MSACL 2017 US
9th Annual Conference & Exhibits
Palm Springs, CA
January 22-26
MSACL 2017 US

The 9th Annual North American Congress of The Association for Mass Spectrometry: Applications to the Clinical Lab

Palm Springs, California

January 22 - 26, 2017

Renaissance Hotel & Palm Springs Convention Center

The Association is a non-membership, non-profit 501(c)(3) tax-exempt California Corporation with the mission of furthering education in the field of mass spectrometry.

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Thursday @ 9:00 AM in Room 6 (SmokeTree)

• SESSION 6 • TRACK 1 • Insights into Antimicrobial Resistance

Thursday @ 2:15 PM in Room 1 (Mojave Learning Center)

• SESSION 6 • TRACK 2 • Calcium Metabolism

Thursday @ 2:15 PM in Room 2 (Catalina)

• SESSION 6 • TRACK 3 • Proteomics and 'The Emperor of All Maladies'

Thursday @ 2:15 PM in Room 3 (Madera)

• SESSION 6 • TRACK 5 • Metabolism and Drugs

Thursday @ 2:15 PM in Room 5 (Sierra)

• SESSION 6 • TRACK 6 • Optimizing Data Analysis

Thursday @ 2:15 PM in Room 6 (SmokeTree)

• SESSION 7 • TRACK 1 • New Technologies for Clinical Applications of Metabolomics

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Thursday @ 3:30 PM in Room 2 (Catalina)

• SESSION 7 • TRACK 3 • Discovery Proteomics

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• SESSION 7 • TRACK 4 • Therapeutic Drug Monitoring

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• SESSION 7 • TRACK 5 • Closing Keynote - 45 min

Thursday @ 3:30 PM in Room 5 (Sierra)

POSTER PRESENTATIONS

POSTERS BY TOPIC

POSTERS BY NUMBER

PRESENTER INDEX
## Sponsorship & Travel Grant Support

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<th>Sponsor</th>
<th>Amount</th>
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</thead>
<tbody>
<tr>
<td>Platinum</td>
<td>Thermo Scientific</td>
<td>$18,900</td>
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<td>Gold</td>
<td>Shimadzu</td>
<td>$12,600</td>
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<tr>
<td>Silver</td>
<td>Indigo bioAutomation Agilent Technologies</td>
<td>$6,300</td>
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<tr>
<td>Bronze</td>
<td>Bruker Chromsystems PerkinElmer SCIEX</td>
<td>$3,150</td>
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<tr>
<td>Travel Grant Support</td>
<td>Thermo Scientific</td>
<td>$10,000</td>
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<tr>
<td></td>
<td>Cambridge Isotope Laboratories, Inc. Isotope.com</td>
<td>$2,000</td>
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</tbody>
</table>
## Scientific Committee

**Chair**: David Herold, MD, PhD  
*University of California, San Diego*  
*VA Medical Center, San Diego*

### Endocrinology

- **Dan Holmes, MD** (Lead)  
  *St. Paul’s Hospital*
- **Michael Chen, MD**  
  *McGill University*
- **Brian Rappold**  
  *Essential Testing*
- **Shannon Haymond, PhD**  
  *Ann and Robert H. Lurie Children’s Hospital of Chicago, Northwestern University, Feinberg School of Medicine*

### Metabolomics

- **Rick Yost, PhD** (Lead)  
  *University of Florida*
- **Tim Garrett, PhD**  
  *University of Florida*
- **Gary Patti, PhD**  
  *Washington University*

### Microbiology

- **Susan Butler-Wu, PhD** (Lead)  
  *University of Southern California*
- **Pieter Dorrestein, PhD**  
  *University of California, San Diego*
- **Carey-Ann Burnham, PhD**  
  *Washington University*
- **Vanessa Phelan PhD**  
  *University of Colorado*
- **Nathan Ledeboer, PhD**  
  *Medical College of Wisconsin*

### Proteomics

- **Cory Bystrom, PhD** (Lead)  
  *Cleveland Heart Lab*
- **Mari DeMarco, PhD**  
  *The University of British Columbia*
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<tr>
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<th>Regulations &amp; Standards</th>
<th>Tissue Imaging</th>
<th>Toxicology / TDM / Pain</th>
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<tr>
<td>Rob Fitzgerald, PhD (Lead)</td>
<td>Julianne Botelho, PhD (Lead)</td>
<td>Livia Eberlin, PhD (Lead)</td>
<td>Kara Lynch PhD (Lead)</td>
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<tr>
<td>University of California, San Diego</td>
<td>CDC</td>
<td>University of Texas at Austin</td>
<td>University of California, San Francisco</td>
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<tr>
<td>Judy Stone, PhD</td>
<td>Victoria Zhang, PhD</td>
<td>Jeff Spraggins, PhD</td>
<td>Mark Marzinke, PhD</td>
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<tr>
<td>University of California, San Diego</td>
<td>University of Rochester</td>
<td>Vanderbilt University</td>
<td>Johns Hopkins University</td>
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<tr>
<td>Hubert Vesper, PhD</td>
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<td>Jennifer Colby, PhD</td>
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Please join us at MSACL 2017!
Visit us at Booth 24 to speak with a specialist and to collect your favorite style from our assortment of “Be someone's hero” pins.

Workshops

Wednesday – January, 25, 2017   8:00 – 8:45am  Location: Catalina
Can you reduce drug testing reimbursement challenges? A case study using HRMS for simultaneous analyte screening and quantitation
Speaker: Ana Grenier, Ph.D., Dominion Diagnostics, North Kingstown, RI, U.S.A

Wednesday – January, 25, 2017   1:00 – 1:30pm  Location: Catalina
Paperspray MS in clinical research: early experiences in a U.K. clinical laboratory
Speaker: Lewis Couchman, Viapath Analytics, Kings College Hospital, London, UK.

Thursday – January, 26, 2017   8:00 – 8:45am  Location: Catalina
Speeding up the cancer biomarker discovery: Advanced Clinical Proteomics workflow with High Resolution MS
Speaker: Sebastien Gallien, Ph.D., Former researcher at CRP-Santé LIH Luxembourg Institute of Health

Find out more at thermofisher.com/ClinicalResearchSolutions

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**Be sure to attend our workshops:**

**Shimadzu Mass Spec Automation Lunch Workshop:**
Integration & Implementation of Fully Automated Sample Preparation for Mass Spectrometry
Wednesday, January 25th, 1:00 – 1:30 pm in the Pasadena Room
Presentation by Isabel Cabruja (CEO, Shimadzu Italy) and Manoj Tyagi, Ph.D., FACB, NRCC-CC (Medical Lab Director, Captiva LLC)

**Shimadzu Microbiome Breakfast Workshop:**
Advances in Human Microbiome Science: Metabolic Disease
Thursday, January 26th, 8:00 – 8:45 am in the Pasadena Room
Presentation by Stanley L Hazen, MD, Ph.D., Chair of the Department of Cellular & Molecular Medicine at the Cleveland Clinic’s Lerner Research Institute, Section Head of Preventive Cardiology & Rehabilitation at the Cleveland Clinic, Jan Bleekma Chair in Vascular Cell Biology and Atherosclerosis, and the Leonard Krieger Chair in Preventive Cardiology

All attendees will receive a free t-shirt!

Find out more at Booth #41 www.ssi.shimadzu.com

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Automates instrument monitoring
every analyte
every sample
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To learn more about Bruker’s accurate protein quantitation workflows, visit us at booth 38 or www.bruker.com/proteomics

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<table>
<thead>
<tr>
<th>Chromatographic Platform</th>
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<tr>
<td><em>MassChrom® Biogenic Amines/Metabolites in Urine</em> consisting of mobile phases, rinsing solution and analytical column</td>
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<tr>
<th>Sample Prep Sets</th>
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<tbody>
<tr>
<td><strong>Catecholamines</strong></td>
</tr>
<tr>
<td>Free Metanephrines</td>
</tr>
<tr>
<td>Serotonin</td>
</tr>
<tr>
<td>Adrenaline (epinephrine)</td>
</tr>
<tr>
<td>Noradrenaline (norepinephrine)</td>
</tr>
<tr>
<td>Dopamine</td>
</tr>
<tr>
<td>Free metanephrine</td>
</tr>
<tr>
<td>Free normetanephrine</td>
</tr>
<tr>
<td>Free 3-methoxytyramine</td>
</tr>
<tr>
<td>Serotonin</td>
</tr>
<tr>
<td><strong>Total Metanephrines (free + conjugated)</strong></td>
</tr>
<tr>
<td>Total metanephrine</td>
</tr>
<tr>
<td>Total normetanephrine</td>
</tr>
<tr>
<td>Total 3-methoxytyramine</td>
</tr>
<tr>
<td><strong>VMA, HVA, 5-HIAA</strong></td>
</tr>
<tr>
<td>Vanillylmandelic acid (VMA)</td>
</tr>
<tr>
<td>Homovanillic acid (HVA)</td>
</tr>
<tr>
<td>5-Hydroxyindoleacetic acid (5-HIAA)</td>
</tr>
</tbody>
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Be sure to attend our corporate workshops
Location: Sierra

Wednesday, January 25, 8:00am
The Evolution of SelexION® ION Mobility Technology: Past, Present and Future
Michael Jarvis

Wednesday, January 25, 1:00pm
Microflow LC: Improving sensitivity for the quantitation of biopharmaceuticals with LC-MS
Remco Van Soest

Space is limited, so come early to grab a seat!
Register to attend at http://sciex.com/events/msacl-0125

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Continuing Education credits will be available on the MSACL website for the Short Courses and the Scientific Sessions through ACCENT by AACC. Go to: msacl.org > CE Credits > ACCENT > MSACL 2017 US

Conference Badges
Your badge constitutes your admission pass to the Conference, receptions and the Exhibit Hall. **YOU ARE REQUIRED TO DISPLAY YOUR BADGE PROMINENTLY** while attending the conference and at all associated functions. If you do not have your badge you will be escorted to the registration desk to get one, or off the premises.

If you have an **EXHIBITS ONLY** badge **YOU ARE NOT PERMITTED IN THE SCIENTIFIC SESSIONS**, except the Plenaries in the Exhibit Hall. Violation may result in registration revocation without refund.

Yoga
Yoga will be held daily starting **Monday** at 6:00 – 7:00 AM in San Jacinto in the Renaissance Hotel. MSACL will be providing a limited number of yoga mats and other yoga-related accoutrements.

Smoking
*Smoking is prohibited within the conference facility and outside within 50 ft of the building.*

Tape Recording/Video Recording Policy
Please observe the MSACL policy which prohibits operation of tape recorders, video recorders, cameras, or camera phones, except for official association equipment, at all conference sessions, in the Exhibit Hall, and during the plenary sessions

**NOTE:** Throughout Conferences MSACL will be videotaping and taking photographs to be used for promotional or educational purposes by MSACL. If you do not wish to appear on camera, please notify the videographer or photographer and your request will be honored.

Short Course Meals on Monday and Tuesday
If you are registered for a short course, you will receive one or more lunch vouchers when you pick up your registration materials. These voucher are for use Monday (breakfast, lunch) and Tuesday (breakfast) in the Date Restaurant located in the Renaissance Hotel. You MUST present your voucher to enter the restaurant. If you are not taking a short course, you can purchase a meal voucher for $20 for either breakfast or lunch at the restaurant or the MSACL registration desk.
Presenter Info and Guidelines

Podium Presentations

Locations: Rooms 1-6; also known as, Mojave Learning Center, Catalina, Madera, Pasadena, Sierra & SmokeTree.

- If an individual is unable to present or does not show, the presentation time slot will be left open. It will not be filled by the next speaker. The next speaker will begin presenting at his/her scheduled time.
  - Back-Up Presenters: If a presenter does not show, a back-up presenter may be called to fill the open spot. Session Chairs, please contact registration immediately on determining that a speaker may not show so that efforts may be put in place to locate a back-up speaker.
- Speakers: Please make an effort to repeat any questions from the audience before answering.
- Podium presentations are 20 minutes including Q&A.
- PC Laptops are running Windows 7 Pro and Office 365.
- Presenters should check-in at least 15 minutes prior to their Session (NOT their talk) with either the Session Chair or AV Support on-hand to confirm their presentation is functional.
- Presenters may either upload their presentations before they arrive via Dropbox or bring their presentations on thumb (USB) drives for placement on a single presentation computer from which all presenters will access their PowerPoint presentations.
- Laser pointers will be provided.

Poster Presentations

Location: Exhibit Hall

Posters will be placed for the entire conference starting on Tuesday at 4:00 PM and ending on Thursday at 1:30 PM. Posters are only required to be attended for one hour on a selected day (specific to each poster), but are up for the duration of the congress. Please see poster abstract information for attendance details.

- Poster dimensions: 42x42 inches.
- Poster Boards are fabric.
- Push pins will be provided.
## Schedule Overview: Sunday

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<tr>
<td>10:30 AM</td>
<td><strong>BUS PICKUP at HOTEL: Palm Springs Aerial Tram Retreat</strong>&lt;br&gt;Location: Renaissance Hotel Front Entry&lt;br&gt;Sponsored by the Early Career Development Council (ECDC). Catch the bus to the Palm Springs Aerial Tram for a ride up the San Jacinto Mountain.&lt;br&gt;RESERVATION REQUIRED</td>
</tr>
<tr>
<td>11:30 AM - 1:00 PM</td>
<td><strong>NETWORKING LUNCH BUFFET</strong>&lt;br&gt;Location: The Francis Crocker Room at top of Palm Springs Aerial Tram&lt;br&gt;Enjoy a lunch buffet overlooking Palm Springs. For ECDC event guests only.&lt;br&gt;RESERVATION REQUIRED</td>
</tr>
<tr>
<td>11:45 AM - 12:45 PM</td>
<td><strong>ECDC SPEAKERS</strong>&lt;br&gt;Location: The Francis Crocker Room at the top of the Palm Springs Aerial Tram&lt;br&gt;RESERVATION REQUIRED&lt;br&gt;Chair: David Herold&lt;br&gt;(1) Daniel Holmes, MD: On the Necessity of an Interface between Labs Results and Clinicians&lt;br&gt;(2) Thomas Annesley, PhD: On Being a Reviewer&lt;br&gt;(3) Rainer Vollmerhaus, PhD: On Effective Results Management&lt;br&gt;(4) Karen Mahooti, MBA: On Creating Compelling Presentations</td>
</tr>
<tr>
<td>12:45 PM - 1:30 PM</td>
<td><strong>EXPLORE THE MOUNTAIN</strong>&lt;br&gt;Location: Top of Palm Springs Aerial Tram&lt;br&gt;RESERVATION REQUIRED</td>
</tr>
<tr>
<td>1:30 PM - 2:00 PM</td>
<td><strong>1st TRAM DEPARTURE FOR SHORT COURSES</strong>&lt;br&gt;Location: Top of Palm Springs Aerial Tram&lt;br&gt;RESERVATION REQUIRED</td>
</tr>
<tr>
<td>1:45 PM - 3:00 PM</td>
<td><strong>ROTATING BUS PICKUP at TRAM BASE STATION</strong>&lt;br&gt;Location: Tram Base Station&lt;br&gt;RESERVATION REQUIRED</td>
</tr>
<tr>
<td>2:00 PM</td>
<td><strong>LAST TRAM DEPARTURE FOR SHORT COURSES</strong>&lt;br&gt;Location: Top of Palm Springs Aerial Tram&lt;br&gt;RESERVATION REQUIRED</td>
</tr>
<tr>
<td>3:00 PM - 7:00 PM</td>
<td><strong>SHORT COURSES</strong>&lt;br&gt;Location: Various Rooms at Renaissance Hotel</td>
</tr>
<tr>
<td>7:00 PM - 8:30 PM</td>
<td><strong>PRIVATE DISCUSSION GROUP</strong> for Short Course Instructors&lt;br&gt;Location: Chino</td>
</tr>
<tr>
<td>7:00 PM - 10:00 PM</td>
<td><strong>DINNER ON OWN</strong>&lt;br&gt;Location: Your Decision.&lt;br&gt;Haven't decided on a dinner location yet? Head to the Hospitality Lounge at Rocks Patio to meet up with old friends or make new ones over drinks and light appetizers before heading to dinner in Palm Springs.</td>
</tr>
<tr>
<td>7:00 PM</td>
<td><strong>HOSPITALITY LOUNGE</strong>&lt;br&gt;Location: Santa Rosa and Rocks Terrace (if weather is agreeable)</td>
</tr>
</tbody>
</table>

27
## Schedule Overview: Monday

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td><strong>YOGA</strong></td>
</tr>
<tr>
<td>6:00 AM</td>
<td><em>Location: San Jacinto</em></td>
</tr>
<tr>
<td>7:00 AM</td>
<td>Energize yourself for the day! Yoga is a complimentary offering for all MSACL registrants. A limited number of yoga mats will be provided.</td>
</tr>
<tr>
<td></td>
<td><strong>BREAKFAST</strong></td>
</tr>
<tr>
<td>6:00 AM</td>
<td><em>Location: Date Restaurant</em></td>
</tr>
<tr>
<td>9:00 AM</td>
<td><strong>MSACL Meal Voucher required for entry.</strong></td>
</tr>
<tr>
<td></td>
<td>Short Course registrants receive voucher during badge pick-up. Or purchase a voucher at the restaurant from an MSACL representative for $20.</td>
</tr>
<tr>
<td>7:00 AM</td>
<td><strong>BADGE PICKUP</strong></td>
</tr>
<tr>
<td>8:00 AM</td>
<td><strong>SHORT COURSES: Group A</strong></td>
</tr>
<tr>
<td>12:00 PM</td>
<td><em>Location: Various</em></td>
</tr>
<tr>
<td></td>
<td>10 minute Coffee Breaks at every :50, except before lunch and last hour of class. Lunch 12:00 - 1:00 PM at Date Restaurant.</td>
</tr>
<tr>
<td>8:30 AM</td>
<td><strong>SHORT COURSES: Group B</strong></td>
</tr>
<tr>
<td>12:30 PM</td>
<td><em>Location: Various</em></td>
</tr>
<tr>
<td></td>
<td>10 minute Coffee Breaks at every :20, except before lunch and last hour of class. Lunch 12:30 - 1:30 PM at Date Restaurant.</td>
</tr>
<tr>
<td>9:00 AM</td>
<td><strong>SHORT COURSES: Group C</strong></td>
</tr>
<tr>
<td>1:00 PM</td>
<td><em>Location: Renaissance Ballroom Foyer</em></td>
</tr>
<tr>
<td></td>
<td>10 minute Coffee Breaks at every :50, except before lunch and last hour of class. Lunch 1:00 - 2:00 PM at Date Restaurant.</td>
</tr>
<tr>
<td></td>
<td><strong>COFFEE BREAK</strong></td>
</tr>
<tr>
<td></td>
<td><em>Location: Renaissance Ballroom Foyer</em></td>
</tr>
<tr>
<td></td>
<td>Take a break and get a coffee, juice, water and/or small snack to refresh for the next session.</td>
</tr>
<tr>
<td>12:00 PM</td>
<td><strong>LUNCH</strong></td>
</tr>
<tr>
<td>2:00 PM</td>
<td><strong>Short Course Registrants: You have 1 hr for lunch.</strong></td>
</tr>
<tr>
<td></td>
<td><strong>MSACL Meal Voucher required for entry.</strong></td>
</tr>
<tr>
<td></td>
<td>Short Course registrants receive voucher during badge pick-up. Or purchase a voucher at the restaurant from an MSACL representative for $20.</td>
</tr>
<tr>
<td>1:00 PM</td>
<td><strong>SHORT COURSES: Group A</strong></td>
</tr>
<tr>
<td>5:00 PM</td>
<td><em>Location: Various</em></td>
</tr>
<tr>
<td></td>
<td>10 minute Coffee Breaks at every :50, except last hour of class.</td>
</tr>
<tr>
<td>1:30 PM</td>
<td><strong>SHORT COURSES: Group B</strong></td>
</tr>
<tr>
<td>5:30 PM</td>
<td><em>Location: Various</em></td>
</tr>
<tr>
<td></td>
<td>10 minute Coffee Breaks at every :20, except last hour of class.</td>
</tr>
<tr>
<td>2:00 PM</td>
<td><strong>SHORT COURSES: Group C</strong></td>
</tr>
<tr>
<td>6:00 PM</td>
<td><em>Location: Various</em></td>
</tr>
<tr>
<td></td>
<td>10 minute Coffee Breaks at every :50, except last hour of class.</td>
</tr>
<tr>
<td>5:00 PM</td>
<td><strong>PRE-DINNER DRINKS</strong></td>
</tr>
<tr>
<td>5:30 PM</td>
<td><em>Location: Rocks Terrace</em> (COLD/RAIN: Santa Rosa)</td>
</tr>
<tr>
<td></td>
<td>Reception &amp; Dinner in Recognition of Travel Grantees</td>
</tr>
<tr>
<td>5:30 PM</td>
<td><em>Location: Rooms 2-5 and Registration Foyer</em></td>
</tr>
<tr>
<td></td>
<td><strong>This event is open for all registrants.</strong></td>
</tr>
<tr>
<td>7:00 PM</td>
<td><strong>HOSPITALITY</strong></td>
</tr>
<tr>
<td>10:00 PM</td>
<td><em>Location: Santa Rosa and Rocks Terrace (if weather is agreeable)</em></td>
</tr>
<tr>
<td></td>
<td>Drinks and light appetizers provided.</td>
</tr>
</tbody>
</table>
# Schedule Overview: Tuesday

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
</table>
| 6:00 AM    | **YOGA**  
*Location: San Jacinto* |
| 6:00 AM    | **BREAKFAST**  
*Location: Date Restaurant*  
**MSACL Meal Voucher required for entry.**  
Short Course registrants receive breakfast voucher during badge pick-up.  
Or purchase a voucher at the restaurant from MSACL representative for $20. |
| 7:00 AM    | **BADGE PICKUP**  
*Location: Renaissance Ballroom Foyer* |
| 7:00 AM    | **PLACE POSTERS**  
*Location: Exhibit Hall*  
All posters for entire conference to be placed during this period. |
| 7:00 AM    | **SHORT COURSES**  
*Location: Various*  
10 minute Coffee Breaks at every :50, except last hour. |
| 7:00 AM    | **COFFEE BREAK**  
*Location: Renaissance Ballroom Foyer* |
| 12:00 PM   | **POOLSIDE OPENING LUNCH RECEPTION**  
*Location: Poolside, most likely. Unless the weather gets really bad.* |
| 2:00 PM    | **KEYNOTE SCIENTIFIC SESSION 1**  
*Location: Various Track Rooms* |
| 2:00 PM    | **COFFEE BREAK**  
*Location: Renaissance Ballroom Foyer* |
| 3:00 PM    | **SCIENTIFIC SESSION 2**  
*Location: Room 1 - Room 6* |
| 4:00 PM    | **EXHIBITS OPEN**  
*Location: Exhibit Hall* |
| 4:00 PM    | **HAPPY HOUR POSTER SESSION**  
*Location: Exhibit Hall*  
With Pretzels & Popcorn |
| 5:00 PM    | **PLENARY AWARD LECTURE: Catherine Fenselau**  
*Location: Exhibit Hall* |
| 6:00 PM    | **WELCOME & ORIENTATION**  
*Location: Exhibit Hall* |
| 6:30 PM    | **TROUBLESHOOTING GRAND ROUNDS**  
*Location: Exhibit Hall*  
With Foosball Tourney, Heavy Appetizers and Drinks |
| 7:30 PM    | **CMS JOURNAL DISCUSSION GROUP**  
*Location: Room 1 (Mojave)* |
| 7:30 PM    | **HOSPITALITY**  
*Location: Santa Rosa and Rocks Terrace (if weather is agreeable)*  
Drinks and light appetizers provided. |
## Schedule Overview: Wednesday

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>6:00 AM</td>
<td>YOGA</td>
</tr>
<tr>
<td>7:00 AM</td>
<td><strong>Location:</strong> San Jacinto</td>
</tr>
<tr>
<td>6:45 AM</td>
<td>BREAKFAST</td>
</tr>
<tr>
<td>8:00 AM</td>
<td><strong>Location:</strong> Renaissance Ballroom Foyer</td>
</tr>
<tr>
<td></td>
<td>Enjoy a light continental breakfast before exploring a corporate workshop.</td>
</tr>
<tr>
<td>7:00 AM</td>
<td>CORPORATE WORKSHOPS</td>
</tr>
<tr>
<td>7:45 AM</td>
<td><strong>Location:</strong> Room 1 - Room 3</td>
</tr>
<tr>
<td>8:00 AM</td>
<td>CORPORATE WORKSHOPS</td>
</tr>
<tr>
<td>8:45 AM</td>
<td><strong>Location:</strong> Room 1 - Room 5</td>
</tr>
<tr>
<td>8:00 AM</td>
<td>WELCOME COFFEE</td>
</tr>
<tr>
<td>9:00 AM</td>
<td><strong>Location:</strong> Exhibit Hall</td>
</tr>
<tr>
<td>9:00 AM</td>
<td>PLENARY LECTURE: Neil Kelleher</td>
</tr>
<tr>
<td>9:45 AM</td>
<td><strong>Location:</strong> Exhibit Hall</td>
</tr>
<tr>
<td>9:45 AM</td>
<td>POSTERS</td>
</tr>
<tr>
<td>10:45 AM</td>
<td><strong>Location:</strong> Exhibit Hall</td>
</tr>
<tr>
<td>10:45 AM</td>
<td>PLENARY LECTURE: Ron Heeren</td>
</tr>
<tr>
<td>11:30 AM</td>
<td><strong>Location:</strong> Exhibit Hall</td>
</tr>
<tr>
<td>11:30 AM</td>
<td>LUNCH</td>
</tr>
<tr>
<td>1:00 PM</td>
<td><strong>Location:</strong> Exhibit Hall. Seating provided in Exhibit Hall AND Lawn outside Exhibit Hall.</td>
</tr>
<tr>
<td>1:00 PM</td>
<td>CORPORATE WORKSHOPS</td>
</tr>
<tr>
<td>1:30 PM</td>
<td><strong>Location:</strong> Room 1 - Room 5</td>
</tr>
<tr>
<td>1:30 PM</td>
<td>COFFEE BREAK</td>
</tr>
<tr>
<td>1:45 PM</td>
<td><strong>Location:</strong> Renaissance Ballroom Foyer</td>
</tr>
<tr>
<td>13:45 AM</td>
<td>SCIENTIFIC SESSION 3</td>
</tr>
<tr>
<td>14:45 PM</td>
<td><strong>Location:</strong> Room 1 - Room 6</td>
</tr>
<tr>
<td>2:45 PM</td>
<td>TEA-TIME BREAK</td>
</tr>
<tr>
<td>3:00 PM</td>
<td><strong>Location:</strong> Renaissance Ballroom Foyer</td>
</tr>
<tr>
<td>3:00 PM</td>
<td>SCIENTIFIC SESSION 4</td>
</tr>
<tr>
<td>4:00 PM</td>
<td><strong>Location:</strong> Room 1 - Room 6</td>
</tr>
<tr>
<td>4:00 PM</td>
<td>TROUBLESHOOTING GRAND ROUNDS</td>
</tr>
<tr>
<td>5:00 PM</td>
<td><strong>Location:</strong> Exhibit Hall with Foosball Tourney, Pretzels, Popcorn and drinks served.</td>
</tr>
<tr>
<td>5:00 PM</td>
<td>HAPPY HOUR POSTER SESSION</td>
</tr>
<tr>
<td>6:00 PM</td>
<td><strong>Location:</strong> Exhibit Hall with Pretzels, Popcorn and drinks served.</td>
</tr>
<tr>
<td>6:00 PM</td>
<td>DISCUSSION GROUPS</td>
</tr>
<tr>
<td>7:00 PM</td>
<td><strong>Location:</strong> Andreas, Chino, Pueblo, Rm 1 (Mojave), Rm 6 (SmokeTree) and Mesquite H</td>
</tr>
<tr>
<td>7:00 PM</td>
<td>MEXICAN FIESTA DINNER</td>
</tr>
<tr>
<td>8:00 PM</td>
<td><strong>Location:</strong> Rooms 2-5 &amp; Registration Foyer</td>
</tr>
<tr>
<td>8:00 PM</td>
<td>THE OCCASIONALS</td>
</tr>
<tr>
<td>9:00 PM</td>
<td><strong>Location:</strong> Rooms 2-5</td>
</tr>
<tr>
<td>8:00 PM</td>
<td>HOSPITALITY</td>
</tr>
<tr>
<td>10:00 PM</td>
<td><strong>Location:</strong> Santa Rosa and Rocks Terrace (if weather is agreeable)</td>
</tr>
<tr>
<td></td>
<td>Drinks and light appetizers provided.</td>
</tr>
</tbody>
</table>
## Schedule Overview: Thursday

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>6:00 AM</td>
<td>YOGA</td>
</tr>
<tr>
<td>6:45 AM</td>
<td>BREAKFAST <em>(light continental)</em></td>
</tr>
<tr>
<td>8:00 AM</td>
<td>CORPORATE WORKSHOPS</td>
</tr>
<tr>
<td>8:00 AM</td>
<td>WELCOME COFFEE</td>
</tr>
<tr>
<td>9:00 AM</td>
<td>SCIENTIFIC SESSION 5</td>
</tr>
<tr>
<td>10:00 AM</td>
<td>POSTER SESSION</td>
</tr>
<tr>
<td>11:00 AM</td>
<td>PLENARY LECTURE: Garry Nolan</td>
</tr>
<tr>
<td>11:45 AM</td>
<td>POSTER AWARDS</td>
</tr>
<tr>
<td>12:00 PM</td>
<td>LUNCH</td>
</tr>
<tr>
<td>1:30 PM</td>
<td>EXHIBITS CLOSED</td>
</tr>
<tr>
<td>1:30 PM</td>
<td>CORPORATE WORKSHOPS</td>
</tr>
<tr>
<td>2:00 PM</td>
<td>COFFEE BREAK</td>
</tr>
<tr>
<td>2:15 PM</td>
<td>SCIENTIFIC SESSION 6</td>
</tr>
<tr>
<td>2:15 PM</td>
<td>TEA-TIME BREAK</td>
</tr>
<tr>
<td>3:30 PM</td>
<td>SCIENTIFIC SESSION 7</td>
</tr>
<tr>
<td>4:30 PM</td>
<td>PRE-DINNER COCKTAIL</td>
</tr>
<tr>
<td>5:00 PM</td>
<td>BBQ COOKOUT &amp; CLOSING RECEPTION</td>
</tr>
<tr>
<td>6:30 PM</td>
<td>HOSPITALITY</td>
</tr>
<tr>
<td>6:00 PM</td>
<td>PALM SPRINGS VILLAGE FEST</td>
</tr>
<tr>
<td>8:00 PM</td>
<td>CONFERENCE CLOSED</td>
</tr>
</tbody>
</table>
**Plenary Speaker Series**

**MSACL 2017 US - Distinguished Contribution Awardee**

**Rapid Characterization of Microorganisms by Mass Spectrometry: What can be Learned and How?**

Catherine Fenselau  
*University of Maryland*

**Tuesday @ 5:00 PM in Oasis 4 (Exhibit Hall) includes Award Presentation**

Various configurations of MALDI mass spectrometry have been developed for rapid detection of unprocessed microorganisms on the battle field. Recently this direct approach has been approved by the FDA for use in clinical microbiology. Automated data processing has a critical role in both of these applications, and both library matching and proteomic bioinformatics have been developed to identify bacteria based on their mass spectra. This presentation will include a historical overview of the biomarkers, including phospholipids and proteins, which can be observed directly from unprocessed bacteria and yeast using many different ionization methods. Observations will be offered on strategies for sample enrichment. Current limitations and challenges for mass spectrometry-based strategies will be discussed.

---

**Translational Top Down Proteomics in Oncology: from Histones to KRAS and Beyond**

Neil Kelleher  
*Northwestern University*

**Wednesday @ 9:00 AM in Oasis 4 (Exhibit Hall)**

A general theme in translational proteomics that involves first genotyping patients will be presented. Some peptide-driven assays for histone modifications in cancer epigenetics will be presented, along with whole-protein (i.e., top down proteomic) measurements of high value targets like KRAS. Assays deployed in clinical research are typically developed and validated with basic studies of isogenic cell-based models of colorectal cancer, multiple myeloma, and glioblastoma. Current state-of-the-art in whole protein mass spectrometry will be presented, along with the state of play in assessing the value of proteoform-resolved measurements in clinical research and biomarker discovery & verification.
Molecular Tissue-typing: Comprehensive Imaging Mass Spectrometry in Translational Clinical Research
Ron M.A. Heeren
M4I, Maastricht University

Wednesday @ 10:45 AM in Oasis 4 (Exhibit Hall)

A comprehensive understanding of molecular patterns of health and disease is needed to pave the way for personalized medicine and tissue regeneration. The best way to capture disease complexity is to chart and connect multilevel molecular information within a tissue using mass spectrometry and data algorithms. This molecular tissue-typing using imaging mass spectrometry provides unique insights in patterns of health and disease. Mass spectrometry based molecular information is impacting clinical research and diagnosis in various disciplines, ranging from pathology to surgical care. Molecular detail provided by translational imaging mass spectrometry is demonstrated to directly benefit patient cure and care.

A Defined "Structure" for the Immune System That Reflects Immune Surveillance & Mechanistic Processes
Garry Nolan
Stanford University School of Medicine

Thursday @ 9:00 AM in Oasis 4 (Exhibit Hall)

High parameter single cell analysis has driven deep understanding of immune processes. Using a next-generation single-cell "mass cytometry" platform we quantify surface and cytokine or drug responsive indices of kinase target with 45 or more parameter analysis (e.g. 45 antibodies, viability, nucleic acid content, and relative cell size). Similarly, we have developed two advanced technologies that enable deep phenotyping of solid tissue in both fresh frozen and FFPE formats (50 – 100 markers). We have recently extended this parameterization to mRNA with the capability to measure down to 5 molecules per cell in combination with any other set of previously created markers.

I will present evidence of deep internal order in immune functionality demonstrating that differentiation and immune activities have evolved with a definable “shape”. This shape is altered during immune surveillance and “imprinted” during, and after, pathogen attack, traumatic injury, or auto-immune disease. Hierarchies of functionally defined trans-cellular modules are observed that can be used for mechanistic and clinical insights. I will focus upon pathogen attack, traumatic surgical intervention in human, and auto-immune processes for the presentation.
Young Investigator Grants

Young Investigator Travel Grants (n=81) are provided to support trainees (MD/residents/fellows and PhD - students / post-docs) and young faculty members (less than 4 years since appointment) who submitted abstracts that have been accepted for presentation at the conference.

Bernice Agana The Ohio State University
Ravali Alagandula Cleveland State University
Elizabeth Alore Baylor College of Medicine
Michael Andrews Georgia State University
Florian Barré Maastricht University, M4I
Sankha (Bobby) Basu Brigham and Women's Hospital
Timur Baygildiev Lomonosov Moscow State University
Alena Bensussan University of Texas at Austin
Zsolt Bodai Imperial College London
Anne-Claire Boschat Institut Imagine
Adam Burke Imperial College
Joshua Buse University of Calgary
Simon Cameron Imperial College London
Sean Campbell University of Virginia
Siaw Li Chan University of Chicago
Dawn Z Chen Cedar Sinai Medical Center
Meng Han Chiang Chang Gung Memorial Hospital
Christopher Chouinard Pacific Northwest National Laboratory
Lewis Couchman Viapath Analytics, King's College Hospital, London
Christopher Cox Colorado School of Mines
Kendall Cradic Mayo Clinic
Andreas Dannhorn Imperial College London
Sarah Delaney SickKids Hospital/University of Toronto
Sri Ramya Donepudi Baylor College of Medicine
Clara Feider University of Texas at Austin
Erica Forsberg The Scripps Research Institute
Lidong He Florida State University
Clark Henderson University of Washington Medical Center
Basia Hiley NSW Health Pathology
Kelly Hines University of Washington
Hui-Yu Ho Imperial College London
Melissa Hoffman Moffitt Cancer Center/University of South Florida
Tao Huan The Scripps Research Institute
Benjamin Hunter Murdoch University
Robert Jansen Weill Cornell Medicine
Carl Jenkinson Metabolism and Systems Research
Jeffrey Jones Oak Ridge Institute for Science and Education
Audrey Jongen Maastricht University Medical Centre
Raghavi Kakarla Cleveland State University
Guinevere S.M. Kammeijer Leiden University Medical Center
Martin Kaufmann Queen's University
Vathany Kulasingam University Health Network
Arun Babu Kumar University of Washington
Yungkang Lee Berkshire Medical Center
Alisa Li Columbia University
Philip Loziuk North Carolina State University
Madhuri Manohar Johns Hopkins University
Adam McShane Cleveland Clinic
Anna Merrill University of Washington
Wojciech Michno University of Gothenburg
Nicole Morse Queen's University
Antonis Myridakis Imperial College of London
Valentina Pirro Purdue University
Danthasinghe Waduge Piyaratna Baylor College of Medicine
Boone Prentice Vanderbilt University
Adam Rosebrock Stony Brook School of Medicine
Nicholas Saichek Colorado School of Mines
Marta Sans The University of Texas
Ellen Schmitz Eindhoven University of Technology
Lusia Sepiashvili Mayo Clinic
Breland Smith University of California, San Diego
Philip Sobolesky University of California San Diego
Boya Song ARUP Laboratories
Sandra Spencer University of Washington, Department of Genome Sciences
Timothy Toby Northwestern University
Menelaos Tzafetas Imperial College London
Raf Van de Plas Delft University of Technology
Irene van den Broek Cedars-Sinai Medical Center, Advanced Clinical Biosystems Research Institute
Xander van Wijk University of California, San Francisco
Ruta Veigure Institute of Chemistry, University of Tartu
Panagiotis Vorkas Imperial College London
Dajana Vuckovic Concordia University
Clayton Wilburn Houston Methodist Hospital
Vincen Wu Imperial College London
Feng Xian Beijing Institute of Genomics, Chinese Academy of Sciences
Yi Xiao Childrens Hospital Los Angeles
Yifei Yang University of Chicago
Yanbao Yu J. Craig Venter Institute
Min Yu University of Virginia
Shenyan Zhang Cedars Sinai Medical Center
Nazanin Zounemat Kermani Imperial College London
Lab Director Grants

Lab Director Travel Grants (n=26) are provided to individuals leading clinical labs. These individuals have had minimal exposure to mass spectrometry and are interested in gaining more understanding of its clinical applications.

Vilte Barakauskas BC Children's and Women's Health Centre
Allison Chambliss University of Southern California Keck School of Medicine
Jennifer Dien Bard Children's Hospital Los Angeles; University of Southern California
Xiaowei Fu University of Southern California, Children's Hospital Los Angeles
Yang Gao Nankai University
Kristine Glunde The Johns Hopkins University School of Medicine
Stewart Graham Beaumont Health
Ronald Henriquez Walter Reed National Military Medical Center
Thomas Kampfrath Santa Clara County Medical Center
Yuanyu Lee California State University at Long Beach
Zaiping Liu IWK Health Centre, Dalhousie University
Christopher Lowe Providence Health Care
Robert Mason Alfred I duPont Hospital for Children
Denise Milhorn Walter Reed National Military Medical Center
Khushbu Patel Children's Health
Michael Payne Providence Health Care
Jennifer Powers Washington University
Pratistha Ranjitkar Medical College of Wisconsin
Jesse Seegmiller University of Minnesota
Alina Sofronescu University of Nebraska Medical Center
Christophe Stove Ghent University
Craig Sykes UNC-Chapel Hill
Awet Tecleab Staten Island University Hospital
Margrét Thorsteinsdóttir Pharmaceutical Sciences, University of Iceland
Yuan Wang Beijing Institute of Heart Lung and Blood Vessel Diseases
Xiangdong Xu University of California San Diego, VA Medical Center
Trainee Grants

Trainee Grants (n=39) were provided to individuals training to lead clinical labs. These individuals have had minimal exposure to mass spectrometry and are interested in gaining more understanding of its clinical applications.

Ashton Brock University of Virginia
Dustin Bunch Cleveland Clinic
Liyun Cao MD Anderson Cancer Center
Roy Yu-Wei Chen University of British Columbia
Andrew Cho Texas Tech University
Jia Fan Houston Methodist Research Institute
Matthew Feldhammer Emory University
Fatemeh Fouladkou UCSF - San Francisco General Hospital
Howard Gerson McGill University/Jewish General Hospital
Alex Greninger University of Washington
Feng Jin Baylor College Of Medicine
Lisa Johnson University of Minnesota
Rutchanna Jongejan Erasmus Medical Centre Rotterdam
Praveen Kumar Beaumont Health System
David Kemble Dartmouth-Hitchcock Medical Center
Stacy Kenyon Mayo Clinic
Claire Knezevic Johns Hopkins Medical Institutes
Erik Korte University of Louisville
Craig Livie Glasgow Royal Infirmary
Christopher Marquez University of Texas Medical Branch
Haik Mkhikian University of California, Irvine
Abdurehman Mohammed Izmir Institute of Technology
Garrett Mullins University of Virginia
Samia Naccache Children’s Hospital Los Angeles
Dennis Orton Dr. CI Coady Associates
Anjaneyaswamy Ravipati The University of British Columbia
Igor Rodin Moscow State University, Analytical Research Centre
Ashley Sanchez Bridgewater State University
Rohan Shah Cleveland State University
Sydney Strickland University of Virginia
Stephanie Tantzer Nemours/Alfred I. duPont Hospital for Children
Basile Tessier-Cloutier University of British Columbia
Tam Van Children’s Hospital Los Angeles
Chad Vanderbilt University of Colorado, Anschutz Medical Campus
Dan Wang Mount Sinai Hospital
Jeffrey Whitman University of California, San Francisco
Fang Wu University of Utah and ARUP Laboratories
Ali Yilmaz Beaumont Health, Reseach Institute
DeLu (Tyler) Yin University of Louisville
Short Course Overview

The Short Course Program provides a rapid introduction to topics, issues and techniques. Each course is led by one or more distinguished instructors with expertise in the respective course areas.

Clinical MS 301

A Comprehensive Review of Clinical Mass Spectrometry Technology & Techniques, including Miniaturization

Duration: Monday Morning → Tuesday Noon
Location: Rm 2 (Catalina)
Level: 2-3 (Intermediate - Advanced)
Instructor(s): Jack Henion, PhD

This course presents a comprehensive overview of technology and techniques of analytical mass spectrometry and from that foundation extends into exciting, disruptive recent developments.

1. Sample preparation
   - Topics: New types of extraction, Issues to consider, Isolation of proteins from biological samples
     Ultrafiltration, Affinity techniques, Molecularly Imprinted Polymers (MIP?s), Aptamers, Thermo?s MSIA pipette tips, Electro Extraction, Quechers, SISCAPA, Micro extractions: Dried blood spots (DBS), Dried Plasma Spots (DPS).

2. Advanced separation techniques for large molecules
   - Topics: UHPLC, Hydrophobic Interaction Chromatography (HIC), Nano-UHPLC, Micro LC/MS, Size Exclusion Chromatography (SEC), ion exchange chromatography, Capillary Electrophoresis (CE), Differential Mobility Spectrometry (DMS).

3. Ionization techniques for MS
   - Topics: Electrospray ionization (ESI), Nano ESI, Micro ESI, Atmospheric pressure chemical ionization (APCI), Atmospheric pressure photoionization (APPI), Matrix assisted laser desorption ionization (MALDI), LAESI, Electron ionization (EI) and its potential for LC/MS.
   - To Discuss: New ionization techniques which may be used without on-line separation science technology. This area has evolved into a variety of ambient ionization techniques such as DESI, DART, ASAP, etc.

4. Mass Analyzers
   - Topics: Quadrupoles, Ion traps, linear and quadrupole, Time-of-Flight (TOF), Orbitraps, Hybrid mass analyzer systems, Ion mobility spectrometers, and Differential Mobility Spectrometry (DMS).
   - To Discuss: Developments and improvements in mass analyzers including linear ion traps, FTMS, time-of-flight (TOF), orbitraps, and accelerator mass spectrometry (AMS), the latter currently being applied to micro-dosing experiments by the pharmaceutical industry. Issues such as full-scan acquisition rates, high-resolution mass spectrometry (HRMS), the importance and usefulness of exact mass measurements for qualitative and quantitative analysis, and the analytical merits compared with modern SRM LC/MS experiments will be discussed with many practical examples and applications. The latter will include clinical chemistry issues as well as pharmaceutical, food safety, environmental and industrial examples.

5. Imaging and profiling by MS
   - Topics: Applications of recently reported ionization techniques for imaging the location of chemicals in various matrices employing MALDI, DESI, LAESI, LESA and other techniques.

6. High resolution MS
   - Topics: Fundamentals, Mass Defects, Isotopic patterns, Mass axis calibration, Types of HRMS systems, Qual/Quan Analysis, Data mining processes, Future directions
To Discuss: The analytical merits of HRAMS from QTOF as well as orbitraps and FTMS systems will be presented. Instances where either SRM LC/MS or LC HRAMS may be preferred for optimal selectivity due to chemical background or other interference issues.

7. Miniaturization in MS
- Topics: Purdue University "Mini 11", Torion, Microsaic, Advion expression CMS, Waters QDa
- To Discuss: The benefits and limitations of smaller analytical instrumentation systems will be compared. This includes miniaturization of HPLC systems as well as the mass spectrometers themselves. The commercial introduction of chip-based HPLC systems closely integrated with mass spectrometers offers a glimpse of future directions in analytical chemistry.

8. Synergistic Integration
- A systematic overview via specific examples with applications highlighting noted examples of innovative novel and non-standard technologies which demonstrate the analytical potential of new analytical technologies.
- Developing instrumentation and technologies will be important aspects of future mass spectrometry techniques and its expansion to important new applications. An extremely important example is the need for LC/MS bioanalysis (quantitation) of biologics (ADCs, large molecules, RNA, etc.) in biological samples employing both bottom up and top down methods. HRAMS coupled with "protein friendly" chromatography will significantly expand our present analytical capabilities. Ion mobility spectrometry (IMS) and transportable mass spectrometers could lead to point-of-care applications and other far reaching applications of mass spectrometry beyond what we are doing today. The future is very exciting!

Data Science 101

**Breaking up with Excel: A Newbie's Introduction to the R Statistical Programming Language**

**Duration:** Sunday 3PM → Tuesday Noon  
**Location:** Rm 1 (Mojave)  
**Level:** 1-2 (Beginner - Intermediate)  
**Instructor(s):** Daniel Holmes, MD & Stephen Master, MD, PhD (TA: Will Slade, PhD)

Have you ever tried to do Deming regression in Excel only to discover that it is not available? Have you had your figure rejected by a journal because the resolution was not good enough? Have you wished that you could figure out a way to stop manually transcribing your LC-MS/MS results into the LIS?

Well, your wait is over because this year at MSACL we will be offering a course for complete programming newbies that will help you get going analyzing real data related to LC-MS/MS assay development, validation, implementation and publication. The only background expected is the ability to use a spreadsheet program. The skills that you will acquire will allow you to take advantage of the many tools already available in the R language and thereafter, when you see that your spreadsheet program does not have the capabilities to do what you need, you will no longer have to burst into tears. You will be empowe-R-ed.

The course will be run over two days and time will be evenly split between didactic sessions and hands on problem solving with real data sets. Drs Holmes and Master will adopt a “no student left behind policy”. Students will be given ample time to solve mini problems taken from real life laboratory work and focused on common laboratory tasks. All attendees will need to bring a laptop with the R language installed R Studio interface installed. Students may use Windows, Mac OSX or Linux environments. Both R and R studio are free and open-source. No cash required.

Students should be prepared for learning what computer programming is really like. This may involve some personal frustration but it will be worth it.

**Obtaining the Software**

Instructions for installing the R language are here: [http://cran.r-project.org/](http://cran.r-project.org/)  
Instructions for installing R Studio are here: [http://www.rstudio.com/](http://www.rstudio.com/)

**Course Description**
The course will cover:

- The major types of R variables: vectors (numerical, character, logical), matrices, data frames and lists.
- The important classes: numeric, character, list and changing between them.
- Importing data from Excel.
- Dealing with non-numeric instrument data: the “<10”s and “>1000”s.
- Manipulating your data: sub-setting, which, match, sort, unique, cut.
- Simple statistical tests: mean, median, quantiles (normal ranges), t-tests, ANOVA, Wilcoxon.
- Data merges: matching rows between sets.
- Exporting data to Excel-like format.
- Non-linear regressions.
- Looping: Doing things repeatedly.
- Writing your own functions.
- Making highly customized graphs: scatter plots, regression lines, histograms, box plots, qq-plots.
- Putting it all together projects:
  - Preparing method comparison regression and Bland Altman plots.
  - Preparing mass spectrometry data for upload to LIS.

