-Gated LINK CAAR T Cell models for Autoimmune Therapy**; Spencer Jeffries[1]; Morgan Payne[1]; Abby Cheever[1]; Brianna Davis[1]; Scott Weber[1]; Brandon Gassaway[1]; *[1]Brigham Young University, Provo, UT*

TP 725 **CHIMERYS and DDA-MS-dependent proteomics demonstrate that commonly used macrophage-like cell lines distinctly reflect primary macrophage phenotypes**; Yuto Nakamura[1]; Taku Kasai[1]; Gabriel Shlayen[1]; Sasha A Singh[1]; Masanori Aikawa[1]; *[1]Center for Interdisciplinary Cardiovascular*

Sciences, Division of Cardiovascular Medicine, Department of Medicine, Brigham Women's Hospital, Harvard Medical School, Boston, MA

TP 726 **Robustness of mitochondrial biogenesis and respiration underlies overflow metabolism**; Easun Arunachalam[1]; Felix C Keber[1, 2]; Richard C Law[3]; Joseph Crapse[1, 2]; Chirag K Kumar[1, 2]; Yihui Shen[4]; Martin Wühr[1, 2]; Daniel Needleman[5, 6]; Junyoung O Par; [1]*Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ;* [2]*Department of Molecular Biology, Princeton University, Princeton, NJ;* [3]*University of California, Los Angeles, Los Angeles, CA;* [4<]

TP 727 **From Nodes to Networks: Drug-Induced Interactomics and Mutant-Scanning AP-MS Accelerates Target and MOA Discovery**; Chris Adams1; Daniela Flores[1]; Anand Divakaran[1]; Fabian Ortega[1]; Philipp Junk[1]; Animesh Roy[1]; Subrata Shaw[1]; Keelan Guiley[1]; Ali Bashir[1]; Chris Sinz<; [1]*Rezo Therapeutics, San Francisco, CA*

TP 728 **Integrated Serum Proteomic and Metabolomic Profiling Reveals Training Load–Associated Systemic Adaptations in Elite Athletes**; Hophil Min; *Korea Institute of Science and Technology, Seoul, South Korea*

TP 729 **DanCER: A differential elution scoring toolkit for co-fractionation MS**; Monita Muralidharan[1, 2, 3]; Martin Gordon[1, 2, 3]; Benjamin Polacco[1, 2, 3]; Ujjwal Rathore[2]; Manisha Ummadi[1, 2, 3]; Reanna Lao[1, 2, 3]; Michael McGregor[1, 2, 3]; Robyn M Kaak; [1]*Quantitative Biosciences Institute, University of California, San Francisco, San Francisco, San Francisco, United States., San Francisco, CA;* [2]*Gladstone Institute, UCSF, San Francisco, CA;* [3]*Department of Bioengineering an*

WEDNESDAY POSTERS

WP 001 **Breaking the Barriers to Antibody-Oligonucleotide Conjugate (AOC) Site Conjugation Determination by LC-MS**; Samantha Ippoliti[1]; Ying Qing Yu[1]; Nick Pittman[2]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom*

WP 002 **Optimization of Chromatographic Resolution of Individual DAR Species in Native RPLC-HRMS Rapid Characterization of Antibody Drug Conjugates**; A. Carl Sanchez[1]; Juan M Perfetti[1]; James Song[1]; Miklos Czaun[1]; Ismail Rustamov[1]; Cuong Hoang[1]; *[1]Phenomenex, Torrance, CA*

WP 003 **Antibody charge variant characterization via microdroplet digestion post strong cation exchange (SCX) chromatography**; Praneeth Ivan Joel FNU[1]; Yongqing Yang[1]; Timothy Yaroshuk[1]; Md Tanim-Al Hassan[1]; Hao Chen[1]; Harsha P. Gunawardena[2]; Jim Lau[3]; Mike Knierman[3]; Xi Qui[3]; Karen Luo[3]; John Sausen[3]; Hui Zhao[3]; *[1]New Jersey Institute of Technology, Newark, NJ; [2]Johnson & Johnson Innovative Medicine, Spring House, PA; [3]Agilent Technologies, Wilmington, DE*

WP 004 **New peak detection-assisted characterization of light-induced covalent crosslinks in antibody-drug conjugates**; Xinhao Shao; *AbbVie Inc., North Chicago, IL*

WP 005 **Structural characterization of IgG2 disulfide isoforms using cation exchange chromatography coupled to mass spectrometry and peptide mapping**; Yann Leblanc[1]; Nicolas Cauquil[1]; Stéphane Bahraoui[2]; Magali André[1]; Emmanuel Nony[1]; *[1]Servier, Antony, France; [2]Protein Metrics, Boston, MA*

WP 006 **Product Ion Filtering for Comprehensive Profiling of Low-Level Antibody-Drug Conjugate Metabolites in Complex Biological Samples**; Haiying Zhang[1]; Zhigang Lyu[1]; Joe R. Cannon[1]; *[1]Bristol-Myers Squibb R&D, Princeton, NJ*

WP 007 **Aggregates analysis of a bispecific antibody using Orbitrap Excedion Pro BioPharma mass spectrometer with extended mass range**; Xiaoxi Zhang[1]; Reiko Kiyonami[2]; Weijing Liu[3]; Xuepu Li[1]; Min Du[2]; *[1]ThermoFisher Scientific, Shanghai, China; [2]Thermo Fisher Scientific, Lexington, MA; [3]Thermo Fisher Scientfic, San Jose, CA*

WP 008 **Monoclonal Antibodies in the Pathogenesis of Heparin-Induced Thrombocytopenia**; Hossam A Ali[1]; Daniil Ivanov[1]; Aurora Tini[1, 2]; Jared Treverton[3]; Ishac Nazy[3]; Igor Kaltashov[1]; *[1]University of Massachusetts Amherst, Amherst, MA; [2]University of Pavia (Università degli Studi di Pavia), Pavia, Italy; [3]Michael DeGroote School of Medicine, McMaster University, Hamilton, ON*

WP 009 **Native Ion Mobility-Mass Spectrometry Captures Antibody-Cytokine Complexes and Detects Variability Among TNFα Antagonists**; Alyssa M. Erlenbeck[1]; Brandon T. Ruotolo[1]; *[1]University of Michigan, Ann Arbor, MI*

WP 010 **Automated Sample Preparation and Direct Infusion MS: A Platform for Rapid Therapeutic Protein Analysis**; John Chlystek[1, 2]; Austin Z Salome[1, 2]; Craig D Wenger[1]; Alex S Hebert[1, 2]; Scott T Quarmby[1, 2]; Lloyd M Smith[1, 3]; Joshua J Coon[1, 2, 3, 4]; *[1]University of Wisconsin Madison, Madison, WI; [2]National Center for Quantitative Biology of Complex Systems, Madison, WI; [3]CeleramAb Inc., Middleton, WI; [4]Morgridge Institute for Research, Madison, WI*

WP 011 **Identification of Sulfation in an Fc-Fusion Protein by High-Resolution Mass Spectrometry**; Vincent Larraillet[1]; Cornelia Wagner[1]; *[1]Roche Diagnostics GmbH, Penzberg, Germany*

WP 012 **Differential Ion Mobility Spectrometry of Antibodies: Exploring the Dipole Alignment of Intact mAbs**; Hayden A. Thurman[1]; Tobias P. Wörner[2]; Alexander A. Makarov[2]; Alexandre A. Shvartsburg[1]; *[1]Wichita State University, Wichita, KS; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

WP 013 **Discovery and LC-MS/MS Characterization of a Novel Hydroxyproline Modification in a Bispecific Antibody**; Shlomo Zarzhitsky; *Bristol-Myers Squibb, New Brunswick, NJ*

WP 014 **Comprehensive characterization of a trisulfide modification in a bispecific antibody by LC-MS methods**; Wen Chen[1]; Micheal Batt[1]; Joomi Ahn[1]; *[1]Eli Lilly & Company, San Diego, CA*

WP 015 **A sensitive LC/MS/MS method for evaluating the intactness of the antibody for antibody-drug conjugate**; Wei Lu[1]; Xiaoying Zhou[1]; ZhengQuan Zhang[1]; Mao Yin[1]; Ling Xu[1]; *[1]PrimeLink Therapeutics, Suzhou, JIangsu Province, MA*

WP 016 **Simultaneous Quantitation of Antibody-Drug Conjugates and Antibody Components in Human Serum via Hybrid LBA LC-MS/MS**; Zhihui Zhang[1]; Hamza Kandoussi[1]; Jim X Shen[1]; Lina Luo[1]; *[1]Bristol Myers Squibb, Princeton, NJ*

WP 017 **Comparative DAR Analysis by Triple Quadruple MS and HRMS**; Suhong Zhang[1]; Amy Yang[2]; Sean Yu[2]; *[1]Frontage lab, Exton, PA; [2]Frontage Laboratories, Exton, PA*

WP 018 **An Integrated Mass Spectrometry-Based Platform for the Multiplexed Quantification of Antibody-Oligonucleotide Conjugates (AOCs)**; Li Qu[1]; Hongfang Cui[1]; Hefeng Zhang[1]; Zhiyu Li[1]; Lili Xing[1]; Yi Tao[1]; Liang Shen[1]; *[1]WuXi AppTec, Pudong, Shanghai, China*

WP 019 **Determination of DS-8201 in Rat Plasma Using mSPE Magnetic Beads Method Coupled with Liquid Chromatography-Tandem Mass Spectrometry**; Zhiren Yu[1]; Hefeng Zhang[1]; Wenhan Zhang[1]; Hongfang Cui[1]; Li Qu[1]; Weimin Hu[2]; Zhiyu Li[1]; Lili Xing[1]; Yi Tao[1]; Liang Shen[1]; *[1]WuXi AppTec, Pudong, Shanghai, China; [2]WuXi AppTec, Nantong, China*

WP 020 **Development of an Automatic Immunocapture-Based Integrated Mass Spectrometry Platform for Qualitative and Quantitative Study of Fusion Protein Drug**; Zhiyu Li[1]; Li Qu[1]; Hongjing He[1]; Siyu Liu[1]; Lili Xing[1]; Yi Tao[1]; Liang Shen[1]; *[1]WuXi AppTec, Pudong, Shanghai, China*

WP 021 **Elimination of ADC-Related Interferences for the Detection of Free Payloads in Biological Matrices with LC-MS/MS**; Man Yang[1]; Yating Ding[1]; Qing Chang[1]; Yanfu Ren[1]; Zhiyu Li[2]; Lili Xing[2]; Yi Tao[2]; Liang Shen[2]; Xinfa Fu[2]; *[1]WuXi AppTec, Suzhou, China; [2]WuXi AppTec, Pudong, Shanghai, China*

WP 022 **LC-MS-MRM Assay for Site-Specific Antibody-Drug Conjugates with High Drug-to-Antibody Ratio: Heavy and Light Chain Surrogate Peptides Analysis for Pharmacokinetics Quantitation**; Jagadeeshaprasad MG[1]; Chao Gong[1]; John Kellie[1]; *[1]Integrated Bioanalysis, Clinical Pharmacology and Safety Sciences, R&D, AstraZeneca, Gaithersburg, MD*

WP 023 **Expanding ETD-based fragmentation technologies using IR-laser for deeper characterization of monoclonal antibodies on a modified Orbitrap Tribrid mass spectrometer**; Jingjing Huang[1]; Joshua Hinkle[1]; Christopher Mullen[1]; Roberto Gamez[1]; Graeme McAlister[1]; Kristina Srzentic[1]; Rafael Melani[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

WP 024 **Peptide mapping with a novel low-flow ion source and cartridge on a modified Orbitrap Tribrid mass spectrometer**; Jingjing Huang[1]; Katherine Walker[1]; Kevin Yang[1]; Joshua Hinkle[1]; Christopher Mullen[1]; Roberto Gamez[1]; Graeme McAlister[1]; Kristina Srzentic[1]; Rafael Melani[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

WP 025 **Comprehensive LC-MS workflows for antibody drug conjugate (ADC) analysis**; Baiba Cabovska[1]; Ebru Selen[2]; Rathna Veeramachaneni[3]; Eshani Galermo[2]; *[1]SCIEX, Marlborough, MA; [2]SCIEX, Redwood City, CA; [3]KCAS Bio, Olathe, KS*

WP 026 **Native Middle-Down MS Reveals Structural Changes of Monoclonal Antibodies After Being Subjected to Forced Degradation Conditions**; Xuanyu Chen; *University of California, Los Angeles, Los Angeles, CA*

WP 027 **Intact ADC Bioanalysis in Biological Matrices Using Orbitrap-based LC–HRAM MS**; Hao Yang[1]; Gus Hui[2]; Moucun Yuan[2]; Thais De Faria[3]; Claire Dauly[4]; Min Du[5]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]PPD, part of Thermo Fisher Scientific, Henrico, VA; [3]Thermo Fisher Scientific, Eugene, OR; [4]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [5]Thermo F*

WP 028 **Tailored Multi-Omic Workflows for Antigen Discovery Across Varied Biological Matrices**; Sharla Friend[1]; Douglas V Guzior[1]; Ethan Stancliffe[1]; Ashima Mehta[1]; Caitlin Kelly[1]; Monil Gandhi[1]; Sandeep

Acharya[1]; Adam Richardson[1]; Tom Cohen[1]; Kevin Cho[2]; Cassandra G Kempf[2]; Gary J Patti[2]; *[1]Panome Bio, Saint Louis, MO; [2]Washington University in St. Louis, Saint Louis, MO*

WP 029 **Systemic Detection of Cyclosporine Following Sustained-Release Ocular Implantation in Horse**; Ian P. Y. Lam[1]; Yat-Ming So[1]; Wai Him Kwok[1]; Charlynn Yap[1]; Wapi Yau[1]; Celia O. L. Wong[1]; Samuel G. R. Smalley[2]; Bronte S. Forbes[3]; Derek W. Y. Chow[4]; Emmie N. M. Ho[1]; *[1]Racing Laboratory, The Hong Kong Jockey Club, Hong Kong, China; [2]Veterinary Clinical Services, The Hong Kong Jockey Club, China, Hong Kong; [3]Veterinary Regulation, Welfare and Biosecurity Policy, The Hong Kong Jockey Club*

WP 030 **PCR–LC–MS: a Hyphenated Approach to Doping Control Analysis of Transgenes in Horses**; Bruce P.N. Yuen[1]; Emmie N.M. Ho[2]; Wing-Tak Wong[1]; *[1]The Hong Kong Polytechnic University, Hong Kong, Hong Kong; [2]Racing Laboratory, The Hong Kong Jockey Club, Hong Kong, China*

WP 031 **On-Site Detection of Drugs of Abuse and Metabolites Using Miniaturized Mass Spectrometer**; Nan Zhang[1]; Yang Lu[2]; Kun Lu[2]; Nan Wang[1]; Zhengxiang Zhang[1]; Jiexun Bu[1]; Zheng Ouyang[3]; *[1]PURSPEC Technology (Beijing) Ltd., Beijing, China; [2]PURSPEC Technology (China) Ltd., Suzhou, China; [3]Department of Precision Instrument, Tsinghua University, Beijing, China*

WP 032 **Supercritical fluid chromatography coupled to high-resolution mass spectrometry: application to the detection of drugs of abuse in saliva**; Franck SAINT-MARCOUX; *University Hospital of Limoges, Limoges, France*

WP 033 **Development and Validation of an LC-MS Method for Identification and Quantitation of Tianeptine, Mitragynine and 7-Hydroxymitragynine (7-OH) in Dietary Supplements**; Michael Staake[1]; Brian Agan[1]; Jeffrey Wilson[1]; Jennifer Gogley[1]; *[1]US Food & Drug Administration, Irvine, CA*

WP 034 **New insights into metandienone metabolism by untargeted gas chromatography-high resolution mass spectrometry**; Gianluca Barone[1, 2]; Francesco Botrè[1, 3]; Daniel Jardines[1]; Maria Kristina Parr[4]; Xavier De La Torre[1]; *[1]Laboratorio Antidoping, Federazione Medico Sportiva Italiana, Via delle Rupicole 12, 00169, Rome, Italy; [2]Dipartimento di Scienze e Tecnologie Chimiche, Università di Roma “Tor Vergata”, Via della Ricerca Scientifica 000133, Rome, I*

WP 035 **From Nile to Vial: Exploring Ancient Egyptian Ritual and Magic using LC-MS**; Liam Marcelo McEvoy[1, 2]; Veena S. Avadhani[1, 2]; Anthony T. Iavarone[1]; Hoi-Ying Holman[2]; Evan R. Williams[1, 2]; *[1]University of California, Berkeley, Berkeley, CA; [2]Lawrence Berkeley National Laboratory, Berkeley, CA*

WP 036 **GC/MS study of cosmetic powder of the Great Silk Road based found in Kazakhstan**; Olga V Poliakova[1]; Maria Kondratieva[1]; Maria Mednikova[2]; Albert T Lebedev[1]; *[1]Shenzhen MSU-BIT University, Shenzhen, China; [2]Institute of archeology RAS, Moscow, Russia*

WP 037 **New biomarkers for the characterization of ancient wine molecules in archaeological ceramics**; Gazmend Elezi[1]; Kym Faull[2]; Jacques Connan[3]; Hans Barnard[4]; Julian Whitelegge[4]; *[1]UCLA, Los Angeles, CA; [2]USC, Los Angeles, CA; [3]Strasbourg University, Strasbourg, France; [4]UCLA, LOS ANGELES, CA*

WP 038 **Chromatography and Mass Spectrometry Elucidate the Materials in Margarito’s 13th Century Painting Madonna and Child Enthroned with Four Saints**; Daniel D Vallejo[1]; John K Delaney[1]; Kathryn A Dooley[1]; Teresa T Duncan[1]; Kathryn M Morales[1]; Joanna R Dunn[1]; Amar D Risbud[1]; *[1]National Gallery of Art, Washington DC, DC*

WP 039 **SugarMALDI, a software for the MS-based characterization of complex polysaccharides in natural gums applied to historical watercolors**; Marie YAMMINE[1, 2, 3]; Pierre-Alexandre Ho[4]; William Whitney[5]; Stéphanie Flament[4]; Fabrice Bray[4]; Christian Rolando[6]; *[1]Miniaturization for Synthesis, Analysis & Proteomics, UAR 3290, CNRS, University of Lille, 59655 Villeneuve d’Ascq Cedex, France., Lille, Afghanistan; [2]Institut Pasteur, MSBio lab, Paris, France; [3]Université Paris Cité, P*

WP 040 **Collagen Sequences from the Lower Jurassic: Proteomic Evidence for Endogenous Biomolecules in Fossil Crocodylomorph Bone**; Joseph Hubbard[1]; Joscelyn Harris[2]; Steven

Robinson[3]; Brian Thomas[4]; Claire Eyers[2]; Stephen Taylor[4]; *[1]University of Liverpool, Liverpool, United Kingdom; [2]Centre of Proteomic Research, University of Liverpool, Liverpool, United Kingdom; [3]Materials Innovation Factory, University of Liverpool, Liverpool, United Kingdom; <su*

WP 041 **Analysis of Natural Dyes Found in Northern European Textile Artifacts using Mass Spectrometry**; Alison M Trettin[1]; Peppi Toukola[2]; Riikka Räisänen[2]; Nelson R Vinueza Benitez[1]; *[1]North Carolina State University, Raleigh, NC; [2]University of Helsinki, Helsinki, Finland*

WP 042 **A Non-Autoregressive Deep Learning Model for De Novo Peptide Sequencing**; Devanshi C Desai[1]; William S. Noble[1, 2]; Justin Sanders[1]; Wout Bittremieux[3]; *[1]Paul G. Allen School of Computer Science and Engineering, University of Washington, Seattle, WA; [2]Department of Genome Sciences, University of Washington, Seattle, WA; [3]Department of Computer Science, University of Antwer*

WP 043 **pUniFind pushes the limits of mass spectra interpretation with a unified large pre-trained deep learning model**; WEIJIE ZHANG[1]; Hao Chi[2]; Jiale Zhao[2]; *[1]DP Technology, Beijing, China; [2]Institute of Computing Technology, Beijing, China*

WP 044 **AI Parent-to-Metabolite Pathway Predictor**; Savannah M Mason[1]; Paula Cifuentes[1, 2, 3]; Tommaso Palomba[1, 4]; Ismael Zamora[1]; *[1]Mass Analytica, S.L., Sant Cugat del Vallés, Spain; [2]Universitat Pompeu Fabra, Barcelona, Spain; [3]Lead Molecular Design, SL, Sant Cugat del Vallès, Spain; [4]Molecular Discovery, Borehamwood, United Kingdom*

WP 045 **Targeted immunopeptidomics without authentic synthetic peptide standards**; Curt Fischer[1]; Kyle Hoffman[2]; Ailee Aihemaiti[2]; *[1]Decade Bio, Daly City, CA; [2]Bioinformatics Solutions Inc, Waterloo, ON*

WP 046 **De Novo Molecular Structure Generation from MS/MS via Chemically Informed Contrastive Learning and Graph Diffusion**; Nir Cohen[1]; Yonatan Harnik[2]; Lilach Yishai Aviram[3]; Shai Kendler[3, 4]; Nitzan Tzanani[3]; Anat Milo[2]; *[1]Weizmann institute of science, Rhovot, Israel; [2]Ben-Gurion University of the Negev, Be'er Sheva, Israel; [3]Israel Institute for Biological Research, Ness Ziona, Israel; [4]Technion - Israel Institute of Technology*

WP 047 **Generalizing iRT prediction to unseen PTMs with atomic encoding and transfer learning**; Alexandros Pachos[1]; Ignacio Jauregui[2]; An-phi Nguyen[1]; George Rosenberger[3]; Oliver M. Bernhardt[1]; Monika Pepelnjak[1]; Grzegorz Skoraczyński[1]; Dennis Trede[3]; Tejas Gandhi[1]; *[1]Biognosys AG, Zurich, Switzerland; [2]Mestrelab Research S.L., Santiago de Compostela, Spain; [3]Bruker Switzerland AG, Fällanden, Switzerland*

WP 048 **Applying Large Language Models for Mass Spectrometry Data Analysis**; Haoyue Zhang[1]; Wenpeng Zhang[1]; Zheng Ouyang[1]; *[1]Tsinghua University, Beijing, China*

WP 049 **Improving AI models via direct optimization of search identification rates with Evolutionary Strategies**; An-phi Nguyen[1]; Alexandros Pachos[1]; Ignacio Jauregui[2]; George Rosenberger[3]; Tejas Gandhi[1]; *[1]Biognosys AG, Schlieren, Switzerland; [2]Mestrelab Research S.L., Santiago de Compostela, Spain; [3]Bruker Switzerland AG, Fällanden, Switzerland*

WP 050 **JUMPtrans: a transformer model for predicting substrate-kinase relationships**; Dehui Kong[1]; Jiacheng Guo[1]; Aijun Zhang[1]; Zhenserik Shynykul[1]; Ling Li[1]; Jay M. Yarbro[2]; Junmin Peng[2]; Xusheng Wang[1]; *[1]University of Tennessee Health Science Center, Memphis, TN; [2]St. Jude Children's Research Hospital, Memphis, TN*

WP 051 **It takes a village to build a world: Multi-agent LLM pipeline for multi-omic analysis and hypothesis generation**; Carlos Gonzalez[1]; Karen Cheng[1]; Leah Dorman[1]; Carolina Arias[1]; Josh E. Elias[1]; *[1]Chan Zuckerberg Biohub, San Francisco, CA*

WP 052 **Cascadia-tims enables de novo peptide sequencing of timsTOF diaPASEF data**; Michael Dammann[1, 2]; Sander Willems[3]; Bhavyahshree Krishnan[4]; Justin Sanders[4]; Wout Bittremieux[5]; William S Noble[4]; George Rosenberger[6]; Fabian J. Theis[1, 2]; *[1]Helmholtz Munich, Neuherberg, Germany; [2]Technical*

University of Munich, Freising, Germany; [3]Bruker, Kontich, Belgium; [4]University of Washington, Seattle, WA; [5]University of Antwerp, Antwerpen, Belgiu

WP 053 **Learning the shotgun proteomics measurement process enables global absolute protein quantification**; Vyas Pujari[1]; Chirag Kumar[1]; Meera Gupta[1]; Eli Costa[1]; Donovan Cassidy-Nolan[1]; Arjuna Subramanian[1]; Vishu Gupta[1]; Michael Skinnider[1]; Martin Wühr[1]; *[1]Princeton University, Princeton, NJ*

WP 054 **Five Aligned Omics Modalities Enable AI-Assisted Understanding of Host-Pathogen Temporal Dynamics in Dengue and Zika Infections**; Carlos G. Gonzalez[1]; Astrid Anaya[1]; Madhura Bhave[1]; Miguel Cid-Rosas[1]; Leah Dorman[1]; Clarissa Ferolla[1]; Ira Gray[1]; Shivali Kanwar[1]; Sudip Khadka[1]; See-Chi Lee[1]; Sarah Lin[1]; Frank McCarthy[1]; Johnson Truong[1]; Vincent Turon-Lagot[1]; Eileen Wang[1]; Brian C. DeFelice[1]; Karen Cheng[1]; Norma F Neff[1]; Carolina Arias[1]; Joshua E Elias[1]; *[1]Biohub, San Francisco, CA*

WP 055 **Smart Liquid Chromatograph Platform for High Throughput LC-MS workflow**; Xiaofeng Xie[1]; Thy Truong[1]; Nathaniel Axtell[1]; *[1]MicrOmics Technologies, Spanish Fork, UT*

WP 056 **Vibe coding and machine learning for FTICR MS performance optimization and capability improvement**; William Kew[1]; Kevin J. Zemaitis[1]; Piliang Xiang[1]; Rosalie Chu[1]; Yuri E Corilo[1]; John Lindquist[1]; Sai Munikoti[1]; Jan Strube[1]; Tobias P. Woerner[2]; Matthias Biel[2]; Alexander A. Makarov[2]; Ljiljana Pasa-Tolic[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

WP 057 **Predicting Discrete Structural Transformations in Small Molecules from Tandem Mass Spectrometry Using an Edit-Distance Based Deep Learning Framework**; Xianghu Wang[1]; Gwendolyn Kiler[1]; Michael Strobel[1]; Mohammed Reza Shahneh[1]; Daniel Petras[1]; Yasin El Abiead[2]; Vanessa V. Phelan[3]; Mingxun Wang[1]; *[1]University of California, Riverside, Riverside, CA; [2]University of Natural Resources and Life Sciences Vienna, Department of Chemistry, Institute of Analytical Chemistry, Vienna, Austria; [3]University of Colorado Anschutz,*

WP 058 **Toward Foundation Models of Cellular Regulatory State from Chromatin-Bound Proteomics**; Lillian T Tatka[1]; Daniele Canzani[1]; Andrea Gutierrez[1]; Evan E Hubbard[1]; Sebastian J Paez[1]; Anastasiya V. Prymolenna[1]; Julia Robbins[1]; Kyle Siebenthall[1]; Lindsay K Pino[1]; Alexander J Federation[1]; William E Fondrie[1]; *[1]Talus Bioscience, Seattle, WA*

WP 059 **End-to-End Multi-Agent Proteomics Workflow for Degrader Screening**; David Foreman[1]; Nathaniel K Berney[2]; Pooja Saklani[2]; Emily F Leibfritz[2]; Gaurav Chopra[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue Univeristy, West Lafayette, IN*

WP 060 **Practitioner AI for Regulated Biopharmaceutical Science: Accelerating Sequence Variant Analysis of Therapeutic Proteins Using Automated Curation**; Nina Socorro Cortina[1]; Lieza Marie Danan[1]; David Christy Ann Nacar[2]; Renee Kristine Tan[2]; Jerome Asuncion[2]; *[1]LiVeritas Biosciences, South San Francisco, CA; [2]LiVeritas Philippines, Taguig City, Philippines*

WP 061 **Integrative metabolomics and machine learning reveal anti-methanogenic compounds and genetic targets in low-methane-emission forages using mass spectrometry**; Camila Riccio-Rengifo[1]; Gabriel Esteban Velez[1]; Gustavo Adolfo Lara-Cruz[1]; Juliana Chaura[1]; Santiago Ruiz[1]; Diana Carolina Clavijo-Buritica[1]; Alejandra Marin[2]; Jacobo Arango[2]; Andres Jaramillo-Botero[1, 3]; *[1]iÓMICAS Research Institute, Pontificia Universidad Javeriana, Cali, Colombia; [2]Alliance Bioversity and International Center for Tropical Agriculture (CIAT), Cali, Colombia; [3]Chemistry and Chemical Engineering, California*

WP 062 **AI-Driven Chemical Analyses Provides an Opportunity for a Holistic Approach which Includes Point-of-Care and Novice Users**; Sarah N Trimpin[1, 2]; Dushan Kovacevic[3]; Ellen D Inutan[2, 4]; Frank S Yenchick[3]; Sullivan Stimac[1]; Jaden Stanley[1]; Hala Alaswad[1]; Brooklyn Ruffler[1]; Trine G Halvorsen[5]; Barbara S Larsen[6]; Paul M Stemmer[1]; Ken Mackie[7]; John W Tomsho[8]; Milan Pophristic[2, 9]; Charles N McEwen[2, 9]; *[1]Wayne State University, Detroit, MI; [2]MSTM, LLC, Newark, DE; [3]Singidunum, LLC, Detroit, MI; [4]Mindanao State University-Illigan Institute of Technology, Illigan City, Philippines; [5]University of Oslo,* WP 063 **Random Forest-Based Multiple Imputation and Pooling Framework for Missing Values in Proteomics**; Sijia S Qiu[1]; Apekshya Ghimire[1]; Anthony P Yun[1]; Soyoung Ryu[1]; [1]*University of Nevada Reno, Reno, NV*

WP 064 **Generative modelling of small molecule tandem mass spectrometry (MS/MS) with next token prediction**; Luke Zhang[1]; Hannes Rost[1]; [1]*University of Toronto, Toronto, ON*

WP 065 **Automated targeted chemoproteomic analysis of cysteine-containing peptides enabled by real-time peptide identification and retention time prediction**; Tommy K. Cheung[1]; Christopher M Rose[1]; [1]*Genentech, Inc., South San Francisco, CA*

WP 066 **Bond-Resolved Interpretation of Untargeted PFAS MS/MS Data Using Homolog Series and Fragmentation Constraints**; Sanoj Silva[1]; Mihira Kasun[1]; Osanda Hemachandra[1]; Pulasthi Ekanayake[1]; Chamika Perara[1]; Doreen Chrishanthy[2]; [1]*EXPERT Intelligence, Santa Clara, CA;* [2]*Expert Intelligence, Sanat Clara, CA*

WP 067 **ID-Free AI Proteomics for Multi-Cancer Screening**; Moonsu Bok[1, 2]; Seungheun Baek[3]; Kwon-Hee Bok[1, 2]; Chaewon Kang[1, 2]; Jiwon Hong[1, 2]; Tae Won Ko[1, 2]; JeongSu Jo[1, 2]; Su-jin Kim[1, 2]; Jingi Bae[1, 2, 4]; Hokeun Kim[1, 2]; Jueon Park[3]; Sohyun Chung[3]; Eunha Lee[3]; JunSeok Choe[3]; Jaewoo Kang[3, 5]; Sang-Won Lee[1, 2, 4, 6]; YoungRok Choi[7]; Suk Kyun Hong[7]; Jeongseon Kim[8]; Kyung Su Han[9]; So-Youn Jung[10]; Susie Kim[11]; Young-Woo KIM[11]; [1]*Department of Chemistry, Korea University, Seoul, South Korea;* [2]*Center for Proteogenome Research, Seoul, South Korea;* [3]*Department of Computer Science and Engineering, Korea University, Seoul, South Korea;* [4]*Targ*

WP 068 **DelPi: Replacing Handcrafted Scoring with Self-Supervised Learning Substantially Boosts Peptide Identifications Across DIA and DDA**; Jungkap Park[1]; Un-Beom Kang[1]; Sangtae Kim[1]; [1]*Bertis Inc., Gwacheon, South Korea*

WP 069 **The discovery of protein biomarkers associated with vancomycin-resistant in Enterococcus faecium using label-free quantitative proteomics**; Chao-Jung Chen[1]; Hsin-Yi Liao[1]; [1]*China Medical University, Taichung, Taiwan*

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WP 072 **GC×GC/HRMS and chemometric analysis of volatile and semi volatile compounds in Chinese mushrooms**; Albert T Lebedev[1]; Ekaterina Dmitrieva[1]; Olga V Poliakova[1]; Maria Kondratieva[1]; [1]*Shenzhen MSU-BIT University, Shenzhen, China*

WP 073 **High-throughput Untargeted Lipidomics Analysis Using the ZenoTOF 8600 System**; Pengyi Hou[1]; Dandan Si[1]; Zhimin Long[1]; Bingjie Liu[1]; [1]*SCIEX, Beijing, China*

WP 074 **Integrating Ionizing Radiation and Infection Stressors in a Dual-Hit Model to Identify Biomarkers Supporting Novel Nuclear Emergency Biodosimetry Assays**; Evan Pannkuk[1]; Anika Kot[1]; Jerry Angdisen[1]; Morgan DiGiorgio[1]; Lorreta Yun-Tien Lin[1]; Raymond Song[1]; Eric Wang[2]; Igor Shuryak[2]; Albert Fornace, Jr. [1]; Heng-hong Li[1]; [1]*Georgetown University, Washington Dc, DC;* [2]*Columbia University, New York, NY*

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Oluwatosin Daramola[1]; Andrew Reisner[2]; Laura Blackwell[2]; Verma Meena[2]; Yehia Mechref[1]; [1]*Texas Tech University, Lubbock, TX;* [2]*Children's Healthcare of Atlanta, Atlanta, GA*

WP 076 **Plasma Proteomics Across Various Blood Collection Tubes Using Nanotrap PEAK**; Anurag Patnaik[1]; Natalie L Smith[1]; Ben Lepene[1]; Mark Cafazzo[1]; [1]*Ceres Nanosciences, Manassas, VA*

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WP 079 **Mass Spectrometry Profiling of PNS-Tau Reveals Tissue-Specific Signatures in Heart and Kidney**; Monika Renuka Sanotra[1]; Xuemei Zeng[1]; Thomas K. Karikari[1]; [1]*University of Pittsburgh, Pittsburgh, PA*

WP 080 **Proteomic Analysis of Human Saliva for Discovery of Noninvasive Biomarkers of Human Performance**; Elizabeth C. Evin[1]; Hannah L. Whitacre[1]; Chi Yen Tseng[1]; Jessica A. Salguero[1]; Kes A. Luchini[1]; M. Gracie Thornhill[1]; Trevor G. Glaros[1]; Phillip M. Mach[1]; Ethan M. McBride[1]; Brett R. Blackwell[1]; [1]*Los Alamos National Laboratory, Los Alamos, NM*

WP 081 **Targeted LC-MS Analysis of a Mechanistically Anchored TML-Carnitine Signature for Improved Prostate Cancer Diagnosis**; Eric Zhao[1]; Anirudh Kashyap[2]; Morgan Fair[2]; Naseruddin Höti[2]; Raghothama Chaerkady[2]; Liang Zhao[2]; Laura Sena[3]; Qing Wang[2]; [1]*Gilman School, Baltimore, MD;* [2]*Complete Omics, Baltimore, MD;* [3]*Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University, Baltimore, MD*

WP 082 **Mass Spectrometry–Based Multi-Omics Signatures of Early Kidney Damage Biomarkers in Salt-Sensitive Hypertension**; Alessandra Anna Altomare[1]; Giovanna Baron[1]; Lara Davani[1]; Graziano Colombo[1]; Isabella Dalle-Donne[1]; Giulio Fumagalli[1]; Maguie Elboustani[2]; Simone Cardaci[2]; Chiara Lanzani[2, 3]; Lorena Citterio[2]; Paolo Manunta[2, 3]; [1]*University of Milan, Milan, Italy;* [2]*IRCCS San Raffaele Scientific Institute, Milan, Italy;* [3]*Vita-Salute San Raffaele University, Milan, Italy*

WP 083 **Development of a Liquid Chromatography-Mass Spectrometry Assay for Quantification of the DNA Damage Biomarker gammaH2AX in B-cells using Blood Samples**; Feng Jin; *AbbVie, Inc., North Chicago, IL*

WP 084 **Investigating Lipidomic and Glycomic Modifications as Biomarkers of Cardiotoxicity**; Kelsey E Buonodono[1]; Anna Colleen Crouch[1]; Caitlin Tressler[2]; [1]*University of Tennessee, Knoxville, TN;* [2]*Johns Hopkins University, Baltimore, MD*

WP 085 **Efficient Metabolic Fingerprinting of Follicular Fluid: A Novel Approach to Encode Ovarian Reserve and Fertility Potential**; Jiao Wu; *Biomedical Engineering, SJTU, Shanghai, China*

WP 086 **Mass Spectrometry–Based Proteomic Analysis of Breast Milk Proteins for Early Breast Cancer Biomarker Discovery**; Aneeta Arshad[1]; Costel C. Darie[1]; Kathleen F. Arcaro[2]; [1]*Clarkson University, Potsdam, NY;* [2]*University of Massachusetts Amherst, Amherst, MA*

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WP 089 **Proteomic profiling of tissue and serum-derived sEV discriminates rectal cancer patients with different statuses of regional lymph node metastasis**; Anna Wojakowska[1]; Kamil Jakub Frackowiak[1]; Daniel Fochtamn[1]; Łukasz Marczak[1]; Monika Pietrowska[2]; Marcin Zeman[3]; *[1]Institute of Bioorganic Chemistry Polish Academy of Sciences, Poznan, Poland; [2]Center for Translational Research and Molecular Biology of Cancer, Maria Skłodowska-Curie National Research Center and Institute of Oncology Gliwice Bran*

WP 090 **Multi-omics of Hunter syndrome in a mouse model by LC-HRMS/MS**; Nathan Ghafari[1]; Maggy Lepine[1]; Iskren Menkovic[2]; Pamela Lavoie[2]; Christiane Auray-Blais[2]; Michelo Boutin[2]; Lekha Sleno[1]; *[1]University of Quebec in Montreal (UQAM), Chemistry department, Montreal, QC; [2]Department of Pediatrics, Division of Medical Genetics, Faculty of Medicine and Health Sciences, University of Sherbrooke, Sherbrooke, QC, Canada, Sherbro*

WP 091 **Combined Unbiased Discovery and Targeted Proteomics for Enhanced Biological Insight in Alzheimer's Disease**; Ryan Lamers[1]; Khatereh Motamedchaboki[2]; Stephen Pollo[1]; Jenny Samskog[1]; Evgeny Kanshin[3]; Lauren Tang[3]; Dominique Leitner[3]; Thomas Wisniewski[3]; Beatrix Ueberheide[3]; *[1]Olink Proteomics (part of Thermo Fisher Scientific), Waltham, MA; [2]Thermo Fisher Scientific, San Jose, CA; [3]NYU Langone Health, New York, NY*

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WP 093 **Multi-omics Identifies PAGE4 as MED12-Mutant Uterine Fibroid Biomarker**; Yih Tyng Bong[1]; Xiaonan Liu[1]; Yaxin Jing[1]; Iftekhar Chowdhury[1]; Dicle Malaymar Pinar[1]; Salla Keskitalo[1]; Markku Varjosalo[1]; *[1]HiLIFE, University of Helsinki, Helsinki, Finland*

WP 094 **Global Proteomics Uncovers Immune Profiles and Lymph Node Metastasis in Early-Stage Non-Small Cell Lung Cancer by Smoking Status**; Kyujin Song[1, 2]; Minhyung Kim[3, 4]; Qian Yang[3, 4]; Kamya Sankar[5, 6]; Ho-Young Lee[7]; Sukhmani K. Padda[8]; Michael R. Freeman[3, 9]; Kwang Pyo Kim[2, 10]; Sungyong You[3, 4, 6]; *[1]Korea Research Institute of Bioscience and Biotechnology, Daejeon, South Korea; [2]Department of Applied Chemistry, Institute of Natural Science, Kyung Hee University, Yongin, South Korea; [3]Departments of Urology, Cedars-Si*

WP 095 **Mass Spectrometry–Based Atlas of the Blood-Accessible Surface Proteome in Syngeneic Brain Tumor Models**; Domenico Ravazza[1]; Marcel Bühler[2]; Carlotta Dell'Anna Misurale[2]; Samuele Cazzamalli[1]; Emanuele Puca[1]; Michael Weller[2]; Dario Neri[3, 4]; Tobias Weiss[2]; Ettore Gilardoni[1]; *[1]Philochem AG, Otelfingen, Switzerland; [2]Department of Neurology, Clinical Neuroscience Center, University Hospital and University of Zurich, Zurich, Switzerland; [3]Philogen S.p.A., Siena, Italy; [4]Swiss Federal I*

WP 096 **Mass guided isolation of lipids that induce epinephrine autocrine signaling in the secondary metastasis of high grade serous ovarian cancer**; Silvia Xie[1]; Monica Haughan[2]; Hannah Lusk[1]; Joanna Burdette[2]; Laura Sanchez[1]; *[1]University of California, Santa Cruz, Santa Cruz, CA; [2]University of Illinois Chicago, Chicago, IL*

WP 097 **Characterization of Ionizing Radiation-Dependent Substrates of PPM1D Phosphatase**; Lisa M Jenkins[1]; Tapan K Maity[1]; Weiming Yang[1]; Kate Brown[1]; Ettore Appella[1]; *[1]National Cancer Institute, National Institutes of Health, Bethesda, MD*

WP 098 **Proteomics of Bone CarryingMetastatic Breast Cancer Lesions from Archival Formalin-Fixed Paraffin Embedded (FFPE) Tissue Blocks Unveils Striking Skeletal Remodeling**; Charles A Schurman[1]; Gabriel M Pagnotti[2]; Theresa Guise[2]; Birgit Schilling[1]; *[1]Buck Institute for Research on Aging, Novato, CA; [2]MD Anderson Center, Houston, TX*

WP 099 **Scaling Label-Free Single-Cell Proteomics to >1,000 Cells Reveals Distinct Survival and Resistance Responses in Triple-Negative Breast Cancer**; Hsien-Jung L Lin[1]; Chao Wang[1]; Jacob H. Clark[1]; Ella E. Norton[1]; R. J. S. Miercort[1]; Garrett D. Haynie[1]; Kenneth S. Triggs[1]; Joshua L. Andersen[2]; Ryan T. Kelly[1]; *[1]Brigham Young University, Provo, UT; [2]University of Utah, Salt Lake City, UT*

WP 100 **Cross-Laboratory Validation of High-Resolution Ion Mobility Mass Spectrometry for Glycosphingolipid Profiling in PDAC**; Veronika Subrtova[1]; Huong Giang Vo[2]; Robert Jirasko[1]; Ondrej Peterka[1]; Milan Vosmik[3]; Laura Bindila[2]; Michal Holcapek[1]; *[1]University of Pardubice, Faculty of Chemical Technology, Department of Analytical Chemistry, Pardubice, Czech Republic; [2]University Medical Center, Institute of Physiological Chemistry, Clinical Lipidomics Unit, Mainz, Germany; <sup*

WP 101 **Tumor Microenvironment Dynamics in Metastatic High-Grade Serous Ovarian Cancer Revealed by Quantitative Proteomics**; Nicholas Bateman[1]; Jonathan Ogata[1]; Suzanne Jokajtys[1]; Ryan Khan[2]; Tamara Abulez[1]; Brian Hood[1]; Kelly Conrads[1]; Allison Hunt[3]; M Herman Chui[2]; Michelle Wu[2]; Hunter Green[2]; David Bowtell[4]; Kathleen Darcy[1]; Christoper Tarney[1]; Britta Weigelt[2]; Dennis Chi[2]; Thomas Conrads[3]; G. Larry Maxwell[3]; *[1]Gynecologic Cancer Center of Excellence, Annandale, VA; [2]Memorial Sloan Kettering Cancer Center, New York, NY; [3]Women's Health Integrated Research Center, Annandale, VA; [4]Peter MacCallum Cancer Centre, Parkvill*

WP 102 **Multi-Omic Analysis Reveals Metabolic and Signaling Reprogramming of Hormone Therapy Resistant ER+ Breast Cancer**; Adam Graves[1, 2, 3, 4]; Attila Szenasi[2, 3, 4]; Philip Spanheimer[2, 3, 4, 5]; Tigist Tamir[1, 2, 3, 4, 6, 7]; *[1]Department of Biochemistry and Biophysics, Chapel Hill, NC; [2]Lineberger Comprehensive Cancer Center, Chapel Hill, NC; [3]UNC School of Medicine, Chapel Hill, NC; [4]University of North Carolina at Chapel Hill, Chap*

WP 103 **Proteogenomic Mapping of Environmental Exposures and Functional States in Gastric Cancer**; Hsiang-En Hsu[1]; Ya-Hsuan Chang[2]; Tzu-Chan Hong[3, 4]; Kuen-Tyng Lin[1]; Yi-Jing Hsiao[1]; Juanilita T. Waniwan[1]; Rodrigo Espinoza Silva[5]; Yi-Ju Chen[1]; Hao Fang[1]; Pei-Rong Huang[1]; Chia-Li Han[6]; Deng-Chyang Wu[7]; Hsuan-Yu Chen[8]; Sung-Liang Yu[9]; Ming-Shiang Wu[3]; Yu-Ju Chen[1]; *[1]Institute of Chemistry, Academia Sinica, Taipei, Taiwan; [2]Institute of Molecular and Genomic Medicine, National Health Research Institutes, Maioli, Taiwan; [3]Department of Internal Medicine, National Taiwan University Hosp*

WP 104 **Multiomics Oral Rinse Profiling to Identify Host–Microbial Biomarkers Associated With Cancer Risk in Individuals With Fanconi Anemia**; Rachel Uppgaard[1]; Beverly Wuertz[2]; Danielle Weise[3]; Brett Phinney[4]; Subina Mehta[3]; John Wagner[5]; Margaret Macmillan[6]; Tim Griffin[3]; Frank Ondrey[2]; Pratik Dilip Jagtap[3]; *[1]School of Dentistry, University of Minnesota, Minneapolis, MN; [2]Department of Otolaryngology, University of Minnesota, Minneapolis, MN; [3]Department of Biochemistry, Molecular Biology and Biophysics, University of Minnesot*

WP 105 **Integrated mass spectrometry reveals KRAS-dependent regulation of protein secretion in lung cancer cells**; Victoria Gonzalez[1]; Ran Cheng[1]; Janos Demeter[1]; Peter Jackson[1]; *[1]Stanford University, Stanford, CA*

WP 106 **Ultra-high doseω-3 docosahexaenoic acid (DHA) or eicosapentaenoic acid (EPA) block tumorigenesis in a MYCN-driven neuroblastoma model**; Yanning Li[1]; Vishwa Patel[2]; Lorraine-Rana E Benhamou[3]; Hui Gyu Park[3]; Mariya Raleigh[3]; Thomas J. Brenna[2]; John T. Powers[2]; *[1]University of Texas at Austin, Dell Pediatric Research Institute, Austin, TX; [2]University of Texas at Austin, Austin, TX; [3]University of Texas - Austin, Austin, TX*

WP 107 **Rapid Detection of High-Grade Serous Carcinoma In Vivo in Diagnostic and Primary Debulking Surgeries using a Laparoscopic-MSPen**; Charles A. Wolfe[1]; Mary F. Wang[1]; Faith Jackobs[1]; Ashley Montgomery[1]; Barrett C. Lawson[2]; Kelly Rangel[3]; Mario Tanguma[3]; Anil K. Sood[3]; Amir Jazaeri[3]; Livia S. Eberlin[1]; *[1]Department of Surgery, Baylor College of Medicine, Houston, TX; [2]Department of Anatomic Pathology, Division of Pathology & Laboratory Medicine, MD Anderson Cancer Center, Houston, TX; [3]Department of Gynecologic Oncology a*

WP 108 **Multi-omic discovery of system xc inhibition–dependent LRRC58 regulation and function during ferroptosis in lung cancer**; Xuan Mo[1]; Karina Nugroho[1]; Carlo Ramil[1]; Benjamin Ruprecht[1]; An Chi[1]; *[1]Merck & Co., Inc., Cambridge, MA*

WP 109 **A Comparative Analysis of Doxorubicin and Sodium Nitroprusside-Induced Proteomic Alterations in Cancer Cells**; Zahid Hasan[1]; Kamrul Islam[1]; Amit Singh[1]; Zhibo Yang[2]; Nagib Ahsan[1, 3]; *[1]Department of Chemistry and Biochemistry, University of Oklahoma, 73019, Norman, OK; [2]University of oklahoma HSC, Oklahoma city, OK; [3]Mass Spectrometry, Proteomics and Metabolomics Core Facility, Stephenson Life Sciences*

WP 110 **Mapping Glioblastoma Heterogeneity with Fluorescence-Guided Multiple Sampling, Tumor-Matched Primary 3D Models and Spatial Omics**; Adele-Asia Ponzoni[1]; Evangelos Liapis[1]; Lea Anne T. Maristela[1]; Elizabeth E. Ginalis[2]; Kar Fai Chow[1]; Kangmin Lee[1]; George J Kaptain[1]; Claire Louise Carter[1]; *[1]Hackensack Meridian Health, Nutley, NJ; [2]Rutgers New Jersey Medical School, Newark, NJ*

WP 111 **Evaluation of the MasSpec Pen Technology for Molecular Identification of Soft-Tissue Sarcomas and Surgical Margin Assessment**; Ashley E Montgomery[1]; Yasmin Shanneik[1]; Emily Ma[1]; Jacob I Mardick[1]; Charles A. Wolfe[1]; Sarah Bench[1]; Pujita Munnangi[2]; Alicia Gingrich[2]; Sharon Landers[2]; Sintawat Wangsiricharoen[2]; Angela Bhalla[2]; Patrick P Lin[2]; Valerae O Lewis[2]; Bryan S Moon[2]; Shalin Shreyaskumar Patel[2]; Heather Lyu[2]; Heather Lillemoe[2]; Christopher Scally[2]; Emily Keung[2]; Christina L Roland[2]; Kelly K Hunt[2]; Ian McCutcheon[2]; Justin E Bird[2]; Wendong Yu[2]; Keila E Torres[2]; Livia S. Eberlin[1]; *[1]Department of Surgery, Baylor College of Medicine, Houston, TX; [2]MD Anderson Cancer Center, Houston, TX*

WP 112 **Proteomics-Driven Bioinformatics for Drug Discovery and Precision Treatment for Pancreatic Cancer**; Max Shen[1]; Christopher Kevil[1]; Long Jin[1]; Xinggui Shen[1]; *[1]LSU Health Shreveport, Shreveport, LA*

WP 113 **Molecular Profiling of Pediatric Sarcoma Tissues Using the MasSpec Pen and DESI Mass Spectrometry Imaging**; Manoj Kumar[1]; Jacob I. Mardick[1]; Faith E Jackobs[1]; John M. Hicks[2]; Sarah Bench[1]; Yasmin Shanneik[1]; Ashley Montgomery[1]; Dailen Alonso[1]; Ruth Costa[1]; Raul Villacob[1]; Mary Wang[1]; Alessandro Baldan[2]; Nino Rainusso[1, 2]; Sanjeev Vasudevan[1, 2]; Livia S. Eberlin[1]; *[1]Department of Surgery, Baylor College of Medicine, Houston, TX; [2]Department of Pediatrics, Texas Children's Hospital, Houston, TX*

WP 114 **LC-MS Lipidomics Reveals Unique Dysregulation in Temozolomide-MF-438 Combination Treatment of Isocitrate Dehydrogenase 1-Mutant Oligodendroglioma**; Taylor A. Harmon[1]; Lumin Zhang[1]; Mioara Larion[1]; *[1]National Cancer Institute, National Institutes of Health, Bethesda, MD*

WP 115 **Comparing the differences of HSP90α and HSP90β in native protein complex incorporation**; Daryna Serediuk[1]; Luke Botticell[1]; Feixia Chu[1]; Seth McNutt[1]; *[1]University of New Hampshire, Durham, NH*

WP 116 **An Integrative, Ultrasensitive Proteogenomic Framework for Tumor-Specific Cell Surface Proteoform Discovery and Multi-PTM Mapping**; Katarzyna Kulej[1]; Gabriella Casalena[1]; Jinxin Zhang[1]; Asher Preska Steinberg[1]; Andrew McPherson[1]; Alex Kentsis[1]; *[1]Memorial Sloan Kettering Cancer Center, New York, NY*

WP 117 **Identification of Altered RNA N-Glycosylation Patterns in Melanoma Development and Metastasis Using MALDI MSI**; Shaaron Ochoa-Rios[1]; Manon Chadourne[1]; Anand Mehta[2]; Florian Karreth[1]; *[1]Moffitt Cancer Center, Tampa, FL; [2]Medical University of South Carolina, Charleston, SC*

WP 118 **Mapping the RORβ Regulatory Network in Neuroblastoma**; Nereida Abad-Yang[1, 2]; Mi Ra Chang[2]; Patrick R Griffin[1, 2]; *[1]Scripps Research, La Jolla, CA; [2]UF Scripps, Jupiter, FL*

WP 119 **Negligible Chiral Inversion of Bexicaserin (R-enantiomer) to S-enantiomer in Clinical Samples Using a Qualified Chiral Assay**; Raja Reddy Kallem[1]; Rosa Chan[1]; Helen Young[2]; Jonathan Williams[1]; Nuggehally R. Srinivas[1]; *[1]Department of Clinical Pharmacology and Pharmacometrics, Lundbeck*

Pharmaceuticals LLC, Deerfield, IL; [2]*Delivery, York Bioanalytical Solutions (YBS), Upper Poppleton, United Kingdom*

WP 120 **Develop and Validate an Ultra-Sensitive LC-MS/MS Method to Quantify Beraprost in Human Plasma**; Changjian Zhao[1]; Hong Zhong[1]; Chenggang Li[1]; Yuhuan Ji[1]; Laixin Wang[1]; [1]*Resolian, Chongqing, China*

WP 121 **A liquid chromatography-tandem mass spectrometry method for direct detection of 20 kDa and 22 kDa subtypes of growth hormone**; Dan Liu[1]; Yao Hu[2]; Chao Huang[1]; Xianglong Zhao[1]; Bingjie Liu[1]; [1]*SCIEX, Beijing, China;* [2]*Department of Laboratory Medicine, Huashan Hospital, Shanghai Medical College, Fudan University, Shanghai, China*

WP 122 **State-Reflective Metabolomic Signatures Enhance Polygenic Risk–Based Severity Prediction in NTM Pulmonary Disease**; Jungeun Kim[1]; JunHwa Shin[2]; Nakwon Kwak[3]; Joo-Youn Cho[2, 4]; [1]*Seoul National University, Seoul, South Korea;* [2]*Department of Clinical Pharmacology and Therapeutics, Seoul National University College of Medicine and Hospital, Seoul, South Korea;* [3]*Division of Pulmonary and Critical Car*

WP 123 **Enabling Earlier Detection and Screening of Colorectal Cancer via a Paper-Based Immunoassay Integrated with Ambient Ionization Mass Spectrometry**; Hianka J.C. De Carvalho[1]; Stephanee Joy B Zerrudo[1]; Rana Arebi[1]; Abraham K. Badu-Tawiah[1]; [1]*The Ohio State University, Columbus, OH*

WP 124 **LC-MS/MS Profiling of Bromazolam Metabolism in Clinical Toxicology Samples**; Hannah J Lusk[1]; Kara Lynch[1]; Lilly Lim[1]; [1]*University of California San Francisco, San Francisco, CA*

WP 125 **Longitudinal metabolome data reveals aromatic amino acids metabolism linked to differential weight loss after sleeve gastrectomy**; Hoseong Hwang[1]; Hyeon-Seong Lee[1]; Won Kyu Kim[1]; Jaeyoung Kwon[1]; [1]*Korea Institute of Science and Technology, Gangneung, South Korea*

WP 126 **Thyroglobulin Measurements using Vanquish Neo Tandem Direct Injection-Altis Plus**; Jennifer Kemp[1]; Richard Lahr[1]; Anthony Maus[1]; [1]*Mayo Clinic, Rochester, MN*

WP 127 **Maximizing the Sensitivity and Throughput of Acacetin Measurements for Therapeutic Drug Monitoring using a Transcend TLX-4-7500**; Anthony Maus[1]; Adam Girtman[1]; Yubo Chai[1]; Todd Juen[1]; Paul Jannetto[1]; [1]*Mayo Clinic, Rochester, MN*

WP 128 **Tube-Type Interchangeability for Plasma Busulfan TDM: Paired Sodium vs Lithium Heparin Evaluation by LC-MS/MS**; Philip Adrian Dugan[1]; Ning Pan Bernhardt[1]; [1]*National Institutes of Health, Bethesda, MD*

WP 129 **Quantitative mass balance of Oral Administration of AB-106 in Human Biological Samples using (14C)AB-106 as probe by Accelerator Mass spectrometer**; Yu-Nan CHEN[1]; Xu-Yang Shen[2]; Yi-Xuan GU[2]; Xin Zheng[3]; Xin-Ge Cui[3]; Ying-Lin ZHOU[2]; Xin-Xiang Zhang[2]; [1]*Peking University, Beijing, China;* [2]*Peking University, Haidian, China;* [3]*Peking Union Medical College Hospital, Beijing, China*

WP 130 **Development of a semi-quantitative analysis of an Insulin-analogue, Novorapid, in human serum using LC-MS/MS**; Dennis JA Van Den Heuvel[1]; Martine Van De Kamp[2]; Tom Stokhof De Jong[2]; Pascal Mannaert[2]; [1]*Shimadzu Benelux, 's-Hertogenbosch, Netherlands;* [2]*Shimadzu Benelux, ‘s-Hertogenbosch, Netherlands*

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WP 132 **Ultra-Trace Measurement of Testosterone in Human Saliva Using a Robust LC-MS/MS Workflow**; Jenishia Menezes[1]; Anant Lohar[2]; Jessin Mathai[2]; [1]*Shimadzu Middle East and Africa Fze, Dubai, United Arab Emirates;* [2]*Shimadzu Middle East and Africa FZE, Dubai, United Arab Emirates*

WP 133 **High-sensitivity LC-MS/MS for steroid hormones in plasma using micro flow analysis**; Tomoya NIINAE[1]; Eishi IMOTO[1]; Satoshi YAMAKI[1]; Tsuyoshi NAKANISHI[1]; [1]*Shimadzu Co., Kyoto, Japan*

WP 134 **End-to-End Fully Automated LC–MS/MS Analysis of Plasma Metanephrines**; Pengyun Liu[1]; Ziqing Kong[2]; Weijia Wu[3]; Huafen Liu[2]; Jun Xia[4]; Yu Zhou[4]; [1]*Disigns Diagnostics, Hangzhou, China, China;* [2]*Calibra Scientific Inc, HANGZHOU, China;* [3]*3P BioSolutions, Woodbridge, VA;* [4]*Zhejiang Provincial People's Hospital (Affiliated People's Hospital), Hangzhou Medical C*

WP 135 **Fully Automated Integrated Mass Spectrometry System for High-Throughput Routine Clinical and Analytical Testing**; Zhouyang Kang[1]; Xiaoping Liu[1]; Yikun Li[1]; Pengyun Liu[1]; Huafen Liu[1]; Haitao Yu[2]; Rui An[2]; Jun Zhang[2]; [1]*Calibra Scientific Inc, HANGZHOU, China;* [2]*Sir Run Run Shaw Hospital of Zhejiang University School of Medicine, Hangzhou, China, China*

WP 136 **Acidic Aspartic Proteases for Rapid In-Solution and Immobilized Digestion in Bottom-Up Bacterial Identification**; Jakub Kordík[1, 2]; Petr Pompach[3]; Ljubina Adámková[1]; Jana Nováková[3]; Dmitry S. Loginov[1]; Petr Novak[1]; [1]*Institute of Microbiology CAS, Prague, Czech Republic;* [2]*Charles University, Prague, Czech Republic;* [3]*AffiPro s.r.o., Vestec, Czech Republic*

WP 137 **NeoSickle and NeoHemog MALDI-MS platforms for sickle cell disease screening and hemoglobinopathy detection**; Marven El Osta[1]; Yann Gouriou[1]; Pierre Naubourg[1]; Guillaume Crevisy[1]; Cassandre Devos[1]; Stephane Moreau[2]; Yusuke Toyota[1]; Patrick Ducoroy[1]; [1]*Shimadzu Chemistry & Diagnostics, Illkirch-Graffenstaden, France;* [2]*Shimadzu Europa GmbH, Duisburg, Germany*

WP 138 **Accelerated blood histone proteoform screening using liquid chromatography, high-resolution trapped ion mobility spectrometry and tandem electron-based fragmentation mass spectrometry**; Md Shofiul Alam[1]; Kevin Jeanne Dit Fouque[1]; Lilian Valadares Tose[1]; Francisco Fernandez-Lima[1]; [1]*Florida International University, Miami, FL*

WP 139 **Hemoglobin Proteoform screening using liquid chromatography, high-resolution trapped ion mobility spectrometry, and tandem electron-based fragmentation mass spectrometry**; Seoyoung Chung[1]; Md Shofiul Alam[1]; Kevin Jeanne Dit Fouque[1]; Lilian Valadares Tose[1]; Ruben Luo[2]; Francisco Fernandez-Lima[1]; [1]*Florida International University, Miami, FL;* [2]*Stanford University, Stanford, CA*

WP 140 **Ultrasonic Nebulization (USN) MasSpec Pen for Tandem MS Analysis Directly from Human Tissues**; Charles A Wolfe[1]; Tassia V Mendes[1]; Mary F Wang[1]; Livia S. Eberlin[1]; [1]*Department of Surgery, Baylor College of Medicine, Houston, TX*

WP 141 **International Multi-Center Validation of the MasSpec Pen Technology for Intraoperative Diagnosis and Tumor Margin Assessment in Lung Cancer Surgeries**; Yasmin Shanneik[1]; Alberto Antonicelli[2]; Ruth P. Costa[1]; Jacob I. Mardick[1]; Michael D Tuck[1]; Charles A. Wolfe[1]; Sarah Bench[1]; Simon Esteva[1]; Gustavo Goncalves Silva[3]; Kenneth J. Gollob[3]; Amanda B. De Figueiredo[3]; Carlos Eduardo Dos Santos Ferreira[3]; Ricardo M. Terra[3]; Francisca K. F. K.F. Pereira[3]; Nathan Sanders[4]; Justin Wiseman[4]; Maheshwari Ramineni[5]; Brant G. Wang[1]; James W. Suliburk[1]; Reginald Chounoune[1]; Ravi Ghanta[1]; Robert T. Ripley[1]; Shanda Blackmon[1]; Bryan Burt[2]; Livia S. Eberlin[1]; [1]*Baylor College of Medicine, Houston, TX;* [2]*University of California, Los Angeles, Los Angeles, CA;* [3]*Albert Einstein Israelite Hospital, Sao Paulo, Brazil;* [4]*MSPen Technologies, Houston, TX;* [5]*Houston Me*

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WP 143 **The Effect of Weight Loss on Depressive Symptom and Serum Dopamine after Sleeve Gastrectomy**; Hyeon-Seong Lee[1]; Hoseong Hwang[1]; Jaeyoung Kwon[1]; Won Kyu Kim[1]; [1]*Korea Institute of Science and Technology, Gangneung, South Korea*

WP 144 **Targeted mass spectrometry improves medication-history ascertainment in older adults compared with self-report, EMR, and claims data**; Jong Do Seo[1]; Yeo-Min Yun[1, 2]; Kyunghoon Lee[3, 4]; Sang Hoon Song[3, 5]; Hyung-Doo Park[6]; Junghan Song[3, 4]; [1]*Department of Laboratory Medicine, Konkuk*

University Medical Center, Seoul, South Korea; [2]Department of Laboratory Medicine, Konkuk University School of Medicine, Seoul, South Korea; [3]Department of Laboratory Medicine, Se

WP 145 **Semi-automatic LC-MS/MS method for measurement of 3-methoxytyramine, Metanephrine and Normetanephrine in plasma**; Ning Pan Bernhardt[1]; Caroline Nottingham[2]; *[1]NIH, Bethesda, MD; [2]Werfen, S.A., Bedford, MA*

WP 146 **Comparative quantitative cross-linking mass spectrometry analysis of nitric oxide synthase dynamics with sulfo-SDA and DSBU**; Ting Jiang[1]; Changjian Feng[1]; *[1]UNM College of Pharmacy, Albuquerque, NM*

WP 147 **Probing Tryptophan and Methionine Solvent Accessible Surface Area and Protein Conformation with Online Ozonation and Mass Spectrometry**; Keshari Kunwor[1]; Nicholas B. Borotto[1]; *[1]University of Nevada, Reno, NV*

WP 148 **Biochemical Environment Drives Proteoform-Specific Conformational Remodeling of α-Synuclein**; Ashlyn N Dollar[1]; Ian K Webb[1]; *[1]Indiana University Indianapolis, Indianapolis, IN*

WP 149 **Assessment of Protein Conformation via Diazirine-Promoted Oxidation of Methionine and Tryptophan Residues**; Supadach Prertprawnon[1]; Salem R. Neufeld[1]; Nicholas B. Borotto[1]; *[1]University of Nevada, Reno, Reno, NV*

WP 150 **Characterization of Protein Interactions Using Ion-Mobility-Shift-Enhanced Covalent Labeling Mass Spectrometry**; Kanitin Khamnong[1]; Avantika Manikandan[1]; Richard W. Vachet[1]; *[1]University of Massachusetts Amherst, Amherst, MA*

WP 151 **Orbitrap™ Astral™ Enables DIA for Deep and Comprehensive Covalent Labeling–Based Protein Structure Analysis**; Yunyun ZHU[1]; Patric Sadecki[2]; *[1]Thermo Fisher Scientific, Lexington, MA; [2]Immuto Scientific, Madison, WI*

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WP 153 **In-cell mapping of epichaperome higher-order assemblies by chemical-probe enrichment and crosslinking mass spectrometry**; Wang Shujuan[1]; Pengzhi Mao[2, 3]; Chiranjeevi Pasala[1]; Luke Botticell[4]; Chander Digwal[1]; Sahil Sharma[1]; Souparna Chakrabarty[1]; Anna Rodina[1]; Feixia Chu[4]; Mara Monetti[5]; Gabriela Chiosis[1]; *[1]Chemical Biology Program, Memorial Sloan Kettering Cancer Center, New York, NY; [2]Key Laboratory of Intelligent Information Processing of Chinese Academy of Sciences (CAS), Institute of Computing Technology, CAS, Beijing, China; <sup*

WP 154 **Oxidative Labeling Mass Spectrometry as a Method to Distinguish Co-existing Conformational States of Proteins**; Ina F. De La Fuente[1]; Elise M. Blackstock[1]; Griffin A. Weiss[1]; Alicia M. Bergeron[1]; Natalie M. Beydoun[1]; Richard W. Vachet[1]; *[1]University of Massachusetts Amherst, Amherst, MA*

WP 155 **Broadly Active Electrophile-Based Protein Profiling (BAE-BPP) Enables Proteome-wide Druggable Pocket Discovery**; Yunlong Shi; *Bayer US LLC, Cambridge, MA*

WP 156 **Covalent Footprinting of Protein Denaturation in Reversed-Phase Chromatography**; Kimber N. Focke[1]; Brian T. Cooper[2]; *[1]University of Arizona, Tucson, AZ; [2]UNC Charlotte, Charlotte, NC*

WP 157 **Is Manual Validation Still Necessary in Crosslinking Mass Spectrometry? A Benchmarking Study**; Fang Liu[1]; Garvey McKenzie[1]; Casey Powers[1]; Juan Pablo Galindo[1]; Ryan D. Leib[1]; *[1]Stanford University, Stanford, CA*

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WP 160 **OpenLink: beyond conventional cross-linked peptides identification for proteome-wide crosslinking mass spectrometry (XL-MS)**; Jinyang Li[1,2]; Peng-Zhi Mao[1,2]; Adalet Memetimin[3,4]; Meng-Qiu Dong[3,4]; Hao Chi[1,2]; Si-Min He[1,2]; *[1]Institute of Computing Technology, Beijing, China; [2]University of Chinese Academy of Sciences, Beijing, China; [3]National Institute of Biological Sciences, Beijing, China; [4]Tsinghua University, Beijing, China*

WP 161 **Large-Scale Interactome Analysis of Cryptococcus deuterogattii by Crosslinking Mass Spectrometry**; Hulyana Brum[1,2]; Emanuella Castro Andreassa[1]; Amanda Dal Lin[1]; Flavia Coelho Reis[3]; Michel Batista[2]; Giovanna Lopes Araújo[4]; Fabio Cesar Gozzo[4]; Marcio Lourenço Rodrigues[3]; Paulo Costa Carvalho[1]; *[1]Laboratory for Structural and Computational Proteomics, Carlos Chagas Institute, Fiocruz, Curitiba, Brazil; [2]Mass Spectrometry Facility, Carlos Chagas Institute, Fiocruz, Curitiba, Brazil; [3]FIOCRUZ, Carlos Chagas Institut*

WP 162 **Crosslinked peptides are getting to the mass spectrometer. Why aren't we finding more of them?**; Bruno C. Amaral[1]; Nicholas I. Brodie[1]; Morgan F. Khan[1]; D. Alex Crowder[1]; Pauline Douglas[1]; David C. Schriemer[1]; *[1]University of Calgary, Calgary, AB*

WP 163 **Evaluation of a New Chymotrypsin for Protein Epitope Mapping Using Carbene Footprinting**; Huimin Zhong[1]; Laurence Fayadat-Dilman[1]; Jason Hogan[1]; *[1]Merck & Co., Inc., South San Francisco, CA*

WP 164 **LipiX-MS: a novel crosslinking mass spectrometry strategy for studying lipid-protein interactions**; Chia-Lung Tsai[1]; Atiya Tahira Tasnim[2]; Zhenyu Xi[2]; Syuan-Ting Kuo[2]; Ramidi Gopal Reddy[2]; Jiaxin Feng[2]; David H Russell[2]; Xuewu Sui[2]; Xin Yan[2]; *[1]Texas A&M University, College Station, TX; [2]Texas A&M Univesity, College Station, TX*

WP 165 **pLink3 enables unified and high-performance analysis of massive crosslinking proteomics data**; Peng-Zhi Mao[1,2]; Yong Cao[3]; Jin-Yang Li[1,2]; Zhen-Lin Chen[1,2]; Song Ge[3]; Ya-Peng Yuan[1,2]; Ran-Fei Chen[1,2]; Jia-Le Zhao[1,2]; Adalet Memetimin[3]; Hao Chi[1,2]; Meng-Qiu Dong[3,4]; Si-Min He[1,2]; *[1]Key Laboratory of Intelligent Information Processing of Chinese Academy of Sciences (CAS), Institute of Computing Technology, CAS, Beijing, China; [2]University of Chinese Academy of Sciences, Beijing, China; [3]National Inst*

WP 166 **Structural Signature of Plasma Proteins Classifies the Status of Alzheimer's Disease**; Ahrum Son[1]; Hyunsoo Kim[2]; Jolene K. Diedrich[3]; Tom Casimir Bamberger[3]; Robert A. Rissman[4]; Russell H. Swerdlow[5]; John R. Yates III[3]; *[1]Graduate School of Medical Science, University of Ulsan, Ulsan, South Korea; [2]Chungnam National University, Daejeon, South Korea; [3]Scripps Research, La Jolla, CA; [4]Alzheimer's Therapeutic Research Institute, De*

WP 167 **Large-Scale protein-protein interaction mapping in suspended cells using a cell fixation / cross-linking approach**; Fabio C Gozzo[1,2]; Leonardo Rosa Valdo[1]; Giovanna Lopes Araujo[1]; Guilherme Reis-de-Oliveira[3]; Bianca Gonçalez Ferrari[1]; Paulo Costa Carvalho[4]; Diogo Borges[4]; Milan Clasen[5]; *[1]IQ - University of Campinas, Campinas, Brazil; [2]National Institute of Science and Technology in Bioanalytics Lauro Kubota - INCTBio-LK, Campinas, Brazil; [3]Centro Infantil Boldrini, Campinas, Brazil; [4]Instituto*

WP 168 **Covalent Labeling mass spectrometry Enables In-Depth Structural Analysis of Antibody Dimers and High Molecular Weight Species**; Kevin Lam; *Boehringer Ingelheim, Biberach an der Riß, Germany*

WP 169 **BioDiAz: A Novel Chemical Crosslinker for Mapping Protein–RNA Interfaces**; Bibhuti Bhusana Palai[1]; Daniel Ramirez[1]; Carolina Bras Acosta[1]; Emily Zahn[1]; Zongtao Lin[2]; Benjamin Garcia[1]; *[1]Washington University School of Medicine, St. Louis, MO; [2]Rutgers University, Piscataway, NJ*

WP 170 **Evaluation of Astral DIA-MS methodology for global, high-throughput detection of alternative protein isoforms predicted with long-read RNA-sequencing**; Micah D. Lehe[1]; Erin D. Jeffery[1]; Nicholas E. Sherman[2]; Nidhi Sahni[3,4]; Gloria M. Sheynkman[1,5,6]; *[1]Department of Molecular Physiology* *and Biological Physics, University of Virginia, Charlottesville, VA; [2]Biomolecular Analysis Facility Core, University of Virginia, Charlottesville, VA; [3]Department of Neurosurgery, Baylo*

WP 171 **ChatDIA: A zero-shot large language model workflow outperforms conventional DIA tools in noisy proteomics data**; Jiayi Li[1]; Joshua Charkow[1]; Mingxuan Gao[1]; Jiaqing Li[2]; Hannes Röst[1]; *[1]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON; [2]Industrial and Molecular Pharmaceutics, Purdue University, West Lafayette, IN*

WP 172 **Proteome-Wide Analysis and Surface Protein Isolation for Secretome Characterization Reveal Insights into the Biology of the Leaf-Cutter Ant Acromyrmex echinatior**; Penghsuan Huang[1]; Joseph Sardina[2]; Haiyan Lu[3]; Gaspar Bruner-Montero[4, 5]; Cameron R. Currie[2, 5]; Lingjun Li[1, 3]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Bacteriology, University of Wisconsin-Madison, Madison, WI; [3]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [4</]*

WP 173 **Investigating the effects of data-independent acquisition strategies on search sensitivity and detection limits**; William Resager[1]; Antony Harvey[2]; Ignat Shilov[2]; *[1]Protein Metrics, Ridgefield, WA; [2]Protein Metrics, Boston, MA*

WP 174 **Enhancing Proteome Coverage and Quantitative Reproducibility Using Alternative Proteolysis and Enzyme-Specific DIA Libraries**; Michael Krawitzky[1]; Wan-Fang Chou[1]; Aline De Lima Leite[1]; Joshua Beri[1]; Mukul Midha[1]; Andy Phan[1]; Christopher M Hosfield[2]; Michael Rosenblatt[2]; Marjeta Urh[2]; *[1]Bruker Scientific LLC, Billerica, MA; [2]Promega Corporation, Madison, WI*

WP 175 **Characterizing the analytical performance of synchro-PASEF for phosphoproteome profiling**; Dain Ryan Brademan[1]; Angelina Mullarkey[2]; Mia Greeson[1]; Emily Blythe[3]; Ruth Huttenhain[1]; *[1]Stanford University, Stanford, CA; [2]University of California, Berkeley, Berkeley, CA; [3]University of Minnesota, Twin Cities, Minneapolis, MN*

WP 176 **Ion level missing signal inference enables complete and accurate quantification for data-independent acquisition proteomics**; Yingxue Fu[1]; Zuo-Fei Yuan[1]; Stephanie Byrum[1]; Long Wu[1]; Junmin Peng[1]; Xusheng Wang[2]; Anthony A. High[1]; *[1]St. Jude Children's Research Hospital, Memphis, TN; [2]University of Tennessee Health Science Center, Memphis, TN*

WP 177 **EdgeCaseInspector: Rescuing and Correcting Truncated Precursors at the Ion Mobility Boundaries of diaPASEF Data**; Long WU[1]; Zuo-Fei Yuan[1]; Yingxue Fu[1]; Stephanie Byrum[1]; Ya Huang[1]; Vishwajeeth Pagala[1]; Anthony A. High[1]; Junmin Peng[1]; *[1]St. Jude Children's Research Hospital, Memphis, TN*

WP 178 **Stage Resolved Proteomics of Single Drosophila Egg Chambers Links Proteins Dynamics to Fertility**; Merin M Rixen[1]; Andrew Bondoc[2]; Margot Quinlan[2]; Rachel R Ogorzalek Loo[2]; Joseph A Loo[2]; *[1]UCLA, Los Angeles, CA; [2]UCLA, LOS ANGELES, CA*

WP 179 **ZT Scan DIA: The next level of scanning DIA for ultra-sensitive high selectivity proteomics enabling robust quantification at high throughput**; Tim Heymann[1]; Denys Oliinyk[1]; Lukas Henneberg[1]; Michael Baggio Lorenz[1]; Nils Eikmeier[1]; Marvin Thielert[1]; Louisa Grauvogel[1]; Bill Loyd[2]; Yves Le Blanc[2]; Ihor Batruch[2]; Patrick Pribil[2]; Jason Causon[2]; Anjali Chelur[2]; Gordana Ivosev[2]; Katherine Tran[2]; Tatjana Talamantes[2]; Bradley B Schneider[2]; Jose Castro-Perez[2]; Matthias Mann[1]; *[1]Max Planck Institute of Biochemistry, Martinsried, Germany; [2]SCIEX, Concord, ON*

WP 180 **Enhancing DIA Proteomics Analysis with FragPipe: New Capabilities and Optimizations**; Kai Li[1]; Fengchao Yu[1]; Yamei Deng[1]; Alexey I Nesvizhskii[1]; *[1]University of Michigan, Ann Arbor, MI*

WP 181 **Impact of Narrow Q1 Isolation Windows on Identification Depth in ZT Scan DIA**; Anjali Chelur[1]; Gordana Ivosev[1]; Wen Jin[1]; Yang Kang[1]; Yves Le Blanc[1]; Huini Du[1]; Nic Bloomfield[1]; *[1]SCIEX, Concord, ON*

WP 182 **Assessment of the false discovery rate in library-free searches in DIA proteomics using a recombinant protein library**; Kongxin Gu[1]; Naoki Goshima[2, 3]; Shingo Ito[1]; Sumio Ohtsuki[1]; *[1]Kumamoto*

University, Kumamoto, Japan; [2]ProteoBridge Corporation, Tokyo, Japan; [3]National Institute of Advanced Industrial Science and Technology, Tokyo, Japan

WP 183 **FragReporter: A Post-Processing Tool for Multi-Level Quantification in DIA Proteomics and PTMomics**; Yamei Deng[1]; Fengchao Yu[2]; Alexey I. Nesvizhskii[2]; *[1]University of Michigan, US, MI; [2]University of Michigan, Ann Arbor, MI*

WP 184 **Elucidation of co-purification mechanisms of host cell proteins in adeno-associated virus vectors during downstream density gradient ultracentrifugation process using DIA-MS**; Yuma Furuta[1]; Yuki Yamaguchi[1]; Yasuo Tsunaka[1]; Mitsuko Fukuhara[1]; Tetsuo Torisu[1]; Susumu Uchiyama[1]; *[1]Department of Biotechnology, Graduate School of Engineering, The University of Osaka, Suita, Japan*

WP 185 **Expanding sensitivity and dynamic range for label-free proteomics and low-input sample analysis on the Orbitrap Excedion Pro mass spectrometer**; Martins Jansons[1]; William Comstock[2]; Jeff Op de Beeck[3]; Bernard Delanghe[4]; Fernanda Salvato[2]; Joshua Silveira[2]; Katherine Walker[2]; Eloy Wouters[2]; Alec Valenta[2]; Tonya Pekar Hart[2]; Amirmansoor Hakimi[5]; *[1]Thermo Fisher Scientific, Vilnius, Lithuania; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Zwijnaarde, Belgium; [4]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [5]Therm*

WP 186 **Pioneer and Altimeter: Fast and Open-Source Analysis of DIA Proteomics Data Optimized for Narrow Isolation Windows**; Nathan T Wamsley[1]; Emily M Wilkerson[1]; Ben Major[1]; Dennis Goldfarb[1]; *[1]Washington University in St. Louis, Saint Louis, MO*

WP 187 **Quantitative proteomics using high-sensitivity data-independent acquisition on a QTOF platform**; Ihor Batruch[1]; Patrick Pribil[1]; Jason Causon[1]; *[1]SCIEX, Concord, ON*

WP 188 **Reaching new heights in Orbitrap-based data independent acquisition with a modified Tribrid mass spectrometer**; Lilian R Heil[1]; Jingjing Huang[1]; Christopher Mullen[2]; Joshua D Hinkle[1]; Rafael D Melani[1]; Graeme McAlister[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]ThermoFisher Scientific, San Jose, CA*

WP 189 **Orbitrap Astral–Based In-depth Global Proteomics of Human Brain Lysates Identifies Low-Abundance Proteins Associated with Alzheimer's Disease**; Elizabeth T Anderson[1]; Joel Bucci[2]; Qin Fu[1]; Andy Lui[1]; Gary E. Gibson[3]; Sheng Zhang[1]; *[1]Cornell University, Ithaca, NY; [2]ThermoFisher Scientific, Lexington, MA; [3]Weill Cornell Medicine, New York, NY*

WP 190 **Evaluating Resonance CID for Data-Independent Acquisition on a Hybrid Nominal Mass Instrument**; Deanna L Plubell[1]; Philip M. Remes[1]; Bo Wen[2]; Wes Rogers[1]; Cristina C. Jacob[1]; Romain Huguet[1]; Michael J. MacCoss[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]University of Washington, Seattle, WA*

WP 191 **Resonance CID with fine-tuned spectral libraries outperforms HCD for DIA proteomics on a modified Orbitrap Tribrid mass spectrometer**; Chris Hsu[1]; Lilian Heil[2]; Bo Wen[1]; Graeme McAlister[2]; Philip M. Remes[2]; Deanna L Plubell[2]; Michael J. MacCoss[1]; *[1]University of Washington, Seattle, WA; [2]ThermoFisher Scientific, San Jose, CA*

WP 192 **There Will Be (peripheral) Blood (mononuclear cells): interrogating the inflammatory regulome across human donors and perturbations**; Julia E Robbins[1]; Andrea Gutierrez[1]; Kyle Siebenthall[1]; Daniele Canzani[1]; Evan E Hubbard[1]; Anastasiya V. Prymolenna[1]; William E Fondrie[1]; Lillian T Tatka[1]; Sebastian J Paez[1]; Sydney Huff[1]; Gaelle Mercenne[1]; Brian McEllin[1]; Megan Fritz[1]; Alexander J Federation[1]; Lindsay K Pino[1]; *[1]Talus Bioscience, Seattle, WA*

WP 193 **Pre-Sliced diaPASEF: Narrowband accumulation in the first timsCell for Ultra-Sensitive Plasma Proteomics**; Marta L Mendes[1]; Ryan Marisco[2]; Schmit Pierre-Olivier[3]; Gunnar Dittmar[1]; *[1]Luxembourg Institute of Health, Strassen, Luxembourg; [2]Bruker, Billerica, MA; [3]Bruker Daltonique S.A., Wissembourg, France*

WP 194 **Benchmarking DIA vs. DDA Workflows to Enhance Sequence Coverage and Data Completeness in HDX-LC-MS of CRISPR-Cas1-Cas2-DNA Complexes**; Patrycja Szamweber[1]; Kellye A. Cupp-Sutton[1]; Swarmistha D. Aribam[2]; Kole R. Long[2]; Joel B. Langford[2]; Oliver Wu[2]; Tomas Pierce[3]; Nathan Basisty[3]; Rakhi Rajan[2]; Si Wu[1]; *[1]University of Alabama, Tuscaloosa, AL; [2]University of Oklahoma, Norman, OK; [3]National Institute on Aging-NIH, Baltimore, MD*

WP 195 **Proteomic Analysis of Cumulus Oocyte Complexes Improves Understanding of Ovarian Cell Competency**; Christina D King[1]; Caroline E Kratka[2]; Mark A Watson[1]; Jeffrey Pea[2]; Francesca E Duncan[1, 2]; Birgit Schilling[1]; *[1]Buck Institute for Research on Aging, Novato, CA; [2]Northwestern University, Feinberg School of Medicine, Chicago, IL*

WP 196 **Exploiting the Similarity-vs-Difference in MS2 Ion Intensity Ratios Between Different MS Samples to Deconvolute Chimeric XICs for DIA-MS Data Sets**; Gautam Saxena[1]; Qin Fu[2]; Aleksandra Binek[2]; Jennifer E. Van Eyk[2]; *[1]GoldenHaystack Lab, Bethesda, MD; [2]Cedars-Sinai Medical Center, LA*

WP 197 **Jigsaw-PASEF: Building Deeper Proteomes for Cohort Studies, One Random Shot at a Time**; Zixuan Xiao[1]; Stephanie Kaspar-Schönefeld[2]; Philipp Strohmidel[2]; Johanna Tüshaus[1]; Jens Decker[2]; Michael Krause[2]; Moritz Resch[1]; Bernhard Kuster[1, 3]; Dennis Trede[2]; Mathias Wilhelm[1, 3]; *[1]School of Life Science, Technical University of Munich, Freising, Germany; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [3]Munich Data Science Institute (MDSI), Technical University of Munich, Garching, Germany*

WP 198 **Stability Indicating UPLC-PDA Method Development and Validation of Fruquintinib and its degradation impurities: Identification and characterization usingLC-QTOF-MS/MS**; Sachin Dattram Pawar; *Department of Pharmaceutical Quality Assurance, Manipal College of Pharmaceutical Sciences, Manipal Academy of Higher Education, Manipal, India, Manipal, India; Department of Pharmaceutical Quality Assurance, Manipal College of Pharmaceutical Sciences, Ma*

WP 199 **Comprehensive In Vitro ADME and Metabolic Profiling of the Anti-Cancer Alkaloid Narciclasine using a QTRAP mass spectrometry**; Ravi Akkireddy[1, 2]; Srinivas Lenkalapelly[1, 2]; In-Hyoung Yang[1, 2]; Harry May[1, 2, 3]; Min Hee Kang[1, 2]; *[1]Cancer Center, School of Medicine, Texas Tech University Health Sciences Center, Lubbock, TX; [2]Department of Pediatrics, School of Medicine, Texas Tech University Health Sciences Center, Lubbock, TX; [3]Graduate School of B*

