Welcome to the 59th ASMS Conference on Mass Spectrometry and Allied Topics. Conference program activities and exhibit booths are in the Colorado Convention Center. Corporate Member hospitality suites are located in the Hyatt Regency Hotel (across 14th Street from the convention center).

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*Titles in the following sections are provided by authors. The complete abstracts are available online: www.asms.org*
**NEW THIS YEAR**

“MyASMS” is a comprehensive online map, poster/exhibit guide, session locator and scheduler: www.asms.org. The program is compatible with most mobile devices, as well as your computer.

**THIS JASMS SUPPLEMENT** is the only printed program. Bring this to the conference with you.

**REGISTRATION** is open 10:00 am - 8:00 pm on Sunday and 7:30 am - 5:00 pm on Monday through Thursday.

**SUNDAY TUTORIAL SESSION, 5:00 - 6:30 PM**

**Wells Fargo Theatre**

5:00 - 5:45 pm  
*Good Mass Spectrometry and its Place in Good Science: Sometimes Close Enough Is Really Not Good Enough*  
Mark W. Duncan  
University of Colorado Denver, Anschutz Medical Campus

5:45 - 6:30 pm  
*LC and MS: A Match Made in Heaven*  
James Jorgenson  
University of North Carolina

**PLENARY SESSIONS, Wells Fargo Theatre**

**SUNDAY CONFERENCE OPENING, 6:45 - 7:45 PM**

*Our Stellar Origins Revealed by Stardust Grains*  
Ernst Zinner  
Washington University

**MONDAY, 4:45 - 5:30 PM, Robert J. Cotter,**  
Award for a Distinguished Contribution in Mass Spectrometry

**TUESDAY, 4:45 - 5:30 PM, Béla Paizs,**  
Biemann Medal

**THURSDAY, 4:45 - 5:30 PM**

*Why Are We Surprised by Only Some of the Things that We See? Visual Illusions, the Brain, and Baseball*  
Arthur Shapiro  
American University

**ORAL SESSIONS** are 8:30 - 10:30 am and 2:30 - 4:30 pm Monday through Thursday.

- **Session A** (MOA, TOA, WOA, ThOA), Wells Fargo
- **Session B** (MOB, TOB, WOB, ThOB), Room 501
- **Session C** (MOC, TOC, WOC, ThOC), Room 401
- **Session D** (MOD, TOD, WOD, ThOD), Korbel 1-2
- **Session E** (MOE, TOE, WOE, ThOE), Korbel 3-4
- **Session F** (MOF, TOF, WOF, ThOF), Four Seasons 1-2
- **Session G** (MOG, TOG, WOG, ThOG), Four Seasons 3-4

**ORAL PRESENTATIONS** are made from ASMS computers running Microsoft Windows 7 and Office 2007. Speakers are required to use the ASMS computers for their presentations.

**SPEAKERS** must load presentations at least one day prior to their talks. The speaker room is 612 and is open with a technician:

- **Sunday:** 10:00 am - 8:00 pm  
  Monday through Wednesday: 7:30 am - 5:00 pm

**POSTERS AND EXHIBIT BOOTH**s are in Exhibit Hall C-D. The Hall is open:

- **Sunday Reception:** 7:45 - 9:30 pm  
  Monday through Wednesday: 7:30 am - 8:00 pm  
  Thursday: 7:30 am - 3:30 pm

**POSTER SET-UP** is 7:30 am on the day scheduled and removal is 7:30 - 8:00 pm. Thursday posters must be removed by 3:30 pm. Refer to the poster numbers in this final program for board assignments. Presenters are expected to supply pushpins or Velcro to mount their posters. Poster titles begin on page 52.

**POSTER SESSIONS** are 10:30 am - 2:30 pm, Monday through Thursday. Presenters should attend their posters 10:30 am - 2:30 pm on their scheduled day. Presenters who must leave a poster unattended should post a return time. Post-it notes for this purpose are provided at the Poster Supply counter near the entrance to the Poster-Exhibit Hall. Presenters should wear “poster presenter” badges which are also available at the counter.

**Lunch Breaks for poster presenters**

- 11:45 am - 12:15 pm: Break for odd-numbered posters
- 12:15 - 12:45 pm: Break for even-numbered posters

**WORKSHOPS** are 5:45 - 7:00 pm on Monday, Tuesday, and Wednesday. See pages 20 - 22 for schedule. Light refreshments are provided outside Korbel Ballroom for those attending workshops.

**EXHIBIT BOOTH**s must be attended as follows:

- **Sunday Reception:** 7:45 - 9:30 pm  
  Monday through Thursday: 10:30 am - 2:30 pm

**FREE INTERNET ACCESS** is provided in the Poster-Exhibit Hall.

**LUNCH CONCESSIONS** are in the Poster-Exhibit Hall. In addition, there are many restaurants close to the convention center.

**DINNER BREAK, 7:00 - 8:00 PM** is time for a breath of fresh air before the opening of hospitality suites at 8:00 pm. For restaurant suggestions and reservations, visit the Denver Hospitality Counter near the entrance to the Poster-Exhibit Hall.

**CONFERENCE PROCEEDINGS** will be published online. Visit www.asms.org after July 9 to view and download the Proceedings.

**WEB CASTING** will include tutorial lectures, plenary lectures, and oral sessions. Web casting will be available to conference attendees until August 12. Web casting of presentations does not constitute publication and in no way jeopardizes the rights of authors to publish material that has been presented. To access the presentations, go to www.asms.org, select web casting, and enter your last name and the User ID on the back of your conference name badge.
**SOCIAL ACTIVITIES**

- **Welcome Mixer, Sunday, 7:45 - 9:30 PM** Poster-Exhibit Hall. Conference name badge is required.

- **Guest Registration** ($10) includes Sunday evening mixer and name badge. Guests are invited to visit the Denver Hospitality counter near the entrance to the Poster-Exhibit Hall to plan excursions.

- **Closing Toast, Thursday, 5:30 - 6:00 PM** Wells Fargo Lobby is immediately following the closing plenary session.

**Corporate Hospitality Suites** may be open 8:00 – 11:00 pm, Monday through Wednesday. Suites are located in Hyatt Regency Hotel across 14th Street from the convention center.

**Employment Center** is located in the Poster-Exhibit Hall and is open to all conference attendees. Applicants must supply at least 20 résumés. There are computers in the center for searching the database of candidates and positions. There are poster boards to post positions and messages. Interview booths must be reserved one day in advance.

- **Sunday:** 7:45 - 9:00 pm
- **Monday – Wednesday:** 7:30 am – 5:00 pm
- **Thursday:** 7:30 am – 2:30 pm

**Childcare** is available in room 301. Advance reservations are required.

**Conference Hotels**

<table>
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<td>Curtis</td>
<td>303-571-0300</td>
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<tr>
<td>Embassy Suites</td>
<td>303-592-1000</td>
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<tr>
<td>Grand Hyatt</td>
<td>303-295-1234</td>
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<tr>
<td>Hilton Garden Inn</td>
<td>303-603-8000</td>
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<tr>
<td>Hyatt Regency Conv. Ctr.</td>
<td>303-436-1234</td>
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<tr>
<td>Marriott Downtown Denver</td>
<td>303-297-1300</td>
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<tr>
<td>Sheraton</td>
<td>303-893-3333</td>
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</table>

**Transportation**

All hotels are within walking distance of the Colorado Convention Center. The convention center is on 14th Street. A free bus runs the length of 16th Street.

**Conference Regulations**

- **Name badges** are required for all conference sessions, including the exhibit hall and the employment center.
- **No smoking** is permitted in the convention center.
- **Cell phones** must be turned off in oral sessions.
- **No photography or recording** is allowed in oral sessions or in the Poster-Exhibit Hall.
- The **placement of advertising** in the meeting area is strictly limited to Corporate Members. There are poster boards and tables in the Exhibit Hall for corporate member notices and literature. No signs on easels are permitted.
- **Hardware, accessories** or any items for sale may be displayed only in corporate exhibit booths and hospitality suites.
- **No organized activities** (even off-site) other than those approved by ASMS are allowed during the conference week (5:00 pm on Sunday through 6:00 pm on Thursday).
- **Corporate or institutional logos** in slides or posters may appear only one time in the presentation.

**Media Events**

Corporate media events are scheduled on Monday and Tuesday in the Hyatt Regency Hotel. Members of the press and financial institutions are welcome.

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<th>Date and Time</th>
<th>Hyatt Regency Room</th>
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<td>Centennial A-C, 3rd Fl</td>
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<tr>
<td>Agilent Technologies</td>
<td>Monday, 1:30 – 2:30 pm</td>
<td>Capitol 1-4, 4th Fl</td>
</tr>
<tr>
<td>Bruker Daltonics</td>
<td>Monday, 11:00 am – 12:00 pm</td>
<td>Mineral Hall A-C, 3rd Fl</td>
</tr>
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<td>PerkinElmer</td>
<td>Tuesday, 10:00 am – 11:00 am</td>
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<td>Shimadzu</td>
<td>Monday, 9:30 – 10:30 am</td>
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<tr>
<td>Thermo Scientific</td>
<td>Monday, 3:00 – 4:00 pm</td>
<td>Centennial D, 3rd Fl</td>
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<tr>
<td>Waters Corporation</td>
<td>Monday, 4:30 – 5:30 pm</td>
<td>Centennial E, 3rd Fl</td>
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**DON’T MISS:**

- "MyASMS," a comprehensive online map, poster/exhibit guide, session locator and scheduler: www.asms.org. The program is compatible with most mobile devices, as well as your computer.
- Refreshments before the start of workshops on Monday, Tuesday and Wednesday - look for a theme each evening
- A one-hour break between the end of workshops and the opening of corporate hospitality suites to explore "fast" and "fine" restaurants in the area surrounding the convention center
- Hospitality suites in the Hyatt Regency Hotel across 14th Street from the convention center
- Breakfast seminars hosted by some corporate members (reservations required)
President
Scott A. McLuckey
Purdue University
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Northeastern University
Boston, MA

Member at Large for Digital Communications
David R. Goodlett
University of Washington
Seattle, WA

Past President
Gary L. Glish
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ASMS announces the election of these members to the Board of Directors

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Lance Nicolaysen
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Secretary
Rachel O. Loo
University of California, Los Angeles

Member at Large for Publications
Evan R. Williams
University of California, Berkeley

STAFF
Judith A. Sjoberg, Executive Director
Cindi Lilly, Brent Watson
Jennifer Watson, Marin Walker, Miquela Ortiz-Sena

ASMS BOARD OF DIRECTORS
### ASMS Leadership

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- Daniel Austin, ASMS
- Susan E. Abbatiello, ASMS
- Victor Ryzhov, ASMS
- William Wikoff, ASMS
- Chris Turck, ASMS
- Helen J. Cooper, ASMS
- Jennifer Grant, ASMS
- Huo Chen, ASMS

### Interests Group Coordinators

**Analytical Lab Managers**

- John Greaves, University of California, Irvine

**Bioinformatics for MS**

- Marc Kirchner, Chdn's Hospital/Harvard Medical
- Brian Searle, Proteome Software

**Clinical Chemistry**

- Nigel Clarke, Quest Diagnostics
  - Daniele Fabris, SUNY, Albany
  - Herbert Oberacher, Innsbruck Medical University

**Drug Metabolism & Pharmacokinetics**

- Edward Kerns, Discovery ADME
  - Gabriella Szekely-Klepser, Allergen

**Energy, Petroleum & Biofuels**

- David Stranz, Sierra Analytics
  - Wolfgang Schrader, MPI Muelheim

**Environmental Applications**

- Xing-Fang Li, University of Alberta

**Flavor, Fragrance and Foodstuff**

- Eric Handberg, 1st Detect

**Forensics & Homeland Security**

- Karen Wahl, Pacific Northwest Natl. Laboratory

**FTMS Fundamentals**

- Adam Hawkridge, North Carolina State University
- Joshua Sharp, University of Georgia

**Hydrogen Exchange & Covalent Labeling**

- Janna Kieselar, Case Western Reserve
- Michael Chalmers, Scripps Institute

**Imaging MS**

- Felicia Green, National Physical Laboratory (UK)
- Timothy Garrett, Univ. of Maryland Baltimore Cty.

**Ion Mobility MS**

- Brandon Ruotolo, Univ. of Michigan

**Ion Trap MS**

- Joshua Coon, Univ. of Wisconsin

**LC/MS Related Topics**

- Susan E. Abbatiello, Broad Institute

**Metabolomics**

- Lloyd W. Sumner, Noble Foundation
- William Wikoff, Univ. of Calif, Davis

**Metal Ion Coordination Chemistry**

- Victor Ryzhov, Northern Illinois Univ.
  - Grant Johnson, Pacific Northwest Natl. Laboratory

**Peptide Fragmentation**

- Gavin Reid, Michigan State Univ.
  - University of Birmingham (UK)

**Pharmaceuticals**

- Matthew Blatnik, Pfizer
- Chris Turck, Max Planck Institute

**Protein Therapeutics**

- Guodong Chen, Bristol-Myers Squibb

**Quantitative Intact Proteomics**

- Mark Chance, Case Western Reserve

**Regulated Bioanalysis**

- Fabio Garofolo, Algorithmhe Pharma
- Steven Lowes, Advion Biosciences

**Undergraduate Research in MS**

- Jennifer Grant, University of Wisconsin

**Young Mass Spectrometers**

- Huo Chen, Ohio University

### Committees

**Aslomar Conference**

- Rebecca Jockusch, Chair
- Carolyn Cassidy
- Facundo Fernandez
- Gary Glish

**Audit**

- Gary Van Berkel
- John Eyler
- Susan Richardson

**Corporate Liaison**

- Chip Cody, Chair
- Gary Glish
- Carol Harp
- Heather May
- Lance Nicolaysen
- Michael Sabatino
- Heath Collins
- Jon Speak

**Digital Communications**

- David Goodlett, Chair
- Manor Askenazi
- Garry Corthals
- Suzanna Moyer
- Steve Stein

**Education**

- Richard Vachet, Chair
- Christine Hughie
- Karen Jonscher
- Jianhua Ren
- Rong Wang

**Nominating**

- Catherine Costello, Chair
- David Burinsky
- Ragu Ramanathan
- Michael Siu
- Christine Wu

**Publications**

- John Engen, Chair
- Russell Grant
- Lan Huang
- Neil Kelleher
- Lisa Marzilta
- Michael Gross (Ex Officio)

**Sanibel Conference**

- David Burinsky, Chair
- Lucinda Cohen
- Lisa Deterding
- Jianhua Ren

**Archivist**

- Michael Grayson
Tandem mass spectrometry (MS/MS) is a key tool for molecular structure elucidation. Many instrument configurations are feasible for accomplishing gas-phase analyte selection followed by activation and molecule-specific dissociation. Robert J. Cotter is recognized for his invention and development of tandem time-of-flight (TOF/TOF) mass spectrometry that utilizes high-energy collisions (up to 20 keV) for collision-induced dissociation. Cotter’s first instrument design, realized in 1993, incorporated two dual-stage reflectrons (rTOF/rTOF), which were later replaced by single-stage reflectrons for improved focusing of product ions over a wider mass range. This work was followed by the development of the “curved-field reflectron” to enable simultaneous focusing of the entire product ion mass range. The curved-field reflector also gained wide use on post-source decay instruments and was licensed to Kratos Analytical for their Kompact IV, AXIMA CFR and AXIMA CFR+ mass spectrometers and then Shimadzu Confidence mass spectrometers. A simplified instrument configuration, developed in 2004, was commercialized as the Kratos AXIMA TOF, and later the Shimadzu Performance. More than 400 curved field reflectron instruments have been manufactured and sold. The potential benefits of high-energy (20 keV) collisions are now being appreciated, with perhaps the most exciting being the possibility of carrying out “top-down” or “middle-down” protein analyses on a MALDI TOF mass spectrometer.

Dr. Robert J. Cotter is Professor of Pharmacology and Molecular Sciences at the Johns Hopkins University School of Medicine.

Biemann Medal

Award Lecture: 4:45 pm, Tuesday, Wells Fargo Theatre
2011 Recipient: Béla Paizs

Tandem mass spectrometric analysis of peptides, a vital element of proteomics, requires a deep understanding of the complex fragmentation reaction networks occurring in mass spectrometers under various excitation conditions. The focused efforts of Béla Paizs have led to detailed characterization of peptide product ion structures and dissociation mechanisms, and have demonstrated that the principle characteristics of peptide collision-induced dissociation spectra can be understood with basic physical and chemical laws. Paizs’ work combines various experimental techniques (e.g., MS/MS, “action” infrared multiphoton dissociation, ion mobility spectrometry, gas-phase H/D-exchange) with state-of-the-art theoretical methods. “Raw” experimental data (fragmentation patterns, IR spectra, collision cross-sections, etc.) are processed with the help of advanced modeling and provides invaluable structural, thermodynamic, and kinetic data on peptide fragmentation chemistry. Among other achievements, Paizs has characterized the major fragmentation pathways leading to b, y, and a ions, the scrambling chemistry of b fragments, and very recently, he has described a new rearrangement pathway for a fragments. His work has unified diverse dissociation mechanisms into a comprehensive peptide fragmentation model. These achievements have substantially advanced the field of peptide characterization and provide a solid scientific background for developing improved bioinformatics tools for peptide sequencing in mainstream proteomics.

Dr. Béla Paizs is Group Leader, Gas-phase Peptide Chemistry Group at the German Cancer Research Center.

Ron A. Hites Award for Outstanding Research Publication in JASMS

Award Presentation: ASMS Meeting, 4:45 – 5:30 pm, Wednesday, Korbel 1-2

The Ron Hites Award recognizes an outstanding presentation of original research. Selection is based on a paper’s innovative aspects, technical quality, likely stimulation of future research, likely impact on future applications, and quality of presentation. The award is named in honor of Professor Ronald A. Hites of Indiana University, who led the creation of JASMS in 1988 while president of ASMS.

The 2011 award is presented to Prof. Scott A. McLuckey for the article “Top-Down Tandem Mass Spectrometry of tRNA via Ion Trap Collision-induced Dissociation,” Huang, T.-Y., Liu, J., & McLuckey, S. A.; JASMS 2010, Vol. 21(6), 890-898. Prof. McLuckey is in the Department of Chemistry, Purdue University. Prof. McLuckey is donating the award prize of $2,000 toward student travel support.
**AWARDS**

**RESEARCH AWARDS**

ASMS is pleased to announce that Thermo Scientific and Waters Corporation have each increased their Research Awards to $35,000. Awards will be presented at the Biemann Medal Award Lecture, 4:45 pm, Tuesday, Wells Fargo Theatre.

**Sponsored by**

**THermo Scientific**

![Judit Villen](image1.png)

**University of Washington**

**Waters Corporation**

![Brandon Ruotolo](image2.png)

**University of Michigan**

**CALL FOR 2012 RESEARCH AWARD PROPOSALS**

**OBJECTIVE**

To promote academic research by young scientists in mass spectrometry.

**ELIGIBILITY**

Open to academic scientists within four years of joining the tenure-track faculty or equivalent in a North American university. Applicants may not have previously received an award under this program.

**APPLICATION**

Applicants should submit SEVEN collated sets of the following:

1. One-page fiscal proposal and justification
2. List of current research support
3. Three-page proposal, including references and figures
4. Curriculum vitae
5. Two letters of recommendation (may be sent by email, fax or mail to ASMS)

**DEADLINE**

Application materials, including letters of recommendation, must be received in the ASMS office by November 30, 2011. Send to:

ASMS, 2019 Galisteo Street, Building I-1, Santa Fe, NM 87505

**FISCAL**

The awards of $35,000 each will be made to a university in the name of the selected individual and for the researcher’s exclusive use. In accepting this award, the institution will agree not to charge overhead on the funds.

**INFORMATION**

Contact ASMS. Telephone: (505) 989-4517  •  Fax: (505) 989-1073  •  office@asms.org

**RICHARD A. SCHAFFER MEMORIAL FUND GRANTS**

The Richard A. Schaeffer Memorial Fund provides student travel grants of approximately $1,000 each. Information and applications are available at [www.richardschaeffer.org](http://www.richardschaeffer.org).

**Recipients of the 2011 grants for ASMS Conference Travel**

Ryan Dain, Wichita State University
Oscar Martinez, Jr, University of Colorado
Kevin McAvey, University of New Orleans
DON'T MISS THE CORPORATE HOSPITALITY SUITES
Located in the Hyatt Regency Hotel third and fourth levels.
Suites are open
Monday – Wednesday after 8:00 pm.
During the day by appointment.
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<td>AB SCIEX</td>
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STUDENT ASSISTANTS

Graduate students are assisting with many aspects of the conference, including registration, oral and poster sessions, and the employment center. The students each receive a stipend to assist with their conference expenses. Springer Publishing has generously underwritten the student assistant stipends.

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Yingming Zhao

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Karen Wahl
Julian Whitelegge
William Wikoff
PROGRAM OVERVIEW

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<tr>
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<tr>
<td>9:00 AM - 4:30 PM</td>
<td>Short Courses</td>
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<td>2:00 - 5:00 PM</td>
<td>Registration</td>
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<td>Sunday</td>
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<tr>
<td>9:00 AM - 4:30 PM</td>
<td>Short Courses</td>
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<tr>
<td>10:00 AM - 8:00 PM</td>
<td>Registration</td>
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<tr>
<td>5:00 - 6:30 PM</td>
<td><strong>Tutorial Lectures</strong>, Wells Fargo Theatre</td>
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<td>5:00 - 5:45 pm</td>
<td>Good Mass Spectrometry and its Place in Good Science: Sometimes Close Enough Is Really Not Good Enough</td>
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<td>Mark W. Duncan</td>
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<td>University of Colorado Denver, Anschutz Medical Campus</td>
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<td>5:45 - 6:30 pm</td>
<td>LC and MS: A Match Made in Heaven</td>
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<td>James Jorgenson</td>
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<td>University of North Carolina</td>
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<td>6:45 - 7:45 pm</td>
<td><strong>Opening</strong>, Wells Fargo Theatre</td>
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<td><strong>Plenary Lecture</strong></td>
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<td>7:00 - 7:45 pm</td>
<td>Our Stellar Origins Revealed by Stardust Grains</td>
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<td>Ernst Zinner</td>
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<td>Washington University</td>
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<td>7:45 - 9:30 pm</td>
<td><strong>Reception in the Poster-Exhibit Hall</strong>, Exhibit Hall C-D</td>
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## PROGRAM OVERVIEW

### MONDAY

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<td>MOA am:</td>
<td>Systems Biology/Cellular Pathways, Wells Fargo Theatre</td>
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<td>MOB am:</td>
<td>H/D Exchange: New Developments in Hardware, Software and Methodology, Room 501</td>
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<td>MOD am:</td>
<td>Imaging MS: Instrumentation and Ionization Sources, Korbel Ballroom 1-2</td>
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<tr>
<td>MOE am:</td>
<td>Energy, Petroleum and Biofuels, Korbel Ballroom 3-4</td>
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<tr>
<td>MOF am:</td>
<td>Integrated Qualitative and Quantitative LC-MS for Drug Metabolism and Pharmacokinetics, Four Seasons Ballroom 1-2</td>
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<tr>
<td>MOG am:</td>
<td>Protein Therapeutics in Drug Discovery and Development: LC-MS Quantification, Four Seasons Ballroom 3-4</td>
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<td>Post-translational Modifications, Wells Fargo Theatre</td>
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<td>H/D Exchange for Protein Structure and Function, Room 501</td>
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<tr>
<td>MOC pm:</td>
<td>Fundamentals: Ion Spectroscopy, Room 401</td>
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<td>MOD pm:</td>
<td>Imaging MS: Biological Applications, Korbel Ballroom 1-2</td>
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<tr>
<td>MOE pm:</td>
<td>Plant Proteomics, Korbel Ballroom 3-4</td>
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<td>High Resolution MS in Drug Metabolism and Pharmacokinetics, Four Seasons Ballroom 1-2</td>
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<tr>
<td>MOG pm:</td>
<td>Biomarker Quantification: Challenges in Regulated Bioanalysis: LC-MS Quantification, Four Seasons Ballroom 3-4</td>
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</tbody>
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<table>
<thead>
<tr>
<th>10:30 AM - 2:30 PM</th>
<th>AWARD LECTURE, Wells Fargo Theatre</th>
</tr>
</thead>
<tbody>
<tr>
<td>Award Lecture:</td>
<td>Award for a Distinguished Contribution in Mass Spectrometry</td>
</tr>
<tr>
<td></td>
<td>Wells Fargo Theatre</td>
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<tr>
<td></td>
<td>Robert J. Cotter</td>
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<td></td>
<td>Johns Hopkins University</td>
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<table>
<thead>
<tr>
<th>2:30 - 4:30 PM</th>
<th>WORKSHOPS See page 20. There are light refreshments outside Korbel Ballroom.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td>Fundamentals, Room 501</td>
</tr>
<tr>
<td>2.</td>
<td>Challenges in Polymer Mass Spectrometry, Room 505</td>
</tr>
<tr>
<td>3.</td>
<td>The Energy Landscape: Alternatives, Economics, and Analytical Problems in Energy, Petroleum, and Biofuels, Room 401</td>
</tr>
<tr>
<td>4.</td>
<td>Creating a Parts/Knowledge Resource for Older Instruments, Room 405</td>
</tr>
<tr>
<td>5.</td>
<td>Applied Topics in FTMS, Korbel Ballroom 1-2</td>
</tr>
<tr>
<td>6.</td>
<td>Computational Methods for the Interpretation of Ion Mobility-Mass Spectrometry Data, Korbel Ballroom 3-4</td>
</tr>
<tr>
<td>7.</td>
<td>Simultaneous Qual/Quan Workflows: What Are the Optimal Technologies, Methods, Applications and Real-World Productivity Enhancements? Four Seasons Ballroom 1-2</td>
</tr>
<tr>
<td>8.</td>
<td>Practical ETD, Four Seasons Ballroom 3-4</td>
</tr>
<tr>
<td>9.</td>
<td>New Methods for Analysis of Foods, Flavors and Fragrances, Room 607</td>
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</tbody>
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<thead>
<tr>
<th>5:45 - 7:00 PM</th>
<th>DINNER BREAK</th>
</tr>
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<tbody>
<tr>
<td>AFTER 8:00 PM</td>
<td>CORPORATE HOSPITALITY SUITES, Hyatt Regency Hotel</td>
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## PROGRAM OVERVIEW

### TUESDAY

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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</thead>
<tbody>
<tr>
<td>7:00 AM - 5:00 PM</td>
<td><strong>REGISTRATION</strong></td>
</tr>
<tr>
<td>8:30 AM - 10:30 AM</td>
<td><strong>ORAL SESSIONS</strong></td>
</tr>
<tr>
<td></td>
<td>• TOA am: Quantitative Proteomics: Peptides, <em>Wells Fargo Theatre</em></td>
</tr>
<tr>
<td></td>
<td>• TOB am: Unknown Environmental Contaminants: Advanced Mass Spectrometry Technologies, <em>Room 501</em></td>
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<td></td>
<td>• TOC am: Metabolomics, <em>Room 401</em></td>
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<td></td>
<td>• TOD am: Biomolecular Structure Analysis by Covalent Labeling: Future Directions, <em>Korbel Ballroom 1-2</em></td>
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<tr>
<td></td>
<td>• TOE am: Fundamentals: Supramolecular Chemistry/Non-covalent Interactions, <em>Korbel Ballroom 3-4</em></td>
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<td></td>
<td>• TOF am: Mass Spectrometry Analysis of Dried Blood Spot Samples, <em>Four Seasons Ballroom 1-2</em></td>
</tr>
<tr>
<td></td>
<td>• TOG am: Clinical Chemistry: Advances in Separation Technologies, <em>Four Seasons Ballroom 3-4</em></td>
</tr>
<tr>
<td>10:30 AM - 2:30 PM</td>
<td><strong>POSTER SESSION AND EXHIBITS, Exhibit Hall C-D</strong></td>
</tr>
<tr>
<td></td>
<td>Tuesday posters begin on page 87.</td>
</tr>
<tr>
<td>2:30 PM - 4:30 PM</td>
<td><strong>ORAL SESSIONS</strong></td>
</tr>
<tr>
<td></td>
<td>• TOA pm: Informatics: Quantification/Validation, <em>Wells Fargo Theatre</em></td>
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<td></td>
<td>• TOB pm: Environmental Chemistry and Health, <em>Room 501</em></td>
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<td></td>
<td>• TOC pm: Lipids I: Identification and Structural Analysis, <em>Room 401</em></td>
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<td></td>
<td>• TOE pm: Ion Traps and Hybrid Instruments: New Developments, <em>Korbel Ballroom 3-4</em></td>
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<tr>
<td></td>
<td>• TOF pm: Imaging MS: Pharmaceutical Applications, <em>Four Seasons Ballroom 1-2</em></td>
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<tr>
<td></td>
<td>• TOG pm: Advances in Micro- and Nano-scale Separations, <em>Four Seasons Ballroom 3-4</em></td>
</tr>
<tr>
<td>4:45 PM - 5:30 PM</td>
<td><strong>AWARD LECTURE</strong>, <em>Wells Fargo Theatre</em></td>
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<tr>
<td></td>
<td><strong>Biemann Medal</strong></td>
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<td></td>
<td><em>Wells Fargo Theatre</em></td>
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<td></td>
<td><strong>Béla Paiz</strong></td>
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<td></td>
<td><em>German Cancer Research Center</em></td>
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<tr>
<td>5:45 PM - 7:00 PM</td>
<td><strong>WORKSHOPS</strong></td>
</tr>
<tr>
<td></td>
<td><em>See page 21</em>. There are light refreshments outside Korbel Ballroom.</td>
</tr>
<tr>
<td></td>
<td>1. Hydrogen Exchange and Covalent Labeling, <em>Room 501</em></td>
</tr>
<tr>
<td></td>
<td>2. Advances in Mass Spectrometry Driving Drug and Target Identification Efforts, <em>Room 505</em></td>
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<tr>
<td></td>
<td>3. Trans-Proteomic Pipeline and Related Open-source Proteomics Resources, <em>Room 401</em></td>
</tr>
<tr>
<td></td>
<td>4. NIH Grant Opportunities and Mock Study Section, <em>Room 405</em></td>
</tr>
<tr>
<td></td>
<td>5. Metabolomics Current Challenges &amp; Future Directions, <em>Korbel Ballroom 1-2</em></td>
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<tr>
<td></td>
<td>7. Is a Deeper Understanding of Peptide Fragmentation Chemistry Required to Improve MS/MS-based Protein Identification and Characterization Strategies? <em>Four Seasons Ballroom 1-2</em></td>
</tr>
<tr>
<td></td>
<td>8. Upcoming Challenges and Developments in Regulated LC-MS Bioanalysis: Fit-for-Purpose; Emerging Technologies; Stability Issues, <em>Four Seasons Ballroom 3-4</em></td>
</tr>
<tr>
<td></td>
<td>9. LC/MS Library/Libraries for Advancing Environmental Chemistry and Health Sciences, <em>Room 607</em></td>
</tr>
<tr>
<td>7:00 PM - 8:00 PM</td>
<td><strong>DINNER BREAK</strong></td>
</tr>
<tr>
<td>After 8:00 PM</td>
<td><strong>CORPORATE HOSPITALITY SUITES</strong>, <em>Hyatt Regency Hotel</em></td>
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</tbody>
</table>
### PROGRAM OVERVIEW

**WEDNESDAY**

<table>
<thead>
<tr>
<th>7:00 AM - 5:00 PM</th>
<th><strong>REGISTRATION</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ORAL SESSIONS</strong></td>
<td>WOA am: Intact Proteins: Quantitative and Qualitative Analysis, <em>Wells Fargo Theatre</em></td>
</tr>
<tr>
<td></td>
<td>WOB am: Ion Mobility Separations: Fundamentals and Instrumentation, <em>Room 501</em></td>
</tr>
<tr>
<td></td>
<td>WOC am: Lipids II: Profiling and Quantitation, <em>Room 401</em></td>
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<td></td>
<td>WOD am: Glycoproteins: New Approaches for Structure Analysis, <em>Korbel Ballroom 1-2</em></td>
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<td>WOE am: Instrumentation: New Developments in Ionization, <em>Korbel Ballroom 3-4</em></td>
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<td></td>
<td>WOF am: PK Assays: Novel Approaches to Increase LC-MS Throughput, <em>Four Seasons Ballroom 1-2</em></td>
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<td></td>
<td>WOG am: Protein Therapeutics: Structural Characterization, <em>Four Seasons Ballroom 3-4</em></td>
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<tr>
<th>8:30 AM - 10:30 AM</th>
<th><strong>POSTER SESSION AND EXHIBITS, <em>Exhibit Hall C-D</em></strong></th>
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</thead>
<tbody>
<tr>
<td><strong>ORAL SESSIONS</strong></td>
<td>WOA pm: Phosphoproteomics, <em>Wells Fargo Theatre</em></td>
</tr>
<tr>
<td></td>
<td>WOB pm: Ion Mobility Mass Spectrometry: Integration into Structural Biology, <em>Room 501</em></td>
</tr>
<tr>
<td></td>
<td>WOC pm: Fundamentals: Ion-Surface Interactions and Preparative MS, <em>Room 401</em></td>
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<td></td>
<td>WOD pm: Carbohydrates: New Approaches for Structure Analysis, <em>Korbel Ballroom 1-2</em></td>
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<td>WOE pm: Instrumentation: New Developments in Instrumentation, <em>Korbel Ballroom 3-4</em></td>
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<td>WOF pm: Informatics Tools for Pharmaceutical Applications of Mass Spectrometry, <em>Four Seasons Ballroom 1-2</em></td>
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<td></td>
<td>WOG pm: Reactive Metabolites: Novel LC-MS Detection Methods, <em>Four Seasons Ballroom 3-4</em></td>
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<thead>
<tr>
<th>4:45 AM - 5:30 PM</th>
<th><strong>ASMS MEETING, <em>Korbel 1-2</em></strong></th>
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</thead>
<tbody>
<tr>
<td><strong>WORKSHOPS</strong></td>
<td>See page 22. There are light refreshments outside Korbel Ballroom.</td>
</tr>
<tr>
<td></td>
<td>1. Towards Quantitative Imaging, <em>Room 501</em></td>
</tr>
<tr>
<td></td>
<td>2. Nucleic Acids Sequencing: Fundamentals and New Directions, <em>Room 505</em></td>
</tr>
<tr>
<td></td>
<td>4. Quantitative Intact Proteomics (QIP), <em>Room 405</em></td>
</tr>
<tr>
<td></td>
<td>5. Hot Topics in LC-MS Instrumentation Troubleshooting, <em>Korbel Ballroom 1-2</em></td>
</tr>
<tr>
<td></td>
<td>7. Qualitative and Quantitative Techniques for Protein Therapeutics, <em>Four Seasons Ballroom 1-2</em></td>
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<td></td>
<td>8. Career Development in Mass Spectrometry Research, <em>Four Seasons Ballroom 3-4</em></td>
</tr>
<tr>
<td></td>
<td>9. Interaction of Metal Ions and Clusters with Biomolecules, <em>Room 607</em></td>
</tr>
<tr>
<td></td>
<td>10. Group Discussion to Generate Workshop Content to Stimulate Undergraduate Student Interest in Mass Spectrometry, <em>Room 711</em></td>
</tr>
</tbody>
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<thead>
<tr>
<th>7:00 AM - 8:00 PM</th>
<th><strong>DINNER BREAK</strong></th>
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<tbody>
<tr>
<td><strong>AFTER 8:00 PM</strong></td>
<td><strong>CORPORATE HOSPITALITY SUITES, <em>Hyatt Regency Hotel</em></strong></td>
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## Thursday

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>7:00 AM - 5:00 PM</td>
<td><strong>Registration</strong></td>
</tr>
<tr>
<td>8:30 - 10:30 AM</td>
<td><strong>Oral Sessions</strong></td>
</tr>
<tr>
<td></td>
<td>- ThOA am: Informatics: Identification, Wells Fargo Theatre</td>
</tr>
<tr>
<td></td>
<td>- ThOB am: Fundamentals: Ion Structure and Energetics, Room 501</td>
</tr>
<tr>
<td></td>
<td>- ThOC am: Synthetic Polymers: New Methods for Analysis, Room 401</td>
</tr>
<tr>
<td></td>
<td>- ThOD am: Membrane Proteins, Korbel Ballroom 1-2</td>
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<tr>
<td></td>
<td>- ThOE am: High Mass Accuracy/High Performance Instrumentation and Applications, Korbel 3-4</td>
</tr>
<tr>
<td></td>
<td>- ThOF am: Protein Therapeutics: Identification of Metabolites, Impurities and Degradants, Four Seasons Ballroom 1-2</td>
</tr>
<tr>
<td></td>
<td>- ThOG am: Biomarker Analysis and Metabolomics in Drug Discovery, Four Seasons Ballroom 3-4</td>
</tr>
<tr>
<td>10:30 AM - 2:30 PM</td>
<td><strong>Poster Session and Exhibits, Exhibit Hall C-D</strong></td>
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<tr>
<td></td>
<td>Thursday posters begin on page 157.</td>
</tr>
<tr>
<td>2:30 - 4:30 PM</td>
<td><strong>Oral Sessions</strong></td>
</tr>
<tr>
<td></td>
<td>- ThOA pm: Biomarkers/Disease Signatures, Wells Fargo Theatre</td>
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<tr>
<td></td>
<td>- ThOB pm: Fundamentals: Ion/Molecule and Ion/Ion Interactions, Room 501</td>
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<td></td>
<td>- ThOC pm: Microorganisms: Identification and Characterization, Room 401</td>
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<td></td>
<td>- ThOD pm: Oligonucleotides: Structure and Reactivity, Korbel Ballroom 1-2</td>
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<tr>
<td></td>
<td>- ThOE pm: Metal-Biomolecular Complexes: Structure and Reactions, Korbel Ballroom 3-4</td>
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<td></td>
<td>- ThOF pm: Biomarkers of Drug/Metabolite Toxicity: LC-MS Methods, Four Seasons Ballroom 1-2</td>
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<tr>
<td></td>
<td>- ThOG pm: Ambient Desorption Ionization Techniques: New Developments and Applications, Four Seasons 3-4</td>
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<tr>
<td>4:45 - 5:30 PM</td>
<td><strong>Plenary Lecture</strong>, Wells Fargo Theatre</td>
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<td></td>
<td>Why Are We Surprised by Only Some of the Things that We See? Visual Illusions, the Brain, and Baseball</td>
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<td></td>
<td>Arthur Shapiro</td>
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<td>American University</td>
</tr>
<tr>
<td>5:30 - 6:30 PM</td>
<td><strong>Closing Toast</strong>, Wells Fargo Lobby</td>
</tr>
</tbody>
</table>
Workshops are organized on topics of special interest to mass spectrometry. Light refreshments are provided outside Korbel Ballroom.

### Fundamentals
**Daniel Austin** and **Rebecca Jockusch**, presiding  
Room 501
In the tradition of the fundamentals workshop, we will encourage young mass spectrometrists to give short presentations on topics of interest to generate an informal discussion. While the exact topics are dependent on the choice of oral presentations at ASMS, we expect that new developments in the understanding of ionization techniques, ion mobility and ion spectroscopy will feature prominently.

### Challenges in Polymer Mass Spectrometry
**Andrew Hoteling** and **William Erb**, presiding  
Room 505
In this time of energy uncertainty, many potential new sources to supplement or replace the geopetrleum-based energy supply are being explored. This workshop will present, in tutorial format, a review of the current and future energy landscape: sources, alternatives, economics and scalability, and the analytical challenges faced at the research and production levels. Audience participation will be encouraged.

### Creating a "Parts/Knowledge Resource" for Older Instruments
**John Greaves**, presiding  
Room 405
Many instruments are being called on to last well beyond the instrument development cycle. This may mean that after several years use it can become hard to obtain both spares and information on any given model. It is proposed that we discuss how to create and maintain a database of instruments (maybe older than 5 years), locations and users with the aim that a user in trouble may have a source of information/parts resource. The database should include that instrument in the basement that is no longer used but could provide a wealth of parts for others.

### Applied Topics in FTMS
**Adam Hawkridge** and **Joshua Sharp**, presiding  
Room 401
An anonymous web-based survey was conducted in early 2010 which provided members of the FTMS community the opportunity to suggest topics for the 2010 and 2011 Workshops. Based on the responses to this survey, the 2011 Workshop will focus on specific applications and capabilities that are unique to FTMS. The format of the 2011 Workshop will include 3-4 short talks that cover contemporary applications that will allow ample time for discussion.

### Computational Methods for the Interpretation of Ion Mobility-Mass Spectrometry Data
**Brandon T. Ruotolo**, presiding  
Korbel Ballroom 3-4
With the availability of commercial ion mobility-mass spectrometry (IM-MS) instrumentation, the application of IM-MS data to a host of problems in wide-ranging fields is growing at an exponential rate. However, these emerging datasets have highlighted the fact that the growing IM-MS community needs both 1) a deeper understanding of the computational tools already available to analyze IM-MS data and 2) new computational approaches capable of analyzing IM-MS data derived from these emergent datasets. This workshop seeks to showcase both tutorial presentations and cutting-edge research involving the computational analysis of IM-MS data. Discussion in this workshop will be focused on the areas of: molecular modeling/molecular dynamics for the generation of candidate structures in comparison with IM data, theoretical methods for computing the collision cross-section of model structures, and new computational methods that enable the analysis of previously problematic IM-MS datasets.

### Simultaneous Qual/Quan Workflows: What Are the Optimal Technologies, Methods, Applications and Real-World Productivity Enhancements?
**Gabriella Szekely-Klepsner** and **Ed Kerns**, presiding  
Four Seasons Ballroom 1-2
The qualitative identification of xenobiotic metabolites and the quantification of the significant ones together with the parent drug remains an important deliverable for practitioners in this area of the pharmaceutical industry. New instrument platforms are capable of the simultaneous collection of qualitative and quantitative data at low and high resolution enabling more complete understanding of PK/PD relationships and drug disposition. This workshop is going to invite an open discussion on key technological advances, new approaches, and open or controversial questions in these areas. Topics or questions will be presented by the moderators and invited subject matter experts in short (~ 5 min) presentations which will be followed by discussion with the audience.

### Practical ETD
**Katalin Medzhiradszky**, presiding  
Four Seasons Ballroom 3-4
This workshop will focus on the practical aspects of ETD analysis. Invited speakers will make short presentations (max 5 min) to illustrate the advantages and limitations of ETD analysis including: special applications for PTM analysis, database searching strategies, as well as unexpected fragmentations and other practical problems.

### New Methods for Analysis of Foods, Flavors and Fragrances
**Eric Handberg**, presiding  
Room 607
Method developments in mass spectrometry continue to improve for the Food, Flavor and Fragrance Interest Group. These methods include broadly applicable LC-MS/MS methods and new ionization methods, such as surface desorption atmospheric pressure chemical ionization (DAPCI) and extractive electrospray. This workshop aims to bring together analysts and experts to discuss practical applications to volatile compounds important to the flavor, fragrance and food area. Attendees are invited to share relevant challenges and problem-solving techniques in an open discussion format. We hope to use the Interest Group’s Forum page at the ASMS web site for advance discussion of specific topics and techniques.
Workshops are organized on topics of special interest to mass spectrometry. Light refreshments are provided outside Korbel Ballroom.

**Hydrogen Exchange and Covalent Labeling**
Michael Chalmers and Janna Kiselar presiding  
*Room 501*

The workshop will focus on the discussion of new methods and techniques of interest to our members. There will be a brief overview of a new method development, followed by questions and discussion. Topics will be selected to allow interaction between speakers and the audience.

**Advances in Mass Spectrometry Driving Drug and Target Identification Efforts**
Matthew Blatnik and Chris Turck, presiding  
*Room 505*

Current therapeutic strategies are shifting from small molecule to peptide and large molecule based programs. The instrumentation and strategies for investigating new targets and relationships is evolving. This workshop will focus on current mass spectrometry applications in the industry and how they are being used to solve complex biological and therapeutic problems.

**Trans-Proteomic Pipeline and Related Open-Source Proteomics Resources**
Eric Deutsch, presiding  
*Room 401*

This is a tutorial-style presentation on how to use the freely available and open-source suite of software tools for the analysis of proteomics shotgun datasets called the Trans-Proteomic Pipeline (TPP). The presentation will include demonstrations of use of format conversions, PeptideProphet, iProphet, ProteinProphet, and related tools through the TPP graphical user interface, both in a local installation and on the Amazon EC2 cloud computing platform. Next we will present examples of how to use other resources from the Seattle Proteome Center including PeptideAtlas and SRMAtlas for the planning of targeted proteomics experiments. The workshop will conclude with an open discussion on use of the tools, possible improvements, as well as future directions. There will be an opportunity to talk with the developers of the TPP.

**Upcoming Challenges and Developments in Regulated LC-MS Bioanalysis: Fit-for-Purpose; Emerging Technologies; Stability Issues**
Stephen Lowes and Fabio Garofolo, presiding  
*Four Seasons Ballroom 1-2*

Recent public comment from representatives of FDA have indicated forthcoming regulatory guidance will address emerging approaches and techniques for the quantitative bioanalysis of drugs, metabolites and biomarkers. Considering the challenges to current regulatory language that endogenous biomarkers, biotherapeutics and non-triple quadrupole instruments present, makes for lively discussion around the future developments of bioanalysis. This workshop will highlight three areas of particular current interest:
1. Fit-for-Purpose and how to accommodate in a regulated laboratory.
2. Integration of emerging and new technologies for quantitative bioanalysis including dried blood spot assays and application of high resolution instruments.
3. Is it time to re-think our stability method validation experiments? This is an educational forum to discuss issues and applications associated with the LC-MS/MS Bioanalysis. The scientific debate will be led by three panelists who are recognized international experts in the field who will introduce each of the above topics to engage discussion.

**Clinical Protein and Peptide Analysis: When, Where and How?**
Nigel Clarke and Russ Grant, presiding  
*Korbel Ballroom 3-4*

Over the last few meetings we have discussed the current state of play in diagnostics with regards to small molecules and automation. The next frontier is developing validated assays for clinical measurement of proteins and peptides. This is critical to both replace the current RIA's and ICMAs (due to their specificity issues etc) as well as for the development of new disease biomarkers. To this end we will be inviting panelists from academic, industry and regulatory backgrounds to give a brief (5 min) presentation each and then partake in a question and answer discussion with the audience.

**NIGC/ASMS Library/Libraries for Advancing Environmental Chemistry and Health Sciences**
Enrico Davoli and Xing-Fang Li, presiding  
*Room 607*

Research in environmental and health sciences has greatly benefited from the NIST GC/MS library. Many compounds are not volatile or thermally stable to allow for GC/MS detection. This problem can be overcome by advanced LC/MS technologies. However, recent research has shown that identification of unknowns in a sample is a challenge. LC/MS libraries are very useful to confront this challenge. Industrial partners have developed LC/MS libraries with their specific instrumentation, but it is difficult to perform inter-laboratory validation. How can both academic and industry work together to build a unified LC-MS library from the available libraries to advance environmental and health sciences?
Experts will be prepared for general, as well as specific discussions of instrument troubleshooting. Areas of discussion will include use and distribution of an additive in a polymer. This is a powerful tool for disease studies or product development, but there is an increasing need to provide quantitative image analysis. This workshop will discuss the current thinking, ideas and future needs to enable fully quantitative imaging mass spectrometry.

Towards Quantitative Imaging
Felicia Green, presiding
Room 501

The use of mass spectrometry for imaging of surfaces has seen rapid growth in recent years and is capable of providing detailed chemical maps of a drug and/or its metabolites, a peptide, biomarkers or a cosmetic ingredient across a sample of tissue or even the distribution of an additive in a polymer. This is a powerful tool for thermochemistry of metal ion-biomolecule complexes, clustering of carbohydrates, oligonucleotides. Some of the potential topics include weak interactions between metal ions and biomolecules.

Nucleic Acid Sequencing: Fundamentals and New Directions
Herbert Oberacher and Daniele Fabris, presiding
Room 505

Obtaining sequence information is a critical step in the characterization of all biopolymers, including DNA and RNA. Over the years, the MS community has developed gas-phase as well as solution approaches for sequencing nucleic acids and locating their post-transcriptional modifications. The panel will review the fundamentals and discuss the merits of the different approaches. The panel will also present new directions and discuss the changing needs of this field of applications.

Applications and Challenges in Forensics and Homeland Security Related to Mass Spectrometry
Karen Wahl, presiding
Room 401

This workshop will provide information to the attendees on the daily activities and challenges in the fields of forensics and homeland security from various speakers representing government agencies. There are many ways that mass spectrometry tools are applied to help provide information and solutions. Information gained from the chemistry and biology must also be combined with other information such as traditional fingerprint or text analysis or regulations for final solutions and outcomes to problems.

Quantitative Intact Proteomics (QIP)
David Friedman and Julian Whitelegge, presiding
Room 405

We will continue the open forum format that we started with last year, during which the discussion was directed by topics submitted to the QIP Interest Group ahead of time. Major themes from last year’s workshop will be explored further, including experimental design, replicates, variation, resolving multiple proteins identified from 2Dgels, and quantitative issues related to top-down strategies. Additional topics and panel participants will be selected from the presentations given during the “Intact Proteins: Quantitative and Qualitative Analysis” Wednesday morning oral session.

Hot Topics in LC-MS Instrumentation Troubleshooting
Susan Abbatiello, presiding
Korbel Ballroom 1-2

Working from the success of the “Hot Topics” LC-MS workshop in 2010, the 2011 workshop will again focus on problem areas in instrument troubleshooting. Areas of discussion will include use and development of proper standards for LC-MS applications including MS tuning and optimization, troubleshooting low MS signal, ionization source cleaning, and chromatographic irreproducibility. A panel of experts will be prepared for general, as well as specific discussions of problem spots with the current state of technology. In addition, the workshop will begin with three student presentations related to LC-MS research.

Bonding Theory and Application: Algorithm Development and Implementation Licensing
Marc Kirchner and Brian Searle, presiding
Korbel Ballroom 3-4

The Bioinformatics interest group will feature two sets of very brief, pecha kucha-style kick-off talks combined with in-depth discussion sessions. We will debate algorithmic issues associated with peptide- and protein-level quantification (such as the implicit identification problem). In addition, we will attempt to spark some discussion about software licensing and its effects on algorithm implementation availability for academia and industry.

Qualitative and Quantitative Techniques for Protein Therapeutics
Jon Williams and Sheng Gu, presiding
Four Seasons Ballroom 1-2

This workshop is intended to provide a forum to discuss and share new and emerging methodologies used to analyze protein therapeutics by mass spectrometry. The session will be designed to give scientists who work with these materials a chance to share their experiences in qualitative and quantitative analysis of these materials. We will also encourage discussion on regulatory hurdles that need to be overcome for these types of therapeutics.

Career Development in Mass Spectrometry Research
Bich Vu and Hao Chen, presiding
Four Seasons Ballroom 3-4

Scientists in mass spectrometry from both academics and industry will be invited to answer the questions from young scientists who are interested in career development. Short PowerPoint presentations are also in consideration for the workshop.

Interaction of Metal Ions and Clusters with Biomolecules
Grant E. Johnson and Victor Ryzhov, presiding
Room 607

The workshop will serve as an informal venue (especially for young scientists) to discuss metal ion- and cluster-related topics. Typical subjects include ion formation, reactivity, structure and energetics studied by mass spectrometry and complementary techniques (ion spectroscopy and theoretical calculations). The focus of the 2011 workshop will be on the interaction of metal ions and clusters with various classes of biomolecules (amino acids, peptides, proteins, carbohydrates, oligonucleotides). Some of the potential topics include metal ion-assisted fragmentation of biomolecules, structure and thermochemistry of metal ion-biomolecule complexes, clustering of biomolecules around metal ions, hydration of biomolecule/metal ion complexes, and optical properties of metal cluster-biomolecule hybrids.

Group Discussion to Generate Workshop Content to Stimulate Undergraduate Student Interest in Mass Spectrometry
Jennifer Grant, presiding
Room 711

We will use this workshop to generate educational materials to stimulate undergraduate students’ interest in mass spectrometry, taking advantage of colleagues’ specific expertise. This material might be used in future workshops aimed at undergraduates, perhaps at colleagues’ home institutions. The focus will be geared towards promoting mass spectrometric research at undergraduate-focused institutions.
problem spots with the current state of technology. In addition, the experts will be prepared for general, as well as specific discussions of source cleaning, and chromatographic irreproducibility. A panel of instrument troubleshooting. Areas of discussion will include use and working from the success of the “Hot Topics” LC-MS workshop in 2019. Additional topics and panel participants will be selected from the security from various speakers representing government agencies.

Obtaining sequence information is a critical step in the fundamentals and discuss the merits of the different approaches. The characterization of all biopolymers, including DNA and RNA. Over the rapid growth in recent years and is capable of providing detailed chemical maps of a drug and/or its metabolites, a peptide, biomarkers or a cosmetic ingredient across a sample of tissue or even complexes, and optical properties of metal cluster-biomolecule bonding theory and application: algorithm development and implementation licensing and protein-level quantification (such as the implicit identification therapeutics by mass spectrometry. The session will be designed to give scientists who work with these materials a chance to share their experiences in quantitative and qualitative analysis of these.

The Bioinformatics interest group will feature two sets of very brief, subject include ion formation, reactivity, structure and energetics scientists) to discuss metal ion- and cluster-related topics. Typical subjects include ion formation, reactivity, structure and energetics. Scientists are also in consideration for the workshop. We will use this workshop to generate educational materials to help provide information and solutions. Information gained from the workshop will be explored further, including experimental design, activities and challenges in the fields of forensics and homeland security related to mass spectrometry. Fundamentals and discuss the merits of the different approaches.

CONFERENCE OPENING AND PLENARY SESSION
5:00 - 6:30 pm
Susan T. Weintraub, University of Texas Health Science Center, presiding
Wells Fargo Theatre

MOA am 5:45 pm
Good Mass Spectrometry and its Place in Good Science: Sometimes Close Enough Is Really Not Good Enough
Mark W. Duncan
University of Colorado Denver, School of Medicine

5:45 - 6:30 pm
LC and MS: A Match Made in Heaven
James Jorgenson
University of North Carolina

MOA am 6:45 pm
Our Stellar Origins Revealed by Stardust Grains
Ernst Zinner
Washington University

CONFERENCE OPENING AND PLENARY SESSION
6:45 - 7:00 pm
Susan T. Weintraub, University of Texas Health Science Center, San Antonio, presiding
Wells Fargo Theatre

MOA am 8:30
The Role of MS-based Proteomics in Systems Biology: Steven Gysel; Ronghu Wu; Noah E. Dehoure; Wilhelm Haas; Mathew Sowa; Harvard Medical School, Boston, MA

MOA am 8:50
Analysis of the Endogenous Human Regulatory Complexome: Anna Malovannaya; Rainer Lanz; Sung Yun Jung; Nguyen T. Le; Yaroslava Bulynko; Doug W. Chan; Chen Ding; Yi Shi; Yi Wang; Bert W. O’Malley; Jun Qin; Baylor College of Medicine, Houston, TX

MOA am 9:10
A Dynamic Model of Proteome Changes Reveals New Roles for Transcript Alteration in Yeast: M. Violet Lee; Scott Topper; Shane Hubler; Craig Wenger; Audrey Gasch; Joshua J. Coon; University of Wisconsin, Madison, WI

MOA am 9:30
Quantitative Phosphoproteomics Defines Novel Substrates and Functional Modules of the Aurora and Polo-like Kinases in Mitosis; Arminja Kettenbach; Devin Schewepe; Brendan Faherty; Dov Pechenick; Alexandre Pletnev; Scott A. Gerber; Dartmouth Medical School, Hanover, NH

MOA am 9:50
Quantitative Affinity Proteomics Identifies Substrates of RNF146, a Poly(ADP-ribose)-Directed E3 Ubiquitin Ligase that Regulates Axin Degradation and Wnt Signaling; Yue Zhang; Jason Murphy; Elizabeth McWhinnie; Yan Feng; Feng Cong; Markus Schirle; Novartis, Cambridge, MA

MOA am 10:10
Protein Conformational Ensembles and their Utility in Defining Signaling Pathways; Graham M West; Michael J. Chalmers; Bruce D. Pascal; Karsten Melcher; Ellen Y. T. Chien; H. Eric Xu; Raymond C. Stevens; Patrick R. Griffin; ‘The Scripps Research Institute, Scripps Florida, Jupiter, FL; ‘Van Andel Research Institute, Grand Rapids, MI; ‘The Scripps Research Institute, La Jolla, CA
H/D EXCHANGE: NEW DEVELOPMENTS IN HARDWARE, SOFTWARE AND METHODOLOGY
8:30 – 10:30 am
Matthew B. Renfrow, University of Alabama-Birmingham, presiding
Room 501

MOB am 8:30  High Sensitivity On-line Deuterium Exchange Mass Spectrometry Using a Microfluidic Platform; Terry Lee¹; Yunan Miao¹; Kossi Lekpor¹; Reid A. Brennen²; Hongfeng Yin³; Kevin Killeen¹; Sheng Li¹; Tracy Handel¹; Virgil Woods, Jr.³; ³City of Hope, Duarte, CA; ²Agilent Labs, San Jose, CA; ³University of California, San Diego, La Jolla, CA

MOB am 8:50  A Histidine H/D Exchange Strategy for the Thermodynamic Analysis of Protein Folding and Ligand Binding; Duc Tran¹; Michael Fitzgerald; Duke University, Durham, NC

MOB am 9:10  Software for the Analysis of Large HDX Datasets; Bruce D Pascal; Scooter Willis; Michael J Chalmers; Janelle Lauer; Rachelle R Landgraf; Graham M West; Scott Novick; Patrick R Griffin; The Scripps Research Institute, Scripps Florida, Jupiter, FL

MOB am 9:30  Combining ESI Supercharging with Top-Down HDX-MS of Proteins and Complexes; Harry J. Sterling; Catherine A. Cassou; Evan R. Williams; University of California, Berkeley, CA

MOB am 9:50  Expanding the Utility and Flexibility of a Commercial HDX MS Automation Solution; Eric Monroe¹; Peter Smith³; Peter Prevelige²; ¹Univ. Alabama - Birmingham, Birmingham, AL; ²LEAP Technologies, Carrboro, NC

MOB am 10:10  Hydrogen Exchange Analysis at Single-Residue Resolution by ETD and Supplemental Activation in Tandem Travelling Wave Ion Guides; Kasper D. Rand¹; Steven D Pringle³; Michael Morris¹; John R. Engen¹; Jeffery M. Brown¹; ¹Swiss Institute of Bioinformatics, Lausanne, Switzerland; ²Northeastern University, Boston, MA; ³Waters MS Technologies Centre, Manchester, UK

FUNDAMENTALS OF PEPTIDE FRAGMENTATION: ELECTRON, PHOTON- AND COLLISION-BASED PROCESSES
8:30 – 10:30 am
Nicolas Polfer, University of Florida, presiding
Room 401

MOC am 8:30  Structure and Formation of a₅⁺ Ions of Protonated Peptides; Bela Paizs¹; Benjamin Bythell⁵; Alex G. Harrison⁴; Philippe Maitre¹; ¹DKFZ, Heidelberg, Heidelberg, Germany; ²National High Magnetic Field Laboratory, Tallahassee, FL; ³University of Toronto, Toronto, ON; ⁴Laboratoire de Chimie Physique, Orsay, France

MOC am 8:50  Statistical Study of Electron Transfer Dissociation Pairwise Fragmentation Patterns; Wenzhou Li¹; Chi Song⁵; George C. Tseng³; Joshua J. Coon³; Vicki H. Wysocki¹; ¹University of Arizona, Tucson, AZ; ²University of Pittsburgh, Pittsburgh, PA; ³Univ of Wisconsin-Madison, Madison, WI

MOC am 9:10  Excited State Trajectories of Electron-Based Peptide Dissociations; Christopher Moss; University of Washington, Seattle, WA

MOC am 9:30  Negative Ion Electron Capture Dissociation (niECD) of Disulfide-Linked Peptide Anions; Ning Wang; Kristina Hakansson; University of Michigan, Ann Arbor, MI

MOC am 9:50  Femtosecond Laser-induced Ionization/Dissociation Tandem Mass Spectrometry (fs-LID-MS/MS) of Multiply Deprotonated Phosphopeptide Anions; Scott Smith; Li Cui; Gavin E. Reid; Michigan State University, East Lansing, MI

MOC am 10:10  Direct Elucidation of Disulfide Bond Partners Using Ultraviolet Photodissociation Mass Spectrometry; Arun Agrawal⁵; Jolene Diedrich⁵; Ryan R. Jullan¹; ¹University of California at Riverside, Riverside, CA; ²University of CA, Riverside, Riverside, CA; ³University of California, Riverside, Riverside, CA
**IMAGING MS: INSTRUMENTATION AND IONIZATION SOURCES**

**8:30 – 10:30 am**

<table>
<thead>
<tr>
<th>Time</th>
<th>Title</th>
<th>Authors</th>
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<tbody>
<tr>
<td>MOD am 8:30</td>
<td>Strategy for Laser Ablation MS Imaging with Subwavelength Spatial Resolution; Renato Zenobi; Liang Zhu; Thomas Schmitz; Rolf Dietiker; Joachim Koch; Detlef Günter; Frank Krumpe; ETH Zurich, Switzerland</td>
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<tr>
<td>MOD am 8:50</td>
<td>Direct Fragmentation from Tissue by Combining CASI (Continuous Accumulation of Selected Ions) and SORI-CID: Structural Validation of Ion Images; Jeffrey Sprague; Shannon Cornett; Peggi Angel; Richard M. Caprioli; 1Vanderbilt University, Nashville, TN; 2Bruker Daltonics Inc., Fairview, TN</td>
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<tr>
<td>MOD am 9:10</td>
<td>Nanospray Desorption Electrospray Ionization: a New Technique for Ambient Imaging Mass Spectrometry; Julia Laskin; Patrick Roach; Brandi Heath; Jeremie Watrous; Peter Dorrestein; Lisa H. Cazares; Oliver John Semmes; 1Pacific NW National Laboratory, Richland, WA; 2University of California, San Diego, Skaggs School, La Jolla, CA; 3Eastern Virginia Medical School, Norfolk, VA</td>
<td></td>
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<tr>
<td>MOD am 9:30</td>
<td>High Performance Chemical Imaging: C60 SIMS FT-ICR Mass Spectrometry; Donald Smith; Errol Robinson; Aleksy Talmachev; Christian Berg; Ron M.A. Heeren; 1Pacific Northwest National Laboratory, Richland, WA; 2Bruker Daltonics Inc., Billerica, MA; 3FOM Institute AMOLF, Amsterdam, Netherlands</td>
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<tr>
<td>MOD am 9:50</td>
<td>Mass Spectrometry Imaging with High Resolution in Mass and Space (HR²MSI) - A New Level of Information and Validity; Andreas Römpp; Sabine Guenther; Yvonne Schober; Julia Kokesch; Dhaka Bhandari; Zoltan Takats; Bernhard Spengler; Justus Liebig University, Giessen, Germany</td>
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<tr>
<td>MOD am 10:10</td>
<td>Imaging Mass Spectrometry (MS) at Atmospheric and Intermediate Pressure using Laserspray Ionization (LSI); Sarah Trimpin; Wayne State University, Detroit, MI</td>
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**ENERGY, PETROLEUM AND BIOFUELS**

**8:30 – 10:30 am**

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<tbody>
<tr>
<td>MOE am 8:30</td>
<td>Quantitative Analysis of Aromatic Compounds in Petroleum by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry; Hendrik Muller; Hanadi Al-Jawad; Frederick Adam; Adnan Al-Hajji; Saud Aramco, Dhahran, Saudi Arabia</td>
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<td>MOE am 8:50</td>
<td>Investigation on the Formation of Fouling Deposits during Crude Oil Production; Wolfgang Schrader; Dominick Brandin; Max-Planck Inst für Kohlenforschung., Mülheim / Ruhr, Germany</td>
<td></td>
</tr>
<tr>
<td>MOE am 9:10</td>
<td>Comprehensive Petroleomic Characterization of Biomass Pyrolysis Using FT-ICR Mass Spectrometry and its Insights into Bio-oil Aging; Erica Smith; Marge Rover; Sunita Sadula; Christopher Thompson; Robert Brown</td>
<td></td>
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<tr>
<td>MOE am 9:30</td>
<td>Comprehensive Petroleomic Characterization of Fossil Organic Matter using NMR Techniques in Combination with Ultrahigh Resolution Mass Spectrometry; Elodie Salmon; Françoise Behar; Patrick Hatcher; Old Dominion University, Norfolk, VA; 1IFP Energies Nouvelles, Rueil-Malmaison, France</td>
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<tr>
<td>MOE am 9:50</td>
<td>A New Strategy for Molecular Characterization of Algal Biofuel and Feedstocks; F. Omar Holquin; Uriel Ortega-Rodriguez; Tanner Schaub; New Mexico State University, Las Cruces, NM</td>
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### INTEGRATED QUALITATIVE AND QUANTITATIVE LC-MS FOR DRUG METABOLISM AND PHARMACOKINETICS

**MOF am 8:30**  
**High Resolution Mass Spectrometry for Structural Elucidation and Quantitation of Drugs and their Metabolites based on Multiple MS and MS/MS Workflows;**  
Gerard Hopfgartner; Emmanuel Varesio;  
University of Geneva, Geneva, Switzerland

**MOF am 8:50**  
**A New Direction for Integrating Qualitative and Quantitative Bioanalysis;**  
Anthony Barros Jr; Ragu Ramanathan; Yuan-Qing Xia; Mohammed Jemal; Nirmala Raghavan; Asoka Ranasinghe; Timothy Olah; William Humphreys; Suma Ramagiri; Bristol-Myers Squibb Company, Princeton, NJ; AB SCIEX, Concord, ON

**MOF am 9:10**  
**Combining Non-selective and Selective Fragmentation and High Resolution Accurate Mass for Metabolite Screening and Identification in Early in vitro Studies;**  
Tim Stratton; Yingying Huang; Markus Kellmann; Thermo Fisher Scientific, San Jose, CA; AB SCIEX, Concord, ON

**MOF am 9:30**  
**High Throughput Screening of CYP Inhibition using a Cocktail Assay: Application of High-Resolution Mass Spectrometry to Sensitive Metabolite Quantification;**  
Hong Cai; Ming Yao; Jonathan L. Josephs; Mingshe Zhu; Bristol-Myers Squibb, Pennington, NJ

**MOF am 9:50**  
**Enabling 2 Minute Metabolite Identification Workflows using High Resolution UPLC, QTof and MS²;**  
Mark D. Wrona; Jeff Goshawk; Stephen McDonald; Alan Millar; Waters Corporation, Milford, MA; Waters, Manchester, UK

**MOF am 10:10**  
**Bridging the Quant to Qual Gap in Pharmaceutical Research Using a Novel High Speed, High Sensitivity QqTOF Mass Analyzer;**  
Loren Olson; John Maynard; Shaila Hoque; Hesham Ghobarah; Elliott Jones; Heather Zhang; George Tonn; John-Michael Sauer; Patrick J. Rudewicz; AB SCIEX, San Jose, CA; Elan Pharmaceuticals, South San Francisco, CA

### PROTEIN TERAPHEUTICS IN DRUG DISCOVERY AND DEVELOPMENT: LC-MS QUANTIFICATION

**MOG am 8:30**  
**Application of 18O-CASIL (Comparative Analytics using 18O Stable Isotope Labeling) to Biotherapeutic Development;**  
P. Matthew Fesinmeyer; Kenneth Daugherty; Sabine Hogan; Himanshu Gadgil; Amgen, Seattle, WA

**MOG am 8:50**  
**Quantitation of Human Growth Hormone (hGH) in Human Serum using an Immunofinity LC-MRM Hybrid Assay;**  
Shanhua Lin; Kumar Shah; Junlong Shao; Moucin Yuan; Patricia Paterson; Rand Jenkins; PPD, Richmond, VA

**MOG am 9:10**  
**An Improved SPE/LC/MS/MS Platform for the Quantification of Amyloid Beta Peptides in Cerebrospinal Fluid;**  
Erin E. Chambers; Mary E. Lame; Diane Diehl; Sarah Grimwood; Waters Corporation, Milford, MA; Pfizer Global Research & Development, Groton, CT

**MOG am 9:30**  
**LNA Oligonucleotides: Quantitative LC-MS/MS Approaches to Gaining Sensitivity in Various Matrices;**  
Elisabeth Lonie; Dawn Dufield; Pfizer, Andover, MA

**MOG am 9:50**  
**LC-MS/MS to Quantify Therapeutic Antibodies in Preclinical Samples: a Generic Approach Using a Common Antibody Reference Standard and Internal Standard;**  
Michael Hall; Amgen, Thousand Oaks, CA

**MOG am 10:10**  
**Accelerated Method Development for Sensitive, Accurate and Reproducible Quantification of Therapeutic Monoclonal Antibodies in Various Tissues Using Orthogonal-array-optimization and Nano-LC/SRM-MS;**  
Yuan-Qing Xia; Luina Abugayyas; Joseph P. Balthasar; Jun Qu; University at Buffalo, Amherst, NY; CoE in Bioinformatics&Life Sciences, Buffalo, NY
**POST-TRANSLATIONAL MODIFICATION**

MOA pm 2:30 Characterizing Gas-Phase Rearrangements of Arginine-Phosphorylated Peptides and their Influence on Phosphorylation Site Localization; Hongjian Yang; Yanoslav Lytvynskiy; David Good; Roman Zubarev; Karolinska Institutet, Stockholm, Sweden

MOA pm 2:50 Proteome-Wide Detection and Quantification of Isoaspartyl Residues in Blood Plasma of Alzheimer’s Disease Patients; Hongjian Yang; Yanoslav Lytvynskiy; David Good; Roman Zubarev; Karolinska Institutet, Stockholm, Sweden

MOA pm 3:10 Identification and Verification of Lysine Succinylation as a Novel in-vivo Protein Post-Translational Modification; Minjia Tan; Zhihong Zhang; Zhongyu Xie; Lunzhi Dai; Yue Chen; Yingming Zhao; Ben May Department for Cancer Research, The University of Chicago, Chicago, IL

MOA pm 3:30 New Mass Spectrometry Approach to Identify SUMOylated Peptides from Large-scale Proteomics Analyses Using a LTQ-Orbitrap Velos; Eric Bonnell; Chantal Durette; Louiza Mahrouche; Pierre Thibault; IRIC-Université de Montréal, Montréal, Canada; 2Department of Biochemistry, Université de Montréal, Montréal, Canada

MOA pm 3:50 Large-scale Endogenous S-nitrosylation Analysis of Mouse Spleen; Miao Liu; Ibrahim Younos; Hong Peng; Xin Huang; Lin Huang; Kai Fu; Zhixin Zhang; James Talmadge; Shi-Jian Ding; University of Nebraska Medical Center, Omaha, NE

MOA pm 4:10 Quantification of 10,000 Mouse Phosphorylation Sites in Response to Insulin Stimulation by Spike-in SILAC and HCD-Orbitrap MS; Matthias Mann; Max Planck Institute for Biochemistry, D Martinsried, Germany

**H/D EXCHANGE FOR PROTEIN STRUCTURE AND FUNCTION**

MOB pm 2:30 Structural Dynamics of Membrane Proteins and Neurotoxic Aggregates Probed by Conformer-Specific HDX Mass Spectrometry; Lars Konermann; Jingxi Pan; Yan Pan; Leonid Brown; Christoph H. Borchers; Jun Han; 1Univ. of Western Ontario, London, CANADA; 2University of Western Ontario, London, ON; 3University of Guelph, Guelph, ON; 4Uvic-GBC Proteomics Centre, Victoria, BC; 5University of Victoria-Genome BC Proteomics Centre, Victoria, BC

MOB pm 2:50 Activation and Inhibition of Type-I insulin-like Growth Factor Receptor Differentially Alters Conformation and Influences Asymmetric Behavior; Damien Houde; Stephen Demarest; Biogen Idec, Cambridge, MA

MOB pm 3:10 Fragment-based Approach for Inhibitor Design by Amide Hydrogen/Deuterium (H/D) Exchange Mass Spectrometry; Srinath Krishnamurthy; Anna Jansson; Steven A. Cohen; Ganesh Anand; 1National University of Singapore, Singapore, Singapore; 2Nanyang Technological University, Singapore, Singapore; 3Waters Corporation, Milford, MA

MOB pm 3:50 Structure to Function; Use of Limited Proteolysis and Hydrogen Exchange Mass Spectrometry to Understand Virus Capsid Assembly and Entry; Brian Bothner; Navid Movahedi; Vamsi Rayaprolu; Jonathan K. Hilmer; Dewey Brooke; Adam Zlotnick; Mavis Agbandje-McKenna; Montana State University, Bozeman, MT; 1Indiana University, Bloomington, IN; 2University of Florida, Gainesville, FL

MOB pm 4:10 The Utility of Hydrogen Exchange Mass Spectrometry in Structural Genomics: The PGAM5 Story; Sean R. Marciszin; Apirat Chaikuad; Sarah Picaud; Ivan Alfano; Murakami Shiori; Kosuke Takeda; Hidenori Ichijo; Panagis Filippakopoulos; Stefan Knapp; John R. Engen; 1Northeastern University, Boston, MA; 2Structural Genomics Consortium, Oxford, UK; 3University of Tokyo, Tokyo, Japan
### MONDAY AFTERNOON ORAL SESSIONS

#### Fundamentals: Ion Spectroscopy

**2:30 – 4:30 pm**  
Robert C. Dunbar, Case Western Reserve University, presiding  
**Room 401**

- **MOC pm 2:30**  
  **Ion Spectroscopy - an Overview; John R. Eyler**  
  **Ashley Awartani**; Cesar Contreras  
  **Marcus Tirado**; Alfred Young  
  **Jeffrey Steill**; Giel Berden  
  **Jos Oomens**; Nicole Horenstein  
  **University of Florida, Gainesville, FL**;  
  **NASA Ames Research Center, Moffett Field, CA**;  
  **Carelton College, Northfield, MN**;  
  **FOM Rijnhuizen, Nieuwegein, Netherlands**;  
  **Sandia/California, Livermore, CA**;  
  **University of Amsterdam, Amsterdam, Netherlands**

- **MOC pm 2:50**  
  **Structure and Reactivity of Cysteine-Containing Radical Ions Studied by Ion Spectroscopy and Ion-Molecule Reactions; Victor Ryzhov**  
  **Sandra Osburn**; Jos Oomens  
  **Richard A. J. O'hair**;  
  **University of Florida, Gainesville, FL**;  
  **NASA Ames Research Center, Moffett Field, CA**;  
  **University of California, San Diego, Skaggs school, La Jolla, CA**;  
  **University of Bremen, Bremen, Germany**;  
  **University of Amsterdam, Amsterdam, Netherlands**

- **MOC pm 3:10**  
  **Conformation-Specific Spectroscopy of Cold Peptide Fragment Ions; Tobias Wassermann**  
  **Thomas Rizzo**; Ecole Polytechnique Fédérale de Lausanne, Ch-1015 Lausanne, Switzerland

- **MOC pm 3:30**  
  **Fluorescence and Fluorescence Resonance Energy Transfer (FRET) Measurements of Mass-Selected Gaseous Ions; Rebecca A. Jobkusch**  
  **Martin F. Czar**; Francis O. Talbot  
  **University of Toronto, Chemistry Department, Toronto, Canada**

- **MOC pm 3:50**  
  **Spectroscopic Evidence for A Triplet Ground State in Dehydrogenated Polyaromatic Cations; Hector Alvaro Galuè**  
  **Jos Oomens**; FOM Rijnhuizen, Nieuwegein, Netherlands; University of Amsterdam, Amsterdam, Netherlands

- **MOC pm 4:10**  
  **Vibrational Spectroscopy of Dipeptides Using Infrared and Raman Dissociation of Cryogenic, H2-Tagged Ions; Michael J. Van Stipdonk**  
  **Christopher Leavitt**; Michael Kamrath  
  **Etienne Garand**; Arron Wool  
  **Wirchita State University, Wichita, KS**; Yale University, New Haven, CT

#### Imaging MS: Biological Applications

**2:30 – 4:30 pm**  
Rachel O. Loo, UCLA, presiding  
**Korbel Ballroom 1-2**

- **MOD pm 2:30**  
  **2 and 3-Dimensional Mapping of Metabolic Interactions in Microbial Communities; Jeramie Watrous**  
  **Theodore Alexandrov**; Pieter Dorrestein  
  **University of California, San Diego, Skaggs school, La Jolla, CA**;  
  **University of Bremen, Bremen, Germany**;  
  **UCSD, La Jolla, CA**

- **MOD pm 2:50**  
  **MALDI Mass Spectrometry Imaging of Secreted Lipopeptides in a Bacterial Biofilm Colonizing Plant Roots; Delphine Debois**  
  **Emmanuel Jourdan**; Marc Ongena  
  **Edwin De Pauw**;  
  **University of Liege - LSM / GIGA-R, Liege, Belgium**;  
  **University of Liege - CWBI, Liege, Belgium**;  
  **University of Liege - Gembloux Agro-BioTech, Gembloux, Belgium**

- **MOD pm 3:10**  
  **Multiple Changes in Peptide and Lipid Expression Associated with Regeneration in the Nervous System of the Medicinal Leech by MSI; Cédric Meriaux**  
  **Karim Arafah**; Aurélie Tasiemski  
  **Maxence Witsorts**; Jocelyne Brudan  
  **Céline Wichlacz-Boidin**; Annie Desmons  
  **Delphine Debois**; Olivier Laprévote  
  **Alain Brunelle**; Eduardo Macagnano  
  **Isabelle Fournier**; Michel Salzet  
  **FABMS, Université Lille 1, Villeneuve D’Ascq, FRANCE**;  
  **UCSD, La Jolla, CA**;  
  **Centre de Recherche de Gif, ICSN-CNRS, Gif Sur Yvette, France**;  
  **LSM-CART-GIGA-R, University of Liège, Liège, Belgium**;  
  **Université Paris Descartes, Paris, France**;  
  **ImabioTech, Villeneuve D’Ascq, France**

- **MOD pm 3:30**  
  **Alterations of Striatal Dynorphin Peptide Levels in L-DOPA-induced Dyskinesia Revealed by Imaging Mass Spectrometry; Jörg Hanrieder**  
  **Anna Karlsson**; Maria Fälth  
  **Sofie Eriksson-Mammon**; Jonas Bergquist  
  **Malin Andersson**; Uppsala University, Uppsala, Sweden;  
  **German Cancer Research Center, Heidelberg, Germany**

- **MOD pm 3:50**  
  **Mass Spectrometry Visualizes Hypoxia-driven Processes in Breast Tumors; Kamila Chughtai**  
  **Lu Jiang**; Tiffany R. Blackwell  
  **Kristine Giunde**; Ron M.A. Heeren  
  **AMOLF, Amsterdam, Netherlands**;  
  **The Johns Hopkins University School of Medicine, Baltimore, MD**

- **MOD pm 4:10**  
  **Imaging Mass Spectrometry to Uncover Proteomic Differences in Follicular Lymphomas; Kristina Schwamborn**  
  **Ellen Leich**; Andreas Rosenwald  
  **Vanderbilt Univ Sch of Med, Nashville, TN**;  
  **Technical University Munich, Munich, Germany**;  
  **University of Wuerzburg, Wuerzburg, Germany**
MONDAY AFTERNOON ORAL SESSIONS

<table>
<thead>
<tr>
<th>PLANT PROTEOMICS</th>
<th>HIGH RESOLUTION MS IN DRUG METABOLISM AND PHARMACOKINETICS</th>
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<tbody>
<tr>
<td>2:30 – 4:30 pm</td>
<td>2:30 – 4:30 pm</td>
</tr>
<tr>
<td>Paul A. Haynes,</td>
<td>Mustafa Varoglu, Cubist Pharmaceuticals, presiding</td>
</tr>
<tr>
<td>Macquarie University, presiding</td>
<td>Four Seasons Ballroom 1-2</td>
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<tr>
<td>Korbel Ballroom 3-4</td>
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MOE pm 2:30
A Systems Approach for Characterizing the Phosphoproteome and Interactome of Leucine-Rich Repeat Receptor-Like Kinases in Arabidopsis; Srijee Mita; Xiaofeng Wang; Kevin Blackburn; Tara Nash; Ruiqiang Chen; Steven Clouse; Michael Goshe; North Carolina State University, Raleigh, NC

MOE pm 2:50
Proteogenomics: Annotating the Genome of Zea Mays Using Proteomics; Natalie E Castellana; Doruk Beyer; Michelle Facette; Joshua Osborn; Zhourxin Shen; Justin Walley; Laurie Smith; Steven P. Briggs; Vineet Bafna; UCSD, La Jolla, CA; Bilkent University, Ankara, Turkey

MOE pm 3:10
Structural Organization and Function of the Oligomeric Clp Protease in Plants Determined by QConCAT and Spectral Counting-based Quantitative Proteomics; Klaas J. Van Wijk; Paul Dominic B. Olinares; Jitae Kim; Anton Poliakov; Lalit Ponnal; Giulia Friso; Cornell University, Ithaca, NY

MOE pm 3:30
Enhanced Shotgun Proteomic Approach Provides a Systematic Survey of Single Amino Acid Polymorphisms in Populus Leaf, Root, and Stem; Paul Abraham; Rachel Adams; Ranjan Priya; Richard Giannone; Gerald Tuskan; Robert Hettich; Oak Ridge National Lab, Knoxville, TN; GST, University of Tennessee, Knoxville, TN

MOE pm 3:50
Proteomic Responses in Arabidopsis thaliana Seedlings Treated with Ethylene; Bret Cooper; Ruiqiang Chen; Brad Binder; Wesley Garrett; Mark Tucker; Caren Chang; USDA-ARS, Beltsville, MD; University of Maryland, College Park, MD; University of Tennessee, Knoxville, TN

MOE pm 4:10
Online enrichment and Targeted Analysis of Phosphopeptides in Hormone Mediated Plant Signaling; Kelli Kline; J. Bryce Young; Sahana Mollah; Nicole Hebert; Michael R. Sussman; University of Wisconsin, Madison, WI; AB SCIEX, Concord, ON; Eksigent Technologies, Dublin, CA

MOF pm 2:30
Accurate Mass: Why it’s the Best Solution for Metabolite Identification In Discovery, Development and Clinical Applications; Philip Tiller; RMI laboratories, North Wales, PA

MOF pm 2:50
When the Use of High Resolution Mass Spectrometry is Critical for Correct Structural Elucidation of Metabolites: A Few Case Studies; Natalia Penner; Lin Xu; Chandra Prakash; Biogen Idec, Cambridge, MA

MOF pm 3:10
Metabolite Identification in Beagle Dog Bile Collected with the Entero-Test® Device; Peter L. Jacobs; Rianne H.M. Glaudemans-Rijkers; Henk J.M. van Hal; Marlon L.P.S. van Iersel; Eric van der Meulen; MSD, Oss, Netherlands

MOF pm 3:30
Advantages of Single Injection Generic Quant & Qual Workflows using High Resolution Accurate Mass Technology for in-vivo PK analysis; Suma Ramagiri; Tanya Gamble; Jeffrey Miller; Graham Gibson; Hesham Gobarah; Gary Impey; Elliott Jones; Yanou Yang; Nirmala Raghavan; Chiwu Emily Luk; Jonathan L. Josephs; Ragu Ramanathan; William Griffith Humphreys; AB SCIEX, Concord, CANADA; Bristol-Myers Squibb, Princeton, NJ; ABSCIEX, Medford, NJ

MOF pm 3:50
Comprehensive Metabolite Profiling in a Discovery Environment Using a Novel Hybrid Quadrupole-Orbitrap Instrument; Jonathan L. Josephs; Yanou Yang; Chiwu Emily Luk; Kate Comstock; Tim Stratton; Yingying Huang; William Humphreys; Bristol-Myers Squibb, Pennington, NJ; Thermo Fisher Scientific, San Jose, CA

MOF pm 4:10
Rapid Identification of Peptide Hydrolysates Fragments Using Quadrupole Time-of-Flight Mass Spectrometry to Facilitate Optimization of Pharmacokinetic Properties; Hongjuan Zhao; Michelle Dennehy; Panos Hatsis; Novartis, Cambridge, MA
Biomarker Quantification: Challenges in Regulated Bioanalysis

2:30 – 4:30 pm
Fabio Garofolo, Algorithmic Pharma, Inc., presiding
Four Seasons Ballroom 3-4

MOG pm 2:30 A Model Standard Operating Procedure for Quantitative LC-MS Biomarker Assay Validation; Gary A. Schultz; Barry R. Jones; Kathleen A. Cormack; Stephen Lowes; Advion BioServices, Inc., Ithaca, NY

MOG pm 2:50 Quantitation of Aldosterone and Related Steroids by UPLC/MS for In-Vivo Samples; Ling Xu; Lucinda Cohen; Xinchun Tong; DMPK Merck Research Laboratories, Rahway, NJ

MOG pm 3:10 Epitope Mapping and Quantitation of Troponin Biomarker by Targeted Mass Spectrometry; Cheng Zhao; Helen Xie; Jeffrey Fishbaugh; Carol Ramsay; Abbott Laboratories, Abbott Park, IL

MOG pm 3:30 S100 A8, A9 and A12-Multiplex for Monitoring Inflammatory Status – Key Contributions for RA and Related Diseases; Stephane Charmont; Stephan Bek; Nelson Guerreiro; Thomas Vogl; Johannes Roth; Jemima Schuhmann

MOG pm 3:50 Development and Validation of an Online Spe-LC-MS/MS Assay for Quantitation of Urinary Tetranor PGDM and Tetranor PEGEM As Inflammatory Biomarkers; Yizhong Zhang; Guodong Zhang; Philip Clarke; Rick Steenwyk; Joe Zhaosheng Lin; Pfizer, Groton, CT

MOG pm 4:10 Quantitative Analysis of Growth Hormone Biomarker IGF-1 in Human Serum by UPLC-MS/MS: Extraction, Oxidation Stability, and Mass Spectrometry; Mouyun Yuan; Junlong Shao; Michael Tingler; Shanhua Lin; Bruce Hidy; Rand Jenkins; PPD, Richmond, VA

Award Lecture
4:45 - 5:30 pm
Scott A. McLuckey, Purdue University, presiding
Wells Fargo Theatre

Award for a Distinguished Contribution in Mass Spectrometry
Robert J. Cotter
Johns Hopkins University

Quantitative Proteomics: Peptides

8:30 – 10:30 am
Claudia Maier, Oregon State University, presiding
Wells Fargo Theatre

TOA am 8:30 Next Generation Quantification (NGQ): Studying the Mitotic Microtubule Interactome Using a Novel Metabolic 5-Plex Quantification Method; Marc Kirchner; Dominic Winter; Ghazal Ashrafi; Thomas Schwarz; Judith Steen; Hanno Steen; Harvard Medical School/Children’s Hospital Boston, Boston, MA

TOA am 8:50 Comparison of iTRAQ- and mTRAQ-based Peptide Quantification in Global Proteomics and Phosphoproteomics Studies of EGFR-Inducing Phosphoantigens; Philipp Mertins; Namrata Udeshi; Karl R. Clauer; Steven A. Carr; The Broad Institute, Cambridge, MA

TOA am 9:10 Label-Free Internal Reference Peptide Quantification of Phosphorylation Stoichiometry Using MS3 and MS3 Analysis on an LTQ Velos Mass Spectrometer; Amy-Joan L. Ham; Stacy D. Sherrod; Matthew V. Myers; Ming Li; Daniel C. Liebler; Vanderbilt University School of Medicine, Nashville, TN

TOA am 9:30 Investigating the Relationship between Sample Complexity and Accurate Assessment of Quantitative Change - How Uniquely Can an Ion be Measured; Craig Dorschel; Martha Stapels; Scott Geromanos; Waters Corporation, Milford, MA

TOA am 9:50 SWATH-MS: Data Independent Capture of MS/MS Sequences for Quantification of Peptide Kinetics in a Cell Signalling Cascade; Lorne E B Taylor; Stephen A Tate; Yong Zheng; Cunjie Zhang; Ruedi Aebersold; Tony Pawson; Samuel Lunenfeld Research Institute, Toronto, ON; ETH Zurich, Zurich, Switzerland; AB SCIEX, Concord, ON

TOA am 10:10 Meeting the Design, Development and Implementation Challenges of >100-Plex Quantitative Assays for Proteins in Plasma: A Large-Scale, NCIC-PTAC Interlaboratory Study; Susan E. Abbatiello; Birgit Schilling; Brendan Maclean; Pawel Sadowski; Angela M. Jackson; Mousumi Ghosh; Hasmik Keshishian; Terri Addona; Jeffrey Whiteaker; Simon Allen; Michael Burgess; Nell Sedransk; D. R. Mani; Steven C. Hall; Steven A. Carr; CPTAC Network; Lisa Zimmerman; Daniela Tomazela; Broad Inst of MIT and Harvard, Cambridge, MA; Buck Inst for Research on Aging, Novato, CA; Univ of Washington, Seattle, WA; New York Univ; Uvic Genome BC Proteomics Centre, Victoria, BC; Memorial Sloan Kettering Cancer, NY; Fred Hutchinson Cancer Res Ctr, Seattle, WA; Univ of California, San Francisco; NISS, Research Triangle Park, NC; UCSF Sandler-Moore Mass Spectrometry Core Facility, San Francisco; Nati Cancer Inst, Bethesda, MD; Vanderbilt Univ.

