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**Neil Kelleher**  
*Northwestern University*



**Ljiljana Paša-Tolić**  
*EMSL, PNNL*

*Speakers – please arrive ½ hour before your session to load your presentation.*

**THURSDAY, JANUARY 24**

6:00 – 7:00 pm      **Registration, Outside of the Long/Bird/Indian Ballroom**

<p><b>6:30 – 8:00 pm</b> <b>Opening Session</b> <b>Top Down Mass Spectrometry: Past, Present and Future</b> Session Chairs, Neil Kelleher, <i>Northwestern University</i> &amp; Ljiljana Paša-Tolić, <i>EMSL, PNNL</i> <i>Long/Bird/Indian Ballroom</i></p>
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6:30 - 7:15 pm	<p><b>Joseph Loo, UCLA</b> Top-Down Mass Spectrometry – Where are we going? Are we there yet?</p>
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7:15 - 8:00 pm	<p><b>Fred McLafferty, Cornell University</b> Charge Site Mass Spectra: Basic Mechanisms for Electron Capture Dissociation of Both Covalent and Noncovalent Bonds in Ionized Proteins</p>
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<p><b>8:00 - 10:00 pm</b> <b>Reception</b> setup all posters <i>Banyan Breezeway</i></p>
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**FRIDAY, JANUARY 25**

**8:30 – 9:30 am**

**Instrumentation for Top Down Mass Spectrometry**

Session Chair: David Goodlett, *University of Washington*

*Long/Bird/Indian Ballroom*

- 8:30 – 9:00 am **Alan Marshall**, *NHMFL/Florida State University*  
Determination of Site-Specific Protein Disulfide Bond Reduction Potentials by Top-Down FT-ICR MS/MS
- 9:00 – 9:30 am **Mike Senko**, *Thermo Fisher Scientific*  
Orbitrap Instrumentation for Top-Down Analysis
- 9:30 - 9:50 am **Coffee Break**, *Banyan Breezeway*

**9:50 - 11:20 am**

**Targeted strategies I**

**(Characterization of recombinants, immunoglobulins, phosphoproteins, membrane proteins, histones, etc.)**

Session Chair: Lloyd Smith, *University of Wisconsin*

*Long/Bird/Indian Ballroom*

- 9:50 – 10:20 am **Julian Whitelegge**, *UCLA*  
Data-Directed Top-Down Mass Spectrometry for Precise Characterization of Integral Membrane Proteins
- 10:20 – 10:50 am **Yury Tsybin**, *Ecole Polytechnique Federale*  
Top-Down and Middle-Down Mass Spectrometry of Immunoglobulins and Beyond
- 10:50 – 11:20 am **John Yates**, *Scripps Research Institute*  
The CFTR Interactome: the Case for Protein Complex Variations
- 11:20 – 11:40 am **Coffee Break**, *Banyan Breezeway*

**11:40 am - 12:40 pm**

**Targeted strategies II**

**(Characterization of recombinants, immunoglobulins, phosphoproteins, membrane proteins, histones, etc.)**

Session Chair: Julia Chamot-Rooke, *CNRS - Ecole Polytechnique*

*Long/Bird/Indian Ballroom*

- 11:40 am - 12:10 pm **Ying Ge**, *University of Wisconsin*  
Top-Down Targeted Proteomics for Deep Sequencing of Phosphoproteins
- 12:10 - 12:40 pm **Maarten Altelaar**, *Utrecht University*  
Extending the Capabilities of the Orbitrap in Mass Range and Fragmentation Efficiency for Top-Down Proteomics
- 12:40 – 2:00 pm **Group Lunch**, *Garden Courtyard*

**FRIDAY, JANUARY 25**

**2:00 - 3:30 pm**

**Protein Conformation, Charging and Complexation**

Session Chair: Joseph Loo, *UCLA*

*Long/Bird/Indian Ballroom*

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|----------------|---|
| 2:00 - 2:30 pm | <b>Scott McLuckey</b> , <i>Purdue University</i><br>New Gas-Phase Ion Chemistries for Top-Down Tandem Mass Spectrometry |
| 2:30 - 3:00 pm | <b>Kathrin Breuker</b> , <i>University of Innsbruck</i><br>ECD and Protein Structure in the Gas Phase                   |
| 3:00 - 3:30 pm | <b>Evan Williams</b> , <i>UC Berkeley</i><br>Supercharging Approaches for Top-Down Native Mass Spectrometry             |

