

SUNDAY, MARCH 11

Welcome to the Opening Session
TECHNOLOGY ACCELERATING DISCOVERY

Session Chair: Tim Griffin (University of Minnesota)

6:00 – 6:10 pm Opening Remarks
6:10 – 7:00 pm **Ruedi Aebersold**; *ETH Zurich*

7:00 – 8:30 PM: **OPENING RECEPTION**, *Exhibits-Posters*

All attendees are invited to join us for food, drink, and connecting with colleagues.

MONDAY, MARCH 12

8:00 – 8:30 AM: **EARLY MORNING COFFEE & PASTRIES**, *Exhibits-Posters*

8:30 - 9:20 AM: **JPR Distinguished Achievement in Proteomics Award Lecture**, *Ballroom 2*
Session Chair: John Yates (The Scripps Research Institute)

8:30 - 9:20 am **Proteomics in the Hunt Lab: A Brief History of Instrumentation and Methods Development for the the Sequence Analysis of Peptides and Intact Proteins**; Donald F. Hunt; *University of Virginia*

Dr. Hunt is the recipient of this inaugural award funded by JPR and presented at US HUPO. This honor will be awarded annually at future US HUPO conferences.

9:20 - 9:50 AM: **COFFEE BREAK**, *Exhibits-Posters*
Refresh and visit with the exhibitors.

9:50 – 11:10 AM: PARALLEL SESSION
MICROBIOME PROTEOMICS, *Ballroom 2*
Session Chair: Bob Hettich (Oak Ridge National Laboratory)

9:50-10:15 am **Metabolic Activity Within the Gut Microbiome and Its Impact on Human Health**; Kelsey Veldkamp; Kimberleigh Romano; Federico Rey; Daniel Amador-Noguez; *University of Wisconsin, Madison, WI*

10:15-10:40 am **Interrogation of Gut Microbiomes with Chemical Probes and MS Proteomics**; Dennis Wolan, *The Scripps Research Institute*

10:40-10:55 am **Reproducible, Robust Quantitative Functional Analysis of Metaproteomes Using the Galaxy Platform**; Caleb Easterly¹; Joel Rudney¹; James Johnson¹; Carolin Kolmeder²; Andrea Argentini³; Thomas McGowan¹; Bjoern Gruening⁴; Praveen Kumar¹; Subina Mehta¹; Lennart Martens³; Tim Griffin¹; Pratik Jagtap¹; ¹*University of Minnesota, Minneapolis, MN*; ²*Max Planck Institute for Developmental Biology, Tuebingen, Germany*; ³*Ghent University, Ghent, Belgium*; ⁴*University of Freiburg, Freiburg, Germany*

10:55-11:10 am **Influence of the Gut Microbiota on Histone Acetylation through Butyrate Oxidation**; Peder Lund¹; Sarah Smith¹; Johayra Simithy¹; Lillian Chau¹; Elliot Friedman¹; Yedidya Saiman¹; Sophie Trefely²; Zuo-Fei Yuan¹; Kevin Janssen¹; Yemin Lan¹; Nathaniel Snyder²; Gary Wu¹; Benjamin Garcia¹; ¹*University of Pennsylvania, Philadelphia, PA*; ²*AJ Drexel Autism Institute, Drexel University, Philadelphia, PA*

MONDAY, MARCH 12

9:50 – 11:10 AM: PARALLEL SESSION
SIGNALING & PROTEIN INTERACTOMICS, Ballroom 1
 Session Chair: Fernando Bazan (Bio-Techne)

- 9:50-10:15 am **From RNA Granules to Signaling Networks: A Proximity Map of a Human Cell**; Anne-Claude Gingras; *University of Toronto, Toronto, Canada*
- 10:15-10:40 am **Proteome-Scale Profiling of the Human Protein Interaction Landscape**; Edward Huttlin; *Harvard Medical School, Boston, MA*
- 10:40-10:55 am **Integrating Virology and Proteomics to Define Mechanisms of Cellular Innate Immune Signaling during Herpesvirus Infection**; Krystal Lum; Benjamin Diner; Catherina Pan; Timothy Howard; Ileana Cristea; *Princeton University, Princeton, New Jersey*
- 10:55-11:10 Am **Proteomic Analysis Reveals Novel Hydroxyproline-Dependent Cellular Pathways in Cancer Cells**; Luke Erber; Tong Zhou; Yue Chen; *University Of Minnesota, Minneapolis, MN*

11:10 AM – 12:00 PM: PLENARY SESSION
LIGHTNING TALKS – ROUND I, Ballroom 2

High-energy (and brief) presentations selected from poster presentations. 90 seconds max or face the music!