WP 200 **Mass Spectrometric and Cytotoxic Evaluation of narciclasine: Evidence for P-gp-Independent Transport and Anti-Tumor Activity**; SRINIVAS LENKALAPELLY[1, 2]; In-Hyoung Yang[1, 3]; Ravi Akkireddy[1, 2]; Harry May[1, 2, 4]; Min Hee Kang[1, 2]; *[1]Cancer Center, School of Medicine, Texas Tech University Health Sciences Center, Lubbock, TX; [2]Department of Pediatrics, School of Medicine, Texas Tech University Health Sciences Center,, Lubbock, TX; [3]Department of Pedia*

WP 201 **Automated Nanomole Scale LC--MS Purification Accelerating DMTA Cycles in Modern Drug Discovery**; Tanvir A Amit[1]; Sarah Parko[1]; Tanner Burk[1]; Ashwin Pillai[1]; Leigh Ann Alexander[1]; Mark Kershaw[1]; Jonathan Grob[1]; *[1]Valo Health, Lexington, MA*

WP 202 **Ultra-Performance Liquid Chromatography-Tandem Mass Spectrometry Method Development and Pharmacokinetics of NIH972 in Mice**; Amy Q Wang[1]; Natalie R Hagen[1]; Raul R Calvo[1]; Sitanshu S Singh[2]; Juan J Marugan[1]; Udo Rudloff[2]; Xin Xu[1]; *[1]National Center For Advancing Translational Sciences, Rockville, MD; [2]National Cancer Institute, National Institutes of Health, Bethesda, MD*

WP 203 **Leveraging LALA: A generic approach to clinical PK assay development**; Yijun Chen[1]; David Chick[1]; Elsy Philip[1]; Kelly Coble[1]; Emily Werth[1]; David Roos[1]; *[1]Boehringer-Ingelheim, Ridgefield, CT*

WP 204 **Detection of Anti-Drug Antibodies Using a Hybrid IP-LC-MS Approach: A Sensitive and Selective Alternative to Ligand-Binding Assays**; Li Sun[1]; Habib Sistani[1]; Wolfgang Seghezzi[1]; Brad Roadcap[1]; Faye Vazvaei-Smith[1]; *[1]Merck & Co., Inc., Rahway, NJ*

WP 205 **The effect of structural modifications on the in vitro microsomal stability of μ-opioid receptor (MOR) agonist carfentanil**; Li Kong[1]; Andrew J Walz[1]; *[1]Chemical Biological Center, U.S. ARMY, Gunpowder, MD*

WP 206 **AI based metabolite prediction as an aid to MS-based metabolite identification, pharmacokinetics and tissue distribution for a PROTAC drug**; Robert S Plumb[1, 2]; Andrew Leightner[3]; Ian D. Wilson[2, 4]; Steven Lai[3]; Nikunj Tanna[3]; Anthony J Midey[3]; *[1]Waters, Milford, MA; [2]University of Liverpool, Liverpool, United Kingdom; [3]Waters Corporation, Milford, MA; [4]Imperial College London, London, United Kingdom*

WP 207 **Ultra high-throughput analysis of drug metabolites by cytochrome P450 using a triple quadrupole mass spectrometer**; Miho Kawashima[1]; Eishi Imoto[1]; *[1]Shimadzu Corporation, Kyoto, Japan*

WP 208 **Fit-for-Purpose Non-Regulated Bioanalysis Workflow for Targeted Protein Degradation Programs**; Qin C. Ji; *Abbvie, North Chicago, IL*

WP 209 **A Fast Antisense Oligonucleotides (ASOs) Metabolite Identification Workflow using HRMS and Biopharma Finder**; Junfeng Xiao; *Frontage Laboratories, Exton, PA*

WP 210 **High-Efficiency Quantification of Nusinersen Using Streamlined Kit-Based Sample Preparation and LC-MS/MS**; Marian Twohig[1]; Margot Lee[1]; Andrew Leightner[1]; Robert S Plumb[1]; Nikunj Tanna[1]; Mary Trudeau[1]; Courtney Walton[1]; Neil Walsh[2]; Catalin E Doneanu[1]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom*

WP 211 **Productivity, Throughput, and Data Quality in Discovery and Regulated Bioanalysis**; Nikunj Tanna[1]; Kieron Faherty[1]; Neil Walsh[2]; Robert S Plumb[1]; Henry Foddy[2]; Andrew Leightner[1]; Basile Khara[3]; Sally Hannam[3]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Synexa Life Sciences, Manchester, United Kingdom*

WP 212 **Uncertainty-Aware Site-of-Metabolism Prediction from Ambiguous LC–MS Metabolite Identification Data**; Ramon Adàlia[1, 2]; Ismael Zamora[3]; *[1]Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Spain; [2]Lead Molecular Design, SL, Sant Cugat del Vallès, Spain; [3]Mass Analytica, Sant Cugat del Valles, Spain*

WP 213 **From Molecular Structure to Pharmacokinetic Parameters: Autonomizing Quantitative Bioanalysis Across Modalities**; Ismael Zamora[1, 2]; Luca Morettoni[3]; Fabien Fontaine[2]; Kevin Bateman[4]; *[1]Mass Spec Analytica, Sant Cugat del Valles, Spain; [2]Lead Molecular Design, SL, Sant Cugat del Vallès, Spain; [3]Mass Analytica, Sant Cugat del Valles, Spain; [4]2KDAM Consulting, Halifax, NS*

WP 214 **Improved Bioanalytical Performance Using a Simplified 2-Step Oasis™ PRiME HLB Protocol with an Ultra-Short UHPLC Column for UHPLC-MS/MS**; Sonam Panchal[1]; Chelsea Plummer[1]; Nikunj Tanna[1]; Tom Walter[1]; Keil Brinster[1]; *[1]Waters Corporation, Milford, MA*

WP 215 **Characterization of glucuronides by chemical derivatization and structural elucidation of metabolites with EAD fragmentation**; Hlaing (holly) Maw[1]; Robert Blake[2]; *[1]Boehringer Ingelheim Pharmaceuticals, Inc., Ridgefield, CT; [2]Boehringer Ingelheim, Ridgefield, CT*

WP 216 **From Mystery Mass Spec Chromatogram Peaks to Potential Novel Metabolic Pathway**; Nicole Anders[1]; Carla Camou-Sainz[1]; Cody Fullenwider[1]; Brandon Rojas-Aguilar[1]; Drake Russell[1]; Pano Santos[1]; Ann Shih[1]; Will Tao[1]; Chenghong Zhang[1]; *[1]Vividion Therapeutics, San Diego, CA*

WP 217 **Concentration-Dependent Modulation of Fentanyl Metabolism by α2-Adrenergic Agonists in Primary Human Hepatocytes**; Yash Mehta[1]; Dhavalkumar Patel[1]; Lance R. McMahon[1]; Samuel Obeng[1]; *[1]Department of Pharmaceutical Sciences, Texas Tech University Health Sciences Center, Amarillo, TX*

WP 218 **Development of an LC-MS/MS method for quantitation of insulin degludec in rat plasma**; Tilak Chandrasekaran[1]; Ebru Selen[2]; John Gibbons[3]; Eshani Galermo[2]; Rahul Baghla[2]; *[1]SCIEX, Marlborough, MA; [2]SCIEX, Redwood City, CA; [3]SCIEX, Concord, ON*

WP 219 **In vivometabolite identification and pharmacokinetic studies of Nirogacestat in the rat model employing mass spectrometry**; Sayalee Bharati Sanjay Mane; *NIPER Guwahati, Changsari, India*

WP 220 **Evaluation of Echo MS with HRMS for high throughput ADME assays**; Kerri Grove[1]; Mingqing Chen[1]; Rahul Baghla[2]; Patrick Rudewicz[1]; *[1]Novartis Biomedical Research, Emeryville, CA; [2]SCIEX, Redwood City, CA*

WP 221 **Rapid LC-MS/MS compound method development and sample analysis for DMPK workflows**; Bianca Ferreira da Silva[1]; Steve Ainley[2]; Lee Bertram[3]; Jeremy Lawton[2]; *[1]Agilent Technologies, Wilmington, DE; [2]Sound Analytics, Niantic, CT; [3]Agilent Technologies, Santa Clara, CA*

WP 222 **Sensitive MS^n Analysis of PROTAC Therapeutics in Rat Plasma Using a Hybrid Quadrupole Dual-Pressure Linear Ion Trap Mass Spectrometer**; Wes Rogers[1]; Sissi White[2]; Scott M Peterman[1]; Jon Bardsley[2]; Sebastien Morin[3]; Min Du[2]; Romain Huguet[1]; Deanna L Plubell[1]; Cristina C. Jacob[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Lexington, MA; [3]Thermo Fisher Scientific, Mississauga, ON*

WP 223 **Development of an IP-LC-MS Workflow for Quantification of a Low-Abundance Protein in Cynomolgus Monkey Tissues**; Armin Oloumi[1]; Kip Conner[1]; Zhe Wang[1]; *[1]Amgen, South San Francisco, CA*

WP 224 **Dual Approach for Psilocin Analysis: Qualitative Nanodiamond-Assisted MALDI-MS and Novel LC-MS/MS Quantification**; Amir Khajavinia[1]; Deborah Michel[1]; Jordan Reekie[1]; Randall W Purves[1, 2]; Robert B. Laprairie[1]; Anas El-Aneed[1]; *[1]College of Pharmacy and Nutrition, University of Saskatchewan, Saskatoon, SK; [2]Canadian Food Inspection Agency, Saskatoon, SK*

WP 225 **Affinity Selection Mass Spectrometry (AS-MS) Reveals Boost-Free HIV Protease Inhibitors with Enhanced Potency and Metabolic Stability**; Xianshu Yang; *Affinityligand LLC, Belmont, MA*

WP 226 **GLP-1 and Dual GIP/GLP-1 Agonist Suppress Liver Fatty Acid Uptake and β-oxidation in High-Fat Diet-Induced Obese Mice**; Dhavalkumar Patel[1]; Heba A Ewida[1]; Syed Tareq[1]; Ulrich Bickel[1]; MahmoudSalama Ahmed[1]; *[1]Texas Tech University Health Sciences Center, Amarillo, TX*

WP 227 **A simple, sensitive, and high-throughput LC-MS/MS method for the simultaneous quantification of dual payloads in an antibody-drug conjugate**; ZhengQuan Zhang[1]; Wei Lu[1]; Shasha Li[1]; Mao Yin[1]; Ling Xu[1]; *[1]PrimeLink Therapeutics, Suzhou, JIangsu Province, MA*

WP 228 **Unbiased Proteomics Expands the Target Space of CRBN Molecular Glue Degraders**; Wilson Phung[1]; Nicholas Endres[1]; Hanna Budayeva[1]; *[1]Genentech, South San Francisco, CA*

WP 229 **Reliable, Scalable Quantitation of Off-Target Drug Interactions and Toxicity Using a Modified Thermo Fisher Tribrid Mass Spectrometer**; Daniel Delafield[1]; Jichu Pang[1]; Fiona McAllister[1]; *[1]Calico Life Sciences LLC, South San Francisco, CA*

WP 230 **Application of Magnetic Nanobead Affinity Selection for the Discovery of Ligands to the SHIP1 Protein Involved in Alzheimer's Disease**; Daniel D Simchuk[1]; Richard B van Breemen[2]; *[1]Oregon State University, Corvallis, OR; [2]Linus Pauling Institute, Oregon State University, Corvallis, OR*

WP 231 **Automating knowledge production from proteomics with robotics and AI agents**; Yuming Jiang[1]; Cameron Movassaghi[1]; Amanda Momenzadeh[2]; Jose De Jesus Munoz Estrada[2]; Niveda Sundararaman[2]; Jesse Meyer[2]; *[1]Cedars-Sinai Medical Center, Los Angeles, CA; [2]Cedars-Sinai Medical Center, LA*

WP 232 **Acoustic Ejection-Affinity Selection Mass Spectrometry (AE-ASMS) for Non-Covalent Ligand Identification**; Hui Zhang[1]; Hui Yin Tey[2]; Chiu Cheong Aw[2]; Han Wang[2]; Chang Liu[3]; *[1]Iambic Therapeutics, San Diego, CA; [2]SCIEX, Singapore, Singapore; [3]SCIEX, Concord, ON*

WP 233 **Targeted workflow for assessing LLOQ in drug-spiked plasma using a modified Orbitrap Hybrid mass spectrometer**; Christian Klaas[1]; Markus Kellmann[1]; Siddharth Jadeja[2]; Zdeněk Spáčil[2]; Claire Dauly[1]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientific, Brno, Czech Republic*

WP 234 **HRMS QTOF-PRM (Parallel reaction Monitoring) for ultra-trace level quantification of N-Nitroso Moxifloxacin in API and Formulations**; Uday Agarwal[1]; Ashish Pargaonkar[2]; Saikat Banerjee[3]; Vivek Dhyani[4]; Ju-Hwan Lim[5]; Aimei Zou[6]; *[1]Agilent technologies, Gurgaon, India; [2]Agilent Technologies India Pvt. Ltd, Bangalore, India; [3]Agilent India, Hyderabad, India; [4]Agilent India, Mumbai, India; [5]Agilent Technologies Korea Ltd, Seoul,*

WP 235 **LC-MS Bioanalysis to Enable Preclinical Evaluation of Gut-Restricted EP4 Agonists for the Treatment of Inflammatory Bowel Disease**; France Landry[1]; Yongliang Zhang[1]; Josef Ruzicka[1]; Laura Armstrong[1]; Tamara King[1]; Trevor Sherwood[1]; Petia Shipkova[1]; *[1]Bristol Myers Squibb, Princeton, NJ*

WP 236 **SurfaceScout™: A Chemoproteomic Platform for Comprehensive Profiling of Cell Surface Proteins and Macromolecular Uptake Mechanisms**; Raffaela Berger[1]; Anika Kötemann[1]; Barbara Schnitzer[1]; Viktoria Fischer[1]; Catalina Cepeleaga[1]; Maria Ines Faria[1]; Hannes Hahne[1]; *[1]Momentum Biotechnologies, Freising, Germany*

WP 237 **Multiplexed Targeted Proteomics for Selectivity Profiling of Targeted Protein Degraders**; Raffaela Berger[1]; Sandra Poser[1]; Viktoria Fischer[1]; Anika Koetemann[1]; Götz-Norman Hagemann[1]; Christin Zasada[2]; Hannes Hahne[1]; *[1]Momentum Biotechnologies, Freising, Germany; [2]Momentum Biotechnologies, Billerica, MA*

WP 238 **Single-Column Chiral LC–MS Method for Comprehensive Amino Acid Enantiomer Analysis in Synthetic Peptides**; Laura Muehlbauer; *Eli Lilly and Company, Indianapolis, IN*

WP 239 **LC–MS Target Occupancy Quantification of Covalent Small-Molecule Binding to an Endogenous Nuclear Enzyme**; Zhe Wang[1]; Armin Oloumi[1]; Fang Xie[1]; *[1]Amgen, South San Francisco, CA*

WP 240 **Enabling Advanced In vitro/In vivo Correlations Through Quantitative Proteomics to Aid Drug Discovery, Revealing Molecular Initiating Events and Toxicological Pathways**; Gene Ciccimaro[1]; Karen Augustine[1]; Vasanthi Bhaskaran[1]; Catherine Garrison[1]; Paul Levesque[1]; Joshua Nicklay[1]; Bogdan Sleczka[1]; Jacob Zalaznick[1]; Petia Shipkova[1]; *[1]Bristol Myers Squibb, Princeton, NJ*

WP 241 **Mapping FLT3 inhibitor sensitivity to patient subpopulations with different clinical responses using protein expression signatures and ex vivo cell models**; James T Sorrentino[1]; Eduardo S. De Camargo Magalhaes[2]; Salvador Martinez-Bartolome[1]; Mahan Abbasian[1]; Christina Lamm[1]; Antonius Koller[1]; Samanta Catueno[3]; Brandon D Brown[3]; Yihua Qiu[4]; Steven M Kornblau[4]; Pilgrim Jackson[1]; *[1]Yatiri Bio, San Diego, CA; [2]Department of Ageing Biology/ERIBA, University of Groningen, University Medical Center Groningen, Groningen, the Netherlands, Groningen, Netherlands; [3]Department of Pediatrics, The University o*

WP 242 **Pioneering Bioanalytical Strategies to Support a Broad Biotherapeutics Pipeline: In vivo Quantitation, Characterization, and Pharmacokinetic Analyses**; Jaqueline A. Picache[1]; Jake A. Melby[1]; Jason Wang[1]; John F. Kellie[1]; *[1]AstraZeneca, Gaithersburg, MD*

WP 243 **HDX-LC-MS guided drug discovery for ApoE4 protein**; Evgeniy Petrotchenko[1]; Roopa Thapar[2]; Jim Ray[2]; Christoph H. Borchers[1, 3]; *[1]Lady Davis Institute for Medical Research, Montreal, QC; [2]M.D. Anderson Cancer Center, Institute for Applied Cancer Science, Therapeutics Discovery Division, Houston, TX; [3]Gerald Bronfman Department of Oncology, Jewish Ge*

WP 244 **Novel Plasma Proteomics and Phosphoproteomics Platform Captures Pleiotropic Cardiometabolic Spectrum Effects of Semaglutide in Patients with T2D and Atherosclerosis**; Antigoni Manousopoulou[1]; Cory H. White[1]; Sajad Hamal[2]; Raj Nihalani[1]; Matthew J. Budoff[2]; Spiros D. Garbis[1]; *[1]Proteas Health, Inc., Torrance, CA; [2]The Lundquist Institute, Torrance, CA*

WP 245 **DIA-based chemoproteomics discovers covalent NONO inhibitors for metastatic castration-resistant prostate cancer**; Daniele Canzani[1]; Brian McEllin[1]; Julia Robbins[1]; Andrea Gutierrez[1]; Evan E Hubbard[1]; Lillian T Tatka[1]; Sebastian J Paez[1]; Anastasiya V. Prymolenna[1]; Sydney Huff[1]; Margaux McBirney[1]; Kyle Siebenthall[1]; William E Fondrie[1]; Gaelle Mercenne[1]; Lindsay K Pino[1]; Alexander J Federation[1]; *[1]Talus Bio, Seattle, WA*

WP 246 **Investigation of Hits against GLP1 Receptor Identified in an Affinity Selection Mass Spectrometry (ASMS) High-Throughput Screen**; Can Jon Ozbal[1]; Zane Thistleford[2]; Christina Thompson[2]; Jan Kubicek[3]; Barbara Maertens[3]; William LaMarr[2]; *[1]PureHoney Technologies, Billerica, MA; [2]Momentum Biotechnologies, Billerica, MA; [3]Cube Biotech, Monheim, Germany*

WP 247 **MS-Based Proteomics Reveals Superior Efficacy of Degraders over Small Molecule Inhibitors for Challenging Targets: Mechanistic Insights and Therapeutic Implications**; Susanne Breitkopf[1]; Charles L. Howarth[1]; Yogesh Chutake[1]; Joyoti Dey[1]; Rujuta Kshirsagar[1]; Varsha Ananthapadmanabhan[2]; James A DeCaprio[2]; Kirti Sharma[1]; *[1]Kymera Therapeutics, Watertown, MA; [2]Dana-Farber Cancer Institute, Boston, MA*

WP 248 **VISUALIZING SECOND-LINE ANTI-TB DRUG DISTRIBUTION WITHIN GRANULOMAS AT HIGH SPATIAL DETAIL USING DESI-MASS SPECTROMETRY IMAGING**; PREM SHANKAR[1]; David Beaver[1]; Nikolas Shurgaia[2]; Mari Buziashvili[2]; Sergo Vashakidze[2]; Russell Kempker[3]; Brendan Prideaux[1, 4]; *[1]Department of Neurobiology, University of Texas Medical Branch, Galveston, TX; [2]The National Centre for Tuberculosis and Lung Diseases, Tbilisi, Georgia; [3]Department of Medicine, Division of Infectious Disease, School of*

WP 249 **Orbitrap-based Charge Detection Mass Spectrometry to Quantify Heterogeneous Therapeutic Proteins**; Zoltan Szabo[1]; Kyle P. Bowen[2]; Michael W. Senko[2]; Rafael D Melani[1]; Dietmar Reusch[3]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]ThermoFisher Scientific, San Jose, CA; [3]Roche Diagnostics GmbH, Penzberg, Germany*

WP 250 **Application of high-resolution mass spectrometry in the identification of bioactive compounds from marine gastropods**; Tsotlhe Trinity Kereeditsea[1]; Yvan Anderson Tchangoue Ngandjuia[1]; Garland Kagiso More[2]; Adeyemi Ojutalayo Adeeyoa[1]; Karin De Bruynb[2]; Jeraldine Maire Bourletidis How[2]; Ilunga Kamika[1]; Lawrence Mzukisi Madikizelaa[1]; Hlengilizwe Nyoni[3]; Thabo T.I. Nkambule[1]; Titus A.M. Msagati[4]; *[1]Institute for Nanotechnology and Water Sustainability (iNanoWS), College of Science, Engineering and Technology (CSET), UNISA, South Africa, Johannesburg, South Africa; [2]College of Agriculture and Environmental Science Laboratories,*

WP 251 **Cytotoxicity Study of Airborne Particulate Matter by Mass Spectrometry-Based Multi-Omics**; YANHAO ZHANG[1, 2]; Zifang Peng[1]; Shusheng Zhang[1]; Zongwei Cai[2, 3]; *[1]Zhengzhou University, Zhengzhou, China; [2]Hong Kong Baptist University, Hong Kong, Hong Kong; [3]Eastern Institute of Technology, Ningbo, China*

WP 252 **Rapid quantification of 130 perfluorinated and polyfluorinated compounds in water using a high-end triple quadrupole mass spectrometer**; Liuqing Zhao[1]; Yu Xia[2]; Jing Shi[2]; Zong Yang[1]; Bingjie Liu[1]; *[1]SCIEX, Shanghai, China; [2]Suzhou Center for Disease Control and Prevention, Suzhou, China*

WP 253 **Analysis of 6-PPDQ Uptake and Distribution in Radish Tissues by Targeted LC-MS/MS**; Katelyn A Haas[1]; Claire E. Korte[1]; Nevannah B Harlan[1]; Debanjana Ghosh[1]; Kevin R. Tucker[1]; *[1]Southern Illinois University Edwardsville, Edwardsville, IL*

WP 254 **Non-targeted analysis of PFAS isomers in rain and snow by ion mobility mass spectrometry**; Jennifer Faust[1]; Yubin Kim[1, 2]; Bruna Jatoba[1]; Morgan Olsen[3]; Andrew May[4]; Rachel Saylor[5]; Paul Edmiston[1]; Douglas Collins[3]; *[1]College of Wooster, Wooster, OH; [2]University of Michigan, Ann Arbor, MI; [3]Bucknell University, Lewisburg, PA; [4]The Ohio State University, Columbus, OH; [5]Oberlin College, Oberlin, OH*

WP 255 **PFAS Analysis of Leachate: Evaluating Key Sample Preparation and LC–MS/MS Parameters for Improved Performance**; Tiffany Liden[1]; Kate (Xiaomeng) Xia[1]; Evelyn Wang[1]; Om Shrestha[1]; Vikki

Johnson[1]; Ruth Marfilvega[2]; Kevin Schug[3]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Shimadzu Corporation, Kyoto, Japan; [3]University of Texas At Arlington, Arlington, TX*

WP 256 **Using the Fenton reaction, a pH-dependent reaction, to assist in the degradation of environmental pollutants**; Shih-Shin Liang; *Kaohsiung Medical University, Kaohsiung, Taiwan*

WP 257 **Dual-SPE untargeted Orbitrap HRMS profiling of emerging contaminants in a tropical megacity river**; Federico Cristaudo[1]; Debora Fabbri[1]; Claudio Medana[1]; Federica Dal Bello[1]; Paola Calza[1]; *[1]Università degli Studi di Torino, Turin, Italy*

WP 258 **Development of an Advanced LC-MS/MS Method for PFAS Analysis in Automotive Rubber Materials: Adapting KS M 9722 for EU Compliance**; Euichul Jeong[1]; Sujin Min[1]; Byungil Choi[2]; Hyeonho Park[2]; Gyounglyul Jo[2]; Taegyue Ryue[1]; *[1]Korea Testing & Research Institute (KTR), ulsan, South Korea; [2]Korea Testing & Research Institute, Gwacheon, South Korea*

WP 259 **Detection and Quantification of Per- and Polyfluoroalkyl Substances (PFAS) Degradation Products from Advanced Oxidation Processes**; Nan Qiu[1]; Anaira Roman Santiago[2]; Rachel A. Harris[1]; Patrick S. Doyle[2]; Julia Balog[1]; *[1]Waters Corporation, Milford, MA; [2]Massachusetts Institute of Technology, Cambridge, MA*

WP 260 **IC-MS and ISA-DESI-MS Analysis of PFAS Degradation Products from Aqueous Microdroplets**; Samantha Kruse[1]; Nathan R Bays[1]; Mohammad Shohel[1]; Paul R Tumminello[1]; Brynal Benally[1]; Trinity Griffus[1]; David Schafer[1]; Jessica Kustas[1]; Ryan D Davis[1]; *[1]Sandia National Laboratories, Albuquerque, NM*

WP 261 **Single Quadrupole LC-MS with Line-Shape Calibration Enhancement as an Economical Alternative for PFAS Screening**; Ethan R Hain[1]; Aron Jaffe[1]; Yongdong Wang[2]; Ruth Marfil-Vega[3]; Valeria Zerda[1]; Sarah Monti[1]; Lihini Mendis[1]; Landon Wiest[1]; Jacob Smith[1]; Allie Ferranti[1]; Stephen Kurzyniec[1]; Christopher Gilles[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Cerno Bioscience, Las Vegas, NV; [3]Shimadzu Co., Kyoto, Japan*

WP 262 **Accelerating RSSCT tests with Online Sampling Automation and Experimental Design**; Nick Lentz[1]; Emily Parry[2]; Patrick Cronan[2]; Andy Johnson[2]; *[1]Birchtech Corp, Grand Forks, ND; [2]Agilent Technologies, Inc., Wilmington, DE*

WP 263 **High-throughput RPLC-MS/MS Analysis of Bromate, Chlorate, Dalapon, and Haloacetic Acids in Drinking Water Samples by Triple Quadrupole LCMS**; Valeria Zerda-Pinto[1]; Ethan R Hain[1]; Aron Jaffe[1]; Sarah Monti[1]; Lihini Mendis[1]; Landon Wiest[1]; Ruth Marfil-Vega[2]; Jacob Smith[1]; Allie Ferranti[1]; Stephen Kurzyniec[1]; Christopher Gilles[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]Shimadzu Co., Kyoto, Japan*

WP 264 **A novel sample screening approach to resolve analytical challenges in LC-MS workflows for PFAS analysis**; Atis Chakrabarti[1]; Nishaben Patel[1]; Stephanie Pollard[1]; Matt James[2]; Arianne Soliven[2]; Tony Edge[2]; Gemma Lo[2]; Helen Poole[2]; *[1]Avantor, Bridgewater, NJ; [2]Avantor, Theale, United Kingdom*

WP 265 **Quantitation of ultrashort- and short-chain PFAS in beverages by a direct injection LC-MS/MS method**; Simon Roberts[1]; Holly Lee[2]; Craig Butt[3]; Sam Lodge[4]; RenXi Ye[5]; Irina Nistorescu[5]; Cora Young[5]; Trevor VandenBoer[5]; *[1]SCIEX, Golden, CO; [2]SCIEX, Concord, ON; [3]SCIEX, Marlborough, MA; [4]Phenomenex, Torrance, CA; [5]York University, Toronto, ON*

WP 266 **Simultaneous SIM/Scan P&T-GC/MSD for VOCs: Sub-ppb Sensitivity with Full-Scan Confirmation**; Jessica Lehman[1]; Thomas Hartlein[2]; *[1]AGILENT TECHNOLOGIES, Inc, Wilmington, DE; [2]Teledyne Tekmar, Mason, OH*

WP 267 **Accelerating large-panel pesticide analysis and method development with ultrafast MRM acquisition**; Megumi Shimizu[1]; Andrew Folkerson[2]; Michael Deng[2]; Holly Lee[2]; David Cox[2]; Craig Butt[3]; *[1]SCIEX, Golden, CO; [2]SCIEX, Concord, ON; [3]SCIEX, Marlborough, MA*

WP 269 **Analysis of 6PPD-Q in Reagent and River Water Using a Triple Quadrupole LCMS**; Ethan Hain[1]; Aron Jaffe[2]; Valeria Zerda Pinto[2]; Sarah Monti[2]; Lihini Mendis[2]; Landon A Wiest[2]; Ruth Marfil-Vega[3]; Jacob Smith[4]; Allie Ferranti[4]; Stephen Kurzyniec[4]; Christopher Gilles[2]; *[1]Shimadzu Scientific Instruments, Inc., Columbia, MD; [2]Shimadzu Scientific Instruments, Columbia, MD; [3]Shimadzu Corporation, Kyoto, Japan; [4]Shimadzu Scientific Instruments, Carlsbad, CA*

WP 270 **Multiphase Atmospheric PFAS analysis Coupled with LC-MS/MS Analysis**; Kenichi Suzuki[1]; Hiroshi Hayashida[1]; Reika Takahara[1]; Takumi Kunieda[1]; Shigenori Ota[1]; *[1]GL Sciences Inc., Tokyo, Japan*

WP 271 **Automated, Sensitive, and Robust Analysis of PFAS in Soil and Fish**; Ethan R Hain[1]; Brianna Warren[2]; Bendict Liu[2]; Alicia Stell[2]; Om Shrestha[1]; Aron Jaffe[1]; Valeria Zerda[1]; Sarah Monti[1]; Lihini Mendis[1]; Landon A Wiest[1]; Ruth Marfil-Vega[3]; Jacob Smith[1]; Allie Ferranti[1]; Stephen Kurzyniec[1]; Christopher Gilles[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD; [2]CEM Corporation, Matthews, NC; [3]Shimadzu Corporation, Kyoto, Japan*

WP 273 **An Integrated Ion-Mobility Q-TOF MS and FT-ICR MS Workflow for Suspect PFAS Characterization in Drinking-Water Sources**; Hyemi Jang[1, 2]; Mira Choi[1, 2]; Kyoung-Soon Jang[1, 2]; *[1]Korea Basic Science Institute, Cheongju, South Korea; [2]University of Science and Technology, Daejeon, South Korea*

WP 274 **Automated EPA 8270E GC/MS/MS Analysis of 192 Semivolatiles Compounds (SVOC) with Rail Automation: Broad Coverage, Sub-ppb Quantitation, and Reduced Solvent/Waste**; Stefano Maggi[1]; Guido Premoli[1]; Luigi Magno[1]; Anna Calì[2]; Aaron Boice[3]; Sophie Tirat[2]; Marica Beggio[2]; Luca Godina[4]; Anastasia Andrianova[5]; *[1]LabAnalysis, Casanova Lonati, Italy; [2]Agilent Technologies Inc., Cernusco sul Naviglio, Italy; [3]Agilent Technologies, Santa Clara, CA; [4]Agilent Technologies Deutschland GmbH, Waldbronn, Germany; [5]Agi*

WP 275 **From Lab to the Field: Rapid, On-site PFAS Quantitation in Environmental Waters via Automated Bubble Preconcentration and Portable MS/MS**; Zhi-Yang Huang[1]; Chuping Lee[1]; *[1]Department of Chemistry, National Chung Hsing University, Taichung, Taiwan*

WP 276 **Disproportionate Ecological Risks of Emerging Organophosphate Compounds in a High-Altitude River System of the Tibetan Plateau**; Zhenfei Han[1]; Jinze He[1]; Yisheng Xu[2]; Yindong Tong[1]; Hongyang Cui[1]; *[1]School of Environmental Science & Engineering, Tianjin University, Tianjin, China; [2]Waters cooperation, Beijing, China*

WP 277 **Machine Learning-Driven Prioritization of Neurotoxic Emerging Contaminants in Non-Targeted Screening**; Mengyao Ran[1]; Guomao Zheng[1]; *[1]SUSTech, Shenzhen, China*

WP 278 **High-resolution mass spectrometry insights into pharmaceutical partitioning and transformation in aquaculture water-sediment microcosms**; Federico Cristaudo[1]; Debora Fabbri[1]; Jenjira Phuriragpitikhon[2]; Pattamaporn Hemwech[3]; Francesco Giunchino[1]; Benedetto Sicuro[4]; Paola Calza[1]; *[1]University of Turin, Department of Chemistry, Turin, Italy; [2]Department of Service Science, Institute of Standard Development and Conformity Assessment, Bangkok, Thailand; [3]Department of Service Science, Bureau of Laborat*

WP 279 **Fast Headspace GC/MS of Volatiles Analysis (VOC): Sub-7-Minute Separations with Automated Sample Preparation**; Lakshmi Krishnan[1]; Saurabh U Patel[2]; Anastasia Andrianova[1]; *[1]Agilent Technologies, Santa Clara, CA; [2]Agilent Technology, Wilmington, DE*

WP 280 **Ultra-Trace Determination of Epichlorohydrin in Water by Non-Heated Purge and Trap GC–MS**; RENATO ORSINO[1]; Ishii Kazuyuk[1]; Baba Noriyuki[1]; *[1]GL Sciences Inc., Tokyo, Japan*

WP 281 **Mining Milk: A New Non-Targeted LC-IMS-MS Workflow Reveals Novel PFAS Exposure through Lactation**; Kara M. Joseph[1]; Allison N. Fry[1]; Gregory P. Kudzin[1]; Sarah J. Rehm[1]; Madeline G. McNelis[2, 3]; Jane I. Khudyakov[4]; Michael L. Power[3]; Erin S. Baker[1]; *[1]University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]University of California, Santa Cruz, Santa Cruz, CA; [3]Smithsonian's National Zoo and Conservation Biology Institute, Washington, DC; [4]University o*

WP 282 **Automated liquid-liquid extraction workflow for direct ultra-trace analysis of pesticides and PAHs in water matrices using GC-MS/MS**; Andrew P Fornadel; *Thermo Fisher Scientific, Severna Park, MD*

WP 283 **Determination of PFAS in Serum using HRAM-DDA coupled with on-line SPE on LCMS-9050**; Tobias Brosch[1]; Anja Grüning[1]; Sascha Rexroth[1]; [1]*Shimadzu Europa GmbH, Duisburg, Germany*

WP 284 **Elucidating Benzodiazepine Sorption Mechanisms on Virgin, Aged, and Biofilm-Coated Micro and Nanoplastics by MOI-LEI-QqQ Mass Spectrometry**; Achu Kuriakose[1]; Genny Grasselli[1]; Tommaso Grazioso[1]; Wei Zhou[2]; Januz Pawliszyn[2]; Adriana Arigò[1]; Giorgio Famiglini[1]; Achille Cappiello[1, 3]; [1]*University of Urbino Carlo Bo, Urbino, Italy;* [2]*University of Waterloo, Ontario, ON;* [3]*University of Vancouver Island, Nainamo, BC*

WP 285 **Evaluation of Robustness, Sensitivity, and Consistency of Thermo Scientific™ TSQ Certis™ Triple Quadrupole Mass Spectrometer for Pesticides Analysis**; Mindy Gao; *ThermoFisher Scientific, San Jose, CA*

WP 286 **Systematic GC Method Development: A Case Study on Polycyclic Aromatic Hydrocarbons (PAHs)**; Ross Salzberg[1]; Jenny Lewis[2]; Crystal Holt[2]; [1]*Phenomenex, Torrance, CA;* [2]*Phenomenex, Inc. - Torrance, CA, Torrance, CA*

WP 287 **Time- and Tissue-Dependent LC-MS/MS Analysis of Metoprolol in Radish Plants Following Exposure to Local Concentrations in Wastewater Effluent**; Claire E. Korte[1]; Katelyn A. Haas[1]; Chloe I. Koons[1]; Kevin R. Tucker[1]; [1]*Southern Illinois University Edwardsville, Edwardsville, IL*

WP 288 **Pesticide Analysis from Soil, Water, and Air nearby Farmlands by Thermal Desorption and HS-SPME Gas Chromatography Tandem Mass Spectrometry**; Jillian Tonnies[1]; Reagan Guerra[1]; Adriana Martinez[1]; Kevin R. Tucker[1]; [1]*Southern Illinois University Edwardsville, Edwardsville, IL*

WP 289 **Evaluating SSRI Uptake in Crawfish via LC-MS/MS**; Sydney R. Worth[1]; Isabel M. Baldwin[1]; Lauryn E. Rogers[1]; Chloe I. Koons[1]; Karizma Casarez[1]; Isabella L. Mishler-Trerice[1]; Kevin R. Tucker[1]; [1]*Southern Illinois University Edwardsville, Edwardsville, IL*

WP 290 **LC-MS/MS QTOF analysis of river water identifies contaminants of environmental concern by non-targeted profiling**; Alan Barnes[1]; Emily G. Armitage[1]; James Ault[1]; Neil J. Loftus[1]; Melanie Egli[2]; Helena L. Rapp Wright[2]; Leon Barron[2]; [1]*Shimadzu Corporation, Manchester, United Kingdom;* [2]*Imperial College London, London, United Kingdom*

WP 291 **A sensitive method for the quantitation of per- and polyfluoroalkyl substances (PFAS) in pharmaceutical packaging containers**; Santosh Gorti[1]; Lakshmanan Deenadayalan[2]; Sashank Pillai[2]; Rahul Baghla[3]; Eshani Galermo[3]; [1]*SCIEX, Marlborough, MA;* [2]*SCIEX, Bangalore, India;* [3]*SCIEX, Redwood City, CA*

WP 292 **Evaluation of a novel low-diffusion ionization interface for pesticide analysis in water using triple-quadrupole LC–MS**; Yukako Yukawa[1]; Tsuyoshi Nakanishi[1]; Satoshi Yamaki[1]; Kazuhiro Kawakami[1]; [1]*Shimadzu Corp., Kyoto, Japan*

WP 293 **Application of the Sciex 8600 and Bruker timsMetabo for the identification of trace level environmental metabolites**; Jeffrey R Gilbert[1]; Chris Brown[1]; Jesse Balcer[1]; [1]*Corteva Agriscience, Indianapolis, IN*

WP 294 **Evaluation of Compact Ion Trap MS for Trace Residue Analysis to Support Cleaning Validation in Pharmaceutical Manufacturing**; Vishal Mahale[1]; Madhuri Gupta[1]; Subodh Chawan[1]; Priya Singh[2]; Rupesh Kelaskar[2]; Jess Palko[1]; Caleigh R O'Connor[1]; [1]*MassTech Inc., Columbia, MD;* [2]*FDC Limited, Mumbai, India*

WP 295 **Integrating Passive Sampling, Bioassays, and High-Resolution Mass Spectrometry to Characterize Seasonal CEC Mixtures in South African Wastewater and Receiving Rivers**; Ratanang Mlaba-Zwane[1]; Tshepo Joseph Malefetse[1]; Thabo T.I. Nkambule[1]; Hlengilizwe Nyoni[1, 2];

[1]Institute for Nanotechnology and Water Sustainability (iNanoWS), College of Science, Engineering and Technology (CSET), UNISA, South Africa, Johannesburg, South Africa; [2]Institute for Energy and Environmental, Pennsylvania State Uni

WP 296 **Quantitative Detection of Antibiotics in Honeybees and Bee Larva using Mass Spectrometry**; Andrew S Hall[1]; Rebecca Weed[1]; Bradley Metz[1]; *[1]North Carolina State University, Raleigh, NC*

WP 297 **Protein-Affinity-Guided Identification of Bioaccumulative Silanol Quaternary Ammonium Compounds in Indoor Environments and Human Serum**; Zhong Lv[1]; Guomao Zheng[1]; *[1]Southern University of Science and Technology, Shenzhen, China*

WP 298 **Progress Toward Interactome Analysis of Post-Translationally Modified Histone Photoaffinity Probes via Bottom-Up Proteomics**; Kerstin E. Peterson[1]; Joe McPherson[1]; Molly Sneddon[1]; Noelle Olson[1]; Luke Erber[2]; Francisca N. L. Vitorino[3]; Renee Dean[3]; Dani Dahlseid[1]; Jacklyn Artymiuk[1]; Natalia Tretyakova[1]; Benjamin A. Garcia[3]; William C. K. Pomerantz[1]; *[1]University of Minnesota, Minneapolis, MN; [2]University of Kansas, Lawrence, KS; [3]Washington University School of Medicine, St Louis, MO*

WP 299 **Integrative analysis of mass spectrometry screening of HDAC inhibitors and high-throughput sequencing in breast cancer**; Rashmi Karki[1]; Francisca N. L. Vitorino[2]; Richard Searfoss[2]; Joanna Lempiainen[2]; Benjamin Garcia[2]; *[1]Washington University in St. Louis, St. Louis, MO; [2]Washington University in St.Louis, St.Louis, MO*

WP 300 **Quantitative Mass Spectrometry-Based Profiling of Histone Post-Translational Modifications in Oryzias latipes(Medaka) Gonads Following Benzo[a]pyrene Exposure**; Luke A Churchman[1]; Frauke Seemann[1]; Hussain Abdulla[1]; *[1]Texas A&M University-Corpus Christi, Corpus Christi, TX*

WP 301 **Integrated Global Histone Proteoform Profiling Reveals Histone PTM Reprogramming Induced by DNA Damage**; Moshfiqur Rahman[1]; Md Shofiul Alam[1]; Lilian Valadares Tose[1]; Kevin Jeanne Dit Fouque[1]; Richard Searfoss[2]; Francisca N. L. Vitorino[2]; Benjamin Garcia[2]; Manuel A Barbieri[1]; Francisco Fernandez-Lima[1]; *[1]Florida International University, Miami, FL; [2]Washington University School of Medicine, St. Louis, MO*

WP 302 **Top Down Proteomics Discovers a Mechanism that Supersedes Canonical γH2AX DNA Damage Response Catalyzed by a New Class of Protease**; Faith M. Joseph[1]; Mathew V. Holt[1]; Nicolas L. Young[1]; *[1]Baylor College of Medicine, Houston, TX*

WP 303 **Identification of Extractables from Pharmaceutical Packaging by Using GC-MS with EI and Soft Ionization**; Nanako Kato[1]; Azusa Kubota[1]; Masaaki Ubukata[1]; *[1]JEOL Ltd., Akishima, Japan*

WP 304 **Chemical characterization of biliary stent systems using a systematic source tracking strategy combining LC-MS and GC-MS**; Joongsuk Kim[1, 2]; Hyunki Cho[1]; Kwan Joong Kim[1]; Woojin Yang[1]; Kihye Jung[1]; Jee Won Jung[1]; Jun Seok Lee[3]; Jungsuk Pyun[3]; Se Kyung Kim[3]; Jungmin Song[1]; Seung Ho Choi[1]; *[1]Korea Testing & Research Institute, Gwacheon, South Korea; [2]Department of Medical Device Engineering and Management, Yonsei University College of Medicine, Seoul, South Korea; [3]National Institute of Food and Drug Safety E*

WP 305 **Multi-Database Approach for Interlaboratory Extractables and Leachables Study of Medical Device Polymers for Confident Identification**; H. Jamie Kim[1]; Chathurika Rathnayake[1]; Mark Annunziato[1]; Krishna Patel[1]; Eric Miller[1]; Samanthi Wickramasekara[1]; *[1]FDA, Silver Spring, MD*

WP 306 **Targeting Efficiency: A Database and Optimized Method for Sensitive and Reliable Targeted LC/MS Analysis of Extractables and Leachables**; Sierra Durham[1]; David A Weil[1]; Lee Bertram[1]; *[1]Agilent Technologies, Santa Clara, CA*

WP 307 **Advanced High Resolution LC/MS-Based Characterization of Extractables from Food Contact Materials Enabled by a Newly Developed Chemical Database**; David A Weil[1]; Sierra Durham[1]; Matthew Curtis[1]; Sofia Nieto[1]; *[1]Agilent Technologies, Santa Clara, CA*

WP 308 **Quantification of Unknowns in Non-Target LC-MS Analysis Using Experimentally Measured Relative Response Factors**; Rebecca Stevens[1]; Jonathan Wilson[1]; *[1]Smith + Nephew, Andover, MA*

WP 309 **Screening to Quantitation: DDA of extractables to determine markers of interest for quantitation using TOF-MRM with a multi-reflecting TOF platform**; Rachel J Sanig[1]; Lee A. Gethings[1]; Jayne Kirk[1]; Richard Lock[1]; Shashank Jain[2]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

WP 310 **Advancing "polymer-aware" data analysis: extractables and leachables assessment for chemical characterization of medical devices using LC–MS-based non-targeted analysis**; Vittoria Lopez[1]; Thierry Nicolas Jean Fouquet[1]; Orlando Cabarcos[1]; *[1]Bausch and Lomb, Rochester, NY*

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WP 312 **Analysis of Single-Use Plastic Water Bottles for Extractable and Leachable Components by Gas Chromatography with Time-of-Flight Mass Spectrometry**; Joseph E Binkley[1]; Elizabeth M. Humston-Fulmer[1]; David E. Alonso[1]; *[1]LECO Corporation, St. Joseph, MI*

WP 313 **Development of a Standard PFAS Method for the Evaluation of PFAS in Food Contact Materials**; Logan Miller[1]; Michael Deible[2]; Shih-Hung Yang[2]; Jacquelyn Runco[2]; Dominika Gruzsecka[1]; Victoria Johnson[1]; Toshiya Matsubara[1]; *[1]Shimadzu Scientific Instruments, Inc., Columbia, MD; [2]RJ Lee Group, Pittsburgh, PA*

WP 314 **Investigating the Leaching and Transformation of PFAS in AFFF Encapsulated Concrete**; Michael Deible[1]; Logan Miller[2]; Shih-Hung Yang[1]; Jacquelyn Runco[1]; Michael Baker[1]; William Lipps[2]; Victoria Johnson[2]; Toshiya Matsubara[2]; *[1]RJ Lee Group, Pittsburgh, PA; [2]Shimadzu Scientific Instruments, Inc., Columbia, MD*

WP 315 **Response Factor Comparison of Broad Extractable Leachable (E&L) Screening Method by LC-MS-QTOF and LC-MS-Orbitrap**; Vasilia R Spourdalakis; *Baxter International, Round Lake, IL*

WP 316 **Future-proof LC-MS/MS solution for analysis of nitrosamines in esomeprazole API**; Ebru Selen[1]; John Gibbons[2]; Craig Butt[3]; Eshani Galermo[1]; Rahul Baghla[1]; *[1]SCIEX, Redwood City, CA; [2]SCIEX, Concord, ON; [3]SCIEX, Marlborough, MA*

WP 317 **Applying non-targeted analysis workflows to the detection and identification of extractables and leachables in medical device polymers**; Neil J. Loftus[1]; Emily G Armitage[1]; Alan Barnes[1]; Dennis JA Van Den Heuvel[2]; *[1]Shimadzu Corporation, Manchester, United Kingdom; [2]Shimadzu Benelux, 's-Hertogenbosch, Netherlands*

WP 318 **Chemical Characterization of a Transvenous Tachyarrhythmia Lead Using Comprehensive Analytical Techniques for Biocompatibility Evaluation**; Yan Jia[1]; Mikel Roe[1]; Qi Luo[1]; Steven Peterson[1]; Seth Randall[1]; Scott A Citrowske[1]; Robert F Shulfer[1]; *[1]Abbott, St Paul, MN*

WP 319 **Quantitation-Model Bias and Day-of-Analysis RRF Calibration Improve UF/AET Reliability in Medical Device E&L MS**; Michael Rush[1]; David Ricker[1]; *[1]Edwards Lifesciences, Salt Lake City, UT*

WP 320 **A QuEChERS Method to Extract Phthalates from Soil Coupled to Gas Chromatography-Mass Spectrometry**; Jennifer Kobee[1]; Lance E Talbert[1]; *[1]California State University, Bakersfield, Bakersfield, CA*

WP 321 **StayClean™ QSight LC-MS/MS for Analysis of Nitrosamine Impurities in Active Pharmaceutical Ingredient (API)**; Julia Casagrande[1]; Sheng-Suan (Victor) Cai[1]; Jacob Jalali[1]; *[1]PerkinElmer US, LLC, Shelton, CT*

WP 322 **Comparative lipidomics of plant and animal foods reveals food-specific differences in nutritionally relevant lipid profiles across production systems**; Mariana Barboza[1, 2]; Mariana

Villegas-Romero[3]; Natalia Vázquez Manjarrez[3]; Justin Siegel[1, 4]; *[1]Innovation Institute for Food and Health, University of California Davis, Davis, CA; [2]Genome Center, College of Biological Sciences, University of California Davis, Davis, CA; [3]Departmento de Fisiologia de la Nutrición, I*

WP 323 **Metabolic fingerprinting for terroir discrimination and authentication within Virginian and South African wines via HPLC-HRMS**; Taylor G Chambers[1]; Laine S Fine[1]; Connell Cunningham[2]; Xin Ma[1]; *[1]Department of Chemistry, University of Virginia, Charlottesville, VA; [2]Department of Chemistry, Washington and Lee University, Lexington, VA*

WP 324 **The Chemistry of Comfort Food: How Cultivar and Cooking Alter Potato Nutritional Composition**; Jacqueline Michelle Chaparro[1]; Sahar B Toulabi[1]; Rachel R Jones[1]; Stephen C Boyko[1]; Caroline Grey[1]; Beth Messier[1]; David G Holm[1]; Paul MacLean[2]; Jessica E Prenni[1]; *[1]Colorado State University, Fort Collins, CO; [2]University of Colorado Anschutz, Aurora, CO*

WP 325 **Targeted analysis and suspect screening of PFAS pesticides in fruits and vegetables by micro-flow LC-HRMS**; Florencia Jesús[1]; Adrián Rosa García[1]; Francisco José Díaz-Galiano[2]; María Dolores Hernando[3]; Amadeo R. Fernández-Alba[1]; *[1]University of Almeria, Almeria, Spain; [2]UNIVERSITY OF JAEN, Jaen, Spain; [3]Department of Desertification and Geo-ecology, Experimental Station of Arid Zones, CSIC, Almeria, Spain*

WP 326 **Foodomics by high-Throughput DESI Lipid Profiling of Cattle Muscle Biopsies Using On-Plate Surface Extraction and In Situ Cholesterol Derivatization**; Kevin A Perez[1, 2]; Emilio Restrepo Nunez[1, 3]; Yunfei Feng[4]; Ryan T Hilger[4]; Juliana A Torrecilhas[5]; Nicolas M Morato[6]; Luis Artur Loyola Chardulo[5]; Priyanka Ramesh[1]; Christina Ferreira[1]; *[1]Bindley Bioscience Center, Purdue University, West Lafayette, IN; [2]Universidad Nacional de Colombia, Medellin, Colombia; [3]Universidad de los Andes, Bogota, Colombia; [4]Purdue University Dept of Chemistry, West L*

WP 327 **Targeted Lipidomic Analysis in Human Milk using LC-MS/MS Triple Quadrupole**; Hui Zhao[1]; Manorama Tummala[1]; Gaurav Pandey[2]; Lars Bode[2]; *[1]Agilent Technologies, Inc., Wilmington, DE; [2]Human Milk Institute, University of California San Diego, La Jolla, CA*

WP 328 **Profiling of Alpha-Gal Epitopes in Rabbit Red Blood Cells: Characterization of Complex Reagents for the Study of Alpha-Gal Syndrome**; Ying Sheng[1]; Erica Ma[1]; Amanda Atanasio[1]; Yuan Mao[1]; Ning Li[1]; *[1]Regeneron Pharmaceuticals Inc, Tarrytown, NY*

WP 329 **Scenario-Based Quality Control Strategies for Non-Targeted Analysis of Complex Food Matrices**; Karen E Butler[1]; Erica L Bakota[1]; Christine M Fisher[1]; Ann M Knolhoff[1]; *[1]US Food and Drug Administration, College Park, MD*

WP 330 **Natural Food Supplements: Characterization using LC/MS – Ashwagandha, Turmeric and Ginger Examples**; Gordon Fujimoto[1]; Lindsay Hatch[1]; Sarah Dowd[1]; Nicholas Ellor[1]; *[1]Waters Corporation, Milford, MA*

WP 331 **A Non-Targeted Mass Spectrometry–Based Proteomic Workflow for Species-Specific Signature Peptides in Plant-Based Protein Products**; Ada L Madrid Sandoval[1]; Darrin Mckenzie[1]; Robert Graham[1]; Di Wu[1]; *[1]Queen's University of Belfast, Belfast, United Kingdom*

WP 332 **“Genome Guided MALDI TOF for Bacillus cereus Group Species Level Identification and Direct LDI Detectio**; Valentin Ernest Pflüger; *Mabritec, Riehen, Switzerland*

WP 333 **Multi-species identification of plant proteins in complex food matrices by global LC-MS/MS**; Melinda A. McFarland[1]; Matthew M. Miele[1]; *[1]FDA-Human Foods Program, College Park, MD*

WP 334 **Allergenic Potential and Food Safety Evaluation of North American Freshwater Panfish Species**; Kamrul Islam[1]; Douglas Zentner[2]; Zahid Hasan[1]; Amit Singh[1]; Zongkai Peng[3]; Anayat Yousuf[4]; Mohamed S Aborahma[4]; Cal Albirini[4]; Annelise N Huynh[4]; Kareem S Salous[4]; Muhammad A Ali[4]; Mustafa Amir[4]; Maria Gasset[5]; John W Peters[1]; Zhibo Yang[3]; Nagib Ahsan[1, 6]; *[1]Department of Chemistry and*

Biochemistry, University of Oklahoma, Norman, OK; [2]Oklahoma Department of Wildlife Conservation, Oklahoma Fishery Research Laboratory, Norman, OK; [3]Department of Biochemistry and Physiology, Un

WP 335 **Correlation between phenolic contents and in-vitro cytotoxicity in Calvatia lilacina: Comparison of HPLC-MS/MS and colorimetric assays**; Will Leung[1]; Jie-He Guo[2]; Yin-Hung Lai[3]; *[1]National Yang Ming Chiao Tung University, Taipei, Taiwan; [2]Department of Chemical Engineering, National United University, Miaoli, Taiwan; [3]National Yang Ming Chiao Tung University, Beitou Dist., Taiwan*

WP 336 **Bringing LC/MS to the Wellness Aisle: Quantitation of Water Soluble Vitamins in Over-the-Counter Supplements**; Patrick M Batoon[1]; Russell Burge[2]; *[1]Agilent Technologies Inc., Santa Clara, CA; [2]Agilent Technologies, Santa Clara, CA*

WP 337 **A Comprehensive Dilute-and-Shoot Method for Creatine and Creatinine in Commercially Available Sports Nutrition Products Using a Single Quadrupole LCMS**; Aron Jaffe[1]; Dominika Gruzsecka[1]; Ethan R Hain[1]; Landon Wiest[1]; Valeria Zerda-Pinto[1]; Sarah Monti[1]; Christopher Gilles[1]; Lihini Tharanga Mendis[1]; Jacob Smith[1]; Allie Ferranti[1]; Stephen Kurzyniec[1]; *[1]Shimadzu Scientific Instruments, Inc, Columbia, MD*

WP 338 **From unripe to ripe: an untargeted lipidomic view of cocoa maturation by UHPLC–Orbitrap MS**; Eclair Venturini Filho[1, 2]; João Victor Macedo De Almeida[3]; Daniel Stoffle Trancoso[3]; Alan Reinke Pereira[2, 3]; Nathália Santos Conceição[2, 3]; Anna Clara Faleiro Braz[2]; Marcio Vieira Rodrigues[4]; Nayara Araujo dos Santos[2]; Wanderson Romão[2, 3]; *[1]Federal University of Espirito Santo, Vitoria, Brazil; [2]Federal Institute of Education, Science and Technology of Espírito Santo, Vila Velha, Brazil; [3]Federal University of Espirito Santo, Vitória, Brazil; [4]Fed*

WP 339 **Metabolic Profiling of Dietary Fiber Intake in Humans by LC-MS/MS**; Nebiyu Abshiru[1]; Boris Nemzer[1, 2]; *[1]FutureCeutical Inc., Momence, IL; [2]University of Illinois at Urbana-Champaign, Urbana-Champaign, IL*

WP 340 **Bee-yond the Label: Chemical Fingerprinting of Honey from Diverse Origins**; Felix Grun[1]; Anton K. Grun[2]; *[1]University of California Irvine, Irvine, CA; [2]Costa Mesa High School, Costa Mesa, CA*

WP 341 **Manipulation of Ion/Ion Reaction Kinetics for Enhanced Phospholipid Identification in Imaging Mass Spectrometry**; Yingchan Guo[1]; Jonathan T. Specker[1]; Boone M. Prentice[1]; *[1]University of Florida, Department of Chemistry, Gainesville, FL*

WP 342 **Ozonolysis of metal-adducted lipids enables rapid double bond position and stereoisomer identification**; Troy R. Scoggins IV[1]; Samuel C. Brydon[2, 3]; Jackson O. T. Long[2]; Hamayal Shahzad[1]; Stephen J. Blanksby[2, 3]; Boone M. Prentice[1]; *[1]Department of Chemistry, University of Florida, Gainesville, FL; [2]School of Chemistry and Physics, Queensland University of Technology, Brisbane, Australia; [3]Central Analytical Research Facility, Queensland University of*

WP 343 **Direct [2+2] cycloaddition reaction between O2•- and C=C bonds to form dioxetanes**; Shiqi Wei[1]; Xiaoxiao Ma[1]; *[1]Tsinghua university, Beijing, China*

WP 344 **Improved sequence coverage of MALDI-generated protein ions via charge inversion ion/ion reactions and IRMPD**; Matthias-Erich N Born[1]; Boone M. Prentice[2]; *[1]University of Florida, Gainesville, FL; [2]University of Florida, Department of Chemistry, Gainesville, FL*

WP 345 **Parking-Assisted Precursor Accumulation Multiply-charged Ion Attachment Resolves Charge State Distributions of Macromolecular Mixtures**; Boukar K. S. Faye[1]; Nicolas J. Pizzala[2]; Scott A. McLuckey[2]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, West lafayette, IN*

WP 346 **Oligonucleotide Spectral Simplification via Metal Cation Saturation**; Alexander M Koers[1]; Zachary T Kruger[2]; Scott A. McLuckey[3]; *[1]Purdue University, West Lafayette, IN; [2]Purdue University, West lafayette, IN; [3]Purdue University, west lafayette, IN*

WP 347 **Collision Induced Unfolding Detected by Hydrogen/Deuterium Exchange and Charge Stripping Reactions**; Kacy L Black[1]; Ian K. Webb[2]; *[1]Indiana University-Indianapolis, Indianapolis, IN; [2]Indiana University Indianapolis, Indianapolis, IN*

WP 348 **Elucidating protein structural effects of electrospray supercharging using ion mobility and cross-linking mass spectrometry**; Ketakumbure H M D D S Herath[1]; Rebecca Cain[1]; Ian K. Webb[1]; *[1]Indiana University Indianapolis, Indianapolis, IN*

WP 349 **Gas-Phase Reactivity of Naphthyloxenium Cations**; Tianyang Dai[1]; Fan Ji[1]; Hilkka I. Kenttämaa[1]; *[1]Purdue University, Lafayette, IN*

WP 350 **Reactions of Isomeric Singlet and Triplet Pyridyloxenium Cations in the Gas Phase**; Tuong Van Nguyen[1]; John J. Nash[1]; Hilkka I. Kenttämaa[1]; *[1]Purdue University, west lafayette, IN*

WP 351 **Classification of Nonvolatile Oxygen-containing Compounds by Using Tandem Mass Spectrometry Based on Diagnostic Gas-phase Ion-molecule Reactions**; Ashley J Galligan[1]; Meghan A Cortez[1]; Gavin L Wolfmule[1]; Hilkka I Kenttämaa[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

WP 352 **Proton-Driven Click Reactions of Nitrile Imines with Serine and Threonine in Gas-Phase Peptide Ions**; Yingxuan Wei[1]; Dominik Halman[2]; Simona Sedláčková[1]; Chenxun Dai[1]; Karel Lemr[2, 3]; František Tureček[1]; *[1]University of Washington, Seattle, WA; [2]Department of Analytical Chemistry, Faculty of Science, Palacky University, Olomouc, Czech Republic; [3]Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Repub*

WP 353 **Photoelectron Spectra of Molecular Anions Relevant to Nuclear Science and Technology**; Burak A. Tufekci[1]; Taylor Gregory[2]; Nathan Loutsch[3]; Shiying Wang[1]; Kathryn Foreman[1]; Tatsuya Chiba[1]; Lan Cheng[1]; Evangelos Miliordos[2]; Bess Vlaisavljevich[3]; Kit H. Bowen[1]; *[1]The Johns Hopkins University, Baltimore, MD; [2]AUBURN UNIVERSITY, Auburn, AL; [3]The University of Iowa, Iowa City, IA*

WP 354 **Untangling Metal–Peptide Interactions in Alzheimer's-Linked Peptides**; Panagiotis Katechis[1]; Sadia Bari[1, 2]; Lucas Schwob[1]; Laura Pille[1]; Aarathi Nair[3]; Jean-Xavier Bardaud[4]; Debora Scuderi[4]; Alexandre Guiliani[5, 6]; Aleksandar Milosavljevic[5]; *[1]Deutsches Elektronen-Synchrotron DESY, Hamburg, Germany; [2]Zernike Institute for Advanced Materials, Groningen, Netherlands; [3]The Hamburg Centre for Ultrafast Imaging (CUI), Hamburg, Germany; [4]Institut de Chimie*

WP 355 **Deciphering the Structure of Metal-Proline Clusters**; Xianglei Kong; *Nankai University, Tianjin, China*

WP 356 **Vanadium Reactions with O2 and NH3: Bond Dissociation Energies of OV+-O, VN+, and VN+-NH3**; Joshua Ewigleben[1]; Erick Tieu[1, 2]; Brandon Stevenson[1]; Sergei Aksyonov[1]; Michael Morse[1]; *[1]University of Utah Department of Chemistry, Salt Lake City, UT; [2]University of Washington, Seattle, WA*

WP 357 **Beyond Mass Spectrometry: Isomer-specific Photodetachment Spectra of 1-, 2, and 5-cyano-cyclopentadiene Radical Anions and Thermochemistry of the Three Cyano-cyclopentadiene Isomers**; Wilson Gichuhi[1]; Vincent Michuki[1]; Ethan Cummins[1]; *[1]Tennessee Tech University, Cookeville, TN*

WP 358 **Development and Optimization of a Custom IR Action Spectroscopy Platform for Ionic Clusters**; Nwanne D. Banor[1]; Jenna E. Lees[1]; Miyuru M. Wellalage[1]; Thushitha S. Jayasekara[1]; Daniel A Thomas[1]; *[1]University of Rhode Island Chemistry Department, Kingston, RI*

WP 359 **Vibrational Structures and Thermochemistry of Hydroxyacetonitrile, 2-hydroxy-2-phenylacetonitrile and Their Deprotonated Radical Anions**; Ethan S. Cummins[1]; Wilson K. Gichuhi[1]; *[1]Tennessee Technilogical University, Cookeville, TN*

WP 360 **Evaluating Existing Computational Algorithms to Support Structural Interpretation of Enantiomer Differentiation via Noncovalent Complexation and Ion Mobility – Mass Spectrometry**; Emma R. Remish[1]; Benjamin K Blakley[1]; Eric Dybeck[2]; Jody C May[1]; Valeria Guidolin[3]; John A McLean[1];

[1]Department of Chemistry, Center for Innovative Technology, Institute of Chemical Biology, Institute for Integrative Biosystems Research and Education, Vanderbilt University, Nashville, TN; [2]MedDesign, Pfizer, Cambridge, MA; [3]</

WP 361 **CAD mechanisms of isomeric protonated aryl C-nitroso compounds**; Meghan A Cortez1; Annika M Little[1]; Harleigh L Abbott[1]; Hilkka I Kenttämaa[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

WP 362 **Using Variable-Temperature Native Mass Spectrometry to Probe Hydration-Dependent Thermodynamics in Multi-Ligand Protein Complexes**; Kacie A. Evans[1]; Morgan Powers[1]; Robert L. Rider[1]; Carter Lantz[2]; Arthur Laganowsky[2]; Hays Rye[2]; David H. Russell[2]; *[1]Texas A&M University, College Station, TX; [2]Texas A&M Univesity, College Station, TX*

WP 363 **Determination of AAV VP Ratio from Direct Mass Measurements of Intact Capsids and Packaged Genomes by Charge Detection Mass Spectrometry**; Benjamin E Draper[1]; Lohra M Young[1]; Martin F Jarrold[1, 2]; *[1]Megadalton Solutions, Bloomington, IN; [2]Indiana University - Bloomington, Bloomington, IN*

WP 364 **Comparison of standard and high-field Orbitrap mass analyzers for charge detection mass spectrometry (CD-MS) applications**; Tobias P. Wörner[1]; Dmitry Grinfeld[1]; Alexander A. Makarov[1]; *[1]Thermo Fisher Scientific, Bremen, Germany*

WP 365 **Restrained charge state distributions in charge-reducing native mass spectrometry fail to reflect protein unfolding in solution**; Hanlin Ren[1]; Jennifer S. Brodbelt[1]; *[1]University of Texas at Austin, Austin, TX*

WP 366 **Direct Native Mass Spectrometry of Endogenous Large Protein Assemblies in Crude Cell Lysates Using High-Resolution Multi-Turn TOF-MS**; Michiko Tajiri[1]; Sayaka Hokazono[1]; Yusuke Tateishi[2]; Qiuyi Wang[2]; Hiroko Morinaga[2]; Hiroyuki Miura[2]; Masaru Nishiguchi[2]; Daisuke Okumura[2]; Tsuyoshi Konuma[1]; Satoko Akashi[1]; *[1]Yokohama City University, Yokohama, Japan; [2]Shimadzu Corporation, Kyoto, Japan*

WP 367 **DIA Based Native Proteomics of HeLa Cell Lysate**; William Moeller[1, 2]; Zihao Qi[2, 3]; Guijie Zhu[4]; Yun-Jung Hsu[2, 3]; Jorge Colón Rosado[5]; Liangliang Sun[5]; Vicki H. Wysocki[2, 3]; *[1]Georgia Institute of Technology, Atlanta, GA; [2]Native MS Guided Structural Biology Center, Georgia Institute of Technology, Atlanta, GA; [3]School of Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA; <*

WP 368 **Revealing Growth-Dependent Ribosomal Heterogeneity through Charge Detection and Native Mass Spectrometry**; Deshani S Dehiwaththage[1]; Salina Mali[1]; Jared B Shaw[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE*

WP 369 **Infrared photoactivation improves the native top-down and complex-down analysis of macromolecular assemblies**; Cynthia N. Nagy[1]; Linda B. Lieu[1]; Jake T Kline[1]; Joshua D. Hinkle[2]; Luca Fornelli[1]; *[1]University of Oklahoma, Norman, OK; [2]ThermoFisher Scientific, San Jose, CA*

WP 370 **Mapping Heterogeneous Glycoforms at the Complex Level via DIA-ECCR-nMS**; Zhixin Xu[1, 2, 3]; Chen Du[3]; Eduardo Olmedillas[4, 5]; Erica Ollmann Saphire[4, 5]; Vicki H. Wysocki[1, 2, 3]; *[1]Georgia Institute of Technology School of Chemistry and Biochemistry, Atlanta, GA; [2]Native Mass Spectrometry Guided Structural Biology Center, Georgia Institute of Technology, GA 30318, Atlanta, GA; [3]The Ohio State Univer*

WP 371 **Probing structural stability of laser-ablated proteins using circular dichroism (CD) spectroscopy and native ion-mobility mass spectrometry (IM-MS)**; Neda Feizi[1]; Maiah Woodring[1]; Jonathan Clinger[1]; Kermit K. Murray[2]; Touradj Solouki[1]; *[1]Baylor University, Waco, TX; [2]Louisiana State University, Baton Rouge, LA*

WP 372 **Enabling Routine Native Mass Spectrometry for Diverse Biotherapeutics with Automated Online Buffer Exchange**; Mason Chilmonczyk[1]; Casey Vantucci[1]; Carter Asef[1]; Suraj Dhungana[1]; *[1]Andson Biotech, Atlanta, GA*

WP 373 **CDMS and Biophysical Measurements of MDa Ions: Stabilities in the Gas Phase and Solution**; Zachary M. Miller[1]; Evan R. Williams[1]; *[1]University of California, Berkeley, Berkeley, CA*

WP 374 **Complex-up IRMPD and SID workflows reveal proteoform heterogeneity in Escherichia coli ribosomes**; Sachin Tennakoon[1]; Jared B. Shaw[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE*

WP 375 **Ionization via Desorption by Impulsive Vibration Excitation (i-DIVE) for Intact and Native Protein Analysis**; Pei Su[1]; Khaled Madhoun[1, 2]; Semah Keissieh[1]; R. J. Dwayne Miller[2]; *[1]University of California, Riverside, Riverside, CA; [2]University of Toronto, Toronto, ON*

WP 376 **Proteasome Activator Complexes Studied by Charge Detection Mass Spectrometry and Cryo-EM**; Bradley T.V. Davis[1]; Adwaith B. Uday[2]; Anisha Haris[3]; Alex Keszei[4]; Jakub Ujma[3]; David Bruton[3]; Keith Richardson[3]; Mohammad Mazhab-Jafari[4]; Kevin Giles[3]; Natalie Zeytuni[2]; Siavash Vahidi[1]; *[1]University of Guelph, Guelph, ON; [2]McGill University, Montreal, QC; [3]Waters Corporation, Wilmslow, United Kingdom; [4]University of Toronto, Toronto, ON*

WP 377 **ML-driven glycopeptide classifier enables enrichment-free glycoproteomics**; Bingyuan Zhang[1]; The Huong Chau[1]; Kristina Mae Bienes[1]; Hiromu Arakawa[1]; Christopher Ashwood[2]; Hiroyuki Kaji[1]; Rebeca Kawahara[1]; Yusuke Matsui[1]; Morten Thaysen-Andersen[1]; *[1]Nagoya University, Nagoya, Japan; [2]Protea Glycosciences Pty Ltd, NSW, Australia*

WP 378 **Reprising the role of Immobilized Metal Affinity Chromatography (IMAC) in glycoproteomic workflows**; Vanessa Encinas[1]; Tim S. Veth[1]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA*

WP 379 **Mining Domain-Specific O-glycosylation in Human Plasma from Public Glycoproteomic Databases**; Huilin Hao[1]; Robert S. Haltiwanger[1]; *[1]Complex Carbohydrate Research Center, University of Georgia, Athens, GA*

WP 380 **Elucidating the role of altered N-glycosylation patterns on glycoprotein trafficking and localization**; Alexander W Black[1]; Tiffany Ngo[1]; Dominic Ng[1]; Maggie PY Lam[1]; *[1]University of Colorado Anschutz Medical Campus, Aurora, CO*

WP 381 **High-Resolution Liquid Chromatography-Tandem Mass Spectrometry Enables Comparison of Protein Glycosylation Heterogeneity in Patient-Matched Colon Cancer Tissue and Serum**; Kathryn L Kapp[1]; Fernando J. Garcia-Marques[1]; Abel Bermudez[1]; Nikhiya Shamsher[1]; Audrey E. DaDamio[1]; Melissa C. Parra[1]; Chelsea Diaz-Perez[1]; Sharon J. Pitteri[1]; *[1]Stanford School of Medicine, Palo Alto, CA*

WP 382 **Investigating the effects of gas phase fractionation and related parameters for improving glycopeptide identification**; Ruby Zhang[1]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA*

WP 383 **Multiple Accumulation Precursor Mass Spectrometry to Improve the Dynamic Range of Glycoproteome Measurements**; Madeline J Yeh[1]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA*

WP 384 **Deep, Omics-Scale Glycoproteoform Analysis of Hereditary Spastic Paraplegia by Data-Independent Top-Down Mass Spectrometry**; Joshua B Rubin[1]; Carina Alvarez[2]; Neil L Kelleher[1, 3]; Hande P Ozdinler[4]; Steven Patrie[1, 3]; *[1]Chemistry of Life Processes Institute, Northwestern University, Proteomics Center of Excellence, Evanston, IL; [2]Department of Chemistry, University of Illinois Chicago, Chicago, IL; [3]Department of Chemistry and Molecular*

WP 385 **Improved Identification and Localization of N- and O-Linked Glycopeptides with MetaMorpheus**; Cheng-Ruei Yang[1]; Michael R. Shortreed[1]; Lloyd M Smith[1]; *[1]University of Wisconsin-Madison, Madison, WI*

WP 386 **Automated and semi-automated enrichment methods for glycoproteomics**; Kayla Markuson[1]; Chinmayee Deshpande[1]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA*

WP 387 **Extensive Site-Specific Characterization of N-Linked Glycosylation in Human Plasma**; Yi Liu[1]; Yuri Mirokhin[1]; Sergey Sheetlin[1]; Meghan Burke[1]; Xiaoyu Yang[1]; Guanghui Wang[1]; Dmitrii V. Tchekhovskoi[1]; Stephen E. Stein[1]; *[1]NIST, Gaithersburg, MD*

WP 388 **In-depth Glycoproteomic Analysis of Clear Cell Renal Cell Carcinoma Using Patient-Derived Xenograft Tissue and Serum Samples by Mass Spectrometry**; Abel Bermudez[1]; Fernando J. Garcia-Marques[1]; Dalin Zhang[2]; Hongjuan Zhao[2]; James D Brooks[2]; Sharon J. Pitteri[1]; *[1]Canary Center for Cancer Early Detection, Department of Radiology, School of Medicine, Stanford University, Palo Alto, CA; [2]Department of Urology, Stanford University, Palo Alto, CA*

WP 389 **GlycoDiveR: a modular R framework to analyze and visualize highly dimensional glycoproteomics data**; Tim S Veth[1]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA*

WP 390 **Dialing in glycopeptide fragmentation through infrared-activated electron transfer dissociation (IR-ETD)**; Haley M. Schramm[1]; Joshua D. Hinkle[2]; Jingjing Huang[3]; David Bergen[2]; Rafael D. Melani[2]; Graeme C. McAlister[2]; Christopher Mullen[2]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientfic, San Jose, CA*

WP 391 **Cell surfaceome profiling with membrane protein enrichment for elucidation of age-associated alterations to the gut-vascular barrier (GVB)**; Oliver Wu[1]; David S Roberts[1]; Andrew Reiter[2]; Carolyn R Bertozzi[1]; *[1]Stanford University, Stanford, CA; [2]Stanford University, Stanford*

WP 392 **In-depth N-linked and O-linked glycosylation characterization of etanercept using Orbitrap Excedion Pro mass spectrometer with electron-transfer/higher-energy collision dissociation (EThcD) fragmentation**; Xiaoxi Zhang[1]; Roberto Gamez[2]; Reiko Kiyonami[3]; Min Du[3]; *[1]ThermoFisher Scientific, Shanghai, China; [2]Thermo Fisher Scientific, Austin, TX; [3]Thermo Fisher Scientific, Lexington, MA*

WP 393 **Glycopeptide mapping of Untreated and Deglycosylated CUB domain containing protein 1 using LC-MS/MS**; Melissa R Leyden[1]; Scott A Ugrin[2]; Enrico L Digiamarino[2]; Keith Pui-Kei Wu[2]; Yingchun Li[2]; *[1]Abbvie, North Chicago, IL; [2]AbbVie Inc., North Chicago, IL*

WP 394 **Resolving Disease-Linked Plasma Glycoforms Using High-Accuracy Multi-Reflecting Time-of-Flight Mass Spectrometry in Bipolar Disorder and Schizophrenia Cohorts**; Matthew E Daly[1]; Lee A Gethings[1]; Richard Lock[1]; James I Langridge[1]; *[1]Waters Wilmslow UK, Wilmslow, United Kingdom*

WP 395 **Integrating Glycan Database Search and De Novo Sequencing for Unbiased Glycan Discovery**; Weiping Sun[1]; Zheng Chen[1]; Shuyang Zhang[1]; Xiyue Zhang[1]; Zihao Wang[1]; Linting LI[1]; Wenting Li[1]; Baozhen Shan[1]; *[1]Bioinformatics Solutions Inc, Waterloo, ON*

WP 396 **Confident Characterization of N- and O-Linked Glycopeptides Using Electron-Based Dissociation on a timsOmni Platform**; Hongxia Bai[1]; Ioanna Barla[2]; Anastasios Grigoriadis[2]; Kristina Marx[3]; Gadi Armony[4]; Florian Busch[5]; Athanasios Smyrnakis[6]; Greg Chopiuk[7]; Guillaume Tremintin[8]; Dimitris Papanastasiou[6]; Matthew Willetts[9]; *[1]Bruker, Billerica, MA; [2]Fasmatech Science and Technology, Athens, Greece; [3]Bruker Daltonics GmbH & Co.KG, Bremen, Germany; [4]Bruker Nederland B.V., Leiderdorp, Netherlands; [5]Bruker Switzerland AG, Fäl*

WP 397 **Selective Glycopeptide Signal Enhancement Using the Athena Ion Processor in the Collision Cell on a timsTOF Ultra AIP system**; Hongxia Bai[1]; Diego Assis[2]; Kristina Marx[3]; Benjamin Jones[2]; Michael Krawitzky[4]; Matthew Willetts[2]; *[1]Bruker, Billerica, MA; [2]Bruker Scientific LLC, Billerica, MA; [3]Bruker Daltonics GmbH & Co.KG, Bremen, Germany; [4]Bruker Scientific LLC, San Jose, CA*

WP 398 **Therapeutic Antibody Interactions with Serum Characterized by Hydrogen Deuterium Exchange Mass Spectrometry**; Isabel Mariano[1]; Miklos Guttman[1]; Abhinav Nath[1]; *[1]University of Washington, Seattle, WA*

WP 399 **Conformational dynamics of GPR55 across different activation states by HDX-MS**; Chamalee Demalgiriya Gamage[1]; Tobias Claff[1]; Lee Frego[1]; *[1]Boehringer Ingelheim, Ridgefield, CT*

WEDNESDAY POSTERS

WP 400 **Isotopic coding in HDX-MS as a means of monitoring allosteric changes across homomeric, symmetric assemblies**; Madison Turner[1]; Anisha Haris[2]; Verena Filz[3]; Cristina Lento[4]; Jakub Ujma[2]; David Bruton[2]; Keith Richardson[2]; Thomas Böttcher[3]; Kevin Giles[2]; Derek Wilson[4]; Siavash Vahidi[1]; *[1]University of Guelph, Guelph, ON; [2]Waters Corporation, Wilmslow, United Kingdom; [3]University of Vienna, 1090 Vienna, Austria, Vienna, Austria; [4]York University, Toronto, ON*

WP 401 **Native Mass Spectrometry Buffers Directly Influence Protein Dynamics and Behavior in Solution**; Emily Burningham[1]; Carter Lantz[2]; Robert Rider[2]; Arthur Laganowsky[2]; David H Russell[2]; *[1]Texas A&M University, College Station, TX; [2]Texas A&M Univesity, College Station, TX*

WP 402 **Modulation of UBA5 Dimer Equilibrium by Small Molecule Inhibitors Monitored by HX-MS**; Darby J Ball[1]; David Weis[1]; James Mignone[1]; Elizabeth Jurica[1]; Brian Mahon[1]; Dawn Mulligan[1]; Jaclyn Robustelli[1]; Joseph Yanchunas[1]; *[1]Bristol Myers Squibb, Lawrence Township, NJ*

WP 403 **Hydrogen–deuterium exchange mass spectrometry reveals mutation-specific conformational remodelling in STAT5B**; Ayesha Chaudhry[1]; Qirat Ashraf[2]; Cristina Lento[1]; Elvin De Araujo[2]; Patrick Gunning[2]; Derek Wilson[1]; *[1]York University, Toronto, ON; [2]University of Toronto, Toronto, ON*

WP 404 **Histidine HDX-MS EnablesSite-ResolvedQuantification ofMetal-Bound Fractionsin Metalloproteins**; Chenao Zhang[1]; Francesca A. Vaccaro[1]; Katherine J. Franz[1]; Bruce D. Pascal[2]; Michael C. Fitzgerald[1]; *[1]Department of Chemistry, Duke University, Durham, NC; [2]Omics Informatics LLC, Honolulu, HI*

WP 405 **HDX-MS characterization of protein dynamics involved in the recognition of BACH1 by ubiquitin ligase SCF-FBXO22**; Dayana Argoti[1]; Benedikt Goretzki[2, 3]; Martin Schroeder[4]; Maryam Khoshouei[4]; Philipp Hoppe[4]; Sascha Guttmann[4]; Cesar Fernandez[4]; Andreas Frank[1]; *[1]Novartis Biomedical Research, Emeryville, CA; [2]Novartis, Emeryville, CA; [3]Isomorphic Labs, London, United Kingdom; [4]Novartis Biomedical Research, Basel, Switzerland*

WP 406 **Enhanced HDX-MS Analysis of Membrane Protein NINJ1 via Microflow Chromatography and Multi-Reflecting TOF-MS**; Yisheng Xu[1]; Shaofei Cui[2]; *[1]Waters cooperation, Beijing, China; [2]waters cooperation, Shanghai, China*

WP 407 **Virus breathing is critical for establishment of disassembly intermediates in Coxsackie Virus B3 upon receptor binding**; Victoria Brady[1]; Sayan Das[2]; Susan L Hafenstein[2]; Ganesh S Anand[1]; *[1]Pennsylvania State University, University Park, PA; [2]University of Minnesota, Hormel Institute, Austin, MN*

WP 408 **Site-specific epitope mapping of SARS-CoV-2 spike protein using HDX-MS**; Rhona Cowan[1]; Joseph Anacleto[1]; Cristina Lento[1]; Derek J Wilson[1]; *[1]Department of Chemistry, York University, Toronto, ON*

WP 409 **DynaDUB – Structural Dynamics Underlying Deubiquitinase Inhibitor Potency and Selectivity**; Andrea Pierangelini[1]; Hannah Jones[1]; Simeon Draganov[1]; Franziska Guenther[1]; Iolanda Vendrell[1]; Katherine England[1]; Eidarus Salah[2]; Christopher Schofield[2]; Lennart Brewitz[2]; Emma Murphy[1]; Adan Pinto-Fernandez[1]; Andrew Turnbull[3]; Benedikt Kessler[1]; Darragh O'Brien[1]; *[1]University of Oxford Nuffield Department of Medicine, Oxford, United Kingdom; [2]University of Oxford, Department of Chemistry, Oxford, United Kingdom; [3]Cancer Research Horizons, London, United Kingdom*

WP 410 **A microfluidic quench-flow apparatus for PEPS-HDX-**; Isini Ranawake Arachchige[1, 2]; Rohana Liyanage[1, 2]; Wesley Stites[3]; Jackson O. Lay Jr[1, 2]; *[1]University of Arkansas, Fayetteville, AR; [2]Arkansas Statewide Mass Spectrometry Facility, FAYETTEVILLE, AR; [3]Marshall University, HUNTINGTON, VA*

WP 411 **Analysis of 30 volatile Per- and Polyfluoroalkyl Substances from OTM-50 using canisters and a novel cryogenic preconcentrator with GC/TQ**; Eric Fausett[1]; Dan Cardin[2]; Tom Robinson[2]; Eric Park[1]; Victoria Vogel[2]; *[1]Agilent Technologies, Wilmington, DE; [2]Entech Instruments, Simi Vally, CA*

WP 412 **Evaluating Residual Detergent in AAV Production Process**; Khin Myint; *MilliporeSigma, Bedford, MA*

WP 413 **Quantitative PFAS Analysis in Medical Devices Using Triple Quadrupole LC/MS**; Aimei Zou[1]; Auni Wong[2]; Siji Joseph[2]; Andreas Otto[3]; *[1]Agilent Technologies Singapore, Singapore, Singapore; [2]Agilent Technologies, Singapore, Singapore; [3]Agilent Technologies Deutschland GmbH, Waldbronn, Germany*

WP 414 **Comprehensive PFAS Analysis in Textiles Using Triple Quadrupole GC/MS and LC/MS Workflows**; Aimei Zou[1]; Auni Wong[2]; *[1]Agilent Technologies Singapore, Singapore, Singapore; [2]Agilent Technologies, Singapore, Singapore*

WP 415 **Formula Troubleshooting of Particulate Formation in Surfactant-Based Cosmetic Matrices via Liquid Chromatography Mass Spectrometry**; Nicole M Brundridge[1]; Chung-chueh Chang[1]; Ismael Cotte-Rodriguez[1]; *[1]L'Oreal, Clark, NJ*

WP 416 **A novel monodisperse supermacroporous reversed-phase platform enabling unified LC–MS analysis of nucleic acids across a broad size range**; Ke Ma[1]; Shane Bechler[2]; Christof Mitter[3]; Mauro De Pra[4]; *[1]Thermo Fisher, Sunnyvale, CA; [2]Thermo Fisher Scientific, Sunnyvale, CA; [3]Thermo Fisher Scientific, Germering, Germany; [4]Thermo Fisher Scientific, Milan, Italy*

WP 417 **Risk-Based LC–MS Strategy for Classification and Control of Amine Impurities in Peptide Manufacturing**; Pei Wang[1]; Christopher Ciptadjaya[1]; Jie Ding[1]; *[1]Thermofisher Scientific, Middleton, WI*

WP 418 **Automated Gas-Assisted Dynamic Accelerated Solvent Extraction (GA-dASE) Workflow vs. EPA Method 1633A: PFAS in Soil, Biosolids, and Tissues**; Gopal Bera[1]; German Gomez-Rios[1]; Yan Liu[1]; Rooz Golshani[1]; Brian McLaughlin[1]; *[1]Thermofisher Scientific, Sunnyvale, CA*

WP 419 **Development of an SPE-LC-MS/MS Analytical Platform for Trace-Level Quantitation of Nitrosamines in Pharmaceuticals**; Christopher M Jones[1]; Siqi Du[1]; Meredith Spradlin[2]; Fei Chen[1]; Kevin Parker[1]; *[1]AbbVie Inc., North Chicago, IL; [2]Department of Chemistry, The University of Texas at Austin, Austin, TX, 78712, USA, Austin, TX*