MONDAY AFTERNOON and TUESDAY MORNING ORAL SESSIONS
TOB am 8:30  Formation of Highly Toxic Iodo-DBPs in Drinking Water;  
Susan Richardson1; Stephen Duirk1;2; Cristal Lindell3;  
Christopher Cornelson1; Thomas Ternes3; Jennifer Kormos1; Michael Plewa1;  
Emmamarie Smith2; William Mitch2; US EPA, NERL, Athens, GA;  
2Univ of Akron, Akron, OH; 3Federal Inst of Hydrology, Koblenz, Germany;  
4Univ of Illinois, Urbana, IL; 5Yale Univ, New Haven, CT

TOB am 8:50  Ultra-trace Level Metabolite Identification Using the Latest 
Generation of QqTOF, Benchtop Quadrupole-Orbitrap, and LIT-FTMS 
Instrumentation; Jeffrey Gilbert1; Jesse Balcer1; Yelena A. Adelfinskaya1; Kate Comstock1; Suresh Annangudi1; Ayanna Jackson1; Michael Hastings1; Brian Wendelburg1; David McCaskill1; Yingying Huang1; Dow AgroSciences, Indianapolis, IN;  
2Thermo Fisher Scientific, San Jose, CA

TOB am 9:10  Plasma Metabolite Identification using High Resolution LC-MS and HCD 
Fragmentation; Bruce Kristal1; Susan S. Bird1; Matthew Siniatynski1; Diane Sheldon1; Vasant Marur1; Wayne Matson2; Brimmer and women’s Hospital, Boston, MA; 3bedford VA Hospital, Bedford, MA

TOB am 9:30  Exploiting Metabolic Diversity for the Discovery and Elucidation of Triterpene Saponin Biosynthesis; Lloyd W. Sumner1; John H. Snyder1; David V. Huhman1; Dong Sik Yang1; Stacy Allen1; Yuhong Tang1; The Samuel Roberts Noble Foundation, Ardmore, OK

TOB am 9:50  Development of a High-Throughput Mass Spectrometry Method to Identify Malignancy in Patients with Adrenal Tumors; Angelo E. Taylor1; Micheal Bielh1; Beverly Hughes1; Petra Schneider1; David L Smith1; Han Stiekema1; Peter Nightingale1; Cedric HL Shackleton1; Paul M Stewart1; Wiebke Arlt1; 1University of Birmingham, Birmingham, UK; 2University of Groningen, Groningen, The Netherlands; 3University Hospital Birmingham, Birmingham, UK

TOC am 8:30  Automatically Annotating Spectra with Fragmentation Reactions - an Aid for Manual and Automatic Identification of Unknowns; Florian Rasche1; Franziska Hufsky1; Kerstin Scheubert1; Sebastian Böcker1; Friedrich-Schiller-University Jena, Jena, Germany

TOC am 8:50  Chemical Annotation of MassBank ESI-MS2 Data; Takasaki Nishioka1; Masanori Arita1;2; Yuya Ojima1;3; Tasuku Ikeda1;2; Yoshito Nishi1;2; Bird, JST, Tokyo, Japan; 1AB, K; University, Tsuruoka, Japan; 2Grad, Sch., The University of Tokyo, Tokyo, Japan

TOC am 9:10  Determination of Human-Use Pharmaceuticals in Ground- and Surface-Water Samples by Large-Volume Injection, High-Performance Liquid Chromatography/Tandem Mass Spectrometry; Edward T. Furlong1; Mary Noriega1; Mark Burkhardt1; Laura Coffey1; Stephen L. Werner1; National Water Quality Laboratory, U.S.G.S., Denver, CO; 
2U.S. Environmental Protection Agency, Denver, CO

TOC am 9:30  Oxidative Removal of Selected PPCPs and Identification of Oxidative Degradates of PPCPs in Drinking Water Using LC-MS/MS; Yinfu Ma1; Chuan Wang1; Qihua Wu1; Honglan Shi1; Craig Adams1; Terry Timmons1; Missouri S&T, Rolla, MO; Missouri S&T/ERC, Rolla, MO; 1University of Kansas, Lawrence, KS; 2University of Kansas, Lawrence, KS

TOC am 9:50  Development of a High-Throughput Mass Spectrometry Method to Identify Malignancy in Patients with Adrenal Tumors; Angela E. Taylor1; Micheal Bielh1; Beverly Hughes1; Petra Schneider1; David L Smith1; Han Stiekema1; Peter Nightingale1; Cedric HL Shackleton1; Paul M Stewart1; Wiebke Arlt1; 1University of Birmingham, Birmingham, UK; 2University of Groningen, Groningen, The Netherlands; 3University Hospital Birmingham, Birmingham, UK

TOC am 10:10  Discovery of Oxidation Products in Ozonated Carbamazepine Solution by Liquid Chromatography Coupled to Hybrid Triple Quadrupole Linear Ion-Trap Mass Spectrometry; Feng Qin1; Jin Jiang1; Jun Ma1; Yongming Xie1; AB SCIEX, Shanghai, CHINA; 2Harbin Institute of Technology, Harbin, China

TOC am 10:10  Bioregulatory Secretory Proteins in Plasma in Clinical Settings; Yuji Nishio1;2; Martin Scholz1; Christian Hartenberger1; Hiroko Yamamoto1;2; Tobias Schnepp1; Christian Wisniewski1; mathematica, Jena, Germany; 1University of Tübingen, Tübingen, Germany; 2German Cancer Research Center, Heidelberg, Germany
**BIOMOLECULAR STRUCTURE ANALYSIS BY COVALENT LABELING: FUTURE DIRECTIONS**

8:30 – 10:30 am  
Bradford W. Gibson, Buck Institute for Age Research, presiding  
Korbel Ballroom 1-2

**TOD am 8:30**  
Proteinase K Non-Specific Digestion for the Comprehensive Identification of Interpeptide Crosslinks: Application to Prion Proteins; Evgeniy V. Petrochenko¹; Jason J. Serpa; David S. Wishart⁶; Christoph H. Borchers⁴; ¹UVic - Genome BC Protein Centre, Victoria, Canada; ²Departments of Biological Sciences and Computing, Edmonton, Canada

**TOD am 8:50**  
Folding Mechanism of a Membrane Protein Probed by Pulsed Oxidative Labeling and Mass Spectrometry; Yan Pan; Leonid Brown; Lars Konermann; ¹University of Western Ontario, London, Canada; ²University of Guelph, Guelph, Canada

**TOD am 9:10**  
An Integrated High-throughput Workflow for Identification of Crosslinked Peptides from Complex Sample; Bo Yang; Yan-Jie Wu; Ming Zhu; Jin-Zhong Lin; Kun Zhang; Shu-Kun Luo; Li-Yun Xiu; She Chen; Ke-Qiong Ye; Si-Min He; Meng-Qiu Dong; Yue-He Ding; ¹National Institute of Biological Science, Beijing, Beijing, CHINA; ²Key Lab of Intelligent Information Processing, CAS, Beijing, China

**TOD am 9:30**  
Novel structural model for CCL5 (RANTES) Oligomerization Using Hydroxyl Radical Footprinting; Caroline Watson; Xu Wang; Joshua S. Sharp; James H. Prestegard; ¹Complex Carbohydrate Research Center/UGA, Athens, GA; ²University of Georgia, Athens, GA

**TOD am 9:50**  
TUESDAY MORNING ORAL SESSIONS

### MASS SPECTROMETRY ANALYSIS OF DRIED BLOOD SPOT SAMPLES

**8:30 – 10:30 am**

- **Qin Ji, Bristol-Myers Squibb, presiding**
- **Four Seasons Ballroom 1-2**

**TOF am 8:30**

**Highly Sensitive and Specific Clinical Diagnostics of Lysosomal Storage Diseases in Dry Blood Spots by Multiplex Reaction Monitoring Mass Spectrometry**; Claudia cozma1; Christina Mosoarca2; Sebastian Dilly3; Marius-Ionut Iurascu1; Thomas Fritz2; Stefan Maeser3; Alina Zamfir4; Michael Przybylski1; 1Universitat Konstanz, Konstanz, Germany; 2National Institute for Research and Development, Timisoara, Romania; 3Genzyme CEE GmbH, Konstanz, Germany; 4Genzyme GmbH, Neu-Isenburg, Germany

**TOF am 8:50**

**Feasibility of Dried Blood and Plasma Spots to the Enhanced Stability of Glucuronide Metabolites**; Chester L Bowen1; Jessica Cades2; Christopher A. Evans3; 1GlaxoSmithKline, King Of Prussia, PA; 2Drexel University, Philadelphia, PA

**TOF am 9:10**

**A Strategy to Overcome Challenges with Dried Blood Spot Sample Dilution**; Guowen Liu1; Heidi Snapp; Qin Ji; Bristol-Myers Squibb Co., Princeton, NJ

**TOF am 9:30**

**Perforated Dried Blood Spot (PDBS): A Novel Concept for Accurate Micro-sampling**; Fumin Li1; John Zulkoski1; Douglas Fast1; Steven Michael1; Covance Inc., Madison, WI; 2Covance Laboratories, Madison, WI; 3Covance Laboratories, Madison, WI

**TOF am 9:50**

**Paper Spray Mass Spectrometry as an Ambient, Quantitative method for Point of Care Therapeutic Drug Monitoring from Blood**; Ryan Espe1; Nicholas Manicke2; Zheng Ouyang; B. Graham Cooks; Purdue University, West Lafayette, IN

**TOF am 10:10**

**Developing a Fully Automated Dried Blood Spot Direct Analysis Technique for High Sample Throughput Quantitative Bioanalysis**; Paul Abu-Rabie1; Neil Spooner; Philip Denniff2; GlaxoSmithKline R&D Ltd, Ware, UK

### CLINICAL CHEMISTRY: ADVANCES IN SEPARATION TECHNOLOGIES

**8:30 – 10:30 am**

- **Russell Grant, Labcorp, presiding**
- **Four Seasons Ballroom 3-4**

**TOG am 8:30**

**Automated Protein Sample Preparation – Rapid Identification of Single Amino Acid Polymorphisms Amongst a Class of Compounds**; Fred Regnier1; Purdue University, West Lafayette, IN

**TOG am 8:50**

**Vapor-Sorption Induced (Matrix) Crystallization and Protein Arrays for High-Throughput Label-Free Quantitation of Autoantibodies and Enzyme Activities**; Michael Roth1; Jaekuk Kim; Steven Patrie; UT Southwestern Medical Center, Dallas, TX

**TOG am 9:10**

**Profiling of Gangliosides in Brain Tissue and Cell Membranes using nanoHPLC Chip/Q-TOF MS**; Hyeyoung Lee1; Rudolf Grimm2; Carlito Lebrilla1; Bruce German1; 1University of California, Davis, CA; 2Agilent Technologies, Santa Clara, CA

**TOG am 9:30**

**A Novel Multidimensional HILIC Based Proteomic Approach Provides High Resolution Separation Increasing Sensitivity in Proteome Analysis**; Serena Di Palma1; Paul Boersema1, 2; Marc van de Wetering3; Daniel Stange4; Hans Clevers5; Albert J.R. Heck1; Shabaz Mohammed1; 1Utrecht University, Utrecht, Netherlands; 2Max Planck Institute for Biochemistry, Martinsried (Munich), Germany; 3Hubrecht Institute, University Medical Center, Utrecht, The Netherlands

**TOG am 9:50**

**An Empirical Marriage of HILIC and Clinical Diagnostics: Exploration and Expansion of Development, Utility and Doctrine**; Brian Rappold1; Russell Grant; Matthew Crawford; Patricia Holland; Labcorp, Burlington, NC

**TOG am 10:10**

**Standardized High Throughput LC-MS/MS Steroid-Quantification for Clinical Metabolomics - Interlaboratory and Interassay Validation**; Therese Koal1; Diane Schmiederer1; Hai Pham Tuan1; Cornelia Röhring1; Manfred Rauh1; Biocrates Life Sciences AG, Innsbruck, AUSTRIA; 1Universitätsklinikum Erlangen Kinder- und Jugendklinik, Erlangen, Germany
TUESDAY AFTERNOON ORAL SESSIONS

INFORMATICS: QUANTIFICATION/VALIDATION  
2:30 – 4:30 pm  
Brian C. Searle, Proteome Software, Inc., presiding  
Wells Fargo Theatre

TOA pm 2:30  Systematic Biases Affecting Peptide Intensities in Label-Free Proteomic Analyses; Paul Rudnick1; Xia Wang2; Xinjian Yan1; Neil Sedransk1; Stephen Stein1; 1NIST, Gaithersburg, MD; 2National Institute of Statistical Sciences, Research Triangle, NC

TOA pm 2:50  Non-parametric p-values for Differential LC-MS Proteomics Experiments; Gregory Finney; Gennifer Merrihew; Michael J. Maccoss; University of Washington, Seattle, WA

TOA pm 3:10  Changing the Rules of the Game: Next Generation Quantification (NGQ) Enables Complete Isotopic Multiplexing for Quantitative Functional and Dynamic Proteomics; Marc Kirchner; Dominic Winter; Judith Steen; Hanno Steen; Harvard Medical School/Children's Hospital Boston, Boston, MA

TOA pm 3:30  Selecting Peptides Based Upon their Response to Protein Concentration Improves Upon the HI-3 Method for Protein Quantification; Sean McIlwain; Michael Bereman; Michael Mathews; Edwin Rubel; Michael J. Maccoss; William Noble; University of Washington, Seattle, WA

TOA pm 3:50  Bayesian Hierarchical Reconstruction of Protein Profiles Including a Digestion Model; Pierre Grangeat1; Pascal Szacherski1; 1CNRS - IPB, IMS, Talence, France

TOA pm 4:10  mProphet- automated SRM Data Processing and Statistical Error Estimation for Large Scale SRM Experiments; Oliver Rinner1; Lukas Reiter1; Paola Picotti1; Ruth Huettenhain1; Ruedi Aebersold1; 1Biognosys AG, Zurich, Switzerland

ENVIRONMENTAL CHEMISTRY AND HEALTH  
2:30 – 4:30 pm  
Susan Richardson, US EPA, NERL, presiding  
Room 501

TOB pm 2:30  Biodegradation Study of a Fluorotelomer Polymer Product; Barbara S. Larsen1; Robert Buck2; William R Berti2; Edward C. Schaefer1; Raymond L. Van Hoven Van Hoven2; 1The DuPont Company, Wilmington, DE; 2Wildlife International, Ltd., Easton, MD

TOB pm 2:50  Drinking and Swimming with Haloquinones: Liquid Chromatography-Tandem Mass Spectrometry Investigation of Tap Water and Swimming Pools; Yuli Zhao; Wei Wang; Jessica Boyd; Xing-Fang Li; University of Alberta, Edmonton, Canada

TOB pm 3:10  Pollution of Moscow Air in Winter. The GC-MS Study of Snow Samples; Dr. Olga Polyakova; Dmitry Mazur; Albert T. Lebedev; Moscow State University, Moscow, Russian Federation

TOB pm 3:30  Compositional Analysis of BP Deepwater Horizon Oil Contaminated Pensacola Beach Sand by Ultrahigh-Resolution FT-ICR-MS; Brian M. Ruddy1; Amy M. Mckenna2; David C. Podgorski1; Ryan P. Rodgers2; Markus Huettel1; Alan G. Marshall1,2; 1Florida State University, Tallahassee, FL; 2Ion Cyclotron Resonance Prog, Tallahassee, FL

TOB pm 3:50  Determination of Bisphenol A Containing Compounds in Water Samples Taken from Different Countries at Different Stages of Economic Development; M. Paul Chiarelli1; Reichert Matthew1; Deepak Panawennage2; Amy Luke1; Terrence Forrester2; Jacob Plange-Rhule1; 1Loyola University, Chicago, IL; 2University of the West Indies, Mona, Jamaica; 3Kwame Nkrumah University, Kumasi, Ghana

TOB pm 4:10  In-Situ Detection of Agrochemicals from Fruit Using Lens Wipes and a Miniature Mass Spectrometer; Santosh Soparawalla; Fatkhulla Tadjimukhamedov; Joshua Wiley; R. Graham Cooks; Purdue University, West Lafayette, IN
**Lipids I: Identification and Structural Analysis**  
2:30 – 4:30 pm  
Joseph A. Hankin, University of Colorado, presiding  
*Room 401*

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<td>TOC pm 2:30</td>
<td>Unexpected Bioactive Oxysterols in Brain and Cerebrospinal Fluid: Discoveries Using a Charge-Tagging Approach; William James Griffiths; Michael Ogundare; Anna Meljon; Yuqin Wang; Swansea University, Swansea, UK</td>
<td>Brian C. Searle, Proteome Software, Inc.; INFORMATICS: QUANTIFICATION/VALIDATION – CNRS - IPB, IMS, Talence, France; Triangle, NC</td>
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<td>TOC pm 2:50</td>
<td>Tissue Imaging Mass Spectrometry of Sphingolipids; Cameron Sullards; Yanfeng Chen; Ying Liu; Alfred H. Merrill, Jr.; Georgia Institute of Technology, Atlanta, GA; Emory University, Atlanta, GA</td>
<td>Susan Richardson, US EPA, NERL; ENVIRONMENTAL CHEMISTRY AND HEALTH</td>
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| TOC pm 3:10 | Towards the Complete Structure Elucidation of Complex Lipids by Mass Spectrometry: Novel Approaches to Ion Activation; Stephen J Blanksby; Huong Pham Thu; Tony Ly; Berwyck Poad; Adam Trevitt; J. Larry Campbell; Todd W Mitchell; University of Wollongong, Wollongong, NSW, Australia; University of California, San Diego, CA; School of Chemistry, University of Wollongong, Wollongong, AUSTRALIA; AB SCIEX, Concord, ON; Wellcome Trust Centre for Gene Regulation and Expr, Dundee, UK | Patrick R. Griffin, The Scripps Research Institute, presiding  
*Korbel Ballroom 1-2*

**Protein-Ligand Interactions: Characterization by Mass Spectrometry**  
2:30 – 4:30 pm  
Patrick R. Griffin, The Scripps Research Institute, presiding  
*Korbel Ballroom 1-2*

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| TOD pm 2:30 | Protein Interactions and Topologies in Cells; Chunxiang Zheng; Li Yang; Chang Xue; Chad Weisbrod; Juan Chavez; James Bruce; Washington State University, Seattle, WA; University of Washington, Seattle, WA | Gregory Finney; Gennifer Merrihew; Michael Rubel; Michael J. Maccoss; William Noble; Michael Bereman; Michael Mathews; Edwin Giovannelli;  
University of Washington, Seattle, WA |
| TOD pm 2:50 | Monitoring Protein-Ligand Stabilization by Electrospray Ionization Ion Mobility Mass Spectrometry; Sabrina Benchar; Jiang Zhang; Joseph A. Loo; UCLA, Los Angeles, CA | Cameron Sullards; Yanfeng Chen; Ying Liu; Alfred H. Merrill, Jr.; Georgia Institute of Technology, Atlanta, GA; Emory University, Atlanta, GA |
| TOD pm 3:10 | Thermodynamic Analysis of Protein-Ligand Binding Interactions on the Proteomic Scale; Patrick D. DeArmond; Erin C. Strickland; Michael C. Fitzgerald; Duke University, Durham, NC | Brian M. Ruddy; Amy M. Rhule; M. Paul Chiarelli; Reichert 1; NVIDIA 1; Florida State University, Tallahassee, FL; Ion Cyclotron Resonance Mass Spectrometer 2; University of the West Indies, Mona, Jamaica; University of Wollongong,  
Lafayette, IN; 2University of the West Indies, Mona, Jamaica; 3Kwame Nkrumah University, Cape Coast, Ghana; 4Department of Chemistry, University of Wollongong, Wollongong, AUSTRALIA; 5Wellcome Trust Centre for Gene Regulation and Expr, Dundee, UK |
| TOD pm 3:50 | Unravelling the Real Time Assembly Kinetics of Ten Hsp90 Complexes Formed Simultaneously; Nina Morgen; Ima Obong-Ebong; Carol Robinson; University of Oxford, Oxford, UK | Patrick R. Griffin, The Scripps Research Institute, presiding  
*Korbel Ballroom 1-2*

**TUESDAY AFTERNOON ORAL SESSIONS**
TOE pm 2:30  An Ion Mobility-Linear Ion Trap Hybrid Mass Spectrometer For Analysis of Biological Molecules; Sunyoung Lee; Steven M. Zucker; Nathaniel Webber; Stephen J. Valentine; David E. Clemmer; James P. Reilly; Indiana University, Bloomington, IN

TOE pm 2:50  Planar Quadrupole and Coaxial Ion Trap Mass Analyzers: Effects of Field Shape; Daniel Austin; Zhiping Zhang; Brett Hansen; Ying Peng; Brigham Young University, Provo, UT

TOE pm 3:10  Gas-phase Ion/Ion Reactions Eliminate Interference in Isobaric Tag-Based Quantification; Craig D. Wengert; M. Violet Lee; Alexander S. Hebert; Graeme C. McAlister; Aaron R. Ledvina; Douglas H. Phanstiel; Michael S. Westphall; Joshua J. Coon; University of Wisconsin, Madison, WI

TOE pm 3:30  Dipolar and Monopolar DC Potentials Applied to a 3-D Ion Trap; Characterizing CID and the Ion Trap; Boone Prentice; Scott A. Mcluckey; Purdue University, Lafayette, IN

TOE pm 3:50  Evaluation of High Energy Collision-induced Dissociation (HCD) on a Bench Top Linear Ion Trap Mass Spectrometer for Shotgun Proteomics; Michael S. Bereman; Jesse D. Canterbury; Jarrett D. Egerton; Julie Horner; Vlad Zabrouskov; Michael J. MacCoss; University of Washington, Seattle, WA; Thermo Fisher Scientific, San Jose, CA

TOE pm 4:10  Ion Sponge: A 3-Dimensional Quadrupole Ion Trap Array for Ion Trapping, Sorting and Gas-Phase Ion Reactions; Wei Xu; Zhiping Zhang; Zheng Ouyang; Purdue University, West Lafayette, IN

TOF pm 2:30  Integration of Imaging Mass Spectrometry into Drug Development and the Importance of Distribution and Quantitation; David S. Wagner; M. Reid Groseclose; Lauren Richards-Peterson; Peter Gorycki; Steve Castellino; GlaxoSmithKline, RTP, NC

TOF pm 2:50  Could Mass Spectrometry Imaging Be a Drug Quantification Technique?; Gregory Hamm; David Bonnel; Raphael Legouffe; Fabien Pamelard; Jean-Marie Delbos; Francois Boucher; Isabelle Fourrier; Michel Salzet; Jonathan Stauber; ImaBiotech, Villeneuve D’ascq, France; Technologie Servier, Orléans, France; MALDI Imaging Team Université Lille Nord de France, Lille, France

TOF pm 3:10  Absolute Quantification of Drugs In Tissue Sections Using MALDI IMS; Anna Nilsson; Mohammadreza Shariatporjazi; Thomas Fehninger; Lena Gustavsson; Gyorgy Marko-Varga; Per E. Andreén; Uppsala University, Uppsala, Sweden; Lund University, Lund, Sweden; AstraZeneca, Lund, Sweden

TOF pm 3:30  Towards Implementation of MALDI IMS into the Drug Development Workflow: Bridging Histology and Drug Tissue Distributions; Reid Groseclose; David S. Wagner; Steve Castellino; GlaxoSmithKline, RTP, NC

TOF pm 3:50  Mass Spectrometry Imaging (MALDI and TOF-SIMS) and Immunohistological Studies of Benzalkonium Chloride Toxicity in Rabbit Eyes; Nicolas Desbenoit; Christophe Baudouin; Jean-Pierre Both; Alain Brunelle; Isabelle Fournier; Vincent Guérineau; Olivier Laprévote; Raphaël Legouffe; Michel Salzet; Jonathan Stauber; Maxence Wiszorski; Françoise Brignole-Baudouin; Institut de la Vision, INSERM, UMR S968, Paris, France; Centre de recherche de GIF, CNRS, GIF-Sur-Yvette, France; CHNO des Quinze-Vingts, Paris, France; CEA-LIST, GIF-Sur-Yvette, France; LSMBFA, Université de Lille 1, Villeneuve d’Ascq, France; CTAC, EA 446, Université Paris Descartes, Paris, France; ImaBiotech Campus Cité Scientifique, Villeneuve d’Ascq, France

TOF pm 4:10  Liquid Extraction Surface Analysis Mass Spectrometry (LESA-MS) as a Novel Tool for Drug Distribution and Metabolism Analysis: The Terfenadine Example; Daniel Eikel; Marissa Vavrek; Yunsheng Hsieh; Fangbiao Li; Walter Korfmacher; Jack D. Henion; Advion BioSystems Inc., Ithaca, NY; Merck and Company Inc., West Point, PA; Merck Research Laboratories, Kenilworth, NJ
### ion mobility separations: fundamentals and instrumentation

8:30 – 10:30 am  
Brandon Ruotolo, University of Michigan, presiding  
Room 501

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>WOB am 8:30</td>
<td>Interfacing Ion Mobility Spectrometry with Orbitrap: Novel Hyphenated Approach for Biochemical Analysis; Mikhail Beloy; Yehia Ibrahim; William Danielson; Alexander Makarov; Pacific Northwest Nat Lab, Richland, WA; Thermo Fisher Scientific (Bremen) GmbH, Bremen, GERMANY</td>
</tr>
<tr>
<td>WOB am 8:50</td>
<td>A QconCAT Standard for Calibration of Ion Mobility Mass Spectrometry; Ross Chawner; Bryan McCullough; Kevin Giles; Simon J. Gaskell; Claire Eyers; University of Manchester, Manchester, UK; LGC Ltd, Teddington, UK; Waters Corporation, Manchester, UK; Queen Mary University of London, London, UK</td>
</tr>
<tr>
<td>WOB am 9:10</td>
<td>Probing the Limits of Resolution and Accuracy on a Second Generation Travelling Wave Ion Mobility Separator; Yueyang Zhong; Suk-Joon Hyung; Brandon Ruotolo; University of Michigan, Ann Arbor, MI</td>
</tr>
<tr>
<td>WOB am 9:30</td>
<td>Selection of Transport Gas Modifiers in Differential Mobility Spectrometry - Mass Spectrometry (DMS-MS); Stephen L. Coy; Adam B Hall; Bryan M. Wong; Bradley B. Schneider; Thomas R. Covey; Albert J. Fornace Jr.; Paul Vourou; Northeastern University, Boston, MA; Georgetown U Medical Center, Washington, DC; Boston U, Boston, MA; Sandia National Lab, Livermore, CA; AB SCIEX, Concord, ON</td>
</tr>
<tr>
<td>WOB am 9:50</td>
<td>Projected Superposition Approximation: A Fast and Accurate Algorithm for Computing Molecular Collision Cross Sections for Macromolecules; Christian Bleiholder; Thomas Wyttenbach; Michael T. Bowers; University of California Santa Barbara, Santa Barbara, CA</td>
</tr>
<tr>
<td>WOB am 10:10</td>
<td>On the Origin of Peaks in Overtone Mobility Spectrometry (OMS) Distributions: Applications to High-Resolution Mobility Separations; Stephen Valentine; Ruwan Kurulugama; David E. Clemmer; Indiana University, Bloomington, IN; PNNL, Richland, WA</td>
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### lipids II: profiling and quantitation

8:30 – 10:30 am  
Hee-Yong Kim, National Institutes of Health, presiding  
Room 401

<table>
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<tr>
<th>Time</th>
<th>Session</th>
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<tr>
<td>WOC am 8:30</td>
<td>Recent Advances in Lipid Mass Spectrometry; Robert C. Murphy; Univ of Colorado Denver, Aurora, CO</td>
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<tr>
<td>WOC am 8:50</td>
<td>Identifying Novel Components of a Pheromone Synthesis Pathway Using Direct UV-Laser Desorption Ionization Mass Spectrometry of Cuticular Lipids; Joanne Y. Yew; Klaus Dreisewerd; Temasek Life Sciences Laboratory, Singapore, Singapore; National University of Singapore, Singapore, Singapore; University of Muenster, Muenster, Germany</td>
</tr>
<tr>
<td>WOC am 9:10</td>
<td>LC-MS/MS Based Methodology for Identifying Cyclooxygenase-2-Derived Anti-Proliferative Oxidized Lipids; Sumit J. Shah; Xiaojing Liu; Suhong Zhang; Jasbir S. Arora; Nathaniel W. Snyder; Ian A. Blair; University of Pennsylvania, Philadelphia, PA</td>
</tr>
<tr>
<td>WOC am 9:30</td>
<td>Quantitative Profiling of PE, MMPE, DMPE and PC Species by Multiple Precursor Ion Scanning; Mesut Bilgin; Eva Duchoslav; Christer Ejsing; Department of Biochemistry and Molecular Biology, Odense, Denmark; AB Sciex, Concord, ON</td>
</tr>
<tr>
<td>WOC am 9:50</td>
<td>Ultrafast Top-Down Lipidomics by Successive Acquisition of FT-MS(+)/FT-MS(-) Spectra; Kai Schuhmann; Reinaldo Almeida; Ronny Herzog; Mark Baumert; Stefan R. Bornstein; Andrej Shevchenko; MPI-CBG, Dresden, GERMANY; Advion Biosciences, Inc., St Neots, UK; Department of Internal Medicine III, TU Dresden, Dresden, GERMANY</td>
</tr>
<tr>
<td>WOC am 10:10</td>
<td>Defining the Mouse Macrophage Lipidome with CLASS: A Comprehensive Lipidomics Analysis using Separation Simplification; Richard Harkewicz; Edward A. Dennis; University of California, San Diego, La Jolla, CA</td>
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### GLYCOPROTEINS: NEW APPROACHES FOR STRUCTURE ANALYSIS

**8:30 – 10:30 am**

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<th>Time</th>
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<tr>
<td>WOD am 8:30</td>
<td><strong>N-Glycosylation Sites of Influenza A virus Hemagglutinin and Surfactant Protein: Characterization via a Mass Spectrometry Strategy</strong></td>
<td>Nancy Leymarie; Kevan L. Harthorn; Michael Rynkiewicz; Barbara Seaton; Joseph Zaia; Boston University School of Medicine, Boston, MA</td>
</tr>
<tr>
<td>WOD am 8:50</td>
<td><strong>Towards An Automated Glycoproteomics Platform: Using Self-Consistency Rules and a Non-Specific Protease Digest for Enhanced Site-Specific Glycosylation and Glycan Heterogeneity</strong></td>
<td>John S. Strum; Charles C. Nwosu; Scott R. Kronewitter; Richard R. Seipert; Serenus Hu; Robert Bachelor; Kun Wook Park; Jong Shin Yoo; Hyun Joo An; Rudolf Grimm; Carlito B. Lebrilla; Barbara Seaton; Joseph Zaia; Boston University School of Medicine, Boston, MA</td>
</tr>
<tr>
<td>WOD am 9:10</td>
<td><strong>Targeting O-GlcNAc Modification Using HCD/ETD Product Ion Monitoring Approach on a Linear Ion Trap/Orbitrap Mass Spectrometer</strong></td>
<td>Peng Zhao; Chia-Fen Teo; David Horn; Lance Wells; University of California Davis, Davis, CA; Korea Basic Science Institute, Ochang, Korea; Graduate School of Analytical Science and Techn., Daejeon, Korea; Agilent Technologies Inc., Santa Clara, CA; Robert-Mondavi Institute of Food Science UC Davis, Davis, CA; Dept. of Biochem, and Molecular Medicine UC Davis, Davis, CA</td>
</tr>
<tr>
<td>WOD am 9:30</td>
<td><strong>High Level Enrichment and Characterization of Secreted O-Linked Glycopeptides</strong></td>
<td>Zsuzsa Darula; Robert Chalkley; Peter R Baker; A.L. Burlingame; Katalin F. Medzhizdzyk; Laboratory of Proteomics, BRC, Szeged, Hungary; UCSF, San Francisco, CA</td>
</tr>
<tr>
<td>WOD am 9:50</td>
<td><strong>A Fully Automated Workflow for Glycopeptide Analysis</strong></td>
<td>Julian Saba; Rosa Viner; Paul Shan; Lei Xin; Sergei Snovida; Edward Bodnar; Kay-Hoii Khoo; Helene Perreau; Thermo Fisher Scientific, San Jose, CA; Bioinformatics Solutions Inc., Waterloo, ON, Canada; Institute of Biological Chemistry, Academy Sinica, Taipei, Taiwan; University of Manitoba, Winnipeg, MB, Canada</td>
</tr>
<tr>
<td>WOD am 10:10</td>
<td><strong>Comparison of Glycan Distribution in Therapeutic Monoclonal Antibodies by LC-MS using mAb-Glyco-Chip and CE-LIF</strong></td>
<td>Shiew-Lin Wu; Yi Wang; Sam Tep; Zoran Sosic; Yelena Lyubarskaya; Ning Tang; William Hancock; Barry Karger; Northeastern University, Boston, MA; Biogen Idec Inc, Cambridge, MA; Agilent Technologies, Santa Clara, CA</td>
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### INSTRUMENTATION: NEW DEVELOPMENTS IN IONIZATION

**8:30 – 10:30 am**

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<th>Time</th>
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<th>Authors</th>
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<tbody>
<tr>
<td>WOE am 8:30</td>
<td><strong>Improved Performance of Surface Acoustic Wave Nebulization (SAWN) Using an Additional Voltage</strong></td>
<td>Scott Heron; Christophe Masselon; Yue Huang; John Edgar; Sung Hwan Yoon; David R. Goodlett; University of Washington, Seattle, WA; CEA Grenoble, France</td>
</tr>
<tr>
<td>WOE am 8:50</td>
<td><strong>Improving LC-MS Sensitivity by Using a Subambient Pressure NanoESI Source</strong></td>
<td>Koji Tang; Ioan Marginean; Jason S. Page; Ryan T. Kelly; Richard D. Smith; Pacific Northwest National Laboratory, Richland, WA</td>
</tr>
<tr>
<td>WOE am 9:10</td>
<td><strong>Analysis of Carbohydrates and Other Hydrophilic Analytes by Paper Spray Mass Spectrometry</strong></td>
<td>Nicholas Manicke; Zheng Ouyang; R. Graham Cooks; Purdue University, West Lafayette, IN</td>
</tr>
<tr>
<td>WOE am 9:30</td>
<td><strong>Laser Ablation Droplet Capture for Electrospray Ambient Sampling</strong></td>
<td>Kermit K. Murray; Sung Gun Park; Louisiana State University, Baton Rouge, LA</td>
</tr>
<tr>
<td>WOE am 9:50</td>
<td><strong>Inlet Ionization: An investigation into the Mechanism That Produces Ions from an Instrument-Inlet Absent of Lasers, Heat or Voltages</strong></td>
<td>Vincent S. Pagnotti; Charles N. McEwen; University of the Sciences, Philadelphia, PA</td>
</tr>
<tr>
<td>WOE am 10:10</td>
<td><strong>Features and Specifications of Atmospheric Pressure Free Liquid MALDI Mass Spectrometry in Combination with UHPLC</strong></td>
<td>Albert Abdakhanov; Ales Charvat; Bernd Abel; Ostwald-Institute for Physical Chemistry, Leipzig, Germany; Knauer GmbH, Berlin, Germany</td>
</tr>
</tbody>
</table>
**PK Assays: Novel Approaches to Increase LC-MS Throughput**

8:30 – 10:30 am
Ravi Rahavendran, Pfizer Global R&D, presiding
Four Seasons Ballroom 1-2

**WOF am 8:30** Moving Towards Seamless Integration of Automated Sample Preparation with LC-MSMs for PK/PD Analysis; Bernard Chel1, Kyle Lady2, Rong Ling2, Lucinda Cohen3, Chinchun Tong3, Gino Salituro3, 1Merck & Co., Inc., Rahway, NJ; 2University of Michigan, Ann Arbor, MI

**WOF am 8:50** Next Generation Sample Delivery Platform for HT-LC/MS/MS; John Janiszewski1,4; Richard Schneider1; Hui Zhang1; Veronica Zelesky3; Xiaoping Zhou4, William Schramm1; Wayne Lootsma1; Felix Yu1; Pfiizer Inc., Groton, CT; 2Apricot Designs, Covina, CA; 3Sound Analytics, Niantic, CT

**WOF am 9:10** A Strategy for Implementation of Fast SPE-MS/MS into the Workflow of PK and PK/PD Sample Analysis in Drug Discovery; Ann Brown; Novartis, Cambridge, MA

**WOF am 9:30** Use of in vivo Solid Phase Microextraction as a Sample Preparation Strategy for LC-MS; Heather Lord1; Erasmus Cudjoe1; Dajana Vuckovic1, Paul Togunde1; Md Ehsanul Hoque1; Janusz Pawliszyn1; 1University of Waterloo, Waterloo, CANADA; 2University of Toronto, Toronto, ON; 3Trent University, Peterborough, Canada

**WOF am 9:50** Determining Pharmacokinetics Directly from Dosed Tissue Sections by Liquid Extraction Surface Analysis Coupled to Mass Spectrometry; Whitney Parson1; Jamie Erickson1; Roderic Cole1; Robert W Johnson1; Stormy Koeniger1; Nari Talaty1; Annette Schwartz2; Yu Tian2; Christopher Stedman1; Gary J. Van Berkel1, 1Oak Ridge National Laboratory, Oak Ridge, TN; 2Abbott Laboratories, Worcester, MA

**WOF am 10:10** Validation of an Analytical Method to Quantify a Xenobiotic in Rat Plasma Using LDTD-APCI Coupled to Tandem Mass Spectrometry; Fedeli Olivier1; Patricia Moliner1; Beatrice Pradelles1; Laurent Rousseau1; Bernard Julian1; Cyril Bertrand1; Chloe Grosjean1; Marion Layssa1; Christel Marcou1; Patrice Tremblay1; Pierre Picard1; Laurence Fajas1; Freddy Sadoun1; Gerard Fabre1; 1Sanofi-Aventis, Montpellier, France; 2Phytronix Technologies, Quebec, QC

**Protein Therapeutics: Structural Characterization**

8:30 – 10:30 am
Jean W. Lee, Amgen, Inc., presiding
Four Seasons Ballroom 3-4

**WOG am 8:30** Advances in the Use of GeneData Expressionist for the Semi-Automated Assessment of Post-Translational Modifications in Biotherapeutics; Jennifer F. Nemeth1; Steven S. Kaltashov1; 1Centocor R&D, Radnor, PA; 2Centocor Research and Development, Radnor, PA

**WOG am 8:50** Unusual Stability of the Orally Administered Fusion Transferrin-Human Growth Protein and Interaction with its Physiological Partners: A Mass Spectrometry Study; Cedric E. Bobst1; Shunhui Wang1; Wei-Chiang Shen2; Igor A. Kaltashov3; 1University of Massachusetts, Amherst, MA; 2University of Southern California, Los Angeles, CA

**WOG am 9:10** Development of Mass Spectrometric and Informatics Workflows for the Automated Assessment of “Biosimilarity” for a Candidate Biosimilar Antibody; Scott Berger; Asish Chakraborty; Hongwei Xie; Weibin Chen; Waters Corporation, Milford, MA

**WOG am 9:30** Glycomic Perspective of Therapeutic Antibodies; Sureyya Ozcan1; Hyun Joo An2; Ebru Ucakturk1; Kit Lam2; Carlito Lebrilla1; 1UC Davis Chemistry Department, Davis, CA; 2University of California, Davis, CA; 3Faculty of Pharmacy, University of Hacettepe, Ankara, Turkey; 4UC Davis Cancer Center, Sacramento, CA

**WOG am 9:50** Characterizing HIV Specific Antibodies in Sera from Infected Individuals That Do Not Progress to AIDS; Beatrix Ueberheide1,2; Sunnie Myung1,2; David Fenyo1,2; Johannes F Scheid1; Michel C Nussenzweig1; Brian Chait1; 1The Rockefeller University, New York, NY; 2New York University, New York, NY; 3Merck, Union, NJ

**WOG am 10:10** Characterizing Structure of Ion Channel TRPA1 Membrane Protein Using Mass Spectrometry; Liwen Wang; Teresa Cvetkov; Vera Moiseenkov-Bell; Mark R.Chance; Case Western Reserve University, Cleveland, OH
**Phosphoproteomics**

2:30 – 4:30 pm
Arthur Moseley, Duke University, presiding
Wells Fargo Theatre

**Combining PolyMAC-Ti and PolyMAC-Fe for In-Depth Phosphoproteome Analysis of B Cell Signaling**; Anton Iluk1; Keerthi Jayasundera; Rachel Shützenhofer; Renee Killins; Robert Gehlen; WeiGuo Andy Tao; Purdue University, West Lafayette, IN

**Facilitating the Enrichment and Identification of Phosphopeptides Containing Multiple Basic Residues**; Houjiang Zhou1; Teck Yew Low1; Marco Hennrich1; Hanfa Zou2; Albert J. R. Heck1; Shahbaz Mohammed1; Utrecht University, Utrecht, Netherlands; 3Dalain Institute of Chemical Physics, Dalian, China

**High Resolution Separations Increase Sensitivity and Coverage of Phosphoproteome Profiling**; Yueyi Wang; Feng Yang; Therese Clauss; David Stenoien; John Sandoval; Marina Gritsenko; Rui Zhao; Yufeng Shen; David Camp II; Richard Smith; PNLL, Richland, WA

**PhosphoRS, a Novel Phospho-Site Localization Tool Increasing Phosphoproteome Coverage from LC-MS/MS Data Sets**; Thomas Taus1; Thomas Köcher1; Peter Pichler1; Andreas Schmidt1; Hans Grenseman1; Torsten Ueckert1; Bernard Delange1; Karl Mechtler1; 1Research Institute of Molecular Pathology, Vienna, Austria; 2CD Laboratory, MFPL, University of Vienna, Vienna, Austria; 3Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany

**Comparative Proteomic and Phosphoproteomic Profiling of Human Embryonic Stem Cells and their Pure PAX6* Neuroectodermal Derivatives**; Junjie Hou; Ilyas Singic; Andrew Crain; Brian Tobe; Evan Snyder; Laurence M. Brill; Sanford-Burnham Medical Research Institute, La Jolla, CA

**Efficiency and Reproducibility of Phosphoryrosine Peptide Immunoaffinity Capture for Quantitative Mass Spectrometry**; Stacy D. Sherrod1, 2; Amy-Joan L. Ham1; Daniel C. Lieber1, 2; 1Vanderbilt University School of Medicine, Nashville, TN; 2Jim Ayers Institute, Nashville, TN

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**Ion Mobility Mass Spectrometry: Integration into Structural Biology**

2:30 – 4:30 pm
John A. McLean, Vanderbilt University, presiding
Room 501

**The Role of Native Ion Mobility Mass Spectrometry in Studying Virus Structure, Dynamics and Assembly**; Albert J.R. Heck; Utrecht University, Utrecht, Netherlands

**Interpreting Collision Cross Sections of Protein Complexes: Models, Approximations, Errors, and Best Practices**; Matthew F Bush1; Zoe Hall1; Argyris Politis1; Daniel Barsky2; Carol V Robinson1; 1University of Oxford, Oxford, UK; 2Lawrence Livermore National Laboratory, Livermore, CA

**Towards a Structural Understanding of Regulatory Protein-srRNA Complexes by Native Mass Spectrometry Combined With Ion Mobility and Other Biophysical Techniques**; Frank Sobott1; Anastasia Callaghan1; Charlotte Henderson1; Helen Vincent1; 1Center for Proteomics, University of Antwerp, Antwerp, BELGIUM; 2Biological Sciences, University of Portsmouth, Portsmouth, UK

**An Integrated Structural Biology Dataset Reveals Metal-Protein and Protein-Protein Interactions of Critical Importance for Amyloid Formation**; Suk-Joon Hyung; Jonathan J.S. Mayers; Jung-Suk Choi; Jeffrey R. Breder; Ayalusamy Ramamoorthy; Mi Hee Lim; Brandon Ruotolo; University of Michigan, Ann Arbor, MI

**Correlating Structure to Dissociation Patterns with Ion Mobility-CID/SID**; Anne E. Blackwell1; Mowei Zhou; Vicki H. Wysocki; University of Arizona, Tucson, AZ

**Intrinsic Disorder in Proteins: A Challenge for (Un)Structural Biology**; Ewa Jurneczko1; Faye Cruickshank2; Penka Nikolova2; Iain D G Campuzano3; Michael Morris3; Perdita Barran1; 1The University of Edinburgh, Edinburgh, UK; 2Kings College London, London, UK; 3Waters Corporation, Manchester, UK
### Fundamentals: Ion-Surface Interactions and Preparative MS

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<tr>
<td>WOC pm 2:30</td>
<td>In situ Analysis of Chemically Modified Surfaces Prepared by Ion Soft Landing</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
</tr>
<tr>
<td>WOC pm 2:50</td>
<td>Generation of Monolayer Protected Clusters Using Soft-Landing Ion Mobility</td>
<td>Priest2; Julia Laskin1; Chang Ko Liu2</td>
</tr>
<tr>
<td>WOC pm 3:10</td>
<td>Preparation of Atomically Monodisperse Multiply Charged Gold Clusters on Surfaces by Soft Landing of Mass Selected Ions</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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<tr>
<td>WOC pm 3:30</td>
<td>Polysaccharide Degradation by Atmospheric Pressure Thermal Ion Dissociation and Soft-Landing</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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<tr>
<td>WOC pm 3:50</td>
<td>The Study of Ion Transmission and Soft Landing of Macromolecules Using Multiple Quadrupoles Instrument Coupled with MALDI Ion Source</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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<tr>
<td>WOC pm 4:10</td>
<td>Electrospray Ion Beam Deposition for Surface Science in Ultrahigh Vacuum: From Single Molecular Magnets to Proteins</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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### Carbohydrates: New Approaches for Structure Analysis

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<tr>
<td>WOF pm 2:30</td>
<td>Sequencing Intact Bikunin Glycosaminoglycan Chains by FTMS/MS</td>
<td>Franklin E. Leach III1; Tatiana Laremore2; Melissa Ly3; Zhongping Xiao4; John Muchena5; Jeremy Wolff6; Robert J. Linhardt7; Jon Amster8; University of Georgia, Athens, GA; 2Penn State, University Park, PA; 3Rensselaer Polytechnic Institute, Troy, NY; 4Bruker Daltonics, Billerica, MA</td>
</tr>
<tr>
<td>WOF pm 2:50</td>
<td>Characterization of Chondroitin Sulfate and Dermatan Sulfate in Squamous Cell Carcinoma by LC/MS</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
</tr>
<tr>
<td>WOF pm 3:10</td>
<td>A Chemical Derivatization Strategy for Structural Analysis of Isomeric Glycosaminoglycan Oligosaccharides Using Reverse Phase LC-MS5</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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<tr>
<td>WOF pm 3:30</td>
<td>Detailed Studies of the 'Sidedness' of Disaccharide Dissociation in the Negative Ion Mode Using 18O-labeled Structures</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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<tr>
<td>WOF pm 3:50</td>
<td>Rapid Structural Assignment of N-Glycans Using an Annotated Structure Library</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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<tr>
<td>WOF pm 4:10</td>
<td>Mass Spectrometric Quantification of Permethylated Glycans: ESI vs. MALDI</td>
<td>Kevin Schug, University of Texas at Arlington, presiding Room 401</td>
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</table>
INSTRUMENTATION: NEW DEVELOPMENTS IN INSTRUMENTATION

2:30 – 4:30 pm
Joshua J. Coon, University of Wisconsin-Madison, presiding
Korbel Ballroom 3-4

WOE pm 2:30 Performance Investigation of an Orbitrap Mass Analyzer Combined with a Quadrupole Mass Filter; Jan-Peter Hauschild; Ulf Froehlich; Oliver Lange; Alexander Makarov; Eugen Damoc; Sebastian Kanngieser; Frank Czemper; Catharina Crone; Yue Xuan; Markus Kellmann; Andreas Wieghaus; Thermo Fisher Scientific, Bremen, Germany

WOE pm 2:50 From Peptide Anions to Radical Cations: Exploring Ion Activation by UV Photodissociation; Jennifer Brodbelt1; James Medekhan Rebyt; 1University of Texas, Austin, TX; 2University of Texas Austin, Austin, TX

WOE pm 3:10 Photo-SRM: Laser Photo-Dissociation Improves Detection Selectivity of Selected Reaction Monitoring Mode; Quentin Enjalbert1,2; Romain Simon2; Arnaud Salvador3; Rodolphe Antoine1; Sébastien Redon1,4; Mehmet Menaf Ayhan5; Florence Darbour5; Stéphane Chambert1,4; Yann Bretonnière5; Philippe Dugourd6; Jérôme Lemoine7; 1CNRS et Université Lyon 1, UMR5579, LASIM, Villeurbanne, France; 2CNRS et Université Lyon 1 UMR 5180, LSA, Villeurbanne, France; 3INSA-Lyon, Villeurbanne, France; 4ICBMS, UMR5246, CNRS, Université Lyon 1, INSa, CPE, Villeurbanne, France; 5Université de Lyon, Laboratoire de Chimie de l’ENS, Lyon, France

WOE pm 3:30 Incorporation of Surface Induced Dissociation into an Ion Mobility – QTOF Mass Spectrometer for Post-Ion Mobility Activation; Nowei Zhou; Chengwei Huang; Kevin Giles; Anne Blackwell; Vicki Wysocki; 1University of Arizona, Tucson, AZ; 2Waters Corporation, Manchester, UK

WOE pm 3:50 Design and Simulation of a Miniaturized Zaffman Trap for Electrostatic Storage of Ions with < 1 keV of Energy; Ryan T. Hilger; Robert E. Santini; Scott A. McLuckey; Purdue University, West Lafayette, IN

WOE pm 4:10 The Way to Isotopic Resolution for Hundred’s kDa Mass Ions. Experimental Characterization of the New Dynamically Harmonized FTICR Cell; Eugene Nikolayev1,2; Ivan Boldin1,2; Roland Jertz3; M Gokhan Baykut4; 1Institute for Energy Problems of Chemical Physics, Moscow, Russian Federation; 2Institute of biochemical physics Rus. Acad. of Sci, Moscow, Russian Federation; 3The Institute of biomedical chemistry RAMS, Moscow, Russian Federation; 4Bruker Daltonics, Bremen, Germany

INFORMATICS TOOLS FOR PHARMACEUTICAL APPLICATIONS OF MASS SPECTROMETRY

2:30 – 4:30 pm
Xiuxia Du, University of North Carolina-Charlotte, presiding
Four Seasons Ballroom J-2

WOF pm 2:30 A Data Analysis Framework for Label-Free Chemical Proteomics exemplified on the Profiling of Erlotinib and Gefitinib; Jens Lamerz; Angélique Augustin; Guillemette Duchateau-Nguyen; Sabrina Golling; Hélène Meistermann; Nikolaos Berntenis; Manuel Tzuros; Michel Petrovic; Giuseppe Palermo; Barbara Klughammer; Hanno Langen; Laurent Essioux; F. Hoffmann-La Roche Ltd, Basel, Switzerland

WOF pm 2:50 On the Development of a Robust and Transferable Tandem Mass Spectral Library for the Identification of Small Bioorganic Molecules; Birthe Schubert; Herbert Oberacher; Innsbruck Medical University, Innsbruck, Austria

WOF pm 3:10 A Mathematical LC-MS Drift Cancellation Approach for Quantitative Application to High Throughput Dry Powder Inhaler Content Uniformity; Justin Penniston; Joseph Medendorp; Brent Donovan; Merck, Summit, NJ

WOF pm 3:30 Analysis of Drug Metabolites in Wastewater Using LC/Q-TOF MS: Metabolic Profiling as a Possible Tool for Environmental Analysis; Michael Thurman; Imma Ferrer; University of Colorado, Boulder, CO

WOF pm 3:50 Automatic Disulfide Bond Mapping and Reporting in Biotherapeutics by High Resolution LCMS; St John Skilton; Hongwei Xie; Weibin Chen; Waters, Milford, MA

WOF pm 4:10 New Multiple Technique Data Analysis Software for Synthetic Chemists; Alexey Aminov1; Margaret Antler2; Tatiana S. Churanova1; Lorne Fell2; Karim Kassam2; Vitaly Lashin1; Mike McBrien; Graham A. Mcibben2; 1ACD Ltd., Moscow, RUSSIA; 2ACD/Labs, Toronto, Canada

59TH ASMS CONFERENCE ON MASS SPECTROMETRY PAGE 43
WEDNESDAY AFTERNOON and THURSDAY MORNING ORAL SESSIONS

**REACTIVE METABOLITES: NOVEL LC-MS DETECTION METHODS**

WOG pm 2:30  
Fast Profiling and Identification of Reactive Metabolites in Rats Using HR-MS: Applications of Mass Defect Filter-Dependent MS/MS Acquisition; Jie Xing; Kerong Zhang; Fuying Du; Tian Liu; Mingshe Zhu; Shandong University, Jinan, China; 2AB SCIEX, Shanghai, China; 3Bristol-Myers Squibb, Princeton, NJ

WOG pm 2:50  
Investigation of Oxidative and Conjugative Metabolism Reactions With Liquid Chromatography / Accurate Mass High Resolution Mass Spectrometry; Maciej Bromirski; Olaf Schelbner; Helene Faber; Sandra Jahn; Uwe Karst; Hannah Simon; 1Thermo Fisher Scientific, Bremen, Germany; 2University of Munster, Munster, Germany

WOG pm 3:10  
Development of LC-PD-MS and Its Application Towards Identifying Protein Bound Metabolites, Oxidative Stress, and PTMs; Julene K. Diedrich; Ryan R. Julian; University of California, Riverside, Riverside, CA

WOG pm 3:30  
Reactive Metabolite Detection and Characterization Using a QqTOF With Ultra-Fast Data Acquisition and Real-Time Multiple Mass Defect Filtering; Loren Olson; Bud Maynard; Shaila Hoque; Hesham Ghobarah; Elliott Jones; Heather Zhang; George Tonn; John-Michael Sauer; Patrick J. Rudewicz; Elan Pharmaceuticals, South San Francisco, CA; 2AB SCIEX, Foster City, CA

WOG pm 3:50  
LC-MS Identification and Quantification of Electrogenerated Reactive Metabolites and Their Peptide Adducts; Uwe Karst; Helene Faber; Hannah Simon; Anne Baumann; Sandra Jahn; Daniel Melles; University of Münster, Münster, Germany

WOG pm 4:10  
Characterization and Identification of Reactive Metabolites Using Combination of High Mass Accuracy, Polarisation Switching and Target Fragmentation; Bo Wen; David Moore; Hoffmann-La Roche, Nutley, NJ

**INFORMATICS: IDENTIFICATION**

ThOA am 8:30  
Integrating RNA-Seq Data Improves Protein identification in Shotgun Proteomics; Xiaoling Wang; Robbert Slebos; Daniel C. Liebler; Bing Zhang; Vanderbilt University School of Medicine, Nashville, TN

ThOA am 8:50  
Using Subspectral Interval Matching to Make Novel Identifications of ETD Tandem Mass Spectra; Viswanadham Sridhara; Dina L. Bai; An Chi; Jeffrey Shabanowitz; Donald F. Hunt; Lewis Y. Geer; National Library of Medicine, Bethesda, MD; 2University of Virginia, Charlottesville, VA; 3Merck, Boston, MA

ThOA am 9:10  
Identification of two Novel Proteins by de novo Sequencing Using HCD and ETD Spectra; Hao Chi; Ruixiang Sun; Bing Yang; Chun-Qing Song; Chao Liu; Yanmei Zhao; Wei Sun; Long Miao; Si-Min He; Meng-Qiu Dong; 1Institute of Computing Technology, CAS, Beijing, China; 2National Institute of Biological Sciences, Beijing, CHINA; 3Institute of Biophysics, CAS, Beijing, CHINA

ThOA am 9:30  
Gapped Peptide Archives: Scalable Approach for Clustering Billions of Spectra; Ilya Kolykhmatov; Sangtae Kim; Pavel Pevnner; University of California, San Diego, La Jolla, CA

ThOA am 9:50  
Single Protein Digest Spectral Libraries: A New Tool for Quality Control in Proteomics; Qian Dong; Bhaskar Godugu; Lisa E. Kilpatrick; Yuxue Liang; Pedatsur Neta; Xinjian Yan; Stephen Stein; NIST, Gaithersburg, MD

ThOA am 10:10  
A Third Generation Spectra Correlation Algorithm and Its Implementation in Library Search, Identification of Unknowns and Metabolite ID; Juraj Lutisan; Robert Mistrik; HighChem, Ltd., Bratislava, Slovakia

**ASMS MEETING**

4:15 - 5:30 pm  
Scott A. McLuckey, presiding  
Korbel 1-2
THURSDAY MORNING ORAL SESSIONS

**FUNDAMENTALS: ION STRUCTURE AND ENERGETICS**
8:30 – 10:30 am
Veronica M. Bierbaum, University of Colorado, presiding
Room 501

ThOB am 8:30 **Gas-phase Ion-neutral Reaction Chemistry for Charge Manipulation:** Altering the Collision Induced Dissociation Properties of Multiprotein Complexes; Russell Borsheim; Suk-Joon Hyung; Brandon Ruotolo; University of Michigan, Ann Arbor, MI

ThOB am 8:50 **Characterization of Ion Structure and Energetics in the Reactions of 1,3,5-Triazine:** John Garver; Zhibo Yang; Shuji Kato; Scott Wren; Kristen Vogelhuber; W. Carl Lineberger; Veronica M. Bierbaum; 
1University of Colorado, Boulder, Boulder, CO; 2University of Colorado, Boulder, CO; 3JILA, University of Colorado and the NIST, Boulder, CO

ThOB am 9:10 **Structures, Binding Energies, and Coulomb Fission Barriers of Transition Metal Cation-Ligand Complexes:** Mary T. Rodgers; Holliness Nose; Richard Lord; Kevin T. Crampton; Wayne State University, Detroit, MI

ThOB am 9:30 **Pesci [1] Versus Peters [2], Who is the Winner?** Decarboxylation Versus Desulfuration to Generate Coinage Metal Organometallics; George N. Khairallah; Lenka Sraj; Richard A. J. O’hair; 1University of Colorado, Boulder, Boulder, CO; 2University of Melbourne, Melbourne, Australia; 3University of Melbourne, Victoria, Australia

ThOB am 9:50 **b2 Ions: Identification of Their Structure by Their Energetics:** Peter B. Armentrout; Amy Clarke; University of Utah, Salt Lake City, UT

**SYNTHETIC POLYMERS: NEW METHODS FOR ANALYSIS**
8:30 – 10:30 am
Chrys Wesdemiotis, The University of Akron, presiding
Room 401

ThOC am 8:30 **New Structural Insights into a Novel Geometry Polymeric System by Use of Shape-Selective MS Studies:** Charlotte Scarff; Jonathon Snelling; Matthias Knust; James Screvns; 1University of Arkansas, Fayetteville, AR; 2University of Warwick, Coventry, UK; 3Univ of Warwick, Coventry, UK

ThOC am 8:50 **MALDI-TOF Imaging Mass Spectrometry - A Universal Detector for Copolymer Chromatography:** Steffen M. Weidner; Jana Falkenhagen; Fed.Inst.f.Mat.Research, Berlin, Germany

ThOC am 9:10 **From Macrocycles to Molecular Spoked Wheel: Travelling Wave Ion Mobility Analysis of Metallo-Supramolecules and Supramolecular Polymers:** Xiaopeng Li; Jin-Liang Wang; Yi-Tsu Chan; George R. Newkome; Chrys Wesdemiotis; The University of Akron, Akron, OH

ThOC am 9:30 **Proton Sponge Effect for Synthetic Dendrimers in the Gas Phase:** Aura Tintaru; Sabrina Pricl; Ling Peng; Laurence Charles; 1University Aix-Marseille I & III, Marseille Cedex 20, France; 2Aix-Marseille University, Marseille, France; 3Univ de la Mediterranee, Marseille, France; 4University of Trieste, Trieste, Italy

ThOC am 9:50 **MALDI Techniques for Characterization of Ionomers:** Anthony P. Gies; David M. Hercules; 1The Dow Chemical Company, Freeport, TX; 2Vanderbilt University, Nashville, TN

ThOC am 10:10 **ESI-MS and MS/MS of Low Charge State Adduct Ions of high Molar Mass Synthetic (Co)Polymers with Ammonium Compounds:** Andreas Nasioudis; Jan van Velde; Ron M.A. Heeren; 1Akzo Nobel RD&I, Deventer, Netherlands; 2FOM Inst. Atomic/Molecular Phy, Amsterdam, Netherlands
<table>
<thead>
<tr>
<th>Membrane Proteins</th>
<th>High Mass Accuracy/High Performance Mass Spectrometry Instrumentation and Applications</th>
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<tbody>
<tr>
<td><strong>ThOD am 8:30</strong> Proteomic Characterization of the Binding Partners of Dopamine Transporter (DAT) and Functional DAT Mutants</td>
<td>ThOE am 8:30 Targeted Protein Quantification in Urine Samples Using a New Quadrupole-Orbitrap Mass Spectrometer; Sebastien Gallien; Elodie Duriez; Yeon Jin Kim; Bruno Domon; Zhili Hao; Markus Kellmann; Thomas Maehring; Andreas Huhmer; Luxembourg Clinical Proteomics Center, Strassen, Luxembourg; Thermo Fisher Scientific, San Jose, CA; ThermoFisher Scientific, Bremen, Germany</td>
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<tr>
<td>Yingming Zhao, The University of Chicago, presiding</td>
<td>Adam Hawkridge, North Carolina State University, presiding</td>
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<td>Korbel Ballroom 1-2</td>
<td>Korbel Ballroom 3-4</td>
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**ThOD am 8:50** Dysregulated Plasma Membrane Proteins of Adipocytes in Obese Mice Models Influence Their Metabolic Phenotype; Hansjoerg Moest; ETH Zürich, Schwerzenbach, Switzerland

**ThOD am 9:10** Top Down Characterization of Integral Membrane Proteins; Adam Catherman; Dorothy Ahlf; Mingxi Li; John C. Tran; Amanda Berg; Gary Valaskovic; Neil L. Kelleher; Northwestern University, Evanston, IL; New Objective, Inc., Woburn, MA

**ThOD am 9:30** Caught in the Act: Ligand-based Receptor Capturing (LRC) on Living Cells; Andreas Frei; Ock-Youm Jeon; Ruedi Aebersold; Erick Carreira; Bernd Wollscheid; Swiss Federal Institute of Technology, Zurich, Switzerland

**ThOD am 9:50** Human Cell Membrane Glycan Mapping Using Mass Spectrometry; Hyun Joo An; Mary Saunders; Shuai Wu; Jae-Han Kim; Maciej Chichlowski; Lauren Dimapasoc; David Mills; Kit Lam; Carlito Lebrilla; University of California, Davis, CA

**ThOD am 10:10** Mapped Perturbations of the CFTR Interactome Reveals Disease-specific Protein-Protein Interactions as Potential Drug Targets; Sandra Pankow; Casimir Bamberger; William Balch; John Yates; The Scripps Research Institute, La Jolla, CA

**ThOE am 8:30** Targeted Protein Quantification in Urine Samples Using a New Quadrupole-Orbitrap Mass Spectrometer; Sebastien Gallien; Elodie Duriez; Yeon Jin Kim; Bruno Domon; Zhili Hao; Markus Kellmann; Thomas Maehring; Andreas Huhmer; Luxembourg Clinical Proteomics Center, Strassen, Luxembourg; Thermo Fisher Scientific, San Jose, CA; ThermoFisher Scientific, Bremen, Germany

**ThOE am 8:50** How High Mass Accuracy Measurements will Transform Targeted Proteomics; Derek Bailey; Graeme McAlister; Chris Rose; Alex Hebert; Craig Wenger; M. Violet Lee; Michael S. Westphall; Joshua J. Coon; University of Wisconsin, Madison, WI

**ThOE am 9:10** Comparison of Methods for the Determination of Xenobiotics in Biological Samples: Targeted vs. Two Different General Unknown Screening (GUS) Methods; Brad Patterson; Dimitri Gerostamoulos; Olaf Drummer; Jochen Beyer; AB SCIEX, Mulgrave, Australia; Victorian Institute of Forensic Medicine, Melbourne, Australia

**ThOE am 9:30** Liquid Extraction Surface Analysis Mass Spectrometry (LESA MS): Drug Distribution and Metabolism of Diclofenac in Mouse; Simon J. Prosser; Daniel Eikel; Stefan T. Linehan; Mike Batt; Daniel Murphy; Dennis Heller; Patrick J. Rudewicz; Jack D. Henion; Advion BioSystems Inc., Ithaca, NY; XenoBiotic Laboratories Inc., Plainsboro, NJ; Thermo Fisher Scientific, San Jose, CA; Elan Pharmaceuticals, South San Francisco, CA

**ThOE am 9:50** Qualitative and Quantitative Cellular Similarities of the Protein Complement of the Cancer Cell Lines HepG2, PC3 and MDA-MB-231; Scott Geromanos; Hans Vissers; Arthus Moseley; James Langridge; Waters Corporation, Middletown, NJ; Duke University, Durham, NC

**ThOE am 10:10** Characterization of Secondary Plant Metabolites by High Resolution Mass Spectrometry Imaging and Laser Ablation Electrospray Ionization; Arton Berisha; Sabine Guenther; Zoltan Takats; Sebastian Dold; Bernhard Spengler; Andreas Römp; Analytical Chemistry, Justus Liebig University, Giessen, Germany
### Protein Therapeutics: Identification of Metabolites, Impurities and Degradants

<table>
<thead>
<tr>
<th>Session Time</th>
<th>Presentation Title</th>
<th>Speaker(s)</th>
<th>Institution(s)</th>
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<tbody>
<tr>
<td>ThOF am 8:30</td>
<td>The Use of Mass Spectrometry to Assess the Chemical Stability of Therapeutic Proteins during the Discovery Process</td>
<td>Jon Fitchett, Samantha Phan, Mike Batt, Bryan Jones, Scott Wooden</td>
<td>AME/Lilly Inc., San Diego, CA</td>
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<td>ThOF am 8:50</td>
<td>Characterization of A Therapeutic Monoclonal Antibody following Incubation in Plasma or Phosphate-Buffered Saline</td>
<td>Sheng Yin, John T. Stults, Matthew Mazur, David Mahon, Tun Liu, Qinwei Zhou, Richard Crowley</td>
<td>Immunocore, Branchburg, NJ</td>
</tr>
<tr>
<td>ThOF am 9:10</td>
<td>Identification of the Product Related Impurities in a Therapeutic Monoclonal Antibody Samples Using Size Based Fractionation and LC-MS</td>
<td>Richard Seipert, John T. Stults, Matthew Mazur, David Mahon, Tun Liu, Qinwei Zhou, Richard Crowley</td>
<td>Immunocore, Branchburg, NJ</td>
</tr>
<tr>
<td>ThOF am 9:30</td>
<td>Quantitation of Insulin Analogues and Identification of Degradants in Serum</td>
<td>Martha Stapels, Keith Fadgen, Jim Langridge, Thomas Rosano</td>
<td>Waters Corporation, Milford, MA; Albany Medical Center Hospital and College, Albany, NY</td>
</tr>
<tr>
<td>ThOF am 9:50</td>
<td>Top-Down LC-MALDI Identification of Protein in Mixtures of Moderate Complexity and N- and C-terminal Assignments</td>
<td>Anja Resemann, Shannon Cornett, Eckhardt Belau, Detlev Suckau, Bruker Daltonik GmbH, Bremen, Germany; Bruker Daltonics Inc., Fairview, TN</td>
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### Biomarker Analysis and Metabolomics in Drug Discovery

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<thead>
<tr>
<th>Session Time</th>
<th>Presentation Title</th>
<th>Speaker(s)</th>
<th>Institution(s)</th>
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<tbody>
<tr>
<td>ThOG am 8:30</td>
<td>Metabolomic Profiling in Drug Discovery: Understanding the Factors that Influence Metabolomics Studies and Strategies to Reduce Biochemical and Chemical Noise</td>
<td>Mark Sanders, David Peake, Tom McClure, Thermo Fisher Scientific, San Jose, CA</td>
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<tr>
<td>ThOG am 8:50</td>
<td>Pharmacometabonomics of Ginseng Extracts on Vascular Injury Induced by Chronic Homocysteine Treatment</td>
<td>Lui Ed, Hou Jirui, Suma Ramagiri, Takeo Sakuma, Eva Duchoslav, Ron Bonner, Lyle Burton, David Cox, Tom Moy, AB SCIEX, Concord, Canada; University of Western Ontario, London, Canada</td>
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<td>ThOG am 9:10</td>
<td>Identification of Hepatic Toxicity Biomarkers Using Accurate Mass LC/MS and High/Low pH Mobile Phases: A Metabonomics Approach</td>
<td>Rob Plumb, Paul Rainville, Jeremy Nicholson, Waters, Milford, MA; Imperial College, Lonodn, UK</td>
<td></td>
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<tr>
<td>ThOG am 9:30</td>
<td>MS-based Detection and Quantitation of Putative Biomarkers for Ankylosing Spondylitis</td>
<td>Roman Fischer, Moritz Wagner, Paul Bowness, Benedikt Kessler, Centre for Cellular and Molecular Physiology, Oxford, UK; Agilent Technologies, Hewlett-Packard-Strasse, Waldbronn, Germany; Weatherall Institute for Molecular Medicine, Oxford, UK</td>
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<td>ThOG am 9:50</td>
<td>Development of an Electrospray-Mass Spectral Database for Annotating Metabolomics Datasets: Application to the Analysis of the Adult Human Urinary Metabolome</td>
<td>Aurelie Roux, Ying Xu, Jean-François Heiller, Marie-Françoise Olivier, Eric Ezn, Jean-Claude Tabet, Christophe Junot, CEA - Centre d’Etude de Saclay, GIF-Sur-Yvette, France; Institut National de Recherche et de Sécurité, Nancy, France; LCSOB, IPCM, UMR-CNRS 7201, UPMC Paris Universitas, Paris, France</td>
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<td>ThOG am 10:10</td>
<td>Profiling of Indole Alkaloids in Tissues of Medicinal Plants Catharanthus roseus and Rauvolfia serpentina, Using LC-TOF MS</td>
<td>Mary Dawn Celiz, Sarah E. O’Connor, A. Daniel Jones, Michigan State University, East Lansing, MI; Massachusetts Institute of Technology, Cambridge, MA</td>
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### Biomarkers/Disease Signatures

**2:30 - 4:30 pm**  
Chris Turck, Max Planck Institute, presiding  
Wells Fargo Theatre

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<th>Time</th>
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<th>Authors</th>
<th>Affiliations</th>
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<tbody>
<tr>
<td>ThOA pm 2:30</td>
<td>High Resolution Imaging Mass Spectrometry in Arthritic Diseases</td>
<td>Ron M.A. Heeren, Berta Cillero-Pastor, Sanauliah Chungtaï, Gert Eijkel, Donald F. Smith, Jilliana Pasar-Tolic</td>
<td>1MPI of Psychiatry, Munich, GERMANY; 2Pacific NW Nat’l Lab, Richland, WA</td>
</tr>
<tr>
<td>ThOA pm 2:50</td>
<td>Quantitative Proteomic and Metabolomic Profiling of Antidepressant Drug Action Reveals Novel Targets</td>
<td>Christian Webhofer, Philipp Gormann, Stefan Reckow, Vladimir Tolstikov, Giuseppina Maccarone, Walter Ziegglänsberger, Inge Sillaber, Florian Holsboer, Chris Turck</td>
<td>1Affectis Pharmaceuticals, Martinsried, Munich, GERMANY; 2Metabolomics Core, UC Davis, Davis, CA</td>
</tr>
<tr>
<td>ThOA pm 3:10</td>
<td>Meta-analysis of Cardiovascular Disease and Statin Drug Response Biomarkers in Human Patients</td>
<td>William Wikoff, Oliver Fieni, Miles Trupp, Steven Watkins, Rebecca Baillie, Ronald Krauss, Rima Kaddurah-Daouk, University of California Davis, Davis, CA</td>
<td>1University of California Davis, Davis, CA; 2UC Davis, Davis, CA; 3Affectis Pharmaceuticals, Martinsried, Munich, GERMANY</td>
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<tr>
<td>ThOA pm 3:30</td>
<td>Tracking the Proteome/Metabolome Interactions of Potential Biomarkers of Huntington Disease (HD) with LCECA and parallel LCECA/LCMS²</td>
<td>Erika N. Ebbel, Leping Sun, Samantha Matson, Swati Sharma, Stephen Hersch, Wayne R. Matson, Catherine E. Costello, Boston University School of Medicine, Boston, MA; The Edith Nourse Memorial Veterans Hospital, Bedford, MA</td>
<td>Massachusetts General Hospital, Boston, MA</td>
</tr>
<tr>
<td>ThOA pm 3:50</td>
<td>Discovery and Functional Characterization of Epigenetic Signatures of Cancer Pathogenesis</td>
<td>Barry Zee, Gary Leroy, Benjamin Garcia, Princeton, NJ</td>
<td>1University of Pennsylvania, Philadelphia, PA; 2University of California, Los Angeles, CA</td>
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<tr>
<td>ThOA pm 4:10</td>
<td>Measuring Kinase Pathway Activities in Normal and Cancerous Human Prostate Tissue Using an in vitro MS-based Kinase Assay</td>
<td>Robert A. Everley, Ryan C. Kunz, Fiona E. McAllister, Adam S. Feldman, Chin-Lee Wu, Steven P. Gygi</td>
<td>1Harvard Medical School, Boston, MA; 2Massachusetts General Hospital, Boston, MA</td>
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### Fundamentals: Ion/Molecule and Ion/Ion Interactions

**2:30 - 4:30 pm**  
Victor Ryzhov, Northern Illinois University, presiding  
Room 501

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<th>Time</th>
<th>Title</th>
<th>Authors</th>
<th>Affiliations</th>
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<tbody>
<tr>
<td>ThOB pm 2:30</td>
<td>The Effect of α and β Substituents on S₅₂ and E₂ Reactions</td>
<td>Scott Gronert, Samuel Nettey, Christopher Swift, Diogo de Oliveira, Renan Joviliano, Virginia Commonwealth University, Richmond, VA</td>
<td>1University of Wollongong, Wollongong, Australia; 2University of Melbourne, Melbourne, Australia; 3University of Dundee, Dundee, UK; 4University of California, San Diego</td>
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<tr>
<td>ThOB pm 2:50</td>
<td>Reactions of α-carboxylate Radical Anions with Dioxygen</td>
<td>Benjamin B Kirk, Pramesh I Hettiarachchi, Berwyck L J Poad, Adam J Trevitt, Gabriel da Silva, Stephen J Blanksby, University of Wollongong, Wollongong, Australia</td>
<td>1University of Wollongong, Wollongong, Australia; 2University of Melbourne, Melbourne, Australia; 3University of Dundee, Dundee, UK; 4University of California, San Diego</td>
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<tr>
<td>ThOB pm 3:10</td>
<td>Gas-phase Reactivity of Various Didehydroquinolinium and Didehydrosoquinolinium Radicals Toward Aliphatic Amino Acids</td>
<td>Enada F Archibald, Nelson R Vinueza, George Oates, John J Nash, Hilika I Kenttämaa, Purdue University, West Lafayette, IN</td>
<td>1University of Wollongong, Wollongong, Australia; 2University of Wollongong, Wollongong, NSW, Australia</td>
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<td>ThOB pm 3:30</td>
<td>Gas Phase Ozonolysis of Deprotonated Cysteine and Cysteine Containing Peptides: Fundamentals and Potential Applications</td>
<td>Timothy M. Benton, Huong T Pham, Tony Ly, George N. Kharrazi, Stephen J Blanksby, Richard A. J. O’Hair, University of Melbourne, Victoria, Australia; 2Bio21 Inst, Uni of Melbourne, Melbourne, Australia; 3University of Wollongong, Wollongong, NSW, Australia</td>
<td>1University of Melbourne, Victoria, Australia; 2Bio21 Inst, Uni of Melbourne, Melbourne, Australia; 3University of Wollongong, Wollongong, NSW, Australia</td>
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<tr>
<td>ThOB pm 3:50</td>
<td>In-Silico Design of Electron Transfer Dissociation Reagents Evaluated by Q-TOF with Glow Discharge Anion Source</td>
<td>Jeffery M Brown, Keith Richardson, Iain D G Campuzano, Jonathan P Williams, Richard Denny, Barry Dyson, James Langridge, Michael Morris, Waters Corporation, Manchester, UK</td>
<td>1University of Wisconsin, Madison, WI; 2Thermo Fisher Scientific, Charlottesville, VA; 3Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany</td>
</tr>
<tr>
<td>ThOB pm 4:10</td>
<td>Probing ETD Fundamentals Using a Dedicated ETD Reaction Cell and IR Photons on a Hybrid Mass Spectrometer</td>
<td>Aaron Ledvina, Michael S. Westphall, Graeme Mcalister, John E. P. Syka, Jens Griep-Raming, Joshua J. Coon, University of Wisconsin, Madison, WI</td>
<td>1University of Wisconsin, Madison, WI; 2Thermo Fisher Scientific, Charlottesville, VA; 3Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany</td>
</tr>
</tbody>
</table>
### Microorganisms: Identification and Characterization

#### ThOC pm 2:30

**Staphylococcus aureus** Detection and Antibiotic Susceptibility Determination Using 15N-Labeled Bacteriophage Amplification Coupled with Rapid Trypsin Digestion and MALDI-MS; **Jon Rees; Carrie Pierce; John R. Barr; Centers for Disease Control, Atlanta, GA**

#### ThOC pm 2:50

**Modified Proteins in Environmental Microbes;** Rachel O. Loo¹; Deborah R. Francoele¹; Bryan Crable¹; Hosna Mouttaki¹; Robert Gunsalus¹; Michael Mcinerney²; Joseph A. Loo³; UCLA, Los Angeles, CA; University of Oklahoma, Norman, OK

#### ThOC pm 3:10

**Identification of Mechanisms of Extracellular Respiration By Shewanella oneidensis MR-1 Using Imaging Mass Spectrometry;** Brandi Heath¹; Jeremie Watrous²; Peter Dorrestein³; Patrick Roach¹; Lijian Pasa-Tolic¹; Donald Smith¹; zihua zhu¹; Matthew Marshall¹; Julia Laskin²; Pacific Northwest Natl Laboratory, Richland, WA; Univ of California, San Diego, Skaggs school, La Jolla, CA

#### ThOC pm 3:30

**Absolute Quantification of Microbial Proteomes at Different Cellular States by Directed Mass Spectrometry: Application to the Human Pathogen Leptospira Interrogans;** Alexander Schmidt¹; Martin Beck¹; Johan Malmstroem³; Manfred Claassen²; Henry H. N. Lam²; Dave Campbell²; Ruedi Aebersold۴; ۵; Biozentrum, University of Basel, Switzerland; ۶European Molecular Biology Laboratory, Heidelberg, Germany; ۷ETH Zürich, Switzerland; ۸Hong Kong Univ of Science and Technology, Hong Kong, China; ۹Inst for Systems Biology, Seattle, WA; ۱۰Univ of Zurich, Switzerland

#### ThOC pm 3:50

**Comparing the Microbial Species and Metabolic Activities in the Gut Microbiomes of Healthy versus Crohn’s Diseased Matched Human Twins;** Robert Hettich¹; Alison R. Erickson¹; Chongle Pan¹; Nathan C. Verberkmoes¹; Manesh Shah¹; Brandi L. Cantarel²; Regina Lamendella³; Claire Fraser-Liggett³; Janet Jansson⁴; Oak Ridge Natl Laboratory, Oak Ridge, TN; Univ of Tennessee, Knoxville, TN; Univ of Maryland School of Medicine, Baltimore, MD; Lawrence Berkeley Natl Laboratory, Berkeley, CA

#### ThOC pm 4:10

**Comparative Proteome Analyses of Outer Membrane Proteins for The Differentiation of Pathogenic Vs. Nonpathogenic Bacteria Using Mass Spectrometry-Based Proteomics Approach;** Rabih Jabbour¹; Samir Deshpande¹; Mary Wade¹; Michael Stanford¹; Charles Wicking¹; Alan Zulich³; SAIC INC., Apg, MD; Science and Technology Corporation, Edgewood, MD; ECBC, Apg, MD

### Oligonucleotides: Structure and Reactivity

#### ThOD pm 2:30

**Investigation of UV Induced Protein–RNA Cross-Linking by Mass Spectrometry;** Katharina Kramer¹; Florian Richter¹; Caroline Endler¹; Petra Hummel¹; Roland G. Heym³; Alexander Dybkov¹; Xiao Luo ³; Reinhard Lührmann³; Markus C. Wahl³; Dierk Niessing³; Henning Urlaub³; Max Planck Institute for Biophysical Chemistry, Goettingen, Germany; Ludwig-Maximilians-University, Munich, Germany; Free University, Berlin, Germany

#### ThOD pm 2:50

**LC-MS/MS for Assessing the Repair of Purine Cyclonucleosides in Human Cells;** Jin Wang; Changjung You; Bi Feng Yuan; Yinheng Wang; University of California, Riverside, CA

#### ThOD pm 3:10

**Tandem Mass Spectrometry of Platinationed Oligonucleotides;** Adrien Nyakas; Silvan, R. Stucki; Stefan Schuerch; University of Bern, Bern, Switzerland

#### ThOD pm 3:30

**Rapid Extraction of siRNA from Human Serum Using Surface Modified Strong Anion Exchange (SAX) Magnetic Particles;** Guofeng Ye; Michael Beverly; Novartis Institutes for BioMedical Research, Cambridge, MA

#### ThOD pm 3:50

**Pseudouridine Quantification in Transfer and Ribosomal RNAs by Selected Reaction Monitoring Mass Spectrometry;** Balasubrahmanyan Addepalli¹; Patrick A. Limbach; University of Cincinnati, Cincinnati, OH

#### ThOD pm 4:10

**Photoreactivity of Oligonucleotides under UV and VUV Irradiation Frederic Rosu¹; Laure Joly¹; Alexandre Giuliani²; Valerie Gabelica³; Laurent Nahon³; Edwin De Pauw¹; University of Liege, Liege, Belgium; Synchrotron Soleil, Gif-Sur-Yvette, France
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<th><strong>THURSDAY AFTERNOON ORAL SESSIONS</strong></th>
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<td><strong>MATERIAL-BIOMOLECULAR COMPLEXES:</strong></td>
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<td><strong>STRUCTURE AND REACTIONS</strong></td>
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<td>2:30 – 4:30 pm</td>
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<td>Frantisek Turecek, University of Washington, presiding</td>
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<td>Korbel Ballroom 3-4</td>
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<td><strong>BIOMARKERS OF DRUG/METABOLITE TOXICITY:</strong></td>
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<td><strong>LC-METHODS</strong></td>
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<td>Edward Kerns, Discovery ADME, presiding</td>
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<td>Four Seasons Ballroom 1-2</td>
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**THURSDAY AFTERNOON ORAL SESSIONS**

**AMBIENT DESORPTION IONIZATION TECHNIQUES: NEW DEVELOPMENTS AND APPLICATIONS**
2:30 – 4:30 pm  
Daniel Austin, Brigham Young University, presiding  
Four Seasons Ballroom 3-4

**ThOG pm 2:30**  
*In-vivo, Real-time Identification of Tissues During Brain Surgery;* Karl C. Schaefer¹; Julia Balog²; Stefanie Gerbig³; Zoltan Takacs¹; ¹Justus-Liebig-University, Giessen, Germany; ²Semmelweis University, Budapest, Hungary; ³Justus-Liebig-Universität, Giessen, Germany

**ThOG pm 2:50**  
*Synchronized Inductive Desorption Electrospray Ionization Mass Spectrometry;* Guangming Huang; Guangtao Li; Jason S Duan; Zheng Ouyang; R. Graham Cooks; Purdue University, West Lafayette, IN

**ThOG pm 3:10**  
*Ambient Ionization of Unprepared Samples Using Surface Acoustic Waves;* David Go¹; Jenny Ho¹ ²; Ming K. Tan¹; Hsueh-Chia Chang¹; Leslie Yeo²; James Friend²; ¹University of Notre dame, Notre Dame, IN; ²University of Monash, Melbourne, Australia

**ThOG pm 3:30**  
*Microsecond Time-Resolved Desorption Electrospray Ionization-Mass Spectrometry (DESI-MS);* Zhixin Miao; Hao Chen; Ohio University, Athens, OH

**ThOG pm 3:50**  
*Fundamentals and Applications of Inlet Ionization: Ionization Methods for Small and Large Molecules;* Charles N. Mcewen¹; Vincent Pagnotti²; ¹Univ. of the Sciences, Philadelphia, PA; ²University of the Sciences, Philadelphia, PA

**ThOG pm 4:10**  
*Combining Laser Ablation/Liquid Phase Collection Surface Sampling and Electrospray Ionization Mass Spectrometry;* Olga Ovchinnikova; Vilmos Kertesz; Gary J. Van Berkel; Oak Ridge National Laboratory, Oak Ridge, TN

**PLENARY SESSION**  
4:45 - 5:30 pm  
Susan T. Weintraub, University of Texas Health Science Center, presiding  
Wells Fargo Theatre

*Why Are We Surprised by Only Some of the Things that We See? Visual Illusions, the Brain, and Baseball*

Arthur Shapiro  
American University
New Developments in Ionization I, 001 - 021

Ion Mobility: Instrumentation and Fundamentals, 049 - 064
GC-MS: Instrumentation and Applications, 065 - 083
High Mass Accuracy/High Performance MS: Instrumentation, 084 - 108
Atmosphere/Aerosol Chemistry, 109 - 112
Ion-Surface Interactions and Preparative MS, 113 - 114
Small Molecule: Qualitative Analysis, 115 - 136
Small Molecule: Quantitative Analysis, 137 - 167
LC-MS: Chromatography – Small Molecule, 168 - 200
LC-MS: Sample Preparation – Peptides, 201 - 218
LC-MS: Chromatography – Peptides, 219 - 232
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Lipids: General, 254 - 273
Carbohydrates: Characterization, 274 - 293
Nucleic Acids I, 294 - 311
Metabolomics: Sample Preparation, 312 - 318
Metabolomics: Quantitative Analysis, 319 - 338
Diagnostic Clinical Chemistry I, 339 - 357
Elemental Analysis, 358 - 361
Environmental Analysis: General, 362 - 387
Homeland Security, 388 - 401
Food Safety, 402 - 424
Informatics: Fragmentation Mechanism, 425 - 436
Informatics: Peptide Identification and Characterization, 437 - 470
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Phosphopeptides: Enrichment Methods, 477 - 489
Phosphopeptides: Sequence Analysis, 490 - 495
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Microbial Analysis; 530 - 556
Intact Proteins: Sequence Analysis, 557 - 572
Recombinant Proteins: Qualitative Analysis, 573 - 574
Proteomics: Separation, 575 - 583
Proteomics: New Approaches – Instrumentation; 584 - 603
Proteomics: Protein Complexes, 604 - 622
Proteins: Covalent Labeling, 623 - 633
Biomolecular Structure Analysis: Covalent Labeling, 634 - 651
Biomarkers: Quantitative Analysis, 652 - 667
Biomarkers: Discovery-Cancer, 668 - 694

Special 2 Wed & Thurs only. ABRF-sPRG2011 Study:
Development and Characterization of a Comprehensive Standard for Analysis of Post-translational Modifications; Alexander R. Ivanov 1; Christopher Colangelo 2; Craig Dufresne 3; James Farmar 4; David B. Friedman 5; Chris Kinsinger 6; Kathryn S. Lilley 7; Karl Mechtler 8; Brett Phinney 9; Kristie Rose 10; Scott A. Shaffer 11; Susan T. Weintraub 1; 1Harvard University HSPH, Boston, MA; 2Yale University, New Haven, CT; 3Thermo Fisher Scientific, West Palm Beach, FL; 4U. of Virginia, Charlottesville, VA; 5Vanderbilt Univ School of Medicine, Nashville, TN; 6NIH NCI, Gaithersburg, MD; 7IMP Research Institute of MO, Vienna, Austria; 8University of CA, Davis, CA; 9University of Massachusetts Medical School, Worcester, MA; 10Univ. of Texas HSC, San Antonio, TX; 11University of Cambridge, UK

Special 1 Mon & Tues only. PRG-2011: Defining the Interaction Between Users and Suppliers of Proteomics Services; David Hawke 1; Tracy Andacht 2; Maureen K. Burger 3; Cory Bystrom 2; Lawrence Dangott 4; Henrik Molina 5; Robert Moritz 6; Robert Settlage 7; Chris Turck 8; 1Centers for Disease Control and Prevention, Lawrenceville, GA; 2UT- M.D. Anderson Cancer Center, Houston, TX; 3RTI International, Research Triangle Park, NC; 4Quest Diagnostics, San Juan Capistrano, CA; 5Texas A&M University, College Station, TX; 6Centre de Regulacio Genomica (CRG), Barcelona, SPAIN; 7Institute for Systems Biology, Seattle WA; 8Virginia Bioinformatics Institute, Blacksburg, VA; 9Max Planck Institute, Munich, Germany

New Developments in Ionization I, 001 - 021

MP 001 Novel Derivatization Strategies for Biomarker Analysis using APLI MS; Eduard Deibel 1; Ralf Schiewek 2; Klaus J. Brockmann 3; Thorsten Benter 4; 1Oliver J. Schmitz 5; 2University of Wuppertal, Wuppertal, Germany; 3Leiden University Medical Center, Leiden, The Netherlands

MP 002 GC-MS Performance of a Laminar Flow API Source Including APCI/PIAPI, APLI and CAPI for Multi-Mode Operation; Dennis Klink 1; Klaus J. Brockmann 2; Thorsten Benter 3; Oliver J. Schmitz 4; Dennis Klink 5; Thorsten Benter 6; University of Wuppertal, Wuppertal, Germany

MP 003 Ultra-sensitive Gas Chromatographic Analysis of PAHs with a Temperature-controlled APLI-source; Dennis Klink 1; Klaus J. Brockmann 2; Thorsten Benter 3; Oliver J. Schmitz 4; Dennis Klink 5; Thorsten Benter 6; University of Wuppertal, Wuppertal, Germany

MP 004 Photoelectron Induced Atmospheric Pressure Ionization (API) – A Selective Ionization Method for Molecules with High Electron Affinities; Valerie Dermpmann 1; Klaus J. Brockmann 2; Thorsten Benter 3; University of Wuppertal, Wuppertal, Germany

MP 005 In-situ MS Monitoring of Atmospheric Degradation Product Studies of Aromatic Hydrocarbons with APPI and APLI; Jan Barnes 1; Hendrik Kersten 2; Iustinian Bejan 3; Thorsten Benter 4; University of Wuppertal, Wuppertal, Germany

MP 006 Highly Efficient Ionization of Nitro-aromatic Compounds using Photoelectron Induced Atmospheric Pressure Ionization (PAPI); Valerie Dermpmann 1; Hendrik Kersten 2; Hannah Sonderfeld 3; Ralf Koppmann 4; Iustinian Bejan 5; Joerg Kleffmann 6; Thorsten Benter 7; University of Wuppertal, Wuppertal, GERMANY

MP 007 Adjusting the Laser Wavelength to the Peak Absorption of Novel Halogen-substituted MALDI Matrices for Enhanced MS Performance; Thorsten Wolfgang Jaskolla 1, 2; Jens Soltwisch 3; Franz Hillenkamp 4; Michael Karas 5; Klaus Dreisewerd 6; 1University of Muenster, Muenster, Germany; 2Goethe University Frankfurt, Frankfurt am Main, Germany

MP 008 A Novel MALDI Matrix Source Utilizing Soft-Landing Ion Mobility to Rapidly Deposit Ag Nanoparticles for Use as MALDI Matrices;
Monday Posters

MP 009 Matrix-Assisted Inlet Ionization (MAI) Methods Operating Without Voltage or Laser to Produce Highly Charged Ions: What Makes a Matrix a Better Matrix?; Yue Ren; Christopher Lietz; Alicia Richards; Beixi Wang; Ellen D. Inutan; Sarah Trimpin; Wayne State University, Detroit, MI

MP 10 Optimizing Conditions for Multiple Charged Ion Production in AP MALDI; Alexey Kononikhin1,2; Andrea Rocker2; Alexey Boldyrev1; Igor Popov1,3; Alexander Spasskiy2; Eugene Nikolaev1,3; 1Institute for Energy Problems of Chemical Physics, Moscow, Russia; 2Max-Planck Institute for Medical Research, Heidelberg, Germany; 3Emanuel Institute of Biochemical Physics RAS, Moscow, Russia

MP 11 Matrix-Free Laser Desorption/Ionization of Lipid Analyses on Metal Oxide Surfaces; Casey McAlpin; Kent Voorhees; Ryan Richards; April Corpuz; Colorado School of Mines, Golden, CO

MP 12 Characterization of the Potential of UV- and IR-Matrix-Assisted Desorption Ionization (MALDESI) Ionization Source with Air Amplifier; Jeremy Barry; Guillaume Robichaud; David C. Muddiman; North Carolina State University, Raleigh, NC

MP 13 Atmospheric Pressure Laser-Induced Acoustic Desorption Chemical Ionization (API/LIAD-ICI) for Global Hydrocarbon Analysis; Leonard Nyadong; Amy McKenna; Christopher L. Hendrickson; Ryan P. Rodgers; Alan G. Marshall; National High Magnetic Field Laboratory, Tallahassee, FL

MP 14 Highly Charged Protein Ions Generated by an UV Matrix Using Various Laser Wavelengths; Beixi Wang1; Ellen Inutan1; Lu Yan1; James Wager-Miller2; Ken Mackie1; Arthur Suits1; Sarah Trimpin1; 1Wayne State University, Detroit, MI; 2Indiana University, Bloomington, IN

MP 15 Investigating the Instrumental Optimization and Sensitivity of Laserspray Ionization for Protein Analysis; Diana L. Sardelis, Charles N. Mcwuen; Catherine Bentonley; University of the Sciences, Philadelphia, PA

MP 16 A Commercial Intermediate Pressure MALDI-IMS-MS Producing Multiply Charged Laserspray Ionization Ions; Ellen D. Inutan1; Beixi Wang3; James Wager-Miller2; Ken Mackie1; Sarah Trimpin1; 1Wayne State University, Detroit, MI; 2Indiana University, Bloomington, IN

MP 17 An Atmospheric Pressure Photo-ionization Source Based on a Window-less Atmospheric Pressure Spark Discharge; Faezeh Dousty1; Rob O’Brien1; Thorsten Benter1; Hendrik Kersten1; 1UBC Okanagan, Kelowna, Canada; 2University of Wuppertal, Wuppertal, Germany

MP 18 EUV-laser-ablation Mass Spectrometry Depth Profiling of Compound Semiconductor Heterostructures; Ilya Kuznetsov1,2; Feng Dong1,2; Jorge Filevich1,2; Elliot R. Bernstein1,2; Dean C. Crick3; Michael McNeil3; Weilun Chao3; Erik H. Anderson6; Luis Collins, CO; 1Department of Chemistry, CSU, Fort Collins, CO; 2Dept. of Electrical & Computer Engineering, CSU, Fort Collins, CO; 3Department of Microbiology, Immunology and Pathology, CSU, Fort Collins, CO; 4ECCS Dept., University of California, Berkeley, CA; 5Center for x-ray optics, LBNL, Berkeley, CA

MP 19 Photoemission Ambient Pressure Ionization (PAPI) with a UV LED for the Detection of Organic Vapors and Surface Residues; Luke C Short; Pacific Northwest National Laboratory, Richland, WA

MP 20 Windowless Miniature Spark Discharge Light Sources for Efficient Generation of VUV Radiation Below 100 nm for On-capillary APPI; Hendrik Kersten1; Klaus J. Brockmann1; Rob O’Brien2; Thorsten Benter1; 1University of Wuppertal, Wuppertal, Germany; 2UBC Okanagan, Kelowna, BC

MP 21 Miniature Microplasma Discharge-Desorption Atmospheric Pressure Photo-ionization (MD-DAPPI) Source for Ambient Mass Spectrometry; Asiri Galhena; Joshua Symonds; Facundo Fernandez; Thomas Orlando; Georgia Institute of Technology, Atlanta, GA

Direct Ionization: Applications I, 022 - 048

MP 22 The Rapid Identification of the Impurities in 2-Naphthalenamines using Atmospheric Pressure Solids Analysis Probe with Ion Mobility Mass Spectrometry; Hefeng Pan; Göran Lundin; AstraZeneca, Södertälje, Sweden

MP 23 Evaluation of Atmospheric Pressure Solids Analysis Probe Coupled to Mass Spectrometry for the Determination of Cleaning Assay of Budesonide; Göran Lundin; Hefeng Pan; AstraZeneca, Södertälje, Sweden

MP 24 Evaluation of a Hybrid Linear Ion Trap – Triple Quadrupole MS System for Real-Time Monitoring of Ambient Air Pollutants; Nicholas Karellas1; Peter Kvarik1; Jeffery Rivera2; David Cox2; Robert Ellis3; Tom Moy3; Takeo Sakuma3; 1Ontario Ministry of the Environment, Toronto, ON, ON; 2AB SCIEX, Concord, ON

MP 25 Hightroughput Screening of 1,4-butanediol Production in Fermentation Samples using LDTD APCI Ionization Source Coupled to a Benchtop Orbitrap MS; Julia Khandurina1; Patrice Trepagnier2; Nicholas Dukas3; 1Genomatica, San Diego, CA; 2Phytronix Technologies, Quebec, QC; 3ThermoFisher Scientific, Somerset, NJ

MP 26 Direct Mass Spectrometric Analysis of Ozone-initiated Terpene Reaction Products Using Low Temperature Plasma Ionization; Asger Nergaard1; Anni Vibenhold1; Mario Benassi2; Per Axel Clausen1; Peder Wolkoff1; 1Natl Research Centre for the Working Environment, Copenhagen, Denmark; 2Justus-Liebig University, Giessen, Germany

MP 27 Direct Mass Spectrometric Analysis of PM2.5 Filters Sampled in Dwellings using Low Temperature Plasma Ionization; Anni Vibenhold1; Asger W. Nergaard; Per A. Clausen; Peder Wolkoff; 1Natl Research Centre for the Working Environment, Copenhagen, Denmark

MP 28 Detection of Opioids in Breath; Christian Berchtold1; Lukas Meier1; Youssef Daali1; Denis Morel1; Bernard Walder1; Renato Zenobi2; 1ETH Zürich, Zürich, Switzerland; 2University Hospital of Geneva, Geneva, Switzerland
MP 029 Spray Desorption Collection: An Alternative to Swabbing for Pharmaceutical Cleaning Validation; Shashank Jain; Amy Heiser; Andre Venter; Western Michigan Univ, Kalamazoo, MI