**3:30 - 5:30 pm**

**Consortium for Top Down Proteomics**

*Long/Bird/Indian Ballroom*

**7:00 - 8:00 pm**

**Promoted Talks I**

Session Chair: Catherine Costello, *Boston University*

*Long/Bird/Indian Ballroom*

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|----------------|--|
| 7:00 - 7:15 pm | <b>Xibei Dang</b> , <i>Florida State University</i><br><i>Poster 11</i> - Top-Down Analysis of Histone Post-Translational Modifications by Electron Capture Dissociation Fourier Transform Ion Cyclotron Resonance Mass Spectrometry |
| 7:15 - 7:30 pm | <b>Frederik Lermyte</b> , <i>University of Antwerp</i><br><i>Poster 19</i> - Ion Mobility - Mass Spectrometry and top-down Electron Transfer Dissociation of Intact Proteins on a Quadrupole/TOF Instrument                          |
| 7:30 - 7:45 pm | <b>Jared Shaw</b> , <i>University of Texas</i><br><i>Poster 27</i> - 193 nm Ultraviolet Photodissociation in an Orbitrap Elite Mass Spectrometer for Top-Down Proteomics   |
| 7:45 - 8:00 pm | <b>David Horn</b> , <i>Thermo Fisher Scientific</i><br><i>Poster 13</i> - Top-Down Identification of Case in Isoforms using a High Performance Benchtop Quadrupole Orbitrap Mass Spectrometer  |

**8:00 - 10:00 pm**

**Poster Session I**

odd-numbered posters present

*Banyan Breezeway*

**SATURDAY, JANUARY 26**

**8:30 - 10:30 am**

**Intact Protein Separations and Top Down Mass Spectrometry on a Chromatographic Time Scale**

Session Chair: Yury Tsybin, *Ecole Polytechnique Federale*

*Long/Bird/Indian Ballroom*

- 8:30 - 9:00 am **Alan Doucette**, *Dalhousie University*  
How to Analyze Twice as much Sample, in Half the Time
- 9:00 - 9:30 am **Ljiljana Paša-Tolić**, *EMSL, PNNL*  
Defining Bacterial Proteomes from the Top-Down
- 9:30 - 10:00 am **Lloyd Smith**, *University of Wisconsin*  
Proteoform Analysis: New Technologies for Detection and Quantitation of Intact Proteins
- 10:00 - 10:30 am **Neil Kelleher**, *Northwestern University*  
Top Down Proteomics and the Human Proteome Project
- 10:30 - 10:50 am **Coffee Break**, *Banyan Breezeway*

**10:50 am - 12:50 pm**

**Top Down Mass Spectrometry and Human Health**

Session Chair: Ying Ge, *University of Wisconsin*

*Long/Bird/Indian Ballroom*

- 10:50 - 11:20 am **Julia Chamot-Rooke**, *CNRS - Ecole Polytechnique*  
Top-Down Analysis of Bacterial Proteins Involved in Virulence
- 11:20 - 11:50 am **Jeffrey Agar**, *Brandeis University*  
Proteoforms Put in Perspective: Toxic, Therapeutic, and Protective
- 11:50 am - 12:20 pm **Nathan Yates**, *University of Pittsburgh*  
Pharmaceutical Applications of Top-Down Differential Mass Spectrometry
- 12:20 - 12:50 pm **Catherine Costello**, *Boston University*  
Top-Down Analysis of Variant and/or Post-Translationally Modified Proteins
- 1:00 - 7:00 pm **Afternoon Free**  
**or optional trip to the Dali Museum**, shuttle will leave at 1 pm and return at 3:45 pm and 5:00 pm, ask Brent at the registration desk if \$10 shuttle tickets are still available.