WP 420 **Implementing EPA OTM-50: TD-GC-MS/MS Analysis of Volatile PFAS in Air**; Daniela Cavagnino[1]; Terry Jeffers[2]; Lina Mikaliunaite[3]; Nathan Shafer[3]; Manuela Bergna[1]; Lori Dolata[4]; Monica Driscoll[5]; *[1]Thermo Fisher Scientific, Segrate, Italy; [2]Thermo Fisher Scientific, West Palm Beach, FL; [3]Markes International, Sacramento, CA; [4]Thermo Fisher Scientific Inc, Madison, WI; [5]Thermo Fisher Scientific,*

WP 421 **Selected Ion Flow Tube Mass Spectrometry - Real-Time Inline Analysis of VOC Emissions from Plastics Extrusion**; David Mueller[1]; Felix Mehrens[2]; *[1]Syft Technologies GmbH, Darmstadt, Germany; [2]Leibniz Universität Hannover Institut für Kunststoff- und Kreislauftechnik (IKK), Hannover, Germany*

WP 422 **Improved Determination of Fluorotelomer Alcohol Compounds Based on EN17681-1:2025**; Chun-ye Sun[1]; Jia Sheng[1]; Zhi-hui Lin[2]; Lei LV[2]; Sha Wang[3]; *[1]Agilent Technologies (China) Co.,Ltd, Shanghai, China; [2]Agilent Technologies (China) Co.,Ltd, Guangzhou, China; [3]Agilent Technologies (China) Co.,Ltd, Beijing, China*

WP 423 **Early-Stage Risk Screening of Illicit Polyols in Glycerol-Based Systems by SICRIT Mass Spectrometry**; Charles C. Liu[1]; Shun Na[2]; *[1]ASPEC Technologies Limited, Beijing, China; [2]Agilent Technologies (China) Co.,Ltd, Beijing, China*

WP 424 **Expanding Autosampling and LC/MS Integration for Automated Bioreactor Control**; Matthew Wong[1]; James Angelo[1]; Isabel Dunning[1]; Mike Knierman[2]; Bruce Dolby[3]; Christian Lambrecht[3]; Haiko Herschbach[3]; Sebastian Weinig-Berger[2]; *[1]MilliporeSigma, Bedford, MA; [2]Agilent Technologies, Santa Clara, CA; [3]Agilent Technologies Inc., Waldbronn, Germany*

WP 425 **Integrating IEX Separation with Post-Column Denaturation and Reduction for Enhanced Middle-Down Characterization of Antibody CDR Modifications**; Tao Xing[1]; Penghsuan Huang[2]; Yuetian Yan[1]; Shunhai Wang[1]; Ning Li[2]; *[1]Regeneron Pharmaceuticals Inc., Tarrytown, NY; [2]Regeneron Pharmaceuticals Inc, Tarrytown, NY*

WP 426 **Direct headspace-MRR quantitation of ethylene glycol and diethylene glycol contaminants in glycerin**; Alexander V. Mikhonin[1]; Voislav Blagojevic[1]; Roice Michael[2]; René Lovmand[2]; Christopher J. Thompson[3]; Justin L. Neill[1]; *[1]BrightSpec, Inc., Charlottesville, VA; [2]Novo Nordisk A/S, Brennum Park 4M, 3400, Hillerød, Denmark; [3]BrightSpec, Inc., Waltham, MA*

WP 427 **Rapid Analysis of Residual Amines, Nitrosamines, and Pro-Nitrosamine Compounds in Pharmaceutical Products Using Headspace-SIFT-MS**; Claire A. Verbrugge[1]; Leslie P. Silva[2]; Joseph A. Loo[1]; Heath C. Timmons[1, 3]; *[1]UCLA, Los Angeles, CA; [2]Syft Technologies, Studio City, CA; [3]Amgen, Thousand Oaks, CA*

WP 428 **maxiM/Ze: A Novel Image Recognition Approach for Visualizing and Processing Mass Spectrometry Based Metabolomics Data**; Elizabeth R Flammer[1]; Yash Narayan[2]; Timothy J Garrett[1, 2]; *[1]University of Florida, Department of Chemistry, Gainesville, FL; [2]University of Florida, College of Medicine, Department of Pathology, Immunology, and Laboratory Medicine, Gainesville, FL*

WP 429 **AI-enabled metabolomics allows for rapid characterisation and optimization of Syn61, an E coli bioproduction strain with a synthetic genome**; Jack Howland[1]; Amy A Caudy[1]; Baljit K Ubhi[1]; Katherine Raiche[1]; Henry Massey[2]; Markus Englert[2]; Faye Rodgers[2]; Daniel de la Torre[2]; *[1]Matterworks Inc, Sommerville, MA; [2]Constructive Bio, Cambridge, United Kingdom*

WP 430 **A new XIC-centric workflow in NIST MS Search for compound identification from tandem mass spectrometry data using spectral libraries**; Guanghui Wang[1]; Yuri A. Mirokhin[1]; Xiaoyu Yang[1]; Meghan C. Burke[1]; Dmitrii V. Tchekhovskoi[1]; Stephen E. Stein[1]; *[1]NIST, Gaithersburg, MD*

WP 431 **FASSTrecords: Unifying Pan-Repository Metabolomics Data For The Exploration Of The Worldwide Metabolome**; Yasin El Abiead[1]; Jeongin Seo[2]; Wilhan Donizete Gonçalves Nunes[2]; Ozgur Yurekten[3]; Thomas Payne[3]; Eoin Fahy[4]; Shankar Subramaniam[4]; Juan Antonio Vizcaino[3]; Nikiforos Alygizakis[5]; Jeremy Carver[2]; Mingxun Wang[6]; Pieter C. Dorrestein[2]; *[1]University of Natural Resources and Life Sciences Vienna, Department of Chemistry, Institute of Analytical Chemistry, Vienna, Austria; [2]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jo*

WP 432 **Unknown PFAS annotation in complex samples with SIRIUS**; Kai Dührkop[1]; Markus Fleischauer[1, 2]; Marcus Ludwig[1]; Martin Andre Hoffmann[1]; Sebastian Böcker[2]; *[1]Bright Giant GmbH, Jena, Germany; [2]Friedrich Schiller University Jena, Jena, Germany*

WP 433 **The NIST tandem MS library 2026: Instrument methods and spectrum evaluation**; Yuxue Liang[1]; Pedatsur Neta[2]; Xiaoyu Yang[2]; Yi Liu[2]; Tallat Bukhari[2]; Stephen E. Stein[2]; *[1]National Institute of Standards and Technology, Gaithersburg, MD; [2]NIST, Gaithersburg, MD*

WP 434 **Taxonomy-informed libraries for any species, mass accuracy and isotope scoring, and predicted fragmentation to improve metabolomics annotation accuracy**; Corey D Broeckling[1]; Nathan Montgomery[1]; Jeff Nelson[1]; *[1]Colorado State University, ARC-BIO, Fort Collins, CO*

WP 435 **Unraveling Differential Lipids in Aging Tissues Using a Novel Data Analysis Workflow**; Brenna C Keegan[1]; Fernando (Ralph) Tobias[1]; Mark Sartain[1]; Karen Yannell[1]; Almudena Veiga-Lopez[2]; *[1]Agilent Technologies, Santa Clara, CA; [2]University of Illinois Chicago, Chicago, IL*

WP 436 **Differential mass network analysis for systematic discovery of unknown metabolites in large-scale MS/MS datasets**; Mariano Carpena[1]; Camila Riccio-Rengifo[1]; Gabriel Esteban Velez[1]; Gustavo Adolfo Lara-Cruz[1]; Andres Jaramillo-Botero[1, 2]; *[1]iÓMICAS Research Institute, Pontificia Universidad Javeriana, Cali, Colombia; [2]Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, CA*

WP 437 **Can Statistical Normalization Replace Internal Standards in Comparative Lipidomics?**; Thomas Lubinsky[1]; Caitlin Randolph[1]; Shane Tichy[2]; Gaurav Chopra[1]; *[1]Purdue University, West lafayette, IN; [2]Agilent Technologies, Santa Clara, CA*

WP 438 **A Domain Specific AI Assistant for Metabolomics Using SOP and Spectral Library Retrieval**; Rukshan Wijesinghe[1]; Harshani Bandara[1]; Leiver Campeon[1]; Mihira Kasun[1]; Lalin Theverapperuma[1]; *[1]EXPERT Intelligence, Santa Clara, CA*

WP 439 **An Open MS/MS Database of 1.1 Million MS/MS Spectra from 185,000 structurally diverse compounds**; Tobias Kind[1]; Christoph Krettler[1]; Erik DeBloois[1]; James Taylor[1]; Pelle Simpson[1]; August Allen[1]; David Healey[1]; *[1]Enveda Biosciences, Boulder, CO*

WP 440 **OMIXIS: A Graphical Tool for Accurate Quantitation in Untargeted Metabolomics**; I-Chun Chi[1]; Hui-Yin Chang[1, 2]; *[1]Institute of Systems Biology and Bioinformatics, National Central University, Taoyuan City, Taiwan; [2]Department of Biomedical Sciences and Engineering, National Central University, Taoyuan City, Taiwan*

WP 441 **Bridging Complexity and Accessibility in Metabolomics with MetaboApps**; Wilhan D. Goncalves Nunes[1]; Helena Mannochio-Russo[1]; Haoqi Nina Zhao[1, 2]; Kine Eide Kvite[1]; Shipei Xing[1]; Harsha Gouda[1]; Julius Agongo[1]; Ipsita Mohanty[3]; Vincent Charron-Lamoureux[1]; Prajit Rajkumar[1]; Abzer Shah[4]; Axel Walter[4]; Rithi Krishnaraj[5]; Yasin El Abiead[6]; Patrick C. Ferreira[7]; Simone Zuffa[1]; Abubaker Patan[1]; Andres M. Caraballo-Rodriguez[1]; Wout Bittremieux[8]; Daniel Petras[4, 9]; Mingxun Wang[5]; Pieter C. Dorrestein[1, 10, 11, 12]; *[1]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [2]Civil and Environmental Engineering, Stanford University, Stanford, CA; [3]Department of Veterinary & Biomedical Scie*

WP 442 **Resilient Computational Metabolomics Platform with the GNPS2 Federated Network**; Benjamin Bowen[1]; Trent Northen[1]; Brandon Kieft[1]; Ricardo Da Silva[2]; Wout Bittremieux[3]; Sven Nahnsen[4]; Wei-Chih Chin[5]; Yu-Liang Yang[5]; Kyo Bin Kang[6]; Oliver Vining[7]; Daniel Petras[8]; Mingxun Wang[9]; *[1]Lawrence Berkeley National Laboratory, Berkeley, CA; [2]University of Sao Paulo, Sao Paulo, Brazil; [3]University of Antwerp, Antwerpen, Belgium; [4]University of Tuebingen, Tuebingen, Germany; [5]Academia S*

WP 443 **The MZ2Struct database: mapping m/z to substructures for the annotation of small molecules with mass spectrometry**; Aleksandr Zubov[1, 2]; Adrià Olomí[1]; Antoni Del Pino[1]; Núria Canela[1]; Xavier Domingo[1, 2]; *[1]EURECAT - Technology Centre of Catalonia, Reus, Spain; [2]University Rovira i Virgili, Tarragona, Spain*

WP 444 **Pan-cancer metabolomic predictive features enable tissue-agnostic cancer detection from human tissues using direct mass spectrometry technologies**; Jacob I Mardick[1]; Manoj Kumar[1]; Robert Tibshirani[2]; Livia S. Eberlin[1]; *[1]Department of Surgery, Baylor College of Medicine, Houston, TX; [2]Departments of Biomedical Data Sciences and Statistics, Stanford University, Stanford, CA*

WP 445 **MINT: an open-source data analysis software for large-scale metabolomics studies**; Mario E. Valdés-Tresanco[1]; Mario S. Valdés-Tresanco[2]; Ryan A Groves[1]; Nicholas Brodie[1]; Luis F. Ponce[1]; Raied Aburashed[1]; Annegret Ulke-Lemee[1]; Ian A. Lewis[1]; *[1]University of Calgary, Calgary, AB; [2]University of Medellin, Medellin, Colombia*

WP 446 **MetaboGraph: A Framework for Metabolomics and Lipidomics Annotation and Pathway Network Analysis**; Hira Tasqeen[1]; Oluwatosin Daramola[1]; Judith Nwaiwu[1]; Odunayo Oluokun[1]; Mojibola Fowowe[1]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock,, TX*

WP 447 **MSLipidMapper: a lipidomics data mining environment facilitating statistics, pathway, and multiomics analyses**; Takaki Oka[1]; Kozo Nishida[2]; Hiroshi Tsugawa[3]; *[1]Tokyo university of agriculture and technology, Koganei, Japan; [2]RIKEN Center for Biosystems Dynamics Research, Kobe, Japan; [3]Tokyo University of Agriculture and Technology, Koganei, Japan*

WP 448 **Beyond TIC: Improving Tissue-Level Clustering Using RCLR in Multi-Tissue Untargeted LC–MS Metabolomics from People with HIV**; Celia L Ochoa Medina[1, 2]; Giovana Macedo, PhD[1]; Vanessa Gomez-Moreno[2]; Antoine Chaillon, MD, PhD[2]; Sara Gianella, MD[3]; Dennis D Krutkin[3]; Scott T Kelley, PhD[1]; Davey M Smith, MD, MAS, FACP, FIDSA[2]; Laura-Isobel McCall, PhD[1]; *[1]San Diego State University, San Diego, CA; [2]University of California San Diego, San Diego, CA; [3]University of California San Diego, San Diego*

WP 449 **Mascot DIA introduces probabilistic scoring to spectrum-centric analysis of DIA data**; Ville R Koskinen[1]; Richard J Jacob[1]; Patrick A Emery[1]; *[1]Matrix Science, London, United Kingdom*

WP 450 **Hybrid De Novo Sequencing and Database Searching Reveal Endogenous Peptides in Cancer borealis and Callinectes sapidus**; Jiangrong Qin[1, 2]; Lauren Fields[3]; Angel Ibarra[3]; Tong Gao[3]; Tina Dang[4]; Haiyan Lu[4]; Lingjun Li[3, 4, 5, 6]; *[1]Department of Mathematics, University of Wisconsin-Madison, Madison, WI; [2]Department of Statistics, University of Wisconsin-Madison, Madison, WI; [3]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; <su*

WP 451 **Frequency-Based Analysis Reveals Pain-Associated Changes in Neuropeptides**; Elena V Romanova[1]; Xaylie Gray[1]; Jonathan V Sweedler[1]; *[1]University of Illinois at Urbana-Champaign, Urbana, IL*

WP 452 **A de novo sequencing approach enables tumor-wide immunopeptidomic profiling and comprehensive discovery of neoantigens from diverse origins**; Ngoc Hieu Tran[1]; Wenting Li[1]; Kyle Hoffman[1]; Ailee Aihemaiti[1]; Jinghang Zhu[2]; Heng Zhang[2]; Bin Wang[2]; Palaniraja Thandapani[3]; Ming Li[4]; Lei Xin[1]; Baozhen Shan[1]; *[1]Bioinformatics Solutions Inc, Waterloo, ON; [2]BaizhenBio Inc., Wuhan, China; [3]The University of Texas MD Anderson Cancer Center, Houston, TX; [4]University of Waterloo, Waterloo, ON*

WP 453 **Fantastic Mods and How To Find Them: Leveraging Multi-Modification Comet Search for Pooled Screening of Electrophile Libraries**; Kean Hean Ooi[1]; Jimmy K. Eng[2]; Julian Mintseris[3]; Edward L. Huttlin[3]; Ramin Rad[3]; Steven R Shuken[3]; Ka Yang[3]; Joao A Paulo[3]; Steven Gygi[3]; *[1]Harvard University, Boston, MA; [2]University of Washington, Seattle, WA; [3]Harvard Medical School, Boston, MA*

WP 454 **Generalizable Supervised Learning for Spectral Library Searching Rescoring Eliminates Per-Search Model Training**; Hao Xu[1]; Nuno Bandeira[1]; *[1]University of California San Diego, San Diego, CA*

WP 455 **Direct open modification search for data-independent acquisition data**; Fengchao Yu[1]; Daniel A. Polasky[1]; Alexey I. Nesvizhskii[1]; *[1]University of Michigan, Ann Arbor, MI*

WP 456 **QuaVaPeptidePicker: Automated Variant Peptide Selection for Absolute Quantitative Mass Spectrometry**; Constantinos Blidjios[1]; Yassene Mohammed[2, 3, 4]; Pallab Bhowmick[2]; Vincent R. Richard[2]; Christoph H. Borchers[2, 4, 5, 6]; *[1]Segal Cancer Proteomics Center, McGill University, Montreal, QC; [2]Segal Cancer Proteomics Centre, Lady Davis Institute for Medical Research, McGill University, Montreal, QC; [3]Leiden University Medical Center, Leiden, Neth*

WP 457 **FastSpel: A peptide spectrum predictor with deep learning-level performance at a fraction of the computational cost**; Mehdi Bagheri Hamaneh[1]; Yi-Kuo Yu[2]; *[1]Division of Intramural Research, National Library of Medicine, National Institutes of Health, Bethesda; [2]Division of Intramural Research, National Library of Medicine, National Institutes of Health, Bethesda, MD*

WP 458 **Spectral Cruncher: A Visualization Tool Integrating Manual Curation, Ion-Intensity Prediction, and De Novo Tag Generation**; Aline A. M. Martins[1]; Blake L Tsu[2]; Hulyana Brum[3]; Lucas A Sales[3]; Marlon Dias Mariano dos Santos[3]; Juliana de S. da G. Fischer[1]; Stephanie Almeida[1]; Luisa Bulcao Vieira Coelho[1]; Natalia Moreira[1]; Alysson R. Muotri[1]; Paulo C Carvalho[1, 3]; *[1]Integrated Space Stem Cell Orbital Research Center, La Jolla, CA; [2]UCSD, La Jolla, CA; [3]Laboratory for Structural and Computational Proteomics, Carlos Chagas Institute, Fiocruz, Fiocruz, Brazil*

WP 459 **ProteoPRM: An Automated GUI Tool for the Analysis and Quantification of Parallel Reaction Monitoring Proteomics Data**; Mojibola O Fowowe[1]; Sherifdeen Onigbinde[1]; Oluwatosin Daramola[1]; Moyinoluwa Adeniyi[1]; Vishal Sandilya[1]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX*

WP 460 **Extending Casanovo functionality to timsTOF data**; Bhavyahshree Navaneetha Krishnan[1]; Michael Dammann[2]; Sander Willems[3]; Fabian J. Theis[2]; Wout Bittremieux[4]; George Rosenberger[5]; William S Noble[1]; *[1]University of Washington, Seattle, WA; [2]Helmholtz Munich, Neuherberg, Germany; [3]Bruker, Kontich, Belgium; [4]University of Antwerp, Antwerpen, Belgium; [5]Bruker Switzerland AG, Fällanden, Switzerland*

WP 461 **Quetzal: Comprehensive Peptide Fragmentation Annotation and Visualization**; Luis Mendoza[1]; Robert L. Moritz[1]; Eric W. Deutsch[1]; *[1]Institute For Systems Biology, Seattle, WA*

WP 462 **SpectraLens: Interactive, model-based inspection of DIA precursor evidence**; Hojin Yoo[1]; Beomjun Park[1]; Moonjong Shin[1]; Namgil Lee[2]; Heejung Yang[2]; *[1]Bionsight Inc, Chuncheon-si, South Korea; [2]Kangwon National University, Chun Cheon, South Korea*

WP 463 **Spectrum-centric searches with data-matched predicted spectral libraries and Wildcard PTMs**; Florian Seefried[1]; Patroklos Samaras[1]; Michael Graber[1]; Markus Schneider[1]; Samia Ben Fredj[1]; Lizi Mamisashvili[1]; Michelle Tamara Berger[1]; Alexander Hogrebe[2]; Daniel P Zolg[1]; Siegfried Gessulat[2]; Tobias Schmidt[1]; Martin Heinrich Frejno[1]; *[1]MSAID, Garching b.München, Germany; [2]MSAID, Berlin, Germany*

WP 464 **Mascot DIA enables direct comparison of DDA and DIA identification and quantitation results**; Patrick Emery[1]; Richard J Jacob[1]; Ville R Koskinen[1]; *[1]Matrix Science, London, United Kingdom*

WP 465 **Leveraging Insights on Experimental Heterogeneity for Charge State Prediction Generalisation Using a Transformer-based Model**; Ayla Schröder[1]; Omar Shouman[1]; Joel Lapin[1]; Mathias Wilhelm[1, 2]; *[1]Technical University Munich, Freising, Germany; [2]Munich Data Science Institute (MDSI), Technical University of Munich, Garching, Germany*

WP 466 **Characterizing Failure Modes in Label-free Quantification at the Peptide-Level in Data Dependent Acquisition**; Manish Sampath[1]; Nuno Bandeira[1, 2, 3]; *[1]Department of Computer Science and Engineering, University of California San Diego, La Jolla, CA; [2]Center for Computational Mass Spectrometry, La Jolla, CA; [3]Skaggs School of Pharmacy and Pharmaceutical Sciences, Universi*

WP 467 **Improved discovery and quantification of post-translational modifications in single-cell proteomics**; Alexander Solivais[1]; Madeleine Hastings[2]; Lloyd M Smith[2]; *[1]University of Wisconsin-Madison, Chemistry, Madison, WI; [2]University of Wisconsin-Madison Department of Chemistry, Madison, WI*

WP 468 **Peptacular: A ProForma 2.1 Compliant Python Package for Amino Acid Sequence Analysis**; Patrick T Garrett[1]; Titus Jung[1]; John R. Yates III[1]; *[1]Scripps Research Institute, La Jolla, CA*

WP 469 **Towards Real-Time Search For Immunopeptidomics**; Katrina N Peterson[1]; Michael R Hoopmann[1]; Christopher D McGann[1]; Devin K. Schweppe[1]; *[1]Department of Genome Sciences, University of Washington, Seattle, WA*

WP 470 **Timsbuktoolkit Viewer: On-Demand Visualization of Peptide Signals in timsTOF DIA Data**; J. Sebastian Paez[1]; Bo Wen[2]; Evan E Hubbard[1]; Michael J. MacCoss[2]; William S Noble[2, 3]; Alexander J Federation[1]; Lindsay K Pino[1]; William E Fondrie[1]; *[1]Talus Bioscience, Seattle, WA; [2]Department of Genome Sciences, University of Washington, Seattle, WA; [3]Paul G. Allen School of Computer Science and Engineering, University of Washington, Seattle, WA*

WP 471 **Strategies to improve TMT reporter signal in SPS-MS3-based quantitative proteomics**; Zixuan Ye[1]; Fangyi Zhai[2]; Shaoxian Li[2]; Daniel Richards[2]; Qing Yu[2]; *[1]Umass Chan Medical School, Worcester, MA; [2]UMass Chan Medical School, Worcester, MA*

WP 472 **Analysis of Targeted TMT Peptide Panels using the Proteome Discoverer platform**; Kai Fritzemeier[1]; David Horn[2]; Philip Loziuk[2]; Frank Berg[1]; Carmen Paschke[1]; Waqas Nasir[1]; Pedro Navarro[1]; Christoph Henrich[1]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientific, San Jose, CA*

WP 473 **Exploring the potential of data analysis in the cloud to enable large-scale proteomics experiments**; Grzegorz Skoraczyński[1]; Oliver M. Bernhardt[1]; Monika Pepelnjak[1]; Polina Shichkova[1]; Yuehan Feng[1]; Damiano Robbiani[1]; Eduardo Yago Vicent[1]; Tejas Gandhi[1]; *[1]Biognosys AG, Schlieren, Switzerland*

WP 474 **An open source search engine for both DDA and DIA proteomics**; Bo Wen[1]; Chris Hsu[1]; Uri Keich[2]; Michael J. MacCoss[1]; William S. Noble[1, 3]; [1]*Department of Genome Sciences, University of Washington, Seattle, WA;* [2]*School of Mathematics and Statistics, University of Sydney, Sydney, Australia;* [3]*Paul G. Allen School of Computer Science and Engineering, University o*

WP 475 **Enhanced Twister: Gaining and Profiting from a Deeper Understanding of the Data**; Kira Vyatkina; *Sechenov University, Moscow, Russian Federation; Saint Petersburg State University, St Petersburg, Russia; Saint Petersburg Electrotechnical University "LETI", St Petersburg, Russia*

WP 476 **Peptide-3D Mapper: A Multi-Functional Tool for Quantitative Analysis and Visualization of Proteins, Peptides and PTMs onto 3D Protein Structures**; Deeptarup Biswas[1, 2]; Raagasahithi Yarrabadi[2]; Jason Saturno[2]; Hanno Steen[1, 2]; Judith Steen[1, 2]; [1]*Harvard Medical School, Boston, MA;* [2]*Boston children's hospital, Boston, MA*

WP 477 **SageDIA: Peak Shape and Fragment Co-elution Scoring for Enhanced DIA Proteomics**; Robin Park[1]; Tao Xu[2]; Titus Jung[3]; Clarice Park[2]; Vijayaraja Gnanasambandan[2]; Ajay Bharadwaj[4]; Niveda Sundararaman[4]; Hokeun Kim[5]; Sang-Won Lee[5]; Jennifer E. Van Eyk[4]; John R. Yates III[6]; [1]*Chapparal Labs, San Diego, CA;* [2]*Chaparral Labs, Inc., San Diego, CA;* [3]*Scripps Research Institute, La Jolla, CA;* [4]*Cedars-Sinai Medical Center, LA;* [5]*Korea University, Seoul, South Korea;* [6]*Sc*

WP 478 **An RNA-Informed Proteogenomic Workflow for High-Confidence Identification of Infection-Associated Peptides**; Shanji Zhang[1]; Seunghyuk Choi[2]; Eunok Paek[3]; [1]*Hanyang university, Seoul, South Korea;* [2]*kookmin university, Seoul, South Korea;* [3]*Hanyang University, Seoul, South Korea*

WP 479 **Dynamic Search Space Expansion for Comprehensive DIA Proteomics Using SynapSpec™**; Hojin Yoo[1]; Beomjun Park[1]; Moonjong Shin[1]; Namgil Lee[2]; Heejung Yang[2]; [1]*Bionsight Inc, Chuncheon-si, South Korea;* [2]*Kangwon National University, Chun Cheon, South Korea*

WP 480 **Deep Untargeted Lipidomics with Iterative Library Expansion Enables High-Depth, High-Confidence Profiling of Age-Related Brain Lipidome Changes**; Jian Guo[1]; Catherine Heffner[1]; Gilbert Di Paolo[1]; Sonnet Davis[1]; Jung Suh[1]; [1]*Denali Therapeutics, South San Francisco, CA*

WP 481 **Integrating Plasma–Liver–Adipose Lipidomics to Elucidate the Roles of Adipocyte Lipases in MASLD Progression**; Xiang Tian[1]; Erik L Allman[1]; Sonja Hess[1]; Xiao-Rong Peng[1]; Pierre-Damien Denechaud[2]; Dominique Langin[2]; [1]*AstraZeneca, Gaithersburg, MD;* [2]*University de Toulouse, Toulouse, France*

WP 482 **Untargeted UHPLC-HRMS lipidomics reveals lipid class differences between diapause-destined and non-diapause prepupae in the solitary bee Megachile rotundata**; Nilay Saha[1]; Banani Mondal[1]; John Larson[1]; George Yocum[2]; Joseph Rinehart[2]; Rikki Walter[3]; Kendra Greenlee[3]; Franco Basile[1]; [1]*University of Wyoming, Laramie, WY;* [2]*USDA-ARS, Fargo, ND;* [3]*North Dakota State University, Fargo, ND*

WP 483 **The Trans Fat Integrated Hepatic Lipidome**; Jiahao Zhang[1, 2]; Hua Zhang[2]; Shuling Xu[2]; Allen Zhao[2, 3]; Feixuan Wu[2]; Gaoyuan Lu[2]; Judith A. Simcox[3]; Lingjun Li[1, 2, 4]; [1]*Biophysics Program, University of Wisconsin-Madison, Madison, WI;* [2]*School of Pharmacy, University of Wisconsin-Madison, Madison, WI;* [3]*Department of Biochemistry, University of Wisconsin-Madison, Madison, WI;* [4]*D*

WP 484 **mzmine-enabled comparison of DDA and DIA lipidomics on a multi-reflecting time-of-flight mass spectrometer**; Ansgar Korf[1]; Robin Schmid[1]; Steffen Heuckeroth[1]; Lee A. Gethings[2]; Nyasha Munjoma[2]; David Deans[2]; David Heywood[2]; Tomáš Pluskal[1, 3]; [1]*mzio GmbH, Bremen, Germany;* [2]*Waters Corporation, Wilmslow, United Kingdom;* [3]*Institute of Organic Chemistry and Biochemistry of the CAS, Prague, Czech Republic*

WP 485 **A high-coverage workflow for comprehensive profiling of brain sphingolipidomes**; Haiyue Hou[1]; Weishen Zhou[1]; Zhixu Ni[2]; Yu Xia[1]; [1]*Tsinghua University, Beijing, China;* [2]*Tsinghua Shenzhen International Graduate School, Shenzhen, China*

WP 486 **When Motherhood Meets Mass Spectrometry: Multimodal, Isomer-Resolved Lipidomics Reveals Pregnancy and Caregiving Effects in the Alzheimer's Brain**; Caitlin Randolph[1]; Katherine A. Walker[1]; Christina Ferreira[1]; Shane Tichy[2]; Gaurav Chopra[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN; [2]Agilent Technologies, Santa Clara, CA*

WP 487 **Automated Cyclic Ion mobility–Mass Spectrometry MS/MS Workflow and Data Analysis for Shotgun Lipidomics**; Ballal Hossen[1]; Nyasha C Munjoma[2]; Emma Marsden-Edwards[2]; Johannes PC Vissers[2]; Dominik Schwudke[1, 3, 4]; Susan Slade[2]; *[1]Division of Bioanalytical Chemistry, Research Center Borstel - Leibniz Lung Center, Borstel, Germany, Borstel, Germany; [2]Waters Corporation, Wilmslow, United Kingdom; [3]German Center for Infection Research, Thematic Trans*

WP 488 **Simultaneous Analysis of Glycerophospholipids and Eicosanoids in Neutrophils by LC-UVPD-MS**; Andrew Pritchard[1]; Melanie Campbell[1]; Jennifer Brodbelt[1]; *[1]University of Texas - Austin, Austin, TX*

WP 489 **Evaluating the Effects of Viral Sensitizers on the Lipid Dynamics of Lentiviral Vector Production**; Jocelyn Menard[1]; Karlye EA Rudd[2]; Christopher N Boddy[3]; Jean-Simon Diallo[4]; Jeffrey C Smith[2, 5]; *[1]Carleton University, Ottawa, ON; [2]Department of Chemistry, Carleton University, Ottawa, ON; [3]Department of Chemistry and Biomolecular Sciences, University of Ottawa, Ottawa, ON; [4]Ottawa Hospital Research Instit*

WP 490 **Lipidomic Profiling of Mesenchymal Stromal Cell Conditioned Medium as an In-Process, Non-Destructive Approach to Assess Extracellular Vesicle Quality**; Yu-Ting Tseng[1]; Thomas Spoerer[1]; Ross Marklein[1]; Kelly M. Hines[1]; *[1]University of Georgia, Athens, GA*

WP 491 **Linking Inter-Individual and Single-Cell Lipid Variability via LC-MS Lipidomics and High-Throughput MALDI Imaging of ~10,000 Healthy and Trisomy 21 Cells**; Wenxue Li[1, 2]; Shuo Qian[1, 2]; Duo Zhang[1]; Tingting Li[1, 2]; Barbora Salovska[1, 2]; Yansheng Liu[1, 2, 3]; *[1]Cancer Biology Institute, Yale University School of Medicine, Yale University, West Haven, CT; [2]Department of Pharmacology, Yale University School of Medicine, Yale University, New Haven, CT; [3]Department of Biomedical Inf*

WP 492 **Enhancing our understanding of viroceuticals using an optimized mass spectrometry-based lipidomics approach**; Jocelyn A. Menard[1]; Tilia Zinnecker[2]; Joshua Roberts[1]; Elena Godbout[3]; Rozanne Arulanandam[3]; Andrew Chen[3]; Anne Landry[3]; Christopher N Boddy[4]; Udo Reichl[2]; Jean-Simon Diallo[3]; Yvonne Genzel[2]; Jeffrey C. Smith[1, 5]; *[1]Carleton University, Ottawa, ON; [2]Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany; [3]Ottawa Hospital Research Institute, Ottawa, ON; [4]University of Ottawa, Ottawa, ON; [5</]*

WP 493 **A Canine Lipidome-Inspired Framework for PFAS-like Chemical Repellency from Acute Toxin Exposure**; Jana M Carpenter[1, 2]; Ann Kulisiewicz[2]; Lauren Babb[2]; Shawn Stevenson[2]; *[1]Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN; [2]DEVCOM Chemical Biological Center, Aberdeen Proving Ground, MD*

WP 494 **Identifying the Effect of Fasting on Serum Lipidomic Alterations in Biological Pathways Using LC-MS/MS**; Zitu Barman[1]; MD MOSTOFA AL AMIN BHUIYAN[1]; Waziha Tasnim Purba[1]; Oluwatosin Daramola[1]; Haneen S. Dwaib[2]; Ahmed F. El-Yazbi[1, 3, 4]; Yehia Mechref[1]; *[1]Department of Chemistry and Biochemistry, Texas Tech University, Lubbock, TX; [2]Clinical Nutrition Department, Palestine Ahliya University, Bethlehem, Palestine; [3]Department of Pharmacology and Toxicology, Faculty of Pharm*

WP 495 **Untargeted Lipidomic Profiling of Highly Electronegative HDL Reveals Accumulation of Bioactive Lipid Species**; Ming-Hsien Tsai[1]; Hung-Ting Liao[1]; Yun Fan[1]; Wen-Li Hsu[2]; Chu-Huang Chen[3]; *[1]Health Resource Technology, LLC, Kaohsiung City, Taiwan; [2]National Health Research Institutes, Zhunan, Taiwan; [3]The Texas Heart Institute at Baylor College of Medicine, Houston, TX*

WP 496 **A RPLC–HRMS method for identification and quantitation of oxidized lipid profile in aging individuals**; Jie Xu[1]; Nan Meng[1]; Yanjun Liu[1]; Changhu Xue[1]; *[1]Ocean University of China, Qingdao, China*

WP 497 **Untargeted Lipidomic Profiling of Immune Responses to COVID-19 Vaccination in Immunocompromised Individuals**; Dande Aishwarya[1]; Nikhil Pallaprolu[2]; Ramalingam Peraman[2];

[1]NIPER HAJIPUR, Hajipur, India; [2]National Institute of Pharmaceutical Education and Research Hajipur, Hajipur, India

WP 498 **Comprehensive lipid profiling of plant extracts by SFC-HRMS and HPLC-HRMS to analyze stress response**; Maja Kreuznacht[1]; Mayuko Naganawa[2]; Lea Preuß[2]; Till Ischebeck[2]; Heiko Hayen[1]; *[1]Institute of Inorganic and Analytical Chemistry, University of Münster, Münster, Germany; [2]Institute for Plant Biology and Biotechnology, University of Münster, Münster, Germany*

WP 499 **Comparison of the Lipid Composition in Alternative Skin Models and Excised Human Skin using LC/HRMS-based Lipidomics**; Jinchun Sun[1]; Sadegh Modaresi[1]; Alec T. Salminen[1]; Kelly J. Davis[1]; Robert P. Felton[1]; MacKean Maisha[1]; Richard Beger[1]; Luísa Camacho[1]; *[1]NCTR / USFDA, Jefferson, AR*

WP 500 **Impact of Lipid Extraction Protocols on Lipid Class Detection and Profiling Analysis in Bovine Skeletal Muscle**; Nicole Tucci[1]; Rebeca Soares Nogueira[1]; Juliana Akamine Torrecilhas[2]; Ryan T Hilger[3]; Rogerio Abdallah Curi[4]; Luis Artur Chardulo[2, 4]; Christina Ferreira[5]; Guilherme Luis Pereira[1, 4]; *[1]College of Agricultural Sciences, São Paulo State University (UNESP), Botucatu, Brazil; [2]College of Veterinary and Animal Science, São Paulo State University (UNESP), Botucatu, Brazil; [3]Purdue University, Department of Ch*

WP 501 **LC-SICRIT-MSMS Method for Double-Bond Placement and MSn Structure Elucidation of Unsaturated Lipids**; Ciara Conway[1, 2]; Markus Weber[1]; Jan-Christoph Wolf[1]; Christoph Haisch[3]; *[1]Plasmion, Augsburg, Germany; [2]Technical Universitiy of Munich, Freising, Germany; [3]Technical University of Munich, Freising, Germany*

WP 502 **Targeted data mining strategies of PASEF data for in-depth lipid and glycolipid markers identification in Parkinson's Disease**; Huong Giang Vo[1]; Dhanwin Baker[1]; Nikolas Kessler[2]; Mathew Lewis[3]; Sven W. Meyer[2]; Laura Bindila[1]; *[1]Univ Medical Center of the JGU Uni Mainz, Mainz, Germany; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [3]Bruker Daltonics GmbH & Co. KG, Greater London, United Kingdom*

WP 503 **Neural aging drives coordinated lipid reprogramming in the central nervous system**; Jazmyn Miro[1]; Fernanda Sousa Monteiro[1, 2]; Petra Hermann[1]; Willem Carel Wildering[1]; Adriana Zardini Buzatto[1, 2, 3]; *[1]University of Calgary, Calgary, AB; [2]Calgary Metabolomics Research Facility (CMRF), Calgary, AB; [3]Alberta Centre for Advanced Diagnostics (ACAD), Calgary, AB*

WP 504 **Lipid Insight Unblocked: Combining Nontargeted LC/MS Chemometrics With Automated Lipid Annotation**; Mark Sartain[1]; Emma E. Rennie[1]; Sarah M. Stow[1]; Julie Horner-Buxton[1]; Jeremy P. Koelmel[2, 3]; *[1]Agilent Technologies, Santa Clara, CA; [2]Yale University, West Haven, CT; [3]Innovative Omics, Sarasota, FL*

WP 505 **Untargeted LC-MS Lipidomics Analysis of Optic Nerve Regeneration in Xenopus laevis**; Isabella Moceri[1]; Ava J. Udvadia[2]; Fiona L. Watson[3]; Sanjoy K Bhattacharya[1]; *[1]Bascom Palmer Eye Institute, Miller School of Medicine, University of Miami, Miami, FL, USA, Miami, FL; [2]Appalachian State University, Boone, NC; [3]Washington and Lee University, Lexington, VA*

WP 506 **A Spatiotemporal Lipidome Atlas to Decode Human Brain Aging**; Zhijun Zhu[1]; Alina Isakova[1]; Monther Abu-Remaileh[1]; *[1]Stanford University, Stanford, CA*

WP 507 **ZT Scan DIA Enhances Plasma Lipidomics Coverage and Quantitative Reproducibility**; Pradeep Narayanaswamy[1]; Hieu Cuong Le[2]; Anjali Chelur[3]; Eva Duchoslav[4]; *[1]Sciex, Singapore, Singapore; [2]Associate Research Scientist, Sciex, Concord, ON; [3]Associate Staff Research Scientist, Sciex, Concord, ON; [4]Senior Staff Research Scientist, Concord, ON*

WP 508 **From sea to cell: In-vitro anticancer screening and metabolomics profiling of Sargassum wightii Grevilleagainst breast cancer**; H M CHANDRA MOULI[1]; Preethi K Raman[1]; Nivedita Singh[2]; Ezhilmathe A[1]; Raghuveer Varma Pemmadi[3]; Hara Prasad Padhy[1]; Rahul Laxman Gajbhiye[4]; Anupam Jana[4]; Chandraiah Godugu[1]; Gananadhamu Samanthula[1]; *[1]NIPER Hyderabad, Hyderabad, India;*

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WP 509 **Metabolome of Aging Rat Brain and Its Correlation with Cognitive Performance**; Haiyi Yi[1]; Jo Aan Goon[1]; Suzana Makpol[1]; Jen Kit Tan[1]; *[1]Department of Biochemistry, Faculty of Medicine, Universiti Kebangsaan Malaysia (UKM), Kuala Lumpur, Malaysia*

WP 510 **OPTIMIZED ION-PAIRED CHROMATOGRAPHY TOWARDS POLAR METABOLOMICS**; Anna R. Tarach[1]; Abigail E. Ellis[2]; Megan R. Gendjar[2]; Nathan Lanning[3]; Amber Ide[3]; Stephanie Grainger[3]; Amy A. Caudy[4]; Ryan D. Sheldon[1]; *[1]Mass Spectrometry Core, Van Andel Institute, Grand Rapids, MI; [2]Van Andel Institute, Grand Rapids, MI; [3]Department of Cell Biology, Van Andel Institute, Grand Rapids, MI; [4]Caudy Bioanalytical Advisory, Indianap*

WP 511 **Brewed Awakenings – food metabolome analysis comparing high flow to low flow LC-MS**; Surbhi Gupta[1]; Huaxu Yu[1]; Tong Shen[1]; Luis Valdivez[1]; Uri Keshet[1]; Oliver Fiehn[1]; *[1]University of California Davis, Davis, CA*

WP 512 **Integrated Metabolomics and Volatilomics Combined with 18S rRNA Sequencing Reveal Strain-Specific Metabolic Phenotypes of Food-Derived Yeasts**; Noeul Song[1]; Jeonghyun Yun[1]; Sunhee Kang[1]; Hyunsol Cho[1]; Jang-Eun Lee[1]; *[1]Korea Food Research Institute, Iseo-myeon, South Korea*

WP 513 **Derivatization of Carboxyl-Containing Metabolites Enhances Specificity and Sensitivity Using Liquid Chromatography–Trapped Ion Mobility Spectrometry–Mass Spectrometry**; Alan K. Jarmusch[1]; Kaylie I. Kirkwood-Donelson[1]; *[1]National Institute of Environmental Health Sciences, National Institutes of Health, Research Triangle Park, NC*

WP 514 **Isobaric Peptide-Tag Strategy for LC–MS Characterization of Structurally Diverse Metabolites**; Martha Ortega Zepeda[1]; Stephanee Joy B Zerrudo[1]; Abraham Badu-Tawiah[1]; *[1]The Ohio State University, Columbus, OH*

WP 515 **Impact of LC solvent composition on the ionization of 300+ different metabolites by Heated ESI, SICRIT and microflow ESI**; Atsuhiko Toyama; *Shimadzu R&D Center Boston, Newton, MA*

WP 516 **Underivatized Amino Acid Profiling in Fermentation Samples with Novel High- Resolution Mass Spectrometry Platform with Bio-Compatible Column and LC**; Rachel A. McAllister[1]; Sierra D. Durham[1]; Cathyrin Simmermaker[1]; Olivier P. Chevallier[1]; Andre Szczesniewski[2]; *[1]Agilent Technologies, Santa Clara, CA; [2]Agilent Technlogies, Wood Dale, IL*

WP 517 **Incorporating Unlabeled and Stable Isotope-Labeled Bile Acid Mixtures to Automate Quantitative and Quality Control Phases of HRMS Metabolomics**; Andrew J. Percy[1]; James Campbell[2]; J. Michael Ramsey[2]; J. Scott Mellors[2]; J. Will Thompson[2]; *[1]Cambridge Isotope Laboratories, Inc., Tewksbury, MA; [2]Move Analytical LLC, Carrboro, NC*

WP 518 **Spatial and Bulk Metabolomics of Lung Squamous Cell Carcinoma Reveals Redox- and Inflammation-Associated Small-Molecule Signatures**; Vanessa Y. Rubio[1]; Ashley Lui[1]; Isis Narváez-Bandera[1]; Yonatan Ayalew Mekonnen[1]; Guohui Li[1]; Min Liu[1]; Eric Haura[1]; Gina DeNicola[1]; Elsa Flores[1]; John M. Koomen[1]; Paul Stewart[2]; *[1]Moffitt Cancer Center, Tampa, FL; [2]Huntsman Cancer Institute, University of Utah, Salt Lake City, UT*

WP 519 **A hybrid workflow combining targeted and untargeted metabolomics enabled by biocrates' MxQuant kit on timsMetabo LC-TIMS-HRMS**; Aiko Barsch[1]; Cristian De Gobba[2]; Tuan Hai Pham[3]; Guido Dallmann[3]; Matthew R. Lewis[4]; *[1]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [2]Bruker Nordic Denmark, Filial of Bruker Nordic AB, Copenhagen, Denmark; [3]Biocrates Life Sciences GmbH, Innsbruck, Austria; [4]Bruker UK Ltd., Coventry, United Kin*

WP 520 **MetabolomicsHub: International Data Exchange and Data Representation Standards for Metabolomics**; Ozgur Yurekten[1]; Thomas Payne[1]; Jonathan Hunter[1]; Naveen Raj Kookkal Polliapram[1]; Callum Martin[1]; Eoin Fahy[2]; Mano Maurya[2]; Srinivasan Ramachandran[2]; Brian C. DeFelice[3]; Carlos G.

Gonzalez[3]; Joshua E. Elias[3]; Nils Hoffmann[4]; Yasin El Abiead[5, 6]; Pieter C. Dorrestein[5]; Shankar Subramaniam[2]; Juan Antonio Vizcaino[1]; *[1]European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, Hinxton, United Kingdom; [2]Department of Bioengineering, and San Diego Supercomputer Center, University of California, San D*

WP 521 **Untargeted Metabolomic and Genomic Insights into Bacterial Endophyte-Mediated Suppression ofNeopestalotiopsisdiseasein Strawberry**; Chengyu Gao[1]; Stephen W. Muhindi[2]; Shin-Yi L. Marzano[2, 3]; *[1]Campus Chemical Instrument Center, The Ohio State University, Columbus, OH; [2]Application Technology Research Unit, U.S. Department of Agriculture, Toledo, OH; [3]Ohio Controlled Environment Agriculture Center, The Ohio Stat*

WP 522 **Improving confidence in surrogate internal standards-based normalization in single-replicate experiments**; Olivia Taverniti[1]; Andrew T. Quaile[1]; J. Rafael Montenegro-Burke[1]; *[1]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON*

WP 523 **LC-MS platform for metabolic epidemiology: Opening the door to large cohort studies via harmonized sample preparation, sample processing, data analysis**; Ian Lewis; *University of Calgary, Calgary, AB*

WP 524 **Repository scale semi-automated adduct annotation**; Yourae Shin[1]; Michael Strobel[1]; Yasin El Abiead[2]; Kambria Phillips[1]; Stilianos Papadopoulos Lambidis[3]; Daniel Petras[4]; Mingxun Wang[1]; *[1]University of California, Riverside, Riverside, CA; [2]University of Natural Resources and Life Sciences Vienna, Department of Chemistry, Institute of Analytical Chemistry, Vienna, Austria; [3]Max Planck Institute for Biology*

WP 525 **Direct Characterization of B6 Vitamers in PLP-Dependent Transaminase**; Michael Xiao[1]; Owen S. Skinner[1]; *[1]Northeastern University, Boston, MA*

WP 526 **Evaluation of probe electrospray ionization-mass spectrometry for the analysis of in vitro enzyme reaction system**; Nobuyuki Okahashi[1]; Takeo Taniguchi[1]; Takuma Suzuki[1]; Takanari Hattori[2]; Hidenori Takahashi[2]; Kohsuke Honda[1]; Fumio Matsuda[1]; *[1]The University of Osaka, Suita, Japan; [2]Shimadzu Corporation, Kyoto, Japan*

WP 527 **A method for comprehensive ceramide profiling using SFC/MS/MS**; Noriyuki Tomiyasu[1]; Yuki Taya[1]; Yusuke Aratsu[1]; Yukihiro Nomura[1]; *[1]Shionogi & Co., Ltd., Osaka, Japan*

WP 528 **Development of an On-Line Two-Dimensional Chemical Isotope Labeling (CIL) LC–MS Platform for Comprehensive Metabolomic Profiling**; Xian Luo[1]; Liang Li[2]; *[1]The Metabolomics Innovation Centre, Edmonton, AB; [2]Department of Chemistry, University of Alberta, Edmonton, AB*

WP 529 **Creation of a LC-MS/MS Method for 2'-O-Methyladenosine and Isomers from Dried Urine Strips**; Jazmin Gutierrez-Hernandez[1]; Alan K. Jarmusch[1]; *[1]National Institute of Environmental Health Sciences, National Institutes of Health, Research Triangle Park, NC*

WP 530 **Systematic Cross-Site, Cross-Vendor MS Optimization to Maximize Biologically Relevant Metabolite Detection in Limited-input Samples**; Sahil Sharma[1]; Ira Gray[2]; Anthony Goering[1]; Josh Elias[2]; Brian DeFelice[2]; Ryan McClure[1]; *[1]Biohub, Chicago, IL; [2]Biohub, San Francisco, CA*

WP 531 **Unveiling the Impact of Cell Sorting Techniques on Metabolic Profiles**; Lidiia Rumiantseva[1, 2]; Oscar Fornas[3, 4]; Eva Julià[3, 4]; Dharshini Raju[2, 5]; Sandrine Schmutz[6]; Lotte Carr[7]; Alessia Zotta[8, 9]; Massimiliano Mazzone[8, 9]; Jochen Lamote[2, 5]; Bart Ghesquiere[1, 10]; *[1]Laboratory of Applied Mass Spectrometry, Department of Cellular and Molecular Medicine, Biomedical Sciences Group, KU Leuven, Leuven, Belgium; [2]VIB-KU Leuven Center for Cancer Biology, Departement of Oncology, Biomedical Sciences Gr*

WP 532 **Laser Microdissection-Enabled Spatial Metabolomics for Cell-Type Resolved Metabolite Profiling**; Isabel Alcazar[1]; Hardik Shah[1, 2]; Leonhard Donle[1]; Maria Francesca Allega[1]; Ernst Lengyel[1]; *[1]Department* *of Obstetrics and Gynecology, Section of Gynecologic Oncology, University of Chicago, Chicago, IL; [2]Metabolomics Platform, Comprehensive Cancer Center, University of Chicago, Chicago, IL*

WP 533 **Investigation of Varietal Classification Method for Coffee Beans Using Aroma Compounds**; Nozomi Maeshima[1]; Yoshihiro Saito[1]; Takehito Sagawa[1]; Samantha Olendorff[2]; Dominika Gruszecka[2]; Manami Kobayashi[1]; *[1]Shimadzu corporation, Kawasaki, Japan; [2]Shimadzu Scientific Instruments, Columbia, MD*

WP 534 **Targeted Analysis of Methionine Cycle Metabolites to Understand Cellular Methylation Potential under Methionine Restriction and Cancer**; Ella Kim[1]; Ajaatshatru Sisodia[1]; Bill Web[1]; Anna Popova[1]; Gary Siuzdak[1]; James Williamson[1]; *[1]Department of Integrative Structural and Computational Biology and Scripps Center for Metabolomics, The Scripps Research Institute, La Jolla, CA*

WP 535 **MetaboLights - Open Data Repository for Metabolomics**; Thomas Payne[1]; Noemi Tejera[1]; Jonathan Hunter[1]; Mark Williams[1]; Ibrahim Karaman[1]; Felix Xavier Amaladoss[1]; Callum Martin[1]; Naveen Raj Kookkal Polliapram[1]; Ozgur Yurekten[1]; Juan Antonio Vizcaino[1]; *[1]EMBL-EBI, Hinxton, United Kingdom*

WP 536 **Fast polarity-switching untargeted metabolite workflow in a short run powered by Orbitrap Tribrid technology**; Sunandini Yedla[1]; Brandon Bills[1]; Rahul R. Deshpande[1]; Bashar Amer[1]; Rafael D Melani[1]; Susan S. Bird[1]; *[1]ThermoFisher Scientific, San Jose, CA*

WP 537 **Integrated multiomics reveals PGC-1α-driven metabolic remodeling in mouse placenta**; Birgitta Ryback[1]; Erica M Forsberg[2]; Amanda L Smythers[3]; Taylor A Covington[3]; Xuejun Peng[4]; *[1]Bruker Scientific LLC, Billerica, MA; [2]Bruker Daltonics, San Jose, CA; [3]Dana-Farber Cancer Institute, Boston, MA; [4]Bruker Scientific LLC, San Jose, CA*

WP 538 **SICRIT® as Complementary Ionization for Untargeted LC–MS Metabolomics**; Katharina Hohenwallner[1]; Christina Brenner[2, 3]; Ciara Conway[1, 4]; Yasin El Abiead[5]; Jan-Christoph Wolf[1]; Gunda Koellensperger[3]; *[1]Plasmion GmbH, Augsburg, Germany; [2]University of Vienna, Vienna Doctoral School in Chemistry (DoSChem), Vienna, Austria; [3]University of Vienna, 1090 Vienna, Austria, Vienna, Austria; [4]Technical University of Mu*

WP 539 **Optimizing non-ion-pairing liquid-chromatography high-resolution accurate-mass spectrometry workflows for polar metabolites in an Academic Core Facility**; John A Haley[1]; Jaedon Sadler[1]; Caroline A Lewis Chidley[1]; *[1]UMass Chan Medical School, Worcester, MA*

WP 540 **Metabolic responses to prolonged fasting areconserved in zebrafish**; Mun-Gu Song[1]; Madelyn M Jackstadt[2]; Kevin Cho[2]; Triston Groff[2]; Leah Shriver[2]; Gary J Patti[2]; *[1]Washington University in St.Louis, Saint Louis, MO; [2]Washington University in St.Louis, St.Louis, MO*

WP 541 **Metabolomic Profiling of Squid Chromatophores Reveals Differential Biochemical Fingerprints across Red, Yellow, and Brown Colors**; Ketki Bagwe; *Northeastern University, Boston, MA*

WP 542 **Deep-coverage single-cell metabolomics enabled by ion mobility-resolved mass cytometry**; Zhengjiang Zhu; *Shanghai Institute of Organic Chemistry, Chinese Academy of Sciences, Shanghai, China*

WP 543 **The Metabolome Atlas of 22 Tissues in Aging Mice Reveals a Switch in Thermogenesis from Brown Fat to Skeletal Muscle**; Min Liu[1]; Jian Ji[2]; Anthony David[1]; Huaxu Yu[1]; Tong Shen[1]; Yuanyue Li[3]; Lydia Yang[1]; Oliver Fiehn[1]; *[1]University of California, Davis, CA; [2]Jiangnan University, Wuxi, China; [3]Zhejiang University, Hangzhou, China*

WP 544 **Large Extracellular Vesicles Carry a Specialized Metabolic Cargo Associated with Breast Cancer Brain Metastasis**; Ayobami O. Oluokun[1]; Mojibola Fowowe[1]; Odunayo O. Oluokun[1]; Waziha Tasnim Purba[1]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX*

WP 545 **Untargeted Metabolomics to Characterize Proteins of Unknown Function in Pathogens**; Daniel J Breiner[1]; Vanessa V. Phelan[1]; [1]*CU Anschutz Skaggs School of Pharmacy and Pharmaceutical Science, Aurora, CO*

WP 546 **Chemical Cartography and Metabolic Elasticity Scoring Reveal Organ-Specific Responses to Trypanosoma cruzi**; Jeffrey Agyapong[1]; Azadeh Nasuhidehnavi[2]; Kayla Poirier[1]; Joseane Godinho[1]; Giovana Macedo[1]; Guilherme MP Carrara[1]; Caitlyn Middleton[1]; Luis Ernst[1]; Ariel Pernela[1]; Godwin Kwakye-Nuako[1]; Jordan Edens[1]; Monica Ness[1, 3]; Jarrod Laro[1, 3]; Laura-Isobel McCall[1]; [1]*Department of Chemistry and Biochemistry, San Diego State University, 92182, San Diego, CA;* [2]*Department of Pharmaceutical Sciences, Binghamton University, 13902, Binghamton, NY;* [3]*Department of Chemistry and Biochemistry,*

WP 547 **Closing the Loop: Operationalizing Untargeted Metabolomics for Actionable Raw Material Insights by Leveraging Artifical Intelligence**; Chong Ou[1]; Francesca Sajedi[1]; Malik Padellan[1]; Bryan Woh[1]; [1]*Regeneron Pharmaceuticals, East Greenbush, NY*

WP 548 **Host metabolic consequences of intracellular infection by members of the ESKAPE pathogens**; Blanca Lorente-Torres[1]; Helena Á. Ferrero[1]; Pablo Castañera[1]; Sergio Fernandez Martinez[1]; Steffen Braekling[2]; Mohamed Elsadig[3]; Eliska Ceznerova[4]; Sonja Klee[2]; Valesca Anschau[5]; Matthew R. Lewis[6]; Volker Behrends[7]; Michal Latek[1]; [1]*Universidad de León, Leon, Spain;* [2]*TOFWERK, Thun, Switzerland;* [3]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [4]*Bruker Switzerland AG, Fällanden, Switzerland;* [5]*Bruker Scientific LLC, Billerica, MA;*

WP 549 **Insight Profiler streamlines analysis of non-targeted metabolomics data from LCMS or direct injection in a single software solution**; Doug Carlton[1]; Emily G Armitage[2]; Alan Barnes[2]; Neil J. Loftus[2]; [1]*Shimadzu Scientific Instruments, Columbia, MD;* [2]*Shimadzu Corporation, Manchester, United Kingdom*

WP 550 **Machine Learning Guided Analysis of Cardiac and Hepatic Metabolic Remodeling in Chronic Trypanosoma cruzi Infection**; Demetrius I Tillery[1]; Godwin Kwakye-Nuako[2]; David J Tweardy[3]; Cristina Poveda[4]; Maria Elena Bottazzi[5]; Peter J Hotez[5]; Kathryn Jones[5]; Laura-Isobel McCall[2]; [1]*Department of Chemistry and Biochemistry, San Diego State University, 92182, San Diego, CA;* [2]*San Diego State University, San Diego, CA;* [3]*Department of Infectious Diseases, Infection Control & Employee Health, Division of*

WP 551 **4D-Metabolomics Profiling of Lung Adenocarcinoma using timsMetabo with complementary separation techniques**; Edward Rudt[1]; Qiuqin Zhou[2]; Tobias Bausbacher[2]; Railmara Pereira Da Silva[2]; Birgitta Ryback[3]; Marc A. Schneider[4, 5]; Ursula Klingmüller[5, 6]; Jeroen Krijgsveld[7, 8]; Stefanie Wernisch[1]; Carsten Hopf[2, 8, 9]; Matthew R. Lewis[10]; [1]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [2]*CeMOS Research and Transfer Center, Mass Spectrometry and Optical Spectroscopy, Technische Hochschule Mannheim, Mannheim, Germany;* [3]*Bruker Scientific LLC, Billerica, MA; <*

WP 552 **Untargeted wound metabolomics by GC-MS: Analysis of obese vs. healthy mice**; Robin Sven Obrist[1]; Sonja Klee[2]; Steffen Braekling[2]; Heiko Neuweger[3]; Ilmari Krebs[3]; Nikolas Kessler[3]; Matthew R. Lewis[3]; Timm Hettich[1]; Yousef Maali[4]; Kristyna Filipova[4]; Maria Luisa Balmer[4]; Stefan Gaugler[1]; [1]*FHNW Muttenz, Muttenz, Switzerland;* [2]*TOFWERK, Thun, Switzerland;* [3]*Bruker Daltonics GmbH & Co KG, Bremen, Germany;* [4]*Institute for Infectious Diseases, University and University Hospital Bern, Bern, Switzerland*

WP 553 **Custom optimization of enhanced dynamic range scan mode to improve metabolome depth and cancer cell-line discrimination in untargeted metabolomics**; Esther Zaal[1]; Demi Rijlaarsdam[1]; Michal Kaczmarek[2]; Christian Klaas[2]; Susan Bird[2]; Celia Berkers[1]; [1]*Utrecht University, Utrecht, Netherlands;* [2]*Thermo Fisher Scientific, Bremen, Germany*

WP 554 **Modernizing Metabolomics: A Rugged and Robust Metabolomics Workflow**; Richard John Robinson[1]; Bradley C. Cochran[1]; Trevor M. Casserly[1]; Brenan Durainayagam[1]; Ray Moran[1]; Janice C. Jones[1]; Josh Wilson[1]; Matthew W. Mitchell[1]; Thomas Houseman[1]; [1]*Metabolon, Durham, NC*

WP 555 **From DDA to ZT Scan: Passing the Torch for High-Fidelity Metabolomics**; Jinal Patel[1]; Gordana Ivosev[1]; Pradeep Narayanaswamy[2]; David Cox[1]; Huini Du[3]; Anjali Chelur[1]; Hieu Cuong Le[1]; Eva Duchoslav[1]; Lyle L Burton[1]; Adam Lau[1]; *[1]SCIEX, Concord, ON; [2]SCIEX, Singapore, Singapore; [3]SCIEX, Redwood City, CA*

WP 556 **Towards High Throughput Ovarian Cancer Lipidomics: Evaluation of a Multi-Reflecting Time-of-Flight LC-MS Platform Using Papanicolaou Tests**; Thomas M. Knehans[1]; Elisabeth M. Schwiebert[1]; Ying Liu[1]; David A. Gaul[1]; Kristin L. M. Boylan[2]; Amy P. N. Skubitz[2]; Facundo M. Fernandez[1]; *[1]Georgia Institute of Technology, Atlanta, GA; [2]University of Minnesota, Minneapolis, MN*

WP 557 **Retrospective Analysis of Existing Metabolomics Data for Identification of Lipid Alterations**; Hailemariam Abrha Assress[1, 2]; Caiden Brigido[1]; Aline Andres[1, 2]; Andrew J Morris[1, 2]; Colin Kay[1, 2]; Renny S. Lan[1, 2]; *[1]Arkansas Children's Nutrition Center, Little Rock, AR; [2]University of Arkansas for Medical Sciences, Little Rock, AR*

WP 558 **MS-Emblator: an ensemble learning model to facilitate metabolite annotation of tandem mass spectra**; Taiki Hirose[1]; Taihei Torigoe[2]; Fumio Matuda[3]; Yoshihiro Izumi[2]; Hiroshi Tugawa[4]; *[1]Tokyo University of Agriculture and Technology, Tokyo, Japan; [2]The University of Osaka, Toyonaka, Japan; [3]The University of Osaka, Suita, Japan; [4]Tokyo University of Agriculture and Technology, Koganei, Japan*

WP 559 **Methods for Expanding the NIST Mass Spectral Library with Highly Relevant Compounds**; Tytus D Mak[1]; Stephen E. Stein[1]; *[1]National Institute of Standards and Technology, Gaithersburg, MD*

WP 560 **Normalization of large-scale analysis of mouse plasma for detection and identification of metabolic signatures**; Peter Sajjakulnukit[1]; Li Zhang[1]; Bretton Badenoch[1]; Richard Miller[1]; Costas A Lyssiotis[1]; *[1]University of Michigan, Ann Arbor, MI*

WP 561 **Having your cake and eating it too: A novel quantitative LC-HRAM bile acids workflow incorporating robust quantitative and discovery capabilities**; J. Will Thompson[1]; Bashar Amer[2]; Susan S. Bird[2]; Andrew J. Percy[3]; James Campbell[1]; Scott Mellors[1]; *[1]Move Analytical LLC, Carrboro, NC; [2]ThermoFisher Scientific, San Jose, CA; [3]Cambridge Isotope Laboratories, Inc., Tewksbury, MA*

WP 562 **Masscube resolves batch retention time differences and multiple ion feature forms of conjugated and non-conjugated hydroxybenzoic acids in urine**; Stephen Barnes[1]; Landon S. Wilson[1]; Huaxu Yu[2]; Shaoyong Su[3]; *[1]University of Alabama at Birmingham, Birmingham, AL; [2]University of California, Davis, CA; [3]Augusta University, Augusta, GA*

WP 563 **Optimization of a Novel Untargeted Metabolomics Method Utilizing High Resolution Mass Spectrometry for Discovery of Novel Placental Transporter Substrates**; Rachel Buckley[1]; Oindrila Paul[1]; Chenghui Jiang[1]; Ill Yang[1]; Lauren Aleksunes[1]; Brian Thomas Buckley[1]; *[1]Rutgers University, Piscataway, NJ*

WP 564 **Combating Ion Suppression in CIL LC-MS: A 2DLC Strategy to Enhance Untargeted Metabolome Profiling Efficiency and Depth**; Sicheng Quan[1]; Shuang Zhao[2]; Liang Li[2]; *[1]The Metabolomics Innovation Centre, Edmonton, AB; [2]University of Alberta, Edmonton, AB*

WP 565 **An Automated Sample Preparation Method for Oligonucleotide Bioanalysis Using Mesoporous Magnetic Beads**; Jenny Zhang[1]; Michael Johnson[2]; Jingran Zhang[3]; *[1]Unified Separation Technologies Inc., Newark, DE; [2]BioQual Solution, San Diego, CA; [3]Agile Bio, Suzhou, JIangsu Province, China*

WP 566 **Advanced Superficially Porous Separations Materials for LC/MS Analyses of Synthetic Oligonucleotides**; Barry Boyes[1]; Joshua K McBee[1]; Peter Pellegrinelli[1]; *[1]Advanced Materials Technology Inc,, Wilmington, DE*

WP 567 **Effect of Solvent and Additives on siRNA Ionization and Duplex Gas-Phase Stability**; Paul Lawer-Yolar[1]; Mushfeqa Iqfath[1]; Anthony T. Murphy[2]; Chris M. Wiethoff[2]; Julia Laskin[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN; [2]Eli Lilly & Company, Indianapolis, IN*

WP 568 **Standard Addition technic confirms applicability of non-denaturing IPRP-LC-MS methods for direct quantification of single strand impurities in duplex siRNA therapeutics**; Afrand Kamali[1]; Reza Nemati[1]; Ilia Korboukh[1]; Robert V Kolakowski[1]; Guangnong Zhang[1]; [1]*Novo Nordisk, Lexington, MA*

WP 569 **Unzipping the Duplex: A Plug-and-Play Matrix Strategy for High-Sensitivity chemically denaturing CZE–MS of siRNA**; Samantha H Sarni[1]; Ming Huang[1]; Haibo Qiu[1]; Ning Li[1]; [1]*Regeneron Pharmaceuticals Inc, Tarrytown, NY*

WP 570 **Development of a cGMP-Compliant sgRNA Sequencing Method by Ion-Pairing Reversed-Phase liquid chromatography and Tandem Mass Spectrometry**; Ping Jiang[1]; Elizabeth Tande[1]; Jie Ding[1]; [1]*Thermo Fisher Scientific, Middleton, WI*

WP 571 **Quantitative Differentiation of Poly(A) Tailed and Non-Tailed Intact MDa mRNA with Charge Detection Mass Spectrometry**; Julian Robles[1]; Zachary M. Miller[2]; Evan R. Williams[2]; [1]*University of California Berkeley, Berkeley, CA;* [2]*University of California, Berkeley, Berkeley, CA*

WP 572 **Photoclick Chemistry Led to the Identification of HELLS as a Helicase for DNA G-Quadruplexes**; Yie Woon Chong[1]; Yinsheng Wang[2]; Zi Gao[2]; Xiaomei He[2]; Jun Yuan[2]; [1]*University of California Riverside, Riverside, CA;* [2]*University of California, Riverside, Riverside, CA*

WP 573 **Comparative Evaluation of Low-q CID, HCD, and MS^2 UVPD for Sequence Coverage of Defined RNA Oligonucleotides**; Roberto Gamez[1]; Min Du[2]; Robert L Ross[3]; [1]*Thermo Fisher Scientific, Austin, TX;* [2]*Thermo Fisher Scientific, Lexington;* [3]*Thermo Fisher Scientific, Lexington, MA*

WP 574 **EFFECT OF NITRIC OXIDE ON DNA DAMAGE AS EVIDENCED BY THE ANALYSIS OF HYDROPEROXIDES AND STABLE PRODUCTS BY LC-MS/MS**; Ommay Habiba[1]; Jintana Meesungnoen[1]; Jean-Paul Jay-Gérin[1]; Richard Wagner[1]; [1]*Université de Sherbrooke, Sherbrooke, QC*

WP 575 **LC–MS Characterization of an Antisense Oligonucleotide–Bicyclic Peptide Conjugate via HCD-Mediated Peptide Release and MS^n Analysis**; Hans Gaus[1]; Roberto Gamez[2]; Lendell L. Cummins[1]; Min Du[3]; Robert L Ross[4]; [1]*Ionis Pharmaceuticals, Inc., Carlsbad, CA;* [2]*Thermo Fisher Scientific, Austin, TX;* [3]*Thermo Fisher Scientific, Lexington;* [4]*Thermo Fisher Scientific, Lexington, MA*

WP 576 **Enhanced Metabolite Characterization of Therapeutic siRNAs Using Data Independent, Sequential Windowed Acquisition of all THeoretical (SWATH) Ions, LC-MS/HRMS Methods**; Limin Deng[1]; Andrew May[1]; Apoorva S Metkari[1]; Timothy Snow[1]; Zamas Lam[1]; Ragu Ramanathan[2]; [1]*QPS, LLC, Newark, DE;* [2]*Quest Pharmaceutical Services, Newark, DE*

WP 577 **RNA epitranscriptome profiling across stress-induced RNA condensates with CID and EAD MS/MS**; Carolina Brás Costa[1]; Daniel H Ramirez[1]; Emily Zahn[1]; Bibhuti Bhusana Palai[1]; Benjamin A. Garcia[1]; [1]*Washington University School of Medicine, St. Louis, MO*

WP 578 **Identification of Reader Proteins Interacting with 5-Methyluridine-Modified RNA**; Wenxin Li[1]; Zhouxian Li[2]; Yinsheng Wang[2]; [1]*UC Riverside, Riverside, CA;* [2]*UC Riverside, Riversdie, CA*

WP 579 **Ultra-High Sensitivity Method for Quantitation of siRNA in Human Plasma Using Hybrid LC-MS/MS**; Danyang Wang[1]; Andy (Hongfang) Xue[1]; Kuei-Ting Yang[1]; Aihua Liu[1]; [1]*Resolian Inc, Malvern, PA*

WP 580 **Accurate quantification of in vitro-transcribed mRNA cap nucleosides using UHPLC-MS**; Kaley M. Simcox[1]; Shweta Chhajed[2]; Min Du[2]; Robert T. Kennedy[1]; Kristin S. Koutmou[1]; Robert L. Ross[2]; [1]*University of Michigan, Ann Arbor, MI;* [2]*Thermo Fisher Scientific, Lexington*

WP 581 **Nanopipette ESI emitters improve mass spectral quality for oligonucleotides**; Scott Hale[1]; Emily J Byrd[2]; Feng Guo[3]; Rachel R Ogorzalek Loo[3]; Joseph A Loo[3]; [1]*UCLA, Los Angeles, CA;* [2]*University of Leeds, Leeds, United Kingdom;* [3]*UCLA, LOS ANGELES, CA*

WP 582 **LC-MS/MS/MS for Assessing the Incorporation and Repair of O6-Alkyl-2'-Deoxyguanosine Lesions in Genomic DNA**; Chen Wang[1]; Pengcheng Wang[1]; Lin Li[1]; Yinsheng Wang[1]; [1]*University of California, Riverside, Riverside, CA*

WP 583 **Post-Activated Plasma Electron Detachment Dissociation for Oligonucleotide Sequencing in Deta Dependent LC-MSMS**; Kaoru Karasawa[1]; Takashi Baba[2]; [1]*SCIEX, Tokyo, Japan;* [2]*SCIEX, Concord, ON*

WP 584 **Mapping mRNA sequences with LCMS using a Novel Selective digestion method**; Joshua K McBee[1]; Peter Pellegrinelli[1]; Jacob W McCabe[2]; Matthew T Robey[2]; Kenneth R Durbin[2]; Barry Boyes[1]; [1]*Advanced Materials Technology, Wilmington, DE;* [2]*Proteinaceous, Evanston, IL*

WP 585 **Ion-Pairing Free Characterization of mRNA Poly A Tail Length by Native Mass Spectrometry**; Garret M Rubin[1]; Jeremy Filteau[1]; Hao Chen[1]; Ronnie Wei[1]; Hui Zhou[1]; [1]*Modex Therapeutics, Weston, MA*

WP 586 **Comparison of Sample Preparation Techniques Utilized for the Extraction of N-Acetylgalactosamine (GalNAc)-siRNA Conjugates from Biological Samples Followed by LC-MS/MS Analysis**; Nicholas B. Vera[1]; Nicole Bring[1]; Alexander Krett[1]; Girish Chopda[1]; [1]*Novo Nordisk, Lexington, MA*

WP 587 **Complex conformational landscapes of riboswitch aptamers revealed by native IM-MS: effects of selective cation binding**; Sarah Heel-Juen[1]; Evan R. Williams[1]; [1]*Department of Chemistry, University of California, Berkeley, United States;, Berkeley, CA*

WP 588 **Epitranscriptomic profile of selected human cellular models – a blueprint for future epitranscriptomic or related studies**; Norman Chiu[1]; Frank Shnaider[1]; [1]*University of North Carolina Greensboro, Greensboro, NC*

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WP 590 **METTL3 Orchestrates Histone H3K9 Acetylation via Promoting GCN5's Occupancy to Chromatin**; Xiaomei He[1]; Yen-Yu Yang[1]; Zhouxian Li[1]; Shuyang Zhao[1]; Jun Yuan[1]; Chengjie Ma[1]; Yinsheng Wang[1]; [1]*Department of Chemistry, University of California, Riverside, Riverside, CA*

WP 591 **Sub-stoichiometric modifications of Aplysia californica tRNAs and tRNA fragments revealed by integrating intact analysis and bottom-up mass spectrometry**; Weichen Huang[1]; William M McGee[2]; Erika Stark[2]; Erica Wang[1]; Kevin D Clark[1]; [1]*Tufts University, Medford, MA;* [2]*Waters corporation, Cambridge, MA*

WP 592 **Differentiation of leucine and isoleucine isomeric residues by ExD in de novo peptide sequencing. The case of temporins.**; Ekaterina V. Dmitrieva[1]; Tatiana Yu. Samgina[1, 2]; Yury V. Vasil'ev[3]; Michael C. Hare[3]; Albert T. Lebedev[1, 2]; [1]*Shenzhen MSU-BIT University, Shenzhen, China;* [2]*Lomonosov Moscow State University, Moscow, Russia;* [3]*Agilent Technologies, CORVALLIS, OR*

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WP 594 **Multiple Basic Amino Acid Residues Allow High Tyrosine-O-Sulfate Retention During Collisional Activation**; Elfren Roy T. Noche[1, 2]; Sean D. Dunham[1]; Steven A. DeFiglia[1]; Kristina Hakansson[1, 2]; [1]*National High Magnetic Field Laboratory Department of ICR, Tallahassee, FL;* [2]*Florida State University, Tallahassee, FL*

WP 595 **Comparing library-guided and library-free de novo sequencing for antimicrobial peptide discovery**; Alba Lucia Montoya[1]; Chi Yen Tseng[2]; Brett R. Blackwell[2]; Elizabeth C. Evin[2]; Scottie Alexander[2]; Nidhi K. Parikh[2]; Lance M. Miller[2]; Sangeeta Negi[2]; [1]*LOS ALAMOS NATIONAL LABORATORY, LOS ALAMOS, NM;* [2]*Los Alamos National Laboratory, Los Alamos, NM*

WP 596 **Comparative Evaluation of EAD and CID for Disulfide Bond Mapping in Human Insulin and Filgrastim**; Greg Winter[1]; Qiyao Li[1]; Jennifer Grabowski[1]; Jennifer Belsky[1]; *[1] United States Pharmacopeia, Rockville, MD*

WP 597 **Annotation of c-type Ions in NIST Mass Spectral Libraries Enhances Peptide N-terminal Sequencing**; Meghan Burke[1]; Xiaoyu Yang[1]; Yuxue Liang[1]; Pedatsur Neta[1]; Stephen E. Stein[1]; *[1] NIST, Gaithersburg, MD*

WP 598 **Enhanced De Novo Peptide Sequencing via Me-Cou Derivatization for Non-Targeted Peptidomics**; Luan Hui[1]; Yumiko Toyama[1]; Fumiya Honda[1]; Ryotaro Asai[1]; Saya Nakamura[1]; Toshiro Matsui[1]; Mitsuru Tanaka[1]; *[1] Kyushu University, Nishi-ku, Japan*

WP 599 **Expanding Q-TOF Fragmentation with a Dual-Radical Platform for Oxygen and Hydrogen Attachment Dissociation (OAD/HAD)**; Takeaki Kitawaki[1]; Hidenori Takahashi[1]; Kazutaka Mitsui[1]; Masaji Furuta[1]; Yoshihiro Yamada[1]; Sadanori Sekiya[1]; Koichi Tanaka[1]; *[1] Shimadzu corporation, Kyoto, Japan*

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WP 601 **Feasibility Studies for Characterization ofComplex Therapeutic Peptides using HCD, ETD, and UVPD High-Resolution Mass Spectrometry**; Suresh Annangudi[1]; Christopher Jones[1]; Edith Sharon[1]; *[1] AbbVie Inc., North Chicago, IL*

WP 602 **Comprehensive sequencing of cyclic peptides with top-down MS on a timsOmni platform using next-generation ExD fragmentation**; Christian F. Bartelmus[1]; Jean-François Greisch[2]; Athanasios Smyrnakis[3]; Maria-Aggeliki Kosmopoulou[3]; Detlev Suckau[4]; Guillaume Tremintin[5]; Dimitris Papanastasiou[3]; Michael Greig[5]; *[1] Hoffmann-La Roche Ltd, Basel, Switzerland; [2] Bruker Switzerland AG, Fällanden, Switzerland; [3] Fasmatech Science & Technology, Chalandri, Greece; [4] Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [5] Bruke*

WP 603 **Sharper Peaks and Higher Sensitivity: Advancing Positively Charged Surface Stationary Phase Technology with 2 µm Particles**; Peter Pellegrinelli[1]; Joshua McBee[1]; *[1] Advanced Materials Technology, Wilmington, DE*

WP 604 **LC/MS characterization of GLP-1 receptor agonist oligomers and other elusive impurities**; Rachel Franklin; *Agilent Technologies Inc., Corvallis, OR*

WP 605 **Electron-Activated Dissociation Resolves Leucine/Isoleucine and Reveals Co-existence at a Single Variant Site in Peptide-Mapping LC-MS/MS Analysis**; Fan He[1]; Junhua Wang[1]; Weitao Jia[1]; *[1] Gilead Sciences, Foster City,, CA*

WP 606 **LC-HRMS and LC-MS/HRMS Characterization of Cyclic and Bicyclic Peptides Using CID and EAD with Zeno Trapping**; Keyin Li[1]; Nathan O'Neill[1]; Apoorva S Metkari[1]; Zamas Lam[1]; Ragu Ramanathan[2]; *[1] QPS, LLC, Newark, DE; [2] Quest Pharmaceutical Services, Newark, DE*

WP 607 **Rapid intact-mass profiling and MALDI In-Source Decay top-down sequencing for localization of single amino acid hemoglobin variants on benchtop MALDI-TOF/TOF**; Sandip Chavan[1]; Anikha Bellad[2]; Anjali Alving[3]; Sinduri Vuppala[3]; Gunveen Sachdeva[1]; Joshua Fischer[3]; Akhilesh Pandey[1]; *[1] Mayo Clinic, Rochester, MN; [2] Institute of Bioinformatics, Bangalore, India; [3] Bruker Daltonics, Billerica, MA*

WP 608 **Advanced Mass Spectrometry-Based Characterization of Therapeutic Cyclic Peptides at Single Amino Acid Resolution**; Chen Li[1]; Joshua Mcmanus[2]; Yang Wang[1]; Bing Wang[1]; *[1] CMC Synthetics Platform Analytical Sciences, Sanofi, Cambridge, MA; [2] CMC Synthetics Platform Commercial Process Development, Sanofi, Cambridge, MA*

WP 609 **Very Weak Anion Exchange (VWAX) Chromatography for Negatively Charged Glycopeptide Enrichment and Separation**; Peng-Kai Liu[1]; Danqing Wang[1]; Ting-Jia Gu[1]; Bin Wang[1]; Hung-Yu Chiang[1]; Feixuan Wu[1]; Christopher J. Wike[2]; Lingjun Li[1]; *[1]University of Wisconsin-Madison, Madison, WI; [2]PolyLC Inc., Columbia, MD*

WP 610 **Stereochemical evaluation of cell-cell signaling peptides in Platynereis dumerilii**; Ashley D. Clifton[1]; Alisha Doda[1]; Ryan W. Null[2]; B. Duygu Özpolat[2]; James W. Checco[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE; [2]Washington University in St.Louis, St.Louis, MO*

WP 611 **LC-MS/MS technique for peptide drug development: characterization, and stability assessment**; Neven Mikawy[1]; Ben Niu[1]; Qunying Zhang[1]; *[1]Biologics Analytical R&D, Development Sciences, AbbVie Inc, North Chicago, IL, 60064, North Chicago, IL*

WP 612 **Optimization of DIA-Based Ubiquitinomics Using K-ε-GG Enrichment on the Orbitrap Astral**; Riley K Rowland[1, 2]; Margaret Lea Robinson[2, 3]; Mukesh Kumar[4]; Katherine A. Overmyer[2, 3, 5]; Joshua J. Coon[1, 2, 3, 5]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]National Center for Quantitative Biology of Complex Systems, Madison, WI; [3]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Mad*

WP 613 **High-Fidelity Protease KRysin Enables Comprehensive Post-Translational Modification Analysis**; Cristina Hernandez Rollan[1, 2]; Claire Koenig[2]; Tanveer Singh Batth[1, 2]; Jesper Velgaard Olsen[2]; *[1]KPL ApS, Copenhagen, Denmark; [2]Novo Nordisk Foundation Center for Protein Research, Department of Cellular and Molecular Medicine, Copenhagen, Denmark*

WP 614 **Evaluating Parallel-Accumulation Mobility-Aligned Fragmentation Mode for Phosphoproteomics**; Isabel R Uribe[1]; Liulin Deng[1]; Leonard C. Rorrer III[1]; Lauren Royer[1]; Hasmik Keshishian[2]; Steven A. Carr[2]; Daniel DeBord[1]; *[1]MOBILion Systems, Inc, Chadds Ford, PA; [2]Broad Institute, Cambridge, MA*

WP 615 **A Sweet Solution for Mass Spectrometric Glycan Analysis**; Kiran Iyer[1]; Erin Weisenhorn[1]; Shannon Hayes[2]; Hannah Townsend[2]; Luis Fernández Ruiz[2]; Rosalynn Molden[1]; *[1]Just Evotec Biologics, Seattle, WA; [2]Protein Metrics LLC, Boston, MA*

WP 616 **PTM Analysis using HCD and EThcD on an Orbitrap Excedion Pro Mass Spectrometer**; Brett Larsen[1]; Mikayla Shanafelt[2]; Tonya Pekar Hart[2]; Amirmansoor Hakimi[2]; Joshua P. Kline[2]; Anthony Possemato[3]; Barry Zee[3]; Alissa Nelson[3]; Matthew Stokes[3]; Sean Beausoleil[3]; Mukesh Kumar[3]; *[1]Thermo Fisher Scientific, Mississauga, ON; [2]Thermo Fisher Scientific, San Jose, CA; [3]Cell Signaling Technology Inc, Danvers, MA*

WP 617 **Supercharging reagents facilitates EThcD-based fragmentation and site-specific identification of labile post-translational modifications**; Martin Rykar[1]; Sara Charlotte Buch-Larsen[1]; Michael Lund Nielsen[1]; Jesper Velgaard Olsen[1]; *[1]University of Copenhagen, Copenhagen, Denmark*

WP 618 **Direct quant of PTM's in data through instrument data enrichment**; Yves Le Blanc[1]; Claudia Alvarez[1]; Stephen Tate[1]; *[1]SCIEX, Concord, ON*

WP 619 **Global Profiling of Deamidation Susceptibility and Isoaspartate Formation via PIMT-Mediated Labeling and DIA Mass Spectrometry**; Emily E Johnson[1]; Mark Scalf[1]; Marcel Morgenstern[2]; Lloyd M Smith[1]; Katherine A. Overmyer[2, 3, 4]; Joshua J Coon[1, 2, 3, 4]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [3]Morgridge Institute for Research, Madison, WI; [4]Natio*

WP 620 **High-Resolution Detection of Post-Translational Modifications Using Single-Molecule Protein Sequencing**; Natchanon Sittipongpittaya[1]; Kendrick Nguyen[2]; Andrey Reshetnyak[3]; Muriel Priault[4]; Ajay Vashisht[2]; John Vieceli[2]; Meredith L. Carpenter[2]; Nidhi Sahni[5, 6]; Gloria M. Sheynkman[1, 7]; *[1]Department of Molecular Physiology and Biological Physics, University of Virginia, Charlottesville, VA; [2]Quantum-Si, Branford, CT; [3]St.Jude Children Research Hospital, Memphis, TN; [4]IGBC, Universite de Bordeaux*

WP 621 **Regulation of the hYVH1-HSP70 Cell Survival Complex through Tyrosine Phosphorylation Mediated by the Proto-Oncogene Src Kinase**; Michael Zachary Lozon[1]; Ashley DaDalt[1]; Panayiotis O Vacratsis[1]; *[1]University of Windsor, Windsor, ON*

WP 622 **Overcoming Peptide-Centric DIA Limitations: Discovering Unsuspected Modifications in Narrow-Window DIA Using Mascot Error Tolerant Search**; Richard J Jacob[1]; Ville R Koskinen[2]; Patrick Emery[2]; *[1]Matrix Science Inc., Boston, MA; [2]Matrix Science, London, United Kingdom*

WP 623 **Confident differentiation between citrullination and deamidation using 2D LC-MS/MS with peptide retention prediction in both dimensions**; Alexandre J.J Prefontaine; *University of Manitoba, Winnipeg, MB*

WP 624 **Effects of Glucose and Mannitol on Site-Specific Cysteine Acylation in HK2 Cells**; Jian Cai[1]; Ming Li[2]; Frederick Benz[2]; Craig McClain[2]; Jon Klein[2]; Michael L. Merchant[2]; *[1]University of Louisville, Louisville, KY; [2]University of Louisville, Louisville, KY*

WP 625 **diaPASEF Ubiquitinomics Data Analysis with Various Proteomics Search and Analysis Tools**; Brian D Fries[1]; Johnathan Altom[2]; Liwen Zhang[1]; Sophie Harvey[1]; Francesca Cottini[2]; Christopher M Hadad[1, 3]; *[1]The Ohio State University Campus Chemical Instrument Center, Columbus, OH; [2]The Ohio State University Comprehensive Cancer Center, Columbus, OH; [3]The Ohio State University Department of Chemistry and Biochemistry, Columbu*