Presentation Order

- Mon 01 **A Portable Pathway for Processing Peptide Array Data in KNIME with an Interest in Protein-Protein Interactions**; Lee Parsons; *Univ of Minnesota, Plymouth, MN. See Poster 18.*
- Mon 02 **Development of a Novel Strategy for Measurement of the Neurotoxin Beta-N-Methylamino-L-Alanine in Environmental Samples**; Kaylie Kirkwood; Joshua Beri; Michael Bereman; David Muddiman; *North Carolina State University, Raleigh, NC. See Poster 31.*
- Mon 03 **Adaptation of KALIP for the Development and Prediction of Artificial Peptide Substrates to Monitor FMS-Like Tyrosine Kinase 3 (FLT3) Activity**; Minervo Perez¹; W. Andy Tao³; Laurie L. Parker²; ¹*University of Minnesota, Minneapolis, MN*; ²*University of Minnesota Twin Cities, Minneapolis, MN*; ³*Purdue University, West Lafayette, IN. See Poster 49.*
- Mon 04 **Novel High-Throughput Metabolomic Techniques and Mainstream Tools for the Discovery of Drug Mechanism of Action**; Akos Vertes¹; Albert-Baskar Arul¹; Andrew R. Korte¹; Hang Li¹; Peter Avar¹; Peter Nemes¹; Lida Parvin¹; Sylwia Stopka¹; Sunil Hwang¹; Ziad J. Sahab¹; Deborah I. Bunin²; Merrill Knapp²; Andrew Poggio²; Carolyn L. Talcott²; Brian M. Davis³; Christine A. Morton³; Christopher J. Sevinsky³; Maria I. Zavodszky³; ¹*Dept. of Chem., The George Washington University, Washington, DC*; ²*SRI International, Menlo Park, CA*; ³*GE Global Research, Niskayuna, NY. See Poster 34.*
- Mon 05 **Changes in Glycan and Protein Expression in Aging Brain Nigrostriatal Pathway for Adeno-Associated Virus Mediated Gene Therapy in Parkinson's Disease**; Rekha Raghunathan¹; Nicole Polinski²; Joshua Klein¹; John D. Hogan¹; Chun Shao¹; Kshitij Khatri¹; Deborah Leon¹; Mark McComb¹; Caryl Sortwell²; Joseph Zaia¹; ¹*Boston University, Boston, MA*; ²*Michigan State University, Grand Rapids, MI. See Poster 54.*
- Mon 06 **Approach to the Confident Determination of Elemental Compositions in Mass Spectrometry Imaging Using IR-MALDESI**; Sitora Khodjanizova¹; Milad Nazari¹; Kenneth Garrard¹; Mayara Matos²; Glen Jackson²; David Muddiman¹; ¹*North Carolina State University, Raleigh, NC*; ²*West Virginia University, Morgantown, WV. See Poster 30*
- Mon 07 **Determining Peptide Substrates for Bruton's Tyrosine Kinase Biosensors via the KALIP Process**; Lindsay Breidenbach¹; Minervo Perez²; John B³; Laurie L. Parker⁴; ¹*University of Minnesota, Maple Grove, MN*; ²*University of Minnesota, Minneapolis, MN*; ³*UMN, Minneapolis, MN*; ⁴*University of Minnesota Twin Cities, Minneapolis, MN. See Poster 64.*
- Mon 08 **Application for Nanofluidic Devices Towards Single-Cell Proteomics: A Study with *Xenopus Laevis* Embryos**; Anumita Saha-Shah¹; Melody Esmaeili¹; Peter Klein¹; Benjamin A. Garcia²; ¹*University of Pennsylvania, Philadelphia, Pennsylvania*; ²*University of Pennsylvania School of Medicine, Philadelphia, PA. See Poster 65.*
- Mon 09 **Galaxy-Based Multi-Stage Two-Step Database Searching Pipeline for Improved multi-omics analysis**; Praveen Kumar¹; James Johnson¹; Thomas McGowan¹; Matthew Chambers²; Mohammad Heydarian³; Subina Mehta¹; Caleb Easterly¹; Joel Rudney¹; Pratik Jagtap¹; Timothy Griffin¹; ¹*University of Minnesota, Minneapolis, MN*; ²*Vanderbilt University, Nashville, TN*; ³*Johns Hopkins University, Baltimore, MD. See Poster 78.*

MONDAY, MARCH 12

- Mon 10 **Proteome-Wide Structure-Based Function Prediction Reveals Roles of Proteins Responsible for *E. coli* Fitness;** Chengxin Zhang; Mehdi Rahimpour; Peter Freddolino; Yang Zhang; *University of Michigan, Ann Arbor, MI. See Poster 66.*
- Mon 11 **Applying Proteomics and Metabolomics to Understand the Role Spingolipid Signaling in Pancreatic Cancer and Drug Sensitivity;** Max Jones; Monique Speirs; Connor Holman; John Price; *Brigham Young University, Provo, UT. See Poster 07*
- Mon 12 **iOmicsPASS: Integrative-Omics Approach for Predictive Analysis with Subnetwork Signatures in Breast and Colorectal Cancer Subtypes;** Hiromi Wai Ling Koh¹; Hyungwon Choi^{1,2}; ¹*National University of Singapore, Singapore*; ²*Institute of Molecular Cell and Biology, A*STAR, Singapore. See Poster 22.*
- Mon 13 **Predicting Cell-Line Specific Protein and Phospho-protein Abundances in Cancers;** Hongyang Li; Gilbert Omenn; Yuanfang Guan; *University of Michigan, Ann Arbor, MI. See Poster 24.*
- Mon 14 **Traumatic Brain Injury Proteomics Guides Novel KCC2-Targeted Therapy;** Pavel N. Lizhnyak; Demisha D.L. Porter; John T. Povloshock; Andrew K. Ottens; *Anatomy & Neurobiology, Virginia Commonwealth Univ, Richmond, VA. See Poster 36.*
- Mon 15 **Inhibition of KDM4C Leads to Histone Tail Clipping in a Triple Negative Breast Cancer Context;** Shawn Egri¹; Guillermo Peluffo^{2,3}; Malvina Papanastasiou¹; Kornelia Polyak^{2,3}; Jacob Jaffe¹; ¹*The Broad Institute, Cambridge, Massachusetts*; ²*Dana Farber Cancer Institute, Boston, MA*; ³*Harvard Medical School, Boston, MA. See Poster 10.*
- Mon 16 **New Protocols to Monitor Proteome Dynamics in the Developing Chordate Heart;** Burcu Vitriuel; Lionel Christiaen; Christine Vogel; *New York University, New York, NY. See Poster 09.*
- Mon 17 **Statistical Model for dDetecting dDifferentially Abundant Proteins in Isobaric Labeling-Based Protein Quantification Experiments;** Ting Huang¹; Meena Choi¹; Manuel Tzouros²; Nikhil Pandya²; Balazs Banfai²; Tom Dunkley²; Olga Vitek¹; ¹*Northeastern University, Boston, MA*; ²*Roche Innovation Center Basel, Basel, Switzerland. See Poster 83.*
- Mon 18 **Dynamics of Proteomics Changes in Presence of ER Stress in ALS Relevant Mouse Neuronal Model;** Shuvadeep Maity¹; Disi An²; Justin Rendleman¹; Esteban Mazzoni¹; Christine Vogel¹; ¹*Center for Genomics and System Biology, NYU, New York, NY*; ²*Department of Biology, NYU, New York, NY. See Poster 61.*
- Mon 19 **Impact of Three Different Mutations in Ehrlichia Chaffeensis in Altering the Global Gene Expression Patterns;** Chandramouli Kondethimmanahalli; Roman Ganta; *Kansas State University, Manhattan, KS. See Poster 46.*
- Mon 20 **Finding Proteins Connected to Rheumatoid Arthritis;** Marcus Hadfield¹; David Parkinson¹; Stephen Ames¹; Brad Naylor¹; Lavender Lin¹; Colette Quinn²; Lee Hansen¹; John Price¹; ¹*Brigham Young University, Provo, UT*; ²*TA Instruments, Draper, UT. See Poster 50*

MONDAY, MARCH 12

MONDAY LUNCH SEMINARS

Open to all attendees, but RSVP strongly encouraged (at booth or online) in advance as space is limited.