**4:00 - 6:00 pm**

**Consortium for Top Down Proteomics**

*Long/Bird/Indian Ballroom*

**SATURDAY, JANUARY 26**

**7:00 - 8:00 pm**

**Promoted Talks II**

Session Chair: Evan Williams, *UC Berkeley*

*Long/Bird/Indian Ballroom*

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|----------------|--|
| 7:00 - 7:15 pm | <b>Gary Van Berkel</b> , <i>Oak Ridge National Laboratory</i><br><i>Poster 30 - Spatially Resolved Extraction of Proteins from Tissues and Blood Spots for Top Down Analysis using a Continuous Flow Liquid Microjunction Surface Sampling Probe (LMJ-SSP)</i> |
| 7:15 - 7:30 pm | <b>Christophe Masselon</b> , <i>CEA, Institut de Biologie Structurale Jean-Pierre Ebel</i><br><i>Poster 20 - Top-down MS analysis reveals binding site between S. pneumoniae pilin domains</i>   |
| 7:30 - 7:45 pm | <b>Simone Nicolardi</b> , <i>Leiden University Medical Center (LUMC)</i><br><i>Poster 22 - Top-Down MS Identification of New O-Glycosylated Apolipoprotein-CIII Isoforms in Ultrahigh Resolution Human Serum Profiles</i>                                      |
| 7:45 - 8:00 pm | <b>Zhixin (Michael) Tian</b> , <i>Dalian Institute of Chemical Physics, CAS</i><br><i>Poster 28 - Interpreting Biological Mass Spectra as It Is Using Isotopic Mass-to-charge Ratio and Envelope Fingerprinting</i>  |

**8:00 - 10:00 pm**

**Poster Session II**

even-numbered posters present

*Banyan Breezeway*

**SUNDAY, JANUARY 27**

**8:30 - 10:30 am**

**Bioinformatics**

Session Chair: Scott McLuckey, *Purdue University*

*Long/Bird/Indian Ballroom*

- 8:30 - 9:00 am **Richard LeDuc**, *Indiana University*  
Statistical Consideration for Identification and Quantification in Top-Down Proteomics
- 9:00 - 9:30 am **Pavel Pevzner**, *UCSD*  
MS-Align: Identification of Top-Down Spectra with Unexpected Modifications
- 9:30 - 10:00 am **David Goodlett**, *University of Washington*  
Exploring data-independent top-down proteomics
- 10:00 - 10:30 am **Nathan Edwards**, *Georgetown University*  
Phyloproteomic Classification of Unsequenced Organisms by Top-Down Proteomics
- 10:30 - 11:00 am **Coffee Break**, *Banyan Breezeway*

**11:00 am- 12:00 pm**

**Mass Spectrometry Imaging of Intact Proteins**

Session Chairs, Neil Kelleher, *Northwestern University*

& Ljiljana Paša-Tolić, *EMSL, PNNL*

*Long/Bird/Indian Ballroom*

- 11:00 - 11:30 am **Sarah Trimpin**, *Wayne State University*  
LSI Imaging and Characterization of Endogenous Peptides and Proteins Directly from Tissue on High Resolution Mass Spectrometers
- 11:30 am - 12:00 pm **Jeffrey Spraggins**, *Vanderbilt University*  
Integrating the Spatial Domain and Top-Down Proteomics using Mass Accuracy: Enhancing Protein Mapping for Biological Applications
- 12:00 - 12:30 pm **Closing Remarks**

## Poster List

*All posters are located in the Banyan Breezeway  
odd-numbered posters will be presented on Friday from 8:00 - 10:00 pm  
even-numbered posters will be presented on Saturday from 8:00 - 10:00 pm  
All posters should be set up by 7:00 pm on Thursday  
Remove all posters by 11:00 am on Sunday*