### Lab Medicine 101

**Basics of Laboratory Medicine**

- **Duration:** Monday after Lunch → Tuesday Noon
- **Location:** Rm 7B (Agua Caliente B)
- **Level:** 1 (Beginner)
- **Instructor(s):** Prof. Dr. med. Michael Vogeser

This 1-day course aims to make scientists familiar with the basic concepts of clinical pathology and laboratory medicine. Typical processes and workflows in the various categories of clinical laboratories are described and discussed. Topics that are addressed include in particular:

- Basic technologies (photometry, immunoassays, electrochemical methods, cytometry, immuno-fluorescence, etc.)
- Automation and working characteristics of analyzer configurations including total laboratory automation.
- Concept of total testing process including pre- and post-analytical processes.
- Performance characteristics.
- Quality management.
- Regulatory background.
- Sample materials.
- Clinical decision making, reference ranges, decision levels, diagnostic and clinical algorithms.
- Logistics, sample transport.
- Economic considerations.
- Characteristics of IVD industry.

### LC-MSMS 101

**Getting Started with Quantitative LC-MS/MS in the Diagnostic Laboratory**

- **Duration:** Sunday 3PM → Tuesday Noon
- **Location:** Rm 5 (Sierra)
- **Level:** 1-2 (Beginner - Intermediate)
- **Instructor(s):** Lorin Bachmann, PhD & Grace van der Gugten

Is your laboratory under pressure to purchase an LC-tandem MS or is the ROI you wrote last year haunting you now? This short course is designed for attendees implementing quantitative LC-tandem MS for patient testing who have laboratory medicine experience but no mass spectrometry training - CLS bench analysts, supervisors, R&D scientists, and laboratory directors. Theoretical concepts necessary for a robust implementation of clinical mass spectrometry will be presented – but the emphasis is on practical recommendations for:

- LC-MS/MS system purchasing.
• site preparation and installation
• defining preliminary MSMS and LC parameters for your first method
• selecting and optimizing sample preparation for your first method
• choosing internal standards, solvents, and water, making reagents and calibrators
• adjusting sample preparation, LC and MSMS parameters to achieve the desired assay performance
• establishing data analysis & review criteria and an interface to the LIS
• pre-validation stress testing and method validation
• preventative maintenance and troubleshooting
• maintaining quality in production.

Our goal is to present just enough theory so you can report high quality results, while opening a window to the depth and complexity of clinical mass spectrometry such that your appetite is whetted to learn more.

Previous exposure to the principles of clinical method validation, either didactic or practical, is assumed. A glossary of common LC-MSMS terms/acronyms, and diagrams delineating basic LC and MSMS instrument components and functions will be emailed to attendees a week prior to the beginning of the course. This material will also be addressed at the beginning of the course, but the initial learning curve can be steep and review prior to the course will be beneficial if you have absolutely no previous exposure with LC-MSMS.

**LC-MSMS 201**

**Understanding and Optimization of LC-MS/MS to Develop Successful Methods for Identification and Quantitation in Complex Matrices**

Duration: Sunday 3PM → Tuesday Noon
Location: Andreas
Level: 2 (Intermediate)
Instructor(s): Robert D. Voyksner, PhD

This course is designed for the chromatographer / mass spectrometrist who want to be successful in developing methods, method optimization and solving problems using LC/MS/MS. The course covers the atmospheric pressure ionization (API) techniques of electrospray, pneumatically assisted electrospray and atmospheric pressure chemical ionization (APCI) and atmospheric pressure photo ionization (APPI) using single quadrupole, triple quadrupole, time-of-flight and ion trap mass analyzers.

Discussions of sample preparation and chromatography will target method development and optimization for the analysis of "real-world" samples by LC/MS/MS.

The course highlights the following topics with respect to optimization a method to achieve the best sensitivity, specificity and sample throughput:

1. Optimization ionization in API techniques,
2. understanding and minimizing matrix suppression,
3. relative merits of various LC column lengths, particle sizes and column diameters for LC/MS/MS analysis,
4. introduction into the interpretation of MS/MS spectra,
5. important issues in LC/MS/MS quantitation, and
6. optimization of an quantitative analysis.

Applications of LC/MS/MS to analyze compounds of clinical interest in biological matrices will be discussed throughout the course to emphasize the topics covered.
The general goal of the course is to enable practitioners of LC-MS/MS in the clinical laboratory to quickly recognize and diagnose specific problems with instrumentation, in order to decrease downtime and cost of repairs. The course includes ‘best practices’ for instrumentation installation, upkeep and maintenance, practical troubleshooting workflows for LC and MS, and will use problem sessions to reinforce skillsets. Although the course uses examples from specific instrumentation for demonstration, the content is geared to be vendor-neutral and applicable to all LC-MS systems. Additionally, we will provide an opportunity to have instrumentation troubleshooting questions from your laboratory addressed by the facilitators.

Brief outline of course content:

- **General “Best Practices” for Successful LC/MS Operation**
  1. Best Practices; Getting Started on the Right Foot
  2. Breaking the System Down
  3. System Suitability! What is it, and how do I properly implement?

- **Focus on Liquid Chromatography**
  1. Diagnostics using the “heartbeat” of your Chromatographic system
  2. Key System components and where things go wrong
  3. LC troubleshooting workflow
  4. Maintenance Intervals; service contract or do-it-yourself?
  5. Problem sets

- **Focus on Mass Spectrometry**
  1. Discussion of Source, Transfer Optics, Vacuum and how each is critical to your system
  2. MS Troubleshooting workflow
  3. Ion optics cleaning and upkeep; what is ‘charging’?
  4. Problem sets

- **Integrated System**
  1. Ionization
  2. System Communications
  3. Multi-vendor configurations
  4. Strategies to simplify
  5. Integrated real-lab problem scenarios and team exercises

While some basics of instrument component operation will be covered, it will be most beneficial to scientists with experience actively using LC-MS/MS as an analysis tool. While an in-depth discussion of how to operate each individual instrument is surely outside the scope of any short course, specific system setups will be used as examples and attendees will be encouraged to ask questions about specific systems in their own laboratories.

This 2-day course will briefly introduce the key aspects of the LC-MS/MS experimental workflow and then focus on processes and experimental designs for assay development and analytical validation of assays to be employed within clinical diagnostics.
The first day will describe method development in detail, including how-to guides for initial optimization of mass spectrometry systems, chromatographic development and sample preparation schemes. Techniques and technologies for streamlining analytical performance will also be described. Transitional experiments from development to validation will be discussed in detail to stress test methodologies prior to analytical validation.

Day two will cover all details pertinent in validation of LC-MS/MS analytical workflows. Experimental designs for all aspects of validation, putative acceptance criteria and analytical solutions will be shown. Key validation criteria of selectivity, carry-over, matrix effect, accuracy, precision, linearity, stability and inter-assay correlation will be described using multiple case studies.

**MALDI 102**  
**Practical Considerations for MALDI Imaging Mass Spectrometry**  
**Duration:** Sunday 3PM → Tuesday Noon  
**Location:** Rm 6E (Smoketree E)  
**Level:** 1-2 (Beginner - Intermediate)  
**Instructor(s):** Michelle Reyzer, PhD

This course will provide an introduction to the basic concepts involved in running a MALDI Imaging Mass Spectrometry experiment, including key parameters of sample preparation, matrix application, imaging acquisition, instrumental parameters, data analysis, and imaging processing. The course will focus on MALDI mass spectrometry, but other mass spectrometry sources currently used for imaging will be touched on. This course will be presented at the beginner to intermediate level, and will be appropriate for clinicians/pathologists looking to learn more about IMS as well as for mass spectrometrists looking to apply this technology to more clinical samples.

**Manuscripts 101**  
**Preparing Manuscripts for Publication: Improving Your Chances for Success**  
**Duration:** Sunday 3PM → Monday at Lunch  
**Location:** Rm 7B (Agua Caliente B)  
**Level:** 0 (General Interest)  
**Instructor(s):** Thomas Annesley, PhD

Scientific publication is an important and necessary activity for researchers. Being a good researcher, however, does not automatically make you a good writer. Good science is the foundation of a scientific paper, but how the science is presented also strongly influences whether a paper gets accepted for publication. This session focuses on key elements of writing a scientific paper, starting with the first word put onto a page to the final printed product:

- Choosing the most effective words  
- Writing clear sentences  
- Developing the proper title  
- Creating an informative abstract  
- Organizing the introduction  
- Emphasizing results versus data  
- How to start and end the Discussion  
- Creating clear tables and figures  
- How to correctly use citations and references  
- How to choose the right journal  
- How to respond to reviewer comments  
- Acceptance does not mean the finish line

**Expected Outcomes:**
After this session, participants will be able to:
1. bring greater clarity and consistency to a scientific paper;  
2. describe the features that distinguish papers accepted for publication;  
3. organize the major sections of a scientific paper; and  
4. create more effective tables and figures.
Metabolomics describes the analysis of the small molecules present in our body and ingested from the surrounding environment (i.e., drugs, pesticides, etc.). The analysis of these metabolites has recently been utilized to discover new markers of disease and perturbed metabolic pathways. Metabolomic analyses can be performed with either targeted or untargeted measurements. In targeted studies, only a small subset of metabolites is analyzed and this prevalent in clinical analyses for measurements such as those for newborn screening. Untargeted measurements, however, study all possible small molecules in a single injection and heavily rely on the use of high resolution mass spectrometry to precisely measure the m/z values across many samples. Untargeted measurements are almost always coupled to either gas or liquid chromatography or ion mobility as the retention time or mobility provides an important secondary distinguishing characteristic of each specific metabolite. It is expected that both targeted and untargeted metabolomic measurements will have an important place in future clinical studies.

Given the growth of metabolomics over the past several years, the use of high resolution mass spectrometry has rapidly progressed. High resolution approaches to measure small molecules offer several advantages for clinical analyses such as confirmation via accurate mass of the precursor and product ions and an evaluation of the isotopic abundance. This short course will cover the application of high resolution mass spectrometry to both quantitative and semi-quantitative analyses with a focus on metabolomics.

Topics in this short course include: mass accuracy for identification, tandem mass spectrometry, quantitative aspects of high resolution mass spectrometry, identifying and measuring the metabolome, statistical analysis, ion mobility spectrometry, and liquid and gas chromatography coupled to high resolution MS.

Presentations 101
How to Maximize Your Influence Through Creating Compelling Presentations
Duration: Sunday 3PM → Monday at Lunch
Location: Rm 6D (Smoketree D)
Level: 1-2 (Beginner - Intermediate)
Instructor(s): Karen Mahooti, MBA

Day 1: Walk through interactive training in the full methodology for storyboarding, visual design, and oral delivery.

Day 2: See Presentations 102, below.

You have brilliant ideas with great potential. But it doesn't matter what you know; it matters what you communicate! Knowing how to create and deliver clear and compelling presentation documents can unlock influence and opportunity in your career. And the good news is that because there are so many bad presentations out there, armed with the skills in this course, it will be easy for you to stand out in a good way.

This class teaches you how to develop compelling presentations using storyboarding - a method used by professionals in major management consulting firms and some of the largest companies in the world. This versatile method will work for you whether you are in academics, business, government, or a non-profit and whether your audience is executives, colleagues, students, or investors.

While the course has a LOT of very practical information and tips, it is not a collection of sound bites and "top 10 tricks." It is a complete, proven process for creating memorable, persuasive presentations and shows you step by step exactly how to:

- Structure your content to flow smoothly and logically from start to finish in a way that is highly influential
• Design professional quality slides that make your key points jump off the page. Visual polish goes a long way in establishing credibility. And yes, YOU can do this, even if you are not a graphic designer!
• Orally deliver your presentation in a way that fully engages your audience with your ideas.

Many presentation courses are designed for the person giving a keynote address in front of a large auditorium. But most presentations are created for everyday settings: executive or team meetings, classrooms, and client discussions. And these presentations have very different challenges, which are the focus of this course. They must organize and communicate much larger amounts of information, but in a way that is still engaging and easy to follow. In addition, while they may serve as visual aids for an oral presentation, they must also stand on their own two feet and be clearly understood whether or not you are there to narrate them.

Comments from last year’s course participants:

"Very useful and practical. It can be applied right away."

"It was very well laid out and easy to understand. The audience interaction was great and very engaging."

"The materials we get to take home are so well organized and so clear that I was able to use the method on my own, 4 months after the short course."

"I felt very prepared when I had to make a presentation on a new topic. I spent far less time creating graphics I didn’t use and re-arranging slides with Karen’s method. Ultimately that led to less stress during the process of preparing the slides, and it improved the clarity and strengthened the message of my presentation."

Presentations 102
HANDS ON WORKSHOP: Create Your Own Compelling Presentation
Duration: Monday after Lunch → Tuesday Noon
Location: Rm 6D (Smoketree D)
Level: 1-2 (Beginner - Intermediate)
Instructor(s): Karen Mahooti, MBA

The best way to learn is by doing! This is a hands-on workshop opportunity to apply the methodology in development of an actual presentation document with the benefit of coaching from the instructor in combination with tools and techniques learned from Presentations 101. Each participant should bring a topic for a presentation they would like to develop for future use, as well as a general idea of its basic content. You are welcome to bring a laptop if your content is on the computer or needs to be accessed online, but a computer is not required. You will leave the class with a fully developed storyboard and sketched plan for slide visuals.

Proteomics 101
Introduction to Quantitative Proteomics
Duration: Sunday 3PM → Monday at Lunch
Location: Chino
Level: 1-2 (Beginner - Intermediate)
Instructor(s): Mike MacCoss, PhD, Michael Bereman, PhD & Jarrett Egertson, PhD

This course will introduce the researchers to the basics of performing quantitative peptide measurements by mass spectrometry. We will cover the basics of discovery and targeted methods, sample preparation, quality control, sample preparation, and software for method building and data analysis. To prepare participants for performing quantitative proteomics experiments in their own labs we will focus on the following topics:

• Instrumentation for proteomics
• Basics and challenges of NanoLC
• Introduction to quantitative analysis. Challenges for proteomics measurements
• System suitability and quality control
• Basics of complex protein mixture sample preparation
• Tips and tricks from instructor experience
• Use of Skyline for targeted proteomics method building and data analysis.
• Data Independent Acquisition
• Case studies

Proteomics 201

Clinical Proteomics
Duration: Sunday 3PM → Tuesday Noon
Location: Rm 3 (Madera)
Level: 2-3 (Intermediate - Advanced)
Instructor(s): Andy Hoofnagle, MD, PhD, Cory Bystrom, PhD & Chris Shuford, PhD

This course will explore the background of clinical proteomics and approaches to method development and validation. We will provide the motivation for using mass spectrometry to quantify proteins in clinical research and in clinical care. The promise of mass spectrometry to improve the accuracy and precision of results is only realized with robust methods. In order to prepare participants to begin to develop their own robust methods for quantification we will focus on the following topics:

• Why mass spec for peptides and proteins
• Optimization of digestion and other aspects of the method
• Internal standards
• Calibration
• Immunoaffinity enrichment
• Validation
• Quality control
• Case studies

Results Management 101

Effective Results Management
Duration: Monday after Lunch → Tuesday Noon
Location: Chino
Level: 0 (General Interest)
Instructor(s): Rainer Vollmerhaus, PhD

In this short course, individuals will learn how to get the results they need, while balancing the overwhelming number of initiatives and work experienced every day. By taking a focused look at how to effectively drive individual initiatives to a successful outcome the overall rate of delivery of results will increase, the overall success rate will increase. The amount of open initiatives on our plates will decline, we will produce smarter results as we think more clearly.

The mantra at work is often that everyone is continuously overwhelmed and must look and be busy. If you are not overwhelmed and frantic then you are probably not a ‘good’ employee. However, “busy” does not necessarily correlate with achieving desired results or successful outcomes. At its worst, actual results may even be compromised. The reality is that constant overwhelm decreases our ability to make good decisions and decreases our overall effectiveness and creativity. In this workshop we’ll take a look at some of the pitfalls that take us off track in our day to day activities. You will learn how to focus on getting the results you need, quickly and effectively. As a result you will have more time, be more relaxed. As you are more relaxed, you will make better decisions, you will find better solutions to the next set of tasks you are working on.

As these principles are learned for the individual, they will naturally be extended to teams and to organizations and lead to impactful, sustainable growth and improvement.

Goals

1 - To teach attendees to create Space and Time by driving initiatives to successful outcomes.
2 - Provide attendees with training on Continuous Improvement to assist in them in rapidly and successfully completing initiatives
3 - Teach attendees how to identify and develop solutions with the highest impact
4 - Equip attendees with new tools to support implementation of solutions
5 - Extend the learning to move from the effective individual to effective teams and effective organizations
6 - Have fun!

**Learning Objectives**

Attendees will enjoy learning the basic concepts and tools of continuous improvement. In a team environment, they will learn how to support each other to apply these tools and concepts to successfully implement their strategic plans. By the end of the workshop attendees will be confident and mutually supportive of taking the risk to actually use what they learned.

**Learning Activity Breakdown**

- 20% presentations and lectures
- 20% group exercises
- 20% team challenges
- 30% facilitated application in teams
- 10% reflective conversations

**Workshop Content: Introduction to Continuous Improvement Concepts and Tools.**

In a focused, experiential workshop we will:

- Discuss the organizational need for CI and how this connects to individual and organizational success.
- Take a problem from symptom to root cause to implementation.
- Learn key Continuous Improvement concepts and tools
- Learn how to apply concepts and tools in an organizational setting
- Examples of Key Concepts and Tools from the field of Continuous Improvement:
  - A3 management - a simple, powerful CI process used to gain consensus, focuses groups, capture all information, and drive successful outcomes. It turns a typical unfocused discussion into a focused dialog by capturing relevant information in one simple, structured report. This dramatically reduces the time needed to initiate and complete objectives.
  - Identify and define Current and Future States
  - KPIs (key performance indicators)
  - Relation between Problem, Symptom, and Root Cause
  - 5 Whys analysis - a tool to drive down to root cause
  - Creating and implementing sets of solutions
  - Process Waste - learn how to avoid typical wastes when implementing initiatives
  - PDCA (Plan, Do, Check, Adjust) - learn the benefits of iteration to minimize the time it takes to implement successfully
  - Visual Management - a simple method to track progress during and after implementation of solutions

**Sample Prep 201**

**Sample Preparation and Alternative Matrices for LC-MS Assays**

**Duration:** Sunday 3PM → Tuesday Noon
**Location:** Pueblo
**Level:** Beginner / Intermediate
**Instructor(s):** William Clarke, PhD & Mark Marzinke, PhD

This course will encompass various sample preparation approaches used for LC-MS assays. The course will highlight not only the importance of sample processing in the clinical laboratory environment, but also illustrate the “fit for purpose” application of processing techniques in clinical mass spectrometry. This course will also discuss the theory behind different specimen preparation methods, strengths and weaknesses of each approach, as well as opportunities
for automation. The first 8 hours will serve as a primer of the role of upfront sample management, utilizing examples in blood and urine specimen sources. There will also be an introduction to the application of LC-MS approaches in alternative matrices. The second 8 hours will elaborate on the foundations established in the first half, and expand into newer technologies and automated alternatives for sample processing.

Specific topics to be covered include:

1. Pain points in clinical LC-MS
2. Overview of specimen processing in laboratory medicine
3. Off-line sample processing
4. On-line sample processing
5. Analysis of blood and urine
6. LC-MS of tissue specimens
7. Alternate body fluid specimens (e.g. CSF, breast milk, etc.)
8. Intracellular and metabolite analysis
9. Dried specimens as matrices
10. Automation of sample processing

Topics will be covered through lecture, Q&A, Case Studies, and small group exercises.
Discussion Groups

Tuesday from 7:30 to 8:30 PM

Clinical Mass Spectrometry: Journal Overview
@ Room 1 (Mojave Learning Center)
Lead(s): Chris Herold, Alan Rockwood, Michael Vogeser
An update on the status of the to the journal, Clinical Mass Spectrometry. Includes open discussion on how best to approach its development with the intent of creating a premier literature resource for the field.

Wednesday from 6:00 to 7:00 PM

Practical Training Track Development
@ Chino
Lead: Rob Fitzgerald
Feedback on the Practical Training track. How is it going? What can be improved?

Being a Reviewer
@ Pueblo
Lead: Thomas Annesley
1) Why be a reviewer? and 2) what to look for and how to write up an effective review.

Solutions in Search of a Problem? Making Assays Matter for Patients
@ Room 1 (Mojave Learning Center)
Lead: Stephen Master
Panel Discussion with: a practicing physician (Alyssa Burgart, Pediatric Anaesthesiology, Stanford), an MD clinical chemist (Dan Holmes, University of British Columbia), and a pediatric metabolism specialist (Mike Bennett, Children’s Hospital of Philadelphia).

Even the most advanced MS-based assay will fail if it cannot be translated into a clinical decision. A successful diagnostic should answer an important clinical question, provide adequate performance to support a clinical management decision, be delivered within a clinically relevant time-frame, and be understood by the clinician. Complex biomarker discovery efforts based on sensitive emerging technologies and improved biological understanding must still meet these basic criteria if we want our work to matter for patients. One key is ensuring that the clinical laboratory is adequately integrated with clinicians on a regular basis to understand the true clinical needs and ensure that the strengths and weaknesses of assays are clearly understood.
We will discuss the nature of clinical decision-making, important gaps in current testing capabilities, and paradigms for effective collaboration between the lab and the clinician. Our questions will include: What tests do physicians need, and why? How do assay performance and turnaround time influence the utility of a clinical test? What programs have been successful in ensuring that the lab develops tests that meet clinical need? How can the lab effectively communicate the interpretation of complex, emerging tests? What are the ethical considerations for determining when a test is “useful enough” to justify the cost of its development?

Translating Protein MS Assays into the Clinical Laboratory
@ SmokeTree
Lead: Dobrin Nedelkov
Protein MS assays are assured to be the next-generation tests for precise and enabling measurement of clinical protein biomarkers. Or are they? In the 30 years after the MALDI and ESI invention, only a dozen or so protein MS tests have been translated into clinical laboratories. Analytical performance requirements have been in place for some time, along with small molecules MS clinical tests precedents, so why haven’t more protein MS assays found their ways into clinical labs? Is there anything else missing? What about the clinical and economic drivers? If some of these key drivers have not been met yet, are we to proceed with the protein MS tests translation anyway, anticipating near-term clinical adoption? How do we then pick the biomarker targets for these tests? Many players have a stake in the clinical protein MS tests— from reagents and instruments manufacturers, to clinical labs and diagnostic companies. So
please join us for a lively discussion and confessions of the culpable that may help us answer the ultimate question: Are clinical protein MS tests prophetic or just rhetoric?

**CDC Standardization Programs Forum**
@ Andreas
Lead(s): Julianne Botelho & Hubert Vesper
Participants will discuss how CDC Standardization Programs support laboratories with improving measurements for key hormones such as 25-hydroxyvitamin D, estradiol, and testosterone. Included will be additional discussions about new projects and tools available in CDC Standardization Programs.

**Exhibitor Feedback Meeting**
@ Mesquite H
Lead(s): Amber Herold
Exhibitors, let MSACL know your thoughts on the way the conference is working for you and what we can do to make the experience better in the long run.
# Exhibits Summary

<table>
<thead>
<tr>
<th>Day</th>
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<tr>
<td>Tuesday</td>
<td>8:00 – 16:00</td>
<td>Exhibitor Set-Up (EXHIBITS CLOSED) – Poster Placement for Presenters Permitted.</td>
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<tr>
<td></td>
<td>16:00 – 19:30</td>
<td>Opening Reception in Exhibit Hall</td>
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<td>Wednesday</td>
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<td>Welcome Coffee in Exhibit Hall</td>
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<td>9:45 - 10:45</td>
<td>Posters in Exhibit Hall</td>
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<td>11:30 – 13:00</td>
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<td>16:00 – 18:00</td>
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<td>Thursday</td>
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<td>12:00 – 12:45</td>
<td>Poster Session in Exhibit Hall</td>
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<td>Lunch provided in the Exhibit Hall</td>
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<td>EXHIBITS CLOSE</td>
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<td></td>
<td>14:00 – 18:00</td>
<td>Exhibitor Breakdown and Packing</td>
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<tr>
<td></td>
<td>21:00</td>
<td>Deadline for removal of Exhibits from Exhibit Hall</td>
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![Exhibit Floor Plan](image-url)
Exhibitors

**Advion** Booth #37  
http://www.advion.com

With over 20 years of mass spectrometry and chemistry expertise, Advion offers the expression family of compact mass spectrometers designed for the chemist. The affordability, small size and ease-of-use make them ideal for use directly at the chemist’s bench, giving immediate answers and informed decisions instead of waiting in line at a central analytical service laboratory. Quickly and effortlessly analyze samples from Flash chromatography, Prep-LC, SFC, TLC, (U)HPLC, or manual syringe injection. Now every synthetic chemist can have a mass spec that works the same hours that they do. Learn more at www.expressioncms.com

**Agilent Technologies** Booth #56/57  
http://www.agilent.com/en

Agilent Technologies delivers premiere analytical technologies for clinical research ensuring your success from sample prep to final answer. These include a comprehensive portfolio of innovative automation, chemistries, GC, GC/MS, ICP/MS, LC, and LC/MS solutions which enables the identification and quantification of both endogenous and exogenous substances in complex biological matrices with the utmost accuracy and reliability. Coupled with our dedicated global support network, we will get you to your final answer with minimal ramp-up and maximum productivity.

**ALIFAX** Booth #54  
http://www.alifax.com/

ALIFAX was founded in 1988 for the development of innovative solutions in hematology, microbiology, serology and autoimmunity fields becoming rapidly a global important player in the IVD market with 26 active patents, more then 10,000 installed instruments and 1 bln tests sold worldwide. Alifax Eureka LabDivision recently introduced a brand new ready to use CE-IVD line for Liquid Chromatographs, Gas Chromatographs and Mass Spectrometry platforms for Clinical Chemistry, Pharmacology, Occupational/Forensic Toxicology and Endocrinology Therapeutic Drugs Management applications. The mission is to design, produce and support globally the widest kits range fully compatible with the most popular GC/UHPLC/MS/MS manufacturers.

**Apricot Designs** Booth #31  
http://www.apricotdesigns.com

Apricot Designs specializes in purpose-built equipment providing innovative, accurate, and precise liquid handling technology that reflects the increasing complexity and requirements of biotech, clinical, and pharmaceutical research. As liquid handling experts and specialists in multi-channel micro-volume pipettors, disposable pipette tips, and high-performance evaporators, we focus on the lab automation needs of researchers, scientists and lab professionals worldwide with equipment designed to make lab work more accurate, more precise, more efficient and thus, more productive.

**Biotage** Booth #39  
http://www.biotage.com/

Biotage is a leading provider of sample preparation instrumentation and consumables for a wide range of applications, including pharmaceutical, clinical, forensic, environmental, and agrochemical/food. ISOLUTE® and EVOLUTE® brand solid-phase extraction (SPE) and Supported Liquid Extraction (SLE ) products can be run in either a manual or automated environment. The new RapidTrace+ SPE workstation and TurboVap® Solvent evaporators are ideal for increasing throughput and achieving accurate results. Stop by our booth for the latest innovations and applications for Evaporation and Sample preparation.

**Bruker** Booth #38  
http://www.bruker.com

Bruker Corporation is a leading provider of Chromatography and Mass Spectrometry instruments and solutions for the Analytical Sciences. Our innovative and easy-to-use product families (ESI-QTOF, Ion Trap, FTMS, MALDI-TOF, LC-Triple Quads and GC-Triple Quads) provide the highest performance, ruggedness and value for a wide range of applications in the food, environmental, forensic, industrial, pharmaceutical, and life science research markets.
Cambridge Isotope Laboratories Booth #36
http://www.isotope.com
Cambridge Isotope Laboratories, Inc. is the world leader in the manufacture and separation of stable isotopes and isotope-labeled compounds. CIL offers highly pure compounds that are uniformly or selectively enriched in $^{13}$C, $^{15}$N, D, $^{18}$O or $^{17}$O. CIL's labeled reagents are used in proteomics, metabolomics, metabolism, and environmental applications for quantitative mass spectrometry. Our products include MRM PeptiQuantTM assay kits, SILAC protein quantitation kits, media and reagents, 99% enriched amino acids, MouseExpress$^{a}$ Lys $^{13}$C$_{6}$ and $^{15}$N mouse feed and tissue, $^{15}$N spirulina, intact labeled proteins, growth media for protein expression, cell-free protein synthesis products, environmental contaminants standards for ultratrace analysis, steroids, acylcarnitines, drug metabolites, nucleic acids, lipids and carbohydrates. CIL has GMP capabilities; a majority of substrates can be manufactured to Q7A compliance.

Chrom Tech Booth #48
http://www.chromtech.com
Distributor of Chromatography consumables, instrumentation and supplies. Featuring: Sample Preparation Products, 96 Well Plates for MS, 96-well Multi-Tier™ Micro Plate System with Glass Inserts, Columns, Instrument consumables and replacement parts, Pumps, Gas Generators. Featured Suppliers include: Agilent Technologies, Thermo Scientific, Sigma Aldrich, Idex (Upchurch and Rheodyne), Parker Balston, Hamilton, Restek.

Chromsystems Booth #43
http://www.chromsystems.com
Chromsystems is a leading global company providing ready-to-use reagent kits and supplies for routine clinical diagnostics by HPLC and LC-MS/MS, the latter representing the gold standard for many parameters. Our product portfolio includes complete kits, quality controls and multilevel calibrators, all ensuring highly accurate as well as a cost-effective analysis in the laboratory. They enable any laboratory to introduce HPLC and LC-MS/MS methods into their diagnostic routine without prior technical expertise. Analyses can be started immediately and sample preparations require the minimum of laboratory time. Our products are comprehensively validated, in particular LC-MS/MS methods with all widely used tandem mass spectrometers. They are CE-IVD compliant, satisfying regulatory requirements for the laboratory. We combine these high quality products with an excellent support programme and service for our customers.

DPX Labs Booth #32
http://www.dpxlabs.com/
At DPX Labs we believe that your sample preparation should be fast and easy. That is why we have incorporated the benefits of solid-phase extraction into a simple to use pipette tip. The patented Dispersive Pipette Extraction (DPX) tip functions by dispersive SPE, requiring only seconds of mixing within the DPX tip to complete the sample preparation process. Now anyone can rapidly extract samples with high recoveries prior to LC/MS analysis. Whether your laboratory uses a single channel pipettor or a fully robotic liquid handler, there is a DPX tip compatible with your analysis method and throughput. Contact DPX Labs so we can help you eliminate matrix interferences and make ion suppression a thing of the past.

GenTech Scientific Booth #53
www.gentechscientific.com
Reliability Assured for over 20 years! GenTech Scientific supplies quality refurbished GC, HPLC, MS, SEM/TEM, LCMS, ICP/MS instrumentation. Skilled technicians rigorously inspect and fully refurbish all of our products. Get guaranteed OEM standards at a fraction of the cost of new instruments! Extend your peace of mind with our exclusive GenTech Master Certified Instruments. Beyond simple refurbishment, we certify these products only after they’ve met our stringent criteria. GenTech Master Certified Instruments come with a one year warranty and can be extended to two, three, four or five years. We offer customized training, expert service, depot repair and professional installation. Rent, lease or purchase from our warehouse of meticulously maintained instruments. We provide the options you need to equip your lab for less.
**Gerstel**  Booth #61
http://www.gerstelus.com/
Celebrating 50 Years of Chemical Analysis Solutions: GC/MS, LC/MS sample introduction and stand-alone workstations with the most advanced software control available (MAESTRO). MultiPurpose and PrepStation Autosamplers provide maximum versatility and throughput for liquid injection, SPME, Headspace, ALEX, SPE, dpx®, Dynamic HS, ATEX weighing, centrifugation, and SBSE. Twister® performs solventless extraction and ultra-low detection limits. The most versatile Thermal Desorption System available for all sample types. Cooled (PTV) inlet, Olfactory Detection, Multidimensional Heartcutting, Preparative Fraction Collector.

**Golden West Diagnostics**  Booth #17
http://www.goldenwestdiagnostics.com
Golden West Diagnostics, Inc. addresses the need for quality, cost effective biological raw materials for the development of immunoassays and LC-MS applications. GWD provides manufacturers and laboratories with over 80 products including Vitamin D free human serum, serum for ultra-sensitive testing, HSA, HGG, and RGG. Please visit us at www.goldenwestdiagnostics.com.

**Grenova**  Booth #52
http://www.grenovasolutions.com
Grenova devices offer labs the option to reuse plastic tips several times, cutting associated costs by up to 90%. Grenova TipNovus is a benchtop, high-throughput device that will enable labs to wash and sanitize contaminated pipette tips in large quantities for reuse. TipNovus’ unique method of washing and sanitation is safe for both the lab and environment.

**Hamilton Robotics**  Booth #44
http://www.hamiltonrobotics.com
Hamilton Robotics is dedicated to the design and manufacture of automated liquid handling workstations. We offer a several types workstations for direct sale and OEM. Key to our products is our air displacement pipetting and monitoring technology as well as the software controlling our systems. We believe every laboratory automation project is unique. Our workstations and software serve as a common high precision and flexible base upon which to provide automated solutions. To this end we employ teams of highly skilled and experienced application and hardware customization specialists around the world to provide our customers with unique solutions to automate their assays successfully and within budget. Please come explore our products and contact us to discuss your automated liquid handling needs further.

**Imtakt USA**  Booth #12
http://www.imtaktusa.com
We are advancing HPLC science by creating unique columns with novel chemistries that provide enhanced selectivity and resolution. We offer a wide range of innovative stationary phases compatible with HPLC, UPLC and LC-MS. Our columns have 25-50% lower pressure and excellent batch-to-batch reproducibility. For more information, please visit our website to view our Product Guide and Application Library.

**Indigo BioAutomation**  Booth #58/59
http://www.indigobio.com/
Indigo BioAutomation, founded in 2004, is an established leader in software automation for the applied and health sciences. Indigo's flagship system, ASCENT, is a hosted system for automating the processing, reviewing, and reporting of LC-MS/MS data. ASCENT has helped automate the review of tens of millions of samples, in a variety of clinical/toxicology laboratories. In addition to daily workflows, Indigo's systems also provide laboratory analytics dashboards. Looking ahead, Indigo will continue to create world-class computational decision-making tools and laboratory automation systems.
IsoSciences Booth #49
http://isosciences.com/
IsoSciences, LLC is a world leader in the synthesis of stable isotope labeled vitamins, steroids, drug substances, metabolites and other compounds of interest. IsoSciences is ISO9001 certified and has an extensive catalog of stable isotope labeled standards available for immediate delivery both as solids and as CertiMass™ exact concentrations solutions. IsoSciences has added over 200 new products over the past year including an extensive range of $^{13}$C$_3$ labeled steroids, Vitamin D metabolites, $^{13}$C$_7$-Vitamin B$_{12}$, $^{13}$C$_7$-Vitamin K2 MK4, MK7 and MK9. Contact info@isosciences.com for any internal standard needs you may have!

Kura Biotec Booth #63
http://www.kurabiotec.com/

Metabolomic Technologies Booth #15
http://www.metabolomictechnologies.ca/
Metabolomic Technologies Inc. (MTI) is a spin-off company from the University of Alberta in Edmonton, Alberta, Canada. Established in 2010, MTI is a privately owned company and sole owner and proprietor of PolyDx™. Formed from a research program facilitated by Drs. Haili Wang and Richard Fedorak, who were interested in using metabolomics to explore how colorectal cancer, a leading cause of cancer deaths in North America but curable if identified early, affected cellular metabolism. PolyPDX™ is a spot urine diagnostic test to detect adenomatous (precancerous) polyps, and advances the prevention of CRC. Through a new partnership with Atlantic Diagnostic Laboratories, LLC PolyDx™ is now available in 12 US States.

MilliporeSigma Booth #45/46
http://www.Sigma-Aldrich.com/clinical
MilliporeSigma provides the innovative solutions you need to advance your research, and more importantly, the support and expertise to utilize them successfully in your lab. You'll identify more than analytes, target molecules and contaminants. Our full range of water purification products provides accurate lab results, high reliability, low maintenance, predictable and economical running costs and total support. In cellular analysis, protein detection, separation science and membrane filtration, we continue to set the standard for analytical research by providing the highest quality bioanalysis platforms, sample preparation solutions, essential biochemicals, and analytical separation tools.

Nacalai USA Booth #28
http://www.nacalaiusa.com
Nacalai provides HPLC and SFC columns with alternate selectivity for difficult-to-separate compounds. The core-shell Cosmocore Cholester HPLC column can baseline separate 25-OH vitamin D$_3$ and D$_7$ metabolites and their epimers in isocratic reversed-phase condition. The same Cosmocore Cholester HPLC column can also detect Δ-8 THC and Δ-9 THC and metabolites. Additionally, we provide SunShell HPLC/SFC columns in the US. Free column screening is available in our San Diego lab.

Neoteryx Booth #55
http://www.neoteryx.com
Neoteryx delivers automatable and quantitative microsampling solutions comprising of technologies for minimally invasive, economical specimen collection and transportation, facilities for designing/manufacturing custom remote sampling kits, and services that include extraction method optimization, analytical method development, and turnkey workflow installations.

New England Peptide Booth #25
http://www.newenglandpeptide.com/
New England Peptide (NEP, Gardner, Massachusetts) has designed and produced high quality custom peptides, polyclonal and monoclonal antibodies for research organizations worldwide since 1998. Our chemists and immunological experts have over 100 years of experience and deliver a full range of peptide and antibody services for biotech and pharmaceutical applications. These include custom peptide synthesis, custom peptide arrays, polyclonal antibodies, quantitative proteomics via our NEPTune™ platform, and analytical services such as mass spec and AAA. Learn more at www.newenglandpeptide.com.
Optimize Technologies Booth #47
http://www.optimizetech.com
Optimize Technologies offers a complete line of innovative components and replacement parts for UHPLC, HPLC and LC/MS systems. Products include EXP® Fittings, Filters, Traps and Guards, OPTI-MAX® Check Valves, OPTI-SEAL® Seals, Replacement Pistons, OPTI-GUARD® Guard Columns, OPTI-PAK® Traps, OPTI-SOLV® Filters and OPTI-LYNX™ Quick-Connect packed beds. New products include EXP® hand-tight fittings, UHPLC/MS traps, UHPLC filtration, guard solutions rated to 20,000+ psi and OPTI-TRAPS™ for large molecules, peptides, online desalting and detergent removal. All Optimize EXP® products feature hand-tight holders and EXP® Titanium Hybrid reusable ferrules.

OraSure Technologies Booth #04
http://www.orasure.com
OraSure Technologies manufactures oral fluid devices and other technologies designed to detect or diagnose critical medical conditions. Its innovative products include rapid tests for HIV and HCV antibodies, influenza antigens, testing solutions for detecting drugs of abuse, and oral fluid sample collection, stabilization and preparation products for molecular diagnostic applications.

Orochem Technologies Booth #03
http://www.orochem.com/
Established in 1996, Orochem Technologies Inc. manufactures unique Sample Prep and Chromatography Products for the Bioanalysis, Drug Discovery, and the Genomics and Proteomics markets. Backed with unique expertise in high throughput formats, membranes and surface chemistries, Orochem was one of the first companies to translate the concept of pre-filters from single to high throughput formats, a concept now widely implemented for sample prep plates in the biotech and analytical markets. In the year 2001 Orochem manufactured the first commercially available Protein Crash and Precipitation 96-well plate for Bioanalytical processes. Orochem Technologies serves the clinical diagnostic labs in the areas of drugs of abuse, steroids, vitamin D and metabolites, and proteomics. At this MSACL, we will present our new vitamin D Metabolite Extraction Kit, and new HPLC columns for steroid isomer separation.

Parker Hannifin Booth #09
http://www.parker.com/fns/balstonlabgasgenerators
Our company manufactures high efficiency gas generators to eliminate high pressure cylinders from the laboratory. Gas generators provide increased safety, free up laboratory space, save money and produce ultra high purity gasses for your laboratory instruments. With a gas generator you are in control. These state-of-the-art gas generators continuously produce ultra-high purity gases for LC/MS, GC, FT-IR, TOC, ICP, AA and other instrumentation. All products are backed by fully staffed field sales and service organizations and one-year warranty. Preventative maintenance programs and extended warranties are available for all Parker Balston products.

Peak Scientific Booth #33
http://www.peakscientific.com

PerkinElmer Booth #02
https://www.perkinelmer.com
PerkinElmer, Inc. is a global leader focused on improving the health and safety of people and their environment. PerkinElmer is dedicated to the quality and sustainability of the environment. With our analytical instrumentation, illumination and detection technologies, and leading laboratory services, we focus on improving the integrity and safety of the world we live in.

Phenomenex Booth #40
http://www.phenomenex.com
Phenomenex is a global technology leader committed to developing novel analytical chemistry solutions that solve the separation and purification challenges of researchers in industrial, government and academic laboratories. Phenomenex's core technologies include products for liquid chromatography, gas chromatography, sample preparation, bulk purification chromatographic media, and chromatography accessories and equipment. For more information, visit www.phenomenex.com.
**Phytronix Technologies** Booth #51
http://www.phytronix.com/
The leader in quantitative ultra-fast high-throughput analysis for mass spectrometry presents the new LUXON ION SOURCE with a sample to sample speed below one second. The Luxon process can be integrated with automated liquid handling and robotic transfer arm systems to provide real high-throughput and continuous automation for your laboratory workflow. This patented ionization source offers outstanding analytical performance in pharmaceutical, bioanalytical, forensic, food and environmental industries and performs exceptionally well in other analytical fields. The Luxon Ion Source is the second generation sample introduction and ionization source based on the LDTD® technology to provide the fastest and most robust process in mass spectrometry.

**Prosona** Booth #50
http://www.prosona.com
Prosona’s DESI, Flowprobe and Velox 360 products empower scientists in the pursuit of obtaining better chemical data for better decisions in science and medicine. Our portfolio of scientific analytical tools includes innovative sample introduction systems and intuitive software - all of which are part of workflows that reduce complexity and accelerate results.

**Proton OnSite** Booth #05
http://protononsite.com/
Proton OnSite is the world’s leading supplier of on-site generators for laboratories. Proton Onsite offers a safe, affordable and high performance solution for onsite hydrogen generators, nitrogen generators, air compressors, air generators and zero air purifiers. Proton’s units are manufactured in a wide range of space saving stackable systems and we offer a complete line of advanced equipment for the LCMS and GC lab market.

**Psyche Systems** Booth #30
http://www.psychesystems.com/
Psyche Systems Corporation is a private, profit-driven software company that has focused exclusively on delivering laboratory information software to hospitals, clinics, reference and private labs since 1976. It is this unwavering focus on serving our core customer base that has enabled Psyche to maintain strong customer loyalty and deliver on our commitment to high quality products and services. Psyche Systems’ laboratory information software are best-of-breed products designed to meet the specific needs of Anatomic Pathology, Cytology, Histology, GI, Toxicology, Microbiology, and Molecular laboratories. We at Psyche work closely with our customer base during product development to ensure we are delivering the highest quality products and services at a competitive price. For more information, visit www.psychesystems.com

**RECIPE Chemicals & Instruments** Booth #29
RECIPE was founded in Munich, Germany, in 1982 and is one of the leading companies in HPLC and LC-MS/MS diagnostics today. For mass spectrometry, RECIPE offers CE/IVD labelled ClinMass® LC-MS/MS Complete Kits. Furthermore, several reagents such as ClinMass® Optimisation Mixes and Internal Standards, ClinCal® Calibrators and ClinChek® Controls are available for a reliable and standardised LC-MS/MS analysis. All products are developed and produced in our state-of-the-art production plant in Munich. RECIPE is recognised worldwide as a reliable partner for clinical laboratories and is certified by the quality management standards ISO 9001 and 13485.

**Restek** Booth #35
http://www.restek.com
A leading innovator of chromatography solutions for both LC and GC, Restek has been developing and manufacturing columns, reference standards, sample preparation materials, accessories, and more since 1985. We provide analysts around the world with products and services to monitor the quality of air, water, soil, food, pharmaceuticals, chemicals, and petroleum products. Our experts have diverse areas of specialization in chemistry, chromatography, engineering, and related fields as well as close relationships with government agencies, international regulators, academia, and instrument manufacturers. www.restek.com

**Scientific Systems** Booth #34
http://www.ssihlc.com
Scientific Systems, Inc. (SSI) designs and manufactures a full line of high performance piston pumps and fluid path
components for HPLC, Precision Metering and Process applications. Flow rates range from 1 micro-liter to 300 ml/min, with pressures up to 25,000 psi. Fluid paths are offered in PEEK, Stainless Steel and Titanium, in a wide variety of single piston and dual piston platforms. All SSI pump products are available as stand-alone units or as customized kits for OEM instruments. Since 1967, SSI has provided innovative products to the laboratory and industrial markets, with the highest level of Quality and Customer Service.

**SCIEX Booth #22/23**

http://sciex.com/applications/clinical-research

SCIEX helps to improve the world we live in. SCIEX LC-MS/MS solutions enable clinical researchers to push the limits of analysis across a wide variety of applications, including quantitation of steroids, vitamin D, immunosuppressants or drugs of abuse, by harnessing the power of mass spectrometry through exceptionally simple-to-use tools. SCIEX offers the most comprehensive portfolio of pre-configured LC-MS/MS methods and software for clinical research and toxicology. All based on the proven reliability of SCIEX systems, including the SCIEX QTRAP® 5500 system, the most sensitive LC-MS/MS system for trace level analysis -- all backed by the most comprehensive service and support organization in the industry. For more information, go to www.sciex.com/clinicalresearch

**Shimadzu Booth #41/42**

http://www.shimadzu.com/

Founded in 1875, Shimadzu is a multinational corporation with three major divisions: Medical Diagnostics, Aerospace/Industrial, and Analytical Instruments. The Analytical Division is one of the world’s largest manufacturers of analytical instrumentation, supporting a broad range of applications including life sciences, pharmaceuticals, food safety, environmental, chemicals, and forensics. Shimadzu expanded the scope of its ISO-13485 certification, which covered blood coagulation and automatic clinical chemistry analyzers, to include LCMS and LC instruments. Shimadzu will continue to register medical devices with the FDA, and support the growing demand for LC and LCMS in clinical testing markets. Visit our booth to learn more about new Shimadzu platforms, including our ultra-fast LCMS-8050 triple quadrupole, automated protein digestion workstations and a “lab-on-a-card” technology that generates volumetric plasma from an unmeasured drop of whole blood in minutes.

**SPEware Booth #16**

http://www.speware.com

SPEware Corporation brings advanced separation efficiency to the extraction laboratory using micro-particulate Solid Phase Extraction (SPE) paired with Positive Pressure Manifolds. We have 20 years of experience designing, manufacturing and providing Positive Pressure Processors directly to our customer and to resellers. As the original equipment manufacturer, we have perfected the technology of positive pressure for use with our micro-particulate products as well as developed fully automated extraction procedures. SPEware specializes in customized solutions ranging from traditional extraction problems to unique issues that require a high degree of purification and efficient processing. We strive to provide superior customer service and quick turnaround times. We offer a team of experts that includes our scientific advisory board, analytical chemists, and field application scientists in order to deliver innovative solutions to your SPE needs.

**Thermo Scientific Booth #24/27**

http://www.thermoscientific.com

Thermo Fisher Scientific™ is the world leader in serving science. Our mission is to enable our customers to make the world healthier, cleaner and safer. Your clinical research changes the world one life at a time. And we share that quest with you, providing the tools and confidence to improve lives every day. Leveraging our years of experience to help advance clinical research to routine testing with the most comprehensive, most innovative mass spectrometry-based workflows on the planet. We both know, the faster the results, the faster decisions can be made. Be someone’s hero.