WP 626 **Benchmarking Phosphosite Localization Accuracy in Low-Input Data-Independent Acquisition Phosphoroteomics**; Seth M Kelly[1]; Clayton B Tacker[2]; Chris M Tracy[2]; Brandon M Gassaway[2]; *[1]Brigham Young University, Mapleton, UT; [2]Brigham Young University, Provo, UT*

WP 627 **Using a MS integrated charge variant assay to measure mAb product quality attributes during perfusion cell culture**; Hampus Engstroem[1]; Erin Redman[1]; Scott Miller[1]; René Gantier[1]; Scott Mellors[2]; Will Thompson[2]; *[1]Repligen, Waltham, MA; [2]Move Analytical, Morrisville, NC*

WP 628 **Evaluating the Orbitrap Astral MS for Enhanced Impurity Detection in Biotherapeutic Peptide Mapping Workflows**; Jason L. Richardson[1]; Bhavana Shah[1]; Hao Yang[2]; Min Du[2]; Zhongqi Zhang[1]; *[1]Amgen, Thousand Oaks, CA; [2]Thermo Fisher Scientific, San Jose, CA*

WP 629 **Integrated Metabolomics and Proteomics for Rapid, Deep Characterization of a Contaminated Perfusion Bioreactor**; J. Michael Ramsey[1]; Ethan Bossange[2]; James Campbell[1]; Erin Redman[2]; Michael Ford[3]; J. Will Thompson[1]; J. Scott Mellors[1]; *[1]Move Analytical LLC, Carrboro, NC; [2]Repligen, Waltham, MA; [3]MS Bioworks LLC, Ann Arbor, MI*

WP 630 **Rapid and Comprehensive Characterization of Charge Variants in Therapeutic Proteins Using icIEF-UV/MS**; Alexander Campanelli[1]; Fan He[2]; Junhua Wang[2]; Weitao Jia[2]; *[1]Gilead Sciences, Foster City, CA; [2]Gilead Sciences Inc., Foster City, CA*

WP 631 **Characterizing the Oligomeric Composition of Insulin Under Varying Solution Compositions Using Ion Mobility Mass Spectrometry**; Colton Dixon[1]; Emmanuel Dare[1]; Kenneth W. Lee[1]; *[1]Brigham Young University, Provo, UT*

WP 632 **Effect of Truncation on Eye Lens β-Crystallin Oligomerization and Stability**; Grant D Myers[1]; Nicole Ledendecker[1]; Martin E. Tovar Ramirez[2]; Kirsten J. Lampi[2]; Micah T. Donor[1]; *[1]George Fox University, Newberg, OR; [2]Oregon Health & Science University, Portland, OR*

WP 633 **Determining Biological Consequences of PTBP1 Proteolysis via Affinity Purification Mass Spectrometry (AP-MS)**; Caroline J Canavan[1]; Alexandra C Turmon[1]; Keriann M Backus[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

WP 634 **Mapping the Landscape of Coral Small Heat Shock Proteins using Native Mass Spectrometry**; Siong Chen Meng[1, 2, 3]; Katie Osagwu Rodriguez[1, 2]; Navoneel Sen[1, 2]; Chloe-Marie Hawley[3]; Victoria Buckland[3, 4]; April J Burt[5]; Raphael Gollnisch[4]; Lindsay Turnbull[3]; Justin Benesch[1, 2]; *[1]Kavli Institute for*

Nanoscience Discovery, University of Oxford, Oxford, United Kingdom; [2]Department of Chemistry, University of Oxford, Oxford, United Kingdom; [3]Department of Biology, University of Oxford, Oxford, United

WP 635 **Quantitation of Iron Storage in Ferritin by Charge Detection Mass Spectrometry**; Nicholas G. Rommel[1]; Martin F. Jarrold[2, 3]; David E. Clemmer[2, 3]; *[1]Indiana University, Bloomington, IN; [2]Indiana University Bloomington, Bloomington, IN; [3]Megadalton Solutions, Bloomington, IN*

WP 636 **Characterizing the oligomeric distribution of Insulin Analogs using Cyclic Ion Mobility–Mass Spectrometry and Gas-phase Ion Chemistry**; Emmanuel Dare[1]; Colton Dixon[1]; Kenneth W. Lee[1]; *[1]Brigham Young University, Provo, UT*

WP 637 **Probing avidin-biotin interactions with native top-down mass spectrometry**; Delaynie Brinkman[1]; Kanchan Pathak[1]; Fabio P. Gomes[1]; *[1]Virginia Commonwealth University, Richmond, VA*

WP 638 **Native MS Coupled to UVPD to Investigate Allosteric Modulation and Conformational Changes of New Delhi Metallo-β-Lactamase-1**; Prithvijeet Singh Kharnal[1]; Jennifer S. Brodbelt[1]; Emily L. Que[1]; Mohamed I. Gadallah[1]; Jiaxi Zeng[1]; *[1]University of Texas at Austin, Austin, TX*

WP 639 **Complex-resolved epichaperomics reveals PTM-coded rewiring of HSP90–HSC70–cochaperone scaffolds across cellular states**; Luke A Botticelli[1]; Shujuan Wang[2]; Chander Digwal[2]; Daryna Serediuk[1]; Yue Sun[1]; Kathleen Madison Feener[1]; Anna Rodina[2]; Gabriela Chiosis[2]; Feixia Chu[1]; *[1]University of New Hampshire, Durham, NH; [2]Memorial Sloan Kettering Cancer Center, New York City, NY*

WP 640 **Limited Proteolysis with Native Mass Spectrometry Provides Insight into the Structure and Dynamics of Protein/Ligand Complexes**; Carter Lantz[1]; Leila Minian[1]; Roza Avetisyan[1]; John Schermerhorn[1]; David Russell[1]; *[1]Texas A&M Univesity, College Station, TX*

WP 641 **Elucidating Tagging Characteristics in µMap Photocatalytic Proximity Labeling and Identifying a Novel Photocatalyst BODIPY-FL via Site-Specific Conjugation and Mass Spectrometry**; Miyang Li[1]; Song Nie[1]; Shunhai Wang[1]; Ning Li[1]; *[1]Regeneron Pharmaceuticals Inc, Tarrytown, NY*

WP 642 **nMS for Triage of DEL and ASMS Screening Hits: Accelerating Hit Validation in Drug Discovery**; Xidong Feng[1]; Ian Tolis[1]; Christopher McClendon[2]; Brodie Corless[1]; *[1]Pfizer, Groton, CT; [2]Pfizer, Cambridge, MA*

WP 643 **Rapid complexomics with native gel-mass spectrometry**; Joanne Du[1]; Noah M Lancaster[2, 3]; Benton J Anderson[2, 4]; Felicia Deng[5, 6]; Mitchell D Probasco[6]; Katherine A. Overmyer[2, 4, 6]; Jonathan A Stefely[2, 6]; Joshua J Coon[2, 4, 6, 7]; *[1]University of Wisconsin--Madison, Madison, WI; [2]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [3]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [4]Natio*

WP 644 **Formation, Disassembly and Chromophore Attachment of the Engineered Fluorescent Protein smURFP**; Jessica Hellinger[1]; Devon L Kulhanek[2]; Ross Thyer[2]; Jennifer S. Brodbelt[1]; *[1]University of Texas - Austin, Austin, TX; [2]Rice University, Houston, TX*

WP 645 **Elucidating Pancreatic Cancer Drug Targets Using DDA- and DIA-SPROX**; Natalie M Labbe[1]; Meghan K. Virani[1]; Anushka Jain[2]; Eric Wang[1]; Jinjae Park[1]; Yiquan Zhao[1]; Jiyong Hong[1]; Sina Ghaemmaghami[2]; Michael C. Fitzgerald[1]; *[1]Duke University, Durham, NC; [2]University of Rochester, Rochester, NY*

WP 646 **Native Mass Spectrometry Characterization of PROTAC-Induced Binary and Ternary Complexes of BRD4 and CRBN**; Pete Gabriel L. Ledesma[1]; Varun V. Gadkari[1]; William C. K. Pomerantz[1]; *[1]University of Minnesota - Twin Cities, Minneapolis, MN*

WP 647 **ESI polarity impacts the structural stability and gas-phase conformations of protein-ligand complexes**; Madeline G Bannon[1]; Elyssia S Gallagher[1]; *[1]Baylor University, Waco, TX*

WP 648 **Interaction of substrate and inhibitors with SalmonellaFraB deglycase, a drug target**; Yuan Gao[1,2]; Jamison Law[3]; Venkat Gopalan[3]; Vicki H. Wysocki[1,2]; *[1]School of Chemistry and Biochemistry. Georgia Institute of Technology, Atlanta, GA; [2]Native Mass Spectrometry Guided Structural Biology Center, Georgia Institute of Technology, GA 30318, Atlanta, GA; [3]The Ohio State Unive*

WP 649 **Unraveling Protein Ubiquitylation Pathways through Proteome-scale Experimental Profiling and Structural Modeling of Protein Interactions**; Edward L. Huttlin[1]; Laura Pontano Vaites[1]; Nathan Zuniga Pina[1]; Lana D'Addieco[1]; Austin Fergusson[1]; Fana Gebreab[1]; Emily Hill[1]; Karina Martinez Perez[1]; Mateo Valenzuela-Gutierrez[1]; David Vanderwall[1]; Ramin Rad[1]; Joao A Paulo[1]; David P Nusinow[2]; Donald S. Kirkpatrick[2]; Tyrone Lee[1]; Tram Nguyen[1]; Anthony Christidis[1]; Alex Pickering[1]; Ludwig Geistlinger[1]; Devin K. Schweppe[3]; J. Wade Harper[1]; Steve Gygi[1]; *[1]Harvard Medical School, Boston, MA; [2]Xaira Therapeutics, San Francisco, CA; [3]University of Washington, Seattle, WA*

WP 650 **Background proteome correction reduces false positives in affinity purification-mass spectrometry analyses across changing biological contexts**; Melina A Brunelli[1,2]; Lisa Morishita-Cartwright[1,2]; D. R. Mani[3]; Samuel A. Myers[1,2,4]; *[1]La Jolla Institute for Immunology, La Jolla, CA; [2]University of California San Diego, La Jolla, CA; [3]Broad Institute of MIT and Harvard, Cambridge, MA; [4]Moores Cancer Center, La Jolla, CA*

WP 651 **Non-random mAb Fc sialic acid glycan pairing in Fc-engineered mAbs enhances FcγRIIb binding measured by SEC and LC–MS**; Daniel Woodall[1]; Prashant N Jethva[1]; Andrew B Dykstra[1]; Joshua Tokuda[1]; Pavel V. Bondarenko[1]; *[1]Amgen Inc., Thousand Oaks, CA*

WP 652 **A Rearranged Salt Bridge Explains Why Covalent Bond Cleavage Can Compete with Monomer Ejection in Trimeric Membrane Protein AmtB**; Toy Lemmons[1]; Joseph A Loo[1]; Rachel R. Ogorzalek Loo[1]; *[1]University of California Los Angeles, Los Angeles, CA*

WP 653 **TurboID Proximity Labeling Reveals DHRS4 Interactome: Associations with Transcription Factor Networks and Redox Mechanisms**; SAREEN MUTHYALA[1]; HUGO A AMEDEI[1]; GEONHEE LEE[1]; KEVIN PRASAD[1]; SUNAYANA SYED[1]; KYRIAKOS N PAPANICOLAOU[1]; D. BRIAN FOSTER[1]; *[1]Division of Cardiology, Johns Hopkins University, Baltimore, MD*

WP 654 **Identifying and validating the RORβ interactome in an osteosarcoma overexpression model using double crosslinking rapid immunoprecipitation mass spectrometry**; Nadeska I Montalvan[1,2]; Kuang-Ting Kuo[2]; Mi Ra Chang[2]; Patrick R. Griffin[1,2]; *[1]Scripps Research Institute, La Jolla, CA; [2]The Herbert Wertheim UF Scripps Institute for Biomedical Innovation & Technology, Jupiter, FL*

WP 655 **A Native Mass Spectrometry Protein-Ligand Screening Workflow Enabled by Automated Microfluidic Online Buffer Exchange**; Suraj Dhungana[1]; Casey Vantucci[1]; Carter Asef[1]; Arabella Garcia[1]; Mason Chilmonczyk[1]; *[1]Andson Biotech, Atlanta, GA*

WP 656 **Optimized Low-Field Differential Ion Mobility Separations Employing Flexible Waveforms with High-Resolution Mass Spectrometry for Top-Down Proteomics**; Hayden A. Thurman[1]; Pratima Pathak[1]; Egor Gusachenko[1]; Gordon A. Anderson[2]; Alexandre A. Shvartsburg[1]; *[1]Wichita State University, Wichita, KS; [2]GAA Custom Electronics, Kennewick, WA*

WP 657 **Evaluation of an Orbitrap Astral Zoom Mass Spectrometer for Top-Down Proteomics**; Anna V. Pashkova[1]; Tabiwang N. Arrey[1]; Hamish Stewart[1]; Jake T Kline[2]; Andreia Ferreira De Almeida[3]; Luca Fornelli[2]; Eugen Damoc[1]; *[1]Thermo Fisher Scientific, Bremen, Germany; [2]University of Oklahoma, Norman, OK; [3]IonOpticks, Melbourne, Australia*

WP 658 **Enhancing Protein Sequence Coverage Using Multi-Enzyme Middle-Down and Bottom-Up Mass Spectrometry**; Xingzhao Xiong[1]; Xiaowen Liu[1]; *[1]Tulane University, New Orleans, LA*

WP 659 **Probing non-covalent lipid interactions in membrane proteins with native top-down mass spectrometry**; Kanchan Pathak[1]; Delaynie Brinkman[1]; Sarah Walters[1]; Gustavo Perroti[1]; Brian Fuglestad[1]; Fabio P. Gomes[1]; *[1]Virginia Commonwealth University, Richmond, VA*

WP 660 **Boosting sensitivity in top-down protein studies using Cyclic IMS-enabled Wideband Enhancement**; Catherine Tremblay[1]; Dale A Cooper-Shepherd[2]; Isabella A Jones[2]; Emma Marsden-Edwards[2]; [1]*Waters Corporation, Milford, MA;* [2]*Waters Corporation, Wilmslow, United Kingdom*

WP 661 **Advanced Native and Top-Down MS^n Workflows on the timsOmni Platform Enable Deep Structural Analysis of Membrane Protein Complexes**; Jeremy Norris[1]; Abraham O Oluwole[2, 3]; Mariangela Kosmopoulou[4]; Dodge Baluya[1]; Ioanna Barla[4]; Athanasios Smyrnakis[4]; Dimitris Papanastasiou[4]; Weston Struwe[3, 5]; Carol V Robinson[2, 3]; [1]*Fasmatech Science & Technology, Chalandri, Greece;* [2]*Department of Chemistry, University of Oxford, Oxford, United Kingdom;* [3]*Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom;* [4</]

WP 662 **Definitive Protein Sequencing by Top-Down MS with timsOmni and OmniScape**; Dalila Bensaddek1; Miriam Escarlet Diaz Galicia[2]; Magnus Rueping[2]; Mariangela Kosmopoulou[3]; Athanasios Smyrnakis[3]; George Alevizos[3]; Dimitris Papanastasiou[3]; Maan Amad[1]; [1]*Analytical Chemistry Core Lab, King Abdullah University of Science and Technology, KAUST, Thuwal, Saudi Arabia;* [2]*KAUST Catalysis Center (KCC), Division of Physical Sciences & Engineering, King Abdullah University of Science and Tech*

WP 663 **Proteoform-Level Comparison of Mitochondrial Subpopulations from Human Cardiac Tissue**; Thomas S Weir[1]; Matthew S. Fischer[1]; Holden T. Rogers[1]; Zhan Gao[2]; Genevieve C Sparagna[3]; Carmen C Sucharov[3]; Ying Ge[1, 2, 4]; [1]*Department of Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI;* [3]*Division of Cardiology, Department of Medicine, Universit*

WP 664 **Intact and Bottom-up MS for Analysis of S-nitroso Sites on Hemoglobin in Blood Samples via Benzenesulfinic Acid Substitution**; Ireland Plunkett[1]; Saylor Stottlemyer[1]; Rachel Tan[1]; Phillip Matthew Joyner[1]; [1]*Pepperdine University, Malibu, CA*

WP 665 **Direct Aedes aegypti Histone Proteoform Annotation: From Genome to Proteoform**; Andrea Ramirez Torres[1]; Samantha San Juan[1]; Cassandra Nicole Fuller[1]; Lilian Valadares Tose[1]; Kevin Jeanne Dit Fouque[1]; Richard M. Searfoss[2]; Francisca N. L. Vitorino[2]; Detlev Suckau[3]; Gabriel Bianchin De Oliveira[1]; Fahad Saeed[1]; Francisco Fernandez Lima[1]; [1]*Florida International University, Miami, FL;* [2]*Washington University School of Medicine in Saint Louis, Saint Louis, MO;* [3]*Bruker Scientific LLC, Billerica, MA*

WP 666 **Individual Ion Tandem Mass Spectrometry Reveals a Catenin Phospho-Code for Adherens Junction Organization**; Che-Fan Huang[1]; Taojungeng Su[1]; Nickolas P. Fisher[1]; Jared O. Kafader[1]; Cara J. Gottardi[2]; Neil L. Kelleher[1]; [1]*Northwestern University, Evanston, IL;* [2]*Northwestern University Feinberg School of Medicine, Chicago, IL*

WP 667 **Simplified DMTm Processing and Real-Time Visualization using Automated Calibration and Optimized Ion Handling for Robust, High Coverage Antibody Characterization**; Ryan Fellers[1]; Joseph B Greer[1]; Michael A. R. Hollas[2]; Bryan P. Early[2]; Matthew T Robey[1]; Neil L Kelleher[2]; Kenneth R Durbin[1]; [1]*Proteinaceous, Evanston, IL;* [2]*Northwestern University, Evanston, IL*

WP 668 **Quantitation of intact phosphorylated 4EBP1 proteoforms using multisegment spray-capillary CE-MS and parallel reaction monitoring**; Zhitao Zhao[1]; Trishika Chowdhury[1]; Samin Anjum[1]; Kellye A. Cupp-Sutton[1]; Si Wu[1]; [1]*University of Alabama, Tuscaloosa, AL*

WP 669 **Advancing Proteoform Characterization with Next-Gen Software and Instrumentation**; Amy K Carfagno[1]; Taojunfeng Su[2]; Ryan T Fellers[3]; Neil L Kelleher[2]; Luca Fornelli[1]; Ken Durbin[3]; [1]*University of Oklahoma, Norman, OK;* [2]*Northwestern University, Evanston, IL;* [3]*Proteinaceous, Evanston, IL*

WP 670 **Comprehensive Structural Analysis of Large Protein Complexes by Native Top-Down MS on a Modified Orbitrap Tribrid Mass Spectrometer**; Luchen Wuyang[1]; Matthew Kensil[1]; Emily Byrd[1, 2]; Christopher Mullen[3]; Joshua D Hinkle[3]; Kyle Patrick Bowen[4]; Rafael D Melani[3]; Joseph A Loo[1]; [1]*UCLA, Los Angeles, CA;* [2]*University of Leeds, Leeds, United Kingdom;* [3]*Thermo Fisher Scientific, San Jose, CA;* [4]*ThermoFisher Scientific, San Jose, CA*

WP 671 **Denaturing and NativeTop-downProteomicsbySEC–CZE–MS**; Maryam Rahimzadeh Dashtaki[1]; Jorge Colonrosado1[1]; Fei Fang[1]; Liangliang Sun[1]; *[1]Michigan State University, East Lansing, MI*

WP 672 **Optimizing Liquid Chromatography Separations for Intact Proteoforms in Complex Mixtures**; Chloe Gosdin[1]; Patrycja Szamweber[1]; Kellye A. Cupp-Sutton[1]; Zhitao Zhao[1]; Si Wu[1]; *[1]The University of Alabama, Tuscaloosa, AL*

WP 673 **Profiling the heterogeneity of colorectal cancer molecular subtypes using top-down proteomics**; Fei Fang[1]; Fernando (Ralph) Tobias[2]; Emily R. Sekera[2]; Amanda B. Hummon[2]; Liangliang Sun[1]; *[1]Michigan State University, Department of Chemistry, East Lansing, MI; [2]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH*

WP 674 **Application of High-throughput Top-down Thermal Proteoform Profiling to Examine the Effects of Staurosporine Treatment on HeLa Proteoform Stability**; Kellye A Cupp-Sutton[1]; Patrycja Szamweber[1]; Anju Teresa Sunny[1]; Samin Anjum[1]; Si Wu[1]; *[1]The University of Alabama, Tuscaloosa, AL*

WP 675 **Improvement of Throughput and Charge Assignment Accuracy in Orbitrap™-based Charge Detection Mass Spectrometry with Proton Transfer Charge Reduction**; Liangxuan Fu[1]; Michael P. Goodwin[1]; Kyle Patrick Bowen[1]; Christopher Mullen[1]; Graeme C McAlister[1]; Michael Senko[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

WP 676 **A Proteoform-Resolved Atlas of Human Cardiac Histones by Top-down Proteomics**; Zhan Gao[1]; Isabella R. Clemmer[1]; Hsin-Ju Chan[1]; Kwame Osei[1]; Holden T. Rogers[1]; Thomas S Weir[1]; Matthew S Fischer[1]; Rob L Gearhart[1]; Scott Price[1]; Yanlong Zhu[1]; Allan Brasier[1]; Jingshing Wu[1]; Wuqiang Zhu[2]; Ying Ge[1]; *[1]UW-Madison, Madison, WI; [2]Mayo Clinic, Phoenix, AZ*

WP 677 **Development of a perchloric acid (PCA) precipitation workflow for top-down proteomic analysis of low-abundance human plasma proteins**; Kameron N Orel[1]; Jake T Kline[1]; Andreia Ferreira De Almeida[2]; Luca Fornelli[1]; *[1]University of Oklahoma, Norman, OK; [2]IonOpticks, Melbourne, Australia*

WP 678 **Proteoform Identification from Complex Biological Mixtures by Native Top-Down Mass Spectrometry**; Yi Qiao[1]; Andrew Goring[1]; Robert T. Clubb[1]; Joseph A Loo[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

WP 679 **Intact Therapeutic Protein Analysis in Plasma Using Automated 2D-LC/TOF with Multi Heart Cutting**; Linfeng Wu[1]; Li Gu[1]; Guannan Li[1]; *[1]Agilent Technologies, Santa Clara, CA*

WP 680 **Tracking Progressive Liver Cirrhosis through a new Assay for >1500 Plasma Proteoforms across More than 200 Subjects**; Aniel Sanchez[1]; Nhat Hoang Van Le[1]; Indira Pla[1]; Paola Barrios[2]; Katrina N Peterson[1]; Troy D Fisher[1]; Vincent White[1]; Che-Fan Huang[1]; Eleonora Forte[3]; Vijaya Lakshmi Kanchustambham[1]; Michael A. R. Hollas[1]; Jes M Sanders[2]; Therese Banea[2]; Zachary Dietch[2]; John P McGee[1, 4]; Michael Caldwell[1]; Daniela P Ladner[2]; Neil L Kelleher[1, 2]; *[1]Northwestern University, Evanston, IL; [2]Feinberg School of Medicine, Northwestern University, Chicago, IL; [3]University of Illinois Chicago, Chicago, IL; [4]ImmPro, Inc., Evanston, IL*

WP 681 **Leveraging Model Populations of RAS by Top-Down LC-MS/MS to Optimize Proteoform-Specific Parameters and Evaluate Data Analysis Pipelines**; Alexandria L. Sohn[1]; Grace M. Scheidemantle[1]; Matthew R. Drew[1]; Min Hong[1]; Ashley Mitchell[1]; Kayla Russell[1]; Jenna Hull[1]; Katie Powell[1]; Shelley Perkins[1]; Scott Eury[1]; Jennifer Mehalko[1]; John-Paul Denson[1]; Simon Messing[1]; Vanessa Wall[1]; William Burgan[1]; Carissa Grose[1]; Dominic Esposito[1]; Frank McCormick[1, 2]; Dwight V. Nissley[1]; Caroline J. DeHart[1]; *[1]Frederick National Lab for Cancer Research, Frederick, MD; [2]Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, CA*

WP 682 **Proteoform Barcode: An Intuitive Visualization Framework for Top-Down Proteomics Results**; Yifan Yue[1]; Guijie Zhu[1]; Fei Fang[1]; Mehrdad Falamarzi Askarani[1]; Seyed Amirhossein Sadeghi[1]; Reyhane Tabatabaeian Nimavard[1]; Guangyao Gao[1]; Jorge Colonrosado[1]; Maryam Rahimzadeh Dashtaki[1]; Lance Thorp[1]; Liangliang Sun[1]; *[1]Michigan State University, Department of Chemistry, East Lansing, MI*

WP 683 **Systematic and Quantitative Investigation of Newly Synthesized Proteins Reveals Distinct Ion Homeostasis and Mitochondrial Changes between Cuproptosis and Ferroptosis**; Yue Wu[1]; Ronghu Wu[1]; *[1]Georgia Institute of Technology, Atlanta, GA*

WP 684 **Synergistic Arg-C Ultra and Lys-C Digestion for Quantitative Proteomics**; Vyas Pujari[1, 2]; Joseph Crapse[1, 2]; Connor Nisbet[1, 2, 3]; Gloria Bao[1, 2]; Wessley Ferguson[1, 2]; Christopher M Hosfield[4]; Michael Rosenblatt[4]; Felix Keber[1, 2]; Martin Wühr[1, 2]; *[1]Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ; [2]Department of Molecular Biology, Princeton University, Princeton, NJ; [3]Department of Chemistry, Princeton University, Princeton, Princ*

WP 685 **Mass Spectrometry–Based Proteomics to Define Therapy-Induced Senescence in Triple-Negative Breast Cancer (TNBC)**; Maryam Nikpayam[1]; Stanislau Stanisheuski[2, 3]; Siva Kolluri[4, 5]; Jacob Kreitzer[4, 5]; Claudia Maier[1, 3]; *[1]Department of Chemistry, Oregon State University, Corvallis, OR; [2]Department of Biochemistry & Biophysics, Oregon State University, Corvallis, OR; [3]Mass Spectrometry Center, Oregon State University, Corvallis, OR;* [4<]

WP 686 **Proteomic Remodeling Induced by Low-Intensity Pulsed Ultrasound in Human Cortical Organoids**; Juliana de S. da G. Fischer1; Natalia C Dos Santos[1]; Blake Tsu[1]; Stephanie Santos De Almeida[1]; Paulo C Carvalho[1, 2]; Stuart Hameroff[1]; Alysson Muotri[1]; Aline Martins[1]; *[1]Integrated Space Stem Cell Orbital Research, San Diego, CA; [2]Carlos Chagas Institute, Fiocruz, Curitiba, Brazil*

WP 687 **Evaluation of Proteomic Differences between First- and Second-Generation Spheroids Using Mass Spectrometry**; Ali Fraase[1]; Nicole Platzer[1]; Catherine B. Whitney[1]; Amanda B. Hummon[1]; *[1]Ohio State University, Columbus, OH*

WP 688 **Unleash the power of Hybrid-DIA with AI-driven software for Biomarker Discovery and Validation**; Qing Zhang[1]; Zia Rahman[1]; Tabiwang N Arrey[2]; Sophia Steigerwald[2]; Kyle Le Huray[2]; Max Hoek[2]; Philip M. Remes[3]; Eugen Damoc[2]; Baozhen Shan[1]; Yue Xuan[2]; *[1]Bioinformatics Solutions Inc, Waterloo, ON; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]Thermo Fisher Scientific, San Jose, CA*

WP 689 **Trans Fatty Acids Remodel the Hepatic Mitochondrial Proteome and Suppress Bioenergetic Pathways**; Allen Zhao[1, 2]; Jiahao Zhang[2, 3]; Feixuan Wu[2]; Lingjun Li[2, 3, 4]; *[1]Department of Biochemistry, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Biophysics Program, University of Wisconsin-Madison, Madison, WI; [4]D*

WP 690 **Focused Identification and Analysis of O6-Me-dG Binding Proteins**; Michelle Wang[1]; Andrew Kellum[2]; Ting Zhao[2]; *[1]501 West Big Springs Rd, Riverside; [2]University of California Riverside, Riverside, CA*

WP 691 **Quantitative Isotopically Labeled Tags for Precise Proteomic Analysis via Mass Spectrometry**; Michael Girgis[1]; Mikell Paige[1]; Gregory M Petruncio[1]; Miloslav Sanda[2, 3]; *[1]George Mason University, Manassas, VA; [2]Max Planck Institute for Heart and Lung Research, Bad Nauheim, Germany; [3]Georgetown University, Washington, DC*

WP 692 **Variance-Modeled DIA Improves Quantitative Precision Across Global and Phosphoproteomic Workflows**; Amanda L Smythers[1, 2]; Joao A Paulo[1]; Gina Turco[3]; Nimrod Rubinstein[3]; Jonathon O'Brien[3]; Steven P Gygi[1]; *[1]Harvard Medical School, Boston, MA; [2]Dana-Farber Cancer Institute, Boston, MA; [3]Golgi Biotechnology Research, San Francisco, CA*

WP 693 **ALKBH5 Interacts with the NuRD Complex to Modulate Histone Acetylation in Chromatin**; Xingyuan Chen[1]; Chengjie Ma[1]; Yinsheng Wang[1]; *[1]University of California, Riverside, Riverside, CA*

WP 694 **A proteomics workflow for isoform-resolved subcellular localization analysis**; Alicia L Richards[1, 2, 3]; Justin McKetney[1, 2, 3]; Gary R Dixon[4]; Reanna Lao[4]; Martin Kampmann[4]; Nevan J Krogan[1, 2, 3]; Danielle L Swaney[1, 2, 3]; *[1]Department of Bioengineering and Therapeutic Sciences, UCSF, San Francisco, CA; [2]Gladstone Institute, UCSF, San Francisco, CA; [3]Quantitative Biosciences Institute, University of California, San Francisco, San Francisco, S*

WP 695 **METTL1 interacts with U2AF2 to regulate RNA splicing**; Zhongwen Cao[1]; Xingyuan Chen[1]; Yinsheng Wang[1]; [1]*University of California, Riverside, Riverside, CA*

WP 696 **Multiplexed DIA platform based on highly deuterated dialkylation up to 8-plex**; Kang-Seok Yun[1]; Dong-Gi Jang[1]; Jae-Yoon Jo[1]; Jong-Seo Kim[1]; [1]*School of Biological Sciences, Seoul National University, Seoul, South Korea*

WP 697 **Harnessing the enhanced speed and sensitivity of the Orbitrap Astral Zoom MS for simultaneous targeted quantitation and comprehensive proteome coverage**; Yeva Mirzakhanyan[1]; William J Comstock[2]; Katie Peterson[1]; Amirmansoor Hakimi[2]; [1]*Thermo Fisher Scientific, West Palm Beach, FL;* [2]*Thermo Fisher Scientific, San Jose, CA*

WP 698 **Proteomic Insights into Enhanced Productivity of Enriched CHO Cell Subpopulations**; Li Wang[1]; Andy Nelson[1, 2]; Dorothy Ahlf Wheatcraft[1]; Erik L Allman[1]; Lina Chakrabarti[1]; Sonja Hess[1]; [1]*AstraZeneca, Gaithersburg, MD;* [2]*Johns hopkins university, baltimore, MD*

WP 699 **Cell-SysQuan: using SILAC cells for proteome-wide absolute quantitation**; Quinn K. Neale[1, 2]; Victor Spicer[1]; Elyssa Baker[3]; Timon Geib[3]; Javad Alizadeh[1]; Prasanta Paul[1]; Peter Kubiniok[4]; Helen Jiang[1]; Robert Popp[5]; Christoph H. Borchers[3, 6]; René P. Zahedi[1, 2, 7, 8]; [1]*Manitoba Centre for Proteomics and Systems Biology, Winnipeg, MB;* [2]*Department of Biochemistry and Medical Genetics, University of Manitoba, Winnipeg, MB, Canada, winnipeg, MB;* [3]*McGill University - Lady Davis Institute, Mo*

WP 700 **Profiling Cell Proteomics Using a New Micro-Pillar Array Column**; Yuan Lin[1]; Jia Tang[2]; Chieh Wen Lo[3]; Kevin Yang[4]; Runsheng Zheng[5]; [1]*Thermo Fisher Scientific, Sunnyvale, CA;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*Department of Medicine, Division of Infectious Diseases and Geographic Medicine, Stanford University, Stanford, CA;* [4]*Thermo Fis*

WP 701 **TMTc-Based Multiplexed DIA with Improved Complementary Ion Generation and Deconvolution Algorithms**; Hiroshi Nishida[1]; Kosuke Ogata[1]; Yasushi Ishihama[1]; [1]*Kyoto university, Kyoto, Japan*

WP 702 **Spatiotemporal Thermal Proteome Profiling to Monitor CHO Cell Stress Responses**; Harsha Gunawardena[1]; Gihoon Lee[1]; Joshua Justice[1]; Lateef Aliyu[1]; Lauren Kraft[1]; Hirsh Nanda[1]; [1]*JOHNSON AND JOHNSON, Spring House, PA*

WP 703 **Comparison of Analytical Methods for Absolute Quantitation of Synthetic Peptides**; Eileen Tudorica[1]; Peter Kubiniok[2]; Maria Trawkina[3]; Evgeniy V. Petrotchenko[1]; Christoph H. Borchers[1, 3, 4]; [1]*Lady Davis Institute for Medical Research, Montreal, QC;* [2]*Quantivum Inc., montreal, QC;* [3]*MRM Proteomics Inc, Montreal, QC;* [4]*Gerald Bronfman Department of Oncology, Jewish General Hospital, Department of Patholo*

WP 704 **Evaluating SagePRM for Automated, High-Throughput Peak Integration in Large-Cohort Targeted Proteomics**; JIHYEON LEE[1]; Robin Park[2]; Qin Fu[3]; Ali Haghani[3]; Tao Xu[2]; Titus Jung[4]; Vijayaraja Gnanasambandan[2]; Dermot McGovern[1]; John R. Yates III[4]; Jennifer E. Van Eyk[3]; [1]*Cedars Sinai Medical Center, Los Angeles, CA;* [2]*Chaparral Labs, Inc., San Diego, CA;* [3]*Cedars-Sinai Medical Center, Los Angeles, CA;* [4]*Scripps Research Institute, La Jolla, CA*

WP 705 **On the cusp of global apolipoprotein standardization through multiplex LC-MRM-MS quantitation**; Renee Ruhaak[1, 2]; Ernst Leijnse[2, 3]; Nicolaas Van Neer[3]; Nina Diederiks[3]; Christa Cobbaert[2, 3, 4]; [1]*Leiden University Medical Center, Leiden, Netherlands;* [2]*Leiden Apolipoprotein Reference Laboratory, Department of Clinical Chemistry and Laboratory Medicine, Leiden University Medical Center, Leiden, Netherlands;* [3]*Departm*

WP 706 **Spatial Proteomic Profiling of OVCAR8 Spheroids by Serial Trypsinization**; Nicole E. Platzer[1]; Amanda B. Hummon[1]; [1]*The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH*

WP 707 **Molecular Glue–Mediated Interaction and Conformational Dynamics of CSN-CRL Complexes Revealed by Integrative Structural Proteomics**; Xiaorong Wang[1]; Clinton Yu[1]; Huigang Shi[2]; Fenglong

Jiao[1]; Haibin Mao[2]; Ning Zheng[2]; Lan Huang[1]; *[1]University of California-Irvine, IRVINE, CA; [2]University of Washington, Seattle, WA*

WP 708 **High-throughput single-fiber proteomics identifies a dysregulated fiber state enriched in aged human skeletal muscle**; Cameron Movassaghi[1]; Simion Kreimer[1]; Isabell Dobrzycki[2]; Laura E Teigen[2]; Carlos S Zepeda[2]; Yuming Jiang[1]; Chrisopher W Sundberg[2]; Jesse Meyer[1]; *[1]Cedars Sinai Medical Center, Los Angeles, CA; [2]University of Wisconsin--Madison, Madison, WI*

WP 709 **Evaluating EpiTAC degradation of multi-pass transmembrane drug targets using DIA mass spectrometry**; Danica-Mae Manalo-Hebert[1]; Audrey Garces[1]; Jacob Cohen[1]; Kim Hoi[1]; Sara Yan[1]; Noah Solomon[1]; Andrew Goodrich[1]; Josef Gramespacher[1]; Lisa Marshall[1]; Ken Flanagan[1]; Maia Vinogradova[1]; Isaac Rondon[1]; Shyrai Gardai[1]; Lichao Zhang[1]; *[1]EpiBiologics, San Mateo, CA*

WP 710 **Hydraplexing: Signal Amplification via Multi-Isobaric Tagging for Multiomics**; Ailing Li[1]; Navid Ayon[1]; Peter Nemes[1]; *[1]Department of Chemistry & Biochemistry, University of Maryland, College Park, College Park, MD*

WP 711 **GPR110-Dependent Alteration of the Mouse Amygdala Proteome Revealed by Differential Proteomics**; Bill Huang[1]; Mariam Melkumyan[1]; Hee-Yong Kim[1]; *[1]NIAAA/NIH, Rockville, MD*

WP 712 **Current generation high-resolution mass spectrometry reveals inefficiencies of standard proteolytic processing in quantitative bottom-up proteomic experiments**; Jeffrey F Kuhn[1]; Greg Waitt[1]; Erik J. Soderblom[1]; *[1]Duke University School of Medicine, Durham, NC*

WP 713 **Differentiating CRBN-based Degrader Drugs from IMiDs : Derisking Potential Off-Target neosubstrate degradation using Quantitative Targeted and Discovery Proteomics**; Eric Kuhn[1]; Sarah Martinez[1]; Yatao Shi[1]; Chris Browne[1]; Yi-Ting Wang[1]; Xinbo Luo[1]; Guang Liu[1]; Brad Enerson[1]; Xiaozhang Zheng[1]; Matt Weiss[1]; Dirk Walther[1]; Kirti Sharma[1]; *[1]Kymera Therapeutics, Watertown, MA*

WP 714 **Comparing substrate scopes of human and mouse ATE1 isoforms using ATE1-based Arginylation Profiling (ABAP)**; Changfeng Deng[1]; Thilini Abeywansha[2]; Dominic Scopelliti[3]; Mingyang Jiang[1]; Sambavi Elangovan[1]; Benjamin Garcia[3]; Yi Zhang[2]; Zongtao Lin[1]; *[1]Rutgers University, Piscataway, NJ; [2]Case Western Reserve University, Cleveland, OH; [3]Washington University in St.Louis, St.Louis, MO*

WP 715 **Structure-Activity-Relationship (SAR) Study to Explore the Cause of Thermo-Induced Potency Reduction of Adeno-Associated Virus for Gene Therapy**; Yu Zhou; *MilliporeSigma, Carlsbad, CA*

WP 716 **An optimized limited proteolysis method to quantify VP1u Externalization from AAV Capsids under different stress conditions**; Ruiyi Dong[1]; Gabriella S López-Pérez[2]; Xiang Ye[1]; Yunli Hu[1]; Haibo Qiu[1]; Ning Li[1]; *[1]Regeneron, Tarrytown, NY; [2]MIT, Cambridge, MA*

WP 717 **Degradation analysis of recombinant adeno-associated virus by charge-detection mass spectrometry**; Yuki Yamaguchi[1]; Zhuolun Yang[1]; Emily Christofi[2]; Anisha Haris[2]; Xiaofang Lyu[1]; Yasuo Tsunaka[1]; Susumu Uchiyama[1]; *[1]The University of Osaka, Osaka, Japan; [2]Waters Corporation, Wilmslow, United Kingdom*

WP 718 **Viral Membrane Protein Multi-Functionality Orchestrated by Phosphorylated Proteoforms**; Yennifer Delgado[1]; Andrea Chan[1]; Min Hur[1]; Shipra Sharma[1]; Prashant Kaushal[1]; Alexia Andrikopoulos[1]; Katherine Vineall[1]; Immy Ashley[1]; Danielle Schmitt[1]; Mehdi Bouhaddou[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

WP 719 **Charge Detection Mass Spectrometry for Evaluation of Influenza Vaccines in an Orbitrap Mass Spectrometer**; Malcolm A. Barnard[1]; Jennifer S. Brodbelt[1]; *[1]University of Texas at Austin, Austin, TX*

WP 720 **Global Landscape of Human Protein Complexes Remodeled During Viral Infection**; Shipra Sharma[1, 2, 3]; Anne Zaiss[4]; Arjit V Jeyachandran[4]; Brandon Jolly[5]; Callie Phung[1, 2, 3]; Kareem A Alba[1, 2, 3]; Monita Muralidharan[6, 7, 8]; Yennifer Delgado[1, 2, 3]; Immy Ashley[1, 2, 3]; Sophie Lin[1, 2, 3]; Vijaya Pandey[9, 10];

Adarsh K Mayank[9, 10]; Ignacia Echeverria[11]; Vaithilingaraja Arumugaswami[4]; Mehdi Bouhaddou[1, 2, 3]; *[1]Department of Microbiology, Immunology and Molecular Genetics, University of California, Los Angeles, Los Angeles, CA, USA., LOS ANGELES, CA; [2]Institute for Quantitative and Computational Biosciences, University of California, Los A*

WP 721 **Lineage-prevalence peptide databases and mutation discovery enable sensitive viral detection in oral fluid metaproteomics**; Yanjia Zhang[1]; Michael R. Shortreed[2]; Aaron T. Timperman[1]; *[1]University of Pennsylvania, Philadelphia, PA; [2]University of Wisconsin-Madison Department of Chemistry, Madison, WI*

WP 722 **What's Inside a Vaccine? A Closer Look Using Charge Detection Mass Spectrometry**; Anisha Haris[1]; Lohra M Young[2]; Benjamin E Draper[2]; Jakub Ujma[1]; Keith Richardson[1]; Martin F Jarrold[2]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Megadalton Solutions, Bloomington, IN*

THURSDAY MORNING ORALS

ThP 001 **A Decision Support Scheme for Clinical Implementation of Mass Spectrometry-Based Tissue Pathology Determination to Guide Brain Cancer Care**; Darah Vlaminck[1]; Alexa Fiorante[1]; Michael Woolman[1]; Francis Talbot[2]; David Munoz[3]; Farshad Nassiri[2]; Gelareh Zadeh[2]; Sunit Das[3]; Howard Ginsberg[3]; Chris McIntosh[2]; Scott Hopkins[4]; Arash Zarrine-Afsar[1]; *[1]University of Toronto, Toronto, ON; [2]University Health Network, TORONTO, ON; [3]Unity Health Toronto, Toronto, ON; [4]University of Waterloo, Waterloo, ON*

ThP 002 **Development of an ambient ionization mass spectrometry technique for rapid on-skin screening of environmental exposures**; Forough Doustkhahvajari[1]; Stephanie Rankin-Turner[1]; *[1]University of Pittsburgh, Pittsburgh, PA*

ThP 003 **Quantitative analysis of cannabinoids by zone heat-assisted DART-MS with in-situ flash derivatization**; Wen Dong[1]; Mengliang Zhang[1]; *[1]Ohio University, Athens, OH*

ThP 004 **Extraction-free TLC-DESI-MSI enables reproducible metabolomic and lipidomic profiling of cultured cell pellets**; Wei Chen[1]; Chiara Urban[2, 3]; Hakan Taskiran[3, 4]; Chenyue Dai[5, 6]; Kıvanç Görgülü[6, 7]; Julia Jellusova[3, 4]; Nicole Strittmatter[1]; *[1]Department of Bioscience, School of Natural Sciences, Technical University of Munich, Munich, Germany; [2]Institute of Clinical Chemistry and Pathobiochemistry, School of Medicine and Health, University Hospital of Technical University of Munich, Munich, Germany; [3]TranslaTUM, Center for Translational Cancer Research, Technical University of Munich, Munich, Germany; [4]Institute of Clinical Chemistry and Pathobiochemistry, Technical University of Munich, TUM University Hospital, Munich, Germany; [5]Institute for Tumour Metabolism, Comprehensive Cancer Center München, School of Medicine and Health, University Hospital of Technical University of Munich, Munich, Germany; [6]Institute of Metabolism and Cell Death, Helmholtz Zentrum München, Neuherberg, Germany; [7]Comprehensive Cancer Center Munich, Technical University of Munich, TUM University Hospital, Munich, Germany*

ThP 005 **Fatty Acid Identification by HPLC–EESI–MS/MS via Online In-Source Derivatization**; Richard Frimpong[1]; Victor Ryzhov[1]; *[1]Northern illinois University, DEKALB, IL*

ThP 006 **High-Throughput DESI-MS Workflows for Rapid PFAS Recovery and Screening in Beef Biopsies**; Kevin Andres Perez Bastidas[1, 2, 3]; Emilio Restrepo Nunez[1, 4, 5]; Yunfei Feng[6]; Steven Lai[7]; Jinxi Li[8]; Anthony Midey[7]; Ryan T Hilger[6]; Nicolas Mauricio Morato Gutierrez[1, 9]; Christina Ferreira[4, 10]; *[1]Purdue University, west lafayette, IN; [2]Bindley Bioscience Center, Purdue University, West Lafayette, IN, west lafayette, IN; [3]Universidad Nacional de Colombia, Medellin, Colombia; [4]Bindley Bioscience Center, Purdue University, West Lafayette, IN; [5]Universidad de los Andes, Bogota, Colombia; [6]Purdue University Dept of Chemistry, West Lafayette, IN; [7]Waters, Milford, MA; [8]Waters Corporation, Costa Mesa, CA; [9]Purdue Institute for Cancer Research, West Lafayette, IN; [10]Purdue University, West Lafayette, IN*

ThP 007 **Optimizing rapid identification of prohibited substances in sport using ASAP-MS and an advanced data-analysis workflow**; Alisha Henderson[1]; Oliver Krug[2]; David Douce[3]; Ashley Sage[3]; Scott Campbell[4]; John Moncur[4]; Mario Thevis[2]; Liam Heaney[1]; *[1]Loughborough University, Loughborough, United Kingdom; [2]German Sport University Cologne, Cologne, Germany; [3]Waters Corporation, Wilmslow, United Kingdom; [4]SpectralWorks Ltd, Runcorn, United Kingdom*

ThP 008 **Exploration of native DESI for the direct characterization and discovery of metal bound metabolites using hybrid Orbitrap-FTICR mass spectrometry**; Kevin J. Zemaitis[1]; Bryson Gibbons[1]; Erin Bredeweg[1]; Tobias P. Woerner[2]; Matthias Biel[2]; Alexander A. Makarov[2]; Ljiljana Pasa-Tolic[1]; William Kew[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

ThP 009 **High-Throughput Quantitation of Plasma Trimethylamine N-oxide Using Desorption Electrospray Ionization Mass Spectrometry for Rapid Cardiovascular Disease Screening**; Kai-Yuan Chiu[1, 2]; Hao Chen[1]; Yun-Chen Hsieh[2]; Hsin-Bai Zou[2]; Hsien-Li Kao[3]; Wei-Kai Wu[3]; Cheng-Chih Hsu[2]; *[1]New Jersey Institute of Technology, Newark, NJ; [2]National Taiwan Univeristy, Taipei city, Taiwan; [3]National Taiwan University Hospital, Taipei, Taiwan*

ThP 010 **Evaluation of DBDI-HRMS tools for rapid and accurate authentication of the geographical origin of honey**; Carmela Zacometti; *Istituto Zooprofilattico Sperimentale delle Venezie, Vicenza, Italy*

THURSDAY MORNING ORALS

ThP 011 **Rapid Semiquantitative Screening of Anabolic Agents Using Dielectric Barrier Discharge Ionization**; Jana Knytlová[1, 2]; Alžběta Nemeškalová[1, 2]; Iveta Šilhánková[1]; Petra Dinisová[3]; Martin Kuchař[1]; Michael Volný[1, 2]; *[1]University of Chemistry and Technology, Prague, Czech Republic; [2]Institute of Microbiology CAS, Prague, Czech Republic; [3]Pragolab s.r.o., Prague, Czech Republic*

ThP 012 **Spatially Defined Direct Surface Scanning of HPTLC Plates by DART-MS for Correlated Chromatographic–Mass Spectrometric Profiling**; Yanfang Li[1]; Jianghao Sun[2]; Wilmer H. Perera[3]; Mengliang Zhang[1]; *[1]Department of Chemistry and Biochemistry, Ohio University, Athens, OH; [2]Methods and Application of Food Composition Laboratory, Beltsville Human Nutrition Research Center, U.S. Department of Agriculture, Beltsville, MD; [3]CAMAG Scientific Inc., Wilmington, NC*

ThP 013 **Spontaneous α-C−H Carboxylation of Ketones by Gaseous CO2 at the Air-water Interface of Aqueous Microdroplets**; Sinchan Mukhopadhyay[1]; Pallab Basuri[1]; K. S. S. V. Prasad Reddy[1]; Keerthana Unni[1]; Spoorthi B.K. [1]; Jenifer Shantha , Kumar[1]; Sharma S. R. K. C. Yamijala[1]; Thalappil Pradeep[1]; *[1]IIT Madras, Chennai, India*

ThP 014 **Detection of nerve agent hydrolysis marker phosphonates using laser ablation rapid evaporative ionisation mass spectrometry**; Lucy Noyes[1, 2]; Ingvild Comfort Hvinden[3]; William J C Francis[2]; Peter Biggins[4]; Daniel Simon[5]; Lauren Ford[1]; Zoltán Takats[1, 5]; Robert T. Murray[2]; *[1]Department of Metabolism, Digestion and Reproduction, Imperial College London, London, United Kingdom; [2]Department of Physics, Imperial College London, London, United Kingdom; [3]Norwegian Defence Research Establishment (FFI), Instituttveien 20, Kjeller, Norway; [4]Centre for Active Resilience and Security, Department of Civil Engineering, Imperial College London, London, United Kingdom; [5]Institute for Multimodal Imaging of Intercellular Communication, Universität Regensburg, Regensburg, Germany*

ThP 015 **Rapid Quantification of the Foxy Odorants Methyl Anthranilate and o-Aminoacetophenone in Grapes Using Cartridge–Based Headspace Extraction with DART-MS**; Andre P Kalenak[1]; Matthew W Scimeca[2]; Jack N Tsai[1, 3]; Gavin L Sacks[1]; Terry L Bates[2]; *[1]Cornell University, Ithaca, NY; [2]Quantera Analytical, Ithaca, NY; [3]Emory University, Atlanta, GA*

ThP 016 **In Situ SICRIT-HRMS Enables Polarity-Resolved Fingerprinting and Differential Ion Discovery in Complex Soy Sauce Matrices**; Charles C. Liu[1]; Shujie Zou[1]; Echo W. Jia[1]; Xiaokun Duan[1]; *[1]ASPEC Technologies Limited, Beijing, China*

ThP 017 **Evaluation of a Novel Multibarrel Electrospray Probe for Direct Infusion Metabolomics**; Lucie Davidová[1]; Ingela Lanekoff[1]; *[1]Uppsala University, Uppsala, Sweden*

ThP 018 **Ambient Ionization Mass Spectrometric Detection of Aroma Released During Gummy Chewing**; Ayako Nomura[1]; Takehito Sagawa[2]; Akihiro Suzuki[3]; Teruhisa Shiota[3]; Manami Kobayashi[4]; *[1]Shimadzu corporation, Kawasaki-city, Japan; [2]S&B FOODS INC, Tokyo, Japan; [3]AMR, Inc., Tokyo, Japan; [4]Shimadzu corporation, Kawasaki, Japan*

ThP 019 **Event-Resolved Molecular Profiling of Cigarette Flavor Capsules by SICRIT-HRMS**; Zhenxing Li[1]; Wei Ke[1]; Weimin Ouyang[2]; Xiaokun Duan[3]; Wenhao Yu[1]; Yachang Xu[1]; Charles C. Liu[3]; Yu-An Sun[1]; *[1]Zhengzhou University of Light Industry, Zhengzhou, China; [2]Beijing Lumiere Tech Ltd, Beijing, China; [3]ASPEC Technologies Limited, Beijing, China*

ThP 020 **From Rapid Screening to Spatial Lipidomics: Multi-Scale Ambient Ionisation Mass Spectrometry Reveals Chemotherapy-Induced Phospholipidosis and Lipid Reprogramming in Ovarian Cancer**; Stefania Maneta-Stavrakaki[1]; Maria Paraskevaidi[1]; Duncan Roberts[1]; Samantha Hardman[1]; Liying Wan[1]; Lucy Noyes[1]; Apostolia Galani[1]; Laura Burney Ellis[1, 2]; William J. C. Francis[1]; Erika Dorado[1]; Yuchen Xiang[1, 3]; Robert T Murray[1]; Maria Kyrgiou[1, 2]; Zoltan Takats[1, 3]; *[1]Imperial College London, London, United Kingdom; [2]Imperial College Healthcare NHS Foundation Trust, London, United Kingdom; [3]University of Regensburg, Regensburg, Germany*

ThP 021 **A method for assessing the extent of postmortem tissue deterioration to validate autopsy specimens as a source of medical information**; Stanislav Pekov[1]; Ekaterina Parochkina[1]; Andrey Temnov[1]; Denis Zavorotnyuk[1]; Denis Bormotov[1]; Igor Popov[1]; *[1]MIPT, Dolgoprudny, Russian Federation*

ThP 022 **Time-Resolved SICRIT–HRMS Reveals Reversible Molecular Trajectories in Human Oral Headspace Following Rinse Application**; Shujie Zou[1]; Xiaokun Duan[1]; Echo W. Jia[1]; Charles C. Liu[1]; *[1]ASPEC Technologies Limited, Beijing, China*

ThP 023 **Rapid Ambient MS Screening of Lovastatin in Food Supplements for Regulatory Compliance**; Alzbeta Nemeskalova[1, 2]; Hana Mezlova[1]; Jana Knytlova[1, 2]; Michael Volny[1, 2]; *[1]University of Chemistry and Technology Prague, Prague, Czech Republic; [2]Institute of Microbiology CAS, Prague, Czech Republic*

ThP 024 **Data-Driven Differentiation and Marker Discovery of Real-World Samples by SICRIT-HRMS and Multivariate Analysis**; Echo W. Jia[1]; Shujie Zou[1]; Xiaokun Duan[1]; Charles C. Liu[1]; *[1]ASPEC Technologies Limited, Beijing, China*

ThP 025 **Reconsidering Quantitative Pyrazine Analysis by Chromatography-Free Ambient Ionization Mass Spectrometry**; Hongbo Gao[1]; Yuan Zhuang[1]; Echo W. Jia[2]; Bingjie Liu[3]; Xiaojie Sun[3]; Xiaokun Duan[2]; Charles C. Liu[2]; *[1]China National Research Institute of Food and Fermentation Industries, Beijing, China; [2]ASPEC Technologies Limited, Beijing, China; [3]SCIEX, Beijing, China*

ThP 026 **New approach for the quantitation of conjugated payloads by LC-MS from dual-payload ADCs in preclinical samples**; Luca M. Barbero; *RBM MercK, Colleretto Giacosa, Italy*

ThP 027 **Developing Advanced Online Two-dimensional Liquid Chromatography-Mass Spectrometry Technique for Hydrophobic Interaction Chromatography Peak IDs of Antibody Drug Conjugates**; Qianyi Wang[1]; Xiaoying Ye[1]; Chunlei Wang[1]; *[1]AstraZeneca, Gaithersburg, MD*

ThP 028 **Streamlining the Upstream and Downstream Analytical Processes**; Jinlai Wei[1]; Jonathan Le[1]; Renee Yu[1]; Ishmael Ordonez[1]; Yuanzhong Li[2]; Leon Pybus[3]; Hasmik Grigoryan[1]; *[1]FUJIFILM Biosciences, Irvine, CA; [2]Bioscience & Engineering Laboratories, Fujifilm Corporation, Kaisei, Kanagawa, Japan; [3]FUJIFILM Biotechnologies, Billingham, United Kingdom*

ThP 029 **Optimizing Use of the Novel Chymotrypsin rChymoSelect for Improved Peptide Mapping Workflows**; Alba Katiria González Rivera[1]; Thomas Nylandsted Krogh[2]; Michael Rosenblatt[1]; Sergei Saveliev[1]; Marjeta Urh[1]; *[1]Promega Corporation, Madison, WI; [2]Novo Nordisk A/S, Måløv, Denmark*

ThP 030 **Characterization of an antibody-oligonucleotide conjugate using native mass spectrometry and electron-activated dissociation (EAD)-based peptide mapping approaches**; Haichuan Liu[1]; Jingwen Ding[1]; Roxana Eggleston-Rangel[2]; Sujatha Chilakala[2]; Pham Tran[2]; Zoe Zhang[1]; *[1]SCIEX, Redwood City, CA; [2]Phenomenex, Torrance, CA*

ThP 031 **Characterization of antibody-drug conjugate (ADC) and in vivo biotransformation by a novel automated immunocapture and microflow LC-MS platform**; Jixing Lyu[1]; Haiting Zhang[1]; Olav Olsen[1]; William Olson[1]; Marc Cao[1]; *[1]Regeneron Pharmaceuticals Inc, Tarrytown, NY*

ThP 032 **Structure-Function Characterization of Therapeutic mAb Using Forced Degradation Studies**; Weihan Wang[1]; Qing Mike Tang[1]; Ping Hu[1]; *[1]Johnson & Johnson Innovative Medicine, Malvern, PA*

ThP 033 **Analog Chymotrypsin with Narrow Specificity Advances Antibody Peptide Mapping and PTM Quantitation**; Prashant N Jethva[1]; Alba Katiria González Rivera[2]; Sergei Saveliev[2]; Daniel W Woodall[1]; Pavel Bondarenko[1]; Andrew B. Dykstra[1]; *[1]Amgen, Thousand Oaks, CA; [2]Promega Corporation, Madison, WI*

ThP 034 **A High-Throughput Screening Workflow for the Quantification of Antibody Modifications**; Jennifer T. Aguilan[1]; Carlos Madrid-Aliste[1]; Fereshteh Zandkarimi[2]; Alexey Makarov[3]; Alycia Shoultz[4]; Umme Ayesa[4]; Hang Hu[4]; Zachary E. X. Dance[4]; Anumita Saha-Shah[4]; Simone Sidoli[1]; *[1]Albert Einstein College of Medicine, Bronx, NY; [2]Columbia University, New York, NY; [3]Merck & Co., Inc., Boston, MA; [4]Merck & Co., Inc., Rahway, NJ*

ThP 035 **Enzymatic-Assisted RP-LC-MS Characterization of Unpaired Disulfide Bonds in Monoclonal Antibodies with Engineered Cysteines**; Fan Zhang[1]; Xiangfeng Niu[1]; Manish Hudlikar[1]; Alycia Uyeoka[1]; Laurence Fayadat-Dilman[1]; Jason Hogan[1]; *[1]Merck & Co., Inc., South San Francisco, CA*

ThP 036 **Investigation Strategies of the ADC Payload with the Thiol Group in In Vivo Samples**; Hongmei Wang[1]; Jiaming Jiang[1]; Yafei Gao[1]; Min Lv[1]; Menghan Li[1]; Manman Dai[1]; Yingjun Ma[2]; Zhiyu Li[1]; Lili Xing[1]; Yi Tao[1]; Liang Shen[1]; *[1]WuXi AppTec, Pudong, Shanghai, China; [2]WuXi AppTec, Cranbury, NJ*

ThP 037 **Characterization of mAbs and ADCs by direct coupling of capillary isoelectric focusing with mass spectrometry**; Gianni Vandenborre[1]; Jasmin Schairer[1]; Esther Devloo[1]; Thu Ba Nguyen[2]; Tao Bo[3]; Tiemin Huang[3]; Mabelle Meersseman[1]; Pat Sandra[1]; Koen Sandra[1]; *[1]RIC Group, Kortrijk, Belgium; [2]Isogen Life Science BV, Utrecht, Netherlands; [3]Advanced Electrophoresis Solutions Ltd, Cambridge, ON*

ThP 038 **LC-MS/MS implementation and optimization for mAb released N-glycan**; Kelly Cavalcanti Machado[1]; Thiago Bousquet Bandini[1]; Hulyana Brum[1]; Laura Helena Schroeder Borges[1]; Anna Erika Vieira De Araujo[2]; Iaralice Medeiros De Souza[2]; Michel Batista[1]; *[1]Mass Spectrometry Facility, Carlos Chagas Institute, Fiocruz, Curitiba, Brazil; [2]Institute of Technology in Immunobiologicals, Fiocruz, Rio de Janeiro, Brazil*

ThP 039 **Evaluation of disulfide bond scrambling in monoclonal antibodies by peptide mapping in non-reducing conditions**; Esther Devloo[1]; Gianni Vandenborre[1]; Arnd Brandenburg[2]; James Duffy[3]; Catherine Evans Joines[2]; Laura Radu Parlog[2]; Tom Merchiers[1]; Nathan Cardon[1]; Nathan Gérard[1]; Mabelle Meersseman[1]; Pat Sandra[1]; Koen Sandra[1]; *[1]RIC Group, Kortrijk, Belgium; [2]Genedata AG, Basel, Switzerland; [3]Genedata Ltd, Cambridge, United Kingdom*

ThP 040 **Identification of isomeric amino acids in the antigen binding region of a monoclonal antibody by electron capture dissociation**; Gianni Vandenborre[1]; Esther Devloo[1]; Christian Klein[2]; Julie Horner-Buxton[3]; Rachel Franklin[4]; Sonja Schneider[2]; Jonathan Vandenbussche[1]; Mabelle Meersseman[1]; Pat Sandra[1]; Koen Sandra[1]; *[1]RIC Group, Kortrijk, Belgium; [2]Agilent Technologies Deutschland GmbH, Waldbronn, Germany; [3]Agilent Technologies, Inc., Santa Clara, CA; [4]Agilent Technologies, CORVALLIS, OR*

ThP 041 **Rapid Assessment of Antibody Aggregates using SEC-MS and a Multi-Pronged Sliding Window Deconvolution Approach**; Matthew T Robey[1]; Tong Ding[2]; Hugo C. R. De Jesus[2]; Jacob W McCabe[1]; Aaron O Bailey[2]; Kenneth R Durbin[1]; *[1]Proteinaceous, Evanston, IL; [2]AbCellera Biologics, Vancouver, BC*

ThP 042 **Quantification of Antibody-Conjugated Drug in Cleavable ADCs: A Universal, Automated, and Cost-Effective LC-MS/MS Platform**; Mimi Wan[1]; Huiting Xu[1]; Yihui Zhu[1]; Pin Jiang[1]; Jian Ge[1]; *[1]DMPK Department, Shanghai Medicilon Inc., Shanghai, China*

ThP 043 **A comprehensive MS-based strategy to understand protein–protein interfaces and the mechanisms of dimer/high molecular weight (HMW) formation**; Jusung Lee[1]; Chumsae Chris[2]; Balakrishnan Gurusamy[3]; Michael L. Gross[1]; *[1]Washington University in St.Louis, St.Louis, MO; [2]Bristol Myers Squibb, Devens, MA; [3]Bristol-Myers Squibb, New Brunswick, NJ*

ThP 044 **De-Novo Drug Antibody Ratio Quantification for Antibody Drug Conjugates with Deep Learning**; Vishnu R. Tejus[1]; David S. Roberts[1]; Andrew H. Reiter[1]; Carolyn R. Bertozzi[1, 2]; *[1]Stanford University, Stanford, CA; [2]Howard Hughes Medical Institute, Chevy Chase, MD*

ThP 045 **Evaluating critical quality attributes of bispecific antibodies by multi-level mass spectrometry**; Kyle Hoffman[1]; Jacquelyn Jhingree[1]; Wenting Li[1]; Weiwu Chen[1]; Yandong Zhu[1]; Baozhen Shan[1]; *[1]Bioinformatics Solutions Inc, Waterloo, ON*

ThP 046 **Comprehensive MS Characterization Strategies to Support Cell Line Development for Non-Standard Modalities**; Gong Cheng; *Asimov Inc, Boston*

ThP 047 **Redefining Antibody Diagnostics of Viral Infections through Proteome-Wide Serology**; Zoe Turner[1]; Yasmine Rais[1]; Andrei Drabovich[1]; [1]*Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB*

ThP 048 **SISCAPA-LC–MS/MS for Bioanalysis of Biotherapeutics in Human Serum**; Eric W. Ma[1]; David Cui[1]; Minghao Sun[1]; William Mylott[1]; [1]*PPD, part of Thermo Fisher Scientific, Henrico, VA*

ThP 049 **Expanding upon sheath gas modifiers to enable routine use of strong ion pairing agents in chromatographic separations for LCMS**; Jon M Reed[1]; Chamalee Demalgiriya Gamage[1]; Shiyu Dong[1]; Kristina Gueneva-Boucheva[1]; Angela LaCroix-Fralish[1]; Savon Vigil[1]; Lee Frego[1]; [1]*Boehringer Ingelheim, Ridgefield, CT*

ThP 050 **Predicted Peptide Spectral Libraries Enhances High-Confidence Sequence Variants Analysis in Therapeutic Antibodies**; Shivkumar Raidas[1]; Yunlong Zhao[1]; Yuan Mao[1]; Ning Li[1]; [1]*Analytical and Biological Mass Spectrometry, Regeneron Pharmaceuticals Inc., Tarrytown, NY*

ThP 051 **Characterizations of antibody oligonucleotide conjugates utilizing robust SEC and IEX LC separations and UV, MALS and MS detection strategies**; Shilin Cheung[1]; Roxana Eggleston-Rangel[1]; Sujatha Chilakala[1]; Jacey Yan[2]; Lois Luo[2]; Daniel Meng[2]; [1]*Phenomenex Inc., Torrance, CA;* [2]*VectorBuilder China, Guangzhou, China*

ThP 052 **The Effect of Different Mobilizer Additives on Sample Stability and Subsequent MS Analysis with DynaChip X1 Online Buffer Exchange**; Will McElroy[1]; Casey Vantucci[2]; Suraj Dhungana[2]; Christopher Heger[1]; Mason Chilmonczyk[2]; Francisco Ramirez[1]; [1]*ProteinSimple a Bio-Techne Brand, San Jose, CA;* [2]*Andson Biotech, Atlanta, GA*

ThP 053 **Revealing mAb Oligomers that Skew Concentration in High Protein mAb Formulations Using CG-MALS and Native IM-MS to Improve Dose Accuracy**; Kristine F. Parson[1]; Benjamin Pizio[1]; Madison White[1]; Adam Connor[1]; Clara Smith[1]; [1]*FUJIFILM Biotechnologies USA, Inc., Morrisville, NC*

ThP 054 **Rapid characterization of charge variants in therapeutic proteins using orthogonal CE-MS and 2D-LC-MS Methodologies**; Conner P Swearingen[1]; Junhua Wang[2]; Weitao Jia[2]; [1]*Gilead Sciences, Inc., Foster City, CA;* [2]*Gilead Sciences Inc., Foster City, CA*

ThP 055 **Credibility in Modern Science: How Researchers Can Evaluate What to Trust**; Amy Nguyen; *Phenomenex, Torrance, CA*

ThP 056 **Extracting High-Confidence Subsequence Tags from De Novo Sequencing Predictions**; Justin Sanders[1]; Devanshi Desai[1]; William S Noble[1]; [1]*University of Washington, Seattle, WA*

ThP 057 **Virtual High-Resolution Mass Spectral Library Generated by a Transfer Learning-Based Neural Network for PFAS Characterization**; Yi-Chi Chen[1]; Hsin-Yi Wu[2]; Man-Ni Zhuang[1]; Chen-Ming Yi[3]; Wei-Sheng Wu[4]; Pao-Chi Liao[1]; [1]*Department of Environmental and Occupational Health, College of Medicine, National Cheng Kung University, Tainan, Taiwan;* [2]*Instrumentation Center, National Taiwan University, taipei, Taiwan;* [3]*Institute of Computer and Communication Engineering, National Cheng Kung University, Tainan, Taiwan;* [4]*Department of Electrical Engineering, National Cheng Kung University, Tainan, Taiwan*

ThP 058 **Embedding fusion for accurate, compact, and fast acquisition-aligned peptide spectral libraries**; Siegfried Gessulat[1]; Lizi Mamisashvili[2]; Tobias Schmidt[2]; Daniel P Zolg[2]; Martin Heinrich Frejno[2]; [1]*MSAID, Berlin, Germany;* [2]*MSAID, Garching bei München, Germany*

ThP 059 **Building FoxMHC for peptide-HLA contrastive learning and shared neoepitope discovery**; Wen-Feng Zeng; *Westlake University, Hangzhou, China*

ThP 060 **Vibe Coding Mass Spectrometry Tools (I'm Sorry)**; Jonathan Katz; *USC, Los Angeles, CA*

ThP 061 **Image-Based AI for metabolomics data processing: Direct Ion Map Classification Enables Fast Phenotype Prediction**; Songjie Chen[1]; Yang Li[1]; Peter Zhang[2]; Bo Yuan[1]; Maria Madeira[1]; Li Li[1]; Rosa

Sanchez[3]; *[1]Merck & Co., Inc., South San Francisco, CA; [2]Merck & Co., Inc., Cambridge, MA; [3]Merck & Co., Inc., West Point, PA*

ThP 062 **Transformer-Based Model Powered by Large-Scale Multi-Instrument Data Enables Generalization to Challenging New Instruments with Minimal Calibration**; Circe Hsu[1]; Sophia C. Carroll[1]; Luke S. Ferro[1]; Jennifer S. Campbell[1]; Ana S. H. Costa[1]; Craig Knisley[1]; Antonio H. de O. Fonseca[1]; *[1]Matterworks, Somerville, MA*

ThP 063 **Probabilistic Deconvolution of Polymicrobial MALDIMassSpectra Using Maximum Likelihood Decomposition**; Anthony Lavertu[1, 2]; Kanae Teramoto[3]; Zhiqiang Pang[1, 4]; Jacques Corbeil[1, 2, 4]; *[1]Université Laval, Quebec, QC; [2]Linearis Labs, Quebec City, QC; [3]Shimadzu Corporation, Kyoto, Japan; [4]MILA Quebec Artificial Intelligence Institute, Montreal, QC*

ThP 064 **Can generative AI take over? Evaluation of complex PTR-TOF-MS data utilizing two popular chatbots**; Alfons Jordan[1]; Bea Rosenkranz[1]; Rene Gutmann[1]; Andreas Mauracher[1]; Christian Lindinger[1]; Philipp Sulzer[1]; *[1]IONICON Analytik GmbH., Innsbruck, Austria*

ThP 065 **Hivebot: An Interactive AI Assistant Integrating ML-Based Peak Detection for MS Data Analysis**; Ipputa Tada[1]; Kazuto Mannen[1]; Mitsuhiro Kanazawa[1]; Atsushi Ogiwara[1]; *[1]Reifycs Inc., Tokyo, Japan*

ThP 066 **DIA-CLIP: a universal representation learning framework for zero-shot DIA proteomics**; Yucheng Liao[1]; Han Wen[2]; Weinan E[1, 2]; Weijie Zhang[2]; *[1]Peking University, Beijing, China; [2]AI for Science Institution, Beijing, China*

ThP 067 **PhosSight: A Unified Deep Learning Framework Boosting and Accelerating Phosphoproteomic Identification to Enable Biological Discoveries**; Xinpei Yi; *National Facility for Protein Science in Shanghai, Shanghai Advanced Research Institute, Chinese Academy of Sciences, Shanghai, China*

ThP 068 **AlphaXtract: A Deep Learning Framework for Scalable Targeted Proteomics Enabling >3,000 Multiplexed Targets**; Michael Baggio Lorenz[1]; Tim Heymann[1]; Maria Wahle[1]; Georg Wallmann[1]; Johannes Müller-Reif[1]; Kyle Le-Huray[2]; Sophia Steigerwald[2]; Max Hoek[2]; Johannes Petzoldt[2]; Philip M. Remes[3]; Christian Hock[2]; Matthias Mann[1]; *[1]Max Planck Institute of Biochemistry, Planegg, Germany; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]Thermo Fisher Scientific, San Jose, CA*

ThP 069 **Software-Aided Prediction of Key Peptide Properties Using LC–MS Data**; Paula Cifuentes[1, 2, 3]; Ramon Adàlia[2, 3, 4]; Lisa A. Vasicek[5]; Richard Gundersdorf[5]; Abigail Wheeler[5]; Paul Harradine[5]; Ismael Zamora[3]; *[1]Universitat Pompeu Fabra, Barcelona, Spain; [2]Lead Molecular Design, SL, Sant Cugat del Vallès, Spain; [3]Mass Analytica, S.L., Sant Cugat del Vallés, Spain; [4]Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Spain; [5]Merck & Co., Inc., West Point, PA*

ThP 070 **Predicting Electron Ionization Mass Spectra Using a Deep Neural Network to Aid in Critical Evaluation of Spectral Libraries**; Lewis Geer; *NIST, Gaithersburg, MD*

ThP 071 **An AI-Driven Adaptive Temporal Acquisition Method for FT-ICR Mass Spectrometry Imaging**; Mithunjha Anandakumar[1, 2]; Timothy J Trinklein[2, 3]; Jonathan V Sweedler[1, 2, 3]; Fan Lam[1, 2]; *[1]Department of Bioengineering, University of Illinois Urbana Champaign, Urbana, IL; [2]Beckman Institute for Advanced Science and Technology, University of Illinois Urbana Champaign, Urbana, IL; [3]Department of Chemistry, University of Illinois Urbana Champaign, Urbana, IL*

ThP 072 **Assessing the toxicity of unidentified chemicals through MS2 spectra embeddings**; Yvonne Kreutzer[1]; Anneli Kruve[1]; *[1]Stockholm University, Stockholm, Sweden*

ThP 073 **Laser Desorption Mass Spectrometry and Machine Learning for the Detection of Potential Extraterrestrial Microbial Signatures**; Ashley M. Hanna[1]; Rohan Pattnaik[2]; Jill A. Mikucki[3]; Vedran Lekic[1]; *[1]University of Maryland, College Park, MD; [2]Johns Hopkins University, Baltimore, MD; [3]University of Tennessee, Knoxville, TN*

ThP 074 **AI-Powered Custom Visualization Generation: Enabling Flexible Scientific Exploration in Mass Dynamics 3.0**; Mansi Aggarwal[1]; Sean Brady[1]; Aaron Triantafyllidis[1]; Andrew I. Webb[1]; Giuseppe Infusini[1]; *[1]Mass Dynamics, Melbourne, Australia*

ThP 075 **Physically-Grounded Morphological Clustering Conditioned on Text Criteria for AI-based Quality Control of LC–MS**; Daniel Siegismund[1]; Arnd Brandenburg[1]; Reto Ossola[1]; Stephan Steigele[1]; *[1]Genedata AG, Basel, Switzerland*

ThP 076 **A Deep Learning Model for De Novo Sequencing of Intact N-linked Glycopeptides from Tandem Mass Spectra**; Qingyang Xiao[1]; Haixu Tang[1]; *[1]Indiana University Bloomington, Bloomington, IN*

ThP 077 **Nanoparticle-Enhanced Mass Spectrometry Coupled with Machine Learning: Dual-Biofluid Metabolomic Stratification of BPH Drug Resistance**; Shilong Liu; *Shanghai Jiao Tong University, Shanghai, China*

ThP 078 **Training a de novo sequencer to distinguish leucine from isoleucine**; Gwenneth Straub[1]; Wout Bittremieux[2]; Miklos Guttman[3]; William S Noble[1, 4]; *[1]Department of Genome Sciences, University of Washington, Seattle, WA; [2]Department of Computer Science, University of Antwerp, Antwerp, Belgium; [3]Department of Medicinal Chemistry, School of Pharmacy, University of Washington, SEATTLE, WA; [4]Paul G. Allen School of Computer Science and Engineering, University of Washington, Seattle, WA*

ThP 079 **In-Depth Plasma Proteome Profiling Reveals Disease-Associated Signatures in a Colorectal Cancer Pilot Study**; Quentin Enjalbert[1]; Zehan Hu[1]; Sandra Schaer[2]; Katharina Limm[1]; Roland Bruderer[2]; Nils A Kulak[1]; *[1]PreOmics GmbH, Martinsried, Germany; [2]Biognosys AG, Schlieren, Switzerland*

ThP 080 **In-depth characterization of the P2 Plasma Enrichment Workflow**; Arthur Viodé[1]; Sandra Schär[1]; Liliana Malinovska[1]; Polina Shichkova[1]; Martin Mehnert[1]; Wouter Van Bergen[1]; Alan Shomo[2]; Jan Muntel[2]; Christopher Below[1]; Yuehan Feng[1]; Roland Bruderer[1]; *[1]Biognosys AG, Schlieren, Switzerland; [2]Biognosys Inc., Newton, MA*

ThP 081 **Rethinking Microbiome Readouts: What Plasma Metabolomics Can Reveal**; Jessica C Little[1]; Ramanujam Ramaswamy[1]; Angelica Moran[1, 2]; Sabrina Imam[3]; Antonio Hernandez[1]; Amber Rose[1]; Ashley Sidebottom[1]; David Moran[1]; Victoria Burgo[1]; Shanna Banogon[1]; Huaiying Lin[1]; Mark D'Souza[1]; Jinyue Wang[3]; Olatoyosi Odenike[3]; Bhakti Patel[3]; Krysta Wolfe[3]; Eric Pamer[1, 4]; Matthew Odenwald[3]; Christopher Lehmann[3]; *[1]Duchossois Family Institute, University of Chicago, Chicago, IL; [2]Department of Pathology, University of Chicago Medicine, Chicago, IL; [3]Department of Medicine, University of Chicago Medicine, Chicago, IL; [4]Department of Medicine, Section of Infectious Disease and Global Health, University of Chicago Medicine, Chicago, IL*

ThP 082 **A Scalable Multi-omic Workflow Linking Circulating and Tissue Proteomes with Complementary Transcriptomics for High-Confidence, Whole-Patient Biomarker Discovery**; Danielle Gutierrez[1]; Jessica L Moore[1]; Jaison Arivalagan[1]; Tiffany Louie[1]; Kyra Richardson[1]; Yukta Bhurke[1]; Alejandra Stihel[1]; Nripesh Prasad[1]; Don Skifter[1]; Ryan Lamers[2]; Jenny Samskog[2]; Khatereh Motamedchaboki[3]; *[1]Discovery Life Sciences, Huntsville, AL; [2]Olink Proteomics (part of Thermo Fisher Scientific), Waltham, MA; [3]Thermo Fisher Scientfic, San Jose, CA*

ThP 083 **Multiomics analysis of human saliva for identification of noninvasive biomarkers of human performance**; Brett R. Blackwell[1]; Elizabeth C. Evin[1]; Samuel I. Koehler[1]; Kes A. Luchini[1]; Phillip M. Mach[1]; Ethan M. Mcbride[1]; Jessica A. Salguero[1]; Grace M. Thornhill[1]; Chi Yen Tseng[1]; Hannah L. Whitacre[1]; Trevor G. Glaros[1]; *[1]Los Alamos National Laboratory, Los Alamos, NM*

ThP 084 **4,5-dihydroxyhexanoic acid is a robust circulating and urine marker of mitochondrial disease and its severity**; Owen Skinner[1]; Maria Miranda[2]; Fangcong Dong[3]; Tessa Struhl[3]; Melissa Walker[3]; Grigorij Schleifer[4]; Matthew Henke[5]; Jon Clardy[6]; Michio Hirano[7]; Darryl DeVivo[7]; Eric Schon[7]; Kristin Engelstad[7]; Stephanie Siegmund[8]; Catherine Laprise[9]; Christine Des Rosiers[10]; Vamsi Mootha[2]; Rohit Sharma[2]; *[1]Northeastern University, Boston, MA; [2]Massachusetts General Hospital & Harvard Medical School, Boston, MA; [3]Massachusetts General Hospital & Harvard Medical School, Charlestown, MA; [4]University Hospital Bonn, Bonn, Germany; [5]University of Illinois Chicago, Chicago, IL; [6]Harvard Medical School,* *Boston, MA; [7]Columbia University, New York, NY; [8]Brigham and Women's Hospital, Boston, MA; [9]University of Quebec, Chicoutimi, QC; [10]University of Montreal, Montreal, QC*

ThP 085 **Protein corona based P2 enrichment beyond EDTA-Plasma : A Dedicated Enrichment Approach Enables Deeper Serum and Heparin-/citrate-plasma Proteomics**; Sandra Schär[1]; Arthur Viodé[1]; Xaver Wurzenberger[2]; Leander S. Runtsch[2]; Patrick Schreiner[2]; Nils A Kulak[2]; Roland Bruderer[1]; *[1]Biognosys AG, Schlieren, Switzerland; [2]PreOmics GmbH, Martinsried, Germany*

ThP 086 **Characterizing Preadipocyte Surfaceome Changes in Response to Vascular Endothelial Signals**; Samuel Bollinger; *Stanford University, Stanford, CA*

ThP 087 **From Global Metabolomics to Targeted Validation: A Cross-Validated LC–MS Strategy for Serum Biomarker Discovery**; Joseane Godinho[1]; Liu Zongyuan[2]; Jarrod A. Laro[1,2]; Kelly DeToy[3]; Steffany Vucetic[3]; Jordan R. Edens[1]; Jessy Condori[4]; Carolina Duque[5]; Gustavo Durán Saucedo[6]; Manuela Verastegui[4]; Paula Carballo-Jimenez[4,7]; Brandon N. Mercado-Saavedra[8]; Freddy Tinajeros[6]; Edith S. Málaga-Machaca[4]; Rachel Marcus[9]; Robert H. Gilman[3]; Natalie M. Bowman[10]; Laura-Isobel McCall[1]; *[1]San Diego State University, San Diego, CA; [2]University of Oklahoma, Norman, OK; [3]Johns Hopkins Bloomberg School of Public Health, Baltimore, MD; [4]Universidad Peruana Cayetano Heredia, Lima, Peru; [5]Johns Hopkins University, Baltimore, MD; [6]IFHAD: Innovation for Health and Development, Lima, Peru; [7]FASPA: Faculty of Public Health and Administration, Universidad Peruana Cayetano Heredia, Lima, Peru; [8]Universidad Católica Boliviana San Pablo, San Pablo, Bolivia; [9]Medstar Union Memorial Hospital, Baltimore, MD; [10]University of North Carolina at Chapel Hill, Chapel Hill, NC*

ThP 088 **Detection of an Ibuprofen-Carnitine Conjugate in a Mouse Model of Birth Injury: Implications for NSAID Metabolism and Function**; Aubreyana E Mcmaugh[1]; Jasmine Zemlin[2,3,4]; Leila Abolfathi[1,4]; Abubaker Patan[2,3]; Pieter C. Dorrestein[2,3]; Lindsey A. Burnett[4]; *[1]University of California San Diego, La Jolla; [2]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [3]Collaborative Mass Spectrometry Innovation Center, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [4]Department of Obstetrics Gynecology and Reproductive Sciences, University of California San Diego, La Jolla, CA*

ThP 089 **Routes of cannabis administration differentially shape gut-brain metabolic signatures resolved by Orbitrap Astral Zoom SQUAD**; Steven Danielson[1]; Bashar Amer[1]; Nichole Reisdorph[2]; Katrina Doenges[3]; Michael Armstrong[3]; Rahul Deshpande[4]; Susan S. Bird[4]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]University of Colorado Anschutz Medical Campus, Aurora, CO; [3]Department of Pharmaceutical Sciences, Skaggs School of Pharmacy and Pharmaceutical Sciences, Aurora, CO; [4]Thermo Fisher Scientfic, San Jose, CA*

ThP 090 **Exploiting Protease Susceptibility under Native Conditions for Deep Plasma Proteomics**; Eisuke Kanao[1,2]; Hiroto Kakiuchi[1]; Taiki Asaba[1]; Yasushi Ishihama[1,2]; *[1]Kyoto university, Kyoto, Japan; [2]National Institutes of Biomedical Innovation, Health and Nutrition, Osaka, Japan*

ThP 091 **Spatial Proteomics Reveals Prognostic Biomarkers for Neoadjuvant Therapy in Triple-negative Breast Cancer**; Jiayi Peng[1,2,3]; Zheng Linfeng[4]; Yu Chengkun[1,2,3]; Su Dan[4]; Liu Siqi[1,2,3]; *[1]College of Life Sciences, University of Chinese Academy of Sciences, Beijing, China; [2]BGI-Shenzhen, Shenzhen, China; [3]HIM-BGI Omics Center, Zhejiang Cancer Hospital, Hangzhou Institute of Medicine (HIM), Chinese Academy of Sciences (CAS), Hangzhou, China; [4]Department of Pathology, Zhejiang Cancer Hospital, Hangzhou Institute of Medicine (HIM), Chinese Academy of Sciences, Hangzhou, Zhejiang 310022, China., Hangzhou, China*

ThP 092 **Bronchoalveolar lavage proteomics in exacerbation of bronchiectasis**; Ju Yeon Lee[1]; Jiyoul Yang[2]; Jin Young Kim[1]; Yeji Do[3]; Min-Sik Kim[3]; Dong Eun Kye[2]; Geonhui Min[4]; In-Sook Jeon[2]; Eung-Gook Kim[2]; Joong Kook Choi[2]; Minjae Choi[2]; Hyun Lee[5]; Bumhee Yang[2]; *[1]Korea Basic Science Institute, Ochang, Cheongju, South Korea; [2]Chungbuk National University College of Medicine, Cheongju, South Korea; [3]DGIST, Daegu, South Korea; [4]Chungbuk National University, Cheongju,, South Korea; [5]Hanyang University College of Medicine, Seoul, South Korea*

ThP 093 **Metabolomic Profiling via Mass Spectrometry Reveals Biomarkers for Diabetic Kidney and Cardiovascular Complications in Indian Cohorts**; Sneha A Rana[1]; Aviral Singh[2]; Manisha Sahay[3];

Milind Gurjer[1]; Renuka Munshi[4]; Rakesh Sahay[3]; Pramod P Wangikar[1, 2]; [1]*Indian Institute of Technology Bombay, Mumbai, India;* [2]*Clarity Bio Systems India Pvt. Ltd., Pune, India;* [3]*osmania medical college, Hyderabad, India;* [4]*Topiwala National Medical College and Bai Yamunabai Laxman Nair Charitable Hospital, Mumbai, India*