- 1 **N-terminal Top-Down Protein Sequencing by ETD-UHR-TOF Mass Spectrometry;** Christian Albers, Ralf Hartmer, Wolfgang Jabs; *Bruker Daltonik GmbH, Bremen, Germany*
- 2 **LC-MS Analysis of Intact Enzymes using the Synapt G2 Mass Spectrometer;** Ioana M. Barbu, Michiel Akeroyd, Rob A.M. van der Hoeven, Maurien M.A. Olsthoorn, Marcel W.E.M. van Tilborg; *DSM Biotechnology Center, Analysis Department, Delft, The Netherlands*
- 3 **Identification of MALDI Imaging MS peaks by Top-Down Proteomics;** Marshall Bern, Christopher Becker, Yong J. Kil, Peggi Angel, Kristie Rose, David Anderson, Dhananjay Sakrikar, Kevin Schey and Richard Caprioli; *Protein Metrics Inc., San Carlos, CA; Mass Spectrometry Research Center, Vanderbilt University, Nashville, TN*
- 4 **Top-Down Proteomics using High Resolution Mass Spectrometry and Online Core-Shell HPLC Protein Separation;** Christopher Bolcato<sup>1</sup>; Xianglin Yuan<sup>1</sup>; Matthew Maust<sup>1</sup>, Amy Flynn<sup>1</sup>; Matthew Powell<sup>1</sup>; <sup>1</sup>*Protea Biosciences Group, Inc., Morgantown, WV*
- 5
- 6 **MS based Characterization of Soluble and Membrane-Bound Forms of Synaptic Proteins;** Ann Brinkmalm<sup>1</sup>, Gunnar Brinkmalm<sup>1</sup>, William G. Honer<sup>2</sup>, Henrik Zetterberg<sup>1</sup>, Joel Jakobsson<sup>1</sup>, Kaj Blennow<sup>1</sup>, and Annika Öhrfelt<sup>1</sup>; <sup>1</sup>*Institute of Neuroscience and Physiology, The Sahlgrenska Academy at University of Gothenburg, Sahlgrenska University Hospital, Mölndal, Sweden*  
<sup>2</sup>*Centre for Complex Disorders, Department of Psychiatry, University of British Columbia, Vancouver General Hospital Research Pavilion, Vancouver, BC, Canada*
- 7 **Comprehensive Characterization of Amyloid  $\beta$  Peptides – from Endogenous Peptides in Cerebrospinal Fluid to Synthetic Dimers;** Gunnar Brinkmalm<sup>1</sup>, Ann Brinkmalm<sup>1</sup>, Tiernan O'Malley<sup>2</sup>, Erik Portelius<sup>1</sup>, Maria Olsson<sup>1</sup>, Jessica M. Mc Donald<sup>2</sup>, Dominic M. Walsh<sup>2</sup>, Henrik Zetterberg<sup>1</sup>, and Kaj Blennow<sup>1</sup>; <sup>1</sup>*Institute of Neuroscience and Physiology, The Sahlgrenska Academy at University of Gothenburg, Sahlgrenska University Hospital, Mölndal, Sweden*  
<sup>2</sup>*Brigham and Women's Hospital, Harvard Medical School, Boston, MA*
- 8 **Characterising the Mouse Protamine PTMome\* using Bottom-Up and Top-Down Proteomics \* PTMome (pē tē em-ōm) = the Entire Set of Post-Translational Modifications (PTMs) on Proteins Expressed by a Genome, Cell, Tissue or Organism;** Andrea M Brunner<sup>1</sup>, Paolo Nanni<sup>2</sup>, Isabelle M Mansuy<sup>1</sup>; <sup>1</sup>*Brain Research Institute, UZH/ETHZ*, <sup>2</sup>*Functional Genomics Center Zurich, UZH/ETHZ, Switzerland*
- 9 **Comparison of 193 nm UVPD, ETD, HCD and CID for Characterization of Multiple Engineered Green Fluorescent Protein Isoforms with Varying Isoelectric Points;** Joe Cannon, Christian Kluewe, Andrew Ellington and Jennifer Brodbelt; *University of Texas, Austin, TX*
- 10 **Comparative Study of Fractionation Methods for Top-down Analysis of Complex Protein Mixtures;** Avantika Dhabaria<sup>1</sup>; Yan Wang<sup>1</sup>; Catherine Fenselau<sup>1</sup>; Nathan Edwards<sup>2</sup>; <sup>1</sup>*University of Maryland, College Park, MD* <sup>2</sup>*Georgetown University Medical Center, Washington, D. C.*