MP 030 Strategies for Rapid Screening and Analysis of Pesticides in Food and Water Matrix using DAPCI-MS and DESI-MS; Joseph H. Kennedy; Brian C. Laughlin; Justin Wiseman; Prosolia, Inc, Indianapolis, IN; Prosolia, Inc., Indianapolis, IN

MP 031 Simultaneous Analysis of Saturated and Unsaturated, Non-polar and Polar Hydrocarbons by Using Saturated Hydrocarbon Solvents in HPLC/APCI Mass Spectrometry; Inthanakorn Gao; David Barton; Benjamin Owen; Zhicheng Jin; Hilika Kenttamaa; Chemistry Department of Purdue University, West Lafayette, IN; Johns Hopkins University, Baltimore, MD

MP 032 Thermal Desorption / Tandem Quadrupole MS for Rapid Analysis of Complex Heterogeneous Mixtures for Active Components and Degradation By-Products; Tim Jenkins; Eleanor Riches; Peter Lee; Michael Oleary; Waters Corporation, Manchester, UK; Waters Corp, Milford, MA

MP 033 Rapid Characterization of The Proteins Stored in Solutions by Liquid Electrospray Laser Desorption Ionization (ELDI) Mass Spectrometry; Yi-Tzu Chao; Jentaie Shia; National Sun Yat-Sen Univ., Kaohsiung, TAIWAN

MP 034 Direct Electrospray Probe (DEP) Mass Spectrometry for Characterizing the Chemical Compounds Absorbed in Fibers; Minzong Huang; Jentaie Shia; National Sun Yat-Sen Univ., Kaohsiung, Taiwan

MP 035 On-Line Monitoring Aldol Reaction by Liquid Electrospray Laser Desorption/Ionization Mass Spectrometry; Chu-Ning Chen; Jentaie Shia; National Sun Yat-Sen Univ., Kaohsiung, Taiwan

MP 036 1D and 2D Spatial Chromatographic Readout with Liquid Microjunction Surface Sampling Probe/Electrospray Ionization Mass Spectrometry Systems; Matthew Walworth; Oak Ridge National Lab/Department of Chemistry UTK, Knoxville, TN

MP 037 Analysis of Tissue Samples by Liquid Extraction Surface Analysis (LESA) Coupled to Differential Ion Mobility (DMS) High Resolution MS/MS; David Cox; Thomas Covey; J.C. Yves Leblanc; Brad Schnieder; Gary J. Van Berkel; Vilmos Kertesz; Paul Moench; Jimmy Flarakos; AB SCIX, Concord, CANADA; Oak Ridge National Laboratory, Oak Ridge, TN; Oak Ridge National Lab, Oak Ridge, TN; Novartis (NIBR), East Hanover, NJ

MP 038 Quantitative Structural Changes in Hindered Amine Light Stabilizers within Coil Coatings by Desorption Electrospray Ionization-Mass Spectrometry; Martin R. L. Paine; Philip J. Barker; Stephen J Blanksby; University of Wollongong, Wollongong, Australia; BlueScope Steel Research, Port Kembla, Australia

MP 039 Application of WASAP and EESI Ionization Approaches Coupled with Traveling Wave Ion Mobility Mass Spectrometry; James Scrivens; Charlotte Scarborough; University of Warwick, Coventry, UK; University of Arkansas, Fayetteville, AR

MP 040 Venturi Easy Ambient Sonic Spray Ionization Monitoring of Multicomponent Reactions; Vanessa Goncalves Dos Santos; Thais Regiani; Maria Narciso Godoi; Mirela B. Coelho; Rodrigo O. M. A. de Souza; Simon J. Garden; Marcos N Eberlin; Thermo Mass Spectrometry Laboratory, Campinas, Brazil; Federal University of Rio de Janeiro, Rio de Janeiro, Brazil

MP 041 Thermal Assisted Easy Ambient Sonic-Spray Ionization (T-EASI) for Analysis of Triacylglycerides (TAG) in Meat Matrices; Marcos N Eberlin; Minzong Duque de Caxias, RJ, Brazil; Thomas Covey; National Institute of Metrology, Standardization and Allied Research, New Delhi, India; Dance de Caxias, RJ, Brazil; Thermo Mass Spec Lab, UNICAMP, Campinas, SP, Brazil; Department of Chemistry, Purdue University, West Lafayette, IN; Department of Chemistry, Purdue University, West Lafayette, IN

MP 042 Measurement of Biodiesel/Diesel Blend Levels by Easy Ambient Sonic-spray Ionization Mass Spectrometry; Ildefonso S. Cunha; Rosana Maria Alberici; Rosineide Costa Simas; Anna Maria A. P. Fernandes; Gilberto de Sa; Romeo Daroda; Marcos N Eberlin; Thermo Mass Spectrometry Laboratory, UNICAMP, Campinas-SP, Brazil; University of Pernambuco, Recife - PE, Brazil; National Institute of Metrology, Standardization and Allied Research, New Delhi, India; Thermo Mass Spec Lab, UNICAMP, Campinas, SP, Brazil; Universidade Federal de Pernambuco, Recife-PE, Brazil

Effects of Triacylglyceride Molecular Structure on Ionization Efficiency in the Easy Ambient Sonic-spray Ionization Technique; Rosana M. Alberici; Anna Maria A. P. Fernandes; Ildefonso S. Cunha; Rosineide Costa Simas; Daniel Barrera-Arellano; Marcos N. Eberlin; Thermo Mass Spectrometry Laboratory, UNICAMP, Campinas-SP, Brazil; University of Pernambuco, Recife - PE, Brazil; National Institute of Metrology, Standardization and Allied Research, New Delhi, India; Thermo Mass Spec Lab, UNICAMP, Campinas, Brazil; Fats and Oils Laboratory, UNICAMP, Campinas, Brazil

MP 043 Calculated Layer-by-Layer Gold Nanoparticle Array for Direct Detection of Peptides and Small Molecules through Surface Assisted Laser Desorption/Ionization Mass Spectrometry; Chih-Yuan Chen; Pacific Bioscience, CA

MP 044 Direct Detection of Fatty Acid Ethyl Esters using Low Temperature Plasma (LTP) Ambient Ionization Mass Spectrometry for Rapid Bacterial Differentiation; Jingyao (Isabella) Zhang; Anthony Costa; Wei Guo Andy Tao; R. Graham Cooks; Department of Chemistry, Purdue University, West Lafayette, IN; Department of Biochemistry, Purdue University, West Lafayette, IN

MP 045 Direct and Quantitative Analysis of Acylcarbiniles in Serum and Whole Blood Using Paper Spray Mass Spectrometry; Qian Yang; Nicholas Manicke; Chris Petucci; R. Graham Cooks; Zheng Ouyang; Purdue University, West Lafayette, IN; Sanford-Burnham Medical Research Institute, Orlando, FL

MP 046 Direct Analysis of Therapeutic Drugs in Dried Blood Spots using Paper Spray and a Miniature Mass Spectrometer; Zhiping Zhang; Nicholas Manicke; Wei Xu; R. Graham Cooks; Zheng Ouyang; Center for Biomedical Engineering, Purdue Un, West Lafayette, IN; Department of Chemistry, Purdue University, West Lafayette, IN; Department of Biochemistry, Purdue University, West Lafayette, IN; Center for Biomedical Engineering, Purdue University, West Lafayette, IN

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MONDAY POSTERS
MONDAY POSTERS

Analytical Instrumentation Development, West Lafayette, IN

MP 048  Direct Analysis of Biological Tissue by Paper Spray Mass Spectrometry; He Wang; Nicholas Manicke; Qian Yang; Lingxing Zheng; Rui Shi; R. Graham Cooks; Zheng Ouyang; Purdue University, West Lafayette, IN

MP 049  Ion Mobility Mass Spectrometry combined with a Laser Induced Liquid Beam/Droplet Desorption Source; Alexis Charvat1; Albina Abdrahmanova2; Bernd Abel1;2Ostwald-Institute for Physical Chemistry, Leipzig, Germany; 2Knauer GmbH, Berlin, Germany

MP 050  An Electrospray Ionization-Ion Mobility-Mass Spectrometry with Modular Periodic-Focusing DC Ion Guide; Junho Jeon; Ryan Blase; Chamindika M. Gamage; David H. Russell; Texas A&M University, College Station, TX

MP 051  Improving the Apparent Resolution of Differential Mobility Separation-Mass Spectrometry (DMS-MS) using Principle Component Variable Grouping (PCVG); Chris Lock; Gordana Ivosev; J.C. Yves Leblanc; Ron Bonner; Brad Schneider; Thomas Covey; AB Sciex, Concord, ON

MP 052  Modifier and Field Effects for Differential Mobility Spectrometry Separations of Protonated Isomeric Dipeptides; Hassan Javaheri1; Vosilav Blagojevic1; Alexander Chramow1; Bradley Schneider1; Thomas Covey1; Diether K. Bohme1; 1AB SCIEX, Concord, Canada; 2York University, Toronto, ON

MP 053  Optimization of High Field Asymmetric Waveform Ion Mobility Spectrometry (FAIMS) Separations; Samantha L. Isenberg; Paul M. Armistead; Gary L. Glish; University of North Carolina, Chapel Hill, NC

MP 054  Linked Scanning of the Carrier Gas Composition and Compensation Voltage to Increase Resolution of a Planar FAIMS Device; Alice Pil1; Mark Ridgeway1; Andrew Hampton1; Samantha Isenberg2; Desmond Kaplan1; Melvin A. Park1; Gary L. Glish1; 1University of North Carolina, Chapel Hill, NC; 2Bruker Daltonics, Inc., Billerica, MA

MP 055  Trapped Ion Mobility Spectrometry – Mass Spectrometry (TIMS-MS) for the Analysis of Biomolecules; Desmond Kaplan1; Francisco Fernandez-Lima2; Melvin A. Park1; 1Bruker Daltonics, Inc., Billerica, MA; 2Texas A&M University, College Station, TX

MP 056  Characterization of a High Field FAIMS System; Michael Belford; Jean-Jacques Dunyach; Salendra Prasad; Thermo Fisher Scientific, San Jose, CA

MP 057  Increased Ion Capacity of a Circular Drift Tube in Frequency Scanning Mode; Rebecca S. Glaskin; Jeffrey A. Everett; Stephen J. Valentine; David E. Clemmer; Indiana University, Bloomington, IN

MP 058  Design Requirements for Quantitative DMS/MS with Chemically Modified Separations; Bradley Schneider; Thomas Covey; AB Sciex, Concord, Canada

MP 059  Modification of Ion Mobility Separation using Volatile Organic Dopants on a Quadrupole- Ion Mobility-Orthogonal Time-of-Flight Mass Spectrometer; Martin Green; Kevin Giles; Keith Richardson; Martin Palmer; Waters Corporation, Manchester, UK

MP 060  Ion Mobility-Mass Spectrometry Studies of Transition Metal-ligand Complexes; Victoria Wright1; Fernando Castro-Gomez2; Carles Bo1;2 Steven Christie1; Colin Creaser1; Loughborough University, Loughborough, UK; 2Institute of Chemical Research of Catalonia, Tarragona, Spain; 3Universitat Rovira i Virgili, Tarragona, Spain

MP 061  Internal Energy of Ions in Travelling Wave Ion Mobility Spectrometry; Denis Morsa; Edwin De Pauw; Valerie Gabelica; University of Liege, Belgium, Liege, Belgium

MP 062  Effect of Charge-induced Gas Polarization on the Measured Electrical Mobilities of Spherical, Multiply-charged Ionic Liquid Nanodrops; Juan Fernandez Garcia; Juan Fernandez de la Mora; Yale Univ, New Haven, CT

MP 063  Trapped Ion Mobility Spectrometry – Mass Spectrometry (TIMS-MS); Francisco A. Fernandez-Lima1; Desmond Kaplan1; Juergen Suetering1; Melvin A. Park2; 1Texas A&M University, College Station, TX; 2Bruker Daltonics, Inc., Billerica, MA

MP 064  A Comparison of Laserspray Ionization with Electrospray Ionization for Structural Characterization of Ubiquitin Protein Ions; Cory Manly; Ellen D. Inutan; Christopher Lietz; Sarah Trimpin; Wayne State University, Detroit, MI

GC-MS: INSTRUMENTATION AND APPLICATIONS, 065 - 083

MP 065  GC/APCI-FTMS – A Novel Tool for the Analysis of Volatile Compounds in Complex Mixtures; Matthias Witt; Bruker Daltonik GmbH, Bremen, Germany

MP 066  Characterization of Hydrogenation Reactions and Products of 1,4-bis(phenethyl)benzene (DEB) with Ambient Gas Chromatography and High-resolution Mass Spectrometry; Steven Christie1; Colin Creaser1; 1Unicamp, Campinas, SP, Brazil

MP 067  Development of a Low Power Gas Chromatograph-Mass Spectrometer for In-Situ Detection of Organics in Martian Soil; Veronica Pinnick1;2; Arnaud Buch2; Friso H. W. Van Amerom2; Ryan M. Danell3; William Brinkerhoff2; Paul Mahaffy4; Robert J. Cotter1; 1Middle Atlantic MS Laboratory, Baltimore, MD; 2NASA/Goddard, Greenbelt, MD; 3NASA/Goddard, Greenbelt, MD; 4Knauer Spectrometry, Bergisch Gladbach, Germany; 5Prosolia, Inc., Indianapolis, IN

MP 068  Challenging Applications Analysis by GC-MS with Supersonic Molecular Beams – An Alternative to LC-MS; Aviv Amirav; Alexander Gordin; Alexander B. Fialkov; Tel-Aviv University, Tel-Aviv, Israel

MP 069  Gas Chromatography-Mass Spectrometry Combined with Hollow Fiber Drop-to-drop Solvent Microextraction for Determination of Antidepressants Drugs in Human Urine Sample; Kavita Tapadia; National, Rairpur(Cq), India
MP 070  Determination of Furan by Isotope Dilution Method with Solid-Phase Microextraction-Gas Chromatograph/Mass Spectrometer in Heat-processed Foods; Cheon-Ho Jo; Sung-Kug Park; Junghyuck Suh; Ock-Jin Paek; Young-Woon Kang; Hoon Choi; Meehye Kim; Korea Food and Drug Administration, Cheongwon, South Korea

MP 071  Development of a Sensitive and Reliable Method for the Measurement of VOC Migration from Food Packaging; GC-TOF/MS vs. GC-Quadropole/MS; Petra Gerhardt1; Manfred Möller1; Pierre Schanen1; Gerhard Horner1; 1ALMSCO International, Llantrisant, UK; 2UK-Aachen, Aachen, Germany

MP 072  Characterization of Post-Injection Ion Kinetic FT-ICR MS of Protein Complex Ions by using Ammonia Positive Chemical Ionization; Ying Zhang1; Herbert Tobias1; Richard J. Auchus1; J. Thomas Brenna1; 1Cornell University, Ithaca, NY; 2University of Texas Southwestern Medical Center, Dallas, TX

MP 073  Comprehensive GCxGC TOFMS Method for Simultaneous Analysis of Dioxins, PBDEs and PCBs; Anthony Adeuya; Jeffrey Archer; Arkansas Regional Laboratory, US FDA, Jefferson, AR

MP 074  Improvement of IR irradiation Performance in QqTOF MS of Protein Complex Ions by using Pulsed Gas and q0 Trapping; Ayman El-Faramawy1, 2; Yuzhu Guo2; Udo Verkerk2; Bruce Thomson3; K W Michael Siu4; 1AB SCIEX, Concord, Canada; 2CRMS, York University, Toronto, ON

MP 075  Analysis of Bisphosphonates as their Dimethylsilyl Derivatives Via GC/MS; Thomas P. Mawhinney; Deborah Chance; James Waters; University of Missouri, Columbia, MO

MP 076  Gas Chromatography/Electrospray Ionization Combined with High Resolution Mass Spectrometry (GC-ESI/HRMS) to Characterize Volatile Organic Compounds; Sy-Chyi Cheng1; Chun-Chi Chen1; Jentaie Shiea1; 1National Sun Yat-Sen Univ., Kaohsiung, TAIWAN; 2Institute of Forensic Medicine, Ministry of Justice, Taipei, Taiwan

MP 077  Mass Spectra of Derivatives of hydroxy-, mercapto- and aminobenzenecarboxylic acids; Nino Todua1; Kirill Treytyakov; Stephen Stein; Anzor Mikaiia; National Institute of Standards and Technology, Gaithersburg, MD

MP 078  Identification of Sex Pheromones from Male and Female African Brown House Snakes, Lampropolis Fuliginosus by GC/MS and GC/MS/MS; Jan Crowley1; Robert Aldridgde1; John Turk1; Anthony Wilmes1; 1Washington University, St Louis, MO; 2St Louis University, St Louis, MO

MP 079  Development of a Sensitive Method for the Measurement of Nitrosamines in Rubber Articles using GC-PCI-MS/MS; Joerg Riener; Agilent Technologies, Waldbronn, Germany

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MP 081  Accurate Mass GC/MS for the Structural Elucidation of Impurities Observed in Intermediates from the Synthesis of the y-Secretase Inhibitor BMS-708163; Michael Peddicord; John Thornton; Bristol-Myers Squibb, New Brunswick, NJ

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MP 083  Simple Equilibrium Distribution Sampling Device for Calibration of GC-MS Systems; Xiaofeng Xie1; Tai Truong1; Brian Sparano2; Anthony Rands3; Edgar Lee4; Dennis Tolley5; Milton Lee6; 1Brigham Young University, Provo, UT; 2Smiths Detection, Danbury, CT; 3Torian Technologies, American Fork, UT

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MP 086  Characterization of Post-Injection Ion Kinetic Energy and Spatial Distribution in External Source FT-ICR Mass Measurement; Joshua Savory1; Nathan Kaiser2; Brian Ruddy3; Steve Beu4; John Paul Quinn5; Chris Hendrickson6; Alan G. Marshall1; 1National High Magnetic Field Laboratory, Tallahassee, FL; 2S C Beu Consulting, Austin, TX

MP 087  Improved Trap and Trapping of Ions for FT-ICR MS; Nathan Kaiser1; Joshua Savory1; John Paul Quinn5; Steve Beu4; Chris Hendrickson6; Alan G. Marshall1; 1National High Magnetic Field Laboratory, Tallahassee, FL; 2S C Beu Consulting, Austin, TX

MP 088  MagnetoField Inhomogeneity; Measurement, Consequences, and Compensation for Improved FT-ICR Mass Measurement; Joshua Savory1; Nathan Kaiser2; Brian Ruddy3; Steve Beu4; John Paul Quinn5; Chris Hendrickson6; Alan G. Marshall1; 1National High Magnetic Field Laboratory, Tallahassee, FL; 2S C Beu Consulting, Austin, TX

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MP 090  Development of a Sensitive and Robust Accurate Mass Analysis of Small Molecules Using a Dual-Spray Thermal Gradient Focusing Electrospray Ionization (ESI) Source; Shane E. Tichy; Craig Love; Alex Mordehai; Agilent Technologies, Santa Clara, CA

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MP 114 Efficient Reactive Landing of Dendrimer Ions Compatible with Non-volatile Salts Applied to Morgantown, WV Direct FexOy Speciation in Solid State Characterization of Non-enzymatic Acylation Shigeo Ikegawa1; Mitchell; Piriya Wongkongkathep; Alessandra Jennifer Loughmiller-Newman2; Asher Newsome 2; Michael Tolocka1; Gary L. Liver Cytosolic Fraction acetylcysteine Conjugated Bile Acids by a Rat Characterization of Sulfation of Formation of H2 Takashi Iida2; Alan F. Hofmann3; Kuniko Mitamura1; Eriko Aoyama1; 1Kinki University, Higashi-Osaka, Japan; 2University of Colorado at Boulder, Boulder, CO; 3University of Frankfurt, Frankfurt, Germany

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MP 124 Validity of Liquid Chromatography-Tandem Mass Spectrometry Method for Determination of Total Nitrofuran Metabolites in Shrimp in APCI Mode; Mark Henry; Haejung An; Teresa Cain; Bichlsa Tran; John Cheng; Han C. Paek; Dennis Farley; U of Delaware, Department of Art Conservation, Newark, DE; 2Winterthur Museum, Garden & Library, Wilmington, DE; 3Bruker Daltonics, Fremont, CA

MP 125 Advanced Application of a High Resolution Quadrupole Time-of-Flight Mass Spectrometer to Resolve Chemical Noise in Regulated Bioanalysis; Jean-Nicholas Mess1; Louis-Philippe Morin1; Suma Ramagiri2; Mauro Aiello2; Johnny Cardenas2; Milton Furtado1; Fabio Garofolo1; 1Algorithmre Pharma Inc., Laval (Montreal), Quebec, Canada; 2AB SCIEX, Concord, ON

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MP 154 Quantitative Analysis of Phytoestrogens and Phytosterogens Glucosides in Urine by Trap-and-Elute HPLC-ESI-MS; Aaron Morgan; Samuel Yang; Kevin Schug; University of Texas at Arlington, Arlington, TX

MP 155 Validated LC-MS/MS Method and Pharmacokinetics Behavior of Alibendol in Human Plasma; Sookie La1; Hyun Jin Bae2; KKC; KRCT, Daejeon, South Korea

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MP 166 An Ultra Sensitive Method for the Determination of Albuterol in Human Plasma by LC/MS/MS; Brad Bessette1; Meng Min2; Denny Liu1; Cojocaru Laura1; Spencer Carter1; 1Tandem Labs - SLC, Salt Lake City, UT; 2Tandem Labs - NJ, West Trenton, NJ

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MP 172 Novel Assay with Phospholipids Column Trapping and Switching Valve System for the Determination of Carboplatin in Human Plasma by LC/MS/MS; Yifei Liu; Roger Demers; Daria Wentzel; Erika Hess; Laura Cojocaru; Tandem Labs, West Trenton, NJ

MP 173 LC/ESI-MS/MS Method for Focusing Metabolome of Bile Acid Conjugates; Masamitsu Maekawa1; Masaru Mori1; Hiroyuki Suzuki1; Takashi Iida2; Miki Shimada2; Nariyasu Mano3; 1Tohoku University Hospital, Sendai, Japan; 2Nihon University, Tokyo, Japan

MP 174 Development of a Column-Based High-Throughput Assay for Assessment of Small Molecule Binding to Alpha-1-Acid Glycoprotein Using LC/MS; Yu Tian; Genfu Chen; Baoliang Cui; John Maull; Youngjae Kim; Brian Bettencourt; Heather Blanchette; Roderic Cole; Abbott Laboratories, Worcester, MA

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MP 175 An LCMS Method to Simultaneously Measure an Investigational Compound and Urea, an Endogenous Dilution Marker, in Bronchoalveolar Lavage and Plasma; Kelly Wang; Eugene J. Eisenberg; Jaclyn Hayes; Jianhong Wang; Gerry Rhodes; Gilead Sciences, Inc., Foster City, CA

MP 176 Method Development and Validation of Letrozole in Human Plasma by LC-MS/MS; Young Rim Jung; Bio-Medieng, Seongnam-Si, South Korea

MP 177 Pharmacokinetic Characteristics of Limaprost in the Healthy Korean Volunteers by LC-MS/MS; Young Rim Jung; Ji-Young Lee; Bio-Medieng, Seongnam-Si, South Korea

MP 178 Determination of Crenolinib (CP-868,596) in Human Plasma and Serum by Liquid Chromatography Electrospray Ionization Tandem Mass Spectrometry (LC-ESI-MS/MS); Feng Bai1; Jennifer Johnson1; Mohamed Elmeliegy1;2; Abhhit Ramachandran1; Clinton Stewart1;2; 1St. Jude Children’s Research Hospital, Memphis, TN; 2University of Tennessee, Memphis, TN; 2AROG Pharmaceuticals, Dallas, TX

MP 179 Detection and Identification of Components from Extracts of Cornus Officinalis by Liquid Chromatography Hybrid Ion Trap Time-of-Flight Mass Spectrometry; Jinting Yao1; Gang Cao1; Yuki Hashi1; Shimadzu Global COE, Shanghai, China; 2Zhejiang Chinese Medical University, Hangzhou, China

MP 180 A New Method for Simultaneous Determination of Eight Adulterants in Slimming Functional Foods by HPLC-ESI-MS/MS; Yingt Shi1; Bo Gao1; Chenjun Sun1; Aimin Sun1; 1West China School of Public Health, Sichuan Univ, Chengdu, China; 2Analytical & Testing Center, Sichuan University, Chengdu, China

MP 181 A Sensitive LC/MS-MS Method for the Quantitation of Telmisartan in Human Plasma; Srividya Kailasam; Agilent Technologies (India) Pvt. Ltd., Bangalore, India

MP 182 Determination, Characterization and Stability Studies of Pigments from Bougainvillea spp; Rash Di Kochchar; Shimadzu, Mumbai, INDIA

MP 183 Is Your LC separation Specific Enough for Herb Extracts Quantification?--Accurate LC/LC-MS/MS Quantification of 4 Polyphenolic Isomers; Xiaochuan Li1; Kim B. Platli1; Uwe Christians1; 1Univer, Dortmund, Germany; 2University of Colorado HSC, Denver, CO

MP 184 Identifying Alkamides of Echinacea by FT-ICR Electrospray Ionization; Ann Perera1; 1; Ludmila Rizhsky1; Basili J. Nikolau2; 2; W. M. Keck Metabolomics Research Laboratory, Ames, IA; 1The Office of Biotechnology, Iowa State University, Ames, IA; 2Dept of Biochem Biophysics and Molecular Bio, Ames, IA

MP 185 LC-MS/MS-MRM of Organic Residues in Archaeological Ceramics to Corroborate the Presence of Wine; Hans Barnard1; 1Alek N. Dooley1; Kym. F. Faull1; UCLA, Los Angeles, CA; 1Integrated Gulf Biosystems, Cairo, Egypt

MP 186 Study of Abrine as a Chemical Marker from Plants of Indian Origin using LC-MS/MS; Shruti Raju; Shimadzu, Mumbai, India

MP 187 Immobilized Enzyme Reactor Screening of Complex Mixtures to Identify Protein-Binding Ligands Using Tandem Mass Spectrometry; Erica Forsberg; McMaster University, Hamilton, Canada

MP 188 Meet the Challenge of HPLC Carryover: A Systemic Case Study; Lan Gao; Merck, Rahway, NJ

MP 189 Reduction of HPLC Valve and Injector Carryover by Chemical Oxidation of Analyte with Sodium Hypochlorite; Barry Lutzke; Bradley L. Ackermann; Eli Lilly & Company, Indianapolis, IN

MP 190 Rapid, Simultaneous Screening of 38 Benzodiazepines and Related Compounds in Biological Fluids by LC/MS using a Core-shell C18 Column; Liming Peng; Tividar Farkas; Phenomenex Inc., Torrance, CA

MP 191 Use of Supercritically-Poised Columns for Walk-up LC-MS-Crystalline Analysis; Joachim Azzi; Kachicholu Agu; Stephen Johnston; Broad Institute, Cambridge, MA

MP 192 Evaluation of PEG-bonded Stationary Phase for Rapid Elution of Phospholipids in LC-MS/MS Bioanalysis; Donghui Bao; Michael Sofia; Pharmasset, Princeton, NJ

MP 193 Analysis of Synthetic Polymers using a pseudo 2D Chromatogram Integrated by LC-ESI-MS Data from Two Different Chromatographic Columns; Hirota Hisatomi; Yukari Nishimoto; Tomoyuki Ozawa; Hideya Kawasaki; Koichi Ute; Ryuichi Arakawa; Kansai University, Osaka, Japan; 2The Nippon Synthetic Chemical Industry Co. Ltd., Osaka, Japan; 3Nissan Chemical Industries, Ltd., Chiba, Japan; 4The University of Tokushima, Tokushima, Japan

Orthogonal Characterization of Premarin®Intravenous and its Degradation Products; Hien Nguyen; Lauren Tedmon; James Simpkins; Jane Wiggins; David Maas; Joshua Gatson; Kevin Schug; University of Texas at Arlington, Arlington, TX; 2University of North Texas Health Science Center, Fort Worth, TX; 3University of Texas at Southwestern, Dallas, TX

Development of a Rapid and Sensitive Quantitation Method for Adenosine and Guanosine by Ultra-High Performance Liquid Chromatography-Mass Spectrometry; Yung-Hsien Chen; Xiao Ding; Chialin Hsu; Flavius Martin; Brian Dean; Genentech, Inc, South San Francisco, CA

Systematic evaluation of Acetone and Acetonitrile for Use in HILIC Coupled with ESI Mass Spectrometry of Basic Small Molecules; Michael Jones1; 1; James Heaton; Norman Smith; 2Cristina, Legido-Quiroga; 1Waters Corporation, Milford, MA; 2King’s College, London, UK

Fast Quantitation of Biomarkers N-Acetylaspartate and N-Acetylaspartylglutamate in Mouse Brain Homogenates Using HILIC and Tandem Mass Spectrometry; Monica Germann; Kendall Powell; Tandem Labs, Durham, NC

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Analyzing PETN by LC-MS, DUIS Mode; Anna Marie Giambra; Geoffrey W. Brown; Los Alamos National Laboratory, Los Alamos, NM

Homolog Analysis of Aged Pentenarythritol Tetranitrate by Liquid Chromatography – Mass Spectrometry; Geoffrey W. Brown; Anna Marie Giambra; Mary M. Sandstrom; Los Alamos National Laboratory, Los Alamos, NM

A New High Throughput Microchromatography System for Protein Sample Prep; Scott Fulton; BioSystem Development, LLC, Madison, WI

Rapid Removal of Detergents using Online LC-MS for Intact Protein Characterization; Jun Liu; Shuai Zuo; Cheemartner, Lafayette, CA

Evaluation of the Effect of Varying Cellular Lysis and Biomass Quantities on Fractionation Based Proteome Measurement of Microbial Isolates; Ritin Sharma; Brian Dill; 2Nathan VerBerkmoes; Robert Hettich; 1UT/ORNL Graduate Program in Genome Sci. & Tech., Knoxville, TN; 2Oak Ridge National Laboratory, Oak Ridge, TN

A High Yield Method for the Removal of Detergents from Low Concentration Protein or Peptide Samples for MS Analysis; Babu Antharavally; Michael Rosenblatt; Krishna Mallia; John C. Rogers; Paul Haney; Thermo Fisher Scientific, Rockford, IL

Enhanced Protein Extraction for Microbial (meta)Proteomics of Defined Laboratory and Environmental Samples; Xiaolin Liu; Karuna Choure; Silke Nissen; Abigail Green; Shulei Sun; Stephanie Conn; Victoria Orphan; Frank Loeffler; Robert Hettich; 1UT – ORNL Genome Science & Technology, Knoxville, TN; 2Oak Ridge National Lab, Oak Ridge, TN; 3University of Tennessee, Knoxville, TN; 4Caltech, Pasadena, CA; 5UCSD, San Diego, CA

IPG-IEF Fractionation of Peptides Prior to LC/MS: Off-gel Separation vs. In-gel Separation Followed by Peptide Elution; Tom Berkelman; Bio-Rad Laboratories, Hercules, CA

Compatibility of Gel Electrophoresis Stains with ElectroSpray – Tandem Mass Spectrometry; Tim Wehr; Robin Baginski; Aran Paulus; Dennis Yee; Bio-Rad Laboratories, Hercules, CA

Top-Down Analysis by LC-MS/MS (ETD) of Spatially-Resolved Tissue Section Extracts for Protein Identification in MALDI Imaging Experiments; Kristie Lindsey Rose; David Anderson; Kevin L. Schey; Vanderbilt University, Nashville, TN

Nano-flow Hydrophilic Interaction Liquid Chromatography (HILIC): Implications for Automated Gel-based Proteomics; Dörte Hesse; Olaf Jahn; Proteomics Group, MPI Experimental Medicine, Goettingen, Germany

Effect of Sample and Matrix Loading on Signal Response in LC-MS Bioanalysis; Mark Woodruff; Ken Butchard; Ken Saunders; Marc Elliott; 1Forts Technologies Ltd., Cheshire, UK; 2Pfizer, Sandwich, UK; 3Resolution Systems, Inc., Holland, MI

Use of Ammonium Formate to Modify Reversed-Phase LC-MS Analyses of Peptides and Tryptic Digests; Barry Boyes; Darryl...
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Johnson2; Stephanie Schuster1; Jack Kirkland1; Ron Orlando2; 1Advanced Materials Technology Inc., Wilmington, DE; 2Complex Carbohydrate Research Center, UGA, Athens, GA

MP 221 Improving Nanobore Column Duty Cycle via Trap-Column Injection: Evaluating the Effect of Trap-Column Injection Flow Rate on Analytical Separation; Carla Marshall-Waggett1; Helena Svobodova; Gary Valaskovic; Amanda Berg; New Objective, Inc., Woburn, MA

MP 222 Evaluation of 150 μm ID Packed Tip Columns for Quantitative Peptide Analysis by LC-MS/MS; Stanley Durand; Helena Svobodova; Amanda Berg; Gary Valaskovic; New Objective, Inc., Woburn, MA

MP 223 LC-MS Analysis of Biomolecules Applying ZIC-HILIC and RP Monolithic Silica Capillaries; Stephan Altmayer1; Jessica Wohlgemuth2; Wen Jiang3; Sven Andrecht4; 1Merck KGaA, Darmstadt, Germany; 2Merck Sequant AB, Umea, Sweden; 3Abbott GmbH & Co. KG, Ludwigshafen, DE

MP 224 Optimizing Particle Size and Column Length, What is the Best Way to Utilize Nano UHPLC in Proteomics?; Evert-Jan Sneekes; Karsten Dekker; Bjorn de Haan; Remco Swart; DIONEX Corporation, Amsterdam, Netherlands

MP 225 Applying Online Nano-UHPLC to Proteomics; Lasse G Falkenby1; Ole Hoerning1; Christian Ravnborg1; Jakob Bunkenborg1; Jens S Andersen1; 1CEBL, University of Southern Denmark, Odense, Denmark; 2Thermo Fisher Scientific, Odense C, Denmark

MP 226 Coupling High Speed Separations with LC-MS/MS for Protein Identification; Darryl Johnson1; Barry Boyes2; Taylor Fields3; Rachel Kopkin4; Ron Orlando5; 1University of Georgia, Athens, GA; 2Advanced Materials Technology Inc., Wilmington, DE

MP 227 Two-dimensional Predictive Chromatography using Orthogonal Stationary Phases for Improved MS/MS-based Peptide Identification; Eugene Moskovets1; Anton Goloborodko2; Mikhail V. Gorskikh3; 1MassTech Inc, Columbia, MD; 2INEPCEP, Moscow, Russian Federation

MP 228 A Database-derived Approach for Peptide Retention Prediction in Reversed-phase HPLC: N-terminal Amino Acid Addition/Deletion; Janice Reimer; Marine Grigoryan; Vic Spencer; Oleg V. Krokhin; University of Manitoba, Winnipeg, Canada

MP 229 Total Retention Liquid Chromatography for Maximum Protein Sequence Coverage by Mass Spectrometry; Mark E. Jennings II; Jolanta Krudzys-Amblo; Kenneth G. Mann; Saulius Butenas; Dwight E. Matthews; University of Vermont, Burlington, VT

MP 230 Differential Coverage of the Digestion-Resistant Peptidome Explored through Comparisons of Pentfluorophenylpropyl and C18 Stationary Phases using LC/TOF MS; Siobhan Shay; A. Daniel Jones; Michigan State University, East Lansing, MI

MP 231 Increased Protein Identifications Using an Improved Microfluidic Chip; Hongfeng Yin1; Jose-Angel Mora2; Christine Miller3; Jose Meza4; Nortan Kitagawa5; Lukas Trojer6; Wilfred Tang7; Kirill Gromadski2; Kevin Killeen2; Patrick D. Perkins8; 1Agilent Technologies, Santa Clara, CA; 2Agilent Labs, Santa Clara, CA; 3Agilent Technologies GmbH, Waldbronn, Germany

MP 232 Long microcapillary Columns at Elevated Temperatures and Pressures for Proteomic and Metabolomic Applications; Edward Franklin1; Brenna Richardson1; 1J. Will Thompson1; M. Arthur Moseley2; James Jorgenson3; 1University of North Carolina at Chapel Hill, Chapel Hill, NC; 2Duke University, Durham, NC

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MP 233 Detection of TAG-Estolides from Plant and Fungal Oils with Matrix-Assisted Laser Desorption Ionization Time-Of-Flight Mass Spectrometry (MALDI-TOF-MS); Haixia Zhang; Doug J. Olson; Mark A. Smith; Randy W. Purves; NRC-PBL, Saskatoon, SK Canada

MP 234 Characterizing Lipid A and its Modifications by 193 nm UVVP; James Madsen; Thomas Cullen; Jessica Hankins; M. Stephen Trent; Jennifer Brodbelt; University of Texas Austin, Austin, TX

MP 235 Structure Characterization of Glyosphingolipids in Human Milk by LTQ Orbitrap MS; Ying Zhou1; David S. Newburg2; Joseph Zaia3; Catherine E. Costello4; 1Boston University School of Medicine, Boston, MA; 2Boston College, Boston, MA

MP 236 Identification of Phospholipids in Mouse Brain by using MALDI TOF-TOF; Young Seung Park1; Kwang Pyo Kim2; Young Hwan Kim1; 1Korea Basic Science Institute, Cheongwon-gun, South Korea; 2Konkuk University, Seoul, South Korea; 3GRAST in Chungnam National University, Deajeon, South Korea

MP 237 Structure Determination of Complex Plant Glycosphingolipids by Tandem Mass Spectrometry; Jean-Marie Schmitter; Corinne Buré; Jean-Luc Cacas; Fen Wang; Sébastien Mongrand; University of Bordeaux, Bordeaux, France

MP 238 Collisionally Induced Decomposition of Hydroperoxy Cholesteryl Ester Ammonium Adducts; Patrick Hutchins; Robert C. Murphy; Univ of Colorado Den, Aurora, CO

MP 239 Characterization and Identification of Long-Chain and Short-Chain Phospholipid Oxidation Products by MALDI-MS; Whitney L. Stutts1; Kerolyn S. Valente2; Timothy J. Garrett3; Paolo Di Mascio4; Richard A. Yost5; 1Department of Chemistry, University of Florida, Gainesville, FL; 2Department of Biochemistry,University of São Paulo, São Paulo, Brazil; 3College of Medicine, University of Florida, Gainesville, FL

MP 240 Structural Analysis of Complex Lipids using MALDI-TOF-TOF Tandem MS with High Precursor-ion Selectivity; Ayumi Kubo1; Yoshiyuki Itoh2; Masaaki Ubuukata3; Masahiro Hashimoto4; Jun Tamura5; Juyn Onodera6; Robert A. Dipasquale7; 1JEOL Ltd., Tokyo, Japan; 2JEOL USA Inc., Boston, MA

MP 241 Biosynthesis of cysteinyl-containing 14,15-hepoxilins through the 15-lipoxygenase-1 Pathway in Human Cells; Åsa Brunström1; Mats Hamberg9; William J. Griffiths10; Hans-Erik Claesson11; 1Department of Medicine, Karolinska
Evidenced by Deuterium Labeling Steroids in Negative Ion Electrospray MS as Regiospecific Decompositions of Bifunctional Mannosylerythritol Lipid (MEL) Czech Republic of Organic Chemistry and Biochemistry, Prague, Jennifer T. Saville1; Zhenjun Zhao2, 3; Mark D.P. Stephen J Blanksby3; Acoustic Wave Nebulization (SAWN) Structural Analysis of Lipid A using Surface Hwan Yoon Cole

Radical Directed Dissociation for Lipid Structural Identification; Huang Phong Thu1; Tony Ly2; Adam J Trevitt1; Todd W Mitchell3; Stephen J Blanksby3; 1School of Chemistry, University of Wollongong, Wollongong, Australia; 2Welcome Trust Centre for Gene Regulation and Expr, Dundee, UK; 3University of Wollongong, Wollongong, Australia

Development of Workflows Towards Combining Online LC, OzID and CID for Structural Elucidation of Phospholipid Isomers; Rachel Kozlowski2; Todd W Mitchell3; Stephen J Blanksby3; University of Wollongong, Wollongong, Australia

Localization of Double Bonds in Fatty Acids Utilizing Acetonitrile-Related Adducts Generated in the APCI Source; Vladimir Vrksoslav; Michal Hoskovec; Josef Vacvak; Institute of Organic Chemistry and Biochemistry, Prague, Czech Republic

Regioselective Anion Attachment and Regiospecific Decompositions of Bifunctional Sialic Acid via Negative Ion Electrospray MS as Evidenced by Deuterium Labeling; Richard B. Cole; Nalaka S. Rannulu; University of New Orleans, New Orleans, LA

Identification of Lysoglycerophosphocholine in Caenorhabditis elegans using Reversed Phase Liquid Chromatography – Quadrupole Orthogonal Time-of-Flight Mass Spectrometry; Hyejung Park; Catherine E. Costello; Boston University School of Medicine, Boston, MA

Towards Complete Structural Identification and Quantification of (O-acyl)-ω-hydroxy Fatty Acids in Human Tears, Meibum and Contact Lens Deposits; Simon H.J. Brown1; Jennifer T. Saville2; Zhenjun Zhao2, 3; Mark D.P. Wilcox2, 3; Stephen J. Blanksby2; Todd W. Mitchell3; 1School of Chemistry, University of Wollongong, Wollongong, Australia; 2Brian Holden Vision Institute, Sydney, Australia; 3School of Optometry and Vision Science, UNSW, Sydney, Australia; 4School of Health Science, University of Wollongong, Wollongong, Australia

Cross Correlation Score Aids Objective Lipid A Structure Assignment; Ying Sonia Ting1; Roberto M. Barkley1; Miguel Gijon1; Joseph A. Hankin1; Peter M. Henson2; Robert C. Murphy1; 1University of Colorado Denver, Aurora, CO; 2National Jewish Health, Denver, CO

Sample Preparation for Lipidomics: SPE-based Selective Lipids Extraction; Pradeep Narayanawamy1; Edison1; Federico Torta1; Evelyn Goh1; Stephen Wong2; Mark Ritchie2; 1National University of Singapore, Singapore, Singapore; 2Columbia University, New York, NY

Multidimensional Lipid Analysis using Novel Workflows based on High Resolution Mass Spectrometry or High Peak Capacity Separation Techniques; Markus Himmelsbach; Emmanuel Varesio; Gerard Hopfgartner; University of Geneva, LSMS, Geneva, Switzerland

Shotgun Analysis of Phospholipids in Milk Samples by Hydrophilic Interaction Chromatography/Tandem Mass Spectrometry; Marcus Mreyen; -, Duisburg, Germany

Very Long-Chain Polynsaturated Fatty Acids (VLC-PUFAs) Analysis by Liquid Chromatography-Mass Spectrometry; Paolo Lecchi; Vinod Tarwade; Marcus Obeng; Bindi Dangi; Norman Salem, Jr; Krishna Raman; Martek Biosciences, Columbia, MD

Egg Yolk Phospholipid and Oil Triglyceride Degradation Studies using LC Coupled with UV-MS Detection. Impact on Lipid Emulsion Formulation; Louis-Philippe Labranche; Anne Danion; Yves G. Leblanc; Alain Carrier; Sandoz, Boucherville, Canada

MALDI Imaging Mass Spectrometry of Phospholipids in the Mouse Lung; Karm A. Zemski-Berry1; Bilan Li2; Susan D. Reynolds2; Robert M. Barkley1; Miguel Gijon1; Joseph A. Hankin1; Peter M. Henson2; Robert C. Murphy1; 1University of Colorado Denver, Aurora, CO; 2National Jewish Health, Denver, CO

A Sensitive Method for the Spatial Quantification of PI(4)P and PI(4,5)P2 in Eukaryotic Cells; Federico Torta1; Robin B Chan2; Lukas B Tanner1; Markus R Wenk1; Michael P Sheetz1, 2; 1National University of Singapore, Singapore, Singapore; 2Columbia University, New York, NY

Sample Preparation for Lipidomics: SPE-based Selective Lipids Extraction; Pradeep Narayanawamy1; Edison1; Federico Torta1; Evelyn Goh1; Stephen Wong2; Mark Ritchie2; 1National University of Singapore, Singapore, Singapore; 2Columbia University, New York, NY

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Very Long-Chain Polynsaturated Fatty Acids (VLC-PUFAs) Analysis by Liquid Chromatography-Mass Spectrometry; Paolo Lecchi; Vinod Tarwade; Marcus Obeng; Bindi Dangi; Norman Salem, Jr; Krishna Raman; Martek Biosciences, Columbia, MD
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MP 274 Determining the Excretion Balance and Metabolic Fate of Human Milk Oligosaccharides; Stephanie Gaerlan1; M. Lorna De Leoz1; Lauren Dimasposoc1; Mark Underwood2; Rudolf Grimm2; David Mills3; Bryan Braun4; Carlito Lebrilla5; 1University of California, Davis, CA; 2Agilent Technologies, Santa Clara, CA

MP 275 Rapid Determination of Human Milk Oligosaccharide Variation Between Lewis Blood Type and Seasonal Changes; Sarah M. Gutierrez1; Shuai Wu1; Nannan Tao2; Angela Zivkovic3; Andrew M. Prentice3; J. Bruce German4; Carlito Lebrilla5; 1University of California Davis, Davis, CA; 2London School of Hygiene & Tropical Medicine, London, UK

MP 276 Assessing Gut Health of Infants by Quantitative Analysis of Fecal Oligosaccharide Signatures; M. Lorna De Leoz1; Karen Kalanetra2; Stephanie Gaerlan3; John Strum2; Mark Underwood2; Rudolf Grimm2; David Mills3; Bryan Braun4; Carlito Lebrilla5; 1University of California, Davis, CA; 2Agilent Technologies, Santa Clara, CA

MP 277 Rapid Structure Identification of Milk Oligosaccharides in Primates; Shuai Wu1; Nannan Tao2; Jaehan Kim2; Hyun Joo An3; Katie Hinde4; Michael Power5; Pascal Gagneux6; Rudolf Grimm6; 2Department of Chemistry, UC Davis, Davis, CA; 3Department of Viticulture and Enology, UC Davis, Davis, CA; 4Smithsonian National Zoological Park, Washington DC, DC; 5Department of Cellular Molecular Medicine, UCSD, La Jolla, CA; 6Agilent Technologies, Santa Clara, CA; 7Department of Food Science Technology, UC Davis, Davis, CA

MP 278 High Sensitivity Glycomic Analysis of Core 2 O-glycan-Deficient Mice; Mohd Nazri Ismail1; 1Genome Institute of Singapore, Singapore; 2Bristol-Myers Squibb, Princeton, NJ; 3University College, Antwerp, Belgium; 4University of Antwerp, Antwerp, Belgium

MP 279 Structure Characterization of a Novel Heparan Sulfate-Derived Saccharide Found in the Murine Model of Mucopolysaccharidosis Type I; Wei Wei1; Milady R. Ninonuevo2; Rebecca J. Holley2; Audrey Deligny3; H. Angharad O’Leary4; Brian W. Bigger2; Lena Kjellén3; Sarah Trimpin1; Robert M. Barkley1; Miguel Gijon1; Joseph A. Wager-Miller2; Ken Mackie2; Sarah Trimpin1; 1School of Chemistry, University of Bristol, Bristol, UK; 2Department of Biochemistry, University of Wollongong, Wollongong, NSW, Australia; 3Biocrates Life Sciences AG, Innsbruck, Austria; 4Department of Chemistry, Indiana University, Bloomington, IN

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**MP 280** Comparative Glycomics of Human and Bovine Milk Glycosaminoglycans; **Yang Mag**1; David Newburg1; Catherine E. Costello1; Joseph Zaia1; 1Boston University School of Medicine, Boston, MA; 2Boston College, Chestnut Hill, MA

**MP 281** LC-MS and LC-MS/MS Study of Heparan Sulfate Oligosaccharides Processed by Human Sulf-2; **Yu Huang**; Xiaofeng Shi; Joseph Zaia; Boston University School of Medicine, Boston, MA

**MP 282** Structural Analysis of Francisella tularensis Cell Surface Carbohydrates using High Resolution and Accuracy Mass Spectrometry; **Qi Wang**; Xiaofeng Shi; Nancy Leymarie; Guillermo Madico; Jacqueline Sharon; Catherine E. Costello; Joseph Zaia; Boston University School of Medicine, Boston, MA

**MP 283** Characterization of BRP 3 Erythropoietin N-Glycosylation Reveals Large Poly-N-acetyl Lactosamine Extensions; **Jonathan Bones**1; 2; Stefan Mittermayr1; Naobh O'Donoghue1; Mark Hilliard2; Kieran Wynne2; Pauline M. Rudd2; Barry L. Karger1; 1Northeastern University, Boston, MA; 2NIBRT Dublin-Oxford Glycobiology Laboratory, Dublin, Ireland; 3UCD Conway Institute Proteome Research Centre, Dublin, Ireland

**MP 284** A Novel Method for Relative Quantitation of N-glycans by Isotopic Labeling using H218O; **Shiguang Tao**; Ron Orlando; University of Georgia, Athens, GA

**MP 285** The Development of Stable Isotope-Labeled Hydrazide Reagents for the Relative Quantification of N-linked Glycans in Spontaneous Ovarian Adenocarcinoma Model; **Hunter Walker**; Januka Budhathoki-Uprety; Bruce Novak; David C. Muddiman; North Carolina State University, Raleigh, NC

**MP 286** LC-ESI-MS and LC-MALDI MS of Permethylated Glycans derived from Esophageal Adenocarcinoma Human Blood Serum Samples; **Yunli Hu**; Janie DeSantos-Garcia; Yehia Mchref; Texas Tech University, Lubbock, TX

**MP 288** Graphitised Carbon LC-MS/MS Identification of Cancer Specific Glycosylation of uPAR and Integrin β6 from Colorectal Cancer Cells; **Ruby Estrella**1; Alison Kan1; David Cantor1; Iveta Slapetova1; Leon McQuade1; Mark Baker1; 1Macquarie University, Sydney, Australia; 2Australian Proteome Analysis Facility (APAF), Sydney, Australia

**MP 289** Characterization of the N-linked Glycome from Ascites as an Early Indicator for Ovarian Cancer; **Francis Murphy**; Michael A. Finan; Rodney P. Rocconi; Lewis K. Pannell; University of South AL, Mitchell Cancer Institute, Mobile, AL

**MP 290** Negative ion MALDI CID and Ion Mobility Separations of N-glycans: Application to gp120 from the Human Immunodeficiency Virus; **David J. Harvey**1; 2; Charlotte A. Scarff1; Christopher N. Scanlan1; Max Crispin1; Camille Bonomelli1; Frank Sobott1; James H. Scrivens1; 1Department of Biochemistry, University of Oxford, Oxford, UK; 2School of Life Sciences, University of Warwick, Coventry, UK; 3Center for Proteomics, University of Antwerp, Antwerp, Belgium

**MP 291** Glycosylation Profile of Therapeutically Active Glycoproteins: Identification of Glycans in Recombinant Factor IX using Directed MALDI-QIT-TOF-MSn and a Glycan Database; **Matthew Oppenshaw**1; Daniel Spencer2; Louise Royle1; Katharina Pock2; Omar Belgacem2; 1Shimadzu, Manchester, UK; 2Ludger Ltd, Oxford, UK; 3Octapharma Pharmazeutika Produktions GesmbH, Vienna, Austria

**MP 292** Effect of Yeast on Floral Attractiveness - LC-MS/MS Quantitation of Sugars and Amino Acids in Floral Nectar; **Karolina M. Krasinska**; Kabir G. Pey1; Yuen L. Tam2; Tadashi Fukami2; Alis S. Chien1; 1SUMS, Stanford University, Stanford, CA; 2Department of Biology, Stanford University, Stanford, CA

**MP 293** Identifying Enzyme Resistant Xylo-oligomers from Processing Switchgrass to Bioethanol; **Michael Bowman**; Bruce Dien; Ronald Hector1; Gautam Sarathi2; Michael Cotta1; 1USDA, Agricultural Research Service, NCAUR, Peoria, IL; 2USDA, Agricultural Research Service, Lincoln, NE

**MP 294** A Comparison of HPLC and UPLC for the LC-MS/MS Analysis of Transfer Ribonucleic Acids (tRNAs); **Collin Wetzel**; Patrick A. Limbach; University of Cincinnati, Cincinnati, OH

**MP 295** Maldi-TOF and Maldi-TOF/TOF Mass Spectrometry as a Method to Test RNA as Substrates of RNA Modifying Enzymes; **Vincent Guérineau**1; Amandine Guelorget2; Djemel Kabir G. Peay2; Yuen L. Tam1; Tadashi Fukami2; Alis S. Chien1; 1SUMS, Stanford University, Stanford, CA; 2Department of Biology, Stanford University, Stanford, CA

**MP 296** Development of Tissue Specific Isolation and Analysis Methods for Oligonucleotide Therapeutics and their Metabolites by LC/MS; **Michael McInerney**1; Mark Hail1; Greg Scott1; 1Phenomenex, Torrance, CA; 2Novartia, Monmouth Junction, NJ

**MP 297** Comparison of Methods for Purifying and Desalting Polymerase Chain Reaction Products Prior to Electrospray Ionization Mass Spectrometry; **Helene Manduzio1; Armelle Martelet1; Eric Ezan1; Swaroop Samant2; France; 2LEBS CNRS, Gif sur Yvette, France

**MP 298** Femtomole Sensitivity RNA Analysis Based on Ion-pairing Reverse Phase nanoLC with Microfluidic Device; **Zoltan Timar**1; Travis Betz2; James A. Appel1; Hongfeng Yin1; 1Agilent Laboratories in Boulder, Boulder, CO; 2Agilent Nucleic Acid Solutions Division, Boulder, CO

**MP 299** Screening Platform Consisting of Mass Calculator and UPLC-MS Method for Fast Characterization of Related Substances of Synthetic Oligonucleotide Drugs; **William Van Dongen**; Proxy Laboratories, Leiden, Netherlands
MP 322
Quantitative Strategies in Targeted Metabolomics; Mine G. Palazoglu; Sangeeta Kumari; Wan Ling Tan; Mimi Swe; Oliver Fiehn; UC Davis, Davis, CA

MP 323
Quantitative Metabolomics: The Quantitative Measurement of Redox Coupled Metabolites using Reverse Phase Ion-pairing LC-MS; James Cox; Joel Pieper; Alex Coffman; University of Utah, Salt Lake City, UT

MP 324
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MP 442 Top-Down Precursor Acquisition Independent From Ion Count (PACIFIC); Elizabeth Nguyen; Dave Goodlett; Sonia Ying; Jimmy Eng; Patrick Langridge-Smith; Logan Mackay; 1University of Washington, Seattle, WA; 2SIRCAMS, School of Chemistry, Edinburgh University, Edinburgh, Scotland

MP 443 Influence of Search Parameters and Mass Spectrometry Data Quality on Search Engine Performance in Shotgun Proteomics: A Systematic Study; Lev I. Levitsky; Anton A. Goloborodko; Mikhail V. Gorshkov; Institute for Energy Problems of Chemical Physics, Moscow, Russian Federation

MP 444 Partially Hydrolyzed Organisms, Decoy Searches and False Discovery Rates; Bjorn Victor; Sarah Gabriël; Kirezi Kanobana; Katja Polman; Pierre Dorny; André Deelder; Magnus Palmblad; 1Leiden University Medical Center, Leiden, Netherlands; 2Institute of Tropical Medicine, Antwerp, Belgium

MP 445 Peptide Search Algorithm by Selecting and Rescoring Reliable Peaks for MS (n>1) Spectra; Kentaro Morimoto; Masaki Murase; Tsuyoshi Tabata; Shigeki Kajihara; Yoshiya Oda; Koichi Tanaka; Shimadzu corporation, Kyoto, Japan; Eisai Product Creation Systems, Tsukuba, Japan

MP 446 Chromatographic Elution Time Based Clustering for Data-Independent Mass Spectrometry; HuiSon Pak; Carla Pasquarello; Alexander Scherfl; Markus Mueller; 1University of Geneva, Geneva, Switzerland; 2Swiss Institute of bioinformatics, Geneva, Switzerland

MP 447 Unbiased False Discovery Rate Estimation After Peptide- and Protein-level Integration of Shotgun Proteomics Search Results; Yong J. Kii; PeiZhi Shi; Marshall W. Bern; 1Palo Alto Research Center, Palo Alto, CA; 2Applied Mathematics, University of Washington, Seattle, WA

MP 448 An Examination of the Impact of Database Sequence Similarity on Differences in Protein Grouping Across Software Packages; Thomas McGowag; Pratik Jagtap; Sean L. Seymour; Leann Higgins; Sriharan Bandhakavi; Tim Griffin; 1University of Minnesota, St. Paul, MN; 2Minnesota Supercomputing Institute, UMN, Minneapolis, MN; 3AB SCIEX, Foster City, CA; 4Bio-Rad Laboratories, Hercules, CA

MP 449 Mining Millions of Assigned Peptides in Order to Identify Characteristics of Incomplete Protein Sequence Coverage; Dylan Storey; Brian Erickson; Rachel Adams; Sally Ellingson; Rick Weber; Harry Richards; Robert Hettick; 1SCALE-IT, University of Tennessee, Knoxville, TN; 2Oak Ridge National Laboratory, Oak Ridge, TN

MP 450 Spec2spec – A Spectrum-to-Spectrum Search Engine Using Protein-wide Spectral Libraries; Chia-Yu Yen; Stephane Houel; Natalie Ahn; William Old; 1University of Colorado at Boulder, Boulder, CO; 2Howard Hughes Medical Institut, Boulder, CO

MP 451 Improving Confidence in Peptide Identification by CID and ETD through Combined Use of Trypsin and Carboxypeptidase B; Ross Chawner; David Wedge; Simon J. Gaskell; Claire Eyers;
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MP 452 Improvement of Peptide-Spectrum Match Validation Techniques Using an Enriched XCorr-based Feature Set; Marina Spivak; Jason Weston; William Stafford Noble; "University of Washington, Seattle, WA; Google Research, New York, NY

MP 453 Breaking the 2000 Proteins Barrier in a Standard LC Run using a New Benchtop Orbitrap Instrument and Multiple Search Engines; Carmen Paschke; Yue Xuan; Eugen Damoc; Torsten Ueckert; Ute Comberg; Hans Grensemann; Markus Kellmann; Bernard Delagrange; Thermo Fisher Scientific, Bremen, Germany

MP 454 Improved Middle-Down Proteomics with High Mass Accuracy Tandem Mass Spectrometry and Mass Accuracy Sensitive Database Search; Jia You1; Michael A. Freitas2; Hua Xu2; 1Ohio State University, Columbus, OH; 2Case Western Reserve University, Cleveland, OH

MP 455 ROCCIT: A Next Generation MS/MS Protein Database Search Engine; Michael J Sweredoski; Geoffrey T Smith; Anastasia Kalli; Robert Lj Graham; Sonja Hess; Caltech, Pasadena, CA

MP 456 Blocked Pattern Matching Problem and its Applications in Computational Proteomics; Julio Ng; Pavel Pevzner; UCSD, La Jolla, CA

MP 457 PeaksDB: New Software for Substantially Improved Peptide Identification from Orbitrap ETD Mass Spectrometry; Jing Zhang1; Baozhen Shan2; Lei Xin1; Bin Ma2; 1Bioinformatics Solutions Inc., Waterloo, Canada; 2University of Waterloo, Waterloo, Canada

MP 458 Enabling the Generation of Long and Accurate Gapped Peptides; Kwokwon Jeong; Pavel Pevzner; UCSD, La Jolla, CA

MP 459 gMacro: GPU-CPU Computing for High Throughput Peptide Spectral Matching; Brendan Faherty; Jeffrey Milloy; Scott A. Gerber; Dartmouth Medical School, Lebanon, NH

MP 460 Dispelling the Protein Inference Nightmare for Identification and Quantification: Marc Vaude1; René P Zahedi2; Albert Sickmann2; Julia M Burkhart1; Lennart Martens2; 1ISAS, Dortmund, Germany; 2University of Gent, Gent, Belgium

MP 461 Constrained De Novo Sequencing of Peptides with Application to Conotoxins; Swapnil Bhata1; Yong Kil1; Beatrix Ueberheide1; Brian Chait1; Lemmlou Tiao2; 1Purdue University, West Lafayette, IN; 2Birck Nanotechnology Institute, Purdue University, West Lafayette, IN

MP 462 De Novo Sequencing vs. Database Search; Jing Zhang1; Bin Ma2; 1Bioinformatics Solutions Inc., Waterloo, Canada; 2University of Waterloo, Waterloo, Canada

MP 463 Large Improvements in MS/MS Based Peptide Identification Rates using a Hybrid Analysis: William Cannon1; Mitchell Rawlins1; Douglas Baxter2; Ananth Kalyanaraman2; Mary Lipton1; Stephen J. Callister1; Donald Bryant3; 1Pacific NW National Lab, Richland, WA; 2Washington State University, Pullman, WA; 3Pennsylvania State University, University Park, PA

MP 464 RAID_aPS: MS/MS Analysis with Multiple Scoring Functions and Spectrum-Specific Statistics; Gelio Alves; Aleksey Y Ogurtsov; Yi-Kuo Yu; National Center for Biotechnology Information, NLM, Bethesda, MD

MP 465 New Effects of Mass Defect from Complete Mapping of all Theoretically Possible Peptide Masses and from Post-Translational Modifications; Indranil Mitra1; 2; 1Dept of Biochemistry and Molecular Biology, UTMB, Galveston, TX; 2Sealy Center for Molecular Medicine, UTMB, Galveston, TX

MP 466 "Identify Me", Says the Alien Peptide! Combining Publicly Available Mass Spectrometry Repositories and Clustering Tools is How!; Gerben Menschaert; Eiseuke Hayakawa; Geert Baggerman; K.U.Leuven, Leuven, Belgium

MP 467 Exposing the Target-decoy Approach for Peptide Identifications: Lessons from Examples; Sanatae Kim; Nuno Bandeira; University of California, San Diego, La Jolla, CA

MP 468 Quality of Database Matches for MS/MS Spectra Can Be Computed Analytically; Andrey Genn; Robert M. Day; Nikita D. Arnold; Tamah Fridman; Oak Ridge National Laboratory, Oak Ridge, TN

MP 469 BPDA2D – An Improved Bayesian Peptide Detection Algorithm for Mass Spectrometry; Youting Sun1; Jianqu Zhang2; Ulisses Braga-Neto3; Edward R. Dougherty4; 1Texas A&M University, College Station, TX; 2University of Texas at San Antonio, San Antonio, TX

MP 470 PILOT_PROTEIN: A Novel Approach for Modified Protein Identification via High Resolution Tandem Mass Spectrometry and Integer Linear Optimization; Richard C. Ballaban; Peter A. Dimaggio; Mariana D. Plaza-Mayorca; Benjamin Garcia; Christodoulo A. Fioudas; Princeton University, Princeton, NJ

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MP 471 Mass Spectral Imaging of Neurotransmitters and Neuropeptides in the Central Nervous System of Lobster Homarus americanus at Multiple Developmental Stages; Xiaoyue Jiang; Hui Ye; Lingjun Li; School of Pharmacy, University of Wisconsin-Madison, Madison, WI

MP 472 Monolithic Based Immobilized-pH Gradient Capillary Isoelectric Focusing and Monolithic Liquid Chromatography for Neuropeptide Analysis; Zichuan Zhang; Junhua Wang; Aaron Cook; Hui Ye; Michael P. Nusbaum1; Lingjun Li1; 1Univ. of Wisconsin-Madison, Madison, WI; 2University of Pennsylvania, Philadelphia, PA

MP 473 Discovery and Functional Study of a Novel Tachykinin from Callinectes sapidus via a Multi-faceted MS Approach; Limei Hui1; Yuzhuo Zhang1; Junhua Wang1; Aaron Cook1; Hui Ye1; Michael P. Nusbaum1; Lingjun Li1; 1Univ. of Wisconsin-Madison, Madison, WI; 2University of Pennsylvania, Philadelphia, PA

MP 474 Dimethylated Leucine Isobaric Tags for Relative Quantitation of Crustacean Neuropeptides at Multiple Feeding States;
Medical Research China Medical University, Taichung, Taiwan

MP 493 Extensive Phosphoproteomic Comparison Between Orbitrap HCD and Ion-trap CID Fragmentation Types Renders over 20,000 Murine Brain Sites; Mark Jedrychowski1; Wilhelm Haas; Edward Hutlin; Mathew Sowa; John Rush; Steven Gygi; 1Harvard Medical School, Boston, MA; 2Cell Signaling Technology, Danvers, MA

MP 494 Pinpointing Phosphorylation: Quantitative Filtering and a Novel Site-specific X-ion Fragment; Christian Kelstrup; Omid Hekmat; Chiara Francavilla; Jesper V. Olsen; CPR, University of Copenhagen, Copenhagen N, Denmark

MP 495 Improving the Confidence in Phosphorylation Site Assignment using a Maximum Confidence Approach (MCA); René Zahedi; Florian Beck; Marc Vaudel; Albert Sickmann; ISAS, Dortmund, Germany

MP 496 A High Throughput Quantitative Peptidomic Approach for the Discovery of Plant Signaling Peptide; Yun-Wei Ku1; 2; Ying-Lan Chen1; 2; Chih-Yu Lin1; Han-Jia Lin1; Yet-Ran Chen1; 2, 1ABRC, Academia Sinica, Taipei, Taiwan; 2Institute of Bioscience and Biotechnology, NTOU, Keelung, Taiwan; 3Institute of Plant Biology, NTU, Taipei, Taiwan

MP 497 Does External Microbes Affect the Synthesis of Amphibian Defense Peptides?; Vladimir Gorskhov; Galina El-Registan; Tatiana Samgina; Yegor Vorontsov; Roman Zubarev; Sergey Ogorustsov; Elena Demkina; Albert T. Lebedev; 1Moscow State University, Moscow, Russian Federation; 2Karolinska Institute, Stockholm, Sweden; 3Microbiology institute RAN, Moscow, RU

MP 498 Characterization of Peptidic Natural Products (PNPs); Wei-Ting Liu; Hosein Mohimani; Pavel Bilgin; Amin Behrang; Steve Rapp; M. DeVol; K. Scholz; J. Liu; RCSI, Smurfit Science and Technology Park, Dublin, Ireland

MP 499 Using LC-ESI-MS-MRM Methods to Identify D-Amino Acids in Endogenous Neuropeptides; Lu Bai; Jonathan Sweeney; University of Illinois at Urbana-Champaign, Urbana, IL

MP 500 Natural Product Peptidogenomics (NPP): A Mass Spectrometry-Guided Genome Mining Approach for Peptidic Natural Product Discovery; Roland D. Kersten1; Michael A. Fischbach; Bradley S. Moore; Pieter C. Dorrestein; 1SIO-UCSD, La Jolla, CA; 2UCSF, San Francisco, CA; 3SSPPS-USCD, La Jolla, CA

MP 501 The Quest for Small Non-tryptic Peptides: Food Bioactives; Alexandre Panchaud; Michael Affolter; Sophie Lagache; Irma Silva Zolelli; Martin Kussmann; Nestlé Research Center, Lausanne, Switzerland

MP 502 Native Peptides from Plasma: Top-Down Identifications using ETD and HCD Mass Spectrometry; Hans-Dieter Zucht; Stephan Jung; Sasa Koncarevic; Karsten Kuhn; Marco Schärfer; Petra Budde; Proteome Sciences R&D GmbH & Co. KG, Frankfurt, Germany

MP 503 Simple and Generic Approach for the Absolute Quantification of Large and Undigested Peptides in Plasma using a Particular LC-MS/MS set-up; Bilgen Vatansever1; Hamid Reza Sobhi1; Arno Wortmann1; Eric Grouzmann2; Bertrand Rochat1; 1QMSF - CHUV, Lausanne, Switzerland; 2Clinical Pharmacology - CHUV, Lausanne, Switzerland

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Comparison of CE-MS and LC-MS Peptide Profiling Method for Clinical Application; Min-Jung Kang; Chang No Yoon; Young Sook Yoo; KIST, Seoul, South Korea

MP 505 Heat Stabilization Enhances Detection of Hormones in the Mouse Thymus; Henrik Alm; Olof Sköld; Mats Borén; Birger Scholz; Marcus Söderquist; Karl Sköld; Kim Kultima; 1Denator, Göteborg, Sweden; 2Uppsala University, Uppsala, Sweden

MP 506 Top-Down Label-Free LC-MALDI Analysis of the Peptidome during Neural Progenitor Cell Differentiation Identifies Progenitor Cell Markers; Daniel Maltman; Sven Brand; Eckhard Belau; Peter Brechlin; Detlev Suckau; Paaper Rainer; Stefan Przyborski; 1Durham University, Durham, UK; 2Bruker Daltonik GmbH, Bremen, Germany

MP 507 Oxytontmodulin-analog Intact Peptide Quantitation from Rat Brain Tissue by LC/MS/MS Analysis; Evaluating and Optimizing Tissue Sample Preparation Techniques; Katherine Wright; Mengmeng Wang; Lei Sun; Jennifer Spencer-Pierce; Dawn Dufield; Pfizer, Andover, MA

Comparison of Neuropeptides Stability using Different Preparation Protocols for Mass Spectrometry-based Targeted Peptidomic Analysis; Floriane Pailleux; Francis Beaudry; Université de Montréal, St-Hyacinthe, Canada

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MP 509 SILAC Zebrafish Enables in vivo Monitoring of Cardiac Morphogenesis; Anne Konzer; Helene Braun; Aaron Ruhis; Benno Jungblut; Thomas Braun; Marcus Krüger; Max-Planck-Institute for Heart and Lung Research, Bad Nauheim, Germany

Quantitative Mass Spectrometry to Study the Effect of Histone H4 Acetylation; Diana Lang; Dirk Schwarzar; Eberhard Krause; Inst Mol Pharm Berlin, Berlin, Germany

MP 511 Relative Quantitation of Osteocalcit Proteome using 3 PIex SILAC; Eunkyung An; Sung Kyu Park; Ronald Germain; 1; Aleksandra Nita-Lazar1; 1NIH/NIAID/PSIIM, Bethesda, MD; 2The Scripps Research Institute, La Jolla, CA

Quantitative Proteomic and Interaction Network Analysis of Drug Resistance in HeLa Cells; Álvaro Chavez; Michael R. Hoopmann1; Chad Weisbrod; Kohji Takara1; James. Bruce1; 1University of Washington, Seattle, WA; 2Himeji Dokkyo University, Himeji, Japan

Middle Down Histone Quantification using Stable Isotope Labeling by Amino Acids in Cell Culture; Barry Zee; Nicolas L. Young; Peter A. Dimaggio; Benjamin Garcia; Princeton University, Princeton, NJ

Mass Spectrometry Detects SHARPIN-Dependent Linear Ubiquitylation on NEMO; Mirta Franz-Wachtel1; Fumiyo Ikeda2; Nicole Sessler1; Karsten Krug1; Sjoerd van Wijk2; Ivan Dikic2; Boris Macke1; 1Proteome Center Tuebingen, Germany

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MP 505 Quantitative Analyses Of Silac-Labeled Proteomes Using MASCOT, InSpecT and ProteoIQ; Oliver Fregoso1; Brent Weatherly1,3; Cornelia Ghiban2; Benjamin Weindoerf1; Adrian Krainer1; Cristian I. Ruse2; Darryl Pappin1; Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; NuSep, Inc, Bogart, GA; University of Georgia, Athens, GA

Automated Approach to Detect Peptide Level Changes Within SILAC LC-MS/MS Data Sets; Xiaoyan Guan; Neha Rastogi; Mark R. Parthun; Michael A. Freitas; Ohio State University, Columbus, OH

OFFGEL Fractionation of SILAC Labeled Proteins after Stimulation of Jurkat cells with Human Serum from Ankylosing Spondylitis Patients; Roman Fischer1; Moritz Wagner2; David Trudigan1; Paul Bowness1; Benedikt Kessler1; Centre for Cellular and Molecular Physiology, Oxford, UK; Agilent Technologies, Hewlett-Packard-Strasse, Waldbronn, Germany; Weatherall Institute for Molecular Medicine, Oxford, UK

Improved Quantification of Labeled LC-MS; Long Chen1; Jianqiu Zhang1; Univ. of Texas at San Antonio, San Antonio, TX; University of Texas at San Antonio, San Antonio, TX

Direct Comparison of Stable Isotope Labeling by Amino Acids in Cell Culture and Label Free Spectral Counting for Quantitative Proteomics; Timothy S. Collier1; Prasenjit Sarkar; William L. Franck; Balaji M. Rao; Ralph A. Dean; David C. Muddiman; North Carolina State University, Raleigh, NC

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Trends for Nominal Mass Isobars in Proteomics; Long Yu; Nicolas Polfer; University of Florida, Gainesville, FL

Derivation of Five Essential Factors to Predict Peptide Tandem Mass Spectrometric Detectability; Sunhee Jung1; Samuel Danziger2; Alexandre Panchaud3; Priska von Haller1; John Altchison2; David R. Goodlett1; University of Washington, Seattle, WA; Institute for Systems Biology, Seattle, WA; Nestle Research Center, Lausanne, Switerland

Y not B? The Occurrence of b-ions on Different Mass Spectrometers Platforms; Daniel Waldner; Anja Stefanakis; Sebastian Link; Anke Schnabel; Helmut E. Meyer; Kai Stühler; Medizinisches Proteom-Center, Bochum, Germany

Renaissance of Reporter Ions; Helena Barysz; Lutz Fischer; Zhuo Chen; Salman Tahir; Jurri Rappsilber; University of Edinburgh, Edinburgh, UK

Gas Phase Covalent Modification of Tryptic Peptides and Poorly Fragmenting Cyclic Peptides via Ion/Ion Reactions; John Stutzman; Purdue University, West Lafayette, IN

Evaluation of the Selectivity of Histidine-Containing Peptides for Transition Metals by ESI-MS, along with Isotopic and Gradient HPLC-UV; Doug Carlson1; Heather Tippens1; Robert Rayford1; Eunice Murage2; Jung-Mo Ahn3; Kevin Schug1; The University of Texas at Arlington, Arlington, TX; The University of Texas at Dallas, Dallas, TX

An Investigation of Factors Influencing the Detection of Peptides by Laser Desorption/Ionization (LDI) Mass Spectrometry; Christopher C. Lai1; Qian Sun; James A. Kelley; Chemical Biology Laboratory, NCI/NIH, Frederick, MD

A Novel Sample Preparation Method for Quantitative Analysis of Insulin Analogues Using Liquid Chromatography-Tandem Mass Spectrometry; Huan-Shen Chen; Xinchun Tong; Lucinda Cohen; John Lawrence1; Peptide-in-a-Tip: An Optimized Protocol for High-throughput Peptide Synthesis using Tips Packed with Chromatographic Media; Mukta Shukla1; Johannes Hewel2; Dirk Winkler3; Eva-Maria Keidel4; Maria Mangos5; Glygen Corp., Columbia, MD; Donnelly Centre, University of Toronto, Toronto, ON; Kinexus Bioinformatics Corporation, Vancouver, Canada; MPI of Biochemistry, Munich, Germany; University of Toronto, Ontario Cancer Inst, Toronto, Canada

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MP 521 Trends for Nominal Mass Isobars in Proteomics; Long Yu; Nicolas Polfer; University of Florida, Gainesville, FL

MP 522 Derivation of Five Essential Factors to Predict Peptide Tandem Mass Spectrometric Detectability; Sunhee Jung1; Samuel Danziger2; Alexandre Panchaud3; Priska von Haller1; John Altchison2; David R. Goodlett1; University of Washington, Seattle, WA; Institute for Systems Biology, Seattle, WA; Nestle Research Center, Lausanne, Switerland

MP 523 Y not B? The Occurrence of b-ions on Different Mass Spectrometers Platforms; Daniel Waldner; Anja Stefanakis; Sebastian Link; Anke Schnabel; Helmut E. Meyer; Kai Stühler; Medizinisches Proteom-Center, Bochum, Germany

MP 524 Renaissance of Reporter Ions; Helena Barysz; Lutz Fischer; Zhuo Chen; Salman Tahir; Jurri Rappsilber; University of Edinburgh, Edinburgh, UK

MP 525 Gas Phase Covalent Modification of Tryptic Peptides and Poorly Fragmenting Cyclic Peptides via Ion/Ion Reactions; John Stutzman; Purdue University, West Lafayette, IN

MP 526 Evaluation of the Selectivity of Histidine-Containing Peptides for Transition Metals by ESI-MS, along with Isotopic and Gradient HPLC-UV; Doug Carlson1; Doug Carlson1; Heather Tippens1; Robert Rayford1; Eunice Murage2; Jung-Mo Ahn3; Kevin Schug1; The University of Texas at Arlington, Arlington, TX; The University of Texas at Dallas, Dallas, TX

MP 527 An Investigation of Factors Influencing the Detection of Peptides by Laser Desorption/Ionization (LDI) Mass Spectrometry; Christopher C. Lai1; Qian Sun; James A. Kelley; Chemical Biology Laboratory, NCI/NIH, Frederick, MD

MP 528 A Novel Sample Preparation Method for Quantitative Analysis of Insulin Analogues Using Liquid Chromatography-Tandem Mass Spectrometry; Huan-Shen Chen; Xinchun Tong; Lucinda Cohen; John Lawrence1; Peptide-in-a-Tip: An Optimized Protocol for High-throughput Peptide Synthesis using Tips Packed with Chromatographic Media; Mukta Shukla1; Johannes Hewel2; Dirk Winkler3; Eva-Maria Keidel4; Maria Mangos5; Glygen Corp., Columbia, MD; Donnelly Centre, University of Toronto, Toronto, ON; Kinexus Bioinformatics Corporation, Vancouver, Canada; MPI of Biochemistry, Munich, Germany; University of Toronto, Ontario Cancer Inst, Toronto, Canada

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Mon 530 Quantitative Proteomics of Intracellular Campylobacter Jejuni Reveals Metabolic Reprogramming; Xiaoyun Liu1; Beile Gao; Veronica Novik; Jorge Galan; Yale University School of Medicine, New Haven, CT

MP 531 Addressing Protein Degeneracy Using MS-based Proteomics and a Model Human Gut Microbiota of 12 Bacterial Species Established in Gnotobiotic Mice; Alison R. Erickson1,2; Nathan P. McNulty1; Patricia Carey2; Nathan C. Verberkmoes3; Jeffrey I. Gordon4; Robert L. Hettich5; University of Tennessee, Knoxville, TN; Oak Ridge National Laboratory, Oak Ridge, TN; Washington University School of Medicine, St. Louis, MO

MP 532 Systematic Comparison of Spectral Counting, Metabolic Labeling, and Chemical Labeling Approaches for Quantitative Proteomics on LTQ-Orbitrap-Velos; Zhou Li1; Rachel Adams1; Karuna Chourey2; Robert Hettich3; Chongle Pan4; UT-ORNL Graduate School of Genome Science and Tech, Knoxville, TN; Oak Ridge National Laboratory, Oak Ridge, TN

MP 533 Unraveling Metabolic Pathways in Haloalkaliphilic Sulphur Bacteria using Proteomics; Martin Pinkse1; Qiao Hua; Dmitry Sorokin1; Gerard Muijzer2; Peter Verhaerens3; Delft University of Technology, Delft, Netherlands

The Proteome of Chlamydomonas reinhardtii Under Stress; Hong Hanh Nguyen1; Cristian Piras2; Janette Kropat3; Melissa Sondej1; Paola Roncada1; Sabeeha Merchant1; Joseph A. Loo2; Rachel O. Loo1; UCLA, Los Angeles, CA; University of Sassari, Sardinia, Italy; Istituto
Sperimenterale Italiana Lazzaro Spallanzani, Milan, Italy

MP 535 Bottom-up Proteomic Analysis of Free Living and Symbiotic Nostoc punctiforme; Diana Tran; John C. Meeks; Elsie Campbell; Barrett Smith; Brett S. Phinney; 1UC Davis Proteomics Core, Davis, CA; 2Section of Microbiology, University of California, Davis, CA

MP 536 Comprehensive Proteomic Profiling of C. difficile Spores; Lu Yu; Chinyere Okoro; Trevor Lawley; Gordon Dougan; Joity Choudhary; Wellcome Trust Sanger Institute, Hinxton, UK

MP 537 Identification and Label-Free Quantification of Archaeaon *Ghost* Proteins; Nailea Ramnulu 1; Deborah R. Francolien; Jonathan Erde; Anne Henstra; Lars Rohlin; Robert P. Gunsalus; Michael Daly; Rachel O. Loo; Joseph A. Loo; 1UCLA, Los Angeles, CA; 2Waters Corp, Oakland, CA

MP 538 Characterizing the Novel Flagellin and Pilin Glycoproteins Expressed by the Archaeaon, Methanothermobacter maripaludis; John F. Kelly; Evgueny Vinogradov; Sandy Ng; Divya Nair; John Wu; Luc Tessler; Anna Robotham; Kaoru Uchida; Susan Logan; Shin-Ichi Aizawa; Ken Jarrell; 1National Research Council of Canada, Ottawa, Canada; 2Queen’s University, Kingston, Ontario, Canada; 3Prefectural University of Hiroshima, Hiroshima, Japan

MP 539 Escherichia coli Exhibits a Membrane Related Response to a Small Arginine- and Tryptophan-rich Antimicrobial Peptide; Benjamin Fränzel; Dirk Wolters; Analytical Chemistry, University of Bochum, Bochum, Germany

MP 540 The Secretome of Streptococcus Pneumoniae; Shobha Ravipaty; Lokto Sham; Malcolm E. Winkler; James P. Kelly
1Department of Chemistry, Indiana University, Bloomington, IN; 2Department of Biology, Indiana University, Bloomington, IN

MP 541 Genomic and Proteomic Analyses of Respiratory Viruses; Kai Tang; Nanyang Technological University, Singapore

MP 542 In-vivo MS Profiling and Imaging of a Growing Bacterial Colony Directly from Nutrient Agar using nanoDESI Mass Spectrometry; Jeramie Watrous; Brandi Heath; Patrick Roach; Julia Laskin; Pieter Dorrestein 1; 1University of California, San Diego, La Jolla, CA; 2Pacific Northwest National Lab, Richland, WA; 3University of California, San Diego, Skaggs School, La Jolla, CA

MP 543 Rapid Detection of Polymicrobial Composition Pathogenic Bacterial Cultures using Secondary Electrospray Ionization-mass Spectrometry (SESI-MS); Jiangjiang Zhu; Heather Bean; Yin-Ming Ku; Jane Hill; University of Vermont, Burlington, VT

MP 544 Thermal Desorption–Gas Chromatography–Mass Spectrometry Characterization of Novel Microbial Volatile Organic Compounds Produced by Chaetomium and Cladosporium Molds; Syveda S. Quadri; Michael J. Ferriss; Jim E. Cutler; Richard B. Cole; 1University of New Orleans, New Orleans, LA; 2Children’s Hospital, New Orleans, LA

MP 545 Simultaneously Analysis of Cardiolipin and Lipid A from Helicobacter pylori: Structure Alteration under ex vivo Gastric Conditions; Jianjun Li; Ping Zhou; Rui Hu; Vandana Chandan; Wangxue Chen; Rhonda KuolLee; Eleonora Allman; National Research Council, Ottawa, Canada

MP 546 Microorganism Detection by MALDI in the Presence of Inteferents; Juaneka Hayes; Kermit K. Murray; Louisiana State University, Baton Rouge, LA

MP 547 A Novel Test for Rapid Diagnosis of MRSA (Meticillin Resistant Staphylococcus aureus) using Mass Spectrometry (MS); Pranav Somaiya; Michael Charlesworth; Steve Davies; 1National Dong Hwa University, Shoufeng, Hualien, TAIWAN; 2Tzu Chi University, Hualien, Taiwan

MP 548 Rapid Identification of Acinetobacter Species with Nanodiamond; Chih-Jen Yeh; Chu-Wei Chen; Kai-Chih Chang; Wen-Ping Peng; 1National Dong Hwa University, Shoufeng, Hualien, TAIWAN; 2Tzu Chi University, Hualien, Taiwan

MP 549 Rapid Discrimination of Methicillin-resistant and Vancomycin-intermediate Staphylococcus Aureus from Methicillin-sensitive Staphylococcus Aureus Strains by MALDI-TOF; Chao-Jung Chen; Fuu-Jen Tsai; Yu-Ching Liu; Cheng-Mao Ho; Jing-Jhu Lu; 1China Medical University, Taichung, Taiwan; 2China Medical University Hospital, Taichung, Taiwan

MP 550 Detection of pathogens in nymphal ticks from the Czech Republic using PCR/ESI-MS; Chris Crowder; Megan Rounds; Heather Matthews; Vaclav Honig; Libor Grubhoffer; Dave Ecker; Benjamin Luft; 1Ibis Biosciences, Carlsbad, CA; 2Institute of Parasitology, Ceske Budejovice, Czech Republic; 3SUNY at Stony Brook, Stony Brook, NY

MP 551 Development and Validation of a Broad Biothreat (BT) Identification Strategy using PCR/ESI-MS; Ranga Sampath; Niveen Muliholland; Nicholas Heng; Nicole Wehrbright; Robert Lovari; Debra Rubio-Aparicio; Mark Frinder; Irene Yasuda; Fong Li; Roberta Housley; Thomas Hall; Steven Hofstadler; Christian Massire; Lawrence Blyn; David Ecker; 1Ibis Biosciences, Inc., Carlsbad, CA; 2Institute of Parasitology, Ceske Budejovice, Czech Republic

MP 552 RT-PCR/ESI-MS for Simultaneous Rapid Detection of Biothreat (BT) and Common Respiratory Pathogens in Bronchoalveolar Lavages (BALs); Kevin Jeng; Helen Won; Lawrence Blyn; Stephen Peterson; Justin Hardick; Alexander Valsamakis; Richard Rothman; Charlotte Gaydos; Karen Carroll; 1Johns Hopkins University, Baltimore, MD; 2Ibis Biosciences, Carlsbad, CA

MP 553 The Development of a Mass Coding based Pathogen Detection Platform for Clinical Research; Gavin Fischer; Craig Monell; Natalia Novoradovskaya; Scott Basehore; Dan-Hui Dorothy Yang; Yves Konigshofer; Michelle Cayouette; Sarah Hamilton; Yuan Shau; Yoon Rhee; Katie Felts; Denise Rhodes; Carsten Carstens; Roger H. Taylor; Marilyn Marx; Lynde Nottebaum; Anging Fan; Yinghang Yang; Holly
Molds Produced by Chaetomium and Cladosporium

Microbial Volatile Organic Compounds

Nutrient Agar using nanoDESI Mass Growing Bacterial Colony Directly from Germany
Ottawa, Canada; 2Queen’s University, Kingston, John Wu2; Luc Tessier1; Anna Robotham1; Kaoru
Ontario, Canada; 3Prefectural University of Malcolm E. Winkler2; James P. Reilly1; 
1National Research Council of Canada, Jarrell2; 
2Waters Corp, Oakland, Michael Daly2; Rachel O. Loo 1; Joseph A. Loo1; 
2; Deborah  R. Francoleon1; Jonathan Erde1; Anne 
1UC Davis Proteomics Analytical

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Combining UV Absorbance and Diagnostic CID Fragment Ions to Identify and Distinguish Isobaric Chromophores on Phycobiliproteins; Loubna Hammad 1; Animesh Shukla1; Avijit Biswas2; Yuening Zhang2; David 

Kehoe3; Wendy Schluchter2; Jonathan A. Karty2; 
1; Marcus Macht1; Braniislav Kovacech2; 
Andrej Kovac2; 1Bruker Daltonik GmbH, Bremen, Germany; 2Inst. of Neuroimmunol., Slovak 
Academy of Sciences, Bratislava, Slovakia; 3Bruker Daltonik Scientific Instruments, Houston, TX

A-, B-, C-, D-, W-, Y- and Z-type Ions Generated Simultaneously by MALDI In-

Source Decay; Kai Scheffler2; Tabiwan Arrey2; Kerstin Strupat1; 
1Thermo Fisher Scientific GmbH, Dreieich, Germany; 2Thermo Fisher Scientific 
GmbH, Bremen, Germany

Top-Down Proteomics of Protein Mixtures using MALDI-In Source Decay with Software to Simultaneously Sequence Multiple Proteins; Tyler A. Zimmerman1; Gabriel D 
Mazzucchelli1; Delphine Debois1; Edwin De 
Pauw1; 1University of Liege, Liege, Belgium; 2MS Lab, GIGA, Liege, Liege, Belgium; 3Liege 
University, Liege, Belgium

Protein Sequence and Size Variation Effects on MALDI In-Source Decay Fragmentation Efficiency; Huiling Liu; Ben Bolanos6; Michael Greig; 1Pfizer Global R&D- La Jolla, San Diego, CA

A Rapid and Universal Approach to the Verification of Protein Termini Using In-
source Decay; Yutian Gan; Corey Bakalarски; Peter Liu; Jennie Lill; Wendy Sandoval; 
Genentech, Inc., South San Francisco, CA

Single-scan, Top-down Intact Protein Analysis on a Velos Orbitrap Modified with a Dedicated High-capacity Ion/Ion Reaction Cell; Jason D. Russell1; Aaron R. Ledvina 1; 
Graeme C. McAlister2; Michael S. Westphall1; John E. P. Syka3; Jens Gries-Raming3; Joshua J. Coon3; 
1University of Wisconsin, Madison, WI; 2Thermo Fisher Scientific, San Jose, CA; 3Thermo Fisher 
Scientific GmbH, Bremen, Germany

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Stability Evaluation of HIV Type 1 Protease Constructs by High-Resolution Mass Spectrometry; Jan Mitchell S. De Vera3; Gail E. 