**Thomson Instrument Co Booth #26**

http://htslabs.com/

Thomson Instrument Company is a leading-edge manufacturer and supplier of consumable products for the Chemistry and Biological fields. Our SINGLE Step Filter Vials (450uL capacity), Nano Filter Vials (10uL minimum sample volume), and eXtreme Filter Vials (>30% particulates) are used in many labs for all your sample preparation needs and are compatible with most standard autosamplers for HPLC, GC, LC/MS. We provide a number of simple standard and custom products to meet our customer’s needs. Please look at our website at www.htslabs.com. We are committed to
competitive pricing and quality customer service. Ph: 800-541-4792 or 760-757-8080 Fax: 760-757-9367 E-Mail: folks@htslabs.com

UCT Booth #01
http://www.unitedchem.com
UCT is a vertically integrated manufacturer of high quality Sample Prep and HPLC column products. We combine this with world class technical support. Product lines include Solid Phase Extraction (SPE) cartridges/well plates, QuEChERS tubes, Selectra® HPLC columns, manifolds, Selectrasil® reagents and enzymes, and newly launched Ultra Flash® purification columns. Also, UCT in collaboration with Obotics and Hudson Robotics are excited to present OB-1, the world’s first truly intelligent robotic lab assistant. This automated platform provides a complete solution that fully accommodates the needs of the forensic toxicology community.

UTAK Laboratories Booth #11
http://www.utak.com
Since 1973, UTAK Laboratories, Inc., has been connecting Research and Commercial Laboratories with the most comprehensive menu of Stock and Custom manufactured Quality Controls available. Our Products offer complete commutability with many methods of evaluation including: Immunoassay, ELISA, HPLC, UHPLC, ICPMS, GC/MS, and LC/MS, TOF, etc. Our entire line of 100% REAL Human Matrix products along with our Specialty Matrix (SMx™) products come together to offer Laboratorians a true 3rd party Quality Control, especially for Laboratory Developed Tests or LDT’s. Ask us about QC for your LDT. UTAK, createCONTROL

Veritomyx Booth #62
http://www.veritomyx.com
Veritomyx® delivers unprecedented breakthroughs in biomarker discovery and exploitation, through innovative advanced signal processing and identification algorithms applied to raw mass spectral data. Our flagship PeakInvestigator™ software detects and deconvolves overlapped peak data, increasing mass-analyzer resolution by 3-4x, and revealing critical hidden information with large sensitivity and precision improvements. This more accurate, complete and precise information helps to minimize inefficient misdirected R&D, by accelerating correct metabolomic and proteomic biomolecular identifications. PeakInvestigator’s resolution-multiplying impact operates upon raw profile MS data from ion trap, TOF, Orbitrap and FTICR mass analyzer outputs. Veritomyx’ second product, PeptideDetective™ software (alpha collaborations phase), outperforms current market leaders in de novo peptide identifications, yielding further important improvements in biochemical identifications efficiency.

Waters Booth #13/14
http://wwmc.waters.com
At Waters Corporation, we understand the factors necessary to succeed at each stage of the health sciences continuum, from the challenges of biomarker discovery and translation to validation and commercialization of innovative clinical diagnostics. We draw on first class scientific expertise to bridge the translation gap and help further the understanding and management of disease. Driven by purposeful innovation, we have created a comprehensive line of scientific products and services designed to support the entire continuum of biomedical research. These include state of the art analytical tools such as chromatography and mass spectrometry, associated informatics, and supportive sample preparation and diverse column chemistries. www.waters.com/msacl

Zef Scientific Booth #60
http://www.zefsci.com
• Is your Mass Spectrometer showing the uptime that you expect? • Do the different vendors tend to blame each other—or your method—for an issue? • Are you looking for a more harmonized and seamless experience in maintaining your LC-MS/MS? ZefSci is the country’s premier independent LC-MS/MS engineering firm. A network of experienced field service and qualification engineers are strategically positioned nationwide supplying our customers with the highest level of services on AB/Sciex, Thermo, Waters, Agilent, and Shimadzu. 1- Service Contracts 2- Preventative Maintenance 3- Repair 4- GxP Compliance IQ/OQ/PQ
Corporate Workshops

Corporate Workshops - Wednesday Early AM
7:00 - 7:45 AM

MSACL - Room 1 (Mojave)
Ensuring the future of innovation in laboratory medicine
Chair: Stephen Master
Panel: Drs. Michael Bennett (President, AACC), Richard Friedberg (President, CAP), Steve Gonias (Chair of Pathology, UCSD)

The development of clinical laboratory medicine over the past century has been driven by advancements in the range of analytes measured and the analytical performance provided by novel technologies. The discipline has continued to create and implement new diagnostic modalities, with mass spectrometry being the most recent example of a technology that provides fundamental improvements in clinical testing capabilities. This historical success in clinical translation has depended on an adequately trained group of clinical laboratorians (both MD and PhD-level leadership as well as technologists) with the resources to perform assay development and optimization. However, the need for trained personnel has also spurred commercial development of turnkey (or even Point-of-Care) versions of these technologies. Paradoxically, this may reduce the willingness of medical centers to support trained personnel and the development infrastructure that is required for the further advancement of diagnostics through advanced mass spectrometry, informatics, and other emerging technologies.

In light of this issue, it will be important for professional societies and organizations dedicated to clinical chemistry and laboratory medicine to develop effective and cooperative strategies to ensure the ongoing intellectual vitality of the field. Specifically, a number of questions will need to be addressed: How do we provide adequate training in novel assay development for laboratorians? How do we identify and strategically support emerging technologies? What are the roles of academic medical centers, large reference labs, and IVD companies in technology development pipelines? How do we effectively advocate for funding sources that can encourage translational diagnostic development? How do we ensure that test development addresses significant medical needs? How do we communicate this value to health care payers? If technology development is centralized at a small number of centers, is this adequate for robust and creative development of technology?

Spark Holland - Room 2 (Catalina)
1. A Dried Plasma Spot Device for the Collection and Automated On-Line LC/MS/MS Bioanalysis of Micro Blood Samples, 2. The Hematocrit Issue in Dried Blood Spot Analysis: Still an Issue?
1. Jack Henion, Ph.D. Emeritus Professor, Cornell University, 2. Christophe Stove, Ph.D. Professor, Ghent University

Major Dried Blood Spot (DBS) uses include screening for inborn metabolomic errors, epidemiological surveys (e.g. HIV monitoring), TDM, and toxicology. Implementing dried blood microsamples in an analytical workflow offers advantages, including simplification of sample collection, transport, storage and processing, as well as automation. Furthermore, it enables collection by non-medically trained persons in remote areas or at home. However, DBS also introduces challenges, such as a need for sensitivity and extensive method validation. Quantitative DBS analysis suffers from issues that continue to limit its breakthrough into routine bioanalysis. Amongst these are spot volume, spot inhomogeneity, and influence of hematocrit. The latter has proven especially problematic for widespread DBS acceptance. Recently, several approaches to accommodate the hematocrit issue have been developed, the pros and cons of which will be discussed in these presentations.

Biotage - Room 3 (Madera)
Practical Considerations for LC/MS Method Development of a Comprehensive Urine Pain Panel
Stephanie J. Marin, Ph.D.

There has been increased interest in the clinical laboratory to develop comprehensive LC-MS/MS assays for urine drug testing, with 50 or more drugs and metabolites from multiple drug classes in a single method. These panels can increase throughput and improve laboratory efficiency, but create many challenges. Considerations for developing robust sample preparation methods for acidic, basic and neutral drugs for pain management and compliance testing in hydrolyzed urine specimens will be discussed. Method development strategies depending upon the compounds of interest will be presented.
Corporate Workshops -  Wednesday AM  
8:00 - 8:45 AM

Brucker - Room 1 (Mojave)  
(1) Rapid Response: Precision Microbiome Detection, (2) Implementing the MicroFlex in the Clinical Laboratory to Identify Monoclonal Proteins in Serum  
(1) Alexander A. Aksenov, Ph.D., Project Scientist, Skaggs School of Pharmacy and Pharmaceutical Sciences, UCSD, (2) David Barnidge, Ph. D., Clinical Development Associate, Mayo Clinic  
‣ (1) The goal of the Rapid Response Precision Microbiome (RRPM) initiative at UCSD is to enable under 48-hour integrated "omics" reporting to the physician. We will highlight what it takes to achieve such rapid turn-around on microbial molecules, host status, antibiotic resistance and/or drug metabolism, but also demonstrate points for optimization. (2) Introduction of a mass spectrometer into a clinical lab unfamiliar with the platform can be challenging. Here we discuss implementation of the Bruker MicroFlex MALDI-TOF into a protein immunology lab where the results obtained by mass spectrometry are compared to gel electrophoresis for specific clinical tests. The talk will present results observed using the MicroFlex in combination with automated liquid sample handling and matrix spotting for samples taken from a serum tube.

Thermo Scientific - Room 2 (Catalina)  
Can you reduce drug testing reimbursement challenges? A case study using HRMS for simultaneous analyte screening and quantitation.  
Ana Grenier, Ph.D.  
‣ Continuing to manage healthcare cost constraints and monitoring therapy adherence and abstinence from non-prescribed drugs are important aspects to consider when physicians prescribe drugs with the potential of misuse, abuse, and addiction. Typically, drug monitoring is performed by screening urine using an immunoassay technique, and confirmed by mass spectrometry methodologies (GC/MS or LC MS/MS). Innovations in mass spectrometry technologies, such as resolution power, have made possible to improve the accuracy of testing in the clinical research market. Here, we present the clinical research evaluation for the simultaneous screening for analytes of interest and to quantify 47 drugs in urine by Liquid Chromatography-High Resolution Mass Spectrometry utilizing the Q Exactive™ instrument.

Waters - Room 3 (Madera)  
Low-flow Immunoaffinity Mass Spectrometry for the Masses and Implications for Biomedical Research  
Michael Lassman, Principle Scientist, Merck  
‣ Only 4-5 years ago, neither low-flow mass spectrometry, nor immunoaffinity mass spectrometry (IA-LC/MS) could be considered routine platforms. These techniques, championed by specialized laboratories were only applied within a small number of academic research groups. High sensitivity platforms such as nanoflow mass spectrometry which measured proteins and peptides in in vitro cell lines, could not be easily incorporated into translational or clinical research. Leap forward half a decade, and IA-LC/MS is not simple, but is applied in many academic, research, government and hospital laboratories, allowing specific and robust quantitation of proteins and peptides in complex matrices that could only be measured previously using immunoassays. The value of IA-LC/MS in biomedical research will be explored as will implications on how IA-LC/MS may enable improved clinical research and patient care.

Indigo BioAutomation - Room 4 (Pasadena)  
The Batch and Beyond - LCMS Result Automation Strategies and Analytics  
Jim Edwards  
‣ The utilization of self-aware peak processing algorithms, a comprehensive quality architecture, and a streamlined, exception-based data/result review process have proven to be a successful strategy for improving both quality and throughput of LCMS analysis. The positive impacts of these batch-oriented optimizations can be significantly magnified by an additional layer of analytics and visualization which provide comprehensive information across instruments, assays, and batches over time. Please join us for a discussion on how these analytics are used to diagnose and prevent issues, target quality improvement efforts where they will be most effective, improve the quality and speed of automated result release, and align both the business and science aspects of the laboratory for an elevation in the efficiency and effectiveness of both.
**The Evolution of SelexION® ION Mobility Technology: Past, Present and Future**

*Michael Jarvis*

> Since its introduction in 2011, a growing list of LC-MS/MS applications in Clinical Research, Lipidomics, and Forensics have benefited from the use of SelexION(R) ion mobility technology. In this workshop we will present an overview of the technology, a history of the evolution of the product, and key examples of applications that have benefited from the use of this unique technology. We will also offer an exciting glimpse into the future, with a sneak peek at enhanced capabilities currently under development. Please join us for this exciting presentation!

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**Corporate Workshops - Wednesday PM**

1:00 - 1:30 PM

**Thomson Instrument Co - Room 1 (Mojave)**

**Detection of THC in oral fluid: the bane of a toxicologist’s existence.**

_Jill Yeakel, Lehigh Valley Toxicology_

> This presentation will review the comparison of two sample preparation techniques used for the analysis of THC in oral fluid samples. Due to the chemical composition of THC, many scientists struggle to achieve both clean extractions and sensitive detection. The difference between solid phase extraction and filter vial preparations will be discussed to determine the optimal procedure prior to injection on a liquid chromatograph tandem mass spectrometer (LC-MS/MS). The instrumental parameters for analysis on the LC-MS/MS will also be provided to illustrate the most advantageous process for sensitively detecting THC along with a multitude of other drugs in a single method.

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**Thermo Scientific - Room 2 (Catalina)**

**Paperspray MS in clinical research: early experiences in a U.K. clinical laboratory**

_Lewis Couchman, Viapath Analytics, Kings College Hospital, London, UK._

> Paperspray MS offers a unique opportunity for clinical laboratories in which dried samples collected onto filter papers are analysed directly, and rapidly, without any prior sample extraction or preparation. In this workshop, our early experiences using Paperspray MS in conjunction with high-resolution, accurate mass detection (Q Exactive MS) will be discussed. Considerations for the development of targeted quantitative applications from dried blood samples will be covered, including possible approaches to calibrate and add internal standards to account for paperspray and 'extraction' variability. Secondly, the use of Paperspray MS as an analytical screening tool for drugs of abuse in dried urine samples will be discussed. Approaches for MS data acquisition to maximize the possibility of compound identification will be covered.

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**Phenomenex - Room 3 (Madera)**

**Demystifying a Couple of Challenging Assays**

_Seyed Sadjadi_

> In this workshop we discuss the use of stationary and mobile phase modifications to overcome chromatographic challenges in two quantitative assays: EtS/EtG and Chiral Amphetamines. First, we discuss the use of new LC stationary phases and mobile phases to solve the issues of polarity, isobaric urine interference, and retention in Ethyl Glucuronide (EtG) and Ethyl Sulfate (EtS). Next we will discuss the role of mobile phase pH in the chiral separation of methamphetamine and related compounds. The result of this investigation will be better understanding of how minor adjustments can make major improvements in assay performance.

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**Shimadzu - Room 4 (Pasadena)**

**Integration & Implementation of Fully Automated Sample Preparation for Mass Spectrometry**

_Isabel Cabrera (CEO, Shimadzu Italy) and Manoj Tyagi, PhD. FACB, NRCC -CC (Medical Lab Director, Captiva LLC)_

> The direct detection of disease related biological compounds and drugs in blood, urine, or other biological samples are possible thanks to mass spectrometry. The bottleneck, however, remains sample preparation, which is often tedious, increases contamination and introduces errors. This interactive workshop will take a closer look at the implementation of full sample preparation automation for triple quadrupole mass spectrometry. The Shimadzu CLAM-2000 is the first system in the world able to perform all steps fully automated from pretreatment of the sample to LCMS analysis We will demonstrate successful integration of sample prep automation for several assays, and Dr. Manoj Tyagi (Captiva Labs) will join us to present a fully automated approach to quantitative clinical toxicology and drug analysis from oral fluid matrix.
**Microflow LC: Improving sensitivity for the quantitation of biopharmaceuticals with LC-MS**  
*Remco Van Soest*

- The utilization of Microflow LC is increasing in LC-MS due to the potential to increase sensitivity in comparison to traditional flow LC-MS. This workshop will focus on the successful application of MicroLC in the quantitation of peptide and protein drugs in plasma.

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**Corporate Workshops - Thursday AM**  
8:00 - 8:45 AM

**Hamilton Robotics - Room 1 (Mojave)**

*Automated Dispersive Pipette Extraction Tips for Rapid Analysis of Serum and Urine Specimens using a Hamilton Microlab NIMBUS and Microlab STARlet Workstations*  
*Daniel B. Kassel, PhD., Founder & CEO, SciAnalytical Strategies, Inc., La Jolla, CA and Dylan Bach, PhD, MD, CEO, Bach Diagnostics*

- Novel methods for the automated extraction and isolation of steroids in serum and drugs of abuse in urine are reviewed. Analyses of steroids includes a patent pending protein crash method based on dispersive pipette extraction that streamlines the entire process from serum extraction to LC-MS/MS analysis without the need for centrifugation and vortex mixing. Up to 96 serum samples are processed simultaneously in ~10 minutes on an automated liquid handler, providing clean extracts, immediately ready for LC-MS/MS analysis. For urine, extraction is complete in ~5 minutes after hydrolysis. Extracts are clean in a low eluate volume and do not require solvent evaporation and reconstitution. The automated DPX method allows for seamless throughput without downtime for LC column maintenance, which is commonly found with dilute and shoot methods.

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**Thermo Scientific - Room 2 (Catalina)**

*Speeding up the cancer biomarker discovery: Advanced Clinical Proteomics workflow with High Resolution MS*  
*Sebastien Gallien, Ph.D.*

- Adoption of cancer biomarkers in clinical labs has been plagued by the speed with which these biomarkers are discovered and validated for clinical use. Clinical proteomics approaches where the use of predefined set of surrogate peptides for proteins has been helpful in systematically identifying these markers. Targeted analyses using parallel reaction monitoring (PRM), performed on high resolution and accurate-mass (HRAM) quadrupole-orbitrap mass spectrometers, present the selectivity and sensitivity to confidently quantify peptides in complex samples. The internal standards (IS) used for isotope dilution quantification were recently leveraged to actually drive the acquisition ("internal standard triggered-parallel reaction monitoring", IS-PRM), thus improving the acquisition efficiency. Learn how to uncover biomarkers faster.

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**Restek - Room 3 (Madera)**

**Ultra-rapid LC-MS/MS analysis**  
*Lewis Couchman, Toxicology Unit, Department of Clinical Biochemistry, Viapath Analytics, King’s College Hospital, London, UK.*

- Typically, targeted quantitative LC-MS/MS analyses using gradient elution are carried out at the rate of a few minutes per injection. In this workshop, an approach to ultra-rapid LC-MS/MS analysis using Raptor biphenyl columns will be demonstrated in which complete injection-to-injection cycle-times are approximately 30 seconds without the requirement for LC multi-plexing. Despite such short analysis times, chromatographic efficiency is typically maintained (e.g. for drugs and metabolites), and the approach has been shown to be applicable to a range of compounds. Retention time reproducibility of more than 1,500 injections on a single short column has been shown to be excellent. Practical considerations and requirements for this approach will be demonstrated using a range of analytes for which therapeutic drug monitoring is advocated.
Shimadzu - Room 4 (Pasadena)

**Advances in Human Microbiome Science: Metabolic Disease**

Stanley L Hazen, MD, PhD (Chair of the Department of Cellular & Molecular Medicine at the Cleveland Clinic’s Lerner Research Institute, Section Head of Preventive Cardiology & Rehabilitation at the Cleveland Clinic, Jan Bleeksma Chair in Vascular Cell Biology and Atherosclerosis, and the Leonard Krieger Chair in Preventive Cardiology)

Dr. Hazen’s laboratory focuses on understanding mechanisms through which inflammation contributes to diseases such as atherosclerosis. His work has led to numerous discoveries in multiple areas of cardiovascular disease research. His discovery of a mechanistic link between gut microbes and cardiovascular disease was awarded as an Inaugural recipient of a “Top 10 Clinical Discovery of the Year (2011)” award by the Clinical Research Forum (April, 2012), which is comprised of leadership at NHLBI, academia and industry. His further studies on the gut microbe – cardiovascular disease connection were recognized by the American Heart Association and the American Stroke Association in 2014 as a “2013 top 10 advances in heart disease and stroke science”. Dr. Hazen will present on mass spectrometry based applications to human microbiome analysis.

MilliporeSigma - Room 5 (Sierra)

**Facilitating LC/MS Method Development: Impact of Stationary Phase Chemistry**

David S. Bell, PhD

Problems encountered executing LC/MS methods are often a result of the choice of column chemistry employed. Many analysts will reach for their C18 upon commencement of method development; however C18s are often not the best tool for a given separation. There are many choices of alternative stationary phase chemistries that render the phase decision difficult. In this work stationary phase classes and chromatographic modes which are highly complementary to alkyl phases are discussed. An understanding of the contrasting interactions that these classes of stationary phase chemistries provides guidance regarding the choice of phase that may be most appropriate for a given task. This critical information promises to facilitate LC/MS method development and generate simpler, more reliable separations.

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Corporate Workshops - Thursday PM

1:30 - 2:00 PM

Neoteryx - Room 1 (Mojave)

**Microsampling Workshop | A Look at the Implementation of Dried Blood Microsampling from Convenient Patient Collection to Reliable, Automated Specimen Processing**

Thierry Dervieux, PharmD., PhD., DABCC, CSO & Medical Director, Exagen Diagnostics & Julia Colletti, Scientist, Mass Spectrometry R&D, Quest Diagnostics

Examine how two clinical diagnostic organizations have implemented volumetric absorptive microsampling (VAMS™) to capitalize on patient benefits of improved comfort from a fingerstick and increased convenience of at-home collection. Furthermore, the presenters will share how they generate results similar to those from venous blood, resolve the volumetric hematocrit assay bias, and fully automate the assay on a Hamilton® STAR™ workstation.

1. Therapeutic Drug Monitoring of Disease Modifiers in Rheumatic Diseases: Implementation Using VAMS Collection Method | **Exagen Diagnostics**
2. Automated Method for the Sample Preparation and LC-MS/MS Analysis of Steroids in Dried Blood using Mitra Microsampling Devices | **Quest Diagnostics**

Agilent Technologies - Room 2 (Catalina)

**A robust triple-quadrupole ion-paired reverse-phase metabolomics workflow for turn-key analysis of central metabolic pathways.**

Adam Rosebrock

Mass-spectrometry analysis of endogenous metabolites, metabolomics, has emerged as a powerful tool to directly examine biochemical state. Advances in LC separation and mass spectrometry instrumentation permit efficient and sensitive separation and detection, enabling the parallel analysis of hundreds of compounds in a single run. Despite the promise of metabolomic analysis, the wide chemical diversity of analytes presents many challenges for method development and a resulting hurdle for setting up metabolic assays. For Research Use Only. Not for use in diagnostic procedures.
Matrix Effects and Matrix Affects: The Impact of Different Sample Matrices on Sample Preparation and Chromatographic Analysis

Jonathan Danaceau, Ph.D, Principal Applications Chemist, Waters Corporation

- This workshop will discuss many challenges that analysts face when working with a variety of complex sample matrices. The analysis of 3 compounds will be described with an emphasis on how the sample pre-treatment, SPE protocols and chromatographic methods must change depending on the sample matrix. Four different sample matrices will be used including urine, whole blood, plasma and oral fluids. Suggestions will also be provided for method developers concerned with these types of matrices.

Biognosys - Room 4 (Pasadena)

Best of both worlds: combining quantitative targeted proteomics with high-content discovery proteomics

Fadi Abdi, Florian Marty

- Biognosys is the leading next generation proteomics company. Using our proprietary HRM-MS approach we have recently identified over 9,000 proteins in a single shot DIA measurement of mouse cerebellum tissue. Here, we present a workflow that combines the quantitative power of stable isotope-labelled reference peptides with the discovery potential of HRM-MS. Using the reference peptides from our PlasmaDive and PlasmaDeepDive panels we have obtained absolute quantitative information of 173 proteins in un-depleted plasma. Additionally, over 400 plasma proteins were identified in a single shot experiment and can be quantified over a large cohort with high reproducibility. Further, the quantification values obtained for the SIS peptides can be used to extrapolate the absolute quantitative values of all proteins identified.

MilliporeSigma - Room 5 (Sierra)

Quantitation of Proteins and Antibodies In Serum by LC-MS/MS Using Full-Length Stable Isotope Labeled Internal Standards and Certified Reference Materials

Kevin Ray and Uma Sreenivasan

- LC-MS/MS is becoming a powerful tool for the quantitation of proteins in plasma. Such methods typically utilize stable isotope labeled (SIL) peptide internal standards. For more accurate quantitation, a full-length SIL protein can be added to the sample at the initial stage of the assay workflow. To enable this approach, we have developed SIL monoclonal antibodies, including SIL-Infliximab, as well as SIL versions of clinically-relevant human proteins, such as Thyroglobulin. We will demonstrate that the use of a SIL proteins and SILuMAB internal standards allows for more accurate and rapid quantitation of therapeutic antibodies and human protein biomarkers in plasma by LC-MS/MS. We will also discuss development and certification of proteins as Certified Reference Materials for accurate quantitation in clinical applications.
Podium Presentations

Tuesday, Wednesday & Thursday

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The Olympic Drug Testing System

Don Catlin - Anti-Doping Research Institute (dcatlin@ucla.edu)

In the sixties a group of members of the International Olympic Committee (IOC) noted that drugs were being used to enhance the performance of Olympic athletes. They successfully persuaded the IOC to appoint a Medical Commission (MC). The IOC-MC proposed the anti-doping rules, developed and maintained the prohibited list of drugs, selected and inspected the testing laboratory in the host city and certified every positive case. The most intense and serious testing took place at the German Olympics in 1992 where gas chromatographs (GCs) were used to detect Stimulants. Anabolic steroids were first tested for by immunoassay at the Montreal summer games in 1976. Subsequent to the Games, these cases were confirmed by GC/MS in the first instance of GC/MS at the Olympic Games. The U.S. did not attend the 1980 Olympic Games where the detection of testosterone use was suspected based on the T/Epitestosterone (T/E ratio). In 1984 the IOC asked us to perform an analysis by GC/MC and perform a carbon isotope ratio test if the T component of T/E was elevated. Erythropoietin and Growth Hormone continue to be difficult to test for.
Tuesday @ 2:00 PM in Room 2 (Catalina)

New Frontiers for Hormone Testing by Mass Spectrometry

**Stefan Grebe - Mayo Clinic** (grebe.stefan@mayo.edu)

* During the last two decades, mass spectrometry (MS) has revolutionized clinical testing of low molecular weight hormones. Due to superior specificity and lesser susceptibility to interferences, MS is now regarded the best testing method for steroids, biogenic amines, and most vitamins. The last decade has seen an extension of MS to the clinical measurement of peptide and protein hormones, while most recently, clinical laboratories have started to experiment with metabolomics MS applications. High resolution, accurate mass MS and antibody-mediated enrichment of the targeted analytes have been key facilitators of these more recent expansions of clinical MS.
Tuesday @ 2:00 PM in Room 3 (Madera)

**Translational Mass Spectrometry**

*Amanda Paulovich - Fred Hutchinson Cancer Research Center* (apaulovi@fhcrc.org)

Proteins carry out the biological functions of our cells and form the basis of diagnostic tests and treatments, yet over 95% of human proteins can’t be studied because we lack reliable laboratory assays for quantifying their abundances. This lack of standardized assays for quantifying the majority of human proteins has left the proteome clinically inaccessible, contributed to poor inter-laboratory reproducibility of preclinical research, and is the biggest impediment to translating novel protein diagnostics into clinical use. Selected/multiple reaction monitoring mass spectrometry (S/MRM), especially coupled to the enrichment of target analytes, promises to relieve this limitation by offering a robust platform that enables efficient generation of highly sensitive, multiplex-able assays that are standardized to support high reproducibility across laboratories and platforms.
**Advancing Whole-Plant Cannabis Clinical Interests**

*Jeffrey Raber* - *The Werc Shop* (jeff@thewercshop.com)

Cannabis sativa L. is an exceptionally diverse plant rapidly rising in acceptance as a physiologically useful tool for alleviating numerous chronic ailments. The use of whole-plant cannabis products often offers greater therapeutic effectiveness than single molecule cannabinoid approaches. This presents unique challenges in determining product chemical compositions required for entering the clinic. Furthermore, metabolic profiling of these compositions can be exceptionally complex and require the development of advanced analytical methodologies to provide useful clinical insight. As new laws and regulations around cannabis continue to develop we will undoubtedly see many diverse whole-plant products begin to enter the clinic.
Tuesday @ 2:00 PM in Room 5 (Sierra)

**Mass Spectrometry for Image Guided Neurosurgery and Drug Development**

*Nathalie Agar - Harvard Medical School* (Nathalie_Agar@dfci.harvard.edu)

- Mass spectrometry provides multiple options for the direct characterization of tissue to support surgical decision-making, and provides significant insight in the development of drugs targeting tumors of the central nervous system (CNS). Using an array of mass spectrometry (MS) applications, we rapidly analyze specific tumor markers such as metabolites, fatty acids, lipids, and proteins from surgical tissue for surgical guidance and rapid diagnosis. Using similar clinical protocols, we visualize drug and metabolites penetration in brain tumor tissue and correlate with tumor heterogeneity and response to support drug development.
A Multi-Omic Analysis of Pre-Eclampsia and Related Conditions using Ion Mobility-Mass Spectrometry

Christopher Chouinard - Pacific Northwest National Laboratory (christopher.chouinard@pnnl.gov) -- Young Investigator Grantee*

- Pre-eclampsia, gestational diabetes mellitus (GDM), and other complications arising during pregnancy lead to increased morbidity and mortality in both pregnant women and their fetuses, potentially causing long-term effects. Such conditions have been studied extensively and, although some treatments have been determined, the precise cause of these conditions remains uncertain. However, there appears to be a link with pre-existing conditions such as obesity. In this study, ion mobility-mass spectrometry (IMS-MS) was used to investigate plasma metabolomic, lipidomic, and proteomic changes in pregnant women that developed GDM or preeclampsia compared with control pregnancies. Ion mobility allowed an additional mode of identification and separation for potential biomarkers in these samples.

Targeted Full-Scan LC-MS Metabolomic Workflow Enables Robust Quantitation of Known Compounds and Prospective Compound Discovery Across Large Sample Sets

Adam Rosebrock - Department of Pathology, Stony Brook School of Medicine (adam.rosebrock@stonybrookmedicine.edu) -- Young Investigator Grantee*

- Full-scan LC-MS analysis is gaining widespread use in metabolomic applications, but is often viewed as secondary platform for routine quantitation in favour of inherently targeted triple-quadrupole approaches. We have developed a workflow using a biologically-derived, isotopically labeled reference and an integrated software platform for robust quantitation on time-of-flight instruments. In addition to quantitation of known compounds, our approach enables simultaneous data mining for discovery and analysis of new mass spectral features. We have applied our tools to analysis of central carbon metabolites and other organic acids from patient derived cell lines and biofluids in the context of large, multi-site glioblastoma multiforme project. In addition to greatly improved quantitation and reproducibility, our approach has enabled identification of previously unknown metabolites.

Development of a High-Throughput Information Rich LC-MS Platform for Large Cohort Epidemiology & Biomedical Research Studies

Robert Plumb - Imperial College London (r.plumb@imperial.ac.uk)

- The detection, identification and validation of biomarkers for biomedical research and discovery requires a robust, reliable and information rich analytical platform. Metabolic Phenotyping of large cohort epidemiological and pre-clinical studies provides a metabolic insight into disease mechanism, treatment efficacy and toxicity. Analysis of these large cohort batches by UHPLC-MS is time consuming and often results in batch to batch variations due to subtle analytical batch variation. A high-throughput microbore UPLC-MS method has been developed providing an analytical platform for the metabolic phenotyping of biofluids from large sample cohorts. This approach has demonstrated high throughput reproducibility and the ability to identify biomarkers of toxicity.
Diagnosis of Adrenocortical Carcinoma by LC-HRAM Urine Steroid Profiling
Ann Rivard - The Mayo Clinic (rivard.ann@mayo.edu)

Incidental adrenal tumors are found in approximately 5% of the 80 million CT scans performed in the U.S each year. While most masses are benign adrenal adenomas, those with indeterminate imaging characteristics will require additional diagnostic workup to exclude adrenocortical carcinoma. To address these issues we developed a liquid chromatography-high resolution accurate mass spectrometry 24-hour urine panel of 26 steroid metabolites to distinguish ACC from benign ACAs. This non-invasive method allows for an accurate, rapid, and cost-effective means of diagnosis. Here we present the analytical validation. This method decreases the need for more aggressive diagnostic procedures which most often includes surgery as well as biopsies, provocative hormone driven testing, and repeated imaging. This method brings significant improvement to both physician diagnosis and patient safety.

Some Like it Hot: Moving from Cold to Harmony in the Plasma Renin Activity Assay
William Slade - LabCorp (sladew@labcorp.com)

Plasma renin activity (PRA) has been traditionally measured using immunoassays for angiotensin I (AngI) with little attention paid to inter-method harmonization. These methods require generation steps of 3-18 h and include a portion of the specimen evaluated as a “cold sample” to account for AngI generation prior to analysis. Both of these requirements decrease throughput. We present manual and automated methods using a single internal standard to quantify PRA by LC-MS/MS. Our method development employed a double internal standard approach to evaluate the effect of generation conditions and pre-analytical processing on AngI recovery. Automation will be discussed. Finally, we demonstrate harmony with the LC-MS/MS method of St. Paul’s Hospital, Vancouver, despite numerous methodological differences.

The Role of LC-MS/MS in the Diagnosis of Munchausen Syndrome Presenting as Factitious Hypercortisolism
Joshua Buse - University of Calgary (joshua.buse@cls.ab.ca) -- *Young Investigator Grantee*

Immunoassays (IAs) are invaluable for routine use, but suffer from lower specificity compared to LC/MS-MS. Here we present a case report of a 30 year old woman with no clinical evidence of Cushing Syndrome who had consistent and marked elevation of salivary cortisol by IA, but indeterminate tests for elevation of plasma cortisol. Intensive investigation by LC-MS/MS determined that cortisone was present at supraphysiological concentration and prednisone was present in very high concentrations in the patient’s salivary sample, explaining the high IA results. The limitations of test methods to report false positive results due to interferences can result in erroneous diagnoses or exploited by patients with Munchausen syndrome.
Putting the Top Down and Taking Proteomics for a Spin
Tuesday @ 3:00 PM in Room 3 (Madera)
Session Chair: Cory Bystrom - Cleveland Heart Lab

Tuesday @ 3:00 PM in Room 3 (Madera)
Analysis of Monoclonal Antibodies in Human Serum for Monoclonal Gammopathy Diagnosis by use of 21 Tesla FT-ICR Top-Down and Middle-Down MS/MS
Lidong He - Florida State University (lhe@magnet.fsu.edu) -- *Young Investigator Grantee*

- Monoclonal gammopathy is a B cell proliferative disorder characterized by a plasma cell clonal expansion. If there is clinical suspicion of a monoclonal gammopathy, serum and urine are tested for the presence of elevated levels of a monoclonal immunoglobulin secreted by clonal plasma cells. Here, we describe top-down and middle-down analysis of immunoglobulins in serum with the advantages of fast sample preparation, ultrahigh mass accuracy, and extensive residue cleavages by use of 21 tesla FT-ICR MS/MS. To our knowledge, this is the first time that extensive top-down cleavages for both variable and constant regions have been achieved for mAbs in a human serum background.

Tuesday @ 3:20 PM in Room 3 (Madera)
Detection of an Unreported Hemoglobin Variant by LC-MS/MS Intact Protein Characterization
Donald Hunt - University of Virginia (dfh@virginia.edu)

- Hemoglobin Charlottesville, a previously unreported hemoglobin variant, contains a S138X (X= I or L) substitution on the alpha subunit. The presence of the variant hemoglobin was detected during manual review of cation exchange HPLC and capillary electrophoresis data. The identity of the variant was assigned through LC-MS/MS analysis of the intact globin subunits, using novel techniques for intact protein interrogation: sequential ion/ion reactions and multiple fills of the ion/ion reaction products into the C-trap prior to Orbitrap analysis. The resulting sequence coverage of the alpha variant (141 residues, 15.1 kDa) was 80%. Coupled with HCD MS3 analysis of the C-terminal residues, 86.5% sequence coverage of the alpha variant was achieved.

Tuesday @ 3:40 PM in Room 3 (Madera)
Translational Top-Down Proteomics as a Path Forward to Improved Diagnostics in Liver Transplant Rejection
Timothy Toby - Northwestern University (TimothyToby2018@u.northwestern.edu) -- *Young Investigator Grantee*

- Opportunities for top-down proteomics in translational research are beginning to expand as clinicians discern the value of proteoform-resolved measurements. We have developed a comprehensive pipeline applying top-down proteomics to multiple phases of the biomarker discovery workflow for proteoforms, including global discovery modes and high-throughput validation modes. Here, we present an example application of this pipeline in peripheral blood to elucidate proteoform biomarkers of clinical rejection in liver transplantation, a patient phenotype that lacks non-invasive diagnostic measures. Label-free quantitation yielded an initial discovery panel of putative markers of rejection in a cohort of 30 patients. Additionally, a novel method for targeted quantitation, proteoform reaction monitoring, is presented for an early model biomarker.
Tuesday @ 3:00 PM in Room 4 (Pasadena)

Anodyne by Design; Esoteric Designer Opiates in Pain Management

**Gregory Janis - MedTox / Labcorp** (janisg@labcorp.com)

- Abuse of a multifarious collection of designer opiates has recently emerged. Novel fentanyl analogs, and a variety of esoteric, structurally unique opiate agonists such as U-47700 and IC-26 have been identified as street drugs. It is postulated that opiate seeking individuals within pain management settings may be among the earliest experimenters of this emerging drug class. We devised and validated independent LC-MS/MS screening and confirmation methods targeting 20 designer opiates and their respective metabolites. The methodologies were then employed to survey identified heroin users within pain management programs. A variety of fentanyl analogs were prevalent within this population.

Tuesday @ 3:20 PM in Room 4 (Pasadena)

Comparison of Untargeted Methods using GC-MS and LC-TOF-MS/MS for Analysis of K2/Spice Synthetic Cannabinoids in Herbal Products

**Shijun Lu - Wadsworth Center, NYS DOH** (shijun.lu@health.ny.gov)

- The abuse of synthetic cannabinoids (SCs) or K2/spice in herbal products has become a significant public health issue. The detection and identification of the new SCs in the routine drug testing lab are difficult since they are constantly modified. It is necessary to develop an untargeted method which is capable of detecting all possible drugs of abuse. Herein, we propose a GC-MS approach for SCs screening. Based on the 43 K2/Spice herbal products results, 13 of SCs were identified and then semi-quantified. The results of GC-MS screening approach were confirmed by and in good agreement with those of LC-HRMS analysis.

Tuesday @ 3:40 PM in Room 4 (Pasadena)

Quantification of Soapberry Toxins and their Urinary Metabolites by HPLC-MS/MS

**Samantha Isenberg - Centers for Disease Control and Prevention** (sisenberg@cdc.gov)

- Hypoglycin A (HGA) and methylenecyclopropylglycine (MCPG) are naturally-occurring amino acids found in soapberry (Sapindaceae) fruits. HGA is found in ackee fruit and is known to cause Jamaican Vomiting Sickness, or ackee poisoning. MCPG is a structural analogue of HGA and was recently implicated as the causative agent of seasonal hypoglycemic encephalopathy outbreaks in India. To verify the role of soapberry fruits in these outbreaks, we developed an agricultural method to quantify HGA and MCPG in fruit arils as well as a clinical method to quantify the urinary metabolites of both toxins.
Tuesday @ 3:00 PM in Room 5 (Sierra)

Comparison of Radiative and Conductive Rapid Evaporation Ionisation Mass Spectrometry on Healthy and Cancerous Breast Tissue for Real-Time Tissue Identification

Zsolt Bodai - Imperial College London (z.bodai@imperial.ac.uk) -- *Young Investigator Grantee*

- Intraoperative tissue identification has been a long-standing problem in cancer surgery. Both surgical diathermy and LASER dissection coupled with REIMS can provide tissue specific signal from cancerous and healthy breast tissue with excellent tissue classification and identification rate. Spectrum acquired from the surgical plume from both techniques were similar and the found the same significant biomarkers. This potentially means that the previously built REIMS databases constructed from the diathermy technique can be used for LASER dissections. Laser REIMS using a breast cancer diathermy model was tested on normal and cancerous patient samples and provided 100% correct tissue identification.

Tuesday @ 3:20 PM in Room 5 (Sierra)

Solid Phase Microextraction – High Resolution Mass Spectrometry: Integrated Platform for Multilevel Clinical Analysis

Barbara Bojko - Nicolaus Copernicus University (bbojko@cm.umk.pl)

- Analysis of clinical samples, particularly tissues, is troublesome and time consuming procedure. In the past few years progress in mass spectrometry enforced development of fast and simple methods of sample collection and introduction to MS platforms. Using brain tumor and liver and kidney graft studies as the examples of clinical applications, the presentation will demonstrate how in vivo and in situ solid phase microextraction (SPME) addresses requirements for tissue sample preparation prior targeted and untargeted LC-MS and MS analysis emphasizing features of the technology, which complement more conventional protocols. This will include phenomenon of chemical biopsy and tissue sample collection-free extraction, low invasiveness and balanced analyte coverage. It will be also discussed what areas of medicine could benefit from the proposed solution.

Tuesday @ 3:40 PM in Room 5 (Sierra)

Touch Spray-Mass Spectrometry with Medical Swabs for in Vivo Analysis of Surgical Margins during Brain Tumor Resection

Valentina Pirro - Purdue University (vpirro@purdue.edu) -- *Young Investigator Grantee*

- Surgical intervention is primary treatment option for brain tumors. The best patient outcomes are dependent on absolute tumor resection, ideally minimizing damage to adjacent normal tissue, and reducing surgery time. Touch-spray mass spectrometry (MS) with medical swabs allows for in vivo - minimally invasive - sampling of brain tissue at the surgical margins. Small quantity of tissue is transferred to the swab tip by touch. Glycerophospholipids and metabolites indicative of cancer are detected by generating an electrospray directly from the swab tip. Here we show proof-of-concept results demonstrating the ability to detect molecular-based diagnostic information in a few seconds.
Tuesday @ 3:00 PM in Room 6 (SmokeTree)
The Basics of Clinical Mass Spectrometry: Why Many Call it the “Gold Standard”
Alec Saitman - Providence Regional Laboratories (alec.saitman@providence.org)
 › This session talk is designed for the absolute beginner with little to no previous experience with clinical mass spectrometry. Mass spectrometry is a broad scientific area and this section will focus on one of the most relevant clinical applications, the use of liquid chromatography tandem mass spectrometry in the clinical laboratory.

Tuesday @ 3:20 PM in Room 6 (SmokeTree)
Clinical Mass Spectrometry: A Gold Standard in Routine Applications
Alicia Hutcherson Wright - Providence Health & Services (Alicia.Wright@providence.org)
 › Over the past few years, clinical laboratories have been increasingly adopting liquid chromatography with tandem mass spectral detection (LC-MS/MS) for a myriad of applications. With the increase in routine utilization, there may still stand the question of what exactly makes this technology appealing for clinical use? This presentation will describe several benefits to implementing this valuable ‘gold standard’ technique in routine applications.

Tuesday @ 3:40 PM in Room 6 (SmokeTree)
Where the Rubber Meets the Road: Clinical Mass Spectrometry Case Studies
Matthew Feldhammer - Emory University (mfelh2@emory.edu) -- *Young Investigator Grantee*
 › This talk in the fundamentals of Mass spectrometry beginners track will explore how mass spectrometry is utilized in the clinical laboratory to provide actionable clinical information to healthcare providers. This session will highlight the power of mass spectrometry to resolve discrepancies and false results that can occur in traditional immunometric based platforms and provide a barrier to patient health. By exploring several real world case studies we will demonstrate how mass spectrometry is quickly becoming the gold standard platform for the modern clinical laboratory alleviating many of the inconsistencies that have plagued the laboratory medicine community in the past.
Rapid Evaporative Ionisation Mass Spectrometry (REIMS): A Platform for Microbial Identification, Functional Classification, and Direct from Sample Analysis

Simon Cameron - Imperial College London (s.cameron@imperial.ac.uk) -- *Young Investigator Grantee*

- Mass spectrometry (MS) has revolutionised the workflow of microbiology laboratories; leading to a substantial reduction in diagnosis times. Unlike commercially available MS platforms, rapid evaporative ionisation MS (REIMS) requires no sample preparation, such as the addition of a matrix, before sample analysis. We have developed an automated, high-throughput REIMS platform which is capable of analysing up to 5,000 microbial colonies in 24 hours. This platform classifies isolates with an accuracy of >99% for Gram, >95% for genus, and >93% for species. This presentation will cover the ongoing technical optimisation of the platform, including the addition of laser REIMS and optimised monopolar diathermy electrodes, the development of a reference spectral database to allow identification of unknown isolates, and phenotypic classifications including antimicrobial resistance profiles.

Diagnostic Identification of Clinical Yeasts and Molds by Metal Oxide Laser Ionization Mass Spectrometric Fatty Acid Profiling

Christopher Cox - Colorado School of Mines (crcox@mines.edu) -- *Young Investigator Grantee*

- Diagnostic MALDI is an important tool for clinical pathogen ID. While relatively effective for bacteria, MALDI protein profiling has had little impact on fungal diagnosis because it often cannot differentiate closely related isolates expressing similar or identical proteins. This results in mis-ID or failure to ID, necessitates additional lengthy biochemical tests, and delays treatment. New approaches are needed to improve accuracy and reduce turnaround. We investigated Metal Oxide Laser Ionization (MOLI) MS fatty acid analysis for ID of clinical yeasts and molds that are historically difficult or impossible to ID with commercial MALDI instruments. The energy inherent to the MALDI laser allowed for in situ metal oxide-catalyzed lipid fragmentation into taxonomically useful fatty acids. This resulted in near 100% accurate ID of Candida, Cryptococcus, Rhodotorula and Saccharomyces.

Identification of Mycobacterium to Species Level using MALDI-TOF MS and ASTA MycoDB

Hyung Soon Park - ASTA Inc. (hspark@astams.com)

- Over 170 species in the Mycobacterium genus confers the limitation of precise identification with a single test. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) based identification has been successfully implemented in clinical laboratories for bacteria identification and might change the standard identification methods of mycobacteria in clinical laboratories. Here we introduce a linear type MALDI-TOF mass spectrometer, Tinkerbell LT (ASTA, Korea), a mycobacteria MALDI-TOF mass spectrum database, MycoDB v.1.10 (ASTA, Korea) and its evaluation for identification of mycobacteria isolates. MycoDB v.1.10 contains more than 90 species-specific spectra covering most of mycobacterial species that frequently isolated in clinical laboratories in Korea.
Design of Experiments for Optimization of LC-MS/MS Clinical Diagnostic Assays
Margrét Thorsteinsdóttir - Pharmaceutical Sciences, University of Iceland (margreth@hi.is)
Method optimization of liquid chromatography-tandem mass spectrometry (LC-MS/MS) for quantification of biomarkers for support of clinical diagnosis and therapeutic drug monitoring can become much more efficient by utilizing design of experiments (DoE). This approach offers many advantages including performing experiments in accordance to predefined plan, modelling by empirical functions and graphical visualization. This paper will illustrate that using DoE for optimization of LC-MS/MS methods is much more efficient with only fraction of experiments that would be required by changing one-factor-at-time (COST) approach. Example will be given to illustrate how DoE works for optimization of LC-MS/MS clinical diagnostic assay.

Min Yu - University of Virginia (my7m@virginia.edu) -- *Young Investigator Grantee*
The volume of mass spectrometric testing in clinical laboratories has increased tremendously in recent years, leading to a need to enhance workflow. Automation of workflow has been achieved in sample preparation, data collection and processing, but turnaround time and productivity are hampered by time-consuming manual data review. Our aim is to develop a software tool that can automate the process of review of quality data. Using cannabinoids as an example, we demonstrate the use of software to speed and enhance review and show that the Support Vector Machines algorithm is superior to other classifiers in its ability of distinguish results that need further investigation from results that can be released without further review. Replacing the traditional manual review with this approach may increase throughput and increase efficiency while maintaining confidence in reported results.

Take Back Your Techs’ Time by Letting Your Data Flow
Shannon Haymond - Northwestern University (shaymond@luriechildrens.org)
Though automation of sample preparation and analyses are becoming more common in clinical mass spectrometry laboratories, much of the data review and transfer are still performed manually. This is time-consuming and error prone, easily exceeding the limits of human capacity for effective parallel processing. Other problems exist when sample data fields and results are manually transcribed, some repeatedly across multiple points in the testing process. Therefore, systematic, automated methods for reviewing and transferring data throughout the testing process have a tremendous effect on operational efficiency and quality. This presentation will describe our efforts to automate data flow in our LC-MS/MS lab from test order to result. Approaches for the various points of automation that we and others have used will be described with discussion of associated challenges.
Wednesday @ 1:45 PM in Room 3 (Madera)

**Using Mass Spectrometry to Monitor IgG Heavy Chains: A Continuation of MS-Based Immunoglobulin Analysis in the Clinical Laboratory**

*David Barnidge* - *Mayo Clinic College of Medicine* (barnidge.david@mayo.edu)

In this abstract we present the next-generation of MS based immunoglobulin monitoring focusing on the heavy chain of IgG; the most abundant immunoglobulin isotype making up approximately 75% of all immunoglobulins in circulation. Using the commercially available immunoglobulin-degrading enzyme from Streptococcus pyogenes (IdeS) we show that heavy chain variable and constant regions from IgG, including post-translational modifications such as glycosylation, can be easily monitored in a single assay using LC-MS. We also show that top-down MS can be used to determine the N-terminal amino acid sequence of IgG Fc fragments originating from endogenous enzymes, mutated heavy chains, along with the expression level of different IgG allotypes. We demonstrate the use of this approach in 20 normal donors and patients with an autoimmune disorder.