12:15 – 1:30 PM: **BRUKER**, *Deer-Elk Lake*



If you have not already registered in advance, please stop by booth Sunday night or Monday morning to RSVP.

During this informative seminar the technology behind the new timsTOF Pro, a novel QTOF instrument with a Trapped Ion Mobility Spectrometry (TIMS) front end, using the Parallel Accumulation Serial Fragmentation (PASEF) method will be described. In addition, exciting new applications in shotgun proteomics enabled by the technology described in the first talk will be discussed.

Highest Sensitivity, Highest Speed and Robust DDA Shotgun Proteomics with the timsTOF Pro Powered by PASEF
Gary Kruppa, *Ph. D., Vice President Proteomics, Bruker Daltonics Inc., Billerica MA*

Applications of PASEF on the timsTOF Pro for High Sensitivity Proteomics, Proximity Ligation Workflows and Multiplexed Analysis

Chris Adams, *Ph. D., Director of Proteomics, Stanford University Mass Spectrometry (SUMS)*

12:15 – 1:30 PM: **Biognosys**, *Maple-Pine Lake*



Taking a Leap to Quantifying the Proteome

If you have not already registered in advance, please stop by booth Sunday night or Monday morning to RSVP.

Next generation proteomics based on data independent acquisition (DIA) enables deep and reproducible quantification of thousands of proteins in a single measurement experiments (Bruderer et al., 2015, 2017).

DIA workflows overcome the technical limitation of sampling speed of mass spectrometers by isolating broad ranges of peptide ions in parallel-- because of this, powerful data deconvolution algorithms must be utilized. This enables DIA technology to become only limited by the sensitivity of the detector, and not the sequential speed of the mass spectrometer.

Strategies and Challenges for Large-Scale SWATH-MS Dataset Generation and Analysis for Quantitative Discovery Proteomics

Dr. Mukul K. Midha, *Institute for Systems Biology, Seattle*

Latest Advancements in Data Independent acquisition (DIA) Using Spectronaut Pulsar

Dr. Florian Marty, *Biognosys AG, Schlieren, Switzerland*

MONDAY, MARCH 12

1:30 – 3:00 PM: **POSTER SESSION**, *Posters-Exhibits*

3:00 – 4:20 PM: PARALLEL SESSION
INFORMATICS: EMERGING & NEW APPROACHES, *Ballroom 2*
Session Chair: Bobbie-Jo Webb-Roberstson (PNNL)

- 3:00-3:25 pm **Alexey Nesvizhskii**; *University of Michigan, Ann Arbor, MI*
- 3:25-3:50 pm **Next Generation MaxQuant: Machine Learning Enhanced Quantitative Proteomics**; Juergen Cox; *Max-Planck Institute*
- 3:50-4:05 pm **Improved Protein Inference for Multiple Protease MS Data Using a Single Database Search**; Rachel Miller¹; Connor Hoffmann¹; Gloria Sheynkman^{2, 2}; Robert Millikin¹; Stefan Soltsev¹; Anthony Cesnik¹; Michael Shortreed¹; Lloyd Smith^{1, 3}; ¹*University Wisconsin-Madison, Madison, Wisconsin*; ²*Center for Cancer Systems Biology (CCSB), Boston, MA*; ³*Genome Center of Wisconsin, Madison, WI*
- 4:05-4:20 pm **A Sampling of Perceptions in the Field of Mass Spectrometry Data Processing Software**; Rob Smith; *University of Montana, Missoula, MT*

3:00 – 4:20 PM: PARALLEL SESSION
PROTEOMICS OF CANCER & DISEASE, *Ballroom 1*
Session Chair: Lingjun Li (University of Wisconsin-Madison)

- 3:00-3:25 pm **Proteomic Analysis of Stalled Replication Forks**; Anja Bielinsky¹; Ya-Chu Chang¹; Rebecca Rivard²; Yee Mon Thu¹; Susan Kaye Van Riper¹; LeeAnn Higgins²; Todd Markowski¹; Katarzyna Kulej²; Jack Hedberg¹; Luke Erber¹; Yue Chen¹; Eric Brown²; ¹*University of Minnesota, Minneapolis, MN*; ²*University of Pennsylvania, Philadelphia, PA*
- 3:25-3:50 pm **Hunting Circulating Mediators of Systemic Vascular Dysfunction after Carbon Nanotube Exposure**; Andrew Ottens; *Virginia Commonwealth University, Richmond, VA*
- 3:50-4:05 pm **Polycomb Loss Enhances Oncogenesis But Leads to Therapeutic Vulnerabilities in Malignant Peripheral Nerve Sheath Tumors**; John Wojcik^{1, 2}; Dylan Marchione^{1, 2}; Simone Sidoli^{1, 2}; Ben Garcia^{1, 2}; ¹*University of Pennsylvania, Philadelphia, PA*; ²*University of Pennsylvania School of Medicine, Philadelphia, PA*
- 4:05-4:20 pm **A Proteomics Approach to Understand the Role of Autophagy in Colorectal Cancer and Enhance Chemosensitivity**; Monique Speirs; Emily Cannon; John Price; *Brigham Young University, Provo, Utah*

4:30 – 5:50 PM: PARALLEL SESSION
QUANTITATIVE PROTEOMICS I, *Ballroom 2*
Session Chair: Sarah Parker (Cedars-Sinai Medical Center)

- 4:30-4:55 pm **Drug Target Identification by Label-Free Differential Mass Spectrometry**; Nathan Yates; *University of Pittsburgh, Pittsburgh, PA*;
- 4:55-5:20 pm **Targeted Peptide Quantification Using Data Independent Acquisition**; Michael MacCoss; *University of Washington, Seattle, WA*
- 5:20-5:35 pm **FlashLFQ: Ultrafast Label-Free Quantification of Peptides in Proteomics**; Robert J. Millikin; Stefan K. Soltsev; Michael R. Shortreed; Lloyd M. Smith; *University of Wisconsin, Madison, WI*
- 5:35-5:50 pm **Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results**; Florian Marty; Roland Bruderer; Lukas Reiter; *Biognosys AG, Schlieren, Switzerland*