ThP 094 **Evaluating the "Dark" Proteome for Prostate Cancer Urine Biomarker Discovery**; Jilin He[1]; Chenghao Zhu[2]; Vladimir Ignatchenko[1]; Lydia Y. Liu[1]; Brian P. Main[3]; John Semmes[3]; Danny Vesprini[4]; Stanley K. Liu[4]; Julius O. Nyalwidhe[3]; Paul C. Boutros[2]; Thomas Kislinger[1]; [1]*Princess Margaret Cancer Centre, Toronto, ON;* [2]*Sanford Burnham Prebys NCI-designated Cancer Center, San Diego, CA;* [3]*Old Dominion University, Norfolk, VA;* [4]*Sunnybrook Odette Cancer Centre, Toronto, ON*

ThP 095 **CPa8/9-HNE: Discovery and Validation of Novel Circulating Neo-Epitope Biomarkers for Neutrophil-Mediated Tissue Destruction in Inflammatory Bowel Disease**; Shujia Dai[1]; Mahmud Hossain[1]; Laura Parisi[1]; Bailin Zhang[1]; [1]*Sanofi, Cambridge, MA*

ThP 096 **CAT-APP: Contamination Analysis and Tempering—An Automated Online Platform for Plasma Proteomics with Biomarker Rescuing Capabilities**; MingMing Niu[1]; Dong Zhang[1]; Zhiwei Zhou[1]; Jiaqi Zhang[1]; Hong Wang[1]; [1]*CAS Peking Union Medical College, Tianjin, China*

ThP 098 **Throughput versus Depth in Cerebrospinal Fluid (CSF) DIA-MS Proteomics: Comparing 100SPD and 30SPD Evosep Gradients for Biomarker Discovery**; Caroline M Watson[1]; Lenora Higginbotham[1]; Anantharaman Shantaraman[1]; Qi Guo[1]; Eddie Fox[1]; Pritha Bagchi[1]; Fang Wu[1]; James J Lah[1]; Allan I. Levey[1]; Nicholas T. Seyfried[1]; [1]*Emory University School of Medicine, Atlanta, GA*

ThP 099 **Integrative re-analysis of Parkinson's Disease mass spectrometry proteomics data across multiple cohorts using bayesian graphical models identifies novel biomarker candidates**; Maximilian Burq[1]; Dejan Stepec[1]; Charlie Kim[1]; Peter Cimermancic[1]; [1]*Tesorai, MOUNTAIN VIEW, CA*

ThP 100 **Development of red blood cells and plasma-based diagnostic lipid biomarker panel for Parkinson's disease**; Shaima Muhammed Nazaar[1]; Anne M. Roberts[1]; Malcolm Horne[2]; Stephan Klatt[3, 4]; Christopher J Fowler[3]; Colin L. Masters[5, 6]; James D. Doecke[7, 8]; Blaine Roberts[1, 9]; [1]*Emory University School of Medicine, Atlanta, GA;* [2]*Bionics Institute, East Melbourne, Australia;* [3]*The Florey Institute of Neuroscience and Mental Health, Victoria, Australia;* [4]*BASF Metabolome Solutions GmbH, Berlin,, Berlin, Germany;* [5]*University of Western Australia, Perth, Australia;* [6]*Alzheimer's Research Australia, Perth, Australia;* [7]*Australian E-Health Research Centre, Herston, Australia;* [8]*Centre for Precision Health, School of Medical and Health Sciences, Western Australia, Australia;* [9]*Department of Neurology, Emory University, Atlanta, GA*

ThP 101 **Characterization of glycosylated recombinant human epididymis protein 4 (HE4) standard using top-down proteomics**; Alyssa A Williams[1]; Cynthia N Nagy[1]; Jake T Kline[1]; Luca Fornelli[1]; [1]*University of Oklahoma, Norman, OK*

ThP 102 **Proteomics of mechanotransduction in cancer associated fibroblasts identify mechanosensing pathways driving inflammatory, senescent and profibrotic phenotypes**; Carlo Ramil[1]; Hongwei Han[2]; Neal Smith[2]; Isabela Joy Kernin[2]; Frank Urena[2]; Alejandro Scaffa[1]; Milena Hornburg[1]; Aleksandra Olow[1]; Xin Yu[1]; Marta Wlodarska[1]; David Lagares[2]; An Chi[1]; [1]*Merck & Co., Inc., Rahway, NJ;* [2]*Harvard Medical School, Boston, MA*

ThP 103 **Real-time SESI-HRMS volatilomics and 13C tracing reveal glutathione-linked markers of lung cancer and therapy**; Jiangjiang (Chris) Zhu; *The Ohio State University, Columbus, OH*

ThP 104 **Integrated Proteomic and Phosphoproteomic Profiling of Butyrate Driven Cellular Remodeling in Clear Cell Renal Cell Carcinoma**; Yu-Hao Shih[1]; Yen-Chieh Wang[2, 3]; Chi-Jung Huang[1, 2]; Wei-Chi Ku[3]; [1]*National Defense Medical University, Taipei City, Taiwan;* [2]*Cathay General Hospital, Taipei city, Taiwan;* [3]*Fu Jen Catholic University, New Taipei City, Taiwan*

ThP 105 **New insights on lung cancer drug resistance in patients undergoing osimertinib/local ablative therapy by phospho-proteomic analysis of cancer tissues**; Tapan Maity[1]; Xu Zhang[1]; Udayan Guha[1]; Lisa M Jenkins[1]; [1]*National Cancer Institute, National Institutes of Health, Bethesda, MD*

ThP 106 **Biodegradable intra-arterial drug-eluting implants achieve sustained focal delivery, quantified by LC-MS/MS**; Anil Bhatia[1]; Manas Kinra[2]; Ruoyu Sheng[3,4]; Yiqing Chen[2,3]; Amancio Jose De Souza[1]; Garrett Sakomizu[5]; Jinrui Tan[3]; Dongwei Sun[3,4]; Edward Zagha[2]; Huinan Liu[3,4]; *[1]UCR Metabolomics Core Facility, Institute for Integrative Genome Biology, University of California at Riverside, Riverside, CA; [2]Department of Molecular, Cell and Systems Biology, University of California at Riverside, Riverside, CA; [3]Department of Bioengineering, University of California at Riverside, Riverside, CA; [4]Materials Science & Engineering Program, University of California at Riverside, Riverside, CA; [5]Department of Microbiology and Plant Pathology, University of California at Riverside, Riverside, CA*

ThP 107 **Spatially Resolved Proteomic Profiling Reveals Immune Phenotype–Specific Signatures in Gastric Neuroendocrine Carcinomas**; Kyunggon Kim[1,2]; Jiyoung Yu[2]; Bokyung Kim[1]; Bokyung Ahn[3]; Seung-Mo Hong[3]; Chang Seok Ko[4]; Beom-su Kim[4]; *[1]Department of Medical informatics and Statistics, BK21 Project, University of Ulsan College of Medicine, Seoul, South Korea; [2]Clinical Proteomics Core Lab, Convergence Research Center, Asan Medical Center, Songpa-gu, Seoul, South Korea; [3]Department of Pathology, Asan Medical Center, University of Ulsan College of Medicine, Seoul, South Korea; [4]Division of gastrointestinal surgery, Department of surgery, Asan Medical Center, Seoul, South Korea*

ThP 108 **Conserved remodeling of cardiolipin acyl chain composition across aggressive pediatric CNS and non-CNS tumors**; Adele-Asia Ponzoni[1]; Evangelos Liapis[1]; Lea Anne T. Maristela[1]; Katharine Offer[2]; Derek Hanson[1,2,3]; Claire L. Carter[1,4]; *[1]Hackensack Meridian Health Center for Discovery and Innovarion, Nutley, NJ; [2]Joseph M. Sanzari Cancer Center, Hackensack University Medical Center, Hackensack, NJ; [3]Department of Pediatrics, Hackensack Meridian School of Medicine, Nutley, NJ; [4]Department of Pathology, Hackensack Meridian School of Medicine, Nutley, NJ*

ThP 109 **Clinical Performance of the MasSpec Pen for Surgical Margin Assessment in Breast Cancer: A Multi-Site Study**; Keziah E Liebenberg[1]; Ruth A. P. Costa[1]; Sarah Bench[1]; Emily X. Ma[1]; Brian J Armijo[1]; Mary L. Hutchinson[1]; Faith Jackobs[1]; Jacob I Mardick[1]; Eric J. Silberfein[1]; Cary Hsu[1]; Alastair Thompson[1]; Stacey A. Carter[1]; Nagi Chandandeep[1]; Jing Wang[1]; James W. Suliburk[1]; Livia S. Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX*

ThP 110 **Illuminating melanoma: Repetitive UVB Irradiation Drives Proteome State Transition**; Adrian-Daniel Vasiu[1,2]; Jeroen Krijgsveld[1,2]; *[1]German Cancer Research Center (DKFZ), Heidelberg, Germany; [2]Heidelberg University, Heidelberg, Germany*

ThP 111 **Utilizing Parallel Reaction Monitoring (PRM) Analysis to Identify and Quantify Phosphorylation Sites of BRAF and MEK Proteins**; Grace M Scheidemantle[1]; Robert A. D'Ippolito[1]; Alexandria Sohn[1]; Matthew R. Drew[1]; Kelly Snead[1]; Jenna Hull[1]; Daniel A Ritt[2]; David E Durrant[2]; Nicholas Wright[1]; Hannah Ambrose[1]; Ashley Mitchell[1]; Kayla Russell[1]; Katie Geis[1]; Vanessa Wall[1]; Carissa Grose[1]; Deborah Morrison[1]; Dominic Esposito[1]; Frank McCormick[1,3]; Dwight V. Nissley[1]; Caroline DeHart[1]; *[1]Frederick National Laboratory, Frederick, MD; [2]National Cancer Institute, National Institutes of Health, Bethesda, MD; [3]Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco, San Francisco, CA*

ThP 112 **Evaluating mechanisms of resistance to thiol-containing anticancer drugs using targeted mass spectrometry**; Connor P Jewell[1]; Michelle Kwarteng[1]; Robert W Robey[1]; Michael M Gottesman[1]; Lisa M Jenkins[1]; *[1]Laboratory of Cell Biology, National Cancer Institute, Bethesda, MD*

ThP 113 **Bulk and Single-Cell Proteomics Reveal PRC1-Dependent Oxaliplatin Sensitivity in PDAC**; Anthony E. Johansen-Sallee[1]; Alexa M. Barber[1]; Nikitha Murugavel[1]; Jose Trevino[2]; Robert E. Lewis[1]; Sunil Hingorani[3]; Nicholas T. Woods[1]; *[1]Department of cancer Research, University of Nebraska Medical Center, Omaha, NE; [2]Department of Surgical Oncology, Virginia Commonwealth University, Richmond, VA; [3]Director of the Pancreatic Cancer Center of Excellence, University of Nebraska Medical Center, Omaha, NE*

ThP 114 **Orthogonal Proteomics Reveals Mutant-Resolved SWI/SNF Interactomes and Metabolic Rewiring in ccRCC**; Waikeong Un[1]; Daoyun Sun[2]; Zhihua Wang[1]; Xing Zeng[1]; Chunlin Hao[2]; Yufeng Yao[3]; *[1]Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China; [2]Wuhan University, Wuhan, China; [3]HuaZhong University of Science and Technology, Wuhan, China*

ThP 115 **A multiplexed PRM-based panel for potential use in patient selection and pharmacodynamic profiling for antibody-drug conjugate responses**; Kristine A Tsantilas[1]; Jeffrey R Whiteaker[1]; Rose C Pletcher[1]; Jeremy Hoog[2]; Lei Zhao[1]; Hong Wang[1]; Max Short[1]; Regine M Schoenherr[1]; Uliana J Voytovich[1]; Richard G Ivey[1]; ChenWei Lin[1]; Foluso O Ademuyiwa[2]; Cynthia X Ma[2]; Amanda G Paulovich[1]; *[1]Fred Hutchinson Cancer Center, Seattle, WA; [2]Washington University School of Medicine, St Louis, MO*

ThP 116 **Variant-Resolved Membrane Proteomics Dissects Immune-Tumor Crosstalk under EGFR-TKI Resistance**; Yu-Teng Jheng[1]; Morgan Kamanga[2]; Chia-Li Han[2]; *[1]National Taiwan Univeristy, Taipei, Taiwan; [2]Taipei Medical University, Taipei, Taiwan*

ThP 117 **Phosphoproteomic Analysis of Chimeric Antigen Receptor Signaling in Natural Killer Cells**; Yukiko Higa[1]; Lei Tian[2]; Jianhua Yu[2]; Stacey Finley[1]; Nicholas Graham[1]; *[1]University of Southern California, Los Angeles, CA; [2]University of California, Irvine, Irvine, CA*

ThP 118 **Global and Single-Nucleus Proteomics to Uncover Nuclear-Cytoplasmic Protein Dynamics upon EZH2 Degradation**; Anastasiia Sergeeva[1]; Syed Azmal Ali[1]; Selin Ulukaya[1]; Qianying Yang[1]; Jeroen Krijgsveld[1, 2]; *[1]German Cancer Research Center (DKFZ), Division of Proteomics of Stem Cells and Cancer, Heidelberg, Germany; [2]Heidelberg University, Medical Faculty, Heidelberg, Germany*

ThP 119 **Spatial lipidomic profiling of a patient-derived xenograft triple-negative breast cancer model**; Yongjin Lim[1]; Chloe AK White[1]; Thomas J Velenosi[1]; *[1]University of British Columbia, Vancouver, ON*

ThP 120 **Characterization and Statistical Classification of Rectal Cancer Molecular Signatures in Tissues and Surgical Margins using the MSPen and MS Imaging**; Raul Villacob[1]; Trevor Godfrey[1]; Roshan Raza[1, 2]; Atif Iqbal[1, 2]; Livia S Eberlin[1, 2]; *[1]Baylor College of Medicine, Houston, TX; [2]Baylor St. Luke's Medical Center, Houston, TX*

ThP 121 **Multi-omic Single cell MALDI-MSI reveals N-glycome and lipidome remodeling in PBMCs and TCR-engineered Cells**; Lyndsay E.A. Young[1]; Lauren E. Hill[1]; Satyajit Das[1]; James W. Dressman[1]; Muhammed F. Bayram[1]; Shikhar Mehrotra[1]; Anand Mehta[1]; Richard R. Drake[1]; *[1]Medical University of South Carolina, Charleston, SC*

ThP 122 **Under the Sea: A Multiomics Characterization and Mechanistic Evaluation of a Marine-Derived Nutraceutical for Anticancer Activity**; Crystal L. Pace[1]; Angie L. Mordant[1]; Scott P. Lyons[1]; Natalie K. Barker-Krantz[1]; Aurora Cabrera[1]; Thomas S. Webb[1]; Michael P. East[1]; Aaron Ebbs[2, 3]; Albert Baldwin[2, 3]; Andrew Satterlee[4, 5, 6]; Laura E. Herring[1]; Whitney L. Stutts[1]; *[1]UNC Metabolomics & Proteomics Core, Department of Pharmacology, University of North Carolina at Chapel Hill, Chapel Hill, NC; [2]UNC Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Chapel Hill, NC; [3]Department of Biology, University of North Carolina at Chapel Hill, Chapel Hill, NC; [4]Screening Live Cancer Explants Program and Core Facility, Eschelman School of Pharmacy, University of North Carolina, Chapel Hill, NC; [5]Eshelman Innovation, University of North Carolina, Chapel Hill, NC; [6]Division of Pharmacoengineering and Molecular Pharmaceutics, Eshelman School of Pharmacy, University of North Carolina, Chapel Hill, NC*

ThP 123 **Time-resolved, tissue-specific multi-omic profiling of near-complete breast cancer tumor reduction via induction of short-term hibernation**; Alexandria S. Battison[1]; Adrian Gomez[1]; Yue Wu[1]; Sonam Tamrakar[2]; Jill Habel[1]; Amanda Bjertenes[1]; Jennifer Liddle[2]; Marina Sherman[1]; Jeremy Balsbaugh[2]; Michael Lukey[1]; Jeremy Borniger[1]; *[1]Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; [2]University of Connecticutt, Storrs, CT*

ThP 124 **Histology Resolved Proteomic Characterization of the Triple Negative Breast Cancer Tumor Immune Microenvironment**; Allison L. Hunt[1, 2]; Fei Wang[3]; Tamara Abulez[2, 4]; Xue Wang[5]; Baoliang Cui[3]; Liang Jin[3]; Jan Schejbal[3]; Suzanne Coberly[6]; Jonathan Ogata[2, 4]; Katlin N Wilson[2, 4]; Kelly Conrads[2, 4]; Brian Hood[2, 4]; Nicholas W. Bateman[2, 4]; Tamar Uziel[7]; Josue A Samayoa[5]; Thomas Conrads[1, 2]; Yu Tian[3]; *[1]Women's Health Integrated Research Center, Inova Women's Service Line, Inova Health System, Annandale, VA; [2]Gynecologic Cancer Center of Excellence and the Women's Health Integrated Research Center, Department of Gynecologic Surgery and Obstetrics, Uniformed Services University and Walter Reed National Military Medical Center, Bethesda, MD; [3]AbbVie Bioresearch Center,* *Worcester, MA; [4]The Henry M. Jackson Foundation for the Advancement of Military Medicine, Inc., Bethesda, MD; [5]AbbVie Inc., South San Francisco, CA; [6]Bristol Myers Squibb, San Francisco, CA; [7]AbbVie Inc., North Chicago, IL*

ThP 125 **Ligand field stabilization energy of divalent transitionmetals influences fragmentationof anomeric carbohydrates**; Alexes N. Thurman[1]; Lyssa A. Garber[1]; Elyssia S. Gallagher[1]; *[1]Baylor University, Waco, TX*

ThP 126 **Ion intensities of Co(II)-adducted sialylated glycans increase in the presence of formic acid during electrospray ionization**; Holly T. Wilson[1]; Elyssia S. Gallagher[1]; *[1]Department of Chemistry and Biochemistry, Baylor University, Waco, TX*

ThP 127 **Unraveling the Complexity of Microalgal EPS: A Multi-Analytical Approach to Polysaccharide Composition and Characterization**; Bat-hen Eylon[1, 2]; Itai Kolsky[2]; Ivan Plyushchenko[2]; Nataly Barger[2]; Tali Mass[2]; Tal Luzzatto Knaan[1, 2]; *[1]The Interdisciplinary Center for Metabolomics, University of Haifa, Haifa, Israel; [2]Department of Marine Biology, The Leon H. Charney School of Marine Sciences, University of Haifa, Haifa, Israel*

ThP 128 **Differentiation of carbohydrate stereoisomers using logically derived sequence tandem mass spectrometry**; Chi-Kung Ni[1]; Hock-Seng Nguan[2]; *[1]Academia Sinica, Taipei, Taiwan; [2]Academia Sinica, Institute of Atomic and Molecular Sciences, Taipei, Taiwan*

ThP 129 **Dissecting Rare Isomeric Disaccharides via Porous Graphitic Carbon Chromatography Coupled to Contained Electrospray Ionization Mass Spectrometry**; Santosh Raman Acharya[1]; Abraham Badu-Tawiah[1]; *[1]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH*

ThP 130 **HILIC-Based high-resolution mass spectrometry method for comprehensive characterization of hyaluronic acid hydrogel degradation products**; Annija Vaska[1]; Kolia Moret[2]; Ivan Ivanenko[1]; Anna Rubina[1]; Kristine Salma-Ancane[1]; Kristaps Klavins[1]; *[1]Riga Technical University, Riga, Latvia; [2]University of Applied Sciences and Arts of Western Switzerland, Valais-Wallis, Delémont, Switzerland*

ThP 131 **Comprehensive Structural Characterization of Intact Glycosphingolipids by Electronic Excitation Dissociation Tandem MS^{n}**; Chaoshuang Xia[1]; Cheng Lin[1]; Kelly A. Dingess[2]; Bernd Stahl[1, 2, 3]; Catherine E. Costello[1]; *[1]Center for Biomedical Mass Spectrometry, Boston University Chobanian & Avedisian School of Medicine, Boston, MA; [2]Danone Global Research and Innovation, Utrecht, Netherlands; [3]Department of Chemical Biology & Drug Discovery, Utrecht Institute for Pharmaceutical Sciences, Utrecht University,, Utrecht, Netherlands*

ThP 132 **Unlocking the prebiotic activity of Coastal Chardonnay pomace oligosaccharides through mass spectrometry: insights into functionality by targeted glycoprofiling**; Bruna Paviani[1]; Han Peng[1]; Ishita Shah[1]; Mara Baller[1]; Daniela Barile[1]; *[1]University of California, Davis, Davis, CA*

ThP 133 **Automated Rapid-Throughput Monosaccharide Analysis Using Liquid-Handling Robotics**; Simon Ellison[1]; Aaron Stacy[1]; Carlito B. Lebrilla[1]; *[1]UC Davis, Davis, CA*

ThP 134 **Benchmarking the Performance of an Electrostatic Linear Ion Trap (ELIT) Charge Detection Mass Spectrometer (CDMS) for Natural Polymer Analysis**; Helin Zhuang[1]; Xinmiao Guo[1]; Anisha Haris[2]; Kate Yu[3]; Stephen McDonald[2]; Yuanjiang Pan[1]; Bin Wu[1]; Mowei Zhou[1]; Qi Cai[4]; *[1]Zhejiang University, Hangzhou, China; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Waters Corporation, Milford, MA; [4]Waters China Limited, Harbour City, Hong Kong*

ThP 135 **Direct Mass and Charge Characterization of Large Polysaccharides by Charge Detection Mass Spectrometry**; Lohra M Young[1]; Benjamin E Draper[1]; Matthew Lauber[2]; Keith Richardson[3]; Jakub Ujma[3]; Martin F Jarrold[1, 4]; *[1]Megadalton Solutions, Bloomington, IN; [2]Waters Corporation, Milford, MA; [3]Waters Wilmslow UK, Wilmslow, United Kingdom; [4]Indiana University Bloomington, Bloomington, IN*

ThP 136 **Electron-activated dissociation on a linear ion trap-pulsing Q-TOF enhances selectivity in clinical toxicology testing**; Morgan W Mann[1]; Lilly Lim[1]; Emilio Mejia[1]; Kara Lynch[1]; *[1]University of California San Francisco, San Francisco, CA*

ThP 137 **Methylmalonic Acid in Serum by LC-MS/MS for Clinical Research Using Supported Liquid Extraction**; Haroon Rehmani[1]; Rajashree Chakravarti[2]; Stephanie J Marin[2]; [1]*Phenomenex, Torrance;* [2]*Phenomenex, Torrance, CA*

ThP 138 **A minimally invasive Covalent Protein Painting (CPP) assay enabling pre-symptomatic detection of amyloid-driven heart failure (ATTR-CM)**; Sandra Pankow[1, 2]; Gabriel Kline[1, 2]; Jihyeon Lee[3]; Patrick T Garrett[2]; Robert O'Neill[2]; Titus Jung[2]; Lauren E Ives[4]; Prem Soman[5]; Mazen Hanna[4]; Jennifer E. Van Eyk[3]; Jeffrey Kelly[2]; John R. Yates III[2]; [1]*3D BioAnalytiX, San Diego, CA;* [2]*The Scripps Research Institute, La Jolla, CA;* [3]*Cedars-Sinai Medical Center, Biomedical Sciences, LOS ANGELES, CA;* [4]*Cleveland Clinic, Cleveland, OH;* [5]*UPMC, Pittsburgh, PA*

ThP 139 **A MALDI-ToF IVD Scanner for IP-MS Protein Biomarker Screening of Alzheimer's Disease (AD) and Other Disease Protein Biomarker Pannels**; Jun J Hu[1]; Zhiruo Chang[1]; Haixuan Sun[2]; Jun Qian[2]; [1]*Ningbo University, Ningbo, China;* [2]*Suzhou Institute of Biomedical Engineering and Technology, CAS, Suzhou, JIangsu Province, China*

ThP 140 **Rapid Quantification of Clinically Relevant Compound Classes by Chromatography-Free DART-MS/MS**; Arnd Ingendoh[1]; Jeffrey Zonderman[2]; Artem Filipenko[2]; Sam Putnam[2]; Zahuindanda Aventura[1]; Lukas Brunner[3]; Gernot Wolfram[3]; Christopher Elicone[2]; [1]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [2]*Bruker Scientific LLC, Billerica, MA;* [3]*Recipe Chemicals & Instruments GmbH, Munich, Germany*

ThP 141 **Advancing Lysosomal Disease Newborn Screening: Updated LC-MS/MS Assays and Expanded Quality Assurance Materials**; Samantha L Isenberg[1]; Elya Courtney[1]; C. Austin Pickens[1]; Samyukta Sah[1]; Daquille Peppers[1]; Christian Freeman[1]; Timothy Lim[1]; Carla Cuthbert[1]; Rachel Lee[1]; Konstantinos Petritis[1]; [1]*Centers for Disease Control and Prevention, Atlanta, GA*

ThP 142 **High-Throughput Vitamin K1 Quantification in Serum Using LDTD-MS/MS**; Pierre Picard[1]; Serge Auger[1]; Mégane Moreau[1]; Sarah Demers[1]; Jonathan Rochon[1]; Jean Lacoursiere[1]; [1]*Phytronix Technologies, Inc., Quebec, QC*

ThP 143 **Low-Level LC-MS/MS Analysis of Steroid Hormones in Human Serum and Plasma**; Haley Berkland[1]; Jared Burkhart[1]; [1]*Restek Corporation, Bellefonte, PA*

ThP 144 **Ex vivo degradation of fibrinopeptides: potential interference with quantitating coagulation progress and profiling dipeptides and amino acids in blood serum**; Evgenii B Serebriakov[1]; Chau Tran[1]; Igor A. Kaltashov[1]; [1]*University of Massachusetts Amherst, Amherst, MA*

ThP 145 **Ponatinib LC–MS/MS PK Assay Governance Across the Lifecycle: Phase 1 Fit-for-Purpose Through Global Cross-Validation and Platform Upgrades**; Ewa Sokol-Blond[1]; Kerri Smith[1]; Anson Pierce[1]; Mike Baratta[1]; [1]*Takeda Development Center Americas Inc., Cambridge, MA*

ThP 146 **Rapid Diagnosis of Hemoglobinopathies from Whole Blood Samples using Fast Protein Hydrolysis and Mass Spectrometry**; Zikang Li[1]; Wenpeng Zhang[1]; Zheng Ouyang[1]; [1]*State Key Laboratory of Precision Measurement Technology and Instruments, Department of Precision Instrument, Tsinghua University, Beijing 100084, P. R. China, Beijing, China*

ThP 147 **Rapid and Comprehensive Therapeutic Drug Monitoring (TDM) Using SPME-Based Ambient Ionization and a Miniaturized Mass Spectrometer**; Nan Zhang[1]; Weixu Fan[1]; Jian Zhao[1]; Wenpeng Zhang[2]; Jiexun Bu[1]; Zheng Ouyang[2]; [1]*PURSPEC Technology (Beijing) Ltd., Beijing, China;* [2]*Department of Precision Instrument, Tsinghua University, Beijing, China*

ThP 148 **Comparative evaluation of DDM-mediated single-pot and SP3 workflows for low-input clinical FFPE proteomics**; Ashley Frankenfield[1]; Camille Lombard-Banek[1]; Christopher Richardson[1]; David C Chain[1]; Steve Sweet[1]; Yeoun Jin Kim[1]; Andrew Chambers[1]; [1]*AstraZeneca, Gaithersburg, MD*

ThP 149 **A sensitive LC-MS/MS method for the quantitative determination of Ethinyl Estradiol and Norethindrone in human plasma**; Aiping Zhu[1]; Haiping Liu[1]; Shuyu Hou[1]; Tian-Sheng Lu[1]; [1]*Medpace, Cincinnati, OH*

ThP 150 **High-Throughput Serum Steroid Quantification via Fully Automated LC-MS/MS**; Fangjun Chen[1]; Zhouyang KANG[2]; Pengyun Liu[2]; WEI GUO[1]; HUAFEN LIU[2]; *[1]Department of Laboratory Medicine, Zhongshan Hospital, Fudan University, Shanghai, China; [2]Calibra Scientific Inc, HANGZHOU, China*

ThP 151 **Development of the LC-MS/MS method for the determination of long chain fatty acids in DBS samples**; Tomasz Bienkowski[1]; Konrad Kowalski[1]; Malgorzata Rogozinska[1]; Joanna Kucharska[1]; Renata Halak[1]; Olga Nalewajko[1]; Aleksandra Zalewska[1]; Bogdan Radwanski[1]; Michal Michalak[2]; *[1]Masdiag Sp. z o.o., Warszawa, Poland; [2]Institute of Organic Chemistry of the Polish Academy of Sciences, Warszawa, Poland*

ThP 152 **High-throughput multiplexed Online SPE LC-MS/MS for quantitation of dopamine, epinephrine, and norepinephrine in plasma using simple sample pretreatment**; Eishi IMOTO[1]; Daiki FUJIMURA[1]; Satoshi YAMAKI[1]; Tsuyoshi NAKANISHI[1]; *[1]Shimadzu Co., Kyoto, Japan*

ThP 153 **Design and Evaluation of Comprehensive Internal Standard Kits for First and Second Tier Newborn Screening**; Daquille Peppers[1]; Samantha L Isenberg[1]; Timothy Lim[1]; C. Austin Pickens[2]; Carla Cuthbert[1]; Rachel Lee[1]; Konstantinos Petritis[1]; *[1]Centers for Disease Control and Prevention, Chamblee, GA; [2]Waters, Milford, MA*

ThP 154 **Sequencing of M-protein from Multiple Myeloma Patients using Individual Ion Fragmentation**; Nickolas P Fisher[1]; Taojunfeng Su[1]; Jared Kafader[1]; Sabine Allam[2]; Jean Baptiste Alberge[2]; Irene Ghobrial[2]; Neil L Kelleher[1, 3]; *[1]Northwestern University, Evanston, IL; [2]Dana-Farber Cancer Institute, Boston, MA; [3]Chan Zuckerberg Biohub Chicago, Chicago, IL*

ThP 155 **Analysis of free testosterone from serum using SEC tips**; William Brewer; *DPX Technologies, Inc., Columbia, SC*

ThP 156 **Generalizability of machine-learning–identified metabolites for breast cancer diagnosis across MS platforms and clinical sites**; Laura Min Xuan Chai[1]; Tzu-Yin Wan[1]; Un Cheng Loi[1]; Hsiang-Wei Huang[2]; Li-Wei Tsai[2, 3, 4]; Wei-Ning Chiu[5]; Chiao Lo[5]; Ming-Yang Wang[2]; Cheng-Chih Hsu[1, 6]; *[1]Department of Chemistry, National Taiwan University, Taipei, Taiwan; [2]Department of Surgical Oncology, National Taiwan University Cancer Center, Taipei, Taiwan; [3]Graduate Institute of Clinical Medicine, National Taiwan University College of Medicine, Taipei, Taiwan; [4]Department of Surgery, National Taiwan University College of Medicine, Taipei, Taiwan; [5]Department of Surgery, National Taiwan University Hospital, Taipei, Taiwan; [6]Leeuwenhoek Laboratories Co. Ltd., Taipei, Taiwan*

ThP 157 **Lipidomics for Clinical Diagnosis of Acute Kidney Injury in Orthotopic Liver Transplant Patients Using ESI(+)-LTQ MS and UFLC-ESI(+)microTOF-QII-MS/MS**; Larissa Motta[1]; Brenda A. Vieira[2]; Camila M. Almeida[3]; Bruno A. Lessa[3]; Maritina Blank[4]; Vanessa Oliveira[4]; Hernán F. Terenzi[4]; Ana Paula C. F. Neves[5]; Cecília G. Ravetti[5]; Vandack A. Nobre Junior[5]; Valério G. Barauna[1]; Paula F. Vassallo[5]; Valdemar Lacerda Junior[3]; Wanderson Romão[2]; *[1]Federal University of Espirito Santo, Vitória, Brazil; [2]Federal Institute of Espírito Santo, Vitória, Brazil; [3]UFES, vitória, Brazil; [4]Federal University of Santa Catarina, Santa Catarina, Brazil; [5]Federal University of Minas Gerais, Belo Horizonte, Brazil*

ThP 158 **Enabling Plasma Extracellular Vesicle Proteomics Using Lipid Nanoprobe Technology**; Hongzhang He; *Captis Diagnostics, Pittsburgh, PA*

ThP 159 **A Sensitive LC–MS Bioanalytical Method for Simultaneous Quantification of Structurally Similar Cyclic Tetrapeptides at the Picogram Level**; Wenchuan Ma[1]; Min Fang[1]; QingCong Lin[1]; Benjiamin Wei[1]; Nilesh Sonawane[1]; *[1]Medicilon, Lexington, MA*

ThP 160 **Systematic optimization of PISA expands proteome-wide detection of bioactive peptide interactions**; Dan Richards[1]; Fangyi Zhai[1]; Shaoxian Li[1]; Qing Yu[1]; *[1]UMASS Chan Medical School, Worcester, MA*

ThP 161 **Advanced Mass Spectrometry Reveals Natural Antibiofilm Compounds Targeting Fungal Pathogens**; Oscar E Romero[1]; Rahul Deshpande[2]; Susan S. Bird[2]; Brandon Bills[2]; Stephanie N. Samra[2]; Jennifer Geddes-McAlister[1]; *[1]University of Guelph, Guelph, ON; [2]Thermo Fisher Scientific, San Jose, CA*

ThP 162 **A Generic Ion-Pairing Reagent-Free HILIC-MS/MS Method for Simultaneous Quantification of Six Approved GalNAc-siRNAs in Human Plasma**; Xiaofei Wu[1]; Ranran Jia[1]; Hongyun Wang[1]; [1]*Peking Union Medical College Hospital, Beijing, China*

ThP 163 **Quantitative analysis of NDMA at Ultra-trace level in Empagliflozin-Metformin ER tablets while DMF interference is resolved using LC/TQ**; Vikrant Goel[1]; Vivek Dhyani[2]; Parul Thakur[3]; Ju-Hwan Lim[4]; [1]*Agilent Technologies, Gurgaon, India;* [2]*Agilent Technologies, Mumbai, India;* [3]*Agilent Technologies, Hyderabad, India;* [4]*Agilent Technologies Korea Ltd, Seoul, South Korea*

ThP 164 **Direct Analysis of THC containing edibles using Py-GC/MS**; Fatma Mohammed AlMadani[1]; Mohammad Jamal[1]; Samar Gewily[1]; Adnan Lanjawi[1]; Hind Alshuhomi[1]; Rashed Alremeithi[1]; [1]*Dubai Police, Dubai, United Arab Emirates*

ThP 165 **Molecular Glue (MG) Discovery: Integrating Affinity Selection Mass Spectrometry (ASMS) with the D2B Platform to Drive Hit Identification**; Naifu Zhang[1]; Jiawei Li[1]; Yayue Ling[1]; Weiqiang Mo[1]; Ning Chen[1]; Wenzhang Chen[1]; Weihui Guo[1]; [1]*WuXi Apptec, Shanghai, China*

ThP 166 **Integration of HT LC with QToF MS to Rapidly Assess Optimal Reaction Conditions in Synthetic Molecule Drug Development**; Mercedes Biven[1]; Brock Juliano[1]; Kevin McGee[1]; Matthew Martin[2]; [1]*Eli Lilly, Indianapolis, IN;* [2]*Cogent Scientific, Indianapolis, IN*

ThP 167 **Accelerating Drug Discovery with Interactomic Technologies: Optimizing Proximity Labeling Enzymes and Bait Architectures for Induced Proximity Therapeutics**; Peter Liu[1]; Tess Branon[1]; [1]*Genentech Inc, South San Francisco, CA*

ThP 168 **From data to decisions: Accelerating proteomics insight in drug discovery with metadata-aware, interactive visualizations**; Jana Zecha[1]; Matthew S. Glover[1]; Stewart MacArthur[2]; Sonja Hess[1]; [1]*CGR-Dynamic Omics, Centre for Genomics Research (CGR), Discovery Sciences, Biopharmaceuticals R&D, AstraZeneca, Gaithersburg, MD;* [2]*Bioinformatics, Centre for Genomics Research (CGR), Discovery Sciences, BioPharmaceuticals R&D, AstraZeneca, Cambridge, CB2 0AA, United Kingdom*

ThP 169 **Identifying Metabolites from Protein-Peptide Conjugates Using Intact and bottom-up LC-MS with PEAKS Finder**; Christopher Kovach[1]; Xianyin Lai[1]; [1]*Eli Lilly & Company, Indianapolis, IN*

ThP 170 **A Robust LC-MS/MS Method for Determination of Schiff-Base Forming Reversible Covalent Inhibitors in Whole Blood**; Xuejing Guan[1]; Xinfa Fu[1]; Yanfu Ren[1]; Zhiyu Li[2]; Lili Xing[2]; Yi Tao[2]; Liang Shen[2]; [1]*WuXi AppTec, Suzhou, China;* [2]*WuXi AppTec, Pudong, Shanghai, China*

ThP 171 **Discovery and validation of > 150 novel CRBN neosubstrates by high-throughput deep proteomic screening of 960 molecular glue degrader drugs**; Uli Ohmayer[1]; Martin Steger[1]; Bachuki Shashikadze[1]; Björn Schwalb[1]; Patrick Zanon[1]; Ines Scheller[1]; Denise Winkler[1]; Anastasia Bednarz[1]; Sophie Machata[1]; Tobias Graef[1]; Denis Bartoschek[1]; Henrik Daub[1]; [1]*NEOsphere Biotechnologies, Planegg, Germany*

ThP 172 **LC-MS/MS Method Development and Validation for Oligonucleotide Bioanalysis in Rat Plasma**; Krishani K Rajanayake[1]; Alexander Serafini[1]; Lucas Wilson[1]; Dhruba Bhattarai[1]; Jonathan Bissland[1]; Philip Joyce[1]; Kevin Douglass[1]; [1]*Charles River Laboratories, Mattawan, MI*

ThP 173 **A Novel LC-MS/MS Method for the Determination of the AAV Peptide in Human and Mouse Liver**; Christina Chang[1]; Veronica Viramontes[1]; Matt Mazur[1]; Donald Chun[1]; Zhili Li[1]; [1]*Insmed, Bridgewater Township,, NJ*

ThP 174 **Resolving Drug-Induced Protein Turnover Kinetics in Intestinal Organoids via dSILAC for Applications in ADME**; Mario Leutert[1]; Elisabeth Gill[2, 3]; Nikolche Gjorevski[2]; Jitao David Zhang[3, 4]; Marcus Bantscheff[1]; [1]*360 Labs, Strategy, Portfolio & Operations, Roche Pharma Research and Early Development, Roche Innovation Center Basel, Basel, Switzerland;* [2]*Institute of Human Biology (IHB), Roche Pharma Research and Early Development, Roche Innovation Center Basel, Basel, Switzerland;* [3]*Pharmaceutical Sciences, Roche Pharma Research and Early Development, Roche Innovation Center*

Basel, Basel, Switzerland; [4]Computational Sciences Center of Excellence, Roche Innovation Center Basel, Basel, Switzerland

ThP 175 **Accelerating Molecular Glue Discovery: Hybrid DIA Unites PRM-Level Precision with Unbiased Global Proteome Profiling**; Jin Wang[1]; Adebowale Abiodun Alade[1]; Hanfeng Lin[1]; Sung Yun Jung[1]; Yue Xuan[2]; Helen Sun[3]; Fernanda Salvato[4]; *[1]Baylor College of Medicine, Houston, TX; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]ThermoFisher Scientific, San Jose, CA; [4]Thermo Fisher Scientific, San Jose, CA*

ThP 176 **An automated workflow for in vitro metabolite identification of insulin**; Kevin He[1]; Lakshmanan Deenadayalan[2]; Sashank Pillai[2]; Rahul Baghla[1]; Eshani Galermo[1]; *[1]SCIEX, Redwood City, CA; [2]SCIEX, Bangalore, India*

ThP 177 **Application of Inductively Coupled Plasma Mass Spectrometry (ICP-MS) for Detecting Metal Nanomaterials in Biological Matrices**; Qingmei Li[1]; Zengpu Yue[1]; Li Gao[1]; Yanfu Ren[1]; Zhiyu Li[2]; Lili Xing[2]; Yi Tao[2]; Liang Shen[2]; *[1]WuXi AppTec, Suzhou, China; [2]WuXi AppTec, Pudong, Shanghai, China*

ThP 178 **High Resolution LC MS Characterization of Tirzepatide Forced Degradation Pathways Using the Xevo MRT Mass Spectrometer**; Jonathan E Fox[1]; Andrew Ball[1]; *[1]Waters Corporation, Wilmslow, United Kingdom*

ThP 179 **High-Throughput Affinity Screening Using DESI-MagMASS**; Gee Yin Bryan Wong[1]; Elizabeth Want[1]; Zoltan Takats[1]; Lauren Ford[1]; *[1]Imperial College London, London, United Kingdom*

ThP 180 **Discrimination of different constrained ethyl nucleotides by electron-mediated MS2/MS3 fragmentation strategies**; Stephen W. Holman[1]; Andrew D. Ray[1]; Athanasios Smyrnakis[2]; Mariangela Kosmopoulou[2]; Christian Albers[3]; Heidi Vitrac[4]; Konrad Winkels[3]; Dirk Wunderlich[3]; Dimitris Papanastasiou[2]; *[1]AstraZeneca, Macclesfield, United Kingdom; [2]Fasmatech Science and Technology, Athens, Greece; [3]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [4]Bruker Scientific LLC, San Jose, CA*

ThP 181 **A Robust LC–MS/MS Method for Quantitative Bioanalysis of siRNA Antisense Strand in Mouse Serum and Liver**; Yingjun Ma[1]; Hsuanshen Chen[1]; Shaoting Zhang[1]; Jiangchao Chen[1]; Lili Xing[1, 2]; Yi Tao[1, 2]; *[1]DMPK Department, WuXi AppTec, Lab Testing Division (New Jersey), Cranbury, NJ; [2]DMPK Department, WuXi AppTec, Lab Testing Division, Shanghai, China*

ThP 182 **Bridging the Gap Between Screening and Localization: An Integrated Workflow Enabling High-Throughput Detection and Localization of Covalent Protein–Ligand Interactions**; Jacob W McCabe[1]; Matthew T Robey[1]; Kenneth R Durbin[1]; *[1]Proteinaceous, Evanston, IL*

ThP 183 **A Novel Screening Strategy to Characterize Ligandable Cysteines and Binding Pockets of Deubiquitinases**; Nicholas Girardi; *Harvard University - DFCI, Boston, MA*

ThP 184 **A New High Throughput Hydrogen-Deuterium Exchange Study Using Acoustic Ejection-Mass Spectrometry**; Erwin Abucayon[1]; Chang Liu[2]; Alexey Makarov[1]; Yuan Jiang[1]; Michael Wleklinski[1]; Suman Luthra[1]; Juncai Meng[1]; *[1]Merck & Co., Rahway, NJ; [2]SCIEX, Concord, ON*

ThP 185 **Mass spectrometry and bioactivity driven machine learning for discovering analgesic cannabinoids**; Elizabeth R. Milner[1, 2]; Inah Gu[1, 2]; Parker Rianda[3]; Jaewoo Choi[4, 5]; Heidi Kloefkorn[6]; Claudia Maier[4, 5]; Kevin S. Brown[1]; Jan F. Stevens[1, 2, 5, 7]; *[1]Department of Pharmaceutical Sciences, Oregon State University, Corvallis, OR; [2]Linus Pauling Institute, Oregon State University, Corvallis, OR; [3]Bioresources Research Program, College of Agricultural Sciences, Oregen State University, Corvallis, OR; [4]Department of Chemistry, Oregon State University, Corvallis, OR; [5]OSU Mass Spectrometry Center, Oregon State University, Corvallis, OR; [6]Department of Chemical, Biological, and Environmental Engineering, Oregon State University, Corvallis, OR; [7]Global Hemp Innovation Center, Oregon State University, Corvallis, OR*

ThP 186 **Rethinking In Vitro Cell Permeability Prediction with EPSA and IAM**; Newton Wu[1]; Huy Nguyen[1]; *[1]Genentech Inc, South San Francisco, CA*

ThP 187 **Untargeted Multiple Reaction Monitoring (uMRM) Pharmacology**; Elizabeth M. Billings[1]; Robert Plumb[2, 3]; Bill Webb[1]; Linh Hoang[1]; Winnie Uritboonthai[1]; Aries Aisporna[1]; Mary E. Spilker[4]; Gary Siuzdak[1]; *[1]Scripps Research, La Jolla, CA; [2]University of Liverpool, Liverpool, United Kingdom; [3]Waters Corporation, Milford, MA; [4]Pfizer, La Jolla, CA*

ThP 188 **Anintegrated metabolomics and lipidomics study of the effect of PPARδ agonist GW501516 in plasma of diabetic mice**; Li Xiang[1]; Jingchun Shi[1]; Zongwei Cai[1]; *[1]Hong Kong Baptist University, Hong Kong, Hong Kong*

ThP 189 **Metabolic Studies of Nandrolone Decanoate in Castrated Horses and Its Relevance to Equine Doping Control**; Chris K. L. Wong[1]; Yat-Ming So[1]; Wai Him Kwok[1]; Christina W. Y. Tang[1]; Stella M. S. Yuen[1]; Celia O. L. Wong[1]; Emmie N. M. Ho[1]; *[1]Racing Laboratory, The Hong Kong Jockey Club, Hong Kong, China*

ThP 190 **In-Vitro Metabolic Profiling of Simvastatin, a Potent Competitive HMG-CoA Reductase Inhibitor, Using Ion Trap and QqQ LC-MS/MS**; Wencui Yin[1]; Reem I Al-Wabli[1]; A. F. M. Motiur Rahman[1]; Adnan A Kadi[1]; *[1]Department of Pharmaceutical Chemistry, College of Pharmacy, King Saud University, Riyadh, Saudi Arabia*

ThP 191 **Streamlining Bottom-Up LC-MS Approach for Large Molecule Metabolite Identification**; Haley K Malone[1]; Joseph Mwangi[1]; Michael Berna[1]; Lukasz Chlewicki[1]; *[1]Eli Lilly & Company, Indianapolis, IN*

ThP 192 **Comparative Lifetime Evaluation of Kinetex™ Endura vs Standard Kinetex™ Columns for a Pain Management Drug Panel Analysis by LC-MS/MS**; Rajashree Chakravarti[1]; Stephanie J Marin[1]; Jason A Anspach[1]; Gareth Friedlander[1]; Sarah Rhoads[2]; Shalena Utterback[2]; Kavinda DeSilva[2]; Frances Morris[2]; *[1]Phenomenex, Torrance, CA; [2]Molecular testing labs, Vancouver, WA*

ThP 193 **Development of a hybridization mass spectrometry method to increase sensitivity and quantification of siRNA drug modalities and their metabolites**; Avery M Runnebohm[1]; Ryan C Hill[1]; Michael J Berna[1]; *[1]Eli Lilly & Company, Indianapolis, IN*

ThP 194 **Rapid PRM Method Development Enabled by Intelligent Software for Ultra-Sensitive Metabolite Quantification on hybrid quadropole linear ion trap (HQLIT) MS**; Sissi White[1]; Wes Rogers[2]; Kirstin Faoro[3]; Min Du[1]; *[1]ThermoFisher Scientific, Lexington, MA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, Austin, TX*

ThP 195 **Glass insert enabled LC–MS method for detecting low intracellular drug levels on an Orbitrap Exploris 240**; Luis Ernst[1]; Laura-Isobel McCall[1]; *[1]San Diego State University, San Diego, CA*

ThP 196 **Comprehensive Characterization of ADC Biotransformation in In Vitro Plasma Using UPLC-HRMS**; Juntao Wang[1]; Ruixing Li[1]; Liqi Shi[1]; Weiqun Cao[1]; Yi Tao[1]; Liang Shen[1]; *[1]DMPK Department, WuXi AppTec, Shanghai, China*

ThP 197 **Addressing the challenge of rapid drug metabolite identification using Cyclic Ion Mobility Mass Spectrometry**; Nyasha C Munjoma[1]; Paul Kowalski[2]; Robert S Plumb[2]; Emma Marsden-Edwards[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters, Milford, MA*

ThP 198 **A comprehensive in-vitro S9 and LC-MS based approach for analyzing pesticide metabolism in early discovery stages.**; Kundi Yang; *Corteva Agriscience, Indianapolis, IN*

ThP 199 **Online Backflush for Improving Ion Suppression: A 2D-LC/MS/MS Method for Measuring Enrofloxacin and Ciprofloxacin in Beagle Plasma**; Jingduan Chi[1]; Melissa Mofikoya[1]; *[1]Thermo Fisher Scientific Inc, Madison, WI*

ThP 200 **End-to-End High-Throughput Biotransformation Workflow: Automated Data Acquisition and Processing of Sub-Second UHPLC Peaks Using Multi-Reflecting Time-of-Flight Mass Spectrometry and Data-Mining**; Ismael Zamora[1]; Hania Khoury-Hollins[2]; Richard Lock[2]; David Pickles[2]; Robert S Plumb[2]; Ian Wilson[3]; Ludovic Pelligand[4]; Elizabeth Mann[5]; *[1]Mass Spec Analytica, Sant Cugat del Valles, Spain; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Imperial College London, London,* *United Kingdom; [4]Royal Veterinary College, London, United Kingdom; [5]Pharmaron UK Ltd, Rushden, United Kingdom*

ThP 201 **Peptide drug metabolic stability and degradation pathways in human liver lysosomes using high resolution mass spectrometry**; Nadya Benson[1]; Leah Logan[1]; Seema Muranjan[1]; Joanna Barbara[1]; *[1]BioIVT, Kansas City, KS*

ThP 202 **Simultaneous Quantitation of 1-Methylnicotinamide and Two Metabolites in Human Plasma Via LC/MS/MS**; Moo-Young Kim[1]; Xiangyang Liu[1]; Sha Sahil[1]; Md Akteruzzaman[1]; Melissa Mofikoya[1]; *[1]PPD, part of Thermo Fisher Scientific, Middleton, WI*

ThP 203 **Development of a Bimodal UPLC-UV-ESI-MS/MS Method in Human Plasma for the Simultaneous Quantification of Dolutegravir and Fluoxetine/Norfluoxetine for Pharmacokinetic Studies**; Alhaji Simon Ekere[1]; Waheed Adedeji[2]; Connor E. Gould[1]; Jill S. Hochreiter[1]; Robin DiFrancesco[1]; Gene D. Morse[1]; Troy D Wood[1]; *[1]University at Buffalo, Buffalo, NY; [2]University of Ibadan, Ibadan, Nigeria*

ThP 204 **Potential Risk Assessment of Drug Candidates for Human Aldehyde Oxidase Susceptibility Using Mass Spectrometry in Early Drug Development**; Kazuko Inoue; *Eisai Co.,Ltd., Tsukuba, Japan*

ThP 205 **A high resolution Cyclic™ ion mobility-based workflow for pinpointing isomeric amino acids in GLP-1 agonist peptides**; Gary Harland[1]; Dale A Cooper-Shepherd[1]; Isabella A Jones[1]; Emma Marsden-Edwards[1]; *[1]Waters Corporation, Wilmslow, United Kingdom*

ThP 206 **Drug Screen Suite: Streamlined LC-HRMS Toxicological Screening for Routine and Post-Mortem Casework**; Birgit Schneider[1]; Juergen Kempf[2]; Laura M. Huppertz[2]; Carsten Baessmann[1]; Eva Niehaus[3]; Sam Putnam[4]; *[1]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [2]Institute of Forensic Medicine, Medical Center - University of Freiburg, Freiburg, Germany; [3]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [4]Bruker Scientific LLC, Billerica, MA*

ThP 207 **Untargeted Profiling of Beetroot Metabolites using Biphasic Extraction and High-Resolution LC-Q-TOF-MS**; Kiran Subedi[1]; Mufeed M. Basti[2]; Anupama Tuladhar[3, 4]; Heba Alfares[2]; Xuejun Peng[5]; *[1]NCAT, Greensboro, NC; [2]Chemistry Department, NCATSU, Greensboro, NC; [3]College of Agriculture and Environmental Sciences, NCATSU, Greensboro, NC; [4]Department of Agricultural Engineering, An-Najah National University, Nablus, Palestine; [5]Bruker Scientific LLC, San Jose, CA*

ThP 208 **Diagnosing Extraction Artifacts in LC–MS/MS PK Assay: HRMS Evidence for pH/Temperature Labile Mobocertinib Metabolites in Clinical Bioanalysis**; Ewa Sokol-Blond[1]; Feng Yin[2]; Mike Baratta[2]; *[1]Takeda Development Center Americas Ltd., Cambridge, MA; [2]Takeda Development Center Americas Inc., Cambridge, MA*

ThP 209 **A key public health insecticide, chlorfenapyr, prevents development and transmission of malaria parasites**; Natalie M Portwood[1]; Alanna R Condren[2]; Kevin Walz[1]; Lilian P. Dorner[1]; Buyuan He[1]; Antonia L. Böhmert[1]; Morgan McCauley[2]; Harsha Vardhan Reddy[1]; Rhiannon A.E. Logan[1, 3]; Shouxun Zhao[2]; Susanne Stutz[4]; David Malone[5]; Friederike-Nora Vögtle[1, 6]; James W. Austin[7]; Friedrich Frischkenecht[1, 3]; Victoria A. Ingham[1]; *[1]Center for Integrated Infectious Diseases, Heidelberg University Medical Faculty Heidelberg,, Heidelberg, Germany; [2]BASF, Wyandotte, MI; [3]Partner site Heidelberg, German Center for Infection Research (DZIF), Heidelberg, Germany; [4]Professional & Specialty Solutions, BASF SE, Limburgerhof, Germany; [5]Bill & Melinda Gates Foundation, Seattle, WA; [6]Center for Molecular Biology of Heidelberg University (ZMBH), Heidelberg, Germany; [7]BASF Agricultural Solutions US LLC, Research Triangle Park, NC*

ThP 210 **A Holistic View of GLP-1R Agonist–Mediated Cellular Response Revealed Through Orthogonal Technologies**; Mark Sartain[1]; Rebecca Mongeon[1]; Lisa Winer[1]; Paul Held[1]; Natalia Romero[1]; Joe Clayton[1]; Daniel Cuthbertson[1]; *[1]Agilent Technologies, Santa Clara, CA*

ThP 211 **Development of an LC-MS/MS Method for the Quantitative Analysis of VX-765 and Its Active Metabolite VRT-043198 in Biological Matrices**; Cristina Arciniega[1]; Brandie M. Ehrmann[1]; *[1]The University of North Carolina at Chapel Hill, Chapel Hill, NC*

ThP 212 **Structural Elucidation of Metabolites from Positive Control Nitrosamine Drug Substance-Related Impurities in the Enhanced Ames Test using High-Resolution Mass Spectrometry**; Jarod Fincher[1]; Ping Lu[2]; Joel Christensen[2]; Katherine McGettigan[2]; Mark Powley[2]; Zhanna Sobol[2]; Patricia Escobar[2]; Bennett Ma[2]; *[1]Merck & Co., West Point, PA; [2]Merck & Co, Rahway, NJ*

ThP 213 **Effect of column chemistry, temperature, inert flow path, and mobile phase on the separation of GLP-1 peptides and their impurities**; Ace G. Galermo[1]; Oscar Potter[1]; Charu Kumar[1]; Randall Robinson[2]; Mohammad-Aref Khalily[3]; Shawn Ehlers-Cheang[1]; Chenchen He[4]; Yucheng Huang[4]; Changjun Fan[4]; Jordy Hsiao[1]; Ta-Chen Wei[4]; *[1]Agilent Technologies, Inc., Santa Clara, CA; [2]Agilent Technologies, Inc., Folsom, CA; [3]Agilent Technologies LDA UK Limited, Church Stretton, United Kingdom; [4]Agilent Technologies, Inc., Wilmington, DE*

ThP 214 **Determination of Dolutegravir in Human Peripheral Blood Mononuclear Cells**; Yourong (Zoe) Geng[1]; Florence Marzan[1]; Emma Gunderson[1]; Liusheng Huang[1]; Amelia N. Deitchman[1]; *[1]University of California San Francisco, San Francisco, CA*

ThP 215 **Development of an LC-MS method for detecting banned veterinary drug residues in liver**; Jana Kinar[1]; Bryn O Shurmer[1]; Randall W Purves[1]; *[1]Canadian Food Inspection Agency, Saskatoon, SK*

ThP 216 **Target Peptide Refinement for a Multi-Tree Nut Mass Spectrometry Method for Food Allergen Detection and Quantification**; Jerry Kahu[1]; Philip Johnson[1]; Melanie L. Downs[1]; *[1]Food Allergy Research and Resource Program, Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE*

ThP 217 **Spectral Stitching Improves the Performance of Flow Injection-Nano-ESI-Mass Spectrometry for Food Authentication: An Example of Pomegranate Juice**; Yaxi Hu[1]; Hieu Le[1]; Ruixi Xie[2]; Terry Koerner[2]; *[1]Carleton University, Ottawa, ON; [2]Health Canada, Ottawa, ON*

ThP 218 **Fingerprinting Flavor: Nontargeted GC-MS/O Analysis of Sriracha Sauces**; Tiffany L Crawford[1]; Michael Horton[1]; James G Redwine[1]; *[1]Kalsec Inc, Kalamazoo, MI*

ThP 219 **Determination of PFAS Residues in Shellfish by Low Residual Liquid Chromatography Coupled with Tandem Mass Spectrometry**; Chien-An Lin[1]; Hui-Chi Lin[1]; Chi-Chun Li[1]; Wei-Yun Chen[1]; Yung-Ching Fan[1]; Hsueh-Ching Lin[1]; *[1]Department of Health, Kaohsiung City Government, Kaohsiung City, Taiwan*

ThP 220 **Comparison of black and white sesame seeds and selection of sesame-specific peptides by global LC-MS/MS**; Matthew M. Miele[1]; Karen E. Butler[1]; Melinda A. McFarland[1]; *[1]U. S. Food and Drug Administration, College Park, MD*

ThP 221 **Characterizing “Nature’s Ozempic™”: Non-targeted screening of berberine supplements using ion mobility high-resolution mass spectrometry**; Lindsay Hatch[1]; Sarah Dowd[1]; Gordon Fujimoto[1]; *[1]Waters Corporation, Milford, MA*

ThP 222 **Single-Run Non-Targeted and Wide-Targeted Food Aroma Analysis by Simultaneous Scan/MRM Acquisition with Triple Quadrupole GC-MS/MS**; Kazuhiro Kawamura[1, 2]; Yukihiko Kudo[1]; *[1]Shimadzu Corporation, Kyoto, Japan; [2]Osaka University, Osaka, Japan*

ThP 223 **Automated PAL3–8890 GC–FID/LUMA Workflow for Rapid, Reproducible FAME Profiling in Edible Oils**; Saurabh U Patel; *Agilent Technology, Wilmington, DE*

ThP 224 **Qualitative and Quantitative Determination of Furanocoumarins in Citrus Oils by MS/ToF**; Bita Alipour Parvizian[1]; Sue D'Antonio[2]; John Wright[2]; Tracy Blethen[3]; Michael Adams[4]; *[1]Agilent, Santa Clara, CA; [2]Agilent Technologies, Santa Clara, CA; [3]Agilent Technologies, Chicago, IL; [4]CWC Labs, Cedar Creek, TX*

ThP 225 **Next-generation HRMS multiresidue pesticide analysis for food safety on Modified Orbitrap MS: boosting MS1 performance via Enhanced Dynamic Range acquisition**; Amadeo R. Fernández-Alba[1]; Florencia Jesús[1]; Adrián Rosa García[1]; *[1]University of Almeria, Almeria, Spain*

ThP 226 **Enhanced Sensitivity in Multi-Residue Pesticide Analysis by LC-MS/MS Using High-Pressure Feed Injection**; Tarun Anumol[1]; M. Lorna De Leoz[2]; Peter Kornas[3]; Edgar Naegele[3]; *[1]Agilent Technologies, Wilmington, DE; [2]Agilent Technologies, Inc., Wilmington, DE; [3]Agilent Technologies Deutschland GmbH, Waldbronn, Germany*

ThP 227 **Streamlined EMR LC-MS/MS Approach for Sensitive PFAS Determination in Alcoholic Beverages**; M. Lorna De Leoz[1]; Limian Zhao[1]; *[1]Agilent Technologies, Inc., Wilmington, DE*

ThP 228 **High Resolution Mass Spectrometric Analysis of Vitamin B12 Opens the Door to Structural Identification of Cobalamin Impurities**; Dennis Gessmann[1]; Paul Brown[2]; Celena Josephitis[3]; Marianne Bertrand[3]; *[1]Tolmar, North Chicago, IL; [2]Paul Brown Consulting Services, Columbia, MO; [3]Tolmar, Fort Collins, CO*

ThP 229 **A Unified Method for Quantifying Multiple Free Fatty Acids in Cricket Powders by Using SPE-HPLC/HRMS**; Philip L Duvall[1]; Grace Greene[1]; Hilkka Kenttämaa[1]; *[1]Purdue University, Department of Chemistry, West Lafayette, IN*

ThP 230 **Comparing volatile compositions of coffee and its substitutes using a high-resolution GC/MS and flavor and fragrance accurate mass library**; Sofia Nieto[1]; Yuanyuan Ke[2]; Lei Tao[1]; Li Sun[1]; *[1]Agilent Technologies, Inc., Santa Clara, CA; [2]Agilent Technologies, Inc., Chengdu, Sichuan, China*

ThP 231 **Profiling the Proton Affinity of Vicine—A Toxic Faba Bean Glycoside—Through Competitive Dissociation of Proton-Bound Dimers via TOF-MS**; Carlos Lucero; *Ingredion Inc., Bridgewater, NJ*

ThP 232 **Direct injection mass spectrometry for high throughput beer quality analysis of typical flavor aging markers**; Pedro Martinez Noguera[1]; Marco Cardin[1]; Mikael Agerlin Petersen[1]; Jesper Harholt[2]; Cecilie Bay Wirenfeldt[3]; Roberto Schimmenti[3]; Sylvester Holt[1]; Artem Leonov[3]; Trine Tving Jensen[3]; Kenneth Heide Preisler[3]; *[1]University of Copenhagen, Copenhagen, Denmark; [2]Novonesis, Copenhagen NV, Denmark; [3]Carlsberg, Copenhagen NV, Denmark*

ThP 233 **AI-Driven Non-Targeted Metabolomics for Comprehensive MS-Based Characterization of Bioactive Constituents in Coffee Byproducts**; Gui-Ru Xie[1]; Hong-Jhang Chen[2]; *[1]National Taiwan Univeristy, Taipei, Taiwan; [2]National Taiwan University, Taipei, Taiwan*

ThP 234 **Unlocking Microbial Aromas: Prioritization of Key Compounds in Food Science using GC-ecTOF**; Lucie K. Tintrop[1]; Steffen Braekling[2]; Sonja Klee[2]; Helena Saehrendt[1]; Ueli Von Ah[1]; Pascal Fuchsman[1]; *[1]Agroscope, Bern, Switzerland; [2]TOFWERK, Thun, Switzerland*

ThP 235 **Hybrid Targeted-Untargeted GC-MS/MS Captures Quantified Non-Volatiles and Aroma Markers for Comparative Wine Profiling**; Archana Kumari[1]; Sayeree Joardar[2]; Deepti Sahasrabuddhe[2]; Sushil Dhital[3]; Pramod P. Wangikar[1, 2]; *[1]Clarity Bio Systems India Pvt. Ltd., Pune, India; [2]Indian Institute of Technology Bombay, Mumbai, India; [3]Monash University, Clayton, Australia, Melbourne, Australia*

ThP 236 **Comparative Analysis of Fibril Forming Collagens by Charge Detection Mass Spectrometry**; Polycarp C Ofoegbu[1]; Martin F Jarrold[2]; *[1]Indiana University Bloomington, Bloomington, IN; [2]Indiana University - Bloomington, Bloomington, IN*

ThP 237 **Characterization of Gene Delivery Systems with XevoTM Charge Detection Mass Spectrometry (CDMS)**; Benjamin E. Draper[1]; Lohra M Young[1]; Erin M. Panczyk[2]; Stephen McDonald[2]; *[1]Megadalton Solutions, Bloomington, IN; [2]Waters Corporation, Milford, MA*

ThP 238 **Relative sn-isomer quantification of phosphatidylglycerol using manganese complexation and electrospray ionization tandem mass spectrometry**; Sara Amer[1]; Xilai Li[1]; Haven Wilson[1]; Julia Laskin[1]; *[1]Purdue University, west lafayette, IN*

ThP 239 **Mild and efficient coupling reactions enabled by in situ electrolytically generated Cu(I) cation catalyst in nanoelectrospray**; Annesha Sengupta[1]; Disni Gunasekera[1]; Gopal Reddy Ramidi[1]; Mia Beaudoin[1]; Shiqing Xu[1, 2]; Xin Yan[1]; *[1]Department of Chemistry, Texas A&M University, College Station, TX; [2]Department of Pharmaceutical Sciences, Texas A&M University, College Station, TX*

THURSDAY MORNING ORALS

ThP 240 **A Reductionist Approach to Understanding Group II Organometallic Chemistry: Gas-Phase Reactivity of Group II Metal Methide Cations**; Ashley Caputo[1]; Samuel Lenze[1]; Madeline Handel[1]; Theodore Corcovilos[1]; Michael Van Stipdonk[1]; [1]*Duquesne University, Pittsburgh, PA*

ThP 241 **Structural investigation of the proton-bound dimers of arginine analogs using HDX, IRMPD, and DFT**; JC Poutsma[1]; Bennett Clark[1]; Helen Lu[1]; Trinh Ton[1]; Paul Wenthold[2]; [1]*College of William & Mary, Williamsburg, VA;* [2]*Purdue University, west lafayette, IN*

ThP 242 **Anion in a Heterocyclic Ring Environment: Surprising Strength to the Relationship**; Najma Benelouald[1]; Jane S Murray[2]; Gabriel Gaiffe[3]; Maxime Bridoux[3]; Philippe Maître[4]; Richard B Cole[1, 2]; [1]*Sorbonne Université - Faculté des Sciences et Ingénierie, Paris Cedex 05, France;* [2]*University of New Orleans, New Orleans, LA;* [3]*CEA-DAM, Bruyères-le-Châtel,, France;* [4]*Université Paris-Sud, Orsay, France*

ThP 243 **An assessment of the Internal Energy Distribution of ions generated in Picosecond Infrared Laser Mass Spectrometry**; Laurentiu Dabija[1, 2]; Anna Ye[2]; Arash Zarrine-Afsar[1, 2]; [1]*University of Toronto, Toronto, ON;* [2]*University Health Network, TORONTO, ON*

ThP 244 **Guided Ion Beam Mass Spectrometry Evaluation of Tb+ Oxidation and Collision-Induced Dissociation of TbO+: the Terbium (Tb) Chemi-ionization Reaction**; Talley A. Fenn[1]; Brandon C. Stevenson[1]; Elijah Bliss[1]; Sara Rockow[1]; Peter B. Armentrout[1]; [1]*University of Utah Department of Chemistry, Salt Lake City, UT*

ThP 245 **Mechanistic Characterization of Ethyl and Allyl Cation Adduct Fragmentation upon Methane Chemical Ionization of Aromatic Oxygen-Containing Compounds**; Bridger Johnston[1]; Grace Greene[1]; Hilkka I. Kenttämaa[1]; [1]*Purdue University, Department of Chemistry, West Lafayette, IN*

ThP 246 **Phosphorous Upcycling from Collisional Activation of Gas-phase Phosphate Clusters**; Peishan Cai[1]; Aidan G Purcell[1]; Ryan R. Julian[1]; [1]*University of California, Riverside, Riverside, CA*

ThP 247 **Dynamic Spray Ionization Mass Spectrometry: High-throughput Multidimensional Reaction Screening Platform**; Purva S Damale[1]; Alex P Zumock[1]; Riley Ferguson[1]; Abraham Badu-Tawiah[1]; [1]*The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH*

ThP 248 **Probing Molecular Flexibility Via Energy- and Time-Resolved Collision Cross Section Measurements on Host-Guest Complexes**; Emily D. Richards[1]; Wyatt Hansen[1]; Sanaz Mohammadzadeh Koumleh[1]; Statton Sparks[1]; David V Dearden[1]; [1]*Brigham Young University, Provo, UT*

ThP 249 **The Curious Behavior of Organosulfur Compounds in the DART Gas Stream: Implications for the Interpretation of Disulfide DART Mass Spectra**; Rabi A Musah[1]; Benedetta Garosi[1]; Parandaman Arathala[1]; [1]*Louisiana State University, Baton Rouge, LA*

ThP 250 **When Binary, Group II Metal Hydride Cations Meet Ketones: Ion-Trap Mass Spectrometry Insights into Native, Solvent-Free Chemistry**; Madeline R Handel[1]; Samuel J Lenze[1]; Emma Nicholson[1]; Theodore A Corcovilos[1]; Michael J Van Stipdonk[1]; [1]*Duquesne University, Pittsburgh, PA*

ThP 251 **Differentiating glycan isomers based on linkage memory and proton affinity via proton transfer charge reduction**; William I Eisen[1]; Haley M Schramm[1]; Miklos Guttman[1]; Nicholas M. Riley[1]; [1]*University of Washington, Seattle, WA*

ThP 252 **Microdroplet Magic? OH•no! Mechanisms for hydroxyl formation in droplets and will they impact my analysis?**; Casey J. Chen[1]; Matthew S. McPartlan[1]; Pyeongeun Kim[2]; Kevin R. Wilson[2]; Evan R. Williams[1]; [1]*University of California, Berkeley, Berkeley, CA;* [2]*Lawrence Berkeley National Laboratory, Berkeley, CA*

ThP 253 **Energy Resolved Ion Mobility Mass Spectrometry of Natural Product Diastereomers**; William Crandall[1, 2, 3]; Lester Manly[4]; Eric Gier[5]; Zoltan Takats[6, 7]; Facundo Fernandez[5]; Dean Jones[2]; Cassandra Quave[3, 8, 9]; Bela Paizs[6, 7, 10]; [1]*Molecular and Systems Pharmacology, Emory University., Atlanta, GA;* [2]*Department of Medicine: Pulmonary, Allergy, Critical Care, and Sleep Medicine, Emory University.,* *Atlanta, GA; [3]Department of Dermatology, Emory University., Atlanta, GA; [4]Department of Biochemistry, Emory University, Atlanta, GA; [5]School of Chemistry and Biochemistry. Georgia Institute of Technology, Atlanta, GA; [6]Faculty of Medicine, Department of Metabolism, Digestion and Reproduction, Imperial College London, W12 0NN, UK, London, United Kingdom; [7]deShape ltd., London, United Kingdom; [8]Center for the Study of Human Health, Emory University., Atlanta, GA; [9]Emory University Herbarium, Emory University., Atlanta, GA; [10]The Rosalind Franklin Institute, Building R113 Rutherford Appleton Laboratory, Harwell Campus, Didcot, Oxfordshire, OX11 0QX, UK, Didcot, United Kingdom*

ThP 254 **Unmasking Group 12 Hydride Reactivity: Intrinsic Gas-Phase Chemistry from Combined MS and Computation**; Allison P Zeiss[1]; Madeline R Handel[1]; Samuel J Lenze[1]; Michael Van Stipdonk[1]; *[1]Duquesne University, Pittsburgh, PA*

ThP 255 **A model correlating peptide helicity and deprotonated D/L-cysteine residue in the gas-phase**; Shiyuan Wang[1]; Jianhua Ren[1]; *[1]University of the Pacific, Stockton, CA*

ThP 256 **Hydroxide or Hydride? Ligand-Controlled Reactivity of Al(III)-formate Cations**; Jake Hartman[1]; Samuel J Lenze[1]; Madeline R Handel[1]; Michael J Van Stipdonk[1]; *[1]Duquesne University, Pittsburgh, PA*

ThP 257 **Resolving Lipid Positional Isomers via Dissociation Kinetic Measurements of Lipid-Metal-Ligand Ion Types**; Narayanan Chelakkara Venkiteswaran[1]; Troy R. Scoggins IV[1]; Julia R Bonney[2]; Boone M. Prentice[1]; *[1]University of Florida, Department of Chemistry, Gainesville, FL; [2]Harvard Medical School, Boston, MA*

ThP 258 **Reaction Acceleration in Droplet-Based Ionization Methods: Local Acidity Enhancement and Surface-Mediated Neutralization Pathways**; Styliani Consta[1]; Jihong Shi[2]; Han Nguyen[2]; *[1]University of Western Ontario, London, ON; [2]The University of Western Ontario, London, ON*

ThP 259 **Loss of core fucosylation in hepatocytes can aid in the identification of liver cancer biomarkers**; Andrew Bauer[1, 2]; Hongyan Liang[1]; Mengjun Wang[1]; Shaaron Ochoa-Rios[1, 3]; Anand Mehta[1]; *[1]Medical University of South Carolina, Charleston, SC; [2]Clemson University, Clemson, SC; [3]Moffitt Cancer Center, Tampa, FL*

ThP 260 **Isomeric Profiling of N-Glycans Elucidates N-Glycosylation Pathways in Drosophila melanogaster**; Yen-Ting Lin[1]; Yi-Chun Huan[1]; Hsin-Ho Sung[1]; Cheng-Ting Chien[1]; Chi-Kung Ni[1]; *[1]Academia Sinica, Taipei, Taiwan*

ThP 261 **Towards decoding sialic acid N-glycan isomer complexity in biological tissues with the Structure of Lossless Ion Manipulations (SLIM)**; Christopher Harrilal[1]; Heidi Vandyk[1]; Dusan Velickovic[2]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]PNNL, Richland, WA*

ThP 262 **Integrated Glycocentric Omics to Decipher the Brain Glycan Code and Molecular Signatures of Specific Cell Types**; Myung Jin Oh[1, 2]; Dongtan Yin[1, 3]; Ji Woong Bae[4]; Kyung-Seok Han[4]; Hyun Joo An[1, 2]; *[1]Graduate School of Analytical Science and Technology, Chungnam National University, Daejeon, South Korea; [2]Asia-Pacific Glycomics Reference Site, Daejeon, South Korea; [3]Asis-Pacific Glycomics Reference Site, Daejeon, South Korea; [4]Department of Biological Sciences, Chungnam National University, Daejeon, South Korea*

ThP 263 **Dose-Dependent Inhibition of Protein Glycosylation Reveals Crosstalk Between Glycosylation and Phosphorylation in EGF Signaling Pathways**; Hongyi Liu[1]; Ding Chiao Lin[1]; Yingwei Hu[1]; Zhenyu Sun[1]; Yuanyu Huang[1]; Yuanwei Xu[1]; Hui Zhang[1]; *[1]Johns hopkins university, baltimore, MD*

ThP 264 **Systemic and Brain-Specific O-Glycan Alterations in Alzheimer's Disease**; Yehia Mechref[1]; Joy O Solomon[1]; Sherifdeen B. Onigbinde[1]; Sofia Sepulveda[1]; Moyinoluwa Adeniyi[1]; Odunayo O. Oluokun[1]; Fabricio Meneses[1]; Sarah Sahioun[1]; *[1]Texas Tech University, Lubbock, TX*

ThP 265 **High-Fat Diet Modulates Cardiac Glycosylation After Traumatic Brain Injury: Insights from LC-MS/MS Glycomics**; Abiodun M Adewolu[1]; Oluwatosin Daramola[1]; Esther O. Oji[1]; Abderrahmane Koraich[1]; Judith Nwaiwu[1]; Stanley Ibeh[2]; Sarin Mekhjian[3]; Firas H. Kobaissy[4]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Dalhousie University, Halifax, NS; [3]American University of Beirut, Beirut,* *Lebanon; [4]Center for Neurotrauma, Multiomics & Biomarkers (CNMB) Morehouse School of Medicine, Atlanta, GA*

ThP 266 **Organelle-Specific Glycosylation Patterns in Breast Cancer and Glioblastoma Cells: Implications for Cell Biology and Cancer Biology**; Stephen Awuku[1]; Mojibola O Fowowe[1]; Joy O Solomon[1]; Moyinoluwa Adeniyi[1]; Odunayo O. Oluokun[1]; Sarah Sahioun[1]; Vishal Sandilya[1]; Waziha Tasnim Purba[1]; Judith Ijeoma Nwaiwu[1]; MD MOSTOFA AL AMIN BHUIYAN[1]; Favour M. Chukwubueze[1]; Esther O. Oji[1]; Ayobami O. Oluokun[1]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX*

ThP 267 **Site-Specific O-Glycoproteomics and Molecular Dynamics Reveal Functional Roles of Tear Fluid O-Glycans**; Vincent Chang[1]; Ryan Chen[1]; Isaac Lian[1]; Keira Mahoney[1]; Stacy Malaker[1]; *[1]Yale University, New Haven, CT*

ThP 268 **"HILIC-Based Enrichment of O-Linked Glycopeptides from Human Serum"**; Jyoti Kannoujia[1]; Kurt Ian Boleman[2]; Gabriel William Cohen[2]; Andrew Dewitt Couse[2]; Jonathan Cyboski Trinidad[2]; *[1]Indiana University, BLOOMINGTON, IN; [2]Indiana University, Bloomington, IN*

ThP 269 **Isobaric Multiplex Labeling Reagents for Carbonyl-Containing Compound (SUGAR) Tagging with MnESI-MS Platform Enable Isomeric Separation and Quantification of α2,3/α2,6-Sialylated Glycopeptides**; Ching-Yuan Yang[1]; Penghsuan Huang[2]; Peng-Kai Liu[1]; Yajing Lu[2]; Alexander Nassar[2]; Zicong Wang[3]; Lingjun Li[1, 2, 3]; *[1]Biophysics Program, University of Wisconsin-Madison, Madison, WI; [2]Department of Chemistry, University of Wisconsin-Madison, Madison, Wisconsin 53706, USA., Madison, WI; [3]School of Pharmacy, University of Wisconsin-Madison, Madison, WI*

ThP 270 **Functional validation of an in vitro IgA1 expression system with CRISPR/dCas9-mediated gene modulation by LC-MS glycopeptide profiling**; Iwona Borošak[1]; Goran Josipović[1]; Jasminka Krištić[1]; Sara Monteiro-Martins[2]; Anna Köttgen[2, 3]; Gordan Lauc[1, 4]; *[1]Genos Glycoscience Research Laboratory, Zagreb, Croatia; [2]Institute of Genetic Epidemiology, Faculty of Medicine and Medical Center–University of Freiburg, Freiburg, Germany; [3]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD; [4]Department of Biochemistry and Molecular Biology, Faculty of Pharmacy and Biochemistry, University of Zagreb, Zagreb, Croatia*

ThP 271 **Development of a High-Sensitivity Glycoproteomics Approach for Fc-Specific Quantification of IgG Core Fucosylation in Traumatic Brain Injury**; Abdulrahman Abdulmumin[1]; Sherifdeen B. Onigbinde[1]; Joy Solomon[1]; Vishal Sandilya[1]; Oluwatosin Daramola[1]; Mojibola Fowowe[1]; Moyinoluwa Adeniyi[1]; Firas H. Kobeissy[2]; Stefania Mondello[3]; Ava Puccio[4]; Yehia Mechref[1]; *[1]Texas Tech University, USA, Lubbock, TX; [2]Centre for Neurotrauma, MultiOmics & Biomarkers (CNMB) Morehouse School of Medicine, Atlanta, GA; [3]University of Messina, Messina, Messina, Italy; [4]University of Pittsburgh, Pittsburgh, Pittsburgh, PA*

ThP 272 **FAIMS-Enhanced Orbitrap LC-MS Molecular Phenotyping of Native Sialylated Galactose-Deficient IgA1 O-Glycoforms in Serum of Patients with IgA Nephropathy**; Mukta Saurabh Gulavane[1]; Mary A Cunningham[1]; Olivia Schou[1]; Stacy D Hall[2]; Zhengrong Yang[3]; Hogan Morton[1]; Dana V Rizk[4]; Bruce A. Julian[4]; Jan Novak[2]; Matthew B Renfrow[1]; *[1]Department of Biochemistry and Molecular Genetics, University of Alabama at Birmingham, Birmingham, AL; [2]Department of Microbiology, University of Alabama at Birmingham, Birmingham, AL; [3]Department of Biochemistry and Molecular Genetics,University of Alabama at Birmingham, Birmingham, AL; [4]Department of Medicine, Division of Nephrology, University of Alabama at Birmingham, Birmingham, AL*

ThP 273 **GlypPRM: An Automated Analyzer and Quantification Tool for Glycopeptides Parallel Reaction Monitoring**; Oluwatosin Daramola[1]; Sherifdeen Onigbinde[2]; Moyinoluwa Adeniyi[2]; Cristian D Gutierrez Reyes[2]; Mojibola Fowowe[2]; Vishal Sandilya[2]; Yehia Mechref[2]; *[1]Texas Tech University, Lubbock, TX; [2]Texas Tech University, Lubbock,, TX*

ThP 274 **Characterizing integrin glycosylation using a real-time decision-making platform**; Anna G. Duboff[1]; Kathryn Kothlow[1]; Tim S. Veth[1]; Jacob H. Russell[1]; Katrina N. Peterson[1]; Fengchao Yu[2]; Daniel A. Polasky[2]; Alexey I. Nesvizhskii[2]; Devin K. Schweppe[1]; Nicholas M. Riley[1]; *[1]University of Washington, Seattle, WA; [2]University of Michigan-Ann Arbor, Ann Arbor, MI*

ThP 275 **Proteomic and glycoproteomic analyses of low-abundance IgA1-containing immune complexes in serum by (FAIMS) Orbitrap Ascend LC-MS**; Olivia J Schou[1]; Mary A Cunningham[1]; Mukta Saurabh Gulavane[1]; Zhengrong Yang[1]; Stacy D Hall[2]; Hogan Morton[1]; Dana V Rizk[3]; Bruce A. Julian[3]; Jan Novak[2]; Matthew B Renfrow[1]; [1]*Department of Biochemistry and Molecular Genetics,University of Alabama at Birmingham, Birmingham, AL;* [2]*Department of Microbiology, University of Alabama at Birmingham, Birmingham, AL;* [3]*Department of Medicine, Division of Nephrology, University of Alabama at Birmingham, Birmingham, AL*

ThP 276 **LacNAc-ase enabled glycoproteomics: an enzymatic strategy to uncover poly-LacNAc modified glycoproteins using endo-beta-galactosidase**; Jacob H Russell[1]; Nicholas M. Riley[1]; [1]*University of Washington, Seattle, WA*

ThP 277 **A catch and release strategy for cell surface glycoproteomics with intact glycosite information**; Emmajay Sutherland[1]; Nicholas M. Riley[1]; [1]*University of Washington, Seattle, WA*

ThP 278 **Integrated Mass Spectrometry-Based Proteomic and Intact N-glycoproteomic Analysis of Acquired Glucocorticoid Resistance in Pediatric Acute Lymphoblastic Leukemia**; Ao Wang[1]; Fernando Garcia-Marques[2]; Yuxuan Liu[1]; Abel Bermudez[2]; Milton Merchant[1]; Sharon Pitteri[2]; Kara L Lynn[1]; [1]*Department of Pediatrics, Hematology-Oncology, School of Medicine, Stanford University, Palo Alto, CA;* [2]*Canary Center for Cancer Early Detection, Department of Radiology, School of Medicine, Stanford University, Palo Alto, CA*

ThP 279 **N-Glycosylation Patterns Across Major Human Milk Proteins**; Rachna Chaddha[1]; David E. Clemmer[2]; Jonathan Cyboski Trinidad[2]; Sarah Joelle Cox-Vazquez[2]; Xuyao Zeng[2]; Morgan Elizabeth Lane[2]; Andrew Dewitt Couse[3]; [1]*Indiana University, Bloomington, IN;* [2]*Indiana University Bloomington, Bloomington, IN;* [3]*Indiana University - Bloomington, Bloomington, IN*

ThP 280 **Integrated CID-EAD LC-MS/MS Strategy for Precise Site-Specific Localization of Immunogenic α-Gal Epitopes in Advanced Biotherapeutics**; Juhui Baek[1, 2]; Hye Kyeong Jeong[1, 2]; Myung Jin Oh[1, 2]; Hyun Joo An[1, 2]; [1]*Asia-Pacific Glycomics Reference Site, Daejeon, South Korea;* [2]*Graduate School of Analytical Science and Technology, Chungnam National University, Daejeon, South Korea*

ThP 281 **Improved Serum Glycoproteome Coverage via EGCG-Based Extracellular Vesicle Isolation**; Geul Bang[1]; Jong Hyun Seol[1]; Su-Min Lee[1]; Bao Tan Nguyen[1]; Seungjin Na[1]; Jin Young Kim[1]; [1]*Korea Basic Science Institute, Cheongju, South Korea*

ThP 282 **Automated and High-Throughput Strategy for Site-Specific Clinical Plasma Glycoproteome Profiling**; Jung Hoon Choi[1]; Jin Young Kim[1]; Geul Bang[1]; [1]*Korea Basic Science Institute, Ochang, Cheongju, South Korea*

ThP 283 **Finding unanticipated modifications to N-glycans in glycoproteomics data**; Alyssa Tang[1]; Wilfred Tang[2]; [1]*Proof School, San Francisco, CA;* [2]*Protein Metrics, Boston, MA*

ThP 284 **High-Throughput Plasma IgA Enrichment and Site-Specific Glycosylation Profiling for Cohort Studies**; Jelena Simunovic[1]; Sinisa Habazin[1]; Jerko Stambuk[1]; Natali Nakic Bedekovic[1]; Filip Klicek[1]; Sara Monteiro-Martins[2]; Anna Kottgen[2, 3]; Gordan Lauc[1, 4]; [1]*Genos Glycoscience Research Laboratory, Zagreb, Croatia;* [2]*Institute of Genetic Epidemiology, Faculty of Medicine and Medical Center–University of Freiburg, Freiburg, Germany;* [3]*Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Johns Hopkins University, Baltimore, MD;* [4]*Department of Biochemistry and Molecular Biology, Faculty of Pharmacy and Biochemistry, University of Zagreb, Zagreb, Croatia*