Wednesday @ 2:05 PM in Room 3 (Madera)

**Quantification of Disease Burden and Therapeutic Antibody Levels in Multiple Myeloma Patients**

*Melissa Hoffman* - *Moffitt Cancer Center/University of South Florida* (Melissa.Martinez@moffitt.org) -- *Young Investigator Grantee*

Multiple myeloma tumor burden is evaluated using the levels of the monoclonal immunoglobulin (M-protein) secreted by the cancer cells; numerous methods have been applied to this clinical biomarker measurement. Treatment strategies have improved both rates and depths of response, requiring improvement in the sensitivity disease detection. Furthermore, treatment with therapeutic antibodies can interfere with clinical assays, resulting in a false positive. Therefore, we use a proteogenomics approach with RNA-sequencing to determine the M-protein variable region sequences from the disease-specific monoclonal Ig followed by quantification using reaction monitoring mass spectrometry. MS quantification demonstrates improved sensitivity and specificity, eliminating biotherapeutic interference.

Wednesday @ 2:25 PM in Room 3 (Madera)

**Quantitation of Intact Light Chains by the Q-Exactive Produces a Sensitive and Rapid Assay for Therapeutic Monoclonal Antibodies**

*Kendall Cradic* - *Mayo Clinic* (cradic.kendall@mayo.edu) -- *Young Investigator Grantee*

Quantitation of therapeutic monoclonal antibodies is important for monitoring loss of response to therapy. Mass spectrometry assays have been developed for specific antibodies, mostly utilizing tryptic digest methodologies. We developed an assay for quantitation of vedolizumab intact light chains using the Q-Exactive Orbitrap mass spectrometer. The linear range (1-150 mcg/mL) is consistent with the therapeutic range and precision at 1 mcg/mL is less than 10%. Method comparisons with a tryptic digest method (Immunodiagnostik, Bensheim, Germany) showed a slope of 1.002 with an intercept of -0.70 (r=0.991; n=84). The assay provides a simple, rapid, and accurate means to monitor vedolizumab.
Wednesday @ 1:45 PM in Room 4 (Pasadena)

**Data Dependent or Data Independent Acquisition: Evaluation of SWATH for Drug Screening**

*Kara Lynch* - *University of California San Francisco* (kara.lynnch@ucsf.edu)

- High resolution mass spectrometry has become increasingly common for drug screening in clinical and forensic toxicology laboratories. Data-dependent strategies are commonly used for automated data acquisition (DDA). For this study two data-independent acquisition (DIA) methods using Sequential Windowed Acquisition of all Theoretical fragment-ion spectra (SWATH) were developed (fixed and variable window isolation) and compared to a DDA method using a QTOF mass spectrometer. Limits of detection, matrix effects, and the ability to identify 115 drugs/metabolites in 50 patient samples, using the three methods, were evaluated. SWATH was deemed comparable to DDA with increased detection for some low abundance compounds.

Wednesday @ 2:05 PM in Room 4 (Pasadena)

**‘Chromatogra-Free’: Ultra-Rapid LC-MS/MS Analysis Demonstrated using Clozapine and Norclozapine**

*Lewis Couchman* - *Viapath, King’s College Hospital* (lewis.couchman@nhs.net) -- *Young Investigator Grantee*

- Typically, targetted quantitative LC-MS/MS analyses using gradient elution are carried out at the rate of a few minutes per injection. In this paper, an approach for ultra-rapid LC-MS/MS analysis will be described in which the complete injection-to-injection cycle-time is just 36 seconds, or one 96-well plate per hour. This cycle time is more akin to that of direct injection methods such as flow-injection analysis, but includes efficient chromatographic separation of target analytes and matrix components. Practical considerations and requirements for this approach will be demonstrated using two target analytes, clozapine and norclozapine, following automated extraction from plasma samples.

Wednesday @ 2:25 PM in Room 4 (Pasadena)

**Use of Automation to Achieve High Performance Solid Phase Extraction**

*Mark Hayward* - *ITSP solutions* (Mark.Hayward@ITSPsolutions.com)

- Despite >40 yr of SPE using LC sorbents, LC principles have been ignored due to the lack of flow control in SPE devices. Variable flow results in variation in results. Internal standards are used to achieve meaningful results. Measuring absolute recovery against external standards to demonstrate absence of matrix effect (gold standard) isn’t done. With a new SPE device, this is changed. It uses a syringe to achieve both automation & accurate flow. With PAL autosamplers, SPE & LC/MS/MS is automated in a single parallel workflow. van Deemter curves are measured & SPE performed at flow achieving >99% absolute recovery. As a micro device, sample dry down isn’t needed for enrichment up to 200x. SPE is performed efficiently, economically, & with performance matching all LC knowledge of the last 50 yr. Examples of clinical measurement using reverse phase & ion exchange SPE are provided.
Eicosanoid Detection in Cancer using DESI-imaging

Renata Soares - Imperial College London (r.filipe-soares@imperial.ac.uk)

Desorption Electrospray Ionisation Mass Spectrometry Imaging (DESI-MSI) has been extensively used for the analysis of cancer samples. One major advantage of DESI-MSI is that spatial distribution of molecules can be obtained, which can allow for the further investigation of cancer environment. Eicosanoids are considered inflammatory molecules that play an important role in cancer. In this work, cancerous samples have been analysed by DESI-MSI and the spatial distribution of eicosanoid classes was assessed in different types of tissues. It was observed that different classes of eicosanoids are present depending on the tissue type. Hence, highlighting another usage of this ambient imaging technique.

Novel Mass Spectrometry Imaging (MSI) Biomarkers of Breast Tumor Aggressiveness

Kristine Glunde - The Johns Hopkins University School of Medicine (kglunde@mri.jhu.edu)

Breast cancer is a molecularly and spatially heterogeneous disease that continues to escape today’s treatment options. On the road towards personalized medicine, it is paramount to obtain detailed molecular tissue images of cancerous regions that seamlessly integrate with histopathology as well as the clinical workflow of histopathology. We have shown that mass spectrometry imaging (MSI) can be employed to obtain distinct biomolecular signatures, which include metabolites, lipids, and proteins, from aggressive hypoxic and metabolically de-regulated regions of preclinical breast tumor models. Our body of preclinical work has built a framework from which we will be able to translate our preclinical findings directly to large patient cohorts.

Molecular Markers of Serous Ovarian Cancer Aggressiveness and Surgical Outcome by Ambient Ionization Mass Spectrometry Imaging

Marta Sans - The University of Texas (msans@utexas.edu) -- *Young Investigator Grantee*

High-grade serous ovarian cancer (HGSOC) and borderline serous tumors (BOTs) present underlying differences regarding tumor invasion and prognosis. Surgical resection is a key component of HGSOC treatment but post-operative disease adversely impacts patient survival. Here, desorption electrospray ionization (DESI) mass spectrometry imaging (MSI) together with multivariate statistical analysis was used to diagnose HGSOC, and tumor overall with 96.4% and 96.2% agreements, respectively. Molecular markers of cancer aggressiveness were also identified and selected as significant contributors for HGSOC and BOT classification. Finally, metabolic profiles were used to predict HGSOC patients at high risk for residual disease after surgery.
Evaluation of Quantitative Proteomic Methods

Clark Henderson - University of Washington Medical Center (cmhene@uw.edu) -- *Young Investigator Grantee*

Along with peptide selection and proper development of calibration curves, other experiments should be performed to evaluate the analytical performance of a quantitative proteomic method. This session will discuss some of the fundamental experiments that should be used to evaluate an LC-MS/MS method for reliable and robust quantification of proteins.

Selection of Optimal Peptides for Targeted Proteomic Experiments

James Bollinger - Washington University School of Medicine (james.bollinger@wustl.edu)

This session discusses an empirical pipeline for the selection of peptides for a targeted proteomic experiment. Using plasma and cerebrospinal fluid as sample biological matrices, we will walk through a handful of examples and address the key considerations for assay design in bottom-up proteomics. By the conclusion of this session, participants should be able to: 1) Discuss the important physiochemical properties of a “proteotypic” peptide 2) Understand the difference between gene product and proteoform in the context of the limitations of bottom-up proteomics 3) Discuss the advantages and drawbacks of using recombinant or native protein standards 4) Select an appropriate protease to analyze their proteoform-of-interest 5) Discuss strategies for screening digested matrices for proteotypic peptides 6) Design simple experiments to optimize digestion conditions.

How NOT to Calibrate Your Protein Assay

Christopher Shuford - Laboratory Corporation of America (shuforc@labcorp.com)

When trying to quantify an endogenous protein biomarker, why would one calibrate with a synthetic peptide? Does it matter? Why even calibrate? In this presentation, the pros and cons will be discussed regarding the continuum of options for both bottom-up (digestion) and top-down (intact) “absolute” protein quantification.
A New Pathway for Glutaminolysis in *Mycobacterium tuberculosis*

**Robert Jansen - Weill Cornell Medicine** (rsj2005@med.cornell.edu) -- *Young Investigator Grantee*

- *Mycobacterium tuberculosis* (MTB) is the leading cause of deaths due to an infectious agent, killing 1.5 million people in 2014. Genetic screens have shown that the gene Rv3722c is essential for MTB, but its function is unknown. Using activity-based metabolite profiling and untargeted metabolomics, we show that Rv3722c is an aminotransferase that converts glutamine into its keto acid oxoglutarate. Comparative genomics revealed that another gene of unknown function, Rv0480c, functions as an omega-amidase that hydrolyzes oxoglutarate to alpha-ketoglutarate and free ammonia. Together, Rv3722c and Rv0480c constitute a non-canonical pathway for glutaminolysis that affects the carbon-nitrogen balance in MTB.

A Biomarker Metabolomic Signature Defines Motor Skill Sets in Sargramostim Treatment of Parkinson’s Disease

**Erica Forsberg - The Scripps Research Institute** (forsberg@scripps.edu) -- *Young Investigator Grantee*

- Parkinson’s Disease (PD) is a neurodegenerative disorder involving progressive loss of nigrostriatal neurons and altered effector T cell functions. Research in animal models demonstrated neurodestructive effector T cells can be pharmacologically transformed to regulatory neuroprotective T cells. To translate animal models to human we used sargramostim for PD treatment to assess immune modulatory functions. A phase I double blind placebo controlled study demonstrated this transformation with improvements in cortical neurophysiological activities. This incited mechanistic questions on whether a metabolomics disease signature exists. Our works demonstrated that global metabolomics isolated tryptophan and vitamin D metabolism as key treatment pathways. Targeted metabolomics was used to quantify dysregulated metabolites, providing insights into potential neuroprotective actions.

Metabolic Profiling Reveals a Potential Novel Pathway of Macrophage Foam Cell Apoptosis in Atherogenesis

**Panagiotis Vorkas - Imperial College London** (p.vorkas09@imperial.ac.uk) -- *Young Investigator Grantee*

- Atherosclerosis remains the leading cause of mortality and morbidity in the western world. Here, UPLC-MS-based metabonomics were utilized for the analysis of human atherosclerotic tissue. A panel of established pathways were identified being dysregulated, such as free cholesterol (FC), oxidized cholesteryl esters, purines, pyrimidines, sphingolipids and acylcarnitines. A previously unassociated sphingolipid, namely phosphatidylethanolamine-ceramide (PE-Cer), was detected with high statistical significance (p=9.8x10^{-12}) and 2-fold reduction in disease. PE-Cer also demonstrated the highest inverse correlation to FC. Pilot studies in primary human monocyte-derived macrophage foam cells demonstrated elevated apoptosis, accompanied by 2-fold reduction of SAMD8, the enzyme responsible for PE-Cer synthesis. This provides insight for the role of PE-Cer in foam cell formation and atherogenesis.
**Native Matrix/Surrogate Analyte Calibration: Quantifying Testosterone with Deuterated Testosterone Calibrators**

**Joshua Hayden - Weill Cornell Medical College** (jah9108@med.cornell.edu)

- Our objective was to develop a calibration approach that does not require analyte-free matrix. Towards this end, we validated a testosterone assay that utilizes deuterated testosterone in pooled patient serum as calibrators. The assay involved a simple liquid-liquid extraction and carbon-13 labeled testosterone as the internal standard. Testosterone values for patient samples were obtained with standard calibrators and native matrix/surrogate analyte calibrators (deuterated testosterone in pooled patient serum). Accuracy of the native matrix/surrogate analyte approach was confirmed by comparison with the traditional calibration approach (slope 1.04, R²=0.99) and an established LC-MS/MS assay (slope 1.07, R²=0.996). The success of this approach suggests that authentic matrix/surrogate analyte could be a useful approach for samples where analyte-free matrix is challenging to obtain.

**Universal Calibration: Populations Don’t Lie, People Do**

**Matthew Crawford - LabCorp** (crawfm1@labcorp.com)

- LC-MS/MS calibration can have compounding error as they rely on gravimetric weighing of materials and the quality of material. As such in-house gravimetry was undertaken with materials from 3 different vendors and compared against the reference method via samples of assigned concentrations. Beyond gravimetry, internal standard based calibration will be shown by setting IS response at 6 clinical cut-offs. Finally, the concept of calibration using normal patient sample pools will be demonstrated. Pools were collected for age and gender specific reference intervals. Value assigned for each population pool will be explored. To conclude all mechanisms of calibration were challenged against value assigned reference method samples.

**Authentic or Analogue Calibration: Is there a Difference for Protein Quantification?**

**Russell Grant - LabCorp** (grantr@labcorp.com)

- Fully-tryptic stable-isotope labeled (SIL) peptides, cleavable SIL peptides, and a full-length SIL protein were compared as internal calibrators for quantifying 3 forms of unlabeled thyroglobulin (Tg) by protein cleavage-isotope dilution mass spectrometry using multiple digestion conditions. All SIL calibrators and unlabeled proteins were standardized by amino acid analysis to allow confident assignment of accuracy. Collectively, the results demonstrate lack of commutability for peptide calibrators across digestion conditions and potential for different proteoforms to provide disparate concentration assignments due to variations in the peptide formation despite altering denaturation/digestion stringency. Nonetheless, these results still support the use of recombinant, full-length proteins as calibrators and internal standards, in favor of pseudo-protein calibrators.
ADAM(TS13) and Eve: Clinical Proteomics Taking Yet Another Bite of the Apple with the Irresistible LC-MS/MS Technique

Christopher Shuford - Laboratory Corporation of America (shuforc@labcorp.com)

Thrombotic Thrombocytopenic Purpura (TTP) is a life-threatening disease characterized by acute and severe decrease in the activity of ADAMTS13, the enzyme responsible for cleaving von Willebrand factor. Despite the acuity of TTP, the complexity and cost of ADAMTS13 activity testing necessitate that most institutions use reference laboratories rather than in-house assays, which leads to delayed testing results that can impact patient management. To counter this delay as a reference laboratory, we are developing a simple LC-MS/MS assay capable of STAT testing through the use of historical (e.g., biweekly) calibration. Key elements in development and validation of the STAT LC-MS/MS assay will be presented.

Targeted Proteomic Estimation of High Density Lipoprotein Function is Associated with Cardiovascular Disease

Cory Bystrom - Cleveland HeartLab, Inc. (cbystrom@clevelandheartlab.com)

High density lipoprotein (HDL) plays many roles in vascular biology. Cholesterol efflux capacity (CEC) is one functional role that has been linked to cardiovascular disease in cell-based studies. Here we present a targeted method for the quantitation of 21 HDL-associated proteins from which a mathematical model for the prediction of CEC was discovered. This model was further refined for the stratification of patients with coronary artery disease and healthy controls, and confirmed in a separate experiment. The results of this work is a rapid, scalable, precise prototype assay that enables further exploration of the relationship between HDL and vascular biology.

A Critical Evaluation of a Clinically Utilized Immunoassay for Assessing Cardiovascular Risk

Celalettin Topbas - Cleveland Heart Lab (jtopbas@clevelandheartlab.com)

Lipoprotein Associated Phospholipase A2 (Lp-PLA2), is an enzyme associated with vascular inflammation. Both the concentration and the activity of Lp-PLA2 in serum are used clinically to assess risk of coronary heart disease. We compared an in-house proteomic LC-MS/MS (SISCAPA®) concentration assay, a fully validated LDT for LP-PLA2 activity and the FDA approved Lp-PLA2 concentration assays to investigate their relationship. The ELISA showed a weak correlation with both concentration and activity while the first two compared well. Further investigation revealed that the immunoassay suffers from a substantial interference and unpredictably detects only a fraction of the total Lp-PLA2 in human serum.
Development and Application of Novel, Nondestructive Dried Blood Spot-Based Hematocrit Prediction Methods using Noncontact Diffuse Reflectance Spectroscopy

Christophe Stove - Ghent University (christophe.stove@ugent.be)

The hematocrit (Hct) effect is generally considered as one of the most crucial issues in dried blood spot (DBS) based quantitation, as it is known to impact the accuracy of the results and hence, correct interpretation. As an improvement to a previously developed Hct prediction method, based upon the potassium content of a DBS extract, we now developed non-contact methods that enable Hct prediction in mere seconds, allowing complete sample preservation. The methods are based on the hemoglobin content of DBS, measured via noncontact diffuse reflectance spectroscopy, either by using the reflectance spectrum between 500 and 700 nm or by using reflectance at a single wavelength (589 nm). The methods were thoroughly validated, used to predict the Hct from DBS and applied to correct for the Hct-induced bias seen in DBS-based LC-MS/MS analysis of two model compounds, caffeine and paraxanthine.

Do DBS and DPS Micro Sampling Techniques have a Place in the Clinical Laboratory?

Jack Henion - Q2 Solutions (henionj@advion.com)

Dried blood spot (DBS) and dried plasma spot (DPS) micro sampling techniques offer several benefits for the clinical diagnostic laboratory. These include small sample volumes, minimally invasive sample collection, point-of-care/home patient sample collection and economical sample shipping/and storage. To-date DBS techniques for newborn screening are well accepted, but DBS techniques have not been generally accepted in the clinical laboratory. This presentation will show how DBS techniques and a novel book-type DBS/DPS card provides a dried spot of red blood cells and the corresponding dried spot of plasma from the same micro sample can be analyzed by LC/MS/MS bioanalysis.

Validation of Creatinine in Dried Blood Spots: Remote Monitoring in Pediatric Renal Transplant Patients

Jane Dickerson - Seattle Children’s Hospital (jane.dickerson@seattlechildrens.org)

We have previously described implementing a clinical dried blood spot program for monitoring immunosuppressants. Improving compliance in the adolescent population is a major effort of the clinical team. To assist their efforts, we developed and validated a liquid chromatography-mass spectrometry (LC-MS/MS) assay for quantitation of creatinine in dried blood spots (DBS). The method correlated well with plasma creatinine measured on an Ortho Vitros. We believe this research will improve the clinical utility of remote collection of dried blood spots for renal transplant patients by monitoring both immunosuppressant and creatinine levels.
Wednesday @ 3:00 PM in Room 5 (Sierra)

Mass Spectrometry Imaging Combined with in vivo Luminescent Imaging Reveals the Molecular Panels of Different Treatment Responses in Lymphoma Models

Florian Barré - Maastricht University, M4I (f.barre@maastrichtuniversity.nl) -- *Young Investigator Grantee*

- Diffuse large B-cell lymphoma (DLBCL) is a biologically aggressive disease and up to one-third of patients will ultimately become refractory to initial therapy or relapse after treatment and display poor survival outcome. The high mortality rate in patients with relapsed or refractory DLBCL highlights the urgent need for novel therapeutic approaches based upon selective molecular targets. We propose to combine in vivo luminescent/fluorescent DLBCL xenograft models with mass spectrometry imaging (MSI) analysis to study the tumor characteristics during R-CHOP treatment. The aim is to investigate changes in the chemical composition during tumoral development, treatment response and identify yet uncharacterized targets that could become alternative targets for therapy.

Wednesday @ 3:20 PM in Room 5 (Sierra)

Advances in Data-Driven Image Fusion for Imaging MS: Novel Image Modality Combinations Targeting Distinct Biomolecular Classes

Raf Van de Plas - Delft University of Technology (raf.vandeplas@tudelft.nl) -- *Young Investigator Grantee*

- Data-driven multi-modal image fusion enables integration of imaging mass spectrometry (IMS) with other imaging technologies. Applications include the estimation of molecular distributions in tissue that is not physically measured by IMS, and prediction of ion distributions to a spatial resolution that exceeds that of measured ion images by ten times or more. The ability to predict an ion’s localization using another modality depends on whether that ion species has a detectable relationship to the other modality. We examine for different biomolecular classes, including lipids and proteins, the relationship between fusion performance and the modality type that IMS is integrated with.

Wednesday @ 3:40 PM in Room 5 (Sierra)

Multimodal Imaging of Ad-Associated Lipid Species in Structurally Distinct Plaques

Wojciech Michno - Sahlgrenka Academy at University of Gothenburg (wojciech.michno@neuro.gu.se) -- *Young Investigator Grantee*

- Alzheimer’s disease (AD) is a neurodegenerative disease, of which the underlying pathological mechanism is still not understood. The disease is characterized by accumulation of Amyloid-β peptides into different extracellular plaques. Plaques have also been found in non-demented pathological aging patients. Therefore, discrimination between structural and molecular plaque architecture are of interest to resolve plaque pathology in AD. MALDI IMS was utilized to elucidated lipid environment in AD tissue. Then, a hyperspectral imaging paradigm employing Amyloid-β aggregate binding LCOs and an in-house software was used to differentiate between different types of plaques. Clear localization of several sphingolipids in plaques and their surroundings, as well as lipid composition differences between the different plaques, were identified through a true multimodal imaging paradigm.
LC-MS/MS Troubleshooting: An Introduction
Imir Metushi - LabCorp/Esoterix (imirmetushi@gmail.com)

Liquid chromatography is a critical component during LC-MS analysis and it accounts for the larger portion of troubleshooting problems during a LC-MS run. This presentation will talk about some general approaches to ensure good LC workflow, some of which include guard column choices, ferrule connections, tubing etc. Two short cases will be used to illustrate the basic concepts presented.

Investigation of Peak Shape Degradation and Retention Time Shifts
Breland Smith - University of California San Diego (bes003@ucsd.edu) -- *Young Investigator Grantee*

LC system pressure is affected by various factors including mobile phase composition, column length and internal diameter, particle composition, temperature, and flow rate which are also modulated to affect peak resolution and retention time. There is often a compromise in optimizing separation efficiency while maintaining proper system pressure. This session will discuss the relationship between these factors, system pressure, and separation as well as demonstrate how a system leak can affect analytical separation by describing a case study that involves LC method failure due to a small, high pressure leak following annual maintenance. In addition, this presentation will give insight into how to investigate and diagnose an unexpected change in separation performance.

Naturally Occurring Isotopes Affecting the Calibration Curve: A Case Study
Philip Sobolesky - UCSD (psobolesky@ucsd.edu) -- *Young Investigator Grantee*

Selecting unique transition ions for quantification by tandem mass spectrometry using stable isotopically labeled standards is essential for accurate and consistent results. It is important to understand how the structure of your target compound and the contribution of naturally occurring isotopes can affect the mass to charge ratio. This session will discuss a troubleshooting case that involved the selection of a quantifier ion for deuterated lorazepam that resulted in a non-linear calibration curve due to the contribution of naturally occurring isotopes of lorazepam to the deuterated standard.
Bioactive Lipids as Pharmacodynamic Biomarkers of Mast Cell Activity in the Clinic

Veronica Anania - Genentech, Inc. (ananiav@gene.com)

- Although it is recognized that mast cells are important in asthma, biomarkers to measure mast cell activity in clinical samples are lacking. Additionally, bioactive lipids produced by mast cells play an important role in airway inflammation, yet these lipids are not measured in clinical trials due to lack of robust assays. To address this issue, we developed a multiplexed mass spectrometry assay to quantify bioactive lipids in several biological sample types including bronchoalveolar lavage (BAL) fluid, nasal mucosal lining fluid, and urine. Based on this in vitro and in vivo data, urinary lipids have been included as exploratory biomarkers in several ongoing asthma clinical studies. In conclusion, our study indicates that bioactive lipids represent a novel class of clinical pharmacodynamic biomarkers that can be utilized to assess mast cell activity in the context of a clinical trial.

Worldwide Newborn Screening for Lysosomal Storage Diseases by Tandem Mass Spectrometry

Michael Gelb - Univ. of Washington (gelb@chem.washington.edu)

- Our lab developed tandem mass spectrometry for multiplex analysis of several enzymes in dried blood spots for newborn screening of lysosomal storage diseases. Recently several US states have expanded their newborn screening programs to include these methods. They are also carried out in Taiwan and Australia. More recently we have put all the assays together into a single multiplex LC-MS/MS assay of 13 lysosomal storage diseases including enzyme assays and biomarkers. Also included are biomarkers for additional diseases for which newborn screening is being considered (bile acid disorders for example). The work shows how mass spectrometry can uniquely address the challenges of newborn screening of several rare and treatable metabolic diseases using a single punch of a dried blood spot and in a high throughput manner appropriate for use in newborn screening laboratories worldwide.

Opportunities for Clinical Metabolomic Analysis of Tissue using Liquid Microjunction Surface Analysis

Timothy Garrett - University of Florida (tgarrett@ufl.edu)

- Liquid microjunction surface analysis (LMSA) is a direct tissue analysis sampling approach that enables the rapid sampling of a tissue surface for many applications such as metabolomics, imaging, and analysis of short lived chemical species. The application to clinical specimens offers a rapid approach to tissue analysis that could improve diagnosis and treatment. We report the use of LMSA on the analysis of melanoma as well as the application to detecting transient chemical signatures produced by deep brain stimulation.
Thursday @ 9:00 AM in Room 2 (Catalina)

**Posttranslationally Modified Proteins as New Targets for Clinical MS Protein Tests**

*Dobrin Nedelkov - Biodesign Institute, Arizona State University* (dobrin.nedelkov@asu.edu)

- The last decade has seen increased efforts to bring MS-based protein tests into clinical labs; however, only a dozen such tests have been adopted thus far. Even when MS approaches result in new protein biomarkers discovery, enzymatic immunoassays oftentimes replace MS in clinical lab tests. One way to drive translation and adoption of MS protein tests is to target protein features that could only be detected with MS - such as post-translational modifications (PTMs) – thus generating both content and demand. Discussed in this presentation will be some viable PTM protein targets and the path forward for these clinical MS protein tests.

Thursday @ 9:20 AM in Room 2 (Catalina)

**Development and Validation of an Immunoaffinity LC-MS Method to Active and Total B-Type Natriuretic Peptide in Human Plasma**

*Michael Lassman - Merck & Co* (michael_lassman@merck.com)

- We have developed and validated a first of its kind immunoaffinity LC/MS assay with sufficient performance characteristics to measure BNP derived fragments as well as “Total BNP” in the plasma of adults diagnosed with heart failure. The following performance characteristics were assessed as part of analytical validation: inter and intra-assay precision, sensitivity, spike recovery, dilution linearity, freeze/thaw stability, and assay recovery. The ratio of active BNP(1-32) to Total BNP in the plasma was found to be low, ranging from below the limit of quantitation to 8%. In addition, we observed that the Total BNP measurement is better correlated ($r^2=0.89$) with the clinical NT-proBNP measurement rather than the more specific IA-LC/MS BNP(1-32) measurement ($r^2=0.06$), leading us to conclude that the accepted clinical based BNP measurements are not indicative of active BNP.

Thursday @ 9:40 AM in Room 2 (Catalina)

**Profiling B-Type Natriuretic Peptide Cleavage Proteoforms in Human Plasma by CE-MS**

*Shenyan Zhang - Cedars Sinai Medical Center* (shenyan.zhang@cshs.org) -- *Young Investigator Grantee*

- B-type Natriuretic Peptide (BNP) is a biologically active circulating hormone whose concentration is routinely used in the diagnosis of heart failure. Multiple enzymes cleave BNP before it binds its natriuretic peptide receptors. We coupled capillary electrophoresis to high-resolution mass spectrometry to profile BNP proteolysis in plasma with a view to assessing its potential relation to heart failure severity. Our method relies on electrophoretic introduction of minimally processed plasma samples to monitor the dynamic generation and breakdown of five BNP proteoforms. Combined with multisegment injection, this method can produce a multi-point BNP proteolysis profile of one patient within an hour.
Accuracy of Volumetric Absorptive Microsampling for Quantification of Protein Biomarkers

Irene van den Broek - Cedars-Sinai Medical Center (Irene@vandenbroek.net) -- *Young Investigator Grantee*

Volumetric absorptive microsampling (VAMS) allows accurate sampling of 10 µL blood from a minimally invasive finger prick and overcomes effects from hematocrit and sample heterogeneity associated with dried blood spots. We describe the first application of VAMS for mass spectrometry-based protein quantification. To achieve the required accuracy for clinical application, specific focus was placed on the realization of automated and high-throughput sample preparation as well as quality control and standardization throughout the assay pipeline. Method validation for six high abundance proteins (apoA-I, apoB, apoC-I, apoC-III, apoE, HSA) includes assessment of sampling precision, short- and long-term storage stability, extraction recovery, intra- and inter-day reproducibility, and comparison to clinical plasma samples using 15N-labeled apoA-I as internal standard.

Quantification of Retinol-Binding Protein (RBP) in Human Serum by LC-MSMS: Considerations for Development and Validation

Anna Merrill - University of Washington (merrilla@u.washington.edu) -- *Young Investigator Grantee*

Retinol-binding protein (RBP), a 21-kDa polypeptide that transports vitamin A from hepatic storage to peripheral target locations, is commonly quantified in the clinical laboratory using nephelometry, a methodology with notable shortcomings. We validated a “plug-and-play” clinical LC-MS/MS assay for RBP that circumvents many of these challenges, improving testing quality and utility for multiple patient groups, including preterm neonates. Assay calibration was accomplished using an external calibration scheme. Both pre-validation and validation studies were carried out according to CLSI document C62-A. During assay validation, we witnessed sporadic failures that were eventually linked to faulty trypsin digestion. Symptoms of this problem will be discussed, along with troubleshooting strategies and suggestions for quality monitoring in high-throughput clinical mass spectrometry assays.

Dried Blood Spot Screening for Primary Immunodeficiencies using Immuno-SRM

Sunhee Jung - Seattle Children (sunhee@uw.edu)

Primary immunodeficiency disorders (PIDDs) are a diverse group associated with defective immune system. Because of the susceptibility to severe infections caused by the immunodeficiency, early detection of life-threatening PIDDs is critical for maximizing patient survival and clinical outcomes. Many of these treatable PIDDs are associated with the absence/reduced levels of a particular protein or a particular immune cell subset that can provide clues to a diagnosis. We herein report a proof-of-concept study demonstrating that the immuno-SRM can detect extremely low abundance marker proteins of CD3e, BTK, and WASP in DBS for three life-threatening PIDDs: Severe Combined Immudeficiency, X-linked Agammaglobulinemia, and Wiskott-Aldrich syndrome, respectively. Our promising data opens up the great potential of a multiplexed immuno-SRM assay for screening a variety of congenital disorders.
CTP Synthase Activity Assay by LC-MS/MS in the Multiple Reaction Monitoring Mode

Anne-Claire Boschat - Institut Imagine (anne-claire.boschat@institutimagine.org) -- *Young Investigator Grantee*

- Cytosine 5’-Triphosphate Synthase (CTPS) is known to be a central enzyme in the de novo synthesis of CTP. Recently, a CTPS loss-of-function homozygous mutation inducing combined immunodeficiency in human was identified. Here we present an analytical method for the measurement of CTPS activity by LC-MS/MS. CTPS activity was measured in peripheral blood mononuclear cells issued from healthy donors, as well as of an immunodeficient patient with a rare recessive homozygous mutation in CTPS1 gene. This assay is a useful tool to better characterize the enzyme and could also provide an effective way of screening new inhibitors of CTPS.

Development and Validation of a LC-MS/MS Method for L-Arginine (ARG) and Asymmetric/Symmetric Dimethylarginine (ADMA/SDMA)

Xander van Wijk - University of California, San Francisco (Xander.vanWijk@ucsf.edu) -- *Young Investigator Grantee*

- Asymmetric and symmetric dimethylarginine (ADMA and SDMA) are involved in endothelial function via inhibition of endothelial nitric oxide synthase. Elevated levels are associated with cardiovascular risk and renal failure. The latter is particularly true for SDMA as renal excretion is the primary route of its elimination. ADMA and SDMA levels are also increased in critically ill and septic patients. In this regard, the L-arginine (ARG)/ADMA ratio is decreased as well. In light of a greater effort of clinically validating new markers for sepsis, we developed and validated a method for ARG, ADMA, and SDMA. The method we describe here is a relatively simple, reversed phase method, without the need for derivatization. We are currently investigating the clinical utility of ARG, ADMA, and SDMA as markers for sepsis.

UPLC-MS/MS Analysis of Disease-Specific Oligosaccharides for Lysosomal Storage Diseases: Diagnosis and Potential Treatment Monitoring

Rongrong Huang - Greenwood Genetic Center (rhuang@ggc.org)

- Several lysosomal storage diseases (LSDs), primarily the glycoproteinoses, are characterized by accumulation of free oligosaccharides as a result of impaired glycoprotein degradation. The typical method used to detect abnormal accumulation of urine oligosaccharides is thin-layer chromatography, which lacks adequate sensitivity and specificity. Our laboratory has developed a UPLC-MS/MS assay for relative quantification of seven disease-specific urine oligosaccharides using samples from 110 unaffected controls and 51 affected LSD patients. The results indicate the assay can be used for sensitive diagnosis of eight different LSDs, and potentially for treatment monitoring. Preliminary data indicates it can also be applied to other biological specimens.
MALDI Imaging: A Promising Tool in Elucidating the Pathophysiology of Colorectal Anastomotic Leakage

**Audrey Jongen** - Maastricht University Medical Centre (a.jongen@maastrichtuniversity.nl) -- *Young Investigator Grantee*

- Colorectal anastomotic leakage (CAL) remains the most dreaded complication after colorectal surgery despite extensive research, the implementation of fast track protocols and new surgical techniques. It occurs with an incidence between 7-12% and is associated with high rates of morbidity and mortality, decreased quality of life and a threefold increase in health care costs. In order to elucidate the pathophysiology of CAL, a discovery based longitudinal experiment was conducted to identify molecular pathways of anastomotic healing and anastomotic leakage using MALDI-IMS. Rat models for anastomotic healing and leakage were used, and clear differences in lipid expression could be observed between different time points and between control and anastomotic tissue. IMS was shown to be a valuable tool to identify molecules involved in the normal healing process and anastomotic leakage.

Rapid Cancer Diagnosis from Fine Needle Aspirate and Touch Imprint Biopsies by Ambient Ionization Mass Spectrometry

**Livia Schiavinato Eberlin** - The University of Texas at Austin (liviae@utexas.edu)

- Ambient ionization MS provides great analytical sensitivity, specificity, and depth of molecular information in real time, directly from tissue samples, thus, the prospect of using this technology in and outside of the operating room is broad and exciting. Yet, is it realistic to expect ambient ionization MS to become an integral clinical technology for biopsy analysis? In this talk, examples of research progress being undertaken towards this goal using ambient ionization MS will be presented, including 1. Pre-operative diagnosis of fine needle aspirate biopsy samples, 2. Intra-operative diagnosis of touch imprint biopsies. Our results suggest that ambient ionization mass spectrometry can be successfully used for rapid cancer diagnosis from small biopsy samples in a profiling mode.

Simulated Breast Cancer Resection Margin Assessment using Desorption Electrospray Ionization (DESI) Mass Spectrometry Imaging (MSI) with Histology Correlation

**Nicole Morse** - Queen's University (11naam@queensu.ca) -- *Young Investigator Grantee*

- Obtaining negative margins in breast cancer surgery is critical in preventing recurrence. We assessed performance of DESI in a simulated resection margin analysis in breast cancer, by imaging frozen sections, and by hematoxylin/eosin staining for histology correlation. Metabolites m/z 215 and m/z 863 were selectively abundant in non-neoplastic tissue and tumor tissue respectively. Furthermore, MSI based on the ratio of m/z 863/215 improved the ability to detect tumor in samples with smaller, more infiltrative nests. This work points to the potential of MSI based on ion intensity ratios to improve correlation between histology and MSI.
Thursday @ 9:00 AM in Room 6 (SmokeTree)

**Understanding Matrix Effects Experiments**

*Grace van der Gugten* - *St Paul's Hospital* (gvandergugten@providencehealth.bc.ca)

- Liquid chromatography-tandem mass spectrometry is highly specific and sensitive, allowing for the measurement of many endogenous and exogenous compounds in biological matrices. Biological matrices are “dirty”, and can cause suppression or enhancement of the signal for the analyte(s) of interest: This is referred to as ‘matrix effects’, which must be assessed during LC-MS/MS method development and validation. This presentation will describe matrix effects, discuss qualitative and quantitative matrix effects experiments, and give examples of each type. Detailed examples of the quantitative matrix effects pre and post spike calculations and results will be shown.

Thursday @ 9:20 AM in Room 6 (SmokeTree)

**Method Development Matrix Effects Case Study**

*Autumn Breaud* - *Johns Hopkins University* (abreaud1@jhmi.edu)

- When developing HPLC-MS/MS methods for therapeutic drug monitoring or toxicology, it is important to work with a sample matrix which closely matches the matrix of unknown samples. Generally, this involves the use of pooled materials for which no demographic information is available. In this session, we discuss the discovery of age-specific matrix interference during the development of an assay for quantification of chlorhexidine, an antiseptic agent used for washing neonatal patients.

Thursday @ 9:40 AM in Room 6 (SmokeTree)

**Matrix Effects: An Interactive Session**

*Grace van der Gugten* - *St. Paul's Hospital* (gvandergugten@providencehealth.bc.ca)

- When developing and validating an LC-MS/MS assay, matrix effects must be assessed. But what should be done when the post column infusion and/or phospholipid scans show undesirable results? And how do we correctly calculate spikes for the quantitative matrix effects experiment? In this interactive session, attendees will work through a problem set to help better understand how to perform matrix effects experiments and interpret the results.
In-Depth Analysis of a Resilient Multi-Drug Resistant Pathogen, KPC27, using High-Throughput Quantitative Proteomics Approach

Yanbao Yu - J. Craig Venter Institute (yayu@jcvi.org) -- *Young Investigator Grantee*

- We analyzed the proteomes of Klebsiella pneumoniae (Kp) strains derived from UTIs by LC-MS/MS. Over 45% of the in silico proteome was identified from analyses of strain KPC27. This strain produces several b-lactamases and a carbapenemase resulting in only a few last-resort antibiotic drugs for therapy of infections. We observed that KPC27 responded to antibacterial effectors with increased expression of iron uptake and transport systems. In addition, we found differences in the use of iron acquisition systems and MFA pathways in the in vivo environment when comparing cultured and in vivo KPC27 proteomes. We hypothesize that iron starvation induces a regulatory shift towards energy metabolism via MFA pathways. Strategies interfering with the regulatory circuit of iron starvation and energy generation could potentially lead to inhibitors that form a new class of antibiotic drugs.

Identification of Altered Lipidome in Lipopeptide-Resistant Bacteria by HILIC-IM-MS

Kelly Hines - University of Washington (kmhines5@uw.edu) -- *Young Investigator Grantee*

- Antimicrobial resistance is a rapidly growing public health crisis, affecting over 2 million people in the USA each year. The rapid identification of antimicrobial-resistant infections is critical to preventing their spread and ensuring proper treatment. Using untargeted lipidomics by HILIC-ion mobility-mass spectrometry, we have distinguished daptomycin susceptible and resistant strains of S. aureus, E. faecalis, and C. striatum based on their lipid profiles. Significant alterations in cell membrane lipids such as phosphatidylglycerols and diglycosyldiacylglycerols were observed among the three strains of resistant bacteria, presenting a potential approach for rapid identification of lipopeptide-resistant strains from clinical isolates.

Simultaneous Identification and Antimicrobial Resistance Determination of Pathogenic Enterococci by Phage-Based MALDI-TOF MS

Nicholas Saichek - Colorado School of Mines (nsaichek@mines.edu) -- *Young Investigator Grantee*

- The continuous emergence of antibiotic resistance in clinically-relevant bacterial strains has driven the need for new clinical diagnostic techniques for identification and resistance profiling. Current methods for Enterococcus identification rely on expensive, time-consuming, and often antiquated techniques which makes accurate identification difficult. In order to address this, our current work demonstrates a phage-based approach coupled with MALDI-TOF MS for rapid, simultaneous identification and resistance determination of Enterococcus. An extensive host range study of vancomycin-resistant and -sensitive strains revealed promising phage candidates which were probed for unique peptide fragments by MALDI-TOF MS. Antibiotic resistance determination was determined by successful phage amplification.
A New Look at Parathyroid Hormone-Related Protein (PTHrP): Possible Role for Calcium Regulation in Brain
Mark Kushnir - ARUP Institute for Clinical & Experimental Pathology (kushnm@aruplab.com)
Calcium plays a role in the nerve signaling and brain function, while PTHrP is involved in intracellular calcium regulation. Limited information is available related to PTHrP expression in brain. We analyzed PTHrP using LC-MS/MS and calcium using ICP-MS in sets of paired serum/CSF samples from individuals without neurologic diseases and patients with elevated albumin indexes, and assessed association between concentrations of PTHrP and calcium, and concentration of nine common CSF biomarkers. We observed association of PTHrP concentrations with age and albumin index, suggesting that PTHrP may play a role in age-related physiologic changes in the brain and in pathologic neurologic conditions.

Separation of Multiple Vitamin D Metabolites using Ultra-Performance Convergence Chromatography Tandem Mass Spectrometry
Carl Jenkinson - IMSR, University of Birmingham (C.Jenkinson@Bham.ac.uk) -- *Young Investigator Grantee*
The aim of this study develop a was to develop a UPC2-MS/MS method to measure multiple vitamin D metabolites, apply supercritical CO2 as part of the mobile phase to determine enhanced resolution and sensitivity compared with an LC-MS/MS method. The mobile phase consisted of supercritical CO2 with methanol/0.1% formic acid mobile phase. Analysis of chromatographic separation revealed the order of elution was reversed based on polarity compared to reversed phase LC, however the C3-epimers, 3-epi-25-hydroxyvitamin(OH)D eluted after 25-hydroxyvitamin D in both methods. Baseline separation of 24OHD2 from 25OHD2 was achieved with UPC2; however this could only be partially separated by LC.

A multiplexed assay to identify CYP24A1 deficiency
Andy Hoofnagle - University of Washington (ahoof@u.washington.edu)
Precursor and active vitamin D hormone are catabolized by CYP24A1, which helps maintain normal concentrations of active hormone in target tissues. Genetic deficiency of CYP24A1 leads to inappropriately high concentrations of hormone and can result in severe hypercalcemia. The diagnosis of deficiency can be made in the setting of elevated plasma concentrations of 1,25-dihydroxyvitamin D and low 24,25-dihydroxyvitamin D compared with 25-dihydroxyvitamin D. Chronic kidney disease also leads to decreased 24,25-dihydroxyvitamin D but also reduced 1,25-dihydroxyvitamin D. We have developed a multiplexed assay that can be used to quantify precursor, active hormone, and catabolite in large epidemiological studies. We have also used it to efficiently screen for genetic deficiency and present a case study of CYP24A1 deficiency in an adult.
Quantitative Proteomic Analysis of HER2 Expression in the Selection of Gastric Cancer Patients for Trastuzumab Treatment

Eunkyung An - NantOmics (eunkyung.an@nantomics.com)

• A wide range of response rates have been reported in HER2-positive gastric cancer (GC) patients treated with trastuzumab. Other HER2-targeted therapies for GC have yet to show efficacy, raising doubt about the ability of standard HER2 diagnostics to accurately identify the GC patients most likely to benefit from anti-HER2 therapy. We applied mass spectrometry-based proteomic analysis to quantify HER2 protein expression in 237 formalin-fixed GC samples. A 115-fold range of HER2 protein expression was observed among patients diagnosed as HER2 positive by standard methods. Trastuzumab-treated patients with HER2 protein levels above a cutoff of 1,825 amol/ug had twice the median overall survival (OS) of their counterparts below the cutoff. A quantitative proteomic cutoff improves selection of GC patients for trastuzumab as compared to current diagnostic methods.

Prostate Specific Antigen Glycomics Assay: Towards a More Specific Tool for Early Detection of Prostate Cancer

Guinevere S.M. Kammeijer - Leiden University Medical Center (g.s.m.kammeijer@lumc.nl) -- *Young Investigator Grantee*

• Prostate specific antigen (PSA) is a well-known biomarker for the early detection of prostate cancer (PCa) however it lacks specificity as many other factors can cause elevation of the PSA concentration in the bloodstream. We established a non-invasive PSA glycomics assay, which allows an in-depth identification of the glycosylation and quantitation of PSA in urine. We are currently evaluating the alterations in glycosylation of PSA for improving diagnosis and prognosis of PCa.

Proteogenomics of Lung Squamous Cell Carcinoma

John Koomen - Moffitt Cancer Center (john.koomen@moffitt.org)

• An integrated proteogenomic study of lung squamous cell carcinomas has been undertaken to produce complete views of tumor architecture and contextual understanding of clinically relevant drug targets and immune-tumor interactions. The individual datasets include standard genotyping, DNA and RNA sequencing, and expression proteomics of 116 tumor tissues. This team science approach combines expertise in clinical medicine, mass spectrometry, genomics, and bioinformatics/biostatistics to enable extensive studies of the tumor proteogenomes, building on previous advances integrating complementary omics approaches to address hypotheses related to chemotherapy resistance, novel drug targets, and cancer signaling networks.
Thursday @ 2:15 PM in Room 5 (Sierra)

**Exploring the Limits of DESI and MALDI MSI for Metabolite Identification**

Andreas Dannhorn - Imperial College London (a.dannhorn16@imperial.ac.uk) -- *Young Investigator Grantee*

› Mass spectrometry imaging (MSI) became a powerful tool in drug discovery applications. In the current study we explored the suitability of desorption electrospray ionization (DESI) and matrix-assisted laser desorption ionization (MALDI) MSI to map the spatial distribution of 4 cassette-dosed drugs and their metabolites in a rat brain, liver and kidney sections. Using these two different MSI techniques, we were able to map the spatial distribution of the 4 drugs and 7 out of 10 metabolites, identified by LC-MS analysis, together with endogenous compounds. Combined DESI full-scan ToF MS and MS/MS imaging experiments were performed to acquire full scan data of the tissue while confirming the identity and localization of the observed drugs and their metabolites.

Thursday @ 2:35 PM in Room 5 (Sierra)

**Application of Imaging Mass Spectrometry to Assess Ocular Drug Transit**

Kerri Grove - Novartis Institutes for BioMedical Research (kerri.grove@novartis.com)

› MALDI imaging mass spectrometry (IMS) is becoming an important technology to determine localization of drug compounds after dosing and has become of interest in the ophthalmology field. For this study, ocular distribution of brimonidine, a drug used to treat glaucoma, was investigated in rabbits following topical instillation. We have developed IMS methods to assess transit of topically administered brimonidine from the anterior chamber to the posterior segment of rabbit eyes. The distribution of brimonidine suggests that the route of transit following topical administration is mainly through the uveal route. This study demonstrates that IMS can be applied to monitor ocular transit and distribution of topically administered drugs.