MONDAY, MARCH 12

4:30 – 5:50 PM: PARALLEL SESSION
PROTEOMICS OF AGING & AGE-RELATED DISEASE, *Ballroom 1*
Session Chair: Birgit Schilling (Buck Institute)

- 4:30-4:55 pm **How Protein PTMs Inspired Pharmacological Chaperones and Crosslinkers That Minimize Dead-End Modifications**; Jeff Agar; *Northeastern University, Boston, MA*
- 4:55-5:20 pm **Understanding the Influence of Aging on Host Response to Infection**; Renā Robinson; *Vanderbilt University, Nashville, TN*
- 5:20-5:35 pm **Proteome-wide Modulation of Degradation Dynamics in Response to Growth Arrest**; Tian Zhang^{1,2}; Kevin Welle²; Jennifer Hryhorenko²; [Sina Ghaemmaghani](#)²; ¹*Harvard Medical School, Boston, MA*; ²*University of Rochester, Rochester, NY*
- 5:35-5:50 pm **Identifying ApoE isoform Dependent Changes for Protein Turnover in the Brain**; [Joseph Creery](#); Joshua Chamberlain; Russell Denton; John Price; *Brigham Young University, Provo, UT*

5:50 – 6:30 PM: **INFORMAL MIXER**, *Exhibits-Posters*

Join exhibitors for snacks and drinks *before the evening workshops*.

EVENING WORKSHOPS

All attendees are invited to participate in Monday evening workshops.

6:30 – 8:00 PM: PARALLEL EVENING WORKSHOP

LINCS WORKSHOP, *Ballroom 2*

Workshop Organizers: Andrea Matlock (Cedars-Sinai Medical Center), Mike MacCoss (University of Washington), and Jenny Van Eyk (Cedars-Sinai Medical Center)

Workshop Chair: Mike MacCoss

The NIH program **Library of Network-Based Cellular Signatures** (LINCS) presents benefits and challenges of large proteomic data sets, current efforts to generate a comprehensive library of signatures representative of chemical and genetic perturbations in cellular systems, as well as analysis tools and platforms for integration across different data types. Paving the road to a shared vision of powerful biological knowledge gains from large proteomic data sets queried individually or combined with omic integration studies, now and into the future.

TUESDAY, MARCH 13

7:00 AM: ZUMBA!!

Have a little early morning fun, join us for a 45-min Zumba session. Come by Registration, sign a quick waiver and we will direct you to the US HUPO Zumba class. There is a free class for US HUPO attendees only. Look for US HUPO President David Muddiman (a Zumba aficionado) to be among the intrepid!

8:00 – 8:30 AM: EARLY MORNING COFFEE & PASTRIES, Exhibits-Posters

**8:30 – 9:20 AM: PLENARY SESSION
AWARD PRESENTATIONS AND LECTURES, Ballroom 2**
Gil Omenn, presiding

- 8:30 – 8:55 am **Gilbert S. Omenn Computational Proteomics Award: Hannes Röst, University of Toronto**
Award presentation followed by 20 minute talk.
- 8:55 – 9:08 am **Robert J. Cotter New Investigator Award: Leslie Hicks, University of North Carolina, Chapel Hill**
Award presentation followed by 20 minute talk.

9:20 - 9:50 AM: COFFEE BREAK, Exhibits-Posters
Coffee and pastries with the exhibitors.

**9:50 – 11:10 AM: PARALLEL SESSION
QUANTITATIVE PROTEOMICS II, Ballroom 2**
Session Chair: Yue Chen (University of Minnesota)

- 9:50-10:15 am **Quantitative Multidimensional Characterization of Protein-Protein Interactions in Cancer; Danielle Swaney¹; Minkyu Kim¹; Margaret Soucheray¹; Kyumin Kim¹; Fan Zheng²; Jennifer Grandis¹; Trey Ideker²; Nevan Krogan¹; ¹University of California, San Francisco, San Francisco, CA; ²University of California, San Diego, San Diego, CA**
- 10:15-10:40 am **Exploring Protein Interactions Networks with High-Throughput Quantitative Proteomics; Wilhelm Haas; Massachusetts General Hospital, Boston, MA**
- 10:40-10:55 am **Quantifying Protein Synthesis Rates During Fetal Development Reveals Temporal and Tissue-Specific Regulatory Networks; Josue Baeza¹; Barbara Coon²; William Peranteau²; Ben Garcia¹; ¹University of Pennsylvania School of Medicine, Philadelphia, PA; ²Childrens Hospital of Pennsylvania, Philadelphia, PA**
- 10:55-11:10 am **The Initiating Events in Direct Cardiomyocyte Reprogramming Involve Temporally Distinct Gene Expression and Proteome Abundance Signatures; Todd Greco¹; Kimberly Sauls²; Li Wang²; Meng Zou²; Michelle Villasmil²; Li Qian²; Frank Conlon²; Ileana Cristea¹; ¹Princeton University, Princeton, NJ; ²Univ of North Carolina McAllister Heart Institute, Chapel Hill, NC**

**9:50 – 11:10 AM: PARALLEL SESSION
INTACT PROTEIN STRUCTURAL ANALYSIS, Ballroom 1**
Session Chair: Lingjun Li (University of Wisconsin)

- 9:50-10:15 am **Analysis of Intact Proteins and Protein Complexes by Ultraviolet Photodissociation Mass Spectrometry; Jennifer Brodbelt; University of Texas at Austin, Austin, TX**
- 10:15-10:40 am **Native MS in Structural Biology: Surface Collisions of Protein Complexes; Vicki Wysocki; The Ohio State University, Columbus, OH**
- 10:40-10:55 am **Linear and Differential Ion Mobility Separations of Middle-Down Proteoforms; Alyssa Garabedian¹; Matthew Baird²; Jacob Porter¹; Kevin Jeanne Dit Fouque¹; Pavel Shliha³; Ole Jensen³; Todd Williams⁴; Francisco Fernandez-Lima¹; Alexandre Shvartsburg²; ¹Florida International University, Miami, FL; ²Wichita State University, Wichita, KS; ³University of Southern Denmark, Odense, Denmark; ⁴University of Kansas, Lawrence, KS**
- 10:55-11:10 am **Characterizing Transmembrane Domains of Membrane Proteins with Top-Down Ultra-Violet Photodissociation (UVPD) High-Resolution Mass Spectrometry; Julian Whitelegge¹; Romain Huguet²; Chris Mullen²; Vlad Zabrouskov²; ¹UCLA, Los Angeles, ; ²Thermo Fisher Scientific, San Jose, CA**

TUESDAY, MARCH 13

11:10 AM – 12:00 PM: PLENARY SESSION

LIGHTNING TALKS – ROUND II, Presidential Ballroom (2nd Level)

High-energy (and brief) presentations selected from poster presentations. 90 seconds max or face the music!