- 11 **Top-Down Analysis of Histone Post-Translational Modifications by Electron Capture Dissociation Fourier Transform Ion Cyclotron Resonance Mass Spectrometry;** Xibei Dang<sup>1</sup>, Jenna Scotcher<sup>2</sup>, Yeqing Tao<sup>1</sup>, Alan G. Marshall<sup>1,2</sup>, and Nicolas L. Young<sup>2</sup>; <sup>1</sup>*Department of Chemistry and Biochemistry, Florida State University, 95 Chieftain Way, Tallahassee, FL;* <sup>2</sup>*Ion Cyclotron Resonance Program, National High Magnetic Field Laboratory, 1800 East Paul Dirac Drive, Tallahassee, FL*
- 12 **Type IV pili of Pathogenic *Neisseria meningitidis* Sickly Sweet Appendages;** Joseph Gault<sup>1</sup>, Christian Malosse<sup>1</sup>, Guillaume Duménil<sup>2</sup>, Catherine Costello<sup>3</sup>, Julia Chamot-Rooke<sup>1</sup>; <sup>1</sup>*Institut Pasteur, CNRS UMR3528, Unité de Spectrométrie de Masse Structurale et Protéomique, Paris 75015, France;* <sup>2</sup>*INSERM U970, Paris Cardiovascular Research Center, Paris 75015, France;* <sup>3</sup>*Center for Biomedical Mass Spectrometry, Department of Biochemistry, Boston University School of Medicine, Boston, MA*
- 13 **Top-Down Identification of Casein Isoforms using a High Performance Benchtop Quadrupole Orbitrap Mass Spectrometer;** David M. Horn, Terry Zhang, Yi Zhang, and Guifeng Jiang; *Thermo Fisher Scientific*
- 14 **Verification of Glycosylation of the Recombinant Human Granulocyte Colony Stimulating Factor (G-CSF) produced in HEK293 cells by Top-down Mass Spectrometry;** Sergei Ilchenko<sup>1</sup>; Alexander V. Gasparian<sup>2</sup>; Janna Kiselar<sup>1</sup>; Natalia D. Tararova<sup>2</sup>, Mark R. Chance<sup>1</sup>; Anton A. Komar<sup>2,3</sup>; <sup>1</sup>*Case Western Reserve University, 2-DAPCEL Inc, 3-Cleveland State University, Cleveland, OH*
- 15 **Mass Spectrometric Immunoassay Workflow for the Determination of Human IGF1;** Urban A. Kiernan<sup>1</sup>, David A. Phillips<sup>1</sup>, Kemmons A. Tubbs<sup>1</sup>, Dobrin Nedelkov<sup>1</sup>, Bryan Krastins<sup>2</sup>, Mary F. Lopez<sup>2</sup>, and Eric E. Niederkofler<sup>1</sup>; <sup>1</sup>*ThermoFisher Scientific, 2155 E. Conference Dr., Suite 104, Tempe, AZ;* <sup>2</sup>*ThermoFisher Scientific BRIMS, 790 Memorial Dr., Cambridge, MA*
- 16 **Top-Down Mass Spectrometry Approach for Structural Analysis of Proteins using Covalent Labeling;** Sergei Ilchenko<sup>1</sup>; Janna Kiselar<sup>1</sup>; Alexandra Klinger<sup>2</sup>, Paul Axelsen<sup>2</sup> and Mark R. Chance<sup>1</sup>; *Case Western Reserve University, Cleveland, OH; University of Pennsylvania, PA*
- 17 **Intact Protein (PTM) Characterization: Top-Down Proteomics Approach;** Ravi K Krovidi, *Agilent Technologies Pvt. Ltd, Bangalore, 560 048, India*
- 18 **Identification of Proteins with Multiple Post-Translational Modifications using Top-Down Tandem Mass Spectra;** Xiaowen Liu<sup>1,3</sup>, Shawna Hengel<sup>2</sup>, Si Wu<sup>2</sup>, Nikola Tolić<sup>2</sup>, Ljiljana Pasa-Tolić<sup>2</sup>, and Pavel A. Pevzner<sup>3</sup>; <sup>1</sup>*School of Informatics, Indiana University-Purdue University Indianapolis;* <sup>2</sup>*Biological Science Division, Pacific Northwest National Laboratory;* <sup>3</sup>*Department of Computer Science and Engineering, University of California, San Diego, CA*
- 19 **Ion Mobility - Mass Spectrometry and top-down Electron Transfer Dissociation of Intact Proteins on a Quadrupole/TOF Instrument;** Lermyte, F.<sup>a,b,c</sup>, Valkenborg, D.<sup>a,c</sup>, Sobott, F.<sup>a,b</sup>; <sup>a</sup>*CFP-CeProMa, University of Antwerp, Belgium;* <sup>b</sup>*Department of Chemistry, University of Antwerp, Antwerp, Belgium ;* <sup>c</sup>*MANT, VITO, Mol, Belgium*
- 20 **Top-Down MS Analysis Reveals Binding Site between *S. pneumoniae* Pilin Domains;** Anne-Marie di Guilmi<sup>1</sup>, Unige Laskay<sup>2</sup>, Yuri Tsybin<sup>2</sup>, Christophe Masselon<sup>3</sup>; *CEA, Institut de Biologie Structurale Jean-Pierre Ebel, F-38027 Grenoble, France; Biomolecular Mass Spectrometry Laboratory, Ecole Polytechnique Fédérale de Lausanne, CH-1015 Lausanne, Switzerland; CEA, IRTSV, Biologie à Grande Echelle, F-38054 Grenoble, France*