Thursday @ 2:55 PM in Room 5 (Sierra)

**Whole Body Skin Imagings of Medicines and Metabolites by Thermal Desorption-Electrospray Ionization/Mass Spectrometry**

Jentaie Shiea - National Sun Yat-Sen University (jetea@fac.nsysu.edu.tw)

› Skin plays a vital role in protecting human being against the attack by pathogenic microorganisms. Metabolites are also released from skin through numerous glands underneath it. Although some metabolites on skin are potential disease biomarkers, current analytical techniques are incapable to efficiently identify them on skin. In this study, TD-ESI/MS, a novel ambient mass spectrometric technique, was used to characterize the skin compounds including drugs, lipids and metabolites without doing any sample pretreatment. Herein, ambient imaging was demonstrated for visualizing the distribution of drugs and metabolites on whole body skin. After medicine was taken by volunteer for a period of time, the distribution of medicines or their metabolites was collected and analyzed.
• Session 6 • Track 6 •
Optimizing Data Analysis
Thursday @ 2:15 PM in Room 6 (SmokeTree)
Session Chair: Josh Hayden - Weill Cornell Medical College

Thursday @ 2:15 PM in Room 6 (SmokeTree)
Challenges in Mass Spectrometry Data Analysis … Why You Can’t Just Weigh Out Your Peaks Anymore
Joshua Hayden - Weill Cornell Medical College (jah9108@med.cornell.edu)
‣ This session will present an overview of the type of data generated in a typical mass spectrometry assay. The session is intended for participants who have limited experience performing these sorts of assays and is designed to give beginners an overview. This overview includes a delineation of data analysis that needs to be performed to ensure reliable quantitation. At the conclusion of this session, participants should have a solid understanding of the scope of data analysis required to ensure reliable quantitation by mass spectrometry.

Thursday @ 2:35 PM in Room 6 (SmokeTree)
Clinical Mass Spectrometry Data Flow: Friend or Foe? Understanding Your Information Technology Options
Patrick Mathias - University of Washington (pcm10@uw.edu)
‣ Managing data flow for clinical mass spectrometry testing is challenging because of the lack of automated commercial solutions. The session is intended for participants who are interested in learning more about opportunities to implement optimized workflows for managing mass spectrometry data, which begins with an order for a laboratory test and ends with an uploaded patient result. This session will explore different design configurations throughout the process that laboratories should examine to improve efficiency. At the conclusion of this session, participants will be able to diagram the steps taken from sample to result and identify opportunities to implement lean solutions.

Thursday @ 2:55 PM in Room 6 (SmokeTree)
Strategies for Human-Proofing High-Throughput Data Analysis
Julia Drees - Kaiser Permanente Regional Laboratories (julia.c.drees@kp.org)
‣ Data analysis and reporting can be an error-prone and time consuming part of LC-MS/MS testing even for low volume clinical laboratories. This session will describe how data analysis software and middleware rules can streamline workflows and reduce errors by automatically flagging samples with quality failures and preventing the uploading of those results. A case study will be presented demonstrating how one high volume clinical laboratory further increased throughput by implementing data review by exception. At the conclusion of this session, participants will be able to assess their own workflows and implement solutions that reduce time and errors spent analyzing data.
New Technologies for Clinical Applications of Metabolomics

Thursday @ 3:30 PM in Room 1 (Mojave Learning Center)
Session Chair: Robert Jansen - Weill Cornell Medicine

**Metabolomics Guided Systems Biology in Clinical Applications**
*Tao Huan - The Scripps Research Institute* (thuan@scripps.edu) -- *Young Investigator Grantee*

- Over the last 15 years, metabolomics has emerged as a powerful technology to interrogate cellular biochemistry, perform diagnostic testing, and characterize biochemical mechanisms of disease. Owing to innovative developments in informatics, analytical technologies and integration of orthogonal biological approaches, it is now possible to expand metabolomic analyses into understanding the systems-level effects of metabolites. In this work, we incorporated systems level technologies into XCMS, a widely used metabolomic platform, to gain insight into the mechanisms of disease progression in clinical applications. Our platform allows users to directly map metabolomic data onto metabolic pathways in “one-click” and carry out multi-omic integration with self uploaded and/or database archived epigenome, genetic variations, genome, transcriptome, and proteome data in a user-friendly approach.

**Ion Mobility/Mass Spectrometry for Metabolomics and Clinical Analysis**
*Richard Yost - University of Florida* (ryost@ufl.edu)

- Ion mobility/mass spectrometry has tremendous potential for metabolomics and clinical analysis. Ion mobility can resolve compounds unresolved by LC/MS/MS, provide additional structural information not available from mass spectrometry, and reduce or even eliminate the need for chromatographic separation. These features offer significant improvements for quantitative targeted metabolomics and clinical analysis, as well as for untargeted (global) metabolomics studies. Techniques to be covered include both classic drift tube ion mobility (IMS) and high-field asymmetric-waveform ion mobility (FAIMS), with various applications including steroids, bile acids, and Vitamin D.

**Applicability of Rapid Evaporative Ionization Mass Spectrometry (REIMS) in Uterine Cervical Pathology — a Proof of Principle Study**
*Menelaos Tzafetas - Imperial College London* (m.tzafetas@imperial.ac.uk) -- *Young Investigator Grantee*

- Cervical cancer and its precancerous form cervical intraepithelial neoplasia (CIN) are common diseases in women of reproductive age. Fertility-sparing treatments are available, however they require precise disease clearance at the margins to balance future oncological and reproductive outcomes for these patients. In our pilot study, we showed REIMS was able to quickly and accurately differentiate between cancerous and normal cervical tissue. We plan to develop this technique in this field and believe it has great potential to improve patient satisfaction and balance oncological and reproductive outcomes.
• Session 7 • Track 2 •
Assay Standardization II
Thursday @ 3:30 PM in Room 2 (Catalina)
Session Chair: Hubert Vesper - CDC

Thursday @ 3:30 PM in Room 2 (Catalina)
Improved Diagnosis and Treatment of Patients Through Accurate and Standardized Estradiol Tests
Julianne Cook Botelho - Centers for Disease Control and Prevention (gur5@cdc.gov)
‣ Accurate and reliable estradiol (E2) measurements are vital to monitor breast cancer patients on aromatase inhibitors and IVF patients on ovarian stimulation therapy as well as to assess risk for estrogen secreting tumors and fractures. CDC is ensuring accurate E2 measurements by maintaining a highly accurate and precise reference method as well as providing serum reference materials through the Hormone Standardization Program (HoSt). E2 requires a method with high sensitivity to address the need for low pg/mL measurements and a method with high specificity, free from potential interferences. CDC is working to ensure that laboratory results in research and patient care are accurate, reliable, and meet the needs defined by stakeholders such as The Partnership for Accurate Testing of Hormones (PATH).

Thursday @ 3:50 PM in Room 2 (Catalina)
The Path Toward Urine Albumin Standardization
Ashley Beasley Green - National Institute of Standards and Technology (ashley.beasley@nist.gov)
‣ Urinary excretion of albumin is a major diagnostic and prognostic marker of renal dysfunction and cardiovascular disease; therefore, accurate measurement of urine albumin is vital to clinical diagnosis. To address urine albumin measurement precision, we have developed the following components of the urine albumin reference measurement system: a multiplexed candidate reference measurement procedure that utilizes isotope dilution-mass spectrometry (ID-MS) and multiple reaction monitoring (MRM) to quantify urine albumin; a primary reference material to be used as a calibrator for higher-order urine albumin methods; and a secondary reference material to be used as a matrix-based quality control for commercially-available urine albumin assays.

Thursday @ 4:10 PM in Room 2 (Catalina)
Lipoprotein Sub-Class Composition, Size and Particle Number in Normal and Dyslipidemic Individuals Measured by Means of Quantitative LC-MS/MS Techniques
Zsuzsanna Kuklenyik - Centers for Disease Control (zkuklenyik@cdc.gov)
‣ Lipoproteins circulating in fasting blood are classified by density into high, low, intermediate and very low density lipoproteins (HDL, LDL, IDL and vLDL). In this work lipoprotein classes/sub-classes were size fractionated using <100 µL serum from 200 donors (normal, hyperglycemia, hypercholesterolemia, hypertriglyceridemia and hyperlipidemia), collecting size fractions of 6-40 nm. Each serum sample and their corresponding 40 size fractions were analyzed parallel by three different quantitative LC-MS/MS methods for measurements of non-polar lipid classes (free cholesterol, cholesterol esters, and triglycerides), five phospholipids classes, and 8 apolipoproteins. The data demonstrate how LC-MS/MS can provide highly effective means to measure lipoprotein sub-class composition in cohort studies, allowing system biology investigations of various dyslipidemias and cardiovascular diseases.
Proteome-Based Mapping of Non-Serous Gynecological Tissue Specimens

Vathany Kulasingam - University Health Network (vathany.kulasingam@uhn.ca) -- *Young Investigator Grantee*

Ovarian cancer (OvCa) is made up of several distinct subtypes, including serous, endometrioid (EC), clear cell (CCC) and mucinous (MC). While serous OvCa mostly arises from the fallopian tube, the origins of the non-serous subtypes remain unclear. In light of this, we have deciphered the proteomes of non-serous OvCa tissues along with their suspected precursors. Overall, the expression profiles of EC and CCC were associated with endometriosis while those of MC were associated with gastrointestinal cancers. In addition, a subgroup of EC correlated well with MC suggesting that the current subtype model based on histopathology may not be sufficient and that proteomic profiling may enhance accurate diagnoses. Most importantly, this work will serve as the basis to unravel the underlying biology of the non-serous subtypes with respect to their extra-ovarian origins.

A Computational Pipeline for Accurate and Reproducible Analysis of Peptides in Data Independent Acquisition MS Data: Application to Human Clinical Samples

Jarrett Egertson - University of Washington (jegertso@uw.edu)

We present a pipeline for automated analysis of data acquired using data independent acquisition (DIA). Beyond removing the potential for human-error, automated peak integration of DIA data is necessary due to the large amount of analytes measured in a single DIA LC-MS/MS run. We present details of the data processing workflow in the context of an application to an Alzheimer’s disease cohort consisting of samples from human brain autopsies. We assess the impact of the pipeline on precision by comparing human and automated analysis of a “5x5” data set with sample assayed repeatedly between and within days. We also demonstrate quality control steps in the form of summary statistics and visualizations for each step of the pipeline. Finally, we discuss containerization and versioning o support repeatable data processing.

Elucidation of Novel Proteoforms of Superoxide Dismutase (SOD1) in Sporadic ALS Patients

Philip Loziuk - NC State University (plloziuk@ncsu.edu) -- *Young Investigator Grantee*

Mass spectrometry offers the most robust and specific platform to discover and characterize biomolecules. In the field of proteomics, there are three main approaches: top-down, middle-down, and bottom-up. This presentation will detail the characterization of SOD1 derived from patients diagnosed with sporadic ALS. The level of molecular detail (100% sequence coverage) using bottom-up proteomics allowed us to discover novel attributes of SOD1 including the incorporation of a nonprotein amino acid, novel nonsynonymous SNPs as well as low abundant PTM’s (<1% occupancy) pertaining to oxidative stress. New materials for the characterization and quantification of novel SOD1 proteoforms will also be presented. Finally, computational modeling of these proteoforms suggests that they have a significant impact on the structure of SOD1 and the progression of motor neuron diseases.
Thursday @ 3:30 PM in Room 4 (Pasadena)
**LC-MS/MS-Based Drug Monitoring in Breast Milk: Understanding the Mechanism of Transport and Risk of Infant Exposure**

**Sarah Delaney** - *SickKids Hospital/University of Toronto* (sarah.delaney@sickkids.ca) -- *Young Investigator Grantee*

- The health benefits of breastfeeding are well described. It has been reported that ~70% of women take medication in the postpartum period; however, little is known about drug excretion into breast milk. Measuring drug concentrations in breast milk will help determine the extent of infant drug exposure and risk for toxicity. We developed two LC-MS/MS assays to measure concentrations of two first line medications, escitalopram and methotrexate, in milk. An animal model, population pharmacokinetics, and physiologically-based pharmacokinetic modeling were used to help provide insight into the risk of infant drug exposure via breast milk.

Thursday @ 3:50 PM in Room 4 (Pasadena)
**Validation of a LC-MS/MS Assay for the Simultaneous Quantitation of 5 Azole Antifungals and 1 Active Metabolite**

**Adam McShane** - *Cleveland Clinic* (mcshana@ccf.org) -- *Young Investigator Grantee*

- Invasive fungal infections are deadly and prevalent in certain high-risk patient populations: patients with hematological malignancies, the immunosuppressed, and the critically ill. Therapeutic drug monitoring of azole antifungal medications may potentially decrease morbidity and mortality in patients undergoing azole treatment. Therefore, a liquid chromatography tandem mass spectrometry method was developed and validated for 6 analytes: fluconazole, voriconazole, posaconazole, isavuconazole, itraconazole, and its active metabolite hydroxyitraconazole. Analytically, simple sample preparation is required, and the injection-to-injection window is less than 2 minutes. The implementation of this method will be a great asset to our infectious disease service.

Thursday @ 4:10 PM in Room 4 (Pasadena)
**Capillary Blood Collected on Volumetric Absorptive Micro Sampler for Therapeutic Drug Monitoring of Hydroxychloroquine**

**Ying Qu** - *Exagen Diagnostic, Inc.* (yqu@exagen.com)

- Volumetric absorptive microsampling (VAMS) blood collection method was successfully applied for the first time to the therapeutic drug monitoring of hydroxychloroquine (HCQ) in rheumatoid arthritis patients. LC-MS/MS workflow for analysis of VAMS sample was developed and validated. Drug concentrations of HCQ and its metabolites in capillary blood on VAMS were compared to those in venous blood. Our results established that VAMS is a simple and accurate sampling device that delivers the benefits of dried blood spots (DBS) sampling while overcoming the issues associated with hematocrit and homogeneity.
Thursday @ 3:30 PM in Room 5 (Sierra)

MALDI Imaging MS: Histology and Beyond

Kristina Schwamborn - Institute of Pathology (kschwamborn@tum.de)

Pathologists face many problems in their day to day practice trying to guide clinicians in finding the precise diagnosis and optimal treatment for a patient. Reliable markers for diagnostic purposes or markers that correlate with disease severity as well as prognosis and therapeutic response are needed. Since MALDI imaging mass spectrometry goes far beyond microscopy and enables the assessment of spatial molecular arrangements in tissue sections it is ideal for this endeavor. Moreover, it has the potential to revolutionize pathology.
Poster Presentations

Location: *Exhibit Hall (Oasis 3-4)*

Posters by Topic: p. 108
Posters by Number *with Abstract*: p. 123
Endocrinology

Implementation and Validation of a LC-MS Method for the Quantification of Total Homocysteine in Plasma, Serum, and Urine
Serim Kim - Green Cross Laboratories

Comparison of Immunoassay and LC-MS/MS for the Determination of Salivary Cortisol
Dajana Vuckovic - Concordia University

A Simple, Robust, and Rugged LC-MS/MS Method for Serum Methylmalonic Acid Measurements
Yungkang Lee - Berkshire Medical Center

LC-MS/MS Quantitative Analysis of the Vitamin K's and Metabolites in Serum
Alexander Cherkassky - Thermo Fisher Scientific, Inc

A Selective Method for Quantitation of Underivatized Methylmalonic Acid (MMA) in Plasma
Laura Snow - Phenomenex, Inc.

Single Assay Measurement of Aldosterone-to-Renin Ratio by UHPLC-MS/MS
Christopher Gilles - Shimadzu Corp., MSBU

Development and Validation of a LC-MS/MS Method for the Measurement of Aldosterone in Serum
Basia Hiley - NSW Health Pathology - SEALS

Value Assignment of Total Thyroxine and Total 3,3',5-Triiodothyronine for SRM 971, Hormones in Frozen Human Serum
Susan Tai - National Institute of Standards and Technology

A Sensitive LC-MS/MS Method for the Simultaneous Determination of 11β-MNT and 11β-MNTDC in Human Serum
Feng Bai - LA BioMed Research Institute

A Simple and Fast Solid Phase Extraction Method for Analysis of Eleven Steroids in Serum using LC-MS/MS
Xiaolei Xie - ThermoFisher Scientific

Clinical Utility of an Ultrasensitive Late Night Saliva Cortisol Assay by Tandem Mass Spectrometry
Lillian Sturmer - Stanford University School of Medicine

Improved Method for Analysis of Thyroid Hormone T3 and Pro-Hormone T4 in Serum
Slobodan Milasinovic - Orochem Technologies, Inc.
Endocrinology | Wednesday 5:00 PM Poster #17C
**LC-MS/MS Analysis of Angiotensin I for Assessment of Plasma Renin Activity in Clinical Research**
*Dominic Foley* - Waters Corporation

Endocrinology | Wednesday 5:00 PM Poster #35C
**Different Composition of Serum Bile Acids in Patients with Type 2 Diabetes Mellitus Compared with Normal Controls**
*Sang-Guk Lee* - Yonsei University College of Medicine

Endocrinology | Wednesday 5:00 PM Poster #40C
**Analysis of Estrogens and their Methoxy- and Hydroxy- Metabolites in Serum using the Sciex Triple Quad ™ 6500+ LC-MS/MS System**
*Michael Jarvis* - Sciex

Endocrinology | Wednesday 5:00 PM Poster #44C
**LC-MS/MS Quantitative Analysis of Endogenous Androgenic and Estrogenic Steroids in Serum**
*Susan DiPietro* - Thermo Fisher Scientific, Inc

Endocrinology | Wednesday 5:00 PM Poster #56C
**Development of a Novel, Fully Automated Robotic Method to Support LC-MS/MS Quantification of a Comprehensive Steroid Hormone Panel from Patient Serum**
*Daniel Kassel* - Scianalytical Strategies, Inc.

Metabolomics | Tuesday 4:00 PM Poster #31A
**Novel Metabolism Pathway in Pancreatic Cancer: Findings from Targeted Metabolomics Study**
*Feng Jin* - Baylor College of Medicine

Metabolomics | Tuesday 4:00 PM Poster #43A
**Comparison of Fresh and Frozen Human Breast Tissue for Analysis by Rapid Evaporative Mass Spectrometry**
*Hui-Yu Ho* - Imperial College London

Metabolomics | Tuesday 4:00 PM Poster #44A
**LC-MS/MS Quantitative Analysis of Polyunsaturated Fatty Acids Omega 3, 6, 7 and 9 in Serum**
*Rory Doyle* - Thermo Fisher Scientific

Metabolomics | Tuesday 4:00 PM Poster #51A
**Identification of Potential Biomarkers in Spontaneous Pre-Term Birth (sp-PTB) Delivery, using an Untargeted Metabolomics Approach Label-Free LC-DIA-MS Approach**
*Shirish Yakkundi* - INFANT Centre, Cork University Maternity Hospital

Metabolomics | Tuesday 4:00 PM Poster #54A
**Phosphatidylinositol Phosphates Profiling from Biological Samples and their Structural Characterization**
*Hyun Ju Yoo* - Asan Medical Center

Metabolomics | Tuesday 4:00 PM Poster #55A
**Profiling of Lipid Changes in Disease States: Searching for New Biomarkers**
*Sean Campbell* - University of Virginia

Metabolomics | Wednesday 9:45 AM Poster #01B
**LC-MS/MS Targeted Profiling of Methylamines**
*Antonis Myridakis* - Imperial College of London

Metabolomics | Wednesday 9:45 AM Poster #06B
**Gastric Fluid Metabolomics Towards Understanding Progression of Esophageal Adenocarcinoma**
*Khyati Pathak* - Translational Genomics Research Institute

Metabolomics | Wednesday 9:45 AM Poster #30B
**Metabolomics in Saliva for Cystic Fibrosis Screening**
*Cibele Esteves* - University of Campinas
Metabolomics | Wednesday 5:00 PM Poster #45C
Metabolomics Reveals Metabolic Changes in Age and Breastfeeding in Infancy
Meng Han Chiang - Chang Gung Memorial Hospital at Linkou, Taiwan

Metabolomics | Wednesday 5:00 PM Poster #49C
Importance of Measuring Amino Acid Concentrations on Tandem Mass Spectrometer in Follow-Up Treatment of Ornithinemia: A Case Report
Marija Zekušić - Univerity Hospital Centre Zagreb

Metabolomics | Thursday 10:00 AM Poster #57D
Lysophospholipidomics Profiling of Media from Platelet Concentrates during Storage
Jeongah Oh - National University of Singapore

Microbiology/Virology

Microbiology/Virology | Tuesday 4:00 PM Poster #23A
Discrimination of Bacillus cereus and Bacillus thuringiensis by Small Molecules Profiling using MALDI-TOF MS
Miyoung Ha - Nonghyup Food Research Institute

Microbiology/Virology | Tuesday 4:00 PM Poster #26A
Development of a UPLC-MS/MS Method to Monitor Second Line Tuberculosis Medications in Serum
Sankha (Bobby) Basu - Brigham and Women

Microbiology/Virology | Wednesday 5:00 PM Poster #38C
Rapid Evaporative Ionisation Mass Spectrometry (REIMS) as a Novel Approach to Pathogen Detection Directly from Clinical Diagnostic Samples
Adam Burke - Imperial College London

Microbiology/Virology | Thursday 10:00 AM Poster #15D
Therapeutic Drug Monitoring of Antibiotics in Plasma: A Novel, Seamlessly Automated Solution to Increase Traceability and Routine Throughput
Luigi Motti - Alifax

Microbiology/Virology | Thursday 10:00 AM Poster #20D
Direct Extractive Sampling from Microbial and Related Samples for Real-Time Characterization
Mariam ElNaggar - Prosolia

Proficiency, Regulations, Standards

Proficiency, Regulations, Standards | Tuesday 4:00 PM Poster #01A
Clinical LC-MS/MS – Electrospray Ionization Mass Spectrometry and Inter-Lab Data Variability: Root Causes
Eduard Rogatsky - Wadsworth Center

Proficiency, Regulations, Standards | Wednesday 9:45 AM Poster #29B
Odds Results of HbA1c with Normal Hemoglobin on using Five Routine Methods
Yeo-Min Yun - Konkuk University School of Medicine

Proteomics

Proteomics | Tuesday 4:00 PM Poster #06A
An Assay for Measurement of Kinase Activity from Biological Samples
Sandra Spencer - University of Washington

Proteomics | Tuesday 4:00 PM Poster #14A
Optimization of the Linear Quantification Range of an On-Line Trypsin Digestion Coupled LC-MS/MS Platform
Christopher Toth - Centers for Disease Control and Prevention

Proteomics | Tuesday 4:00 PM Poster #47A
Quantification of HMGB1, a “Difficult” Serum Protein and its Post Modifications, by Immunoaffinity Tandem Mass Spectrometry
Dawn Z Chen - Cedars Sinai Medical Center
Proteomics | Tuesday 4:00 PM Poster #52A
Absolute Quantification of Apolipoproteins in Serum and the Efficacy of Trypsin while Utilizing UPLC-IDMS
Michael Andrews - Centers for Disease Control and Prevention

Proteomics | Tuesday 4:00 PM Poster #56A
Effects of Ultracentrifugation on Plasma Lipoprotein Particle Size Distribution
Jeffrey Jones - Oak Ridge Institute for Science and Education

Proteomics | Wednesday 9:45 AM Poster #04B
Large-Scale Study of Glycated Hemoglobin Levels using Dried Blood Spots and MALDI-TOF Mass Spectrometry
Alan Rockwood - ARUP Laboratories

Proteomics | Wednesday 9:45 AM Poster #17B
Exosomal Protein Profiling Distinguishes Small Cell Lung Carcinoma from Non-Small Cell Lung Carcinoma Cells
Bernice Agana - The Ohio State University

Proteomics | Wednesday 9:45 AM Poster #21B
Affi-BAMS™: A MALDI TOF MS-Based Immunoaffinity Platform for Monitoring Total Protein and PTM Abundance Changes with a Capacity to Multiplex Over 1,000 Analytes
Vladislav Bergo - Adeptrix Corp

Proteomics | Wednesday 9:45 AM Poster #43B
Clinical Potential of Plasma Glutathione S-Transferases Quantification using Affinity Coupling with LC-MS/MS
Feng Xian - Beijing Institute of Genomics

Proteomics | Wednesday 9:45 AM Poster #48B
Quantitative Analysis of MET Tyrosine Kinase Receptor as Prognostic Biomarker of Survival in Gastroesophageal Adenocarcinoma using Clinical Mass Spectrometry
Wei-Li Liao - Nantomics, LLC

Proteomics | Wednesday 9:45 AM Poster #49B
Proteomic Analysis of Therapeutic Biomarkers in Decalcified Bone Metastases
Kerry Scott - NantOomics

Proteomics | Wednesday 9:45 AM Poster #50B
Development of a UPLC-MS/MS Method for Quantification of Hepcidin in Different Anemic Populations
Ellen Schmitz - Eindhoven University of Technology

Proteomics | Wednesday 9:45 AM Poster #51B
Optimizing Liquid Chromatography and Mass Spectrometer Performance using a Peptide Reference Material
Lisa Kilpatrick - National Institute of Standards and Technology

Proteomics | Wednesday 9:45 AM Poster #53B
Development of a Targeted Immuno-Enrichment and LC-MS/MS Proteomics Approach for the Therapeutic Monitoring of Adalimumab
Yifei Yang - University of Chicago

Proteomics | Wednesday 9:45 AM Poster #54B
Quantification of Infliximab in Human Serum by LC-MS/MS using a Full-Length Stable Isotope Labeled Internal Standard
Kevin Ray - MilliporeSigma

Proteomics | Wednesday 9:45 AM Poster #61B
Development of a Robust, Low Flow LC-MS/MS Method for Quantitation of Peptides
Kerry Hassell Forrest - ThermoFisher Scientific
Routine 50ul Serum/Plasma Analysis of Hepcidin-25 using LC-MS/MS: Measurement of Diurnal Variation

Benjamin Hunter - Murdoch University

QuiC - A Fast, Easy to use QC Monitor

Florian Marty - Biognosys

A Highly-Reproducible Automated Proteomics Sample Preparation Workflow

Qin Fu - Cedars Sinai Medical Center

RAIDR: Rapid Ammonium Hydroxide Isobutryic Acid O-Glycan Deglycosylation Reaction

Andrew Cho - Texas Tech University

Longitudinal Monitoring of Systemic Inflammation in Inflammatory Bowl Disease and Irritable Bowel Syndrome using DBS-SISCAPA-MRM

Leigh Anderson - SISCAPA Assay Technologies Inc.

Simplified Immunoaffinity and Protein Digestion: Analysis of the Low-Abundance Plasma Biomarker, in Less Than Four Hours

Suparna Mundodi - ThermoFisher

Certified Reference Materials for LC-MS/MS Quantitation of Thryoglobulin

Lauren Lytwak - MilliporeSigma

Dispersive-Pipette Extraction for Automated Enrichment of IGF-1 from Serum

Andrew Lee - IMCS, LLC

Developing Clinical Assays for Cancer Detection: Exosome Protein Signatures in Cell Culture and Serum

Alisa Li - Columbia University

Multiple Isotopes Improve Precision for Surrogate Peptide Quantitation Mass Spectrometry

Calvin Wiese - Wellspring Clinical Lab, Inc.

Enrichment and Characterization of Immunoglobulin Free Light Chains by MALDI-TOF Mass Spectrometry

Lusia Sepiashvili - Mayo Clinic

A Standardized Method to Produce a Digested Yeast Protein Extract Reference Material for Mass Spectrometry

Candice Johnson - National Institute for Standards and Technology

Assessment of Volatile Nitrosamine Exposure in the U.S. Population- NHANES 2013-14

Tiffany Seyler - CDC
A Sensitive LC-MS/MS Method for the Quantification of Urinary 8-iso-Prostaglandin F2α (8-iso-PGF2α) including Pediatric Reference Interval

Yi Xiao - Children's Hospital of Los Angeles

Intelligent Design of a Toxicology Panel: Let Chemistry be Your Guide

Zlatuse Clark - ARUP Laboratories

Development and Validation of a LC-MS/MS Method for the Quantification of Dapivirine in Human Breast Milk

Madhuri Manohar - Johns Hopkins University

Quantitative Antiepileptic Drug (AED) Panel by Ultra-Performance LC-MS/MS (UPLC-MS/MS)

Mariana Hristeva - University of Michigan Hospital and Health Systems

Single Generic Extraction Method for Analysis of More Than 100 Drugs in Urine by LDTD-MS/MS (Screening) and LC-MS/MS (Confirmation)

Pierre Picard - Phytronix Technologies inc.

Development and Validation of a High-Throughput Quantitative Method for Determination of Vitamin B6 in Serum and Plasma using LC-MS/MS

Boya Song - ARUP Laboratories

An Ultrafast, Dilute and Shoot-Flow Injection Tandem Mass Spectrometric (MRM) Method for Quantification of Phenobarbital and Ethyl-D-Glucuronide (EtG) in Urine

Ravali Alagandula - Cleveland State University

Isomer Interferences Observed during the Development of a 47-Analyte HRAM LC-MS/MS Method for Urine Drug Testing

Ana Grenier - Dominion Diagnostics

A Highly Sensitive Method for the Simultaneous UHPLC-MS/MS Analysis of Sedative Drugs and their Metabolites in Blood Plasma using HFIP as the Eluent Additive

Ruta Veigure - Institute of Chemistry, University of Tartu

Development of a High-Sensitivity LC-MS/MS Serotonin Assay for Assessing Platelet Function using a Minimal Amount of Whole Blood

Siaw Li Chan - University of Chicago

Validation of LC-MS/MS Method for the Determination of Triclocarban in Human Urine Samples

Qi Gavin - CDPH

Quantitation of the Antifungal Agents, Voriconazole and Posaconazole, by LC-MS/MS

Yun Wei - University of Alberta Hospital
Small Molecules / Tox | Tuesday 4:00 PM Poster #33A

**LC-MS/MS Method for Quantitative Analysis of Clozapine, its Major Metabolites (Norclozapine and Clozapine N-Oxide), and Trazodone in Serum or Plasma**

Stephen Merrigan - ARUP

Small Molecules / Tox | Tuesday 4:00 PM Poster #36A

**A Rapid and Robust Sample Preparation Method for Quantitation of Nicotine from Oral Fluid**

Shahana Huq - Phenomenex

Small Molecules / Tox | Tuesday 4:00 PM Poster #37A

**Urinary Analysis of an Olive Oil Metabolite using Liquid Chromatography Tandem Mass Spectrometry**

Jesse Seegmiller - University of Minnesota

Small Molecules / Tox | Tuesday 4:00 PM Poster #38A

**The Rise of Designer Benzodiazepines and their Quantitation in Biological Fluids by LC-MS/MS**

Stephanie Kumor - NMS Labs

Small Molecules / Tox | Tuesday 4:00 PM Poster #40A

**A Problem of Too Many Pills and the Arcane World of Dihydrocodeine**

Anna Miller - MedTox/LabCorp

Small Molecules / Tox | Tuesday 4:00 PM Poster #41A

**Quantification of 11-nor-9-Carboxy-THC in Hair using a Hybrid Triple Quadrupole Linear Ion Trap Mass Spectrometer**

Xiang He - SCIEX

Small Molecules / Tox | Tuesday 4:00 PM Poster #42A

**Development of a Simplified Extraction and HPLC-MS/MS Method for Plasma Propofol Quantitation**

Clayton Wilburn - Houston Methodist Hospital

Small Molecules / Tox | Tuesday 4:00 PM Poster #46A

**Novel Approaches for Methylphosphonic Acid Determination by Various LC-MS/MS Techniques**

Timur Baygildiev - Lomonosov Moscow State University

Small Molecules / Tox | Tuesday 4:00 PM Poster #48A

**Evaluation of the Analytical Parameters for Sensitive and Robust Quantitative Analysis of Catecholamines in Human Plasma with LC-MS for Research**

Mindy Gao - Thermo Scientific

Small Molecules / Tox | Tuesday 4:00 PM Poster #49A

**Assessing Metabolic Distribution of Ketamine, Norketamine, and Dehydronorketamine in Urine**

Erin C. Strickland - Ameritox, LLC

Small Molecules / Tox | Tuesday 4:00 PM Poster #57A

**Analysis of Novel Psychoactive Substances — Synthetic Cathinones and Kratom — using LC-MS/MS**

Oneka Cummings - Ameritox, LLC

Small Molecules / Tox | Tuesday 4:00 PM Poster #60A

**Direct Analysis of Morphine and its Metabolites with Related Compounds in Urine by LC-MS/MS**

Frances Carroll - Restek

Small Molecules / Tox | Tuesday 4:00 PM Poster #61A

**Evaluation of Generic LC-MS/MS-Based High Sensitivity, High-Throughput Quantitation Method of Oral Fluids Towards Therapeutic Drug Monitoring**

Manoj Tyagi - Captiva Lab, LLC

Small Molecules / Tox | Wednesday 9:45 AM Poster #02B

**Morphine Acetyltransferase Activity in Abalone B-Glucuronidase can Generate False Positive 6-Acetylmorphine (6-MAM) Results**

Martin Johnson - Assurance Scientific Laboratories
Fast Analysis of Low ng/dL Level Cortisol in Saliva by Tq LC-MS
Zicheng Yang - Bruker Daltonics

Chiral Separation of Amphetamines using LC-MS/MS
Kavinda De Silva - MTL

Quantitative LC-HRMS Analysis of Dried Blood Spots to Assess Adherence to Cardiovascular Pharmacotherapy
Graham Lawson - De Montfort University

LC-HRMS Analysis of 133 Patients’ Micro-Volume Blood Samples to Allow Clinical Assessment of Medication Adherence
Sangeeta Tanna - De Montfort University

The Determination of Arsenic, Mercury and Lead in Human Hair and Nail Samples by Inductively Coupled Plasma Mass Spectrometry (ICP-MS)
Patrick Day - Mayo Clinic

Total Urinary Cotinine Has a Higher Detection Rate when Compared to Serum Cotinine in Nonsmokers in the US Population: Data from NHANES 2013-2014
Ricky Alexander - Centers For Disease Control and Prevention

LC-MS/MS Analysis of Urinary Benzodiazepines and Z-Drugs via a Simplified, Mixed-Mode Sample Preparation Strategy
Jonathan Danaceau - Waters Corporation

Confirmation of 6-Monoacetylmorphine in Urine: Despite Expectations, Morphine is Often Only Present at Low or Undetectable Concentrations
Benjamin Beppler - TriCore Reference Laboratories

Dilute and Shoot FI-MS/MS for Quantification of Glycocholic Acid in Human Bile using Standard Addition Method
Raghavi Kakarla - Cleveland State University

High-Throughput UPLC-MS/MS Method for the Measurement of Urinary Aromatic Diamines as Biomarkers of Disocynate Exposure
Deepak Bhandari - Centers for Disease Control and Prevention

Approaching a Random Access Calibration Design for a Multi-Component Urine Drug Assay-It’s More Robust Than You Think!
Heather Hochrein - UC San Diego Health

Development of a Twelve Element Panel in Urine using an Automated 96-Well Based ICP-MS Workflow
Rebecca Parker - ARUP Institute for Clinical and Experimental Patho
Method Validation for the Simultaneous Quantification of Three Antiretroviral Drugs in Human Plasma using LC-MS/MS Over a 10,000 Fold Calibration Range

Craig Sykes - University of North Carolina-Chapel Hill

Overcoming Challenges for the Quantitation of Urinary Mono-Hydroxylated Polycyclic Aromatic Hydrocarbons by On-Line SPE-HPLC-Tandem Mass Spectrometry

Yuesong Wang - CDC

A Method for Improved LC-MS/MS Peak Integration by using Multiple Traces and Peak Modeling

John Gibbons - Sciex

Ultra-Fast Forensic Toxicological Screening and Quantitation under 3 Minutes with a QTOF LC-MS/MS System

Amol Kafle - SCIEX

Total Unbound Cysteine/Cystine Assay in Monkey Plasma using LC-MS/MS

Dale Schoener - Intertek Pharmaceutical Services

Quantification of Immunosuppressants in Human Whole Blood by Online SPE LC-MS/MS for Clinical Research

Claudio De Nardi - Thermo Fisher Scientific

LC-MS/MS Analysis of Phytocannabinoids and their Metabolites in Urine, Oral Fluid and Blood

Sherry Gregory - Thermo Fisher Scientific

Screening Method for Methamphetamine and Amphetamine using DART® MS Analysis Followed by Chiral Confirmation for D-Methamphetamine

Emily Barrey - MilliporeSigma

Conversion of Drug Metabolites Due to Contaminants in Commercial β-Glucuronidase Products

Pongkwan (Nikki) Sitasuwan - IMCS

Automated High-Throughput Extraction of Serum Samples for 25-OH-Vitamin D2 and D3 Analysis by LC-MS/MS using DPX Tips with Hamilton Microlab NIMBUS96

William Brewer - DPX Technologies, LLC

Direct Injection of Antiretroviral Drugs in Highly Organic Protein-Precipitated Human Plasma by LC-MS/MS

Sharon Lupo - Restek

Method Optimisation for the Low Level Detection of Vitamin B7 from Human Serum using UPLC-MS/MS Analysis

Lee Williams - Biotage GB Limited

Improved Method for Barbiturates and THC Carboxylic Acid Panel in Urine

Xuejun Zang - Orochem Technologies Inc
Validation of Residual Platinum Detection in Serum and Plasma using a 96-Well Plate Method and Inductively Coupled Plasma-Mass Spectrometry

Kim Kalp - ARUP Laboratories

Comparing Traditional LC-MS/MS to Ultra-Fast SPE-MS/MS for Monitoring of Clobazam and its Active Metabolite N-desmethyl Clobazam (Norclobazam) in Serum

Michael Mbughuni - Mayo Clinic

Drugs of Abuse with Multivariate Intermolecular Properties Analyzed by Polymeric Mixed-Mode Cation Exchange

Dan Menasco - Biotage

Dried Blood Spot Testing for Nine Steroids using LC-MS/MS and Reference Interval Determination in the Korean Population

Hyung-Doo Park - Samsung Medical Center

Simultaneous Extraction of Catecholamine and Metanephrines from Urine Prior to Analysis using LC-MS/MS

Adam Senior - Biotage GB Limited

Repurposing Antibodies: Immunoaffinity Capture Mass Spectrometry for Endogenous Lipid Biomarker Analysis

Paul Kennedy - Cayman Chemical Company

Quantitative Analysis of THC and Related Cannabinoids in Multiple Matrices using a Solid Phase Extraction Sorbent with UPLC-MS/MS for Clinical Research

Kim Haynes - Waters Corporation

Determination of Arsenobetaine in Urine by Isotope Dilution HILIC-MS/MS

Holly VanMetre - Florida Department of Public Health

Germanium Isotopes as an Internal Standard for Clinical ICP-MS Analysis

Joshua Akin - UC San Diego Health

A Proposed Strategy for the Detection of Metabolic Disorders: High Resolution Screening with Reflex to Targeted Quantitation by Tandem Mass Spectrometry

Natalie Rasmussen - ARUP Institute for Clinical and Experimental Path

Automated Hydrolysis and Sample Preparation for the Analysis of 12 Opiates in Urine using the Thomson Extreme Filter Vials® by LC-MS/MS

Lisa Wanders - Thomson Instrument Company

Utilizing Automated Solid Phase Extraction Technologies to Facilitate High-Throughput Ambient Ionization-MS Analysis of Biological Samples

Brian Musselman - IonSense, Inc.
Small Molecules / Tox | Wednesday 5:00 PM Poster #60C
Analysis of Immunosuppressive Drugs from Whole Blood by LC-MS/MS
Ty Kahler - Restek

Small Molecules / Tox | Wednesday 5:00 PM Poster #61C
An Orthogonal Workflow for the Detection of Nicotine and Related Metabolites in Oral Fluid After Vaping Nicotine Free Labeled E-Liquids
Desmond Wichems, Ph.D. - PerkinElmer

Small Molecules / Tox | Wednesday 5:00 PM Poster #62C
Fully Automated Platform for Determination of Antiepileptic Drugs in Serum
Isabel Teresa Cabrura - Shimadzu Italia

Small Molecules / Tox | Thursday 10:00 AM Poster #02D
Evaluation of Three Beta-Glucuronidase Enzymes to Determine the Best Hydrolysis Conditions for Urine Samples in Clinical Toxicology and Pain Management
Stephanie Marin - Biotage

Small Molecules / Tox | Thursday 10:00 AM Poster #35D
A Rapid and Selective Determination of Steroids in Serum Matrix by LC-MS/MS
Evelyn McClure - SCIEX

Small Molecules / Tox | Thursday 10:00 AM Poster #38D
Drug Monitoring of Methotrexate in Rheumatic Diseases: Implementation by Clinical Mass Spectrometry Coupled with Volumetric Absorptive Microsampler
Thierry Dervieux - Exagen Diagnostics

Small Molecules / Tox | Thursday 10:00 AM Poster #44D
Direct Drug Analysis in Serum by Probe Electrospray Ionization/Tandem Mass Spectrometry and its Preliminary Application to a Real-Time Metabolism Study
Kei Zaitsu - Institute for Advanced Research, Nagoya University

Small Molecules / Tox | Thursday 10:00 AM Poster #48D
Development of Microflow LC-MS/MS Method for Vitamins and Steroids in Complex Matrix for Clinical Research
Edward Goucher - Thermo Fisher Scientific

Small Molecules / Tox | Thursday 10:00 AM Poster #52D
Hydrolysis Efficiency Evaluation of Novel Recombinant Limpet and E. coli β-Glucuronidase Enzymes
Jim Blasberg - MilliporeSigma

Small Molecules / Tox | Thursday 10:00 AM Poster #60D
LC-MS/MS Method Development Challenges for the Analysis of 43 Anxiety Medications and Metabolites
Megan Kent - Restek

Tissue Imaging & Analysis

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #18A
Brain Imaging of Down Syndrome Murine Model using DESI-MS
Vincen Wu - Imperial College London

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #19A
Application of Optimised Hierarchical Agglomerative Clustering for Peak Matching of Large High Resolution Clinical Mass Spectrometry Tissue Imaging Data
Nazanin Zounemat Kermani - Imperial College London

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #21A
Ambient Ionization Mass Spectrometry Imaging for Molecular Diagnosis of Endometriosis Lesions and Surgical Resection
Clara Feider - University of Texas at Austin
Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #25A
Desorption Electrospray Ionization Mass Spectrometry Imaging of Melanoma and Metastatic Melanoma in Lymph Node
Alena Bensussan - University of Texas at Austin

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #34A
Neuropeptide Analysis and Identification from Pituitary Gland using LESA-µLC-HDMSE
Lieke Lamont - Maastricht University

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #35A
Correlation of Metabolic Profiles by Desorption Electrospray Ionization Mass Spectrometry with Clinical Stage of Non-Medullary Thyroid Cancer
Elizabeth Alore - Baylor College of Medicine

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #50A
Discriminating Lipid and Metabolite Distribution from Mild Blast Traumatic Brain Injury using DESI and High Resolution Mass Spectrometry
Joseph H Kennedy - Prosolia

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #53A
Distinct Metabolite Profiles Acquired by DESI Mass Spectrometry Imaging Discriminate Between Tumor and Non-Neoplastic Tissue from Multiple Organs
Martin Kaufmann - Queen's University

Tissue Imaging & Analysis | Tuesday 4:00 PM Poster #58A
Tissue Imaging with Laser Assisted Rapid Evaporative Ionization Mass Spectrometry (LA-REIMS)
Haixing Wang - Imperial College London

Tissue Imaging & Analysis | Wednesday 9:45 AM Poster #46B
Absolute Quantification of Pharmaceutical Compounds by MALDI using Multiple TOF/TOF Events in a Single Laser Shot
Boone Prentice - Vanderbilt University

Tissue Imaging & Analysis | Wednesday 5:00 PM Poster #19C
True Distribution of Isobaric N-Glycans Separated by Ion Mobility Directly from FFPE Colon Cancer Tissue by MALDI Imaging
Emmanuelle Claude - Waters Corporation

Tissue Imaging & Analysis | Thursday 10:00 AM Poster #18D
A Multimodal Mass Spectrometry Imaging Approach in Pre-Clinical Breast Cancer Research
Khalid Khan - Waters Corporation

Troubleshooting

Troubleshooting | Tuesday 4:00 PM Poster #11A
Retention Time Shifts with Large Drug Concentrations
Stacy Ordonio - Precision Diagnostics

Troubleshooting | Tuesday 4:00 PM Poster #13A
A Solution to Stable Isotope Labeled Internal Standard Degradation in an On-Line Trypsin Digestion Coupled to LC-MS/MS Platform
Jeffrey Jones - Oak Ridge Institute for Science and Education

Troubleshooting | Wednesday 5:00 PM Poster #11C
Tailing Peaks for a New Method Development on a Sub-2 µm Column
Sharon Lupo - Restek
Centroiding with Statistical Confidence: Mass and Abundance Error Bars from Peakinvestigator™ 2.0
Luke Schneider - Veritomyx, Inc.

Sponge Spray – Direct Ionisation from Mitra Microsampling Devices
Max Hecht - University of Tartu

Retention Time Flag in Phenobarbital
Richard Thomas - Precision Diagnostics

The Case of Decreasing Internal Standard Peak Area for Cyclosporin A
Katerina Sadilkova - Seattle Childrens

Troubleshooting with Grand Rounds

Good Practices for Successful High-Throughput LC-MS Bioanalysis
Joe Di Bussolo - Thermo Fisher Scientific

Systematic Troubleshooting of Assay Weaknesses during Method Development
Russell Grant - Laboratory Corporation of America

Failed Linearity during Validation Due to Analyte Interfering with its Own Internal Standard
Benjamin Beppler - TriCore Reference Laboratories

Matrix Effects and Ion Suppression in Estradiol LC-MS/MS Assay
Yifei Yang - University of Chicago

Various OTHER

Separation and Quantitation of Oxysterol, Secosterols, and Cholesterol Intermediates using LC-MS/MS
Evelyn Wang - Shimadzu Scientific Instruments

Measurement of 7-Alpha-Hydroxy-4-Cholesten-3-One in Serum using LC-MS/MS for the Screening of Bile Acid Malabsorption in IBS-D
Stacy Kenyon - Mayo Clinic

Sensitive and Reproducible LC-MS Quantification of C-Reactive Protein in Plasma
Laks Iyer - Waters

Contamination Potentials of Trace Elements in Serum Specimens Archived by the California Biobank Program
Key-Young Choe - California Department of Public Health

Evaluation of Stable Isotope-Labeled Compound for use as Internal Standard during Quantitation of Pyschosine from Dried Blood Spots
Patrick DeArmond - Nationwide Children's Hospital
Various OTHER | Wednesday 5:00 PM Poster #47C
Design and Development of GALNS Substrate for the Newborn Screening of MPS-IVA using Tandem Mass Spectrometry
Arun Babu Kumar - University of Washington

Various OTHER | Thursday 10:00 AM Poster #21D
Simultaneous LC-MS/MS Quantitation of 20 Antiepileptic Drugs in Human Serum
Vaughn Miller - Agilent Technologies

Various OTHER | Thursday 10:00 AM Poster #54D
Mass Spectrometric Identification of Biomarkers Associated with Fatal Neonatal Liver Disease in the Lipid-Storage Disease Cerebrotendinous xanthomatosis (CTX)
Kenneth Setchell - Cincinnati Children’s Hospital Medical Center

Various OTHER | Thursday 10:00 AM Poster #62D
Metal Oxide Laser Ionization (MOLI) MS for Identification of Bacteria using Intact Lipids for Profiling
Kent Voorhees - Colorado School of Mines
IONIZE AND ANALYZE

The Association for
Mass Spectrometry: Applications to the Clinical Lab
Posters by Number

Poster #01A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Proficiency, Regulations, Standards  
Clinical LC-MS/MS – Electrospray Ionization Mass Spectrometry and Inter-Lab Data Variability: Root Causes  
Eduard Rogatsky - Wadsworth Center (eduard.rogatsky@health.ny.gov)  
‣ In the past decade literature has addressed different methodological questions, related to data variability between immunoassays and LC/MS methods [during clinical assay standardization studies]. However, inter-lab proficiency testing variability, performed only on LC/MS instruments typically are not discussed. While a pipetting inaccuracy limit is typically within 3% interval, reported proficiency testing results produced by well validated LC/MS methods, could be exceeding 20% bias or ± 3σ consensus interval, even if the same method and same instrument brand were used in other laboratories. I present case studies demonstrating the impact of calibration curve design, instrument settings, LC and MS instrumental conditions and analyte source chemistry on test results of specimens, blanks and quality controls.

Poster #01B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Metabolomics  
LC-MS/MS Targeted Profiling of Methylamines  
Antonis Myridakis - Imperial College of London (a.myridakis@imperial.ac.uk) -- *Young Investigator Grantee*  
‣ Methylamines (trimethylamine, trimethylamine-N-oxide etc...) have been correlated with the development of non-alcoholic fatty liver disease, insulin resistance and cardiometabolic diseases. A combination of a broader chromatographic (UPLC-MS/MS) and a faster flow injection (FI-MS/MS) mass spectrometric methods are presented for their determination in human and mice biofluids and tissues. Isotopic dilution has been employed in order to ensure the high accuracy and specificity of the methods. The smaller metabolites are derivatised in order to achieve better mass spectrometric performance and the samples are cleaned up with protein precipitation.