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Fanucci1; Maria Cristina A. Dancel1, 2; 1Department of Chemistry, University of Florida, Gainesville, FL; 2Mass Spectrometry Facility, University of Florida, Gainesville, FL

MP 574 Efficient and Rapid Multienzymatic Limited Digestion Method for Complete Protein Characterization; Gabriel Mazzucchelli1, Nicolas Smargiasso2; Marie-Alice Meuwis3; Michel Degueldred1; Laurent Leclercq2; Edwin De Pauw1; 1University of Liege, MS Lab - GIGA, Liege, Belgium; 2Johnson & Johnson Pharmaceutical R&D, Beerse, Belgium

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MP 575 A Novel Two-Dimensional LC/MS/MS Approach For Automated Analysis of Complex Protein Samples Using Ms Compatible Buffers; R. Ivanov1; 1Bio-Rad Laboratories, Inc, Hercules, CA; 2Agilent Technologies, Santa Clara, CA

MP 576 Elevated Temperature Separation Improves the Depth and Quality of LC-MS-based Analysis of Proteome Digests, PTMs, and Mixtures of Intact Proteins; Eugene Moskovets1, 2; Jane Razumovskya; Emily Freeman1; Alexander R. Ivanov1; 1Harvard University HSPH, Boston, MA; 2S.E.S.I., Columbus, MD

MP 577 Secondary Analysis of SPR Based Arrays by Direct Use in a MALDI Time of Flight Mass Spectrometer; Steve Roth1; Fiona Plows2; Matthew Hammond2; “Bio-Rad Laboratories, Inc, Hercules, CA; “Bio-Rad Laboratories, Inc., Hercules, CA; “Stanford University, Stanford, CA

MP 578 Integrated Strong-Cation Exchange Liquid Chromatographic Procedure for SDS Removal and Peptide Separation for MS-Based Shotgun Proteome Analysis; Difei Sun1; Nan Wang1; Liang Li1; Department of Chemistry, University of Alberta, Edmonton, Canada

MP 579 Development of Multidimensional RPLC-RPLC Separation at the Protein and Peptide Levels Combined with ESI-MS/MS for Comprehensive Mapping of the Phosphoproteome; Xiaoxia Ye1; Liang Li1; University of Alberta, Edmonton, CANADA

MP 580 Porous Graphitic Carbon: A Novel Application as a First-dimension Stationary Phase in the 2D-LC-MS/MS Analysis of Complex Peptide Mixtures; John R. Griffiths1; Simon Perkins1; Yvonne Connolly1; Lu Zhang1; Valeria Barattini1; Luisa Pereira1; Anthony Edge1; Harald Ritchie1; Duncan Smith1; 1Paterson Institute for Cancer Research, Manchester, UK; 2Thermo Scientific, Runcorn, UK

MP 581 Effects of Fractionation on Protein Identifications by Online 2D-UPLC-MS/MS; Stephanie Houlé1; Robert Abernathy1; Scott A. Stuart1; Chia-Yu Yen1; Karen Meyer-Arendt1; William M. Old1; Natalie G. Ahn1, 2, 3; 1Howard Hughes Medical Institute, Boulder, CO; 2University of Colorado at Boulder, Boulder, CO

MP 582 Protemic Exploration of Cyclic Peptide Diversity Among Plants Using Peptide Labelling and Orthogonal Separation Strategies; Aaron Poth1, 2; Michelle Colgrave1; 1IMB, The University of Queensland, St Lucia, Australia; 2CSIRO Livestock Industries, St Lucia, Australia

MP 583 Separation and Mass Spectrometry of Tryptic Peptides at Low and High pH; Mark J. Raftrey; Bioanalytical Mass Spectrometry, Sydney, Australia

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MP 585 Ion Mobility-Assisted Data Independent Analysis with Inter-Analysis Alignment Provides Improved Depth of Proteome Coverage; J. Will Thompson1; Scott Geromanos1; Martha D. Stapels2; Laura G Dubois3; Keith Fadgen4; Cindy Chepanoske5; Erik J Soderblom1; 1University of Illinois at Chicago, Chicago, IL; 2Duke University School of Medicine, Durham, NC; 3Waters Corporation, Milford, MA; 4Ceiba Solutions, Seattle, WA

MP 586 Quantitative Proteomics via Laser Desorption Photoionization Mass Spectrometry: Proof of Principle Study using iTRAQ Tagging; Artem Akhmetov1; Praneeth Edirisinghe1; Jerry F. Moore1; Melvin Blaze M. T.1; 1University of Washington, Seattle, WA; 2Rush University Medical Center, Chicago, IL; 3MassThink LLC, Naperville, IL

MP 587 A Novel Proteomics Approach to Quantitative Direct Sample Infusion: Rapid Protein Identification and Quantification Using Data-Independent Acquisition; John D. Chapman1; Scott Edgar1; Jason L. Shaw1; David R. Goodlett2; 1Duke University Medical Center, Durham, NC; 2University of Illinois at Chicago, Chicago, IL

MP 588 Non-assumptive Identification of Protein Modifications using High Resolution-high Speed Quadrupole TOF-MS/MS Analysis; Lekha Slend1; Xu Guo1; Souade Ben Haddou1; Stephen A Tate1; Brigitte Simons1, 2; UQAM, Montreal, Canada; 2AB SCIEX, Concord, ON

MP 589 Optimizing High Performance at Highest Speeds for Protein Identification in Complex Matrices; Eric Johansen1, 2; Xu Guo1, 2; Scott Stuart1; Sahana Mollah1, 2; Sean Seymour1, 2; Doug Simmons1; 1AB SCIEX, Foster City, CA; 2AB SCIEX, Toronto, Canada; 3University of Colorado at Boulder, Boulder, CO

MP 590 In-Funnel Orthogonal Ion Injection for Highly Sensitive and Accurate Proteome Acquisitions; Artem Akhmetov1; Praneeth Edirisinghe1; Jerry F. Moore1; Melvin Blaze M. T.1; 1University of Washington, Seattle, WA; 2Rush University Medical Center, Chicago, IL; 3MassThink LLC, Naperville, IL

MP 591 An Ion-overfilling Approach that Significantly Improves the Sensitivity of Orbitrap and Application in Highly Sensitive and Accurate Proteomic Profiling; Jun Qiu1; Xiaotao Duan1; Frank Engler1; University at Buffalo, Amherst, NY

MP 592 Calibration of MALDI-TOF-TOF for MS/MS of Non-digested Proteins for Top-down Proteomic Identification; Clifton K. Fagerquist1; Omar Sultan1; USDA, Albany, CA

MP 593 A Top-Down/Bottom-Up Approach for the Differential Proteomic Analysis of a Beta-Arrestin 1,2 Double-Knockout; Jordan Stobaugh1; Kaitlin Fague1; Brenna Richardson2; Kunhong Xiao1; James Jorgenson1; 1University of Rochester, Rochester, NY; 2Memorial Sloan-Kettering Cancer Center, New York, NY
North Carolina at Chapel Hill, Chapel Hill, NC; 2Duke University, Durham, NC

**MP 594**
A Combined Top-down and Bottom-up Proteomics Approach to Detect and Identify Disease Related IgGs; Lennard Dekker1; Si Wu2; Martin Vandijoen3; Nikolai Toic4; Theo Marten Luider1; Lijliana Pasa-Tolic1; Erasmus Medical Center, Rotterdam, Netherlands; Pacific NW Nat’l Lab, Richland, WA

**MP 595**
Efficient Top Down of Yeast Proteins under 70 kDa using a Combination of Dissociation Techniques with LTQ-FT and Orbitrap Instruments; John F. Kellie1; Philip Compton1; Kenneth R. Durbin1; Shannon M Eliuk1; Vlad Zabrouskov1; Neil L. Keller1; Northern Arizona University, Flagstaff, AZ; 2Thermo Scientific, San Jose, CA

**MP 596**
(SWATH) A Method For Collecting MSMS of All Parent Ions in a Sample on an LC Time Scale; Stephen A. Tate1; Alexander Loboda1; Igor Chernushevich2; Ludovic Gillet3; Pedro Navarro4; Ron Bonner1; Ruedi Aebersold1; 1AB SCIEX, Concord, Canada; 2ETH Zurich, Zurich, Switzerland

**MP 597**
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**MP 598**
Increasing LCMs Assay Robustness through Increased Specificity using High Resolution MRM-like Analysis; Christie L Hunter1; Hasim Keshishian1; Steven A. Curr1; 1AB SCIEX, Foster City, CA; 2Broad Institute, Cambridge, MA

**MP 599**
Using Fragmentation at Different Collision Energies for Automated De Novo Sequencing of Peptides in Proteomics; Miguel Garcia1; Cesar Costa Vera2; Andre M. Deelder2; Magnus Palmblad3; 1Escuela Politecnica Nacional / Dept. de Fisica, Quito, Ecuador; 2Leiden University, Leiden, Netherlands

**MP 600**
Increasing Throughput for Quantitative Proteomics by Combining Data-independent Acquisition with Accurate Online 2D-LC; Richard R. Sprenger1; Angel Manteca2; Ole N. Jensen3; 1University of Southern Denmark, Odense, Denmark; 2Universidad de Oviedo, Oviedo, Spain

**MP 601**
Nanomanipulation-Nanospray Ionization-Mass Spectrometry Coupled to Raman Microscopy to Elucidate Astaxanthin-Protein Interaction in Freshwater Copepods; Nicole Wallace1; student; Lewisville, TX

**MP 602**
DBnovo: Information Based Control of Mass Spectrometers for Real-time Analysis of Biopolymers; Andreas Kuhn1; Katja Tham1; Stephan Heymann1; Johann-Christoph Freytag1; Michael W. Linscheid1; Humboldt-Universität zu Berlin, Berlin, Germany; 1Thermo Fisher Scientific, Bremen, Germany

**MP 603**
Multiplexing SIMs on a Novel Bench Top Orbitrap with a Quadrupole Mass Filter to Increase Sensitivity for Peptide Quantitation; Jonathan C. McNally1; ThermoFisher Scientific, San Francisco, CA

**MP 604**
New Methodology to Detect Peptide Toxin-GPCR Interaction by MALDI-TOF Mass Spectrometry; Julien Echtcherille1; Nicola Gilles2; Edwin De Pauw1; Lolic Quinton1; 1University of Liege - Labo. Spectrometrie de Masse, Liege, Belgium; 2IBiTecs, SIMOPRO - CEA, Gil Sur Yvette, France

**MP 605**
Application of a SUPREX-based H/D Exchange Protocol for Thermodynamic Analysis of a Molecular Chaperone Binding to its Unfolded Protein Substrate; Yiqi Xu1; Dana Reichmann1; Ursula Jakob2; Michael C. Fitzgerald1; 1Duke University, Durham, NC; 2University of Michigan, Ann Arbor, MI

**MP 606**
Structural Details of NKR-P1D / C1rb Interaction Elucidated by Chemical Cross-linking and High Resolution Mass Spectrometry; Pavel Hanc1; Daniel Rozbysky1, 2; Josef Chmelik1; Karol Bezouska1; 1Petr Novak1, 2; 2Institute of Microbiology, Prague, Czech Republic; 3Faculty of Sciences, Charles University, Prague, Czech Republic

**MP 607**
Using FAIMS-FTICR/MS to Determine the Effectiveness of a Novel Crosslinker in Identifying Protein-Protein Interactions Sites; Melissa Stoudemayer1; Rachel Parker1; Ruth Furukawa1; Marcus Fecheimer2; Evgeniy V. Petrotenko1; Christoph H. Borchers1; Jon Amster1; 1University of Georgia, Athens, GA; 2Uvic-GBC Proteomics Centre, Victoria, BC

**MP 608**
Mass Spectrometry of Immunodepleted Plasma Derived Humand Serum Albumin to Identify Proteins and Metabolites Non-Specifically Bound to Albumin; Christopher Vanselov1; Vidaraja Bhat2; Sunia Trauger1; Julian Whitelegge1; 1Agilent Technologies, La Jolla, CA; 2Agilent Technologies, Little Falls, DE; 3The Scripps Research Institute, La Jolla, CA; 4University of California, San Diego, CA

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**MP 610**
Tracking and Filtering Interaction Proteomics Data: Prohibs, SAINT and the Total Contaminant Repository for Affinity Purification; Hyungwon Choi1; Guomin Liu2; Datta Mellacheruvu3; Brett Larsen1; Jianping Zhang1; Mike Tyers1; 1Alexey Nesvizhskii1; 2University of Michigan, Austin, TX; 3University of Texas, Austin, TX; 4University of Southern California, Los Angeles, CA

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Characterization of ITAM Peptide Probes Based on Competitive Assay and Quantitative Proteomics; Lianghui Hu1; Andrew Lichk1; Ziniu Zhou1; 1Department of Biochemistry, Purdue University, West Lafayette, IN; 2Department of MCMP, Purdue University, West Lafayette, IN

**MP 612**
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MP 626 Investigation of the Interaction between E. coli Alanyl-tRNA Synthetase with tRNAaa+ and other Ligands by Mass Spectrometry; Jinghu Gue; John D. Dignam; Wendell P. Griffith; university of toledo, Toledo, OH

MP 627 Preferential ETD Cleavage for Facile Mapping of Protein Surface Residue Accessibility; Lisa Vasicek; John O’Brien; Jennifer Brodbelt; The University of Texas, Austin, TX

MP 628 Scrambling of Covalently Labeled Amino Acids During CID; Nicholas Borotto; Yaping Zhou; Richard Vavrinov; University of Massachusetts, Amherst, MA

MP 629 Mass Spectrometry Studies of DNA-protein Cross-linking by Cisplatin; Xun Ming; Colin Campbell; Erin Michaelson; Natalia Tret'yakova; University of Minnesota, Minneapolis, MN

MP 630 Watching Amino Acid Residues Change During Protein Fast Folding; Jiawei Chen; Don L. Rempel; Michael L. Gross; Washington University, St. Louis, MO

MP 631 Does Chemical Cross-Linking Distort the Protein? - Investigations Using Hydrogen-Deuterium Exchange and Ion Mobility Mass Spectrometry; Adam Klein1;2; Derrick L. Morast1;3; R. Sam Houk1;3; Akiko Nakatomi3; Shin-ya Ohki1; Hideya Kasakida2; Ryuichi Arakawa3;1Japan Advanced Institute of Science and Technology, Nomi, Ishikawa, Japan; 2Kansai University, Suita, Osaka, Japan; 3Hokkaido University, Sapporo, Hokkaido, Japan

MP 632 Probing the Structure of Amyloid β-Protein Monomer and Dimer using Radiolytic Labeling and Mass Spectrometry; Eric Pang1;3; Margaret Condron1; Sayan Gupta1; Mark Chance2; David B. Teplow3; Joseph A. Loo1;3; 1UCLA, Los Angeles, CA; 2Case Western Reserve University, Upton, NY; 3David Geffen School of Medic, Los Angeles, CA

MP 633 Influence of Phosphate Concentration on DOTA-NHS Conjugation of an IgG 1 mAb; David Hambley; Keith Bower; Anna Senczuk; Janet Tam; Art Hewig; Peter Prince; Himanshu Gadgil; Aymen Inc., Seattle, WA

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MP 635 Increasing Protein Structural Information during Covalent Labeling with Mass Spectrometric Detection; Yuping Zhou; Richard Vachet; University of Massachusetts, Amherst, MA

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Dan Therrien; Jonathan Burden; Nicole Therrien;
Flathead Valley Comm College, Kalispell, MT

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MP 654 Rapid and Sensitive Determination of Human
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Dietrich A. Volmer; Gero Hoth; Gunter Eckert;
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MP 656 A New Strategy for Identifying Alternative
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Amanda Paulovich; Fred Hutchinson Cancer
Research Center, Seattle, WA; Broad Institute,
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MP 657  Validation of an ImmunoPrecipitation, Digestion and Immunoaffinity LC-MS/MS Assay for Human b-NGF Biomarker and Implementation in Support of Clinical Trials;  
Kathryn M. Porter*; Hendrik Neubert*; Gary Schultz*; 1Advion BioServices, Inc., Ithaca, NY; 2Pfizer Corporation, Andover, MA

MP 658  A microRNA Network Controlled by Oncogenic B-Raf;  
Thomas Lee1, 2; Kasey Couts3; Stephane Houlé1; 2; Emily Anderson1; Maren Mayer1; Kevin Sullivan1; William Old1; Natalie Ahn1, 2; 1University of Colorado, Boulder, CO; 2Howard Hughes Medical Institute, Boulder, CO; 3Dharmacon RNA Technologies, Thermo Fisher, Lafayette, CO

MP 659  LC/MS/MS Quantitation of Pyridinoline and Desmosine Crosslinks from Aorta and Heart as a Biomarker of Heart Failure and Hypertension;  
David R Bush; Randy Vazquez; Douglas F. Larson; Vicki H. Wysocki; University of Arizona, Tucson, AZ

MP 660  Advanced Glycation End Products (AGEs) as Pathology Biomarkers: Microwave Assisted Synthesis and Biological Quantitative Analysis by LC-FTMS;  
Claudio Medana; Sonja Visentin; Federica Dal Bello; Valeria Giancotti; Manuela Aragno; Raffaella Mastroculto; Claudio Baiocchi; University of Turin, Torino, Italy

MP 661  Identification of Ovarian Cancer Biomarkers using Lecithin Microarray and Glycoproteomics;  
Xiaolei Xie1; Jingt Wu2; Yashu Liu2; Jingtang He2; David M. Lubman1; 1Captron Proteomics US LLC, Menlo Park, CA; 2University of Michigan, Ann Arbor, MI

MP 662  Identification of AAL-reactive Species of Immunoglobulin G (IgG) by Quantitative Analysis of N-linked Glyco-isoforms of IgG Using LC-MS/MS;  
Chen Li1; Hongbo Gu2; Patrick Romano1; Anand Mehta1; Timothy Block1; Carthene Bazemore-Walker1; Songming Chen1; 1Institute for Hepatitis and Virus Research, Doylestown, PA; 2Brown University, Providence, RI; 3Drexel University, Philadelphia, PA

MP 663  Identification of Glycoproteins Associated with Glioblastoma Stem Cell Differentiation;  
Jingtang He1; Yashu Liu1; Xiaolei Xie2; Thant Zhu1; Xing Fan1; Fan Xiang3; David M. Lubman1; 1University of Michigan, Ann Arbor, MI; 2Captron Proteomics US LLC, Menlo Park, CA; 3Shimadzu Biotech, Pleasanton, CA

MP 664  A Validated Method for the Definitive Quantitation of Hepcidin 25 in Rat Serum by LC-MS/MS;  
John E. Buckholz; Barry R. Jones; Joseph Koopmeiners2; Tim Griffin1; 1BD Diagnostics, Franklin Lakes, NJ; 2University of Minnesota; Biostatistics, Minneapolis, MN

MP 665  Quantitative Investigation of Peptide Biomarker Stability in Blood Specimens by comparing MS and ELISA Methods;  
Jizu Yi; David Craft; BD Diagnostics, Franklin Lakes, NJ

MP 666  Kinase Inhibition Studies Using a High Resolution/Accurate Mass MS Targeted Approach and Nucleotide Probes;  
Scott Peterman1, 2, 3; Amol Prakash1, 2, 3; Rosa Viner1, 2, 3; Ryan Bogmarden1, 2, 3; John Rogers1, 2, 3; 1Thermo Fisher Scientific, Cambridge, MA; 2Thermo Fisher Scientific, San Jose, CA; 3Thermo Fisher Scientific, Rockford, IL

MP 667  Quantitative Phosphoproteomics in Surrogate Tissues for Pharmodynamic and Target Engagement Biomarkers Development for Kinase Inhibitors;  
An Chi1; Peter R. Strack1; Hongbo Guo2; Jan-Rung Mo1; John F. Reilly1; Ronald C. Hendrickson2; Cloud Paweletz1; 1Merck, Boston, MA; 2University of Toronto, Toronto, ON

MP 668  A CPTAC multisite Lectin-based Analysis of Glycopeptide Biomarker Candidates utilizing Cancer Cell Lines, and Plasma Samples from Patients and Controls;  
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MP 669  Secretome Signature of Invasive Glioblastoma Multiforme;  
Catherine Formolo1; Russell Williams2; Tobey J MacDonald2; Norman H Lee2; Yetrih Hathout1; 1Children's National Medical Center, Washington, DC; 2Department of Pharmacology and Physiology, GWU, Washington, DC; 3Aflac Cancer Center, Emory University, Atlanta, GA; 4Children's Natl. Medical Center, Washington, DC

MP 670  Analysis of Glioblastoma Tumors Using a Trizaic nanoTile based UPLC System in Combination with SYNAP G2 and XEVO TQ-S MS;  
Tony Tegeler; Wendy McDonough; Linda Nagore; Jane Liu; Ashoka D. Polpibya; Michael Berens; Konstantinos Petratis; Translational Genomics Research Institute, Phoenix, AZ

MP 671  Analysis of Human Melanoma Cell Lines Secretomes;  
Livja Malorni1; Micaela Rocco2; Rosaria Cozzolino1; Giuseppe Palmieri1; Carla Ruzzo1; Augusto Parente2; Angela Chambery3; 1CNR Institute of Food Science, Avellino, Italy; 2Second University of Naples, Caserta, Italy; 3Unit of Cancer Genetics CNR-ICB, Sassari, Italy

MP 672  Discovery of Melanoma Autoantibody using Mass Spectrometry and Glycoprotein Microarray;  
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MP 673  Mesoporous Silica Nanochip Fractionation and MALDI-MS Identify Serum Low-Molecular-Weight Peak Profiles Associated with Treatments in Melanoma Mouse Model;  
Adakalam Veilachamy1; Renduo Song2; Ye Hu3; Ann L. Van de Ven1; Diana L. Chan1; Catherine E. Hickman1; Jason C. Hickman1; Jizu Yi1; 1The Methodist Hospital Research Institute, Houston, TX; 2UT M.D. Anderson Cancer Center, Houston, TX

MP 674  Glycoprotein Profiling of Breast Cancer Cell Lines;  
Ten-Yang Yen1; Jodi Wong; Chris Alleyne-Chin1; Christina Litsakos-Chueung; Roger Yen; Leslie
Biomarker Candidates Discovery in a Large, Multi-site Bladder Cancer Patients Cohort, using a Label-free Quantitative Proteomics Approach; Magali Court1; Mourad Mellal1; Madalen Le Gorrec3; Yves Allory4; Núria Malats1; Christophe Bruyère1; Elodie Duriez2; Bruno Domon2; Jérôme Garin1; Christophe D Masselon2; Edyp Laboratory; Greiner, France; AHPH Mondor Hospital, Pathology, Creteil, France; 3Spanish National Cancer Research Centre, Madrid, Spain; 4Luxembourg Clinical Proteomics Center, Luxembourg, Luxembourg

Proteomic Discovery of Gastric Cancer Tissue Biomarkers Using MALDI-IMS and 2D-DIGE; Chun-Chia Cheng1; Chun-Chao Chang1; Shui-Cheng Lee2; Jung-Shan Chang3; Eu-Der Mai4; 1Taipei Medical University, Taipei, Taiwan; 2Institute of Nuclear Energy Research, Taoyuan, Taiwan

Proteomics Biomarker Discovery in Plasma of Mouse Xenografted with Human Colorectal Carcinoma Cells; Svetlana Mihaylova-Todorova1; Elissa L. Devos3; Jian Liu4; Tony Tegeler3; Ashoka D. Polpitiya2; Jeffrey Mackeigan2; Konstantinos Petritis3; Translational Genomics Research Institute, Phoenix, AZ; 2Van Andel Research Institute, Grand Rapids, MI

Protein Profiling for Biomarker Discovery in Patients with Colorectal Cancer using 2D-(RP-RP)-HPLC MS/MS Approach; Peyman Ezzati1; Diego V. Krokhin1; Vic Spencer1; Mohamed Akra1; Ahmed Lemor1; 1University of Manitoba, Winnipeg, Canada; 2CancerCare Manitoba, Winnipeg, Canada

Proteomics Study of Head-And-Neck Squamous Cell Carcinoma Using ITRAQ Labeling and an Iterative LC-MS Analysis; Sebastien Voisin1; Olga Krakovska1; Ajay Matta1; Leroci DeSousa1; Ranj Redarin1; K W Michael Sui1; 1CRM - York University, Toronto, Canada; 2Mount Sinai Hospital, Toronto, Canada

The Salivary Peptidome: Sample Handling/Collection Considerations and Identification of Naturally Occurring Peptide Biomarkers of Oral Cancer; Ebbing De Jong1; Joseph Koopmeiners1; Tim Griffin1; 1University of Minnesota; Biochemistry, Minneapolis, MN; 2University of Minnesota; Biostatistics, Minneapolis, MN

Cancer Genetics-guided Discovery of Serum Biomarker Signatures for Prostate Cancer Diagnosis and Treatment Response; Ralph Schiess1; Igor Cima1; Peter Wild1; Martin Kealin1; Martin Schüffler1; Joseph Buhme1; Thomas Cerny1; Holger Moch1; Silke Gillessen1; Wilhelm Krek1; Ruedi Aebersold1; ETH Zurich, Zurich, Switzerland; 2ProteoMedix Inc., Zurich, Switzerland; 3University Hospital Zurich, Zurich, Switzerland; 4Kantonsspital St Gallen, St Gallen, Switzerland

Evaluation of a High Throughput LC/MS/MS/MS (MS3) Method for Quantitation of NEDD8-MLN4924 Adduct; Ling Xu1; Matthew
MONDAY POSTERS

MP 692  **Targeting Biomarker Discovery via Selective Tissue Proteome Enrichment**; Cheng S. Lee1; Xueping Fang2; Fang He1; Brian Baigley1; Chen Chen Wang3; Ie-Ming Shih4; 1University of Maryland, College Park, MD; 2Calibrant Biosystems, Gaithersburg, MD; 3Johns Hopkins Medical Institutions, Baltimore, MD

MP 693  **Proteomic Analysis of Phenotypes Produced by Cancer-related Mutations**; Patrick J. Halvey1; Bing Zhang1; Haixia Zhang1; Natasha G. Deane1; Ajaz Bhat1; Punita Dhawan1; Lisa J. Zimmerman1; R. Daniel Beauchamp1; Robert J. Coffey1; Daniel C. Liebler1; Robert J. C. Siebos1; Vanderbilt University, Nashville, TN

MP 694  **High-Throughput Native Glycan Chromatographic Profiling with Isomer Separation and Quantitation for the Discovery of Cancer Biomarkers**; Serenus Hua1; Cynthia Williams1; Hyun Joo An1; Sureyya Ozcan1; Grace Ro1; Ning Tang1; Keith Waddell1; Jay Solnick1; Carlito Lebrilla1; 1University of California, Davis, CA; 2Agilent Technologies, Santa Clara, CA
7:30-8:00 am ........................ All Tuesday posters should be set up.
10:30 am-2:30 pm .......... All poster authors should be present.
11:45 am-12:15 pm  . Lunch break for odd-numbered posters.
12:15-12:45 pm ......Lunch break for even-numbered posters.
7:30-8:00 pm ................. Remove all Tuesday posters.

Ionization Mechanisms; 001 - 022

TP 001 From Solution Phase to Spectrometer, an Analytical Model for the Electrospray Process from a Proteomics Perspective; John P. Hayes, Keith Richardson; Waters, Manchester, UK

TP 002 Preservation of Labile Post-Translational Modifications for Peptide Fragmentation during Nanoelectrospray Ionization; Lei Tan 1, Yu Xia 2, 3, 4; 1 graduate student, West Lafayette, IN; 2 Purdue University, West Lafayette, IN

TP 003 Mechanism of Electrospray Ionization Explored by Molecular Dynamics Simulations; Elias Ahadi 1, 2, Lars Konermann 1, 2; 1, 2 Univ. of Western Ontario, London, ON; 3 Univ. of Western Ontario, London, ON

TP 004 Clarifying the Ionization Mechanism of Extractive Electrospray Ionization (EESI); Rui Wang; Swiss Federal Institute of Technology Zurich, Zurich, Switzerland

TP 005 Examining the Influence of Sample Volatility on the Sensitivity of Extractive Electrospray Ionization Mass Spectrometry; Lukas Meier; Renato Zenobi; ETH Zurich, Zurich, Switzerland

TP 006 Reagents for Enhancing Protein Charging for Electrospray Ionization Mass Spectrometry from Organic/Aqueous Solvent Systems; Rajeswari Lakshmanan; Sabrina Benchara; Ivory Peng; Carly Ferguson; Shirley Lomeli; Jiang Zhang; Rachel O. Loo; Joseph A. Loo; UCLA, Los Angeles, CA

TP 007 The Effects of Polypeptide Sequence on Supercharging for ESI-MS and MS/MS; Rudy Alvarado; Rajeswari Lakshmanan; Rachel O. Loo; Joseph A. Loo; UCLA, Los Angeles, CA

TP 008 Investigating the Role of Analyte Partitioning in Protein Supercharging; Kevin Douglass; John Miller; Andre Venter; Western Michigan University, Kalamazoo, MI

TP 009 Role of Anions in Determining Charge State Distributions of Peptides; Xiaohua Liu; Richard B. Cole; University of New Orleans, New Orleans, LA

TP 010 Effect of Protic and Aprotic Solvents on Negative Ion ESI Response for a Physicochemically Diverse Group of Acidic Compounds; Christine A. Hughes; Bruce Wilcox; Daniel Rafferty; Brian Huffman; Evangelyn Brunson; Jenny Phung; James Madison University, Harrisonburg, VA

TP 011 Investigation of Matrix Effect Focused on Interaction among Matrix and Target Molecules; Mequni Wakimoto; Hajime Mizuno; Naohiro Tsuyama; Takano Harada; Tsutomu Masujima; Hiroshima Univ. Grad. Sch. Biomed. Sci, Hiroshima, Japan

TP 012 Optical profiling of an Agilent Jet Stream Technology electrospray by Laser-Induced-Fluorescence Coupled to Mass Spectrometry Measurements; Marion Girod; Rodolphe Antoine; Philippe Dugourd; CNRS Université Lyon 1, Villeurbanne, France

TP 013 Exploring the Molecular Organization in Solvent-Free MALDI Samples by Solid State NMR; Yannis Major 1, Hélène Pizzala 2, Fabio Ziarelli 3, Laurence Charles 4, Aix-Marseille Universities, UMR 6264, SACS, Marseille, France; Spectropole, Féd Sciences Chimiques-CNRS, FR 1739, Marseille, France

TP 014 Simulation of Material Removal in Ambient Laser Desorption Ionization Mass Spectrometry; Fan Huang; Kermit K. Murray; Louisiana State University, Baton Rouge, LA

TP 015 Particle Formation in Atmospheric Pressure Laser Desorption and Ionization; Thabiso Musapelo; Kermit K. Murray; Louisiana State University, Baton Rouge, LA

TP 016 New Insights in the Atmospheric Pressure Photoionization (APPI) Mechanisms Using Tunable Synchrotron VUV Radiation; David Toubl 1; Alexandre Giuliani 2, 3; Julie Allegrand 4; Olivier Laprévote 5, 6; Alain Brunelle 1; Centre de recherche de GIF, ICSN-CNRS, GIF-Sur-Yvette, France; DISCO beamline, Synchrotron Soleil, GIF-Sur-Yvette, FRANCE; Cepia, Institut National de Recherche Agronomique, Nantes, France; CTAC, EA446, Université Paris Descartes, Paris, France

TP 017 Mechanistic Study of Role of Toluene Molecules in Positive Mode APPI of Polycyclic Aromatic Compounds; Arif Ahmed; Cheol-Ho Choi; Sungkyung Kim; Kyungpook National University, Daegu, Republic of Korea

TP 018 Activation of C-C and C-H Bonds in Hydrocarbons by Field-Assisted Nitrogen Atom Insertion; Guangtao Li; Xin Li; Zheng
TP 019  
**Paper Spray Ionization using Solvents of Low Polarity or High Viscosity;**  
Anying Li; He Wang;  
Michael Wleklinksi; Ryan Espy; Zheng Ouyang; R. Graham Cooks; Purdue University, West Lafayette, IN

TP 020  
**Ion Yields and Ion Suppression “Hot-Spots” in Direct Analysis In Real Time Mass Spectrometry;**  
Glenn A. Harris; Caitlin E. Falcone; Facundo Fernandez; Georgia Institute of Technology, Atlanta, GA

TP 021  
**Characterization of the Compound-dependent Mechanisms of APCI using Ultra High Resolution TOF Mass Spectrometry;**  
Matthew Giardina; Timothy Judkins; Vlatcheslav Artaev; LECO Corporation, St. Joseph, MI

TP 022  
**Optimization and Damage Study of Ambient Mass Spectrometry using a PADI rce;**  
Tara La Roche Salter; Felicia Green; Ian Gilmore; James Bradley; National Physical Laboratory, Teddington, UK

TP 023  
**Enhanced Direct Ambient Analysis by Differential Mobility-Filtered Desorption Electrospray Ionization-Mass Spectrometry;**  
Facundo Fernandez; Asiri Galhana; Mark Kwaskin; Glenn A. Harris; Georgia Institute of Technology, Atlanta, GA

TP 024  
**Development of an Endoscopic DESI Sampling Probe;**  
Chien-Hsun Chen; Ziqing Lin; Sandiya Garmimela; Robert Graham Cooks; Zheng Ouyang; Biomedical Engineering, Purdue, West Lafayette, IN; Chemistry, Purdue, West Lafayette, IN

TP 025  
**Leaf Spray: Direct Ambient Ionization for Plant Tissue Analysis;**  
Jingjiang Liu; He Wang; R. Graham Cooks; Zheng Ouyang; Purdue University, West Lafayette, IN

TP 026  
**Ambient Ionization High Resolution Mass Spectrometric Fragmentation Behavior of Chalcone Derivatives Employing Direct Mass Spectrometry in Real Time (DART) Technique;**  
Amirreza Amighi; Nasser Ashgriz; Lisa M. Jewett; Adnan Kadi; Mohamed Attwa; A. F. M. Motiur Rahman; Adnan Kadi; Mohamed Attwa; A. F. M. Motiur Rahman; A. F. M. Motiur Rahman; National Institute for Environmental Administration, Alameda, CA; 2DPX Laboratories, USA, Inc., Peabody, MA; 2IONICS Mass Spectrometry, Peabody, MA; 3Institute of Pharmacy, Riyadh, Saudi Arabia

TP 027  
**Development of an Endoscopic DESI Discharge Ion Source and it's Application in Real Time Ambient Mass Spectrometry;**  
R. Graham Cooks; Zheng Ouyang; T. J. Begley; Charles N. Mcewen; ProSolia, Inc., Indianapolis, IN

TP 028  
**Quantitative Capabilities of DART-Orbitrap MS for Determination of Pesticides on Fruits and Vegetables;**  
Lenin Parrales; Peter T. Palmer; Adam Leung; San Francisco State University, San Francisco, CA; Food & Drug Administration, Alameda, CA

TP 029  
**Transmission-Mode Direct Analysis in Real Time (DART) Quadrupole Time-of-Flight Mass Spectrometry for Fast Untargeted Metabolomic Profiling of Human Serum;**  
Christina Jones; Tingting Hu; Facundo Fernandez; Georgia Institute of Technology, Atlanta, GA

TP 030  
**Intrasurgical Identification of Tissues by Direct Combination of Ultrasonic Surgical Aspiration and Sonic Spray Mass Spectrometry;**  
Karl C Schaefer; Julia Balog; Zoltan Takats; Justus-Liebig-University, Giessen, GERMANY; Medimass Ltd., Budapest, HUNGARY

TP 031  
**Optimisation and Damage Study of Ambient Mass Spectrometry using a PADI rce;**  
Tara La Roche Salter; Felicia Green; Ian Gilmore; James Bradley; National Physical Laboratory, Teddington, UK; 2Liverpool University, Liverpool, UK

TP 032  
**Ambient Mass Spectrometry: Ensuring Consistency in DESI;**  
Felicia Green; Tara La Roche Salter; Ian Gilmore; National Physical Laboratory, Teddington, UK

TP 033  
**Direct Ambient Analysis using Atmospheric Pressure Photoionization (APPI);**  
Kaveh Jorabchi; Sheng-Suan (Victor) Cai; Brian J. Nies; 59th ASMS Conference on Mass Spectrometry
TP 043  Enabling High Throughput Bioanalysis by Transmission Mode DART: In-line Desorption Ionization of Small Molecules from an Array of Samples; Elizabeth Crawford; Joseph Tice; Michael Festa; Brian D. Musselman; IonSense, Inc., Saugus, MA

TP 044  Rapid Sample Cleanup Procedure using Disposable Pipette Extraction (DPX) for Detection of Drugs in Urine by DART; Robert B. Cody; John Dane; William E. Brewer; JEL USA, Inc., Peabody, MA; DPX Laboratories, Columbia, SC

TP 045  Mass Spectrometric Fragmentation Behavior of Chalcone Derivatives Employing Direct Analysis in Real Time (DART) Technique; Adnan Kadi; Mohamed Attwa; A. F. M. Motuir Rahman; King Saud University, College of Pharmacy, Riyadh, Saudi Arabia

TP 046  Detecting Transient Organometallic Catalytic Intermediates on the Millisecond Timescale Using Desorption Electrospray Ionization; Richard H. Percy; Konstantin Chinning; Richard N. Zare; Stanford University, Stanford, CA

TP 047  Surface-Enhanced Desorption Electrospray Ionization Mass Spectrometry of Biomarkers using Silicon Substrates; John O’Brien; Ivan Jewett; Jennifer Brodbelt; The University of Texas, Austin, TX

TP 048  Representative Sampling and Monitoring of the Synthesis of Tetraphenylporphin with Desorption Electrospray Ionization Mass Spectrometry; Jonathan Person; Emily Backhus; Christopher Mulligan; Illinois State University, Normal, IL

TP 049  Rapid Screening of Performance Enhancing Drug Masking Agents in Biological Samples Using Desorption Electrospray Ionization Mass Spectrometry; Alexandra Eldridge; Kyle Vrcks; Eric Flesher; Christopher Mulligan; Illinois State University, Normal, IL

TP 050  Planar Separations and Analysis of Intact Tissue Samples using DESI-MS; Justin Wiseman; Prosolida, Inc., Indianapolis, IN

TP 051  Piezoelectric Driven Microplasma – a Non-Thermal Atmospheric Pressure Ionization Source; Albrecht Brockhaus; Alexander Laue; Albrecht Glasmachers; University of Wuppertal, Wuppertal, Germany

TP 052  Positive and Negative Ion Formation of Amino Acid and its Hydrated Clusters using Ambient Corona Discharge with Micro-devices; Mami Sakai; Mitsuo Takayama; Yokohama City University, Yokohama, JAPAN

TP 053  Dielectric Barrier Discharge Microplasma-Ionization for LC/MS Applications; Heiko Haven; Antje Michel; Bogdan Olenici-Craciunescu; Helma Geltenporth; Joachim Franzke; University of Wuppertal, Wuppertal, Germany; Leibniz-Institut für Analytische Wissenschaften, Dortmund, Germany

TP 054  Double Cylindrical Dielectric Barrier Discharge Ion Source and its Application in Different Fields; Mridul Kanti Mandal; Satoshi Ninomiya; Lee Chiu Chen; Takashi Iwama; Kenzo Hiraoka; University of Yamanashi, Kofu, Japan; The Yamanashi Prefectural Industrial Technology, Kofu, Japan

TP 055  Comparison of Ion Internal Energy Deposition with Surface Acoustic Wave Nebulization (SAWN) and Electrospray Ionization; Yue Huang; Sung Hwan Yoon; Scott Heron; Christophe Masselon; John Edgar; Frantishek Turcek; David R. Goodlett; University of Washington, Seattle, WA; CEA Grenoble, Grenoble, France

TP 056  Combined ESI/LIFDI-Ion Source for a FT-ICR Mass Spectrometer; Jürgen H. Gross; Bernhard Lindemann; Inst. of Organic Chemistry, Heidelberg University, Heidelberg, Germany; Linden CMS, Leeste, Germany

TP 057  Enhanced Rates of Bulk Solution Phase Microdroplets as Reaction Vessels; Abraham K Badu Tawiah; R. Graham Cooks; Purdue University, West Lafayette, IN

TP 058  Visualization of High Flow Electrospray with a Coaxially Flowing Gas; Farnan Sultan; Amirreza Amighi; Nasser Ashgriz; Lisa M. Cousins; Gholamreza Javahery; University of Toronto, Toronto, Canada; JIONICS Mass Spectrometry Group, Inc., Bolton, ON

TP 059  Study of a Labile Post Translational Modification using Alternating Current (AC) Electrospray; Katie Isbell; University of Notre Dame, Notre Dame, IN

TP 060  Theoretical Studies of Swirling Flow and Heating Methods on Droplet Evaporation in a Heated Coaxial Flow APCl Ion Source; Charles Jolliffe; Sergei Savtchenko; George Scott; Nasser Ashgriz; JIONICS Mass Spec Group, Inc., Bolton, ON; University of Toronto, Toronto, ON

TP 061  Super Atmospheric Pressure (P >1 atm) Electrospray Ion Source; Lee Chiu Chen; Mridul Kanti Mandal; Kenzo Hiraoka; University of Yamanashi, Kofu, Japan

TP 062  Vacuum Electrospray Assisted by Laser Irradiation; Satoshi Ninomiya; Lee Chiu Chen; Yuji Sakai; Kenzo Hiraoka; University of Yamanashi, Kofu, Japan

TP 063  Application of a Sheathless Capillary Electrophoresis-Electrospray Ionization-Mass Spectrometry (CE-ESI-MS) Platform for Peptide Analysis: Comparison to nanoLC-ESI-MS; Herbert H. Lindner; Klaus Faserl; Leopold Kremser; Bettina Sarg; Biocenter, Division of Clinical Biochemistry, Innsbruck, Austria

TP 064  Analytes Fractionation in Probe Electrospray Ionization; Kenzo Hiraoka; Mridul Kanti Mandal; Lee Chiu Chen; University of Yamanashi, Kofu, Japan

TP 065  Improving Ion Production and Efficiency with Obstruction Surfaces using Sonic Spray Ionization (SSI) Mass Spectrometry; Nicholas Chubatyi; Charles N. Mcewen; Univ. of the Sciences, Philadelphia, PA

TP 066  Analysis from ‘Non-ESI-Friendly’ Solvents using Continuous Flow-Extractive Desorption Electrospray Ionization-Mass Spectrometry; Li Li; Samuel Yang; Karel Lemr; Vladimir Havlicek; Kevin Schug; University of Texas Arlington, Arlington, TX; Palacky University, Olomouc, CZECH REPUBLIC; Institute of Microbiology, Prague 4, CZECH REPUBLIC

TP 067  Numerical Simulation of the Distribution of Ion Acceptance (DIA) in a commercial API
Source; Walter Wisssor; Matthias Lorenz; Thorsten Benter; University of Wuppertal, Wuppertal, Germany

TP 079 Quadrupole-Time Of Flight Mass Spectrometry as a Robust Tool for Characterizing Transition Metal Organic Complexes in Synthetic Reaction Samples; Tao Bo; Chencben Li; Agilent Technologies, Beijing, China

TP 080 Determination of an iNOS Inhibitor with Simultaneous Metabolite Identification and Endogenous Biomarker Quantituation using Accurate Mass Orbitrap Mass Spectrometry; John G. Swales; Richard T. Gallagher; Raimund Peter; Astrazeneca, Macclesfield, UK

TP 081 A Novel Peptide Mapping Method Using LCMS-IT-TOF with Peptide Accurate Mass Database; Djohan Kesuma; Zhaoqi Zhan; Shimadzu Asia Pacific, Singapore, SINGAPORE

TP 082 A Novel High Throughput Method Using Full Scan High Resolution Accurate Mass and Online Extraction for Plasma Protein Binding Determination; Kevin Cook; Mark Dreyer; Keeley Murphy; Thermo Scientific, San Jose, CA

TP 083 High-Resolution Mass Spectrometry for Analysis of Selected Drugs in Dried Blood Spots; Sangeeta Tanna; Elizabeth Cocks; Graham Lawson; De Montfort University, Leicester, UK

TP 084 The Development of High Resolution ESI-MS Methods for Structural Characterization of the Oligosaccharide Antibiotic Evernixinicin; Li-Kang Zhang; Birendra Pramanik; ‘Merck Research Laboratories, Kenilworth, NJ; ‘Retired, Parsippany, NJ

TP 085 Ultra High Resolution Accurate Mass LC-MS Analysis of Synthetic Cannabinoids (Spice) and their Metabolites in Urine; Kristine Van Natta; Thermo Fisher Scientific, San Jose, CA

TP 086 Profiling Histone H3 Isoforms in Differentiating Human Embryonic Stem Cells using ETD on a dQqC-Orbitrap; Chenxi Yang; Aaron Ledvina; Michael S. Westphall; Justin Brumbaugh; Joshua J. Coon; University of Wisconsin-Madison, Madison, WI

TP 087 A Medium-Throughput in vitro System Incorporating Hepatocyte Cultures and High Resolution Mass Spectrometry for Evaluating Metabolism and Biliary Clearance; Mary Grubb; Bristol-Myers Squibb, Pennington, NJ

TP 088 Characterization of Pepperminnt Essential Oils Grown in Different Areas by Gas Chromatography Ultra High Resolution Time of Flight MS (GC-HRT); Cory Fix; Joe Binkley; Kevin Siek; Jeffrey Patrick; LECO Corporation, St. Joseph, MI

TP 089 Rapid and Integrated Qualitative and Quantitative Metabolite Identification Process using a New Quadrupole Time-of-Flight Mass Spectrometer; Chiwu Emily Luk; Jonathan L. Josephh; William G. Humphreys; Bristol-Myers Squibb Co, Princeton, NJ

TP 090 High Throughput Screening using Multiplexed High Resolution Accurate Mass LC/MS; Keeley Murphy; Thermo Fisher Scientific, San Jose, CA

TP 091 AP MALDI Produced Ions Inspected with an Exact Mass Spectrometer; Kerstin Strupat; Olaf Schelbner; Tatiwang Arrey; Maciej Bromirski;
**TP 092**

**Metabolite Detection and Identification with Triple TOF High Resolution Mass Spectrometry and Metabolitepolite™ Coupled with Ultra Fast HPLC:** Xiaomei Gu; Ming Yao; Ragu Ramanathan; Ramaswamy Iyer; W. Griffith Humphreys; Bristol-Myers Squibb, Princeton, NJ

**TP 093**

**Non-targeted Screening of Psychiatric Substances in Legal Highs by Nano-LC-chip-Q/ToF:** Emilia Formal; Grzegorz Zuczninski; Andrzej Wojtyla; The John Paul II Catholic University of Lublin, Lublin, Poland; Maria Curie-Skodowska University, Lublin, Poland; Institute of Agricultural Science, Poland

**TP 094**

**Pomegranate Sample Profiling using Multivariate Data Analysis, High Resolution Chromatography, UV and Time of Flight MS Detection:** Marian Twok; Jennifer Burgess; Antonietta Gledhill; Kenneth Rosnack; Paul B Young; Dana Krueger; Waters Corporation, Milford, MA; Waters, Manchester, UK; Krueger Food Laboratories, Inc., Billerica, MA

**TP 095**

**High Performance Metabolic Profiling of Plasma Metabolites of Selected Mammalian Species and Mitochondrial Metabolomics:** Youngja Park; James Roede; Fred Strobel; Tianwei Yu; Dean Jones; Emory University, Atlanta, GA

**TP 096**

**The Determination of an Optimized FT-ICR Resolving Power to Achieve the Best Spectral Accuracy for Unknown Identification:** Christopher Thompson; Ming Gu; Bruker Daltonics Inc., Billerica, MA; Cerno Bioscience, Yardley, PA

**TP 097**

**Analysis of Persistent Organic Pollutants in Complex Matrices by Gas Chromatography – High Resolution Time of Flight Mass Spectrometry (GC-HRT):** David Alonso; Joe Binkley; Kevin Siek; Viacheslav Artaev; Leco Corporation, St. Joseph, MI

**TP 098**

**Identification and Quantitation of Strawberry Polyphenols and Their Metabolites in Human Plasma:** Katarzyna Banaszewski; Indika Edirisinghe, Ph.D.; Britt Burton-Freeman, Ph.D.; Jack C. Cappozzo; NCFST/ITT, Summit-Argo, IL

**TP 099**

**Evaluation of the Performance Improvements Needed in an ESI-QTOF-MS System for Qualitative and Quantitative Multi-Target Pesticide Screening in Food:** Carsten Baessmann; Ellen Scherbaum; Rebekka Loetterle; Petra Decker; Oliver Raether; Ilmari Krebs; Bruker Daltonik GmbH, Bremen, Germany; Chemisches und Veterinä runtersuchungsamt Stuttgart, Stuttgart, Germany

**TP 100**

**Higher HCD Energies and Xtract Function Improving Mapping Ubiquitin Sites using LTQ Velos Orbitrap:** Tatiana N. Boronina; Thomas K. Harris; Hassan Al-Ali; Robert N. Cole; Johns Hopkins School of Medicine, Baltimore, MD; University of Miami, Miller School of Medicine, Miami, FL

**TP 101**

**Can Isotopic Fine Structures of Peptides Improve Protein Identification in Proteomics:** Saša M. Miladinović; Anton N. Kozhinov; Michael V. Gorskov; Yuri O. Tsybin; Ecole Polytechnique Féderale de Lausanne, Lausanne, Switzerland; Institute for Energy Problems of Chemical Physics, Moscow, Russian Federation

**TP 102**

**A Strategy for Characterization of the Molecular Weight Distribution of PEG in Biological Samples:** Bethanne Warrack; Mark S. Bolgar; Purnima Khandelwal; Brian Redding; Petia Shipkova; Guodong Chen; Adrienne Tymia k; Bristol-Myers Squibb, Princeton, NJ; Spectrix Analytical Services, Princeton, NJ

**TP 103**

**Disulfide Mapping: Searching Stressed Glycoprotein Therapeutics for Disulfide Scrambled Species:** Cedric E. Bobst; Adriana Z. Kita; Igor A. Kaltashov; Melanie Lin; Paul Salinas; John J. Thomas; Philip J. Savickas; University of Massachusetts, Amherst, MA; Shire Pharmaceuticals, Cambridge, MA

**TP 104**

**A Comprehensive ESI-MS Study of Novel Gold(I) Complexes with Antineoplastic Properties:** Maria Stefanopoulou; Ricardo Rubbiani; Andreas Meyer; Ingo Ott; William S. Sheldrick; Dirk Wolters; Ruhr Universität Bochum, Bochum, Germany; Technische Universität Braunschweig, Braunschweig, Germany

**TP 105**

**Detection of Novel Degradation for Enzymes with ASG Amino Acid Sequence at Active Site:** Fanfei Yan; William S. Hancock; Shiw-lin Wu; Northeastern University, Boston, MA

**TP 106**

**Characterization of the N-terminally Extended Minor Form of a Recombinant Protein by Mass Spectrometry:** Xidong Feng; Kieran F. Geoghegan; Jeanne S. Chang; Kerry Kelleher; Paul W. Wu; Laura Lin; Francis Rajamohan; PharmaTherapeutics Research, Pfizer Inc., Groton, CT; BioTherapeutics Research, Pfizer Inc., Cambridge, MA

**TP 107**

**Analysis of Isoaspartic Acid in Monoclonal Antibodies:** Jian Zhang; Christopher Yu; Albert Lee; Judy H. Chou; Ashraf Amanullah; Genentech-Oceanside Pharma Tech Development, Oceanside, CA; Genentech-Protein Analytical Chemistry, South San Francisco, CA; PRPM, Irvine, CA; Tanvex, San Diego, CA

**TP 108**

**Non-targeted Screening of Psychactive Species and Mitochondrial Metabolomics:** Andreas Meyer; Ingo Ott; William S. Sheldrick; Dirk Wolters; Ruhr Universität Bochum, Bochum, Germany; Technische Universität Braunschweig, Braunschweig, Germany

**TP 109**

**Primary Sequence Determination of a Monoclonal Antibody against alpha-1-Antitrypsin using a Novel Mass Spectrometry-based Approach:** Eric Sossa; Pfizer, Cambridge, MA

**TP 110**

**Protein Therapeutics: Structural Characterization:**

**TP 111**

**Analysis of Isoaspartic Acid in Monoclonal Antibodies:** Min Liu; Janet Cheetham; Nina Cauchon; Judy Ostovic; Da Ren; Zhaohui Sunny Zhou; Amgen, Inc., Thousand Oaks, CA; Northeastern University, Boston, MA

**Analysis of Isoaspartic Acid in Monoclonal Antibodies:** Min Liu; Janet Cheetham; Gina Cauchon; Judy Ostovic; Da Ren; Zhaohui Sunny Zhou; Amgen, Inc., Thousand Oaks, CA; Northeastern University, Boston, MA

**Interaction between Therapeutic Proteins and Acrylic Acid Leachate:** Dengfeng Liu; Yasser Nashed-Samuel; Pavel V. Bondarenko; David N. Brems; Da Ren; Amgen Inc., Thousand Oaks, CA
TP 112  
*Unusual Susceptibility to Oxidation of a -Tryptophan-X-methionine- Amino Acid Sequence Present in the Light Chain of a Monoclonal Antibody;* Jay Charlebois; Matthew Mazur; Tun Liu; Qinwei Zhou; Rick Crowley; Imclone Systems, Branchburg, NJ

TP 113  
*Comprehensive Peptide Mapping of Antibody Protein, IgG by 2D LC/FT-ICR MS;* Kyu Hwan Park; Sang Beom Lee; Min-sun Kim; Hee Young An; Hyo-Jik Yang; Hyun Sik Kim; Korea Basic Science Institute, Daejeon, South Korea

TP 114  
*Sequence Verification Strategy to Enable Biosimilar Monoclonal Antibody Development;* Xian Huang; Anita Colvin; Marie Rose van Hovenrudij; CMC ICOS Biologics, Inc., Bothell, WA

TP 115  
*Identification of both Proteolytic Cleavage and protease in CHO Cell Production of Glucagon-like-peptide-1 Fusion Antibody by Proteomic Approach;* Qiaozheen Lu; Suli Liu; Shilaw-Lin Wu; William Hancock; Mike Tang; Yonghui Wang; Haimanti DoraI; Alex Santiago1; Marguerite Campbell2; Michael Bond3; Michael Lewis1; 1Northeastern University, Boston, MA; 2Centocor R and D, Radnor, PA

TP 116  
*Development of Microwave-Assisted Acid Hydrolysis Combined with MS and MS/MS for Determining Terminal Amino Acid Sequences of Proteins;* Yanan Tang; Liang Li; University of Alberta, Edmonton, Canada

TP 117  
*Characterization of Pertussis toxoid using mass spectrometry;* Manorama Tummala; Almary Chacon; Shwu-Maan Lee; Edward K. Chess; Peifeng Hu; Baxter Healthcare Corporation, Round Lake, IL

TP 118  
*Structural Determination of Drug-substance Related Variants using In-gel Digestion Coupled with Mass Spectrometric Characterization;* Xiaojing Zheng; Nikita Kulkarni; Ning Li; Regeneron Pharmaceuticals, Inc., Tarrytown, NY

TP 119  
*Development of a Tryptic Mapping Method To Optimize the Enzymatic Digestion and Sequence Coverage for a Monoclonal Antibody;* Qile Luo; Shivkumar Raidas; Biao Shen; Thomas Daly; Ning Li; Regeneron Pharmaceuticals, Tarrytown, NY

TP 120  
*Structural Characterization of Antibody Drug Conjugates in Animal Plasma by High Resolution Mass Spectrometry;* Baiyi Xue1; Sandra Alves2; Olivier Pasquier2; Patrick Soubayrol2; Jean-Claude Tabet1; 1University of Paris VI (UPMC), Paris Cedex 05, France; 2Sanofi-Aventis, Chilly-Mazarin, France

TP 121  
*Analysis of Antibodies using a Novel High Resolution Quadrupole Time-of-Flight Mass Spectrometry Platform and Chromatographic Separations;* Jeff Layne; Debbie Garrett; Michael Mcginley; Phenomenex, Torrance, CA

TP 122  
*Developing New Separation Methods for Intact Protein LC/MS Analysis of Large Proteins;* Jeff Layne; Debra Garrett; Michael Mcginley; Phenomenex, Torrance, CA

TP 123  
*Mass Spectrometry and Size Exclusion Chromatography Assisted Optimization of Proteins Conjugation to Transferrin;* Son N. Nguyen; Cedric E. Bobst; Igor A. Kaltashov; University of Massachusetts Amherst, Amherst, MA

TP 124  
*Characterization of Charge Heterogeneity in a Recombinant IgG1 Monoclonal Antibody by Cation Exchange Chromatography and Mass Spectrometry;* Jinhua (Jenny) Feng; Deepthi Sharma; Kenneth De Mel; Methal Albarghouthi; Anthony Shannon; Johnson Varghese; Patricia Cash; MedImmune, Gaithersburg, MD

TP 125  
*Strategies for Coupling of IEC and SEC to MS Detection for the Separation and Characterization of Related Substances in Biopharmaceuticals;* Wim Decroop; Evert-Jan Sneekes; Remco Swart; Dionex Corporation, Amsterdam, Netherlands

TP 126  
*Efficient and Sensitive Characterization of Intact Proteins by High-Performance Sheathless CE-ESI-TOFMS;* Govert Somsen; Rob Haselberg; Gerhardus de Jong; Utrecht University, Utrecht, Netherlands

TP 127  
*Characterization of IgG Charge Heterogeneities by IEF Gel Electrophoresis and Peptide Mapping;* Qing Tang; Mike Nedved; Peter Lisi; Johnson & Johnson, Radnor, PA

TP 128  
*Evaluation of Charge Variant Enrichment Methods for Use in cIEF Profile Characterization;* Zac Yates; Jessica Bjorklund; Justin Kim; Danielle Pace; Angen, Seattle, WA

TP 129  
*Advancements in Microfluidic Chip Technology for Rapid and Sensitive Detection of Sialylated Glycans from Erythropoietin;* Maggie Bynum; Gregory O Staples; Hongfeng Yin; Kevin Killeen; Agilent Laboratories, Santa Clara, CA

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*Analysis of Halogenated Aromatic Compounds by Electron Impact ionisation and Ion Mobility Separation on a GC-EI-Q-IMS-ToF;* Gareth Rhys Jones; Keith Richardson; Martin Green; Waters UK Ltd, Wythenshawe, Manchester, UK

TP 131  
*Characterization of Ortho-, Meta-, and Para-Isomers in POSS Coupling Systems using Travelling Wave Ion Mobility Mass Spectrometry;* Kai Guo1; Xiaopeng Li2; Yiwen Li3; Stephen Cheng2; Chrys Wesdemiotis1; 1Department of Polymer Science, University of Akron, Akron, OH; 2Department of Chemistry, University of Akron, Akron, OH

TP 132  
*Analysis of Isomeric Glucuronide Conjugates by Liquid Chromatography-Ion Mobility Spectrometry with Time-of-Flight Mass Spectrometry;* Joanna E. Barbara; Mark Horrigan; Paul C. Toren; Andrew Parkinson; XenoTech, LLC, Lenexa, KS

TP 133  
*The Determination of the Collision Cross-Section of Oligonucleotides Using Traveling Wave Ion-Mobility;* Christopher K. Bartow; David H. Russell; Texas A&M University, College Station, TX

TP 134  
*In-source Fragmentation of FAIMS-selected Ions in Combination with Time-of-Flight Mass Spectrometry;* Lauren J. Brown1; Robert W. Smith1; Danielle E. Toutoungi1; James C. Reynolds1; Anthony W.T. Bristow1; Andrew D. Ray1; Ashley Sage1; Daniel Weston1; Ian Wilson1;
TP 135 Separation of Isoboronic Steroids using Differential Mobility Spectrometry Tandem Mass Spectrometry; Michael J. Y. Jarvis; Doina Caraiman; J.C. Yves Leblanc; Brad Schneider; Andre Schreiber; Lisa Sapp; Adrian Taylor; AB SCIEX, Concord, Canada

TP 136 Analysis of cis/Trans Isomers of Carotenoids using Ion Mobility and Cation Exchange Chromatography and Mass Spectrometry; Linlin Dong; Henry Shion; Roderick Davis; Richard B. Van Bremen; 1University of Illinois College of Pharmacy, Chicago, IL; 2Waters Corp., Milford, MA; 3Univ. of Illinois at Chicago Research Ctr, Chicago, IL

TP 137 Diastereomer Analysis by Travelling Wave Ion Mobility and Density Function Theory; Iain D G Campuzano; Matthew F Bush; Keith Richardson; Scott Gillingwater; Claire Beaumont; Hyungjun Kim; Waters Corporation, Manchester, UK; 1University of Oxford, Oxford, UK; 2DMPK GlaxoSmithKline, Ware, Hertfordshire, UK; 3Center for Materials Simulations and Design, Daejeon, Republic of Korea

TP 138 Gas Phase Structures of Polyethylene Glycol Ions studied via Ion Mobility and Mass Spectrometry; Carlos Larriba Andaluz; Juan Fernandez De La Mora; 1Yale University, New Haven, CT; 2Yale University - Mechanical Engineering Department, New Haven, CT

TP 139 Separation and Characterization of ‘Protonmers’ by TWIM-MS/(MS); Priscila Lalli; Bernardo Iglesias; Gilberto Sa; Romeo Daroda; Vanderleia Souza; Kotti Araki; Marcos Eberlin; 1Thomson Mass Spectrometry Laboratory, UNICAMP, Campinas, SP, Brazil; 2University of Sao Paulo, Institute of Chemistry, Sao Paulo, SP, Brazil; 3National Institute of Metrology, Inmetro, Duque de Caxias, RJ, Brazil

TP 140 Lipid Profiling and Imaging using a MALDI – Ion Mobility – TOF MS; Gregg M Schieffer; Thomas Egän; Shelley N Jackson; Jeremy D Post; Ernest K. Lewis; J. Albert Schultz; Amina S. Woods; 1NIAID-I/IR, NIH, Baltimore, MD; 2Ionwerks, Inc., Houston, TX

TP 141 High-throughput Proteomics Platform Demonstrated for Liver Disease Progression Biomarker Verification; Erin Baker; Kristin Burum; Daniel Orton; Yehia Ibrahim; William Danielson III; Kevin Crowell; Jon Jacobs; Matthew Monroe; Gordon Sluyss; Anuj Shah; Maria Luna; Marina Gritsenko; David Purdy; Deborah L Diamond; Brian McMahan; Brenna Simons; Gordon Anderson; Michael Katze; Mikkel Behol; Richard D. Smith; 1Pacific Northwest National Laboratory, Richland, WA; 2University of Washington, Seattle, WA; 3Alaska Native Tribal Health Consortium, Anchorage, AK

TP 142 A Mobility Database of Cationized Peptide Ions: Explorations in Metal-Peptide Binding Effects on Structure; Jonathan Dilger; Matt Glover; Stephen Valentine; David E. Clemmer; 1Indiana University, Bloomington, IN; 2Naval Surface Warfare Center, Crane Division, Crane, IN

TP 143 Analysis of Wound Fluid by Ion Mobility-Mass Spectrometry for Biomolecular Signatures of Diabetic Wound Healing; Kelly Hines; Samir Ashfaq; Jeffrey Davidson; Lily Wang; Susan Opaleni; John A. Mclean; 1Vanderbilt University, Nashville, TN; 2Texas A&M, College Station, TX

TP 144 Revealing the High Molecular Diversity of Miller’s Prebiotic Reaction Products by Ultra Performance Liquid Chromatography-Ion Mobility Spectrometry-Mass Spectrometry; Manshui Zhou; Henderson James Cleaves; Jeffrey L. Bada; Facundo M. Fernandez; 1Georgia Institute of Technology, Atlanta, GA; 2Carnegie Institute of Washington, Washington, Washington DC; 3Scripps Institution of Oceanography, UCSD, La Jolla, CA

TP 145 The Use of a Cross Section Database and Intrinsic Amino Acid Size Parameters for the Improvement of Peptide Identification; Michael Ewing; Stephen Valentine; Jonathan Dilger; Matt Glover; Scott Gillingwater; Chris Hughes; David E. Clemmer; 1Indiana University, Bloomington, IN; 2Waters Corporation, Middletown, NJ; 3Waters, Manchester, UK

TP 146 Use of a High-Resolution Ion Mobility Mass Spectrometer for the Separation and Characterization of Small Organic Molecules in Complex Matrices; Jasper Boschmans; Frank Sobott; Paul Van Schil; Ernst de Bruijn; Filip Lemiëre; 1Center for Proteomics, University of Antwerp, Antwerp, Belgium; 2University Hospital of Antwerp, Antwerp, Belgium; 3Catholic University of Leuven, Leuven, Belgium

TP 147 Microfluidic-Coupled Ion Mobility-Mass Spectrometry Platform for Real-Time, Temporally-Resolved Analysis of Excreted Cellular Materials; Jeffrey Enders; Christina Marasco; Cody Goodwin; Jody May; Kevin Seale; John Wikswo; John A. Mclean; 1Vanderbilt University Department of Chemistry, Nashville, TN; 2Vanderbilt University Biomedical Engineering, Nashville, TN; 3Vanderbilt University Department of Physics, Nashville, TN

TP 148 Data independent MALDI Ion Mobility Acquisition for the Analysis of Tryptic Peptides for Proteomic and MALDI Imaging Applications; Emmanuelle Claude; Marie Claude Djidal; Jim Langridge; Waters corporation, Manchester, UK; 2The Institute of Cancer Research, UK, London, UK

TP 149 Coupling Nanospray and High Field Asymmetric Waveform Ion Mobility Spectrometry for Gas Phase Fractionation in Tandem Mass Spectrometry Experiments; Kristian E. Swearingen; Richard S. Johnson; Robert Mottz; Institute for Systems Biology, Seattle, WA

TP 150 3D Wine Analysis by Traveling Wave Ion Mobility Mass Spectrometry; Fiayms Leno Silva; Maia Fasciotti; Priscila Lalli; Claudio Messias; Gilberto Sa; Vanderleia Souza; Romeo Daroda; Marcos Eberlin; 1Thomson Mass Spectrometry Laboratory, UNICAMP, Campinas, Brazil; 2School of Agriculture Engineering, UNICAMP, Campinas, Brazil; 3National Institute of Campinas, Inmetro, Duque de Caxias, Brazil
TP 151  Localization of Modified Sites on Peptides and Proteins using High-Resolution Differential Ion Mobility Spectrometry; Alexandre A. Shvartsburg; David Singer; Ralf Hoffmann; Andrew Creese; Helen Cooper; Richard D. Smith; \textsuperscript{1}PNL, Richland, WA; \textsuperscript{2}Inst. for Bioanalytische Chemie, Univ. Leipzig, Leipzig, Germany; \textsuperscript{3}University of Birmingham, Birmingham, UK

TP 152  Multi-dimensional Separations using Ion Mobility-Mass Spectrometry for Natural Product Discovery; Cody Goodwin; Ruth McNees; Kasia Derewacz; Larissa S. Fenn; John A. Mclean; Brian Bachmann; \textsuperscript{1}Vanderbilt University Department of Chemistry, Nashville, TN; \textsuperscript{2}Vanderbilt Institute of Chemical Biology, Nashville, TN; \textsuperscript{3}Waters Corporation, Cary, NC

TP 153  Tertiary Structure Analysis of IgG Drug Products using Electrospray Quadrupole Ion-Mobility Time-of-Flight Mass Spectrometry; Kimura Mikiko; Isamu Terashima; Nobuhisa Kawakami; Sumiko Okamoto; Akiko Koga; Chugai Pharmaceutical Co.,Ltd, Tokyo, Japan

TP 154  Top-Down Structural Characterization of Protein Using ESI-MS-CID-IM-MS; Nathanael F Zinnel; College Station, TX

TP 155  Disulfide Bonds Assignment and Folding Characterization of Peptide Toxins by Ion Mobility Mass Spectrometry; Loic Quinton; Julien Echterbille; Edwin De Pauw; University of Liege- Labo. Spectrometrie de Masse, Liege, Belgium

TP 156  Structure and Topology of the Escherichia coli Cascade Complex Studied by Native Ion Mobility Mass Spectrometry; Ioana M. Barbu; Esteban Casadesus; Arjan Barendregt; Jelle M. Bultema; Mattijas M. Jore; Magnus Lundgren; Edze R. Westra; Stan J.J. Brouns; Blake Wiedenhof; Jennifer A. Doudna; Egbert J. Boekema; John van der Oost; Albert J.R. Heck; \textsuperscript{1}Biomolecular Mass Spectrometry and Proteomics, Utrecht, Netherlands; \textsuperscript{2}Department of Biophysical Chemistry, Groningen, The Netherlands; \textsuperscript{3}Laboratory of Microbiology, Wageningen, Netherlands; \textsuperscript{4}Howard Hughes Medical Institute, CA

TP 157  On the Two Gas-Phase Conformers of the Large Complex GroEL and the Malleability of Protein Tons; Juan Fernandez De La Mora; Yale University - Mechanical Engineering Dept, New Haven, CT

TP 158  Ion mobility and Time-of-Flight Mass Spectrometry Characterization of Covalent and Non-Covalent Protein Dimerization; Ryan Preston; Michael Bacica; Wade Diehl; Ben Bolanos; Robert Murphy; \textsuperscript{1}Pfizer / CovX, San Diego, CA; \textsuperscript{2}Pfizer Global R & D, San Diego, CA

TP 159  IMS for Characterisation of Impurities in New Biological Entities; Kim F. Haselmann; Rune Salbo; Peter K Nielsen; Novo Nordisk, Maaloev, Denmark

TP 160  Global Deglycosylation in High Throughput LC-MS Glycomics: Comparing Microwave, Barocycling, and Ultrasound Effects on PNGase F with Human Serum; Scott R. Kronewitter; Robert A. Heegel; Daniel J. Orton; Heather M. Brewer; Carrie D. Nicora; Daniel Lopez-Ferrer; Gordon W. Slys; Matthew E. Monroe; Kevin L. Crowell; Brian L. LaMarche; Anuj R. Shah; Ronald J. Moore; Gordon A. Anderson; David G. Camp II; Richard D. Smith; Pacific Northwest National Lab, Richland, WA

TP 161  Systematic Studies towards Microwave-aided O-glycan Release; L. Renee Ruhaak; M. Lorna De Leon; Hyun Joo An; Carillo B. Lebrilla; University of California, Davis, CA

TP 162  Exoglycosidase Digestion of Oligosaccharides on a Stainless Steel MALDI Target; Elisabeth Kast; Elizabeth Higgins; GlycoSolutions, Marlborough, MA

TP 163  Glycan Labeling in Aqueous Solution; Suping Zhang; Steven Becht; PPD, Inc, Middleton, WI

TP 164  Isoliquiritigenin (4,2′,4′-trihydroxychalcone); a New MALDI Matrix for Neutral Oligosaccharides Analysis; shuying liu; Hongmei Yang; Changchun Inst Appl Chem, Changchun, China

TP 165  Relationship between Sweet Spot for Glycopeptides in Matrix-Assisted Laser Desorption/Ionization and Specific Crystal Polymorph of 2,5-dihydroxybenzoic Acid; Hisako Okumura; Takashi Nishikaze; Hiroshi Jinmei; Junko Amano; The Noguchi Institute, Tokyo, Japan

TP 166  Ionic Liquid Assisted Electrospray Ionization of Polysaccharides; Yu-Ling Chang; Yu-Chun Lee; Wen-Bin Yang; Chuan-Hua Chen; \textsuperscript{1}Genomics Research Center, Academia Sinica, Taipei, Taiwan; \textsuperscript{2}The Biology Department, Johns Hopkins University, Baltimore, MD

TP 167  Hydrazide Coated Chip for Capture and on Target Analysis of Glycans; S. Jake Yang; Hui Zhang; Johns Hopkins Medical Institutions, Baltimore, MD

TP 168  Characterization and Quantitation of Synthetic Galactooligosaccharide Isomers by Isotopic Labeling and nanoLC-MS Methods; Kyle Peacock; Mariana Barboza; Man Tsui; Maartje Franse; Bill King; David Mills; Carlito Linhardt; Jon Amster; Geert-Jan Boons; \textsuperscript{1}University of Georgia, Athens, GA; \textsuperscript{2}Rensselaer Polytechnic Institute, Troy, NY

TP 169  Differentiating Carbohydrate Positional and Structural Isomers by Ion Mobility Mass Spectrometry; Weibin Chen; Ying-Qing Yu; Asish Chakraborty; Henry Shion; John Skilton; Waters Corporation, Milford, MA

TP 170  Glycan Structural Elucidation and Glycan Structural Isomer Differentiation Using A Bioinformatics Tool; Julian Saba; Amy Zumwalt; Ningombam Sanjib Meitei; Arun Apte; Rosa Viner; \textsuperscript{1}Thermo Fisher Scientific, San Jose, CA; \textsuperscript{2}PREMIER Biosoft International, Palo Alto, CA

TP 171  Differentiation of the Stereochemistry and Anomeric Configuration for 1,3-Linked Disaccharides via Tandem Mass Spectrometry and 18O-labeling; Chiharu Konda; Brad Bendiaux; Yu Xia; \textsuperscript{1}Purdue University, West Lafayette, IN; \textsuperscript{2}University of Colorado Health Sciences Center, Aurora, CO; \textsuperscript{3}Purdue University, West Lafayette, IN

TP 172  Quantification of Plasma Glucose 2H-enrichment from Deuterated Water by LC-MS/MS; Vera Mendes; Ivan Viegas; Ivana Jarak; John Jones; Bruno Manadas; "Centre CARBOHYDRATES: NEW APPROACHES; 160 - 188
for Neuroscience and Cell Biology, Cantanhede, PORTUGAL; 1IMAR, University of Coimbra, Coimbra, Portugal; 2Department of Life Sciences, University of Coimbra, Coimbra, Portugal

TP 173 Validation of a Surrogate Derivative LC/MS/MS Method for the Determination of Glucose in Human Plasma with [13C6]-Glucose as a Tracer; Taiga Tang; Kemuel Escobar; Fei Zhang; outdoors; 'Xenobiotic Laboratories, Inc., Plainview, NJ; 'XBL-China, Nanjing, P. R. China

TP 174 Quantification of Permethylated N-glycans derived from Human Blood Serum Using Multiple Reaction Monitoring (MRM) LC-MSMS; Janie Desantos-Garcia; Yunli Hu; Yehia Mecrefh; Texas Tech University, Lubbock, TX

TP 175 Negative Electron Transfer Dissociation Fourier Transform Mass Spectrometry of Sulfated Glycosaminoglycan Carbohydrates; Jeremy Wolff; Franklin E. Leach III; Melissa Ly; Sailaja Arungundam; Kanar Al-Mafraj; Andre Venot; Geert-Jan Boons; Robert J. Linhardt; Jon Amstorp; Bruker Daltonics, Billerica, MA; 2University of Georgia, Athens, GA; 3Rensselaer Polytechnic Institute, Troy, NY

TP 176 Electron Transfer Dissociation (ETD) vs. Electron Capture Dissociation (ECD) of Metal-adducted Oligosaccharides; Wen Zhou; Kristina Hakansson; University of Michigan, Ann Arbor, MI

TP 177 Negative Ion Mode Electron Induced Dissociation (EID) of Glycans; Pi Gao; Kristina Hakansson; University of Michigan, Ann Arbor, MI

TP 178 Sulfate Migration during MS Analysis of Sulfated Oligosaccharides; Dharmuji Kenny; Niclas Karlsson; Gothenburg University, Gothenburg, Sweden

TP 179 Electron Transfer Dissociation of Permethylated Oligosaccharides: An Investigation of Different ETD Chemical Reagents for Carbohydrates; Liang Han; Catherine E. Costello; Boston University, Boston, MA; 2Boston University School of Medicine, Boston, MA

TP 180 Mass Spectrometric Method for Determining the Uronic Acid Epimerization in Heparan Sulfate Disaccharides Generated using Nitril Acid; Vanessa Mendoza; Xiaofeng Shi; Joseph Zaia; Boston University School of Medicine, Boston, MA

TP 181 Investigations of Surface-Induced Dissociation for Site-Specific Glycan Mapping; Andrew Vanschoick; Vicki Wysocki; University of Arizona, Tucson, AZ

TP 182 Charge-localization Isomers of a Disaccharide-disulfate Observed by the (-) ESI-MS/MS; Yoko Ohashi; Masayuki Kubota; Hiroshi Hatase; Takashi Hirano; Shojiro Maki; Haruki Niwa; The Univ. of Electro-Communications, Chofu, Tokyo, Japan; 2Brain Sci. Inst., RIKEN, Wako, Saitama, Japan; 3Thermofisher Scientific Co., Yokohama, Kanagawa, Japan

TP 183 Characterizing Mixtures of Glycan Isomers using Multiple Collision Energy Tandem MS; Jayier Satulovsky; Gregory O. Staples; Maggie Bynum; Hongfeng Yin; Kevin Killeen; Agilent Laboratories, Santa Clara, CA

TP 184 Separation and Characterization of Heparan Sulfate Tetrasaccharide Isomers Differing Only in Hexuronic Acid Stereochemistry Using ESI-FAIMS and FTICR-MS/MS with EDD; Muchena J. Kaillema; Franklin E. Leach III; Sailaj Arungundrum; Kanar Al-Mafraj; Andre Venot; Melissa Ly; Tatiana Laremore; Desmond Kavanagh; Kevin A. Park; Robert J. Linhardt; Jon Amstorp; Geert-Jan Boons; 'University of Georgia, Athens, GA; 2Rensselaer Polytechnic Institute, Troy, NY; 3Penn State, University Park, PA; 4Bruker Daltonics, Inc., Billerica, MA

Identification of Sialic Acid Linked to Internal N-acetylhexosamine Residues on Mucin Glycoproteins with Negative Ion Mode CID Fragmentation; Kristina Thomsson; Gunnar C. Hansson; University of Gothenburg, Gothenburg, Sweden

Differentiation of Underivatized Monosaccharides by Atmospheric Pressure Chemical Ionization Quadrupole Time-of-Flight Mass Spectrometry (APCI/QTOF-MS); Zhenqian Zhu; Liuqeng Song; John Bartmess; Department of Chemistry, University of Tennessee, Knoxville, TN

Collision-induced Dissociation versus Electron Transfer Dissociation of Metal-adducted Oligosaccharides; Malikharuna Bogula; Carolyn J. Cassad, A, Park; 2Boston University School of Medicine, Boston, MA; 3University of Alabama, Tuscaloosa, AL

Detection and Quantitation of Intact Anionic Polysaccharides by Ion-Pair Reversed Phase Chromatography and Source-Induced Fragmentation Mass Spectrometry; Christopher Jones; Liqiong Fang; Edward K. Chess; Jeffrey Sauter; Baxter Healthcare Corp., Round Lake, IL

TP 185 TUESDAY POSTERS

TP 186 Positive Ion Mode Electron Induced Dissociation (EID) of Glycans; Di Gao; Kristina Hakansson; University of Michigan, Ann Arbor, MI

TP 187 Negative Ion Mode Electron Induced Dissociation (EID) of Glycans; Pi Gao; Kristina Hakansson; University of Michigan, Ann Arbor, MI

TP 188 Sulfate Migration during MS Analysis of Sulfated Oligosaccharides; Dharmuji Kenny; Niclas Karlsson; Gothenburg University, Gothenburg, Sweden

TP 189 Regioselectivity of Human UDP-Glucuronosyltransferase and Sulfortransferase Isozymes in Flavonoid Biotransformation by Metal Complexation and Tandem Mass Spectrometry; Scott A. Robotham; Jennifer S. Brodbelt; University of Texas at Austin, Austin, TX

TP 190 Identifying Previously Undocumented Glutamine Conjugates Utilizing MS/MS Fragmentation Patterns and Accurate Mass Data; John J. Lennon; Anne M. Evans; Klaus Peter Adam; Matthew Mitchell; Metabolon, Inc., Durham, NC

TP 191 Characterization and Profiling of Novel Diterpene Glycosides from Glandular Trichomes of the Wild Tomato Relative Solanum habrochaites; E.A. Prabodha Ekanayaka; Chao Li; A. Daniel Jones; Michigan State University, East Lansing, MI

TP 192 Regioselectivity of Human UDP-Glucuronosyltransferase and Sulfortransferase Isozymes in Flavonoid Biotransformation by Metal Complexation and Tandem Mass Spectrometry; Scott A. Robotham; Jennifer S. Brodbelt; University of Texas at Austin, Austin, TX

TP 193 Towards Structure Elucidation of Flavonoid Compounds in Complex Mixtures by Higher-
energy Induced Collisional Dissociation (HCD) on an LTQ-Orbitrap; Mikel R. Roe; Jerry D. Cohen; Adrian D. Hegeman

TP 194 Studying Fragmentation Pathways of Multiple-Cyclic Diterpenoid Phytosteroids under CID by Unknown GA Identification; Baichen Zhang; Leslie M. Hicks; Danforth Center, St. Louis, MO

TP 195 Identify Unknown Compounds in GC-MS Based Metabolic Profiling: GC-APCI-TOF Analysis of a Corynebacterium Glutamicum AfpP2D Mutant Strain; Aiko Barsch; Marcus Persicke; Jens Plassmeier; Karsten Niehaus; Gabriela Zurek; Sandy Yates; Bruker Daltonik GmbH, Bremen, Germany; Center für Biotechnologie, Universität Bielefeld, Bielefeld, Germany; Bruker Daltonics, Fremont, CA

TP 196 Disclosing Oxidatively Damaged Metabolites under Homeostatic Control of Mammalian Cells by LC-MS-based Metabolomics: Daiki Setoyama; Yoshinori Fujimura; Kiyoshi Sakai; Kazuhiro Ichikawa; Hiroyuki Wariishi; Daisuke Miura; Kyushu University, Fukuoka, Japan

TP 197 Characterizing Small Molecules in Biological Extracts using IntelliXtract Data Processing on High Resolution Accurate Mass Time-of-Flight Data; Margaret Antles; Graham A. McGibbon; Vitaly Bashin; Jeffrey S. Patick; Kevin Siek; ACD/Labs, Toronto, Canada; LECO Corporation, Saint Joseph, MI

TP 198 Differential Metabolomic Analysis of Corn Leaf Extracts by Liquid Chromatography - High Resolution Time of Flight Mass Spectrometry (LC-HRT); Jan Hazebroek; Pioneer Hi-Bred International, Johnston, IA

TP 199 Mass spectrometric Identification of HOCl-Mediated Heme Degradation Products of Hemoglobin; Jaeman Byun; Dhiman Maitra; Ghassan Saed; Husam Abu-Soud; Subramaniam Pennathur; University of Michigan, Ann Arbor, MI; Wayne State University, Detroit, MI

TP 200 Core-structure of Drug Metabolism Study by MS analysis of Unknown Metabolite Identification; Yimin Wu; Avalyn Lewis; Azeret Zuniga; Liang Li; University of Alberta, Edmonton, Canada

TP 201 Targeted Approach for Data Mining Untargeted Metabolomics Study; Syed Salman Lateef; Sudha Rajagopalan; Siji Joseph; Nilanjan Guha; Yugandhar Reddy; Agilent Technologies India Pvt. Ltd, Bangalore, India

TP 202 An LC-MS/MS Spectral Library Containing Thousands of Compounds Facilitates Metabolite Identification in Yeast Exposed to Immunosuppressant Drugs; Stefan Jenkins; Steven M. Fischer; Theodore R. Sang; Agilent Technologies, Inc, Santa Clara, CA

TP 203 Retention Index as Filter for Molecular Formulas in Derivatization based GC-MS; Sangeeta Kumari; Tobias Kind; Oliver Fiehn; Metabolomics Fiehn Lab, Genome centre, UC Davis, Davis, CA

TP 204 A Workflow for Metabolite Identification from LC-MS/MS data; Bin Zhou; Junfeng Xiao; Habtom Ressom; ECE Department, Virginia Tech, Falls Church, VA; Lombardi Cancer Center, Georgetown University, Washington, DC

TP 205 Development of Algorithm Enabling Data-driven Determination of Elemental Composition based on Isotopic Peak Ratio Observed by Ultra-high-resolution FT-ICR-MS; Tatsuhiko Nagao; Daichi Yukihira; Yosinori Fujimura; Daisuke Miura; Hiroyuki Warishii; Kyushu University, Fukuoka, Japan

TP 206 Fragmentation Patterns and Rat Metabolite Identification of 4-anilinoquinazoline-based Compounds by LC-MS and MS/MS; Alexandre F. Gomes; Silvana A. Rocco; Kleger G. Chordia; Timothy L. Macdonald; Stephen Mcdonald; Mark Wrona; Jeff Goshawk; Mike Kean; Novartis Pharma AG, Basel, Switzerland

TP 207 Diagnostic Neutral Losses and Common Fragment Ions for Putative Identification of Amine-containing Metabolites; Jiamin Zheng; Azeret Zuniga; Avalyn Stanislaus; Liang Li; University of Alberta, Edmonton, Canada

TP 208 Computation of Fragmentation Trees from Metabolite GC/MS Data; Franziska Hufsky; Florian E Rasche; Sebastian Böcker; Friedrich-Schiller-University Jena, Jena, Germany; Max Planck Institute for Chemical Ecology, Jena, Germany

TP 209 Improved Metabolite Identification using Cross-Platform LC-MS Retention Prediction By Flow Rate and Gradient Profile Back-Calculation; Paul G. Boswell; Jonathan R. Schellenberg; Peter W. Carr; Jerry D. Cohen; Adrian D. Hegeman; University of Minnesota, Minneapolis/St. Paul, MN

TP 210 New Developments in the Synthesis of Drug/Xenobiotic Metabolites and the Prediction thereof by Means of On-line Electrochemistry/MS; Joann Purkerson; Agnieszka Kraf; Hendrik-Jan Brouwer; Martin Eysberg; Jean-Pierre Chervet; Antec USA, Palm Bay, FL; Antec, Zouterwoude, Netherlands Direct Detection, Structural Characterization and Isolation of Novel Oxidative Chemical Matter Using an Electrochemistry-MS Platform; Smriti Khera; Chris Fotsch; Joann Purkerson; Paul Schnier; Steve Hollis; Amgen Inc., South San Francisco, CA; Antec (USA), Palm Bay, FL

TP 211 Rapid Generation and Identification of Oxidative Metabolites by Electrochemistry Coupled Online to LC/ESI-MS; Hannah Simon; Uwe Karst; University of Münster, Münster, Germany

TP 212 Simulation of the Metabolism of the Anti-platelet Drug Ticlopidine with Electrochemistry/Liquid Chromatography/Mass Spectrometry; Helene Faber; Uwe Karst; University of Münster, Münster, Germany

TP 213 Investigation of the Skin Sensitizing Potential of Eugenol and Isoeugenol by Electrochemistry Coupled to Liquid Chromatography and Mass Spectrometry; Daniel Mellert; Torsten Vielhaber; Anne Baumann; Raniero Zazzaroni; Uwe Karst; University of Muenster, Muenster, Germany; Unilever, Bedford, UK
TP 215  *Glutathione S-Transferase pi Trapping Approach for the Characterization of Reactive Metabolites in Human Liver Microsomes;* Hideo Yukinaga; Haruo Iwabuchi; Osamu Okazaki; Takashi Izumi; Daiichi Sankyo Co., Ltd., Tokyo, Japan

TP 216  *High Resolution Mass Spectrometry: Screening Strategies Using a Hybrid Linear Ion Trap-Orbitrap to Avoid the Misidentification of Reactive Metabolites;* Regina Nardi; Dilrukshi Ramanathan; Kean University, Union, NJ

TP 217  *A Neutral-Loss Searching Algorithm for High Resolution UPLC-MS Data Processing: Application for Rapid Detection of Glutathione Conjugates;* Xiaochun Zhu; Mike Hayashi; Raju Subramanian; Amgen, Inc., Thousand Oaks, CA

TP 218  *Enaminone as a Reactive Metabolite: Studies towards Understanding of Idiosyncratic Toxicity of Duloxetine;* Min Yang; Mahendra D. Chordia; Timothy L. Macdonald; University of Virginia, Charlottesville, VA

TP 219  *LC-MS/MS Study of Ginseng Metabolism;* Carmai Seto; Suma Ramagiri; Takeo Sakuma; Ed Lui; Matthew Barnes; Liqe Coolen; AB SCIEX, Concord, Canada; Ontario Ginseng Innovation & Research Consortium, London, Canada; University of Western Ontario, London, Canada

TP 220  *Evaluation of Different Trapping Agents used to Identify Reactive Intermediates in Biotransformation Studies;* Michael Kiffe; Werner Gertsch; Reiner Aichholz; Joachim Blanz; Jérôme Dayer; Thierry Delemonté; Philippe Ramstein; Novartis Pharma AG, Basel, Switzerland

TP 221  *Metabolite Identification using Fragment Interpretation Functions Integrated within MetaboLite ID Software;* Alina Dindyal-Popescu; Carmai Seto; Shaokun Pang; Hesham Ghabarah; AB SCIEX, Concord, Canada

TP 222  *Evaluation of Chemically Intelligient Acquisition and Processing Tools as a Platform for Discovery Metabolite Identification;* Russell J Mortishire-Smith; Pascale Proost; Filip Cuyckens; Gary Impye; Hesham Ghabarah; Carmai Seto; Johnson & Johnson PR&D, Beerse, BELGIUM; AB SCIEX, Concord, ON

TP 223  *Assessment of Metabolite Identification using Mass-MetaSite and High Resolution Mass Spectrometry;* Andreas Brink; Ruth Haas; Kirsten Eickhoff; Ismael Zamora; Fabien Fontaine; Axel Paehler; F. Hoffmann-La Roche Ltd, Basel, Switzerland; Lead Molecular Design, Sant Cugat del Valles, Spain

TP 224  *IsoCount: Software-assisted Localization of Biotransformations by High-Resolution Mass Spectrometry;* Wijnand Mooji; Leclercq Laurent; Michael Hartshorn; Russell Mortishire-Smith; Alastair Hill; Filip Cuyckens; Jeff Goshawk; Stephen Mcdonald; Alan Millar; Johnson & Johnson, Beerse, BELGIUM; Waters, Manchester, UK; Dotmatics, Bishops Stortford, UK

TP 225  *Novel Tools for Automated Metabolite Identification, Biotransformation Localization and Quantitation using UPLC-QTOF MSE;* Stephen Mcdonald; Mark Wrona; Jeff Goshawk; Alan Millar; Waters Corporation, Milford, MA; Waters, Manchester, UK

TP 226  *High-resolution Accurate Mass-Measurements and Metabolite Identification: an Automated Approach using Fragment Prediction in Combination with Fragment Ion Search (FISH);* Paul-Geirard Lassahn; Swiss BioAnalytics AG, Birsfelden, Switzerland

TP 227  *Identification of in vitro Lycopene Metabolites using Isotope Pattern Dependent MS-MS;* Jeffrey H. Dahl; Richard B. Van Bremen; Shimadzu Scientific Instruments, Columbia, MD; University of Illinois, Chicago, IL

TP 228  *Elucidating the Metabolism of Oxyntomodulin Like Peptide “A” Using LC/MS/MS and Radiochromatography;* Shakey Quazi; Pfizer, Andover, MA

TP 229  *Characterization of Biliary Metabolites of the Potent 5-HT1D Receptor Antagonist, Elzasonan in Rats by HPLC/RAM/ESI/MS/MS;* Kevin Colizza; Mithat Gunduz; Scott obach; Amin M. Kame1; Novartis Institutes for BioMedical Research, Cambridge, MA; Novartis, Cambridge, MA; Pfizer Global Res.&Dev, Groton, CT

TP 230  *In vitro metabolism Studies of the GABAA receptor partial agonist [14C]CP-409,092 and Sumatriptan in Human Liver Microsomes using HPLC/RAM/ESI/MS/MS;* Amin M. Kame1; Kevin Colizza; Mithat Gunduz; Scott Obach; Novartis Institutes for BioMedical Research, Cambridge, MA; Novartis, Cambridge, MA; Pfizer, Groton, CT

TP 231  *Coupling of UPLC with Fast Fraction Collection-Microplate Scintillation Counting and Mass Spectrometry for Isolating oxidized Metabolites of Drug Metabolites in Biological Matrices;* Wei Tong; Swapan Chowdhury; Mark Wrona; Kevin Bateman; Merck Research Laboratory, Rahway, NJ

TP 232  *Metabolite Identification From Dried Blood Spot Using Capillary LC – High Resolution OrbitrapTM Mass Spectrometry;* Jianwei Shen; Abbott Lab, Abbott Park, IL

TP 233  *Evaluation of an Integrated LC-MS + offline NMR platform In Identification of Drug Metabolites;* Rose Gathungu; Craig Masse; Paul Vouros; Roger Kautz; Northeastern University, Boston, MA; CoNCERT Pharmaceuticals, Leixington, MA

TP 234  *Interspecies Comparison of Metabolite Profiles for Propranolol in Rat and Human Liver Microsomes;* Yi Tao; Quan Li; Wanxian Chen; Jianfeng Huang; Ping Chen; Weiqing Chen; Alicia Du; Chempartner Co., Shanghai, CHINA

TP 235  *Blood-Plasma Partitioning Effects During DBS-Plasma Cross-Validation of a Carboxylic Acid-Containing Compound and its Acyl Glucuronide Metabolite;* Robert Rieger; A. Dale Wright; Jason Neale; Patrice Lee; Ronald Franklin; Array BioPharma, Boulder, CO

TP 236  *Examples of dried Blood Spot Sampling and Analysis to Improve Paediatric Medicine;* Graham Lawson; Hussain Mulla; Parul Pate1; Sangeeta Tanna; De Montfort University, UK
TP 244 | A Simple and Sensitive Method for Determination of Rifampicin and Rifampicin-Quinone in Human Plasma by HR-MS with Target MS/MS Mode; Jun Wang1; Lijia Zhu1; Jiazhang Xu1; Ying Wang1; Weiguo Tan2; Hong'an Kass1; Xiaoli Liu1; Yingzhou Yang1; Shenzhen Center for Chronic Disease Control, Shenzhen, China; 2Agilent Technologies, Shanghai, China

TP 245 | Quantification of Acamprosate in Dog Plasma Using APT-S50 QTRAP Systems under High Resolution with Fast Scan; Guanochun Zhou; Chen-Yu Wang; Urzula Lorent; Erin Goodin; Maria Hackman; Yong-Xi Li; Medpace, Cincinnati, OH

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TP 247 | Quantification of Metabolites in Plasma Samples by UV-MS Correction using a Dual-cell Linear Ion Trap Mass Spectrometer; Yingying Huang; Tim Stratton; Julie Horner; August Specht; Thermo Fisher Scientific, San Jose, CA

TP 248 | Tracking Metabolism of the NSAID Sulindac: From HPLC-UV to HPLC-MS/MS; Alan W. Taylor; Gayle A. Orner; Sharon K. Krueger; Oregon State University, Corvallis, OR

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TP 250 | Application of UPLC Nanotile MS/MS in the Analysis of Samples from Chimberic Mice with Humanised Livers; Richard Gallagher1; Raimund Peter1; Kathryn Pickup1; Kristin Samuelsson1; Ian Wilson1; Leonard Dillon2; David Douce2; 1AstraZeneca, Macclesfield, UK; 2Waters Corp, Manchester, UK

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TP 259 Converting LC/MS/MS Plasma Assay to DBS Assay: Challenges and Comparison of Two Riluzole Assays in Different Matrices; Min Meng; Yue Zhao; Weiwei Yuan; Troy Voelker; Scott Reuschel; Tandem Labs, Salt Lake City, UT

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TP 262 Thickness Monitoring of Ultrathin Layers by Laser Desorption Mass Spectrometry; Natalia Mavrin skaia; Hans Joachim Räder; Klaus Müllen; MPI for Polymer Research, Mainz, Germany

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TP 269 A Novel Automated LCMSMS Method for the Simultaneous Determination of L evothyroxine (T4) and Liothyronine (T3) in Human Serum; Gilles Provencher; François Viel; Nadine Boudreau; Ann Lévesque; PharmaNet Canada, Québec, Canada

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TP 276 Improved Strategies for Analyzing Dried Blood Spots as a Sampling Technique for the Quantitative Determination of Guanfacine in Clinical Studies; Yuanyuan Li1; Daniel Eikel1; Tom Alexander1; Kärin Dillon2; John Buckholz3; Jack Henion1; Richard Abbott2; Phillip Wang3; 1Advin BioServices Inc, Ithaca, NY; 2Shire Pharmaceutical Development Ltd., Basingstoke, UK; 3Shire Development, Inc., Wayne, PA

TP 277 Stability Issues and Method Development of a Polar Phenolic Quaternary Amine Compound in Human Plasma by LCMSMS; Valérie Montmyn; Nicolas Piquet; Sylvain Lachance; Nadine Boudreau; Ann Lévesque; PharmaNet Canada, Québec, Canada

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TP 284 Alaska Heavy Oil Component using Molecular Beam Mass Spectrometry: Temperature Programmed Thermal and Laser Pyrolysis; Kejing Li; Andrew Renehan; Andrew Herring; Matthew Liberator; Colorado School of Mines, Golden, CO

TP 285 Unfolding Molecular Complexity of the Asphaltenes and Heavy Crude Oils by Atmospheric Pressure Laser Ionization (APLI) FT-ICR Mass Spectrometry; Andreas Gaspar; Wolfgang Schrader; Max-Planck Inst für Kohlenforschung, Mülheim / Ruhr, GERMANY

TP 286 Ion Mobility Mass Spectrometry: A New Dimension for Molecular Structure Characterization of Petroleum Products; Kathleen Edwards1; Chunping Wu2; Kuangnan Qian3; Manuel Franciso4; David Russell5; Kyle Fort2; 1ExxonMobil Research & Engineering Co., Annandale, NJ; 2Texas A&M University, College Station, TX

TP 287 Laser Ablation ICP MS of TLC Plate for Total and Speciation Analyses; Mauro Martinez Labrador1; 2; José Chirinos1; Manuel Caetano2; Canine Arnaudguilhem1; Brice Bouysiere1; Ryszard Lobinski2; 1Univ. Pana 3; 2Laboratory of Mass Spectrometer, Caracas, Venezuela

TP 288 Applications of Desorption Electrospray Ionization Mass Spectrometry Imaging to Petroleum and Lipid Analysis; Chunping Wu1; Kuangnan Qian2; Livia S. Eberlin3; Gautam Sharma4; R. Graham Cooks5; 1ExxonMobil Research & Engineering Co., Annandale, NJ; 2Purdue University, West Lafayette, IN