ThP 285 **Beyond N-Glycosylation: Integrated Hybrid DIA-MS Strategy Reveals O-Glycosylation of PD-L1 Protein**; Ching-Hsun Tsai[1]; Yi-Ju Chen[1]; [1]*Department of Biological Science and Technology, College of Engineering Bioscience, National Yang Ming Chiao Tung University, Hsinchu City, Taiwan*

ThP 286 **Integrated hybrid DIA-MS for Sensitive Detection of O-Glycosylation on AXL protein**; Yun-Hsin Kuo[1]; Yi-Ju Chen[1]; [1]*Department of Biological Science and Technology, College of Engineering Bioscience, National Yang Ming Chiao Tung University, Hsinchu City, Taiwan*

ThP 287 **Improving O-Glycopeptide Characterization with IR-ETD and Multi-Protease Digestion**; Annie Jen[1]; Li-Yu Chen[2]; Katherine A. Overmyer[1, 3, 4]; Haley M Schramm[5]; Scott T Quarmby[1, 4]; Graeme C McAlister[6]; Joshua D Hinkle[6]; Christopher Mullen[6]; Nicholas M. Riley[5]; Joshua J Coon[1, 2, 3, 4]; *[1]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [3]Morgridge Institute for Research, Madison, WI; [4]National Center for Quantitative Biology of Complex Systems, Madison, WI; [5]Department of Chemistry, University of Washington, Seattle, WA; [6]Thermo Fisher Scientific, San Jose, CA*

ThP 288 **Delocalization of Analytes as a Function of the Ablation Process in Mass Spectrometry Imaging**; Andrew Bowman[1]; Yongan Tang[1]; Junhai Yang[1]; Nari Talaty[1]; *[1]AbbVie, Inc., North Chicago, IL*

ThP 289 **Development of a Tapping-mode Scanning Probe Electrospray Ionization Platform for Single-Cell MSI of Tissue**; Yoichi Otsuka[1]; Takao Yasuda[1]; Tasuku Kato[1]; Shuichi Shimma[2]; Tomoki Misaka[1]; Takuya Matsumoto[1]; Michisato Toyoda[1]; *[1]The University of Osaka, Toyonaka, Japan; [2]The University of Osaka, Suita, Japan*

ThP 290 **Photochemical Tissue Processing for MALDI Lipid Imaging**; Kermit K. Murray[1, 2]; Kadeem O. Hayes[1]; *[1]Louisiana State University, Baton Rouge, LA; [2]Laser Bioanalytics LLC, Baton Rouge, LA*

ThP 291 **Combining topographical and chemical mapping to advance discovery-driven single-cell and multiomics investigations**; John Sentmanat[1]; Kisurb Choe[1]; Mazdak Taghioskoui[2]; Andrei Fedorov[1]; *[1]Georgia Institute of Technology, Atlanta, GA; [2]Trace Matters Scientific LLC, Bethesda, MD*

ThP 292 **Assessment of HDMSe and HDSMS/MSe for MSI applications using SELECT SERIES™ Cyclic™ ion mobility**; Emmanuelle Claude[1]; Bindesh Shrestha[2]; Joanne Ballantyne[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

ThP 293 **Integration of nano-DESI MSI with infrared laser ion desolvation of proteins and complexes**; Helen Cooper[1]; Oliver J. Hale[1]; *[1]University of Birmingham, Birmingham, United Kingdom*

ThP 294 **Studying the Extraction–Ionization Process of Tapping-Mode Scanning Probe Electrospray Ionization by Monitoring the Spray Current**; Mengze Sun[1]; Yoichi Otsuka[1]; Lee Chuin Chen[2]; Michisato Toyoda[1]; *[1]The University of Osaka, Toyonaka, Japan; [2]University of Yamanashi, Kofu, Japan*

ThP 295 **SIMION-COMSOL Simulation for Plasma Desorption Ion (PDI) Mass Spectrometry for Biological Imaging of Mouse Livers after Ge-Zhi**; Eric Handberg[1]; Shuanglong Wang[1, 2]; Huaxue Xie[1]; Tianchen Zhang[1]; Ni Zhang[3]; Rui Su[3]; *[1]East China University of Technology, Nanchang, China; [2]Evaluation and Research Center of Dao-di Herbs of Jiangxi Province, Nanchang, China; [3]Jiangxi University of Chinese Medicine, Nanchang, China*

ThP 296 **Ion mobility separation of lipids using a prototype cyclic IMS QTof with a MALDI source**; Mark Towers[1]; Emmanuelle Claude[1]; Patricia Prabutzki[2]; Eva Cuypers[2]; Roy Martin[3]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Maastricht University, Maastricht, Netherlands; [3]Waters Corporation, Milford, MA*

ThP 297 **Ultraviolet matrix-assisted laser desorption electrospray ionization imaging mass spectrometry of metabolites**; Andrews Ruano Rosa[1]; Paul Zerebinski[1]; Ruwan T. Kurulugama[2]; Sarah M. Stow[2]; Richard A. Yost[1]; Timothy J. Garrett[1, 3]; Boone M. Prentice[1]; *[1]University of Florida, Department of Chemistry, Gainesville, FL; [2]Agilent Technologies Inc., Santa Clara, CA; [3]University of Florida, College of Medicine, Department of Pathology, Immunology, and Laboratory Medicine, Gainesville, FL*

ThP 298 **Coupling AP-SMALDI MS Imaging technology with a modified Orbitrap Hybrid mass spectrometer**; Julius Wollmann[1]; Christian Schaefer[1]; Stefanie Gerbig[1]; Carolin Morawietz[1]; Max A. Mueller[1]; Bernhard Spengler[1]; Susan S. Bird[2]; Claire Dauly[3]; Kerstin Strupat[3]; *[1]TransMIT GmbH, Giessen, Germany; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

ThP 299 **Dual-mode high sensitivity imaging at ultra-high spatial resolution**; MIKHAIL BELOV[1]; Christoper Anderson[1, 2]; *[1]Spectroglyph LLC, Kennewick, WA; [2]GAA Custom Electronics, Kennewick, WA*

THURSDAY MORNING ORALS

ThP 300 **Influence of cryogenic analysis conditions in combination with water cluster ion beams for biological analysis with secondary ion mass spectrometry**; Simon Uzoni[1]; John S Fletcher[1]; *[1]University of Gothenburg, Gothenburg, Sweden*

ThP 301 **Efficient and Cost-Effective Enzyme Deposition onto Tissues for Mass Spectrometry Imaging of N-Glycans using a Mini-Humidifier**; Erik Sveen[1]; Alyssa Moore[1]; Miranda Weigand[1]; Julia Laskin[1]; *[1]Purdue University, west lafayette, IN*

ThP 302 **The Development of an Expansion Mass Spectrometry Method for Single Cell MALDI-MSI**; Dalia A Riad[1]; Jason Guerrero[2]; Vignesh Venkataramani[3]; Ethan Older[2]; Marouen Zammali[3]; Danielle Latham[3]; Ramita Arampongpun[3]; Lydia Kisley[3]; Laura M Sanchez[2]; *[1]University, Santa Cruz, CA; [2]University of California, Santa Cruz, Santa Cruz, CA; [3]Case Western Reserve University, Cleveland, OH*

ThP 303 **Two-step matrix deposition for improved MS Imaging Resolution**; Francine E Yanchik-Slade[1]; Elizabeth Ko[1]; Nazim Boutaghou[1]; *[1]Shimadzu Scientific Instruments, Columbia, MD*

ThP 304 **Integration of Expansion Microscopy and Imaging Mass Spectrometry via Multimodal Image Fusion for 100-fold Spatial Resolution Enhancement**; Elijah D. Mayo[1]; Jacob M. Samuel[1]; Yingchan Guo[1]; Boone M. Prentice[1]; *[1]University of Florida, Department of Chemistry, Gainesville, FL*

ThP 305 **10-fold Expansion Factor Hydrogels for High Spatial Resolution Lipid Imaging Mass Spectrometry**; Jacob M Samuel[1]; Nana M Baby[1]; Elijah D. Mayo[1]; Sarah J Murphy[1]; Boone M Prentice[1]; *[1]University of Florida, Department of Chemistry, Gainesville, FL*

ThP 306 **Metabolomic Analysis of Ocular and Renal Tissues Affected by Diabetes Mellitus Using Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging**; John Albert Cabanit[1]; Yi-Wen Chang[2]; Wen-Ping Peng[1]; ChengKang Chiang[3]; *[1]National Dong Hwa University, Shoufeng, Taiwan; [2]National Taiwan University Hospital, Taipei, Taiwan; [3]Department of Chemistry, National Dong Hwa University, Shou-Feng, Hualien, Taiwan*

ThP 307 **Measuring pH Microheterogeneity in Biological Tissues using Hydrogen-Deuterium Exchange (HDX) and IR-MALDESI Mass Spectrometry Imaging**; Emily R. Bruce[1]; Eleanor J. Burns[1]; Sean J. Cone[2]; Michael P. Gamcsik[2]; David C. Muddiman[1]; *[1]Biological Imaging Laboratory for Disease and Exposure Research (BILDER), Raleigh, NC; [2]UNC/NCSU Joint Department of Biomedical Engineering, Raleigh, NC*

ThP 308 **Optimizing Organoid Embedding Methods for Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry Imaging Analysis**; Madison E Kjar[1]; Amanda B Hummon[1, 2]; *[1]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH; [2]The Ohio State University Comprehensive Cancer Center, Columbus, OH*

ThP 309 **Multidirectional analysis of cancer-immune-related polyunsaturated fatty acids in a mouse tumor model by MS imaging and oxygen attachment dissociation (OAD)**; Kaoru Nakagawa[1]; Akiko Kubo[2]; Yuki Katoh[3]; Francine Yanchik Slade[4]; Mohamed Boutaghou[4]; Manami Kobayashi[5]; Hidenori Takahashi[6]; *[1]Shimadzu corporation, Kyoto, Japan; [2]Kobe University, Kobe, Japan; [3]Nihon University, Tokyo, Japan; [4]Shimadzu Scientific Instruments, Columbia, MD; [5]Shimadzu corporation, Kawasaki, Japan; [6]Shimadzu Corporation, Kyoto, Japan*

ThP 310 **DESI-MSI Reveals Cholesterol and Lipidomic Differences in Longissimus Dorsi Across Cattle Breeds**; Emilio Restrepo Nunez[1, 2]; Kevin Andres Perez[1, 3]; Priyanka Ramesh[1]; Juliana A Torrecilhas[4]; Nicolas Mauricio Morato Gutierrez[5]; Yunfei Feng[5]; Ryan T Hilger[5]; Christina Ferreira[1]; *[1]Bindley Bioscience Center, Purdue University, West Lafayette, IN, west lafayette, IN; [2]Universidad de los Andes, Bogota, Colombia; [3]Universidad Nacional de Colombia, Medellin, Colombia; [4]Sao Paulo State University, Sao Paulo, Brazil; [5]Purdue University Dept of Chemistry, West Lafayette, IN*

ThP 311 **Thin-Section-Free MSI of Leaf Metabolites and Pesticides Using a Porous Glass-Bead Transfer Plate**; Takamasa Ikeda[1]; Yutaka Takahashi[2, 3]; Mitsutoshi Setou[2]; *[1]Hamamatsu Photonics K.K., Iwata, Japan; [2]Hamamatsu University School of Medicine, Hamamatsu, Japan; [3]Preppers Co., Ltd., Hamamatsu, Japan*

ThP 313 **Spatial Carboxyl-metabolomics On-tissue Using 3-Nitrophenylhydrazine Derivatization and Hydrogel Assistance Strategy**; Chunlu Feng[1, 2]; Wensong Chen[2]; Yuanmao Zhang[2]; Yun Zhao[2]; Wan Sun[2]; Raobo Xu[2]; Lingyun Chen[2]; Zhanlong Mei[2]; Guixue Hou[2]; Jin Zi[2]; Siqi Liu[2, 3]; *[1]Key Laboratory of Systems Health Science of ZhejiangProvince, School of Life Science, Hangzhou Institute for Advanced Study, Hangzhou, China; [2]BGI Genomics, ShenZhen, China; [3]College of Life Sciences, University of Chinese Academy of Sciences, Beijing, China*

ThP 314 **Study of ion suppression phenomena in MALDI for metabolite standards deposited on glass and tissue homogenate**; Enya Murray[1]; Felicia Wirtz[1]; Angeliki Christakopoulou[1]; Alex Dexter[1]; Josephine Bunch[1, 2]; Rory T Steven[1]; *[1]National Physical Laboratory, London, United Kingdom; [2]Imperial College London, London, United Kingdom*

ThP 315 **Investigating alternative derivatization reagents for MALDI-based mass spectrometry experiments**; Abigail Moreno-Pedraza[1]; Kevin J. Zemaitis[1]; Aiko Barsch[2]; Arne Behrens[2]; Nikolas Kessler[2]; Christopher Anderton[1]; Dusan Velickovic[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany*

ThP 316 **Image Fusion Restores Spatial Resolution Following Pixel-Based Signal Averaging in Orbitrap MSI**; Yury Desyaterik[1]; MaryPeace McRae[2]; Konstantin O. Nagornov[3]; Anton N. Kozhinov[3]; Yury O. Tsybin[3]; Angela D.M. Kashuba[1]; Elias P. Rosen[1]; *[1]UNC, Chapel Hill, NC; [2]Virginia Commonwealth University, Richmond, VA; [3]Spectroswiss, Lausanne, Switzerland*

ThP 317 **Sequential MALDI and nano-DESI imaging of lipids and proteins on stretched tissue samples: boosting spatial resolution with high molecular coverage**; Timothy J Trinklein[1]; Mushfeqa Iqfath[2]; Stanislav S Rubakhin[1]; Julia Laskin[2]; Jonathan V Sweedler[1]; *[1]University of Illinois Urbana Champaign, Urbana, IL; [2]Purdue University, Lafayette, IN*

ThP 318 **Optimization of Fixation and Spotting Procedures for Mammalian and Bacterial Cells to Improve Lipid Signal in MALDI-MSI Analysis**; Evelyn E. Minton[1]; Catherine B. Whitney[1]; Arbil Lopez[1]; Amanda B. Hummon[1]; *[1]The Ohio State University Department of Chemistry and Biochemistry, Columbus, OH*

ThP 319 **Super-Resolution Mass Spectrometry Imaging using Correlative SIMS and DESI Data**; Shenghui Ye[1]; Hongzhe Ma[2]; Zhaoying Wang[2]; Xiaoxiao Ma[1]; Zheng Ouyang[1]; *[1]Tsinghua University, Beijing, China; [2]Minzu University of China, Beijing, China*

ThP 320 **High mass and spatial resolution MS imaging of soft fruit sample cross-sections using desorption electrospray ionization (DESI)**; Wei Rao[1]; Cory Scanlan[2]; Mark Towers[1]; Joanne Ballantyne[1]; Joanne Williams[1]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters Corporation, Milford, MA*

ThP 321 **Optimized targeted spatial imaging of Nicotinamide Adenine Dinucleotide (NAD+) via iprm-PASEF confirms metabolic resilience in aged CD38-/- mice**; Sriya Cheruvu[1]; Charles A Schurman[1]; Prasanna Vadhana Ashok Kumaar[1]; Jingqi Fang[1]; Rebeccah Riley[1]; Joanna Bons[1]; Andrea Roberts[1]; Genesis Vega Hormazabal[1]; Nannan Tao[2]; Eric Verdin[1]; Birgit Schilling[1]; *[1]Buck Institute for Research on Aging, Novato, CA; [2]Bruker Daltonics, San Jose, CA*

ThP 322 **Analysis of French Spirit Barrels (Oak Wood) Metabolites by LDI MS imaging**; Diana A. Barrera-Adame[1]; Aline Cournut[2]; Quentin P. Vanbellingen[2]; Matthias Ochs[1]; David Touboul[3]; Veronique Eparvier[4]; Alain Brunelle[2]; Andreas Roempp[1]; *[1]Bioanalytical Sciences and Food Analysis, University of Bayreuth, Bayreuth, Germany; [2]Laboratoire d'Archéologie Moléculaire et Structurale (LAMS), CNRS, Sorbonne Université, Paris, France; [3]Ecole Polytechnique, CNRS, Laboratoire de Chimie Moléculaire, Institut Polytechnique de Paris, Palaiseau, France; [4]Université Paris-Saclay, CNRS, Institut de Chimie des Substances Naturelles, Gif-sur-Yvette, France*

ThP 323 **Enabling subcellular imaging of the Drosophila embryo with femtosecond laser ablation**; Khaled Madhoun[1]; Alexander A.C. Wainwright[1]; Stephen Vanderburgt[2]; Aosheng Gu[1]; Hui Zhang[3]; Tony J.C. Harris[3]; R.J. Dwayne Miller[1, 2]; *[1]Department of Physics, University of Toronto, Toronto, ON; [2]Department of Chemistry, University of Toronto, Toronto, ON; [3]Department of Cell and Systems Biology, University of Toronto, Toronto, ON*

ThP 324 **Improving Detection and Relative Quantitation of Metabolites via Stable Isotope–Enhanced DESI-MS Imaging**; Karolina M. Krasinska[1]; Grzegorz Krzak[2]; Michelle Monje[2,3]; Ryan D. Leib[1]; *[1]SUMS, Stanford University, Stanford, CA; [2]Department of Neurology and Neurological Sciences, Stanford University, Stanford, CA; [3]Department of Psychiatry and Behavioral Sciences, Stanford University, Stanford, CA*

ThP 325 **Normalizing Desorption Electrospray Ionization MS Imaging Data from Tissues to Internal Standards**; Soumika Pinninti[1]; Rachel J. DeHoog[1]; Michael D Tuck[1]; Alyson Black[2]; Livia S. Eberlin[1]; *[1]Baylor College of Medicine, Houston, TX; [2]HTX Technologies, LLC, Chapel Hill, NC*

ThP 326 **Mass Spectrometry Imaging of Sorghum bicolor Organs to Examine Lipid Distribution**; Sara Greenfield[1]; Andrew Crow[1]; Jonathan V Sweedler[1]; *[1]University of Illinois at Urbana-Champaign, Urbana-Champaign, IL*

ThP 327 **The Hunt for Macrophages – Combining High-Throughput and Imaging Ambient Methods for Characterising Cell Populations in Tissues**; Daniel Simon[1]; Yu Wang[2]; Gabriel Stefan Horkovics-Kovats[1]; Istvan Pap[1]; Zahra Nozari[1]; Yuchen Xiang[1]; Robert T Murray[2]; Zoltan Takats[1,2]; *[1]Regensburg University, Regensburg, Germany; [2]Imperial College London, London, United Kingdom*

ThP 328 **Optimizing Array-Based Protein Fingerprinting by MALDI-MS Imaging for High-Throughput Screening Applications**; Akaansha Rampal[1]; Casey Miller[1]; Quinn Roth-Carter[1]; Hope Burks[1]; Ryan McClure[1]; *[1]Chan Zuckerberg Biohub Chicago, Chicago, IL*

ThP 329 **Incorporating a standardized instrument QC framework into large-scale MALDI IMS studies for reproducibility**; Timothy Hendrigsman[1]; Madeline E Colley[2,3]; Megan S Ward[2,4]; Lauren Emmerson[2,5]; Alexis P Pope[2,5]; Jacqueline M Van Ardenne[2,6]; Katerina V. Djambazova[2,3]; Lukasz G Migas[2,7]; Martin Dufresne[2,3]; Raf Van De Plas[2,7,8]; Jeffrey M Spraggins[2,3,5,6,8,9]; *[1]Vanderbilt University, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [4]Chemical and Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [5]Chemical Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [6]Department of Chemistry, Vanderbilt University, Nashville, TN; [7]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [8]Department of Biochemistry, Vanderbilt University, Nashville, TN; [9]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN*

ThP 330 **High-ThroughputSingle-Cell Resolved Spatial Proteomics Enabled by Ordered Colloidal Crystal Column**; Haofei Sun[1]; Yu Liang[1]; Lihua Zhang[1]; Yukui Zhang[1]; *[1]Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Dalian, China*

ThP 331 **Factors Influencing Mass Spectrometry Imaging Performance in Multi-Reflecting Time-of-Flight Mass Spectrometry**; Tristen West[1]; David Lewis[1]; Thomas Knehans[1]; Pooja M. Datta Roy[1]; Facundo Fernandez[1]; Michelle C. LaPlaca[1]; *[1]Georgia Institute of Technology, Atlanta, GA*

ThP 332 **Lipid Double-Bond Tagging Enables Correlated Fluorescence and Mass Spectrometry Imaging with Isomer Resolution**; Leon Li Cyun Chen[1]; Xin Yan[1]; *[1]Texas A&M University, College Station, TX*

ThP 333 **AP/MALDI MS imaging and simultaneous ion mobility of endogenous (neuro)peptides (as well as metabolites) straight off pathologists' FFPE tissue sections**; Peter D. Verhaert[1,2]; Lilian Valadares Tose[3]; Eugene Moskovets[4]; Nivedita Bhattacharya[5]; Marco Giampà[6]; Raf Sciot[2]; Francisco Fernandez-Lima[3]; *[1]ProteoFormiX BV, Vorselaar, Belgium; [2]Department of Imaging and Pathology, University of Leuven, Leuven, Belgium; [3]Florida International University, Miami, FL; [4]MassTech Inc, Columbia, MD; [5]MassTech Inc., Columbia, MD; [6]VIB Metabolomics Core Leuven, VIB Technologies, VIB, Leuven, Belgium*

ThP 334 **A High-Throughput, Reproducible Workflow Integrating MALDI Imaging and Automated LC–MS/MS for Lipid and Metabolite Annotation**; Ryan Coyle[1,2]; Allison B. Esselman-Lawrence[1,2]; Bella Coenen[2]; Lauren Emmerson[2,3]; Madeline E Colley[2,4]; Lukasz G Migas[2,5]; Raf Van De Plas[2,5,6]; Jeffrey M Spraggins[1,2,4,6,7]; *[1]Department of Chemistry, Vanderbilt University, Nashville, TN; [2]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [3]Chemical and Physical Biology*

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ThP 335 **High spatial resolution MALDI mass spectrometry imaging of human tissue samples using custom binary matrix mixtures**; Martin Dufresne[1]; Lukasz G Migas[2]; Thai H Pham[3, 4]; Jade K. Macdonald[3, 4]; Audra M Judd[3, 4]; Jamie L Allen[3, 4]; Anna J Smith[3, 4]; Melissa A. Farrow[3, 4]; Raf Van De Plas[2]; Jeffrey M Spraggins[3, 4, 5, 6, 7]; *[1]Vanderbilt University, Nashville, TN; [2]Delft Center for Systems and Control, Delft University of Technology, Delft, Netherlands; [3]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [4]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [5]Department of Chemistry, Vanderbilt University, Nashville, TN; [6]Department of Biochemistry, Vanderbilt University, Nashville, TN; [7]Department of Pathology, Microbiology, and Immunology, Vanderbilt University Medical Center, Nashville, Nashville, TN*

ThP 336 **Revealing the Spatial Organization of Polyunsaturated Lipids and Bile Salts Across the Zebrafish Body Axis with MALDI Imaging**; Jacquelyn Spathies[1, 2, 3]; Caitlin C Murdoch[2, 3]; Simeon Betapudi[1]; Madeline E Colley[1, 4]; Katherine N Gibson-Corley[3]; Eric P Skaar[2, 3]; Jeffrey M Spraggins[1, 2, 3, 4, 5, 6]; *[1]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [2]Vanderbilt Institute for Infection, Immunology, and Inflammation, Vanderbilt University Medical Center, Nashville, TN; [3]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN; [4]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [5]Department of Biochemistry, Vanderbilt University, Nashville, TN; [6]Department of Chemistry, Vanderbilt University, Nashville, TN*

ThP 337 **FragNovo: A Versatile De novo Peptide Sequencing Model with Adaptation for Customizable PTMs and Diverse Proteomics Acquisition Modes**; Junkang Wei[1]; Kai Li[1]; Fengchao Yu[1]; Alexey Nesvizhskii[1]; *[1]University of Michigan, Ann Arbor, MI*

ThP 338 **TimsRust: A Modular Foundation for Performant timsTOF Data Workflows**; Jonathan Krieger[1]; Jonathan Moss[2]; George Rosenberger[3]; Dennis Trede[4]; Sander Willems[5]; *[1]Bruker Ltd, Milton, Canada, Toronto, ON; [2]Bruker, Preston, Australia; [3]Bruker Switzerland AG, Fällanden, Switzerland; [4]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [5]Bruker, Kontich, Belgium*

ThP 339 **Artificial Intelligence (AI)-based system to evaluate quality spectra in MALDI-TOF mass spectra**; SYED MUHAMMAD ALI FARHAN[1]; Yi-Sheng Wang[1]; *[1]Genomics Research Centre (GRC) Academia Sinica, Taiwan, Taipei, Taiwan*

ThP 340 **Comprehensive top-down mass spectral library enables pan-dataset analysis and top-down spectral prediction**; Kun Li[1]; Kaiyuan Liu[2]; James M. Fulcher[3]; Haixu Tang[2]; Xiaowen Liu[1]; *[1]Tulane University, New Orleans, LA; [2]Indiana University, Bloomington, IN; [3]Pacific Northwest National Laboratory, Richland, WA*

ThP 341 **A real-world public structure elucidation challenge and benchmark, with challenge spectra from hundreds of molecules derived from complex samples**; David Healey[1]; Tobias Kind[1]; Christoph Krettler[1]; Erik DeBloois[1]; James Taylor[1]; Pelle Simpson[1]; Daniel Domingo-Fernandez[1]; August Allen[1]; *[1]Enveda Biosciences, Boulder, CO*

ThP 342 **SenoCETSA software identifies potential targets of senolytics from MS-CETSA data**; Tomas Pierce[1]; Serena Wu[1]; Gisela Altes Bargallo[1]; Martin Salamini Montemurri[1]; Quinn Strassheim[1]; Amit Dey[1]; Delaney Rutherford[1]; Reema Banarjee[1]; Dmitrios Tsitsipatis[1]; Bradley Olinger[1]; Ruin Moaddel[1]; Myriam Gorospe[1]; Alison Herman[1]; Nathan Basisty[1]; *[1]National Institute on Aging, Baltimore, MD*

ThP 343 **Telescope: Open source database search software for real-time mass spectrometry technology development**; Michael R Hoopmann[1]; Jimmy K. Eng[1]; Devin K. Schweppe[1]; *[1]University of Washington, Seattle, WA*

ThP 344 **BayesPeak: A Bayesian Approach of Spectrum-Spectrum Matching for Peptide Identification in Proteomics**; Chun Kit Jason Chung[1]; Henry Lam[1]; [1]*The Hong Kong University of Science and Technology, Hong Kong, Hong Kong*

ThP 345 **PRIME: An Interactive Platform for Integrative Proteomics Analysis**; Yu Sun[1, 2]; Kumar Yugandhar[2]; Yuliang Tang[2]; Yiwen Wang[2, 3]; Katie Munechika[2, 4]; Haiyuan Yu[2, 3]; [1]*Cornell University, Ithaca, NY;* [2]*Weill Institute for Cellular and Molecular Biology, Cornell University, Ithaca, NY;* [3]*Department of Computational Biology, Cornell University, Ithaca, NY;* [4]*Meinig School of Biomedical Engineering, Cornell University, Ithaca, NY*

ThP 346 **LLM-Enabled Automated Data Conversion for Reproducible MSstats Differential Analysis**; Devon Kohler[1]; Anthony Wu[1]; Olga Vitek[1]; [1]*Northeastern University, Boston, MA*

ThP 347 **Isonucleonic Isotopologues and Tensor-Based Isotope Distributions in High-Resolution Mass Spectrometry**; Frédérique Vilenne[1]; Piotr Prostko[1]; Dirk Valkenborg[1]; [1]*Hasselt University, Hasselt, Belgium*

ThP 348 **ModLocalize: A PTM Localization Algorithm with Ambiguity Regions and Integrated FLR Control**; Pisit Wajanasara[1, 2]; Nuno Bandeira[1, 2, 3]; [1]*Center of Computational Mass Spectrometry, University of California San Diego, La Jolla, CA;* [2]*Department of Computer Science and Engineering, University of California San Diego, La Jolla, CA;* [3]*Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA*

ThP 349 **Robustness of charge state determination approaches for processing mass-spectrometry data**; Paul Trusov[1, 2]; Oleg Obolensky[2]; Aleksey Ogurtsov[2]; Yi-Kuo Yu[2]; [1]*Cornell University, Ithaca, NY;* [2]*Division of Intramural Research, National Library of Medicine, National Institutes of Health, Bethesda, MD*

ThP 350 **OAC-PCA: orthogonal adjustment for confounding principal component analysis for metabolomics data mining**; Misaki Kurata; *Tokyo University of Agriculture and Technology, Tokyo, Japan*

ThP 351 **Modular End-to-End TMTpro Proteomics Analysis with Channel-Set Normalization and Reference-Based Control of Deuterated Channels**; Farhad Shakeri[1]; Andreas Buness[2]; Marc Sylvester[3]; Stefan Selzer[1]; David van Meter[1]; Ian Pike[4]; [1]*Proteome Sciences R&D GmbH & Co. KG, Frankfurt am Main, Germany;* [2]*Core Unit for Bioinformatics Data Analysis, University of Bonn, University Hospital Bonn, Bonn, Germany;* [3]*Core Facility Analytical Proteomics, University of Bonn, University Hospital Bonn, Institute of Biochemistry and Molecular Biology, Bonn, Germany;* [4]*Proteome Sciences plc, Coveham, Surrey, UK, Cobham, Surrey, United Kingdom*

ThP 352 **Accurate resolution of proteomics open modification search delta masses to UniMod modifications while allowing for modification site uncertainty**; Astoria Ma[1, 2]; Nuno Bandeira[1, 2, 3]; [1]*Center of Computational Mass Spectrometry, University of California San Diego, La Jolla, CA;* [2]*Department of Computer Science and Engineering, University of California San Diego, La Jolla, CA;* [3]*Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA*

ThP 353 **Comparing prediction matching and artificial intelligence approaches for the interpretation of oligonucleotide sequencing data obtained by tandem mass spectrometry**; Pierre F. Fabris[1]; Daniele Fabris[1, 2]; [1]*RiboDynamics, Manchester, CT;* [2]*University of Connecticut, Storrs, CT*

ThP 354 **Deterministic Inference of Structural Nuclei from Homologous Series Using DBE–Carbon Growth Rules in FT-ICR MS**; Jussara Roque[1]; Lidya Cardozo Da Silva[1]; João Victor Ataide Oliveira[1]; Deborah Victoria Alves De Aguiar[1]; Wilson Cardoso[1]; Hugo Gontijo Machado[1]; Boniek Gontijo[1]; [1]*Universidade Federal de Goias, Goiânia, Brazil*

ThP 355 **Explainable Annotation of Mass Spectra through Chemically Constrained Fragmentation Modeling**; Johannes B.S. Petersen[1]; Akbar Davoodi[1]; Christoph Flamm[2]; Christoph Henrich[3]; Peter F. Stadler[4]; Daniel Merkle[1, 5, 6]; [1]*University of Southern Denmark, Odense, Denmark;* [2]*University of Vienna,*

Vienna, Austria; [3]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [4]Leipzig University, Leipzig, Germany; [5]Algorithmic Cheminformatics, Faculty of Technology, Bielefeld University, Bielefeld, Germany; [6]The Center for Biotechnology (CeBiTec), Bielefeld University, Bielefeld, Germany

ThP 356 **The Last Alignment Frontier: Optimal and Non-Monotonic Alignment Without Standards Across Methods For Signal Amplification**; Allen Hubbard[1, 2]; Louis Connelly[1, 2]; Ivan Baxter[1, 2]; *[1]Metablify, Saint Louis, MO; [2]Donald Danforth Plant Science Center, Saint Louis, MO*

ThP 357 **Evaluation of a Consensus Based MS/MS Library Matching Algorithm and Integration into a Non-Targeted Software Platform for Increasing Exposome Coverage**; David Schiessel[1]; Jeremy Koelmel[1]; Olivier P. Chevallier[2]; David Godri[3]; Randolph R. Singh[4]; Thomas O. Metz[5]; Fanny Chu[5]; Parker Chang[1]; Sheng Liu[1]; Emma E. Rennie[2]; Krystal J. Godri Pollitt[1]; *[1]Yale University, New Haven, CT; [2]Agilent Technologies, Santa Clara, CA; [3]3rd Floor Solutions, Caledon, ON; [4]Columbia University, New York, NY; [5]Pacific Northwest National Laboratory (PNNL), Richland, WA*

ThP 358 **xTracer: A Spectrum-centric Approach for Untargeted Peptide Identification in SLIM-Based PAMAF DIA data**; Jian Song[1]; Liulin Deng[2]; Lauren Royer[2]; Bennett Kalafut[2]; Daniel DeBord[2]; Jesse Meyer[1]; *[1]Cedars-Sinai Medical Center, LA; [2]MOBILion Systems, Inc, Chadds Ford, PA*

ThP 359 **MSMICA: computational metabolite identification in untargeted metabolomics by integrating MS, retention time, and biological evidence**; Jiada Zhan[1, 2]; Jaclyn Weinberg[1]; William J Crandall[1]; Zhaohui Qin[3]; Zachery R Jarrell[1]; Joshua D Preston[1, 2]; Mary Nellis[1]; Sami Teeny[1]; Donghai Liang[4]; Greg S Martin[1]; Nathan L Price[5]; Rafael de Cabo[5]; Viraj Master[6]; Barbara A Cohn[7]; Terrance J Kavanagh[8]; Young-Mi Go[1]; Dean P Jones[1]; *[1]Division of Pulmonary, Allergy, Critical Care, and Sleep Medicine, School of Medicine, Emory University, Atlanta, GA; [2]Nutrition and Health Sciences, Laney Graduate School, Emory University, Atlanta, GA; [3]Department of Biostatistics and Bioinformatics, Rollins School of Public Health, Emory University, Atlanta, GA; [4]Gangarosa Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, GA; [5]National Institute on Aging, Baltimore, MD; [6]Department of Urology, School of Medicine, Emory University, Atlanta, GA; [7]Public Health Institute, Oakland, CA; [8]University of Washington, Seattle, WA*

ThP 360 **Agnostic identification of peptide modifications from MS1 data using mass defect**; Gillian Leach[1, 2]; Abanoub Mikhael[1, 2]; Darryl Hardie[1]; Derek Smith[1]; David R. Goodlett[1, 2]; *[1]UVic Genome BC Proteomics Centre, Victoria, BC; [2]University of Victoria, Victoria, BC*

ThP 361 **From Global FDR to Local Probabilities: Context-Aware Confidence Estimation for Targeted Proteomics**; Ariana E Shannon[1]; Yuqi Zheng[2]; Alex W Joyce[3]; Lilian Heil[4]; Cristina C. Jacob[4]; Philip M. Remes[4]; Lukas Käll[5]; Brian C. Searle[1]; *[1]Mayo Clinic, Rochester, MN; [2]SciLifeLab, Department of Protein Science, KTH, Solna, Sweden; [3]The Toledo Clinic, Toledo, OH; [4]ThermoFisher Scientific, San Jose, CA; [5]KTH Royal Institute of Technology, Stockholm, Sweden*

ThP 362 **Interpolating chromatographic peak shape with log-quadratic fits**; Brian C. Searle; *Mayo Clinic, Rochester, MN*

ThP 363 **Probing the uncertainty and variance of peptide fragment ion intensities**; Damien B Wilburn; *Ohio State University, Columbus, OH*

ThP 364 **Exploring the proteomics capabilities of a new Trapped Ion Mobility Q-TOF designed for enhanced metabolomics performances**; Benoit Fatou[1]; Héléna Alamil[1]; Manuel Chapelle[1]; Verena Tellestroem[2]; Sabine Jourdain[1]; Jocelyn Dupuy[1]; Silke Neustifter[2]; Schmit Pierre-Olivier[3]; *[1]Bruker France SAS, Wissembourg, France; [2]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [3]Bruker Daltonique S.A., Wissembourg, France*

ThP 365 **Optimizing Ion Transfer Across Pressure Stages in a Dual-Field Converging Multipole (Cyclone) Ion Guide**; Tim Woods[1]; Haopeng Wang[1]; Laura Pollum[1]; Patrick M Batoon[1]; *[1]Agilent Technologies, Santa Clara, CA*

ThP 366 **Characterization of a Low-Cost, Open-Source Mass Spectrometer to Biogenic Volatile Organic Compounds**; Shondiin Lawson[1]; Abigail LePinske[1]; Kevin A. Wokosin[2]; Timothy H. Bertram[2]; Steven J Kregel[1]; *[1]Bradley University, Peoria, IL; [2]University of Wisconsin-Madison, Madison, WI*

ThP 367 **Evaluation of System Robustness and Long-Term Stability of the Thermo ScientificTM StellarTM Mass Spectrometer**; Jason D. White[1]; Cristina C. Jacob[1]; Philip M. Remes[1]; Michael V. Ugarov[1]; *[1]Thermo Fisher Scientific, San Jose, CA*

ThP 368 **Quantifying contamination in mass spectrometers using SEM-EDX**; Nigel Gore[1]; Julia Zaks[2]; Xuan Tung Duong[2]; Maozi Liu[1]; Cole Mauws[2]; Allan K. Bertram[2]; *[1]Agilent Technologies, Santa Clara, CA; [2]University of British Columbia, Vancouver, BC*

ThP 369 **Automated Optimization Methods for an Electron-Capture Dissociation Device**; Gareth Rhys Jones[1]; Jeff Brown[1]; Keith Richardson[1]; *[1]Waters Wilmslow UK, Wilmslow, United Kingdom*

ThP 370 **Effects of improved frequency resolution in SWIFT for ion trap isolation on a modified OrbitrapTM TribridTM mass spectrometer**; Lucas Szalwinski[1]; Philip M. Remes[1]; Christopher Mullen[1]; Graeme C McAlister[1]; *[1]ThermoFisher Scientific, San Jose, CA*

ThP 371 **Adding MS/MS Capability to a Single Quadrupole Mass Spectrometer**; Martin Green[1]; Douce David[1]; Witold Niklewski[1]; Ashley Sage[1]; Thomas Moore[1]; *[1]Waters Corporation, Wilmslow, United Kingdom*

ThP 372 **Improved Electron Transfer Dissociation acquisition rates, sensitivity, and product ion yield on a modified Tribrid mass spectrometer enables new workflows**; Christopher Mullen; *Thermo Fisher Scientific, San Jose, CA*

ThP 373 **Ion Funnels, Ion Carpets and Immersion Lenses: A Study of Ion Transfer Through Various Pressure Regimes**; Randall E Pedder[1]; Luke J. Metzler[1]; *[1]Ardara Technologies L.P., Ardara, PA*

ThP 374 **Enhancing Low-Mass Ion Transmission in a Vortex Collision Cell via RF Voltage Optimization**; Dallas Freitas[1]; Haopeng Wang[1]; Laura Pollum[1]; Patrick Batoon[1]; *[1]Agilent Technologies, Santa Clara, CA*

ThP 375 **A compact wireless camera module for visualizing objects within a space limited vacuum environment**; Kisurb Choe[1]; John Sentmanat[1]; Andrei Fedorov[1]; *[1]Georgia Institute of Technology, Atlanta, GA*

ThP 376 **Investigation of the charge distribution of electrospray-generated species and its impact on ambient ion soft landing for nanomaterial surface modifications**; Adam Neuman[1, 2]; Shao-Yu Liang[3]; Marcela Dendisová[1]; Alžběta Nemeškalová[1, 2]; Wen-Ping Peng[3]; Michael Volný[1, 2]; *[1]University of Chemistry and Technology, Prague, Czech Republic; [2]Institute of Microbiology CAS, Prague, Czech Republic; [3]National Dong Hwa University, Shoufeng, Taiwan*

ThP 377 **Simulation of a Jet-damping Lens Combined with a Radio-Frequency Ion Guide at High Pressure**; Mingrui Zhou[1]; Saifei Chen[1]; Xiaoqiang Zhang[1]; Kang Guo[1]; Wenjian Sun[1]; *[1]Shimadzu Research Laboratory (Shanghai) Co. Ltd, Shanghai, China*

ThP 378 **Enhancing Efficiency in Quality Control through Automated High Throughput Systems**; Juliane Kramer[1]; Mareike Myrach[1]; Mareike Prüfer[1]; Susanne Huhmann[1]; Karin Abraham[1]; Carsten Losch[1]; *[1]KNAUER Wissenschaftliche Geräte GmbH, Berlin, Germany*

ThP 379 **13C-Isotope Tracing Structural Lipidomics for Resolving Phospholipid Metabolism Dynamics in Human Breast Cancer Cells**; Zhuoning Xie; *Tsinghua University, Beijing, China*

ThP 380 **Mapping Inter-organ Metabolic Flux via Integrated Arteriovenous Metabolomics and Isotope Tracing**; Hosung Bae[1]; Cholsoon Jang[1]; *[1]University of California Irvine, Irvine CA, CA*

ThP 381 **Novel LC-Orbitrap Method for Quantifying De Novo Lipogenesis: Applications in Circadian Rhythms and Nutritional States in SD Rats**; Peng Li[1]; Yuan Ye[1]; Huan Li[1]; Weiqun Cao[2]; Yi Tao[2];

Liang Shen[2]; *[1]WuXi AppTec (Nanjing) Co., Ltd., Nanjing, China; [2]DMPK Department, WuXi AppTec, Shanghai, China*

ThP 382 **A 13C Labeling Strategy to Distinguish Endogenous and Exogenous Fatty Acids in Staphylococcus aureus Membrane Lipids**; Taeeun Park[1]; Kelly M Hines[1]; *[1]University of Georgia, Athens, GA*

ThP 383 **Automated detection of isotopic incorporation from in vivo stable isotope-labeled time-course experiments reveals changes in transsulfuration with age.**; Phillip Seitzer[1]; Amanda L Gunawan[1]; Bryan King[1]; Bryson D. Bennett[1]; *[1]Calico Life Sciences LLC, South San Francisco, CA*

ThP 384 **Characterizing nutrient-specific drivers of acetylation through a global 13C acetylome tracing approach**; Caroline Hanson; *Dana Farber Cancer Institute, Boston, MA*

ThP 385 **Novel Electroosmotic Flow-Based Probe Enables Online LC-MS Measurement of Leu-Enkephalin Hydrolysis Rate in Rat Hippocampus In Vivo**; Tingyuan Xu[1]; Stephen Weber[1]; *[1]Department of Chemistry, University of Pittsburgh, Pittsburgh, PA, United States, Pittsburgh, PA*

ThP 386 **Rapid Differentiation of Isomeric Bis(monoacylglycerol)phosphates and Phosphatidylglycerols via a Gas-phase Ion/Ion Reaction and Ion Trap Collision-Induced Dissociation**; Rebekah G. Bogle[1]; Sarah T. Nsiah[1]; Caitlin E. Randolph[1]; Scott A. McLuckey[1]; *[1]Purdue University Dept of Chemistry, West Lafayette, IN*

ThP 387 **Comprehensive Structural Elucidation of Branched-Chain Fatty Acids Using TEMPO-MP–Based Radical-Directed Dissociation**; Wen Li[1]; Qiaohong Lin[1]; Wenpeng Zhang[1]; Zheng Ouyang[1]; *[1]State Key Laboratory of Precision Measurement Technology and Instruments, Department of Precision Instrument, Tsinghua University, Beijing, China*

ThP 388 **Deep profiling of corynomycolic acids in C.Glutamicum via chemical derivatization and tandem mass spectrometry**; Jitong Wang[1]; Ying Yang[2]; Zhidan Zhang[2]; Yu Xia[1]; *[1]Tsinghua University, Beijing, China; [2]Tianjin Institute of Industrial Biotechnology, Tianjin, China*

ThP 389 **Multi-LC-MS Platform Plasma Lipidomic Profiling of BRCA1/2 Mutation Carriers and Breast Cancer Risk: A Retrospective Komen Tissue Bank Study**; Elisabeth M. Schwiebert[1]; Katherine J. Kenney[1]; Rana German[2]; Samuel G. Moore[3]; Rahul Deshpande[4]; Bashar Amer[4]; David A. Gaul[1, 3]; Susan S. Bird[4]; Jaeyeon Kim[5]; Facundo M. Fernández[1, 3]; *[1]School of Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA; [2]The Komen Tissue Bank, Indiana University School of Medicine, Indiana University, Melvina and Bren Simon Comprehensive Cancer Center, Indianapolis, IN; [3]Petit Institute of Bioengineering and Bioscience, Georgia Institute of Technology, Atlanta, GA; [4]Thermo Fisher Scientific, San Jose, CA; [5]Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indiana University, Melvin and Bren Simon Comprehensive Cancer Center, Indianapolis, IN*

ThP 390 **Native MS-guided lipidomics reveals endogenous lipid-dependent assembly of fibroblast growth factor receptors**; Xue Sun; *University of Oxford, Oxford, United Kingdom*

ThP 391 **Determination of Carbon-Carbon Double Bond Position in Unsaturated Lipids via In-line Ozonolysis LC-MS with a UV Lamp Ozone Source**; Sophia M. Alonzi[1, 2]; Andrew T. Quaile[1]; J. Rafael Montenegro-Burke[1, 2]; *[1]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON; [2]Department of Chemistry, University of Toronto, Toronto, ON*

ThP 392 **Comparison of Relative Quantification Strategies for LC–MS–Based Lipidomics**; Yasmine Rais[1]; Shuang Zhao[2]; Liang Li[2]; *[1]The Metabolomics Innovation Centre, Edmonton, AB; [2]The Metabolomics Innovation Centre, University of Alberta, Edmonton, AB*

ThP 393 **Comprehensive Structural Elucidation of Unsaturated Phospholipids via MS³ of Cu(II)-Adducted, Oxidized Derivatives**; Dong Zhang[1]; Tak-Wah Dominic Chan[1]; *[1]The Chinese Univ. of Hong Kong, Hong Kong Sar, China*

ThP 394 **Structural Lipidomics System Enables High-Coverage Isomer-Resolved Analysis for Biomedical and Nutritional Research**; Junhan Wu[1]; Yikun Liu[1]; Qiaohong Lin[2]; Zhourui Zhang[1]; Jiexun Bu[3]; Wenpeng Zhang[2]; Zheng Ouyang[2]; *[1]PURSPEC Technology(China) Ltd., Suzhou, China; [2]Tsinghua University, Beijing, China; [3]PURSPEC Technology (Beijing) Ltd., Beijing, China*

ThP 395 **PartialDB database: community-driven resource to support annotation of novel and partially characterized lipids**; Zhixu Ni[1]; Chetin Baloglu[2]; Lauren Cockayne[3]; Miguel Gijón[4]; Simon Andrews[2]; Xueli Guan[5]; Yu Xia[6]; Rosario Domingues[7]; Ondrej Kuda[8]; Valerie O'Donnell[3]; Maria Fedorova[9]; Laura Goracci[10]; *[1]Tsinghua Shenzhen International Graduate School, Shenzhen, China; [2]Babraham Institute, Cambridge, United Kingdom; [3]School of Medicine, Cardiff University, Cardiff, United Kingdom; [4]Cayman Chemical Company, Ann Arbor, MI; [5]Novo Nordisk Foundation Centre for Basic Metabolic Research, University of Copenhagen, Copenhagen, Denmark; [6]Tsinghua University, Beijing, China; [7]University of Aveiro, Aveiro, Portugal; [8]Institute of Physiology, Academy of Sciences of the Czech Republic, Prague, Czech Republic; [9]University Hospital and Faculty of Medicine Carl Gustav Carus of TU Dresden, Dresden, Germany; [10]University of Perugia, Perugia, Italy*

ThP 396 **Enterococcus faecalis strains respond differently to fatty acid isomers based on their susceptibility to daptomycin**; Rebekah L Phelan[1]; Kelly M Hines[1]; Annika L. Silverberg[2]; Michael T Marty[2]; *[1]University of Georgia, Athens, GA; [2]University of Texas - Austin, Austin, TX*

ThP 397 **Database construction for lipid annotation from phytoplankton Calcidiscus leptoporus extracts using a hybrid Orbitrap–21 T FT-ICR mass spectrometer**; Robert Horn[1]; Martha L Aguilera[2]; Leonarda Lazarin[1]; Jelena Godrijan[1]; Blaženka Gašparović[1]; *[1]Ruder Boskovic Institute, Zagreb, Croatia; [2]National High Magnetic Field Laboratory, Tallahassee, FL*

ThP 398 **Inferring Molecular Identity via Multi-Adduct MS/MS Fragment Integration in routine LC-MS/MS**; Jae-Seung Lee[1]; Kyeong-Seog Kim[2]; Jun Hwa Shim[3]; Joo-Youn Cho[1, 3]; *[1]Seoul National University College of Medicine, Seoul, South Korea; [2]University of Liverpool, Liverpool, United Kingdom; [3]Seoul National University College of Medicine and Hospital, Seoul, South Korea*

ThP 399 **High-resolution MS/MS characterization of endogenous steroid fragmentation profiles for structural elucidation**; Nathan Ghafari[1]; Lekha Sleno[1]; *[1]University of Quebec in Montreal, Montreal, QC*

ThP 400 **Development of a Real-time Library Search (RTLS) Method for Improved UVPD Characterization of Unsaturated Aminolipids and Phospholipids in ESKAPE Pathogens**; Melanie J Campbell[1]; Roberto Jhonatan Olea-Ozuna[2]; Joseph M. Boll[2]; Jennifer S. Brodbelt[1]; *[1]University of Texas at Austin, Austin, TX; [2]University of Texas at Dallas, Richardson, TX*

ThP 401 **Investigating Endogenous Odd-Chain Fatty Acid Metabolism under Defined Conditions in a Human Cell Line**; Verne T. Urquhart-Cox[1]; Andrew T. Quaile[1]; J. Rafael Montenegro-Burke[1]; *[1]Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, ON*

ThP 402 **Trapped Ion Mobility Spectrometry Enables Electron-Activated FT-ICR Tandem Mass Spectrometry of Lipid Isobars in Complex Matrices**; Jameson Norton[1, 2]; Steven A DeFiglia[1, 2]; Christopher A. Wootton[3]; Martha L Aguilera[1]; Blaženka Gašparović[4]; Robert Horn[4]; Kristina Hakansson[1, 2]; *[1]National High Magnetic Field Laboratory, Tallahassee, FL; [2]Florida State University, Tallahassee, FL; [3]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [4]Ruder Boskovic Institute, Zagreb, Croatia*

ThP 403 **Pushing the Limits of Structural Lipidomics: Enhanced Sensitivity and MS^3-Driven Annotation on a Modified Orbitrap Tribrid Mass Spectrometer**; Rahul Ravi Deshpande[1]; Bashar Amer[1]; Brandon Bills[1]; Sunandini Yedla[1]; Rafael D Melani[1]; Susan S. Bird[1]; Thomas Moehring[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

ThP 404 **Characterizing phosphoethanolamine glucosylceramides in complex biological samples by two-dimensional chromatography and high-resolution tandem mass spectrometry**; Julia Hillebrand[1]; Anna Gremme[2]; Julia Bornhorst[2]; Heiko Hayen[1]; *[1]University of Münster, Institute of Inorganic and Analytical Chemistry, Münster, Germany; [2]University of Wuppertal, Food Chemistry with focus on Toxicology, Wuppertal, Germany*

ThP 405 **Enhanced Characterization of Bacterial Cell Membrane Lipids Using RPLC-MS/MS**; Andrew Stai[1, 2]; Broquell Wong[3]; Attelia Hollander[2]; Frank Löffler[4, 5, 6]; Brian Davison[2]; Robert L. Hettich[2]; *[1]University of Tennessee, Knoxville, TN; [2]Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN; [3]Department of Biochemistry and Cellular and Molecular Biology, University of Tennessee, Knoxville, TN; [4]Department of Civil and Environmental Engineering, University of Tennessee, Knoxville, TN; [5]Department of Microbiology, University of Tennessee, Knoxville, TN; [6]Department of Biosystems Engineering and Soil Science, University of Tennessee, Knoxville, TN*

ThP 406 **Enabling Broad Metabolite and Lipid Annotation for Imaging Mass Spectrometry Using Optimized timsMetabo Workflows**; Madeline E. Colley[1, 2]; Lauren N. Emmerson[1, 3]; Timothy M.D. Hendrigsman[1, 4]; Megan S Ward[1, 5]; Jeffrey M Spraggins[1, 2, 3, 4, 6, 7]; *[1]Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN; [2]Department of Cell and Developmental Biology, Vanderbilt University, Nashville, TN; [3]Chemical and Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [4]Department of Chemistry, Vanderbilt University, Nashville, TN; [5]Chemical Physical Biology Program, Vanderbilt University School of Medicine, Nashville, TN; [6]Department of Biochemistry, Vanderbilt University, Nashville, TN; [7]Department of Pathology, Microbiology and Immunology, Vanderbilt University Medical Center, Nashville, TN*

ThP 407 **Advancing lipid detection and structural characterization using high resolution ion mobility spectrometry and gas phase ozonolysis**; Dylan H Ross[1]; Josie G. Eder[1]; Christopher Harrilal[1]; Yehia M. Ibrahim[1]; Xueyun Zheng[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

ThP 408 **Online Ion-Funnel Ozonolysis Coupled with LC-Orbitrap MS for Lipid Double-Bond Isomer Profiling**; Shanika Malshani Weerasinghe[1]; Vy T. Tat[1]; Young Jin Lee[1]; *[1]Iowa State University, Ames, IA*

ThP 409 **High-coverage and structurally resolved lipidome analysis via LC-EAD-MS/MS**; Shuling Xu[1]; Tina C Dang[1]; Cameron John Kaminsky[1]; Yuzhuo Zhang[2]; Paul R Baker[2]; Lingjun Li[1]; *[1]University of Wisconsin-Madison, Madison, WI; [2]SCIEX, Redwood City, CA*

ThP 410 **Comprehensive isomer-resolved ganglioside profiling by HILIC-nanoESI-MS/MS**; Robert Ahrends[1]; Nina Nicole Troppmair[1]; Cristina Coman[1]; *[1]University of Vienna, Vienna, Austria*

ThP 411 **Investigating the Infant Nasal Metabolome and Exposome by LC-HRMS**; Sabrina Berger[1, 2]; Jesse T. Peach[1]; Anke Martens[3]; Lukas Wisgrill[3, 4]; Benedikt Warth[1, 2, 4]; *[1]University of Vienna, Department of Food Chemistry and Toxicology, Vienna, Austria; [2]University of Vienna, Vienna Doctoral School in Chemistry (DoSChem), Vienna, Austria; [3]Medical University of Vienna, Division of Neonatology, Pediatric Intensive Care and Neuropediatrics, Comprehensive Center for Pediatrics, Vienna, Austria; [4]Exposome Austria, Research Infrastructure and National EIRENE Node, Vienna, Austria*

ThP 412 **Social Isolation Drives Metabolomic Changes That Impair Pelvic Floor Muscle Recovery After Birth Injury**; Jasmine Jungok Zemlin[1, 2]; Parnaz Boroon[3]; Monique Smith[3]; Pieter C. Dorrestein[1]; Lindsey A. Burnett[2]; *[1]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [2]Department of Obstetrics Gynecology and Reproductive Sciences, University of California San Diego, La Jolla, CA; [3]Department of Neuroscience, University of California San Diego, La Jolla, CA*

ThP 413 **Data Fidelity testing - A method to measure data quality after normalization of MS data**; Chris Beecher[1]; Debasish Ghosh[2]; Felice De Jong[1]; Vladimir Shulaev[2]; *[1]IROA Technologies, Chapel Hill, NC; [2]University of North Texas, Denton, TX*

ThP 414 **Benchmarking enhanced dynamic range scan mode and intelligent MS/MS strategies to expand metabolomics coverage in conventional and low-volume clinical samples**; Ales Kvasnicka[1]; Barbora Pisklakova[1]; Sander Johannes Thorbjørnsen Guttorm[1]; Michal Kaczmarek[2]; Helge Rootwelt[1]; Hanne Bendiksen Skogvold[1]; Elise Sandås Sand[1]; Susan S. Bird[3]; Katja Benedikte Prestø Elgstøen[1]; *[1]Section for Metabolomics and Lipidomics, Oslo University Hospital, Oslo, Norway; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]ThermoFisher Scientific, San Jose, CA*

THURSDAY MORNING ORALS

ThP 415 **A Validated Comprehensive Uremic Solute Assay: From LC-MS/MS MRM Methodology to Pilot Observations in CKD**; Renny Shang-Lun Lan[1, 2, 3]; Lindsay M. Pack[1]; Alexia Lo[1]; Hailemariam Abrha Assress[1, 2]; John M. Arthur[2]; Christian Herzog[2]; Colin Kay[1, 2, 3]; Tiffany Miles[1, 2, 3]; Joseph L. Alge[2, 3]; *[1]Arkansas Children's Nutrition Center, Little Rock, AR; [2]University of Arkansas for Medical Sciences, Little Rock, AR; [3]Arkansas Children's Research Institute, Little Rock, AR*

ThP 416 **Metabolomic Profiling of Prednisone Response in Severe Alcoholic Hepatitis**; Regina L Gasparetto[1, 2, 3, 4]; Vatsalya Vatsalya[3, 5, 6]; Xipeng MA[1, 2, 3, 4]; Jing Feng[1, 2, 3, 4]; Khairul Islam Khan[1, 2, 3, 4]; Jane Frimodig[3, 4]; Xinmin Yin[1, 2, 3, 4]; Liqing He[1, 2, 3, 4]; Eugene Mueller[1]; Seongho Kim[7, 8]; Craig McClain[3, 4, 5, 6, 9]; Xiang Zhang[1, 2, 3, 4, 9]; *[1]Department of Chemistry, University of Louisville, Louisville, KY; [2]Center for Regulatory and Environmental Analytical Metabolomics, Louisville, KY; [3]University of Louisville Alcohol Research Center, Louisville, KY; [4]University of Louisville Hepatobiology & Toxicology Center of Biomedical Research Excellence, Louisville, KY; [5]Department of Medicine, University of Louisville, Louisville, KY; [6]Robley Rex Louisville VAMC, Louisville, KY, Louisville, KY; [7]Karmanos Cancer Institute, School of Medicine, Wayne State University, Detroit, MI; [8]Department of Oncology, School of Medicine, Wayne State University, Detroit, MI; [9]Department of Pharmacology and Toxicology, University of Louisville, Louisville, KY*

ThP 417 **Uncovering Metabolites Associated with Skin Microbiota Alterations in Hidradenitis Suppurativa**; Un Cheng Loi[1]; Yu-Hsuan Chen[1]; Laura Min Xuan Chai[1]; Jia-Fang Tsai[2]; Yi-Hua Liao[2]; Cheng-Chih Hsu[1, 3]; *[1]Department of Chemistry, National Taiwan University, Taipei, Taiwan; [2]Department of Dermatology, National Taiwan University, Taipei, Taiwan; [3]Leeuwenhoek Laboratories Co. Ltd., Taipei, Taiwan*

ThP 418 **Evaluation of Metabolites from Bandage Samples Using LC–MS/MS**; Ariel Pernela[1]; Adrianna Tompros[2]; Carolyn Ibberson[2]; Laura-Isobel McCall[1]; *[1]San Diego State University, San Diego, CA; [2]University of Tennessee, Knoxville, Knoxville, TN*

ThP 419 **Orbitrap Tribrid Real-Time similarity searching of mzCloud library for guided unknown characterization of roasted tea metabolites and lipids**; Brandon Bills[1]; Sunandini Yedla[1]; Rahul Deshpande[1]; Bashar Amer[1]; Susan S. Bird[1]; Rafael Melani[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientfic, San Jose, CA*

ThP 420 **Revealing Hidden Medication Exposures in Human Milk**; Haoqi Nina Zhao[1, 2]; Sydney P. Thomas[1]; Kerri Bertrand[1]; Christina Chambers[1]; Shirley M. Tsunoda[1]; Pieter C. Dorrestein[1]; *[1]University of California San Diego, San Diego, CA; [2]Stanford University, Stanford, CA*

ThP 421 **Discovery of prenylated small molecules through reverse metabolomics**; Thomas N Trybala[1]; Joshua Baccile[1]; *[1]University of Tennessee, Knoxville, Knoxville, TN*

ThP 422 **Structure-Activity Relationship Mass SpectrometryAccelerates the Discovery of Novel Gut Microbiota-Derived Immune-Regulating Metabolites**; Haoduo Zhao[1]; Zhenfa Zhang[1]; Yun-Chung Hsiao[1]; Chih-Wei Liu[1]; Ryan Balfour Sartor[1]; Kun Lu[1]; *[1]UNC chapel hill, chapel hill, NC*

ThP 423 **Chemotaxonomic evaluation of Populus reveals a rare, species-specific metabolite**; Lindsay P Brown[1]; Joshua A. Baccile[2]; Nancy L. Engle[1]; Brian J. Stanton[3]; Rick Stonex[3]; Kathy Haiby[3]; Timothy J. Tschaplinski[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN; [2]University of Tennessee, Knoxville, Knoxville, TN; [3]Poplar Innovations, Inc., Castle Rock, WA*

ThP 424 **From Dark Feature to Pathway Inspiration: Microdroplet Chemistry in Electrospray Ionization Mass Spectrometry Analysis of Metabolites**; Xiaowei Song[1, 2]; Jinheng Xu[2]; Chenglong Sun[3]; Joshua Lyu[2]; Hongqian Kui[4]; Ruiping Zhang[4]; Zeper Abliz[4]; Richard N Zare[2]; *[1]Tsinghua Shenzhen International Graduate School, Shenzhen, China; [2]Stanford University, Stanford, CA; [3]Qilu University of Technology, Jinan, China; [4]State Key Laboratory of Bioactive Substance and Function of Natural Medicines, Institute of Materia Medica, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China*

ThP 425 **Anchored Retention-Time Prediction to Improve Annotation in Untargeted LC-HRMS Metabolomics and Lipidomics**; Paolo Bonini[1]; Sajjan Mehta[1]; Aina Lara Salto[1]; Oliver Fiehn[2]; *[1]Olobion, Barcelona, Spain; [2]West Coast Metabolomics Center, University of California Davis, Davis, CA*

ThP 426 **Pan-Metabolomics Repository Mapping of the Carnitine Landscape**; Helena Mannochio Russo[1]; Patrick C. Ferreira[2, 3]; Kine Eide Kvitne[2]; Abubaker Patan[2]; Victoria Deleray[2]; Harsha Gouda[2]; Wilhan D. Gonçalves Nunes[2]; Shipei Xing[2]; Jasmine Zemlin[2]; Martijn Van Faassen[4]; Erin Reilly[5]; Imhoi Koo[6]; Andrew D Patterson[6, 7, 8]; Shirley M. Tsunoda[2]; Lindsey A. Burnett[2]; Pieter C. Dorrestein[2, 9, 10, 11]; *[1]University of California San Diego, San Diego, CA; [2]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [3]Institute of Chemistry, University of Campinas, Campinas, Brazil; [4]Department of Laboratory Medicine, University of Groningen, University Medical Center Groningen, Groningen, Netherlands; [5]Department of Biochemistry and Molecular Biology, The Pennsylvania State University, University Park, PA; [6]Department of Veterinary and Biomedical Sciences, The Pennsylvania State University, University Park, PA; [7]Center for Molecular Toxicology and Carcinogenesis, Department of Veterinary and Biomedical Sciences, Pennsylvania State University, University Park, PA; [8]One Health Microbiome Center, Huck Life Sciences Institute, The Pennsylvania State University, University Park, PA; [9]Center for Microbiome Innovation, University of California San Diego, La Jolla, CA, 92093, USA, San Diego, CA; [10]Collaborative Mass Spectrometry Innovation Center, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, San Diego, CA; [11]Department of Pharmacology, University of California San Diego, La Jolla, CA*

ThP 428 **The Shin-MassBank project : Efforts to further enhance MassBank using raw metabolome data**; Ryosuke Hayasaka[1]; Yushi Takahashi[2]; Taihei Torigoe[3]; Takaki Oka[4]; Motohiro Ogawa[4]; Yuki Matsuzawa[4]; Takato Kikuchi[2]; Masatomo Takahashi[3]; Akiyasu C Yoshizawa[2]; Yoshihiro Izumi[3]; Hiroshi Tsugawa[4]; Akiyoshi Hirayama[1]; Shujiro Okuda[2]; Fumio Matsuda[5]; *[1]Keio University, Tsuruoka, Japan; [2]Niigata University, Chuo-ku, Japan; [3]The University of Osaka, Toyonaka, Japan; [4]Tokyo University of Agriculture and Technology, Koganei, Japan; [5]The University of Osaka, Suita, Japan*

ThP 429 **Novel data processing workflow including in-silico derivatization for integrated CI/EI MS data acquired with the GC-ecTOF instrument**; Cory Lytle[1]; Heiko Neuweger[1]; Robin Sven Obrist[2]; Timm Hettich[2]; Ilmari Krebs[1]; Nikolas Kessler[1]; Steffen Braekling[3]; Yousef Maali[4]; Maria Luisa Balmer[4]; Stefan Gaugler[2]; Sonja Klee[3]; *[1]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [2]University of Applied Sciences and Arts Northwestern Switzerland (FHNW), Muttenz, Switzerland; [3]TOFWERK, Thun, Switzerland; [4]Institute for Infectious Diseases, University and University Hospital Bern, Bern, Switzerland*

ThP 430 **Building Robust Library Spectra of Bile Acids By Selective Dissociation for Metabolomics**; Sophia N Boor[1]; Rachel Buckley[1]; Brian Thomas Buckley[1]; *[1]Rutgers University, Piscataway, NJ*

ThP 431 **Advanced Laser Control Enables Parallel UVPD Acquisition to Improve Low-Abundance Metabolite Identification on a Modified Orbitrap™ Tribrid™ Ascend™ Mass Spectrometer**; Xiao Wang[1]; Christopher Mullen[1]; Graeme McAlister[1]; *[1]ThermoFisher Scientific, San Jose, CA*

ThP 432 **Untargeted Metabolite Identification Combining LC-MS, NMR, and Ratio Analysis in Complex Biological Samples**; Nagana G.A. Gowda[1, 2]; Elle Harwood[1, 2]; Wentao Zhu[1, 2]; Vadim Pascua[1, 2]; Daniel Raftery[1, 2, 3, 4]; *[1]Northwest Metabolomics Research Center, Seattle, WA; [2]Mitochondria and Metabolism Center, Anesthesiology and Pain Medicine, Seattle, WA; [3]Department of Chemistry, University of Washington, Seattle, WA; [4]Fred Hutchinson Cancer Center, Seattle, WA*

ThP 433 **Geometry-driven Machine Learning for Accurate Collision Cross Section Predictions in Untargeted Metabolomics Workflows**; Rithika Gorrepati[1]; Olatomiwa Bifarin[2]; Facundo M. Fernández[2]; *[1]Georgia Institute of Technology, Atlanta, GA; [2]School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA*

ThP 434 **Charting the Undiscovered Metabolome with Synthetic Multiplexing**; Abubaker Patan[1]; Shipei Xing[2]; Vincent Charron Lamoureux[2]; Zhewen Hu[2]; Victoria Deleray[2]; Julius Agongo[2]; Yasin El Abiead[2]; Helena Russo Mannochio[2]; Ipsita Mohanty[2]; Harsha Gouda[2]; Jasmine Zemlin[2]; Jeongin Seo[2]; Prajit Rajkumar[2]; Carlynda Lee[2]; Daniel Leanos[2]; Noah Weimann[2]; Wataru Tsuda[2]; Sadie Giddings[2]; Tammy Bui[2]; Kine Eide Kvitne[2]; Haoqi Nina Zhao[2]; Simone Zuffa[2]; Vivian Nguyen[2]; Aileen Andrade[2]; Wilhan Nunes[2]; Andrés M. Caraballo Rodríguez[2]; Lurian Caetano David[3]; Nuno Bandeira[2, 4]; Mingxun Wang[5]; Lindsey A. Burnett[6]; Dionicio Siegel[2]; Pieter C. Dorrestein[2, 7, 8, 9]; *[1]Skaggs School Of Pharmacy And Pharmaceutical Sciences,, san diego, CA; [2]Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA; [3]Laboratório de Métodos de Extração e Separação (LAMES), Instituto* *de Química (IQ), Universidade Federal de Goiás (UFG), Campus II – Samambaia, Goiânia, GO, 74045-155, Brasil, Samambaia, Goiânia, Brazil; [4]Department of Computer Science and Engineering, University of California San Diego, La Jolla, CA; [5]Department of Computer Science, University of California Riverside, Riverside, CA, USA, Riverside, CA; [6]Department of Obstetrics Gynecology and Reproductive Sciences, University of California San Diego, La Jolla, CA; [7]Department of Pharmacology, University of California San Diego, La Jolla, CA, 92093, USA, San Diego, CA; [8]Collaborative Mass Spectrometry Innovation Center, Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, San Diego, CA; [9]Center for Microbiome Innovation, University of California San Diego, La Jolla, CA, 92093, USA, San Diego, CA*

ThP 435 **Maximizing Metabolomic Discovery on timsMetabo: MoRE Mode Combined with Met4DX and MetDNA3 Workflow**; Xianming Liu[1]; Yandong Yin[2]; Xiaoyu Wang[1]; Haosong Zhang[2]; Zhengjiang Zhu[2]; *[1]Bruker, Shanghai, China; [2]Interdisciplinary Research Center on Biology and Chemistry, Shanghai Institute of Organic Chemistry, Chinese Academy of Sciences, Shanghai, China*

ThP 436 **From spectra to certainty: end-to-end workflows for confident metabolite identification**; Michał Kaczmarek[1]; Bashar Amer[2]; Rahul Deshpande[3]; Susan S. Bird[3]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientfic, San Jose, CA; [3]Thermo Fisher Scientific, San Jose, CA*

ThP 437 **Small molecule prenylome mapping via reverse metabolomics**; Joshua Baccile[1]; Thomas N Trybala[2]; *[1]The University of Tennessee, Knoxville, TN; [2]University of Tennessee, Knoxville, TN*

ThP 438 **Automated Two-Step Derivatization Workflow for Untargeted Metabolomics of Murine Wound Samples Using GC-ecTOF**; Robin Sven Obrist[1]; Hagen M. Gegner[2]; Tiantian Li[2]; Oliver Frank[2]; Günter Böhm[2]; Sonja Klee[3]; Steffen Bräkling[3]; Timm Hettich[1]; Erik Hunziker[1]; Dominik Meinel[1]; Stefanie Wernisch[4]; Martin Poloczek[4]; Axel Maibaum[4]; Matthew R. Lewis[4]; Maria Luisa Balmer[5]; Stefan Gaugler[1]; *[1]University of Applied Sciences and Arts Northwestern Switzerland (FHNW), Muttenz, Switzerland; [2]CTC Analytics AG, Zwingen, Switzerland; [3]Tofwerk, Thun, Switzerland; [4]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [5]Institute for Infectious Diseases, University and University Hospital Bern, Bern, Switzerland*

ThP 439 **Fecal metabolomics coverage by LC-HRMS/MS using different sample preparation workflows, capturing volatile and non-volatile organic compounds**; Oriana Zambito[1]; Lekha Sleno[1]; *[1]University of Quebec in Montreal, Montreal, QC*

ThP 440 **Extraction protocol for formalin-fixed and paraffin-embedded (FFPE) archival human tissue for untargeted metabolomics**; Jacob J. Haffner[1]; Seidu Adams[2]; Hani Habra[1]; David Irabor[3]; Akinfemi Akingboye[4, 5]; Patrick Huck[6]; Oloruseun O. Ogunwobi[2]; Maryam Goudarzi[1, 2]; *[1]Mass Spectrometry and Metabolomics Core, Michigan State University, East Lansing, MI; [2]Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI; [3]Department of Surgery, University of Ibadan, Ibadan, Nigeria; [4]College of Life Sciences and Aston Medical School, Aston University, Birmingham, United Kingdom; [5]The Dudley Group Foundation NHS Trust, West Midlands, Dudley, United Kingdom; [6]Osteopathic Surgical Specialties, Michigan State University, East Lansing, MI*

ThP 441 **Si-Trap™: A simultaneous, detergent-free multi-omics platform with high throughput and reproducibility**; John Wilson[1]; Tyler Scherzi[1]; *[1]ProtiFi LLC, Fairport, NY*

ThP 442 **Vision-Guided Robotics for High-Throughput, Supervised LC–MS Analyte Quantification**; Jerrica Yang[1]; Liang Li[1, 2]; *[1]University of Alberta, Edmonton, AB; [2]The Metabolomics Innovation Centre, Edmonton, AB*

ThP 443 **Comprehensive Acylcarnitine Profiling by Online-Solid Phase Extraction and LC-MS/MS**; Lucas Ortmann[1]; Hannah Waldmann[1]; Paula Wigger[1]; Torben Meiners[2]; Julia Bornhorst[2]; Heiko Hayen[1]; *[1]University of Münster, Münster, Germany; [2]University of Wuppertal, Wuppertal, Germany*

ThP 444 **Comprehensive Evaluation of Sampling and Preservation Strategies for Multi-Omics Analysis of Human Fecal Samples**; Po-Cheng Kuo[1]; Chen-Syuan Yen[2]; Cheng-Chih Hsu[2]; *[1]National Taiwan University, Taipei, Taiwan; [2]National Taiwan Univeristy, Taipei, Taiwan*

ThP 445 **Development of a MOF-Coated Blade Spray Ion Source for Rapid Screening of Complex Biological and Food Matrices**; Adolfo Fernandez-Gomez De Enterria[1]; Priscilla Rocio-Bautista[2]; Kiran Kamboj[1]; Idaira Pacheco-Fernández[2]; Jorge Pasan[2]; Alberto Paradela[3]; Fernando Corrales[3]; Daniel Lopez Ferrer[1]; Veronica Pino[2]; *[1]Montara BioLabs, Las Rozas de Madrid, Spain; [2]Laboratorio de Materiales para Análisis Químico (MAT4LL), Departamento de Química, Unidad Departamental de Química Analítica, Universidad de La Laguna (ULL), San Cristóbal de La Laguna, Spain; [3]Functional Proteomics Laboratory, Centro Nacional de Biotecnología, CSIC, Madrid, Spain*

ThP 446 **Assessing the low-molecular-weight peptidome for breast cancer diagnostics: Mass spectrometric profiling of a 10 kDa serum fraction**; Pathea S Bruno[1]; Ethan C. Freedley[1]; Shaelee I. Torres[1]; Sarah E. Abbott[1]; Costel C. Darie[1]; *[1]Clarkson University, Potsdam, NY*

ThP 447 **Cocaine Withdrawal-Induced Alterations of Neuropeptide Expression Revealed by Investigation of the Rat Brain Peptidome**; Kendra G Selby[1]; Gaoyuan Lu[2]; Fengfei Ma[2]; Vu Ngoc Huong Tran[2]; Pingli Wei[1]; Min Ma[2]; Brian Baldo[3]; Lingjun Li[1, 2]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Department of Psychiatry and Neuroscience Training Program, University of Wisconsin-Madison, Madison, WI*

ThP 448 **Advancing MHC-Associated Peptide Proteomics Assay for Predicting Immunogenicity of Protein Therapeutics**; Bin Wang[1]; Marilyn Wang[1]; Minchao Chen[1]; Kristina Najjar[1]; Li Li[1]; Christina Shen[1]; *[1]Merck & Co., Inc., Rahway, NJ*

ThP 449 **Mass Spectrometric Profiling and Discovery of Disulfide-Bonded Neuropeptides in the American Lobster Homarus americanus Nervous System**; Margot S Beaver[1]; Vu Ngoc Huong Tran[1]; Sonal Kedia[2]; Thao Duong[3]; Ziyi Sun[3]; Gaoyuan Lu[1]; Eve Marder[2]; Lingjun Li[1, 3]; *[1]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [2]Biology Department and Volen Center, Brandeis University, Waltham, MA; [3]Department of Chemistry, University of Wisconsin-Madison, Madison, WI*

ThP 450 **Comprehensive Neuropeptidome Profiling of the Jellyfish Clytia hemisphaerica via High-Resolution Mass Spectrometry**; GAOYUAN LU[1]; Brian P Grone[2]; Vu Ngoc Huong Tran[1]; Shuling Xu[1]; Brandon Weissbourd[2]; Lingjun Li[1]; *[1]University of Wisconsin-Madison, Madison, WI; [2]Massachusetts Institute of Technology, Cambridge, MA*

ThP 451 **Comparative Neuropeptidomic Profiling of Jonah Crab Hemolymph by Direct Withdrawal and In VivoMicrodialysis**; Ziyi Sun[1]; Vu Ngoc Huong Tran[2]; Gaoyuan Lu[2]; Michael Nusbaum[3]; Lingjun Li[1, 2]; *[1]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [2]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [3]Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA*

ThP 452 **TuttiPepti: A web platform for fast and robust assessment of antigen tumor specificity using GTEx RNA-seq data**; Yujin Choo[1]; Shanji Zhang[1]; Seunghyuk Choi[2]; Eunok Paek[1]; *[1]Hanyang University, Seoul, South Korea; [2]kookmin university, Seoul, South Korea*

ThP 453 **Optimization of Evosep Tip Loading Protocols to Enhance Hydrophilic Peptide Retention in MHC-Associated Peptide Proteomics (MAPPs)**; Jason LaMar[1]; Arun Tailor[1]; M. Violet Lee[2]; Alisa Arata[1]; Ola M Saad[1]; *[1]Genentech, Inc., South San Francisco, CA; [2]Genentech Inc, South San Francisco, CA*

ThP 454 **AI-Driven immunopeptidome analysis and neoantigen discovery of the ASFV**; Chao Peng[1]; Ping Wu[2]; Haofei Miao[1]; *[1]BaizhenBio Inc., Shanghai, China; [2]BaizhenBio Inc., Wuhan, China*

ThP 455 **Ultra-Sensitive-Data-Independent Acquisition Enables Robust MHC peptide quantification in Low-Input Samples**; Hem R Gurung[1]; Justin Gibson[1]; Jill Schartner[1]; Susan Klaeger[1]; *[1]Genentech Inc., South San Francisco, CA*

ThP 456 **Proteoform Characterization of Biologics and Microproteins: Novel Technologies Enable Sensitive, Robust nanoLC-MS Middle- and Top-down Proteomics**; Helena Svobodova[1]; Amanda Berg[2]; Gary Valaskovic[2]; Nicholas Cheung[3]; Xun Bao[3]; Kyle Brown[3]; Robert Salzler[3]; *[1]New Objective, Inc., Littleton, MA; [2]New Objective inc, LITTLETON, MA; [3]Regeneron Pharmaceuticals Inc, Tarrytown, NY*

ThP 457 **Translating Peptide Evidence into Immunotherapy Targets: Modified Tribrid MS Delivers High-Confidence Spectral Annotation**; Fernanda Salvato[1]; Patience Sanderson[2]; Christopher Mullen[1]; Joshua Hinkle[1]; Graeme McAlister[3]; Anastasia K Klenke[4]; Katie S. Peterson[2]; Rafael Melani[1]; Tonya Pekar Hart[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, West Palm Beach, FL; [3]Thermo Fisher Scientfic, San Jose, CA; [4]Thermo Fisher Scientific, Rockford, IL*

ThP 458 **PROTEOMIC ANALYSIS OF IMMUNO-MODULATORY PROTEINS IN PRO-BIOTIC TREATED XENOPUS LAEVIS TISSUE EXTRACTS USING TANDEM MASS SPECTROMETRY**; Joan Rozario[1]; Barney Bishop[1]; Paul Russo[1]; Carly Muletz Wolz[2]; Leon Grayfer[3]; *[1]George Mason University, Manassas, VA; [2]NIST, Gaithersburg, MD; [3]George Washington University, Washington DC, DC*

ThP 459 **Real-time artificial intelligence prediction of peptide characteristics and MSFragger search improves multiplexed quantification of shared, non-canonical HLA-I peptides**; Kristin Leskoske[1]; Ana Marcu[1]; Fengchao Yu[2]; Alexey I Nesvizhskii[2]; Susan Klaeger[1]; Christopher M Rose[1]; *[1]Genentech, South San Francisco, CA; [2]University of Michigan, Ann Arbor, MI*

ThP 460 **Large-scale clinical peptidomics of 2,200 plasma samples reveals stroke-associated and treatment-induced proteolytic signatures**; Andreas Zellner[1]; Steffen Tiedt[2]; Christina Ludwig[3]; Bernhard Kuster[4]; Chien-Yun Lee[1]; *[1]School of Life Sciences, Technical University of Munich, Freising, Germany; [2]Institute for Stroke and Dementia Research (ISD), LMU University Hospital, LMU Munich, Munich, Germany; [3]Bavarian Center for Biomolecular Mass Spectrometry (BayBioMS), Technical University of Munich, Freising, Germany; [4]Chair of Proteomics and Bioanalytics, Technical University of Munich, Freising, Germany*

ThP 461 **Sensitive Antigen Discovery Using Library-Free DIA with Integrated In-Source Fragmentation Detection**; Monika Pepelnjak[1]; Oliver M. Bernhardt[1]; Grzegorz Skoraczyński[1]; Monika Puchalska[1]; Arthur Viodé[1]; Roland Bruderer[1]; Anamarija Pfeiffer[1]; Tejas Gandhi[1]; *[1]Biognosys AG, Schlieren, Switzerland*

ThP 462 **Comprehensive and Automatable MHC Class I and II Immunopeptide Enrichment with LC-MS Analysis**; Anastasia K Klenke[1]; Joanna Geddes[1]; Fernanda Salvato[1]; Ellen Casavant[2]; Tonya Pekar Hart[2]; Pierre Thibault[3]; Joel Lanoix[3]; Katherinne Sofia Herrera Jordan[3]; Bhavin Patel[1]; *[1]Thermo Fisher Scientific, Rockford, IL; [2]Thermo Fisher Scientific, San Jose, CA; [3]University of Montreal, Montreal, QC*

ThP 463 **Identification and Quantification of Immunopeptides from Low-Input Samples**; Ritu Raj[1]; Jenny Ho[2]; H Irem Baymaz[1]; Tiaan Heunis[1]; Andrew W Jones[1]; Yoanna Ariosa-Morejon[1]; Helena Ring[1]; Sergio Regufe Da Mota[1]; Ricardo J Carreira[1]; *[1]Immunocore Ltd., Abingdon, United Kingdom; [2]Thermo Fisher Scientific, Hemel Hempstead, United Kingdom*

ThP 464 **Uncovering weathered polyethylene microplastic induced changes in the neuropeptidome of Cancer borealis**; Paul Corsetti[1]; Hridyesh Tewani[2]; Tina C Dang[3]; Angel E. Ibarra[4]; Thao U Duong[4]; Lauren Fields[4]; Pavana Prabhakar[2]; Lingjun Li[1, 3, 5]; *[1]Molecular and Environmental Toxicology, University of Wisconsin-Madison, Madison, WI; [2]Department of Civil & Environmental Engineering, University of Wisconsin-Madison, Madison, WI; [3]School of Pharmacy, University of Wisconsin-Madison, Madison, WI; [4]Department of Chemistry, University of Wisconsin−Madison, Madison, WI; [5]Department of Chemistry, University of Wisconsin-Madison, Madison, WI*

ThP 465 **Next-generation immunopeptidomics: comprehensive identification with optimized DIA and quantitative impact with hybrid DIA**; Fernanda Salvato[1]; Patience Sanderson[2]; Anastasia K Klenke[3]; Bhavin Patel[3]; Katie S. Peterson[2]; Tonya Pekar Hart[4]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, West Palm Beach, FL; [3]Thermo Fisher Scientific, Rockford, IL; [4]ThermoFisher Scientific, San Jose, CA*

ThP 466 **Deep MHC II Immunopeptidomics: Optimized Enrichment and DDA-PASEF Enable High-Confidence Detection from Minimal Input**; Dorothy Ahlf Wheatcraft[1]; Xiaoxu Wang[1]; Kristina Archer[1]; Matthew S. Glover[1]; Rajat Varma[1]; Sonja Hess[1]; *[1]AstraZeneca, Gaithersburg, MD*

ThP 467 **Optimized dia-PASEF-based immunopeptidomics for enhanced detection of the MHC-II ligandome**; Petra Erdmann Gilmore[1, 2]; Anthony N. Vomund[1, 2]; Michael Krawitzky[3]; Cheryl F. Lichti[1, 2];

[1]Washington University School of Medicine, St. Louis, MO; [2]Bursky Center for Human Immunology and Immunotherapy, St. Louis, MO; [3]Bruker Daltonics, Billerica, MA

ThP 468 **MHCBooster: Harnessing AI to Enhance Immunopeptidome Profiling Sensitivity from DDA and DIA Data**; Ruimin Wang[1]; Mohammad Shahbazy[1]; Valeria Azcoitia[1]; Isabelle Leo[1]; Saketh Kapoor[1]; Etienne Caron[1, 2]; *[1]Department of Immunobiology, Yale School of Medicine, Yale University, New Haven, CT; [2]Yale Center for Immuno-Oncology, Yale Center for Systems and Engineering Immunology, Yale Center for Infection and Immunity, Yale School of Medicine, New Haven, CT*

ThP 469 **Balancing Throughput and Depth in HLA-I Immunopeptidomics Using Orbitrap Astral and Astral Zoom LC–MS Platforms**; Huiling Liu[1]; Barbara Helm[1]; Arnau Peris Cuesta[1]; Na Qiao[1]; Aya A Albittar[1]; Beatriz Alvarado Hernandez[1]; Sachet Ashok Shukla[1]; Sara Zanivan[1]; Dominic Helm[1]; *[1]The University of Texas, MD Anderson Cancer Center, Houston, TX*

ThP 470 **Acquisition-to-Search Optimization for Sensitive MHC Peptide Analysis on the Astral Zoom**; Ioana Clotea[1]; Ritchlynn Aranha[1]; Mark Yarmarkovich[1]; Beatrix Ueberheide[1]; *[1]NYU Langone Health, New York, NY*

ThP 471 **Enhanced Recovery and Peak Shape of Acidic and Phosphopeptides Using Waters BioResolve™ Premier 1 mm ID Columns**; Caitlin M. Hanna[1]; Stephan M. Koza[1]; Balasubrahmanyam Addepalli[1]; *[1]Waters Corporation, Milford, MA*

ThP 472 **Comparison of the SUMS Phosphoproteomics Data-Dependent Acquisition Methods on a ThermoFisher Orbitrap Eclipse Tribrid Mass Spectrometer**; Garvey McKenzie[1]; Casey Powers[1]; Juan Pablo Galindo[1]; Fang Liu[1]; Ryan Leib[1]; *[1]Stanford University Mass Spectrometry, Palo Alto, CA*