Poster #01C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Proteomics  
Routine 50ul Serum/Plasma Analysis of Hepcidin-25 using LC-MS/MS: Measurement of Diurnal Variation  
Benjamin Hunter - Murdoch University (benjaminhunter9@gmail.com) -- *Young Investigator Grantee*  
‣ Hepcidin is a relatively recently discovered peptide with numerous isoforms. Hepcidin is a cysteine rich peptide, demonstrating similar antimicrobial properties and conformation with defensins, tachyplesins and protegrins. The largest isoform, hepcidin-25, is now known as the critical keystone regulator of iron metabolism in mammalian systems, whilst the function(s) of the smaller hepcidins -22 and -20 remain poorly understood. Here we report the quantitative measurement of hepcidin-25, together with the measurement of hepcidins -22 and -20 by UPLC-MS/MS using a Bruker EVOQ triple quadrupole mass spectrometer operating in positive ion electrospray mode. The developed methods allow interrogation of the diurnal variation of hepcidin-25, 22 and 20 between healthy controls and a hemochromatosis patient by both finger prick and venesection blood collection.

Poster #02A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Small Molecules / Tox  
Assessment of Volatile Nitrosamine Exposure in the U.S. Population- NHANES 2013-14  
Tiffany Seyler - CDC (tvh2@cdc.gov)  
‣ VNAs are established teratogens and carcinogens in animals and classified as probable and possible carcinogens in humans. Several large epidemiology studies associate VNA exposure with increased risk of insulin-resistance, diabetes, non-alcoholic steatohepatitis, and neurodegenerative disease such as Alzheimer’s disease. Therefore, VNA exposure assessment among the US population would be useful given the toxicity and high values of cancer indexes of VNAs. Our laboratory measured the levels of six VNAs in a representative sampling of the US population, using the NHANES 2013-14 (1/3 subset plus all adult smokers). The six VNAs were: NDMA, NMEA, NDEA, NPIP, NPYR, NMOR. This is the first time these compounds are monitored and reported in the US population.
Poster #02B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox

**Morphine Acetyltransferase Activity in Abalone B-Glucuronidase can Generate False Positive 6-Acetylmorphine (6-MAM) Results**

*Martin Johnson* - Assurance Scientific Laboratories (mjohnson@ncpmr.com)

- A conclusive indicator of heroin use is 6-acetylmorphine (6-MAM). The analysis of patient urine samples (using high pressure liquid chromatography mass spectrometry) identified a number of low level 6-MAM results in specimens with high morphine concentrations. Kinetic and heat inactivation studies demonstrated that 6-MAM was being produced enzymatically (morphine acetyltransferase activity) during deglucuronidation. Four sources of commercially available abalone b-glucuronidase were examined with similar results. Substituting sodium citrate instead of sodium acetate as the mediating buffer abrogated 6-MAM production. Collectively, these studies identify the source of potential false-positive 6-MAM results which can result in severe social, financial and legal ramifications.

Poster #02C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Proteomics

**QuiC - A Fast, Easy to use QC Monitor**

*Florian Marty* - Biognosys (florian.marty@biognosys.com)

- QuiC is a fast, easy to use QC monitor that generates QC readouts in real time from raw files of various vendors and workflows including MRM, PRM, DIA and DDA. LC-MS based proteomics has become the method of choice for identification and quantification of a high number of proteins in large sample sets. Robust and accurate quality controls (QC) during data acquisition are essential to ensure that high quality data with low systematic errors is collected. Biognosys has developed a QC tool that is simple, easy to use and interpretable by non-mass spec experts. The tool handles all proteomics workflows across different vendors.

Poster #02D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Small Molecules / Tox

**Evaluation of Three Beta-Glucuronidase Enzymes to Determine the Best Hydrolysis Conditions for Urine Samples in Clinical Toxicology and Pain Management**

*Stephanie Marin* - Biotage (stephanie.marin@biotage.com)

- Kura, Campbell, and IMCSzyme beta-glucuronidase enzymes were evaluated to determine conditions for optimal hydrolysis of drugs in urine samples. Four glucuronides (morphine-3-beta-D-glucuronide, norbuprenorphine glucuronide, oxazepam glucuronide, 11-nor-9-carboxy-THC glucuronide) were spiked into drug free urine. Samples were hydrolyzed at 55°C and 65°C for 30 minutes and 60 minutes. A spiked sample containing 56 “free” drugs and metabolites was also prepared and analyzed to evaluate potential suppression caused by the enzymes. The IMCSzyme and Kura enzymes provided the best overall hydrolysis of the four glucuronides. For the majority of the free drug compounds, the recoveries were comparable across all enzymes.

Poster #03A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox

**A Sensitive LC-MS/MS Method for the Quantification of Urinary 8-iso-Prostaglandin F2α (8-iso-PGF2α) including Pediatric Reference Interval**

*Yi Xiao* - Children’s Hospital of Los Angeles (yxiao@chla.usc.edu) -- *Young Investigator Grantee*

- Oxidative stress has been implicated in numerous diseases, including arthritis, atherosclerosis, Alzheimer’s disease, cancer, diabetes, and inflammation. 8-iso-PGF2α, a member of the F2 isoprostane family, has been well-accepted as a valuable biomarker for the assessment of oxidative stress. We developed and validated an ultra-sensitive LC-MS/MS assay for urinary 8-iso-PGF2α measurements in pediatric population (selectivity, linearity, LLOD, LLOQ, accuracy, precision, recovery, matrix effect, ion suppression, stability, etc.). Reference interval were established to be <0.5 ng 8-iso-PGF2α/mg creatinine from a group of pediatric population (2 months-18 years, n=136). The test will allow for accurate assessment of oxidative stress in pediatric population.
Poster #03B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
**Topic: Small Molecules / Tox**  
**Fast Analysis of Low ng/dL Level Cortisol in Saliva by Tq LC-MS**  
**Zicheng Yang** - Bruker Daltonics (zicheng.yang@bruker.com)  
- Saliva testing is one of the easiest, cost-effective and most accurate ways to measure the presence of free cortisol in human body. Collecting saliva sample is relatively non-invasive and easier. A rapid and sensitive method for the quantification of free cortisol was developed using Bruker TQ LC/MS system. Excellent sensitivity, linearity and dynamic range were obtained with a LOD of 1 ng/dL, r² > 0.99, and 3.5 orders of linear dynamic range with a total run cycle time of 5 minutes. The method with low ng/dL level detection with wide dynamic detection range is for suitable clinical research use.

Poster #03C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
**Topic: Small Molecules / Tox**  
**Method Optimisation for the Low Level Detection of Vitamin B7 from Human Serum using UPLC-MS/MS Analysis**  
**Lee Williams** - Biotage GB Limited (lee.williams@biotage.com)  
- This poster evaluates method development strategies to achieve low level detection of vitamin B7 in human serum. LC-MS/MS analysis was performed using a Waters ACQUITY UPLC I-Class and Xevo TQ-S triple quadrupole MS. Due to its carboxylic acid functionality both positive and negative ionization were evaluated using compatible LC mobile phase options. Various solid phase extraction chemistries demonstrated recoveries greater than 80 % with RSDs below 10 %. Post column infusion and phospholipid analysis was performed to gauge optimum cleanliness. Calibration curves from 25 to 1000 pg/mL demonstrated good linearity and r² values greater than 0.99 in human serum.

Poster #04A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
**Topic: Small Molecules / Tox**  
**Intelligent Design of a Toxicology Panel: Let Chemistry be Your Guide**  
**Zlatuse Clark** - ARUP Laboratories (zlatuse.d.clark@arulab.com)  
- Inclusion of specific analytes in a given LC-MS/MS assay in the clinical laboratory is often driven organically in concert with the addition of new drugs and their metabolites over time. We sought a complete redesign for a given list of urine toxicology tests to determine if chemistry, rather than ordering patterns or related metabolism, is a superior driver of panel design. Using a strategy for internal test design based on chromatographic retention time we were able to identify three separate groups of compounds (early, mid and late eluting), and develop a pilot 23-analyte “mid-eluter” panel method utilizing automated extraction, fast polarity switching, and scheduled MRM data acquisition. Using existing arrival rates, process times, and instrumentation capacity we were able to predict a potential 4.5-fold increase in overall capacity while reducing the turnaround time.

Poster #04B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
**Topic: Proteomics**  
**Large-Scale Study of Glycated Hemoglobin Levels using Dried Blood Spots and MALDI-TOF Mass Spectrometry**  
**Alan Rockwood** - ARUP Laboratories (alan.rockwood@arulab.com)  
- Presented here are the results from a large-scale study on the quantification of hemoglobin glycation from dried blood spots based on MALDI-TOF mass spectrometry. The method quantifies the extent of glycation from both the alpha and beta hemoglobin subunits. Certain hemoglobin variants like sickle cell hemoglobin are detected in the same analysis. Sample preparation requires mere dilution from whole blood extracted from a 1/8” hole-punch of a standard blood card. Statistics garnered from three analytical replicates and six technical replicates of each sample are used to demonstrate the precision and accuracy of the methodology.

Poster #04C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
**Topic: Small Molecules / Tox**  
**Improved Method for Barbiturates and THC Carboxylic Acid Panel in Urine**  
**Xuejun Zang** - Orochem Technologies Inc (june@orochem.com)  
- Many labs use dilute and shoot method for barbiturates and THC carboxylic acid panel, but their methods show high matrix effect and long term deterioration of the LC column and mass spectrometer. General reversed phase solid phase extraction method partially cleans up salts but shows lower recovery of THCA with high matrix effect in early elute of barbiturates. We tested several SPE stationary phases and procedures, and developed a quick and low cost sample preparation process and UPLC-MS/MS method with lower matrix effects and higher recovery.
Poster #05A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
Development and Validation of a LC-MS/MS Method for the Quantification of Dapivirine in Human Breast Milk
Madhuri Manohar - Johns Hopkins University (madhurimanohar9@gmail.com) -- *Young Investigator Grantee*

- Dapivirine (DPV) is a non-nucleoside reverse transcriptase inhibitor, currently being evaluated for HIV prevention as a topical microbicide. In order to completely characterize the compartmentalized pharmacokinetics of the drug, we developed a liquid chromatographic-tandem mass spectrometric (LC-MS/MS) method to quantify dapivirine in human breast milk, which is critical to understanding DPV pharmacokinetics in nursing mothers. The method is short (3 minutes), requires low sample volume (200 µL) and is highly sensitive, with a lower limit of quantification of 10 pg/mL. The method was validated in accordance with the FDA, Guidance for Industry: Bioanalytical Method Validation guidelines, and is currently being used to support NIH-funded clinical trials.

Poster #05B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Endocrinology
Development and Validation of a LC-MS/MS Method for the Measurement of Aldosterone in Serum
Basia Hiley - NSW Health Pathology - SEALS (barbara.hiley@health.nsw.gov.au) -- *Young Investigator Grantee*

- Measurement of aldosterone plays an important role in screening hypertensive patients for the presence of primary aldosteronism. Immunoassay methods are traditionally used for screening, however these are known to suffer from lack of specificity due to antibody cross-reactivity. We have developed and validated a sensitive and specific LC-MS/MS method for the quantitation of aldosterone in serum. The use of 96 well SLE plates enables the introduction of sample robotics for preparation of sample extracts to minimise manual labour and error. The negative bias seen in comparison to immunoassay results reflects the known problems with specificity associated with immunoassay.

Poster #05C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Small Molecules / Tox
Validation of Residual Platinum Detection in Serum and Plasma using a 96-Well Plate Method and Inductively Coupled Plasma-Mass Spectrometry
Kim Kalp - ARUP Laboratories (kimberly.j.kalp@aruplab.com)

- Platinum-based antineoplastic drugs are commonly used in cancer treatment. 50 µL of plasma or serum was mixed with 450µL of diluent containing internal standard in 96-well plates. The Teledyne MVX-7100 low volume autosampler was used to introduce sample into an Agilent 7900 ICP-MS with a total sample time of < 1.2 minutes. Plasma platinum concentrations in 571 patients had an average concentration of 90.2 ng/L, minimum concentration of < 5 ng/L, and maximum concentration of 2582.3 ng/L. Based on 96.3% average recovery of platinum in plasma samples, the method originally validated for serum proved acceptable for plasma specimens as well.

Poster #06A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Proteomics
An Assay for Measurement of Kinase Activity from Biological Samples
Sandra Spencer - University of Washington (sespence@uw.edu) -- *Young Investigator Grantee*

- Regulation of protein activity often occurs through post-translational modification, phosphorylation/dephosphorylation being the most common reversible modification and dysregulation of kinase activity has been implicated in a wide variety of human diseases including diabetes, Alzheimer’s, cardiovascular and neurological disease, and a variety of cancers. We have employed a kinase activity assay to measure the activity of two cancer-relevant kinases; Bruton’s tyrosine kinase and MAPKs. Enrichment of histidine tagged reporter proteins, phospholipase-γ 2 and HIF1-α, respectively, was used to decrease sample complexity prior to measurement of the fraction of phosphorylated reporter. Inhibition studies showed that the reporter proteins are specifically phosphorylated by the kinase of interest. This method is promising for application to whole blood or dried blood spot samples.
**Poster #06B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**

**Topic:** Metabolomics

**Gastric Fluid Metabolomics Towards Understanding Progression of Esophageal Adenocarcinoma**

*Khyati Pathak - Translational Genomics Research Institute (kpathak@tgen.org)*

- Esophageal adenocarcinoma (EA) is an aggressive disease with poor prognosis and survival rates. We employed a comprehensive targeted approach to query metabolic alterations in gastric fluid of 119 patients with gastroesophageal reflux disease (GERD), metaplasia, dysplasia and EA. Metabolite profiles distinguished dysplasia and EA from GERD and metaplasia with significant dysregulations in amino acid, lipid and energy metabolism.

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**Poster #06C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**

**Topic:** Small Molecules / Tox

**Comparing Traditional LC-MS/MS to Ultra-Fast SPE-MS/MS for Monitoring of Clobazam and its Active Metabolite N-desmethyl Clobazam (Norclobazam) in Serum**

*Michael Mbughuni - Mayo Clinic (mbughuni.michael@mayo.edu)*

- Clobazam is an anti-epileptic drug approved to treat seizures associated with Lennox-Gastaut Syndrome in patients who are >2 years old. Therapeutic monitoring of Clobazam and its metabolite Norclobazam is recommended. This study compared the performance of a traditional LC-MS/MS system and an Ultra-Fast SPE-MS/MS system for the quantitative determination of Clobazam and Norclobazam in serum. Performance characteristics including; turn-around time (TAT), accuracy, precision, carry-over, analytical sensitivity/specificity were compared. While acceptable methods were shown on both platforms based on accuracy, analytical sensitivity, and interferences. The data showed less imprecision and carry-over on the traditional LC-MS/MS, but shorter analysis time on the Ultra-Fast SPE-MS/MS system.

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**Poster #07A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic:** Endocrinology

**Implementation and Validation of a LC-MS Method for the Quantification of Total Homocysteine in Plasma, Serum, and Urine**

*Serim Kim - Green Cross Laboratories (srkim1982@gmail.com)*

- Increased total plasma or serum homocysteine is an important risk factor for cardiovascular disease. We implemented and validated a rapid LC-MS/MS method for quantifying total homocysteine based on the analysis of 100 mL of plasma, serum and urine with 10 ìmol/L homocysteine-d8 as an internal standard. Sample preparation is based upon a chemical reduction with dithiothreitol, followed by precipitation with a formic acid/ trifluoroacetic acid/ acetonitrile solution. Linearity, accuracy, precision, carry over, and inter-method comparison to immunoassay and HPLC were evaluated to validate the method. The LC-MS/MS homocysteine assay showed excellent performances and well correlated with the other methods.

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**Poster #07C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**

**Topic:** Small Molecules / Tox

**Drugs of Abuse with Multivariate Intermolecular Properties Analyzed by Polymeric Mixed-Mode Cation Exchange**

*Dan Menasco - Biotage (dan.menasco@biotage.com)*

- The need to provide larger and more comprehensive panels for drugs of abuse (DOA) for the detection of patient adherence to pain management programs and clinical monitoring necessitates the use of robust, high-throughput sample clean-up strategy. While many classes among DOA possess homologous intermolecular traits, such as functional amines, others remain chemically neutral and insensitive to pH adjustment or derivatization. Within this work, we demonstrate that the careful utilization of organic wash proportions allows for both carisoprodol and meprobamate, which lack functional groups that respond to ion-exchange mechanisms, can be isolated and successfully recovered within a panel of 44 DOA using mixed-mode cation-exchange solid phase extraction.
**Poster #08A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic: Small Molecules / Tox**

**Quantitative Antiepileptic Drug (AED) Panel by Ultra-Performance LC-MS/MS (UPLC-MS/MS)**

*Mariana Hristeva - University of Michigan Hospital and Health Systems (marianah@umich.edu)*

- Epilepsy, a disorder resulting in unpredictable and unprovoked recurrent seizures causes a variety of mental and physical comorbidities. It is one of the most common neurological conditions affecting more than 3 million people in the United States. Antiepileptic drug (AED) therapy and their therapeutic monitoring is a mainstay for optimal clinical management of epilepsy and to manage overdosed patients. We validated an UPLC-MS/MS assay using a simple sample preparation method amenable for quantitation of all commonly used AEDs and their relevant metabolites in serum including lamotrigine, oxcarbazepine, carbamazepine epoxide, carbamazepine, levetiracetam, topiramate and zonisamide.

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**Poster #08C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**

**Topic: Endocrinology**

**Improved Method for Analysis of Thyroid Hormone T3 and Pro-Hormone T4 in Serum**

*Slobodan Milasinovic - Orochem Technologies, Inc. (slobodan@orochem.com)*

- Thyroid hormones T3 and T4 are analyzed to understand the functionality of thyroid gland and how well the thyroid treatment is working. Recently, mass spectrometry analysis has become a routine method for testing of these hormones. However, there are several challenges, such as strong protein binding of T3 and T4, instability of T4 in matrix and during analysis, and matrix effect of phospholipids on mass spectrometry. We tested several types of sample preparation procedures, such as protein crash, phospholipids depletion, and solid phase extraction. The optimized method overall showed low matrix effect with good recovery.

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**Poster #11A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic: Troubleshooting**

**Retention Time Shifts with Large Drug Concentrations**

*Stacy Ordonio - Precision Diagnostics (stacy.ordonio@precisiondxlab.com)*

- We ran into a problem where the retention times for amphetamine-D4 and pregabalin were out of range. We traced the interference to large quantities of gabapentin, in many cases the estimated concentration was greater than 1,000,000 ng/ml. Dilution of two to fifty-fold resolved 42 of the 50 cases; however, in 8 of the cases we were unable to resolve the retention time shift. In these cases, the estimated pregabalin concentrations were below our lower limit of quantitation.

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**Poster #11B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**

**Topic: Troubleshooting with Grand Rounds**

**Good Practices for Successful High-Throughput LC-MS Bioanalysis**

*Joe Di Bussolo - Thermo Fisher Scientific (joe.dibussolo@thermofisher.com)*

- As LC-MS systems are designed to measure part-per-trillion amounts of analytes in biological samples, steps must be taken to prevent sample and system contamination and degradation to ensure reliable results. Precautions include dusting off reagent bottles before use, adding antimicrobial reagents to aqueous mobile phases, preventing contact of solvent lines and filters with contaminated surfaces, protecting columns from buildup of interfering sample components and avoiding residue buildup in MS ion sources. The application of these and other good practices to conventional, multi-dimensional and multi-channel LC-MS systems used for high-throughput bioanalysis are summarized in this presentation.

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**Poster #11C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**

**Topic: Troubleshooting**

**Tailing Peaks for a New Method Development on a Sub-2 µm Column**

*Sharon Lupo - Restek (sharon.lupo@restek.com)*

- Severe peak tailing was observed during method development for several cardiac drugs on a sub-2 µm column. Peak tailing persisted regardless of mobile phase composition, pH, or column phase used. When using a sub-2 µm particle column, it is imperative to minimize extra system volume in order to realize the benefits of a small particle. Recently, the HPV rotor and stator had been replaced on the LC autosampler. The entire sample flow path was re-plumbed to ensure all fittings were properly seated following the repair. The analysis was repeated under identical conditions and the peak shapes were drastically improved.
Poster #11D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Troubleshooting
Retention Time Flag in Phenobarbital
Richard Thomas - Precision Diagnostics (richard@precisiondxlab.com)
• We ran into a problem where retention time (RT) shift in Phenobarbital caused its retention time to exceed relative RT deviation limits of ±2.5%, and be flagged as out of range. Review indicated that RT deviation limits of ±2.5% for Phenobarbital were too narrow. Possible reason for RT shift is column overload from gabapentin in patient samples, or from using injection volume of 10 µL. The latter caused broadening and poor peak shape of Phenobarbital. Widening limits to ±6%, and using Phenobarbital-D5 as internal standard eliminated potential RT flag. Lowering injection volumes to 2 µL restored peak shape back to normal, and removed RT flag.

Poster #12C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Troubleshooting with Grand Rounds
Failed Linearity during Validation Due to Analyte Interfering with its Own Internal Standard
Benjamin Beppler - TriCore Reference Laboratories (benjamin.beppler@tricore.org)
• During validation of an updated assay for anti-rejection drugs, the initial linearity evaluation for Cyclosporine A failed badly, following a nearly perfect power law rather than the expected straight line. The problem was confirmed to be caused by naturally occurring isotopes interfering with the d4-cyclosporine used as the internal standard. Due to the structure of cyclosporine, the M+4 isotope composes approximately 1.7% of the sample, resulting in augmentation of the true d4-cyclosporine internal standard concentration and suppression of the true analyte concentration by up to 19%. The problem was eliminated by choosing an internal standard representing an M+11 mass difference.

Poster #12D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Troubleshooting
The Case of Decreasing Internal Standard Peak Area for Cyclosporin A
Katerina Sadilkova - Seattle Childrens (katerina.sadilkova@seattlechildrens.org)
• We observed that the second set of cyclosporine A quality controls at the end of the whole blood immunosuppressant run was failing repeatedly (high) due to decreased internal standard (I.S.) peak area. The same problem was detected on two separate LC-MS/MS systems, using two different types of LC columns on each platform. We considered the possibility for deuterium-hydrogen exchange in the source, since we recently switched to deuterated I.S. for cyclosporine A. After performing a series of tests overnight, the intensity improved. We implemented a series of water blanks to be injected with each run, a pre- and post-run column and source cleaning procedure, and weekly cleaning of the source and probe tip. Performance was monitored for one month, and the issue was resolved.

Poster #13A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Troubleshooting
A Solution to Stable Isotope Labeled Internal Standard Degradation in an On-Line Trypsin Digestion Coupled to LC-MS/MS Platform
Jeffrey Jones - Oak Ridge Institute for Science and Education (JJones13@cdc.gov) -- *Young Investigator Grantee*
• In order to achieve the workflow throughput required in our lab, we have moved to an automated online tryptic digestion system coupled to a LC-MS/MS platform. However, when we started to do calibrated, targeted proteomics in serum using stable isotope labeled peptides as internal standards, we observed that our calibration curves had a significant positive curvature for most analytes. We examined the data and found the IS count was decreasing as we moved to higher concentrations of serum. We were able to prevent the loss by heating the samples before adding the IS to deactivate any enzymes. However, this substantially slowed down our workflow, so we switched from adding the internal standard to the well to injecting it from a pretreatment vial into the sample loop alongside our samples, which solved the problem by preventing degradation of the IS by proteases in serum.
Poster #13B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Troubleshooting with Grand Rounds
Systematic Troubleshooting of Assay Weaknesses during Method Development
Russell Grant - Laboratory Corporation of America (Grantr@labcorp.com)
- Development of a Multi-analyte psychostimulant panel comprising Fluphenazine, Chlorpromazine, Risperidone, 9-OH Risperidone, Methylphenidate and Haloperidol was undertaken using TFC-LC-MS/MS. The assay development posed an initial challenge related to assay LLOQ (0.1ng/mL for Fluphenazine and 10ng/mL for Chlorpromazine) with a common measurement range (250 fold). Sequential observations were resolved including phospholipid removal (TFC loop injection and LC gradient modulation), transition detuning (and selection for equivalent response ranges), transition summing (least sensitive ionization/transmission efficiency analyte focus), improved imprecision/accuracy (echo transition summing, scheduled MRM and differential transition selection between IS and analyte) and determination of LC eluent stream multiplexing (staggered parallel LC compatibility).

Poster #13C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Troubleshooting
Centroiding with Statistical Confidence: Mass and Abundance Error Bars from Peakinvestigator™ 2.0
Luke Schneider - Veritomyx, Inc. (luke_schneider@targetdiscovery.com)
- PeakInvestigator™ (Veritomyx, Inc.) utilizes a new algorithm for fully-automated mass spectral centroiding and peak deconvolution. The latest version 2.0 provides statistically-valid mass and abundance error bars for every peak called. Presented are two examples of how this information can prove invaluable for downstream mass spectral analyses. The first example utilizes the mass precision error for building more accurate chromatographic peaks in an LC/MS experiment. The second shows how mass abundance precision can be used to discriminate between isotopic peaks that could not be discriminated by mass alone in peptide sequencing.

Poster #14A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Proteomics
Optimization of the Linear Quantification Range of an On-Line Trypsin Digestion Coupled LC-MS/MS Platform
Christopher Toth - Centers for Disease Control and Prevention (ctoth@cdc.gov)
- Tandem mass spectrometry (MS/MS) based proteomic workflows with the bottom-up approach require enzymatic digestion of proteins to peptide analytes, usually by trypsin. On-line coupling of trypsin digestion of proteins, using immobilized enzyme reactor (IMER), with liquid chromatography (LC) and MS/MS techniques is becoming a frequently used approach. However, finding IMER digestion conditions that allows quantitative analysis of proteins requires optimization of multiple interactive parameters; including digestion buffer flow rate, injection volume, sample dilution, and surfactant type/concentration. We present a design of experiment (DoE) approach to the optimization of an integrated IMER-LC-MS/MS platform. Through multivariate surface response modeling and consideration of diffusion controlled immobilized enzyme kinetics, the optimal set of digestion conditions were determined.

Poster #14B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
Quantitative LC-HRMS Analysis of Dried Blood Spots to Assess Adherence to Cardiovascular Pharmacotherapy
Graham Lawson - De Montfort University (glawson@dmu.ac.uk)
- The analysis of dried blood spot samples (DBS) by liquid chromatography – high resolution mass spectrometry (LC-HRMS) for assessing adherence to candidate cardiovascular therapeutic drugs was investigated. To evaluate the method 8 mm discs were punched from each DBS and extracted followed by subjecting to LC-HRMS analysis. Trials using the top 11 UK prescribed cardiovascular drugs are reported demonstrating the ability of the system to detect the target analytes during the 24 hour repeat prescription cycle. The system responded successfully to challenges by samples from volunteers of known adherence or receiving no medication. Examples of non-adherence to different medications were identified.
Poster #14C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Troubleshooting
**Sponge Spray – Direct Ionisation from Mitra Microsampling Devices**
*Max Hecht* - University of Tartu (hecht@ut.ee)
- Microsampling for the home application and clinical studies has evolved beyond dried blood spots. Neotyrex® Mitra microsampling devices are sponge like tips able to take up fixed amount (such as 10 µL or 20 µL) of sample. These devices have now been successfully subjected to direct ionisation of antimicrobials. A linear dependence of concentration vs signal in standard solution could be confirmed. The analysis of dried blood/plasma as well as immediate analysis of wet samples are planned. This combines the advantages of volumetric blood microsampling and direct analysis of the sample via ambient mass spectrometry.

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Poster #14D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Proteomics
**Multiple Isotopes Improve Precision for Surrogate Peptide Quantitation Mass Spectrometry**
*Calvin Wiese* - Wellspring Clinical Lab, Inc. (cwiese@sprynet.com)
- The precision of surrogate peptide quantitation mass spectrometry can be improved through the use of multiple isotopic internal standards. We present our analysis of the impact on precision measurement of C-reactive protein associated with increasing the number of isotopic internal standards compared to a single isotopic internal standard.

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Poster #15A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Endocrinology
**Comparison of Immunoassay and LC-MS/MS for the Determination of Salivary Cortisol**
*Dajana Vuckovic* - Concordia University (dajana.vuckovic@concordia.ca) -- *Young Investigator Grantee*
- The assessment of cortisol in saliva is useful in the screening of neuroendocrine dysregulation such as adrenal insufficiency or stress. The assessment of cortisol in saliva is routinely executed using immunoassay (ELISA) or liquid chromatography-tandem mass spectrometry (LC-MS/MS). The objective of this work was to compare the performance of these two methods for cortisol. We developed and validated LC-MS/MS method for the assessment of cortisol and cortisone in saliva with the limit of quantitation of 0.31 ng/mL. We compared this method to ELISA using patient samples, analytical and commercial ELISA standards. ELISA demonstrated negligible cross-reactivity to cortisone alone. Our study confirms that cortisol is over-estimated by ELISA in saliva and that this over-estimation is not due to cross-reactivity to cortisone.

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Poster #15B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
**LC-HRMS Analysis of 133 Patients’ Micro-Volume Blood Samples to Allow Clinical Assessment of Medication Adherence**
*Sangeeta Tanna* - De Montfort University (stanna@dmu.ac.uk)
- 133 DBS card/Mitra micro-volume blood samples were analysed by LC-HRMS to determine if therapeutic levels of the prescribed cardiovascular (CVD) drugs were present. This research focussed on the top 11 UK prescribed CVD drugs. Calibration samples, prepared from spiked human whole blood, were extracted and analysed by LC-HRMS. This method was validated and applied to volunteer and patient samples. The system successfully identified the prescribed drugs in volunteer’s samples who were known to be adherent. Non-detection of a prescribed drug indicated non-adherence to prescription: a situation identified for 12% of the volunteers and 36% of the patients.

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Poster #15C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Proteomics
**A Highly-Reproducible Automated Proteomics Sample Preparation Workflow**
*Qin Fu* - Cedars Sinai Medical Center (qin.fu@cshs.org)
- Sample preparation for proteomic analysis of complex biological samples by mass spectrometry is a tedious and time-consuming process with many steps where technical variations can be introduced and propagated. We describe an automated trypsin digestion workflow that yields uniformly-processed samples in less than 5 hours. Reproducible quantitation of hundreds of peptides from numerous proteins was seen across replicates, days, instruments, and laboratory sites, demonstrating the broad applicability of this approach.
Poster #15D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Microbiology/Virology
Therapeutic Drug Monitoring of Antibiotics in Plasma: A Novel, Seamlessly Automated Solution to Increase Traceability and Routine Throughput
Luigi Motti - Alifax (luigi.motti@alifax.com)
‣ Antimicrobials prescription tuning is more and more required by Clinicians to improve patients with severe infection outcome and to reduce the development of antimicrobial resistance. TDM must be used to optimize the efficacy and minimize the toxicity of a antimicrobial therapy by individual patient. UHPLC-MS/MS shows higher sensitivity and specificity compared to other technologies, however this approaches shows lack in standardization due complex sample preparation procedures that involves long time-consuming and errors risks due to the several required manual steps. The use of a novel ready to use kit for antibiotic applied to a sample prep sampler seamlessly connected to an UHPLC-MS/MS platform shows the impressive increase of the data quality and of the clinical sensitivity with an impressive TAT improvement.

Poster #16A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
Single Generic Extraction Method for Analysis of More Than 100 Drugs in Urine by LDTD-MS/MS (Screening) and LC-MS/MS (Confirmation)
Pierre Picard - Phytronix Technologies inc. (p.picard@phytronix.com)
‣ Toxicology laboratories are looking for new ways to improve their analysis by lowering operating costs and increasing throughput all the while maintaining quality data reporting. To increase the sample throughput, LDTD-MS/MS was used employing the generic sample extraction. Presumptive positive samples were transferred to LC-MS/MS for confirmation using the same sample extract. A Generic extraction method for all drug polarities and concurrent is used for presumptive and definitive testing method. More than 100 drugs in urine from different classes are analyzed simultaneously, with quantitative screening results obtained in less than 9 seconds per sample. Using the same extract LC-MS/MS analysis were performed for the confirmation analysis.

Poster #16B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
The Determination of Arsenic, Mercury and Lead in Human Hair and Nail Samples by Inductively Coupled Plasma Mass Spectrometry (ICP-MS)
Patrick Day - Mayo Clinic (day.patrick@mayo.edu)
‣ An inductively coupled plasma mass spectroscopy (ICP-MS) method was developed to quantify arsenic, mercury and lead in human hair and nail samples. Chronic exposure to arsenic, mercury, and lead continues to be a world-wide health problem and hair or nails provide a suitable matrix to monitor this exposure. Therefore a method to measure these elements in hair and/or nails with minimal weight (0.01 grams) was validated using ICP-MS technology with a Peltier cooler and kinetic energy discrimination analysis mode. The method had an analytical measurement range of 2-2000 ng/mL for arsenic, 1-2000 ng/mL for lead and 10-200 ng/mL for mercury, respectively. Accuracy, precision, recovery and reportable range studies were conducted to confirm sensitivity, specificity and reliability of the assay.

Poster #16C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Small Molecules / Tox
Dried Blood Spot Testing for Nine Steroids using LC-MS/MS and Reference Interval Determination in the Korean Population
Hyung-Doo Park - Samsung Medical Center (nayadoo@hanmail.net)
‣ We developed a novel screening method by LC-MS/MS (Agilent 1200 and Agilent 6490, Agilent Technologies) for nine metabolites in steroid pathway. Test items were as follows: cortisol, 17-hydroxyprogesterone, 11-deoxycortisol, 21-deoxycortisol, androstenedione, corticosterone, 11-deoxycorticosterone, testosterone, and progesterone. A total of 1,080 dried blood spots were used to determine reference intervals in the Korean population. The LLOQ were 0.5 ng/mL for 21-deoxycortisol and corticosterone, 1.0 ng/mL for cortisol, and 0.25 ng/mL for the other steroids, respectively. The reference intervals were comparable with the previous reports. As we know, this is the first time to measure testosterone and progesterone in dried blood spots from Korean newborns.
Development and Validation of a High-Throughput Quantitative Method for Determination of Vitamin B6 in Serum and Plasma using LC-MS/MS

Boya Song - ARUP Laboratories (songby914@gmail.com) -- *Young Investigator Grantee*

A quantitative HPLC-MS/MS method for Vitamin B6 (pyridoxal 5′-phosphate) analysis in serum/plasma was developed and validated for high-throughput testing to handle large sample volume. Vitamin B6 in serum/plasma was extracted by protein precipitation, followed by HPLC-MS/MS with spiked isotopic-labeled internal standard for quantitative analysis. Quantifier and qualifier MRM transitions were 248/150 and 248/94 (PLP), 251/153 and 251/97 (PLP-d3). Cycle time for PLP separation and measurement was 2.5 min. The assay eliminates the time-consuming derivatization step required for conventional HPLC-fluorescence. The short cycle time provides much higher throughput and the one-step sample preparation makes it highly compatible with automated operation.

Exosomal Protein Profiling Distinguishes Small Cell Lung Carcinoma from Non-Small Cell Lung Carcinoma Cells

Bernice Agana - The Ohio State University (agana.1@osu.edu) -- *Young Investigator Grantee*

Lung Cancer is the most prevalent cause of cancer-related deaths worldwide and the main classes are Small Cell Lung Carcinoma (SCLC) and Non-Small Cell Lung Carcinoma (NSCLC). Most patients are usually at the advanced stage at the time of diagnosis, and prognosis of the disease is poor. Here we explore label-free quantitative mass spectrometry to study the protein expression profiles of SCLC and NSCLC cell lines. Pathway analysis reveal very distinct protein signatures in exosomes isolated from these cell lines. This study provides evidence of the potential of exosome protein profiling as a multi-marker phenotyping tool for clinical diagnostics as well as for pathological correlations.

LC-MS/MS Analysis of Angiotensin I for Assessment of Plasma Renin Activity in Clinical Research

Dominic Foley - Waters Corporation (dominic_foley@waters.com)

We have developed a LC-MS/MS method for the measurement of angiotensin I as a marker of plasma renin activity (PRA) for clinical research activities involving biomarkers of hypertension. Following incubation of plasma samples for 3 hours at 37°C, an offline automated sample preparation method was performed using µElution Solid Phase Extraction (SPE) in 96-well plate format, reducing sample preparation time and optimizing analytical sensitivity. This offline automated method demonstrates good linearity, precision, and accuracy, while providing high sample throughput and sample tracking capabilities. For Research Use Only, Not for use in diagnostic procedures.

Brain Imaging of Down Syndrome Murine Model using DESI-MS

Vincen Wu - Imperial College London (v.wu15@imperial.ac.uk) -- *Young Investigator Grantee*

Down syndrome (DS) is one of the most common genetic birth defects, caused by an extra copy of chromosome 21. Despite the strong link between genotype and phenotype, little is known about DS metabolic alterations and brain metabolomic profile. Recent advances allowed to analyse metabolites distribution within the brain, using imaging techniques such as DESI-MS. For this study, brain sections from two groups of young adult mice (euploid vs. trisomic) were analysed by DESI-MS and compared using multivariate analysis, towards the profiling of altered metabolites.
Poster #18B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Small Molecules / Tox  
**Total Urinary Cotinine Has a Higher Detection Rate when Compared to Serum Cotinine in Nonsmokers in the US Population: Data from NHANES 2013-2014**  
*Ricky Alexander - Centers For Disease Control and Prevention (jra0@cdc.gov)*  
- We measured cotinine in 3145 matched pairs of serum and urine specimens from nonsmoker participants in the 2013-2014 National Health and Nutrition Examination Survey (NHANES) using isotope dilution LC/MS/MS. The detection rate in serum was 47% and in urine it was greater than 98%. Regression analysis showed a good correlation between urine and serum measurements (R-squared > 0.6) with urine cotinine concentrations about 7.5 times the concentration in serum. This is the first time urinary cotinine has been measured in the NHANES population.

Poster #18C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Small Molecules / Tox  
**Simultaneous Extraction of Catecholamine and Metanephrines from Urine Prior to Analysis using LC-MS/MS**  
*Adam Senior - Biotage GB Limited (adam.senior@biotage.com)*  
- This poster discusses the impact of optimization of various parts of the method development process to maximise assay performance while delivering a combined assay for the analysis of urine catecholamines and metanephrines. This included optimization of sample loading volume, pH and ionic content to allow for the efficient measurement of a wide range of analyte concentrations. LC-MS/MS analysis was performed using a Shimadzu Nexera UHPLC system coupled to an AB SCIEX 5500 triple quadrupole MS. SPE methods demonstrated average recoveries of over 80 % with RSDs below 10 %. Calibration curve ranges varied from analyte to analyte based on the approximate level expected in urine. This ranged from 0.1 to 25 ng/mL of epinephrine through to 2.5 to 625 ng/mL of dopamine. All demonstrated good linearity and r2 values of greater than 0.99 were returned for all analytes.

Poster #18D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM  
Topic: Tissue Imaging & Analysis  
**A Multimodal Mass Spectrometry Imaging Approach in Pre-Clinical Breast Cancer Research**  
*Khalid Khan - Waters Corporation (khalid_khan@waters.com)*  
- Breast cancer is a complex and heterogeneous disease that has distinct biological features and clinical characteristics. In the last few years, the understanding of breast cancer progression has greatly profited from research using genetically modified mouse models. MSI is an established analytical tool for bimolecular research which can accurately determine the spatial location of molecules in a tissue section. Initially, MALDI was used, but in the last few years, other techniques like DESI have been applied to tissue imaging. In this study, we present data comparing and contrasting MALDI and DESI ionisation techniques for MS imaging cancer tissue. In the studies described we have used normal and tumour samples from the polyoma middle T oncprotein (PyMT) mouse model of breast cancer which closely replicates the tumour progression found in the human disease.

Poster #19A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Tissue Imaging & Analysis  
**Application of Optimised Hierarchical Agglomerative Clustering for Peak Matching of Large High Resolution Clinical Mass Spectrometry Tissue Imaging Data**  
*Nazanin Zounemat Kermani - Imperial College London (n.zounemat-kermani13@imperial.ac.uk) -- *Young Investigator Grantee*  
- Mass spectrometry imaging is a technology that enables the acquisition of chemical profiles from surfaces in a spatially resolved manner. It allows the investigation of proteins, metabolites and lipid composition of tissues. Fast and efficient processing techniques to make MSI data comparable and manageable are necessary. Peak matching of MSI spectrum is of particular significance compared with other preprocessing steps. Here, application of hierarchical agglomerative clustering is extended from being applicable to a small set of low-resolution mass spectra to a large set of high-resolution MSI data. This technique is evaluated against clinical datasets from a large colorectal cancer study.
Poster #19C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Tissue Imaging & Analysis
True Distribution of Isobaric N-Glycans Separated by Ion Mobility Directly from FFPE Colon Cancer Tissue by MALDI Imaging
Emmanuelle Claude - Waters Corporation (emmanuelle_claude@waters.com)
* Research studies have reported extensive alterations in protein glycosylation patterns in cancer tissues, like in colon cancer which is the third most common cancer in the United States. However during these studies, tissues are homogenized and the spatial information showing the localization of the glycans is lost. Mass spectrometry imaging (MSI), can accurately determine the spatial location of molecules in a tissue section. Recently, methods have been developed to determine released N-Glycans directly from tissues. A major challenge in the analysis of N-glycans is the large number of isobaric glycans resulting from their complex structures with branched chains and multiple additions residues. Here we report the ability of ion mobility separation to differentiate isobaric N-glycans in a MALDI MSI workflow used for the analysis of human FFPE colon cancer tissue.

Poster #19D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Proteomics
Enrichment and Characterization of Immunoglobulin Free Light Chains by MALDI-TOF Mass Spectrometry
Lusia Sepiashvili - Mayo Clinic (Sepiashvili.Lusia@mayo.edu) -- *Young Investigator Grantee*
* The aim of this study is to fill a clinical need to directly detect serum monoclonal free light chains (FLCs) autonomously of the abnormal Kappa/Lambda FLC (K/L) ratio. For some patient subgroups (e.g. light chain multiple myeloma), this ratio is used as the sole indicator of a low abundance monoclonal plasma cell clone that is, in most cases, undetectable by other established lab methods including serum protein electrophoresis and immunofixation electrophoresis. Affinity enrichment of IgG, IgM, IgA, total K or L LCs, and Free K or L LCs was performed (n=129 sera) and purified specimens were subjected to MALDI-TOF MS. Analysis of resulting spectra demonstrated the potential of this method to (i) differentiate monoclonal free light chains from intact monoclonal immunoglobulins, and (ii) to detect low abundance monoclonal FLC clones.

Poster #20A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Toxicology
An Ultrafast, Dilute and Shoot-Flow Injection Tandem Mass Spectrometric (MRM) Method for Quantification of Phenobarbital and Ethyl-D-Glucuronide (EtG) in Urine
Ravali Alagandula - Cleveland State University (ravali5990@gmail.com) -- *Young Investigator Grantee*
* LC-MS/MS is the gold standard of urine drug testing (UDT), However, LC is time consuming, limiting the throughput of MS-based testing and increasing the cost. This is particularly a problem for quantification of drugs such as phenobarbital and EtG, ionized in the negative ESI mode, hence they are often analyzed in 3 separate LC-MS/MS runs. Hence we developed a robust and simple dilute and shoot-flow injection MS/MS method without LC separation to quantify phenobarbital and EtG by negative ESI MS/MS system operated on MRM mode with the stable isotope-labeled internal standards. The developed method was validated according to FDA guidelines and was found to be precise and reliable. Run time for one sample was 2 minutes, and the method can robustly quantify phenobarbital and EtG in urine without LC separation with dilution as sample preparation.

Poster #20B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Endocrinology
Value Assignment of Total Thyroxine and Total 3,3’,5-Triiodothyronine for SRM 971, Hormones in Frozen Human Serum
Susan Tai - National Institute of Standards and Technology (susan.tai@nist.gov)
* Thyroxine (T4) and 3,3’,5-Triiodothyronine (T3) are hormones produced by the thyroid gland to regulate many cellular functions including oxygen consumption, carbohydrate metabolism, and protein synthesis. Both elevated and decreased thyroid output of these hormones are relatively common conditions. Accurate and precise quantitative evaluations of T4 and T3 are important for reliable diagnosis and appropriate treatment of diseases. NIST has recently certified total T4 and total T3 in SRM 971 using isotope-dilution LC-MS/MS reference measurement procedures previously developed and recognized by JCTLM. This SRM can serve as an accuracy base for routine methods of total T4 and total T3 used in clinical laboratories.
Poster #20C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Small Molecules / Tox  
Repurposing Antibodies: Immunoaffinity Capture Mass Spectrometry for Endogenous Lipid Biomarker Analysis  
**Paul Kennedy** - *Cayman Chemical Company* (pkennedy@caymanchem.com)  
> Immunoaffinity based diagnostic assays are a well-established tool in the clinical laboratory however the promiscuous nature of antibodies and indirect measurement methods of the assays can make it difficult to ensure appropriate specificity. Mass Spectrometry offers an improvement in specificity over Immunoassays but sample enrichment is often required to meet sensitivity requirements. The benefits of combining antibody enrichment with mass spectrometry will be discussed and the development of antibody enrichment materials and methods for several clinically relevant lipid biomarkers will be described.

Poster #20D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM  
Topic: Microbiology/Virology  
Direct Extractive Sampling from Microbial and Related Samples for Real-Time Characterization  
**Mariam ElNaggar** - *Prosolia* (elnaggar@prosolia.com)  
> The flowprobe system facilitates continuous in situ microextractive sampling at atmospheric pressure and without additional extensive preparation for targeted profiling as well as arrayed analysis. Characterizations of surfaces bound growth by way of direct extraction, ionization, and identification of molecules of interest also is possible for cytological preparations in such a way that the samples are preserved and useful for subsequent orthogonal analysis. Presented here is an overview of some microbial and cytological applications of the sample introduction technique at the levels of basic and quantitative research, biomarker discovery, drug deposition analysis, and clinical use.

Poster #21A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Tissue Imaging & Analysis  
Ambient Ionization Mass Spectrometry Imaging for Molecular Diagnosis of Endometriosis Lesions and Surgical Resection  
**Clara Feider** - *University of Texas at Austin* (clfeider@utexas.edu) -- *Young Investigator Grantee*  
> Here, we apply multiple ambient ionization mass spectrometry imaging techniques towards the molecular analysis of endometriosis lesions and surrounding normal tissues which are often involved in endometriosis resection operations. By analyzing these tissues and obtaining lipid, metabolite, and protein abundance and distribution information, species that are indicative of endometriosis that could potentially be used as disease biomarkers for diagnosis and detection. The information gathered in this studied could be used to better understand the pathogenesis of endometriosis, but also could be useful for intra-surgical lesion border evaluation in order to aid surgeons during conservative endometriosis operations to prevent disease recurrence due to incomplete endometriosis resection.

Poster #21B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Proteomics  
Affi-BAMS™: A MALDI TOF MS-Based Immunoaffinity Platform for Monitoring Total Protein and PTM Abundance Changes with a Capacity to Multiplex Over 1,000 Analytes  
**Vladislav Bergo** - *Adeptrix Corp* (vbergo@adeptrix.com)  
> We have developed a novel analytical platform (Affi-BAMS™), which provides straightforward integration of multiplexed immunoaffinity enrichment with MALDI TOF MS. In this study, we utilized 20 commercially available western blot antibodies to assemble an Affi-BAMS™ bead assay for profiling selected sites within the mTOR signaling pathway. Both the total protein and phosphospecific antibodies achieved highly efficient enrichment of their corresponding targets from protease digested cell lysates. MALDI TOF MS analysis of proteolytic peptides was used to quantify abundance changes for the target proteins between normal and stress-induced cell culture conditions. The Affi-BAMS™ assay platform has been designed to easily accommodate at least 1,000 different protein targets for rapid screening of protein or peptide biomarkers.
Poster #21C in Exhibit Hall - attended for 1 hr on Wednesday starting at 5:00 PM

**Topic:** Various OTHER

**Sensitive and Reproducible LC-MS Quantification of C-Reactive Protein in Plasma**

*Laks Iyer - Waters* (laks_iyer@waters.com)

- The ability to detect and quantify plasma C-Reactive Protein (CRP) as a marker of inflammation is of high interest. For LC-MS protein quantification, enzymatic digestion and analysis of resulting peptides is often employed. These workflows are complex and laborious, with enzymatic digestion’s often taking 24 hours to achieve sensitive and accurate quantification. This work describes a total workflow that can be completed in <3 hours using commercially available digestion and peptide purification kits and generic protocols for the accurate quantification of CRP from only 35 µL of plasma. Quantification limits between 0.025-0.1 µg/mL were achieved with a dynamic range from 0.025-100 µg/mL.