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TP 290 Spreading the ElectrospRAY Umbrella: Ionization Reagents that Extend Negative Ion ESI Coverage to Low Polarity Analytes in Complex Organic Mixtures; Vladislav V. Lobodin1; Ryan P. Rodgers1; 2; Alan G. Marshall1; 2National High Magnetic Field Laboratory, Tallahassee, FL; 2Department of Chemistry and Biochemistry, FSU, Tallahassee, FL

TP 291 Comprehensive Analysis of NSO-compounds in Diesel Submitted to HDT under Different Operational Conditions by ESI-FT-ICR MS: Boniek Gontijo Vaz1; Rosana Cardoso Lopes Pereira1; Sandra Shirley Ximeno Chiaro1; Rosineide Costa Simas1; Clécio Klitzke2; Helaira Lopes Nascimento1; Yuni E Corilo1; Marcos NV Eberlin2; 1PETROBRAS, Rio De Janeiro, Brazil; 2UNICAMP, Campinas, Brazil

TP 292 Temperature Controlled Separation of Volatile Compounds of Crude Oil by Direct Probe APCI-FTMS: Matthias Witt; Thomas Arthen-Engeland; Jochen Friedrich; Bruker Daltonik GmbH, Bremen, Germany

TP 293 Solvent Extraction Combined with Derivatization to Selectively Characterize N-Species in Crude Oil; Fabiane Nachtigall; Wolfgang Schrader; Max-Planck Inst für Kohlenforschung, Mülheim / Ruhr, Germany

TP 294 Direct Simultaneous Determination of Fluorinated Benzoic Acids at the Femtomolar Levels in Oil Reservoir Waters by UPLC-MSMS: Coralie Serres-Piole1; Ryszard Lobinski2; Navid Moradi-Tehrani1; 2; Christophe Allicani; Hugues Preud’homme1; 1LCABIE - UMR 5254 - CNRS - University of Pau, Pau, France; TOTAL, Pau, France

TP 295 Contribution of Mass Spectrometry to Assess Quality of Petroleum Fractions; Patricia Araujo Pantolla1; Maria Anita Mendes1; 2; Claudio Augusto Oller do Nascimento1; 2; 1University of Sao Paulo, Sao Paulo, Brazil; 2CEPEMA-USP, Sao Paulo, Brazil

TP 296 Application of Normal Phase APCI LCMS for the Analysis of Diesel Fuel and Fuel Dyes; Richard B. Lucke1; Bob W. Wright; Pacific Northwest National Laboratory, Richland, WA

TP 297 LC/MS/MS Analysis of Three Oil Spill Dispersants in Sea Water: Robert Ellis1; Takeo Sakuma1; Kenichi Suzuki2; Masatoshi Takahashi2; Curtis Campbell2; Chris Borton1; Deolinda Fernandes1; Becky Wittrig1; Stacy Temretin1; Fouad Khalaf1; 2AB SCIEX, Concord, Canada; 1Shimadzu Scientific Instruments, Columbia, MD; 2GL Sciences Inc, Tokyo, Japan

TP 298 Silicon Speciation by Gas Chromatography/Mass Spectrometry: Applications in Petroleum Products and Artifacts; Fabien Chaintet1; Charles-Philippe Lieman1; Jeremie Ponthus1; Marion Courtiade1; Olivier Francois Xavier Donard1; 1IFP Energies Nouvelles, Solaize, France; 2IPREM, Pau, France

TP 299 Identification of Silicon Compounds in Gasolines by FT-ICR/MS: Towards the Speciation by Kendrick Plot; Fabien Chaintet1;
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LC-MS-MS Analysis of VX from Tape Stripping Samples following Percutaneous Exposure of Hairless Guinea Pigs; Christopher Byers1; Christopher Whalley1; Edward Clarkson1; Lucille Lumley1; E. Michael Jakubowski, Jr.3; US Army ECBC, APG, MD; 2US Army Institute of Chemical Defense, APG, MD

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Proteomic Study of Escherichia coli treated with Distamycin Analogs Bispyrrole-Pyridine; Jia-Ying Yang1; Jingyueh Jeng2; Chun-yeu Lin3; Chih Wei Ong3; National Sun Yat-sen University, Kaohsiung, TAIWAN; Chia Nan University of Pharmacy and Science, Tainan, Taiwan

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Simultaneous Quantification of Five DNA Adducts in Human Saliva by Stable Isotope Dilution NanoLC-Nanospray Ionization Tandem Mass Spectrometry; Wen-Peng Lin; Hauh-Jyun Candy Chen; National Chung Cheng University, Ming-Hsiao, Chia-Yi, TAIWAN

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Sensitive Detection of 11-nor-D9-Tetrahydrocannabinol-9-Carboxylic Acid in Hair; David Engelhart1; Fred Feyerherm2; Stephan Baumann3; Omega Laboratories, Mogadore, OH; 2Agilent Technologies, Inc., Santa Clara, CA

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TP 330  MALDI-TOF detections of Single- and Double-Stranded Polynorbornenes; Zhen-Yu Xie1; Nai-Ti Lin1; Lei Zhu2; Ching-Hsuan Chen3; Tien-Yau Luh1; 1Genomics Research Center, Academia Sinica, Taipei, Taiwan; 2Department of Chemistry, National Taiwan University, Taipei, Taiwan

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TP 332  Meeting the Challenges of Pre-Polymer, Polymer and Polymer Additive Analyses with APPI and ASAP Ionisation Techniques; Eleanor Riches1; Michael O’Leary1; Peter Lee2; 1Waters Corporation, Manchester, UK; 2Waters Corp., Milford, MA

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TP 334  Application of ASAP Mass Spectrometry Capabilities for Polymeric Materials Characterization; Andrew Melhuish1; William Nichols2; 1Bausch + Lomb, Inc., Rochester, NY; 2Eastman Kodak Company, Rochester, NY

TP 335  Evaluation of Atmospheric Pressure Solids Analysis Probe (ASAP) MS for the characterisation of synthetic polymers; Michael Smith1; Jackie Mosely1; Neil Cameron1; Peter Stokes1; David Parker1; Durham University, Durham, UK

TP 336  In situ Analysis of Polymers by MALDI-MS following Calorimetry or Controlled Thermal Aging using Microfabricated Platforms for Heating and MS; Curtis Mowry1; Matthew Moorman1; Jeff Reich1; Amy Allen1; John Anderson1; Sandia National Laboratories, Albuquerque, NM

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TP 340  Preliminary Imination in Structure Determination of Amine Group Containing Polymers by MALDI-Tof Mass Spectrometry; Roman Borisov; Nikolai Polovkov; Vladimir Zaikin; Topchiev Institute of Petrochemical Synthesis, Moscow, Russia

TP 341  Confirmation of the Absence of Bisphenol A in Copolymers by Polymer Hydrolysis in Combination with LC-MS/MS and LC-FLD; Curtis D. Cleven; Warren Jackson; Eastman Chemical Company, Kingsport, TN

TP 342  Analysis of Recycled Polymers using SEC-MALDI and Precipitation Method; Yuzo Yamazaki; Shimadzu Corporation, Kyoto, JAPAN

TP 343  Differential Analysis in Polysulfide Silane Coupling Agents by High Mass Accuracy MS and Multivariate Statistical Technique; Hiroki Nakajima; Takahiro Goda; Satoshi Yamaki; Tsutomo Nishine; Yuko Sekine; Fumito Yatsuyanagi; Shimadzu Corporation, Kyoto, Japan; 2The Yokohama Rubber CO., LTD., Kanagawa, Japan

TP 344  Poly(Methyl Methacrylate) Characterization by High-resolution Ion Mobility Spectrometry-Mass Spectrometry; Junkan Song; Christian Grün; Ron M.A. Heeren; Hans-Gerd Janssen; Oscar F. Van Den Brink; 1AkzoNobel R&D, Deventer, The Netherlands; 2Unilever R&D, Vlaardingen, The Netherlands; 3FOM Inst. Atomic/Molecular Phy, Amsterdam, The Netherlands; 4University of Amsterdam, Amsterdam, The Netherlands

TP 345  Structural Analysis and Accurate Mass Measurements for Synthetic Polymers and Additives with MALDI/TOF-TOF and High-Energy CID; Masaaki Ubukata; Robert B. Cody; John Dane; Ayumi Kubo; Yoshiyuki Itoh; Masahiro Hashimoto; Yosuke Fujino; Jun Onodera; 1JEOL USA, INC., Peabody, MA; 2JEOL Ltd., Tokyo, Japan

TP 346  The Analysis of Synthetic Polymer by High Energy CID using High Precursor Ion Selectivity MALDI-TOF-TOF, Takaya Satoh; Ayumi Kubo; Yoshiyuki Itoh; Masahiro Hashimoto; Masaaki Ubukata; Jun Tamura; Takaumi Satoh; James Doug Meinhardt; 1JEOL Ltd., Akishima, Japan; 2JEOL USA, Inc, Peabody, MA

TP 347  Characterization of Cyclic Polymers by Mass and Tandem Mass Spectrometry; Aleer M. Yel; Shih-Fan Wang; Boyd A. Laurent; Mark D. Foster; Scott M. Grayson; Roderic P. Quirk; Chrys Wesdemiotis; 1The University of Akron, Akron, OH; 2Tulane University, New Orleans, LA

TP 348  Peptoid fragmentation under tandem mass spectrometry conditions; Kiran Kumar Morisetti; Scott Russell; Xiaoning Zhao; David Robinson; Jianhua Ren; 1University of the Pacific, Stockton, CA; 2CSU Stanislaus, Turlock, CA; 3Sandia National Laboratory, Livermore, CA

TP 349  PLUMS - a Software for Analyzing Homopolymer Tandem Mass Spectra; Kerstin Scheuber; Bernhard Pfetsch; Anja Baumgartel; Ulrich Schubert; Sebastian Böcker; 1Friedrich-Schiller-University, Jena, Germany; 2Dutch Polymer Institute, Eindhoven, Netherlands

TP 350  Effect of Experimental Variables on the Attachment of Metal Cation Attachment to Non-Tonic Surfactants. AN ESI Mass Spectrometric Study; Khaled Edbye; Graine Moran; Gary D. Willett; 1Benghazi, LIBYA; 2Chifley, NSW, Australia

**Food Safety; 351 - 375**

TP 351  Non-Targeted Screening for Food Residues using High Resolution Accurate Mass LC-MS/MS and Statistical Data Processing; Andrea Schreiber; Yun Yun Zou; Kai Zhang; Jon Wong; AB SCIEX, Concord, CANADA; 2FDA-CFSAN, College Park, MD

TP 352  Bisphenolic Can Coating Migrants Interfering with BPA: Accurate Mass/NMR Identification and Levels in Canned Food; Luke K. Ackerman; Gregory O. Noonan; Timothy H. Begley; FDA Center for Food Safety and Applied Nutrition, Bethesda, MD

TP 353  Migration of Perfluoroalkyl Acids from Food Packaging to Food Simulants; Yichuan Xu; Gregory Noonan; Timothy Begley; Gregory Diachenko; FDA ORS, College Park, MD

TP 354  Determination of Dioctylsulfoxosuccininate (DOSS) in Oysters using Single Quadrupole Mass Spectrometry; Marcus Miller; Jinyuan Wang; William C. Schnute; Dionex Corporation, Sunnyvale, CA

TP 355  Environmental and food safety screening of persistent organic pollutants (POPs) by GC(xGC)-TOFMS without dependence on extensive sample clean-up; Nick Bukowski; Kurt Thaxton; Dan Cooper; ALMSCO International, Llantrisant, UK

TP 356  Analysis of mycotoxins in grain products by QuEChERS combined with liquid chromatography-tandem mass spectrometry; Pin-Jen Yu; Wang-Ming Lee; National Chung-Hsing University, Taichung, TAIWAN

TP 357  Determination of PAHs in Edible Oil By Automated On-line Clean-up GPC-GCMS System; Lai Chin Loi; Cynthia Melanie Lahey; Gee Sing Ling; Jie Xing; Mylene Taduran; Katsuhiro Nakagawa; Shimadzu Asia Pacific Pte. Ltd., Singapore, SINGAPORE; Shimadzu Philippines Corporation, Makati City, Philippines; Shimadzu Corporation, Kyoto, Japan

TP 358  Determination of five mycotoxins by using QuEChERS method and LC/MS/MS in processed foods; DonGisK Jeong; Daehyun Kim; JongHo Lee; SeungRim Baek; CheongTae Kim; NONGSHIM Co., Ltd., Seoul, SOUTH KOREA

TP 359  Simultaneous, rapid analysis of melamine and its analogues in various processed foods by LC-MS/MS; DaeHyun Kim; DongSik Jeong; SeungRim Baek; JongHo Lee; Jongsun Park; CheongTae Kim; NONGSHIM Co., Ltd., Seoul, SOUTH KOREA; Euro Science Co., Ltd., Sungnam City, South Korea

TP 360  Simultaneous Determination of Monensin and Salinomycin in Animal Tissue, Milk and Egg by Liquid Chromatography-Tandem Mass
The detection of Trenbolone and Pouponneau2; Loic Beyet Faber2; Tallahassee, FL; 2FL and Fish Wildlife Conservation Monitoring Tea Extract Using Automated Online Sample Screening Method for 30 Pesticides in Green Analysis of Oysters, Crabs and Shrimp From Zhang2; Jon Wang2; GERMANY; Goethe University Frankfurt, Frankfurt/Main, 2LABERCA, Nantes, France

Improved Sequence Tagging Infrastructure Datasets; of Medecine, Boston, MA; 2Boston University School of Medicine, Boston, MA

Differential Analysis of Tandem Mass Spectrometry Profile Data from the Perspective of Network Topology; Han Hu1; Yu Xia2; Nancy Leymarie 3; Joseph Zaia2; 1Boston University School of Medicine, Boston, MA

An Automated Tool for Detecting Modification-Specific Marker Ions to Improve the Sensitivity of Modified Peptide Identification; 1Han-Yin Yang1; Chih-Chiang Tsou1; Yi-Ju Chen1; Yen-Yi Lin1; Yu-Ju Chen2; Ting-Yi Sung1; Wen-Lian Hsu1; 1Institute of Information Science, Academia Sinica, Taipei, Taiwan; 2Institute of Chemistry, Academia Sinica, Taipei, Taiwan

Shotgun Protein Sequencing with Meta-Datasets; 1Case Western Reserve University, Cleveland, OH; 2University of Edinburgh, Edinburgh, UK

Quantitative Mass Spectrometry Data - A New Tool for Protein Identification and Screen for Linear/Disordered Motifs Using Mass Spectrometry based Proteomics; 1Le Ma1; Ting Liu2; Haijian Wang2; Francois A. Macherone; Marcus Kim; Agilent Technologies, Wilmington, DE

Quantitative Determination of Ultra-trace N-Methyl Carbamates in Rice Samples by Accelerated Solvent Extraction (ASE) and UHPLC-MS/MS; Jinyuan Wang; Marcus Miller; William C. Schnute; Dionex Corporation, Sunnyvale, CA

A Comparative Label-Free Mass Spectrometry Analyses Using MALDI-TOF Imaging MS (IMS) and Tandem Mass Spectrometry Datasets; Morte Rasmussen; Peter Højrup; University of Southern Denmark, Odense M, DENMARK

Sequence-tag and de novo Search Strategies for Detection of Whole Saliva Native Peptides and Amino Acid Modifications; Leean Higgin 1; Pratik Jagtap2; Matthew Stone 3; Ebbing De Jong1; Thomas McGowan1; Tim Griffin1; 1University of Minnesota, Minneapolis, MN; 2Minnesota Supercomputing Institute, UMN, Minneapolis, MN

TowardsFully Identifying a Benchmark Dataset of Tandem Mass Spectra with an Integrated Modification Discovery Pipeline; Yan Fu; Ding Ye; Institute of Computing Technology, CAS, Beijing, China

An Iterative Search Algorithm for Protein Identification from Complex Patterns of Post-Translational Modifications; Xiu Huang1; Lin Huang1; Peng Hong1; Weihua Xue1; Miao Liu1; Kai Fu1; Zhixin Zhang1; Shi-Jian Ding1; 2Department of Pathology and Microbiology, UNMC, Omaha, NE; 3Mass Spectrometry Proteomics Core Facility, UNMC, Omaha, NE

Improved Sequence Tagging Infrastructure for Peptide Modification Hunting in Clinical Cancer Samples; Surendra Dasari; Dong Wang; Matthew Chambers; David Tabb; Vanderbilt University, Nashville, TN

Systematic Evaluation of Alternative Acquisition of CID and ETD Spectra for Phosphoproteomics; Min-Sik Kim1; Jun Zhong1; Kumaran Kandasamy1; Bernard Delanghe2; Akhilesh Pandey1; 1Johns Hopkins University, Baltimore, MD; 2University of Kentucky, Lexington, KY
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TP 384
The isotopic Distribution: Still a Useful Tool for Tomorrow’s MS Instruments?; Dirk Valkenberg; VITO, Mol, Belgium

TP 385
Identification of Protein Isoforms in Fungi by Mass Spectrometry Analyses Using Alternative Splicing Databases; Kun-Yen Chang; Emine Gokce; William L. Franck; Ralph A. Dean; David C. Muddiman; North Carolina State University, Raleigh, NC

TP 386
Shotgun Protein Sequencing with Meta-Contig Assembly; Adrian Guthals; Karl R. Clausler; Nuno Bandeira; University of California, San Diego, La Jolla, CA; Broad Institute of MIT and Harvard, Cambridge, MA

TP 387
Quantitative Phosphoproteomic Analysis to Elucidate Signaling Networks of Yeast Filamentous Growth; Yan Zhang; Hye Kyong Kweon; Christian Shiverly; Anuj Kumar; Philip Andrews; University of Michigan, Ann Arbor, MI

TP 388
Clustering by Homology Increases Confidence in Protein Identifications and Quantification in Populus Proteomics; Rachel Adams; Richard J. Giannone; Paul Abraham; Gerald Tuskan; Chongle Pan; Robert Hetlich; Oak Ridge National Laboratory, Oak Ridge, TN; GST, University of Tennessee, Knoxville, TN

TP 389
Identification of Proteins from Biological Samples by MALDI Peptide Mass Fingerprinting without Protein Separation; Kenneth Parker; Stephen J. Hattan; Jie Du; VIC Instruments Corporation, Sudbury, MA

TP 390
De Novo Sequencing of Antimicrobial Peptides from the Leukocytes of the American Alligator (Alligator mississippiensis); Lancia N.F. Darville; Mark E. Merchant; Kermit K. Murray; Louisiana State University, Baton Rouge, LA; McNeese State University, Lake Charles, LA

TP 391
Proteogenomic Validation of Small and Orphan Polypeptides from Pathogenic Mycobacteria using non-biased Translation; Matthew Champion; Erliang Zeng; University of Notre Dame, Notre Dame, IN

TP 392
Deciphering the Proteome in Colostrum and Mature Milk; Anh Le; Doug Barton; Sarah Maria; Robert McMahon; David Parsi; Kevin Hakala; Philip Serwer; Susan T. Weintraub; UT Health Science Center at San Antonio, San Antonio, TX

TP 393
Label-free MS Determination of Protein Stoichiometry using Bacteriophages as a Model System; Stephen C. Hardies; Donald Perez; David Parsi; Kevin Hakala; Philip Serwer; Susan T. Weintraub; UT Health Science Center at San Antonio, San Antonio, TX

TP 394
Expanding the MDM2 Interactome Using Quantitative Mass Spectrometry Data - A Screen for Linear/Disordered Motifs; Judith Nicholson; Perdita Barran; Alexander Scherl; Ted Hupp; University of Edinburgh, Edinburgh, UK; Centre Medical Universitaire (CMU), Geneva, Switzerland

TP 395
Quantification of Intact Chemical Cross-Links on Proteins Using Isobaric Mass Tags and Tandem Mass Spectrometry; Hua Xu; Pang-Hung Hsu; Case Western Reserve University, Cleveland, OH; National Taiwan Ocean University, Keelung, Taiwan

TP 396
A Comparative Label-Free Mass Spectrometric Evaluation of Phosphatidylglycerol’s Impact on Protein Expression in Cyanobacteria; Tatiana Talamanes; Mihaly Kis; Idikô Domonkos; Zoltan Gombos; Laszlo Prokai; UNT Health Science Center, Fort Worth, TX; Institute of Plant Biology, BRC, Szeged, Hungary

TP 397
Drug Target Identification from Protein Dynamics Using Quantitative Pathway Analysis; David Good; Roman Zubarev; Karolinska Institutet, Stockholm, Sweden; Karolinska Institute, Stockholm, Sweden

TP 398
Salivary Metaproteomics - A Two-Step Workflow for Analyzing Oral Microbiome in a High-Density Human Saliva Dataset and its Clinical Significance; Pratik Jagtap; Thomas McGowan; Joel Kroonen; Sricharan Bandhakavi; Sean L. Seymour; Joel Rudney; Tim Griffin; Minnesota Supercomputing Institute, UMN, Minneapolis, MN; University of Minnesota, Minneapolis, MN; Bio-Rad Laboratories, Hercules, CA; AB SCIEX, Foster City, CA

From Mass Spectrometry based Proteomics to System Biology; Martin Dambo; Alexandre Podtelevnikov; Jacob Kristensen; Erik Nielsen; Christian Ravnsgorp Ingrell; Thermo Fisher Scientific, Odense, Denmark

TP 400
Mathematical Modeling of Yeast Osmotic Stress Responses from Proteomic and Transcriptional Data Suggests Coordination of Transcription, Translation, and Cell Division; Shane L. Hubler; M. Violet Lee; Scott Topper; Craig Wenger; Audrey Gasch; Joshua J. Coon; University of Wisconsin, Madison, WI

TP 401
Mining of Mass Spectrometry Proteomics Experiments through Integration of Spectral Libraries; Sarah Killcoyne; Institute for Systems Biology, Seattle, WA

TP 402
Applications of Global Distance Metric for Tandem Mass Spectrometry Datasets; Magnus Palmblad; André M. Deelder; Leiden University Medical Center, Leiden, Netherlands

TP 403
Normalization in MALDI-TOF Imaging of Proteins; Soeren-Oliver Deininger; Claus Koester; Shannon Cornett; Rainer Paape; Michael Becker; Charles G. Pineau; Sandra Rauser; Axel Walch; Eryk Wolski; Bruker Daltonik GmbH, Bremen, Germany; Bruker Daltonics Inc., Billerica, MA; Inserm U625, Rennes, France; Institute of Pathology, Helmholtz Zentrum München, Munich, Germany

TP 404
Absolute Quantification of Drugs and Peptides in Brain Tissue Section using MALDI Imaging MS (IMS); Patrik Kalbac; Mohammadreza Shariatgorji; Nicoletta Schintu; Per Svenningsson; Per E. Andreu; Uppsala university, Uppsala, Sweden; Karolinska Institutet, Stockholm, Sweden

TP 405
Development of a Data Processing and Analysis Software for Mass Spectrometry Imaging; Xingchuang Xiong; Xiang Fang; You Jiang; Zejian Huang; Yukui Zhang; Zheng Ouyang; Beijing Institute of Technology, Beijing,
TP 406 Software for Peak Picking using Common Peak Method for Imaging Mass Spectrometry Data; Masaru Usuihija; Shigeki Kajihara; Kurindo Hosaka; Takahiro Hayasaki; Naoko Goto-Inoue; Akiko Yuba-Kubo; Masanori Waku; Ikuko Yamamoto; Matsunori Semba; Masaaki Matsuura; 1Japanese Foundation for Cancer Research, Tokyo, Japan; 2Shimadzu Corporation, Kyoto, Japan; 3Kansai Medical University, Osaka, Japan; 4Hamamatsu University School of Medicine, Shizuoka, Japan; 5Keio University, Tokyo, Japan

TP 407 Exploring MS Imaging Data in a Semi-Supervised and Interactive Manner; Jocelyne Bruand; Theodore Alexandrov; Maxence Wiszortski; Céline Meriaux; Michel Salzet; Isabelle Fournier; Eduardo Macagno; Vineet Bafna; 1University of California, San Diego, La Jolla, CA; 2University of Bremen, Germany; 3FABMS, Université Lille 1, Villeneuve d’Ascq, France; 4Bruker Daltonik GmbH, Bremen, Germany

TP 408 Modelling Approach to Optimize Chemical Imaging using a Continuously Moving Proximal Probe in Thermal Desorption/Secondary Ionization Mass Spectrometry; Vílmós Kertesz; Olga Ovchinnikova; Gary J. Van Berkel; 1Oak Ridge National Laboratory, Oak Ridge, TN; 2University of Tennessee, Knoxville, TN

TP 409 Online Public Resource for Imaging Mass Spectrometry Data; Theodore Alexandrov; Janina Jaeger; Jerame Watrous; Pieter Dorrestein; 1University of Bremen, Bremen, Germany; 2Steinbeis Innovation Center SCiLS, Bremen, Germany; 3University of California at San Diego, La Jolla, CA; 4University of California, San Diego, Skaggs school, La Jolla, CA

TP 410 Improved Peak Picking for Mass Spectral Imaging by Integrating Localized Wavelet Information; Nico Verbeek; Bart De Moor; Etienne Waelkens; Raf Van de Plas; Katholieke Universiteit Leuven, ESAT-SCD, Leuven, Belgium; 2Katholieke Universiteit Leuven, Mol. Cell Biology, Leuven, Belgium; 3Katholieke Universiteit Leuven, ProMeta, Leuven, Belgium; 4Vanderbilt University, MS Research Center, Nashville, TN

TP 411 Improved Principal Component Analysis for Mass Spectral Imaging by Means of a Maximum Likelihood Estimator; Yossef El Alam1, 2; Nico Verbeek1, 2; Bart De Moor1, 2; Etienne Waelkens1, 2; Raf Van de Plas1, 2; Katholieke Universiteit Leuven, ESAT-SCD, Leuven, Belgium; 2Katholieke Universiteit Leuven, IBBT-Future Health, Leuven, Belgium; 3Katholieke Universiteit Leuven, Mol. Cell Biology, Leuven, Belgium; 4Katholieke Universiteit Leuven, ProMeta, Leuven, Belgium; 5Vanderbilt University, MS Research Center, Nashville, TN

TP 412 Automated MALDI Matrix Spraying System for Coating Multiple Tissue Samples in Imaging Mass Spectrometry Analysis; William Mounfield; Timothy Garrett; University of Florida, Gainesville, FL

TP 413 High-Throughput Imaging Mass Spectrometry: Experiment Definition, Auto-

TP 414 Alignment and Quality Control; Enryis Jones; Alexandre van Remoortere; René van Zeijl; André Deelder; Liam McDowell; Parasitology, Leiden University Medical Center, Leiden, the Netherlands

TP 415 Continuous Laser Raster Sampling for High-Speed and High-Spatial Resolution Imaging Mass Spectrometry; Erik Todd; Jeffrey Spraggins; Andrey I. Zavalin; Richard M. Caprioli; 1Vanderbilt University, Nashville, TN; 2Vanderbilt Univ Sch of Med, Nashville, TN

TP 416 Profiling and Automatic Sub-Cellular Imaging Mass Spectrometry with 1 μm Spatial Resolution; Andrey I. Zavalin; Richard M. Caprioli; 1Vanderbilt University, Nashville, TN; 2Vanderbilt Univ Sch of Med, Nashville, TN

TP 417 Development and Evaluation of New Stigmatic Mass Microscope with High Mass and Spatial Resolving Power using Multi-Turn Time-of-Flight Mass Spectrometer; Jun Aoki; Hirofumi Nagao; Michisato Toyoda; Kunio Awa; Katsuyoshi Masuda; Kenichi Fujii; Yasuhide Naito; Graduate School of Science, Osaka University, Toyonaka, Osaka, Japan; Graduate School of Engineering, Osaka University, Suit, Osaka, Japan; GPI, Hamamatsu, Shizuoka, Japan; Suntory Institute for Bioorganic Research, Mishima-gun, Osaka, Japan; Osaka Institute of Technology, Hirakata, Osaka, Japan; OIST, CREST, Chiyoda-ku, Tokyo, Japan

TP 418 Observation of Tissue Sections Using a Stigmatic Mass Microscope with a Multi-turn Time-of-flight Mass Spectrometer; Hisanao Hazama; Hirofumi Nagao; Michisato Toyoda; Katsuyoshi Masuda; Kenichi Fujii; Toshio Tashima; Yasuhide Naito; Kunio Awa; Graduate School of Engineering, Osaka University, Suita, Osaka, Japan; Graduate School of Engineering, Osaka University, Toyonaka, Osaka, Japan; 2Renovation Center, Osaka University, Totonaka, Osaka, Japan; 3Suntory Institute for Bioorganic Research, Mishima-gun, Osaka, Japan; 4Osaka Institute of Technology, Hirakata, Osaka, Japan; 5GPI, Hamamatsu, Shizuoka, Japan; 6Japan Science and Technology Agency, CREST, Chiyoda-ku, Tokyo, Japan

TP 419 Predicting Collision-Induced Dissociation Spectra of Peptides with Post-Translational Modifications; Christine Contrepois; Eric Ezan; Carl Mann; Francois Plath; Benjamin Garcia; 1University of Virginia, Charlottesville, VA; 2University of Muenster, Muenster, Germany; 3University of Wuppertal, Wuppertal, Germany; 4Institute of Technology, Hirakata, Osaka, Japan; 5JST, CREST, Chiyoda-ku, Tokyo, Japan

TP 420 Identification and Quantification of Lysine Modifications; Eric Chan; Gary Leroy; Barbara Bryant; 1University of Tennessee, Knoxville, TN; 2University of Wuppertal, Wuppertal, Germany; 3University of Munich, Munich, Germany; 4Institute of Technology, Hirakata, Osaka, Japan; 5JST, CREST, Chiyoda-ku, Tokyo, Japan

TP 421 Determination of Kinetic Energy Distributions of Different Materials versus Ion Transfer Efficiency for Spatially Resolved SIMS on Crossbeam Devices; Michel Aliman; Alex Mantz; Alexander Laue; Albrecht Glasmachers; 1Johns Hopkins University, Baltimore, MD; 2University of Muenster, Muenster, Germany; 3Forschungszentrum Juelich, Juelich, Germany; 4National Institute of Metrology, Beijing, China; 5Protea Biosciences, Inc., Morgantown, WV; 6GPI, Hamamatsu, Shizuoka, Japan; 7Japan Science and Technology Agency, CREST, Chiyoda-ku, Tokyo, Japan

TP 422 Imaging MS: Instrumentation; 441 - 445

TP 423 Automated MALDI Matrix Spraying System for Coating Multiple Tissue Samples in Imaging Mass Spectrometry Analysis; William Mounfield; Timothy Garrett; University of Florida, Gainesville, FL

TP 425 Direct Imaging of Sample Surfaces with Digital Imaging Mass Spectrometry; Casimir Bamberg1; Andreas Bamberg2; 1The Scripps Research Institute, La Jolla, CA; 2Albert-Ludwigs University of Freiburg, Freiburg, Germany

TP 426 Determination of Kinetic Energy Distributions of Different Materials versus Ion Transfer Efficiency for Spatially Resolved SIMS on Crossbeam Devices; Michel Aliman; Alex Mantz; Alexander Laue; Albrecht Glasmachers; 1Johns Hopkins University, Baltimore, MD; 2University of Muenster, Muenster, Germany; 3Forschungszentrum Juelich, Juelich, Germany; 4National Institute of Metrology, Beijing, China; 5Protea Biosciences, Inc., Morgantown, WV; 6GPI, Hamamatsu, Shizuoka, Japan; 7Japan Science and Technology Agency, CREST, Chiyoda-ku, Tokyo, Japan

TP 428 A UV/IR-MALDI Sample Stage Integrating Scanning Knife-Edge and Slit Devices for Laser Beam Analysis; Jens S. Andersen; Eric Chan; Gary Leroy; Barbara Bryant; 1University of Virginia, Charlottesville, VA; 2University of Tennessee, Knoxville, TN; 3University of Munich, Munich, Germany; 4Institute of Technology, Hirakata, Osaka, Japan; 5JST, CREST, Chiyoda-ku, Tokyo, Japan
TP 422 Probing Liquid Surfaces in situ under Vacuum Using TOF SIMS; Li Yang1; Xiao-Ying Yu1; James Cowin2; Zhihua Zhu3; Martin Iedema1; Pacific Northwest National Laboratory, Richland, WA; Cowin In-Situ Science, L. L. C., Richland, WA

2D and 3D Imaging of Biological Samples Using a Novel Integrated LAESI-MS Source; Brent Reschke; Callee Walsh; Pamela Williams; Holly Henderson; Matthew Powell; Protea Biosciences, Inc., Morgantown, WV

Online Sample Manipulation and Preparation within Liquid Extraction Based Surface Sampling Probes; Mariam Elnagar; Gary J. Van Berkel; Oak Ridge National Laboratory, Oak Ridge, TN

Direct Analysis of Lipids in Animal and Human Tissue by MALDI Imaging and LMJ Surface Sampling Coupled to Nano-Electrospray MS; Josephine Bunch; Rian Griffiths; Rebecca Edwards; Helen Cooper; Sumera Karim; Patricia Lator; University of Birmingham, Birmingham, UK

Metalloproteine Microscopy for Quantitative Imaging of Metals and Metallomics Studies in Neurosciences; Johanna Sabine Becker; Forschungszentrum Juelich, Juelich, Germany

TP 427 Characterization of N1 – A Histone Chaperone Involved in Establishing the Embryonic Epigenetic State in Xenopus laevis; Joseph Struk1; Paromita Mukherjee2; Joshua Nicklay3; Jeffrey Shabanowitz1; David Schechter2; Donald Hunt1; University of Virginia, Charlottesville, VA; The Albert Einstein College of Medicine, Bronx, NY

The Dynamic Epigenome of Induced Pluripotent Stem Cells Controls Cellular Fate; Michelle Gonzales1; Rupa Sridharan2; Kathrin Plath1; Benjamin Garcia1; Princeton University, Princeton, NJ; Broad Stem Cell Center, Univ of California, Los Angeles, CA; David Geffen School of Medicine, Univ California, Los Angeles, CA

TP 428 Capillary Electrophoresis-Electrospray Ionisation-Mass Spectrometry (CE-ESI-MS) for PTM Analysis of H1 Histones: Strengths and Limitations; Klaus Faser; Bettina Sarg; Bernhard Halfinger; Herbert Lindner; Innsbruck Medical University, Innsbruck, AUSTRIA

Compendium Proteomic-Transcriptomic Analysis of Epigenetic Features in Human Cell Lines; Eric Chan1; Gary Leroy1; Barbara Bryant2; Patrick Trojer3; Benjamin Garcia1; Princeton University, Princeton, NJ; Constellation Pharmaceuticals, Inc., Cambridge, MA

Bottom-Up Proteomic Analysis of PTM changes on Histones through Prostate Cancer Progression; John Lapek1; Lisabeth Hoffman1; Gregory Tornbr1; Alan Friedman1; University of Rochester, Rochester, NY; University of Georgia, Athens, GA

Comparative Analysis of Histone Post-Translational Modification Patterns Obtained by Mass Spectrometry on Intact Proteins, Asp-N/Glu-C and tryptic peptides; Kevin Contrepois1; Eric Ezan1; Carl Mann1; Francois Fenaille1; CEA, IBi Tec-S, SPI, GIF sur Yvette, France; CEA, IBi Tec-S, SBIGeM, GIF sur Yvette, France

Identification and Quantification of Histone PTMs on Nucleosomes Isolated with Bromodomain and Chromodomain Containing Proteins; Gary Leroy1; Iouri Chepelev2; Nicolas L. Young3; Peter A. Dimaggio5; Kiji Zhao5; Benjamin Garcia1; Princeton University, Princeton, NJ; National Institutes of Health (NIH), Bethesda, MD

Comparison of Age and Calorie-Restricted Yeast Histone PTM Profiles using Isotopic Derivatization and High Resolution Mass Spectrometry; Elisabeth Hersman1; Junbiao Dai1; Jeff D. Boeke1; Robert J. Cotter2; Johns Hopkins Medical Institute, Baltimore, MD; Middle Atlantic MS Laboratory, Baltimore, MD

Identification and Quantification of Lysine Acetylation on Histones From High Glucose Grown Rat Retinal Muller Cells; Chandra Sekhar Rao Kadiyal; Yunpeng Du; Timothy Kern; Masaru Miyagi; Case western reserve University, Cleveland, OH

MS/S MS of Synthetic Peptides Is Not Sufficient to Verify New Types of Protein Post-Translational Modifications; Sangkyu Lee; Minjia Tan; Lunzhi Dai; Yue Chen; Yingming Zhao; The University of Chicago, Chicago, IL

Validation of Peptide and PTM Identifications by Chemical Proteomics; Jakob Bunkensbasse; Lasse G. Falkenbye; Lea M. Harder; Jens S. Andersen; CEBI, University of Southern Denmark, Odense, Denmark

Probabilistically Assigning Sites of Protein Modification with Scaffold PTM; Brian G. Searle; Mark Turner; Proteome Software Inc., Portland, OR

Generalized Approach for Determination of False Localization Rates in Post-Translational Modification Site Assignments; June Snedecor1; Banu Dost1; Vineet Bafna1; Mark Lortie1; Claudio Albuquerque1; Nuno Bandeira1; University of California, San Diego, La Jolla, CA; Univ. Cal. San Diego, San Diego, CA

Modification Site Localization Scoring Integrated into a Search Engine; Peter R Baker; Jonathan C. Trinidad; Katalin F. Medzihradzky; A.L. Burlingame; Robert Chalkley; UCSF, San Francisco, CA

New Computational Method for Identifying Peptides with Unspecified Modifications; Lin He1; Xi Han1; Lei Xin1; Baozhen Shan1; Bin Ma1; University of Waterloo, Waterloo, Canada; Bioinformatics Solutions Inc., Waterloo, Canada

Prediction of Collision-Induced Dissociation Spectra of Peptides with Post-Translational or Process-Induced Modifications; Zhongqi Zhang; Amgen, Inc., Thousand Oaks, CA

Software and Algorithm for Differential Characterization of Post-Translational Modifications; Viveck N. Bhatia1; David H. Perlman1; Catherine E. Costello2; Mark E. Mccomb1; Boston University School of Medicine, Boston, MA; Princeton University, Princeton, NJ

A Comprehensive Analysis of Protein Post-Translational Modifications, Disulfide Bonds, Mutations, and Novel Types of Modifications;
TP 445  High Levels of Iron Adducts Contribute to Unassigned Peaks in Database Searches; Jonathan Blandford; Lindsay Schambeau; Cristina Di Poto; Lewis K. Pannell; Mitchell Cancer Institute, Mobile, AL; University of Alabama at Birmingham, Birmingham, AL

TP 446  iTRAQ and Label-Free Quantitative Proteomics of Two Chlamydomonas Strains using LTQ-Orbitrap Velos; Honoxia Wang; Sophie Alvarez; Leslie M. Hicks; Donald Danforth Plant Science Center, St. Louis, MO

TP 447  Development and Validation of 8-Plex N,N-Dimethyl Leucines as Novel Tandem Mass Tags for Quantitative Proteomics and Peptidomics; Tyler J. Greer; Xiong Cai; Dustin Frost; Lingjun Li; University of Wisconsin-Madison, Madison, WI

TP 448  Measurement of Lysine Acetylation Occupancy Rates using Deuterated Acetylation Labeling Approach; Yong Chen; Marjan Gucek; NIH/NHLBI, Bethesda, MD

TP 449  Utilization of 4H-Labeled Synthetic Peptides or Proteomes in Targeted Quantitative Proteomics; Bekim Bajrani; Xudong Yao; University of Connecticut, Storrs, CT

TP 450  Quantitative Top-Down and Bottom-Up Profiling of the Proteomic Response to Ionizing Radiation; Shchema Hengel; Zhixin Tian; Joshua T. Aldrich; Gordon Sylisz; Gordon A. Anderson; Nikola Tolić; Matthew Monroe; Anil K. Shukla; Si Wu; Errol Robinson; David L. Stenoien; Ljiljana Pasa-Tolic; Pacific Northwest National Laboratory, Richland, WA

TP 451  High Precision Quantitative Proteomics for Identifying the Regulation of Proteins in Microglia by miRNAs using Tandem Mass Tags; Seema Sharma; Shantel Gushue; Debra Parchialiuk; Julian Saba; Mark Sanders; Stephanie Booth; Thermo Fisher Scientific, San Jose, CA

TP 452  Understanding the Role of TRK Receptors in Neuroblastoma using Quantitative Phosphoproteomics Approaches; Michael Rosenblatt; Megan Dobbs; Douglas Hughes; Ryan Bomgardner; Eugene Cichon; Garrett Brodeur; John C. Rogers; Thermo Fisher Scientific, Rockford, IL; The Children’s Hospital of Philadelphia, Philadelphia, PA

TP 453  Mass Spectrometric Analysis of Hematopoietic Stem Cell Regulation; Andrew Williamson; Anthony Whetton; Manchester Uni, Manchester, UK

TP 454  Quantitative Peptidomics of Spinal Cord and Striatum from Mice Deficient in Endothelin Converting Enzyme-2; Xiaowen Hou; Lydia Miller; Lakshmi Devi; Jonathan Sweedler; University of Illinois Urbana-Champaign, Urbana, IL; Mount Sinai School of Medicine, New York, NY

TP 455  Quantitative proteomic profiling of tamoxifen response in breast cancer cells via pH dependent RP-RP-HPLC-Chip/Q-TOF analysis; Michael Gormley; Vadiraja Bhat; Andrew Quong; Thomas Jefferson University, Philadelphia, PA; Agilent Technologies, Wilmington, DE

TP 456  Quantitative proteomic analysis of healthy dentate and edentulous saliva: Assessing the GCF content of saliva; Andrew Creese; Melissa Grant; Marko de Jager; Helen Cooper; Iain Chapple; University of Birmingham, Birmingham, UK; Philips Oral Healthcare, Saronikos, Greece

TP 457  Identification of novel cisplatin induced MHC-peptides in ovarian cancer by immunoproteomics; Vivekananda Shetty; Gomathinayagam Sinnathamby; Zacharie Nickens; Julie Hafner; Michael A Morse; Ramila Philip; Immunotope, Inc., Doylestown, PA; Department of Medicine, Duke University Med Cent, Durham, NC

TP 458  Quantitative Proteomics of Epigenetically Altered Lines of Brachypodium distachyon Exposed to Brome Mosaic Virus; David Shearer; Vic Spicer; Oleg Krokhin; Steve Haber; University of Manitoba, Winnipeg, Canada; Agriculture Canada, Winnipeg, Canada

TP 459  A combined SILAC/TMT labeling strategy for higher order multiplexed quantitative analysis of the yeast TOR pathway; Noah E. Dephoure; Harvard Medical School, Boston, MA

TP 460  Tandem Mass Tags for Relative Quantitation using Higher Energy CID on a Dual Pressure Linear Ion Trap; Julia A. Horner; Roger G. Biringer; Andreas F.R. Huhmer; August A. Specht; Philip M Remes; Jae C. Schwartz; Thermo Fisher Scientific, San Jose, CA

TP 461  Stable isotopes in large-scale quantitative proteomics: merits and drawbacks of isobaric tagging and SILAC; M. Violet Lee; Justin Brumbaugh; Doug Phanstiel; Craig Wenger; Edward Huttlin; Steven Gygi; Joshua J. Coon; University of Wisconsin, Madison, WI; Harvard Medical School, Boston, MA

TP 462  Statistical evaluation of iTRAQ quantitative mass spectrometric data proven from two separation techniques and obtained with two fragmentation methods; Paolo Soffientini; Andrea DiFonzo; Theodora Manousidou; Gabriela Grigorean; Cogentech, Milan, Italy; Instituto Europeo Oncologico, Milan, Italy

TP 463  OFFGEL Peptide Fractionation without Glycerol; Na Li; Dodge Baluya; Jhoana Mendoza; Rong Wang; Mount Sinai School of Medicine, New York, NY

TP 464  Identification of the apelin peptides in Bovine Colostrum using Liquid chromatography-High resolution mass spectrometry; Cédric Mesmin; François Becher; François Fenaille; Eric Ezan; CEA Saclay/BI-Tec-S/SP, GIF sur Yvette, France

TP 465  Comparative Analysis of De Novo Sequencing Solutions Utilizing High Mass Accuracy Data and Computational Algorithms; Jared D. Leszyk; Stephanie Maniatis; Scott A. Shaffer; University of Massachusetts Medical School, Worcester, MA

TP 466  Improving peptide sequence characterization using electron-capture dissociation and collision-induced dissociation; Eisuke Hayakawa; Gerben Menschaert; Geert Baggerman; Walter Luyten; Liliane Schoofs; Philips O/H Care, Brussels, Belgium; University of Antwerp, Antwerp, Belgium
Characterization of Conformational Epitopes of a Therapeutic Antibody by Hydrogen-Deuterium Exchange (HDX) and Top-down Mass Spectrometry; Bin Wang; Protein Analytics (pRED), Roche Diagnostics GmbH, Penzberg, Germany

Experimental and Theoretical Studies of Gas-Phase H/D Exchange Reactions on Protonated Mitorrubin Azaphilones and Derivatives under ESI Conditions; Ljubica Svilari; Vesna Stankov-Jovanovic; Héloïse Soldi-Lose; Denis Lesage; Sandra Alves; Jean-Claude Tabet; UPMC, Paris, France; Faculty of Science and Mathematics, Nis, Serbia

Hydrogen/Deuterium Exchange Mass Spectrometry Reveals Quaternary Conformational Changes for AMP Activated Protein Kinase upon Binding of Small Molecules; Rachelle R Landgraf; Michael J Chalmers; Francis Rajamohan; Melissa S Harris; Rachelle Magyar; Ravi G Kurumbail; Patrick R Griffin; The Scripps Research Institute, Jupiter, FL; Pfizer, Inc., Groton, CT

Mechanistic Studies of Retinoic Acid Receptor-related Orphan Receptor Modulators by Hydrogen-Deuterium Exchange Mass Spectrometry; Janelle Lauer; Naresh Kumar; Michael Chalmers; Ruben Garcia-Ordonez; Patrick R Griffin; The Scripps Research Institute, Jupiter, FL

Dissecting Estrogen Receptor Modulator Selectivity with Hydrogen / Deuterium Exchange Mass Spectrometry and X-ray Crystallography; Michael Chalmers; Yong Wang; Scott Novick; Bruce Pascal; Sato Masahiko; Henry Brant; Chahrazad Montrose-Rafizdah; Jeffrey Dodge; Patrick Griffin; Lilly Research Laboratories, Indianapolis, IN; The Scripps Research Institute, Scripps Florida, Jupiter, FL

Hydrogen Exchange Mass Spectrometry Analysis of an Inactivating Mutant of Fes SH2-kinase; Thomas E. Wales; Panfilipakopoulos; Stefan Knappe; John R. Engen; Northeastern University, Boston, MA; SGC, University of Oxford, Oxford, UK

Conformational Dynamics Studies of PEGylated and Non-PEGylated Granulocyte Colony Stimulating Factor by Hydrogen/Deuterium Exchange Mass Spectrometry; Hut Wei; Joomi Ahn; Ying-Qing Yu; Guodong Chen; Adrienne Tymaki; Bristol-Myers Squibb, Princeton, NJ; Waters Corporation, Milford, MA

Histidine HDX Mass Spectrometry: Relationship between the HDX Rate Constants and the pKa Values; Vennela Mullangi; Takashi Nakazawa; David Ball; David Anderson; Masaru Miyagi; Ceville State University, Nara, Japan; Cleveland State University, Cleveland, OH; Case Western Reserve University, Cleveland, OH; ‘Case Western Reserve Univer, Cleveland, OH

Utility of Hydrogen/Deuterium Exchange (H/D-Ex) for Epitope Mapping of Large, Highly Modified Antigens in Biotherapeutic Drug Development; Steven C. Pomerantz; Sheng-Jiun (Sam) Wu; Jinquan Luo; Sook Yun
Conformational Dynamics in Peptides and Gas-phase Hydrogen-Deuterium Exchange

Hydrogen/Deuterium Exchange FT-ICR Mass Spectrometry; Tallahassee, FL; 2Florida State University, St. Louis, MO

Deuterium Exchange – Mass Spectrometry Method for Improved Determination of Proton Exchange Sites in Insulin under Amyloid Fibril Forming Conditions; Teerapat Rojialakul; Fred King; West Virginia University, Morgantown, WV

Structural Characterization of Coagulation Factor XII and Activated Forms of FXIII by Hydrogen-Deuterium Exchange Mass Spectrometry; Mette Dahl Andersen; Johan H. Faber; Novo Nordisk A/S, Maaloev, Denmark

Gas-phase Hydrogen-Deuterium Exchange Coupled with ECD to Investigate Conformational Dynamics in Peptides and Proteins; Kevin B. Tung; Aaron Highley; Eizadora Yu; Sidney Elmer; Yooli Light; Darryl Sasaki; Ken Sale; Joseph Schoeniger; Sandia National Laboratories, Livermore, CA

HDX-Mass Spectrometry Study of Amyloid beta (Aβ 1-42) Peptide Oligomer; Ying Zhang; Washington University in St. Louis, St. Louis, MO

Solvent Accessibility of the Active Site Loop and the Oligomerization Interface of Peroxiredoxins Studied using Synapt HDMS UPLC HDX Technology; Sasidhar N Nirudodhi; Claudia Maier; Oregon State University, Corvallis, OR

A Top-Down Approach to Investigate Protein Structure and Protein-Protein Interactions using H/D Exchange and FT-ICR Mass Spectrometry; Michaela J. Levy; Pei-Jing Pai; David H. Russell; David P. Barondeau; Texas A&M University, College Station, TX

A Study on the Conformational Analysis of Big-Size Peptides Using H/D Exchange Combined with ESI and ETD-MS; Chhabil Dass; Raghu K Chitta; "The University of Memphis, Memphis, TN; "Bayer, Berkeley, CA

Investigation of the Opening Mechanism of E. coli DNA Polymerase Processivity Clamp by Hydrogen Exchange Mass Spectrometry; Jing Fang; Penny; J Beuning; John R. Engen; Northeastern University, Boston, MA

Characterizing Disordered Proteins by H/D Exchange Mass Spectrometry (H/D-MS); Theodore Keppel1; Farai Rusingwa; Victoria Dunlap2; Julie Rumi-Masante3; Trevor Creamer4; David Weis5; 1University of Kansas, Lawrence, KS; 2University of Kentucky, Lexington, KY

Major Conformational Change Correlated with Novel Function of Human Lysyl-tRNA Synthetase Revealed by Hydrogen/Deuterium Exchange FT-ICR Mass Spectrometry; Huimin Zhang1; Alan G. Marshall2; Pengfei Fang3; Paul Schimmel3; Xiang-Lei Yang4; Min Guo5; "NatI High Magnetic Field Lab, Tallahassee, FL; "Florida State University, Tallahassee, FL; "The Scripps Research Institute Florida, Jupiter, FL; "The Scripps Research Institute, La Jolla, CA

Conformational Selection in Heat-stable Nucleoid (H-NS)-mediated Gene Silencing in Bacteria by Ion Mobility and Amide H/D Exchange Mass Spectrometry; Ganesh S. Anand1; Gao Yunfeng2; Mark Ritchie3; Yan Jie4; Linda Kenney5; "NUS Singapore, Singapore; Singapore; "Waters Pacific Pty Ltd, Singapore, Singapore; "University of Illinois at Chicago, Chicago, IL

Structural Studies of Signal Transduction in a Transmembrane Protein; Kathleen Molnar; University of Pennsylvania, Philadelphia, PA

Kinetic H/D Exchange and ECD Evidence for the α-Helix as a Basic Structural Element of Gaseous Protein Ions; Sergio Castro1; Kathrin Breucker2; Owen S. Skinner3; Xianglei Kong4; Fred W. McLafferty5; 1Cornell University, Ithaca, NY; 2University of Innsbruck, Innsbruck, Austria; 3Nankai University, Tianjin, China

Interaction between BRCT Domains of Ligase IV and XRCC4 Studied by H/D Exchange Coupled to Mass Spectrometry; Martial Rey; Yu Yaping; Susan Lemon; David D. Lienheimer; University of Calgary, Calgary, Canada

Investigating Insulin Oligomers by Native Spray H/D Exchange and Top-Down Mass Spectrometry; Yining Huang; Weidong Cui; Michael L. Gross; Washington University, St. Louis, MO

Hydrogen Exchange-Mass Spectrometry Enables the Facile Measurement of Stapled Peptide Folding Dynamics and the Optimization of Stapled Peptide Drug Properties; Xiangguo (Eric) Shi1; Thomas Wales2; Carl Elkin3; Noriyuki Kawahata4; John R. Engen5; Allen Amis6; 1Aileron Therapeutics, Inc., Cambridge, MA; "Northeastern University, Boston, MA

Quantitative Assessment of Protein Models by Comparison of H/D Exchange MS Data with Exchange Behavior Accurately Predicted by DXCOREX; Tong Liu1; Dennis Pantazatos2; Sheng Li1; Yoshitomo Hamuro3; Vincent Hilser4; Virgil Woods Jr.5; 1UCSD, La Jolla, CA; "COBRE Center for Cancer Research and Development, Providence, RI; 2ExSAR Corporation, Monmouth Junction, NJ; 3USDA-ARS at Cornell University, Ithaca, NY; 4USDA-ARS at Cornell University, Ithaca, NY; 5USDA-ARS at Cornell University, Ithaca, NY

Bacterial Mechanism of Iron Uptake and Release by Hydrogen/Deuterium Exchange; Leslie Silva; University of Calgary, Calgary, Canada

Probing the Structure and Peptide-Peptide Interaction of Fusogenic Peptide Oligomer using nES MS and H/D Exchange experiments; John D. Gehman; Richard A. J. O'Hair; Hadi Lino; University of Melbourne, Parkville, Australia

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TP 508 LC-MS/MS Biopharmaceutical Glycoanalysis: Comparison of Pronase Digestion and 2-AB Labeling; John Schiel; Jennifer Au; Hua-Jun He; Karen Phinney; NIST, Gaithersburg, MD

TP 509 Mass Spectrometric Approach for Characterization of Kinetics and Site-specificity of a Glycosyltransferase Initiating O-glycosylation of IgA1 Hinge Region; Kazuo Takahashi1; Milada Horynova1,2; Milan Raska1,2; Stacy D. Hall1; Archer D. Smith IV1; Bruce A. Julian1; Zina Moldoveanu1; Jiri Mestecky1; Matthew B. Renfrow1; Jan Novak1; University of Alabama at Birmingham, Birmingham, AL; Palacky University in Olomouc, Olomouc, Czech Republic

TP 510 A Relationship between IgY(Dfc) and the Endangered White-Wood Winged Ducks High Susceptibility to Mycobacterium Avium; Tessianna Misko; Phil D’Amico; Sarah Stevens; Jody Modarelli; Hiram College, Hiram, OH

TP 511 Capillary Electrophoresis Coupled to Advanced QTOF Mass Spectrometer for the Study of Glycopeptides in Monoclonal Antibodies; Suresh Babu CV1; Ravindra Gudihal1; Ning Tang1; Tobias Preckel1; Martin Greiner1; Agilent Technologies India Pvt. Ltd, Bangalore, INDIA; 2Agilent Technologies, Santa Clara, CA; 3Agilent Technologies-R&D and Mkkg, GmbH & Co.KG, Waldbronn, Germany

TP 512 Deglycosylation Study of Murine IgG1, IgG2a, IgG2b and Humanized IgG1 Monoclonal Antibodies; Megan Ellis; John Lambert; Alex Lazar; Immunogen Inc., Waltham, MA

TP 513 Improved Mass Spectrometric Analysis of IgG molecule and its Posttranslational modifications; Sara Marron; Erika Lattova; Helene Perreault; University of Manitoba, Winnipeg, Canada

TP 514 Glycosylation Characterization of Human IgA1 by UPLC-ESI QTOF MS through Differential Deglycosylation; Song Klupoetke; Steven Becht; PPD, Middleton, WI

TP 515 Ion Mobility MS of Glycopeptides from the Fc Regions of Different IgG Subclasses; Yoshinao Wada1; Michiko Taji1; Kenji Hirose2; Osaka MCHRI, Osaka, Japan; 2Nihon Waters K.K., Osaka, Japan

TP 516 Developmentally Regulated Posttranslational Modification of Histone H1; Simon Moon1; Jose E. Meza2; Carol Ball2; Roger A. Avey1; California State University, Long Beach, CA; 2Agilent Technologies, Santa Clara, CA

TP 517 The Analysis of Subcellular Fractions from Mycobacterium tuberculosis for the Presence of Glycosylated Proteins; Geoffrey T Smith1; Christina Bell1; Michael J Sweredoski1; Sonja Hess1; Caltech, Pasadena, CA; 2University of Montreal, Montreal, QC

TP 518 Analyses of Fungal Glycophotobyes by MS and MS2; Teresa Hong; Diana Diaz Arevalo; Karine Bagramyan; Roger Moore; Gabriel Gugui; Markus Kalkum; City of Hope, Duarte, CA

TP 519 Characterization of N-linked Glycosylated Proteins in Complex Tomato Fruit Extracts Coupling HILIC with Precursor Ion Scanning and MS2; Wei Chen1; Robert Sherwood2; James Mccardle1; Eliel May2; Jocelyn Rose3; Theodore Thannhauser2; Sheng Zhang1; 1Proteomics & Mass Spec Facility, Cornell University, Ithaca, NY; 2Department of Plant Biology, Cornell University, Ithaca, NY; 3USDA-ARS at Cornell University, Ithaca, NY

TP 520 Glycation Sites Determination of the Synthetic Neoglycoconjugate Tetrasaccharide from Bacillus Anthracis Kellomycin B: Its Conjugation to the BSA using LC-ESI-Qq-TOF-MS and MALDI-TOF/TOF-MS/MS; Farid Jahoub1; Shu-jie Hou2; Paul Kovac3; Joseph Banoub1,2; 1Memorial University of Newfoundland, St John’s, Canada; 2NIDDK, LBC, National Institutes of Health, Bethesda, MD; 3Department of Fisheries and Oceans, St John’s, Canada

TP 521 Comparative Glycoproteomics of N-Linked Complex-Type Glycoforms Containing Sialic Acid in Human Serum; Wonryeun Cho; Kwanyoung Jung; Fred Regnier; Purdue University, West Lafayette, IN

TP 522 Characterization of Glycoproteins Associated with Esophageal Adenocarcinoma through Lectin Chromatographic Enrichment and LC-MS/MS; Ehwang Song; Swetha Pyreddy; Yehia Mechref; Texas Tech University, Lubbock, TX

TP 523 Alteration of Glycoprotein Expression in Breast Ductal Epithelial Cells; Evelyn H. Kim; Vladimir Galchev; Kathleen M. Woods Ignatowski; David E. Misek; University of Michigan, Ann Arbor, MI

TP 524 Characterization of Wheat Germ Agglutinin-Enriched Proteins from Non-Human Primate Cerebrospinal Fluid; Ronald A. Miller; Shahriar Niroumand; Jacob Marcus; Joel B. Schachter; Daniel S. Spellman; Bonnie J. Howell; Merck and Co., Inc., West Point, PA

TP 525 A Mass Spectrometric Assay for Analysis of Haptoglobin Fucosylation in Pancreatic Cancer; Zhenxin Lin1; Diane Simeone1; Michelle Anderson2; Randall Brand2; Xiaolei Xi2; Kerby Sheddien3; Mack Ruffin1; David Lubman1; 1University of Michigan, Ann Arbor, MI; 2University of Pittsburgh, Pittsburgh, PA

TP 526 Applications of the IDAWG Technique to Quantitative Glycomics of Human Embryonic Stem Cells; Meng Fang; Jae-Min Lim; Michael Kulik; Sandii Brimble; Jun Han; Will York; Stephen Dalton; Lance Wells; Complex Carbohydrate Research Center, Athens, GA

TP 527 Concurrent Global Analysis of the Proteome and N-linked Glycome of Differentiating Human Embryonic Stem Cells: Shan M. Randall1; Steven H. Walker1; Prasenjit Sarkar1; Balaji Rao1; Timothy S. Collier1; David C. Muddiman1; 1North Carolina State University, Raleigh, NC; 2Washington University, St. Louis, MO

TP 528 Simple Workflow For Glycosylation Pattern Analysis In Human Plasma; Oliver Ozohanics; Jilla Turik; Laszlo Orosz; Karoly Vekky; Hungarian Academy of Sciences, Chemical Research C, Budapest, HUNGARY

TP 529 Identification of Novel Phosphorylation Sites of CBP in the beta-catenin Interacting N-terminus; Mingquan Guo; Zanxian Xie; Hong Ma; University of Southern California, Alhambra, CA

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**TP 532** First Time Identification of Phosphorylation Sites in C. Maxima Phloem Small RNA Binding Protein 1 by Hybrid High-accuracy MS; Weitao Jia; Liu Liu; Milady Ninonuevo; William J. Lucas; Julie A. Leary; Dept. of Molecular and Cellular Biology, U.C.Davis, Davis, CA; Dept. of Plant Biology, U.C.Davis, Davis, CA

**TP 533** A Proteomic Strategy to Identify Protein Kinase Substrates and Substrate Specificity of Differential Phosphorylation in Response to ABA by Hybrid High-accuracy MS/MS; Liang Xue; Wenhorng Wang; Lianghai Hu; Anton Iluk; Shuai Yu; Robert Geahlen; Andy Tao; Department of Biochemistry, Purdue University, West Lafayette, IN; Department of Med. Chem. and Mol. Pharm, Purdue, West Lafayette, IN

**TP 534** Mouse Liver Phosphopeptide Analysis with Comparative Mascot Scoring; Ling Zhang; Mark J. Raftery; Bioanalytical Mass Spectrometry, Sydney, Australia

**TP 535** Identifying WNK1 Phosphorylation Sites within WNK4 Reveals a Switch Mechanism to Control Sodium Reabsorption and Potassium Secretion; Orlando Yarborough; Peng Yue; Wen-Hui Wang; Richard Litton; Jesse Kinehart; Yale University, New Haven, CT; New York Medical College, Valhalla, NY

**TP 536** Highly Sensitive Phosphoproteome Analysis of a Minute Number of Cells; Takeshi Masuda; Yasuyuki Igarashi; Masaru Tomita; Jun Namiki; Naoyuki Sugiyama; Yasushi Ishihama; Institute for Advanced Biosciences Keio University, Tsuruoka, Japan; Keio University School of Medicine, Tokyo, Japan; Kyoto University, Kyoto, Japan

**TP 537** Investigation of the Impact of Phosphorylation on Top-down Electron Capture Dissociation Mass Spectrometry of Large Proteins; Xiaoguo Guo; Fangmin Xu; Han Zhang; Huseyn Guner; Ying Ge; University of Wisconsin-Madison, Madison, WI

**TP 538** Comparison of ATP/ADP Probes versus Kinobeads for the Enrichment of Kinases from Complex Lysates; Simone Lemeer; Kristian Kohl; John C. Rogers; Bernhard Kuster; Technische Universität München, Freising, Germany; Thermo Fisher Scientific, Rockford, IL

**TP 539** Application of Sheathless CE-ESI-MS for the Identification of Phosphorylation Sites of Cadmusen after Incubation with Myosin Light Chain Kinase; Bettina Sarg; Leopold Kremser; Aporilsky Sobieszek; Bernhard Haflinger; Herbert H. Lindner; Div. of Clin. Biochemistry, Biocenter Innsbruck, Innsbruck, Austria; Institute for Biomedical Aging Research, Innsbruck, Austria

**TP 540** Identification of Phosphorylation Sites in the Gap Junction Protein Connexin45; Richard Y-C. Huang; Evelyn M. Kanter; Henry W. Rohrs; Kathryn A. Yamada; R. Reid Townsend; Washington University, St Louis, MO

**TP 541** Comprehensive Phosphoproteome Analysis of INS-1 Pancreatic Beta-Cells by Various Digestion Strategies Coupled with Liquid Chromatography-Tandem Mass Spectrometry; Dohyun Han; Sungyoung Moon; Hyunsoo Kim; Ekwon Kim; Ho-Pil Min; Youngsoo Kim; Seoul National University, Seoul, South Korea; Seoul National University College of Medicine, Seoul, South Korea

**TP 542** Increasing Phosphoproteomic Coverage through Sequential Digestion by Complementary Proteases; Jason M. Gilmore; Arminja Kettenbach; Scott A. Gerber; Dartmouth Medical School, Lebanon, NH

**TP 543** Identification of ABCA4 Phosphorylation by Mass Spectrometry; Benlian Wang; Krzysztof Palczewski; Mark Chance; Center for Proteomics and Bioinformatics, Cleveland, OH; Department of Pharmacology, Cleveland, OH; Ophthalmology and Visual Sciences, Cleveland, OH

**TP 544** Phosphorylation of the Human E3 Ubiquitin-Protein Ligase EDD; Jennifer R Bethard; Lawton Roberts; Hui Zheng; Scott Eblen; Musc, Charleston, SC

**TP 545** Identification of Novel Post-translational Modifications on c-Src Using Tandem Mass Spectrometry; Kuntong (Kevin) Xiao; Teng-Yi (Roy) Huang; Kevin Alexander; Chetan B Patel; Santosh Shanmuga; Howard A Rockman; Duke University Medical Center, Durham, NC

**TP 546** Comprehensive Mapping of Phosphorylation Sites in Origin-Recognition Complex; Cristian I. Ruse; Sylvain Mitelheiser; Samantha Peacock; Bruce Stillman; Cold Spring Harbor Laboratory, Cold Spring Harbor, NY

**TP 547** Identification of Phosphorylated Substrates of Specific Cyclin-CDK Complexes; Yinvin Li; Brian Chait; The Rockefeller University, New York, NY

**TP 548** Large-Scale Analyses of Phosphorylation and N-linked Glycosylation Post-translational Modifications in W. casei Saffold; Matthew Stone; Sun Yat-Sen University, Guangzhou, PR China

**TP 549** Spatial and Temporal Proteomics Reveals that apKPC Phosphorylates LIN-5/NUMA to Position the Mitotic Spindle during Asymmetric Division; Javier Munoz; Matilde Galli; Vincent Portegeis; Mike Boxem; Sander van den Heuvel; Albert J.R. Heck; Utrecht University, Utrecht, Netherlands

**TP 550** Proteomic Characterization and Functional Analysis of Myosin II Motor Proteins during Tumor Cell Migration; Giridharan Gokulrangan; Venkiah Betapudi; Thomas Egelope; Mark Chance; Center for Proteomics and Bioinformatics, CWRU, Cleveland, OH; The Lerner Research Institute, Cleveland Clinic, Cleveland, OH

**TP 551** Analysis of Receptor Phosphorylation during Development and Activity; Ry Tweedie-Cullen; Sashu Singh; Judith Lawton; Harvard Medical School/CHB, Boston, MA; Harvard Medical
TP 552  Human Cell-Line Phosphoproteome Mapping using a Dual-Funnel ETD Ion Trap; Schmit Pierre-Olivier; Brunker Daltonique S.A., Wissembourg, France

TP 553  Subcellular Fractionation for Increased Proteome Coverage in Multi-dimensional Top Down Mass Spectrometry; Dorothy Ahlf; Adam Catherman; John C. Tran; Nathan R. Bohn; Paul Thomas; Neil L. Kelleher; Northwestern University, Evanston, IL

TP 554  Modifications of Proteins in the Ribosome in Acquired Drug Resistance; Karen Lohnes; Faith Hays; Jaclyn Wolfe; Alexey Petrov; Yan Wang; Jonathan Dinman; Catherine Fensela; University of Maryland, College Park, MD

TP 555  Proteomic Analysis of Intact Apolipoproteins in Human HDL using Immunoaffinity Chromatography and Top-Down High Resolution Mass Spectrometry; Li Jing1; Donald Puppione2; Christopher Ryan1; Christopher Vanselov; Kym Faull3; Julian Whitelegge; UCLA, Los Angeles, CA; Agilent Technologies, San Diego, CA

TP 556  Identification of Combinatorial Histone Post-Translational Modifications from Mouse ES Cells to iPSC Cells; Kai Zhang; Nankai University, Department of Chemistry, Tianjin, China

TP 557  Integration of Intact Protein and Peptide Measurements for the Characterization of the Extracellular Proteins of Clostridium Thermocellum; Priyanka Mishra1,2; Robert Hettich3; 1University of Tennessee, Knoxville, TN; 2Oak Ridge National Laboratory, Oak Ridge, TN

TP 558  Top-down and Bottom-up MS Evidence for Sulfur Trafficking by the Pseudomonas aeruginosa PA1036 Protein; Gregory Tombline; Johanna Schwingel; John Lapek; Michael Maguire; Nadine VanAlst; Alan Friedman; Barbara Iglewski; University of Rochester Medical Center, Rochester, NY

TP 559  Interrogating the Molecular Details of p53 Redox-Regulation Using Top-down FT-ICR Mass Spectrometry; Jenna Scocher1; David J Clarke; Stefan Weid1; Ted Hupp2; Peter J Sadler12; C. Logan Mackay; Pat Langridge-Smith1; 1SIRCAMS, School of Chemistry, Edinburgh University, Edinburgh, EH9 3JJ, UK; 2Cancer Research Centre, Edinburgh University, Edinburgh EH4 2RX, UK; 3Department of Chemistry, University of Warwick, Coventry CV4 7AL, UK

TP 560  Identification and Characterization of Intact Proteins in Complex Mixtures using Online ETD Fragmentation on a High Resolution Mass Spectrometer; Shannon Elku1; John F. Kelle1; Neil L. Kelleher; Vlad Zabrouskov; Thermo Fisher Scientific, San Jose, CA; 1Northwestern University, Evanston, IL

TP 561  Mapping the Binding Sites of Platinum Anticancer Drugs to Calmodulin; Huilin Li; Tzu-yung Lin; Ana Pizarro; Peter Sadler; Peter O’Connor; University of Warwick, Coventry, UK

TP 562  Analysis of Histone Post-Translational Modifications Specific to Rett Syndrome by FT-ICR Mass Spectrometry; Muhammed Karim; John Connelly; Pat Langridge-Smith; Adrian P. Bird; C. Logan Mackay; 1SIRCAMS School of Chemistry, Edinburgh University, Edinburgh, UK; 2Wellcome Trust Centre for Cell Biology, Edinburgh, UK

TP 563  Quantitative Proteomic Analysis of S-Nitrosylated Proteins in Microglial BV-2 Cells Under Nitrosative/Oxidative Stress; Antioxidant Effects of the Green Tea (-)-epigallocatechin-3-gallate; Zezong Gu1; Fanjun Meng1,2; Wenwen Sheng1,2; Justin Purdy1; Fan Wei1; Siqi Liu1; Grace Y. Sun1,2; 1University of Missouri School of Medicine Pathology, Columbia, MO; 2University of Missouri School of Medicine Biochem, Columbia, MO; 3Beijing Institute of Genomics, Chinese Acad. Sci., Beijing, China

TP 564  Absolute Quantification and Identification of Intact Proteoforms: Separated by HILIC and Detected by Native UV-Induced Fluorescence and Top-Down Mass Spectrometry; Daniel T. Ladror; Jason D. Russell; Brian L. Frey; Mark A. Scalf; Joshua J. Coon; Lloyd M. Smith; University of Wisconsin-Madison, Madison, WI

TP 565  A Novel Approach for Quantifying Allergenic Lipid Transfer Proteins, in Maize Kernels by LC-UV/MS; Scott Young; Krishnamoorthy Kuppannan; Barry Schafer; Dave Albers1; Demetris Dielman; 1The Dow Chemical Company, Midland, MI; 2Dow AgroSciences, Indianapolis, IN

TP 566  Analysis of Signaling Pathways Modulated by PTEN Phosphatase using Combined DIGE-MS and MudPIT; Todd W. Miller; Sipranchan Chanthaphaychith; Carlos L. Arteaga; Sarah Stuart; Salisha Hill; Kristie L. Rose; W. Hayes McDonald; David B. Friedman; Vanderbilt University School of Medicine, Nashville, TN

TP 567  Constructing a Comprehensive Catalogue of Human Salivary Gland-Derived Intact Proteome using Top-down MS; Si Wu1; Joseph Brown1; Haizhen Zhang2; Nikola Tolic2; Rui Zhao2; Da Meng; Ron Moore; Richard D. Smith; Susan Fisher2; Lijiliana Pasa-Tolic; 1PNRL, Richland, WA; 2FHCRC, Seattle, WA; 3University of California San Francisco, San Francisco, WA

TP 568  A Dimethyl Isotopic Labeling Strategy Enables in vitro Quantitative Comparisons of Diverse Red Blood Cell Membrane Proteomes; Matthew Berberich; Yelena Maksimova; Patrick Gallagher; Jesse Rinehart; Yale University, New Haven, CT

TP 569  Quantification of Membrane Protein Antigens using Liquid Chromatography Tandem Mass Spectrometry to Support Vaccine Bioprocess Optimization; John T. Mehl; Merck, West Point, PA

TP 570  High-Throughput Pipeline for the Purification and Identification of Desulfovibrio vulgaris (Hildenborough) Membrane Protein Complexes; Simon Allen; Peter J. Walian; Lucy Zheng; Haichuan Liu; Evelin D. Szakal; Steven C. Hall; Susan J. Fisher; Ralph Santos; Bonita Lam; Jill T. Geller; John-Marc Chandonia; Terry C. Hazen; Bing K. Jap; Mark D. Biggin; H. Ewa Witkowska; 1University of California, San Francisco, San Francisco, CA; 2Lawrence Berkeley National Laboratory, Berkeley, CA
TP 571  Quantitative Analysis of S-Fatty Acylation of Membrane Proteins by Mass Spectrometry and Fluorescence Imaging; Hongying Zhong; Central China Normal University, Wuhan, China

TP 572  Structure and Dynamics of Membrane Proteins using HDX: How to Cope with Detergents; Shahid Mehmoody; Martial Rey; Benjamin Clemenzy; Ludovic Pelosi; Jean-Michel Jault; Petar Man; Eric Forest; Inst. for Structural Biology, Grenoble, France; 2CEA, Grenoble, France; 3Institute of Microbiology, Prague, Czech Republic

TP 573  Comparison of Cationic Nanoparticle Pellicles for Exploring Plasma Membrane Proteome; Waewaloei Chokswangkarn; University of Maryland, College Park, College Park, MD

TP 574  Development of an Efficient Strategy for Purification of Plasma Membrane Proteins; Hsiang-Ju Chen; Academia Sinica, Taipei, Taiwan

TP 575  Chemical Crosslinking of a Membrane Fractin Yields Integral Membrane Protein/Cytoskeleton Interactions; Zhen Wang; Kevin L. Schey; Vanderbilt University, Nashville, TN

TP 576  Detergent Assisted Lectin Affinity Chromatography for Membrane Glycoproteomics; Dustin Frost; Xin Wei; Lingjun Li; University of Wisconsin-Madison, Madison, WI

TP 577  Cyanobacterial Membrane-specific Proteome Analysis by Combining Complete Membrane Purification with 1-D SDS/PAGE and Nano-LC/MS; Kun Cho; Hyun Ju Park; Sang Oh Kwon; Seoung Il Kim; Jong-Soon Choi; Young Hwan Kim; Division of Mass Spectrometry, KBSI, Ochong, SOUTH KOREA; 2Division of Life Science, KBSI, Daejeon, SOUTH KOREA

TP 578  Multienzymatic Strategy for Increased Sequence Coverage of Membrane Proteins using Optimized nLC-MALDI-MS/MS; Dominic Baumlisberger; Marion Rohmer; Tabiwang N. Arrey; Benjamin F. Mueller; Tobias Beckhaus; Michael Karas; Goethe University, Frankfurt Am Main, Germany

TP 579  Quantitative Analysis of Seizure-Induced Rat Brain Proteins using Antibody-Dependant and Independent Approaches; Je-Hyun Baek; James Trimmer; 1NBP (UCD), Davis, CA; 2NPB/PMB (UCD), Davis, CA

TP 580  The Neutrophil Derived Oxidant HOCI Selectively Oxidizes Functionally Important Proteins of the Red Blood Cell Membrane; Grady Blacken; Thomas Jordan; Yi Wang; Xiaoyun Fu; 1Research Division, Puget Sound Blood Center, Seattle, WA; 2Department of Medicine, University of Washington, Seattle, WA

TP 581  Isolation and Mass Spectrometric Analysis of Native Protein Complexes in Rat Liver Mitochondrial Contact Sites; Kwanwon Lee; Janos Kerner; Charles Hoppel; Case Western Reserve University, Cleveland, OH

TP 582  Cardiac Protein-Protein Interaction Networks of Long QT Syndrome Membrane Proteins; Alicia Lundby; Jesper Velgaard Olsen; Center for Protein Research, Copenhagen, Denmark

TP 583  Two Dimensional Liquid Chromatography Followed by MALDI-ToF Mass Spectrometry of Intact Membrane Proteins for Differential Proteomic Analysis; Brian Matthew; James Jorgenson; University of North Carolina, Chapel Hill, NC

TP 584  Characterizing Human Respiratory Cilia Using Data-Independent LC/MS²: Identification and Quantification of Membrane Proteins; Kevin Blackburn; Kristin Thompson; Lawrence Ostrowski; Michael Goshe; North Carolina State University, Raleigh, NC; University of North Carolina, Chapel Hill, NC

TP 585  Using Mass Spectrometry to Update Regulated Influenza Vaccine Production; Carrie Pierce; Tracie Williams; James Pirkle; John R. Barr; Centers for Disease Control and Prevention, Atlanta, GA

TP 586  Quantitative proteomics analysis for DHA-enhanced proliferation of neural stem cells; Bill Huang; Masanori Katakura; Hee-Yong Kim; NIAAA/NIH, Rockville, MD

TP 587  Quantitative Proteomic Analysis of Mouse Brain Membrane Proteins upon Lipopolysaccharide Treatment; Fa-Yun Che; Cong Zhang; Jihyeon Lim; Edward Nieves; Louis Weiss; Ruth H Angeletti; Harris Goldstein; Albert Einstein College of Medicine, Bronx, NY

TP 588  Protein Glycosylation Profiling in Pancreatic Cancer Tissue using Lectin Affinity Enrichment and nano-UPLC-LC-MS/MS; Evelyn H. Kim; Vladimir I. Galchev; David E. Misek; Department of Surgery, University of Michigan, Ann Arbor, MI

TP 589  Impact of Tissue Stabilization Technology on in vivo Shotgun Phosphoproteome Analysis; Hiroyuki Katayama; Lynn Chellarajan; Tyler Teceno; Laurette Burgess; John Lindsay; Keith Wilcoxen; Yoshiya Oda; Eisai Inc., Biomarkers and Personalized Medicine, Andover, MA; Eisai Inc., Life Sciences, Andover, MA; Denator AB, Westford, MA

TP 590  Oxidative Stress Related Post Translational Modifications in Postmortem Brain Tissue of Individuals Diagnosed with HIV and HIV-Encephalitis; Lerna Uzasci; Avindra Nath; Robert J. Cotter; Johns Hopkins University School of Medicine, Baltimore, MD

TP 591  Systematic Evaluation of Protein Identities for Species with Unsequenced Genomes; Joel Chick; Steven Gygi; Harvard medical school, Boston, MA

TP 592  Mass Spectrometry based Approach to Measure and Quantify Protein Degradation and Protease Activity in Tissue Samples; Christoph Stigl; Frederike G.I. van Vilsteren; Mats Borén; Katarina Alenäs; Jacques J. Bergman; Theo M. Luider; 1Erasmus Medical Center, Rotterdam, Netherlands; 2Academic Medical Center, Amsterdam, The Netherlands; 3Denator AB, Gothenburg, Sweden

TP 593  Development of a Microwave-assisted Shotgun Analysis Protocol for Proteome Profiling of Formalin-fixed, Paraffin-embedded (FFPE) Tissues; Nan Wang; Liang Li; Department of Chemistry, University of Alberta, Edmonton, Canada

TP 594  Characterization of Early and Late Stage Ovarian Carcinomas Using Formalin Fixed Paraffin Embedded Tissue; Katherine Heaton;
| TP 595 | Multiple Reaction Monitoring Assay for Pre-eclampsia Related Calcybin Peptides in Formalin-Fixed Paraffin-Embedded Placenta; Coskun Güzeli; Nicolette Uremse; Lennard Dekker; Pieter Derkx; Jos Joore; Evert van Dijk; Gerard Lichtvoort; Eric Steegers; Theo Luider; Eramus Medical Center, Rotterdam, Netherlands; Pepscan Presto BV, Lelystad, Netherlands |
| TP 596 | Proteomic Investigation on the Response of Prostate Cancer to Oxidative Stress Induced by Photodynamic Therapy; Dan Dan Xu; William Chi-Shing Cho; Hon-Ming Lam; Albert Wing Nang Leung; The Chinese University of Hong Kong, Shatin, Hong Kong; Queen Elizabeth Hospital, Kowloon, Hong Kong |
| TP 597 | Fragmentation Patterns of Immunoglobulin (Ig) Light Chain (LC) Proteins Deposited in Human Subcutaneous Fat Tissues; Yanyan Lu; Brian H. Spencer; Roger Theberge; Pamela T. Soo Hoo; Lawrene H. Connors; Catherine E. Costello; Boston University School of Medicine, Boston, MA |
| TP 598 | Disparate Reactivity of the Mitochondrial Thiol Proteome from Heart; Jing Wang; Claudia Maier; Oregon State University, Corvallis, OR |
| TP 599 | Use of iTRAQ Labeling Reagents for Relative Quantitation of MACS2A vs. MACS2B in Human Mitochondrial Extracts by Tandem LC-MS; Alexander Barnakov; William J. Jones; Ingrid Deckman; Andy Mahan; John A. Masucci; Johnson & Johnson Pharmaceutical, Spring House, PA |
| TP 600 | Preliminary Results on the Characterization of Host-Microbiome Proteome of Ear Infection; Linda Nagore; Lance Price; Cindy Liu; Rick Friedmann; Anil Lalwani; Konstantinos Petrits; Translational Genomics Research Institute, Phoenix, AZ; Northern Arizona University, Flagstaff, AZ; House Ear Institute, Los Angeles, CA; New York University School of Medicine, New York, NY |
| TP 601 | Mass spectrometric Characterization of the HIV-1 Preintegration Complex; Pawel Ciborowski; Cameron Schweitzer; Teena Jagadish; Rufina Dominic Savio; Mike Belshan; University of Nebraska Medical Center, Omaha, NE; Creighton University, Omaha, NE |
| TP 602 | Identification of Crkl-SH3 Binding Proteins from Embryonic Murine Brain: Implications for Reelin Signaling during Brain Development; Muleeburahman Cheerrathodi; Bryan Ballif; University of Vermont, Burlington, VT |
| TP 603 | Altered Protein Trafficking Quantified in the Synapse of Schizophrenic Post-Mortem Brain using LC-SRM/MS and a Labeled Mouse Brain Standard; Eugene F. Ciccarelli; Matthew L. Macdonald; Scott Peterman; Amol Prakash; Ian A. Blair; Chang-Gyu Hahn; ThermoFisher Scientific, Somerset, NJ; University of Pennsylvania, Philadelphia, PA |
| TP 604 | Analysis of Membrane and Hydrophilic Proteins Simultaneously Derived from the Mouse Brain Using Cloud-Point Extraction; Magnus Wetterhall; Ganna Shevchenko; Konstantin Artemenko; Marcus Stödlin; Jonas Bergquist; Uppsala University, Uppsala, Sweden |
| TP 605 | Nodes and Pathways in PPAR gamma Cognitive Rescue in the Tg2576 Mouse Model of Alzheimer’s Disease; Sigmund Haidacher; Rovshan Sadygov; Jonathan Starkey; Yingxin Zhao; Bruce Luxon; Jennifer Rodriguez-Rivera; Kelly Dineley; Vadiraja Bhat; Nalini Sadagopan; Larry Denner; UTMB, Galveston, TX; Agilent Technologies, Fremont, CA; Agilent Technologies, Houston, TX |
| TP 606 | Proteomic Analysis of Adriamycin-treated Mice Using Isotopic Labeling to Assess Effects on Immunity; Adam Evans; Teresa Noel; Daret St. Clair; Allan Butterfield; Rena A. S. Robinson; University of Pittsburgh, Pittsburgh, PA; University of Kentucky, Lexington, KY |
| TP 607 | Sensitive Protein Knockdown Measurements of ACLY, GPAT and Apo B in Mouse Liver by SRM; Ekaterina G. Devanova; James Loderstedt; Heather Zhou; Myung Shin; Alain vanGool; Thomas Vogt; Brian Hubbard; Nathan Yates; Ronald Hendrickson; Merck & Co Inc., Rahway, NJ; MSD, Singapore, Singapore |
| TP 608 | Identification of Primary Targets for Protein Nitration in Cortical Mitochondria through Chemoprecipitation and Liquid Chromatography-Tandem Mass Spectrometry; Jia Guo; Katalin Prokai-Tatrai; Laszlo Prokai; University of North Texas Health Science Center, Fort Worth, TX |
| TP 609 | Response of the Mitochondrial Proteome of Rat Renal Proximal Convoluted Tubules to Chronic Metabolic Acidosis; Dana M. Freund; Scott J. Walmsley; Norman P. Cuthroys; Jessica E. Prenni; Colorado State University, Fort Collins, CO |
| TP 610 | Identification of Primary Targets for Protein Nitration in Cortical Mitochondria through Chemoprecipitation and Liquid Chromatography-Tandem Mass Spectrometry; Jia Guo; Katalin Prokai-Tatrai; Laszlo Prokai; University of North Texas Health Science Center, Fort Worth, TX |
| TP 611 | A Proteomic Study of Bacterial Symbionts in Lignocellulose Degradation in the Shipworm Bankia setacea; Colleen O’Neill; Elizabeth Lamkin; Jennifer Fung; Jack S. Benner; Daniel Distel; New England Biolabs, Ipswich, MA; Ocean Genome Legacy, Ipswich, MA |
| TP 612 | A Meta-analysis of Quantitative Proteomics Data from Honeybees Reveals Secrets behind a Better Learning Performance; Florian Wolschin; Christina Tolsfien; Gro Amdam; UMB, Aas, Norway; Arizona State University, Tempe, AZ; Climate and Pollution Agency, Oslo, Norway |
| TP 613 | Proteomics of Olfaction: Identification and Relative Quantification of Odorant Binding Proteins in the Antennae of Drosophila melanogaster; Taufika Islam Williams; Shilpa Swarup; Shanshan Zhou; Robert Anholt; North Carolina State University, Raleigh, NC |
| TP 614 | Quantitative Proteomics and Phosphoproteomics Approach to Investigate the Effects of Botanicals on Insulin Sensitivity; Peter Scherp; Lauren Kelley; William T. Cefalu; Indu Kherpatel; Pennington Biomedical Research Center, LSU System, Baton Rouge, LA; Louisiana College, Pineville, LA |
| TP 615 | Cross-referencing a Mass Spectrometry-Derived Proteomic Signature for TUESDAY POSTERS
Invasive Ductal Breast Carcinoma with Tissue Image Analysis and Clinical Investigations; Claudia Roewer1; Cornelia Koy1; Björn Ziems2; Annegret Radtke1; Oliver Schmitt5; Toralf Reimer1; Hans-Juergen Thiesen2; Bernd Gerber2; Michael O. Glocke2;3; Proteome Center Rostock, Rostock, Germany; 2Institute of Immunology, Rostock, Germany; 3Partnerschaft der Fachakademie für Pathologie, Rostock, Germany; 4Department of Anatomy, University of Rostock, Rostock, Germany; 5Department of Obstetrics and Gynecology, Rostock, Germany

TP 616 Label Free Quantitative Proteomics of Formalin Fixed Embedded (FFPE) Tissue Sections from Temporal Giant Cell Arteritis Patients; Helen Ge1; Guey Shuang Wu2; Roger Moore3; Nursing Rao; Terry Lee1; Gabriel Gujulu1; 1City of Hope, Duarte, CA; 2Doheny Eye Institute, Los Angeles, CA

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TP 617 Proteome Characterization of Enterohemorrhagic Escherichia coli O157:H7 using High Resolution Mass Spectrometry; Raghotthama Chaerkady1;2; Anne-Marie Hansen3; Nandini Sahasrabuddhe1;2; Santosh Renuse1;2; Vadiraja B. Bhat1; James B. Kaper1; Akhilesh Pandey1;3; Johns Hopkins University, Baltimore, MD; 2Institute of Bioinformatics, Bangalore, India; 3University of Maryland, Baltimore, MD; 4Agilent Technologies, Wilmington, DE

TP 618 Analysis of Proteome Response of Mycobacterium Smegmatis and Mycobacterium Tuberculosis in an Integrated Stress Environment; Prathad Rao; UIC, Chicago, IL

TP 619 Identifying the Effects of L-telluriummethione on the Proteome of Escherichia coli by Nano-ESI/qTOF/MS; Sarah Brinkley; Tennessee Tech, Cookeville, TN

TP 620 Quantitative Tracking of Isotope Flows in Proteomes of Microbial Communities; Chongle Pan1; Curt Fischer2; Doug Hyatt1; Benjamin Bowen1; Robert Hetrick1; Jillian Banfield1; Oak Ridge National Laboratory, Oak Ridge, TN; 2University of California, Berkeley, Berkeley, CA; Lawrence Berkeley National Laboratory, Berkeley, CA

TP 621 Comparison of Direct and Indirect Extraction Methods for Deep Metaproteomics Characterization of the Gut Microbiota; Kristen Corrier1; Alison Erickson1; Regina Lamendella1; Brandi Cantarel1; Manesh Shah1; Claire Fraser-Liggett1; Robert Hetrick1; Janet Jansson1; Marcelo Sztein1; Nathan Verberkmoes1; Oak Ridge National Laboratory, Oak Ridge, TN; 2University of Maryland School of Medicine, Baltimore, MD; 3Lawrence Berkeley National Laboratory, Berkeley, CA

TP 622 Proteogenomic Analysis and Genome Annotation of Mycobacterium smegmatis using High Resolution Mass Spectrometry; Jagadeesha Maharudraiah1; Ken Miller2;1; Santosh Renuse1;2; Raju Ravikumar3; Raghotthama Chaerkady1;2; Vadiraja B. Bhat1;3; H. C. Harsha1; Akhilesh Pandey1; 1Institute of Bioinformatics, Bangalore, India; 2Agilent Technologies, Santa Clara, CA; 3Agilent Technologies, Wilmington, DE; 4Johns Hopkins University, Baltimore, MD; 5NIMHANS, Bangalore, India

TP 623 Quantitation of Membrane Proteome Dynamics under Diauxie Growth Conditions in Escherichia coli Using 13N-Metabolic Labeling and Unique Tri-Phasic Protein Fractionation; Grzegorz Sabat; Gregory A. Barrett-Wilt; Heather L. Burch; Michael R. Sussman; University of Wisconsin, Madison, WI

TP 624 Large scale Identification of Coordinate Mitotic Proteins; Dominic Winter; Sasha Singh; Marc Kirchner; Hanno Steen; Judith Jehanathirajah Steen; Harvard Medical School/Children’s Hospital Boston, Boston, MA

TP 625 Towards Proteomic Approach for the Identification of Heart Kinetically Stable Proteins; Gishan Lin; Jinghua Zhu; University at Albany, Rensselaer, NY

TP 626 Measurement of Cellular Post-Translational Modification Perturbation in Response to HIV Infection using Copper (I)-catalyzed Cycloaddition Protein Labeling; David Colihougn1;2; Veronica Aquino1; Allexey Lyashkov1; Ceereena Mohien1; Rachel Doolaslan1; Brian Agnew2; David Graham2; National Hopkins Bloomberg School of Public Health, Baltimore, MD; 2Johns Hopkins School of Medicine, Baltimore, MD; 3Life Technologies-Molecular Probes, Eugene, OR

TP 627 Proteins in Paintings: Investigation on their Chemical Modifications Due to Local Environment and Aging; Caroline Tokarski; Christian Roland; Univ. de Lille 1, Sciences et Technologies, Villeneuve D’ascq, France

TP 628 Qualitative and Semi-Quantitative Proteomic Characterization of Three Types of Basement Membranes in the Human Eye; Guy Uchchi; Yuchen Lu; Emanuel Schreiber; John Cardamone; Willi Halfert; Manimala Balasubramani; University of Pittsburgh, Pittsburgh, PA

TP 629 Terminal Proteomics for Biomarker Exploration of Plasma Proteome; Taro Kishimoto1;2; Jun Kondo; Takako Takai-Igarashi3; Hiroshi Tanaka1; Molecule Corporation, Kanagawa, Japan; 2Mitsubishi Pharma Corporation, Kanagawa, Japan; 3Tokyo Medical and Dental University, Tokyo, Japan

TP 630 Studying Infection Kinetics of Swine-Origin H1N1 (SOIV) Influenza in Cynomolgus Macaques using Mass Spectrometry-based Proteomics; Arti Navare1; Eric Y. Chan1; David Purdy1; Alexei L. Krasnoslesky1; Jose Meza2; Arivusudar Marimuthu1; Keith Hebner1; William Hancock2; Brian Agnew3; David Graham2; National Institutes of Health, Hamilton, MT; 2Johns Hopkins School of Medicine, Baltimore, MD; 3Agilent Technologies, Santa Clara, CA

TP 631 Studying the Proteome Turnover at a Large-Scale Using Stable-Isotope Labeled Mice; Antonius Koller1; Jenne Relucio1; Sara Nik1; Banu Dost1; Holly Colognato1; Nuno Banderia1; Emily Chen1; 1Stony Brook University, Stony Brook, NY; 2Stony Brook University, Proteomics Center, Stony Brook, NY; 3University of California, San Diego, La Jolla, CA

TP 632 Proteomics Analysis of Dynamic Changes in a CHO Cell Culture; Tyler D Carlage1; Li Zang1; Rashmi Kshirsagar1; Vijay Janakiram1; Andy Weiskopf1; William Hancock2; Brian Agnew3; Stony Brook, Cambridge, MA; 2Northeastern University, Boston, MA