ThP 473 **Enhancing phosphoproteomics depth and quantitative performance through integrated noFAIMS–FAIMS analysis**; Byoung-Kyu Cho[1]; Antonia Zamacona Calderon[1]; Young Ah Goo[1]; *[1]Washington University in St.Louis, St.Louis, MO*

ThP 474 **Regulation of the Myotubularin Family of Lipid Phosphatases by Mitogen-Activated Protein Kinases**; Dylan Ing[1]; Grace Querbach[1]; Kaitlyn Hand[1]; Panayiotis O Vacratsis[1]; *[1]University of Windsor, Windsor, ON*

ThP 475 **Accessible IMAC Strategies for Discovery of Endogenous Phosphorylated Neuropeptides in Crustacean Neural Tissues and Hemolymph**; Zachary P Del Mundo[1]; Lukas P Quinones[1]; Thao Duong[2]; Vu Ngoc Huong Tran[1]; Feixuan Wu[1]; Lingjun Li[1, 2]; *[1]University of Wisconsin-Madison School of Pharmacy, Madison, WI; [2]University of Wisconsin-Madison Department of Chemistry, Madison, WI*

ThP 476 **Dissecting kinase signalling networks at 500 phosphoproteomes per day**; Denys Oliinyk[1]; Tim Heymann[1]; Elisabeth Zollbrecht[1]; Matthias Mann[1]; *[1]Max Planck Institute of Biochemistry, Planegg, Germany*

ThP 477 **Automation of Extracellular Vesicle Phosphoproteomics Pipeline via coupling magnetic- and membrane-based high throughput procedures**; Nathaniel M Miller[1]; Yi-Kai Liu[1]; Gregory A Davidson[2]; Xiaohui Zhang[2]; Guotao Lu[2]; Anton Iliuk[1, 3]; W. Andy Tao[1, 3, 4, 5]; *[1]Department of Biochemistry, Purdue University, West Lafayette, IN; [2]CDS Analytical LLC, Oxford, PA; [3]Tymora Analytical Operations, West Lafayette, IN; [4]Purdue Institute for Cancer Research, West Lafayette, IN; [5]James Tarpo Jr. and Margaret Tarpo Department of Chemistry, Purdue University, West Lafayette, IN*

ThP 478 **From Native Complexes to Proteoform Maps: Multi-Dimensional MS Workflows for Kinase Drug Targets**; Boris Krichel[1, 2, 3]; Hsin-Ju Chan[4]; Marius JC Natsch[1, 2]; Stuart Pengelley[5]; Susanne Alfken[5]; Detlev Suckau[5]; Athanasios Smyrnakis[6]; Eduardo Carrascosa[5]; Amalia Apalategui[5]; Dimitris Papanastasiou[6]; Charlotte Uetrecht[1, 2]; Ying Ge[3, 4]; *[1]CSSB Centre for Structural Systems Biology, Deutsches Elektronen-Synchrotron DESY & Leibniz Institute of Virology (LIV), Hamburg, Germany; [2]University of Lübeck, Lübeck, Germany; [3]Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI; [4]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [5]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [6]Fasmatech Science & Technology, Athens, Greece*

ThP 479 **Evaluation of OptiSpray Technology against Lab-Fabricated Capillary Columns for Phosphoproteomics**; Drew Jordahl[1]; John S. Chlystek[1]; Daniel J. Nesbitt[2]; Jonathan Tai[3]; Stephanie McGregor[4]; Katherine L. Walker[5]; Runsheng Zheng[5]; Scott T. Quarmby[1, 6]; Katherine A. Overmyer[1, 6, 7]; Joshua J. Coon[1, 2, 6, 7]; *[1]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [2]Department of Chemistry, University of Wisconsin-Madison, Madison, WI; [3]Department of Biochemistry, University of Wisconsin-Madison, Madison, WI; [4]Department of Pathology and Laboratory Medicine, University of Wisconsin-Madison, Madison, WI; [5]Thermo Fisher Scientific, San Jose, CA; [6]National Center for Quantitative Biology of Complex Systems, Madison, WI; [7]Morgridge Institute for Research, Madison, WI*

ThP 480 **High-throughput, multiplexed phosphoproteomics with automated Fe-NTA enrichment and targeted quantification on Orbitrap Tribrid MS**; Dustin Frost[1]; Amarjeet Flora[1]; Leigh Foster[1]; Bhavin Patel[1]; Ryan D Bomgarden[1]; *[1]Thermo Fisher Scientific, Rockford, IL*

ThP 481 **The KinoPlex Structural Atlas Decodes Kinase Substrate Specificity Across The Human Proteome**; David R Vanderwall[1]; Edward L. Huttlin[2]; Julian Mintseris[2]; Tomer M Yaron-Barir[3, 4]; Jared L Johnson[2, 3]; Kevin D Dong[2]; Alex J Bott[2]; Yuchen He[2]; Christina Schroeter[2]; Geordon Frere[2]; Mohamed Uduman[5]; Harin Lee[5]; Sean Beausoleil[5]; Joao A Paulo[2]; Lewis C Cantley[2, 6]; Steven P Gygi[2]; *[1]St. Jude Children's Research Hospital, Memphis, TN; [2]Harvard Medical School, Boston, MA; [3]Dana Farber Cancer Institute, Boston, MA; [4]Boston Children's Hospital, Department of Pediatrics, Boston, MA; [5]Cell Signaling Technology Inc, Danvers, MA; [6]Dana-Farber Cancer Institute, Boston, MA*

ThP 482 **Benchmarking Phosphopeptide Enrichment Workflows: Depth, Specificity, and Reproducibility**; Bushra Amin[1]; Nishat I Tabassum[2]; Xiangru Cheng[2]; Yibo Fan[2]; Xiangyuan Peng[2]; Thiruma V Arumugam[2]; *[1]LA Trobe University, Melbourne, Australia; [2]Department of Microbiology Anatomy Physiology and Pharmacology, LA Trobe University, Melbourne, Australia*

ThP 483 **Enabling absolute phosphosite quantitation with a highly multiplexed PRM workflow on the Stellar Mass Spectrometer**; Cristina Jacob[1]; Hasmik Keshishian[2]; Philip M. Remes[1]; Michael W. Burgess[2]; Nikita Kormshchikov[2]; Romain Huguet[1]; Steven A. Carr[2]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Broad Institute, Cambridge, MA*

ThP 484 **Optimized FFPE sample preparation enabled deeper insights into cancer signaling pathway via phosphoproteomics**; Johanna Wallner[1]; Kathrin Grundner-Culemann[1]; Johanna Thiery[2]; Oliver Schilling[2]; Jörg W. Bartsch[3]; Stephan Axel Sieber[4]; Jan Muntel[1]; Hannes Hahne[1]; *[1]Momentum Biotechnologies, Freising, Germany; [2]Institute of Surgical Pathology, University Medical Center Freiburg, Freiburg, Germany; [3]Department of Neurosurgery, Philipps-University Marburg, Marburg, Germany; [4]Chair of Organic Chemistry II, TUM School of Natural Sciences, Technical University Munich, Garching, Germany*

ThP 485 **Spatially directed phospho-bioproximity analysis of STK17B kinase in multiple myeloma cells**; Tricia C Ho[1]; Zhannan Han[2]; Greg Waitt[1]; Zhibo Yan[2, 3]; Mikhail Nikiforov[2, 3]; Erik J Soderblom[1]; *[1]Proteomics and Metabolomics Core Facility, Duke University School of Medicine, Durham, NC; [2]Department of Biomedical Engineering, Pratt School of Engineering, Duke University, Durham, NC; [3]Department of Pathology, Duke University School of Medicine, Durham, NC*

ThP 486 **ELUCIDATING DNA DAMAGE REPAIR SIGNALING ACTIVATED BY DNA TRANSPOSASE-GENE PGBD5 IN HUMAN CELLS USING FUNCTIONAL PHOSPHOPROTEOMICS**; Helen S Mueller[1]; Kaisha Garvin[1]; Sophia Rha[1]; Katarzyna Kulej[1]; Alex Kentsis[1]; *[1]Memorial Sloan Kettering Cancer Center, NY, NY*

ThP 487 **Proximity Phosphoproteomics Reveals the Spatial Organization of DNA Damage Responses**; Mateusz Wagner[1]; Ruiheng Wu[1]; Marcus B Smolka[1]; *[1]Cornell University, Ithaca, NY*

ThP 488 **Mass Spectrometry Imaging Reveals Hemicellulose-Rich Sieve Tubes Driving Ambient-Pressure Water Permeation in Moso Bamboo**; Shan Li; *International Centre for Bamboo and Rattan, Beijing, China*

ThP 489 **Proteomic Profiling Reveals Differential Protein Patterns in Galdieria sulphuraria extracts replacing fetal bovine serum in muscle cell culture**; Svenja Hütker[1]; Hanna Wellkamp[1]; Imke Lang[1]; Felicitas Berger[1]; Verena Tellstroem[2]; Shourjo Ghose[3]; *[1]Bremerhaven University of Applied Sciences, Institute EcoMaterials, Bremerhaven, Germany; [2]Bruker Daltonics GmbH & Co KG, Bremen, Germany; [3]Bruker Scientific LLC, Billerica, MA*

ThP 490 **Revealing Plant Chemistry: Cryogenic Water Cluster Secondary Ion Mass Spectrometry (SIMS) for 2D and 3D High Resolution Label-Free Molecular Imaging**; Naoko Sano[1]; Kate McHardy[1]; Paul Blenkinsopp[1]; Hua Tian[2]; *[1]Ionoptika Ltd, Eastleigh, United Kingdom; [2]Columbia University, New York, NY*

ThP 491 **Mitochondrial Homeostasis in Long-Term Stress-Adapted Tobacco BY-2 Cells**; Lukasz Marczak[1]; Maria Tomys[2]; Tomasz Skrzypczak[3]; Agnieszka Szuba[4]; Przemyslaw Wojtaszek[2]; Anna Kasprowicz-Maluski[2]; *[1]Institute of Bioorganic Chemistry Polish Academy of Sciences, Poznan, Poland; [2]Department of Molecular and Cellular Biology, Adam Mickiewicz University, Poznan, Poland; [3]Centre of Advanced Technologies, Adam Mickiewicz University, Poznan, Poland; [4]Institute of Dendrology Polish Academy of Sciences, Kornik, Poland*

ThP 492 **Assessment of the New Shimadzu TQ8050 Atmospheric Monitoring Triple Quadrupole Real-Time Mass Spectrometer (3Q-RTMS) with Real-Time LifeStream (RTLS) Time-Lapse Video**; Karl K Weitz[1]; Bryson Gibbons[1]; Aivett Bilbao[1]; Andrea Harrison[1]; David Hall[1]; Rosalie Chu[1]; Mary S. Lipton[1]; *[1]Pacific Northwest National Laboratory (PNNL), Richland, WA*

ThP 493 **Extended Capillaries Facilitating High-Resolution icIEF-MS Online and High-Yield Fractionation with LC-MS/MS Peptide Mapping for protein Heterogeneity**; Simin Yang[1]; Teresa Kwok[1]; Chengmeng Sun[1]; Victor Li[1]; Tiemin Huang[1]; Tao Bo[1]; *[1]Advanced Electrophoresis Solutions Ltd, Cambridge, ON*

ThP 494 **Hybrid Cross-Linking Mass Spectrometry Coupled with Computational Modelling for Rapid Biotherapeutic Candidate Selection**; Thomas J Powell[1]; Martin Ebner[1]; Andrew Creese[1]; *[1]Immunocore, Abingdon, United Kingdom*

ThP 495 **An improved workflow for enrichment and identification of biologics charge variants**; Yunpeng Lan; *AstraZeneca, Gaithersburg, MD*

ThP 496 **Kinetic and Structural Characterization of Filgrastim and its Biosimilar Fiprima® Under Forced Degradation by Enzymatic Digestion and HRMS**; Felipe C Lecher[1]; Giovanny Carvalho Dos Santos[1]; Luiz Felipe de Oliveira Faria[1]; Nathalia D'Elboux Bernardino[1]; Carlos Eduardo Carelli Junior[1]; *[1]Eurofarma Laboratórios, Itapevi, Brazil*

ThP 498 **Unraveling Disulfide Isoforms in Multispecific Proteins Using high-resolution LC/MS**; Shuai Wu[1]; Stephen Kok[2]; Nick DeGrann-Weber[2]; *[1]Amgen, Thousand Oaks, CA; [2]Genedata Inc, San Francisco, CA*

ThP 499 **A workflow for comprehensive characterization of highly-complex N-glycans in a glycoprotein with automated data analysis**; Zhongqi Zhang[1]; Bhavana Shah[1]; *[1]Amgen Inc., Thousand Oaks, CA*

ThP 500 **At-line monitoring of biotherapeutic production and quality, using native ion mobility-mass spectrometry directly from crude spent media**; Hari Newnham[1, 2, 3]; Kristine F Parson[4]; John Raven[5]; Mason Chilmonczyk[6]; Jessica Kane-Fidgeon[5]; Leon Pybus[5]; Perdita E Barran[1, 2, 3]; *[1]Michael Barber Centre for Collaborative Mass Spectrometry, Manchester, United Kingdom; [2]Manchester Institute of Biotechnologies, Manchester, United Kingdom; [3]The University of Manchester, Manchester, United Kingdom; [4]FUJIFILM Biotechnologies, Morrisville, NC; [5]FUJIFILM Biotechnologies, Billingham, United Kingdom; [6]Andson Biotech, Atlanta, GA*

ThP 501 **Increasing sensitivity in peptide-level studies; Cyclic™ IMS-enabled Wideband Enhancement of CID and ECD product ions**; Ramin Rabbani[1]; Dale A Cooper-Shepherd[2]; Isabella A Jones[2]; Emma Marsden-Edwards[2]; *[1]Waters Corporation, Milford, MA; [2]Waters Corporation, Wilmslow, United Kingdom*

ThP 502 **Integrated Experimental and Computational Workflow Enabled by In-Source Reduction for "Truly Complete" Disulfide Mapping**; He Zhu[1]; Zhiqing Jiang[1]; Yongsheng Xiao[1]; [1]*Wuxi Biologics, Wuxi, China*

ThP 503 **Evaluation of a New Platform for Ultra-Fast Direct-Infusion Peptide Mapping of Monoclonal Antibodies**; Pei Liu[1]; Benjamin Cutak[1]; Kevin Ray[1]; [1]*MilliporeSigma, St. Louis, MO*

ThP 504 **Driving Consistency and Data Quality in Protein Mapping Through Rule-Based Automation**; Cece Cui[1]; Magdalena Szczygiel-Buchner[2]; Arnd Brandenburg[3]; [1]*Genedata Inc, Boston, MA;* [2]*Genedata GmbH, Munich, Germany;* [3]*Genedata AG, Basel, Switzerland*

ThP 505 **Integrated Single-Column LC-MS Workflow for Deep Structural Characterization of Complex TCR-Fab Bispecific Antibodies**; Kia Ngee Low[1]; Yee Jiun Kok[1]; Claudia Alvarez[2]; Stephen Tate[2]; Xuezhi Bi[1]; [1]*Bioprocessing technology Institute, Singapore, Singapore;* [2]*SCIEX, Concord, ON*

ThP 506 **Minimizing artificial modifications in antibody proteomics via rapid sequential digestion**; Dmitry S. Loginov[1]; Jakub Kordik[1, 2]; Petr Novak[1]; [1]*Institute of Microbiology CAS, Prague, Czech Republic;* [2]*Charles University, Prague, Czech Republic*

ThP 507 **Infrared Photon-Activated Electron Transfer Dissociation and Automated Data Analysis for Improved Characterization of Fab Antibody Subunit Mixtures**; Amy Carfagno[1]; Linda B Lieu[1]; Jingjing Huang[2]; Jake T Kline[1]; Kenneth R Durbin[3]; Rafael D Melani[2]; Luca Fornelli[1]; [1]*University of Oklahoma, Norman, OK;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*Proteinaceous, Evanston, IL*

ThP 508 **Towards In-Process Monitoring of Cell Therapies: Online Buffer Exchange for Cell Culture Media Analysis**; Casey Vantucci[1]; Carter Asef[1]; Arabella Garcia[1]; Suraj Dhungana[1]; Mason Chilmonczyk[1]; [1]*Andson Biotech, Atlanta, GA*

ThP 509 **Online Buffer Exchange with Nanoflow Infusion Streamlining Ensemble and Charge Detection Native Mass Spectrometry**; Weijing Liu[1]; Carter Asef[2]; Suraj Dhungana[2]; Mason Chilmonczyk[2]; [1]*Thermo Fisher Scientific, San Jose, CA;* [2]*Andson Biotech, Atlanta, GA*

ThP 510 **LC–MS analysis of intact and subunit-level monoclonal antibodies enabled by a novel monodisperse supermacroporous reversed-phase platform**; Audrius Zvirblis[1]; Odeta Dembovskyte[1]; Ke Ma[2]; Christof Mitterer[3]; Mauro De Pra[4]; Frank Steiner[5]; [1]*Thermo Fisher Scientific, Vilnius, Lithuania;* [2]*Thermo Fisher Scientific, Sunnyvale, CA;* [3]*Thermo Fisher Scientific, Langerwehe, Germany;* [4]*Thermo Fisher Scientific, Milan, Italy;* [5]*Thermo Fisher Scientific, Germering, Germany*

ThP 511 **Characterizing Unknown Critical Impurity in Cyclic Peptide Ligand for Oligonucleotide Therapeutics**; Rajeswari Lakshmanan[1]; Andy Rodriguez[1]; Phil Olsen[1]; Stilianos G. Roussis[1]; Daniel Capaldi[1]; Claus Rentel[1]; [1]*Ionis Pharmaceuticals, Inc., Carlsbad, CA*

ThP 512 **ATP-Regulated Druggable Sites: A New Paradigm for Targeting Neuronal Solute Carriers**; Idlir Liko[1]; Katharina Duerr[2]; Srinath Krishnamurthy[3]; Fernando Goncalves De Almeida[1]; [1]*EIT, Oxford, United Kingdom;* [2]*University Of Oxford, Oxford, United Kingdom;* [3]*OMass Therapeutics, Oxford, United Kingdom*

ThP 513 **MS^n Characterization of Chemical Modifications in Pharmaceutical Protein Byproducts Using the timsOmni Platform**; Kim F. Haselmann[1]; Max Edmund Kraner[1]; Heidi Jensen[1]; Tine Nygaard Vinther[1]; Athanasios Smyrnakis[2]; Mariangela Kosmopoulou[2]; Konrad Winkels[3]; Dodge Baluya[4]; Christian Albers[5]; Dimitris Papanastasiou[2]; [1]*Novo Nordisk A/S, Måløv, Denmark;* [2]*Fasmatech Science and Technology, Athens, Greece;* [3]*Bruker Daltonics GmbH & Co. KG, Bremen, Germany;* [4]*Bruker Scientific LLC, San Jose, CA;* [5]*Bruker Daltonik GmbH, Bremen, Germany*

ThP 514 **Advancing bispecific antibody development with orthogonal LC-MS workflows**; Matthew J Amaral[1]; Andrew Mahan[1]; Jingwen Ding[2]; Michael Poltash[1]; Haichuan Liu[2]; Zoe Zhang[2]; Hirsh Nanda[1]; [1]*Johnson & Johnson Innovative Medicine, Spring House, PA;* [2]*SCIEX, Redwood City, CA*

ThP 515 **Identification of the Root Cause of Visible Particle Formation in a Therapeutic Monoclonal Antibody by LC-MS-Based Approaches**; Amareth Lim[1]; Andrew G. Werner[2]; Brandon L. Doyle[2];

William D. Holmes[2]; Andrew W. Carr[2]; Chi A. Nguyen[2]; Suzanne E. Stone[2]; Elisabeth Krug[2]; [1]*Eli Lilly and Company, Indianapolis, IN;* [2]*Eli Lilly & Company, Indianapolis, IN*

ThP 516 **Development of an Impurity Profiling Method for GLP-1 Analogs Using Reverse-Phase Chromatography, Exact Mass Analysis, and EThcD Fragmentation**; Felicia Riordan[1]; Kwasi Mawuenyega[1]; Kevin Ray[1]; [1]*MilliporeSigma, St. Louis, MO*

ThP 517 **Developing a Two-Step Non-Reduced Digestion Protocol under Acidic Conditions for Disulfide Bond Characterization**; Yasmine Bouchibti[1]; Shuai Wu[1]; Iain D. G. Campuzano[1]; [1]*Amgen, Thousand Oaks, CA*

ThP 518 **Glucagon-like peptide-1 agonist therapeutics: a compliant-ready monitoring strategy using RP-HRAM MS**; Sara Carillo[1]; Corentin Beaumal[1]; Silvia Millan Martin[1]; Kai Scheffler[2]; Jonathan Bones[1, 3]; [1]*NIBRT, Dublin, Ireland;* [2]*Thermo Fisher Scientific, Germering, Germany;* [3]*School of Chemical and Bioprocess Engineering, University College Dublin, Dublin, Ireland*

ThP 519 **Utilising ProA-IEX-MS for the measurement of charge variants of biotherapeutic proteins directly from Cell Culture Supernatant**; Matthew J Edgeworth[1]; Sara Carillo[2]; Jonathan Bones[2]; Felipe Guapo[2]; James Graham[1]; Karina Bora[1]; [1]*LONZA, Slough, United Kingdom;* [2]*NIBRT, Dublin, Ireland*

ThP 520 **Comprehensive Domain-specific N-Glycan Characterization of a Monoclonal Antibody**; Qi Hu[1]; Oliver Silerio[1]; Ally Liu[1]; Sean Shen[1]; Lian Yi[1]; Tawnya Flick[1]; [1]*Gilead Sciences, Oceanside, CA*

ThP 521 **Ultrasensitive nHDX-MS for high-throughput analysis of challenging protein-ligand and protein-protein interactions**; Shaunak Raval[1]; Yuqi Shi[2]; Daniel Rosen[1]; Jaechan Lee[1]; Siddhant U. Jain[3, 4]; Cigall Kadoch[3, 4]; Nir Hacohen[1]; Steven A. Carr[1]; Malvina Papanastasiou[1]; [1]*Broad Institute, Cambridge, MA;* [2]*Thermo Fisher Scientific, San Jose, CA;* [3]*Dana-Farber Cancer Institute, Boston, MA;* [4]*Harvard Medical School, Boston, MA*

ThP 522 **Breathing dynamics of intrinsically disordered viral capsid proteins by integrative structural mass spectrometry and cryo-EM**; Amanda J Gramm[1]; Ebere Precious Orji[2, 3]; Caroline H Langley[2, 3]; Hyunwook Lee[3]; Kyle J Messina[3]; Carol M Bator[3]; Matt Swulius[4]; Sarah Brendle[4, 5]; Neil D Christensen[4, 5]; Susan L Hafenstein[2, 3, 6]; Ganesh S Anand[1]; [1]*Pennsylvania State University, University Park, PA;* [2]*University of Minnesota, Minneapolis, MN;* [3]*University of Minnesota, Hormel Institute, Austin, MN;* [4]*Pennsylvania State University College of Medicine, Hershey, PA;* [5]*The Jake Gittlen Laboratories for Cancer Research, Hershey, PA;* [6]*Department of Infectious Disease, Mayo Clinic, Rochester, MN*

ThP 523 **Probing Tau Conformations and Early Aggregates Using Native Mass Spectrometry**; Isabella M. Rossetti[1]; Vanessa L. Stahl[1]; Emma L. Poirier[1]; Richard W. Vachet[1]; [1]*University of Massachusetts Amherst, Amherst, MA*

ThP 524 **Development of a high-throughput device for oxidative labeling of biomolecules using singlet oxygen**; Lada Fialová[1, 2]; Marta Cruz[2, 3]; Jan Rasl[2]; Petr Novák[2]; Alžběta Nemeškalová[1, 2]; Michael Volný[1, 2]; [1]*University of Chemistry and Technology, Prague, Czech Republic;* [2]*Institute of Microbiology CAS, Prague, Czech Republic;* [3]*Charles University, Prague, Czech Republic*

ThP 525 **Native and Hydrogen–Deuterium Exchange Mass Spectrometry Elucidate Lipid Binding and Conformational Regulation of Endogenous Human Glucose Transporter 1**; Siyuan Song[1, 2]; Xingyu Qiu[1, 2]; Di Wu[1, 2]; Carol V Robinson[1, 2]; [1]*Department of Chemistry, University of Oxford, Oxford, United Kingdom;* [2]*Kavli Institute for Nanoscience Discovery, University of Oxford, Oxford, United Kingdom*

ThP 526 **Exploiting a declustering ion guide and Cyclic™ IMS-enabled Wideband Enhancement for native top-down studies**; Isabella A Jones[1]; Stephen Griffin[2]; Dale A Cooper-Shepherd[3]; Emma Marsden-Edwards[3]; [1]*University of Birmingham, Birmingham, United Kingdom;* [2]*Waters, Milford, MA;* [3]*Waters Corporation, Wilmslow, United Kingdom*

ThP 527 **Limited Proteolysis and Ion-Mobility Mass Spectrometry Provides Insight into the Physiochemical Properties of the Myoglobin/Heme Complex**; Leila Nazira Minian[1]; Roza Grigoryevna Avetisyan[1]; Carter Lantz[1]; David Russell[1]; [1]*Texas A&M Univesity, College Station, TX*

ThP 528 **Automated & Multiplexed Protein Footprinting for Higher Order Structure Elucidation**; Wenzhou Li[1]; Thao Nguyen[1]; Jichu Pang[1]; Niclas Olsson[1]; Leanne J Chan[1]; Jason Smith[1]; Emily Chea[2]; Charles Mobley[2]; Scot R Weinberger[2]; Fiona E McAllister[1]; *[1]Calico Life Sciences LLC, South San Francisco, CA; [2]GenNext Technologies Inc, Half Moon Bay, CA*

ThP 529 **Probing Conformational Changes Induced by PROTACs Using Plasma Induced Modification of Biomolecules (PLIMB) and Limited Proteolysis Mass Spectrometry**; Sangeeta Pandey[1]; Gregory K Potts[1]; Tiffany A Thibaudeau[1]; Aaron C Ehlinger[1]; Alla V Korepanova[1]; Judith A Ronau[1]; Jon D Williams[1]; Nathaniel L Elsen[1]; *[1]AbbVie Inc., North Chicago, IL*

ThP 530 **Enhanced Structural Resolution in HRPF: Integrating AutoFox with Astral Zoom DIA for Comprehensive Small Molecule Binding Site Characterization**; Charles Mobley[1]; Emily Chea[1]; Yuqi Shi[2]; Weijing Liu[2]; Scot R Weinberger[1]; *[1]GenNext Technologies, Half Moon Bay, CA; [2]Thermo Fisher Scientific, San Jose, CA*

ThP 531 **Integrated HRPF Workflows Combining Flash Oxidation with End-to-End Data Processing for Structural MS**; Michelle English[1]; Thomas Botzanowski[2]; Emily Chea[3]; Charles Mobley[3]; Scot R Weinberger[3]; Albert Van Wyk[2]; *[1]Genedata Inc, Boston, MA; [2]Genedata AG, Basel, Switzerland; [3]GenNext Technologies, Half Moon Bay, CA*

ThP 532 **Spatiotemporal analysis of protein conformations and interactions in live cells by CXMS**; Qun Zhao[1]; Lihua Zhang[1]; *[1]Dalian Institute of Chemical Physics, ACS, Dalian, China*

ThP 533 **Structural Insights into Metabotropic GABAB Receptor Dynamics and Pharmacological Modulation by Auxiliary Subunits**; Yi-An Chen[1]; Yuqi Shi[2]; Yi-Quan Wang[1]; Ning-En Chang[1]; Hsin-Yung Yen[1, 3]; *[1]Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan; [2]Thermo Fisher Scientific, San Jose, CA; [3]Institute of Biochemical Sciences, National Taiwan University, Taipei, Taiwan*

ThP 534 **Deciphering the oligomerization mechanism of human mitochondrial ClpP protease by charge detection and H/D exchange mass spectrometry**; Monica M Goncalves[1]; Anisha Haris[2]; Jakub Ujma[2]; David Bruton[2]; Keith Richardson[2]; Kevin Giles[2]; Aaron D. Schimmer[3]; Siavash Vahidi[1]; *[1]University of Guelph, Guelph, ON; [2]Waters Corporation, Wilmslow, United Kingdom; [3]Princess Margaret Cancer Centre, Toronto, ON*

ThP 535 **Dissecting ribonucleoproteins by native top-down mass spectrometry**; Lasini Amunugama[1]; Sachin Tennakoon[1]; Weijing Liu[2]; Boldsaikhan Boldbayar[1]; Shilla O. Ansah[1]; Catherine D. Eichhorn[1]; Jared B Shaw[1]; *[1]University of Nebraska-Lincoln, Lincoln, NE; [2]ThermoFisher Scientific, San Jose, CA*

ThP 536 **Comparative crosslinking mass spectrometry (CX-MS) studies examining the structure of the cytoplasmic domain of the human α1 glycine receptor**; Erica Maney[1]; Michael Cascio[1]; *[1]Duquesne University, Pittsburgh, PA*

ThP 537 **X-Ray Footprinting / Mass Spectrometry Provides a New, Detailed View of Intrinsically Disordered Proteins and Disorder-Containing Complexes**; Darren N Kahan[1]; Sayan Gupta[2]; Aditya Udupa[1]; Max V Staller[1]; Corie Y Ralston[2]; Susan Marqusee[1]; *[1]UC Berkeley, Berkeley, CA; [2]Lawrence Berkeley National Laboratory, Berkeley, CA*

ThP 538 **Nucleosome Binding Alters Progesterone Receptor Dynamics and Acetylation Signatures**; Matthew David Mann[1]; Phoebe S. Tsoi[2]; Michael P. Suess[2]; Raj Kumar[3]; Dean P. Edwards[2]; Patrick R. Griffin[4]; *[1]Scripps Research, Jupiter, FL; [2]Baylor College of Medicine, Houston, TX; [3]Touro College of Pharmacy, Touro University, New York, NY; [4]UF Scripps, Florida, Jupiter, FL*

ThP 539 **Mass Spectrometry Informs on Chemically Ambiguous Electron Diffraction Density in Protein Crystals**; Cameron W Flowers[1]; Tim Low-Beer[2]; Purna Chandra Rao Vasireddy[3]; Michael Martynowycz[3]; Jose A. Rodriguez[4]; Joseph A Loo[4]; *[1]UCLA, Los Angeles, CA; [2]University at Buffalo, Buffalo, NY, United States, Buffalo, NY; [3]University at Buffalo, Buffalo, NY; [4]UCLA-DOE Institute for Genomics and Proteomics, University of California, Los Angeles, Los Angeles, CA*

THURSDAY MORNING ORALS

ThP 540 **IC-FPOP on Peripheral Blood Mononuclear Cells (PBMCs): The Advancement of Structural Biology in Primary Human Samples**; Lisa M Jones; *University of California San Diego, La Jolla, CA*

ThP 541 **Beamline 3.3.1 of Advanced Light Source, LBNL: A National Resource for X-ray mediated hydroxyl radical Footprinting and Mass Spectrometry**; Sayan Gupta[1]; Line G Kristensen[1]; Brandon Russell[1]; Darren N Kahan[2]; Corie Y Ralston[1]; *[1]Lawrence Berkeley National Laboratory, Berkeley, CA; [2]University of California, Berkeley, Berkeley, CA*

ThP 542 **Mapping the dynamic conformational landscape of hyperactive STAT5B by X-ray Footprinting Mass Spectrometry (XFP-MS)**; Qirat Ashraf[1, 2]; Erik R Farquhar[3]; Balmiki Kumar[1]; Elvin De Araujo[1]; Patrick Gunning[1, 2, 4]; *[1]University of Toronto, Mississauga, ON; [2]University of Toronto, Toronto, ON; [3]Case Western Reserve University, Cleveland, OH; [4]University of Glasgow, Glasgow, United Kingdom*

ThP 543 **Insights into targeted protein degradation by chemical crosslinking, quantitative mass spectrometry and computational modeling**; Franz Herzog[1]; Benjamin Neuditschko[1]; Stefanie Brandstetter[1]; Klaus Rumpel[2]; *[1]IMC University of Applied Sciences Krems, Krems, Austria; [2]Boehringer Ingelheim RCV GmbH & Co KG, Vienna, Austria*

ThP 544 **Conformational dynamics of a membrane-associated ancestral cytochrome P450 monooxygenase revealed through X-ray footprinting mass spectrometry**; Line G. Kristensen[1]; John C Hackett[2]; Sayan Gupta[1]; Corie Y. Ralston[1]; *[1]Lawrence Berkeley National Laboratory, Berkeley, CA; [2]Florida International University, Miami, FL*

ThP 545 **Integrating Mass Spectrometry-Based Footprinting and Molecular Docking to Analyze Ebola Protein-Host Binding Interfaces**; Xinyi Cynthia Kuang[1]; Grace Uwase[2]; Nicole D Wagner[1, 2]; Daisy W Leung[2]; Gaya K Amarsinghe[2]; Michael L. Gross[1]; *[1]Washington University in St. Louis, University City, MO; [2]Washington University School of Medicine, St. Louis, MO*

ThP 546 **LC-MS/MS-based chemoproteomics and lipidomics reveal liposomes directly modulate metabolic serine hydrolase activity**; Payton E Lowrey[1]; Olivia Murtagh[1]; Maddie Gunawardena[2]; Rudra Pangeni[2]; Qingguo Xu[2]; Ku-Lung Hsu[1]; *[1]University of Texas at Austin, Austin, TX; [2]Virginia Commonwealth University, Richmond, VA*

ThP 547 **What's the (melting) point? Detergents alter thermal stability of lysate proteomes: implications for thermal profiling**; Catherine Sniezek[1]; Veronika Glukhova[1]; Christian Schmitz[1]; Katarina Vlajic[1]; Devin Schweppe[1]; *[1]University of Washington, Seattle, WA*

ThP 548 **Proteome Mapping of Formaldehyde-derived Modifications and Cross-links by Real-time Isotopic Signature Targeted Profiling**; Tianyu Feng[1]; Guogeng Jia[1]; Yicheng Liu[1]; Linghao Kong[1]; Ruobing Liang[2]; Chu Wang[1, 3]; *[1]College of Chemistry and Molecular Engineering, Peking University, Beijing, China; [2]College of Chemistry, Nankai University, Tianjin, China; [3]Peking-Tsinghua Center for Life Sciences, Academy for Advanced Interdisciplinary Sciences, Peking University, Beijing, China*

ThP 549 **Stability-Based Proteomic Methods Add Value toActivity-Based Protein Profiling Studies**; You Zou[1]; Diego J. Sanson[1]; Jianli Wu[1]; Gibeom Nam[1]; Ssu-Yu Chen[1]; Jiyong Hong[1]; Jen-Tsan Ashley Chi[1]; Michael C. Fitzgerald[1]; *[1]Duke University, Durham, NC*

ThP 550 **The Functionalisation of Light, Medium, and Heavy Reagents with Tandem Mass Tags to Enable 105plex Cysteine Chemoproteomic Compound Screening**; Katrina H Andrews[1]; Nikolas R Burton[1]; Dustin R Frost[2]; Erum Raja[2]; Brett Larsen[3]; Rosa Viner[4]; Ryan D Bomgarden[2]; Keriann M Backus[1]; *[1]University of California, Los Angeles, Los Angeles, CA; [2]Thermo Fisher Scientific, Rockford, IL; [3]Thermo Fisher Scientific, Mississauga, ON; [4]Thermo Fisher Scientific, San Jose, CA*

ThP 551 **Systematic identification of confounding factors influencing reactive cysteine profiling across lysate- and live cell-based chemoproteomics platforms**; Shaoxian Li[1]; Bohui Li[1]; Dan Richards[1]; Fangyi Zhai[1]; Ka Yang[2]; Qing Yu[1]; *[1]UMASS Chan Medical School, Worcester, MA; [2]Harvard Medical School, Boston, MA*

ThP 552 **Chemoproteomics reveals irreversible inhibition of mouse CYP2E1 by diethyldithiocarbamate through heme perturbation**; Durgalakshmi Sivasankar[1]; Wensheng Yang[1]; Jeffrey Agar[1]; *[1]Northeastern University, Boston, MA*

ThP 553 **Integrated cysteine and phosphoproteomic profiling enables systems-level analysis of signaling adaptation to covalent molecules**; Laura J Keller[1]; Thijs J Hagenbeek[1]; Carsten Peukert[1]; Vasumathi Kameswaran[1]; Alissa D Guarnaccia[1]; Christopher M Rose[1]; Bence Daniel[1]; Anwesha Dey[1]; Hanna Budayeva[1]; *[1]Genentech Inc., South San Francisco, CA*

ThP 554 **Fe–S Cluster Proteins as Antibacterial Targets of the Isocyanide Natural Product B371**; Sara Berndl[1]; Daniel Bak[2]; Mara Hebeis[3]; Alexandra Geißler[1]; Ingrid Span[3]; Eranthie Weerapana[2]; Stephan Sieber[1]; *[1]Chair of Organic Chemistry II, Technical University Munich, Garching bei München, Germany; [2]Boston College, Boston, MA; [3]Friedrich Alexander University Erlangen-Nürnberg, Erlangen, Germany*

ThP 555 **neo-N-terminal SP3 Pyridine Carboxaldehyde Enrichment (N-SPyCE) identifies T cell activation dependent cleavage events**; Alexandra C. Turmon[1]; Caroline J. Canavan[1]; Andrew P. Becker[1]; Nicole Wilkinson[1]; Nithesh Perumal[1]; Avani Pammidimukkala[1]; Lisa Boatner[1]; Beatrice Polli[1]; Alexander W. Sun[1]; Charlotte Nyland[1]; Douglas Black[1]; Maureen Su[1]; Keriann M. Backus[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

ThP 556 **Large-scale Mass Spectrometry-Based Chemical Proteomics Screen for the Identification of Kinase-Substrate Relationships**; Bernhard Kuster[1]; Florian Bayer[2]; *[1]Technical Universitiy of Munich, Freising, Germany; [2]Technical University of Munich, Freising, Germany*

ThP 557 **Atarget-driven, reactive cysteine profiling method using parallel reaction monitoring (PRM) on the Orbitrap Astral**; Ka Yang[1]; Yuchen He[1]; Steven P Gygi[1]; *[1]Harvard Medical School, Boston, MA*

ThP 558 **Proteome-wide, unmodified fragment screening using Limited Proteolysis coupled Mass Spectrometry**; Maximilian Dünnebacke[1]; Evgenia Elizarova[2]; Bruno Correia[2]; Paola Picotti[3]; *[1]ETH Zurich, Zürich, Switzerland; [2]EPFL, Lausanne, Switzerland; [3]ETH Zürich, Zurich, Switzerland*

ThP 559 **Advancing High-Throughput TMT-Multiplexed Chemoproteomics Through Enhanced Orbitrap Tribrid Performance**; Amanda M Tallon[1]; Ryan Lumpkin[1]; Nicole Hinkle[1]; Dylan C MItchell[1]; *[1]Expedition Medicines, Cambridge, MA*

ThP 560 **Chemoproteomic profiling of lysosomal enzyme activity and luminal content in human aging and disease**; Seth R Allen[1]; Mahbubur Rahman[1]; Ruben Elias[1]; Derek Rhoades[1]; Dan Garza[1]; Jeffery W Kelly[1]; *[1]Scripps Research, La Jolla, CA*

ThP 561 **Improved synthesis and validation of sCIP-DiLeus, a click-compatible 29plex set of isobaric chemoproteomic reagents**; Aditya Sivakumar[1]; Chau Ngo[1]; Katrina H Andrews[1]; Nikolas R. Burton[1]; Keriann M. Backus[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

ThP 562 **Silyl-ether enabled precise and high coverage chemoproteomic interaction site mapping**; Chau Ngo[1]; Sho Takechi[2, 3]; Aditya Sivakumar[2]; Keriann M. Backus[2]; *[1]University of California Los Angeles, Los Angeles, CA; [2]UCLA, Los Angeles, CA; [3]R&D Division, Daiichi Sankyo Co., Tokyo, Japan*

ThP 563 **A Novel Small Molecule VDAC Ligand Inhibits ERAD and Induces Selective Cancer Cell Death via Disruption of Calcium Homeostasis**; Dingyin Tao[1]; Wenjing Yan[2]; Yanyan Qu[1]; Yuhong Fang[1]; Valentine V Courouble[1]; Christopher A LeClair[1]; Shengyun Fang[2, 3]; *[1]NIH/NCATS, Rockville, MD; [2]Department of Pharmacology and Physiology, University of Maryland School of Medicine, Baltimore, MD; [3]Program in Oncology, UM Greenebaum Comprehensive Cancer Center, University of Maryland School of Medicine, Baltimore, MD*

ThP 564 **Benchmarking DIA and TMT Strategies for Cysteine-Focused Activity-Based Proteome Profiling**; Taylur Ma[1]; Christy Ong[1]; Anwesha Dey[1]; Zhenru Zhou[1]; Hanna Budayeva[1]; *[1]Genentech, Inc., South San Francisco, CA*

ThP 565 **Investigation of ClpXP inhibition as an antivirulent strategy in Staphylococcus aureus**; Marianne Pandler[1]; Davide Boldini[1]; Ursula Bilitewski[2]; Axel Mogck[3]; Stephan Axel Sieber[1]; *[1]Chair of Organic Chemistry II, TUM School of Natural Sciences, Technical University Munich, Garching, Germany; [2]Helmholtz-Zentrum für Infektionsforschung (HZI), Braunschweig, Germany; [3]Zentrum für Molekulare Biologie (ZMBH), Heidelberg University, Heidelberg, Germany*

ThP 566 **Proximity Proteomic Labeling of Suspension Cells Using Antibody-Directed IF-POCA**; Hanna G. Goldberg[1]; Elijah B. Biletch[1]; Keriann M. Backus[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

ThP 567 **High Throughput Screening of Cysteine-engaging Electrophiles by DIA and Two-dimensional Pooling**; Yuchen He[1]; Ka Yang[1]; David Vanderwall[1]; Geordon A. Frere[1]; Edward L. Huttlin[1]; Steve P. Gygi[1]; *[1]Harvard Medical School, Boston, MA*

ThP 568 **A Proteome-Wide Map of Ligandable Cysteine Pockets Enabled by Stereochemistry and Protein Language Models**; Sameek Singh[1]; Maja Wierzbińska[1]; Yue Dou[1]; Jonathon O'Brien[2]; John H. Bushweller[1]; Tian Zhang[1]; *[1]University of Virginia, Charlottesville, VA; [2]Golgi Biotechnology Research, San Francisco, CA*

ThP 569 **Investigating the function and ligandability of mutant STAT3 using LC-MS/MS based global, phospho- and chemoproteomics**; Mikayla L. Horvath[1]; Wesley J. Wolfe[1]; Madeleine L. Ware[1]; Ku-Lung Hsu[1]; *[1]The University of Texas at Austin, Austin, TX*

ThP 570 **Isotopic Cysteine Proteomics Maps Local Redox States within Biomolecular Liquid–Liquid Phase Separated Condensates, Revealing Regulators of Phase Separation Dynamics**; Halime D Yilmaz[1]; Ashley Julio[2]; Keriann Backus[2]; Robert Damoiseaux[2]; Ela Erkan[2]; Lucia Liu[2]; *[1]University of California, Los Angeles, Los Angeles, CA; [2]UCLA, LOS ANGELES, CA*

ThP 571 **Identifying the comprehensive list and functional roles of elastase and elastase-like proteins in the luminal proteome related to IBD**; Elias K Zegeye[1]; Christopher M Rose[1]; *[1]Proteomic and Genomic Technologies, Genentech, South San Francisco, CA*

ThP 572 **CysScout: A flexible high-throughput and ultra-deep chemoproteomic screening platform for global identification of ligandable cysteine sites**; Michael Zollo[1]; Gözde Kibar[1]; Janine Sequeira[1]; Theresa Keil[1]; Melanie Holzner[1]; Maria Ines Faria[1]; Catalina Cepeleaga[1]; Christin Zasada[1]; Johannes Krumm[1]; Hannes Hahne[1]; *[1]Momentum Biotechnologies, Freising, Germany*

ThP 573 **An Automated Limited Proteolysis Mass Spectrometry Workflow for Scalable, Unbiased Proteome-Wide Target Identification**; Keith D Rivera[1]; Ella G Sobieszczyk[1]; Cameron G Lian[1]; Namrata D Udeshi[1]; Steven A. Carr[1]; *[1]Broad Institute, Cambridge, MA*

ThP 574 **Identification and development of a selective NGLY1 inhibitor to tackle Nrf1 driven resistance in Glioblastoma**; Bilal Saqib[1]; Geordon Frere[2]; Elvin De Araujo[1]; Jason Moffat[3]; Sheila Singh[4]; Naman Patel[1]; Patrick Gunning[1]; *[1]University of Toronto, Mississauga, ON; [2]Harvard Medical School, Boston, MA; [3]SickKids SPARC BioCentre, Toronto, ON; [4]McMaster University, Hamilton, ON*

ThP 575 **Library-Scale Chemoproteomics for Protein Pocket Finding and Covalent Ligand Discovery**; Zhen Chen[1]; John Venable[1]; Ansgar Brock[1]; Guray Kuzu[1]; *[1]Biomedical Research, Novartis, San Diego, CA*

ThP 576 **Visible Light Driven Proteomic Labeling as a New Tool for Mapping Reactive Interfaces**; Harendra Sheshma[1]; Ankita Rai[1]; *[1]Jawaharlal Nehru University, Delhi, India*

ThP 577 **Investigations on the mode of action of the antitubercular cyanine dye Cy3**; David Podlesainski[1, 2]; Violetta Krisilia[3]; Tim Richter[1]; Farnusch Kaschani[1]; Rainer Kalscheuer[3]; Markus Kaiser[1]; *[1]University of Duisburg-Essen, Essen, Germany; [2]Ruhr University Bochum, Bochum, Germany; [3]Heinrich Heine University Düsseldorf, Düsseldorf, Germany*

ThP 578 **Discovery of a novel PTM mediated by bile acid**; Yanqi Wang[1]; Chang Zheng[2]; Ziming Tang[3]; Chu Wang[3]; *[1]Peking University, Beijing, China; [2]2, Chengdu, China; [3]1, Beijing, China*

ThP 579 **Development of covalent Prolyl Endopeptidase inhibitors**; Tim Richter[1]; Werner W.A. Tabak[1]; Farnusch Kaschani[1]; Robert Huber[1, 2, 3]; Markus Kaiser[1]; *[1]University of Duisburg-Essen, Essen, Germany; [2]Max Planck Institute of Biochemistry, Martinsried, Germany; [3]TUM Senior Excellence Faculty, Technical University of Munich, Munich, Germany*

ThP 580 **Achieving High Sensitivity and Quantitative Accuracy with Trigger-free, Multiplexed Targeted Chemoproteomics on a Modified Orbitrap Tribrid Mass Spectrometer**; Amanda M. Tallon[1]; Ryan Lumpkin[1]; Nicole Hinkle[1]; Dylan C. Mitchell[1]; *[1]Expedition Medicines, Cambridge, MA*

ThP 581 **Overcoming Tradeoffs between Proteome Coverage and Target Quantification for PROTAC Analysis with Hybrid-DIA on the Orbitrap Astral**; Jaison Arivalagan[1]; Yukta Bhurke[1]; Cavin Ott[1]; Jessica L Moore[1]; Shawn Fahl[1]; Don Skifter[1]; Danielle Gutierrez[1]; *[1]Discovery Life Sciences, Huntsville, AL*

ThP 582 **Enrichment of Apolipoprotein A-IV from Serum Using Affinity Chips Prepared by Ambient Ion Soft-Landing**; Mikulas Vlk[1]; Ales Hnizda[2]; Petr Pompach[3, 4]; Petr Novak[5]; Michael Volny[4, 5, 6]; *[1]Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Republic; [2]First Faculty of Medicine, Charles University, Prague, Czech Republic; [3]Institute of Biotechnology CAS, Vestec, Czech Republic; [4]AffiPro s.r.o., Vestec, Czech Republic; [5]Institute of Microbiology CAS, Prague, Czech Republic; [6]University of Chemistry and Technology Prague, Prague, Czech Republic*

ThP 583 **Large-Scale Proteomic Analysis of Serum to Identify Biomarkers Associated with the Progression of Age-Related Macular Degeneration (AMD)**; Christopher A LeClair[1]; Yanyan Qu[1]; Claire Weber[2]; Gleysin Cabrera-Herrera[2]; Ravi Tharakan[1]; Yuhong Fang[1]; Susan Vitale[2]; Tiarnan D Keenan[2]; Souvick Mukherjee[2]; Wathudurage De Silva[2]; Ewy Mathé[1]; Fei Liu[3]; T Michael Redmond[2]; Dingyin Tao[4]; Emily Chew[2]; *[1]National Center for Advancing Translational Sciences, NIH, Rockville, MD; [2]National Eye Institute, NIH, Bethesda, MD; [3]Department of Medicine, Brigham Women's Hospital, Havard Medical School, Boston, MA; [4]National Center For Advancing Translational Sciences, Rockville, MD*

ThP 584 **Spatially resolved proteomic profiling of the human macula reveals molecular signatures in age-related macular degeneration**; Byoung-Kyu Cho[1]; Jessica K Lukowski[1]; Antonia Zamacona Calderon[1]; Young Ah Goo[1]; *[1]Washington University School of Medicine, St Louis, MO*

ThP 585 **Exosome-Based Proteomics to Predict Inflammation-mediated Diseases and Prevent Organ Damage**; Evelyn Hammer[1]; Antonio Piras[1]; Rudolf Napieralski[1]; Catharina Strube[1]; Sabrina Richter[1]; Christoph Krisp[2, 3]; Gary Kruppa[4]; Gabriele Schricker[1]; Bastian Hoechst[5]; Valter Bergant[6, 7]; Andreas Pichlmair[6]; Olaf G. Wilhelm[1]; Percy A. Knolle[5]; *[1]therawis diagnostics GmbH, Munich, Germany; [2]Bruker Daltonics GmbH & Co. KG, Bremen, Germany; [3]MDC-Bruker Center of Excellence for Single Cell Omics, Max Delbrück Center for Moleculare Medicine in the Helmholtz-association, Berlin, Germany; [4]Bruker Daltonics GmbH & Co. KG, Fahrenheitstr. 4, 28359, Bremen, Germany; [5]Institute of Molecular Immunology, TUM University Hospital, TUM, Munich, Germany; [6]Institute of Virology, TUM, Munich, Germany; [7]National Institute of Chemistry, Ljubljana, Slovenia*

ThP 586 **Impact of variations in blood-to-plasma standard operating procedures on nanoparticle-dependent plasma proteome recovery**; Taku Kasai[1]; Luisa Weiss[1, 2]; Jessica Wohlfahrt[3]; Joan T, Matamalas[1]; Gabriel Shlayen[1]; Zachary Kirsch[4]; Matt Willetts[4]; Masanori Aikawa[1, 5, 6]; Elena Aikawa[1, 6]; Sasha A. Singh[1]; *[1]Center for Interdisciplinary Cardiovascular Sciences, Division of Cardiovascular Medicine, Department of Medicine, Brigham Women's Hospital, Harvard Medical School, Boston, MA; [2]SPHERE Research Group, Conway Institute, School of Biomolecular and Biomedical Sciences, University College Dublin, Dublin, Ireland; [3]PreOmics Inc., Billerica, MA; [4]Bruker Scientific LLC, Billerica, MA; [5]Center for Excellence in Vascular Biology, Division of Cardiovascular Medicine, Department of Medicine, Brigham and Women’s Hospital, Harvard Medical School, Boston, MA; [6]Channing Division of Network Medicine, Department of Medicine, Brigham Women's Hospital, Harvard Medical School, Boston, MA*

ThP 587 **Translational Mass Spectrometry Maps Spatially Regulated PSMA N-Linked Glycoforms with Prognostic Relevance in Prostate Cancer**; Stephen Mackay[1]; Ian O Oduor[2]; Janette Lockett[1]; Julius O Nyalwidhe[1, 3]; *[1]Department of Biomedical and Translational Sciences, Virginia Health Sciences Eastern Virginia Medical School at Old Dominion University, Norfolk, VA; [2]Department of Neurology,* *Children's Hospital of the Kings Daughters,, Norfolk, VA; [3]Virginia Health Sciences Eastern Virginia Medical School at ODU, Norfolk, VA*

ThP 588 **Nanoparticle Enrichment of Volumetrically Accurate Microsampled Blood for Enhanced Proteomic Analysis of Dried Blood**; Amanda Campbell[1, 2]; Lindsey Becker[1]; Matthew Ayres[1]; Simion Kreimer[1]; Janice Emmanuella[1]; Koen Raedschelders[1]; Jennifer E. Van Eyk[1]; *[1]Cedars-Sinai Medical Center, Los Angeles, CA; [2]Department of Clinical Biochemistry, Odense University Hospital, Odense, Denmark*

ThP 589 **Development and Validation of an LC-MS/MS Assay for Measuring KEAP1 Cys151 Target Engagement in Tumor Biopsies**; Brandon T Ebright[1]; Egor Vorontsov[2]; Seth Negron[1]; Stephanie Ballweg[2]; Katrin Rottluff[2]; Michael Bremang[2]; Stefan Selzer[2]; Antje Berfelde[2]; Christie Eissler[1]; Stephen McComish[1]; Emma Masteller[1]; Marielena Mata[1]; Gabriel Simon[1]; Matthew Patricelli[1]; David Van Meter[2]; Ian Pike[2]; Melissa Hoffman[1]; *[1]Vividion Therapeutics Inc., San Diego, CA; [2]Proteome Sciences R&D GmbH & Co. KG, Frankfurt, Germany*

ThP 590 **A novel workflow for high-throughput bacterial identification**; Chitralekha Sen Roy[1]; Dipankar Malakar[1]; Rashmisnata Barman[2]; DilipKumar Reddy Kandula[3]; *[1]SCIEX India Private limited, Bangalore, India; [2]Dr. B. Borooah Cancer Institute, Guwahati, India; [3]SCIEX, Marlborough, MA*

ThP 591 **Liquid Chromatography–Mass Spectrometry Optimization for Urinary Intact Proteins in Multiple Myeloma**; Lancia N.F. Darville-Bowleg[1]; Baylee Holcomb[1]; Tyanna Legoute[1]; Glen L. Hortin[1]; John M. Koomen[1]; *[1]Moffitt Cancer Center, Tampa, FL*

ThP 592 **Improved mycobacterial species and subspecies identification using DIA MS/MS coupled with PEP-TORCH**; Allen Po[1]; Bo Ning[1]; Jia Fan[1]; *[1]Tulane University, New Orleans, LA*

ThP 593 **Bridging Drug Sensitivity and Resistance: Elucidating MET-HER3 Crosstalk Through Phosphoproteomics and Proximity Labeling**; Morgan A Payne[1]; Jaime Schneider[2, 3, 4]; Yutong Dai[3]; Jinpeng Chen[3]; Summer Helvey[1]; Brandon M Gassaway[1, 5]; *[1]Brigham Young University, Provo, UT; [2]Dana-Farber Cancer Institute, Boston, MA; [3]Harvard Medical School, Boston, MA; [4]Mass General Brigham, Boston, MA; [5]Harvard University, Boston, MA*

ThP 594 **LFQ proteomics and hydrodynamic size-based fractionation of human synovial fluid enabled the discovery of biomarkers of protein aggregates in arthritis**; Cristina C Clement[1]; Barbara Roda[2]; Valentina Marassi[2]; *[1]Weill Cornell Medicine, New York, NY; [2]Department of Chemistry G. Ciamician, University of Bologna, Bologna, Italy*

ThP 595 **Proteomic Profiling of Inflammation-Associated Proteins in an Inflammatory Bowel Disease Model**; Michelle Hayunga[1]; William Lafon[1]; Saiful M Chowdhury[1]; *[1]University of Texas At Arlington, Arlington, TX*

ThP 596 **A Time-Course Analysis of the Normal Mesothelial Cell Secretome via Mass Spectrometry**; Rachel L Watkin[1]; Jennifer R Damicis[1]; Avedis A Kazanjian[1]; Elizabeth Yohannes[1]; *[1]DHA, MADIGAN Army Medical Center, Tacoma, WA*

ThP 597 **Divergent Proteomic Landscapes Underlying Lethal and Neuropathic Phenotypes in SCO2-Related Mitochondrial Disorders**; Anastasia Alexandridou[1]; Andreas Hentschel[1]; Andrea Gangfuss[2]; Ulrike Schara-Schmidt[2]; Andreas Roos[2, 3, 4, 5]; Albert Sickmann[1, 6]; *[1]ISAS, Dortmund, Germany; [2]University of Duisburg-Essen, Essen, Germany; [3]Heinrich Heine University Düsseldorf, Düsseldorf, Germany; [4]Ruhr University Bochum, Bochum, Germany; [5]University of Ottawa, Ottawa, ON; [6]Ruhr Universität Bochum, Bochum, Germany*

ThP 598 **A Scalable Skyline-based Targeted Proteomics Workflow for Profiling Plasma Protein Changes in Non-Arteritic Anterior Ischemic Optic Neuropathy (NAION)**; Mengying Fu[1]; Linfeng Wu[2]; Anas Alkhabaz[1]; Yaping Joyce Liao[1]; Yuqin Dai[1]; *[1]Stanford University, Stanford, CA; [2]Agilent Technologies, Santa Clara, CA*

ThP 599 **Development of a nanoHPLC-HRMS-based method for the proteomic profiling of biological samples of patients with endometriosis**; Rafael López Romero[1]; Serena Arpaia[1]; Andrea Magnani[1]; Eleonora Robba[1]; Stefano Domenico Cosma[1]; Federica Dal Bello[1]; *[1]Università degli Studi di Torino, Turin, Italy*

ThP 600 **Peptide level mapping of mouse plasma apolipoproteins using data independent acquisition mass spectrometry**; Mahmoud Elhusseiny Mostafa[1]; Constance Delwarde[1]; Taku Tasaki[1]; Yuto Nakamura[1]; Masanori Aikawa[1, 2, 3]; Sasha A Singh[1]; *[1]Center for Interdisciplinary Cardiovascular Sciences, Division of Cardiovascular Medicine, Department of Medicine, Brigham Women's Hospital, Harvard Medical School, Boston, MA; [2]Center for Excellence in Vascular Biology, Division of Cardiovascular Medicine, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, MA; [3]Channing Division of Network Medicine, Department of Medicine, Brigham Women's Hospital, Harvard Medical School, Boston, MA*

ThP 601 **Arachidonic Acid Supplementation Alleviates Cognitive Impairment Associated with Organophosphate Exposure and Pre-Diabetes**; Ronny M Barrera[1]; Vishal Sandilya[1]; Rowan E Arida[2, 3]; Sherifdeen B. Onigbinde[1]; Sarah Sahioun[1]; Favour Chukwubueze[1]; Hadi Al Sheikh[1]; Heba-Tallah Abd El-Rahim Abd Elkader[2]; Salwa A Abuiessa[2]; Mahmoud Agami[3]; Mai M. Helmy[2]; Ahmed F. El-Yazbi[2, 3]; Yehia Mechref[1]; *[1]Texas Tech University, Lubbock, TX; [2]Alexandria University, Alexandria, Egypt; [3]Alamein International University, Alamein, Egypt*

ThP 602 **Development and qualification of an ultra-sensitive SISCAPA-MS assay for UBE3A quantification in human CSF for Angelman Syndromeresearch**; Luca Räss[1]; Simonas Savickas[1]; Richard Yip[2]; Andrew Hettle[2]; Allyson Berent[3]; Jennifer Panagoulias[3]; Leigh Anderson[2]; Terry Pearson[2]; Demet Kekilli-Kuzma[1]; Maik Müller[1]; Erik Baier[4]; Yuehan Feng[1]; Jakob Vowinckel[1]; Roland Bruderer[1]; Morteza Razavi[2]; *[1]Biognosys AG, Schlieren, Switzerland; [2]SISCAPA Assay Technologies Inc., Washington, DC; [3]Foundation for Angelman Syndrome Therapeutics (FAST), Austin, TX; [4]Biognosys Inc., Newton, MA*

ThP 603 **CD14 Blockade Modulates Toll-Like Receptor Signaling in Renal Ischemia-Reperfusion Injury: Insights from Proteomics with Translational Relevance**; Stephanie Almeida[1]; Alana Hawkes[2]; Juliana de S. da G. Fischer[1]; Blake Tsu[1]; Paulo Costa Carvalho[1, 3]; Isabelle Luz[1]; Alysson R. Muotri[1]; Dianne McKay[2]; Aline Martins[1]; *[1]Integrated Space Stem Cell Orbital Research, San Diego, CA; [2]Scripps Research Institute, La Jolla, CA; [3]FIOCRUZ, Carlos Chagas Institute, Curitiba, Brazil*

ThP 604 **Distinct Proteomic Stoichiometry of Electronegative L5 and H5 Reveals Shared Pathogenic Signatures and Divergent ApoA1 Remodeling**; Ching-Hsun Wang[1]; Sin-Hong Lew[1]; Wen-Li Hsu[2]; Chu-Huang Chen[3]; Ming-Hsien Tsai[1]; *[1]Health Resource Technology, LLC, Kaohsiung City, Taiwan; [2]National Health Research Institutes, Zhunan, Taiwan; [3]The Texas Heart Institute at Baylor College of Medicine, Houston, TX*

ThP 605 **Proteomics-Driven Discovery of SPARC as a Diagnostic Biomarker and WEE1 as a Therapeutic Target in Uterine Leiomyosarcoma**; Yani Gu[1, 2]; Renjun Zhang[1, 2]; Siyuan Wang[1]; Catherine CL Wong[1]; *[1]Peking Union Medical College Hospital, Beijing, China; [2]Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China*

ThP 606 **Nanotrap PEAK Enrichment Enables Deep and Reproducible Proteomic Analysis of Synovial Fluid**; Patrick Acer[1]; Ben Lepene[1]; Lauren Saunders[1]; Lauren Dixon[2]; Gabriela Grigorean[2]; *[1]Ceres Nanosciences, Manassas, VA; [2]UC Davis, Davis, CA*

ThP 607 **AI-Accelerated Acoustic FFPE Proteomics Identifies ATP5IF1-Linked Mitochondrial Remodeling as a Defining Feature of Acral Melanoma**; Peter Horvatovich[1]; Diana Lashidua Fernandez-Coto[2]; Marisol Ayala[3]; Ramiro Alonso[2]; Alicia Palmqvist[3]; Henriett Oskolas[3]; Lukas Christersson[3]; Livia Fulöp[4]; Balazs Szigeti[4]; Matilda Marko-Varga[3]; Johan Malm[3]; Leticia Szadai[3, 5]; Roberto Herrera-Goepfert[6]; Attila Marcell Szasz[7]; Sergio Encarnación-Guevara[2]; György Marko-Varga[3, 8, 9]; Jeovanis Gil[3]; *[1]University of Groningen, Groningen, Netherlands; [2]Center for Genomic Sciences, National Autonomous University of Mexico, Cuernavaca, Mexico; [3]Department of Translational Medicine, Lund University, Lund, Sweden; [4]Deptartment of Pathology, National Koranyi Institute of Pulmonology, Budapest, Hungary; [5]Department of Dermatology and Allergology, Albert Szent-Györgyi Medical School, University of Szeged, Szeged, Hungary; [6]Surgical Pathology Department, Instituto Nacional de Cancerología, Mexico City, Mexico; [7]Department of Internal Medicine and Oncology, Semmelweis University, Budapest, Hungary;*

[8]Department of Biotechnology, College of Life Science and Biotechnology, Yonsei University, Seoul, South Korea; [9]1st Department of Surgery, Tokyo Medical University, Tokyo, Japan

ThP 608 **MS-based proteomic analysis shows PTGR2 inhibition improves insulin sensitivity through endogenous PPARγ activation**; Fu-An Li[1]; Ling Hui Wang[1]; *[1]Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan*

ThP 609 **Integrated Multi-platform Proteomics Defines Progression-associated Immune Signatures and an Immune-Axonal Regulatory Axis in Amyotrophic Lateral Sclerosis (ALS)**; Xueying Yang[1, 2]; Yani Gu[2]; Siyuan Wang[2]; Lei Cai[3]; Hao Zhang[4, 5, 6]; Catherine C.L. Wong[1, 2]; *[1]Tsinghua-Peking Center for Life Sciences, School of Medicine, Tsinghua University, Beijing, China; [2]State Key Laboratory for Complex, Severe and Rare Diseases, Peking Union Medical College Hospital, Chinese Academy of Medical Science & Peking Union Medical College, Beijing, China; [3]AskhelpU ALS Patient Platform, Beijing, China; [4]Department of Neurology, Affiliated Hangzhou First People's Hospital, School of Medicine, Westlake University, Hangzhou, China; [5]Motor Neuron Disease Diagnosis and Treatment Center, Affiliated Hangzhou First People's Hospital, School of Medicine, Westlake University, Hangzhou, China; [6]Department of Neurology, The Fourth School of Clinical Medicine, Zhejiang Chinese Medical University, Hangzhou First People's Hospital, Hangzhou, China*

ThP 610 **Identification of Longitudinal Plasma Protein Signatures Driving Sarcopenia Progression**; Gyuri Park[1, 2, 3]; Hong-Beom Park[2, 3, 4]; Minhyeok Kang[1, 2, 3]; Yerin Kim[1, 2, 3]; Eunseo Kim[2, 3, 4]; Jin Lee[2, 3, 4]; Jiho Lee[2, 3]; Woosol Chris Hong[2, 3]; Jiyeon Choi[2, 3]; Yiseo Rho[1, 2, 3]; Ok Hee Jeon[5]; Ji Yeon Kim[5]; Jinhee Kim[6]; Seung Shin Park[7]; Hak Chul Chang[8, 9]; Chang Won Won[10, 11]; Miji Kim[12]; Sung Hye Kong[8, 9]; Dohyun Han[2, 3]; *[1]Molecular Medicine and Biopharmaceutical Sciences, WCU Graduate School of Convergence Science and Technology Seoul National University, Seoul, South Korea; [2]Proteomics and metabolomics core facility, Biomedical Research Institute, Seoul National University Hospital, Seoul, South Korea; [3]Department of transdisciplinary medicine, Seoul National University Hospital, Seoul, South Korea; [4]Department of Biomedical Sciences, College of Medicine, Seoul National University, Seoul, South Korea; [5]Department of Biomedical Sciences, Korea University College of Medicine, Seoul, South Korea; [6]Departmet of Preventive Medicine and Public Health, Ajou University School of Medicine, Seoul, South Korea; [7]Department of Internal Medicine, Seoul National University Hospital, Seoul, South Korea; [8]Department of Internal Medicine, Seoul National University Bundang Hospital, Seongnam, South Korea; [9]Department of Internal Medicine, Seoul National University College of Medicine, Seoul, South Korea; [10]Departmet of Family Medicine, Kyung Hee University Medical Center, Seoul, South Korea; [11]Elderly Frailty Research Center, Department of Family Medicine, College of Medicine, Kyung Hee University, Seoul, South Korea; [12]Departmet of Health Sciences and Technology, College of Medicine, Kyung Hee University, Seoul, South Korea*

ThP 611 **Fast and deep proteome profiling with the SCIEX ZenoTOF 8600 mass system**; Feixuan Wu[1]; Haiyan Lu[1]; Patrick Pribil[2]; Ihor Batruch[2]; Sahana Mollah[2]; Tatjana Talamantes[2]; Paul RS Baker[2]; Zoe Zhang[2]; Elliott Jone[2]; Amanda Souza[2]; Remco Vansoest[2]; Lingjun Li[1, 3, 4]; *[1]School of Pharmacy, University of Wisconsin-Madison, Madison, WI, Madison, WI; [2]SCIEX, Redwood City, CA; [3]Department of Chemistry, University of Wisconsin-Madison, Madison, Wisconsin 53706, USA., Madison, WI; [4]Biophysics Program, University of Wisconsin-Madison, Madison, WI*

ThP 612 **Deep Temporal Phosphoproteomic Profiling of LPS-Stimulated iBMDMs using Data-Independent Acquisition**; Doeun Kim[1]; Sung Hwan Yoon[1]; Aleksandra Nita-Lazar[1]; *[1]National Institutes of Health, Bethesda, MD*

ThP 613 **High-throughput drug screening combined with Proteome Integral Solubility Alteration defines mechanisms of action for novel antifungal compounds against Cryptococcus neoformans**; Michael J P Woods[1]; Davier Gutierrez-gongora[1]; Mary Adofo[1]; Chelsea Reitzel[1]; Jason A McAlister[1]; Jonathan Sayewich[2]; Jared Deyarmin[3]; Stephanie N. Samra[3]; J Patrick Murphy[4]; Jennifer Geddes-McAlister[1]; *[1]University of Guelph, Guelph, ON; [2]SPARC Drug Discovery Centre, Hospital for Sick Children, Toronto, ON; [3]Thermo Fisher Scientific, San Jose, CA; [4]University of Prince Edward Island, Charlottetown, PE*

ThP 614 **Blood Feeding Triggers the Terminal Differentiation of Precursor Cells in Tick Salivary Glands**; Sazzad Mahmood[1]; Stephen Lu[2]; Ana Beatriz Barletta Ferreira[3]; Markus Berger[2, 4]; Oladele Oluwayiose[5]; Christine Schneider[6]; Jacqueline Leung[7]; Melina Guizzo[8]; Yixiang Zhang[9]; Randall Johnson[10, 11]; Kevin

Cormier[10, 11]; Motoshi Suzuki[10]; Nathan Brandes[9]; Gwendolyn Cooper[9]; Joshua Gold[9]; Benjamin Schwarz[9]; Lisa Olano[10]; Justin Jack[5]; Carolina Barillas-Mury[3]; José Ribeiro[8]; Lucas Tirloni[1]; *[1]Tick-Pathogen Transmission Unit, Laboratory of Bacteriology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, hamilton, MT; [2]Tick-Pathogen Transmission Unit, Laboratory of Bacteriology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, Hamilton, MT, USA, hamilton, MT; [3]Mosquito Immunity and Vector Competence Section, Laboratory of Malaria and Vector Research, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, Rockville, MD; [4]Centro de Pesquisa Experimental, Hospital de Clínicas de Porto Alegre (HCPA), Universidade Federal do Rio Grande do Sul (UFRGS), Porto Alegre, Brazil; [5]Integrated Data Sciences Section, Research Technologies Branch, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD; [6]Electron Microscopy Unit, Research Technologies Branch, Division of Intramural Research National Institute of Allergy and Infectious Diseases, National Institutes of Health, hamilton, MT; [7]Electron Microscopy Unit, Research Technologies Branch, Division of Intramural Research National Institute of Allergy and Infectious Diseases, hamilton, MT; [8]Vector Biology Section, Laboratory of Malaria and Vector Research, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD; [9]Proteins & Chemistry Section, Research Technologies Branch, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, hamilton, MT; [10]Proteins & Chemistry Section, Research Technologies Branch, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health,, Rockville, MD; [11]Integrated Data Sciences Section, Research Technologies Branch, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, Rockville, MD*

ThP 615 **Spatially guided nanoscale proteomics for direct detection of microbial proteins in host tissues**; Kenneth Weke[1]; Angela Jackson[1]; Hope Maron[2]; Darryl Hardie[1]; Alexandre Giraud-Gatineau[3]; Mathieu Picardeau[3]; David R. Goodlett[1, 2]; Helena Pětrošová[1]; *[1]UVic Genome BC Proteomics Centre, Victoria, BC; [2]Biochemistry & Microbiology, University of Victoria, Victoria, BC; [3]Institut Pasteur, Paris, France*

ThP 616 **Proteomics reveals brilacidin's antifungal mechanisms in Cryptococcus species**; Barbara T. Bezerra[1]; Daniel A. Mellón[1]; Cássia M. Souza[1]; Rafael F. Castelli[1]; Amanda Caroline Camillo De Andrade[1]; Marlon Dias Mariano Dos Santos[1, 2]; Paulo C Carvalho[1]; Marcio L. Rodrigues[1, 3]; Haroldo C. De Oliveira[1, 4]; *[1]Carlos Chagas Institute, Fiocruz Paraná, Curitiba, Brazil; [2]Analytical Biochemistry and Proteomics Unit, Instituto de Investigaciones Biológicas Clemente Estable, Institut Pasteur de Montevideo, Montevideo, Uruguay; [3]Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil; [4]Department of Microbiology, Immunology, and Parasitology, Discipline of Cellular Biology, Federal University of Sao Paulo, São Paulo, Brazil*

ThP 617 **Stress-induced Remodeling of the Translatome and Ribosome Composition in Leishmania**; Cristian Rodríguez-Almonacid[1]; Christian Bustamante[1]; Elena Tikhonova[1]; Sammy Pardo[2]; Dana Molleur[2]; Andrey Karamyshev[1]; Susan T. Weintraub[2]; Zemfira Karamysheva[1]; *[1]Texas Tech University Health Sciences Center, Lubbock, TX; [2]University of Texas Health Science Center at San Antonio, San Antonio, TX*

ThP 618 **Finding a Needle in a Haystack: Untargeted Discovery of Microorganisms in Complex Metaproteomes**; Nicholas Bollis[1]; Yanjia Zhang[2]; Michael R. Shortreed[3]; Aaron T. Timperman[2]; Lloyd M Smith[3]; *[1]University of Wisconsin Madison, Madison, WI; [2]University of Pennsylvania, Philadelphia, PA; [3]University of Wisconsin--Madison, Madison, WI*

ThP 619 **Longitudinal whole-blood proteomics reveals persistent expression of ISG-15 following recovery from COVID-19 infection**; Sarah M. Shapley[1]; Youwei Chen[2]; Patty J. Lee[3]; Coral X. Giovacchini[2]; David J. Shaz[2]; Lingye Chen[2]; A Ian Wong[2]; Timothy J. McMahon[2]; Loretta G. Que[2]; Matthew W. Foster[1, 2]; *[1]Proteomics and Metabolomics Core Facility, Duke University School of Medicine, Durham, NC; [2]Division of Pulmonary, Allergy and Critical Care Medicine, Duke University School of Medicine, Durham, NC; [3]Division of Pulmonary, Critical Care, and Sleep Medicine, Icahn School of Medicine at Mount Sinai, New York City, NY, United States, New York City, NC, United States, New York City, NY*

ThP 620 **An AI Framework for Antiviral Discovery Through the Analysis of Dynamic Protein-Protein Interaction Networks and Comparative Virology**; Tavis J Reed[1]; Olga Troyanskaya[1, 2]; Ileana Cristea[1]; *[1]Princeton University, Princeton, NJ; [2]Flatiron Institute, New York City, NY*

THURSDAY MORNING ORALS

ThP 621 **Comparative Proteomics Reveals Divergent Antiviral Landscapes Controlling Ebola Virus Replication**; Jyothirmai Simhadri[1]; Andrey Ivanov[1]; Bersabeh Tigabu[2]; Namita Kumari[1]; Colette Pietzsch[2]; Xionghao Lin[1]; Alexander Bukreyev[2]; Sergei Nekhai[1]; *[1]Howard University, Washington, DC; [2]University of Texas Medical Branch, Galveston, TX*

ThP 622 **Determining the Impact of RNA Replication on Host Proteome Dynamics**; Alyssa Cruz[1]; Joseph A Loo[1]; William Gelbart[1]; Yu Chen[1]; *[1]University of California, Los Angeles, Los Angeles, CA*

ThP 623 **Proteomics-integrated characterization of the mitochondrial electron transport chain as a putative antifungal target in the fungal pathogen Cryptococcus neoformans**; Matthew Rennie[1]; Brianna Ball[1]; Norris Chan[1]; Michael Woods[1]; J Patrick Murphy[2]; Jonathan Sayewich[3]; Chris Fladd[3]; Jared Deyarmin[4]; Stephanie N. Samra[4]; Jennifer Geddes-McAlister[1]; *[1]University of Guelph, Guelph, ON; [2]University of Prince Edward Island, Charlottetown, PE; [3]SickKids SPARC BioCentre, Toronto, ON; [4]Thermo Fisher Scientific, San Jose, CA*

ThP 624 **A quantitative cross-species atlas of alphavirus protein phosphorylation across host cell types**; Declan Winters[1]; Erin Kim[1]; Justin Selby[2]; Evan Wynn[1]; Valerie Vandersall[1]; Pablo Alvarez[1]; Sara Makanani[1]; Kristen Zarella[3]; Prashant Kaushal[1, 4]; Thomas E Morrison[3]; Suchetana Mukhopadhyay[5]; Melody MH Li[1]; Mehdi Bouhaddou[1]; *[1]UCLA, Los Angeles; [2]UCLA, LOS ANGELES, CA; [3]University of Colorado Anschutz Medical Campus, Aurora, CO; [4]Washington University School of Medicine, St. Louis, MO; [5]Indiana University, Bloomington*

ThP 625 **Host Protein Turnover Dynamics and PTM Crosstalk in Macrophages During Salmonella Typhimurium Infection**; Sandhini Saha[1]; Aleksandra Nita-Lazar[1]; *[1]NIH/NIAID, Bethesda, MD*

ThP 626 **Seceretome analysis and global proteomic investigation of the macrophage response to toll-like receptor 4 stimulation using lipid A variants**; Sung Hwan Yoon[1]; Doeun Kim[1]; Hyojik Yang[2]; Robert K Ernst[2]; Aleksandra Nita-Lazar[1]; *[1]NIH/NIAID, Bethesda, MD; [2]University of Maryland Baltimore, Baltimore, MD*

ThP 627 **Proteolytic Mapping of Bacteriophages E215, LUZ19, and PYO2 Using Liquid Chromatography Tandem Mass Spectrometry**; Connor E. Gould[1]; Alhaji Simon Ekere[1]; Thomas D. Nguyen[1]; Jacob T. Sanborn[1]; Liang Chen[1]; Dwayne R. Roach[2]; Troy D Wood[1]; Nicholas M. Smith[1]; *[1]University at Buffalo, Buffalo, NY; [2]San Diego State University, San Diego, CA*

ThP 628 **Subcellular-Temporal Proteomics Reveals Receptor-Specific Spatial Signaling Programs in Activated Macrophages**; Vanya Bhushan[1]; Aleksandra Nita-Lazar[1]; *[1]National Institutes of Health, Bethesda, MD*

ThP 629 **DIA LC-MS Reveals Inducible Proteome Adaptations in a Voriconazole-resistant Aspergillus fumigatus Strain Lacking cyp51A Mutations**; Catalina Avendano[1]; Daniel Röth[1]; Lotus Lofgren[2, 3]; Sanjeet Dadwal[1]; Jason E Stajich[2]; Markus Kalkum[1]; *[1]City of Hope, Duarte, CA; [2]Department of Microbiology and Plant Pathology, University of California at Riverside, Riverside, CA; [3]University of California, Berkeley, Berkeley, CA*

ThP 630 **Using the miniTurbo Biotinylation Pull-Down Strategy to Investigate Protein-protein Interaction in the Lyme Disease Agent Borrelia burgdorferi**; Declan Houlihan[1]; Cooper D. Wilkinson[1]; Adam Slamin[1]; Mynaja Fergusson[2]; Jason J. Evans[3]; Constantin Nicolae Takacs[1]; *[1]Northeastern University, Boston, MA; [2]University of Massachusetts Boston, Dorchester, MA; [3]University of Massachusetts Boston, Boston, MA*

ThP 631 **Mass spectrometry enabled discovery of viral entry receptors using Molecular Clamp2 for rapid response vaccine development**; Elsje Ferreira[1]; Noushin Jaberolansar[1]; Jake S O'Donnell[1, 2]; Nicolas Tardiota[1]; Diego Pilati[1]; Connor Scott[2]; Varsha Kommajosyula[1]; Mikaela Bell[1]; Rhiannon Dalrymple[1]; Martina Jones[1]; Courtney McAleese[1]; Kym Hoger[1]; Justin Goh[1]; Alexsander Pinder[1]; Karen Hughes[1]; Benjamin Hughes[1]; Daniel Watterson[2, 3]; Benjamin Schulz[2]; Keith J Chappell[1, 2, 3, 4]; *[1]The Australian Institute for Bioengineering and Nanotechnology, The University of Queensland, Brisbane, Australia; [2]The School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Australia;*

[3]*Vicebio, Adelaide, Australia;* [4]*Australian Infectious Disease Research Centre, The University of Queensland, Brisbane, Australia*

ThP 632 **First SaD then HAPPY: Towards blood serum antibody analysis from dried serum spots with ITEM-SIX mass spectrometry**; Mihaela Tanas[1]; Manuela Russ[2]; Cornelia Koy[2]; Charles A Okai[3]; Kwabena F.M. Opuni[4]; Lucian Hritcu[1]; Michael O. Glocker[2]; [1]*Faculty of Biology, Laboratory of Animal Physiology, Alexandru Ioan Cuza University of Iasi, Iasi, Romania;* [2]*Proteome Center Rostock, Rostock, Germany;* [3]*Department of Laboratory Technology, Faculty of Health Sciences, Kumasi Technical University, Kumasi, Ghana;* [4]*Department of Pharmaceutical Chemistry, School of Pharmacy, College of Health Science, University of Ghana, Legon, Ghana*

ThP 633 **Simultaneous Characterization of Intact Proteins and Polar Metabolites From a Single Extraction Using Hydrophilic Interaction Liquid Chromatography Mass Spectrometry**; Helena Rittenhouse[1]; Owen S. Skinner[1]; [1]*Northeastern University, Boston, MA*

ThP 634 **Resolving the Complex Human Proteome by Gel Prefractionation and Photocleavable Surfactant–Enabled Top-Down Proteomics**; Hsin-Ju Chan[1]; Isabella R. Clemmer[1]; Wangqin Ge[2]; Holden T. Rogers[1]; Zhan Gao[3]; Matthew S. Fischer[1]; Ying Ge[1, 3, 4]; [1]*Department of Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*Department of Biochemistry, University of Wisconsin-Madison, Madison, WI;* [3]*Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI;* [4]*School of Medicine and Public Health, University of Wisconsin-Madison, Madison, WI*

ThP 635 **Structural and Functional Insights into Aging Heart Proteoforms via Methionine Oxidation Footprinting in Intact Proteins**; Anju Teresa Sunny[1]; Kellye A. Cupp-Sutton[1]; Patrycja Szamweber[1]; Weronika Zarzycka[2]; Ying Ann Chiao[2]; Si Wu[1]; [1]*University of Alabama, Tuscaloosa, AL;* [2]*Oklahoma Medical Reserach Foundation, OMRF, Oklahoma City, OK*

ThP 636 **High-Sensitivity Top-Down Proteomics of Phospholamban Proteoforms from Biopsy-Equivalent Cardiac Tissue**; Isabella R Clemmer[1]; Holden T. Rogers[1]; Zhan Gao[2]; Mallory C Wilson[1]; Ying Ge[1, 2]; [1]*Department of Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI*

ThP 637 **MOF-Enabled Selective Depletion of Abundant Plasma Proteins for Native Top-Down MS**; Kwame Osei[1]; Hsin-Ju Chan[1]; Matthew S Fischer[1]; Emily A Reasoner[2]; Shravani Goel[1]; Song Jin[1]; Ying Ge[1, 3, 4]; [1]*Department of Chemistry, University of Wisconsin-Madison, Madison, WI;* [2]*Department of Chemistry, University of Wisconsin-Madison., Madison, WI;* [3]*Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI;* [4]*Human Proteomics Program, School of Medicine and Public Health, University of Wisconsin-Madison, Madison, WI*

ThP 638 **High-flow method development for high-throughput top-down proteomics**; Purvi Saxena[1]; Owen S. Skinner[2]; [1]*Northeastern University, Boston, MA;* [2]*Chemistry and chemical biology, Northeastern University, Boston, MA*

ThP 639 **Top-down Proteomics of Bronchoalveolar Lavage Fluid**; Anna G Towler[1]; Zhan Gao[2]; Rob L Gearhart[1]; Matthew S Fischer[1]; Andrew J Perciaccante[1]; Kwame Osei[1]; Hsin-Ju Chan[1]; Yanlong Zhu[3]; Carole L Wilson[4, 5]; Lynn M Schnapp[4, 5]; Ying Ge[1, 2, 3]; [1]*Department of Chemistry, University of Wisconsin−Madison, Madison, WI;* [2]*Department of Cell and Regenerative Biology, University of Wisconsin-Madison, Madison, WI;* [3]*Human Proteomics Program, School of Medicine and Public Health, University of Wisconsin-Madison, Madison, Wisconsin 53705, USA., Madison, WI;* [4]*Pulmonary and Critical Care Medicine, University of Wisconsin-Madison, Madison, WI;* [5]*Department of Medicine, University of Wisconsin-Madison, Madison, WI*

ThP 640 **Specific and efficient native top-down MS3 of proteins in tissues using synchronous precursor selection and photoactivation.**; Oliver J. Hale[1]; Helen J. Cooper[1]; [1]*University of Birmingham, Birmingham, United Kingdom*

ThP 641 **Comprehensive characterization of diverse antibody formats using top-down fragmentation on the timsOmni: CDR sequencing, quality control, and structural analysis**; Iuliia Stroganova[1, 2]; Simon Ollivier[1, 2, 3]; Athanasios Smyrnakis[4]; Maria-Aggeliki Kosmopoulou[4]; Jean-François Greisch[5]; Dimitris

Papanastasiou[4]; Albert J.R. Heck[1, 2]; [1]*Biomolecular Mass Spectrometry and Proteomics, Bijvoet Centre for Biomolecular Research and Utrecht Institute for Pharmaceutical Sciences, Utrecht University, Utrecht, Netherlands;* [2]*Netherlands Proteomics Center, Utrecht, Netherlands;* [3]*Univ Rouen Normandie, Rouen, France;* [4]*Fasmatech Science & Technology, Chalandri, Greece;* [5]*Bruker Switzerland AG, Fällanden, Switzerland*

ThP 642 **Capillary Electrophoresis–Mass Spectrometry Enabling Charge Detection Top-Down Analysis**; Ke Ma[1]; James Xia[2]; Yuqi Shi[1]; Jia Tang[3]; Weijing Liu[3]; [1]*Thermo Fisher Scientfic, San Jose, CA;* [2]*CMP Scientific Corp, Brooklyn, NY;* [3]*Thermo Fisher Scientific, San Jose, CA*