Presentation Order

- Tues 01 **Spritz: An RNA-Seq Analysis Engine that Enables Proteogenomics on Windows;** Anthony Cesnik; Michael Shortreed; Brian Frey; Lloyd Smith; *UW-Madison, Madison, WI. See Poster 17.*
- Tues 02 **Connecting the Dots Between Metabolic Reprogramming and Protein Function in Cancer;** Emily Cannon; Monique Pare Speirs; Max Jones; John Price; *Brigham Young University, Provo, UT. See Poster 03.*
- Tues 03 **A Novel Approach for Isolating Exosomes From Clinical Sample;** Blake Ebert; Alex J Rai, PhD; *Columbia University Medical Center, New York, NY. See Poster 06.*
- Tues 04 **A Quantitative Evaluation of Algorithms for Isotopic Trace Extraction via Ion Chromatogram Clustering;** Mathew Gutierrez; Amber Yascavage; Rob Smith; *University of Montana, Missoula, MT. See Poster 14.*
- Tues 05 **Detection of Post-Translational Modifications Using Mass Spectrometry;** Nathan Zuniga; Marcus Hadfield; Lavender Lin; David Parkins; John Price; *Brigham Young University, Provo, UT. See Poster 48.*
- Tues 06 **Big Data: Ensuring Integrity of Differential Analyzes From Large Scale DIA-MS Experiments;** Andrea Matlock¹; Erin Crowgey²; Vidya Venkatraman¹; Victoria Dardov¹; Jennifer Van Eyk¹; *¹Cedars-Sinai Medical Center, Los Angeles, CA; ²Nemours Children's Health System, Wilmington, DE. See Poster 52.*
- Tues 07 **PTM Knowledge Networks and LINCS Multi-Omics Data for Kinase Inhibitor Drug-Analytcs in Lung Cancer;** Xu Zhang¹; Karen Ross²; Jake Jaffe³; Michele Forlin⁴; Cathy Wu⁵; Udayan Guha¹; *¹CCR, NCI, NIH, Bethesda, MD; ²Georgetown University Med. Ctr., Washington DC, Washington DC; ³Broad Institute of Harvard and MIT, Cambridge, MA; ⁴University of Miami, Coral Gables, FL; ⁵University of Delaware, Newark, DE. See Poster 04.*
- Tues 08 **Investigation of the Effect of Reduced Synthesis and Degradation on in Vivo Protein Stability;** Lavender Hsien-Jung Lin; Marcus Hadfield; Nathan Zuniga; John C Price; *Brigham Young University, Provo, UT. See Poster 58.*
- Tues 09 **Phosphoproteomic Investigation of the Mechanism of Calorie Restriction Attenuation by Dietary Protein Signaling;** Joshua Mcphie¹; Marco Hadisurya²; Aaron Moss³; Richard Carson¹; John Price¹; *¹Brigham Young University, Provo, UT; ²Brigham Young University - Hawaii, Laie, HI; ³Brigham Young University - Idaho, Rexburg, ID. See Poster 60.*
- Tues 10 **Integrated Proteogenomic Analyses Reveal Extensive Tumor Heterogeneity and Validate Expression of Somatic Mutations in Lung Adenocarcinoma;** Xu Zhang¹; Paul Rudnick²; Shaojian Gao¹; Shivangi Awasthi¹; David Fenyo³; Udayan Guha¹; *¹CCR, NCI, NIH, Bethesda, MD; ²Spectragen Informatics LLC, Bainbridge Island, WA; ³NYU School of Medicine, New York, NY. See Poster 75.*
- Tues 11 **Large Datasets and You: Using Proteomics to Design a Biosensor;** John B¹; Minervo Perez²; Laurie L. Parker³; *¹UMN, Minneapolis, MN; ²University of Minnesota, Minneapolis, MN; ³University of Minnesota Twin Cities, Minneapolis, MN. See Poster 63.*
- Tues 12 **Development of Hydrogen-Deuterium Exchange Methodology Coupled to Top- and Middle-Down Mass spectrometry Enables High-Resolution Analysis of Histone Dynamics;** Kelly Karch; Mariel Coradin; ZhongYuan Kan; Ben Black; Benjamin Garcia; *University of Pennsylvania School of Medicine, Philadelphia, PA. See Poster 67.*
- Tues 13 **Antibody-Antigen Interaction Characterization Using Stopped Flow Assisted Hydrogen Deuterium Exchange Mass Spectrometry;** Zhe Wang¹; Kellye Sutton¹; Michael Ashby¹; Kenneth Smith²; Si Wu¹; *¹University of Oklahoma, Norman, OK; ²Oklahoma Medical Research Foundation, Oklahoma City, OK. See Poster 68.*
- Tues 14 **Development of A High-Performance Sheathless CZE-MS Interface for Top-Down Proteomics;** Lushuang Huang; Zhe Wang; Si Wu; *University of Oklahoma, Norman, OK. See Poster 70.*
- Tues 15 **MetaMorpheus for Enhanced Global PTM Discovery (G-PTM-D) and Quantitative Proteomics;** Stefan Soltsev; Michael Shortreed; Brian Frey; Lloyd Smith; *University of Wisconsin, Madison, WI. See Poster 51.*
- Tues 16 **Improved Protein Sequence Analysis by 21 Tesla FT-ICR MS/MS and Advanced Mass Spectral Interpretation;** Lissa Anderson¹; Jeffrey Shabanowitz²; Chad Weisbrod¹; Greg Blakney¹; Donald Smith¹; Donald Hunt²; Christopher Hendrickson¹; *¹NHMFL, Tallahassee, FL; ²Dept. of Chemistry University of Virginia, Charlottesville, VA. See Poster 72.*