TP 633 Measurement of Cellular Post-Translational Modification Perturbation in Response to HIV Infection using Copper (I)-catalyzed Cycloaddition Protein Labeling; David Colihougn1;2; Veronica Aquino1; Allexey Lyashkov1; Ceereena Mohien1; Rachel Doolaslan1; Brian Agnew2; David Graham2; National Hopkins Bloomberg School of Public Health, Baltimore, MD; 2Johns Hopkins School of Medicine, Baltimore, MD; 3Life Technologies-Molecular Probes, Eugene, OR

TP 634 Large scale Identification of Coordinate Mitotic Proteins; Dominic Winter; Sasha Singh; Marc Kirchner; Hanno Steen; Judith Jehanathirajah Steen; Harvard Medical School/Children’s Hospital Boston, Boston, MA

TP 635 Towards Proteomic Approach for the Identification of Heart Kinetically Stable Proteins; Gishan Lin; Jinghua Zhu; University at Albany, Rensselaer, NY

TP 636 Measurement of Cellular Post-Translational Modification Perturbation in Response to HIV Infection using Copper (I)-catalyzed Cycloaddition Protein Labeling; David Colihougn1;2; Veronica Aquino1; Allexey Lyashkov1; Ceereena Mohien1; Rachel Doolaslan1; Brian Agnew2; David Graham2; National Hopkins Bloomberg School of Public Health, Baltimore, MD; 2Johns Hopkins School of Medicine, Baltimore, MD; 3Life Technologies-Molecular Probes, Eugene, OR

TP 637 Proteins in Paintings: Investigation on their Chemical Modifications Due to Local Environment and Aging; Caroline Tokarski; Christian Roland; Univ. de Lille 1, Sciences et Technologies, Villeneuve D’ascq, France

TP 638 Qualitative and Semi-Quantitative Proteomic Characterization of Three Types of Basement Membranes in the Human Eye; Guy Uchchi; Yuchen Lu; Emanuel Schreiber; John Cardamone; Willi Halfert; Manimala Balasubramani; University of Pittsburgh, Pittsburgh, PA

TP 639 Terminal Proteomics for Biomarker Exploration of Plasma Proteome; Taro Kishimoto1;2; Jun Kondo; Takako Takai-Igarashi3; Hiroshi Tanaka1; Molecule Corporation, Kanagawa, Japan; 2Mitsubishi Pharma Corporation, Kanagawa, Japan; 3Tokyo Medical and Dental University, Tokyo, Japan

TP 640 Studying Infection Kinetics of Swine-Origin H1N1 (SOIV) Influenza in Cynomolgus Macaques using Mass Spectrometry-based Proteomics; Arti Navare1; Eric Y. Chan1; David Purdy1; Alexei L. Krasnoslesky1; Jose Meza2; Arivusudar Marimuthu1; Keith Hebner1; William Hancock2; Brian Agnew3; David Graham2; National Institutes of Health, Hamilton, MT; 2Johns Hopkins School of Medicine, Baltimore, MD; 3Agilent Technologies, Santa Clara, CA

TP 641 Studying the Proteome Turnover at a Large-Scale Using Stable-Isotope Labeled Mice; Antonius Koller1; Jenne Relucio1; Sara Nik1; Banu Dost1; Holly Colognato1; Nuno Banderia1; Emily Chen1; 1Stony Brook University, Stony Brook, NY; 2Stony Brook University, Proteomics Center, Stony Brook, NY; 3University of California, San Diego, La Jolla, CA

TP 642 Proteomics Analysis of Dynamic Changes in a CHO Cell Culture; Tyler D Carlage1; Li Zang1; Rashmi Kshirsagar1; Vijay Janakiram1; Andy Weiskopf1; William Hancock2; Brian Agnew3; Stony Brook, Cambridge, MA; 2Northeastern University, Boston, MA

TP 643 Quantitation of Membrane Proteome Dynamics under Diauxie Growth Conditions in Escherichia coli Using 13N-Metabolic Labeling and Unique Tri-Phasic Protein Fractionation; Grzegorz Sabat; Gregory A. Barrett-Wilt; Heather L. Burch; Michael R. Sussman; University of Wisconsin, Madison, WI
TP 633 Mass Spectrometry Analysis of Ancient Bone from Columbian Mammoth; Ryan Hill; Monika Dziectakowska; Kirk Hansen; Univ. of CO. Denver, AMC, Aurora, CO

TP 634 Isolation of Rat Neuronal Nuclei using Expression Microdissection for Mass Spectrometry-based Proteomic Analysis; Bing Gao; Kimberly Tran; Michale Tangrea; Carolyn Olt; Nicole Morgan; Anthony Makusky; Robert Bonner; Thomas Pohida; Aubri Gillespie; Eugenia Romantseva; Michael Emmert-Buck; Jennifer Lippincott-Schwartz; Sanford Markley; National Institutes of Health, Bethesda, MD

TP 635 Identification of Potential Targets of mir200b Using SILAC-based Proteomic Approach; Arivusudar Marimuthu; Keith Waddell; Santosh Renuse; Praveen Kumar; Nandini Sahasrabuddhe; Lakshmi Dhevi Selvan; H.C. Harsha; Akhilesh Pandey; Institute of Bioinformatics, Bangalore, India; Agilent Technologies, Santa Clara, CA; Johns Hopkins University School of Medicine, Baltimore, MD

TP 636 Proteomic Profiling of Urinary Samples Focalized on IEF Gels in the Screening of EPO in Anti-doping Laboratories; Paule Emilie Groleau; Philippe Desharnais; INRS-Doping control, Laval, Canada

TP 637 Metabolic Labeling Proteomics of Nascently Synthesized Proteins: Proteomic Response of Mouse Macrophages to Stimulation by LPS and Interferon; Roger Ebanks; Andrew Leslie; Kirsten Kukula; Michael Morash; Michelle Euloth; NRC - Institute for Marine Biosciences, Halifax, Canada; Dalhousie University, Halifax, Canada

TP 638 Zebrafish Proteogenomics; Raagothama Chaerkady; Elayne Provost; Babylakshmi Muthusamy; Dhanashree Kelkar; Derese Getnet; Nandini A Sahasrabuddhe; Jun Zhong; Praveen Kumar; Chieh-Huei Wang; Vadiraja Bhat; Min-Sik Kim; Santosh Renuse; Steven Leach; Akhilesh Pandey; Johns Hopkins University, Baltimore, MD; Institute of Bioinformatics, Bangalore, India; Agilent Technologies, Wilmington, DE

TP 639 From Climate Change to Crops: Redox-Proteomics of Ozone-Induced Responses in Soybean; Leslie M. Hicks; Ashley Galant; Elizabeth Ainsworth; Joseph M. Jez; Danforth Center, St. Louis, MO; USDA ARS Photosynthesis Research Unit - UIUC, Urbana-Champaign, IL

TP 640 Proteomics of Small Proteins from Plant Tissues; Greg Hurst; Patricia Lankford; Xiaohua Yang; Ting Li; David Weston; Sara Allen; Timothy Tschaplinski; Gerald Tuskan; Oak Ridge National Laboratory, Oak Ridge, TN

TP 641 Analysis of the Cancer Secretome by N-Glyco FASP; Paul J. Boersema; Tamar Geiger; Dorota F. Zielinska; Jacek R. Wiśniewski; Matthias Mann; Max Planck Institute for Biochemistry, Martinsried, Germany

TP 642 Quantitative Analysis of Differentially Expressed Saliva Proteins in HIV-1 Seropositive Individuals; Nawei Zhang; Daniel Malamud; Lingi Zhang; Haiteng Deng; Rockefeller University, New York, NY; Tsinghua University, Beijing, China; New York University, New York, NY

TP 643 Investigating the Oxidative Stress Mechanism of Death for Macrophages Exposed to Anthrax Lethal Toxin using DMPO and Mass Spectrometry; Allison N. Schorzman; Jeffrey F. Kuhn; Kenneth B. Tomer; NIH Research Triangle Park, NC; INIHE/SRA, Garner, NC

TP 644 Comprehensive Label-Free Quantitative Proteomic Analysis of the Corynebacterium Pseudotuberculosis Exoproteome and the Implications on Pathogenicity and Resistance to Stress; Susan E. Slade; Luis Pacheco; Christopher Dowson; Martin Feehlic; James Scrivens; Vasco Azevedo; University of Warwick, Coventry, UK; Universidade Federal de Minas Gerais, Belo Horizonte, Brazil

TP 645 A Pattern Plus Identity Based Proteomic Approach for Molecular Epidemiology in Infectious and Other Endemic Disease; Bushdy Ahmad; D. R. Mani; Michael Gillette; Margaret Pyle; Frode Berven; Raval Adusumilli; Steven A. Carr; Broad Institute of Harvard and MIT, Cambridge, MA; University of Bergen, Bergen, Norway; Dana-Farber Cancer Institute, Boston, MA

TP 646 Using SESI-MS to Determine Volatile Biomarkers Released from Pseudomonas aeruginosa under Antibiotic Stress; Yin-Ming Ku; Jane Hill; University of Vermont, Burlington, VT

TP 647 Mass Spectrometry-Based Analysis of Mice Infected with Aspergillus fumigatus; Chensu Huang; Jason McCarthy; Marta Feldmesser; Vicki H. Wysocki; Universa, Tucson, AZ; Albert Einstein College of Medicine, Bronx, NY

TP 648 MS-based Screening for Klebsiella Proteins in Urine Samples of Klebsiella pneumoniae Patients; Zhenlian Ke; Francisco J. Dieguez-Acuna; Nathan G. Hatcher; Daniel S. Spellman; Ronald C. Hendrickson; Bonnie J. Howell; Merck & Co, West Point, PA

TP 649 Quality Control on MALDI-TOF RPC18 Profiles of Urinary Peptides from Renal Cell Carcinoma Patients; Erica Gianazza; Yuri E.M. Van Der Burgt; Marco R. Bladergroen; Hans Dalebout; Italo Zoppis; Cilizia Chinello; Valeria Squeo; Gianpaolo Zanetti; Giancarlo Mauri; Massimiliano Borsani; Stefano Signorini; Marzia Galli Kienle; Fulvio Magni; André M. Deelder; Leiden University Medical Center, Leiden, Netherlands; University of Milan-Bicocca, Monza/Milan, Italy; University of Milano Ospedale Maggiore Policlinico, Milano, Italy

TP 650 Relative Quantification of Proteins in Urinary Exosomes from Patients with Polycystic Kidney Disease; Kenneth L. Johnson; Roman M. Zenka; M. Cristine Charlesworth; Benjamin J. Madden; H. Robert Bergen, III; Peter C. Harris; Christopher J. Ward; Marie C. Hogan; Mayo Clinic, Rochester, MN

TP 651 High-resolution Liquid Chromatography-Mass Spectrometry to Identify Urinary Biomarkers of Autism; Zachary Fine; Troy Wood; University at Buffalo, Buffalo, NY
TP 652 Proteomic Analysis of Lipid Rafts of Abca1-/- Macrophages Reveals Novel Signaling in Lipid Rafts; Saiful M. Chowdhury; Xuewei Zhu; Jason Williams; B. Alex Merrick; Leesa J. Deterding; John S. Parks; Kenneth B. Tomer; Michael B. Fessler; NEHS, NIH, RTP, NC; Wake Forest University School of Medicine, Winston-Salem, NC

TP 653 Peptide and PTM Biomarkers of Cardiovascular Disease in a Mouse Model; Mark E. McComb; Vivek N. Bhatia; Deborah A. Siwik; Nancy M. Leymarie; David H. Perlman; Richard A. Cohen; Wilson Colucci; Catherine E. Costello; Boston University School of Medicine, Boston, MA

TP 654 Radiation-Induced Changes to Endothelial Cell Surface Proteins in the Pursuit of Targets for Vascular Therapies; Margaret Simonian; Macquarie University/ School of Advanced Medicine, Sydney, Australia

TP 655 Biomarker Discovery in Duchenne Muscular Dystrophy Using Parallel Nanotechnology Based Affinity Capture Enrichment; Sree Rayavarapu; Brian Feild; Ben Lepene; William Coley; Yetrib Hathout; Eric Hoffman; Faith Hays; Kanneboyina Nagaraju; The George Washington University, Washington, DC; Children’s National Medical Center, Washington, DC; Shimadzu Scientific Instruments, Columbia, MD; Ceres Nanosciences, Inc., Manassas, VA

TP 656 Metabolomics Analysis of Alcohol on Mice Fed with Unsurfated Fat Diet Using LTQ-FTMS and GC×GC-MS; Xue Shi; Xiaoli Wei; Wenlong Sun; Xinmin Yin; Xiang Zhang; University of Louisville, Louisville, KY

TP 657 Metabolomics Analysis Reveals that Fats Transport Back to Liver from Adipose Tissue in Mice Fed with Alcohol; Wenlong Sun; Xiaoli Wei; Xue Shi; Bogdan Bogdanov; Xiang Zhang; University of Louisville, Louisville, KY

TP 658 MetSign: An Analysis Platform for High Resolution Mass Spectrometry based Metabolomics; Xiaoli Wei; Wenlong Sun; Xiang Zhang; University of Louisville, Louisville, KY

TP 659 Identifying Citrullinated Peptides by Unbiased Protein-Proteome Analysis; A. Jimmy Ytterberg; Dorothea Rutschhauser; Elena Ossipova; Anca Catrina; Per-Johan Jakobsson; Lars Klareskog; Roman Zubarev; Karolinska Institute, Stockholm, SWEDEN

TP 660 Juvenile Idiopathic Arthritis Patients at Risk of Disease Extension Segregated by Synovial Proteome Analysis; David Gibson; Keri Newell; Gwen Manning; Stephen Pennington; Mark Duncan; Madeleine Rooney; Queen’s University Belfast, Arthritis Research, Belfast, UK; University of Colorado Denver, Proteome Resource, Aurora, CO; University College Dublin, Conway Institute, Dublin, Ireland

TP 661 Label Free Comparative Secretome Proteomics of an Amyotrophic Lateral Sclerosis Cellular Model using Human ESC-derived astrocytes; Robert Sturm; Robert Krenck; Su-chun Zhang; Jingjun Li; University of Wisconsin-Madison, Madison, WI

TP 662 Hydrophobic Metabolites Associated with Type II Diabetes in Human Plasma; Jared Bowden; Edward Dratz; Montana State University, Bozeman, MT

TP 663 Use of Novel “Omic” Based Platforms to Enhance Understanding of Pathophysiology in Diabetes; Tracey Friss; Min Du; Rangaprasad Sarangarajan; Vivek K. Vishnuudas; Shen Luan; Niven R. Narain; Berg Diagnostics, Boston, MA; Berg Biosystems, Boston, MA

TP 664 Novel Insight into the Underlying Pathophysiology of Cardiovascular Dysfunction Using the Berg Interrogative BiologyTM Discovery Platform; Min Du; Tracey Friss; Rangaprasad Sarangarajan; Vivek K. Vishnuudas; Shen Luan; Niven R Narain; Berg Diagnostics, Boston, MA; Berg Biosystems, Boston, MA

TP 665 Type-2 Diabetes and Innate Immunity: Connections Revealed by Multi-Dimensional Fractionation of Blood Plasma; Scott Laffoon; Duane Mooney; Edward Dratz; Paul Grieco; Montana State University, Bozeman, MT; Zdye LLC, Bozeman, MT

TP 666 Label-free Quantification of the Platelet Membrane Proteome in Alzheimer’s Disease; Laura Donovan; Eric Dammer; William Levey; James La; Nicholas Seyfried; Department of Biochemistry, Atlanta, GA; Department of Neurology, Atlanta, GA; Emory School of Medicine, Atlanta, GA

TP 667 Discovery and Validation of a Potential Serum Biomarker for Presymptomatic Alzheimer’s Disease; Linda Desselts; Lennard J. Dekker; Christoph Stingl; Marcel M. van der Weiden; Albert Hofman; Johan M. Kros; Peter J. Koudstaal; Peter A.E. Sillevis Smitt; Monique M.B. Breiteler; Theo M. Luider; Erasmus University Medical Center, Rotterdam, Netherlands

TP 668 Enabling Absolute Quantification to Take Flight: An Exploration of Winged Peptides and their Digestion Properties; Susan E. Abbatielo; Naomi Choodnovsky; Michael Burgess; Tyra J. Cross; Derek Smith; Leigh Anderson; Steven A. Carr; Broad Institute of Harvard and MIT, Cambridge, MA; UVic-Genome BC Proteomics, Victoria, BC; Plasma Proteome Institute, Washington, DC

TP 669 Targeted Biomarker Screen for Secreted Breast Tumor Proteins from a Xenograft Model of Primary Human Breast Cancer; Nicholas Bateman; Michael Lewis; Christine Wu; University of Pittsburgh School of Medicine, Pittsburgh, PA; Baylor College of Medicine, Houston, TX

TP 670 Determination of Protein Turnover in Infants Diagnosed with Respiratory Distress Syndrome using SIL Tracers and SRM Mass Spectrometry; Michael Bereman; Daniela Tomazela; Hilary Heins; Bruce Patterson; Aaron Hamvas; F. Sessions Cole; Michael J. MacCoss; University of Washington, Seattle, WA; Washington University, St. Louis, MO

TP 671 Multiple Reaction Monitoring for Absolute Quantitation of Low Abundant Protein in Whole Cell Lysate; Junseok Kim; Functional Proteomics Center, KIST, Seoul, SOUTH KOREA

TP 672 Dynamic MRM Measurements of Multi-biomarker Proteins by Triple-Quadrupole Mass Spectrometry with Nanoflow HPLC-Microfluidics Chip; Eun Sun JI; Mi Hee Cheon;
TP 663 Enhanced Detection of Low Abundance Human Plasma Proteins using Tandem IgY14-SuperMix Immunoaffinity Depletion and LC-ESI-Q-TOF; Mahboud Hossaini; Athina A. Schepmoe; Thomas L. Fillmore; Tao Liu; Errol W. Robinson; Ronald J. Moore; Keqi Tang; David G. Camp II; Richard D. Smith; Wei-Jun Qian; Pacific Northwest National Laboratory, Richland, WA

TP 674 Biomarker Pattern Discovery Related to Alzheimer’s Disease using Quantitative Proteomics; Lei Wang; Keith Wilcoxen; Ken Aoshima; Hiroyuki Katayama; Yoshiyuki Oda; Eisai Inc. Andover, MA

TP 675 Evaluation of CSF beta-2-microglobulin, VGF, and Cystatin-C as Diagnostic Biomarkers of Alzheimer’s Disease using SRM Assay; Leic Davoy1; Darragh P. O’Brien1, 2; Emma L. Schofield1, 2; James Campbell1; Sanna-Kaisa Herukka1; Merja Hallikainen1; Simon Lovestone3; Hilka Soininen2; Malcolm A. Ward4; Proteome Sciences plc, London, UK; 1Kuopio University and University Hospital, Kuopio, Finland; 2MRC Centre for Neurodegeneration Research, London, UK

TP 676 MRM Analyses for Quantitation of Biomarkers in Urinary Exosomes; Kevin L. Schev; Kristie Rose; Junhua Wei; J. Matthew Luther; Xiaoqiang Wang; Bing Zhang; David L. Hachey; Vanderbilt University, Nashville, TN

TP 677 Precursor and Product Ion Number Effects on LC-MS/MS Quantification Variability; Eric Kilpatrick1; Karen Pinney2; Lisa Kilpatrick3; 1National Institute of Standards and Technology, Gaithersburg, MD; 2NIST, Gaithersburg, MD

TP 678 Simultaneous Quantitation of Apolipoprotein(a) Concentration and Total Kringle IV2 Repeat in Plasma by UPLC/MS/MS; Theresa McLaughlin; Michael Lassman; Hailong Zhou; Lauretta LeVoci; Timothy Fisher; Thomas Roddy; Merck & Co., Inc., Rahway, NJ

TP 679 Targeted Analysis of Protein Expression in Human Lymphoblast Cell Lines; Adele Blackler; Ruby Fried; Pablo Moya; Dennis L Murphy; NIMH, Bethesda, MD

TP 680 Targeted Protein Quantitation Using High Resolution, Accurate Mass Precursor Ion Scanning with scheduled MS/MS; Reiko Kiyonami; Amol Prakash1; Vlad Zabrouskov1; 1ThermoFisher Scientific, San Jose, CA; 2Thermo Fisher Scientific BRIMS center, Cambridge, MA

TP 681 Absolute Quantification of Therapeutic Antibodies in Biofluids by Nano Liquid Chromatography and Triple Quadrupole Linear Ion Trap MS Technology; Jenny Albanese; Christie L. Hunter; All SCIEX, Foster City, CA

TP 682 Optimization of Nanospray Voltage and Spray Stability: Impact on Chromatographic Peak Area for Analyte Quantitation; Amanda Berg1; Mike S. Lee1; Gary Valaskovic; 1New Objective, Inc., Woburn, MA; 2Milestone Development Services, Newtan, PA

TP 683 Verification of a QSOX1 Peptide as Cancer Biomarkers Using Selected Reaction Monitoring; Jian Lu1; Kwasi Antwi2; Tony Tegeler3; Linda Nagore1; Ashoka D. Polpitiya1; Ben Katchman1; Rafaela Zappardo2; Michael Demeure1; Martina Cavestro1; Douglas Lake2; Konstantinos Petritis1; 1Translational Genomics Research Institute, Phoenix, AZ; 2School of Life Sciences, Arizona State University, Tempe, AZ; 3San Raffaele Hospital, Milan, Italy

TP 684 Quantitation of Cystine and Profiling of related Metabolites in White Blood Cells using a High Resolution Accurate Mass Spectrometry Approach; Na Pi1; Shane E. Tichy2; 1; 2A. Jimmy Van der Weiden; 1Sweedish University of Technology, Kista, Sweden; 2Vanderbilt University, Nashville, TN

TP 685 Multiple Reaction Monitoring MS Protein Analysis of Formalin-Fixed Paraffin-Embedded Tissue; Robert Sprung1; Mary Kay Washington; Amy Joan Ham; Daniel Lieder; Vanderbilt University Medical Center, Nashville, TN; 1Berg Diagnostics, Boston, MA; 2NIST, Gaithersburg, MD

TP 686 AD TMT-SRM Assay Delivering Simultaneous Quantitation of 9 Key Plasma Proteins in Clinical Cohorts Relevant to AD Research; Darragh P. O’Brien1; Helen L. Byers1; James Campbell1; Loic Davoy1; Andreas Guntert1; Karsten Kuhn1; Rufina Leung1; Simon Lovestone1; Malcolm A. Ward1; Proteome Sciences plc, London, UK; 1MRC Centre for Neurodegeneration Research, London, UK

TP 687 Hypothesis-driven Biomarker-Verification in Acute Pancreatitis; Stephan Bek; Novartis, Basel, Switzerland

TP 688 Advances in Multiplexed Quantification of Proteins: Inter- and Intra-laboratory Evaluation of Multiplexed Peptide MRM-MS Assays using Peptide Immunoaffinity Enrichment; Eric Kuhn1; Jeffrey Whiteaker2; Angela Jackson1; Lei Zhao2; Matthew Pope3; Keith Rivera1; Derek Smith1; D. R. Mani1; Leigh Anderson1; Terry Pearson4; Amanda Paulovich6; Steven A. Carr5; 1Broad Institute, Cambridge, MA; 2Fred Hutchinson Cancer Research Center, Seattle, WA; 3Uvic Genome BC Proteomics Centre, Victoria, BC; 4University of Victoria, Victoria, BC; 5Plasma Proteome Institute, Washington, DC

TP 689 The Development of a Targeted Quantitation Assay for Cerebral Spinal Fluid Proteins; Derek Smith1; Monica H Elliott2; Darryl Hardie3; Mert Pekcan4; Dominik Domanski5; Angela Jackson1; Juncong Yang1; Alex Camenzind1; Tyra Cross2; Christoph H. Borchers2; 1Ankara University, Faculty of Veterinary medicine, Ankara, Turkey; 2Uvic-Genome BC Proteomics Centre, Victoria, BC; 3University of Victoria, Victoria, BC; 4Plasma Proteome Institute, Washington, DC

TP 690 Developing Diagnostic Biomarkers for Secondary Progressive Multiple Sclerosis using Selected Reaction Monitoring; Yan Jia1; Christine Jelinek1; Scott Newsome2; John Ratchford2; Avindra Nath3; Robert Cotter2; 1Johns Hopkins University, School of Medicine, Baltimore, MD; 2Johns Hopkins University, Department of Neurology, Baltimore, MD

TP 691 A Suite of Multiple Reaction Monitoring (MRM) Assays to Analyze Cancer-Related Metabolic Pathways; Lisa J. Zimmerman;
Patrick J. Halvey; Bing Zhang; Haixia Zhang; Robbert J. C. Slebos; Daniel C. Liebler; Vanderbilt University, Nashville, TN

TP 692 Identification and Quantitative Analysis for Clinical Proteomics by LC-ESI/MS Using Stable Isotope-labeled Iodoacetamide; Sadamurug1, 2, Yuka Kaneko1, 2, Shuji Matsuura1, Satomi Niwayama1; 1Osaka University, Osaka, Japan; 2Wako Pure Chemical Industries, Ltd., Osaka, Japan

TP 693 Measuring H218O Tracer Incorporation on a QQQ-MS Platform Provides a Rapid, Transferable Screening Tool for Relative Protein Synthesis; James Conway; Douglas Johns; Sheng-Ping Wang; Nykia Walker; Thomas McAvoy; Xuemei Zhao; Stephen Previs; Thomas Roddy; Nathan Yates; Brian Hubbard; Ronald Hendrickson; Merck Research Laboratories, Rahway, NJ

TP 694 Quantitation of Glucagon-like Peptide-1, GLP-1 (7-36) Amide, and the DPP4-catalyzed Degradation Product GLP-1 (9-36) Amide by LC/MS; Rong-Sheng Yang; Yan-Hui Liu; Aileen Soriano1; Joyce Hwa1; Merck Research Laboratories, Rahway, NJ; Merck, Kenilworth, NJ

TP 695 Comparative Temporal Proteomics Analysis of OCT4-Induced Melanoma Stem Cell Differentiation; Suresh Kumar; Vadiraja B. Bhat; Xiaowei Xu; University of Pennsylvania, Philadelphia, PA; Agilent Technologies, Wilmington, DE

TP 696 Pattern Recognition Classification of Mass Spectral Profiles as a Tool in Systems Biology: Application to Drug Addiction; Elena Romanova; Justin Rhodes; Jonathan Sweedler; University of Illinois, Urbana, IL

TP 697 Long-term Effects of High-Fat Diet on Metabolic Pathways in 129Sv and C57Bl6/J Mouse Livers: A Proteomics Approach; Eduard Sabido1; Thomas Porstmann1; Shuji Da1; Chunhua Wang1; Anthony J. Rossomando2; Barry L. Karger1; Northeastern University, The Barnett Institute, Boston, MA; A*Star Biotherapeutics, Cambridge, MA

TP 700 Quantitative Proteome of Poxvirus-Infected vs. -Uninfected Human Cells; Wayne Cheung; Tuan Ngo; Paul Gershon; UC-Irvine, Irvine, CA

TP 701 Characterization of the Macaque Sperm Proteome; Timothy Karr1; Sheri Skergt2; Matthew Rosenow2; Konstantinos Petritis2; 1Arizona State University, Tempe, AZ; 2Translational Genomics Research Institute, Phoenix, AZ

TP 702 Applying Isobaric Multiplexing Technology to Unravel Proteome Wide Environmental Stress Adaptation in Budding Yeast; Joshua T. Wilson-Grady; Wilhelm Haas; Steven Gygi; Harvard Medical School, Boston, MA

TP 703 Integrated Microarray and Quantitative Proteomic Analysis Identifies Proteostasis Network Changes in a Mouse Model of Huntington’s Disease; Benbo Gao1; Ken Longo1; Eric Roskelley1; Mark P. Jedrychowski2; Edward L. Huttlin1; Steven P. Gygi2; Walter Newman3; Dan Garza1; Brad Geddes1; Peter H. Reinhart1; Hui Ge1; 1Proteostasis Therapeutics Inc., Cambridge, MA; 2Department of Cell Biology, Harvard Medical School, Boston, MA

TP 704 Revealing the Dynamics of the Acute Promyelocytic Proteome During Remission Using Pulsed SILAC and Mass Spectrometry; Tony Ly; Francois-Michel Boisvert; Yasmeen Ahmad; Mark Larance; Angus Lamond; Welcome Trust Centre for Gene Regulation and Expr, Dundee, UK

TP 705 Systems Immunobiology of HIV and HCV: A Proteomics Approach; Daniela Schlatter1; Donald D. Anthony1; Yawen Chen1; Matthias Mann2; Max-Planck-Institute of Biochemistry, Munich, Germany; 1Max-Planck-Institute of Biochemistry, Martinsried, Germany; 2Thermo Electron (Bremen) GmbH, Bremen, Germany

TP 706 Use of Spectral Counting and AMT to Quantify Changes in Renal Proximal Convoluted Tubules during Onset of Metabolic Acidosis; Scott Walmsley; Norman Curthoys; Colorado State Univ, Fort Collins, CO

TP 707 Quantitative Proteomics of the Yeast Cell Cycle in Single LC MS/MS Runs on a Novel Quadruple Orbitrap Mass Spectrometer; Nagarjuna Nagarajan1; Annette Michalski1; Juergen Cox1; Richard Scheltema1; Oliver Lange1; Eugen Damoc1; Stevan R. Horning1; Matthias Mann2; 1Max-Planck-Institute of Biochemistry, Munich, Germany; 2Thermo Fisher Scientific, Bremen, Germany

TP 708 Differential Proteomic Analysis of Hypoxic Tumor Microenvironment in vivo in Fibrosarcoma Inoculated Mice Breathing Ambient or Hyperoxic Oxygen; Shujia Dai1; Kengo Moriyama2; Dmitry Lukashev2; Zhenke Liu1; Michael Sitkovsky2; Barry L. Karger1; 1Barnett Institute, Northeastern University, Boston, MA; 2Bouvé College of Health Sciences, Boston, MA

TP 709 Differential Expression Proteomic Phenotyping of Enhanced Survivability of Bacillus pumilus following 18-Month Extraterrestrial Exposure Aboard the International Space Station; Arthur Moseley1; Laura Dubois1; Erik Soderblom2; Will Thompson3; Lisa Carrell1; George Fox1; Gerda Horneck4; Parag Vaiashampayan5; Kasthuri Venkatasureswaran5; 1Duke University Medical Center, Durham, NC; 2NASA Langley Research Center, Hampton, VA; 3University of Houston, Houston, TX; 4Aerospace Medicine, DLR German Aerospace Center, Koeln, Germany; 5Thermo Fisher Scientific India Pvt.Ltd, Bangalore, India
TP 710  Functional Proteomics Reveals a Novel Regulator of Breast Cancer Growth and Metastasis; Miao Liu; Saeid Jami; Xin Huang; Rakesh Singh; Shi-Jian Ding; University of Nebraska Medical Center, Omaha, NE

TP 711  SILAC-based Quantitative Proteomics in the Nematode C. elegans; Mark Larance; Aymeric Bailley; Anton Gartner; Angus Lamond; Wellcome Trust Centre for GRE, Dundee, UK

TP 712  Mass Spectrometric Studies on Epigenetic Interaction Networks in Cell Differentiation; Lei Xiong; Agus Darwanto; Seema Sharma; Jason Herring; Maria Filippova; Valery Filippov; Yinsheng Wang; Chien-Shing Chen; Penelope J. Duerksen-Hughes; Lawrence C. Sowers; Kangling Zhang; Loma Linda University, Loma Linda, CA; University of California, Riverside, CA; Thermo Fisher Scientific, San Jose, CA

TP 713  PKC Phosphorylation of Cardiac Troponin I is Up-regulated in Spontaneously Hypertensive Heart Failure Rat; Xintong Dong; Jiang Zhang; Yi-chen Chen; Marius Sumandea; Ying Ge; University of Wisconsin-Madison, Madison, WI; University of Kentucky, Lexington, KY

TP 714  A Proteomics Approach to Uncover Steroid Hormone Signaling Pathways; Karen Sap; Karel Bezstarosti; Dick Dekkers; Peter Verrijzer; Jeroen Demmers; Erasmus Medical Center, Rotterdam, Netherlands

TP 715  A New Approach to Strain Engineering Using Quantitative Proteomics; Miryam Kadkhodayan; Timothy Cole; Ezhilkani Subbian; Jeanne Benoit; Shannon Gladen; Yoram Barak; Jeffrey Colbeck; Soni Shukla; Guillaume Cottarel; Giselle Janssen; Codexis, Inc., Redwood City, CA

TP 716  Genome-wide Phenotyping of Escherichia coli by High Throughput, Accurate Mass Metabolomics; Nicola Zamboni; Tobias Fuhrer; Boris Begemann; Uwe Sauer; ETH Zürich, Zürich, Switzerland

TP 717  Combinatorial Expression of n-butanol Responsive Genes to Explore Stress Resistant Phenotypes in Escherichia coli; Becky Rutherford; Rafael Rosengarten; Robert Dahl; Peter Benke; Aindrila Mukhopadhyay; Jay D. Keasling; University of California, Berkeley, CA; Joint BioEnergy Institute, Emeryville, CA

TP 718  Activity Based Protein Profiling to Measure Changes in Enzymatic Activity of Anaerobic, Cellulolytic Bacteria; Peter McQueen; Tom Rydzak; Dmitri Shamshurin; Namita Kanwar; Richard Sparling; David Levin; Oleg Krokhin; John Wilkins; University of Manitoba, Winnipeg, Canada; MB Centre for Proteomics and Systems Biology, Winnipeg, Canada; Department of Microbiology, Winnipeg, Canada; Department of Biosystems Engineering, Winnipeg, Canada
### ION/MOLECULE, ION/ION, ION/ELECTRON INTERACTIONS; 001 - 024

**WP 001** Backbone Cleavage versus Sidechain Dissociation in Electron Detachment Dissociation (EDD) of Multiply Deprotonated Proteins; Barbara Ganis1; Monika Taucher; Kathrin Breuker; University of Innsbruck, Innsbruck, Austria

**WP 002** Study of Electron Transfer Dissociation Fragment Ion Structures Using Ion Mobility Mass Spectrometry; Unigwe A. Laskay1; Jeffery M. Brown2; Wenzhou Li3; Vicki H. Wysocki4; 1University of Arizona, Tucson, AZ; 2Waters Corporation, Manchester, UK

**WP 003** Experimental and Theoretical Investigations of Electron Capture and Transfer Dissociation of Protonated and Alkaliated Model Peptides; Bogdan Bogdanov; Jianhua Ren; University of the Pacific Department of Chemistry, Stockton, CA

**WP 004** Electron Transfer Dissociation (ETD) of Cysteine-Containing Peptide Complexes; Jia Dong1; Desmond Kaplan1; Richard Vachet2; 1University of Massachusetts, Amherst, MA; 2Bruker Daltonics, Billerica, MA

**WP 005** Using Electron Capture Dissociation to Define Charge Site Location in Protein Ions; Natalie J. Thompson; David M. Crizer; Takashi Baba; Gary L. Glish; University of North Carolina, Chapel Hill, NC

**WP 006** Selective Ion-Ion Charge Reduction of Multiply Protonated Heterogenous ESI Ions; Jeffery M Brown2; Michael Morris3; Bill Gigante1; 1University of Leipzig, Leipzig, Germany; 2Waters Corporation, Manchester, UK

**WP 007** Comparison of CID, ETD, and Metastable Atom-Activated Dissociation (MAD) of Phosphorylated Peptides. ; Glen Jackson1; Shannon Cook2; Carolyn M. Zimmermann2; Ralf Hoffmann3; 1Ohio University, Athens, OH; 2University of Leipzig, Leipzig, Germany; 3University of Texas at Austin, Austin, TX

**WP 008** Electron Transfer Dissociation (ETD) of Phosphatidylcholine Derivatives for Improved MSI Imaging and Targeted Mass Spectrometric Detection; John Hwang1, 2; Scott Cole1; Xiaoqiao Ma2; 1Purdue University, West Lafayette, IN; 2Tsinghua University, Beijing, China

**WP 009** Electron-induced Ionization Provides Information on Cross Sections and Ionization Energies of Gaseous Multiply Charged Proteins; Aleksey Vorobyev; Yury O. Tsybin; Ecole Polytechnique Federale, Lausanne, Switzerland

**WP 010** Effects of Counterion on Sodium and Acid Adduction to Proteins: Implications for the ESI-MS of Proteins and Complexes; Samuel Merenbloom; Tawnya Flick; Evan R. Williams; University of California, Berkeley, CA

**WP 011** The Utilization of Ion/Ion Reactions for Improved MS/MS Spectral Purity; Catherine Vincent; Aaron Ledvina; Michael S. Westphall; Joshua J. Coon; University of Wisconsin, Madison, WI

**WP 012** Suppression of Analyte Ionization during Electrospray LC-MS-MS by Plasma Matrix Phospholipids; Yongchao Li2; Richard B. Van Bremen1; Min Chang3; 1University of Illinois, Chicago, IL; 2Biogen Idec, San Diego, CA

**WP 013** Going Negative in Metal Ion Chemistry; Jason DiMuzio; Sharon Curtis; Paul Michael Mayer; University of Ottawa, Ottawa, Canada

**WP 014** A Mechanistic Study on Electron Capture Dissociation of Metal-Adducted Oligosaccharides; Yiqun Huang1; Xiang Yu2; 1University of Massachusetts, Boston, MA; 2University of Ottawa, Ottawa, Canada

**WP 015** Analysis of Small Inhibitory RNA (siRNA) Using Negative IOn Electron Transfer Dissociation in Linear Ion Trap; Zhiqiao Hao1; Derek Bailey2; Jason Russell2; Laurance Lee2; 1University of Illinois, Chicago, IL; 2Biogen Idec, San Francisco, CA

**WP 016** Detection of Chemical Warfare Agent Simulants Using Ion-Molecule Reactions in a
 WP 017 Ion-Molecule Reactions as a Tool to Locate the Solvent Dependent Charge-Sites of Ions Generated by Electrospray Ionization; Frenell Jarwala; Athula B. Attygalle; Stevens Institute of Technology, Hoboken, NJ

 WP 018 Laboratory Studies of Carbon Containing Ions and Their Reactions in the Interstellar Medium; Cesar Contreras; Claire Ricketts; Farid Salama; NASA, Moffett Field, CA

 WP 019 DIAM: A New Experimental Set-Up Designed for the Investigation of Irradiation of Nanosystems in the Gas Phase; Guillaume Bruny1; Victor Buridon1; Khalid El Farkh2; Sam Eden1; Stefan Feil1; Mahdi M. Harb1; Cécile Teyssier1; Hassan Abdoul-Carime1; Berndette Farizon1; Michel Farizon1; Said Ouaskit1; Tilman D. Mäkl1; CNRS/IN2P3, UMR5822, IPNL - Université Lyon 1, Villeurbanne, France; CNRS (URAC 10), Faculté des sciences Ben M’sik, Casablanca, Morocco; 2Leopold Franzens Universität, InP, Innsbruck, Austria

 WP 020 On the Mechanism of the aza-Morita-Baylis-Hillman Reaction (aza-MBH): The ESI-MS Fishing of a New Unique Intermediate; Thais Rejam1,2; Vanessa Gonçalves dos Santos1; Marla Narciso Godoi1; Boneik Gontijo Vaz1; Fernando Coelho1; Marcos Vagner Eberlin1; Themos Mass Spectrometry Lab, Campinas, Brazil; 2Lab of Synthesis of Natural Products and Drugs, Campinas, Brazil

 WP 021 Reactivity of an Aromatic σ,σ,σ-Triradical: the 2,4,5-Tridehydropropyridinum Cation; Mohammad Sabir Aqueel1; Brian A. Niedzwiecki1; John Nash1; Hilkka Kenttamaa1; Purdue University, West Lafayette, IN

 WP 022 Comparison of the Reactivity of Isomeric Hydroxy-Substituted Dehydropropyridinium Ions Toward Methanol in Solution and in the Gas Phase; Peggy Williams1; Fanny Widjaja1; Zhicheng Jin1; Jennifer Reece1; Bartlomiej Jankiewicz1; Hilkka Kenttamaa1; John Nash1; Purdue University, West Lafayette, IN

 WP 023 Gas Phase Reactions of H Atoms with Anionic Carbon-nitrogen Species and Polycyclic Aromatic Hydrocarbons; Zhibo Yang1; Nicholas Demarais1; Oscar Martinez Jr1; Callie Cole1; Theodore P. Snow1; Veronica M. Bierbaum1; University of Colorado, Boulder, CO

 WP 024 Proton Affinities of the Cyclic Peptides; Xiaoning Zhao1; Jianhua Ren1; University of the Pacific, Stockton, CA

 WP 025 Dissociative Photoionization of Peptide Ions in the Gas Phase Probed by Synchrotron Radiation; Francis Canon1; Aleksandar Milosavljevic1,2; Matthieu Réfrégiers1; Laurent Nahon1; Alexandre Giudici1,2,3; Synchrotron SOLEIL, Saint-Aubin, France; 2CNRS, Institute of Physics Belgrade, Belgrade, Yugoslavia; 3CEPIA, INRA, Nantes, France

 WP 026 A Mechanistic Look at Femtosecond Laser-Induced Ionization/Dissociation (fs-LID) of Protonated α-Amino Acids and Peptides; Christine L. Kalcic1; Gavin E. Reid1; Marcos Dantus1; Michigan State University, East Lansing, MI

 WP 027 Negative Electron Transfer Dissociation with Supplemental Collisional or Infrared Photoactivation of Multiply Charged Peptide Anions; Jared Shaw1; Jennifer Brodbelt1; The University of Texas at Austin, Austin, TX

 WP 028 Enhanced Photodissociation Efficiency of Cysteine Peptides by Attachment of Thiol- Reactive Chromophores; Victoria Dominguez1; Jennifer Brodbelt1; University of Texas at Austin, Austin, TX

 WP 029 193 nm Ultraviolet Photodissociation of Oligosaccharides; Byoung Joon Ko1; Jennifer Brodbelt1; The University of Texas, Austin, TX

 WP 030 Characterization of Heme c using Matrix Assisted Laser/Desorption Ionization Mass Spectrometry; Hyo-Yik Yang1; Kyu Hwan Park2; Hyun Sik Kim1; Jeongkwn National University, Daejeon, South Korea; Korea Basic Science Institute, Daejeon, South Korea

 WP 031 Differentiating Isobaric Steroid Hormone Metabolites Using Multi-Stage Tandem Mass Spectrometry; Lauren Tedmon1; Hien Nguyen2; Kevin Schu2; James Simpkins2; 1University of Texas at Arlington, Arlington, TX; 2University of Texas at Southwestern, Dallas, TX; 3University of North Texas Health Science Center, Fort Worth, TX

 WP 032 Fragmentation of Xanthene Dyes by Laser and Collisional Activation in a High Resolution FT-ICR Mass Spectrometer; Jonathan Peters1; Jurgen Grotenreyer1; Christian-Albrechts-Univ., Kiel, Germany

 WP 033 Bond Dissociation Energy Determinations of Group-11 (Cu, Ag, Au) Cyanide Complexes using Electrospray Ionization Mass Spectrometry and Collision Induced Dissociation; Barbara Walton1; Guido F. Verbeck1; University of North Texas, Denton, TX

 WP 034 Structures and Collision-induced Dissociation Pathways of Protonated 2'-Deoxyribonucleoside-5'-Monophosphates Investigated by Guided Ion Beam Tandem Mass Spectrometry and Theoretical Calculations; Ranran Wu1; Yuan-wei Nie1; Yu Chen1; Mary Rodgers2; Wayne State University, Detroit, MI

 WP 035 Q0 DC Dipolar Activation in a Linear Ion Trap Time of Flight Instrument; Ian Webb1; Purdue University, West Lafayette, IN

 WP 036 A Comparison of the fragmentation Pathways of First Generation Protonated Nitrile and Amine Terminated PPI Dendimers; William D. Price1; Jacob Kibel2; Jennifer J. Maloney1; Marshall University, Huntington, WV

 WP 037 Relative Stability of Sequence Ions Generated by Tandem Mass Spectrometry; Benjamin J. Bythell1,2; Christopher L. Hendrickson1,2; Alan G. Marshall3,4; National High Magnetic Field Laboratory, Tallahassee, FL; Florida State University, Department of Chemistry, Tallahassee, FL

 WP 038 Exploding C-Alpha Amide Radicals as Model Systems for Simple Z-Ions; Joshua A Gregersen1; Frantisek Turecek1; University of Washington, Seattle, WA

 WP 039 Isomeric Distinction of Small Oligosaccharides: A Bottom-Up Approach using the Kinetic Method; Mohamed Major1; Thierry Fouquet1; Laurence Charles1; Aix-
WP 040 Metastable Atom-Activated Dissociation Mass Spectrometry (MAD-MS) of Phosphopeptide and Sulfopeptide Anions; Shannon Cook; Robert Deimler; Glen Jackson; Ohio University, Athens, OH

WP 041 Study of Measurement of Se Isotopes with MC-ICP-MS and CRM; Ren Tongxiang; National Institute of Metrology, Beijing, China

WP 042 Development of Complementary Methods for 3-O-methyl-D-glucose and D-glucose in Clinical Samples using GC/MS and GC/IRMS; Manisha Shrestha; Peter Walter; NNDDK/NIH, Bethesda, MD

WP 043 Determination of Chromium Species and Mass Balance in Food Supplements using Speciated Isotope Dilution Mass Spectrometry; G. M. Mizanur Rahman1, 2; Naudia Martone1; H. M. Skip Kingston1; Matt Pamuku2; 1Duquesne University, Pittsburgh, PA; 2Applied Isotope Technologies, Inc., Sunnyvale, CA

WP 044 The Quantitative Proteome of the Chlamydia-Infected Cell, Early and Late during Infection; Christopher Rolling; Wayne Chou; Luis DeLa Maza; Paul Gershon; UC-Irvine, Irvine, CA

WP 045 Absolute Measurement of carbon Isotope Ratios with Accelerator Mass Spectrometry; John Vogel; Jason Giacomo; Stephen Duerker; Vitalea Science, Davis, CA

WP 046 Measuring Protein Half Life in vivo While Compensating For Tissue-Dependent Amino Acid Tracer Absorption Rate Differences; Nicholas Shulman; Gennifer Merrierh; Doo-Fu Dai; Evelyn S. Vincow; Leo Pallanck; Peter Rabinovitch; Michael J. Maccoss; University of Washington, Seattle, WA

ION STRUCTURE/ENERGETICS: 047 - 068

WP 047 Thermochemical Properties of Fluorinated Borohydrides; Jamelle Williams; Paul G. Wenthold; Purdue University, West Lafayette, IN

WP 048 Experimental Determination of the Gas-Phase Heat of Formation of 2,3 and 3,4-Pyridyne N-oxide; Nathan Ray; Paul Wenthold; Purdue University, West Lafayette, IN

WP 049 Nazarov Cyclization of 1,5-Bis-(2-methoxyphenyl)-1,4-pentadien-3-one in the Gas and Condensed Phases: An Experimental and Theoretical Study; George Mathai1; June Cyricac; Daryl Giblin1; Michael L. Gross1; 1Sacred Heart College, Kochi, India; 2Washington University, St Louis, MO

WP 050 Cyclization and Fragmentation of Protonated Natural Curcumin: An Experimental and Theoretical Study; Daryl Giblin1; June Cyricac; George Mathai1; Michael L. Gross1; 1Washington University, St Louis, MO; 2Sacred Heart College, Kochi, India

WP 051 Xenon Trapping: A Novel Method for Stabilizing Host-Guest Complexes of Decamethyllumcurbit[5]uril With Alkali Metals; Daniel Mortensen; David V. Dearden; Brigham Young University, Provo, UT

WP 052 Formation and Characterization of Cadmium Clusters Containing Sulfides and Bisulfides Using CID and Vibrational Spectroscopy; Kaitlin Papson1; Giel Berden2; Ios Oomens2; Douglas P. Ride1; 1University of Delaware, Newark, DE; 2FOM Institute for Plasma Physics Rijnhuizen, Nieuwegein, Netherlands

WP 053 EIMS of Alkylated Sulfobenzamides: Quantum Chemistry of an Unusual Rearrangement; Karl Irikiura; Nino Touda; Kirill Treytakov; Anзор Мика; Stephen Stein; National Institute of Standards and Technology, Gaithersburg, MD

WP 054 Dissociation Kinetics of Protein-fatty Acid Interactions in the Gas Phase; Lan Liu1; Klaus Michelsen1; Elena Kitova2; Paul Schnier1; Alex Brown1; John Klassen3, 4; Amgen, Thousand Oaks, CA; 2University of Alberta, Edmonton, Canada

WP 055 Comparison of the Dissociation Kinetics of the Streptavidin-Biotin Interaction in Solution and in the Gas Phase; Lu Deng; Elena Kitova; John Klassen; University of Alberta, Edmonton, Canada

WP 056 Investigating the Fe3O Active Site of C–H Bond Activating Enzymes in the Gas Phase; William A. Donald1; Christine J. Mckenzie2; Richard A. J. O’hair1; 1University of Oxford, Oxford, UK; 2University of Melbourne, Melbourne, Australia; 3The University of Southern Denmark, Odense, Denmark

WP 057 An Investigation of the Energetics and Conformations of Polymer/Substrate Complexes Studied with RRKM Modeling, Molecular Dynamics and Ion-Mobility Spectrometry; Justin Renaud; Paul Michael Mayer; University of Ottawa, Ottawa, Canada

WP 058 Energies of Small Polycyclic Aromatic Hydrocarbons; Interstellar Molecules; Brandi West; Paul Michael Mayer; University of Ottawa, Ottawa, Canada

WP 059 Superhalogen Anion KF+; Vertical Electron Detachment and Dissociation Energies; Seydina Lo; Alan Hopkinson; CRMs/YORK University, Toronto, Canada

WP 060 Exotic Molecules on Titan? Structural Characterization of Unsaturated C4H4N2 Species by Negative Ion FT-ICR MS and MS/MS for Laboratory Made Tholins; Arpad Somogyi1; Mark Smith1; Roland Thissen2; Veronique Vuitton2; 1University of Arizona, Tucson, AZ; 2UJF-Grenoble, CNRS-INSU, Institut de Planetologie, Grenoble, France

WP 061 Mass Spectrometry of 1,1-Diamino-2,2-dinitroethene (FOX-7); Miroslav Polasek1; Jan Zabka1; Zdenek Jalovy1; J. Heyrovsky Institute of Physical Chemistry, Praha 8, Czech Republic; 2University Pardubice, Pardubice, Czech Republic

WP 062 Study of Fragmentation Pathways of Persistent Free Radical Ions: Examples of SG1 and TEMPO; Cathie Marchal; Christophe Cherdo; Laurence Charles; Vincent Ledentu; Didier Sirl; Denis Bertin; Didier Gignes; University Aix-Marseille 1 & III, Marseille Cedex, France

WP 063 Formation of Diphosphine-Protected Gold Clusters: Cationic Cluster Formation from Digid Complexes as a Platform for Growth; John Pettibone1; Jeffrey W. Hudgens1; Thomas Selttle1; Denis Bergeron1; 1NIST, Rockville, MD; 2Notre Dame University, Notre Dame, IN

WP 064 Fragmentation Mechanisms of Peptide’s Cation-Radicals Formed in Collision with 59th ASMS Conference on Mass Spectrometry
Electrons of Well-Determined Energies; Yuri V Vasile'yev; Douglas F. Barofsky; Max L. Deinzer; Oregon State University, Corvallis, OR

WP 065 Intercluster Reactions Show that Sulfur Betaine is a Better Methyl Cation Donor than Nitrogen Betaine; Linda Feketeova; Ellie Jung-Hwa Yoo; George N. Khairallah; Richard A. J. O'Hair; The University of Melbourne, Melbourne, Australia

WP 066 Number of Fragment Spectrum in CID of Mass Selected Ions: A New Tool for Ion Characterisation in the MS-MS Frame; Khalid El Farkhi1; Guillaume Bruny2; Victor Buridon1; Stefan Feil1; Mahdi M. Harb1; Cécile Teysssier1; Hassan Abdou-Carime1; Bernadette Farizon1; Michel Farizon1; Tilmann D. Märkl2; 1CNRS/IN2P3, UMR5822, IPNL - Université Lyon 1, Villeurbanne, France; 2Leopold Franzens Universität, IFP, Innsbruck, Austria

WP 067 An Ion Structure Calculation Package; David M. Criner; Alessandra Ferzoco; Gary L. Gilsh; University of North Carolina, Chapel Hill, NC

WP 068 Influence of Salt Bridge Interactions in the Gas Phase peptide-DNA Complex Stability; Bessem Brahim; Sandra Alves; Jean-Claude Tabet; Université Paris VI, Paris, France

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WP 069 Deciphering the Cell Envelope Proteome of Escherichia coli; Malvina Papanastasiou1; Georgia Orfanoudaki1,2; Marios Frantzeskos-Saridis1,2; Panagiotis Mavroudis1,2; Spyridoula Karamanou1; Anastasios Economou1,2, 1Inst of Molecular Biology, Iraklio-Crete, Greece; 2Department of Biology, UoC, Iraklio-Crete, Greece

WP 070 High Mass Accuracy Provides Enhanced Selectivity for the GC/MS Analysis of Pesticides in Food; Thomas P. Doherty; Phil Wylie; Chris Sandy; Bill Russ; Agilent Technologies, Santa Clara, CA

WP 071 Evaluation of a Novel Ion Trap Based Higher Energy Collision Induced Dissociation for Structure Elucidation of Mid-Molecular Weight Compounds; Silvi Chacko1; Jonathan Josephs1; Julie Horner2; August Specht3; 'Bristol-Myers Squibb, Pennington, NJ; 'Thermo Fisher Scientific, San Jose, CA

WP 072 Simultaneous Analysis of Hydroxylated and Non Hydroxylated Polymethylphenyl Ether by LC-APPI-HRMS; Charlotte Marteau1; Sylvie Chevolleau1; Isabelle Jouanin1; Bruno Le Bizec2; Daniel Zalko3; Laurent Debrouwer1; Jean-Philippe Antignac3; UMR 1331 Toxalim INRA INP, Toulouse Cedex 3, France; 'ONIRIS USC 2013 INRA LABERCA, Nantes, France

WP 073 A Method for the Accurate Determination of Monoisotopic Precursors in High-Resolution Mass Spectra; ZuoFei Yuan1, 2; Chao Liu1, 2; Haipeng Wang1, 2; Ruixiang Sun1, 2; Yan Fu1, 2; Leiheng Wang3; Hao Chi1, 2; You Li1, 2; Liyun Xiu1, 2, 1University of Washington, Seattle, WA; 2University of Notre Dame, South Bend, IN; 3NASA Goddard Space Flight Center, Greenbelt, MD

WP 074 Qualitative Comparison of Wine Process Samples with UHPLC and Ultra High Resolution TOF-MS; John Chakel; Joe Binkley; Matthew Giardina; John R. Heim; Jeffrey Patrick; Kevin Siek; LECO Corporation, St Joseph, MI

WP 075 High Resolution Mass Spectrometry for Non-Targeted Analysis: Chromatographic Implications; Timothy R. Coley1; Kevin D. White2; John H. Callahan3; Steve Musser4; 1FDA, College Park, MD; 2US FDA/CFSAN, College Park, MD; 3FDA/CFSAN, College Park, MD; 4US FDA, College Park, MD

WP 076 Improving Proteomics Mass Accuracy by Optimized Offline Lock Mass; Ying Zhang; Zhihui Wen; Laurence Florens; Michael Washburn; Stowers Institute for Medical Research, Kansas City, MO

WP 077 Evaluation of Quantitative Performance for Testosterone Analysis in Plasma on a Novel Quadrupole Orbitrap Mass Spectrometer; Xiang He; Marta Kozak; ThermoFisher Scientific, San Jose, CA

WP 078 Improving Comprehensiveness, Sensitivity, and Retrospectiveness of Doping Controls using a Benchtop Quadrupole-Orbitrap MS for Plasma and Dried Blood Spot Analysis; Mario Theviš1; Andreas Thomas1; Catharina Crone2; Markus Kellmann3; Thomas Möhring4; Stevan Horning4; Wilhelm Schänzer4; 'German Sport University, Cologne, Germany; 'Thermo Fisher Scientific, Bremen, DE

WP 079 High-Throughput Caco-2/TC7 Human Intestinal Absorption Screening using Laser Diode Thermal Desorption-Aerosol Mass Spectrometry Chemical Ionization Coupled to Exact Benchtop Orbitrap; Bernard Julian1; Cyril Bertrand1; Olivier Fedeli1; Patricia Moliner1; Chloe Grosjean1; Marion Layssac1; Christel Marcou2; Patrice Tremblay1; Pierre Picard1; Marie-Pierre Pavageau1; Laurence Fajas1; Gerard Fabre1; Freddy Sadoun1; 'Sanofi-Aventis, Montpellier, France; 'Phytronix Technologies, Quebec, QC; 'Phytronix Technologies, Inc., Quebec, QC; 'ThermoFisher, Paris, France

WP 080 Modern Proteomics with CE-MS : Fast, High Resolution Peptide Separations by Capillary Electrophoresis with LTQ Orbitrap Velos and Bruker Quadrupole Time-of-Flight; Rozsa Woicik1; Michael Maccoss2; William Boggess2; Norman J. Dovich2; 'University of Washington, Seattle, WA; 'University of Notre Dame, Notre Dame, IN

WP 081 Application of Absorption-mode Data Analysis to Biological FT-ICR Mass Spectrometry; Feng Xiang1; Christopher L. Hendrickson1, 2; Gregory T. Blakney2; Steven C. Beu3; Alan G. Marshall1, 2; 'Department of Chemistry, Florida State University, Tallahassee, FL; 'ICR Program, National High Magnetic Field Laboratory, Tallahassee, FL; 'S C Beu Consulting, Austin, TX

WP 082 A Quadrupole Orbitrap Mass Spectrometer with Very High Sequencing Speed Applied to Shotgun Proteomics; Annette Michalski1; Nagarjuna Nagaraj1; Juergen Cox2; Eugen Damoc3; Oliver Lange3; Andreas Wieghaus3; Alexander Makarov3; Matthias Mann1; Stefan R. Horning1; 'Max Planck Institute of Biochemistry, Martinsried, Germany; 'Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany
WP 083 Animal Glues in Paintings: Identification of the Animal Species by Proteomics; Sophie Dallongeville1; Nicolas Garnier2; Caroline Tokarski1; Christian Rolando1; "Univ. de Lille 1, Sciences et Technologies, Villeneuve D'ascq, France; 2Laboratoire Nicolas Garnier, Vic le Comte, France

WP 084 Clinical Toxicology Screening using Accurate-Mass Identification and MS/MS Library Searching on the AB SCIEX TripleTOF™ 5600 LC/MS/MS System; Lisa Sapp1,2; Michael J. Y. Jarvis1,3; Adrian Taylor1,3; AB SCIEX, Framingham, MA; 2AB SCIEX, Concord, Canada

WP 085 Optimizing Chromatography for Maximizing Protein Identifications and Sample Throughput; Shixin Sun1,2; Eastwood Leung3; 1Baylor College Of Medicine, Houston, TX; 2ABS CIEX, Framingham, MA

WP 086 Highly Selective and Specific High Resolution Optimizing Chromatography for Maximizing Isolation Windows Allowing Unlimited SRM-Pipeline for Biomaker Discovery and the Animal Species by Proteomics; Eduard Denisov3; John C. Tran1; Andreas Sleighter3; Joshua Marsh1; Vanessa Bosch3; Amanda Grannas2; Patrick Hatcher1; Amanda Grannas2; Patrick Hatcher1; 1Old Dominion University, Norfolk, VA; 2Villanova University, Villanova, PA

WP 087 Molecular Characterization of Dissolved Organic Matter from Greenland Ice Cores by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry (FTICR-MS); Rachel Swederski; Sonja Hess; Caltech, Pasadena, CA

WP 088 High Resolution TOF MS Quantification of Large Array Pooling for High Throughput LCMS; Elliott Jones; Shaokun Pang; Richard Laumen; Loren Olson; AB Sciex, Foster City, CA

WP 089 A Comparative Top-Down Proteomics Pipeline for Biomarker Discovery and Validation; Steven Patrie; Michael Roth; Jaekuk Kim; Daniel Smith; UT Southwestern Medical Center, Dallas, TX

WP 090 Top-Down Proteomics on Orbitrap-Based Mass Spectrometers; Philip Compton1; Eugen Damoc;1 Eduard Denisov2; John C. Tran3; Andreas Wieghaus3; Michael W. Senko4; Stevan R. Hornig5; Alexander Makarov6; Neil L. Kelleher7; 1Northwestern University, Chicago, IL; 2Thermo Fisher Scientific, San Jose, CA; 3Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany

WP 091 Swath MS: A Novel Data Independent Acquisition Method with Sequential Precursor Isolation Windows Allowing Unlimited SRM-like Data Analysis and Quantification; Ludovic Gillet1; Pedro Navarro2; Stephen Tate3; Hannes Röst4; Ron Bonner5; Ruedi Aebersold6; 1IMS B - ETH, Zurich, Switzerland; 2AB SCIEX, Concord, ON

WP 092 Highly Selective and Specific High Resolution Accurate Mass Quantification for Drug Discovery to Clinical; Suma Ramapir1; Jeffrey Miller1; Hesham Ghabarah1; Mauro Aiello1; Johnny Cardenas1; Graham Gibson1; Yuan-Qing Xia1; Ragu Ramathan1; William Griffith Humphreys2; Timothy Ohl3; AB SCIEX, Concord, CANADA; 4AB SCIEX, Medford, NJ; 5Bristol-Myers Squibb, Princeton, NJ; 6Bristol-Myers Squibb Company, Lawrenceville, NJ

WP 093 Analysis of Parabens in Hand Lotion; David Negrotti; PerkinElmer, Shelton, CT

WP 094 Application of LC-Direct-EI-MS in in vitro Dermal Absorption Study: Quantitative Determination of trans-Cinnamaldehyde; Achille Cappiello1; Giorgio Famiglietti1; Pierangela Palma1; Veronica Termopoli1; Helga Trufelli1; Raniero Zazzeroni1; Sandrine Jacquilliet2; Lucia Radi1; Ouadar Salb1; LC-MS Laboratory, Disteva, University of Urbino, Urbino, Italy; 3Safety & Environmental Assurance Centre, Unilever, Bedford, UK

WP 095 UPLC-MS/MS Analysis of Bimatoprost and Its Free Acid Metabolite from Minipig Skin; Lisa Ford1; Kevin Wilkinson2; Mike Allen2; Lisa Borbridge2; 1Tandem Labs, Durham, NC; 2Enthalpy Analytical, Durham, NC, 3Allergan, Irvine, CA

WP 096 Solvent-free Sample Preparation for LC-MS/MS Confirmatory Analysis of Veterinary Drugs in Equine Urine Matrix; Tania Pessalli; Alejandro Rodriguez; Universidad de la Republica, Pando, Uruguay

WP 097 LC-MS/MS Method for Determination of Total Active Gentamicin in Brown Norway Rat Lung Tissue; Xiaodong Zhu1; Helmin Tara2; Andreas Sleighter3; Gregory Poch; Mike Sullivan; Orlando Espinoza; Ravi Orugunt; Edward Wells; Steve Unger; Worldwide Clinical Trials, Austin, TX

WP 098 Simultaneous Quantification of 8 Bioactive Polyphenolic Compounds in EDTA Rat Plasma by a High Throughput LC-MS/MS Method; David Gingrich1; Hong Zhou1; Xiaochuan Li1; Kim B. Plath4; Uwe Christians4,5; Isaac Cohen2; Yan Ling Zhang1,3; 1Bionovo, Aurora, CO; 2Bionovo, Inc, Emeryville, CA; 3University of Colorado HSC, Denver, CO

WP 099 PEG Precipitation of Abundant Proteins in Extracting PEGylated Recombinant Human Erythropoietin from Equine Plasma; F. Guan1; Cornelius Uboh2; Lawrence Soma2; George Maylin2; Zbin Jiang2; Jinwen Chen2; 1University of Pennsylvania, Kennett Square, PA; 2PA Equine Toxicology and Research Center, West Chester, PA; 3Cornell University, Ithaca, NY

WP 100 Application of Supported Liquid Extraction for Response Normalization of Hemolyzed Bioanalytical Samples in LC-MS/MS Analysis; Jim Shen1; Xiaorong Wei2; Jennifer Cuniffe; Merck Research Laboratories, Summit, NJ

WP 101 Development and Validation of a High Throughput Method for the Determination of Atorvastatin and its Hydroxy-metabolites in Human Plasma; David J Browne; Mohammed Abrar; Pratap Davuluri; Jeremy Cook; Unilabs YBS, York, UK

WP 102 Biological Sample Cleanup using Phospholipids Removal Tips on the Hamilton Microlab STAR; Jie Zhang1; David Ayres1; Xiaoning Lu2; Harold T Smith1; Francis LS Tse1; 1Novartis Institutes for BioMedical Research, East Hanover, NJ; 2Supelco Division of Sigma-Aldrich Corp., Bellefonte, PA

WP 103 Using a Unique Approach to Sample Preparation to Increase the Selectivity of an LC/MS/MS Assay for Ethinylestradiol; Jessalynn Wheaton; Erin Chambers; Diane Diehl; Waters Corporation, Milford, MA

WP 104 Multi-function Impurity Adsorption SPE (MAS), a Novel Sample Preparation Device
for Improved Phospholipid Removal in Bioanalysis Assays for Zwitterionic Analytes; Qihui Ni; Wan Wang; Jerry Wang; Bonna-Agela Technologies, Inc., Wilmington, DE

WP 105 Errors in Bioanalysis Due to Phospholipids - Definitive Measurement, Mechanism, and Management; Russell Grant; Brian Rappold; Matthew Crawford; Patricia Holland; Labcorp, Burlington, NC

WP 106 Magnetic NTA-Based Affinity Mass Spectrometry for Rapid Detection of Indigenous Porphyrins; Fu-Lien Huang; National Taiwan University, Taipei, Taiwan

WP 107 Utilization of Fine Isotope Structures to Facilitate Unknown Identification Based on High Mass Accuracy and High Spectral Accuracy; Ming Gu1, 2; Yongdong Wang1, 2; Hongliang (Leo) Xu1, 2; 1Cerno Bioscience, Yardley, PA; 2Cerno Bioscience, Danbury, CT

WP 108 Comprehensive Study of the Steroidal Saponins from Fenugreek Seeds Using Non-targeted Sample Profiling Strategy by UPLC/orTOF MS2; Liping Kang1; Pang Xu1; Kate Yu2; Heshui Yu1; Yang Zhao1; Chenqi Xiong1; Dawi Tan1; Yue Gao1; Feng Wang1; Alan Millar2; Baiping Ma1; 1Beijing Institute of Radiation Medicine, Beijing, China; 2Waters Corporation, Milford, MA; 3Waters China Ltd, Shanghai, China

WP 109 The Addition of ‘Prototype Biotransformations’ to a Knowledge-based Software Program to Speed up the Elucidation of Uncommon Metabolites; Sian Ives; Ernest Murray; M. Ash Ali; Catherine O’Leary-Steele; Lhasa Limited, Leeds, UK

WP 110 “Meta Effect” in Fragmentation of Gaseous Ions Derived from Substituted Benzene Derivatives; Athula B. Altygalle; Upul Nishshanka; Carl S. Weisbecker; Stevens Institute of Technology, Hoboken, NJ

WP 111 Mass Spectral Characterization of Antioxidant Additives in Copolymers and Lubricants; David Aaserud1; Christina Jasieczek Mastromatteo2; Michael J. Polce3; 1Lubrizol Advanced Materials, Brecksville, OH; 2The Lubrizol Corporation, Wickliffe, OH

WP 112 Identification of Fatty Acids as Microsomal Degradation By-Products in the Presence and Absence of Bovine Serum Albumin by using CAD/ESI/MS/MS; Jennifer Bushee; Gujing Liang; Upendra Argikar; Shawn Harriman; Novartis Institute of Biomedical Research, Cambridge, MA

WP 113 LC-ESI/MS/MS Study of Sulfate-Conjugated Steroid Estrogens: Focusing on Identification and Simultaneous Analysis of Isomers; Seriou P. Palij; Margaret O. James; Sriram Ambadapadi; University of Florida, Gainesville, FL

WP 114 Confirmation of the Identity of a Previously Unknown Alkaloid of Commercial Significance by EI and Other Mass Spectral Techniques; Q. David Sparkman1; Patrick R. Jones2; Matthew Curtis2; Manali Aggrawal1; Liang Xue1; Christine Vandervoort2; 1University of the Pacific, Stockton, CA; 2Michigan State University, East Lansing, MI

WP 115 Showing the Mechanism of Forming Unexpected Fragment Ions by Secondary and Tertiary Aliphatic Alcohols that Were Subjected to Electron Ionization; Patrick Balloon; Patrick R. Jones; Matthew Curtis; O. David Sparkman; University of the Pacific, Stockton, CA

WP 116 Targeted and Non-targeted Approaches Using High-Resolution Accurate-Mass LC-MS-TOF to Characterize Pharmaceutical Stability in Various Excipients; Stephen Sembelow1; Keith Goodman1; Johnie Brown2; Jeff Miller2; 1Credo Inc, New Castle, DE; 2AB SCIEX, Framingham, MA

WP 117 Detection of the Kappa Opioid Receptor (KOR) Antagonists in Mouse Brain Weeks after Administration using LC-MS/MS; Kshitij A. Patkar; Michelle. Ganne-Sherwood; Nicollete Ross; Jay McLaughlin; Harinder Sigh; Torrey Pines Institute for Molecular Studies, Port St. Lucie, FL

WP 118 An Evaluation of Strategies for Small-Molecule Analysis by MALDI Mass Spectrometry: What Are the Limits?; Christopher C. Lai1; Qian Sun1; Lawrence R. Phillips2; James A. Kelley1; 1Chemical Biology Laboratory, CCR, NCI, NIH, Frederick, MD; 2Biological Testing Branch, DTP, NCI, NIH, Frederick, MD

WP 119 Utilization of Tandem Mass Spectrometry, High Resolution Mass Spectrometry, and Synthetic Design for Identification of Unusual Degradant in Hydromorphone Formulation; Sam Molesworth; Daniel Stegner; Christopher McGinley; Todd Schwier; Esther Hwang; Hospira, Wchita, KS

WP 120 Infusion Based Selective Detection of Metabolites using Chemical Effect and Differential Ion Mobility (DMS); Mauro Aiello1; J.C. Yves Leblanc1; Doina Caraiman2; Brad Schneider1; J. Larry Campbell1; 1AB SCIEX, Concord, ON; 2AB SCIEX, Concord, ON


WP 122 Capillary Electrophoresis Coupled to Time-of-Flight Mass Spectrometry for Fingerprint Study of Bio-Active Alkaloids from Traditional Chinese Medicines; Zheng-Xiang Zhang; Tao Bo; Jianqiu Mi; Agilent Technologies (China), Beijing, China

WP 123 Discovery and Lead Structure Optimization of a Non-Secosteroid Binding Partner for the Vitamin D Receptor; Jerry White1; Mark Cushman2; Richard B. van Bremen3; 1University of Illinois, Chicago, IL; 2Purdue University, West Lafayette, IN

WP 124 The Comparison of SCFA Levels in Hamsters Infected with Clostridium Difficile using Atmospheric Pressure Gas Chromatography (APGC) Mass Spectrometry; Gillian Douce1; Janice Spencer1; Anthony Buckley1; Leonard Dillon2; David Douce2; 1Glasgow University, Glasgow, UK; 2Waters (MS Technologies), Manchester, UK

WP 125 Calibration Method for Creating Inter-instrumental and Inter-laboratory Spectral Databank; Farid Ichou1; Denis Lesage1; Xavier Machuron-Mandard2; Christophe Junot1; Jean-
WP 126 Determination of Free and Total Doxorubicin and Doxorubicinol in Human Plasma by HPLC-MS/MS; Xi Chen; Jiongwei Pan; Bibo Xu; Primera Analytical Solutions Corp., Princeton, NJ

WP 127 A Simple and Reliable Method for Simultaneous Quantification of Antiepileptic Drugs in Plasma using LC-MS/MS Combined with Direct Injection Column; Kwang Youl Kim; Cheol Woo Kim; Ju Hee Kang; Moon Suk Nam; Inha University Hospital Clinical Trial Center, Incheon, South Korea

WP 128 Development of an LC-MS/MS Based Biochemical Assay to Evaluate Isopenrylcysteine Carbonyl Methyltransferase (ICMT) as a Cancer Target; Patrick Bingham; Pfizer, San Diego, CA

WP 129 Ultrasensitive Method for Urinary Lignans Analysis in a Unsupplemented Population; Kimberly Clark1; Joshua Prey2; Gerald Fetterly2; Lilian Thompson1; Chi-Chen Hong1; Swati Kulkarni1; Susan McCann1; Roswell Park Cancer Institute, Buffalo, NY; University of Toronto, Toronto, Canada

WP 130 Ultrasensitive Quantitation of the EGFR Inhibitor, Erlotinib and its Active Metabolite OSI-420 Using LC/MS/MS; Kimberly Clark; Gerald Fetterly; Roswell Park Cancer Institute, Buffalo, NY

WP 131 LC/MS/MS Method for the Quantitative Determination of Kevetrin in Dog Plasma; Joseph Pav1; Sylvia Holden2; Krishan Menon2; Toxikon, Bedford, MA; Cellexutix Pharmaceuticals, Beverly, MA

WP 132 Qualitative Analysis of Formoterol in Human Plasma by Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometry; Chang Hun Park; Severance Hospitai, Seoul, South Korea

WP 133 A New Method of Assay of Ketosteroids in Plasma Based on UHPLC-MSMS and Microwaerolysis-Derivatization; Leonardo Di Donna; Benadelkamel Hicham; Fable Mazzotti; Anna Napoli; Donatella Aiello; Giovanni Sindona; Università della Calabria, Dipartimento di Chimica, Arcavacata Di Rende, Italy

WP 134 Endogenous Compound Analysis: Measurement of Cytidine Level in Rodont; Angela Shen; Agilux Laboratories, Worcester, MA

WP 135 A Rapid LC-MS/MS Alternative to the Isotope Dilution GC-MS/MS Reference Measurement Procedure for Determining Glucose in Human Plasma; Brian Beato1; Michael Pugh1; David Hulbert1; AIT Bioscience, Indianapolis, IN; Roche Diagnostics, Indianapolis, IN

WP 136 Evaluation of Matrix Effects from Urine for Estrogen Metabolites using HILIC Coupled with ESI-MS; Heather Tippen; Hien Nguyen; Kevin Schug; University of Texas at Arlington, Arlington, TX

WP 137 Dry Blood Spot Sampling Technology Evaluated for LDTD-MS/MS Analysis; Patrice Tremblay; Serge Auger; Pierre Picard; Phytronix Technologies, Quebec, Canada

WP 138 A New Data Review Software Application and Multiple LC Columns Increase Throughput with High Resolution Accurate Mass Spectrometry; Keeley Murphy; Paul Palma; Nick Duczak; Jim Kapron; Thermo Fisher, San Jose, CA

WP 139 Two Dimensional PFE/PEX Extraction Coupled With Three Dimensional HPLC/UP/LC/MS/MS For Assay 500 fg/mL LLOQ Assay; Troy Voelker1; Lin Tan1; Andrew Acheampong1; John Lings2; Gabriella Szekely-Klepers2; Min Meng1; Tandem Labs, Salt Lake City, UT; Allergan Pharmaceuticals, Irvine, CA

WP 140 Method Development and Validation of 6-Sulfatoxymelatonin (aMT6s) Quantitation in Human Urine; Rachel Sun; Jordan Nally; BASI, West Lafayette, IN

WP 141 Overcoming Glass Vial Adsorption Effects for Trace Analysis of Basic Compounds by LC/MS/MS; Jeremy Shia; Jane Xu; Brian Murphy; Erin E. Chambers; Waters Corpora, Milford, MA

WP 142 Fundamental Characteristics of Small Molecule Analysis using Ultra Low Dynamic Flow; Ben Ngo1; Shaokia Yu2; Mike S. Lee2; Jingtao Wu1; Gary Valaskovic1; New Objective, Inc., Woburn, MA; Millennium Pharmaceuticals, Inc., Cambridge, MA; Milestone Development Services, Newtown, PA

WP 143 Application of DBS to the Pharmacokinetic Evaluation of Compounds with Various Blood to Plasma Ratios Using LC-MS/MS; Phadnis; Earl Moore; Roger pham; Tom Huang; Mary Wells; Christopher James; Timothy Carlson; Gulffen Xu Amgen, South San Francisco, CA

WP 144 LDTD-MS/MS in GLP Environment: What Should be Done?; Jean Lacoursière; Patrice Tremblay; Serge Auger; Pierre Picard; Phytronix Technologies, Quebec, Canada

WP 145 Determination of Chlorpyrifos and Its Metabolites in Cell Media using Liquid Chromatography/Electrospray Ionization Tandem Mass Spectrometry; Alvin Terry; Michael G. Bartlett1; University of Georgia, Athens, GA; Medical College of Georgia, Augusta, GA

WP 146 A Robust and Selective Method for Two Omega-3 Fatty Acids (Eicosapentaenoic Acid and Docosahexaenoic Acid) in Several Matrix Species; Guy Havard1; Nathalie Pelletier1; Sylvain Lachance1; Nadine Boudreau1; Aurélie Levesque1; PharmaNet Canada, Québec, Canada; Acasti Pharma Inc., Laval, Canada

WP 147 Quantitative Analysis of Phytosterols in Cocoa and Vegetable Oils Using Liquid Chromatography-tandem Mass Spectrometry; W. Jeffrey Hurst1; Richard B. Van Breemen1; University of Illinois College of Pharmacy, Chicago, IL; Hershey Company, Hershey, PA


WP 149 Quantification of Dihydropyridine Calcium Channel Blocker A by High-performance Liquid Chromatography Coupled to Mass Spectrometry; Yanan Yang2; Richard B. van Breemen1; Erinn E. Chambers; Keeley Murphy; Paul Palma; Rick Duczak; Richard Kapron; Alltech, Lexington, KY; 3Milestone Development Services, La Jolla, CA
WP 150  Low pg/ml Detection of Underutilized 17β-Estradiol in Serum through Increased Ion Sampling Efficiency using LC/MS/MS; Anabel Fandino; Agilent Technologies, Santa Clara, CA

WP 151  High Precision LC-MS/MS Using Nanoelectrospray Ionization Combined with Full-Scan Accurate Mass Spectrometry; Gary A. Schultz; Jack D. Henion; Steve Lowes; Advin Biosciences, Inc., Ithaca, NY; Advin Biosciences, Inc., Ithaca, NY

WP 152  Quantitative Analysis of Bisphenol A in Rat Serum by LC-MS-MS; Yang Yuan; Xi Qiu; Yinan Yang; Richard B. van Breenen; University of Illinois College of Pharmacy, Chicago, IL; Agilent Technologies, Inc, Santa Clara, CA

WP 153  Ionization Suppression and Charge State Shifting from Biological Matrices during Electrospray Ionization; Richard Wong; Baomin Xin; Timothy Olah; Bristol-Myers Squibb, Pennington, NJ; Bristol-Myers Squibb Company, Lawrenceville, NJ

WP 154  Determination of Urinary Creatine and Guanidinoacetate by Hydrophilic Interaction Liquid Chromatography and Tandem Mass Spectrometry; Marlene F. Madeira; Karina Helena M. Cardozo; Fernando Kok; Valdemir M. Carvalho; Fleury Group, São Paulo, Brazil; School of Medicine, University of São Paulo, São Paulo, Brazil

WP 155  Immobilized Liquids for Simple and Rapid Preparation of Clinical Samples for Quantification by LC-MS/MS; Michal Svoboda; Robert Wohleb; Michael Vogser; Roland Geyer; TECAN AG, Maennedorf, Switzerland; ILE Inc., Ferndale, CA; University Hospital Munich, Munich, Germany

WP 156  Comparison between a High Resolution Reactive and a Triple Quadrupole MS for Quantitative Analyses of Drugs and Clinical Biomarkers; Bertrand Rochat; Hamid Reza Sobhi; Olaf Scheibner; Maciej Bromirski; Hugues Henry; CHUV-UNIL, Lausanne, Switzerland; Thermo Fisher Scientific, Bremen, Germany

WP 157  Development of a Semi-quantitative, High-throughput Method for Simultaneous Detection of Commonly Prescribed Cardiovascular Drugs in Hospitalized Patients; Eduardo Dias; Usha Menon; Dan Roden; Nancy Brown; Richard M. Caprioli; Vanderbilt Univ Sch of Med, Nashville, TN

WP 158  Quantification of Topiramate by Liquid Chromatography and Tandem Mass Spectrometry; Karina Helena M. Cardozo; Valdemir M Carvalho; Fleury Group, São Paulo, Brazil

WP 159  Revealing the Influence of Possible Endogenous and Exogenous Interferences on HPLC-MS/MS Based Quantification of THC and THCOOH in Oral Fluid; Caroline Bylda; Andreas Leinenbach; Roland Thiele; Roche Diagnostics GmbH, Penzberg, Germany

WP 160  High-Throughput Analysis of Tacrolimus in Whole Blood Using Ultra-fast SPE-MS/MS; Kari E. Schlicht; Eric W. Korman; Vaughn P. Miller; Christine L. Snozek; Frank W. Crow; Loralie J. Langman; William A. Lamarr; BIOCIS Life Sciences Inc., Wakefield, MA; Mayo Clinic, Rochester, MN

WP 161  High-Throughput Analysis of Levetiracetam in Serum Using Ultra-fast SPE-MS/MS; Michelle Romm; Eric Korman; Vaughn Miller; Christine Snozek; Frank W. Crow; Loralie Langman; William A. Lamarr; BIOCIS Life Sciences, Inc., Wakefield, MA; Mayo Clinic, Rochester, MN

WP 162  Ultra-fast Analysis of Benzodiazepenes in Human Urine using Dilute and Shoot Methodology and SPE-MS/MS; Laurent Frick; Michelle Romm; Vaughn Miller; William A. Lamarr; BIOCIS Life Sciences, Inc., Wakefield, MA

WP 163  Simultaneous Quantitation of Insulin-like Growth factor-I and II in Human Serum Using Liquid Chromatography High Resolution Mass Spectrometry; Shijun Sheng; Cory Bystrom; Richard Reitz; Nigel Clarke; Quest Diagnostics, San Juan Capistrano, CA

WP 164  Multiplexed SRM (selected-reaction-monitoring) of formalin-fixed-paraffin-embedded (FFPE) Samples from Clinical Trial Patient Biopsies; Sheeno Thyyrambil; Wei-Li Liao; David Krizman; Marlene D. Darfler; Bharat Jasani; Richard Adams; Todd Hembrough; Jon Burrows; Expression Pathology Inc., Rockville, MD; Cardiff University, Cardiff, UK

WP 165  Identification and Characterization of Hemoglobinopathies Using Automated Mass Spectrometry Methods in Clinical Applications; Frank W. Crow; Patricia Wendt; Swanson Kenneth; Ryan Morse; Jennifer Oliveira; James Hoyer; Jose Meza; Mayo Clinic, Rochester, MN; Agilent Technologies, Santa Clara, CA

WP 166  Quantification of IgG Immunoglobulin Subclasses by LC-MS/MS; David Barnidge; Robin Karras; David Murray; Mayo Clinic / DLMP, Rochester, MN

WP 167  Direct MALDI-TOF Mass Analysis of Histopathological Sections with Imaging Mass Spectrometry Convolution Software; Tsukyo Yag; Masanori Yamada; Kurando Hosaka; Takahiro Hayasaka; Masaru Ushijima; Masaaki Matsuura; Mitsutoshi Setou; Seiji Ito; Kansai Medical University, Osaka, Japan; Hamamatsu University School of Medicine, Shizuoka, Japan; Genome Center of JFCR, Tokyo, Japan

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| WP 197 | Development of a MALDI MSI Based Methodology for the Identification of Sexual Assault Suspects; Robert Bradshaw 2; Rosalind Wolstenholme 1; Leesa Ferguson 1; Malcolm Clench 1; Robert Blackledge 1; Simona Francesc 1; Sheffield Hallam University, Sheffield, UK; formerly of Sheffield Hallam University, Sheffield, UK; formerly of the U.S. NCISRF Laboratory, San Diego, CA

| WP 198 | Analysis of Bile Acids in Bear Bile Products by Liquid Chromatography-Ion Trap Mass Spectrometry; Su-Hui Huang; Investigation Bureau, Ministry of Justice, New Taipei City, Taiwan

| WP 199 | Characterization of Vehicle Paints Containing Polystyrene using pyrolysis-GC/MS for Forensic Applications; Sheng-Hsiung Yang; Jermiah Y. Shen; Matt S. Chang; Gaston J. Wu; Chemistry Dept., National Taiwan Normal University, Taipei, Taiwan

| WP 200 | International Effort to Monitor Toy Safety Using Inexpensive Dual Use Military/Civilian Wear Sensors Incorporating DART Mass Spectral Dyes; Ronny Robbins 1; James McCarty M.D. 1; 1US Army, Gunpowder, MD; 2Springs of Grace Church, Mogó, Mexico

| WP 201 | Guidelines for Minimal Destructive Forensic Examination of Inkjet Printer Documents with (MA)LDI Mass Spectrometry and Raman Spectroscopy; Laetitia Heud 1; Delphine Debois 1; Laurent Kohler 1; Franck Partouche 1; Bernard Gilbert 1; Edwin De Paauw 1; 1University of Liege, Liege, Belgium; 2National Institute Criminalistics and Criminology, Brussels, Belgium; 3Criminal Investigation Dpt of National Gendarmerie, Rosny Sous Bois, France

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| WP 203 | Rapid Dating of Silk Fabric by CE-MS Analysis of D/L Amino Acids; Kathryn Klauenberg; Mehdi Moin; Smithsonian Institution, Suitland, MD

| WP 204 | Real Time Thermal Desorption of Airborne Solid Phase Explosive Particulate; William Stott; Edison Cerda; MSdetection, Bolton, ON, Canada

| WP 205 | Analysis of Ammonium Nitrate/Urea Nitrate with Crown Ether and Sugar as Modifiers; Chia-Wei Tsai 1; Anthony Midey 2; Ching Wu 2; Richard A. Yost 1; 1University of Florida, Gainesville, FL; 2Excellims Corporation, Acton, MA

| WP 206 | Characterization of Cannabinomimetic Compounds in Synthetic Cannabis Products by Gas Chromatography-High Resolution Time of Flight Mass Spectrometry (GC-HRT); Joe Binkley; Kevin Siek; Cory Fx; Viatcheslav Artuev; LECO Corporation, St. Joseph, MI

| WP 207 | Confirmation of Drugs of Abuse in Pseudo Drug Mixes using UHPLC-ESI TOF MS; Joshua Wilhide 1; William R. LaCourse 1; Hayley Crowe 1; 1Univeristy of Maryland Baltimore County, Baltimore, MD; 2Perkin Elmer, Waltham, MA

| WP 208 | Development of a Fast Product & Neutral Loss Scanning Method to detect Designer Drugs that Pass Conventional Screening; Jeffrey H. Dahl; Robert Closson; Shimadzu Scientific Instruments, Columbia, MD

| WP 209 | Fast and Sensitive Target Compound Quantification and Confirmation with a New Triple Quad Acquisition Function; Michael Flanagan; Tim Schlabach; Doug McIntyre; Anabel Pandino; Agilent Technologies, Santa Clara, CA

| WP 210 | Detection of Flunitrazepam in Alcoholic Beverages via DESI-MS; Paul D’aliose; Ohio University, Athens, OH

| WP 211 | Determination of the Elemental Composition for Forensic Related Compounds using Low Resolution (GC/MS) and High Resolution Mass Spectrometer (LTQ-Orbitrap); Esphar Jagerde; Jason E. Schaff; Marc A. LeBeau; FBI Laboratory Chem Unit, Quantico, VA

| WP 212 | Sulfur Counting and Spectral Accuracy Capabilities of the LTQ-FT and the LTQ-Orbitrap for Small Molecule Analysis; Samantha Blake; Hunter Walker; David C. Muddiman; David Hinks; Keith Beck; North Carolina State University, Raleigh, NC

| WP 213 | Forensic Isotope Ratio Analysis of Human Hair; Yan An; Glen Jackson; Ohio University, Athens, OH

| WP 214 | Differential Mobility Spectrometry as a Tool to Improve Mass Spectral Library Searching Scores by Removal of Isobaric Interferences; David J. Laytaro; Adrian Taylor; Michael J. Y. Jarvis; Doina Caraiman; Brad Schneider; J.C. Yves Leblanc; AB SCIEX, Concord, Canada

| WP 215 | Nutraceutical Evaluation of Diverse Green Tea Cultivars on the Basis of Metabolic Profiling; Yoshinori Fujimura 1; Kana Kurihara 2; Megumi Ida 2; Reia Kosaka 2; Daisuke Miura 1; Hiroyuki Wariishi 1, 2; Mari Maeda-Yamamoto 3; Atsushi Nesumi 2; Takeshi Saito 2; Tomomasa Kanda 3; Koji Yamada 2; Hirofumi Tachibana 1, 2; 1ICMRN, Kyushu University, Fukuoka, Japan; 2Faculty of Agriculture, Kyushu University, Fukuoka, Japan; 3Bio-Architecture Center, Kyushu University, Fukuoka, Japan; 4NIVTS, NARO, Japan
WP 216 Detection of Metabolic-based Serum Biomarkers for Human Esophageal Cancer using LC-MS; Jian Zhang1; Lingyan Liu1; Siwei Wei1; G.A.Nagana Gowda2; Jeremiah Bowers3; Zane Hammoud1; Daniel Raftery1; *Purdue University, West Lafayette, IN; **Henry Ford Hospital, Detroit, MI

WP 217 Metabolomics Study of the Systemic Signal Transduction in Tomato Wound Response; Ying-Lan Chen1; 2; Yet-Ran Chen1; *ABRC, Academia Sinica, Taipei, Taiwan; **Institute of Plant Biology, NTU, Taipei, Taiwan

WP 218 Liquid Chromatography Mass Spectrometry (LC-MS) Based Metabolomics Reveals Novel Metabolic Pathways Regulated by P3K Kinases; Vinotihni Sivarajah1; Pedro Cutillas2; Barts Cancer Institute, London, UK

WP 219 Metabolomics of Phalaenopsis by LC-DAD-MS; Jen Tse Liang1; Chien-Chung Cheng2; Shan-Te Hsu1; Kuo-Lung Ku1; National Chiayi University, Chiayi City, Taiwan

WP 220 GC-MS-based Comparative Metabolomics Analysis of Pathogenic Salmonella enterica serovar Typhimurium Grown under Host Environment Conditions; Young-Mo Kim1; Heather M. Brewer1; Afshan Kidwai2; Qibin Zhang1; Karl K. Wetzl2; Charles Ansong2; Richard D. Smith2; Fred Heffron3; Joshua N. Adkins3; Thomas O. Metz1; Pacific Northwest National Laboratory, Richland, WA; 2Oregon Health & Science University, Portland, OR

WP 221 High Resolution Profiling of Ginseng Extracts using Triple-Quadrupole-Time-of-Flight Mass Spectrometry Technology; Xu Guo1; Eva Duchoslav1; Edmund Lui2; Hua Pei3; Takeo Sakuma4; Yun Yun Zou1; Byung-Hee Shin2; Sung Hoon Yeo3; Daeseung Lee3; Youngchang Kim4; Robert Ellis5; 1AB SCIEX, Concord, Canada; 2OGIRC, University of Western Ontario, London, Canada; 3AB SCIEX (KOREA), Seoul, Korea; 4Ginseng Research Division, NIHHS, RDA, Seoul, Korea

WP 222 Wine Country of Origin Classification – Application of a Metabolomics Workflow; Friedrich Mandel1; Thomas Glauer2; Jerry Zweigenbaum3; Ondrej Lacina3; Lukas Vaclavik3; Jana Hajslova3; *Agilent Technologies GmbH, Waldbronn, Germany; **Agilent Technologies, Inc., Wilmington, DE; 3Institute of Chemical Technology, Prague, Czech Republic

WP 223 Mass Spectrometry-based Metabolomics for Phenotypic Differentiation between Four Citrus Fruits; Jun Han1; 2; Darryl Hardie1; 2; Christoph H. Borchers1; 3; *University of Victoria-Genome BC Proteomics Centre, Victoria, BC, Canada; **Department of Biochemistry & Microbiology, University of Victoria, Victoria, BC, Canada

WP 224 Evaluation of the Impact of Food and Time-of-Day on Plasma Metabolites in a mouse Model using Liquid Chromatography-Mass Spectrometry (LC-MS); Joo Ern Ang1; Alan Henley1; Victoria Revelle1; Debra Skene1; Florence Raynaud1; *Institute of Cancer Research, Sutton, UK; **University of Surrey, Guildford, UK

WP 225 Metabolomic Profiling of Coffees using UHPLC-QTOF LC/MS and Multivariate Analysis Tool; Akio Hayashi1; Hirokazu Sawada1; Agilent Technologies, Hachioji, Japan

WP 226 A Workflow for Determination of the Elemental Compositions and Metabolic Profiling with FT-ICR MS; Kazunori Saito1; Tatsuhiko Nagao1; Daisuke Miura2; Noriyuki Iwasaki1; Takashi Nirasawa1; Hiroyuki Warishii1; 1Bruker Daltonics K.K., Yokohama, Japan; 2Kyushu University, Fukuoka, Japan

WP 227 Characterization of Asthma Phenotypes in Children by Metabolomics Approach with LC-MS on Exhaled Breath Condensate; Giuseppe Giordano1; Silvia Cerraro1; Matteo Stocchero1; Fabiano Reniero1; Iole Maria Di Gangi1; Antonina Gucciardi1; Paola Pirillo1; Eugenio Baraldi1; 1Pediatrics Department Padova University, Padova, Italy; 2European Commission, JRC, Institute IHCP, ST Unit, Ispra, Italy; 3IN Informatic Solutions, Vicenza, Italy

WP 228 Non-targeted Metabolomics using Nanospray Mass Spectrometry as a Tool to Understand the Growth of Axillary Buds in Tomato Plants; Chloe Steels1; Steve Coates2; Andrew Fleming3; Mike Burrell1; The University of Sheffield, Sheffield, UK; 2Advanced Technologies (Cambridge) Limited, Cambridge, UK