- 21 **Structure Determination, Specificity and Affinity of Fibril- Inhibiting  $\beta$ -Amyloid Epitopes Recognized by Serum Anti-A $\beta$ -Autoantibodies;** Claudia Cozma<sup>1</sup>, Adrian Moise<sup>1</sup>, Marius Iurascu<sup>1</sup>, Gabriela Paraschiv<sup>1</sup>, Madalina Maftel<sup>1</sup>, Alina Petre<sup>1,3</sup>, Gabor Mezo<sup>4</sup>, Ferenc Hudecz<sup>4</sup> Marilena Manea<sup>1,2</sup>, Michael Gross<sup>3</sup> and Michael Przybylski<sup>1\*</sup>; <sup>1</sup>*Department of Chemistry, Laboratory of Analytical Chemistry and Biopolymer Structure Analysis, and* <sup>2</sup>*Zukunftskolleg, University of Konstanz, Konstanz, Germany;* <sup>3</sup>*Department of Chemistry, Washington University St. Louis, St. Louis, MO;* <sup>4</sup>*Department of Peptide Chemistry, Hungarian Academy of Sciences, Budapest, Hungary*
- 22 **Top-Down MS Identification of New O-Glycosylated Apolipoprotein-CIII Isoforms in Ultrahigh Resolution Human Serum Profiles;** Simone Nicolardi\*, Yuri E.M. van der Burgt, Manfred Wuhrer, Paul J. Hensbergen, and André M. Deelder; *Leiden University Medical Center (LUMC), Technology Focus Area Proteomics & Metabolomics, Albinusdreef 2, 2300 RC, Leiden, The Netherlands*
- 23 **Examining the Charge State - Protein Conformation Relationship by H/D Exchange - Electrospray Ionization and Electron Capture Dissociation Mass Spectrometry;** Teerapat Rojsajjakul, Fred L. King\*; *C. Eugene Bennett Department of Chemistry, West Virginia University, Morgantown, WV*
- 24 **Protein Unfolding & Refolding in the Gas Phase;** Moritz Schennach, Kathrin Breuker; *Institute of Organic Chemistry and Center for Molecular Biosciences Innsbruck (CMBI); University of Innsbruck, Innrain 80/82, 6020 Innsbruck, Austria*
- 25 **Suggestions for a Protein Species Terminology;** Hartmut Schlüter (1), Peter Jungblut (2), Hermann-Georg Holzhütter (3), Rolf Apweiler (4); (1) *University Medical Center Hamburg-Eppendorf, Germany.* (2) *Max Planck Institute of Infection Biology, Berlin, Germany.* (3) *Charité - University Medicine, Berlin, Germany.* (4) *EMBL Outstation European Bioinformatics Institute, Hinxton, Cambridge, Great Britain.*
- 26 **193 nm Ultraviolet Photodissociation in an Orbitrap Elite Mass Spectrometer for Top-Down Proteomics;** Jared B. Shaw and Jennifer S. Brodbelt; *The University of Texas, Austin, TX*
- 27 **The Ugly Duckling of Top-Down Mass Spectrometry;** Shannon Cornett, Detlev Suckau, Rainer Paape and Anja Resemann; *Bruker Daltonik GmbH, Bremen, Germany*
- 28 **Using Isotopic Mass-to-charge Ratio and Envelope Fingerprinting to Decode Biological Mass Spectra;** Li Li, Zhixin Tian; *Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Liaoning 116023, China*
- 29 **Top-Down Analysis of Histone H4;** Jeremy J. Wolff and Christopher J. Thompson; *Bruker Daltonics, Billerica, MA*
- 30 **Spatially Resolved Extraction of Proteins from Tissues and Blood Spots for Top Down Analysis using a Continuous Flow Liquid Microjunction Surface Sampling Probe (LMJ-SSP);** Gary J. Van Berkel,<sup>1</sup> Vilmos Kertesz,<sup>1</sup> Joshua J. Nicklay,<sup>2</sup> Kristie L. Rose,<sup>2</sup> Kevin L. Schey,<sup>2</sup> Richard M. Caprioli<sup>2</sup> and Jeremy L. Norris<sup>2</sup>; <sup>1</sup>*Oak Ridge National Laboratory, Oak Ridge, TN;* <sup>2</sup>*Mass Spectrometry Research Center, Vanderbilt University School of Medicine, Nashville, TN*