TUESDAY, MARCH 13

- Tues 17 **Examination of the Specific Binding of Cytochrome c on MPA-Coated Gold Nanoparticles via Protein Footprinting;** Emily Tollefson¹; Xi Zhang²; Nikita Rozanov³; Caley Allen³; Rigoberto Hernandez³; Catherine Murphy²; Erin Carlson¹; ¹University of Minnesota, Minneapolis, MN; ²University of Illinois Urbana Champaign, Urbana, IL; ³Johns Hopkins University, Baltimore, MD. **See Poster 73.**
- Tues 18 **Active Kinase Characterization Using an Isobaric Labeling Activity-Correlated Protein Profiling Platform (TMT-ACPP);** Hongyan Ma; Paul Sims; Si Wu; University of Oklahoma, Norman, OK. **See Poster 77.**
- Tues 19 **A High-throughput Omics Pipeline for Comprehensive Analysis of Challenged Human Cells;** Danielle Gutierrez¹; Carrie Romer¹; Jamie Allen¹; Yuan-Wei Nei²; Melissa Farrow³; Randi Gant-Branum¹; Stacy Sherrod¹; Nicole Muszynski¹; Eric Spivey¹; Salisha Hill¹; Kristie Rose¹; John Wikswo¹; John McLean¹; Eric Skaar³; D. Borden Lacy³; Jeremy Norris¹; Richard Caprioli¹; ¹Vanderbilt University, Nashville, TN; ²Quest Diagnostics, Chantilly, VA; ³Vanderbilt University Medical Center, Nashville, TN. **See Poster 79.**

TUESDAY LUNCH SEMINARS

Open to all attendees, but RSVP strongly encouraged (at booth or online) in advance as space is limited.

12:15 – 1:30 PM: **THERMO FISHER SCIENTIFIC**, Deer-Elk Lake

ThermoFisher
SCIENTIFIC

If you have not already registered in advance, please stop by booth Sunday night or Monday morning to RSVP.

In this seminar, the use of TMT based multiplexing quantitative proteomics for profiling subcutaneously implanted breast cancer patient-derived xenografts (PDXs) will be discussed. PDXs are the best model of primary human tumors and enable cancer researchers to study drug response and tumor biology. The stroma plays an important role in breast cancer progression. In PDX models, the tumor-associated stroma is mouse-derived and can be differentiated from the tumor (human-derived) by analysis of species-unique peptides. Precise and accurate TMT-based multiplexed quantitative proteomics enabled us to discover, in a cohort of 21 breast PDX tumors, that the education of the stroma was highly individualized but biologically coordinated. In particular, proteins involved in immune signaling varied in a subtype- and stage-specific manner. These findings may have future implications for treatment stratification and provide a platform from which to understand tumor-stroma interactions on a large-scale protein level.

Multiplexed Mass Spectrometry Solutions for Cancer Proteomics

Translational proteomics workflows place much greater emphasis on biological replicate analysis of large, well-defined cohorts instead of fewer samples and greater numbers of technical replicates. These also need to be quantitative, with changes across cohorts of samples measured to be precise and accurate. Multiplexed tandem mass tag (TMT) solutions offer greater parallelization potential in quantitative mass spectrometry experiments resulting in greater throughput.

Jason Held, Ph.D., Assistant Professor, Washington University School of Medicine, Departments of Medicine, Oncology Division and Department of Anesthesiology

12:15 – 1:30 PM: **SCIEX**, Birch-Pine Lake

SCIEX

If you have not already registered in advance, please stop by booth Sunday night or Monday morning to RSVP.

Many challenges exist in realizing the potential of Precision Medicine, especially in producing robust, reproducible quantitative proteomics measurements. This workshop will address many of the challenges that currently exist in making these measurements in a high-throughput, industrialized fashion:

- Microflow LC for enhanced workflow robustness and sample throughput
- Cloud-based data processing to address the challenges of large data file and large sample numbers
- Integration with other 'omics data to provide more complete biological insight

Accelerating Quantitative Proteomics – microflow SWATH® Acquisition

Speaker: Arianna Jones & Guest Speaker

TUESDAY, MARCH 13

1:30 – 3:00 PM: **POSTER SESSION**, *Posters-Exhibits*

3:00 – 4:20 PM: PARALLEL SESSION
METABOLISM AND DISEASE, *Ballroom 2*
Session Chair: Ben Garcia (University of Pennsylvania)

- 3:00-3:25 pm **Defining Mitochondrial Protein Function through Systems Biochemistry**; David Pagliarini; *Morgridge Institute for Research, Madison, WI*
- 3:25-3:50 pm **Chemical-Proteomic Strategies to Investigate Reactive Cysteines**; Eranthii Weerapana; *Boston College, Boston, MA*
- 3:50-4:05 pm **Mapping the Changes to the Serum and Urinary Proteomes when the Pancreas is Removed**; Tue Bjerg Bennike^{1, 2}; Melena Bellin⁴; Saima Ahmed^{1, 2}; Zobeida Cruz-Monserrate³; Darwin Conwell³; Hanno Steen^{1, 2}; ¹*Boston Children's Hospital, Boston, MA*; ²*Harvard Medical School, Boston, MA*; ³*The Ohio State University Wexner Medical Center, Columbus, OH*; ⁴*University of Minnesota Medical Center, Minneapolis, MN*
- 4:05-4:20 pm **Sirtuin-Regulated Lipoylation is an Evolutionarily Conserved Mediator of Metabolic Health and Disease**; Elizabeth Rowland; Todd Greco; Caroline Snowden; Cora Betsinger; Ileana Cristea; *Princeton University, Princeton, NJ*

3:00 – 4:20 PM: PARALLEL SESSION
IMMUNOPEPTIDOMICS, *Ballroom 1*
Session Chair: Melanie Patterson (AbbVie)