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Poster #21D in Exhibit Hall - attended for 1 hr on Thursday starting at 10:00 AM

**Topic:** Various OTHER

**Simultaneous LC-MS/MS Quantitation of 20 Antiepileptic Drugs in Human Serum**

*Vaughn Miller - Agilent Technologies* (vaughn.miller@agilent.com)

- LC/MS/MS is particularly suited to the simultaneous analysis of multiple compounds. Further, it's detection range spans several orders of magnitude, which can enable concurrent quantification even when compounds occupy disparate concentration ranges. Here, an LC/MS/MS method was used to measure a large panel of antiepileptic drugs in human serum, rather than the small number often assayed historically due to wide concentration discrepancies. Samples were protein precipitated and diluted into water. Injection, separation of analytes, column cleaning, and column reequilibration were accomplished in <10 minutes. The analytical method was accurate (accuracies within 20% at the lowest concentration and 15% at higher concentrations), sensitive (LODs of low ng/mL), reproducible (CVs <15%, with most <10%), and robust. For Research Use Only. Not for use in diagnostic procedures.

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Poster #22A in Exhibit Hall - attended for 1 hr on Tuesday starting at 4:00 PM

**Topic:** Small Molecules / Tox

**Isomer Interferences Observed during the Development of a 47-Analyte HRAM LC-MS/MS Method for Urine Drug Testing**

*Ana Grenier - Dominion Diagnostics* (agrenier@dominiondiagnostics.com)

- In this work, we present potential opioid interferences discovered during the development of a 47-compound HRAM LC-MS/MS UDT method that could be present in most opioid assays, including those using tandem quadrupole and HRAM LC-MS/MS instrumentation, C18 and phenyl chromatographic stationary phases, and SPE or dilute-and-shoot sample preparation. These interferences were only observed when the method was challenged with patient specimens containing metabolites that are not typically monitored as analytes. This work highlights the importance of challenging a method with patient specimens early in the method development process.

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Poster #22B in Exhibit Hall - attended for 1 hr on Wednesday starting at 9:45 AM

**Topic:** Endocrinology

**A Sensitive LC-MS/MS Method for the Simultaneous Determination of 11β-MNT and 11β-MNTDC in Human Serum**

*Feng Bai - LA BioMed Research Institute* (fbai@labiomed.org)

- We have developed and validated a sensitive and accurate LC-MS/MS assay for the measurement of 11β-MNT and 11β-MNTDC for clinical research purposes in human serum. The two analytes (289.3/109.1 and 501.3/271.1) with their deuterated IS (295.2/133.0 and 507.2/277.2) were separated on a PFP column within 10 minutes with a gradient profile from 48% to 100% methanol at 0.5 mL/min. The calibration curve was linear over a concentration range of 0.5 to 100 ng/mL for 11β-MNT, and 5 to 2000 ng/mL for 11β-MNTDC. The intra-assay and inter-assay precision expressed as coefficient of variation (%CV) were less than 10. The accuracy were from 95.0% to 110.1%, respectively spanning different concentrations.
Quantitative Analysis of THC and Related Cannabinoids in Multiple Matrices using a Solid Phase Extraction Sorbent with UPLC-MS/MS for Clinical Research
Kim Haynes - Waters Corporation (kim_haynes@waters.com)

Cannabis continues to be a highly abused recreational drug. In addition, the increasing number of states legalizing it for medical use, combined with the trend towards legalization for recreational purposes means that analytical methods for the quantification of Δ9-tetrahydrocannabinol (THC), its metabolites and related cannabinoids continue to be necessary. Matrix effects can be a challenge and can vary significantly in different biological matrices. This work uses a novel reversed-phase solid phase extraction (SPE) sorbent, which has been developed to enable simpler and faster SPE protocols. 3 step load-wash-elute SPE protocols, eliminating conditioning and equilibration, were successfully employed to extract THC, OH-THC and COOH-THC from multiple matrices, including plasma, oral fluid, whole blood and urine, followed by direct analysis by UPLC/MS/MS.

MALDI-TOF MS is a rapid, accurate, and relatively inexpensive technique that is becoming increasingly important in microbiology diagnostics to conventional biochemical identification method. However, commercial database for MALDI-TOF MS pathogenic identification is based on ribosomal protein spectra which cannot distinguish closely related species in 16S rRNA sequences. In this study, we demonstrated the applicability of MALDI-TOF MS database for discrimination of closely related two species, food borne pathogen B. cereus and insect pathogen B. thuringiensis which have high degree of genetic homogeneity for food safety control. MALDI-TOF was employed to acquire mass spectra of small molecules from the reference strains that were verified by morphological, biochemical, and genetic identification. Then, we analyzed specific mass peaks to distinguish between B. cereus and B. thuringiensis.

Benzodiazepines are commonly prescribed drugs used for their sedative, anxiolytic, and hypnotic properties. So-called “Z-drugs” (zolpidem and zopiclone) are commonly used sleep aids that act in a similar manner to benzodiazepines. This method analyzes 18 benzodiazepine drugs and metabolites, along with zolpidem, zopiclone and N-desmethyl zopiclone. Strong cation exchange micro elution plates were used to rapidly extract these compounds from urine samples. All sample preparation steps, including enzymatic hydrolysis, were performed within the wells of μElution plates, eliminating sample transfer steps, and the extraction method is simplified by eliminating conditioning and equilibration. Quantitative results were accurate and precise for all analytes across the entire calibration range.

The potential for trace element contamination during serum collection was evaluated for serum separator tubes used for the California Biobank Program. Human serum was added to the tubes and monitored for 13 trace-element levels up to 26 days. The time series data suggest that the highest relative contamination was observed for Cr, Mn, Co, Sb, Pb, and U, followed by As, Sr, Mo, Hg and Tl. In contrast, contamination levels of Se and Cd appeared to be relatively low.
A Highly Sensitive Method for the Simultaneous UHPLC-MS/MS Analysis of Sedative Drugs and their Metabolites in Blood Plasma using HFIP as the Eluent Additive

Ruta Veigure - Institute of Chemistry, University of Tartu (rutaveigure@gmail.com) -- *Young Investigator Grantee*

In intensive care units, precise administration of sedatives and analgesics is crucial for appropriate pain control. This is very important in the case of pediatric patients, and dose-response relationships require study using pharmacokinetic-pharmacodynamic modelling. We developed and validated a rapid and simultaneous ultra-high performance liquid chromatographic-tandem mass spectrometric method for analysis of three sedative and analgesic agents: morphine, clonidine, midazolam, and their metabolites (morphine-3-glucuronide, morphine-6-glucuronide and 1’-hydroxymidazolam) in blood plasma at trace level concentrations. The analytes were chromatographically separated using C18 column with weak ion-pairing additive 1,1,1,3,3,3-hexafluoro-2-propanol and methanol. The lower limit of quantification for the method was 50 pg/mL for all analytes using only 100 μL of blood plasma.

Confirmation of 6-Monoacetylmorphine in Urine: Despite Expectations, Morphine is Often Only Present at Low or Undetectable Concentrations

Benjamin Beppler - TriCore Reference Laboratories (benjamin.beppler@tricore.org)

The ability to ascertain recent heroin use in patients is of critical concern to many clinicians. Due to its extremely short half-life, confirmatory urine testing generally targets the active metabolite 6-Monoacetylmorphine (6MAM). Historically, confirmatory testing of 6MAM was initiated or reported only if sufficient levels of morphine were present, as 6MAM rapidly metabolizes into morphine and its glucuronidated compounds. However, we have shown that over a quarter (26.5%) of our confirmed 6MAM samples contain morphine < 2000 ng/mL, with a majority (21.9% of all positives) containing morphine < 50 ng/mL. Workflow adjustments in many labs may be necessary to avoid 6MAM clinical false negatives.

Desorption Electrospray Ionization Mass Spectrometry Imaging of Melanoma and Metastatic Melanoma in Lymph Node

Alena Bensussan - University of Texas at Austin (alena.bensussan@utexas.edu) -- *Young Investigator Grantee*

Current diagnostic methods for melanoma rely on the histologic evaluation by pathologist to distinguish the morphological patterns of various melanoma subtypes in tissue samples. However, due to the large diversity of cell morphology, diagnoses of melanoma and metastatic melanoma in lymph nodes can be a challenge. Unfortunately, patients whose lymph nodes are positive for melanoma are then subjected to a second surgery for further re-excision. Thus, the availability of a diagnostic technique that could provide real time assessment of the presence of metastatic melanoma in lymph node tissues could significantly improve clinical management of patients. Here, we investigated the potential of desorption electrospray ionization mass spectrometry (DESI-MS) for molecular diagnosis of melanoma tissues.

Dilute and Shoot FI-MS/MS for Quantification of Glycocholic Acid in Human Bile using Standard Addition Method

Raghavi Kakarla - Cleveland State University (r.kakarla@vikes.csuohio.edu)

Cholangiocarcinoma, was associated with changes in the levels of conjugated bile-acids like Glycocholic acid in bile. We aimed at developing and validating a high-throughput, flow injection-MS/MS method to quantify GCA in human bile using an internal standard. A standard addition strategy was utilized to minimize the matrix effect, allowing for the flow injection of the diluted sample into ESI source without HPLC separation and thus reducing the run time and cost. Linearity was achieved in the range of 12.5 to 200 ng/mL and the method was also validated for matrix effect, inter and intra-day precision, LLOQ and stability.
Development of a UPLC-MS/MS Method to Monitor Second Line Tuberculosis Medications in Serum

Sankha (Bobby) Basu - Brigham and Women (sbasu@bwh.harvard.edu) -- *Young Investigator Grantee*

- Multi-drug resistant tuberculosis (MDR-TB) is a rapidly growing problem in many parts of the world. Unfortunately, the medications required to treat MDR-TB have significant pharmacokinetic variability due to poor absorption and drug-drug interactions. Here, we developed a UPLC-MS/MS method to measure eight anti-tuberculosis medications (capreomycin, kanamycin, pyrazinamide, cycloserine, PAS, prothionamide, levofloxacin and moxifloxacin) in human serum. Assay features included a total run time of four minutes, using 50 µL of serum. Serum samples from patients at a Partners in Health site in Lesotho were analyzed to monitor drug levels over several hours of treatment and demonstrated significant inter-patient variability.

High-Throughput UPLC-MS/MS Method for the Measurement of Urinary Aromatic Diamines as Biomarkers of Diisocyanate Exposure

Deepak Bhandari - Centers for Disease Control and Prevention (dbhandari@cdc.gov)

- Aromatic diisocyanates are toxic chemicals that react with polyols to form polyurethanes used extensively in the production of commercial and consumer products including mattresses, foam cushions, pillows, car seats, adhesives, paints, and coatings. In vivo, these aromatic diisocyanates are metabolized into their corresponding aromatic diamines, which can be measured in human urine. We report on the development and validation of an ultra-performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS) method for measuring five aromatic diamines—4,4’-methyleneedianiline (MDA), 2,4-toluenediamine (4TDA), 2,6-toluenediamine (6TDA), 1,5-naphthalenediamine (NDA), and p-phenylenediamine (PPDA)—in human urine.

Determination of Arsenobetaine in Urine by Isotope Dilution HILIC-MS/MS

Holly VanMetre - Florida Department of Public Health (holly.vanmetre@flhealth.gov)

- Arsenobetaine (AsB) is generally regarded as the non-toxic fraction of total arsenic in urine. Human exposure to AsB occurs predominately through dietary consumption of seafood or shellfish. Traditional LC-ICP-MS arsenic speciation methods that use ion-pairing reverse phase or anion-exchange chromatography do not retain AsB (pKa = 2.2), which exists as a zwitterion under most chromatographic pH conditions and is extremely polar. Described is a method that retains AsB by hydrophilic interaction liquid chromatography (HILIC), and detected by positive-polarity electrospray ionization tandem mass spectrometry (ESI-MS/MS). The method is simple, rapid, sensitive, and more selective than traditional LC-ICP-MS arsenic speciation methods.
Approaching a Random Access Calibration Design for a Multi-Component Urine Drug Assay - It's More Robust Than You Think!

Heather Hochrein - UC San Diego Health (hhochrein@ucsd.edu)

- Increased workload and conventional batched liquid chromatography-mass spectrometry (LC-MSMS) have led to increased turn-around times for urine drug confirmation testing. We analyzed our amphetamine production data retrospectively to define the stability of quantitative and qualitative elements and derive and validate an alternative calibration strategy with higher productivity. We chose to preserve extracting a 5-point calibrator set once a month with update from a cutoff calibrator extracted with every batch. Concentrations were within 20% of the conventional method, with no positive/negative discrepancies, and all qualitative elements met the acceptance criteria. Adaptation to a historical 5-point calibration with an in-batch extracted one-point calibrator will decrease turn-around time, increase productivity, and preserve method performance.

Germanium Isotopes as an Internal Standard for Clinical ICP-MS Analysis

Joshua Akin - UC San Diego Health (jakin@ucsd.edu)

- We evaluated three germanium isotopes as internal standards for arsenic whole blood ICP-MS analysis and identified challenges with using Ge70 and Ge72. Ge70 was subject to matrix effects and caused significant variability in calculated concentrations for whole blood samples but not for aqueous samples. The presence of iron oxide (FeO) at mass 72 poses a potential isobaric interference to Ge72 analysis in whole blood. We reproduced this phenomenon by spiking an iron standard into native whole blood samples, which exhibited a dose-response increase in m/z 72 proportional to the concentration of the iron spike. Iron in lysed whole blood samples could account for the formation of interfering oxides in the ionization process. When selecting an internal standard for ICP-MS analysis, it is important to take into consideration polyatomic interferences that may differ with matrix type.

Development of a High-Sensitivity LC-MS/MS Serotonin Assay for Assessing Platelet Function using a Minimal Amount of Whole Blood

Siaw Li Chan - University of Chicago (schan6@bsd.uchicago.edu) -- *Young Investigator Grantee*

- This study was undertaken to expand the study of platelet dense granule secretion. 200 µL of whole blood was incubated with deuterated serotonin (D45-HT) for uptake, then subjected to a variety of classic platelet stimuli. Platelet releasate is then used to assay D45-HT secretion. The use of exogenous, non-radioactive, isotopic serotonin has allowed us to construct a highly sensitive serotonin release assay to assess platelet function. This approach offers a means of overcoming serious limitations of current platelet function testing by expanding the availability of such testing both to pediatric patients and to adult or pediatric with decreased platelet counts.

Development of a Twelve Element Panel in Urine using an Automated 96-Well Based ICP-MS Workflow

Rebecca Parker - ARUP Institute for Clinical and Experimental Patho (rebecca.parker@arulab.com)

- Historically, our laboratory used three separate methods to measure twelve elements in urine, including arsenic, cadmium, cobalt, chromium, copper, mercury, manganese, nickel, lead, selenium, thallium, and zinc. This required a minimum of five minutes per patient, 300 microliters of patient sample, and balancing run times with laboratory test volumes. The reported method describes a simplified process, using a single assay for all analytes, two minutes per sample, and only 50 microliters of urine to achieve the same end results. Benefits include increased efficiency and standardization of the workflow while maintaining acceptable assay performance.
Poster #28C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Small Molecules / Tox  
**A Proposed Strategy for the Detection of Metabolic Disorders: High Resolution Screening with Reflex to Targeted Quantitation by Tandem Mass Spectrometry**  
**Natalie Rasmussen** - ARUP Institute for Clinical and Experimental Path (natalie.rasmussen@aruplab.com)  
Considering the complexity required for sample preparation, separation of analytes of interest from interferences and required detection levels with existing LC-MS/MS methods in amino acid analysis, we explored the possibility of using a LC-QTOF-MS system run in TOF mode as a higher throughput, simplified, qualitative screen for the detection of metabolic disorders such as Phenylketonuria (PKU) in human plasma. The results were analyzed using the Agilent Mass Hunter Qualitative Analysis and compared with an existing quantitative LC-MS/MS method. Acceptable agreement was found between the two methods. The screening technique enables easy method set up without precursor ion selection and fragmentation conditions. Using the QTOF platform as the screen provides retrospective interrogation of collected MS data which can be revisited without re-injection of sample.

Poster #29A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Small Molecules / Tox  
**Validation of LC-MS/MS Method for the Determination of Triclocarban in Human Urine Samples**  
**Qi Gavin** - CDPH (qi.gavin@cdph.ca.gov)  
Previously, we developed an LC-MS/MS method to analyze 13 environmental phenols in human urine specimen. In this study, we expanded our method to analyze triclocarban (TCC) along with previous analytes. Briefly, samples were processed using enzymatic de-conjugation of glucuronides, followed by solid phase extraction (SPE) on a C18 cartridge. Analytes were separated by reversed-phase HPLC, detected by atmospheric pressure chemical ionization (APCI) MS/MS (QTRAP5500) in negative ion mode, and quantified by isotope dilution method. The method proved to be accurate, precise and without obvious matrix effects. The limits of detection are in the low ng/mL range.

Poster #29B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Proficiency, Regulations, Standards  
**Odds Results of HbA1c with Normal Hemoglobin on using Five Routine Methods**  
**Yeo-Min Yun** - Konkuk University School of Medicine (ymyun@kuh.ac.kr)  
We evaluated the odds results of HbA1c with normal Hb showing flag signs on five routine HbA1c assays by comparing with the IFCC reference measurement procedure (RMP). A total of 59 normal Hb samples were showing warning flags or no results on five routine HbA1c assays; Sebia Capillaries 2 Flex Piercing, Roche Tina-quant HbA1c Gen. 2, and three HPLC HbA1c assays (Bio-Rad Variant II Turbo 2.0, ADAMS HA-8180, Tosoh G8 standard mode), and compared with those of IFCC RMP using LC-MS. Hb electrophoresis (EP) is used to identify variant Hb for all of samples. Unacceptable results of samples with Hb variants were 3.4% for Capillarys 2, 5.1% for Tina-quant, 3.4% for Variant II Turbo 2.0, 35.6% for G8 standard mode, and 0% for HA-8180. Laboratories should be aware of the limitation of their methods with respect to interference chemically modified derivatives found commonly.

Poster #29C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Proteomics  
**RAIDR: Rapid Ammonium Hydroxide Isobutryic Acid O-Glycan Deglycosylation Reaction**  
**Andrew Cho** - Texas Tech University (andrew.cho.0223@utexas.edu) -- *Young Investigator Grantee*  
The RAIDR (Rapid Ammonium hydroxide Isobutryic Acid O-glycan Deglycosylation Reaction) approach was developed as another technique to release O-linked glycans from glycoproteins. It was able to selectively release O-glycans from glycoproteins, and furthermore preserved proteins in the original sample which allows for further analysis of N-glycans and peptide sequencing. Moreover, this method is relatively easy and fast and can be performed with basic laboratory equipment. Also, it can be applied to different sample matrices. Released O-glycans are then analyzed using mass spectrometry.
**Poster #30A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic:** Endocrinology

**A Simple, Robust, and Rugged LC-MS/MS Method for Serum Methylmalonic Acid Measurements**

**Yungkang Lee - Berkshire Medical Center** (hugolee@alumni.usc.edu) -- *Young Investigator Grantee*

- Serum/plasma methylmalonic acid (MMA) is a superior marker for assessing patient vitamin B12 status. The authors here present a simple, fast, economic, and yet robust and rugged UPLC-MS/MS method that performed exceedingly well in its validation study as recommended by FDA and CLSI guidelines, and achieved baseline separation between MMA and succinic acid. Assay linearity is 50-1,200 nmol/L and assay throughput with all manual processing and a single UPLC-MS/MS instrument is 250 samples per 8-hour shift, of which 7 hours are for automated analytical runs.

**Poster #30B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**

**Topic:** Metabolomics

**Metabolomics in Saliva for Cystic Fibrosis Screening**

**Cibele Esteves - University of Campinas** (czesteves@gmail.com)

- Cystic fibrosis is an autosomal recessive disease whose detection may not always be readily performed, as many variables are involved in its accurate diagnosis. This contribution aims at establishing biomarkers for the early detection of cystic fibrosis most common variant, F508del, within a biochemical context that makes sense on the pathways that are the most affected by this condition. We used high-resolution mass spectrometry as the analytical main tool, associated with partial least squares discriminant analysis to provide statistical robustness to the obtained data, leading to 90% of specificity and 68% of sensitivity for cystic fibrosis screening.

**Poster #31A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic:** Metabolomics

**Novel Metabolism Pathway in Pancreatic Cancer: Findings from Targeted Metabolomics Study**

**Feng Jin - Baylor College of Medicine** (fjin@bcm.edu) -- *Young Investigator Grantee*

- LC-MS/MS was used to identify biomarker for pancreatic cancer from patients. 480 metabolites were profiled through our targeted approach from 30 cases and 30 controls. 28 metabolites were found to be significantly different in cases versus control. In addition, depletion of tryptophan along kynurenine pathway was associated with immunosuppression in tumor microenvironment in pancreatic cancer.

**Poster #31B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**

**Topic:** Small Molecules / Tox

**Method Validation for the Simultaneous Quantification of Three Antiretroviral Drugs in Human Plasma using LC-MS/MS Over a 10,000 Fold Calibration Range**

**Craig Sykes - University of North Carolina-Chapel Hill** (craig_sykes@unc.edu) -- *Young Investigator Grantee*

- A large calibration range is highly desirable in clinical bioanalysis but is limited to the linear range of the mass spectrometer. Here, we present a validated LC-MS/MS method for dolutegravir, maraviroc, and rilpivirine in human plasma over a 1-10,000ng/mL range. Highly sensitive transitions are used for the 1-200ng/mL range while less sensitive transitions are monitored for the 50-10,000ng/mL range. This approach avoids saturation at high concentrations and the overlap from 50-200ng/mL ensures no value falls outside of both curves. This expanded range assay is especially advantageous in dose escalating studies, adherence monitoring, and studies where concentrations span a large analytical range.

**Poster #32A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic:** Small Molecules / Tox

**Quantitation of the Antifungal Agents, Voriconazole and Posaconazole, by LC-MS/MS**

**Yun Wei - University of Alberta Hospital** (yun.wei@ahs.ca)

- Voriconazole (VORI) and posaconazole (POSA) are triazole antifungal agents used to treat patients with invasive fungal infections. There is an increased clinical need to determine serum drug concentrations to more effectively manage patients including those not responding adequately to therapy, those exhibiting signs and symptoms of toxicity, and when there is a concern for drug interactions. A simple and rapid quantitative method using protein precipitation as sample preparation technique was developed and validated for simultaneous measurement of VORI and POSA in serum samples submitted to the clinical laboratory using LC-MS/MS. The excellent correlation of patient comparison with a reference lab and successful performance of quality control and proficiency testing results demonstrated the presented method is accurate, sensitive and reliable.
Poster #32D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Proteomics

A Standardized Method to Produce a Digested Yeast Protein Extract Reference Material for Mass Spectrometry

Candice Johnson - National Institute for Standards and Technology (candice.johnson@nist.gov)

Currently, there are very few reference materials available that can be used to evaluate the performance of the various steps in proteomics workflows. The yeast proteome is a well-characterized complex mixture of proteins and has been used as a model proteome. RM 8313 Digested Yeast Protein Extract is being developed as a quality control material for mass spectrometry-based workflows used to identify tryptic digested peptides in complex protein samples. Preparation of a yeast based complex tryptic peptide material required optimization of factors such as yeast cell growth and protein expression, protein extraction, protein digestion, and finally LC-MS analysis of the material produced. By producing RM 8313 we intend to provide a digested yeast protein material to support measurements used to identify tryptic peptides in complex protein mixtures in mass spectrometry based workflows.

Poster #33A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox

LC-MS/MS Method for Quantitative Analysis of Clozapine, its Major Metabolites (Norclozapine and Clozapine N-Oxide), and Trazodone in Serum or Plasma

Stephen Merrigan - ARUP (stephen.d.merrigan@aruplab.com)

The LC-MS/MS method discussed is for the quantitative analysis of clozapine, norclozapine, clozapine N-oxide, and trazodone in serum or plasma. Clozapine is an atypical antipsychotic drug for the treatment of severely ill schizophrenic patients and also in schizophrenics with suicidal behavior. Trazodone is an antidepressant chemically unrelated to other known antidepressant agents such as tricyclic or tetracyclic and is also used to treat insomnia. The 2.5 minute analytical method shows good correlation to in-house and/or reference laboratory LC-MS/MS methods for clozapine, norclozapine, and trazodone. The second metabolite, clozapine N-oxide, was evaluated using blinded spikes samples. Results met all parameters for assay validation for all analytes.

Poster #34A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Tissue Imaging & Analysis

Neuropeptide Analysis and Identification from Pituitary Gland using LESA-µLC-HDMSE

Lieke Lamont - Maastricht University (l.lamont@maastrichtuniversity.nl)

Ion suppression is one of the major challenges within the field of clinical mass spectrometry imaging (MSI) due to the presence of salts and competing endogenous compounds in the tissue sample. This is a problem in traditional imaging techniques, e.g. MALDI and DESI. Liquid chromatography (LC) has proven itself to lower the occurrence of ion suppression significantly and, as a result, to improve the reproducibility. Additionally, LC also allows for isomeric separation, that cannot be obtained with traditional MALDI/DESI imaging. Here we present the combination of high spatial resolution sampling using a modified liquid extraction surface analysis (LESA) approach and LC-MS.

Poster #35A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Tissue Imaging & Analysis

Correlation of Metabolic Profiles by Desorption Electrospray Ionization Mass Spectrometry with Clinical Stage of Non-Medullary Thyroid Cancer

Elizabeth Alore - Baylor College of Medicine (alore@bcm.edu) -- *Young Investigator Grantee*

The clinical staging of non-medullary thyroid cancer yields information on patient prognosis as well as helps direct treatment and surgical options. Limitations in current diagnostic procedures limit availability of staging information preoperatively, often resulting in inadequate initial extent of resection being performed on index surgical approach. The use of desorption electrospray ionization mass spectrometry (DESI-MS) has been employed in the rapid, sensitive and specific diagnosis of tissue pathology based on unique molecular signatures. We hypothesize that DESI-MS imaging can be utilized preoperatively in non-medullary thyroid cancer to determine clinical stage in order to direct patient treatment and improve patient care.
Poster #35C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Endocrinology  
**Different Composition of Serum Bile Acids in Patients with Type 2 Diabetes Mellitus Compared with Normal Controls**  
*Sang-Guk Lee - Yonsei University College of Medicine (comforter6@yuhs.ac)*

- We recruited 72 T2DM patients, 97 patients with impaired fasting glucose (IFG) and 75 healthy control subjects and stored the residual serum samples. We measured fifteen kinds of BAs in serum, including colic acid (CA), chenodeoxycholic acid (CDCA), deoxycholic acid (DCA), ursodeoxycholic acid (UDCA), lithodeoxycholic acid (LCA), and their respective taurine and glycine conjugates in samples stored at -70°C. When we compared differences of each serum BA median concentrations according to the diabetic status (healthy control, IFG, and T2DM), GCDCA had P value of less than 0.05. Other glycine conjugated bile acids, GCA, GDCA, and GUDCA also showed decreasing trends with progression of insulin resistance. In addition, total glycine conjugated BAs had P values of 0.05 or smaller for the median differences among groups divided by diabetic status.

Poster #35D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM  
Topic: Small Molecules / Tox  
**A Rapid and Selective Determination of Steroids in Serum Matrix by LC-MS/MS**  
*Evelyn McClure - SCIEX (evelyn.mcclure@sciex.com)*

- Steroid researchers investigating inborn errors of metabolism are increasingly turning to LC-MS/MS as a tool due to the high selectivity and sensitivity of this technique. Despite the inherent selectivity of LC-MS/MS measurements, interferences from related steroid compounds present an on-going challenge. A rapid LC-MS/MS method was developed, enabling the chromatographic separation of a panel of steroids, using a Triple Quad™ 6500+ system for MS/MS detection. Separation of cortisol, 11-deoxycortisol, 21-deoxycortisol, 17-hydroxyprogesterone, and androstenedione was achieved in a run time of 4.5 minutes. Known interferences to the analytes were also chromatographically resolved and monitored. The LOQ for all analytes was 0.1 ng/mL, allowing for accurate quantitation of all present steroids in anonymized serum samples.

Poster #36A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Small Molecules / Tox  
**A Rapid and Robust Sample Preparation Method for Quantitation of Nicotine from Oral Fluid**  
*Shahana Huq - Phenomenex (ShahanaH@phenomenex.com)*

- Nicotine is the active ingredient in tobacco and related products that is highly addictive. Cotinine a metabolite of nicotine, and anabasine has been used as a tool for detection of tobacco exposure. Test development of drugs from Oral fluid specimen has been emerging as a preferred matrix over other fluids. In this communication, we present an efficient solid phase extraction and LC/MS/MS method for detection of nicotine and its metabolite from oral fluid samples using a polymeric sorbent Strata-X-C, in conjunction with Kinetex® 2.6u, EVO C18 column to obtain the best selectivity between the two isomeric compounds nicotine and anabasine.

Poster #36B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Small Molecules / Tox  
**Overcoming Challenges for the Quantitation of Urinary Mono-Hydroxylated Polycyclic Aromatic Hydrocarbons by On-Line SPE-HPLC-Tandem Mass Spectrometry**  
*Yuesong Wang - CDC (ywang6@cdc.gov)*

- Mono-hydroxylated polycyclic aromatic hydrocarbons (OH-PAHs) can be used as biomarkers of exposure to PAHs, ubiquitous environmental pollutants linked to a variety of adverse health effects. A fully automated on-line SPE-HPLC-MS/MS method was previously developed to quantify OH-PAHs in urine. However, certain analytical challenges (e.g., analyte binding to container surfaces, stability of quality control (QC) materials) remained to be addressed to ensure accurate and reproducible quantification. We evaluated the impact of several procedures to prepare analytical standards and QC materials, and optimized conditions to improve overall accuracy and precision.
Poster #37A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
Urinary Analysis of an Olive Oil Metabolite using Liquid Chromatography Tandem Mass Spectrometry
Jesse Seegmiller - University of Minnesota (jseegmil@umn.edu) -- *Young Investigator Grantee*
- Clinical studies have shown benefit for the Mediterranean diet supplemented with olive oil to decrease incidence of stroke and heart attack. One of the primary compounds of interest in olive oils is oleuropein. In an attempt to ensure patient compliance for olive oil consumption a metabolite of oleuropein, hydroxytyrosol, is monitored in urine. However, stability of the hydroxytyrosol compound is problematic in synthetic urine calibrators. This study focused on solutions to help stabilize this compound for quantitative analysis in liquid chromatography tandem mass spectrometry.

Poster #38A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
The Rise of Designer Benzodiazepines and their Quantitation in Biological Fluids by LC-MS/MS
Stephanie Kumor - NMS Labs (stephanie.kumor@nmslabs.com)
- Designer benzodiazepines are an emerging class of new psychoactive substances (NPS) used as an alternative to prescription-only benzodiazepines in the recreational drug world. They were first detected in 2012 and have been rapidly evolving since, creating a challenge for toxicology laboratories. Their structural similarities can trigger positive results for clinical benzodiazepine immunoassay testing, and certain designer benzodiazepines also metabolize to active prescription benzodiazepines. This report presents the development and validation of a quantitative LC-MS/MS method for the detection of designer benzodiazepines with analytical confirmation in toxicology casework.

Poster #38C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Microbiology/Virology
Rapid Evaporative Ionisation Mass Spectrometry (REIMS) as a Novel Approach to Pathogen Detection Directly from Clinical Diagnostic Samples
Adam Burke - Imperial College London (a.burke@imperial.ac.uk) -- *Young Investigator Grantee*
- Mass spectrometry is now an essential part of workflow of diagnostic microbiology laboratories, improving clinical outcomes and efficiency through reduced turnaround times. However, current commercial MS systems rely on pure microbial culture isolation, followed by subsequent sample preparation for MALDI-ToF, and suffer from poor identification accuracy when more than one microbial species is present. Rapid evaporative ionisation mass spectrometry (REIMS) has shown robust identification at the species level for a range of clinically important microorganisms. Here, we present work to identify species specific biomarkers for pathogen detection directly from clinical urine and faecal samples. Species specific biomarkers have begun to be identified in clinical samples, and work is underway to optimise the direct application of REIMS, removing the requirement for isolation and culturing.

Poster #38D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Small Molecules / Tox
Drug Monitoring of Methotrexate in Rheumatic Diseases: Implementation by Clinical Mass Spectrometry Coupled with Volumetric Absorptive Microsampler
Thierry Dervieux - Exagen Diagnostics (tdervieux@exagen.com)
- Therapeutic drug monitoring (TDM) is recognized as important for dosing optimization of methotrexate (MTX) therapy in autoimmune diseases. The purpose of the study was to develop a clinical mass spectrometry method for quantitative determination of MTX polyglutamates (MTXPGs) from blood collected on volumetric absorptive microsampler (VAMS). The LC-MS/MS method was validated in a population of patients with rheumatoid arthritis receiving MTX. MTXPGs levels determined from capillary blood were similar to those recovered from venous blood. A patient survey indicated that the majority of subjects would favor the collection of capillary blood on VAMS compared to blood collected by venipuncture.
Developing Clinical Assays for Cancer Detection: Exosome Protein Signatures in Cell Culture and Serum

Alisa Li - Columbia University (alisa.li221@gmail.com) -- *Young Investigator Grantee*

- Exosomes are small, cell-derived vesicles found in many human body fluids and contain RNA, DNA, and proteins. The protein content of exosomes is of particular interest because of their potential roles in cancer. Antibodies targeting exosome-related proteins were tested and confirmed to be functional when used on several cell lines and exosomes isolated using three different methods. We found that heat shock proteins and CD63 are the most promising markers for exosomal preparations. Knowledge of the exosomal protein content could lead to a future clinical assay which can detect cancer progression and/or metastasis, in a consistent and non-invasive manner.

A Problem of Too Many Pills and the Arcane World of Dihydrocodeine

Anna Miller - MedTox/LabCorp (milla20@labcorp.com)

- Dihydrocodeine holds analytical interest both as an active metabolite of hydrocodone and itself a pharmaceutical agent. The analysis of dihydrocodeine in urine is complicated by the presence of other administered opiates and overlapping convergent metabolism. Assays targeting a single compound or small group of compounds lack sufficient detail to distinguish dihydrocodeine from potential interfering species. To best discriminate administered dihydrocodeine from other opiates, a broad panel assay was employed collecting additional, supporting information which was utilized to definitively identify a presumptive peak as dihydrocodeine through the presence or absence of unique compounds and metabolites.

A Method for Improved LC-MS/MS Peak Integration by using Multiple Traces and Peak Modeling

John Gibbons - Sciex (john.gibbons@sciex.com)

- LC/MS/MS assays that require a higher level of certainty often monitor multiple fragment ions of the analyte precursor ion as separate precursor to product ion transitions. The ratio of the chromatographic peak areas for each transition having a common precursor relative to the same ratio observed in a standard provides greater confidence in the identity and purity of the integrated chromatographic peak. Since the response for each of the related transitions is derived from the same analyte precursor ion, the chromatographic features critical to proper peak integration such as retention time, peak shape, peak start and end should all be the same. By processing the fragment extracted ion chromatograms with a common precursor as a set, we are able to make use of the chromatographic relatedness to improve peak finding, peak integration consistency, and detection.

Analysis of Estrogens and their Methoxy- and Hydroxy- Metabolites in Serum using the Sciex Triple Quad™ 6500+ LC-MS/MS System

Michael Jarvis - Sciex (michael.jarvis@sciex.com)

- Increased exposure to estrogens is associated with increased risk of breast cancer. Researchers have postulated that certain estrogen metabolites are genotoxic, while others are anti-proliferative, and so there is a growing interest in developing accurate and sensitive methods to measure estrogens and their methoxy- and hydroxy- metabolites in serum. We have developed an LC-MS/MS method for the measurement of Estrone (E1), Estradiol (E2), Estriol (E3), 2-Methoxyestrone (2ME1), 2-Methoxyestradiol (2ME2), 16α-Hydroxyestrone (16αHE1), 4-Methoxyestrone (4ME1), and 4-Methoxyestradiol (4ME2) in serum. Chromatographic separation of the analytes was achieved in a run-time of 12 minutes. Using the SCIX Triple Quad™ 6500+ system, the Limit of Quantitation (LOQ) was determined to be 1.0 pg/mL for 4-Methoxyestrone and 4-Methoxyestradiol, and 0.5 pg/mL for the remaining analytes.
**Poster #41A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic:** Small Molecules / Tox

**Quantification of 11-nor-9-Carboxy-THC in Hair using a Hybrid Triple Quadrupole Linear Ion Trap Mass Spectrometer**

**Xiang He - SCIEX** (xiang.he@sciex.com)

- Hair has become an important matrix of choice for selected forensic testing applications. Hair testing allows the investigation of past exposure and history of drug use. In order to confirm drug presence with confidence, parent drugs and their metabolites can both be monitored in hair, despite some analytical challenges. For instance, the carboxy metabolite of tetrahydrocannabinol (THC-COOH) requires a unique mass spectrometric analysis (MS3) that can be reliably achievable on a hybrid triple quadrupole linear ion trap mass spectrometer. We will also discuss a single LC-MS/MS method approach for simultaneous identification and confirmation of a 22-compound panel in hair.

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**Poster #41B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**

**Topic:** Small Molecules / Tox

**Ultra-Fast Forensic Toxicological Screening and Quantitation under 3 Minutes with a QTOF LC-MS/MS System**

**Amol Kafle - SCIEX** (Amol.Kafle@sciex.com)

- Recently, there has been an increasing demand of using the high resolution and accurate mass LC-MS/MS systems for drug screening in forensic toxicological setting. More notably, a fast method that can detect an unlimited number of analytes with all necessary information, such as mass accuracy, retention time, and MS/MS spectral matching, is ideal. In this study, we present an ultra-fast forensic screening method using SCIEX X500R QTOF LC-MS/MS system. The LC runtime of this method is 2.5 min. Two different non-targeted data acquisition methods were compared, both of which yielded data that could be analyzed retrospectively.

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**Poster #41C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**

**Topic:** Proteomics

**Longitudinal Monitoring of Systemic Inflammation in Inflammatory Bowl Disease and Irritable Bowel Syndrome using DBS-SISCAPA-MRM**

**Leigh Anderson - SISCAPA Assay Technologies Inc.** (leighanderson@siscapa.com)

- Inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) collectively affect more than 46 million people in the US. While the symptoms for the two conditions are similar, the clinical manifestation in terms of the severity of inflammation in the bowel is widely different between the two. Inflammatory markers like CRP are routinely used to differentiate between the two conditions and in the case of IBD monitor progression of disease. However, infrequent sampling can be problematic and lead to sub-optimal management of symptoms. Here we report the development of a DBS-based panel that utilizes the SISCAPA workflow to precisely measure a set of 10 inflammatory protein biomarkers in IBD and IBS patients. The results indicate an aberrant inflammatory response in IBD but not in IBS.

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**Poster #42A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**

**Topic:** Small Molecules / Tox

**Development of a Simplified Extraction and HPLC-MS/MS Method for Plasma Propofol Quantitation**

**Clayton Wilburn - Houston Methodist Hospital** (crwilburn@houstonmethodist.org) -- *Young Investigator Grantee*

- A closed-loop propofol infusion device that adjusts dosing through monitoring plasma propofol levels to maintain appropriate depth of sedation has been developed and tested in rabbits. To validate the device’s quantitation accuracy, we developed a liquid chromatography-tandem mass spectrometry assay to serve as a gold-standard for measurement of plasma propofol. Sample preparation included extraction with simplified liquid extraction cartridges with addition of 0.5% tetrabutylammonium hydroxide in methanol to prevent loss of propofol. Assay was linear over the measuring range of 0.1-20.0 μg/mL. LOQ was 0.1 μg/mL with a CV <15% and LOD was 0.08 μg/mL. Recovery ranged from 90-120%.
**Poster #42B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**
**Topic: Small Molecules / Tox**

**Total Unbound Cysteine/Cystine Assay in Monkey Plasma using LC-MS/MS**

*Dale Schoener* - Intertek Pharmaceutical Services (dale.schoener@intertek.com)

*Unbound total cysteine/cystine is a pharmacodynamic biomarker for an engineered human enzyme therapeutic that degrades cysteine/cystine. Unbound cysteine refers to cysteine not bound to plasma proteins. A bioanalytical procedure was developed for the determination of unbound total cysteine/cystine in monkey plasma. Proteins are precipitated with a 40% trichloroacetic acid solution. After neutralization cystine is reduced to cysteine with dithiothreitol. Cysteine is subsequently derivatized with bromobimane. Standards are prepared using cystine and the internal standard is cystine-d6. The standard curve range is 0.5 to 100 µM as cysteine. Detection is by LC-MS/MS on an API-4000 triple quadrupole mass spectrometer in positive ion mode.*

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**Poster #43A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**
**Topic: Metabolomics**

**Comparison of Fresh and Frozen Human Breast Tissue for Analysis by Rapid Evaporative Mass Spectrometry**

*Hui-Yu Ho* - Imperial College London (h.ho15@imperial.ac.uk) -- *Young Investigator Grantee*

*Metabolomic analysis of unprocessed human tissue is possible using Rapid Evaporative Mass Spectrometry (REIMS). Whether the metabolomics features of fresh tissue and frozen tissue are comparative is unclear. We conducted this experiment to clarify the characters of both tissue storage types. Results demonstrate that fresh and frozen breast tissue can be used simultaneously for REIMS analysis in order to build a tissue type database for future intelligent knife model building.*

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**Poster #43B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**
**Topic: Proteomics**

**Clinical Potential of Plasma Glutathione S-Transferases Quantification using Affinity Coupling with LC-MS/MS**

*Feng Xian* - Beijing Institute of Genomics (xianfeng@big.ac.cn) -- *Young Investigator Grantee*

*GSTs, regarded as the indicators related with pathological changes, widely involve in many biological functions. The GST quantities are generally measured by ELISA or enzyme activity. Due to the high homology of GSTs, the traditional approaches could not perform globally quantitative evaluation towards individual members. Herein, we proposed a quantitative measurement to GSTs in human plasma through a combination of affinity chromatography and LC-MS/MS. With optimization of several parameters, now we can identify 8 GSTs using 200L human plasma and the method will be further used to evaluate the absolute quantities of GSTs in clinical samples by MRM.*

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**Poster #44A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**
**Topic: Metabolomics**

**LC-MS/MS Quantitative Analysis of Polyunsaturated Fatty Acids Omega 3, 6, 7 and 9 in Serum**

*Rory Doyle* - Thermo Fisher Scientific (rory.doyle@thermofisher.com)

*An LC-MS/MS analytical method was developed for the quantitation of Polyunsaturated Fatty Acids Omega 3, 6, 7 and 9. A simple acidified hexane extraction sample preparation technique was evaluated. A Thermo Fisher Endura tandem mass spectrometer in negative Electrospray mode with a Vanquish Horizon HPLC system was used for this analysis. 200 µL of serum with an Accucore Vanquish 100 x 2.1 mm, 1.5 µm using a water:acetonitrile mixture containing ammonium acetate achieved baseline chromatographic separation within 10 minutes. The limits of detection and quantitation were determined to range from 10 to 25 ng/ml with very good reproducibility observed.*
Poster #44B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
Quantification of Immunosuppressants in Human Whole Blood by Online SPE LC-MS/MS for Clinical Research
Claudio De Nardi - Thermo Fisher Scientific (claudio.denardi@thermofisher.com)

• An analytical method for clinical research for the quantification of Cyclosporin A, Everolimus, Sirolimus and Tacrolimus in human whole blood is reported. The method involves a simple protein precipitation step followed by online SPE using a Thermo Scientific™ Transcend™ II system; a Thermo Scientific™ TSQ Endura™ triple quadrupole mass spectrometer with heated electrospray ionization is used for detection by single reaction monitoring (SRM) using isotopically labeled internal standards for each analyte. Method performance was evaluated using the MS1100 ClinMass® LC-MS/MS Complete Kit for Immunosuppressants in Whole Blood, advanced – On-Line Analysis from RECIPE, to obtain limits of quantification, linearity ranges, accuracy and intra- and inter-assay precision for each analyte.

Poster #44C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Endocrinology
LC-MS/MS Quantitative Analysis of Endogenous Androgenic and Estrogenic Steroids in Serum
Susan DiPietro - Thermo Fisher Scientific, Inc (susan.dipietro@thermofisher.com)

• An LC-MS/MS analytical method was developed for the quantitation of endogenous Androgenic and Estrogenic Steroids in serum. Simple protein crash and liquid-liquid extraction sample preparation techniques with and without derivatization were evaluated. A Thermo Fisher Quantiva tandem mass spectrometer in positive and negative Electrospray mode with a Vanquish Horizon HPLC system was used. 500 µl of serum with an Accucore Vanquish 100 x 2.1 mm, 1.5 µm using water:methanol mixture containing formic acid achieved baseline chromatographic separation within 10 minutes. The limits of detection and quantitation were determined to the pg/ml levels with very good reproducibility observed for all compounds.

Poster #44D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Small Molecules / Tox
Direct Drug Analysis in Serum by Probe Electrospray Ionization/Tandem Mass Spectrometry and its Preliminary Application to a Real-Time Metabolism Study
Kei Zaitsu - Institute for Advanced Research, Nagoya University (kzaitsu@med.nagoya-u.ac.jp)

• This study demonstrated the application of PESI/MS/MS not only to direct drug analysis in serum, but also to in vivo real-time monitoring of cocaine metabolism in liver. PESI/MS/MS achieved high sensitive and ultra-fast analytical method for drugs in serum without sample preparation. Quantitativity of the method was validated, resulting in sufficient linearity as well as high accuracy and precision values. We successfully expanded the method to rapid drug screening for 161 compounds. We also succeeded in the real-time monitoring of cocaine metabolism in a living mouse liver by PESI/MS/MS through observing the increase in the enzymatic metabolite EME peak.

Poster #45A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Endocrinology
LC-MS/MS Quantitative Analysis of the Vitamin K's and Metabolites in Serum
Alexander Cherkassky - Thermo Fisher Scientific, Inc (alexander.cherkassky@thermofisher.com)

• An LC-MS/MS analytical method was developed for the quantitation of the Vitamin K’s and metabolites. Simple liquid-liquid hexane:ethyl acetate extraction and protein crash sample preparation technique were evaluated. A Thermo Fisher Endura tandem mass spectrometer in positive Electrospray mode with a Vanquish Horizon HPLC system was used for this analysis. 500 µl of serum with an Accucore PFP 100 x 2.1 mm, 2.6 µm using a water:methanol mixture containing 0.1% formic acid achieved baseline chromatographic separation within 6 minutes. The limits of detection and quantitation were determined to range initially from 10 to 25 pg/ml with very good reproducibility observed.
Poster #45B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Endocrinology
A Simple and Fast Solid Phase Extraction Method for Analysis of Eleven Steroids in Serum using LC-MS/MS
Xiaolei Xie - ThermoFisher Scientific (xiaolei.xie@thermofisher.com)
* Over the past few years there has been a growing interest to use liquid chromatography-tandem mass spectrometry (LC-MS/MS) to measure steroids in serum. We developed a simple and fast solid phase extraction (SPE) sample preparation method for an 11-steroid panel (11-deoxycortisol, 17-OH progesterone, aldosterone, androstenedione, corticosterone, cortisol, cortisone, estradiol, estrone, progesterone and testosterone) and evaluated the analytical performance on an LC-triple quadrupole MS/MS system. The entire SPE process takes less than 20 minutes, and no pre-conditioning, evaporation or reconstitution is required. The total LC run time is 7 min. Lower limit of quantitation (LOQ) ranges from 1 to 10 pg/mL. Recovery rate ranged from 42% to 95%.