- 31 **Elucidating the Sites of Metal Binding Important in Fibrillation of  $\alpha$ -Synuclein by Top-Down Mass Spectrometry;** Piriya Wongkongkathap, Sheng Yin, and Joseph A. Loo;  
*Department of Chemistry and Biochemistry, UCLA, Los Angeles, CA*
- 32 **Top-down Study for Heterocyclic Amine Hemoglobin Adducts;** Min Yang<sup>1</sup>, Neelam Zahoor<sup>2</sup>, Maria Ospina<sup>2</sup>, Hubert Vesper<sup>2</sup> ;<sup>1</sup> *Battelle Memorial Institute, Atlanta, GA 30345*, <sup>2</sup> *Division of Laboratory Sciences, National Center for Environmental Health, Centers for Disease Control and Prevention, Atlanta, GA*
- 33 **Systematic Evaluation of Ultrahigh Resolution MS Instrument Parameter to Optimize Topdown Analysis;** Martin Zeller, Mathias Mueller, Eugen Damoc, Eduard Denisov, Dirk Nolting and Thomas Moehring *Thermo Fisher Scientific, Bremen, Germany*
- 34 **Optimization of the High Performance Liquid Chromatography (HPLC) Separation for Characterization and Quantitation of Histone Proteoforms;** Zhaorui Zhang<sup>1</sup>, Si Wu<sup>1</sup>, Rui Zhao<sup>1</sup>, Nikola Tolić<sup>1</sup>, David L. Stenoien<sup>2</sup>, Rosalie K. Chu<sup>1</sup> and Ljiljana Paša-Tolić<sup>1</sup>;  
*Environmental Molecular Science Laboratory, Pacific Northwest National Laboratory; Fundamental & Computational Sciences Division, Pacific Northwest National Laboratory*