- 3:00-3:25 pm **Immunopeptidomics: Accelerating the Development of Personalized Cancer Immunotherapy**; Michal Bassani-Sternberg; *CHUV, Lausanne, Switzerland*
- 3:25-3:50 pm **Chemical Biology to Investigate the Immunopeptidome**; Stephanie Jensen; Greg Potts; Melanie Patterson; *AbbVie, Chicago, IL*
- 3:50-4:05 pm **Characterizing the Intracellular Peptidome to Define Protein Areas Efficiently Processed and Presented across Multiple HLAs**; Julie Boucau¹; Carl Kadie²; David Heckerman²; Sylvie Le Gall¹; ¹*Ragon Institute of MGH, MIT and Harvard, Cambridge, MA*; ²*Microsoft Research, Redmond, WA*
- 4:05-4:20 pm **Improved Discovery of Post-Translationally Spliced Peptides Using Separate b- and y-Ion Databases**; Zach Rolfs; Stefan Solntsev; Michael Shortreed; Brian Frey; Mark Scalf; Alan Attie; Lloyd Smith; *University of Wisconsin, Madison, Wisconsin*

TUESDAY, MARCH 13

4:30 – 5:50 PM: PARALLEL SESSION
PTMs: NEW APPROACHES AND APPLICATIONS, Ballroom 2
Session Chair: Chris Barnes (NovoNordisk)

- 4:30-4:55 pm **Peptide Biosensors for Measuring Kinase Activity in Cells;** Laurie Parker; *University of Minnesota, Minneapolis, MN*
- 4:55-5:20 pm **Judit Villen;** *University of Washington, Seattle, WA*
- 5:20-5:35 pm **Deciphering the Human Sirtuin 3 Antiviral Functions and the Temporal Mitochondrial Acetylome during Herpesvirus Infection;** Xinlei Sheng; Laura Murray; Morgan Sly; Ileana Cristea; *Princeton University, Princeton, NJ*
- 5:35-5:50 pm **Human Succinyl-CoA Ligase Deficiency Causes Widespread Protein Hyper-Succinylation in Patient-Derived Fibroblasts and Myotubes;** Philipp Gut^{1, 2}; Jesse G. Meyer³; Sanna Matilainen⁴; Chris Carrico³; Pieti Pällijeff⁴; Birgit Schilling³; Anu Suomalainen⁴; Eric Verdin³; ¹*Gladstone Institutes, UCSF, San Francisco, CA*; ²*Nestle Institute of Health Sciences, Ecublens, Switzerland*; ³*Buck Institute, Novato, CA*; ⁴*University of Helsinki, Helsinki, Finland*

4:30 – 5:50 PM: PARALLEL SESSION
GLYCOMICS FOR CLINICAL APPLICATIONS, Ballroom 1
Session Chair: Hui Zhang (Johns Hopkins University)

- 4:30-4:55 pm **Integrated Workflows for Intact Glycopeptide Analysis;** Sharon J. Pitteri; *Stanford University, Palo Alto, CA*
- 4:55-5:20 pm **Assignment of Site-Specific Glycosylation in Complex Proteoglycan Samples;** Joshua Klein; Le Meng; Joseph Zaia; *Boston University, Boston, MA*
- 5:20-5:35 pm **Immunoglobulin G Fc Region N-linked Glycosylation as a Clinical Biomarker for Insulin Resistance;** Andrew Lipchik^{1, 2}; Michael Snyder^{1, 2}; ¹*Stanford University, Stanford, CA*; ²*Stanford University, Stanford, CA*
- 5:35-5:50 pm **N-Glycopeptide Feature Identification by Revealing Trends Between Analyte Composition and Compensation Field Through FAIMS-Coupled MS Platform;** Daniel Delafield¹; Zhe Wang¹; Matthew Baird²; Alexandre Shvartsburg²; Si Wu¹; ¹*University of Oklahoma, Norman, OK*; ²*Wichita State University, Wichita, KS*

TUESDAY, MARCH 13

6:00 –7:30 PM: **CAREER DEVELOPMENT EVENT**
Deer-Elk Lake

This special event is sponsored by Bio-Techne

The logo for biotechne, featuring the word "biotechne" in a bold, blue, sans-serif font. The letter "i" is lowercase and has a dot, while the rest of the letters are lowercase. A registered trademark symbol (®) is located at the top right of the word.

A special program coordinated by a committee of young researchers (Kyle Delaney, *University of Chicago*; Joey Huang, *University of Chicago*; Kevin Janssen, *University of Pennsylvania*; Matthew Perez-Neut, *University of Chicago*) with Laurie Parker. All are invited, but the target participants are graduate students, post-docs, and other early career researchers. The program will feature a panelist poster session followed by a reflection exercise and discussion.

7:30-9:00 PM: **SOCIAL EVENT**
Atrium

This special event is sponsored by Pressure BioSciences

Join all attendees for a supper style event featuring live jazz!

The logo for Pressure BioSciences Inc. It features the letters "PBI" in a large, stylized font with a red-to-blue gradient. To the right of "PBI", the words "Pressure BioSciences Inc." are stacked vertically in a blue, serif font.

WEDNESDAY, MARCH 14

8:00 – 8:30 AM: **EARLY MORNING COFFEE & PASTRIES**, Foyer

8:30 – 9:20 AM: PLENARY SESSION
ANNOUNCEMENT OF BEST STUDENT AND POST-DOC POSTER AWARD WINNERS

TIPS & TRICKS (TECHNOLOGY FOCUS) LIGHTNING SESSION

Ballroom 2

Five-minute presentations selected from poster presentations.

Focus is on work-arounds, hacks, and new technology. Posters will be on display in foyer during the coffee break.