Poster #45C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Metabolomics
Metabolomics Reveals Metabolic Changes in Age and Breastfeeding in Infancy
Meng Han Chiang - Chang Gung Memorial Hospital at Linkou, Taiwan (0914.neo@gmail.com) -- *Young Investigator Grantee*
* Metabolic processes of age relating rapid growth and effect of breastfeeding patterns on the change of metabolites in young infants are still lacking. The aim of this study was to investigate the metabolic changes of age as well as different breastfeeding patterns in healthy children during early infancy. In this study, 30 healthy children were recruited from a birth cohort followed up from birth to the age of 2 years. Spot urine samples were collected and urinary metabolites were analyzed by 1H-nuclear magnetic resonance spectroscopy at 6 months, and 1 and 2 years of age. Our results show that metabolic profiles associated with breastfeeding patterns appear to be significantly different at 6 months of age. Furthermore, urinary metabolites significantly change across age especially within the first year of life, indicating the importance of infant nutrition on rapid growth in early life.

Poster #46A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
Novel Approaches for Methylphosphonic Acid Determination by Various LC-MS/MS Techniques
Timur Baygildiev - Lomonosov Moscow State University (timurbaychem@gmail.com) -- *Young Investigator Grantee*
* Organophosphorus nerve agents are one of the most dangerous chemical weapons and methylphosphonic acid is the most stable hydrolysis product of them. Methylphosphonic acid determination is a direct proof of chemical weapons application. Here we describe novel analytical approaches, developed in our laboratory, that allows to determine methylphosphonic acid in different matrices with use of reversed phase, anion-exchange and hydrophilic interaction liquid chromatography with tandem mass spectrometric detection. Every approach is characterized by good metrological characteristics and in most cases limits of detection are lower than those described in the literature.

Poster #46B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Tissue Imaging & Analysis
Absolute Quantification of Pharmaceutical Compounds by MALDI using Multiple TOF/TOF Events in a Single Laser Shot
Boone Prentice - Vanderbilt University (boone.m.prentice@vanderbilt.edu) -- *Young Investigator Grantee*
* Matrix-assisted laser desorption/ionization imaging mass spectrometry (MALDI IMS) allows for the visualization of molecular distributions within tissue sections. While providing excellent molecular specificity and spatial information, absolute quantification by MALDI IMS remains challenging. Especially in the low molecular weight range, analysis is complicated by matrix interferences. Though tandem mass spectrometry (MS/MS) can be used to ensure chemical specificity and improve sensitivity, typical MALDI MS/MS modalities only scan for a single MS/MS event per laser shot. Herein, we describe TOF/TOF instrumentation that enables multiple fragmentation events to be performed in a single laser shot, allowing the intensity of the analyte to be referenced to the intensity of the internal standard in each laser shot while maintaining the benefits of MS/MS.
**Poster #46C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**
**Topic: Proteomics**

**Simplified Immunoaffinity and Protein Digestion: Analysis of the Low-Abundance Plasma Biomarker, in Less Than Four Hours**

_Suparna Mundodi_ - ThermoFisher (suparna.mundodi@thermofisher.com)

- LC-MS/MS analysis was used to allow single-run multiplexed quantification of multiple isoforms of Klotho, a transmembrane β-glucuronidase, which is an important biomarker in aging. As a proof of principal, rapid LC-MS/MS analysis of Klotho from murine plasma is demonstrated here using an integrated immunoaffinity/digestion platform, SMART Digest ImmunoAffinity (IA), enabling results in four hours. The use of an immunoaffinity step prior to the digestion is utilized to purify the target biomarker for increased sensitivity and is able to purify all the isoforms of the biomarker.

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**Poster #47A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**
**Topic: Proteomics**

**Quantification of HMGB1, a “Difficult” Serum Protein and its Post Modifications, by Immunoaffinity Tandem Mass Spectrometry**

_Dawn Z Chen_ - Cedars Sinai Medical Center (chenzh@cshs.org) -- *Young Investigator Grantee*

- Quantification of secreted tumor markers plays important roles in determining the treatment for cancer and Multiple reaction monitoring (MRM) mass spectrometry targeting on the measurement of the signature peptides to reflect the endogenously derived proteins is becoming more indispensable besides immunoassays in clinical applications. However, while MRM takes the advantages of monitoring multiple proteins to correlate to a unique biological state, MRM alone has potential technical challenges, especially for the proteins with low abundance in complex biological samples. To address the limitations, this study uses HMGB1 to present the strategies for MRM assays development for a “not an ideal” protein.

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**Poster #47B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**
**Topic: Small Molecules / Tox**

**LC-MS/MS Analysis of Phytocannabinoids and their Metabolites in Urine, Oral Fluid and Blood**

_Sherry Gregory_ - Thermo Fisher Scientific (Sherry.Gregory@thermofisher.com)

- An LC-MS/MS analytical method was developed for the quantitation of Phytocannabinoids and their metabolites. Simple sample preparation techniques including dilute and shoot, protein crash and liquid-liquid extraction were evaluated. A Thermo Fisher Endura tandem mass spectrometer in positive and negative Electrospray mode with a Vanquish Horizon HPLC system was used. 100 µl of each matrix using an Accucore C18, 100 x 2.1 mm, 2.6 µm with a water:acetonitrile mixture containing ammonium acetate achieved baseline chromatographic separation within 5 minutes. The limits of detection and quantitation were determined to range from 0.25 to 2.5 ng/ml with very good reproducibility observed.

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**Poster #47C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**
**Topic: Various OTHER**

**Design and Development of GALNS Substrate for the Newborn Screening of MPS-IVA using Tandem Mass Spectrometry**

_Arun Babu Kumar_ - University of Washington (arunk@uw.edu) -- *Young Investigator Grantee*

- Tandem mass spectrometry (MS/MS) has emerged as a most dependable tool for the early detection and diagnosis of lysosomal storage diseases (LSDs) through newborn screenings (NBS). Herein we report the design and development of a synthetic GALNS substrate for the NBS of MPS-IVA using tandem mass spectrometry. By mimicking the natural substrate of galactose 6-sulfatase (GALNS) and incorporating a bisamide unit that is hypothesized to readily protonate in the gas phase, we were able to develop a molecular probe that has a 200 fold improvement in ion counts (in MS/MS, compared to previous methods) for the diagnosis of MPS-IVA. This massive (almost 20000%) increase in ion counts will offer the NBS of MPS-IVA with better robustness and the ability to differentiate the newborns with pseudo-deficiency from MPS-IVA patients.
Poster #48A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
**Topic**: Small Molecules / Tox  
**Evaluation of the Analytical Parameters for Sensitive and Robust Quantitative Analysis of Catecholamines in Human Plasma with LC-MS for Research**  
*Mindy Gao* - Thermo Scientific (mindy.gao@thermofisher.com)  
‣ We evaluated an analytical method to support analysis of catecholamines (epinephrine, norepinephrine and dopamine) in human plasma for research. The method used SPE for sample preparation, a 9 min gradient chromatographic separation and a triple quadrupole mass spectrometer collecting two SRM for each analyte to calculate ion ratio. The limit of quantitation in donor plasma was 5 pg/mL for dopamine and 25 pg/mL for epinephrine and norepinephrine. Method precision obtained for RECIPETM QC samples was better than 4.6% and accuracy ranged from 86.6-119%. Ionization suppression was observed only for epinephrine and it was corrected by deuterated internal standard.

Poster #48B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
**Topic**: Proteomics  
**Quantitative Analysis of MET Tyrosine Kinase Receptor as Prognostic Biomarker of Survival in Gastroesophageal Adenocarcinoma using Clinical Mass Spectrometry**  
*Wei-Li Liao* - Nantomics, LLC (Wei-Li.Liao@nantomics.com)  
‣ Numerous signaling pathways are activated by interaction of HGF/MET. Aberrant MET activity has been ubiquitously reported across cancers; the underlying activating mechanism typically involves MET and/or HGF protein overexpression, MET gene amplification, or, rarely, domain-specific sequence mutations/translocations. We applied mass spectrometry-based targeted proteomic analysis to quantify MET protein expression in 282 FFPE GEC tissues. We detected a broad range of MET expression (<200-3246 amol/µg), with 51/282 (18.1%) having detectable levels. Patients with MET protein overexpression (≥400 amol/µg) (HR 1.76; 95% CI 1.06-2.90) was an independent negative prognostic biomarkers predicting worst overall survival in multivariate analyses. Moreover, the results suggest that proteomic analysis of MET may better direct treatment, and in particular MET-targeted therapies for GEC.

Poster #48C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
**Topic**: Small Molecules / Tox  
**Automated Hydrolysis and Sample Preparation for the Analysis of 12 Opiates in Urine using the Thomson Extreme Filter Vials® by LC-MS/MS**  
*Lisa Wanders* - Thomson Instrument Company (lisa.wanders@htslabs.com)  
‣ The use of hydrolysis in the analysis of opiates in urine has become standard practice in drug testing labs. Many laboratories currently use solid phase extraction or solid liquid extraction techniques in the sample preparation of urine for the analysis for opiates. This improved automated sample preparation method evaluates the robustness for the quantitative measurement of opiates in urine without the need for SPE/SLE. Thomson eXtreme Filter Vials provide a simple and efficient extraction technique that has demonstrated adequate analyte recovery, reduced matrix interferences and the elimination of solvent waste and other consumables.

Poster #48D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM  
**Topic**: Small Molecules / Tox  
**Development of Microflow LC-MS/MS Method for Vitamins and Steroids in Complex Matrix for Clinical Research**  
*Edward Goucher* - Thermo Fisher Scientific (ed.goucher@thermofisher.com)  
‣ Analyzing vitamins and steroids in complex matrices has shown to be a challenge. The ionization of these compounds is not very efficient and the chemical structure similarities prove to be difficult to separate chromatographically. This work investigates the ability to use UHPLC and triple quadrupole mass spectrometry to quantitate vitamins and steroids in a complex matrix for clinical research. For LC/MS analysis a flow rate of 5 µL/min was delivered from a Thermo Scientific™ UltiMate™ 3000 RSLC Nano configured with a capillary flow meter. The LC flow was directed to a Thermo Scientific™ TSQ Quantiva™ triple quadrupole mass spectrometer. Calibration curves of neat samples were performed on both forms of Vitamin D2 and D3, the metabolites 25-OH-Vitamin D, and 1,25-OH Vitamin D. The fifteen minute method gave baseline resolution of all isomers having great analytical performance.
Assessing Metabolic Distribution of Ketamine, Norketamine, and Dehydronorketamine in Urine

Erin C. Strickland - Ameritox, LLC (erin.strickland@ameritox.com)

- Ketamine is a dissociative anesthetic that has been used as an anesthetic induction agent, for veterinarian use, or illicit recreational purposes. However, recent interest in ketamine for the treatment of mental health conditions, such as PTSD and depression has reinvigorated interest in this drug. Previous, studies into the metabolites of ketamine had been inconclusive as to whether dehydronorketamine (DNK) is a real metabolite via dehydrogenation of norketamine or an artifact of analysis. Our data suggests the former and that DNK is the most prevalent in urine. In a set of 45 patient specimens 38 were positive for DNK, of which 17 were negative for ketamine and/or norketamine. Median concentrations for ketamine, norketamine, and DNK were found to be at 59, 79, and 123 ng/mL, respectively. This indicates that DNK should be included in the analysis of ketamine in urine specimens.

Proteomic Analysis of Therapeutic Biomarkers in Decalcified Bone Metastases

Kerry Scott - NantOmics (Kerry.Scott@nantomics.com)

- Decalcification of bone destroys protein and can preclude molecular analysis. We assessed the effects of acid decalcification on proteomic analysis of tumor samples. We also quantified protein biomarkers in decalcified bone metastases of cancer patients. Microdissected tumors were solubilized for selected reaction monitoring mass spectrometry. Non-bone tumor samples decalcified for 0, 1, 3, 12, and 24 hours yielded similar amounts of total protein (range: 19.2-24.1 µg) and of all 20 biomarkers detected. Bone metastases (N=21) expressed 19 of 27 proteins tested; bone tumors overexpressed EGFR and hENT1 (marker of gemcitabine therapy) in lung cancer patients and AR, hENT1, EGFR and TOPO1 in genital cancer patients. A breast cancer patient’s bone tumor overexpressed hENT1 (129 amol/µg) and HER2 (5750 amol/µg). Proteomic analysis of decalcified bone metastases may inform treatment decisions.

Importance of Measuring Amino Acid Concentrations on Tandem Mass Spectrometer in Follow-Up Treatment of Ornithinemia: A Case Report

Marija Zekušić - University Hospital Centre Zagreb (zekusicm@yahoo.com)

- Gyrate atrophy of the choroid and retina is a rare autosomal recessive disease that occurs due to the lack of the mitochondrial enzyme ornithine aminotransferase (OAT). Hyperornithinemia causes degeneration of the retina with the symptoms of disease like myopia, reduction in night vision and progressive resolution of vision loss. Our patient is an 8-year old girl with impaired vision and strabismus. As part of the metabolic check-up, analysis of amino acids in plasma revealed significantly increased concentration of ornithine (1039 µmol/L; normal: 20-155 µmol/L). Molecular genetic analysis detected the homozygous mutation in exon 7 of the OAT gene that has not been described as yet (c.868_870delCTT p.Leu290del). The success of low-protein diet and response to pyridoxine was monitored by measuring ornithine concentration for more than one year. Plasma ornithine levels decreased by 30-40%.

Discriminating Lipid and Metabolite Distribution from Mild Blast Traumatic Brain Injury using DESI and High Resolution Mass Spectrometry

Joseph H Kennedy - Prosolia (kennedy@prosolia.com)

- The determination of the distribution of lipids and metabolites in tissue samples has been utilized in understanding disease and biochemistry. DESI imaging provides objective molecular information in histological context without perturbing the integrating of the tissue. In this study, rats were subjected too concussive conditions, sacrificed 24 hours post injury, and the frontal lobes of the rats brain examined to determine differences in lipid profiles. Comparison of Blast versus Control (Sham) rodent brain indicated differences in lipid profile between left and right nodes. Phosphatidylserine (m/z 788.57) levels were depressed in the brain node where the blast was focused as compared to Sham. Differences in levels of some ceramides and diacylglycerols were also observed. Examples illustrating differences in rodent brains before and after blast will be presented.
Development of a UPLC-MS/MS Method for Quantification of Hepcidin in Different Anemic Populations

Ellen Schmitz - Eindhoven University of Technology (e.m.h.schmitz@tue.nl)  --  *Young Investigator Grantee*  

- Hepcidin is a peptide hormone that regulates iron homeostasis. Its diagnostic value is not established yet, because accurate quantification is challenging. We therefore developed a UPLC-MS/MS assay for hepcidin quantification. First, we synthesized hepcidin and its labeled internal standard containing two [13C9,15N]Phe. Calibrators and control samples were made by spiking rabbit serum. Solid phase extraction was performed before analysis. Recovery and matrix effects were 61% and -16%, respectively. Linearity of the UPLC-MS/MS assay was excellent (R^2 = 0.9999). Limits of detection (LOD) and quantification (LOQ) were 0.56 and 1.0 ng/mL, respectively. Within- and between-run imprecision were ≤5.6% and ≤5.7%. Also, median hepcidin levels of normal subjects, patients with iron deficiency anemia and anemia of chronic disease were determined (15, 5.4 and 53 ng/mL, respectively).

Identification of Potential Biomarkers in Spontaneous Pre-Term Birth (sp-PTB) Delivery, using an Untargeted Metabolomics Approach Label-Free LC-DIA-MS Approach

Shirish Yakkundi - INFANT Centre, Cork University Maternity Hospital (shirish.yakkundi@ucc.ie)  

- The BiomarkErs FOR Early Birth project is looking to exploit metabolomics for identification of a useful early pregnancy-screening test for sp-PTB. Birth before 37 weeks’ gestation is the single biggest cause of neonatal deaths in the world. Samples consisting of 20-week heparinised plasma from women whose pregnancies reached term gestations (Control) as compared to pregnancies subsequently complicated by sp-PTB prior to 34 weeks’ gestation (Case) were used. Samples were extracted and analysed along with pooled QCs using LC-MS on a hybrid quadrupole oa-TOF mass spectrometer. The label-free data were normalised processed and database searched using Progenesis QI.

Optimizing Liquid Chromatography and Mass Spectrometer Performance using a Peptide Reference Material

Lisa Kilpatrick - National Institute of Standards and Technology (lisa.kilpatrick@nist.gov)  

- High-throughput, bottom-up proteomics experiments typically involve identifying thousands of peptides eluted during a shallow gradient on a reverse phase column. Mass spectrometer performance for these types of analyses is typically optimized for speed with the aim of identifying the greatest number of unique peptides from the most proteins. Because of the complexity of this analysis process, there are many parameters that may be changed leading to variations in instrument performance. RM 8321 Peptide Mixture for Proteomics, a mixture of 440 peptides at different concentrations, is used in this study to evaluate and optimize reverse phase chromatography and MS parameters for Orbitrap Elite and QTOF mass spectrometers.

Absolute Quantification of Apolipoproteins in Serum and the Efficacy of Trypsin while Utilizing UPLC-IDMS

Michael Andrews - Centers for Disease Control and Prevention (wnc4@cdc.gov)  --  *Young Investigator Grantee*  

- Apolipoprotein A-1 (ApoA-1) and B-100 (ApoB-100) serum levels are two of the strongest measurable predictors for cardiovascular disease (CVD) risk. Our laboratory has developed a method to quantify ApoA-1 and ApoB-100 using liquid chromatography (UPLC) coupled isotope dilution mass spectrometry (IDMS) approach in a manner that is traceable to universal peptide and protein reference standards while avoiding time consuming reduction/alkylation steps of typical proteomic workflows. The method serum for trypsin digestion in the presence of acid labile detergent followed by UPLC-IDMS analysis using peptide calibrators. The method throughput is high enough for application in epidemiologic studies. The reproducibility of the method yields good coefficients of variation (CV) over the course of 21 days (2-3% CV intra-day and <7% CV inter-day).
Poster #52B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
**LC-MS/MS Analysis of Fentanyl and Related Analogs using Biocompatible Solid Phase Microextraction**

**David Bell** - MilliporeSigma (dave.bell@sial.com)

- The extraction mechanism for Biocompatible Solid Phase Micro Extraction (BioSPME) was used to detect fentanyl and some of its related analogs at low levels by LC/MS/MS. Improved sample preparation techniques, along with the use of labeled internal standards, allowed for reproducible and accurate quantitation of the compounds at low levels. Fast and adequate resolution was achieved on a biphenyl HPLC column with separation of all 9 compounds in less than three minutes. Advantages over current methodologies with respect to the time of preparation, chromatographic separation, interference removal and pre-concentration of the analytes to achieve low detection limits will be presented.

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Poster #52D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Small Molecules / Tox
**Hydrolysis Efficiency Evaluation of Novel Recombinant Limpet and E. coli β-Glucuronidase Enzymes**

**Jim Blasberg** - MilliporeSigma (jim.blasberg@sial.com)

- Urine drug testing has become an important tool to monitor compliance and detect the presence of illicit drugs. The primary metabolites of many such drugs are glucuronides, which offer analytical challenges due to their hydrophilic nature and poor ionization efficiencies. β-glucuronidase is often utilized for enzymatic hydrolysis of glucuronide metabolites back to their parent drug, simplifying the analytical workflow. Here we evaluate the hydrolysis efficiencies of two novel recombinant β-glucuronidase enzymes against a traditionally difficult opioid substrate, Codeine-6-β-D-glucuronide, and a less typical quaternary amine substrate, Amitriptyline-N-β-D-glucuronide, in comparison to a naturally-derived limpet enzyme. Additionally we evaluated esterase activity for the three enzymes by measuring conversion of 6-Monoacetylmorphine (6MAM) to Morphine.

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Poster #53A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Tissue Imaging & Analysis
**Distinct Metabolite Profiles Acquired by DESI Mass Spectrometry Imaging Discriminate Between Tumor and Non-Neoplastic Tissue from Multiple Organs**

**Martin Kaufmann** - Queen’s University (martin.kaufmann@queensu.ca) -- *Young Investigator Grantee*

- Intraoperative diagnosis is a challenging aspect of pathology practice that would benefit from DESI mass spectrometry imaging to supplement conventional techniques. We compared metabolite profiles in pathologically-validated cancers of the breast, liver, and kidney in comparison to adjacent non-neoplastic tissue using both DESI and hematoxylin and eosin staining. A range of ions selectively abundant in malignant (m/z 309, 331, 788) versus non-neoplastic (m/z 215, 277, 790) were able to differentiate between tumor and benign tissue in each case. Our results reveal the utility of DESI MSI in pathology practice and the potential to inform intraoperative, real-time mass spectrometry approaches.

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Poster #53B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Proteomics
**Development of a Targeted Immuno-Enrichment and LC-MS/MS Proteomics Approach for the Therapeutic Monitoring of Adalimumab**

**Yifei Yang** - University of Chicago (yifeiyang@uchicago.edu) -- *Young Investigator Grantee*

- The anti-tumor necrosis factor alpha therapeutic monoclonal antibodies, adalimumab (ADA) is widely used in the treatment of rheumatoid arthritis, and Crohn’s disease. In order to monitor their therapeutic effects, we aim to develop and validate a quantitative and targeted proteomic assay to determine the concentrations of ADA. Since the therapeutic effects of the drugs can be attenuated by anti-adalimumab autoantibodies generated by the patients’ immune system, our method is designed to quantify the bioavailable form of ADA in patient serum samples.
Poster #53C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Proteomics  
Certified Reference Materials for LC-MS/MS Quantitation of Thyroglobulin  
Lauren Lytwak - MilliporeSigma (lauren.lytwak@cerilliant.com)  
- Native and stable isotope labeled (SiL) Thyroglobulin solution standards have been prepared as Certified Reference Materials (CRM) for use as LC-MS/MS calibrators and internal standards. Both standards are prepared in the synthetic serum diluent SigMatrixTM. The certification process includes certification of the raw material protein content by amino acid analysis (AAA) and gravimetric dilution to the final certified concentration. The final solution is homogenized and packaged in flame-sealed ampoules. Analytical concentration verification is performed by LC-MS/MS assay comparison against an independently prepared 5-point calibration curve. Accelerated stability studies were conducted to support solution stability. Concentration of the solutions is traceable to NIST-SRM-2389a and IRMM BCR®-457.

Poster #54A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Metabolomics  
Phosphatidylinositol Phosphates Profiling from Biological Samples and their Structural Characterization  
Hyun Ju Yoo - Asan Medical Center (yoohyunju@amc.seoul.kr)  
- Phosphoinositides Phosphates (PtdInsPs) analysis using liquid chromatography-tandem mass spectrometry (LC-MS/MS) has remained challenging due to the strong hydrophilicity of these lipids. We developed a simple LC-MS/MS method for structural identification of sn-1 and sn-2 fatty acids of PtdInsPs and their relative quantitation. Using precursor ion scans of sn-1 MAG and neutral loss scans of headgroups, major PtdInsPs in cells and tissues were successfully identified with structural information of sn-1 and sn-2 fatty acids, and their relative amounts in different samples were compared. Signal enhancement using ammonium adduction helped more PtdInsPs observed.

Poster #54B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Proteomics  
Quantification of Infliximab in Human Serum by LC-MS/MS using a Full-Length Stable Isotope Labeled Internal Standard  
Kevin Ray - MilliporeSigma (kevin.ray@sial.com)  
- Infliximab, a chimeric monoclonal antibody, is used to treat rheumatoid arthritis, psoriatic arthritis, Crohn’s disease, and other autoimmune diseases. Clinical responses are different among patients due to inadequate amount of drug circulating in the blood. Therefore, there is a growing demand for reliable LC-MS/MS assays to support quantification of serum Infliximab in clinical applications. The accurate quantitation of Infliximab is enabled by early introduction of an internal standard that behaves identically to the native target protein throughout the analytical workflow. We have developed and characterized a full-length stable isotope labeled Infliximab internal standard and demonstrate its use to achieve sensitive, accurate, and reproducible quantification of serum Infliximab in an LC-MRM assay.

Poster #54C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Small Molecules / Tox  
Utilizing Automated Solid Phase Extraction Technologies to Facilitate High-Throughput Ambient Ionization-MS Analysis of Biological Samples  
Brian Musselman - IonSense, Inc. (musselman@ionsense.com)  
- Several solid phase extraction technologies have been integrated with an thermal desorption enabled ambient ionization (DART®) mass spectrometry system to permit rapid, reliable determination of drugs in biological samples. We demonstrate the utility of SPE- and SPME-based isolation of small molecules from matrix that results in small volumes of solvent more amenable to deposition on the substrates used for direct ionization. Utilizing a combination of DART®-HR/MS, a precision pipettor (Apricot Design iPipettor® Pro), automated sample positioner and laser-cut wire mesh consumable we demonstrate high-throughput analysis of 96-sample achieved in less than 18 minutes with RSD values of under 3%.
**Mass Spectrometric Identification of Biomarkers Associated with Fatal Neonatal Liver Disease in the Lipid-Storage Disease Cerebrotendinous xanthomatisis (CTX)**

*Kenneth Setchell* - *Cincinnati Children's Hospital Medical Center* (kenneth.setchell@cchmc.org)

- Cerebrotendinous xanthomatisis (CTX; OMIM#213700) is a treatable inherited autosomal recessive lipid-storage disorder usually diagnosed in the 2nd or 3rd decades of life and rarely in infancy. It is caused by mutations in sterol 27-hydroxylase (CYP27A1) that impairs bile acid synthesis. We describe 8 infants with CYP27A1 mutations that presented with severe cholestasis, 5 of whom died from liver failure. Mass spectrometry analysis showed their urine was enriched in bile alcohol sulfates and double conjugates with glucuronic acid rather than bile alcohol mono-glucuronides that are the typical biomarkers for the diagnosis of CTX in later life. These sulfated bile alcohols appear to be associated with a poor clinical outcome and highlight that CTX as a cause of neonatal cholestasis may be overlooked if classical biochemical markers are sought.

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**Profiling of Lipid Changes in Disease States: Searching for New Biomarkers**

*Sean Campbell* - *University of Virginia* (stc2m@Virginia.edu) -- *Young Investigator Grantee*

- Lipid analysis for clinical applications has typically been very limited, mostly due to the difficulty inherent in the separation and quantification of lipid species. In addition, the diversity of lipid species present in biological samples makes individual analysis quite daunting. However, with the proper extraction techniques and the help of mass spectrometry, our group has been making gains in both the determination of individual protein effects on cellular lipid pools as well as changes in lipids in disease states, with the eventual goal of the creation of a mass-spec based method to perform lipid profiles and targeted lipid analysis in patient populations.

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**Screening Method for Methamphetamine and Amphetamine using DART® MS Analysis Followed by Chiral Confirmation for D-Methamphetamine**

*Emily Barrey* - *MilliporeSigma* (emily.barrey@sial.com)

- Using Biocompatible Solid Phase Micro Extraction (BioSPME), methamphetamine and amphetamine were directly analyzed by Direct Analysis in Real Time (DART*-MS) from urine samples. By employing a fast and accurate screening method, the amount of samples that require chiral separation can be reduced and laboratories can increase throughput and decrease costs associated with their drug screening programs. Only the positive samples will require the LC/MS/MS chiral confirmatory method for the detection of D-methamphetamine (illicit form) or L-methamphetamine (OTC product form). This lessens the sample load on the higher cost and time consuming LC/MS method.

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**Evaluation of Stable Isotope-Labeled Compound for use as Internal Standard during Quantitation of Psychosine from Dried Blood Spots**

*Patrick DeArmond* - *Nationwide Children's Hospital* (patrick.dearmond@nationwidechildrens.org)

- The use of deuterium-labeled psychosine was evaluated for use as an internal standard in the quantitation of psychosine from dried blood spots, a quick method used to support the biochemical diagnosis of Krabbe disease. Various figures of merit, including bias, precision, and selectivity, were evaluated, and the use of the stable isotope-labeled standard provided adequate accuracy, selectivity, and bias for the quantitation of psychosine from dried blood spots. No observed matrix effects or significant changes in recoveries were observed under various tested sample conditions (e.g., lipemia, icterus, hemolysis, hyperproteinemia). Because PSY-d5 would be expected to better account for any unforeseen matrix effects, recoveries, and/or chromatographic abnormalities, we believe that the PSY-d5 is better suited for use as an internal standard than non-stable isotope-labeled standards.
Poster #56A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Proteomics
Effects of Ultracentrifugation on Plasma Lipoprotein Particle Size Distribution
Jeffrey Jones - Oak Ridge Institute for Science and Education (JJones13@cdc.gov) -- *Young Investigator Grantee*

- Lipoproteins are natural liposome carriers of lipids and proteins that are central to numerous physiological functions throughout the body. The most prevalent method of fractionating these particles is ultracentrifugation, where components in plasma are separated on the basis of density into the various subclasses. This work utilizes Asymmetric Flow Field-Flow Fractionation (AF4), a comparatively gentle technique, to physically separate the different lipoprotein sub-classes and collect fractions for targeted LC-MS/MS analysis, making it an ideal technique to show changes in sub-class distribution before and after ultracentrifugation. It is shown that there are significant changes occur during ultracentrifugation, which may confound quantification of the sub-class distribution of HDL and LDL particles and subsequent understanding of their atherogenic properties.

Poster #56B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
Conversion of Drug Metabolites Due to Contaminants in Commercial β-Glucuronidase Products
Pongkwan (Nikki) Sitasuwan - IMCS (nikki@imcstips.com)

- Small molecule drugs undergo phase II glucuronidation and sulfation in the liver to be excreted in various biological fluids. β-glucuronidase and sulfatase are used to hydrolyze the metabolites, enabling more sensitive and accurate quantitation of the metabolites by mass spectrometry (MS). Any contamination in these enzymes affects not only the effectiveness of the enzyme but also alters the analytes which can skew the outcome. We demonstrate esterase contamination in various commercial β-glucuronidase enzymes using a fluorescent substrate. Contaminated enzymes show the conversion of 6-monoacetylmorphine (6-MAM), a specific metabolite of heroin, to morphine, skewing the readout to false negative for heroin usage.

Poster #56C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Endocrinology
Development of a Novel, Fully Automated Robotic Method to Support LC-MS/MS Quantification of a Comprehensive Steroid Hormone Panel from Patient Serum
Daniel Kassel - Scianalytical Strategies, Inc. (dkassel@scianalytical.com)

- A robust liquid handling method for the processing of serum and the subsequent isolation of testosterone and related hormones has been developed. Serum is transferred robotically to a deep well microtiter plate onto the deck of a liquid handling robot. Extraction solvent is directly added to the serum using a specially designed wide-bore transfer pipette. Following thorough in-well mixing, the serum extract and precipitate are transferred directly to a second, specially designed filter tip that allows for removal of the serum precipitate incorporating a novel “tip on tip” clean up strategy. The supernate is subjected to automated SPE clean using a custom Wax-S tip, allowing for isolation of the steroid hormones. The organic layer is transferred to an analytical plate for LC-MS-MS analysis. The system has been evaluated for a panel of 6 steroid hormones and the data is presented.

Poster #57A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
Analysis of Novel Psychoactive Substances — Synthetic Cathinones and Kratom — using LC-MS/MS
Oneka Cummings - Ameritox, LLC (oneka.cummings@ameritox.com)

- A liquid chromatography/tandem mass spectrometry (LC/MS/MS) method was developed to analyze illicit substances—mitragynine (kratom) and nine synthetic cathinones. This LC/MS/MS quantitative and definitive analytical method has a cycle time of merely 2.5 minutes while ensuring chromatographic baseline separation of isobars. The analysis was conducted on samples diluted 5X with internal standard solution in the absence of any sample preparation/clean-up steps. This assay monitors two transitions for each of the ten analytes and two internal standards.
Poster #57B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM  
Topic: Small Molecules / Tox  
**Automated High-Throughput Extraction of Serum Samples for 25-OH-Vitamin D2 and D3 Analysis by LC-MS/MS using DPX Tips with Hamilton Microlab NIMBUS96**  
*William Brewer - DPX Technologies, LLC* (bill.brewer@dpxlabs.com)  
▶ A novel, fully automated sample preparation method for the analysis of 25-OH-vitamin D2 and D3 in serum was developed using DPX tip technology on a Hamilton NIMBUS96 platform. Hamilton air-displacement technology and support of 1 mL wide bore tips on the 96-channel Multi Probe Head streamlines high throughput extraction. This method avoids off-line centrifugation by using online mixing and innovative tip-on-tip filtration. The precipitate-free filtrate is then extracted with DPX WAX-S tips. This liquid-liquid solid phase extraction technique provides an analyte rich acetonitrile layer for LC-MS/MS analysis. This “hands-off” method prepares 96 samples in less than ten minutes while maintaining high reproducibility, accuracy, and sensitivity.

Poster #57C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM  
Topic: Proteomics  
**Dispersive-Pipette Extraction for Automated Enrichment of IGF-1 from Serum**  
*Andrew Lee - IMCS, LLC* (lee@imcstips.com)  
▶ Accurate and robust quantification of insulin-like growth factor 1 (IGF-1) from serum using mass spectrometry (MS) is challenging due to its high complexity and dynamic range. Low cost, high throughput enrichment method for such low abundant proteins from the serum is required to enrich target proteins prior to MS analysis. We report a high-throughput sample preparation method using reverse phase micro-solid phase extraction enrichment on robotic liquid handling system and demonstrated over 71% recovery from serum for 96 samples in less than 30 minutes. IGF-1 levels in serum correlates well to other published methods that involve longer processing times.

Poster #57D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM  
Topic: Metabolomics  
**Lysophospholipidomics Profiling of Media from Platelet Concentrates during Storage**  
*Jeongah Oh - National University of Singapore* (jeongah.oh@u.nus.edu)  
▶ Accumulation of specific lipid mediators in media of blood products were discussed as potential factors for side-effects of transfusions, including transfusion-related lung injury (TRALI) and immunomodulation (TRIM). Lysophosphatidylcholines (LPC), platelet-activating factors (PAF) and Lyso-PAF have been shown to have immunomodulatory effects and to prime neutrophil activation that is implicated in TRALI and to accumulate in platelet concentrates. We performed an in-depth targeted lipidomics profiling of media from apheresis platelet concentrates during storage using a rapid MRM (multiple reaction monitoring)-based LC-MS approach. The concentrations of different lysophosphatidylethanolamines (LPE) and LPC species were found to either increase, decrease or remain unchanged during storage. All detected, except very long-chain, lyso-PAF species significantly accumulated during storage.

Poster #58A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM  
Topic: Tissue Imaging & Analysis  
**Tissue Imaging with Laser Assisted Rapid Evaporative Ionization Mass Spectrometry (LA-REIMS)**  
*Haixing Wang - Imperial College London* (haixing.wang@imperial.ac.uk)  
▶ Laser assisted rapid evaporative ionization mass spectrometry (LA-REIMS) with a surgical carbon dioxide laser (wavelength, 10600 nm) was applied for tissue imaging for the first time in this study. Similar mass spectra were obtained both with electrosurgical (iKnife) and laser assisted REIMS which indicates similar ionization mechanism, however, LA-REIMS can be easily automated for high spatial resolution dissection. The distribution differences of lipids and sub-anatomical features in the tested tissue samples were also detected. These promising results demonstrated the capability of the LA-REIMS to build histologically assigned spectral libraries for iKnife application.
Clinical Utility of an Ultrasensitive Late Night Saliva Cortisol Assay by Tandem Mass Spectrometry

**Lillian Sturmer** - Stanford University School of Medicine (lsturmer@stanfordhealthcare.org)

- Late night saliva cortisol measurement is gaining clinical importance as a screening test for Cushing’s syndrome. LC-MS/MS based assays are superior to conventional immunoassays due to improved sensitivity and specificity. Our objective was to modify an existing LC-MS/MS method to improve the measurement of saliva cortisol in adult and pediatric patients. Method validation assessed assay imprecision, linearity, lower limit of detection, lower limit of quantitation, accuracy, interference, and reference interval. Our modified assay has enhanced sensitivity, specificity and linearity with an analytical measurement range of 5-5000 ng/dL. This method exemplifies satisfactory clinical performance for the screening of late night saliva cortisol.

A Selective Method for Quantitation of Underivatized Methylmalonic Acid (MMA) in Plasma

**Laura Snow** - Phenomenex, Inc. (laurasn@phenomenex.com)

- Methylmalonic acid (MMA) is a small dicarboxylic acid. This hydrophilic molecule can present chromatographic challenges both in achieving adequate retention under reversed phase conditions as well as resolution from the isomeric/isobaric species such as succinic acid. To combat these challenges, many published LC/MS/MS methods require a sample derivatization step. Here, we present a fast, reproducible LC/MS/MS method to analyze underivatized MMA by utilizing a unique mixed-mode UHPLC C18 column. The method runtime is 5 minutes including column re-equilibration. The sample preparation procedure uses weak anion exchange solid phase extraction to produce a clean sample from plasma. Analyte detection was performed using negative mode electrospray ionization of a triple quadrupole MS.

Separation and Quantitation of Oxysterol, Secosterols, and Cholesterol Intermediates using LC-MS/MS

**Evelyn Wang** - Shimadzu Scientific Instruments (ehwang@shimadzu.com)

- Monitoring oxysterol levels has become increasingly popular, as potential links between oxysterol levels and certain neurodegenerative disorders and cancer are being explored. To meet the increasing demand, a LCMS oxysterol separation and quantitation method was developed using a Shimadzu LCMS-8060 liquid chromatography triple quadrupole mass spectrometer. Detection and quantitation limits were determined using APCI, ESI, and Dual Ion (DUIS) sources with multiple reaction monitoring (MRM) mode for each of the sixteen oxysterols and cholesterol related compounds in a mixture. The DUIS source was shown to be the optimal ionization source due to its ability to quantify all compounds within a single run while preserving the low detection limits achieved by the APCI and ESI. Human serum with spiked standards was analyzed to show feasibility of future clinical research applications.

Direct Analysis of Morphine and its Metabolites with Related Compounds in Urine by LC-MS/MS

**Frances Carroll** - Restek (frances.carroll@restek.com)

- The analysis of total morphine is typically conducted by first subjecting urine samples to acid or enzymatic hydrolysis in order to cleave the glucuronide conjugate from the parent drug prior to analysis. With the glucuronide moiety removed, morphine is much less polar and is therefore more amenable to traditional reversed-phase chromatography. Both hydrolysis procedures can cost the analyst time and result in sample variability due to incomplete hydrolysis or analyte conversion. By utilizing the retention characteristics of the Restek Force™ Biphenyl column, direct analysis of the metabolites of morphine and related compounds using “dilute and shoot” sample preparation was performed.
Poster #60B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM
Topic: Small Molecules / Tox
Direct Injection of Antiretroviral Drugs in Highly Organic Protein-Precipitated Human Plasma by LC-MS/MS
Sharon Lupo - Restek (sharon.lupo@restek.com)

- A typical protein precipitation protocol produces an extract containing approximately 75% organic solvent. When injected into a reversed-phase liquid chromatography system, distortion of early eluting peaks can result due to strong solvent effects. To counteract these effects, evaporation and reconstitution or dilution with a weaker solvent is performed prior to injection. The benefits and limitations of diluting protein precipitated plasma prior to analysis versus injecting it directly will be assessed by comparing peak shapes, intensities, and recovery values for 5 antiretroviral (ARV) drugs in human plasma. Analysis was performed using liquid chromatography coupled to a quadrupole mass spectrometer.

Poster #60C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM
Topic: Small Molecules / Tox
Analysis of Immunosuppressive Drugs from Whole Blood by LC-MS/MS
Ty Kahler - Restek (ty.kahler@restek.com)

- Cyclosporin A, tacrolimus, sirolimus, and everolimus are four of the most commonly used drugs in organ transplantation therapy. Due to their pharmacokinetic variabilities and narrow therapeutic indexes, time-sensitive and highly accurate therapeutic drug monitoring is necessary, not only to prevent rejection but also minimize toxic side effects. Therefore, a fast and accurate measurement of drug concentration is critical to assist the clinicians for timely and proper treatment of the patients. By combining a simple sample preparation step and chromatographic analysis with a Raptor™ Biphenyl column, a high-throughput analysis was established for simultaneous measurement of these four drugs in human whole blood.

Poster #60D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM
Topic: Small Molecules / Tox
LC-MS/MS Method Development Challenges for the Analysis of 43 Anxiety Medications and Metabolites
Megan Kent - Restek (megan.kent@restek.com)

- The use of liquid chromatography coupled with mass spectrometry (LC-MS/MS) has become a routine method of analysis in forensic and clinical labs and provides sensitivity, speed, and specificity when analyzing drugs in complex biological matrices. Anxiety medications are used to treat a variety of conditions and are often abused in conjunction with other drugs. The presence of isomers and the need to collect data in positive and negative ion modes can present the analyst with significant chromatographic challenges. A comprehensive method has been developed to assay medications used to treat anxiety including benzodiazepines, muscle relaxers, hypnotics, sedatives, z-drugs, and barbiturates on the Raptor Biphenyl column.

Poster #61A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM
Topic: Small Molecules / Tox
Evaluation of Generic LC-MS/MS-Based High Sensitivity, High-Throughput Quantitation Method of Oral Fluids Towards Therapeutic Drug Monitoring
Manoj Tyagi - Captiva Lab, LLC (manoj@captivalab.com)

- Oral fluid is the promising matrix for the drug treatment. SPE based MS/MS provides a way to selectively differentiate the presences of drug(s) in oral fluids, while screening is being used for presumptive testing. However, ease of sample preparation is the key in providing LC-MS/MS analytical sensitivity by reducing matrix effects at lower cut off. We have developed CLAM 2000 coupled LC-MS/MS approach for analysis of drugs testing from oral fluids, using a dilute shoot method. Extraction, analytical sensitivity and high throughput capability have been explored, which has shown that for a generic approach to quantitative clinical toxicology and drug analysis from oral fluid matrix. Despite its strength & limitations, by utilizing hi-sensitivity, high throughput quantitation CLAM 2000 coupled LC-MS/MS based oral fluid testing could become the most prevalent matrix for the drug testing.
**Poster #61B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**
**Topic:** Proteomics

**Development of a Robust, Low Flow LC-MS/MS Method for Quantitation of Peptides**

*Kerry Hassell Forrest - ThermoFisher Scientific (kerry.hassell@thermofisher.com)*

- For biomolecule analysis, LC-MS/MS is the technology of choice because of its speed, selectivity, sensitivity, and cost benefits. Capillary and microflow (1-50µL/min) rates are an excellent compromise in terms of both sensitivity and robustness required for routine bioanalytical analysis. This work investigates the sensitivity improvements made by using narrow bore columns at low flow rates for quantitating peptides with a wide range of hydrophobicities.

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**Poster #61C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**
**Topic:** Small Molecules / Tox

**An Orthogonal Workflow for the Detection of Nicotine and Related Metabolites in Oral Fluid After Vaping Nicotine Free Labeled E-Liquids**

*Desmond Wichems, Ph.D. - PerkinElmer (Desmond.Wichems@PERKINELMER.COM)*

- An emerging threat to public health related to nicotine in nicotine free labeled products is currently being investigated. Candidate samples of vaping e-liquids were identified at Boston University (Boston, MA). The samples were split and sent to PerkinElmer (Downers Grove, IL) for screening by DSA-TOFMS and Arcadia University (Willow Grove, PA) for confirmation analysis by GC-MS. Oral fluid samples were collected at Boston University (Boston, MA) in accordance with IRB protocol for the protection of human subjects in non-invasive sampling. De-identified samples were collected with Quantisal (Immunalysis) kits and shipped to PerkinElmer (Shelton, CT) for analysis by UPLC-ESI-MS/MS.

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**Poster #62A in Exhibit Hall - attended for 1hr on Tuesday starting at 4:00 PM**
**Topic:** Endocrinology

**Single Assay Measurement of Aldosterone-to-Renin Ratio by UHPLC-MS/MS**

*Christopher Gilles - Shimadzu Corp., MSBU (CTGilles@shimadzu.com)*

- The Aldosterone-to-Renin ratio (ARR) is a useful tool for screening of primary aldosteronism. Aldosterone is measured in blood or urine while renin can be quantified in blood directly by immune-assay or by the mean of its enzymatic activity. While these parameters are usually assayed separately, here we present a method able to quantify both aldosterone concentration and plasma renin activity. Aldosterone and the renin enzymatic product (angiotensin-I) are measured together after incubation with a single injection by UHPLC-MS/MS in 100 µL of plasma. The method proved to cover the sensitivity needs to assess low aldosterone levels or low renin activities.

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**Poster #62B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**
**Topic:** Various OTHER

**Measurement of 7-Alpha-Hydroxy-4-Cholesten-3-One in Serum using LC-MS/MS for the Screening of Bile Acid Malabsorption in IBS-D**

*Stacy Kenyon - Mayo Clinic (kenyon.stacy@mayo.edu) -- *Young Investigator Grantee***

- Bile acid malabsorption (BAM) occurs when bile acids are inadequately reabsorbed in the small intestine leading to persistent diarrhea and excess fecal bile acids. Current laboratory methods for detecting BAM require timed fecal collections and measurement of bile acid species that are inconvenient for the patient and technically challenging for the laboratory. The bile acid precursor 7-alpha-hydroxy-4-cholesten-3-one (7aC4) can be measured in fasting serum samples and has been shown to be elevated in patients with BAM. Here we describe a LC-MS/MS assay to measure serum 7aC4 and report its clinical performance as a screening test for patients with suspected BAM.
**Poster #62C in Exhibit Hall - attended for 1hr on Wednesday starting at 5:00 PM**  
Topic: Small Molecules / Tox  
**Fully Automated Platform for Determination of Antiepileptic Drugs in Serum**  
*Isabel Teresa Cabruja - Shimadzu Italia (icabruja@shimadzu.it)*  
- The pharmacological therapy of Epilepsy is performed by the use of a variety of antiepileptic drugs. The results of therapeutic drug monitoring for these molecules are crucial to set the correct dose for each patient. Liquid chromatography coupled to tandem mass spectrometry (LC–MS/MS) shows high sensitivity and specificity, but however also shows a lack of standardization, since predominantly sample preparation procedures involving complex offline extraction methods are required. To increase the data quality, safety, and throughput of LC-MS/MS quantitation of antiepileptic drugs, a fully automated platform for the analysis of antiepileptic drugs in serum has been introduced (the present work is intended for research use only).

**Poster #62D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM**  
Topic: Various OTHER  
**Metal Oxide Laser Ionization (MOLI) MS for Identification of Bacteria using Intact Lipids for Profiling**  
*Kent Voorhees - Colorado School of Mines (kvtv@comcast.net)*  
- MALDI mass spectrometry has become ubiquitous in the clinical laboratory for rapid bacterial identification by protein profiling. In this poster, we describe an extension of matrix-assisted laser desorption ionization MALDI MS for analysis of intact lipids using modified metal oxide nanoparticles as a matrix free platform. The goal of this work was to investigate salt-doped cerium oxide as a means of eliminating catalytic cleavage. By doping samples with alkali salts we observed a shift from the molecular ions to sodium and potassium adducts of intact bacterial lipids. The success for this technique will be compared to other bacterial identification approaches.

**Poster #7B in Exhibit Hall - attended for 1hr on Wednesday starting at 9:45 AM**  
Topic: Small Molecules / Tox  
**Chiral Separation of Amphetamines using LC-MS/MS**  
*Kavinda De Silva - MTL (kavindad@moleculartestinglabs.com)*  
- Methamphetamine is a stereoisomer drug and is available in two forms: d- and l-. The d- form is most frequently used as a prescription stimulant and appetite suppressant. The l- form is available over-the-counter as the active ingredient of the Vicks inhaler and is a metabolite of certain prescription medications such as Selegiline. A method was developed for cost effective, dilute and shoot assay with linear ranges of 20 - 5,000 ng/mL for selective drugs with R2 > 0.99 using LC-MS/MS.

**Poster #8D in Exhibit Hall - attended for 1hr on Thursday starting at 10:00 AM**  
Topic: Troubleshooting with Grand Rounds  
**Matrix Effects and Ion Suppression in Estradiol LC-MS/MS Assay**  
*Yifei Yang - University of Chicago (yifeiyang@uchicago.edu) -- *Young Investigator Grantee*  
- Our LC-MS/MS high-sensitivity estradiol assay provides significant improvement in precision and accuracy in the low concentration ranges (< 20 pg/ml). Nevertheless, this routine assay sometimes suffers from ion suppression effects in some patient samples. We hypothesized that the ion suppression was due to the pH altering substance(s) in the samples. We tested dilution and pH adjustment after sample extraction, and its effects on reducing ion-suppression. While such strategy can reduce the matrix effects, it does not provide reliable quantification results for patient samples containing extremely low concentrations of the estradiol (< 5 pg/ml).
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