WP 229 Integrated LC/MS Metabolic Investigation of Changes in the Rat Serum Metabolite Profile Induced by Acetaminophen; Jinchun Sun1; Yosuke Ando1; 2; Xi Yang1; James Greenhaw1; Laura Schnackenberg1; Lisa Pence1; 1; 2OGIRC, University of Western Ontario, London, ON

WP 230 Protein and Metabolite Profiling of Arabidopsis Glutathione S-Transferase Knockout Mutants using LC/MS and Collision Induced Dissociation; Jiaoying Bao1; 2; A. Daniel Jones; Michigan State University, East Lansing, MI

WP 231 High-throughput Metabolic Profiling and in situ Metabolite Imaging by MALDI Mass Spectrometry; Daisuke Miura1; Daichi Yukihira; Yoshinori Fujimura1; Hiroyuki Wariishi1; Kyushu University, Fukuoka, Japan

WP 232 Defining the Metabolome using GCMS - Quantitation of Compromises Resulting from Temperature Gradient and Scan Rate in Quadrupole Systems; Catherine Rawlinson1; Hayley White2; Garth Maker1; 2; Bruce Fraser2; Paul Wynne2; John Hewetson2; Robert Trengove2; 1Metabolomics Australia, Murdoch University Node, Perth, Australia; 2Murdoch University, Murdoch, Australia; 3Shimadzu Scientific Instruments (Oceania) Pty Ltd, Melbourne, Australia

WP 233 Metabolomic Signature Profiles Indicative of Acute Radiation Exposure; Catherine E. Petersen1; James A Campbell1; David L Stenoien1; Battelle/PNRL, Richland, WA

WP 234 Analysis of Human Skin Tissue after Exposure to Ionizing Radiation Enabled by LC-MS based Metabolomics; Zeping Hu1; Young-Mo Kim1; William Morgan1; Richard D. Smith2; Tom
Theresa O. Metz, Friedrich Mandel, Thomas Glauner, Jerry Mass Spectrometry-based Metabolomics for Technology, Prague, Czech Republic
Christoph H. Borchers, Hoon Yeo, Daeseung Lee, Youngchang Kim, Duchoslav 1, Edmund Lui, Hua Pei, Takeo Zweigenbaum, Ondrej Lacina, Lukas Vaclavik, Wei, G.A. Nagana Gowda, Jeremiah Bowers, 1Institute of Cancer Research, Sutton, UK; 2Advanced Technologies, University of Victoria, Victoria, BC, Canada; 1AB SCIEX, Concord, Canada; 1Agilent Technologies GmbH, Germany; 1Pediatrics Department Padova University, Padova, Italy; 2Innovation 2 Unit, Yuhan Corporation, Seoul, Republic of Korea

Identification and Quantification of YH4808 Metabolites in Human Urine by Liquid Chromatography-Mass Spectrometry (LC-MS); Hwa Suk Kim; Seo Hyun Yoon; Kyung-Sang Yu; In-Jin Jang; Joo-Youn Cho; Seoul National University College of Medicine, Seoul, Republic of Korea; 2Innovation 2 Unit, Yuhan Corporation, Seoul, Republic of Korea

Simultaneous Determination of Theophylline, Caffeine and their Metabolites in Urine by LC-MS/MS for Pediatric Pharmacokinetic study; Young Mi Kim; Sun Hwa Kim; Seo Hyun Yoon; Kyung-Sang Yu; In-Jin Jang; Joo-Youn Cho; Seoul National University College of Medicine, Seoul, South Korea

Pharmacokinetic Characterization of Rosiglitazone and Its Metabolites in Diabetes Animal Model; Sung-Hoon Ahn; Jin Sook Song; Myung Ae Bae; KRICT, Daejeon, South Korea

Determination of Low Levels of Testosterone and Dihydrotestosterone in Human Serum by LC-MS/MS; Chen-Yu Wang; Yan Xu; Kathryn Barnett; Kristin Miller; Yong-Xi Li; Medpace Bioanalytical Laboratories, Cincinnati, OH

Quantitation of Maternal and Fetal Lopolinar Exposure in a Rat Model of Gestational Diabetes by LC-MS/MS; Gregory J. Anger; Michelle E. Young; Matthew W. Forbes; Micheline Piquette-Miller; Faculty of Pharmacy, University of Toronto, Toronto, Canada; 2Department of Chemistry, University of Toronto, Toronto, Canada

Simultaneous Determination of Estrone and Equilin in K EDTA Human Plasma by LC-MS/MS; Ming Zuo; Qiaoling Yu; Zhi Liu; Jianyao Wang; Wenzhe Lu; Daniel Tang; Harry Zhao; Zhongping (John) Lin; 2Frontage Laboratories, Malvern, PA; 3Frontage Laboratories Inc. (Shanghai), Shanghai, China

Use of LC-MS-MS to Assess Induction of Human CYP1A2 and CYP3A4 by Hops; Xi Qiu; Yang Yuan; Richard B. Van Breemen; University of Illinois College of Pharmacy, Chicago, IL

Determination of 5-Hydroxy Omeprazole and Omeprazole Sulfone in Human Plasma by LC-MS/MS; Weimin Wang; Haizhi Lin; Wei Zhang; Futian Han; Harry Zhan; Zhongping (John) Lin; Mike-Qingtao Huang; Naidong Weng; 2Frontage Laboratories, Malvern, PA;
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WP 255 Quantitative LC-MS/MS Methods for Characterizing Metabolites of Drugs Levofloxacin and Cyclosporin A in Human Microdose Plasma Samples; Sanggoo Kim; Joohee Jung; Jinwoo Jung; Jongbok Seo; Korea Basic Sci. Institute, Seoul, South Korea

WP 256 LC-MS/MS for the Assessment of the Biological Implications of Carboxyalkylation of Guanine in the Nucleotide Pool; Lijuan Fu; University of California, Riverside, Riverside, CA

WP 257 Quantitation by LC-MS/MS of Psychotropic Drugs in Different Mice Tissues; Bruno Manadas1, 2, 3; Vera M. Mendes1, 2, 3; Ana I.S. Ferreira1, 2, 3; Sandra Rocha1, 2, 3; Jorge Costa Pereira1, 2, 3; Graça Baltazar1, 2; David Cotter1, 2; Mike J. Dunn1, 2; 1Center for Neuroscience and Cell Biology, Cantanhede, Portugal; 2UCD Conway Institute, Dublin, Ireland; 3Chemistry Department, University of Coimbra, Coimbra, Portugal; Centro de Investigação em Ciências da Saúde, Covilhã, Portugal; 3Department of Psychiatry, Royal College of Surgeon, Dublin, Ireland

WP 258 An LC-MS/MS Analytical Method for Mephedrone and Naphrynone Analysis in Urine; Theresa Lee; Witold Woroniecki; John McFarlane; AB SCIEX, Foster City, CA

WP 259 Development of a Bioanalytical Workflow to Support an Enhanced P-glycoprotein (P-gp) Inhibition Assay; Ying Li; Anthony Pawa; Janet Kolb; Aaron Walker; Andrew Wagner; Xianmei Cai; Harold Weller; John Herbst; Wilson Shou; Bristol-Myers Squibb Company, Wallingford, CT

WP 260 An LC-MS/MS Method for Simultaneously Determining Formoterol and Budesonide in Human Plasma with Dual HPLC System; Yingping Morikawa1; Jorg Morikawa1; Lillian Choi; Dawei Zhou2; 1XenoBiotic Laboratories, Inc., Plainsboro, NJ; 2Zef Scientific Inc., San Diego, CA

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WP 262 Development of a Mass Spectrometry Assay to Identify Compounds Forming Reactive Metabolites with La Antigen Protein in Microsomal Mixtures; Damien Ready1; Nari Talaty2; Laura Miesbauer; Robert W. Johnson; Melanie J. Patterson; Abbott Laboratories, Abbott Park, IL

WP 263 Metabolite Identification of Rifampicin in Human Urine by Modern Tools of Liquid Chromatography–Mass Spectrometry; Jun Wang1; Lilja Zhu1; Ying Wang1; Jiazhang Xu1; Weiguoi Tan1; Rong’an Li1; Yingzhou Yang1; Xiaoli Liu2; 1Shenzhen Center for Chronic Disease Control, Shenzhen, China; 2Agilent Technologies, Shanghai, China

WP 264 Untargeted Metabolomic Profiling using LC-QTOF MS in Human Urine Treated with Rifampicin; HyangHee Yang; SeungHwan Lee; SeoHyun Yoon; KyungSang Yu; JinJin Jang; JooYoun Cho; Seoul National University College of Medicine, Seoul, Republic Korea

WP 265 Metabolic Stability of Leucine-Based gamma–Lactone Prodrugs Developed for the Treatment of Alzheimer’s Disease; Andrew Lampkins; Gregory Gorman; Lori Coward; Erika Cretton-Scott; Samford University, Birmingham, AL

WP 266 Metabolites of Thalidomide Using the Humanized CYP3A Transchromosomal Mouse Liver Microsomes, Detected by LC–MS/MS system; Shin-ichiro Nitta1; Yasuko Tsukazaki1; Naoto Senda1; Toshiyuki Yamazaki2; Masato Aoshima1; Tsutomu Nakai2; Kinya Kubo2; Yasuhiro Kazuki1; Mitsuo Oshimura1; 1Mitubishi Chemical Medience Corporation, Tsukuba, Japan; 2K. A. Boehringer Ingelheim Pharma GmbH & Co.KG, Biberach, Germany

WP 267 Introduction of UPLC/High Resolution Mass Spectrometry combined with Ion Mobility Separation/MS2–Techniques for the Analysis of in vivo Drug Metabolism Studies; Stefan Blech; Ralf Laux; Boehringer-Ingelheim Pharma GmbH & Co.KG, Biberach, Germany

WP 268 Combined Application of Hybrid Triple Quadrupole Linear Ion Trap and High Resolution Accurate Mass Systems for Metabolite Identification Workflows; Hua-Fen Liu; Alexandre Wang; Elliott Jones; AB SCIEX, Foster City, CA

WP 269 Troglitazone Metabolism in a Chimeric Mouse Model with Humanized Livers Determined by High Mass Accuracy MSn Analysis; Alan Barnes1; Neil Loftus1; Ian Wilson1; Timothy Schulz-Utermoehl2; Michopoulos Filippos2; Yoshio Morikawa1; 1Shimadzu ISS MS/BU, Manchester, UK; 2Astra Zeneca, Alderley Park, Cheshire, UK; 3PhoenixBio Co. Ltd, Higashi-Hiroshima, Japan

WP 270 High Sensitivity Characterization of Propanolol and Associated Metabolites Utilizing Intergated Microfluidic LC/MS/MS; Paul Rainville1; Michael Tomany1; James Murphy1; Norman Smith1; Robert Plumb1; 1Waters Corporation, Milford, MA; 2Kings College London, London, UK; 3Imperial College, London, UK

WP 271 Comparative study of in-vitro Metabolites of Investigational Anticancer Agents using RLMs, Rat Hepatocytes and HepG2 by LC-Ion Trap Mass Spectrometry; Mohamed Attwa; Adnan Kadi; King Saud University, College of Pharmacy, Riyadh, Saudi Arabia

WP 272 Leveraging a Mixed Platform Approach for Confident Characterization and Identification of Drug Metabolites; Ming Q1; Mark Gohdes; Joseph T. Marin1; Xiaohong Liu; Heiko Junga; Donald L. Mckenzie1; 1Lamina Research Centre, MD; 2Covance Laboratories, Madison, WI

WP 273 The use of UPLC-MS/MS for Separation and Identification Diastereomeric Hydroxylated Metabolites of GS-9667 in vivo and in vitro; Chungwen Chen1; Nevena Mollitor; Eve-Irene Lepist; Kwan Leng; Gilead Sciences, Inc., Palo Alto, CA
WP 274  Human Metabolism of AMS-36, a Retinoid X Receptor-alpha Ligand; Lian Chen1; Martin Conda-Sheridan2; Mark Cushman; John M. Pezzuto3; Richard B. van Breemen1; 1University of Illinois College of Pharmacy, Chicago, IL; 2School of Pharmacy, Purdue University, West Lafayette, IN; 3College of Pharmacy, University of Hawaii at Hilo, Hilo, HI

WP 275  The Use of a LTQ-XL Linear Ion Trap to Detect 21 Metabolites in a Single Injection; Todd Baughman; GlaxoSmithKline, Research Triangle Park, NC

WP 276  Linear Ion Trap MS vs. High Resolution Quadrupole TOF-MS: Which Provides More Useful Data in a Drug Discovery Program?; Richard Schneider1; Veronica Zelesky; Brenda Kapinos3; Alfin Vaz2; James A. Ferguson1; 1Pfizer Global R&D, Groton, CT; 2AB Sciex, Framingham, MA

WP 277  Characterisation of Melarsoprol, an Arsenic-containing Pharmaceutical, and Its Metabolites by HR-MS/MS; Reinhard Raml1; Georg Raber2; Theresa A. Shapiro; Rahul Bakshi3; Kevin A. Francesconi; Christoph Magnes; 1Joanneum Research-Health, Graz, Austria; 2Institute of Chemistry, Karl-Franzens University, Graz, Austria; 3Department of Medicine, John Hopkins University, Baltimore, MD

WP 278  Characterization of [6]-Gingerol Metabolism in Rat by LC-MS/MS and Accurate-Mass TOF; Marie-Lou Gauthier1; Jennifer Douat2; Pascal Vachon4; Francis Beaudry1; 1Université de Montréal, St-Hyacinthe, Canada; 2Institut de Chimie Pharmaceutique Albert Lespagnol, Lille, France

WP 279  LC/MS/MS Analysis of in vivo Intraacellular Metabolites in Rat Liver Tissue after Administration of INX-189, a Potent HCV Inhibitor; Jerry Muhammad1; Jin Wang; Aleksandr Obikhd; C. Robin Walters4; Damound Hunley5; K. Dawn Bryant; Stan Chamberlain; Christopher McGuigan6; Karolina Madela7; John Vernachio; Elena Gorovits; 1Inhibitex, Inc., Alpharetta, GA; 2Welsh School of Pharmacy, University of Oklahoma, Oklahoma City, OK

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Visualizing the Vaginal Distribution of Tenofovir by Imaging Mass Spectrometry: Quantitation of Tenofovir Biodistribution in Rabbit Vaginal Tissue; Michelle L. Reyzer; Jamie Allen; Patrick Kiser; Richard M. Caprioli; Vanderbilt University, Nashville, TN; University of Utah, Salt Lake City, UT

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Spatial Profiling of Anticancer Drug in Brain Tumor Tissue using MALDI MS Spectrometric Imaging; Dodge L. Balyua; Yioti Sharma; James M. Gallo; Rong Wang; Mount Sinai School of Medicine, New York, NY

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Visualization of Cellular Energy Status and Oxidative Stress by using Multiple Metabolite Ions in Imaging Mass Spectrometry; Yuki Sugiipla; Mitsutoshi Setou; Hamamatsu University School of Medicine, Hamamatsu, Japan; Keio University, Tokyo, Japan

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Accurate Mass Drug Imaging for Metabolite Distribution: Extra Information with Little Extra Effort; Cristina Quiñon; Katherine A. Korte; Brett A. Haberl; William W. Cramer; Maxence Wiszorski; Laboratoire de Biologie marine, Université de Mons, Mons, Belgium; FABMS, Université Lille 1, Villeneuve d’Ascq, France; Imabiotec, Villeneuve d’Ascq, France

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A Comparative Study of DESI and MALDI for the Imaging of Pharmaceuticals in Tissue; Andrew J. Blessire; Stacey R. Oppenheimer; Justin M. Wiseman; Pfizer, Inc., Groton, CT; Prosolia, Inc., Indianapolis, IN

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MALDI Imaging of Fungal Interactions: A Tool to Facilitate the Isolation of Fungal Inhibitors from Marine Bacteria; Wilna Moree; Xiling Zha; Marcelino Gutierrez-Guevara; Pieter Dorrestein; UCSD, Skaggs School of Pharmacy, La Jolla, CA; INDICASAT, Clayton, Panama

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Microbial Metabolic Exchange within a Zebrafish Host; Samantha Mascuch; UC San Diego, La Jolla, CA

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Examination of Titanium Dioxide Nanoparticle Absorption into Skin by Laser Desorption Ionisation Mass Spectrometry Imaging; Rajvir Wadhawan; Malcolm Clench; Sheffield Hallam University, Sheffield, UK

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Simultaneous Imaging Low Molecular Weight Metabolites in Mouse Brain Using TiO2 Nanoparticles in Nano-PALDI-IMS; Kamillesh Shrivas; Takahiro Hayasaki; Yuki Sugiuara; Mitsutoshi Setou; Hamamatsu University School of Medicine, Hamamatsu, Japan

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MALDI MS Imaging of Cereals; Tabiwa Arrey; Maria C. Prieto Conaway; Huy Bui; Thomas Moehring; Kerstin Strupat; Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; Thermo Fisher Scientific, San Jose, CA

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Single-Cell Level MALDI Imaging MS of Metabolites in Maize, a C4 Photosynthesis Plant; Andrew Korte; J Hyun Jun; Marna Nelson; Edward Yeung; Young Jin Lee; BASIL

WP 426
Probing Medicinal Plant Phytochemical Factors through in situ MALDI Tissue Imaging using Quadrupole Ion Mobility Time-of-Flight Mass Spectrometry; David Gang; Laurence Davin; Mwafaq Ibdah; B. Markus Lange; Norman Lewis; Gunn Tunn-Steen; Henry Shion; Greg Witkop; Don Harris; Alan Millar; Washington State University, Pullman, WA; Waters Corp., Milford, MA

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Indirect DESI Imaging of Secondary Metabolites in Plant Material; Christian Janflett; Janina Thunig; Bin Li; Steen H. Hansen; University of Copenhagen, Copenhagen, Denmark

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Imaging Bacterial Biofilms using Laser Desorption Postionization Mass Spectroscopy: Comparing 10.5 eV to 7.87 eV Photoionization; Chhavi Bhardwaj; Jerry F. Moore; Gerald L. Gasper; Yang Cui; Hans Bernstein; Ross P. Carlson; Luke Hanley; University of Illinois, Chicago, Chicago, IL; Dept. of Chemical and Biological Engineering, Center for Biofilm Engineering, Montana State Uni., Bozeman, MT; MassThink, Naperville, IL

MALDI MSI, A New Tool to Understand Marine Life: An Example of the Study of a Chemical Defense Mechanism; Séverine Vandyck; Patrick Flammang; Céline Meriaux; Emmanuelle Claude; Simona Francese; M. Nicola Nanney; Fabien Cramers; Melissa Smith; Department of Biochemistry & Microbiology, University of Victoria-Genome BC, University of Victoria, Genomics BC, Vancouver, BC; School of Medicine, University of Victoria, Victoria, BC, Canada

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MALDI Imaging Mass Spectrometry Reveals Elevated Nigral Levels of Dynorphin Peptides in L-DOPA-induced Dyskinesia; Anna Karlsson; Jörg Hanrieder; Maria Faith; Jonas Bergquist; Malin Andersson; Uppsala University, Neurotoxicology, Uppsala, Sweden; German Cancer Research Center, Heidelberg, Germany; Uppsala University, Analytical chemistry, Uppsala, Sweden

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Time Dependant Lipid Profile Changes in Controlled Cortical Impact Rat Model; Jeremy Post; Shelley N Jackson; Benoit Colsch; Gregg Schieffer; Gregory Bull; Brian Cox; Amina S. Woods; NIH/NIDA-IRP, Baltimore, MD; Uniformed Services University of Health Sciences, Bethesda, MD

MALDI-MSI Analysis of Lipidomic and Proteomic Responses of Human Skin to Sensitizing and Irritant Chemicals, Utilising Ion Mobility Technology; Philippa Hart; Emmanuelle Claude; Simona Franceschi; M. Nicola Woodroofe; Malcolm Clench; Sheffield Hallam University, Sheffield, UK; Waters corporation, Manchester, UK

MALDI MSI Imaging of Brain Tissue from Patients with Alzheimer’s Disease; András Kiss; Anna Carrano; Donald Smith; Saskia M. van der Vies; Ron M.A. Heeren; FOM Institute AMOLF, Amsterdam, The Netherlands; VU University Medical Center, Amsterdam, The Netherlands; Netherlands Proteomics Center, Utrecht, The Netherlands

WP 432
Mass Spectrometry Imaging of Brain Tissue from Patients with Alzheimer’s Disease; András Kiss; Anna Carrano; Donald Smith; Saskia M. van der Vies; Ron M.A. Heeren; FOM Institute AMOLF, Amsterdam, The Netherlands; VU University Medical Center, Amsterdam, The Netherlands; Netherlands Proteomics Center, Utrecht, The Netherlands

WP 433
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WP 434  Localization and Identification of Biomarkers in Human Cartilage by MALDI Imaging Mass Spectrometry; Berta Cillero Pastor1; Francisco J. Blanco García1; Ron M.A. Heeren1; 1FOM Institute AMOLF, Amsterdam, The Netherlands; 2INIBIC- CHUC, A Coruña, Spain

WP 435  MALDI Mass Spectrometry Imaging - A Prospective Tool for Tumor Border Region Identification; Brian Flatley1, 2; Elizabeth Johnson1; Fawaz Musa1; Peter Malone2; Rainer Cramer1; 1University of Reading, Reading, UK; 2Harold Hopkins Department of Urology, Royal Berkshire NHS Foundation Trust Hospital, Reading, UK; 3Department of Pathology, Royal Berkshire Hospital, Reading, UK

WP 436  Differentiation of Diagnostically Challenging Tumors in Multiple Patient Samples Using Multiplex Multivariate Agreement Analysis; Emrys A. Jones1; Nicole Schmitz2; Cathelin Waaier1; Alexandra van Remoortere1; René J.M. van Zeijl1; André M. Deelder2; Judith V.M.G. Bovée2; 1Eindhoven University of Technology, Eindhoven, The Netherlands; 2Parasitology, Leiden University Medical Center, Leiden, the Netherlands; 3Pathology, Leiden University Medical Center, Leiden, the Netherlands

WP 437  Molecular Diagnosis of Metastatic Potential in Human Soft Tissue Sarcoma; Erin H. Seeley; Ginger E. Holt; Richard M. Caprioli1; Vanderbilt University, Nashville, TN

WP 438  Visualizing Breast Cancer Heterogeneity Using Nanostructure-Initiator Mass Spectrometry (NIMS); Wolfgang Reindl; Ben Bowen; Trent Northen; Lawrence Berkeley National Lab, Berkeley, CA

WP 439  Microscopic MALDI Imaging Revealed Heterogeneous Distribution of Metabolites in and Around Colon Cancer Metastasis of Human Colon Cancer Xenograft in Mice; Akiko Kubo1; Mitsuyo Ohmura1; Takako Hishiki1; Masatoshi Wakui1; Mitsuru Murata1; Mitsutoshi Setou1; Makoto Suematsu1; 1Keio University, Tokyo, Japan; 2Hamamatsu University School of Medicine, Shizuoka, Japan

WP 440  An Imaging Approach to Investigate the Therapeutic Effects of Decoy Oligonucleotide Drugs in Cancer; Rita Casandonte1; Joseph M. Amann1; Jennifer R. Grandis2; David P. Carbone1; Richard M. Caprioli1; 1Vanderbilt University, Nashville, TN; 2University of Pittsburgh, Pittsburgh, PA

WP 441  Analysis of Glomerular Proteins by High Spatial Resolution MALDI Imaging Mass Spectrometry; Kerri Grove; Paul Voziyan; Roberto Vanacore; Raymond Harris; Billy Hudson; Richard M. Caprioli; 1Vanderbilt University, Nashville, TN

WP 442  Human Glioma Classification using Desorption Electrospray Ionization Mass Spectrometry Imaging and Statistical Analysis; Livia S. Eberlin1; Allison L. Dill1; R. Graham Cooks1; Isaiah Norton1; Sandro Santagata2; Nathalie Y. R. Agar2; 1Purdue University, West Lafayette, IN; 2Harvard Medical School, Pathology, Boston, MA; 3Harvard Medical School, Neurosurgery, Boston, MA

WP 443  In-situ Tryptic Digestion of Bacterial Biofilms for Protein Identification and Imaging by MALDI Mass Spectrometry; Melvin Blaze M.T; Berdan Sevinc; Luke Hanley; University of Illinois at Chicago, Chemistry, Chicago, IL

WP 444  MALDI-MSI to Investigate Treatment Response in Tumour Vascular Targeted Therapy; Laura Cole1; Marie Claude Djidja2; Joanne Bluff2; Emmanuelle Claude2; Vikki Carolan1; Martyn Paley1; Gillian Tozer1; Malcolm Clench1; 1Sheffield Hallam University, BMRC, Sheffield, UK; 2The Institute of Cancer Research, London, UK; 3University of Sheffield, Sheffield, UK; 4Waters Corporation UK, Manchester, UK

WP 445  Profiling of α-Crystallin Distribution in Cornea by MALDI Mass Spectrometry Imaging Mass Spectrometry Reveals Localization and Identification of Biomarkers for Protein Identification and Imaging by MALDI Mass Spectrometry; Yuntao Zhang; Yasuaki Hiromasa; Takeo Iwamoto; John Tomich; Gary Conrad; Kansas State University, Manhattan, KS

WP 446  Imaging Rheumatoid Arthritis: Novel MS Investigation of an Old Disease; Sananullah Chughtai; Kamila Chughtai; Andras Kiss; Berta Cillero Pastor2; Luke MacAleese; Ron M.A. Heeren; AMOLF, Amsterdam, Netherlands

WP 447  Investigation of Tuberculosis Infection in Monkeys: Evaluation of Drug, Protein, and Lipid Localization in Tissue Samples using Imaging Mass Spectrometry; M. Lisa Manier1; Michelle L. Reyzer1; JoAnne L. Flynn1; Clifton E. Barry1; Richard M. Caprioli1; 1Vanderbilt University, Nashville, TN; 2University of Pittsburgh School of Medicine, Pittsburgh, PA; 3Alida/NIH, Bethesda, MD; 4Vanderbilt Univ Sch Med, Nashville, TN

WP 448  Spatial Detection of Phospholipids in Human Pressure Ulcers by Imaging Mass Spectrometry; Domenico Taverna1; Lillian B Nanney1; Alons C. Pollins2; Jeffrey M. Spraggins2, 3; Giovanni Sindona1; Richard M Caprioli2, 3; 1Univerista della Calabria, Dept. of Chemistry, Arcavacata Di Rende, Italy; 2Vanderbilt University, Dep. of Biochemistry, Nashville, TN; 3University of Victoria, Victoria, BC, Canada

WP 449  Evaluation of Dithanol as MALDI Matrix for Tissue Imaging of Endogenous Metabolites by Fourier-Transform Mass Spectrometry; Cuong H. Le1, 2; Jun Han1, 2; Christoph H. Borchers1, 2; 1University of Victoria-Genome BC Proteomics Centre, Victoria, BC, Canada; 2Department of Biochemistry & Microbiology, University of Victoria, Victoria, BC, Canada

WP 450  Distinct Distribution of Hydroxylated and Non-hydroxylated Sulfatide in Human Cerebral Cortex; Dai Yuuki1; Yuki Sugiyama2; Nobuhiro Zaima1; Hiroyasu Akatsu3; Masami Fujiwara1; Keikichi Sugiyama1; Mitsutoshi Setou1; 1Lion Corporation, Tokyo, Japan; 2Hamamatsu school of medicine, Hamamatsu, Japan; 3National Institute of Health, Tokyo, Japan; 4Ritsumeikan University, Kyoto, Japan

WP 451  Direct Visualization of Heterogeneous Distribution of Lipid Molecules in Cotton Embryos by MALDI-LTQ-Orbitrap; Jessica Lim1; Andrew Korte1, 2; Purnima Neogi1; Patrick Horn1; Kent Chapman1; Young Jin Lee1, 2; 1Iowa State
WP 456 Evaluation of a Nanospray Atmospheric Pressure - Electron Capture Dissociation (AP-ECD) Ionization Source for the Analysis of Post-Translational Modifications; Davin Carter1; Jason Held; Steven Danielson; Bradford Gibson; Buck Inst for Research on Aging, Novato, CA

WP 457 Mass Spectrometric Method Development to Analyze Sequence and Structural Influences on Tyrosine Nitration Site Selectivity; Kent Seeley; Stanley M. Stevens, Jr; University of South Florida, Tampa, FL

WP 458 Combined Isotopic and Isobaric Labeling Strategies for the Identification and Quantitation of 3-nitrotyrosine-modified Proteins; Adam R. Evans; Renã A. S. Robinson; University of Pittsburgh, Pittsburgh, PA

WP 459 Confident Identification of 3-Nitrotyrosine Modifications Using an Experimentally Defined Set of Criteria; Bensheng Li; Jason Held; Birgit Schilling; Steven Danielson; Bradford Gibson; Buck Inst for Research on Aging, Novato, CA

WP 460 Determination of S-nitrosylation Occupancy Rates Using cys-TMT Tags; Angel Aponte1, 2; Mark Kohler; Elizabeth Murphy1; Marjan Gucek1, 3; 1Proteomics Core Facility, Bethesda, MD; 2Laboratory of Cardiac Physiology, Bethesda, MD; 3National Heart Lung and Blood, NIH, Bethesda, MD

WP 461 A Monoclonal Antibody Cocktail as an Enrichment Tool for Acetylation Analysis; Patrick Shaw1; Raghothama Chaerkady2; Nancy Davidson2; Akhilade Pandey1; Johns Hopkins University, Baltimore, MD; 2University of Pittsburgh Cancer Institute, Pittsburgh, PA

WP 462 A Mass Spectrometric Approach for Characterizing and Quantitating Acetylation Sites on the Mitochondrial Pyruvate Dehydrogenase Complex; Salisha Hill; Kristie Lindsey Rose; Sarah Stuart; Joshua Fessel; James West; Charles R. Flynn; Vanderbilt University, Nashville, TN

WP 463 Lysine Acetyltransferase Substrate Discovery by in vitro Enzymatic Reactions and High Resolution Quantitative Acetylimics; Alex Hebert; Derek Bailey; Justin Brumbaugh; Joshua J. Coon; Univ of Wisconsin-Madison, Madison, WI

WP 464 Novel Application of PROTOMAP and AQUA Approaches to Quantify Acetylated CheY, a Response Regulator in Chemotaxis of Escherichia coli; Tevie Mehlman1; Bassem Ziadeh1; Gabriel Simon2; Atim Atte Enyenih3; Milana Fraibergh4; Michael Eisenbach4; Roman Zubarev5; Alla Shainskaya6; 1Biol MS Facility, Weizmann Institute of Science, Rehovot, Israel; 2Washington University in St. Louis, St. Louis, MO; 3Molecular Biometry Lab, Karolinska Institutet, Stockholm, Sweden; 4BioChem Department, Weizmann Institute of Science, Rehovot, IL

WP 465 Development of Methods for Quantitation of Acetylated Peptides; Matthew Rardin; Birgit Schilling; Jason Held; Bradford W. Gibson; Buck Institute for Age Research, Novato, CA

WP 466 Identification and Characterization of New o-Acetylated Peptides; Qian Cai; Riverside, CA

WP 467 An Innovative Dual-enzyme and Dual-activation Strategy for Comprehensive and Accurate Characterization of Protein Arginine-methylation in Trypanosoma brucei; Hao Wang; Jun Li; Jun Qu; University at Buffalo SUNY, Buffalo, NY

WP 468 Proteomics Mapping of Yeast RNA Polymerase II Post-translational Modifications and Investigating Their Biological Significance; Sreenivas Rao Ramessety1; Amber L. Mosley; Michael Washburn1; 1Flowers Institute for Medical Research, Kansas City, MO; 2Indiana University School of Medicine, Department, Indianapolis, IN

WP 469 Bottom-up and Top-down Analysis of Post-translational Modifications in Myelin Basic Protein; Chunghao Zhang; Robert Zand; Philip Andrews; Univ. of Michigan, Ann Arbor, MI

WP 470 Simultaneous Identification of Unmodified Tryptic Peptides and Phosphopeptides, Glycopeptides, and Deamidated Peptides by Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) and LC-MS/MS; Piliang Hao1; Jingru Qian1; Wei Meng1; Wei Meng1; Yan Ren1; Andrew J. Alpert2; Siu Kwan Sze2; 1University of North Carolina, Chapel Hill, NC; 2Stowers Institute for Medical Research, Kansas City, MO

WP 471 Analysis of Phosphorylated Neuropeptides by 3D-ERLIC-HILIC-RP Chromatography and ETD MS Detection - Evaluation of Separation and Detection Conditions; Goran Mitulovic; Verena Trettter; Medical University of Vienna, Vienna, Austria

WP 472 MS-identified Phosphorylation Sites in Homer2 Regulate Binding to Metabotropic Glutamate Receptors; Rob Helton1; Santiago Farias2; Karen K. Szulminiski3; Christine C. Wu1; 1University of Colorado, Aurora, CO; 2University of California Santa Barbara, Santa Barbara, CA; 3University of Pittsburgh School of Medicine, Pittsburgh, PA

WP 473 Comparing and Contrasting Scanning and Fragmentation Methods for Analyzing the Phosphoproteome; Chia-Feng Tsai1; Pei-Yi Lin1; Chris Hughes1; Johannes PC Vissers2; James I Langridge2; Yu-Ju Chen1; 1National Taiwan University, Taipei, Taiwan; 2Academia Sinica, Taipei, Taiwan; 3Waters Corporation, Manchester, UK

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WP 464 Novel Application of PROTOMAP and AQUA Approaches to Quantify Acetylated CheY, a Response Regulator in Chemotaxis of Escherichia coli; Tevie Mehlman1; Bassem Ziadeh1; Gabriel Simon2; Atim Atte Enyenih3; Milana Fraibergh4; Michael Eisenbach4; Roman Zubarev5; Alla Shainskaya6; 1Biol MS Facility, Weizmann Institute of Science, Rehovot, Israel; 2Washington University in St. Louis, St. Louis, MO; 3Molecular Biometry Lab, Karolinska Institutet, Stockholm, Sweden; 4BioChem Department, Weizmann Institute of Science, Rehovot, IL
WP 474  Vibrational and Ion-Electron Activation Methods for Negative Ion Mode MS/MS Analysis of Sulfoproteins; Catherine E. Hersberger; Kristina Hakansson; University of Michigan, Ann Arbor, MI

WP 475  A Top-Down Proteomic Analysis of PTM Changes on Histones through Prostate Cancer Progression; Lisabeth Hoffman; John Lapek; Gregory Tomblin; Alan Friedman; 1University of Rochester Medical Center, Rochester, NY; 2University of Rochester, Rochester, NY

WP 476  Toward Comprehensive Unbiased Analysis of Histone Combinatorial PTMs in Human Centromeric Chromatin; Aaron Bailey; Tatyana Panchenko; Limin Liu; Todd Stukenberg; 1University of Rochester, Rochester, NY

WP 477  C-terminal Sequencing of Sodium Cationized FMOC Derivatized Peptides; Alessandra L. Ferzoco; Gary L. Glish; University of North Carolina, Chapel Hill, NC

WP 478  Investigation of Mass Spectrometry Signal Yields for Phenylisothiocyanate Derivatization of Peptides; Pamela Ann Diez; Xudong Yao; University of Connecticut, Storrs Mansfield, CT

WP 479  Disulfide Bond Scrambling in CID of [M+OH+nH]+ Ions and ETD of [M+nH]+ Ions Formed from Peptides Containing Two Disulfide Bonds; Xiaoxiao Ma; Kit Durand; Chelsea Plummer; Xinrong Zhang; Yu Xia; 1Tsinghua University, Beijing, China; 2Purdue University, West Lafayette, IN

WP 480  Studying Peptide Fragmentation Differences Based on Cysteine Modifications on a Quadrupole-Linear Ion Trap Instrument; Souade Ben Haddou; Andre Leblanc; Tze Chieh Shiao; René Roy; Lekha Sileno; UQAM, Montreal, Canada

WP 481  Facile Hydrogen Atom Migration within Cationic Radical Peptides: Arginine Facilitated Isomerization and Radical-Induced Dissociation; Tao Song; Chun Ming Dominic Ng; Minjie Xu; Chi-Kit Siu; Ivan K. Chu; 1The University of Hong Kong, Hong Kong, China; 2City University of Hong Kong, Hong Kong

WP 482  Effect of Gas Phase Structure on Radical Migration and Subsequent Fragmentation in Peptides; Xing Zhang; Ryan R. Julian; University of California, Riverside, CA

WP 483  An Arginine Residue Can CONTROL the Side-chain Cleavage of c(254excited)-ionylneuclide/isoleucine Radical Cations by Facilitating α-Radical Migrations; Chun Ming Dominic Ng; Qiang Hao; Quan Quan; Song Tao; Chi-Kit Siu; Ivan Keung Chu; 1The University of Hong Kong, Hong Kong, China; 2City University of Hong Kong, Hong Kong, China

WP 484  Roles of Radicals and Charges in the Neutral H2PO3 Loss of Molecular Phosphorylated Peptide Radical Cations; Quan Quan; Ricky P. W. Kong; Shu-Im Siu; Cheu-Kuen Lai; Dominic C. M. Ng; Qiang Hao; Chi-Kit Siu; Ivan K. Chu; 1The University of Hong Kong, Hong Kong; 2City University of Hong Kong, Hong Kong

WP 485  Radical a-ions in ECD – An Untold Story; Roman Zubarev; 1David Good; Mikhail Savitski; Karolinska Institute, Stockholm, Sweden; 2Cellzone, Heidelberg, Germany

WP 486  The Effects of Basic Residues of Peptides on Electron-transfer Dissociation Mass Spectrometry; Changgeng Feng; Carolyn J Cassady; University of Alabama, Tuscaloosa, AL

WP 487  Influence of Peptide Structure on the ECD Fragmentation Pathways; Renjie Hu; Guillaume van der Rest; Gilles Frison; Julia Chamot-Rooke; DCMR - Ecole Polytechnique, Palaiseau, France

WP 488  Electron Transfer Dissociation of Transition Metal-peptide Complexes; Heather M. Watson; Carolyn J. Cassady; University of Alabama, Tuscaloosa, AL

WP 489  From z− to z−: Recruiting Hydrogens to the C-terminal in Electron-transfer Dissociation; Samantha Bokatzian-Johnson; Carolyn J. Cassady; University of Alabama, Tuscaloosa, AL

WP 490  Capture Dissociation and Collision-induced Dissociation Mass Spectrometry of S-nitrosylated Peptides; Andrew Jones; Helen Cooper; University of Birmingham, Birmingham, UK

WP 491  On the Mechanism of Loss of Formamide from a2 Ions and Loss of Methyl Mercaptan from a2 Ions Containing Methionine; Yamil Simon; Pedatsur Neta; Xiaoay Yang; Lisa E. Kilpatrick; Stephen E. Stein; NIST, Gaithersburg, MD

WP 492  Low Energy CID Fragmentation Channels of Proline-containing Peptides: Chaminda M. Gamage; Kevin Kmiec; Christopher Barlow; David H. Russell; Texas A&M University, College Station, TX

WP 493  Fragmentation of Proline Containing Peptides via High Energy Collision Induced Dissociation and 193-nm Photo-activation TOF-TOF Mass Spectrometry; Kevin Kmiec; Chaminda M. Gamage; David H. Russell; Texas A&M University, College Station, TX

WP 494  A Mechanism of the Lz Formations Involving the “Gly-ization” of the Thr Sidechain in Melittin in MALDI-QIT-TOF MS; Kazumi Saikusa; Susumu Yoshioka; Shunshke Izumi; Graduate school of scienee, Hiroshima University, Kogashihiroshima, Japan; 2Yokohama City University, Yokohama, Japan

WP 495  Sequence Dependence of Peptide Rearrangement During Collision Induced Dissociation in a Quadrupole Ion Trap; Sandra Spencer; Alessandra Ferzoco; Meredith Arnold; Jeffrey Stellmacher; Joseph L. Glish; 1University of North Carolina, Chapel Hill, NC; 2FOM Rijnhuizen, Nieuwegein, Netherlands
WP 498 Complementary Methods to Probe the Chemical Structures of CID Product Ions: HDX & IRMPD Spectroscopy; Marcus Tiradq 1; Xian Chen 1; Alfred Yeung 1; Jeffrey Steill 1; Jos Oomens 1; Nicolas Polfer 1; 1University of Florida, Gainesville, FL; 2FOM Rijnhuizen, Nieuwegein, Netherlands.

WP 499 Calculations and Measurements of Ion Intensity Relationships in Mass Spectra of Short Peptides; Oleg Obolensky 1; Wells W. Wu 1; Rong-Fong Shen 1; Yi-Kuo Yu 1; 1National Center for Biotechnology Information, NLM, Bethesda, MD; 2NIA/NIH, Baltimore, MD.

WP 500 Quantum Mechanical Analysis of the Wu 2; Rong-Fong Shen 2; Yi-Kuo Yu 1; 1University of Florida, Gainesville, FL; 2FOM Rijnhuizen, Nieuwegein, Netherlands.

WP 501 Fragment Ions in CID, HCD and PQD MSMS Spectra of Doubly Charged Penta-peptides, versus Theoretical Calculations of Their Relative Intensities; Tibor Pechan 1; Martin Beck 5; Johan Malmstroem 3; Reto Abbatiello 2; Chenwei Lin 2; Jeffrey Whiteaker 2; Travis Lorentzen 2; Eric Kuhn 2; Karl R. Clauser 2; Hasmik Keshishian 2; Keith Rivera 2; Naomi Choodnovskiy 2; Youngsoo Kim 2; Ho-Pil Min 4; Pei Wang 2; Leigh Anderson 2; Steven J Skates 2; Steven A. Carr 2; Amanda Paulovich 1; 1Fred Hutchinson Cancer Research Center, Seattle, WA; 2Tufts University, Medford, MA; 3College of Medicine, Seoul Nat’l Univ, Seoul, South Korea; 4Massachusetts General Hospital, Boston, MA.

WP 502 Influence of Side Chain Chemistry on Fragmentation Pathways of P5-45 Ions; Meredith Arnold 1; Alessandra Ferzoco 1; Sandra Spencer 1; Gary L. Glish 1; University of North Carolina, Chapel Hill, NC.

WP 503 Influence of Basic and Acidic Residues on b n Peptide Fragment Ion Structure; Ashley Gucinski 2; 1; Julia Chamilot-Rooke 2; Arpad Somogyi 1; Vicki H. Wysocki 1; 1University of Arizona, Tucson, AZ; 2DCMR - Ecole Polytechnique, Palaiseau, France.

WP 504 Investigation of the Nonvolatile Thermal Products of Bradykinin Using Liquid Chromatography Tandem Mass Spectrometry; Mohammed Meetani 1; Osama Zahid 1; J. Michael Conlon 1; 1United Arab Emirates University, Al Ain, United Arab Emirates; 2Biochemistry Dept., FMHS, UAE University, Al Ain, UAE.

WP 505 Oviating the Need for Transition Optimization in SRM Assays to Detect and Quantify any Protein of the Human Proteome; Caroline S. Chu 1; Jeffrey Stevens 1; Ulrike Kusebaech 2; Eric Deutsch 2; David S Campbell 2; Christine Carapito 2; 1AB SCIEX, Foster City, CA; 2PharmaCadence Analytical Services, LLC, Hatfield, PA.

WP 506 Automation of a Multiplexed SISCAPA Magnetic Bead Workflow for Protein Biomarker Quantitation by Mass Spectrometry; Leigh Anderson 1; Matt Pope 2; Morteza Razavi 2; Terry Pearson 2; Peter Werner 2; Keith Waddell 2; Christine Miller 2; Andrew Forschung Group, Washington, DC; 2University of Victoria, Biochemistry Department, Victoria, BC, Canada; 3Agilent Technologies, Santa Clara, CA.

WP 507 Employing Mass Spectrometry for Large-scale, Targeted, and Quantitative Protein Measurements in Tumor Tissue and Cancer Cell Lines; Jacob Kennedy 1; Ping Yan 1; Susan E. Abbatiello 2; Chenwei Lin 2; Jeffrey Whiteaker 2; Travis Lorentzen 2; Eric Kuhn 2; Karl R. Clauser 2; Hasmik Keshishian 2; Keith Rivera 2; Naomi Choodnovskiy 2; Youngsoo Kim 2; Ho-Pil Min 4; Pei Wang 2; Leigh Anderson 2; Steven J Skates 2; Steven A. Carr 2; Amanda Paulovich 1; 1Fred Hutchinson Cancer Research Center, Seattle, WA; 2Tufts University, Medford, MA; 3College of Medicine, Seoul Nat’l Univ, Seoul, South Korea; 4Massachusetts General Hospital, Boston, MA.

WP 508 Targeted Protein Quantification using High-Resolution MS - MS/MS Transitions in a VELOS-Orbitrap; Johannes Hewel 1; Jian Liu 1; Daniele Merico 1; Ruth Isserlin 1; Carl White 1; Anthony Gramolini 1; Gary Bader 1; Andrew Emili 1; Donnelly Centre, University of Toronto, Toronto, Canada; 2University of Toronto, Toronto, ON.

WP 509 Quantification of Urinary Apolipoprotein A-I and Apolipoprotein A-II by LC-MS MS and Two Immuno-based Quantitative Assays; Yi-Ting Chen 1; Hsiao-Wei Chen 1; Derek S. Smith 1; Chih-Ching Wu 1; Chien-Lun Chen 1; Ting Chung 1; Yu-Sun Chang 1; Christoph H. Borchers 1; Jau-Song Yu 1; 1Chang Gung University, Taoyuan, Taiwan; 2Victoria University, Victoria, British Columbia, Canada; 3Chang Gung Memorial Hospital, Taoyuan, Taiwan.

WP 510 Absolute Quantification of Urinary Endogenous Peptides Using Selective Reaction Monitoring; Xiaolin Li 1; Daniela Schlatter 1; Mark Chance 1; Case Western Reserve University, Cleveland, OH.

WP 511 Developing Quantitative of Urine UMOD by a Multiplexed Liquid Chromatography – Targeted Mass Spectrometry; Qin Fu 1; Weihu Ji 1; Jie Zhu 1; Pingbo Zhang 1; Josef Coresh 1; Jennifer Van Eyk 1; Johns Hopkins University, Baltimore, MD; 2Johns Hopkins Bloomberg School of Public Health, Baltimore, MD.

WP 512 Increasing the Throughput of Biomarker Verification using Peptide Immunoaffinity Enrichment and Quantitative Mass Spectrometry; Jeffrey Whiteaker 1; Lei Zhao 1; Ping Yan 1; Chenwei Lin 1; Amanda Paulovich 1; Fred Hutchinson Cancer Research Center, Seattle, WA.

WP 513 Investigation of Recovery and Stability of Peptides in LC/MS/MS Analysis; Shu-Chi Zhang 1; Jeffrey Whiteaker 1; Ping Yan 1; Regine Schoenherr 1; Amanda Paulovich 1; Fred Hutchinson Cancer Research Center, Seattle, WA.

WP 514 A Global Approach for the Targeted LC-MS/MS Quantitation of Highly-Modified Proteins; Peter A. DiMagno 1; Nicolas L. Young 1; Benjamin Garcia 1; Princeton University, Princeton, NJ.

WP 515 Estimation of Absolute Protein Quantities by Selected Reaction Monitoring of Unlabeled Proteins; Kwan Leung 1; Claire Somogyi 1; Weidong Li 1; Nick Keener 1; Gang Huang 1; Izydor Apostol 1; Bramwell-German 2; Jennifer Van Eyk 1; Johns Hopkins University, Baltimore, MD; 2Department of Computer Science, ETH Zürich, Switzerland; 3Établissement Français du Sang Nord de France, Lille, France; 4Medical College of Wisconsin, Milwaukee, WI; 5Plasma Proteome Institute, Research Triangle Park, NC; 6Massachusetts General Hospital, Boston, MA.
WP 516 Novel Proteomics Approach for Absolute Quantification using Polytopeptides Containing a Reporter as Internal Standards: Yeoun Jin Kim; Elodie Duriez; Sebastien Gallien; Bruno Domon; Luxembourg Clinical Proteomics Center, Strassen, Luxembourg

WP 517 AQUA Strategy Applied to a Thermal Degradation Marker of Transfusion Plasma: Plasma Retinol Binding Protein 4; Latifa Richa; Alexa Ortiz; Cathy Lane; Carole Minisini; Christine Defer; Dominique Denis; Jean-Jacques Huart; Caroline Tokarski; Christian Rolando; 1Univ. de Lille 1, Sciences et Technologies, Villeneuve D’ascq, France; 2ABSCIEX, Warrington, England; 3Etablissement Français du Sang Nord de Lille, Lille, France

WP 518 The Generation and Application of Targeted Mass Spectrometry Assays to ~750 Human Transcription Factors and Regulatory Proteins: Andrew B. Stergachis; Kristen Lee; John A. Stamatoyannopoulos; Michael J. Maccoss; University of Washington, Seattle, WA

WP 519 Probing Mass Spectrometric Strategies for High Sensitivity Quantitation of Clinically Relevant Peptides: Sahana Mallah; Jeff Chisholm; Nevena Mollova; Kwan Leung; Claire Bramwell-German; 1AB SCIEX, Foster City, CA; 2Gilead, Foster City, CA

WP 520 Utilizing Oxidative Stress Modifications of Human Serum Albumin as Markers for Premyocardial Infarction Cardiac Ischemia; Christine A. Jelinek; Yan Jia; Rebekah L. Gundy; Jennifer VanEyk; Robert J. Cotter; 1Johns Hopkins School of Medicine, Baltimore, MD; 2Medical College of Wisconsin, Milwaukee, WI

WP 521 Quantification of Posttranslational Modifications in Recombinant Protein Using Stable Isotope Labeled Internal Standard and Mass Spectrometry: Quanzhou Luo; Xinhao Jiang; Xin Zhang; Shun Luo; Matt Jerums; Jeff Lewis; Nick Keener; Gang Huang; Izzyor Apostol; Jette Wypych; Amgen Inc, Thousand Oaks, CA

WP 522 Proteome Profiling and Quantification of Mouse Lipid Droplets by using 13C-labelled Quantitative Peptide Concatamers (qCAT): Chen Ding; Benny Hung; Jun Chang; Anna Malovannaya; Lan Li; Yi Shi; Yi Wang; Lawrence C B Chan; Jun Qin; Baylor College of Medicine, Houston, TX

WP 523 A Comparison of the Effects of Different Sample Matrices on Peptide Quantification by MRM: Thomas Y.K. Lau; Susan E. Abbatielo; Hasmik Keshishian; Keith D. Rivera; Steven A. Carr; Broad Institute, Cambridge, MA

WP 524 Evaluation of Protein-level Separation as Sample Preparation for Absolute Protein Quantification by LC-MS/MS: Carmen L. Fernandez-Metzler; Jeremy L. Norris; Chuck Witkowski; Richard King; PharmaCadence Analytical Services, LLC, Hatfield, PA; Protein Discovery, Inc., Knoxville, TN

WP 525 Assessment of Different Protein Digestion Protocols for Quantitative Mass Spectrometry: Timo Glatter; Christina Ludwig; Albert JR Heck; Alexander Schmidt; 1Biozentrum, University of Basel, Basel, Switzerland; 2Institute of Molecular Systems Biology, Zürich, Switzerland; 3Utrecht Institute for Pharmaceutical Sciences, Utrecht, Netherlands

WP 526 Application of Fast MS3 Scanning for Absolute Protein Quantification: Richard King; J. Larry Campbell; J.C. Yves Leblanc; Bruce Collings; Carmen L. Fernandez-Metzler; 1PharmaCadence Analytical Services, LLC, Hatfield, PA; 2AB SCIEX, Concord, ON

WP 527 Comparison of the Novel High Resolution MRMth Assay to the sMRM Assay for Quantifying the Dynamic Signalling Network of ShCa; Cunjie Zhang; Yong Zheng; Lorne Taylor; Karen Colwill; Tony Pawson; Mount Sinai Hospital, Toronto, Canada

WP 528 Utilization of IPG-IEF-LC-MS/MS to Characterize Proteomic Differencs Following Sibillin Treatment on Normal and Malignant Prostate Cells; Kristin West; Maureen Bunger; Nikhil Gare; Xinxin Zhang; Research Triangle Institute, Research Triangle Park, NC

WP 529 Differential Protein Expression in the Life Cycle of the Rice Blast Fungus Magnaporthe oryzae; Emine Gokce; William L. Franck; Yeen Yee Oh; Ralph A. Dean; David C. Muddiman; NCSU, Raleigh, NC

WP 530 Quantification of Collagen in Tissues Using Stable Isotope Labeling and LC-MS; Po-Chih Chang; Sin-Yi Chang; yen-Peng Ho; National Dong Hwa University, Hualien, Taiwan

WP 531 Quantification of eicosanoid Pathway Proteins in Human Cerebrospinal Fluid using a Dual Pressure Linear Ion Trap Mass Spectrometer; Roger G. Biringer; Julie Horner; Alfred Fonteh; Stephen Kaufman; Andreas Huhmer; August Specht; Michael Harrington; 1Thermo Fisher Scientific, San Jose, CA; 2Huntington Medical Research Institutes, Pasadena, CA

WP 532 Fourier Transform Ion Cyclotron Resonance Mass Spectrometry of Intact Heterogeneous Non-Covalent Protein Complexes; Weidong Cui; Hao Zhang; Michael L. Gross; Washington University, St. Louis, MO

WP 533 A Simple Electrostatic Model for the Fragmentation of Protein Complexes in the Gas Phase; Stephen Sculte; JiangJiang Liu; Lars Konermann; The University of Western Ontario, London, Canada

WP 534 MS-based Approaches to define Protein Interactions in Dynamic Systems: Application to Bacterial Circadian Clocks; Rebecca Rose; Utrecht University, Utrecht, Netherlands

WP 535 Characterization of Histone Multimers by ESI-MS; Shingo Shimoyama; Yuki Asano; Kyoei Takahashi; Hiroaki Tachiwana; Aritaka Nagadoi; Hitoshi Kurumizaka; Yoshifumi Nishimura; Satoko Akashi; 1Yokohama City University, Yokohama, Kanagawa, Japan; 2Waseda University, Tokyo, Japan

WP 536 Declustering of Protein Complexes by Trapping in the RF-ion Guide of a Hybrid Qq-
WP 558  LC Column Effects on Deuteron Back Exchange When Performing HDX Measurements;  Julie Cichelli;  Xin Zhu;  Susanne Moyer;  Joe Hedrick;  Agilent Technologies,  Wilmington, DE

WP 559  Methodological Advancements in Studying Proteins that Interact with Lipid Membranes;  Xiaomeng Tan;  Kasper Pedersen;  Mikiyung Kim;  Elias Reinhertz;  John Engen;  1Northeastern University,  Boston, MA;  2Swiss Institute of Bioinformatics,  Lausanne, Switzerland;  3Dana Farber Cancer Institute,  Boston, MA

WP 560  The Use of SFC/ESI/MS and SFC/APPI/MS for Structural Elucidation and Determination of Exchangeable Hydrogens Using Deuterated Modifiers;  Mark A. Olsen;  Kristin Krupa;  Catherine DeBrosse;  Emily Kordwitz;  Cephalon, Inc., Malvern, PA;  2University of Pittsburgh,  Pittsburgh, PA;  3Temple University,  Philadelphia, PA

WP 561  An Improved Measurement of the Isotopic Ratio by High Resolution Mass Spectrometry;  Sanae Ischenko;  Stephen Previs;  Rachid Ouali;  Nadia;  Mark Chance;  Takhar Kasumov;  Case Western Reserve University,  Cleveland, OH;  2Cleveland Clinic Foundation,  Cleveland, OH

WP 562  Pepsin-cotaining Nylon Membranes for Controlled Protein Digestion Prior to Analysis of Hydrogen/Deuterium Exchange by Mass Spectrometry;  Yujing Tan;  Xiao Zhou;  Merlin Bruning;  Michigan State University,  East Lansing, MI

WP 563  Probing Conformation and Dynamics of Large Disulfide-rich Proteins Using a Middle-down HDX/MS Approach: Elimination of Chemical Reduction and LC Separation;  Rinat R. Abzalimov;  Cedric E. Bobst;  Igor A. Kaltashov;  University of Massachusetts,  Amherst, MA

WP 564  Structurally Resolved Conformational Dynamics on the Millisecond Timescale Using a Microfluidic Device Incorporating TRESI, HDX and Rapid Proteolytic Digestion;  Tamanna Rob;  Derek Wilson;  York University,  Toronto, Canada

WP 565  Ion Mobility Enhanced Hydrogen-Deuterium Exchange Mass Spectrometry;  Michael Eggertson;  Keith Fadgen;  Martha Stapels;  John R. Engen;  Thomas Wales;  1Waters Corporation,  Milford, MA;  2Northeastern University,  Boston, MA

WP 566  High-throughput Flexible Automated Hydrogen/Deuterium Exchange Mass Spectrometry (DXMS) Sample Preparation/Processing Apparatus that has Produced Data for More than 52 Publications;  Sheng Li;  Tong Li;  Kossi Lekpor;  Yunan Miao;  Terry D Lee;  Virgil L Woods Jr.;  1University of California,  San Diego,  La Jolla, CA;  2Beckman Research Institute of the City of Hope,  Duarte, CA

WP 556  Software for Identification of Disulfide-Linked Peptides via CID and ETD of Mass Spectra and Protein Sequence Database;  Matthew Leitch;  Rovshan Sadygov;  Chen Li;  Shiaw-Lin Karon;  1Northeastern University,  Boston, MA;  2University of Texas Medical Branch,  Galveston, TX

WP 557  Protein Modification and Crosslinking of Allergens in Thermal Processing of Peanuts;  Christine M. Hebling;  Melinda A. McFarland;  Mark H. Ross;  John H. Callahan;  FDA-CFSAN, College Park, MD

WP 558  3D Protein Structure Through Chemical Cross-linking, H/D-exchange, Mass-spectrometry and Software-assistedModelling;  Morten Rasmussen;  Jan Refsgaard;  Li Peng;  Sanne Boet;  Sabine Amon;  Thomas Jørgensen;  Peter Hojrup;  1University of Southern Denmark,  Odense M, Denmark;  2Statens Serum Institut,  Copenhagen, Denmark;  3IMBB-FORTH, Heraklion, Greece

WP 559  Effect of Chemical Cross-Linking on Protein Structure Investigated by Travelling-Wave Ion Mobility Mass Spectrometry and Molecular Dynamics Simulations;  Fabio C Gozzo;  Alexandre F. Gomes;  Paulo C. T. Souza;  Munir S. Skaf;  IQ - University of Campinas, Campinas, Brazil

WP 560  Chemical Cross-linking and Mass Spectrometry applied to Structural Modeling of the Focal Adhesion Kinase and d8Crystalline Complex;  Alana Dos Reis Figueiredo;  Michelle Bueno de Moura Pereira;  Sean Mcllwain;  William Stafford Noble;  Kleber Gomes Franchini;  Fabio Cesar Gozzo;  1State University of Campinas, Campinas, Brazil;  2Brazillian National Laboratory of Synchrotron Light, Campinas, Brazil;  3Dep. of Genome Sciences, University of Washington, Seattle, WA

WP 561  Chemical Cross-linking Coupled to Mass Spectrometry Applied to the Characterization of the Interaction Region in EBM-Myosin Complex;  Mariana Fioramonti;  Alina Mara Santos;  Kleber Gomes Franchini;  Fabio Cesar Gozzo;  1State University of Campinas, Campinas, Brazil;  2Brazilian National Laboratory of Synchrotron Light, Campinas, Brazil

WP 562  The Designed Peptide that has the Difficult Sequence Showed Different Mass Spectra among Different Instruments;  Akiyoshi Hirata;  Takeshi Kasama;  Ruediger Pipkorn;  Kiyoshi Nokihara;  1HiPep Laboratories,  Kyoto, Japan;  2Tokyo Medical and Dental University,  Tokyo, Japan;  3German Cancer Research Center (DKFZ), Heidelberg, Germany

WP 563  Identification of Disulfide-bridges in Human Serum Proteins Using Mass Spectrometry and Concatenated Peptide Databases;  Stephanie Maniatis;  Karin Green;  John D. Leszyk;  Scott A. Shaffer;  University of Massachusetts Medical School, Worcester, MA

WP 564  Reactivity, Mechanism and Stability of the Formaldehyde Cross-linking Reaction of Proteins Revealed by Mass Spectrometry-based Studies;  Xuan Ding;  Savita Srinivasan;  2Agilent Technologies,  Wilmington, DE

WP 565  A Simple Measure to Monitor the Progress of Chemical Cross-linking of Protein-protein Noncovalent Interactions;  Stefanie Maeder;  Ruizhu Huang;  Elisabetta Boeri Erba;  Renato Zenobi;  ETH Zurich,  Zurich, Switzerland

WP 566  Mass Spectrometric Characterization of Gelsolin and Its Interacting Domains;  Gwenaël Pottie;  Arielle Burns;  Nicole Haverland;  Wojciech Rozek;  Paweł Ciborowski;  University of Nebraska Medical Center, Omaha, NE
Jürgen Kast; The University of British Columbia, Vancouver, Canada

WP 578 Structure and Organization of Small Heat Shock Protein-Substrate Complexes Investigated by Cross-linking and Mass Spectrometry; Heather O'Neill; Wenzhou Li; Vicki Wysocki; Elizabeth Vierling; University of Arizona, Tucson, AZ; University of Massachusetts, Amherst, MA

WP 579 An Enhanced Protein Crosslink Identification Strategy using CID-Cleaveable Chemical Crosslinkers and LC/MS; Fan Liu; Cong Wu; Jonathan Sweedler; Michael Goshe; NC State University, Raleigh, NC; University of Illinois, Urbana-Champaign, IL

WP 580 Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-linked Peptides using Tandem Mass Spectrometry; Xiuxia Du; UNC-Charlotte, Kannapolis, NC

WP 581 Structural Studies of sBBI/Trypsin Non-Covalent Complex using Cross-linking Reactants; Ekaterina Daril; Guanalin Saravanamuthu; Jean-Claude Tabet; Ivo G. Gut; CEA/IG/CNV, Evry, France; CNAG, Barcelona, Spain; Université Paris 6 (UPMC), Paris, France

WP 582 Intra- and Inter-Molecular Cross-Linking of Peptide Ions in the Gas-Phase Using N-hydroxysulfosuccinimide Based Reagents; Marija Mentinova; Scott A. Mcluckey; Purdue University, West Lafayette, IN

WP 583 Estimation of False Discovery Rates in Cross-linking Datasets; Thomas Walzthoeni; Alexander Lettmann; Franz Herzog; Friedrich Förster; Manfred Claassen; Martin Beck; Ruedi Aebersold; Institute of Molecular Systems Biology, Zurich, Switzerland; Max Planck Institute of Biochemistry, Munich, Germany; European Molecular Biology Laboratory, Heidelberg, Germany

WP 584 Structural Analysis of a Prokaryotic Ribosome using a Novel Aminating Cross-Linker; Matthew Lauber; James P. Reilly; Indiana University, Bloomington, IN

WP 585 Preferential Cleavage of Diethyl Suberthioimidate (DEST) Cross-linked Peptides and Its Application in Identification of Cross-linking Products by Tandem MS; Yi Hg; Matthew Lauber; James P. Reilly; Indiana University, Bloomington, IN

WP 586 Identification of Specific Glutamine Acceptor Sites and Lysine Donor Sites Involved in Fibrin Cross-Linking; Weixun Wang; Merck Research Labs, Rahway, NJ

WP 587 Sampling the Topography of Multiprotein Complexes by Reductive Akylation Crosslinking in Conjunction with High Resolution ETD-MS/MS Analysis; Michael Trnka; Peter R Baker; A.L. Burlingame; University of California San Francisco, San Francisco, CA

WP 588 Mass Spectrometric Strategies for Improved Identification of Cross-linked Peptides; Pragya Singh; Richard A. Pfluetzer; Samuel I. Miller; David R. Goodlett; University of Washington, Seattle, WA

WP 589 Development of an LC-MS Method for the Quantitation of Pancreatic Cancer Biomarkers in Human Serum; Angela Y Wehr; Kenneth Yu; Jan A. Blair; University of Pennsylvania, Philadelphia, PA; Memorial Sloan-Kettering Cancer Center, New York, NY

WP 590 The Development of Rapid Diagnostic Approaches for the Characterisation of Hemoglobin Disorders; Krisztina Rady; Charlotte A. Scarff; Susan E. Slade; Nisha A. Patel; James H. Scribens; University of Warwick - Life Sciences, Coventry, UK

WP 591 Comparison of Label-free Strategies for Quantifying Proteins from Diseased Human Brain Tissue; James A Atwood III; Laura Donovan; Marla Gearing; Allan Levy; James Lah; Nicholas Seyfried; Archer Smith IV; D Brent Weatherly; Paul L. Sipes; Inc, Bogart, GA; Emory University, Atlanta, GA; University of Georgia, Athens, GA

WP 592 Relative Quantification of Glycation Sites in Human Serum Albumin by 18O Labeling and MALDI-TOF MS; Omar Barnaby; Ronald L. Cerny; David Hage; Saint Louis University, St. Louis, MO; University of Nebraska - Lincoln, Lincoln, NE

WP 593 Novel, Efficient and Sensitive Method for Protein Recovery from Laser Capture Microdissected Cells Isolated from Formalin Fixed Paraffin Embedded Biopsies; John Shapiro; Mary Severin; Gerard Lozanski; Michael A. Freitas; Ohio State University, Columbus, OH

WP 594 A Novel Approach for Characterization of Histone Isoform Distribution Across Cellular Compartments; Sean W. Harshman; Amy J. Johnson; John C. Byrd; Michael A. Freitas; Ohio State University, Columbus, OH

WP 595 A Mass Spectrometry-Based Quantification Method for the Detection of Bound and Free Therapeutic Antibodies in Patient Serum Samples; Cornelia Koy; Metin Konus; Peter Lorenz; Susanne Drynda; Joern Kekow; Hans-Juergen Thiesen; Michael O. Glöcker; Proteome Center Rostock, Rostock, Germany; Institute of Immunology, University of Rostock, Rostock, Germany; Clinic of Rheumatology, University of Magdeburg, Germany

WP 596 Development of a Mass Spectrometry-Based Assay for Measurement of Angiotensin I and Plasma Renin Activity to Diagnose Secondary Hypertension; Jennifer D. Reid; D. Randal Mason; Carol E. Parker; Daniel T. Holmes; Christoph H. Borchers; UVic Genome BC Proteomics Centre, Victoria, Canada; St. Paul’s Hospital, Vancouver, Canada

WP 597 Biosynthetic Concatenated Labeled Peptides are Useful Alternatives to Whole Labeled Proteins: Human Serum Albumin as a Case Study; Jacqueline Cole; Dhaval Nanavati; Cai Chen; Brian Martin; Anthony J. Makusky;
WP 599 Quantilabel-free Method of Proteomic Profiling to Detect Novel Proteins for Systemic Lupus Erythematosus (SLE) Kidney Damage during Disease Flaring: [In vivo] Qb; Hermine Brunner; Michael Bennett; Prasad Devarajan; Shannen Nelson; Prasad Devarajan; John Schlager; Pavel Shiyavon; 1HIF - 711HPW/RHPB, US Air Force Research Lab, Wright-Patterson Air Force Base, OH; 2Cincinnati Children’s Hospital Medical Center, Cincinnati, OH

WP 600 Developing System Suitability Criteria and Evaluation Methods for Proteomics Experiments: Daniela Tomazela; Jesse D. Canterbury; Gennifer Merrihew; Brendan Maclean; Michael J. Maccoss; University of Washington, Seattle, WA

WP 601 Predicting Treatment-Response for HCV Therapy: Successful Translation from Discovery LC/MS to Verification LC/MRM: Laura G. Dubois; J. Will Thompson; Joseph E. Lucas; Keyur Patel; Jeanette McCarthy; M. Arthur Moseley; 1Duke University School of Medicine, Durham, NC; 2Duke Clinical Research Institute, Durham, NC

WP 602 Human Growth Hormone Quantitation In Serum By Isoform Ratio Analysis Using Nanoparticle Capture/Multiple Reaction Monitoring-Mass Spectrometry: Paul Russo; Taha Rezaei; Amol Prakash; Mary F Lopez; Davide Tamburro; Claudia Fredolini; Lance Liotta; Emanuel Petricoin; George Mason University, Manassas, VA; 2Thermo Scientific BRIMS, Boston, MA

WP 603 Analysis of Esophageal Inflammation using a Novel Proteomics-Based Approach: Karen Jonscher; Agnieszka Kendrick; Sophie Fillon; Zachary Robinson; Joanne Masterson; Steven Ackerman; Glenn Furuta; 1University of Colorado Denver, Aurora, CO; 2University of Illinois at Chicago, Chicago, IL; The Children’s Hospital, Aurora, CO

WP 604 Global and Pulsed SILAC in the Elucidation of the Effects of Sunitinib, a Multi-targeted Receptor Tyrosine Kinase Inhibitor: Robert Li Graham; Michael J Sweredoski; Sonja Hess; CalTech, Pasadena, CA

WP 605 Identification and Affinity Characterization of Lactose Binding Epitopes in Rat gαlectin-5 by Proteolytic excision- MS and Bioaffinity Analysis: Frederike Eggers; Adrian Moise; Michael Przybylski; University of Konstanz, Konstanz, Germany

WP 606 Using Cysteinyl-Peptide Capture to Increase the Depth of Coverage in Protein Expression Analysis: Christie Hunter; Vojtech Tambor; Juraj Lenco; Sean L. Seymour; Lydia Nyuyvayis; Marian Kacerosky; AB SCiEX, Foster City, CA; 2University of Defence, Hradec Kravale, Czech Republic; 3University Hospital, Hradec Kravale, Czech Republic

WP 607 Exploring Nucleotide-binding Proteins at the Whole Proteome Scale using Affinity-labeled Nucleotide Probes: Yongsheng Xiao; University of California, Riverside, Riverside, CA

WP 608 Improved Experimental Protocols and Data Analysis Tools for High-Throughput Protein Complex Identification in Bacteria Using a Quantitative ‘Tagless’ Strategy: Haichuan Liu; Ming Dong; Lee L Yang; Maxim Shatsky; Megan Choi; Nikita Kharina; Maria Limon; Evelin D Szakal; Steven C Hall; Susan J Fisher; Terry C Hazen; Jil T Geller; Mary E Singer; John-Marc Chandonia; Jian Jin; Mark D Biggin; H Ewa Witkowska; University of California at San Francisco, San Francisco, CA; Lawrence Berkeley National Laboratory, Berkeley, CA; 2University of California at Berkeley, Berkeley, CA; 3Consultant, Framingham, MA

WP 609 Peptide Enrichment in Protein Complex Cross-Linking Analysis of a Model Homodimeric Protein Using Mass Spectrometry: Funing Yan; Fa-Yun Che; Edward Nieves; Louis Weiss; Ruth Hogue Angeletti; Andras Fiser; Albert Einstein College of Medicine, Bronx, NY; 2Albert Einstein College of Medicine, Bronx, NY

WP 610 Isolation, Characterization, and Imaging Analysis of Human Mediator Complexes Using HaloTag Technology: Danette Daniels; Richard Jones; David Allen; Ravi Amunugama; Michael Ford; Nancy Murphy; Marie Schwinn; Jacqui Mendez; Helene Benink; Marijeta Urb; MS Bioworks, LLC, Ann Arbor, MI; Promega Corporation, Madison, WI

WP 611 Knock-in AP-MS for Sensitive Identification of Protein Complexes at Physiological Levels: Jing Song; Zhanwen Du; Yujun Hao; Zhenghe Wang; Rob Ewing, Case Western Reserve University, Cleveland, OH

WP 612 Tagging Lysine with N-Acetyl Dipeptides for Quantification of Proteins Using High-Mass Isotope-Coded Signals: Seung Koo Shin; Jongcheel Seo; Hye-Joo Yoon; POSTECH, Pohang, South Korea

WP 613 A Versatile, Multiplexed, Mass Spectrometry Based, in vitro Assay for Measuring Protease Activities: Fiona F McCullister; Ryan Kunz; Woong Kim; Stephen Gygi; Harvard Medical School, Boston, MA

WP 614 MS Strategy for Protein-Ligand Binding Analysis Using An Isotope Labeling Technique: Hai-Tsang Huang; Patrick D. DeArmond; Graham M. West; Michael C. Fitzgerald; Duke University, Durham, NC

WP 615 Profiling the Serine Hydrolase Superfamily using Activity-based Probes: Ryan Bomgarden; Rosa Viner; Chris Etienne; John C. Rogers; 1Thermo Fisher Scientific, Rockford, IL; 2ThermoFisher Scientific, San Jose, CA

WP 616 Identifying Specific Protein-substrate Interactions by a Comparative IP and Enzymatic Approach: John Paul Savary; Mark White; Thomas Zahrt; Brian Halligan; Scott Terhune; 1Medical College of Wisconsin, Milwaukee, WI; 2Biotechnology and Bioengineering Center, Milwaukee, WI; 3Center for Infectious Disease Research, Milwaukee, WI

WP 617 Protein Cleavage, Disulfide Bonds Reduction, Signal Enhancement and More using Electrochemistry/MS: Jean-Pierre Chervet; 1
WP 620 A Novel Recombinant Lys-C Protease for Proteomic Sample Preparation; Sergei S. Savelyev; James R. Hartnett; Rebecca L. Godat; Alexander S. Hebert; Joshua J. Coon; Marjeta Urh; Promega Corporation, Madison, WI; UW-Madison, Madison, WI

WP 621 The Optimization of Protein Digestion Methods using Trypsin or LysC or Both for Decision-Tree Driven MS/MS; Junjie Hou; Laurence M. Brill; Sanford-Burnham Medical Research Institute, San Diego, CA

WP 622 A Replaceable Microreactor for On-line Protein Digestion in a Two-dimensional Capillary Electrophoresis System with Tandem Mass Spectrometry Detection; Yihan Li; University of Notre Dame, Notre Dame, IN

WP 623 Development of Immobilized Pepsin Microreactor for Rapid Protein Identification by Hydrogen/Deuterium Exchange and NanoElectrospray Mass Spectrometry; Ying Long; Troy Wood; SUTF at Buffalo, Buffalo, NY

WP 624 A Microfluidic Cell Culture Chip for Proteomics; Pratap Reddy Machavaram Siva; Steven A. Soper; Kermit K. Murray; Louisiana State University, Baton Rouge, LA

WP 625 Thermal Degradation Products of Phosphopeptide; Lian Li; Franco Basile; University of Wyoming, Laramie, WY

WP 626 Formation of Cross-Linked Products during the Pyrolysis of Peptides; Chenglin Li; Franco Basile; University of Wyoming, Laramie, WY

WP 627 Selective Exploration of Protein Phosphorylation, Glycosylation and Disulfide Bridges by Mass-Pair Detection; He-Hsuan Hsia; Hsin-Yu Hsieh; Henning Urlaub; 1Biological Mass Spectrometry Group, MPIbpc, Goettingen, Germany; 2Genomics Research Center, Academia Sinica, Taipei, Taiwan

WP 628 Optimization of Parameters for Coverage of Low Molecular Weight Proteins; Stephan Müller; Tibor Kohajda; Sven Findeiß; Peter F. Stadler; Stefan Waschet; Manolis Kellis; Martin von Bergen; Stefan Kalkof; Heilmoltz-Centre UFZ, Leipzig, Germany; 2University Leipzig, Leipzig, Germany; 3Massachusetts Institute of Technology, Cambridge, MA

WP 629 A New High Capacity MALDI Target Format for Improved LC-MALDI Analysis of Complex Proteomics Samples; Arndt Asperger; Martin Schurenberg; Detlev Suckau; Marcus Macht; Bruker Daltonik GmbH, Bremen, Germany

WP 630 Comparison between Different Extraction Methods in Spirulina Maxima Using a Proteomics Approach; Hee-Joung Lim; Jong Kim; MJoung Kim; Jee Young Lee; Bora Kim; Na-Young Han; Tran Huyen Trang; JIn Hyun Jun; Joong-Hoon Kim; HooKeun Lee; Hee-Gyoo Kang; 1Eulji University, Sungnam, South Korea; 2Korea University, Seoul, South Korea; 3Gachon University, Incheon, South Korea; 4Kanso Co. Ltd, Sungnam, South Korea

WP 631 An Automated Serum Depletion Process Designed to Inject and Fractionate Samples Using a Commercially Available HPLC System; Eric Bell; Dariusz Janecki; Steven C. Pomerantz; Jennifer F. Nemeth; Centocor R&D, a division of J&JPRD LLC, Radnor, PA

WP 632 Plasma Protein Fractionation by Semi-Selective Precipitation at Different pH for Increased Proteome Coverage; Ekaterina Mostovenko; Hannah C Scott; Andre M Deelder; Magnus Palmblad; 1Leiden University Medical Center, Leiden, Netherlands; 2Leiden University, Leiden, Netherlands

WP 633 Accurate Quantitative Determination of the Reproducibilities and Efficiencies of Cartridge and Column-based Depletion Methods for Plasma Proteins using Multiplexed MRM; Alexander G Camenzind; Monica H Elliott;ensburg Yang; Angela M Jackson; Derek Smith; Christoph H Borchers; UVIC Genome BC Proteomics Centre, Victoria, BC

WP 634 Use of Enrichment and Depletion Approaches to Increase Serum Proteome Coverage in Quantitative Proteomics Experiments; Min-Sik Kim; Nandini A. Sahasrabuddhe; Julie Wight; Akhilesh Pandey; Johns Hopkins University, Baltimore, MD; 1Institute of Bioinformatics, Bangalore, India; 2Agilent Technologies, Columbia, MD

WP 635 Investigation of Denaturants on Digestion Efficiency and Reproducibility: What are the "Best" Digestion Conditions? James Markell; Susan E. Abbatil; Corbin Whitwell; Lisa Zimmerman; Paul Rudnick; Stephen Stein; Birgit Schilling; Steven C. Hall; Steven A. Carr; Broad Institute of MIT and Harvard, Cambridge, MA; 2Vanderbilt University, Nashville, TN; NIST, Gaithersburg, MD; 3Buck Institute for Research on Aging, Novato, CA; 4UCSF Sandler-Moore Mass Spectrometry Core Facility, San Francisco, CA

WP 636 The Use of Mass Spectrometry Combined with mTRAQ™-Labelled Surrogate Standards to Compare Enrichment Strategies for Target Peptides in Plasma; David N. Potter; John R. Griffiths; Richard D. Unwin; Ralf Hoffmann; Anthony D. Whetton; The University of Manchester, Manchester, UK; 2Paterson Institute for Cancer Research, Withington, UK; 3Central Manchester University Hospitals NHS Foundation, Manchester, UK; 4Philips Research, Eindhoven, The Netherlands

WP 637 Investigation of Proteins that Accumulate during Blood Storage using a Label-free Semi-quantitative Mass Spectrometry Based Approach; Monika Dzieciatkowska; Marguerite Kelher; Christopher Silliman; Anirban Banerjee; Kirk Hansen; University of Colorado Denver, Denver, CO; 2Denver Health Medical
WEDNESDAY POSTERS

WP 638 Monitoring Plasma and Serum Integrity Using Quantitative Mass Spectrometry; Maria Hassis; Miles Braten; Matthew Albertolle; Jennifer Adibi; Richard Niles; Susan Fisher; Katherine Williams; UCSF, San Francisco, CA

WP 639 Systematic Identification of Alternative Fractionation Methods for Biomarker Discovery and Targeted Quantitative MRM Analysis using Human Plasma; Zhijun Cao; Hsin-Yao Tang; Tony Chang-Wong; Lynn A. Beer; Nicole Gorman; Won-A Joo; Huan Wang; David W. Speicher; The Wistar Institute, Philadelphia, PA

WP 640 Quantitative Plasma Proteome Profiling to Understand Age-related Effects in Sepsis Patients; Zhivun Cao; Sachin Yende; John A. Kellum; Rena A. S. Robinson; University of Pittsburgh, Pittsburgh, PA

WP 641 Highly Multiplexed MRM Assay for the Rapid Profiling of 158 Plasma Proteins per Run using an Agilent 6490 TQMS; Angela M Jackson; Juncong Yang; Tyra J Cross; Alexander G Camenzind; Dominik Domanski; Alexander Smith; Leigh Anderson; Christoph H Borchers; UVic GBC Proteomics Centre, Victoria, BC; Plasma Proteome Institute, Washington, DC

WP 642 Rapid Data-independent Acquisition for Protein Identification from Immunodepleted Human Sera; Karin Giron; Stephanie Mathis; Andre Kopoyan; Scott A. Shaffer; University of Massachusetts Medical School, Worcester, MA

WP 643 Establishing Quality Control Metrics for Immunodepletion of High-abundance Plasma Proteins and Applying to a Large Clinical Cohort; Meredith Turner; Erik J. Soderblom; J. Will Thompson; Laura G. Dubois; M. Arthur Moseley; Duke University School of Medicine, Durham, NC

WP 644 Global Proteome Dynamics through 2H-metabolic Labeling; Ling Li; Cleveland Clinic Foundation, Cleveland, OH

WP 645 Search for novel Chemical Warfare Agents Exposure Biomarkers using LC-MS/MS; Koichiro Tsuge; Mieko Kanamori-Kataoka; Isaac Ohawa; Takafumi Sato; Takeshi Ohmori; Yasuo Seto; Nat. Res. Inst. of Police Science, Kashiwa, JAPAN

WP 646 Hemoglobin: 5-hydroxymethylfurural Adducts Top-down and Bottom-up Study; Gerhard Kummerow; Maria Osipina; Hubert Vesper; Centers for Disease Control and Prevention, Atlanta, GA

WP 647 Brain Nitrosative Stress in Second Hand Smoke Rat Model; Joy Guingab; Firas Kobaissy; Stanley M. Stevens, Jr.; John Anaghi; Kevin Wang; Banyan Biomarkers, Inc., Alachua, FL; University of South Florida, Tampa, FL

WP 650 Fatty Acid Ratio as a Potential Biomarker in Identification of Lard Using Gas Chromatography-Mass Spectrometry (GC-MS); Che Ninh Binti Man; National Poison Centre, Penang, Malaysia

WP 651 Comparison of Chicken Light and Dark Meat using LC MALDI Mass Spectrometry as a Model System for Biomarker Discovery; Jie Du; Stephen J. Hattan; Kenneth Parker; VIC Instruments Corporation, Sudbury, MA

WP 652 Enhanced Tryptic Digestion in under 10 Minutes using AFA Technology; Isa Isaac; William K. Russell; David H. Russell; Covaris, Inc., Woburn, MA; Texas A&M University, College Station, TX

WP 653 MALDI-FTICR-MS Precision Profiling of Human Serum Peptides; Simone Nicolardi; Yuri E.M. Van Burgt; Magnus Palmblad; Rob A.E.M. Tollenaar; André M. Deelder; Leiden University Medical Center, Leiden, Netherlands

WP 654 Identification of DNP Metabolites for Exposure Marker Discovery using in vitro/in vivo Metabolism and Signal Mining Strategy with LC-MS Data; Pao-Chi Liao; Jing-Fang Hsu; Li-Wen Peng; National Cheng-Kung Univ., College of Medicine, Tainan, TAIWAN

WP 655 Selective Enrichment and Sensitive Detection of Peptide/Protein Biomarkers in Human Serum Using Polymeric Reverse Micelles and MALDI-MS Analysis; Nadnudda Rodthongkum; Rajasekharreddy Ramireddy; Sankaran Thayumanavan; Richard Vachet; University of Massachusetts, Amherst, MA

WP 656 New Isoforms of HDL apolipoprotein C-1 In Individuals with Coronary Heart Disease; Ronald D. Macfarlane; Texas A & M University, College Station, TX

WP 657 Development of an Internal Standard for Studies of Human Plasma by Label Free Quantitative Analysis; Timothy Radabaugh; Haili Xu; George Tsapralis; Zhenqiang Lu; Junmei Liu; Dean Bilheimer; Donata Vercelli; Marilyn Halonen; Serrine S Lau; Southwest Environmental Health Sciences Center, Tucson, AZ; Dept. of Pharm/Tox, College of Pharmacy, Tucson, AZ; Statistics Consulting Laboratory, Tucson, AZ; Dept. of Pharmacology, Tucson, AZ; Arizona Respiratory Center, Tucson, AZ; Arizona Center for the Biology of Complex Disease, Tucson, AZ; Dept. of Agricultural and Biosystems Engineering, Tucson, AZ; Center for Toxicology, The University of Arizona, Tucson, AZ

WP 658 Integrative Effects of Precursor Ion Exclusion and Multi-Dimensional Fractionation on In-Depth Identification of Plasma Biomarkers; Wells W. Wu; Rong-Fong Shen; Josephine M. Egan; Luigi Ferrucci; Sung-Soo Park; Yu Zhou; Stuart Maudsley; Bronwen Martin; NIH (NIA), Baltimore, MD
WP 659 Proteomic Analysis of ePTF-Collected Pancreatic Fluid to Investigate Chronic Pancreatitis; Joao Paulo1,2; Peter Banks1; Darwin Conwell1; Hanno Steen1,3; 1Harvard Medical School/Brigham & Women’s Hospital, Boston, MA; 2Pancreas Center at Children’s Hospital Boston, Boston, MA; 3Harvard Medical School/Children’s Hospital Boston, Boston, MA

WP 660 From SHOTGUN to SNIPER – Pipeline for Discovery and Validation of Human Wound Fluid Biomarkers; Christoph Kriso1,2; Matthew McKay1; Dirk Wolters1; Mark Mollov1,2,3; 1Ruhr University Bochum, Bochum, Germany; 2Macquarie University, Sydney, Australia; 3APAF, Sydney, Australia

BIOMARKERS: QUANTITATIVE ANALYSIS

WP 661 Aqueous Normal Phase LC/QqQ MS Quantification of Protein-bound Chlorotyrosine and Nitrotyrosine in the Colon Tissue of Rag2-/- Hh Mouse; Yu Zeng1; John S. Wishnok2; James Fox3; Steve Tennenbaum1,3; 1Department of Biological Engineering, MIT, Cambridge, MA; 2Division of Comparative Medicine, MIT, Cambridge, MA; 3Department of Chemistry, MIT, Cambridge, MA

WP 662 High-Throughput Ultra-Performance Liquid Chromatography/Tandem Mass Spectrometry Quantification of Endogenous Adrenal Steroids in Biological Samples; Yongxin Zhu1; Bristol-Myers Squibb Company, Princeton, NJ

WP 663 Ultra Sensitive Measurement of Epinephrine and Norepinephrine in Human Plasma using LC/MS/MS; Guodong Zhang1; Zhaosheng Lin2; Yizhong Zhang3; Chengjie Ji4; Thomas McDonald4; Justin Walton1; Rick Steenwyk1; Pfizer Inc., East Lyme, CT

WP 664 LC-MS Quantitative Analysis of Acylcarnitines in Serum from Mice Dosed with Acetaminophen; Lisa Pence1; Shubhra Chaudhuri1,2; Laura James1,2; Sandra McCullough1,2; Rick Beger1,2; 1FDA-National Center for Toxicological Research, Jefferson, AR; 2University of Arkansas for Medical Sciences, Little Rock, AR; 3Arkansas Childrens Hospital, Little Rock, AR

WP 665 Determination of Low Levels of 1H-labeling using High-resolution Mass Spectrometry (HR-MS): Application in Studies of Lipid Flux and Beyond; Kithsiri Herath1; Jiong Yang2; Wendy Zhong1; Alison Kulick1; Rory Rohm1; Michael Lassman3; Jose Castro-Perez1; Abllat Mahsud2; Keiana Dunn1; Douglas Johns1; Stephen Previs1; Brian Hubbard1; Thomas Roddy1; Merck & Co., Inc., Rahway, NJ

WP 666 Detection of Phosphatidylethanol Homologues in Liver Samples as Biomarkers for Alcohol Treated Rats and Mice; Simon Ashton; Neil J Loftus1; Alan Barnes1; Filippos Michopoulos1,2,3; Ian D. Wilson1; Georgios Theodoridis4; Cheng Ji3; Neil Kaplowitz3; 1Shimadzu, Manchester, UK; 2Astra Zeneca, Alderley Park, Cheshire, UK; 3University of Thessaloniki, Thessaloniki, Greece; 4University of Southern California, Los Angeles, CA

WP 667 Determination of an Endogenous Biomarker - 4β-Hydroxycholesterol - in K562 Human Plasma by LC/MS/MS; Weisheng Lin1; Wei Zhang1; Jing Ke1; Harry Hao1; Zhongping (John) Lin1; Mike-Qingtao Huang2; Naidong Weng3; 1Frontage Laboratories, Malvern, PA; 2Johnson & Johnson Pharmaceutical R & D, LLC, Raritan, NJ

WP 668 Validation of 25-Hydroxyvitamin D3 an Endogenous Biomarker in Human Serum using LC/APCI/MS/MS; Themis Flarakos; Marie-Noelle Lepage; Lorella Di Donato; CIRION Clinical Trial Services Inc., Cambridge, Canada

WP 669 Quantification of LTE4 in Human Urine with a 2 pg/mL LLOQ using a UPLC and LC/MS/MS; Lin Tan1; Troy Voelker1; Katherine Wright2; Joe Palandra2; 1Tandom Labs, Salt Lake City, UT; 2Pfizer, Andover, MA

WP 670 Determination of Dopamine, Serotonin and their Metabolites in the Striatum Tissues from Rat and Mouse Brain Using UPLC-MS/MS; Changyu Quang1; Alison E. Johnson1; Nichole R. Myers1; William C. Nethero1; Melissa J. Beck1; Farhad Sayyarpour2; Kuldip D. Dave2; 1WIL Research, Ashland, OH; 2The Michael J. Fox Foundation, New York, NY

WP 671 An Ultra-sensitive and Simple Approach to Analyze Biomarker-Aldeosterone in a Super Micro-volume of Rat Plasma at Low Picogram; Ilonogiwei Pan1; Bibo Xu2; Primera Analytical Solutions Corp., Princeton, NJ

WP 672 Quantification of Thyroxine (T4) in Dried- serum Spots by Tandem Mass Spectrometry; Victor De Jesus2; Donald H. Chace3; Elizabeth Hall1; Tamara Ganka1; Shannon O’Brien1; Joanne Mei1; Carlotta Cuthbert2; 1Centers for Disease Control and Prevention, Atlanta, GA; 2Pediatric Analytical, Pittsburgh, PA

WP 673 Quantifying Glutathione as a Urinary Biomarker; Charmion Cruickshank; Troy Wood; University at Buffalo, Buffalo, NY

WP 674 Quantification of 2-Hydroxyglutarate in Patients with Glioblastoma by Stable Isotope Dilution Mass Spectrometry; Christopher D. Ryals; Guodong Zhang1; Zhaosheng Lin2; Yizhong Zhang3; Chengjie Ji4; Thomas McDonald4; Justin Walton1; Rick Steenwyk1; Pfizer Inc., East Lyme, CT

WP 675 Pseudo-SRM Conditions Improve Detection of Aβ3-ethenoarginine in DNA; Esra Mutlu1; Leonard Collins1; Matthew Stout2; Patricia Upton1; Laura Daye1; Darrell Winsett1; Gary Hatch1; Paul Evansky2; James Sweeney1; 1UNC - Chapel Hill, NC; 2USEPA NHEERL, Research Triangle Park, NC

WP 676 Organ- and Lesion-dependent Biases in the Spectrum of Inflammation-induced DNA Damage in Colon and Liver from Helicobacter hepaticus-infected Rag2-deficient Mice; Wenjie Ye1; Aswin Mangerich2; James Fox1,3; Peter Dedon1,3; Steven Tennenbaum1,3; Koli Taghizadeh1; Erin Prestwich1; John Wishnok1; Liang Cui4; 1Department of Biological Engineering, MIT, Cambridge, MA; 2Division of Environmental Health Science, MIT, Cambridge, MA; 3Division of Comparative Medicine, MIT, Cambridge, MA; 4SMART Centre, MIT, Singapore, Singapore

WP 677 Development of HILIC/MS/MS Method for Simultaneous Measurement of Tobacco-specific Nitrosamines 4-(methylamino)-1-(3-pyridyl)-1-butanol (NNAL) and Its Glucuronide NNAL-Glucuronide; John Lee1,2; Lijuan Peng3; Robert Turesky1; Todd M. Layne2; Nathanols 3; 1Centers for Disease Control and Prevention, Atlanta, GA; 2Battelle, Columbus, OH; 3Applied Research and Innovation Services, North Carolina State University, Raleigh, NC
WP 678 Quantification of F2-isoprostanes in Urine by a Liquid Chromatography Tandem Mass Spectrometry (LC-MS/MS) Method; Alireza Arabshahi; Jeevan K. Prasain; Scott Sweeney; Doyle Ray Moore II; Stephen Barnes; University of Alabama at Birmingham, Birmingham, AL

WP 679 Quantification of Reduced and Oxidized Glutathione without Calibration Curves by LC/MS/MS using Speciated Isotope Dilution Mass Spectrometry; Timothy Fahrenholz; Scott Faber; Hemasudha Chatragadda; Yosip Pineda; John Kern; Matt Pamukcu; H. M. Skip Kingston; 1Duquesne University, Pittsburgh, PA; 2The Children’s Institute, Pittsburgh, PA; 3Applied Isotope Technologies, Sunnyvale, CA

WP 680 Identification and Characterization of Serum Albumin Adducts of 2-Amino-1-methyl-6-phenylimidazo[4,5-b]pyridine by Ultra Performance Liquid Chromatography/Mass Spectrometry; Julian Peng; Robert Turesky; Wakewood Center, NYS Department of Health, Albany, NY

WP 681 Single Extraction Multicolumn LC-MS Analysis for Quantitation of Chemically Diverse Biomarker Candidates of Insulin Resistance; Klaus Peter Adam; Andrew Thompson; Walter Gail; Matthew Mitchell; Michael Milburn; John Ryals; Metabolon Inc., Durham, NC

WP 682 Development of a LC/MS-Based Assay for Simultaneous Analysis of Corticosterone and Drug Molecules and the Application in PK/PD Studies; Yu Tian; Youngjae Kim; Rachel Twomey; Li Chun Wang; Kevin Cusack; Robert Stoffel; Lisa Olson; Roderic Cole; Abbott Laboratories, Worcester, MA

WP 683 Determination of 2-Hydroxyglutarate in Glioma Primary Cell Cultures by HPLC-MS/MS Using In-Line SAX Coupled with Ion Pair Reverse Phase Chromatography; Melissa D. Carter; M. Wade Calcutt; J. Gerardo Valadez; Vandana K. Grover; Sunday A. Abiria; Michael K. Cooper; David L. Hachey; Vanderbilt University, Nashville, TN

WP 684 Reproducibility of Comprehensive Two-dimensional Gas Chromatography Mass Spectrometry; Aijin Fang; Xiang Zhang; University of Louisville, Louisville, KY

WP 685 High-throughput Determination of Urea and Glucose in Serum Samples by High Performance Liquid Chromatography Tandem Triple Quadrupole Mass Spectrometry; Xiaorong Ran; Tao Bo; Agilent Technologies (China), Beijing, CHINA

WP 686 Liquid Chromatography-Mass Spectrometry of Pre-ionized Girard P Derivatives for Quantifying Estrone and its Metabolites in Postmenopausal Women’s Serum; Kannan Rangiah; Sumit Shah; Eugene F. Ciccirmino; Anil Vachani; Clementina Mesaros; Ian A. Blair; 1University of Pennsylvania, Philadelphia, PA; 2ThermoFisher Scientific, Somerset, NJ

WP 687 Quantitative Analysis of 18-β-Glycyrrhetinic Acid, Cortisol and Cortisone by LC-MS/MS for Determination of 11 β-HSD2 Enzyme Activity in Patients; Margret Thorsteinsdottir; Baldur Bragi Sigurdsson; Amdis Sue-Ching Löve; Helga Ágústa Sigurjónsdóttir; 1University of Iceland, Reykjavík, Iceland; 2ArcticMass, Reykjavik, Iceland; 3Landspitali University Hospital, Reykjavik, Iceland

WP 688 Development of a Multiplex MRM Method for Measuring Proteins in High Density Lipoprotein Particles; Thomas J. Lukas; at Western University, Chicago, IL

WP 689 Acyl-coenzyme A Profile Study in Tissues of Wild Type and Short-Chain hydroxyacyl-CoA Dehydrogenase (SCHad) Knockout Mice by Tandem Mass Spectrometry; Jie Chen; Andrew Palladino; Staci Kallish; Srinivas Narayan; Michael Bennett; Children’s Hospital of Phil, Philadelphia, PA

WP 690 Surrogate Analyte Parallelism of Endogenous Amino Acids in Plasma by LC/MS/MS; Barry R. Jones; Kristen M. Bearup; Gary A. Schultz; James A. Eckstein; Bradley L. Ackermann; 1Advion BioServices, Inc., Ithaca, NY; 2Eli Lilly & Company, Indianapolis, IN

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WP 691 Towards Dissecting the Role and Substrates of Yeast Ubiquitin Receptor Proteins: A Comparison using SILAC and TMT Labeling; Lily Ting; Wilhelm Haas; Daniel J. Finley; Steven P. Gygi; Harvard Medical School, Boston, MA

WP 692 Illustrating Dynamics of Metabolic System using High-throughput Metabolomics and Dynamic Correlation Analysis; Daichi Yukihira; Daisuke Miura; Hiroyuki Warishi; Kyushu University, Fukuoka, JAPAN

WP 693 Proteomics of Dicer-knockout SILAC Mice Reveals Altered Lipid Metabolism in Small Intestine; Tai-Chung Huang; Nandini Sahasrabuddhe; Yi Yang; Rahgorthoama Chaerkady; Jonathan Peterson; Guang William Wong; Vadiraja Bhat; Akhilesh Pandey; 1Johns Hopkins University School of Medicine, Baltimore, MD; 2Agilent Technologies, Wilmington, DE

WP 694 Mapping Microbial Metabolism Using Untargeted Metabolite Profiling; Richard Baran; Benjamin Bowen; Nicholas Bouskill; Eoin Brodie; Steven Yannone; Trent Northen; LBML, Berkeley, CA

WP 695 A Systems Analysis of Pathways in Breast Cancer; Xinyan Wu; Rahgorthoama Chaerkady; Nandini Sahasrabuddhe; Santosh Renuse; Saraswati Sukumar; Ben H. Park; Akhilesh Pandey; Johns Hopkins University, Baltimore, MD

WP 696 Phosphoproteome Profiling of HEK 293 Cells Exposed to High NaCl; Rong Wang; Joan D. Ferraris; Guanghui Wang; Marjan Gucek; Maurice M. Burg; NHLBI, NIH, Bethesda, MD

WP 697 Dynamics of Subcellular Proteomes during Brain Development; Dan McClatchy; Lujian Liao; Sung Kyu Park; John Yates; The Scripps Research Institute, La Jolla, CA

WP 698 Proteome-wide Profiling of Deubiquitylating Enzymes in Saccaromyces Cerevisiae by Quantitative Mass Spectrometry; Ton Wriedt Poulsen; Peter Henriksen; Katherine Beck Sylvestersen; Christian Toft Madsen; Michael Lund Nielsen; CPR, University of Copenhagen, Copenhagen, Denmark

WP 699 A Proteomic Investigation of Intermediate HSV-1 Virion Structures Containing the Inner Tegument Protein pUL37; Todd M.
WP 700
Novel Protein Interactors of PS37; Steve Nguyen; 1; 2; Sofia Maier; 3; Matthias Mann; 2; 1Pfizer, Mystic, CT; 2Max Planck Institute for Biochemistry, Muenchen, Germany

WP 701
Quantitative Proteomic Dissection of the Dynamic Hoxcode; Harsha P Gunawardena; 1, 2; Yanbao Yu; 1, 2; Xian Chen; 1, 2

WP 702
Absolute Quantification and Stoichiometry Determination of Protein Complexes Involved in Sister Chromatid Cohesion; Johann Holzmann; 1; Johannes Fuchs; 1; Georg Petzold; 1; 1Research Institute of Molecular Pathology, Vienna, Austria; 2Christian Doppler Laboratory for Proteome Analysis, Vienna, Austria; 3Institute of Molecular Biotechnology, Vienna, Austria

WP 703
Molecular Architecture and Protein Interaction Networks of Dense-core Secretory Vesicles from Human Adrenal Pheochromocytoma: Implications in Stress and Neuropeptide Secretion; Steven Bark; 1; Jill Wegryn; 1; Qi Ma; 1; June Snedecor; 1; Laurent Taupenot; 1; Daniel O’Connor; 1; Vivian Hook; 1; 1UCSD Skaggs School of Pharmacy, La Jolla, CA; 2UCSD Bioinformatics Graduate Program, La Jolla, CA; 3UCSD Department of Medicine, La Jolla, NC

WP 704
Characterization of the Human Sigma-1 Receptor Interactome Using Label-Free Quantitative Chemical Proteomics; Hongbo Gu; 1; Carthene Bazemore-Walker; 2; Brown University, Providence, RI

WP 705
Proteomic Analysis of LEDGF/p75 Interactions with the Nuclear Proteins; Robert L. Graham; 1; Christopher Mckee; 2; Michael J Sweredoski; 1; Mamuka Kvaratskhelia; 1; Sonja Hess; 1; 1Caltech, Pasadena, CA; 2The Ohio State University, Columbus, OH

WP 706
Dynamic Analysis of the Scaffold Protein ShC2-mediated Signaling Network by Targeted Proteomics; Yong Zheng; 1; Cunjie Zhang; 1; Soliman Mohamed; 1; Adrian Pascaulescu; 1; Ryan Williams Williams; 1; Lorne Taylor; 1; 1Wayne State University, Detroit, MI; 2FOM Institute for Systems Biology Rijnhuizen, Nieuwegein, Netherlands; 3University of Sheffield, Sheffield, UK; 4FOM Rijnhuizen, Nieuwegein, Netherlands; 5Van’t Hoff Institute for Molecular Physics, Amsterdam, Amsterdam, THE Netherlands

WP 707
SWATH Quantitation of Protein Phosphatase Interactions across the Cell Cycle; Nicole St-Denis; 1; Brett Larsen; 1; Stephen A Tate; 1; Ron Bonner; 1; Zhen Yuan Lin; 1; Ludovic Gillet; 1; Pedro Navarro; 1; Ruedi Aebersold; 1; Anne-Claude Gingras; 1; 1Samuel Lunenfeld Research Institute, Mount Sinai H, Toronto, Canada; 2AB SCIEX, Concord, ON; 3IMSB-ETH Zurich, Zurich, Switzerland

WP 708
Impact of Histone Modifications on Global Protein Expression in Saccharomyces cerevisiae; Linan Wang; Neha Rastogi; Mark R. Parthun; Michael A. Freitas; Ohio State University, Columbus, OH

WP 709
Sequence-specific Capture of Protein-DNA Complexes for Mass Spectrometric Protein Identification; Lloyd Smith; 1; Siyuan Chen; 1; Marla Chesnik; 2; Lisa Cirillo; 2; Mark A Scalf; 2; Regina Cole; 2; Mindy Dwisnifl; 2; Brian Frey; 2; Hector Guillen Ahlers; 2; Brian Halligan; 2; Rachel Knoener; 2; Gloria Kreitinger; 2; Jozef Lazar; 2; Mark Levenstein; 2; Amy Ludwig-Kubinski; 2; Isaac Matus; 2; Shama Minz; 2; Ashlan Musante; 2; Akua Oduro; 2; Michael Zickus; 2; Molly Pelletier-Hahn; 2; Michael R. Shortreed; 2; Andrew Vallejo; 2; Cheng-Hsien Wu; 2; Yuan Yuan; 2; Michael Olivier; 2; 1University of Wisconsin, Madison, WI; 2Medical College of Wisconsin, Milwaukee, WI

WP 710
Bottom Up, Middle Down and Genomic Analysis of Histone Variants, Their Nucleosomal Binding Partners and Post-Translational Modifications; Nicolas L. Young; Gary Leroy; Peter A. Dimaggio; Barry Zee; Benjamin Garcia; Princeton University, Princeton, NJ
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10:30 am-2:30 pm ...... All poster authors should be present.
11:45 am-12:15 pm .. Lunch break for odd-numbered posters
12:15-12:45 pm ...... Lunch break for even-numbered posters
After 2:30 pm .............. Remove all Thursday posters.