Presentation Order

- Wed 01 **High Pressure Denaturation Improves Protein Digestion by Trypsin**; Vera Gross; Nicole Cutri; Gary Smejkal; Alexander Lazarev; *Pressure BioSciences, Inc., South Easton, MA. See Poster 45.*
- Wed 02 **Abundant Protein Depletion and Multiplexed Protein Quantitation of Human Plasma Samples – A Reproducibility and Scaling Study**; Sergei Snovida; Katherine Herting; Ramesh Ganapathy; Ryan Bomgardner; Barbara Kaboord; Chris Etienne; Monica O'Hara; John Rogers; *Thermo Fisher Scientific, Rockford, IL. See Poster 01.*
- Wed 03 **High-Throughput Untargeted Data-Independent Analysis of Misoprostol Challenged HL60 Cells as a Model for Chemical Threat Assessment**; Roy Martin¹; Brad Williams¹; Danielle Gutierrez²; Jeremy Norris²; ¹Waters, Beverly, MA; ²Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN. **See Poster 90.**
- Wed 04 **Optimizing Collision Energy in Collision-Induced Dissociation for Peptide Sequencing**; Nandhini Sokkalingam; Luke Schneider; William Wright; Siamak Ashrafi; Adam Tenderholt; Jeffrey Peterson; *Veritomyx Inc., Palo Alto, CA. See Poster 19.*
- Wed 05 **Development of a Novel LC Concept for Clinical Proteomics**; Nicolai Bache¹; Philipp Geyer²; Ole Hoerning¹; Lasse Falkenby¹; Peter Treit²; Sophia Doll²; Igor Paron²; Florian Meier²; Ole Vorm¹; Matthias Mann²; ¹Evosep, Odense, Denmark; ²Max-Planck Inst. for Biochemistry, Martinsried, Germany. **See Poster 40.**
- Wed 06 **timsTOF Pro Powered by PASEF for High Speed and Sensitive Shotgun Proteomics**; Gary Kruppa¹; Juergen Cox²; Heiner Koch³; Scarlet Koch³; Baozhen Shan⁴; ¹Bruker Daltonics Inc., Billerica, MA; ²Max Planck Inst. of Biochem., Martinsried, Germany; ³Bruker Daltonik, GmbH, Bremen, Germany; ⁴Bioinformatics Solutions Inc, Waterloo, ON, Canada. **See Poster 42.**
- Wed 07 **Stroma Liquid Biopsy – Pan-Cancer Dysregulation of the Serum Proteome**; Matthew Kuruc¹; Haiyan Zheng²; Amenah Soherwardy²; Swapam Roy¹; ¹Biotech Support Group LLC, Monmouth Junction, NJ; ²Rutgers Center for Proteomics, Piscataway, NJ. **See Poster 05.**
- Wed 08 **Liquid Extraction Surface Analysis (LESA) and LESAPlus Chromatography as Novel Surface Analysis Tools for Mass Spectrometry**; Daniel Eikel; *Advion, Ithaca, NY. See Poster 44.*

9:20 - 9:50 AM: **COFFEE BREAK**, Foyer
Tips & Tricks posters will be featured in the foyer.

WEDNESDAY, MARCH 14

9:50 – 11:10 AM: PARALLEL SESSION

NEXTGEN CLINICAL MS-BASED PROTEOMICS, Ballroom 2

Session Chairs: Victoria Zhang (University of Rochester Medical Center) and Henry Rodriguez (NIH, NCI)

- 9:50-10:15 am **Adapting Proteomics for Patient Care**; Mari DeMarco^{1, 2}; ¹University of British Columbia, Vancouver, Canada; ²Providence Health Care, Vancouver, Canada
- 10:15-10:40 am **Mass Spectrometry Imaging for Surgical Neuropathology and Neurooncology**; Nathalie Agar; Brigham and Women's Hospital, Harvard Medical School, Boston, MA
- 10:40-10:55 am **Selecting Patients with Colorectal Cancer for 5-fluorouracil-based Adjuvant Chemotherapy Using Quantitative Proteomic Analysis**; Yuan Tian¹; Dongyao Yan¹; Ji Hyung Hong²; Hee Yeon Lee²; Jae Ho Byun²; Fabiola Cecchi¹; Sarit Schwartz¹; Wei-li Liao¹; Eunkyung An¹; Todd A. Hembrough¹; ¹Nantomics, Rockville, MD; ²Incheon St. Mary's Hospital, Incheon, Incheon, South Korea
- 10:55-11:10 am **Optimization of Sample Preparation Methods for Using Residual Pap Test Fixatives for Mass Spectrometry-Based Proteomic Identification of Ovarian Cancer Biomarkers**; Anna Rogers¹; Kristin Boylan¹; Melissa Geller¹; Peter Argenta¹; Samantha Hoffman¹; Timothy Griffin¹; Nasrin Perskvist²; Amy Skubitz¹; ¹University of Minnesota, Minneapolis, MN; ²Karolinska Institute, Stockholm, Sweden

9:50 – 11:10 AM: PARALLEL SESSION

INTEGRATIVE 'OMICS: MULTI-OMICS, Ballroom 1

Session Chair: David Fenyo (New York University)

- 9:50-10:15 am **Identifying Therapeutic Targets in Cancer using Proteogenomics**; Kelly Ruggles; New York University, New York, NY
- 10:15-10:40 am **From Raw Data to New Discoveries: Towards a Complete Proteogenomic Informatics Solution**; Praveen Kumar, James E. Johnson, Thomas McGowan, Matthew C. Chambers, Subina Mehta, Caleb Easterly, Ray Sajulga, Shane Hubler, Candace R. Guerrero, Pratik D. Jagtap and Timothy J. Griffin; University of Minnesota, Minneapolis, MN
- 10:40-10:55 am **Identification of Protein Isoforms Resulting from Alternative pre-mRNA Splicing by the Integration of Mass Spectrometry and RASL-Seq**; Laura Agosto^{1, 2}; Simone Sidoli^{1, 2}; Amber K. Weiner^{1, 2}; Kristen W. Lynch¹; Benjamin A. Garcia^{1, 2}; ¹University of Pennsylvania School of Medicine, Philadelphia, PA; ²Epigenetics Institute, Philadelphia, PA
- 10:55-11:10 am **Multi-Omic Molecular Profiling of Lung Cancer Risk in Chronic Obstructive Pulmonary Diseases**; Brian Sandri¹; Adam Kaplan¹; Shane Hodgson²; Mark Peterson¹; Svetlana Avdulov¹; LeeAnn Higgins¹; Todd Markowski¹; Ping Yang³; Andrew Limper³; Tim Griffin¹; Peter Bitterman¹; Eric Lock¹; Chris Wendt²; ¹University of Minnesota, Minneapolis, MN; ²Veterans Affairs Medical Center, Minneapolis, MN; ³Mayo Clinic, Rochester, MN

11:10 AM – 12:00 PM: **PLENARY LECTURE + CLOSING SESSION, Ballroom 2**

Session Chair: Josh Coon (University of Wisconsin)

- 11:10 -11:55 am **Spatiotemporal Proteome Organization of the Human Cell**; Emma Lundberg, KTH Royal Institute of Technology
- 11:55 am-12:00 pm Closing Remarks