ThP 643 **Top-down proteomics driven by high-sensitivity CID and EAD MS/MS fragmentation**; Remco van Soest[1]; Richard M. Searfoss[2]; Benjamin A. Garcia[2]; Patrick Pribil[3]; [1]*SCIEX, Redwood City, CA;* [2]*Dept. of Biochemistry and Molecular Biophysics, Washington University School of Medicine, Saint Louis, MO;* [3]*SCIEX, Concord, ON*

ThP 644 **High-Accuracy Single-Molecule Quantification of Tau Proteoforms across Isoforms and Phosphorylation States**; Andreas FR Huhmer[1]; Zhengjiang Zhang[1]; James Joly[1]; Vivek Budamagunta[1]; Brittany Nortman[1]; Shafraz Shafraz[1]; Katie Winters[1]; Hannah Lee[1]; Maryam Jouzi[1]; Sonal Tonapi[1]; Nicholas Devanney[2]; Samah Shah[2]; Joanna Bons[2]; Jamie Kuhar[1]; Lisa M Ellerby[2]; Birgit Schilling[2]; Kara Juneau[1]; Parag Mallick[1]; [1]*Nautilus Biotechnology, San Carlos, CA;* [2]*Buck Institute for Research on Aging, Novato, CA*

ThP 645 **Location, Location, Location…Native Top-Down Mass Spectrometry Provides Binding Site Information for Protein-Ligand and Protein-Protein Interactions**; Athanasios Smyrnakis[1]; Maria-Aggeliki Kosmopoulou[1]; Dimitris Papanastasiou[1]; Michael Greig[2]; Isin Sakallioglu[3]; Matthew Kensil[4]; Joseph A. Loo[4]; [1]*Fasmatech Science & Technology, Chalandri, Greece;* [2]*Bruker Scientific LLC, San Jose, CA;* [3]*Bruker Scientific LLC, Billerica, MA;* [4]*UCLA, Los Angeles, CA*

ThP 646 **Prevalent Thiol Radical Loss in Top-Down Electron Capture and Transfer Dissociation: Implications for Fragment Ion Annotation**; Marek Polak[1]; Lissa C Anderson[1, 2]; Steven A DeFiglia[1, 2]; Chad R. Weisbrod[1]; Kristina Hakansson[1, 2]; [1]*Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, Tallahassee, FL;* [2]*Department of Chemistry and Biochemistry, Florida State University, Tallahassee, FL*

ThP 647 **Robust Proteoform-Resolved Mapping of Endogenous p53 with Dynamic Modifications under Cellular Stress via Top-down Individual Ion Mass Spectrometry**; Jared Kafader[1]; Raveena Gupta[1]; Taojungeng Su[1]; Nickolas Fisher[1]; Philip Compton[2]; Neil L Kelleher[1]; [1]*Northwestern University, Evanston, IL;* [2]*Integrated Protein Technologies, Carlsbad, CA*

ThP 648 **Next Generation Top-Down Proteomics: FLASHIda:Refine Enables Deep Real-Time Proteoform Characterization using Intelligent Multi-Stage MSnAcquisition**; Tom D Müller[1, 2]; Philipp T Kaulich[3]; Oliver Kohlbacher[2, 4, 5]; Andreas Tholey[3]; Kyowon Jeong[2, 4]; [1]*University of Tübingen, Tübingen, Germany;* [2]*Institute for Bioinformatics and Medical Informatics, University of Tubingen, Tubingen, Germany;* [3]*Systematic Proteome Research & Bioanalytics, Institute for Experimental Medicine, Christian-Albrechts-Universität zu Kiel, Kiel, Germany;* [4]*University of Tuebingen, Tuebingen, Germany;* [5]*Translational Bioinformatics, University Hospital Tübingen, Tübingen, Germany*

ThP 649 **Filling the gaps: multi-experiment de novo tag integration for confident top-down protein characterization in OmniScape**; George Alevizos[1]; Mariangela Kosmopoulou[1]; Georgia Orfanoudaki[1]; Detlev Suckau[2]; Athanasios Smyrnakis[1]; Liliane Soares[3]; Dimitris Papanastasiou[1]; [1]*Fasmatech Science & Technology, Chalandri, Greece;* [2]*Bruker Daltonics GmbH & Co KG, Bremen, Germany;* [3]*Bruker, San Diego, CA*

ThP 650 **A New Software Workflow for Automating Top-Down Proteoform Characterization**; Joseph B Greer[1]; Matthew T Robey[1]; Jacob W McCabe[1]; Abdul R Basharat[1]; Ryan T Fellers[1]; Kenneth R Durbin[1]; [1]*Proteinaceous, Evanston, IL*

ThP 651 **Improved characterization of high molecular weight proteoforms via targeted PTCR using IR photon-assisted fragmentation methods**; Jake T Kline[1]; Jingjing Huang[2]; Christopher Mullen[2]; Andreia

Almeida[3]; Joseph Greer[4]; Kenneth R Durbin[4]; Luca Fornelli[1]; *[1]University of Oklahoma, Norman, OK; [2]Thermo Fisher Scientific, San Jose, CA; [3]IonOpticks, Melbourne, Australia; [4]Proteinaceous, Evanston, IL*

ThP 652 **Toward Database-Independent DIA Top-Down Proteomics via Natural Log-Space Mass Difference Networks**; Lissa C. Anderson[1, 2]; Chad R. Weisbrod[1]; Noor Mohammad Talukder[3]; Greg T. Blakney[1]; Nathan K. Kaiser[1]; Xian Mallory[3]; *[1]NHMFL-FSU, Tallahassee, FL; [2]Department of Chemistry and Biochemistry, Florida State University, Tallahassee, FL; [3]Department of Computer Science, Florida State University, Tallahassee, FL*

ThP 653 **Top-Down Mass Spectrometry identifies complementary hits to proteomics for the identification of polyclonal UniAbs from UniRat serum**; Elizabeth Hecht[1]; Trishika Chowdhury[2]; Alexandr Baryshev[3]; Anthony Tang[3]; Tian Tian[1]; Emma Pelegri O'Day[1]; Yoan Machado Hernandez[3]; Christopher M Murawsky[3]; Iain D. G. Campuzano[4]; *[1]Amgen Inc., South San Francisco, CA; [2]University of Alabama, Tuscaloosa, AL; [3]Amgen, Inc., Burnaby, BC; [4]Amgen, Thousand Oaks, CA*

ThP 654 **Proteoform-Resolved Mapping of Soluble and Insoluble Brain Proteomes Across α-Synuclein Co-Pathologies Using Multidimensional Top-Down MS with Data-Independent Acquisition (DIA)**; Joshua B. Rubin[1]; Neil L Kelleher[1, 2]; Laura Brasseur[3]; Michael X. Henderson[3]; Steven Patrie[1]; *[1]Northwestern University, Evanston, IL; [2]Northwestern University Feinberg School of Medicine, Chicago, IL; [3]Van Andel Institute, Grand Rapids, MI*

ThP 655 **Fair Comparison of Mixed-Mass Protein Intensities in FTMS**; Konstantin Nagornov[1]; Nina Khristenko[2]; Natalia Gasilova[3]; Laure Menin[3]; Anton N. Kozhinov[1]; Yury O. Tsybin[1]; *[1]Spectroswiss, Lausanne, Switzerland; [2]Spectrotech, Lyon, France; [3]EPFL, Lausanne, Switzerland*

ThP 656 **An Integrated Data-Driven Acquisition Pipeline for Maximizing Intact Protein Characterization**; Abdul Rehman Basharat[1]; Troy D Fisher[2]; Michael A R Hollas[2]; Ryan T Fellers[1]; Jacob W McCabe[1]; Joseph Greer[1]; Matthew T Robey[1]; Kenneth R Durbin[1]; *[1]Proteinaceous, Evanston, IL; [2]Northwestern University, Evanston, IL*

ThP 657 **Evaluate the Effects of DDM on Top-down Thermal Proteome Profiling of Complex Biological Samples**; Ashlyn Solenberger[1]; Trishika Chowdhury[1]; Anju Teresa Sunny[1]; Mai A. Atallah[1]; Patrycja Szamweber[1]; Kellye A. Cupp-Sutton[1]; Si Wu[1]; *[1]The University of Alabama, Tuscaloosa, AL*

ThP 658 **Waterfall Spectral Subtraction Boosts Product Ion Assignment in Top-Down Mass Spectrometry**; Nina A. Khristenko[1]; Konstantin O. Nagornov[2]; Anton N. Kozhinov[2]; David P.A. Kilgour[3]; Yury O. Tsybin[1, 2]; *[1]Spectrotech, Lyon, France; [2]Spectroswiss, Lausanne, Switzerland; [3]Vibrat-Ion, Aberystwyth, United Kingdom*

ThP 659 **Targeted multi-omics analysis of plasma samples for investigating focal segmental glomerulosclerosis and related kidney diseases**; Jake T Kline[1]; Amal M Kamal[1]; Amy K Carfagno[1]; Philip M. Remes[2]; Cristina C. Jacob[2]; Brittany Lee[2]; Lilian Heil[2]; Eleonora Forte[3]; Romain Huguet[2]; Lorenzo Gallon[3]; Luca Fornelli[1]; *[1]University of Oklahoma, Norman, OK; [2]Thermo Fisher Scientific, San Jose, CA; [3]University of Illinois, Chicago, IL*

ThP 660 **Quantitative Proteomics Reveals RNA Control of a Central Metabolic Enzyme**; Songbo Wei[1]; Yinsheng Wang[1]; *[1]UC RIVERSIDE, Riverside, CA*

ThP 661 **A Proteomic Analysis of the Mouse Retina Reveals Molecular Changes Induced by Drug Addiction**; Woojin Son[1]; Hyunjeong Jin[2]; Eunkyeoung Kim[3]; Dongyoon Shin[3, 4]; Young June Jeon[1]; Da-Yeon Lee[1]; Youngsoo Kim[4]; Heh-In Im[2]; Sangyong Jung[3]; Junho Park[3, 4]; *[1]Department of Life Sciences, CHA university, Seongnam-si, South Korea; [2]Center for Braine Function, Braine Science Institute, Korea Institute of Science and Technology, Seoul, South Korea; [3]Department of Medical Science, School of Medicine, CHA University, Seongnam-si, South Korea; [4]AI-Omics center, CHA Research Institute, Seongnam-si, South Korea*

ThP 662 **Assessing Quantification Performance in Differential Expression Workflows for Parallel Accumulation Mobility-Aligned Fragmentation (PAMAF) Data Independent Acquisition**; Liulin

Deng[1]; Isabel Uribe[1]; Leonard C. Rorrer III[1]; Lauren Royer[1]; Olga Vitek[2]; Daniel DeBord[1]; [1]*MOBILion Systems Inc., Chadds Ford, PA;* [2]*Northeastern University, Boston, MA*

ThP 663 **A Multiplexed LC-PRM-MS Method for the Quantification and Stoichiometric Determination of Protein Complex Subunits**; Jiaxi Cai[1]; Ziyi Wang[2]; Huilin Zhou[3]; Raymond T Suhandynata[4, 5]; [1]*Shu Chien-Gene Lay Department of Bioengineering, University of California San Diego, La Jolla, CA;* [2]*University of California San Diego, San Diego, CA;* [3]*Department of Cellular and Molecular Medicine East, University of California San Diego, La Jolla, CA;* [4]*Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA;* [5]*Department of Pathology, University of California San Diego, La Jolla, CA*

ThP 664 **FAIMS-PRM TIC-based total peptide quantification assay for post-acquisition PRM normalization**; Camille Lombard-Banek[1]; Ashley Frankenfield[2]; Mary Melkie[2]; Andrew Chambers[2]; Christopher Richardson[2]; David C Chain[2]; Yeoun Jin Kim[2]; Steve Sweet[2]; [1]*Astrazeneca, Gaithersburg, MD;* [2]*AstraZeneca, Gaithersburg, MD*

ThP 665 **Assessing Targeted Versus Untargeted Proteomics for Chemoproteomics Workflows Using a Sciex ZenoTOF 8600 System**; Evan E Hubbard[1]; Daniele Canzani[1]; Ihor Batruch[2]; Lyle L Burton[2]; Katherine Tran[2]; Jason Causon[2]; Tatjana Talamantes[3]; Christa Feasley[4]; Adam Campbell[4]; Elliott Jones[4]; Sebastian J Paez[1]; Alexander J Federation[1]; Lindsay K Pino[1]; [1]*Talus Bioscience, Seattle, WA;* [2]*SCIEX, Concord, ON;* [3]*SCIEX, Marlborough, MA;* [4]*SCIEX, Redwood City, CA*

ThP 666 **Exploring Toxin Pathogenesis of Human Hosts via Proteomic Analysis of Palytoxin-Exposed Multi-Organ-on-a-Chip Systems**; Gabrielle Rizzo[1]; Daniel J Angelini[1]; Priscilla E Lee[1]; Raquel L Shortt-Jackson[2]; Jana M Carpenter[2]; Paul S Demond[2]; Allison E Clay[2]; Conor C Jenkins[1]; [1]*DEVCOM Chemical Biological Center, Aberdeen Proving Ground, MD;* [2]*Precise Systems Inc., Lexington Park, MD*

ThP 667 **Multiplexed Targeted Profiling for Plasma Proteomics in a Single-Shot Adaptive Real-Time Library Search Workflow**; Thao Nguyen[1]; Niclas Olsson[1]; Fiona McAllister[1]; [1]*Calico Life Sciences, South San Francisco, CA*

ThP 668 **Quantitative Multiplexed Proteomics Using a Standalone Ion Trap**; Qi Zhang[1, 2]; Edward Cruz[2, 3]; Vyas Pujari[2, 3]; Andrea Mariossi[2, 3]; Wessley Ferguson[2, 3]; Martin Wühr[1, 2, 3]; [1]*Department of Chemical and Biological engineering, Princeton University, Princeton, NJ;* [2]*Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ;* [3]*Department of Molecular Biology, Princeton University, Princeton, NJ*

ThP 669 **Proteome of the photoreceptor outer-inner segment junction characterized by protein correlation profiling**; Nikolai P. Skiba[1]; Margaux J. Kreitman[2]; Greg Waitt[3]; Erik J. Soderblom[3]; Vadim Y. Arshavsky[2]; [1]*Department of Ophtalmology, Duke University School of Medicine, Durham, NC;* [2]*Department of Ophthalmology, Duke University School of Medicine, Durham, NC;* [3]*Proteomics and Metabolomics Core Facility, Duke University School of Medicine, Durham, NC*

ThP 670 **Comparative LC-MS/MS Proteomics Reveals Dimensionality-Driven Remodeling in PC3 and DU145 Prostate Cancer Cells**; Odunayo O. Oluokun[1]; Joy Solomon[1]; Moyinoluwa Adeniyi[1]; Amani Yehya[2]; Fatima Ghamlouche[2]; Abderrahmane Koraich[1]; Tanjina Akter Suma[1]; Firas H. Kobeissy[3]; Wassim Abou-Kheir[2]; Yehia Mechref[1]; [1]*Texas Tech University, Lubbock, TX;* [2]*American University of Beirut, Beirut, Lebanon;* [3]*Center for Neurotrauma, Multiomics & Biomarkers (CNMB) Morehouse School of Medicine, Atlanta, GA*

ThP 671 **LC-MS/MS Proteomic Characterization of Agave Fructan-Mediated Protein Regulation in Atopic Dermatitis**; Esther O. Oji[1]; Sherifdeen B. Onigbinde[1]; Eva Salinas[2]; Marcela Rios-Carlos[2]; Mojibola Fowowe[1]; Cristian D Gutierrez Reyes[1]; Yehia Mechref[1]; [1]*Texas Tech University, Lubbock, TX;* [2]*Universidad Autonoma de Aguascalientes, Aguascalientes, Mexico*

ThP 672 **NRicher™: Targeted Proteomic Enrichment, Simplified & Diversified**; Matt Kuruc[1]; Haiyan Zheng[2]; Swapan Roy[1]; [1]*Biotech Support Group LLC, Monmouth Junction, NJ;* [2]*Rutgers University, Piscataway, NJ*

ThP 673 **Phosphoproteomic Analysis of Tonic Signaling in CAR-Jurkat T Cells**; Ermioni Charalampopoulou[1]; Long Huynh[2]; Christian Zapata-Sanin[3]; Nicholas Graham[2]; *[1]University of Southern California, Los Angeles, CA; [2]USC, Los Angeles, CA; [3]California Institute of Technology, Pasadena, CA*

ThP 674 **Does Nonsense-Mediated mRNA Decay (NMD) Reshape the Proteome of Saccharomyces cerevisiae under Iron Deficient Conditions?**; Yan Hu[1]; Neda Feizi[1]; Stephnie Nwaiwu[2]; Bessie Kebaara[2]; Touradj Solouki[1]; *[1]Department of Chemistry and Biochemistry, Baylor University, Waco, TX; [2]Department of Biology, Baylor University, Waco, TX*

ThP 675 **Streamlined High-Confidence Plasma Proteomics Reveals Condition-Specific Apolipoprotein E and Fibrinogen Dynamics**; Lawrie Veale[1]; Antony Harvey[1]; Michael Georgoulopoulos[1]; Lukas Tvrdy[1]; *[1]Protein Metrics LLC, Boston, MA*

ThP 676 **Quantification Proteomics for Assessing the PUS7 Interactome**; Yu Wang[1]; Yinsheng Wang[1]; Chenjie Ma[2]; *[1]University of California, Riverside, Riverside, CA; [2]University of California, Riverside, CA*

ThP 677 **High-Precision Label-Free Quantification Enabled by a Modified Orbitrap Hybrid Mass Spectrometer**; Mikayla Shanafelt[1]; Jolene M. Duda[2]; Joshua P. Kline[1]; Amirmansoor Hakimi[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientfic, San Jose, CA*

ThP 678 **High-Resolution Nano LC–MS/MS Proteomic Profiling of Fusarium oxysporum During Early Cotton Root Interaction**; Sarah Metwally[1]; Fang Chen[1]; Mohamed Fokar[1]; Yehia Mechref[1]; *[1]Center for Biotechnology & Genomics, Texas Tech University,, Lubbock, TX*

ThP 679 **Label-Free Thermal Proteome Profiling using Orbitrap Astral DIA to Identify Metabolite-Protein Interactions**; Van Ledermann[1, 2]; Yutong Bao[3]; Katherine A. Overmyer[1, 2, 4]; Andrea Galmozzi[3]; Joshua J. Coon[1, 2, 4, 5]; *[1]Department of Biomolecular Chemistry, University of Wisconsin-Madison, Madison, WI; [2]National Center for Quantitative Biology of Complex Systems, Madison, WI; [3]Department of Medicine, University of Wisconsin-Madison, Madison, WI; [4]Morgridge Institute for Research, Madison, WI; [5]Department of Chemistry, University of Wisconsin-Madison, Madison, WI*

ThP 680 **Efficient multiplexed analysis of proteomic samples on Orbitrap Astral Zoom nLC-MS system using TMTpro 34plex mass tags**; Sergei Snovida[1]; William J Comstock[1]; Rosa Viner[1]; Eugen Damoc[2]; Bernard Delanghe[2]; Tonya Pekar Hart[3]; Dustin R Frost[4]; Amarjeet Flora[4]; Penny Jensen[4]; Bhavin Patel[4]; Ryan D Bomgarden[4]; Amirmansoor Hakimi[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, Bremen, Germany; [3]Thermo Fisher Scientfic, San Jose, CA; [4]Thermo Fisher Scientific, Rockford, IL*

ThP 681 **Distinct Proteomic Signatures of Partial PPARγ Inverse Agonists and Characterization of Subcellular Isoform-Specific Interactomes in Model Systems**; Kuang-Ting Kuo[1]; Yuanjun He[1]; Theodore Kamenecka[1]; Patrick R. Griffin[1]; *[1]The Herbert Wertheim UF Scripps Institute for Biomedical Innovation & Technology, Jupiter, FL*

ThP 682 **Acid-based proteomic profiling identifies and quantifies low-abundance proteins associated with early lactation–dependent changes in human milk**; Amit Singh[1]; Kelsey Hicks[2]; Joan Lien[3]; Jeffrey Eckert[2]; Adam Wilson[2]; Kathryn Burge[2]; Hala Chaaban[2]; Nagib Ahsan[1, 4]; *[1]Department of Chemistry and Biochemistry, University of Oklahoma, 73019, Norman, OK; [2]Department of Pediatrics, University of Oklahoma Health Sciences Centre, Oklahoma City, OK; [3]Department of Pediatrics, University of Washington, Seattle, WA; [4]Mass Spectrometry, Proteomics and Metabolomics Core Facility, Stephenson Life Sciences Research Center, University of Oklahoma, Norman, OK*

ThP 683 **High coverage and accuracy in label-free proteomics using an OptiSpray Ion Source on the Orbitrap Excedion Pro mass spectrometer**; Martins Jansons[1]; William Comstock[2]; Joshua Silveira[2]; Katherine Walker[2]; Eloy Wouters[2]; Alec Valenta[3]; Tonya Pekar Hart[2]; Amirmansoor Hakimi[2]; *[1]Thermo Fisher Scientific, Vilnius, Lithuania; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientfic, San Jose, CA*

ThP 684 **Peptide- and region-resolved absolute plasma proteomics defines a novel analytical dimension for pan-disease profiling**; Fredrik Edfors; *SciLifeLab, Department of Protein Science, KTH, Solna, Sweden*

ThP 685 **Drawing the Line in Proteomics Data Quality**; Leonard B Collins[1]; Taufika Islam Williams[1]; *[1]NCSU, Raleigh, NC*

ThP 686 **Optimization of high-resolution TMTpro 35plex acquisition using dedicated identification and quantitation scans on an Orbitrap Astral Zoom MS system**; Martin Zeller[1]; Julia Kraegenbring[1]; Bernard Delanghe[1]; Christopher Rathje[1]; Eduard Denisov[1]; Robert Ostermann[1]; Tabiwang Arrey[1]; Florian Bonn[1]; Alexander Wagner[1]; Dustin R Frost[2]; Ryan D Bomgarden[2]; Philip Loziuk[3]; David Horn[4]; Max Hoek[1]; Johannes Petzoldt[1]; Hamish Stewart[1]; Eugen Damoc[1]; *[1]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [2]Thermo Fisher Scientific, Rockford, IL; [3]Thermo Fisher Scientific, San Jose, CA; [4]ThermoFisher Scientific, San Jose, CA*

ThP 687 **Nanodiscs can preferentially enrich transmembrane proteins in a bottom-up proteomic analysis workflow**; Hanyu Zheng[1]; Ryan C Bailey[1]; *[1]University of Michigan at Ann Arbor, Ann Arbor, MI*

ThP 688 **Proteome-wide Characterization of Translational Errors in Aneuploid Yeast**; Zhuoxin Shi[1]; Leah E. Escalante[2]; Michael R. Shortreed[1]; Audrey P. Gasch[2]; Lloyd M. Smith[1]; *[1]University of Wisconsin-Madison Department of Chemistry, Madison, WI; [2]Center for Genomic Science Innovation, University of Wisconsin-Madison, Madison, WI*

ThP 689 **Quantitative proteomic profiling of T-cell activation in Jurkat cells**; Utana Umezaki[1]; Dirk H. Siepe[1]; Marian Kalocsay[1]; *[1]University of Texas MD Anderson Cancer Center, Houston, TX*

ThP 690 **Overcoming Reporter-Ion Resolution Limits: 18-Plex TMT on a Multi-Reflecting TOF Analyzer**; Nikki Atwal[1]; Stephen Griffin[2]; Matthew E Daly[3]; Cory Scanlan[2]; Lee A Gethings[3]; Richard Lock[3]; *[1]Waters Corporation, Wilmslow, United Kingdom; [2]Waters, Milford, MA; [3]Waters Wilmslow UK, Wilmslow, United Kingdom*

ThP 691 **Stable isotope tracing of sialic acid reveals metabolic drivers of PDAC hypersialylation**; Miya R Paserba[1]; Minal Nenwani[1]; Olamide Animasahun[1]; Deepak Nagrath[1]; *[1]University of Michigan, Ann Arbor, MI*

ThP 692 **High-throughput LC-MS quantification of isotope-labeled deoxynucleosides from multiplexed DNA-SIP fractions**; Ye Chen[1]; Daniel M. Webber[1]; Tim Seebeck[1]; Jeffrey I. Gordon[1]; *[1]Washington University School of Medicine, Saint Louis, MO*

ThP 693 **Absolute Quantification of Lysosomal Proteins by MRM, SureQuant and QconCAT Standards**; Dhriti Arora[1]; Peter Robert Mosen[2]; Sofia Fajardo-Callejon[1]; Dominic Winter[3]; *[1]Department Metabolism, Senescence and Autophagy Research Center One Health Ruhr, University Alliance Ruhr & University Hospital Essen, Essen, Germany, Essen, Germany; [2]Institute for Biochemistry and Molecular Biology, Rheinische Friedrich-Wilhelms-University of Bonn, 53113 Bonn, Germany, Bonn, Germany; [3]Department Metabolism, Senescence and AutophagyDepartment Metabolism, Senescence and Autophagy Research Center One Health Ruhr, University Alliance Ruhr & University Hospital Essen, Essen, Germany*

ThP 694 **Stable Isotope Labeling with 13C Monosaccharides Reveals Carbon Routing into Serum N-glycosylation Pathways**; Adeola K Adeyemi[1]; Michael Russelle S. Alvarez[1]; Sheryl Joyce G Alvarez[1]; Riya Gogte[2]; Kayla Pakulski[1]; Carlito B. Lebrilla[1]; *[1]University of California, Davis, Davis, CA; [2]University of California Davis, Davis, CA*

ThP 695 **Building a Protein Turnover Atlas of Human Primary Cells**; Götz-Norman Hagemann[1, 2]; Barbara Schnitzer[1, 2]; Viktoria Fischer[1, 2]; Catalina Cepeleaga[1, 2]; Raffaela Berger[1, 2]; Christin Zasada[1, 2]; Hannes Hahne[1, 2]; *[1]OmicScouts GmbH, Freising, Germany; [2]Momentum Biotechnologies, Billerica, MA*

ThP 696 **Identifying methylation sites in MCF7 cell line using fractionation and hmSILAC based proteomics**; Rabin Budhathoki[1]; Charli S Worth[2]; Jessica M Conforti[1]; Joseph H Taube[2]; Elyssia S

Gallagher[1]; *[1]Department of Chemistry and Biochemistry, Baylor University, Waco, TX; [2]Department of Biology, Baylor University, Waco, TX*

ThP 697 **pDANCE: A GPU-Accelerated Hierarchical Bayesian Framework for Protein Turnover Inference**; Yi-Zhi Wang[1]; Jeffrey Savas[1]; *[1]Northwestern University, Chicago, IL*

ThP 698 **Following the Atoms: Mapping Cellular Metabolism with Multiplexed Stable Isotopes on a Modified Orbitrap Hybrid Mass Spectrometer**; Rahul Ravi Deshpande[1]; Claire Dauly[2]; Ayush Midha[3]; Isha Jain[3, 4]; Thomas Moehring[2]; Bashar Amer[1]; Susan S. Bird[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; [3]Gladstone Institute, UCSF, San Francisco, CA; [4]Arc Institute, Palo Alto, CA*

ThP 699 **Targeted U-^{13}C-D-glucose metabolomics maps TCA intermediates and bioenergetic signatures across distinct phases of experimental Chagas disease in mice**; Kayla Poirier[1]; Joseane Godinho[1]; Grace Thygeson[1]; Jarrod Laro[1, 2]; Jeffrey Agyapong[1]; Guilherme MP Carrara[1]; Monica Ness[1, 2]; Giovana Macedo[1]; Caitlyn Middleton[1]; Luis Ernst[1]; Godwin Kwakye-Nuako[1]; Jordan Edens[1]; Laura-Isobel McCall[1]; *[1]San Diego State University, San Diego, CA; [2]University of Oklahoma, Norman, OK*

ThP 700 **Dimethyl labeling facilities comparative protein turnover studies using metabolic labeling with deuterated water**; Henock M Deberneh[1]; Michael E Taylor[2]; Kamil A Kobak[2]; Michael T Kinter[2]; Benjam F Miller[2]; Rovshan G. Sadygov[3]; *[1]The University of Texas Medical Branch Galveston Texas, Galveston, TX; [2]Oklahoma Medical Reserach Foundation, OMRF, Oklahoma City, OK; [3]University of Texas Medical Branch, Galveston, TX*

ThP 701 **Open-search proteomics with metabolic stable isotope labeling reveals selective damage of long-lived proteins in rodents**; Jeffrey N Savas[1]; Robin Park[2]; Yi-Zhi Wang[1]; Eric Young[1]; Yuvraj Joshi[1]; Ewa Bomba-Warczak[3]; *[1]Northwestern University, Feinberg School of Medicine, Chicago, IL; [2]Chaparral Labs, Inc., San Diego, CA; [3]University of Pennsylvania, Perelman School of Medicine, Philadelphia, PA*

ThP 702 **Stable-Isotope Mass Spectrometry Defines Alcohol-Driven Glutathione Flux and Epigenetic Remodeling**; Mirjavid Aghayev[1]; Usman Sabir[1]; Andrea Arias-Alvarado[1]; Serguei Ilchenko[1]; Matthew A. Smith[1]; Laura E. Nagy[2]; Takhar Kasumov[1]; *[1]Northeast Ohio Medical University, Rootstown, OH; [2]Cleveland Clinic, Cleveland, OH*

ThP 703 **LipidTraceR: A tool to identify stable isotope labelled lipid species**; Naruenan Wongreantong[1]; Khanh CK Nguyen[1]; Ming Yuan Zhou[1]; Chloe AK White[1]; Yong Jin Lim[1]; Thomas J Velenosi[1]; *[1]University of British Columbia, Vancouver, BC*

ThP 704 **Quantitative Proteomics of Protein Turnover: Dissecting Autophagy–Proteasome Crosstalk and Substrate Selectivity**; Zi Gao[1]; Qiang Xiao[1]; Evan Powers[1]; Jeffrey Kelly[1]; *[1]Scripps Research, La Jolla, CA*

MONDAY NETWORKING SESSION, 12:00 - 1:00 pm

All are welcome to attend.

Networking Session A: Celebrating Women Mass Spectrometrists

Presiders: Lorna De Leoz, Jennifer Krone, Fanny Caroline Liu

Poster-Exhibit Hall, *look for Networking Session A space in the far-left corner*, 12:00-1:00 pm

Join us for the ninth edition of this annual networking session highlighting the achievements and impact of women mass spectrometrists, organized in collaboration with Females in Mass Spectrometry.

- The session opens with a discussion panel featuring leaders from academia and industry, who will share insights from their professional journeys and discuss strategies on managing conflict and difficult workplace situations.
- Participants will then engage in facilitator led small group discussions using one of three case studies on conflict resolution. Groups will have the opportunity to exchange approaches, practice collaborative problem solving, and share key takeaways.
- The session concludes with group reflection and networking time-an opportunity to connect with peers, celebrate the contributions of women mass spectrometrists, and strengthen our connections across career stages.

All conference attendees are welcome. Come learn practical tools for managing conflict, build confidence through hands on case studies, and be inspired by the women trailblazers in mass spectrometry.

MONDAY EVENING WORKSHOPS, 5:45 -7:00 PM

Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

01 DIA for PTMs: Ready for Primetime?

Bioinformatics MS Interest Group
Presiders: Daniel Polasky, Kai Li
Ballroom 20A

The rapid evolution of Data-Independent Acquisition (DIA) has transformed our ability to perform deep, reproducible proteome profiling. While DIA is becoming a standard for global protein quantification, its application to the complex landscape of chemical and biological peptide modifications (PTMs) presents unique bioinformatic challenges.

This workshop will explore to what degree current computational workflows are truly “ready for primetime” for PTM analysis, including site-specific localization and quantification in DIA data. The session will open with a brief tutorial and overview of the current state of the field, highlighting the transition from traditional DDA-based PTM search strategies to library-based and library-free methods for DIA. We will then host a panel of experts to provide their takes on critical bottlenecks and invite audience questions and participation in an interactive Q&A session. The workshop is for anyone interested in DIA proteomics from novice to expert - come with questions, hot takes, or simply ready to learn.

02 Art, Museums and Archaeology

Art, Museums, and Archaeology Interest Group
Presiders: Paul Haynes, Daniel Vallejo, Alba Alvarez Martin
Ballroom 20BC

The study of archaeological specimens, artworks, and other cultural heritage objects by mass spectrometry requires the adaptation of techniques developed for biomedicine, forensics, or industrial and natural product research, to diverse fields such as anthropology, palaeontology, archaeology, natural history, and art history. This introduces unique issues and challenges and often requires some creative problem-solving. Sharing information on some of the more unusual samples analysed and projects undertaken is helpful for all fellow professionals in the fields, and offers be a unique and inspiring opportunity for other colleagues working on different topics.

This workshop will feature lightning talks selected from ASMS poster abstracts - students and fellows are encouraged to volunteer in advance by contacting the organizers.

Lightning talks will be followed by audience Q&A with a panel of academic, government, public museum and private institution scientists to discuss areas of interest in the field.

Topics may include such things as: ethics and permissions involved in analysing culturally sensitive samples; considerations for historical and contemporary sample contamination; the risk of damage to objects as a result of analysis; the implementation of new minimal invasive sampling techniques; discerning the importance of chemicals identified from an analyte removed from context; sample-limited preparation and recovery approaches for rare and precious analytes; the significance of preservation and prediction of material degradation; the importance of a maintaining fluid communication with conservators and curators; employment, funding, and fellowship opportunities in the field; and much more.

03 Mass Spectrometry Approaches for Characterizing Complex Biotherapeutics Modalities

Biotherapeutics Interest Group
Presiders: Sara Carillo, Elsa Gorre
Ballroom 20D

Emerging biotherapeutic formats-including ADCs, bi and multi-specific antibodies, four chain antibodies, and fusion proteins-exceed traditional monoclonal antibodies in structural complexity. These modalities deliver targeted benefits in oncology and immunology but create novel challenges for design and development.

Mass spectrometry enables detailed characterization of the molecular features of these complex therapeutic modalities and can be applied across development and commercialization. However, broad implementation of mass spectrometry workflows in quality control for therapeutic proteins remains challenging, and adoption is even more limited for complex modalities.

This workshop aims to:
1. Characterize the complexities of emerging biotherapeutic modalities, including ADCs, bispecific antibodies (bsAbs), and fusion proteins.

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

2. Highlight the advantages of mass spectrometry-based analyses for these modalities and review new MS methods being developed to address their specific challenges.
3. Define the technical and practical limits of implementing mass spectrometry workflows in regulated testing environments and discuss considerations for transferring discovery MS methods into routine use.

Join a case study workshop where small focus groups will: dive into advanced characterization techniques, discuss cutting edge mass spectrometry methods, and work through the practical issues of implementing mass spec workflows in regulated analytical testing.

04 Entrepreneurship in Mass Spectrometry: Launching through Bootstrapping and Seed Stage Venture Capital

Independent
Presiders: Paula Burton, Lindsay Pino
Room 6A

Mass spectrometry (MS) and proteomics are driving new frontiers in drug discovery, diagnostics, and biomarker research, creating a growing wave of entrepreneurial ventures. This evening workshop on Entrepreneurship in Mass Spectrometry will focus on our most popular questions from last year, mainly the finances of launching through bootstrapping, non-dilutive external funding, and/or seed stage venture capital. The focus is designed to provide attendees with candid, practical insights into the business side of scientific innovation.

With ASMS 2026 being held in San Diego, a hub for life science startups, we will leverage the strong local ecosystem to host a discussion focused on the real-world experiences of successful MS/proteomics entrepreneurs.

Unlike formal oral presentations, the event will prioritize interaction through a panel discussion format, encouraging audience Q&A and direct dialogue with speakers. While guided by audience Q&A, we anticipate this year's focus will be on the journey from bench science to business, addressing critical commercial realities such as securing funding from early-stage capital to venture investment, budgeting for starting a lab or company including team building, and navigating how to finance the "Minimum Viable Product".

This workshop will foster a collaborative environment for networking and knowledge exchange, demystifying the path for researchers, early-career scientists, and industry professionals interested in launching or joining a scientific venture.

05 Prediction is Not Proof: Structural Mass Spectrometry in the AlphaFold Era

XL/CL/HDX Interest Group
Presiders: Nicholas Borotto, Ian Webb
Room 6B

Recent advances in AI-based protein structure prediction have transformed structural biology, raising a timely question: what is the evolving role of experimental structural mass spectrometry? This workshop will highlight how hydrogen–deuterium exchange (HDX), covalent labeling (CL), and chemical crosslinking (XL-MS) provide critical insights that extend beyond static structural predictions. Short presentations from 4–5 experts will showcase how labeling workflows (i) validate and refine AI-generated models, (ii) capture conformational dynamics and intrinsically disordered regions, (iii) resolve changes in structure arising from PTMs, mutations, and chemical modifications, and (iv) enable structural insight in complex, heterogeneous, and physiologically relevant systems—including those relevant to drug discovery and protein interactions. Speakers will also highlight emerging integrative workflows that combine AI prediction with experimental constraints from labeling MS, pointing toward new hybrid approaches for structural biology.

Following these presentations, the session will transition to a moderated panel discussion focused on big-picture and forward-looking questions: Where does AI succeed, and where does it fail, for higher-order structure? What types of problems are uniquely suited to HDX, CL, and XL-MS? What should experimentalists stop doing, and where should the field invest next? Audience engagement will be a central component of the session. Live polling will be used to capture community perspectives in real time, and the discussion will be guided by several provocative, pre-seeded questions to stimulate debate. The workshop will conclude with an open, audience-driven discussion aimed at defining the future role of labeling-based structural MS in the broader structural biology ecosystem.

06 Young Mass Spectrometrist Workshop: Graduate School Through Early Career Forum

Young Mass Spectrometrists Interest Group
Presiders: John Stutzman, Savannah Snyder
Room 6CF

The Young Mass Spectrometrist (YMS) Workshop has historically been an open forum for graduate students, post-docs, and early career scientists to question and receive career feedback from a diverse panel. A highlight of this workshop is the ability to ask direct questions and receive candid feedback, which has been a consistent theme of positive feedback from attendees. The YMS workshop at the 2026 ASMS conference will continue this practice with some minor changes based on attendee feedback from 2025. Chairs John Stutzman and Savannah Snyder will assemble a diverse panel reflecting multiple sectors and varied backgrounds. At the beginning of the workshop, each panelist will communicate a short introduction to the attendees (approximately 10 minutes total). Once completed, the chairs will start the forum with questions from the attendees (approximately 65 minutes). Attendees' questions may be asked directly through the microphone or ASMS app. Please feel free to submit questions beforehand in the ASMS app, so attendees can focus on the discussion. The chairs will have several preprepared topics and questions to help spark/facilitate discussion if the dialogue begins to slow. Preprepared topics will cover the spectrum of graduate school, post-doctoral positions, finding jobs, and early career topics.

MONDAY EVENING WORKSHOPS, 5:45 -7:00 PM

Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

07 Beyond Accurate Mass: Mobility Separation and Ultrahigh-Resolution FTMS

FT-MS Interest Group
Presiders: Martha Aguilera, Christopher Ruger
Room 6DE

The integration of ion mobility with Fourier transform mass spectrometry (FTMS) represents a significant advance across omics applications, including petroleum and biofuels, dissolved organic matter, emerging contaminants, lipids, and proteins. While mobility platforms such as TIMS-QTOF are well established in structural biology and broader omics workflows, coupling ion mobility separation with ultrahigh-resolution analyzers such as FT-ICR and Orbitrap systems raises important scientific questions. Originally demonstrated in prototype systems by the Fernandez-Lima group, TIMS has evolved into high-field implementations, including 18 Tesla TIMS-FT-ICR platforms. In parallel, complementary technologies such as FAIMS Pro Duo and next-generation mobility front-ends are increasing momentum in the field.

This workshop will examine when mobility separation enhances FTMS workflows and where technical bottlenecks remain. A central focus is what additional information becomes accessible when mobility filtering is followed by isotopic resolution and ultrahigh mass accuracy. Topics will include molecular formula validation after mobility separation, mitigation of ion coalescence in complex mixtures, improved detection of low-abundance species, and the distinction between charge-state filtering and structural characterization. The session will also assess performance tradeoffs, including sensitivity, duty cycle, and data complexity.

Applications spanning lipidomics, environmental analysis, petroleum systems, and biomolecular characterization will be discussed to highlight strengths and limitations. Technical challenges such as collision cross section reproducibility, throughput, and data analysis strategies for mobility-resolved FTMS will be addressed. By bringing together developers, facility operators, and scientists, the workshop aims to define advantages, clarify limitations, and outline future directions for ion mobility-FTMS integration.

08 Million-Dollar Instruments, Lean Times: How to Build a Sustainable Mass Spectrometry Service Portfolio

Analytical Lab Managers Interest Group
Presiders: Maryam Goudarzi, Caroline Chidley
Room 1A

Mass spectrometry service laboratories operate some of the most capital-intensive platforms in science. With increasing service contract costs, rising personnel costs, and tightening federal and institutional budgets, sustainability can no longer be assumed. Strategic portfolio design is essential for long-term viability.

This interactive workshop will bring together a cross-sector panel representing universities, academic medical centers, private research institutes, and industry/CRO settings to examine how different sectors build resilient, growth-ready service models. Rather than a lecture, the session will feature moderated discussion, structured prompts, and live audience polling to benchmark portfolio composition, revenue mix (academic vs. industry), rate-setting strategies, subsidy structures, and realistic cost-recovery expectations.

We will address mass spectrometry-specific challenges including securing capital investment and stakeholder buy-in, service contract burdens, platform obsolescence, and the balance between discovery-driven science and revenue-generating services. Attendees will engage directly with panelists and peers, compare operational models in real time, and leave with practical, peer-informed strategies to strengthen the sustainability and competitiveness of their mass spectrometry service programs.

09 Basics and Beyond: Undergraduate Education, Training, and Mentorship in Mass Spectrometry

Undergraduate Research in MS Interest Group
Presiders: Christopher Tracy, Cay Tressler, Jeff Gilbert
Room 1B

This workshop will focus on advancing undergraduate education, training, and mentorship in mass spectrometry. Through a structured panel discussion and interactive dialogue, we will explore effective strategies for teaching mass spectrometry to undergraduate students, including the use of physical representations of instrumentation, active-learning approaches, and accessible teaching resources that make complex concepts more tangible and engaging.

Panelists will discuss best practices for introducing foundational principles while preparing students to meaningfully participate in research environments. Particular attention will be given to scaffolding learning experiences, from classroom instruction to laboratory training, so that students move confidently beyond the basics and develop both technical competence and conceptual understanding.

A central theme of the workshop will be professional development. Speakers will address the question: What can students do with a strong foundation in mass spectrometry? Perspectives from academia, industry, and related sectors will provide insight into diverse career pathways, emphasizing transferable skills, professional identity formation, and long-term growth in the field. Industry perspectives may be included in a vendor-neutral manner to highlight workforce needs and opportunities.

Finally, the workshop will explore approaches to mentorship and networking within the mass spectrometry community, including ideas for developing or expanding structured mentoring initiatives within ASMS. Attendees will leave with actionable strategies to strengthen undergraduate education, support student success, and cultivate the next generation of mass spectrometrists.

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

10 Advancing DMPK and Bioanalytical Strategies for New Therapeutic Modalities Through Mass Spectrometry

DMPK Interest Group
Presiders: Yongle Pang, Renmeng Liu
Room 2

The continued expansion of complex therapeutic modalities-including antibody-drug conjugates (ADCs), radiolabeled compounds, peptide and oligonucleotide therapeutics-has introduced new analytical and DMPK challenges that require innovative and highly sensitive strategies. This workshop will highlight state-of-the-art mass spectrometry approaches that enable selective, quantitative, and informative analysis of these emerging drug classes.

Experts will showcase advanced product ion filtering strategies for quantifying low-level ADC payload metabolites, addressing sensitivity and selectivity challenges in complex biological matrices. The application of stable-labeled and radiolabeled compounds to support mechanistic understanding and meet regulatory expectations for DMPK studies will also be discussed. In addition, novel LC-MS methodologies for oligonucleotide bioanalysis will be presented, highlighting technological innovations that enhance quantitative performance for these structurally unique therapeutics.

This workshop provides a comprehensive perspective on how modern mass spectrometry technologies are evolving to support next-generation therapeutics across diverse modalities. Attendees will gain practical insights into analytical strategy development, regulatory considerations, and methodological advancements that are shaping the future of DMPK and bioanalysis in both discovery and development settings.

11 Bridging the External and Internal Exposome through Advanced Mass Spectrometry

Exposomics Interest Group
Presiders: Pablo Gago-Ferrero, Haoqi (Nina) Zhao, Ruth Marfil
Room 3

Exposomics has evolved from exploratory, untargeted screening approaches toward integrative and increasingly quantitative strategies that aim to link environmental exposures with internal biological responses. Mass spectrometry plays a central role in this transition, enabling the characterization of complex chemical mixtures across environmental and biological matrices. This workshop will focus on how advances in environmental mass spectrometry, human biomonitoring, and data integration are bridging the external and internal exposome. Rather than discussing definitions, the session will critically examine current methodological limitations, challenges in cross-matrix comparability, the need for improved quantification in untargeted workflows, and the path toward causal interpretation and regulatory relevance. Through perspectives from leading experts, the workshop will highlight conceptual bottlenecks, technological needs, and future directions required to make exposomics more robust, comparable, and actionable.

Workshop will not focus on definitions but on forward-looking challenges and solutions.

12 The NIH and NSF Review and Funding Process

Independent
Presiders: Salvatore Secchi, Cathy Costello, Doug Sheeley, Kenneth Ryan, Kelsey Cook
Room 4

Many ASMS members and conference participants are supported by the National Institutes of Health and the National Science Foundation. During this workshop the general funding and review process of grant applications/proposals will be presented. Issues like identifying the best contacts, writing an effective application/proposal, and responding to the reviewers' criticisms will be discussed. Speakers will explore these issues from the perspectives of the applicant, reviewer, and administrator, with some emphasis on new investigators and training opportunities. Tips on grant writing and insights into the review process will be presented. The session will also provide an opportunity to inquire about the latest NIH and NSF initiatives and priorities. Substantial time will be allotted for discussion and questions. NIH and NSF staff will also be available for individual discussions with investigators during scheduled "Office Hours" in the poster exhibit hall.

TUESDAY NETWORKING SESSION, 12:00 - 1:00 pm

All are welcome to attend.

Networking Session A: Elevating South Asian Leadership in Mass Spectrometry and AI

Presiders: Baljit Ubhi, Prasanna Vadhana Ashok Kumaar
Poster-Exhibit Hall
Look for Networking Session A in the far-left corner
12:00-1:00 pm

Navigating the rapid integration of artificial intelligence (AI) into mass spectrometry presents both exciting opportunities and meaningful moments for visibility and leadership. This session, hosted by South Asians in Mass Spectrometry (SAMS) centers on celebrating and amplifying the contributions of South Asians shaping the evolving intersection of mass spectrometry and AI.
The session will open with an introduction to SAMS, highlighting its mission to foster representation, mentorship, and community while creating space for South Asian scientists and business leaders to be seen and heard. A moderated panel will then feature distinguished professionals across academia, industry, and entrepreneurship who are advancing AI-informed approaches within mass spectrometry. The discussion will focus on leadership journeys, career pivots, innovation pathways, and the broader business and societal impact of AI-driven transformation.

The session will conclude with structured networking designed to foster authentic connections, peer mentorship, and cross-sector collaboration.Ideal for students, early-career professionals, and established leaders, this event offers an inspiring and inclusive space to celebrate South Asian excellence and strengthen community across mass spectrometry and AI.

Networking Session B: Career Opportunities for Chinese Students and Scholars

Presiders: Ling Hao, Bingming Chen
Poster-Exhibit Hall
Look for Networking Session B in the far-right corner
12:00-1:00 pm

With the rapid development of mass spectrometry technologies and the increasing applications to academic research, medicine, industry, and regulatory agencies, a growing number of mass spectrometrists including thousands of Chinese students and scholars are trained. The workshop for Career Development Opportunities for Chinese Students and Scholars aims to provide career perspectives to students and scholars to learn the career paths at different career stages. We will invite four speakers from academia, clinic, industry, and regulatory agencies to share their experiences for career development. We will also assemble a group of discussion panelists to answer questions from the audience. We believe the workshop is beneficial to both students and scholars of all ASMS members and potential employers. The workshop will provide opportunities for students and scholars to prepare for their career development during and after mass spectrometry training and help them to set up career goals in the field of mass spectrometry.

TUESDAY WORKSHOPS, 5:45 -7:00 PM

Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

01 Top-Down Proteomics: Emerging Advances and Future Directions

Top-Down Proteomics Interest Group
Presiders: Corinne Lutomski, Eli Larson, Kellye Sutton
Ballroom 20A

Top-down proteomics (TDP) continues to advance rapidly across all stages of the experimental workflow, including sample preparation, instrumentation, fragmentation strategies, and data analysis. These developments have expanded the applicability of TDP, enabling its increasing adoption in clinical and biopharmaceutical research. This workshop will feature panelists from key areas of innovation in TDP who will share practical insights into both the ongoing development of the field and the application of top-down approaches for targeted analyses across academic and biopharmaceutical settings. The panelists will also discuss anticipated directions for the field over the next five years. Discussion topics will span foundational concepts for newcomers as well as advanced topics for experienced practitioners, making the workshop accessible and valuable to participants at all levels of expertise.

02 Career Paths Beyond Academia: Industry, Government, and Emerging Opportunities

Career Development Interest Group
Presiders: Georgia Charkoftaki, Erica Forsberg
Ballroom 20BC

This workshop will explore diverse career paths beyond academia for scientists trained in mass spectrometry, with perspectives spanning the pharmaceutical industry, biotechnology, national laboratories, and scientific instrumentation. Speakers will share insights into their career paths and day-to-day roles across these sectors. Panelists will discuss how to transition from academia, the skills valued across different environments, and how mass spectrometry expertise can be applied in a range of professional settings. The session will include a moderated discussion and audience Q&A.

Attendees will gain practical guidance on navigating career decisions, identifying transferable skills, and positioning themselves for opportunities beyond academia. The workshop is intended to provide an open and informative forum for trainees and early-career scientists considering diverse career paths.

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

03 High Resolution Ion Mobility: Toward The Need for Standardized Data and Reporting

Ion Mobility MS Interest Group
Presiders: Carlos Larriba-Andaluz, Christopher Chouinard
Ballroom 20D

Ion mobility-mass spectrometry (IM-MS) has matured into a widely used analytical platform across industry and academia. Recent advances in instrument design have driven substantial increases in resolving power, enabling the separation of increasingly subtle structural and isomeric features. However, this rapid evolution has amplified variability across instrument architectures, acquisition strategies, and data processing workflows. As a result, comparing, reproducing, and reusing mobility measurements across laboratories has become increasingly challenging. A growing need exists for shared community practices defining how arrival time distributions, metadata, and derived quantities such as mobilities and collision cross sections (CCS) are reported.

This workshop will introduce a collaborative community effort aimed at establishing standardized reporting practices that support consistent capture, exchange, and interpretation of measurements across platforms. The opening presentation will provide an overview of mobility measurement concepts, highlight current inconsistencies in reporting, and motivate the importance of interoperable data standards for method development, calibration, and future machine-learning applications. It will propose a universal, easy-to-adopt model for mobility data reporting and sharing through a common repository. Brief presentations from vendors and academic groups will follow, each presenting practical perspectives on measurement challenges, data reporting, and implementation barriers.

The workshop will culminate in a panel discussion focused on building consensus around minimum reporting requirements, extensibility, and pathways toward community adoption. Audience input will be actively solicited to identify priorities and unresolved issues. This session aims to establish a simple, one-click, universally interpretable report format generated directly by instrument software and adopted across vendors, industry, journals, and academia.

04 The Past, Present, and Future of Mass Spectral Libraries

Mass Spectral Libraries Interest Group
Presider: Tytus Mak
Room 6A

For decades, mass spectral libraries have served as the essential bedrock of compound and peptide identification, transforming raw machine signals into actionable biological and chemical insight across the wide plethora of fields that depend on mass spectrometry, including environmental chemistry, food science, proteomics, and metabolomics. This workshop offers a comprehensive retrospective and a forward-looking roadmap for the evolution of reference data. The session begins by examining the earliest beginnings, tracing the transition from early printed compilations to the digitized, curated repositories like NIST and Wiley that standardized GC-MS and LC-MS/MS workflows while establishing the scoring algorithms that remain industry standards today. Transitioning into the present, we address the democratization of data through open-access platforms like GNPS, MassBank, and ProteomeXchange, focusing on modern challenges such as curation-at-scale, the integration of orthogonal data such as ion mobility and retention time, and the limitations of search engines in handling increasingly complex, high-resolution datasets. Finally, the workshop explores the future where the boundary between experimental and predicted data blurs through the rise of machine learning and in silico tools like CFM-ID and Prosit. This interactive forum invites researchers and developers to debate how we can ensure tomorrow's libraries are as robust as they are expansive, fostering a collaborative environment to bridge the gap between historical foundations and next-generation discovery.

05 Chemoproteomics: Analytical Rigor, Biological Interpretation, and Translational Application

Independent
Presiders: Lindsay Pino, Jarrod Marto
Room 6B

Chemoproteomics has moved from a niche technique to a central driver of biological discovery and drug development, yet its development and adoption within the broader mass spectrometry community remains uneven. While recent advances have expanded chemical space, throughput, and sensitivity, there remain persistent challenges in analytical rigor, data interpretation, and biological validation that impede deployment at scale. Intellectual investment by the mass spectrometry community can improve the qualitative and quantitative performance as well as scalability of chemical proteomics approaches.

This workshop will provide an informal, discussion-driven forum focused on where chemoproteomics workflows succeed, where they fail, and where investment of domain expertise by the mass spectrometry community can add tremendous value. Rather than formal presentations, the session will center on moderated discussion spanning chemistry, biology, and mass spectrometry perspectives.

We will intentionally avoid focus on any single technology or commercial platform and will feature panelists representing academic, industrial, and translational viewpoints. The goal is to highlight shared pain points, challenge ingrained assumptions, and identify actionable directions where the mass spectrometry community can collectively improve chemoproteomic practice and impact.

06 Real time Mass Spectrometry in Proteomics and Beyond

Independent
Presiders: Nick Riley, Qing Yu, Jesse Canterbury
Room 6CF

The purpose of this workshop is to provide a foundational demonstration of state-of-the-art real-time instrument control through short presentations (5-15 minutes) by invited experts. These presentations lay the groundwork for a panel discussion (30 minutes) that segues into an informal discussion on emerging topics for real-time instrument control (30 minutes). The format offers a unique and exciting opportunity to engage in open discussion, support junior researchers, and identify gaps in the current field that lab- or community-lead efforts can address. The workshop will establish avenues to improve open sharing of data, code, documentation, and methods for the continued development new real-time mass spectrometry tools.

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

Previous speakers include Drs. Livia Eberlin, Chris Rose, Danielle Swaney, Jarrod Marto, Lilian Heil, and John Yates. We covered project topics from multiple instrument vendors (e.g., Bruker and Thermo) and discussions led directly to the development of new real-time instrument control infrastructure for the general community. With 70-85 attendees, the first iteration of this workshop at ASMS 21/22 and the latest iteration in 2025, we believe this workshop has been a successful venue for collaboration and discussions. We will continue to build on this success to generate stimulating discussion, engage a wide range of researchers from industry, vendors, and academia, and enable collaborations between attendees.

07 Mass Spectrometry of Nucleic Acids: Emerging Challenges and New Opportunities

Oligonucleotides and Nucleic Acids Interest Group
Presiders: Kevin Clark, Robert Ross
Room 6DE

This proposal is submitted by Prof. Kevin Clark (Tufts University), Dr. Keeley Murphy (Thermo Fisher Scientific), Dr. Robert Schuster (GSK), and Dr. Robert Ross (Thermo Fisher Scientific) for a workshop hosted by the ASMS Oligonucleotides and Nucleic Acids Interest Group. Mass spectrometry continues to play indispensable roles in the characterization of nucleic acids for biomedical research. This ASMS Interest Group workshop provides a venue for researchers and stakeholders to gather, build community, and exchange insights that advance our field. The 2026 Interest Group Workshop will examine enduring and emerging opportunities in the fields of therapeutic and endogenous nucleic acids in a rapidly changing landscape of health and safety guidance.

Nucleic acids have undeniable momentum as therapeutics, biomarkers, and targets in drug discovery applications. Mass spectrometry characterization is central to efforts in these broad areas, so it is imperative that scientists keep pace with evolving policies and regulations. Our primary goals with this workshop are to (1) underscore the myriad opportunities in nucleic acids mass spectrometry and (2) identify key workforce, technology, and application needs. We will build on the success of our 2025 meeting by assembling a group of 4-6 panelists from academia, industry, and regulatory agencies (if possible) to provide their perspectives. Each panelist will have ~5 min to introduce themselves and their background/expertise and will then describe an emerging challenge they are facing to stimulate discussion. Panelists will have complementary research/professional backgrounds spanning the study of therapeutic and cellular nucleic acids, ensuring a vibrant discussion for all attendees.

08 Software and Data Solutions: A Reivew of Current User-Created Platforms.

Lipids & Lipodomics Interest Group
Presiders: Jeff McDonald, Kim Ekroos
Room 1A

Post-acquisition processing of lipidomics data generated by mass spectrometry remains a significant hurdle for both new and experienced researchers. The increasing use of high-resolution MS, tandem MS, ion mobility, and other advanced analytical tools has further complicated this challenge. Although vendor-provided software solutions are often adequate, they typically lack the flexibility and timely customization needed to keep pace with rapidly evolving technologies.

Custom software solutions have been developed for many years, but historically they have required specialized coding expertise. While several successful platforms exist, their usability and implementation are often limited because they are standalone installations and generally require proficiency in R or Python. The advent of artificial intelligence (AI) and large language models has lowered the barriers to software development, and cloud computing now enables scalable, web-based solutions. The creation of purpose-built tools-whether one-off applications for specific analytical needs or enterprise-level platforms-is more achievable than ever.

In this workshop, we will present several recently developed, user-created software solutions for community evaluation and feedback. This dialogue will be essential as the lipidomics community and instrument vendors navigate the rapidly changing software landscape.

09 JASMS: The Life of a Manuscript and Being a Superstar Reviewer

Independent
Presiders: Jenny Brodbelt, Erin Baker
Room 1B

As the ASMS society's journal, The Journal of the American Society for Mass Spectrometry (JASMS) is a premier science journal that covers all aspects of mass spectrometry, including fundamentals, instrumentation and applications of mass spectrometry in all fields (chemistry, biology, physics, geology, environmental science, and life sciences, and many others). This Workshop will focus on the manuscript submission process and review pipeline of JASMS. It will cover how manuscripts are handled - from the time a manuscript is first submitted to the time the paper is published. The critical role of the reviewers in this process will be emphasized, including tips for being a superstar reviewer.

10 Celebrating 100 Years of Photoionization MS: Early Developments, Modern Applications, and Future Directions

Photoionization MS Interest Group
Presiders: Sven Ehlert, Patrick Mueller
Room 2

On the occasion of the method centenary, the Photoionization Mass Spectrometry Interest Group invites both experienced users and those interested in exploring photoionization mass spectrometry (PI-MS) as an alternative ionization approach to join an engaging workshop on its history, key milestones, and fundamentals. Tracing the field's evolution from its early beginnings to today's technological advances, we will clarify common misconceptions, examine key pitfalls, and highlight emerging opportunities and innovative future applications of PI-MS.

Seasoned scientists who have significantly contributed to the field, together with early-career researchers, will share their perspectives to inspire lively discussion, beginning with a brief history of photoionization that covers the earliest experiments, as well as the coincidental 40th anniversary of the introduction of atmospheric pressure photoionization (APPI) to mass

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

spectrometry, and the 25th anniversary of the commercialization and integration of APPI with liquid chromatography. Afterwards, five-minute flash talks will provide focused insights into contemporary aspects of photoionization mass spectrometry and its interactions with other ionization techniques, including real-time environmental monitoring, ion speciation and its role in ion mobility spectrometry, as well as in the structural elucidation of metabolites, lipids, and molecules of forensic interest.

With this, we aim to honor 100 years of PI-MS by showcasing its unique applications, highlighting opportunities not accessible with other ionization technologies, and concluding the session with an open discussion and audience Q&A, offering attendees a valuable opportunity to exchange ideas, address practical challenges, and explore strategies for implementing PI-MS in modern analytical workflows.

11 Trapping the Future: The Commercial Resurgence of Ion Trap MS

Ion Trap MS Interest Group
Presiders: Kenneth Lee, Hsi-Chun Chao
Room 3

As the breadth of mass spectrometry (MS) applications has grown, there has been a commercial resurgence of unique ion trap technologies, driven by innovations that emphasize functional and mechanistic insight alongside conventional analytical performance. Beyond the more established ion trap technologies of sine-wave driven quadrupole ion traps, Orbitrap, and FT-ICR, more recent commercialization of ion trap technologies include capabilities previously only available on custom-built academic platforms.

The ion trap workshop will feature three academic and industry leaders providing an overview of their ion trap technologies that have recently been advanced into commercial platforms. Dr. Martin Jarrold will describe electrostatic ion traps used for Charge Detection Mass Spectrometry (CDMS), which is now developed by Megadalton Solution and Waters Corporation. Dr. Yuko Fukuyama from Shimadzu will provide an overview of Digital Ion Trap technology and its first commercial implementation as the MALDImini-1 system. Dr. Dimitris Papanastasiou will describe the Omintrap, which combines all common tandem MS approaches into a single technology for powerful and unique structural characterization. The workshop will be conducted as a panel-style session. Each speaker will deliver a focused technical overview of their respective technology, followed by a dedicated QA session. The workshop will conclude with a moderated group discussion addressing the future trajectory of ion trap technology and its anticipated impact on the broader analytical sciences.

12 Advancements in Tools for Studying Materials-Based Catalytic Processes in Polymers and Energy

Polymeric Materials & Energy, Petroleum and Biofuels Interest Groups
Presiders: David Stranz, Christopher Rueger
Room 4

This joint workshop will focus on the combination of mass spectrometry techniques and advanced digital tools for examining complex materials-based catalytic processes in the areas of synthetic polymers and energy. When optimized, catalysts are the driving force behind the control of structure/property relationships and ultimately making the desired product at a competitive price. The key to catalyst optimization is understanding their mechanisms and thoroughly characterizing their resulting products. This crucial information can then be used for process adjustment and dialing-in the desired materials properties. Discussion topics will focus on industrially significant problems that can benefit from the use of advanced digital tools for process optimization. Specific areas of interest include the study of olefin polymerization, asphalt formulations, materials for coatings and foams, and energy production.

The discussion panel will be composed of experts from a variety of mass spectrometry-related disciplines. They will lead discussions on the current challenges, potential solutions, and future needs required to effectively solve these ongoing problems of interest to the Polymer and Petroleum Energy & Biofuels communities.

13 The peptide renaissance: emerging modalities and analytical challenges

Pharmaceuticals Interest Group
Presider: Valeria Guidolin, Josh Johnson, Mack Shih
Room 7AB

Peptide therapeutics are an important class of pharmaceutics bridging the gap between small molecules and biologics. Driven by the clinical success of GLP-1 receptor agonists peptide drug products for diabetes and obesity in recent years, there is an increased interest and resurgence of peptide therapeutics. Breakthroughs in stabilized peptide engineering technologies have transformed peptides from simple linear sequences to complex architectures including nonnative amino acids, cyclization, peptide stapling, and peptide conjugation. These structural changes can dramatically increase the complexity of the peptide structure and introduce unique and interesting challenges when trying to analyze these compounds via mass spectrometry. The ASMS 2026 pharmaceutics workshop aim to explore this “peptide renaissance” in the pharmaceutical industry and the critical use of mass spectrometry in characterizing these next-generation modalities.

Topics will span the analytical lifecycle, beginning with sequence confirmation and structural characterization, where issues such as incomplete fragmentation, near isobaric variants, and amino acid isomerism continue to limit definitive structural assignments. The discussion will extend to intact, middle down and bottom-up MS strategies, charge state complexity, and the interpretability of deconvoluted data for increasingly modified and stabilized peptide designs.

The workshop will also address the evolving role of data analysis software, including automated sequencing, impurity assignment, confidence scoring, and the growing integration of predictive and machine learning-based tools-highlighting both their promise and current limitations. Finally, the session will place these technical challenges within the context of the regulatory landscape for synthetic peptides, where expectations for impurity profiling, comparability, and analytical defensibility continue to evolve alongside the modality.

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

14 Clinical Chemistry Workshop - Small Samples, Big Discussion

Clinical Chemistry Interest Group
Presiders: Matthew Crawford, Renee Ruhaak
Room 8

Microsampling (dried blood spots (DBS), volumetric absorptive microsampling (VAMS), and newer capillary collection devices) promise patient-centric access, remote/self-collection, and reduced pre-analytic burden. At the same time, translating discovery-phase success into routine clinical use requires rigor around equivalency, pre-analytics, and operations. Recent studies show encouraging performance for many chemistry and therapeutic drug monitoring (TDM) analytes, but also analyte-specific biases (e.g., potassium and carbon dioxide) and device-/matrix-dependent effects that must be addressed before clinical deployment. Evidence also continues to expand for VAMS and capillary devices in home-based TDM and safety labs, with clear patient preference advantages, yet clinical validation and bridging to venous matrices remain the critical gate.

This fully discussion based workshop aims to convene professionals from academic, hospital, and reference labs to discuss challenges/solutions in the path from discovery to clinical implementation. Discussion topics to include 1) designing matrix and device specific bridging studies for LC MS/MS assays (capillary serum and DBS/VAMS to venous reference) aligned with ICH M10 and FDA bioanalytical validation expectations, 2) mitigating hematocrit and other pre analytic risks specific to DBS/VAMS in LC MS/MS workflows, 3) implementing CLIA/ISO 15189 controls for remote self collection and documenting analytical/clinical validity for LC MS/MS LDTs under the current oversight landscape, 4) operationalizing microsampling for LC MS/MS, including specimen acceptance criteria, stability/transport of dried vs liquid micromatrices, staff training, and QC/EQA.

WEDNESDAY NETWORKING SESSION, 12:00 - 1:00 pm

All are welcome to attend.

Networking Session A: Hispanics and Latinx in MS

Presiders: Carolina Bras Costa, J. Rafael Montenegro Burke

Poster-Exhibit Hall, look for Networking Session A space in the far-left corner, 12:00-1:00 pm

This networking session will convene scientists, trainees, and professionals who identify as Hispanic and Latinx, as well as colleagues and allies who are committed to fostering inclusion and representation within the mass spectrometry community. The goal of the session is to create an open and welcoming space for connection, visibility, mentorship, and professional exchange.

The session will begin with short research presentations from selected speakers representing diverse career stages and sectors. These talks will highlight cutting-edge work in mass spectrometry and related disciplines while also showcasing the breadth of contributions from Hispanic and Latinx scientists within the field. By centering scientific excellence alongside community building, the session aims to reinforce both professional development and representation.

Following the research talks, the session will transition into a structured networking period designed to facilitate meaningful conversations among attendees. Participants will have the opportunity to connect with peers, mentors, and potential collaborators, discuss career pathways, and share experiences navigating academic, industry, and government environments.

WEDNESDAY WORKSHOPS, 5:45 -7:00 PM

Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

01 Environmental Applications: You Are What You Eat and Breathe

Environmental Applications Interest Group

Presiders: Erin Baker, Carrie McDonough

Ballroom 20A

Chemicals in the environment have a massive impact on our health and well-being. For the many chemicals we are exposed to daily through ingestion, inhalation and dermal absorption, their health impacts are unknown. However, from Paracelsus we know that “the dose makes the poison”, and any chemical, even water, can be toxic if consumed at high enough amounts.

In this workshop, the audience will test their knowledge on the history and current state of chemicals of concern through an interactive quiz (with prizes!!). We will then have several short talks on current developments in environmental measurement approaches and applications, such as novel non-targeted analysis developments and computational workflows, which are allowing us to probe new chemicals of concern that we did not even know existed.

02 When Gas Phase Biomolecular Structure Differs from Solution Phase

Fundamentals & Native Mass Spec Interest Groups

Presiders: Carter Lantz, Jim Prell, Rachel Loo

Ballroom 20BC

Native mass spectrometry and ion mobility narratives typically highlight aspects of gas phase macromolecular analyses that are consistent with known solution phase structure; e.g., the collision cross-section of a charge state that most closely matches the crystal-structure predicted size, product ions or subunits that release from the exterior of a noncovalent complex, or the low m/z charge state distributions produced by electrospraying a folded complex. Certainly, such a focus highlights the ability of electrospray ionization to produce “freeze-dried” biomolecules that retain solution structure and the overall utility of native MS methods to return relevant information on those structures.

Nevertheless, increasing our understanding of the fundamental forces and dynamics relevant to multiply charged, gas phase biomolecules requires an exploration of cases that deviate from expectations, e.g., antibody structures that collapse in the gas phase and release of fragment ions from the interface of protein complexes. This workshop will present and discuss examples of mass spectrometry and ion mobility measurements that suggest differences between gas and solution phase structures, how they should be rationalized, and what, if any, changes should be made in how we think about ESI-generated ions.

03 Advantages of Using Mass Spectrometry Assays (MSA) rather than Ligand Binding Assays (LBA) for the Quantitation of Protein & Peptide Biomarkers

Regulated Bioanalysis Interest Group

Presiders: Fabio Garofolo, Jessica McGregor, Wenkui Li, Adrià Sunyer

Ballroom 20D

The 2026 ASMS Regulated Bioanalysis Interest Group (RBIG) Workshop is focused on an interactive discussion on the Advantages of Using Mass Spectrometry Assays (MSA) rather than Ligand Binding Assays (LBA) for the Quantitation of Protein & Peptide Biomarkers. MSA is recognized as a robust tool for protein & peptide biomarker assessment, offering specificity for distinct protein regions and post-translational modifications. Unlike traditional methods, MSA allows for the simultaneous measurement of multiple biomarkers, significantly enhancing throughput and data consistency. The choice between MSA and LBA depends on factors such as target nature, matrix complexity, and sensitivity. While LBAs are often more sensitive, particularly for low-abundance peptide hormones, they are susceptible to interferences from autoantibodies. Immunoaffinity-Mass Spectrometry (IA-MS also called Hybrid Assays) approaches have been developed, combining the enrichment power of antibodies with the structural precision of MS. However, IA-MS is still limited by the cross-reactivity of capture reagents, restricting

WEDNESDAY WORKSHOPS, 5:45 -7:00 PM

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multiplexing. Future advancements, including reagent-free nano-flow LC, High-Resolution Mass Spectrometry (HRMS) and increased automation, are expected to push the boundaries of sensitivity and structural elucidation. Early collaboration between LBA and MSA teams to align assay design with intended use can ensure that technical and regulatory challenges are addressed during development. This workshop will delve into the Regulated Bioanalysis of protein & peptide biomarker analysis including topics on sample preparation, mass spectrometric and ligand binding methods, Biomarker Assay Validation (BAV) and Context of Use (COU) limitations when used as the only driver of BAV. Experts in the field will share their experiences in this interactive workshop. The discussion will further develop the conclusions from the 2025 White Paper in Bioanalysis: https://www.tandfonline.com/doi/pdf/10.108

04 Careers and Opportunities in Forensic Mass Spectrometry

Forensics & Homeland Security Interest Group
Presiders: Patrick Fedick, Mengliang Zhang
Room 6A

This evening workshop will highlight career pathways in forensic chemistry with a particular focus on the role of mass spectrometry in modern forensic investigations. The session will begin with a moderated career panel featuring notable state and federal forensic chemists who routinely apply advanced mass spectrometry techniques to support criminal investigations, public safety, and national security missions. Panelists will discuss their career journeys, the types of cases and analytical challenges they encounter, and how emerging technologies are shaping the future of forensic science. Topics may include the analysis of seized drugs, toxicological investigations, trace evidence analysis, environmental forensics, and the application of high-resolution and field portable mass spectrometry in evidentiary workflows.

Following the panel discussion, the workshop will transition into an interactive networking and recruitment session designed to connect students, early-career scientists, and postdoctoral researchers with potential employers and mentors. Representatives from federal and state forensic laboratories and investigative agencies will be available to discuss internship programs, postdoctoral opportunities, and full-time employment pathways in forensic chemistry and related analytical science fields.

Participants will have the opportunity to engage directly with practicing forensic scientists, ask questions about required training and professional skills, and learn about the hiring process for government laboratories. The session aims to provide practical guidance for those interested in pursuing careers at the intersection of analytical chemistry, mass spectrometry, and forensic science. By combining expert perspectives with direct networking opportunities, this workshop will serve as a valuable forum for career exploration, mentorship, and workforce development in forensic chemistry.

05 AI in Mass Spectrometry-based Metabolomics

Metabolomics Interest Group
Presiders: Corey Broeckling, Soha Hassoun
Room 6B

Artificial intelligence (AI) is rapidly transforming mass spectrometry-based metabolomics by enabling more accurate, scalable, and automated interpretation of complex spectral data. From peak detection and molecular annotation to structure elucidation and biological interpretation, AI methods-including deep learning, probabilistic modeling, and large language models-are reshaping how researchers extract knowledge from MS and MS/MS data. This workshop will provide an overview of emerging AI-driven approaches across the metabolomics workflow, highlighting advances in deep learning models, de novo molecular generation, and AI-driven scientific discovery. We will also discuss how AI methods are beginning to address longstanding challenges in metabolomics, including incomplete spectral libraries, ambiguous annotations, instrument variability, and the growing scale and heterogeneity of public metabolomics datasets. In addition, the workshop will explore broader directions where AI may play an increasingly important role in metabolomics. These include areas such as retention time and fragmentation prediction, spectral denoising and reconstruction, automated quality control and data curation, multimodal integration with other omics data, biomarker discovery, and intelligent data acquisition and analysis workflows. The workshop will feature presentations and discussion aimed at identifying opportunities, challenges, and emerging needs for integrating AI into metabolomics practice. A moderated interactive discussion will be held following the presentations, where participants will be invited to share their experiences, challenges, and perspectives on applying AI to metabolomics data. Topics may include barriers to adoption, unmet needs in current tools, and opportunities for collaboration between experimental and computational researchers.

06 MS Imaging: Multiplexing and Multimodal Integration for Deeper Insight

Imaging MS Interest Group
Presiders: Stefania Stavrakaki, Angela Kruse, Katerina Djambazova
Room 6CF

Mass spectrometry imaging encompasses a wide range of technologies, amenable to integration with other tissue interrogation workflows, such as microscopy (histology, immunohistochemistry), transcriptomics, spectroscopy, single-cell analyses, and bulk omics. Combining MSI with other modalities can produce uniquely rich datasets, offering a deeper and more comprehensive insight into biological processes. However, there are still key challenges in workflow development, integration of datasets spanning spatial resolutions, data mining, and interpretation. In this workshop, we will cover established and new modalities integrated with MSI to provide orthological measurements, strategies for data integration/mining, data interpretation, and translational work. With these topics in mind, we are interested in discussing challenges and opportunities that arise when developing multimodal workflows. Here, presenters are encouraged to share both positive, negative results, and failed experiments to encourage lively discussions among the workshop presenters and the audience.

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Organization: Similar to previous years, this workshop will comprise two parts. First, multiple invited speakers will briefly describe their methodologies in a series of flash talks. Second, the speakers will serve as a panel for a general discussion with the audience on the challenges that exist within the field, where they will identify opportunities and discuss future strategies. The audience is encouraged to come prepared with questions and ideas. An online tool will be used to ensure direct participation of the audience.

07 Quantitative DIA Data Analysis

Data Independent Acquisition Interest Group
Presiders: Michael MacCoss, Michael Ford

Room 6DE

The remarkable gains in proteome coverage achieved by modern data-independent acquisition (DIA) workflows have transformed discovery proteomics, routinely delivering quantitative measurements for thousands of proteins in a single run. Yet this expanded measurement capacity introduces analytical challenges that the field has only begun to confront. As the number of quantified proteins grows, the multiple hypothesis testing corrections required to control false discovery rates become increasingly stringent, potentially obscuring biologically meaningful changes that would be readily detected in more focused analyses. Critically, maintaining equivalent statistical power to detect a given fold change as proteome coverage expands will likely demand a corresponding increase in the number of biological replicates-a practical constraint with significant implications for experimental design and cost.

These challenges make it essential to carefully control the protein detection FDR itself. A poorly controlled false discovery rate at the identification stage populates quantitative matrices with unreliable measurements, compounding the difficulty of detecting true differential abundance downstream. Noisy or spurious protein detections inflate the testing burden without contributing meaningful biological signal.

This workshop will explore practical strategies for managing these interconnected challenges, including principled approaches to detection FDR control, intelligent filtering, tiered hypothesis testing, and the role of prior biological knowledge in guiding analysis. The discussion will also address emerging signal processing tools-from denoising and deconvolution algorithms to AI-driven spectral and retention time prediction-that promise to improve DIA quantification at its foundation, potentially recovering sensitivity lost to multiple testing correction.

08 De Novo Peptide Sequencing: ongoing opportunities and challenges

Independent
Presiders: Justin Sanders, Will Fondrie, William Noble

Room 1A

In recent years, deep learning-based de novo peptide sequencing has made significant advances, demonstrating remarkable performance in interpreting mass spectrometry data. Despite these successes, researchers still face numerous questions when applying these tools in practice, and adoption remains somewhat limited. This workshop aims to demystify deep learning-based de novo sequencing, providing attendees with a clear understanding of the state of the field, best practices, and practical insights through interactive discussions and live demonstrations. Additionally, we aim to bring together developers and users of de novo tools for a discussion of what roadblocks are limiting the usage of de novo tools today and what future research directions are most critical to drive adoption.

With a growing number of de novo tools and approaches available, researchers often find themselves asking:
What are the best practices for de novo sequencing? We will explore common pitfalls, practical considerations, and specific use cases, including immunopeptidomics and metaproteomics.

Will de novo work for my data? DSince its inception, de novo tools have become much more flexible in handling varied data from different instruments, modifications, etc. However, much still needs to be done to make tools more generalizable. We will provide an overview of what progress has been made on this front, as well as what still needs to be done.

How can I ensure confidence in my results? Unlike sequence database searches, de novo sequencing lacks well-established false discovery rate control methods. We will discuss best practices for assessing confidence and data quality.

Can de novo sequencing solve my specific problem? We invite attendees to bring their own data and explore the power of de novo sequencing in real time. Through live analysis, we aim to uncover unexpected insights together.

Join us for an engaging session where we uncover the potential of deep learning for de novo sequencing.

09 Best Practices for Non-Targeted Analysis - Toward Reproducible Workflows and Defensible Reporting

Independent
Presider: Michael Rush

Room 1B

Nontargeted analysis (NTA) is increasingly used to characterize complex chemical mixtures across environmental, extractables & leachables (E&L), industrial, biomedical, and regulatory applications. However, differences in study planning, data processing, and reporting practices can limit reproducibility, transparency, and confidence in results—particularly when comparing outcomes across instruments, software tools, and laboratories. The Best Practices for Nontargeted Analysis (BP4NTA) working group is a global, volunteer-driven community focused on improving scientific rigor and advancing practical guidance for NTA. This workshop will open with a brief overview of BP4NTA and then transition to actionable ways attendees can engage with ongoing efforts.

The session will spotlight three current BP4NTA activities: (1) the BP4NTA Study Planning Tool to strengthen study design, documentation, and reporting; (2) the GC-NTA technical subcommittee, focused on aligning approaches and terminology

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for gas chromatography-based NTA; and (3) the E&L technical subcommittee, advancing best practices for E&L NTA workflows. Attendees are encouraged to discuss their present challenges and difficulties, which will be compiled in real time. A moderated panel featuring voices from across BP4NTA—spanning government, research, and industry—will respond to the audience-generated topics, highlight practical decision points, and identify where community consensus and resources are most needed. A central outcome of this workshop is to launch participation in an upcoming E&L data-processing round robin: participants will be asked to process a shared dataset using their existing workflows and contribute outputs and metadata for cross-pipeline comparison and community learning.

10 Analytical Selectivity in Ambient Ionization: From Ion Generation to Mass Analysis

Ambient Sampling & Ionization Interest Group
Presiders: Nicolas Morato, Jacob Jordan, Chris Gill
Room 2

This workshop will examine the continuum of ambient ionization mass spectrometry -ion formation, transmission, selection/activation, and mass analysis- to evaluate how analytical selectivity is introduced, intentionally or not. Along with this theme, we will overview fundamental aspects of ion formation in open-air environments, including accelerated droplet chemistry and ion-molecule reactions that can select for certain ions at the point of sampling. We will also cover how ambient ionization sources are interfaced with a variety of instruments, highlighting how the specifics of the desolvation process, inlet geometry, and ion transmission can add additional levels of selectivity. Finally, we will discuss intentional approaches to provide selectivity coupled to ambient ionization, including ion mobility and MS/MS innovations.

The first half of the workshop will consist of flash talks spanning ambient ionization fundamentals, instrumentation, and coupled gas-phase approaches, in the context of analytical selectivity. Talks will also be selected to highlight recent developments in ambient ionization to get participants up to speed on the most recent discoveries within the field. The second half will include a panel discussion with a diverse group of leading scientists working on ambient ionization. By fostering discussion over the most relevant considerations for ion generation in the open air, their transmission through an instrument, and the possibilities surrounding their gas-phase manipulation, we aim to build -together with the audience and the invited speakers- a shared framework for understanding the current limitations and opportunities for higher selectivity or broader coverage in ambient ionization mass spectrometry.

11 Surfing the Next Wave of Metaproteomics: Quantification, Multi-omics and PUFs !

Metaproteomics Interest Group
Presiders: Pratik Jagtap, Timothy Griffin, Robert Hettich
Room 3

Mass spectrometry-based metaproteomics is rapidly emerging as a cornerstone for deciphering the functional dynamics of complex microbiomes, yet the field continues to face analytical and computational challenges that extend beyond traditional proteomics. This evening workshop will convene leading experts and active contributors to global community efforts to discuss the current state of the field, identify unmet needs, and chart a coordinated path forward.

Members of the Metaproteomics Initiative will present updates from recent CAMPI benchmark studies focused on sample preparation and functional annotation, alongside new community-driven projects designed to accelerate methodological standardization and biological insight. These include CAMPI-Quantification, which evaluates reproducibility and quantitative performance across MS platforms using DIA workflows; CAMPI-Multi-omics, which benchmarks integrated omics pipelines using both existing and newly generated datasets; and CAMPI-Proteins of Unknown Function (PUF), which mobilizes the community to identify and characterize conserved yet unannotated proteins within human gut microbiomes.

Through panel discussions and audience engagement, this workshop aims to foster collaboration, refine best practices, and catalyze new initiatives that will deepen our understanding of microbiome function and advance the next decade of metaproteomics research.

WORKSHOP AGENDA:
5:45: Introduction to the Workshop
5:50-6:15: Panel Discussion:
  Introduction to Grand Challenges
  Update on Metaproteomics Quantification Study (CAMPI4)
  Update on Microbiome Multi-omics Study (CAMPI5)
  Update on Proteins of Unknown Functions Study (CAMPI5)
6:15-7:00: Discussion with the attendees:
  Expanding the presence of metaproteomics at ASMS
  Establishing a metaproteomics interest group: vision, structure, organization
  Dedicated oral and poster sessions: structure and organization
  Announcements and Conclusions

12 Charge Detection Mass Spectrometry

Independent
Presiders: Anisha Haris, Victor Cheng Yin, Tessa Reinert, Varun Gadkari
Room 4

Charge Detection Mass Spectrometry (CDMS) has rapidly emerged as a powerful approach for measuring high-mass, highly heterogeneous analytes that exceed the practical limits of conventional mass spectrometry. Growing interest in CDMS reflects advances in instrumentation and expanding applications, including viral vectors, protein assemblies, nanoparticles, and complex macromolecular materials.

This workshop will highlight the unique capabilities and insights enabled by CDMS while providing an interactive forum for the broader mass spectrometry community—ranging from established practitioners to those new to the technique—to examine current performance, share practical experience, and discuss future directions.

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Light refreshments will be available from 5:30 - 5:45 pm in the Sails Pavilion.

A distinguished panel of CDMS pioneers will represent diverse instrument architectures and methodological approaches: Chen Du (Regeneron), John Hoyes (TrueMass), Martin Jarrold (Indiana University, Megadalton Solutions), Shannon Raab (Lilly), Michael Senko (Thermo Fisher Scientific), and Evan Williams (UC Berkeley).

Discussion topics will include reliable single-ion detection, sensitivity optimization, and accurate charge determination. The workshop will compare complementary CDMS implementations to identify current challenges, best practices, and priorities for advancing the field. Emphasis will be placed on barriers to broader adoption, including instrument optimization, sample preparation (e.g., buffer exchange and adduct mitigation), ion transmission, and opportunities for community-driven standardization to improve reproducibility. Integration of CDMS into research, development, and emerging regulatory workflows will also be explored.

Attendees from diverse application areas are encouraged to contribute perspectives and open questions.

13 Flavor, Fragrance, and Foodstuff Discussion: Analyte Identifications and Sample Characterizations with GC& LC-MS and modeling tools

Food, Flavor, and Foodstuff Interest Group
Presiders: Devin Peterson, David Schroeder
Room 7AB

The Flavor Fragrance and Foodstuff Workshop will cover a range of topics related to GC & LC-MS, and sample preparation automation, application enablers, identification, modeling and machine learning tools relevant to these fields. There are a wide range of sample types and analysis objectives within this field, but many application goals are consistent and involve determining reliable identification of analytes and performing exploratory characterization and comparison of data from samples and sets of samples. Both of these topics will be covered in the workshop through application examples from panelists and open discussion. One discussion topic will focus on approaches to identification and will include using acquired spectral information with library databases, using chromatography to improve separation and spectral quality, and connect tentative identification with sensorial descriptions . High-resolution MS data will also be discussed as a support to library matches and as a path towards identifying analytes without library matches. A second discussion topic will focus on data analysis options to compare and characterize data from sets of samples and will include strategies for clustering, machine learning, and various software and modeling tools. Data characteristics, strategies, and software tools will be discussed.

The workshop will be interactive and will cover these topics through application demonstrations from a panel of speakers as well as through open discussion with the panel and attendees.