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**ThP 001**
**Infrared Multiple Photon Dissociation (IRMPD) Spectroscopy of Oxazine Dyes:** Robert J. Niekarz; Jos Ooms; Giel Berden; Pavel Sagulenko; Vladimir Frankevich; Renato Zenobi; ETH Zürich, Zürich, Switzerland; 2FOM Rijnhuizen, Nieuwegein, Netherlands

**ThP 002**
**Tandem-MS and IRMPD-Spectroscopy of Solvated Organozinc Cations in the Gas Phase:** Structure Elucidation of Negishi Cross Coupling Reagents; Frank Dreicker; Jos Ooms; Anthony J.H.M. Meijer; Barry T. Pickup; Richard F.W. Jackson; Mathias Schaefe; 1Department of Chemistry University of Cologne, Koeln, GER; 2University of Amsterdam, Amsterdam, NL; 3Department of Chemistry University of Sheffield, Sheffield, UK; 4FOM Institute for Plasma Physics “Rijnhuizen”, Nieuwegein, The Netherlands; 5Van’t Hoff Institute for Molecular Sciences, Amsterdam, The Netherlands

**ThP 003**
**Infrared Multiple Photon Dissociation Action Spectroscopy of Sodium Cationized Halouracils: Effects of Sodium Cationization on Gas-Phase Conformation:** C. M. Kaczan; R. R. Wu; A. I. Rathur; Y. Chen; C. A. Austin; J. Ooms; C. Berden; M. T. Rodgers; 1Wayne State University, Detroit, MI; 2FOM Institute for Plasma Physics “Rijnhuizen”, Nieuwegein, The Netherlands; 3Van’t Hoff Institute for Molecular Sciences, Amsterdam, The Netherlands

**ThP 004**
**Interconversion of a-2-ion Isomers Derived from Protonated Trialanine: IRMPD Spectroscopy and Density Functional Theory Calculations:** Junfeng Zhao; Udo Verkerk; Jeffrey Steili; Chi-Kit Siu; Jos Ooms; Alan C. Hopkinson; K W Michael Siu; York University, Toronto, Canada; Centre for Research in MS, Toronto, ON; 2City University of Hong kong, Hong Kong, China; 3FOM Rijnhuizen, Nieuwegein, Netherlands; 4Sanedia National Laboratories, Livermore, CA; 5University of Amsterdam, Amsterdam, Netherlands

**ThP 005**
**Structure of Radical Anions and Cations of Cysteine Derivatives Studied by Ion Spectroscopy: A Case Study of N-Acetyl Cysteine:** Sandra Osburn; Giel Berden; Jos Ooms; Richard A. J. O’hair; Victor Ryzhov; 1Northern Illinois University, Dekalb, IL; 2FOM Rijnhuizen, Nieuwegein, the Netherlands; 3University of Melbourne, Victoria, Australia

**ThP 006**
**IRMPD of Triply Charged Lanthanum-Peptide Complexes:** Irine Saminathan; Junfeng Zhao; Udo Verkerk; Jos Ooms; Alan Hopkinson; K. W. Michael Siu; 1CRMS, Chemistry, York University, Toronto, ON; 2FOM Rijnhuizen, Nieuwegein, Netherlands; 3University of Amsterdam, Amsterdam, THE Netherlands

**ThP 007**
**Vibrational Spectroscopy of Protonated Amino Acids and Peptides and Their Collision-Induced Dissociation Products in the Hydrogen Stretching Region:** Kerim Gulyuz; Corey Stedwell; Da Wang; Nicolas Polfer; 1University of Florida, Gainesville, FL

**ThP 008**
**Studying of the Optical Properties of Fluorescent Biological Tags in the Gas Phase:** Pavel Sagulenko; Vladimir Frankевич; Renato Zenobi; ETH Zurich, Zurich, Switzerland

**ThP 009**
**What Happens to Green Fluorescent Protein upon Transfer from Solution to the Gas Phase?:** Vladimir Frankевич; Konstantin Barylyuk; Robert J. Niekarz; Pavel Sagulenko; Renato Zenobi; ETH Zurich, Zurich, Switzerland

**ThP 010**
**Vacuum Ultraviolet and Extreme Ultraviolet Photoionization Mass Spectrometry of Biomolecules:** Elliot Bernstein; Joong-Won Shin; Feng Dong; Michael Grisham; Jorge Roche; Colorado State University, Fort Collins, CO

**ThP 011**
**H2 tagging – A Versatile New Tool for the Vibrational Characterization of Peptides:** Christopher Leaivil; Michael Kamrath; Etienne Garand; Aaron Wolk; Peter Jordan; Scott Miller; Mark Johnson; Yale University, New Haven, CT

**ThP 012**
**Mass Selected Resonant (1+1)-Photodissociation Spectroscopy of Different Iodine Containing Alkanes:** Hannes Schüttig;
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**Measuring the Monolayer Stability of Nanoparticles in Cells Using Laser Desorption/Ionization Mass Spectrometry;** Zheng-Jiang Zhu; Rui Tang; Yi-Cheun Yeh;
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**How Do Matrix Alternatives Compare with DHB in Distinguishing between the Metabolic Footprints from 5 Yeast Mutants using MALDI-MS?**; Lindsay Lai-Rowcroft; Michael Anderson; Roy Goodacre; University of Manchester, Manchester, UK

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Vincent M. Rotello; Richard Vachet; University of Massachusetts, Amherst, MA

A. Versatile MALDI Target Plate Based on Polymer-Filled Reticulated Vitreous Carbon Foam

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[3] Drexel University, Philadelphia, PA

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Simultaneous Determination of Atacamitoxin, Tramodol and O-desmethyltramadol and in Human Plasma by LC-MS/MS; Kyung Hyeon Lee; Yeon Jin Shin; Kyung Hee Cho; Sookie La; Hee Joo Lee; BioCore, Seoul, Korea

Quantitative Determination of Small Pharmaceutical Compound by LDTD/MS/MS, Atmospheric Pressure Chemical Ionization, As Compared to LC/MS/MS of Clinical Study Samples; Azza Waqdy; Serge Auger; Grace E. Kim; Joseph C. Kim; Patrice Tremblay; "Abbott Laboratories, Abbott Park, IL; Phytonix Technologies Inc., Québec, Canada

Simultaneous Determination of Acetaminophen, Tramadol and O-desmethyltramadol and in Human Plasma by LC-MS/MS; R. Van Bremen; Scott G. Franzblau; "Institute for Tuberculosis Research, Chicago, IL; 2University of Illinois at Chicago, Chicago, IL

LC/MS/MS Method for the Quantitative Determination of Ultralow Levels of Ester Prodrug and Acid Metabolite in Human Blood and Plasma; JinJin Shen; Jennifer Keller; Zong-Ping Zhang; Andrew Aceampong; John Ling; Gabriella Szekely-Klesner; Allergan Pharmaceuticals, Irvine, CA; 2PD, Middleton, Wisconsin

Quantification of Tiotropium in Human Plasma with a 1 pg/ml LLOQ using HPLC and LC/MS/MS; Yue Zhao; Stephanie Harrison; Troy Voelker; Min Meng; Tandem Labs, Salt Lake City, UT

LCMS Characterization of Anthroquinones in a mixture. Quantification and Comparison of Detection Limits by Mass Spectrometry and UV-Vis; Christina Jasieczek Mastromatteo; Ben Englehart; Eric Anderson; Perry Matheny; Lubrizol Advanced Materials, Brecksville, OH; 2Promerus LC, Brecksville, OH

Determination of a New Tricyclic Pyrazole Derivative in Rat Plasma and Brain by Liquid Chromatography – Tandem Mass Spectrometry; Giuseppe Peddico; Matteo Falzoi; Barbara Pialli; Giovanni Loriga; Luca Pani; Paolo Lazzari; "Consorzio Elplo, Ed.S, Loc. Piscinamanna, 09101 Pula (CA), Italy; 2PharmaNess Scarl, Ed.5, Loc. Piscinamanna, 09101 Pula (CA), Italy; 3CNR, Istituto di Farmacologia Traslazionale, 09101 Pula (CA), Italy; 4Dip. to Scienze del Farmaco, Università Sassari, 07100 Sassari (SS), Italy

On-the-Fly Gas-Phase Derivatization via Ion/Molecule Reactions: A Novel Strategy for Rapid Analysis of Epoxide Impurities in Active Pharmaceutical Ingredients; Lianning Wu; David Q. Liu; Frederick G. Vogt; Alireza S. Kord; GlaxoSmithKline, King of Prussia, PA

Liquid Chromatography-Mass Spectrometry (LC-MS) Assay for Analysis of Heptanone-Etheno-2′-Deoxyguanosine as Biomarker of Oxidative Stress in Human Urine; Yu Shi; Clementina Mesaros; Jasbir S. Arora; Sumit Shah; Ian A. Blair; University of Pennsylvania, Philadelphia, PA

Development of an LC-MS/MS Method to Quantitate Age Related Differences in Dexamethasone Metabolism in Rhesus Macaques; Sarah Pruettt; M. Kyle Cannon; Vasiliki Michopoulos; Shannon Bouan; Mar Sanchez; 2; Mark E. Wilson; 3; Yerkes National Primate Res. Ctr., Emory University, Atlanta, GA; 4Dept. of Pharmacy and Clinical Sci.,Emory Univ., Atlanta, GA

Determination of Tacrolimus in Rat Whole Blood by Dried Blood Spot Analysis using LC-MS/MS; Gene Ray; Moo-Young Kim; Yansheng Liu; Darid Didad; KACS, LLC, Shawnee, KS

Evaluation of Response Saturation in LC/MS/MS Quantitative Analysis; Zhemin Liang; Hang Zeng; Sreepriya Velanki; Bernd Steinheuber; Stefan Masur; David Moore; Hoffmann-La Roche, Inc., Nutley, NJ; F Hoffmann-La Roche, Basel, Switzerland

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High Throughput Metabolite Identification and Automated Metabolic Soft Spot Analysis by High Resolution Accurate Mass Spectrometry; Ahmed Amann; Barry Press; Suma Ramagiri; Alina Dindyal-Popescu; Shaokun Pang; Eva Duchoslav; Rima Al-awar; AB SCIEX, Concord, Canada; 2Ontario Institute for Cancer Research, MaRS Centre, Toronto, Canada

Selective and Sensitive Recording of MS/MS Spectra of Unknown Drug Metabolites in Complex Matrix Using Mass Defect-Dependent Acquisition; Kerong Zhang; Jie Xing; Yongming Xie; Mingshe Zhu; 2AB SCIEX, Shanghai, China; 2Shandong University, Jinan, China; 2Bristol-Myers Squibb, Princeton, NJ

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Improving Bioanalytical Selectivity in Differential Mobility Spectrometry - Mass Spectrometry using Chemical Effects; J.C. Yves Leblanc; Doina Caraiman; Brad Schneider; J. Larry Campbell; Hesham Gobahar; AB SCIEX, Concord, On, Canada; AB SCIEX, Concord, ON

Quantitation of Small Pharmaceutical Compound by LDTD/MS/MS, Atmospheric Pressure Chemical Ionization, As Compared to LC/MS/MS of Clinical Study Samples; Azza Waqdy; Serge Auger; Grace E. Kim; Joseph C. Kim; Patrice Tremblay; "Abbott Laboratories, Abbott Park, IL; Phytonix Technologies Inc., Québec, Canada

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Simultaneous Measurement of Fifteen Anti-Tuberculosis Compounds Using LC-MS-MS; Yang Song; 1; 2Kuanwei Peng; Nan Zhang; Richard B. Van Bremen; Scott G. Franzblau; "Institute for Tuberculosis Research, Chicago, IL; 2University of Illinois at Chicago, Chicago, IL

LC/MS/MS Method for the Quantitative Determination of Ultralow Levels of Ester Prodrug and Acid Metabolite in Human Blood and Plasma; JinJin Shen; Jennifer Keller; Zong-Ping Zhang; Andrew Aceampong; John Ling; Gabriella Szekely-Klesner; Allergan Pharmaceuticals, Irvine, CA; 2PD, Middleton, Wisconsin

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Selective and Sensitive Recording of MS/MS Spectra of Unknown Drug Metabolites in Complex Matrix Using Mass Defect-Dependent Acquisition; Kerong Zhang; Jie Xing; Yongming Xie; Mingshe Zhu; AB SCIEX, Shanghai, China; 2Shandong University, Jinan, China; 2Bristol-Myers Squibb, Princeton, NJ
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ThP 190  Affinity Mesh Screen Materials for Rapid Drug Discovery Using Transmission Mode Desorption Electrospray Ionization Mass Spectrometry; Samuel Yang1; Sumit Bhawal2; Rajendrasing Dhanikula1; Aruna Wijeratne2; Richard Deshmukh1; Aruna Wijeratne2; Richard Timmons1; Kevin Schug2; 1University of Texas Arlington, Arlington, TX; 2The Department of Cancer and Cell Biology, University of Waterloo, Waterloo, Canada

ThP 191  High Throughput LC/MS Methods Development for in vitro ADME Screening; Veronica Zalesky1; Richard Schneider2; John Janiszewski1; Hui Zhang2; Pfizer Global R&D, Groton, CT

ThP 192  Ultrafast SPE Integrated with TOF-MS Increases the Throughput of Metabolic Stability Assays and Enables Analysis of Metabolites; Nikunj Parikh1; Michelle Romm1; Yuqin Dai1; Vaughn Miller1; William A. Lamar2; Keith Wadde1; Can “Jon” Ozbol1; BIOCUTS Life Sciences, Inc., Wakefield, MA; 2Agilent Technologies, Santa Clara, CA

ThP 193  A Suite of High Throughput in vitro ADME Assays Based on In-Line Solid Phase Extraction and Mass Spectrometry; Cheryl A. Black1; Jeffrey Quinn2; Brett Leclaire3; Eric Sands4; Tonika Bohnet5; Guangqing Xiao6; Ellen Rohde7; Brian Edwards8; Frank Pols9; Richard Timmons1; Kevin Schug1; 1University of Texas Arlington, Arlington, TX; 2The Department of Cancer and Cell Biology, University of Waterloo, Waterloo, Canada

ThP 194  A Software Enabled Relative Quan/Qual Workflow: Acquisition and Automatic Processing of in vitro Screening Data using a Benchtop HRAM MS; Karen Salomon1; Tim Stratton1; Maiciej Bromirski1; Yingying Huang1; 1Thermo Fisher Scientific, San Jose, CA; 2Thermo Fisher Scientific, Bremen, Germany

ThP 195  Reactive Metabolite Screening in Early ADME using Rapid Accurate Mass Technology; James A. Ferguson1; Richard Schneider2; Veronica Zalesky1; Hui Zhang2; 1AB Sciex, Framingham, MA; 2Pfizer Global R&D, Groton, CT

ThP 196  Utilization of Online Dilution Techniques to Improve Quantitative and Qualitative LC/MS Analyses for Drug Discovery; Ari Gritzas1; Helene Maurice2; Ralph Schmidt3; Marie Roumi3; AstraZeneca R&D Montréal, Ville Saint-Laurent, Canada

ThP 197  Characterization of Small Molecule Aggregate Components in Cystine Stages as a Screen for Candidate Stone Inhibitors; Matthew R. Lewis1; Amrik Sahota2; Michael D. Ward2; David S. Goldfarb3; Elaine Holmes4; Elizabeth J Want5; 1Imperial College London, London, UK; 2New York University, New York, NY; 3Rutgers, Camden, NJ

ThP 198  Application of a Novel Bench-top Orbitrap Mass Spectrometer with a Quadrupole Mass Filter for Metabolite Profiling in Drug Discovery; Qian Ruan1; Kate Comstock2; Li Ma3; Tim J Stratton4; Yingying Huang5; Mingshe Zhu6; 1Bristol-Myers Squibb, Princeton, NJ; 2Thermo Fisher Scientific, San Jose, CA

ThP 199  A Comprehensive Approach to the Profiling of the Cooked Meat Carcinogens PhIP, MeIQx and their Metabolites in Human Urine; Dan Gu1; Robert Turesky2; Wadsworth Center, NYS Department of Health, Albany, NY; 2Thermo Fisher Scientific, Wakefield, MA

ThP 200  Modified Polycrylonitrile-Polystyrene-Divinylbenzene 96-Thin-Film SPME System, Capable of Extracting Wide Polarity Range of Metabolites in Biological Fluids; Fatemeh Mirmaghi1; Janusz Pawliszyn2; University of Waterloo, Waterloo, Canada

ThP 201  Using High Sensitivity, High Throughput Rapid Serial Analytical Approaches in ADME for Routine Quantitation and Metabolite ID; Richard Lauman1; John Laycock2; Loren Olson2; 1AB SCIEX, San Jose, CA; 2Amgen, Thousand Oaks, CA

ThP 202  Identifying Chemical Error in Lead Optimization; Timothy Dunne1; Holly McKeith2; David Vlau3; Travis Mathewson3; Rosalia Gonzales3; Pfizer, Groton, CT

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ThP 204  Specificity and Throughput Challenges and Solutions in Protein Biomarker Verification/Validation; Konstantinos Petris1; Mark Holl2; Deirdre Meldrum3; Matthew Rosenow4; 1Translational Genomics Research Institute, Phoenix, AZ; 2Arizona State University, Tempe, AZ

ThP 205  Determination of Ritonavir, Saquinavir and Lopinavir in Dried Blood Spots by LC/MS/MS Comparing Different Automated Extraction Approaches; Thomas Lloyd1; Ravi Orugunty2; Adan Orta3; Andrea Butz4; Steven Hoehne5; Worldwide Clinical Trials, Austin, TX

ThP 206  Approaching 100% LC-MS Duty Cycle with a Three-Column Nano-electrospray Interface; Katie Southwick1; Ben Ngo2; Helene Cardasis1; Mike S. Lee3; Gary Valaskovic2; Nathan Yates2; 1Bristol-Myers Squibb, Princeton, NJ; 2New Objective, Inc., Woburn, MA; 3Milestone Development Services, Newton, PA

ThP 207  High Throughput Low Dead Volume NanoLC-MS Methods Involving a Trap Column; Arthur Fogiel1; Katherine Heaton1; Arthur Fogiel2; 1Sau Lan Tang Staats; Phoenix S&T, Chester, PA

ThP 208  Direct Extraction/Analysis of Dried Blood Spots(DBS): A Fully Automatic System Including Spot Localization, Internal Standard(IS) Application and Multiple Batch Analysis; Matthias Loppacher1; Christoph Fankhauser2; Klaus Schetter2; Urs Schranz1; Manuel Altmeyer1; Agathe Keller3; Bettina Mueller4; Silvio Walpen5; 1CAMAG, Muttenz, Switzerland; 2Institute for Laboratory Technology, Rapperswil, Switzerland

ThP 209  Design of an Agile, High-Throughput Proteomics Pipeline for use in an Industrial Synthetic Biology Setting; Peter Jackson1; Tahera Iqbal1; Manbir Labhan2; Sara P. Gaucher3; Amyris Inc, Emeryville, CA
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ThP 211 Development of a 20 kpsi Enzymatic Digester for High Throughput Proteomic Analysis and Its Application to Membrane Proteinomics; Seok-Won Hyung1; Daniel Lopez-Ferrer2; Daniel J. Orton1; Erika Zink1; Karl K. Weitz1; Rui Zhao3; Ronald J. Moore1; Kim K. Hison1; Edmund Y. Ting1; Alexander V. Lazarev1; Richard D. Smith1; 1Pacific Northwest National Laboratory, Richland, WA; 2Thermo Fisher Scientific, San Jose, CA; 3Thermo Fisher Scientific, San Francisco, CA

ThP 212 Automation of Plasma Processing for High-Throughput Proteomics; Karen Merrell1; Mark Holt1; Konstantinos Petritis1; Darren Lewis1; Kelly Flook1; Yury Agroskin1; Deirdre Meldrum1; 1Arizona State University, Mesa, AZ; 2The Translational Genomics Research Institute, Phoenix, AZ; 3IDEX Corporation, Lake Forest, IL; 4Dionex Corporation, Sunnyvale, CA

ThP 213 Collaborative Methods Development in Drug Discovery; Emily Miller1; Kevin Shirey2; Andrea Clouser-Roche1; Veronica Zelensky2; Kevin Whalen1; Sarah Osgood1; John Janiszewski1; Wayne Loostra1; Anthony Romanelli1; Pfizer Inc., Groton, CT; 1Sound Analytics, LLC, Niantic, CT; 2AB SCIEX, Framingham, MA; 3Pfizer, La Jolla, CA

ThP 214 Bioanalysis without Chromatography: the Evaluation of RapidFire Ultra-fast Online SPE-MS/MS System for Quantitation of Drugs in Biological Matrixes; Wenjing Jian1; Michelle Romm1; Richard W. Edom1; Vaughn Miller1; William A. Lamm1; Naidong Weng1; J&J Pharmaceutical Research & Development, Raritan, NJ; 1BIOCIS Life Sciences, Wakefield, MA

ThP 215 Speeding up the Dry Blood Spot Sampling with One Step Automated Multiple Extractions Combined with LDTD-MS/MS Analysis; Pierre Picard1; Patrice Tremblay1; Serge Auger1; PhytoXnologies Technologies, Quebec, QC

ThP 216 Automated Magnetic Bead Based Sample Purification for High Throughput PCR Product Analysis on an ESI-TOF Mass Spectrometer; Jared Drader1; Jose Gutierrez1; Steven Hofstadler1; Ibis Biosciences, Inc., Carlsbad, CA

ThP 217 Fast Analysis by Mass Spectrometry with Supersonic Molecular Beams – Combining Fast Sampling and Ultra Fast GC-MS; Alexander B. Fialkov1; Alexander Gordin1; Mati Morag1; Aviv Amirav1; Tel-Aviv University, Tel-Aviv, Israel

ThP 218 High Throughput Identification Analysis for Synthetic Chemicals by GC/HRTOFMS Coupling with EI/FI Ion Source; Keisuke Ishii1; Masaaki Ubukata2; Yoshisasa Ueda1; Yujichi Osuga1; Kiyotaka Konom1; JEOI Ltd., Akishima, Japan; 1JEOI USA Inc, Boston, MA

ThP 219 Metabolic Stability and Pharmacokinetic Studies Suggest That the DAP Biomarkers May Lead to Overestimates of Organophosphate Pesticide Exposure; Norman Forsberg1; Rosetta Rodriguez-Proteau2; L. Ma3; Jeffrey Morre1; Mark Christensen1; Claudia Maia2; JJ Jenkins1; Kim Anderson1; Oregon State University, Corvallis, OR

ThP 220 Metabolic Profiling and Imaging Metabolite Distribution of Pea Leaves by Mass Spectrometry; Zhihong Song1; Nickolas A. Hickman2; Young Jin Lee3; Edward S. Yeung4; Basil J. Nikolau4; 1Ames Lab of US DOE/Iowa State University, Ames, IA; 2Iowa State University, Ames, IA; 3Ames Laboratory of US DOE, Ames, IA

ThP 221 Total Biochemical Response Analysis Using Mass Spectrometry and Quadrupole Time of Flight Mass Spectrometry for the Characterization of Small Molecule Aggregate Distribution of Pea Leaves by Mass Spectrometry; Zhihong Song1; Nickolas A. Hickman2; Young Jin Lee3; Edward S. Yeung4; Basil J. Nikolau4; 1Ames Lab of US DOE/Iowa State University, Ames, IA; 2Iowa State University, Ames, IA; 3Ames Laboratory of US DOE, Ames, IA

ThP 222 Development of a Metabolomic Approach Based on LC-HRMS for the Screening of Anabolic Steroids in Equine Urine; Natali Stoiljkovic1; Marie-Agnes Popot1; Yves Bonnaire1; Alain Paris1; Christophe Junot1; Jean-Claude Tabet1; LCH, Verriere le Buisson, France; 1UPMC, Paris, France; 2INRA, Paris, France; 3CEA, Saclay, France

ThP 223 Metabolomics Approach to Profiling Markers Key for Distinctions among Roots of Panax ginseng, Panax quinguefolius and Panax notoginseng by UPLC/oTOFMS; Li Yang1; Han Han1; Kate Yu2; Alan Millar2; Zhengtao Wang1; Shanghai University of TCM, Shanghai, CHINA; 2Pharmacology, Manhattan College, New York, NY

ThP 224 Identification and Authentication of Terminalia species by Comprehensive Profiling Novel Chemical Markers using Metabolomics Strategy with UPLC/TOF MSE; Bharathi Avula1; Kate Yu2; Yan-Hong Wang2; Alan Millar3; Ikhas Khan3; 1NCNP, University of Mississippi, University, MS; 2Waters Corporation, Milford, MA

ThP 225 Metabolomics Profiling of G-Protein-Signaling Mutant Strains of Stagonospora Nodorum by Hybrid Quadrupole Time-Of-Flight Mass Spectrometry; Jeffrey D. Miller1; Joel P.A. Gummers1; John C. Brown1; Beth L. Maker1; Robert Trengove2; Richard P. Oliver3; Peter S. Solomon4; Catherine C. Rawlinson4; 1AB SCIEX, Framingham, MA; 2Separation Science and Metabolomics Laboratory, Perth, WA, Australia; 3School of Biomedical Sciences, University of Western Australia, Perth, WA, Australia; 4School of Biological Sciences, The Australian National University, Canberra, ACT, Australia; 5Aust. Centre for Nectors and Fungal Pathogens, Perth, WA, Australia

ThP 226 Metabolic Analysis of hypercholesterolemic Rats injected with Berberine; Sam Li; National University of Singapore, Singapore, Singapore

ThP 227 Improved Analysis and Profiling of Bile Acid Metabolites in Biological Tissues and Fluids; Hong Yin; Erik Rocheber; Ryan Steeper; John Gounardes; novartis institutes of biomedical research, Cambridge, MA

ThP 228 Grape Seed Extract Metabolite Analysis following Ovariectomy in Rats; John Cutts1; Helen Kim1; UAB, Birmingham, AL

ThP 229 Targeted Metabolomics in Arabidopsis; Evidence for a Role of Vitamin C in Neurotransmitter and Nitric Oxide Synthesis;
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Jay Kirkwood; Katie Lebold; Charlotte Wright; Galen Miller; Carrie Barton; Robert Tanguay; Maret Traber; Fred Stevens; Oregon State University, Corvallis, OR

**ThP 230 Characterization of Echinacea purpurea Alkamides under Positive Electrospray Ionizations and Collision-Induced Dissociations:**

Bandy W. Purves; Jake M. Stout; Stephen R. Purves; 1Michigan State University, East Lansing, MI; 2Iowa State University, Ames, IA

**ThP 231 Novel Approaches to Structure Elucidation and Confirmation for Plant Metabolomics:**

Sven Helling; Gabriela Zurek; Emmanuel Gaggero; Matthias Schoettner; Alain M. Smith; Kevin R. Conard; Burr Binkley; Waters Corp, Milford, MA; 1Michigan State University, East Lansing, MI; 2NanoOncology, Madison, WI

**ThP 232 Identification and Quantification of Short and Mid-Chain Coenzyme as in Hemp (Cannabis sativa) using UPLC and Tandem Mass Spectrometry:**

Connie Jen; Celeste Sandoval; Sara Gaucher; Amyris Inc, Emeryville, CA

**ThP 233 High Throughput Global Strain Interrogation of S Cerevisiae using Targeted Metabolomics For Use in Industrial Systems Biology:**

Nathan Moss; Connie Jen; Celeste Sandoval; Sara Gaucher; Amyris Inc, Emeryville, CA

**ThP 234 A High Throughput Assay for Predicting Human Developmental Toxicity Using Human Embryonic Stem Cells and Metabolomics:**

Paul R. West; Alan M. Smith; Kevin R. Conard; Burr R. Fontaine; Gabriela G. Cezar; April M. Weir; LECO Corporation, St. Joseph, MI

**ThP 235 An Exometabolic Approach for Characterizing Chemically Induced Differentiation Pathways in HL60 Cells:**

Qingfen Zhang; Mark Dodson; Sanofi-Aventis Tucson Research Center, Tucson, AZ

**ThP 236 Global Metabolomics of C. Elegans:**

Yaoling Long; Jungsoo Han; Rebecca Butler; David Powell; Department of Chemistry, University of Florida, Gainesville, FL

**ThP 237 Global Metabolomic Profiles Reveal Aggressive Prostate Cancer Biomarker and Mechanism of Cancer Drug Action Michael Milburn, Chief Scientific Officer Metabolon, Inc; Michael Milburn; Metabolon, Inc., Durham, NC

**ThP 238 Global Metabolomics of Colon Cancer by Analysis of Human Plasma with LC/(+)ESI- MS:**

Noelle M. Elliott; John Koomen; Umut Oguz; Y. Ann Chen; David Shibata; Erin M. Siegel; Richard A. Yost; David H. Powell; 1University of Florida, Gainesville, FL; 2H. Lee Moffitt Cancer Center, Tampa, FL

**ThP 239 Metabolite Biomarkers of Short Term Inflammatory Pain using MALDI-TOF MS:**

Stanislav Rubakhin; Eric J Lanni; Jonathan Sweedler; 1Beckman Institute, UIUC, Urbana, IL; 2Beckman Institute, UIUC, Urbana, IL; 3University of Illinois, Urbana, IL

**ThP 240 Towards a Universal LC-MS Method for Metabolomics:**

Mark Szewcz; Josef Ruzicka; Thermo Fisher Scientific, Somerset, NJ

**ThP 241 Determining the Botanical Origins of Plant Resins Collected by Honey Bees (Apis mellifera) using LC-TOF Fingerprint Analysis:**

Michael B. Wilson; Adrian D. Hegeman; Maria Spivak; Jerry D. Cohen; University of Minnesota, Saint Paul, MN

**ThP 242 LC-MS Based Global Analysis of Detailed Metabolic Dynamics and Regiospecific Variations:**

Miho Irie; Yoshinori Fujimura; Daisuke Miura; Hiroyuki Warishi; kyushu university, Fukuoka, JAPAN

**ThP 243 Efficient Searching of Plant Photo-Response Molecules by the Live Single-Cell MS and Look-Up Metabolic Map Software:**

Takashi Fuji; Hajime Mizuno; Naohiro Tsuyama; Takanori Harada; Tsutomu Masujima; Hiroshima Univ. Grad. Sch. Biomed. Sci, Hiroshima, Japan

**ThP 244 High Throughput Metabolomics using FIA and a Novel MSMS Technique:**

Ron Bonner; Stephen A. Tate; AB SCIEX, Concord, Canada

**ThP 245 Optimising the Use of Quality Control Samples for Signal Drift Correction in Long Term Urine Metabolic Profiling Studies:**

Mhmd Anas Kamleh; Imperial College of London, London, London, UK

**ThP 246 Comprehensive Metabolomic Profiling of Zucker Rat Plasma using LC and GC Ultra High Resolution Time-of-Flight Mass Spectrometry and GCxGC-TOFMS:**

Jeffrey S. Patrick; Kevin Siek; Joe Binkley; Lee Ott; John Heim; LECO Corporation, St. Joseph, MI

**ThP 247 Metabolite Profiling of Deinococcus radiodurans to Discover the Basis for Radiosensitivity Conferred by Endogenous Nitric Oxide:**

Qiuying Chen; Cornell University Medical College, Bronx, NY

**ThP 248 Characterization of Urine Metabolites in Barth Syndrome Patients Employing a Non-Targeted GCMS Screening Approach:**

Yana Sandlers; Stephen Baumann; 1Kennedy Krieger Institute, Baltimore, MD; 2Agilent Technologies, Inc., Santa Clara, CA

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Tiziana Pacchiarotta; LUMC, Leiden, Netherlands

**ThP 250 UPLC-MS Metabolic Profiling for Risk Stratification of Stroke in Human Carotid Atherosclerosis:**

Panagiotis A. Vorkas; Joseph Shahlobh; Claudia Monaco; Elizabeth J. Want; Matthew R. Lewis; Alun H. Davies; Jeremy K. Noble Foundation, Ardmore, OK

**ThP 251 A Metabolomics Analysis of the Effects of Environmental Stress Combination on Arabidopsis Plants:**

Carolina Salazar; David Peake; Michael Aranow; Yingying Huang; Nobuhiro Suzuki; Ron Mittler; Vladimir Shulaev; 1University of North Texas, Denton, TX; 2Thermo Fisher Scientific, San Jose, CA; 3VAST Scientific, Inc., Cambridge, MA

**ThP 252 Untargeted Metabolomics Approach for Studying C. Elegans Embryonic Elongation using a Combination of Aquaeous Normal Phase and Reverse Phase LC-ESI-TOF-MS;**
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**THURSDAY POSTERS**
Supercritical Fluid Chromatography/Tandem Phosphatidylcholines Profiling Method by Duarte, CA; Bascom Palmer Eye Institute, Miami, Ca; UC Davis, Food Science and Technology, San Francisco, San Francisco, CA

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Age-Related Alterations in Human Lens Lipids; Jessica R Hughes; Jane M. Deely; Shane Ellis; Stephen J Blanksby; Roger JW Truscott; Todd W Mitchell; University of Wollongong, Wollongong, Australia; 2Save Sight Institute, University of Sydney, Sydney, Australia

Comparison of Lipid Profiles of Human Meibum from Dry Eye Patients: Drug vs. Placebo Treatment Using ES1-QTOF and MALDI-TOF/TOF-MS; Kari Green-Church; Nan M Kleinehr; Kelly N Nichols; 1The Ohio State University, Columbus, OH; 2HJF/AFLR, Columbus, OH

Multidimensional Mass Spectrometric Analysis of Phospholipids in Alkali Injured Human Cornea; Ashley Crane; Andrew Coggin; Roger Moore; Kossi Lekpor; Byron Lam; Sanjoy Bhattacharya; Gabriel Gniel; City of Hope, Duarte, CA; 2Bascom Palmer Eye Institute, Miami, FL

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Development of Metabolic Profiling Method for Carotenoid Oxidation Products using Supercritical Fluid Chromatography Coupled With Tandem Mass Spectrometry; Atsuki Matsubara; Takato Uchikata; Masakazu Shinohara; Charles Chaltain; Eiichiro Fukusaki; Takeshi Bamba; Dept. Biotech., Grad. Sch. Eng., Osaka Univ., Suita, Japan; 2Grad. Sch. Med., Kobe Univ., Kobe, Japan

The Analysis of Bioactive Lipid Fractions Isolated from Green-Lipped Mussel (Perna canaliculus) using Gas Chromatography-Mass Spectrometry; Glenn Marrow; Catherine Rawlinson; Robert Trengove; Paul Wynne; Nicolette Kalafatis; Theodore Macrides; RMIT University, Melbourne, Australia; 2Metabolomics Australia, Murdoch University Node, Perth, Australia; 3Murdoch University, Murdoch, Australia; 4Shimadzu Scientific Instruments (Ociana) Pty Ltd, Melbourne, Australia

Several Different Approaches for the Analysis in Localization Profile of Lipid Molecular Species by Mass Spectrometry; Ryo Taguchi; Kazutaka Ikeda; Yoko Tajima; Chubu University, Kasugai, Aichi, Japan; 2JST, CREST, Saitama, Japan

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Utilising Normal Phase UPLC for Class Distinct Separation of Lipids in Less Than 10 Minutes; Stephen C.C. Wong; Evelyn M.L. Goh; Mark Ritchie; Waters Pacific Pte Ltd, Singapore, Singapore

A Novel Global Lipid Biomarker Workflow from a Complex Biological Sample; Giorgis Isaac Mezenige; Henry Shion; Stephen McDonald; John P. Shockcor; Alan Milair; Waters Corporation, Mildford, MA

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ThP 303 Analysis of Neurotoxic Mycotoxins in Maize Silage with LC-MS/MS; Annica Teveli Åberg1,2; Alexey Solyakov3; Ann Nymann4; Ulf Bondesson5,6; 1National Veterinary Institute, Uppsala, Sweden; 2Uppsala University, Uppsala, Sweden

ThP 304 Quantitative and Qualitative Measurement of the Small Molecular Weight Proteomes of Sterile and Fertile Maize Anters at Two Developmental Stages; Chris Adams; Dongxue Wang; John Fernandes; Rachel Eggert; Allis Chien; Virginia Walpert; Stanford University, Stanford, CA

ThP 305 Metabolite Profiling of Canola Grown Under Limiting Nitrogen Conditions; Gia C. Fazio; Ndukaku Omelu; Brian Conlin; Wayne Skinner; Jos van Boxtel; Jean C. Kridl; Arcadia Biosciences, Davis, CA

ThP 306 Characterization of the Cell Wall Proteome of Tomato (Solanum lycopersicum) Fruit by Tandem Mass Spectrometry; Miaoming Shen1; Simon Huck2; Kevin Howe3; Michelle Cilia4; Theodore Thanhauser5; 1Boyce Thompson Institute for plant research, Ithaca, NY; 2Cornell University, Ithaca, NY 14853; 3USDA-ARS, RWH Center for Agriculture and Health, Ithaca, NY

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ThP 308 Analysis of Quinolones in Different Food Matrices by Means of LC-MS/MS; Pavel Metalinov; Alexander Komarov; VGNKI, Moscow, Russian Federation

ThP 309 Quantitative Proteomic Analysis of Cold Stress in Rice; Karlie A. Neilson; Michael Mariani; Paul A. Haynes; Macquarie University, North Ryde, Australia

ThP 310 Gas Chromatography-Time of flight – Mass Spectrometry Profiling of Glycosylated Aroma Precursors in Riesling Winegrapes during Berry Ripening; Imelda Ryona; Justine Vanden Heuvel; Gavin Sacks; Cornell University, Geneva, NY

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Analysis of Anthocyanins in Pomegranates using LC/MS/MS; Casey C. Grimm; Steven Lloyd; Rebecca E. Stein; John C. Beaulieu; USDA-ARS-SRRRC, New Orleans, LA

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HPLC-Mass Spectrometry Applied on the Phenolic Compounds Identification in E. globulus, E. grandis, E. urograndis and E. maidenii Bark Extracts; Sónia A. Q. Santos1; Carmen S. R. Freire1; M. Rosário M. Domingues1; Armando J. D. Silvestre1; Carlos Pascoal Neto1; 1Dep. of Chemistry, CICECO, University of Aveiro, Aveiro, Portugal; 2Dep. of Chemistry, QOPNA, University of Aveiro, Aveiro, Portugal

Tandem Mass Spectrometry Structural Characterization of Cyclic Peptides: Revisited; Takemichi Nakamura1; Hiroyuki Koshino1; Ken-ichi Harada1; RIKEN, Wako, Japan; 2Meijo Univ., Nagoya, Japan

Sequencing Cyclic Peptides by Multistage Mass Spectrometry; Hosein Mohimani1; Yu-Liang Yang1; Wei-Ting Liu1; Wei-Pen Hsieh2; Pieter C. Dorrerstein1; Pavel A. Pevzner1; 1University of California, San Diego, La Jolla, CA; 2Chang Gung University, Tao-Yuan, Taiwan

A Natural Cycle — Proteomics Reveals the Biosynthetic Route of Cyclic Peptides while Bioinformatics Provides the Foundations for their Discovery; Michelle Colgrave1; Joshua Mylne1; Aaron Poth1; Hosein Mohimani2; Alun Jones2; Pavel Pevzner2; David Craik2; 1CSIRO, St Lucia, Australia; 2The University of Queensland, Brisbane, Australia; 3University of California San Diego, San Diego, CA

Structural Characterization of c-glycosyl Flavonoids of a Plant Dye from a Latin American Textile by Liquid Chromatography Mass Spectrometry; Nobuko Shibayama1; Jeffrey H. Dahl2; Robert Buco2; Elena Phipps2; Lucy Commoner2; 1Metropolitan Museum of Art, New York, NY; 2Shimadzu Scientific Instruments, Columbia, MD; 3Independent Scholar, New York, NY; 4Cooper-Hewitt National Design Museum, New York, NY

Detection of the Mycotoxin Lolitrem B in Bovine Urine and Feces by LC-MS/MS; Lia Murty; Oregon State University, Corvallis, OR

Real-Time Monitoring of Volatile Organic Compounds from Foods and Beverages by Hybrid Linear Ion Trap – Triple Quadrupole MS System; Fena Zhong; Peter Kovarik; Jeffrey Rivera; Eva Duchoslav; Robert Ellis; Rebecca Wittrig; Takeo Sakuma; AB SCIEX, Concord, Canada

UHPLC-ESI-Q-TOF Analysis of Proanthocyanidins in Grape Seeds and Red Wine; Adéline Del cambre; Yann André; Dawn Visintainer; Richard Barry; Cédric Saucier1; 1University of British Columbia, Kelowna, Canada; 2Agilent Technologies, Santa Clara, CA

Predictive Classification of Contaminants Encountered During the Distillation of Shochu, a Distilled Beverage Native to Japan; Toshiyuki Yamashita1; Takeshi Serino2; David Peterson3; Anthony Gray4; 1Kinyro Electric Co. Ltd., Osaka, Japan; 2Agilent Technologies, Santa Clara, CA

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| ThP 334 | Characterization of Antiproliferative Indole Alkaloids from Geigeria vellusida Bark by LCMS-IT-TOF Technology; Flaurbert Mboukni1; Mary Grace1; Carmen Lategan1; Peter Smith1; Ilya Raskin1; Mary Ann Lila1; 3NC State University, NC Research Campus, Kannapolis, NC; 2University of Cape Town, Cape Town, South Africa; 3Rutgers University, New Brunswick, NJ |
| ThP 335 | Characterization of Siderophores isolated from cell cultures using RPHPLC coupled to Ultra High-resolution Time-of-Flight Mass Spectrometry; Nicholas Hall1; Jeffrey Patrick1; Kevin Siek1; Joe Binkley1; Jeffrey P. Henderson1; Kaveri Chaturvedi1; Jan Crowley1; 3LECO Corporation, St. Joseph, MI; 2Washington University School of Medicine, St. Louis, MO |
| ThP 336 | Development of Signal Ratio Based Antioxidant Index for Assisting Identification of Polyphenolic Compounds by Mass Spectrometry; Jhe-Yi Liao1; Kuo-Lung Ku; National Chiay University, Chiay City, Taiwan |

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| ThP 339 | ESI-MS and ESI-MS/MS as a Toll to Evaluate Upgrading Processes of Bio-Oils; Rosanna Cardoso Lopes Pereira1; Patricia Verardi Abdelnur1; Marco Antonio Gomes Teixeira1; Emmanuelle Sales Retori1; Marlon Brando Bezerra de Almeida1; 1PETROBRAS, Rio De Janeiro, BRAZIL; 2Embrapa Agroenergia, Brasilia, Brazil |
| ThP 340 | Molecular Characterization of Biochar and Laser-induced in situ Fullerene Synthesis; Daniel Cole1; Aasim Azad1; Erica Smith1; Robert Brown1; Young Jin Lee1; 1Chemistry Department, Iowa State University, Ames, IA; 2Ames Lab, US-DOE, Ames, IA; 3CSET, Iowa State University, Ames, IA |
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| ThP 343 | Characterization of Biomass Oils and Fuels: Algae Lipids; Chang Samuel Hsu1; Huan He2; Jie Lu1; Vladislav V. London1; Mark R. Emmett1; 1Alan G. Marshall1; 2Future Fuels Institute, Florida State University, Tallahassee, FL 30310; 3Natl. High Magnetic Field Lab., Florida State Univ, Tallahassee, FL 30310; 4Dept. of Chem. and Biochem., Florida State Univ., Tallahassee, FL |
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**ThP 503** Antibody and MS-based Methods for Identifying SUMO-1 Modified Peptides; Omoruyi Osula1; Caelin Potts2; Michael Matunis3; Robert J. Cotter1,2; 1Johns Hopkins School of Medicine, Baltimore, MD; 2Middle Atlantic MS Laboratory, Baltimore, MD; 3Johns Hopkins School of Public Health, Baltimore, MD

**ThP 504** Characterization of Protein Thioredoxin Incorporated with the Unnatural Amino Acid β-hydroxynorvaline by Escherichia coli Threonyl-tRNA Synthetase; Anand Minajigi1; Bin Deng2; Christopher Franklyn1; University of Vermont, Burlington, VT

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**ThP 506** Profiling Strategy for Relative Quantification of Phosphopeptides from Tissue Extracts: Method Validation and Application to a Cardiovascular Disease Model System; Aruna B. Wijeratne1; Janet Bodmer1; Wendy D. Haffey1; Hongjun Shu1; Jo El J. Schultz2; Kenneth D. Greis3; 1The Department of Cancer & Cell Biology, University of Cincinnati, Cincinnati, OH; 2The Department of Pharmacology & Cell Biology, University of Cincinnati, Cincinnati, OH

**ThP 507** Label-free Phosphoproteomics Method to Investigate Signaling Pathways Downstream of Novel PI3K/mTOR Inhibitors in Cancer Cells; Pedro Casado-Izquierdo1; Juan Carlos Rodriguez-Prados1; Sabina Cosulich1; Sylvie Guichard1; Bart Vanhaesebroeck1; Pedro Cutilias2; 1Barts Cancer Institute, London, UK; 2AstraZeneca, Macclesfield, UK

**ThP 508** Quantitative Phosphoproteomics for Global Profiling of Kinase Activity: a Mass Spectrometry-Based Activitomic Approach to Cell Signaling; Luisa Beltran1; Pedro Cutilias2; 1Barts Cancer Institute, QMUL, London, UK

**ThP 509** Quantitation of Phosphorylation Levels in the TLR Signaling Pathway in Mouse Macrophages using iTRAQ; Virginie Sjoelund1; Aleksandra Nita-Lazar1; NIH/NIAID/PSIIM, Bethesda, MD

**ThP 510** A high-Throughput, in vitro, Multiplexed Kinase Activity Assay with a Benchtop Orbitrap Mass Spectrometer; Ryan Kunz1; 1Harvard Medical School, Boston, MA

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Detection of a Protein Conformational Equilibrium by Electrospray Ionisation-Ion Mobility-Mass Spectrometry; Matthew Jenner; Jacqueline Ellis; Wei-Cheng Huang; Emma Lloyd Raven; Gordon C.K. Roberts; Neil J. Oldham; 1School of Chemistry, University of Nottingham, Nottingham, UK; 2Department of Biochemistry, University of Leicester, Leicester, UK; 3Department of Chemistry, University of Leicester, Leicester, UK

Mobility-Mass Spectrometry Detection of a Protein Conformational ETD-MS Based Mapping of Clustered Glycans on Mucin-Type Glycopeptides; Nottingham, UK; 2Department of Yamauchi; Kenneth B. Tomer; 3Department of Chemistry, University of Wisconsin; 4Department of Environmental Health Science, Research Station, TX

Comparative Studies of Glycoprotein Using TiO2-Enrichment Glycopeptides using LC/MSMS and Multiple Reaction Monitoring (MRM) Mode; Swetha Menon; Liuxi Chen; Aileen Patterson; Ashley Cabecinna; Jun Han; Jason Serpa; David Wishart; Christoph Borchers; UVic-GBC Proteomics Centre, Victoria, CANADA; 2University of Alberta, Alberta, Canada

Structural Flexibility of Glyceraldehyde 3-Phosphate Dehydrogenase Revealed by H/D Exchange and Mass Spectrometry; Tatsuya Yamamoto; Yasuaki Kabe; Seiki Kuramitsu; Makoto Suematsu; Keio University, Tokyo, JAPAN; 2Sueatsu geniology project, ERATO, JST, Tokyo, JAPAN; 3Osaka University, Osaka, JAPAN; 4RIKEN Spring-B Center, Sayo, JAPAN

Study of the Redox Mechanism of Ape 1 by HDX-MS; Jun Zhang; Millie M. Georgiadis; Michael L. Gross; 1Washington University in St. Louis, St. Louis, MO; 2Indiana University School of Medicine, Indianapolis, IN; 3Indian University-Purdue University, Indianapolis, IN

Hydrogen Bond Stabilized Galactocyanose in Collagen Derived O-Linked Glycopeptides is Responsible for Their Anomalous Collision Induced Dissociation Pattern; Irina Perdivara; Lalith Perera; Marnisa Sricholpech; Mitsuo Yamauchi; Kenneth B. Tomer; 1National Institute of Environmental Health Science, Research Triangle Park, NC; 2North Carolina Oral Health Institute, Research Triangle Park, NC

ETD-MS Based Mapping of Clustered O-Linked Glycans on Mucin-Type Glycopeptides; Morten Thaysen-Andersen; Brendan Wilkinson; Richard J. Payne; Nicole H. Packer; Macquarie University, Sydney, Australia; 2Sydney University, Sydney, Australia

Serial Affinity Chromatography As A Selection Tool In Glycoproteomics; Kwanyoung Jung; Wonryeon Cho; Fred Regnier; Purdue University, West Lafayette, IN

Mass Spectrometric Identification and Characterization of Sialylated O-Linked Glycopeptides using TIO2-Enrichment Combined with Enzymatic and Chemical de-Glycosylation; Sara Eun Lendal; Arkadiusz Nawrocki; Peter Højrup; Martin Rassell Larsen; Protein Research Group, Odense, Denmark

Enriching Acidic Glycopeptides with Functionalized Silica; Ed Bodnar; Helene Perreault; University of Manitoba, Winnipeg, Canada

Microfluidic-based NanoLC/TOF for Rapid and Automated Characterization of N-linked Glycans from monoclonal Antibodies; Stephan Buckenmaier; Tom Van De Goor; Lukas Trojer; Agilent Technologies, Waldbrohn, Germany

Microfluidic Chips for Glycopeptide Analysis; Gregory O. Staples; Maggie A. Bynum; Yongfeng Yin; Kevin Killeen; Agilent Laboratories, Santa Clara, CA

Analysis of Protein Glycosylation Using Multi-Dimensional Separation and Multi-Stage Mass Spectrometry; Fan Xiang; Liang Zhao; 1Shimadzu Biotech, Pleasanton, CA; 2University of the Pacific, Stockton, CA

HILIC-MRM Assays Targeting for Analyzing Site-Specific Glycans of Multiple-Sites Glycosylated Proteins and Glycoprotein Mixtures; Hongwei Xie; Joe Riniger; Weibin Chen; 1Waters Corporation, Milford, MA; 2Protein Sciences Corporation, Meriden, CT

Identification and Quantification of glycopeptides using LC/MSMS and Multiple Reaction Monitoring (MRM) Mode; Swetha Pyreddy; Ehwang Song; Yehia Mechref; Texas Tech University, Lubbock, TX

A General Approach for Glycoprotein Analysis by Glycopeptide Mapping and Glycan Semi-Quantitation; Yanning An; John F Cipollo; Food and Drug Administration/CBER, Bethesda, MD

Comparison of PID Product on Synapt HDMS and PI Scan on 4000 Q-trap for Identification of N-linked Glycoproteins; Yong Yang; Robert Sherwood; Wei Chen; Theodore Thannhauser; Sheng Zhang; 1USDA-ARS at Cornell University, Ithaca, NY; 2Proteomics & Mass Spectrometry Facility, Cornell, Ithaca, NY

Comparative Studies of Glycoprotein Using Isotope Labeling and Electrospray Ion Trap Mass Spectrometry; Yi-Chun Ma; Chih-Yu Lin; Guor-Rong Her; 1National Taiwan University, Taipei, Taiwan; 2Academia Sinica, Taipei, Taiwan

Approaching Full Sequence Coverage of Glycoproteins using Multiple Enzymes and Microwave-Assisted Digestion; Marion Rohmer; Dominic Baemulsberger; Benjamin F. Mueller; Tobias Beckhaus; Michael Karas; Goethe University, Frankfurt Am Main, Germany

Automated N-Glycopeptide Lookup from Glycan Databases using Tandem Mass Spectra; Kevin B. Chandler; Petr Pompa; Marshall Bern; Radislav Goldman; Nathan J. Edwards; Georgetown University, Washington, DC; 2Palo Alto Research Center, Palo Alto, CA
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THP 586 GlycoPep Grader-An Automated Analysis Tool to Determine N-linked Glycopeptide Composition from MS/MS Data; Carrie Woodin; David Hua; Morgan Maxon; Kathryn Rebecchi; Eden Go; Heather Desaire; KU Bioanalytical Division, Lawrence, KS

THP 587 Multiplex-MRM Analysis of Human Proteins Obtained from Dried Bloods Spots; Alexander G Camenzind1; Juncong Yang1; Angela M Jackson1; Dominik Domanski1; Derek Smith1; Tim F Oberlander1; Christoph H Borchers1; 1Uvic Genome BC Proteomics Centre, Victoria, BC; 2CFRI, BC Children’s Hospital, Vancouver, BC

THP 588 Quantitative Proteomic Analysis of Doxorubicin Resistance in Ovarian Cancer Cells using SILAC; Shasha Wei1; Xiulan Chen1; Ying Ma1; Xiaoyuan Chen1; Fuquan Yang1; 1Institute of Biophysics, CAS, Beijing, China; 2NIBIB, NIH, Bethesda, MD

THP 589 DifferentiallyExpressed Proteomes of Fibroblast-Derived Pluripotent Stem Cells Using Protein-Based Reprogramming; Ekwon Kim1; Ho-Pil Min1; Sungyoon Moon1; Hyunsoo Kim1; Kyunggon Kim1; Yoowook Kwon1; Hyosoo Kim1; Jonghwa Jin1; Youngsoo Kim1; College of Medicine, Seoul Nat’l Univ, Seoul, South Korea

THP 590 Characterizing Mitochondrial Proteomes in Primary Leukaemic Cells and Cell Lines; Joanne B. Connolly1; Thérèse Mckenna1; Remy Klug1; Gushinder Kaur-Atwal1; Claudia Langlais2; Rebekah Jukes-Jones2; Kelvin Cain2; 1Waters, Manchester, UK; 2MRC Leicester, Leicester, UK

THP 591 Proteomic Analysis of Plasma Microparticles from Patients with Systemic Lupus Erythematosus; Ole Østergaard; Christoffer T Nielsen; Niels H H Heggaard; Statens Serum Institut, Copenhagen, Denmark

THP 592 Proteomic Analyses of EGFR-Interacting Proteins to Elucidate Differences In Signal Transduction Downstream Of Lung Cancer-Specific Mutant EGFRs; Udayan Guha1; Todd M. Greco1; Abhilash Venugopalan1; Harold E. Varmus1,2; Ileana M. Cristea1; 1Medical Oncology Branch, National Cancer Institute, Bethesda, MD; 2Dept. of Molecular Biology, Princeton University, Princeton, NJ; 3National Human Genome Research Institute, Bethesda, MD; 4National Cancer Institute, Bethesda, MD

THP 593 Identification and Relative Quantification of Differentially Expressed Bacterial Proteins after Antibiotic Treatment; Gushinder Kaur-Atwal1; Joanne B. Connolly1; Thérèse Mckenna1; Julia Elisabeth Bandow1; Waters Corporation, Manchester, UK; Ruhr-Universität Bochum, Bochum, Germany

THP 594 Secretome Analysis of Unrestricted Somatic Stem Cells– Identification of Novel Candidate Neurite Outgrowth Factors; Heiner Falkenberg1; Jessica Schira1; Hans Werner Müller2; Heimut E. Meyer1; Kai Stühler1; 1Medizinisches Proteom-Center, Bochum, Germany; 2Molecular Neurobiology, University Hospital, Düsseldorf, Germany

THP 595 Identification of Proteins from Taenia solium Tapeworms in Different Stages of Proglottid Maturation; Miguel Garcia1; Cesar Costa Vera1; Elizabeth Minda1; Richar Rodriguez2; André M. Deelder1; Magnus Palmblad1; 1Escuela Politécnica Nacional / Dept. de Física, Quito, ECUADOR; 2Centro Internacional de Zoonosis-U Central, Quito, Ecuador; 3Leiden University, Leiden, Netherlands

THP 596 Study of ESBL Producing- and Beta Lactam-Sensitive E.coli using MALDI-TOF-MS and Hybrid MALDI-QIT-TOP Mass Spectrometry; Omar Belgacem1; Emmanuel Wey1; Indran Balakrishnan1; Shervanthi Homervanniasinkam1; Valery Edwards-Jones1; Pranav Somaiya1; 1Shimadzu, Kratos, Manchester, UK; 2Royal Free Hospital, London, UK; 3NPMR-UC, London, UK

THP 597 Targeted Proteomic Analysis of Laser Capture Microdissected Breast Cancer Tissues for Exploring Field Effects on Normal Epithelia Adjacent to Tumor; Sangwon Cha1; Shemeica N. Binns1; Dennis C. Sgroi2; Barry L. Karger1; 1Medical Oncology Branch, National Cancer Institute, Bethesda, MD; 2Massachusetts General Hospital, Boston, MA

THP 598 Profiling Changes in the Surface Proteome of Mycobacterium avium During Early Infections by LC-MS/MS; Michael McNamara1; Li Zhang; Shin-Cheng Tzeng; Claudia Maier; Joseph Beckman; Luiz Bermudez; Oregon State University, Corvallis, OR

THP 599 Molecular-Level Elucidation of the Anti-Carcinoma Mechanisms of New Agents via High-Resolution, Comparative Analysis of the Drug- Responsive Proteomic Signatures; Frank
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**ThP 600**
Investigation of Natural HLA-DR Associated Peptides in Rheumatoid Arthritis or Antibiotic-Refactory Lyme Arthritis by Mass Spectrometry; Chunxiang Yao1; Elise E. Drouin2; Robert Seward1,2; Allen C. Steere1; Catherine E. Costello1; 1Boston University School of Medicine, Boston, MA; 2MGH, Harvard Medical School, Boston, MA

**ThP 601**
Histone H1 Phosphorylation as a Biomarker for Invasiveness in Human Bladder Cancer; Kelly H. Telu; Besma Abboua1; Steven K. Clinton; Amir Mortazavi; Michael A. Freitas; Ohio State University, Columbus, OH

**ThP 602**
Protein Differences Associated with Human Papillomavirus Status in Oropharyngeal Squamous Cell Carcinoma (OSCC); Nico Jehmlich1; Brandee Brown2; Wendell Yarbrough3; Daniel C. Liebler4; Robert Siebels5; 1Vanderbilt University, Nashville, TN; 2Ernst-Moritz-Arndt-University, Greifswald, Germany; 3Wheeler2; 4Vanderbilt University, Nashville, TN; 5Vanderbilt School of Medicine, Nashville, TN

**ThP 603**
Proteomics of Human HIV-CSF Based on Multiplex Separation of Intact Proteins; Adriana Bora; Dawn Chen; Carols Anderson; Muznabanu Bachani; Justin McArthur; Ned Sacktor; Avindra Nath; Robert Cotter; Johns Hopkins School of Medicine, Baltimore, MD

**ThP 604**
Protein Expression Signatures of Epidermal Growth Factor Receptor Inhibition; Matt Myers1; Daniel C. Liebler2; 1Vanderbilt University, Nashville, TN; 2Vanderbilt University School of Medicine, Nashville, TN

**ThP 605**
Quantitative Studies of Cancer Epigenetics Using Label-Free Top Down and Bottom Up to Interrogate Histone Modifications; Jeremiah D. Tipton1; Steve M. Sweet; Yupeng Zheng; Kenneth R. Durbin; Mingxi Li; Paul M. Thomas; Neil L. Kelleher; Northwestern University, Evanston, IL

**ThP 606**
Mammalian Sirtuins SIRT1-7: A New Family of Antiviral Genes; Emre Koyuncu1; Yana Miteva1; Hanna Budayeva; Thomas Shenk; Ileana M. Cristea; Princeton University, Princeton, NJ

**ThP 607**
Hemoglobin Variant Analysis Using an LTQ-Orbitrap Top-down Platform with ETD, HCD and LTQ-CID; Roger Theberge; Nancy Leymarie; Mark E. Mccomb; Catherine E. Costello; Boston University School of Medicine, Boston, MA

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**ThP 608**
Label-Free Characterization of a Eukaryotic Protein Corona Enveloping Silver Nanoparticles; Richard A. Eigenheer1; K.E. Wheeler2; A.M. Lampe3; M.Y. Nakamoto3; B.S. Phinney1; 1UC Davis, Davis, CA; 2Santa Clara University, Santa Clara, CA

**ThP 609**
Label Free Proteomics at High Mass Accuracy using a Quadrupole TOF Mass Spectrometer; Matthew McKay; Dylan Xavier; Thiri Zaw; Matthew Fitzhenny; Ardeshrir Amirkhani; Xiaomin Song; Mark Malloy; Australian Proteome Analysis Facility, Sydney, Australia

**ThP 610**
Label-Free Quantification of HPLC Protein Fractions using High-Resolution Precursor Peak Isotope Pattern Matching to Monitor Global Proteome Dynamics; Cuilong Wan; Jian Liu; Andrew Emili; University of Toronto, Toronto, Canada

**ThP 611**
When Every Spectrum Counts: An Integrated Grid and Cloud Enabled Software Pipeline for Identification of Elusive Proteins; Cereena U. Mohien1; David R. Colquhoun1,2; Lindsay A. Parish2; Ravi Tharakan3; Roel R. Dinglasan4; Nathan Edwards5; David R. M. Graham5; 1Johns Hopkins School of Medicine, Baltimore, MD; 2Johns Hopkins Bloomberg School of Public Health, Baltimore, MD; 3Georgetown University Medical Center, Washington, DC; 4Johns Hopkins Bayview Proteomics Center, Baltimore, MD

**ThP 612**
An Isotopic Tagging and Computational Pattern Identification Method for Chemically Directed Proteomics; Krishnan Palaniappan; Austin Pitcher; Brian Smart; Carolyn Bertozzi; UC Berkeley, Berkeley, CA

**ThP 613**
Quantitative Profiling of GTP Binding Proteins Using Label-free Functional Proteomics; Kathrin Bartho; Thomas Lens; Yan Luo; Simon Michaelis; Friedrich Kroll; Michael Seifkow; Mathias Dregel; Sabine Baumgart; Hubert Koester; Bioanalytics GmbH, Berlin, Germany

**ThP 614**
An Ion Mobility Enabled Data Independent Acquisition Strategy for the Quantitative Characterization of Hepatocytes Secreted Rat Exosomes; Eva Rodríguez-Suárez1; Javier Conde-Vancells2; Esperanza González-Jimenez3; Chris Hughes4; Johannes PC Vissers5; James IS Langridge6; Félix Ebrutzma; Bariért 7; José M. Mato8; Juan M. Falcón-Pérez9; 1Proteomic Unit, CIC bioGUNE, Derio, Spain; 2Metabolomic Unit, CIC bioGUNE, Derio, Spain; 3Waters Corporation, Manchester, UK

**ThP 615**
Comparative Study of Label and Label-Free Techniques for Relative Protein Quantification: Precision, Accuracy, and Dynamic Range; Marcus Sjödin; Magnus Wetterhall; Jonas Bergquist; Konstantin Artemenko; Uppsala University, Uppsala, Sweden

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**ThP 616**
Chemoproteomics Profiling of HDAC Inhibitors Reveals Targeting of Multiple HDAC Complexes with Compound Class-Dependent Selectivity; Marcus Bantscheff; Carsten Hopf; Mikhail M. Savitski; Antje Dittmann; Carsten Hopf; Mikhail M. Savitski; Antje Dittmann; Uppsala Applied Science Lab, Uppsala, Sweden

**ThP 617**
Single Gene Analysis Using Chromatin DNA Rehybridization and Mass Spectrometry to Identify Transcription Factors; Huiqing Zhang; Sarah Morse; Jacqueline Mattick; Katherine Southard; Tian Zhang; Linda McGown; Rensselaer Polytechnic Institute, Troy, NY

**ThP 618**
An MRM Study of EZH2 and its Somatic Mutations in Follicular and Diffuse Large B Cell Lymphoma; Annie Moradian1; Damian B. Yap2,4; S.-W. Grace Cheng3; Tobias Berg2; R. Keith Humphries1,6; Samuel A.J. R. Aparicio5; Gregg B. Morin1,5,7; 1Genome Sciences Centre, BC Cancer Agency, Vancouver, Canada; 2Department of Pathology & Laboratory Medicine UBC, Vancouver, Canada; 3Terry Fox Laboratories, BC Cancer Agency, Vancouver, Canada; 4Department of Molecular Oncology, BC Cancer Agency, Vancouver, Canada; 5Department of Medical Genetics, UBC, Vancouver, Canada; 6Department of Medicine, UBC, Vancouver, Canada
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ThP 619  **Mass Spectrometric Analysis of DNA-Bound Proteins From a Complex Matrix**;  
Michael Zickus; Shama Mirza; Hector Guillen Ahlers; Regina Cole; Molly Pellitteri-Hahn; Milena Zelembaba; Mark Scalif; Michael Shortreed; Lloyd M. Smith; Lisa Cirillo; Michael Olivier;  
1Medical College of Wisconsin, Milwaukee, WI; 2University of Wisconsin-Madison, Madison, WI

ThP 620  **Proteo-Genomics for Investigating the Role of Histone H2B Variants in Chromatin Structure**; Rosalynn Menden; Anna Arnaudo; Nicolas Young; Benjamin Garcia; Princeton University, Princeton, NJ

ThP 621  **The Role of Histone H2A Variants in Epigenetic Gene Regulation**; Anna Arnaudo; Rosalynn Menden; Nicolas L. Young; Benjamin Garcia; Princeton University, Princeton, NJ

ThP 622  **Comprehensive Phosphoproteomic Mode of Action Analysis in Cultured Cell Lines and Xenograft Models**; Andreas Tebbe; KINAXO Biotechnologies, Munich, Germany

ThP 623  **2-D DIGE and MS Analysis of Multicellular Tumor Spheroids in Evaluation of Breast Cancer Treatment**; Jennifer Fox; Susanne Grimsby; Anneli Jorsbach; Azita Monazzam; Kofi Nyamekye; Åsa Hagner-McWhirter; GE Healthcare, Piscataway, NJ; GE Healthcare, R&D Bio Technology, Uppsala, Sweden; GE Healthcare, Uppsala Applied Science Lab, Uppsala, Sweden

ThP 624  **Profiling the Interaction of Macrophage Inhibitory Factor with the Idiosyncratically Hepatotoxic Fluoroquinolone, Trovafloxacin**; Hua Tang; Scott E. Warder; Melanie J. Patterson; Paul L. Richardson; Eric A. Blomme; Michael J. Liguori; Shaun M. McLoughlin; Abbott Laboratories, Abbott Park, IL

ThP 625  **Quantitative Proteomics Analysis of the Signaling Pathways that Confer Acquired Radioresistance in Pancreatic Cancer Cells**; Jianzhong Zhou; Yu-Chun Du; University of Arkansas, Fayetteville, AR

ThP 626  **Detection of Caspase Dependent Cleavage Substrates in TRAIL-induced Apoptosis by a Novel SELFCRAB Based Strategy**; Gabrielle Stoehr; Christoph Schab; Johannes Graumann; Matthias Mann; 1MPI for Biochemistry, Martinsried, Germany; 2Kinaxo Biotechnologies, Martinsried, Germany; 3Well Cornell Medical College, Doha, Qatar

ThP 627  **Identification of Biomarkers by Proteomic and Chromosome Comparison of Inflammatory Breast Cancer Cell Lines**; Yue Zhang; Qiaozhen Lu; Shuai-Lin Wu; William Hancock; Barnett Institute, Northeastern University, Boston, MA

ThP 628  **Quantitation of aberrant glycoforms by lectin-coupled multiple reaction monitoring**; Eun Sun Ji; Yeong Hee Ahn; Jong Shin Yoo; Yong-Sam Kim; Jeong Heon Ko; Korea Basic Science Institute, Cheongwon-Gun, South Korea; 2Hannam University, Daejeon, South Korea; 3Daejeon-KRIBB-FHCRC Research cooperation center, Daejeon, South Korea

ThP 629  **Integrated Mass Spectrometry-Based Analysis of Plasma Glycoproteins and Their Glycan Modifications**; Hong Wang; Chee-Hong Wong; Alice Chui; Ayumu Taguchi; Allen Taylor; Sadanori Sekiya; Hidenori Takahashi; Masaki Murase; Shigeki Kajihara; Shinichi Iwamoto; Koichi Tanaka; Samir Hanash; 1Fred Hutchinson Cancer Research Center, Seattle, WA; 2Shimadzu Corporation, Kyoto, Japan; 3Ventana Medical Systems, Inc, Oro Valley, AZ

ThP 630  **Enrichment and Quantitation of 3-Nitrotyrosine-Modified Proteins**; Tasneem Muharib; Deneen Gaynor; Rena A. S. Robinson; University of Pittsburgh, Pittsburgh, PA

ThP 631  **SNO-SNIPE(R): A Surface-functionalized Nanoprobe-based Identification Strategy for Protein S-Nitrosylation Enrichment**; Wei-Chieh Ching; Yi-Ju Chen; Chien-Cheng Chou; Kao-Yu Chou; Chun-Cheng Lin; Yu-Ju Chen; Graduate Institute of Life Sciences, National Defense Medical Center, Taipei City, Taiwan; 2Institute of Chemistry, Academia Sinica, Taipei City, Taiwan; 3IBS, National Taiwan University, Taipei City, Taiwan; 4Institute of Chemistry, National Tsing Hua University, Hsinchu, Taiwan; 5Institute of Chemistry, National Taiwan University, Taipei City, Taiwan

ThP 632  **S-Alkylating Biotin Switch Method Combining Label-free Strategy for Site-specific Quantitation of the S-Nitrosoproteome in Human Colorectal Cancer Tissues**; Yi-Ju Chen; Wei-Chieh Ching; Hsiao-Chiao Chou; Jinn-Shiun Chen; Kay-Hoii Koh; Jenn-Han Chen; Yu-Ju Chen; 1IBS, National Taiwan University, Taipei City, Taiwan; 2Institute of Chemistry, Academia Sinica, Taipei City, Taiwan; 3National Defense Medical Center, Taipei City, Taiwan; 4National Defense Medical Center, Taipei City, Taiwan; 5Colorectal Section, Department of Surgery, Chang Gung Memorial Hospital, Taoyuan, Taiwan; 6JBC, Academia Sinica, Taipei City, Taiwan; 7Institute of Chemistry, National Taiwan University, Taipei City, Taiwan

ThP 633  **A Mass Spectrometry-Based Approach to Determine Linear Kinase Substrate Motifs**; Arminja Kettenbach; Tuabin Wang; Stefan Knapp; Chris Bailey-Kellogg; Scott Gerber; Dartmouth Medical School, Hanover, NH; 1Dartmouth College, Hanover, NH; 2University of Oxford, Oxford, UK

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ThP 634  **Identification and Validation of Vaccine Candidate Proteins by 2-Dimensional Mass Spectrometry Analysis of Group A Streptococcus**; Lori C Stansberry; Angela Payne; Julie Skinner; Loren Schultz; Jon Heinrichs; Eberhard Durr; Merck and Co., West Point, PA

ThP 635  **The Multiplexed Analysis of Two Therapeutic Monoclonal Antibodies and Non-Murine IgG in a Pharmacological Mouse Model by LC-MS/MS**; Mark Jairaj; Lloyd King; UCB, Slough, UK

ThP 636  **Method Optimization on Quantitative LC - MS analysis of a Therapeutic Monoclonal Antibody (Trastuzumab) in Human Serum**; Hua Yang; Catalin Doneanu; Erin Chambers; Weibin Chen; Diane Diehl; Eduard S. P. Bouvier; Waters Corporation, Milford, MA

ThP 637  **MRM Quantification of Host Cell Proteins in Protein Biopharmaceuticals**; Catalin Doneanu; Weibin Chen; Alex Xenopoulos; St John Skilton; Jeff Mazzeo; 1Waters Corporation, Milford, MA; 2Millipore Corporation, Bedford, MA

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**ThP 647**

Label-free Global Proteomics Comparison of Interferon Alpha and Beta Response in Human Liver Carcinoma Huh7 Cells: Relevant to Antiviral Therapy; Kristin E. Burnum; Qi Bai; Yue Zhu; Jennifer Yang; Da Ren; Drew Nichols; Pavel V. Bondarenko; Amgen Inc., Thousand Oaks, CA

**ThP 649**

Using LC-MS/MS for Comparative Analysis of Monoclonal Antibodies and Quantification of Cardiac Troponins In Human Serum; Mark S Lowenthal; John Schiel; Nathan G. Dodder; Hugo Gasca-Aragon; Leslie Bransfield; David M Bunk; National Institute of Standards and Technology, Gaithersburg, MD

**ThP 650**

Mass Spectrometry Analyses of Kappa and Lambda Fractions of IgG Result in Increased Number of Complementarity Determining Regions Identifications; Ingrid Brodman; Dominique De Costa; Christoph Stingl; Lennard Dekker; Martijn VandenBuijn; Jan Lindemans; Rob van Klaveren; Theo Luider; Erasmus Medical Center, Rotterdam, the Netherlands

**ThP 651**

Identification of a Cell Epitope of Diphertheria Toxin by Stable Isotope Tagging and Probing of StERICALLY Hindered Protein Sites; Hugo D. Meirin; Grażyna Sosinska; Joost P. Uittenbogaard; Geert P.M. Mommen; Bernard Metz; Ad P.J.M. de Jong; Natl Inst for Public Health and the Environment, Bilthoven, Netherlands

**ThP 652**

Mass Spectrometric Epitope Mapping without Immobilization of Neither the Antibody nor the Antigen; Reham F. El-Kased; Cornelia Koy; Peter Lorenz; Helen Montgomery; Koichi Tanaka; Hans-Jürgen Thiesen; Michael O. Glocker; Proteome Center Rostock, University of Rostock, Rostock, Germany; 2Institute of Immunology, University of Rostock, Rostock, Germany; 3Shimadzu, Koichi Tanaka MS Research Laboratory, Manchester, UK; 4Koichi Tanaka Research Lab, Shimadzu Corporation, Kyoto, Japan

**ThP 653**

Evaluation of Label-free Quantitation Methods and Targeted Analysis of MHCI Bound Peptides; Manolo D. Plasencia; Henry W. Rohrs; Shirley J. Petzold; Michael L. Gross; Emil R. Unanue; 1Washington University School of Medicine, St. Louis, MO; 2Washington University, St Louis, MO

**ThP 654**

MHC II Peptides as Breast Cancer Immunotherapy Agents; Olelya Chornoguz; Lydia Grima; Joshua Wilde; Alexei Gapeev; Michael O’Neill; Suzanne Ostrand-Rosenberg; UMBC, Baltimore, MD

**ThP 655**

Case study: Application of Mass Spectrometry for Evaluation of N-glycans, Lipids and Protein Impurities in a Plant-Made Influenza VLP Vaccine; Genevieve Mercier; Nathalie Landry; Julie Boisvert; Marc-André D’Aoust; Michele Dargis; François LeMauff; Patrice Lerouge; Louis-P. Vezina; 1Medicago, Quebec, Canada; 2Université de Rouen, Mont Saint Aignan, Cedex, France

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Profiling Caspase-6 HTS Hits Using AQUA and MRM Quantitation Technique; Tommy K. Cheung; Yichin Liu; David Arnott; Qui Phung; Genentech, Inc., South San Francisco, CA

**ThP 657**

Secretome Monitoring in Recombinant CHO-DG44 Cells Using Click Chemistry; Peter G. Slade; Graziella Piras; Margaret Liu; Define C. Koch; Daniela Hutanu; Cheryl Moody-Bartel; Stephen F. Gorffin; 1Life Technologies-Molecular Probes, Eugene, OR; 2Life Technologies-
Development of a Methodology for Quality Human Leukemia Cells
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Pranhitha Reddy; David Hambly; Ronald Gillespie;
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Richard D Smith1;
Washington, Seattle, WA
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1Boston University, Boston, MA; 2Boston
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Observatory, Cape Town, South Africa; 2Centre for
Proteomic & Genomic Research (CPGR),
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Kevin KrocK; Richard B. van Breemen; University of
Illinois College of Pharmacy, Chicago, IL
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McDonald1; Shaun Garnett1; Mare Vlok2; Jonathan
Blackburn1; University of Cape Town,
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Oligomer Formation of Amyloid-β Peptide
and Its Interaction with Other Promoting
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Paul A. Townsend1; Spiros D. Garbis1; 1Academy of Athens, Athens, Greece; 2University of Southampton, Southampton, UK

**ThP 677**

Proteomics Investigation of Archival Lesions of Chronic Pancreatitis and Pancreatic Cancer; Sheng Pan1; Ru Chen1; Tyler Stevens2; Damon May3; Martin McIntosh4; Teresa Brentnall1; 1University of Washington, Seattle, WA; 2Cleveland Clinic Foundation, Cleveland, OH; 3Fred Hutchinson Cancer Research Center, Seattle, WA

**ThP 678**

Large-Scale Comparative Proteomic Analysis of Isolated Colon Cancer Cells from Multiple Patients using a Comprehensive and Reproducible Ion-Current-Based Method; Chengqian Tu1; Jun Li1; Wilfrido Mojica1; Jun Qu1; University at Buffalo SUNY, Buffalo, NY

**ThP 679**

ProtPair: Pairwise Protein Expression Classifier for Candidate Biomarker Discovery; Parminder Kaur1; 1Case Western Reserve Univ., Cleveland, OH

**ThP 680**

Characterization and Comparative Analysis of Proteomic Profiles of Leukemic and Primary Human NK Cells: Did the Cancer Cells Differ?; Mildred Felder1; Manish Patankar1; Lingjun Li1; University of Wisconsin-Madison, Madison, WI

**ThP 681**

The Use of Nitric Oxide as a Radiosensitiser of Hypoxic Prostate Cancer Characterized by Data Independent Label-Free Ion Mobility LC-MS; Grant D Stewart1; Jordan Ingles2; Holger Hus1; Fei Xu3; Craig Dorschel4; 1Johannes PC Visser1; 2James Ross2; 3Edinburgh Urological Cancer Group, Edinburgh, UK; 4Tissue Injury and Repair Group, Edinburgh, UK; 5Waters Corporation, Manchester, UK; 5Waters Corporation, Milford, MA

**ThP 682**

Label-Free Quantitative Proteomic Analysis of Experimental Autoimmune Myocarditis Induced in the Rat; Jong Bok Seo1; Joo Hee Chung1; Sang Goo Kim1; Soo Young Kim1; Eun Jung Bang1; Kwan Soo Hong1; Korea Basic Science Institute, Seoul, South Korea

**ThP 683**

Quantitative Label-Free Protein Profiling of Mouse Hippocampus; Lewis M. Brown1; Joseph B. Rayman2; Alexandre Gornstein3; Eric B. Kandel1; 1Columbia University, New York, NY; 2Columbia University Medical Center, New York, NY

**ThP 684**

Optimizing Specificity and Sensitivity of Label-Free Quantitative Proteomic Biomarker Discovery; Ping Yan1; Shuchua Zhang1; Jeffrey Whiteaker2; Jacob Kennedy1; Chenwei Lin3; Susan E. Abbatangelo2; Karl R. Clauser2; Naomi Chodnovskiy2; Steven A. Carr2; Amanda Paulovich1; 1Fred Hutchinson Cancer Research Center, Seattle, WA; 2Broad Institute of MIT and Harvard, Cambridge, MA

**ThP 685**

Improved Protein Detection and Quantification using Immunodepletion Combined with IEF Fractionation for the Detection of Plasma Biomarkers; Mert Pekcan1; Dominik Domanski2; Darryl B Hardie1; Juncong Yang2; Tyra J Cross2; Derek Smith2; Hilal Karagül1; Christoph H Borchers3; 1Ankara University Faculty of Veterinary Medicine, Ankara, TURKEY; 2Uvic Genome BC Proteomics Centre, Victoria, Canada

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Development of Personalized Quantitative Strategies for Cerebrospinal Fluid Proteomics; 1Hsuan Chen1; Yi-Chung Li1; Chia-Li Han3; Ying-Wei Lu4; Chun-Cheng Lin1; Yu-Ju Chen1; 3National Taiwan Normal University, Taipei, Taiwan; 4Taipei Veterans General Hospital, Taipei, Taiwan; 5Academia Sinica, Taipei, Taiwan; 6National Tsing Hua University, Hsinchu, Taiwan; 7National Taiwan University, Taipei, Taiwan

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Profiling of Differentially Secreted Biomarkers from Isogenic Breast Cancer Cell Lines; Un-Beom Kang1; Bio-Medieng, Seongnam-Si, South Korea

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Identification of Ageing Biomarkers in the Fungus Podospora Anserina; Marthe Chimi1; Stefan Dröse1; Heinrich Heide1; Ilka Wittig2; Mirco Steger1; Andrea Hamann1; Alexandra Werner1; Heinz D. Osiewacz2; Goethe University of Frankfurt, Frankfurt, Germany

**ThP 689**

High Resolution Quantitative Proteomic Analysis for Identification of Gallbladder Cancer Biomarkers; Nandini A. Sahasrabuddhe1, 2; Mustafa A. Barhuiya3; Sneha M. Pinto1; Babylashkhi Muthusamy1; Vishalakshi Nanjappa1; Braj R. Shrivastav1; Pramod K. Tiwari1; Raghothama Dharmadhakty1; Akhilesh Pandey1, 2; 1Institute of Bioinformatics, Bangalore, India; 2Johns Hopkins University, Baltimore, MD; 3Jiwaji University, Gwalior, India; 4Cancer Hospital and Research Institute, Gwalior, India

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A Quantitative Proteomics Timecourse Study to Identify Protein Markers of Niemann-Pick Disease, type C; Stephanie M. Colonna; Xiaosheng Jiang1; Peter S. Backlund1; Christopher A. Wassif2; Howard Schullman3; Daniel Chelsky3; Sushmita Mimi Roy4; 1Capron Proteomics US LLC, Menlo Park, CA; 2New York University, New York, NY; 3Capron Proteomics Inc., Montreal, Quebec, Canada

**ThP 691**

Proteomic Identification of Biomarkers of Chronic Drug Exposure Using Label-Free Differential Profiling; Xiaolei Xie1; Daniel Lopez-Ferrer2; Governed Gil3; Bich Nguyen3; Kenneth Carr4; 1Wistar Institute, Philadelphia, PA; 2University of Pennsylvania, Philadelphia, PA

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Comprehensive Proteome and Transcriptome Analysis of Mouse Organ of Corti; Shi-Jian Ding1, 2; Miao Liu1; Jason Pecka1; Xin Huang2; Kirk Beisel1; 1Department of Pathology and Microbiology, UNMC, Omaha, NE; 2Mass Spectrometry Proteomics Core Facility, UNMC, Omaha, NE; 3Department of Biomedical Sciences, Creighton Univ, Omaha, NE

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Comparison of Primary and Metastatic Melanoma Cells Using SILAC and label-Free LC-MS Reveals Key Metastasis and Autophagy Pathways; Huan Wang1; Shengfu Piao2; Ravi K. Amaravadi3; David W. Speicher4; 1Wistar Institute, Philadelphia, PA; 2University of Pennsylvania, Philadelphia, PA

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Multi-Laboratory Examination of a Set of Designed Quantitation Standard Samples to Establish Benchmark Metrics for Isobaric Label-Based Differential Expression Studies; Sean L. Seymour1; Brian Williamson1; Ignat Shilov2; Rebecca H. Monk2; Matt McKay2; Xiaomin Song3; Mark Molly4; Christie L. Hunter5; 1AB SCIEX, Foster City, CA; 2AB SCIEX, Framingham, MA; 3APAF, Sydney, Australia; 4National Institutes of Health, Bethesda, MD; 5Agilent Technologies, Mass Spectrometry Proteomics Core Facility, UK

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ThP 698 Mass Spectrometric Analysis of Relative Protein Expression Levels in Glioblastoma Multiforme Tissues and Lung Cancer Metastasized to the Brain; Xi Simon Wang1; Leroi Desouza1; Olga Krakovska1; Abhijit Guha2; KM Michael Siu1; 1York University, Toronto, Canada; 2Arthur & Sonia Labatts Brain Tumor Research Center, Toronto, Ontario
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