

Mini Symposium on the Relative Merits of Orthogonal Energy Deposition Modes for Promotion of Fragmentation

Saturday, August 22

3:00
p.m. **Symposium Registration**
 Hotel Nikko, Olympic Room, 25th Floor

Sunday, August 23

Nikko Ballroom

Chair: A. L. Burlingame, University of California, San Francisco, CA, USA

8:30
a.m. **MS.1** New Technology for the Large-scale Proteomic Comparison of Human Embryonic Stem Cells, Induced Pluripotent Stem Cells, and Somatic Cells
 Joshua J. Coon, University of Wisconsin, Madison, WI, USA

9:30 **MS.2** Electron Capture Dissociation in Radio-Frequency-Free Cell
 Douglas F. Barofsky, Oregon State University, Corvallis, OR, USA

10:10 Coffee Break

10:50 **MS.3** Decoding the Histone Code by Quantitative Proteomics
 Benjamin A. Garcia, Princeton University, Princeton, NJ, USA

11:30 **MS.4** Data Processing Algorithms for Analysis of High Resolution MSMS Spectra of Peptides with Complex Post-Translational Modifications
 Shenheng Guan, University of California, San Francisco, CA, USA

12:10
p.m. Lunch

Chair: Shenheng Guan, University of California, San Francisco, CA, USA

1:40 **MS.5** Use of Electron Transfer Dissociation to Analyze Combinations of Histone Post-Translational Modifications on an LTQ-Orbitrap
 Shannon Eliuk, University of California, San Francisco, CA, USA

2:20 **MS.6** Electron Capture Dissociation for Structural Studies of Integral Membrane Proteins and Their Modifications
 Julian Whitelegge, University of California, Los Angeles, CA, USA

3:00 **MS.7** O-GlcNAcylation: The Post-Translational Modification that Best Highlights the Value of ETD
 Robert J. Chalkley, University of California, San Francisco, CA, USA

- 3:40 **MS.8** The Use of ECD for Proteomics-wide Identification and Quantification of iso-Asp Residues
Roman A. Zubarev, Karolinska Institute, Stockholm, Sweden
- 4:00 Symposium Registration
Nikko Ballroom Vestibule
- 4:00 Poster Set-up
Carmel & Monterey Rooms
- 6:00 Opening Reception
Golden Gate Room, 25th Floor

Monday, August 24

- 7:30
a.m. **Registration**
Nikko Ballroom Vestibule

Session 1

Nikko Ballroom

- 8:15 Introduction
A. L. Burlingame, University of California, San Francisco, CA, USA
John Stults, Genentech, Inc., South San Francisco, CA, USA

Plenary Lecture

Chair: John Stults, Genentech, Inc., South San Francisco, CA, USA

- 8:30 **1.1** Global Analysis of Small Molecule Interactions with Proteins
Michael Snyder, Stanford University, Stanford, CA, USA

Chair: Connie R. Jimenez, VU University Medical Center, Amsterdam, The Netherlands

- 9:30 **1.2** Membrane-assisted Sample Preparation for Online ESI-MS Analysis of Biomolecules
Juan Astorga-Wells, Karolinska Institute, Stockholm, Sweden and Biomotif AB, Täby, Sweden
- 10:10** **Coffee Break**
- 10:30 **1.3** Two-Dimensional Liquid Chromatography Coupled with ESI-MS for Protein Identification and Quantification
Jim Langridge, Waters Corporation, Manchester, United Kingdom

11:10 **1.4** Targeted Proteomic Approaches Provide Insights into Virion Assembly and Chromatin Remodeling during Viral Infection
Ilena Cristea, Princeton University, Princeton, NJ, USA

11:50 **1.5** Confident Assignment of Post-Translational Modifications Using Top-Down Mass Spectrometry
Julian Whitelegge, University of California, Los Angeles, CA, USA

12:30
p.m. **Lunch**

Session 2

Chair: Ralph Bradshaw, University of California, San Francisco, CA, USA

2:00 **2.1** Protein Quantification through Targeted Mass Spectrometry: The Way Out of Biomarker Purgatory?
Steven A. Carr, The Broad Institute of MIT and Harvard, Cambridge, MA, USA

2:40 **2.2** Proteomics Targeted to Sub-Cellular Compartments and Integration with Genomics for Candidate Biomarker Discovery in Colorectal Cancer
Connie R. Jimenez, VU University Medical Center, Amsterdam, The Netherlands

3:20 **2.3** Towards the Discovery of Biomarkers in Cerebrospinal Fluid by Combining Peptide Ligand Library Treatment and Label Free Protein Quantification on a LTQ-Orbitrap
Florence Roux-Dalvai, CNRS IPBS, Toulouse University, France

Poster Session A

Co-Chairs: David Maltby, University of California, San Francisco, CA, USA
Shannon Eliuk, University of California, San Francisco, CA, USA

4:00 **Carmel and Monterey Rooms**

A.1 Labeling of Peptide Fragmented Mass Spectra in Proteomic Studies
B. Gerrits*, C. Panse, B. Bodenmiller, and R. Schlapbach

A.2 Exact Quantification of Complex Protein Mixtures Using MeCAT—Metal Coded Tagging
R. Ahrends*, U. Bergmann, S. Pieper, B. Neumann, C. Scheler, and M. W. Linscheid

A.3 On the Reproducibility of a Fractionation Procedure for Fish Muscle Proteomics
P. Rodrigues*, T. Silva, F. Jessen, and J. Dias

A.4 Optimization of Peak Capacity in One and Two-Dimensional NanoLC
S. Eeltink, B. Dolman, R. Swart, and G. Tremintin*

A.5 Improving the Utility of Electron-Transfer Dissociation
K. F. Medzihradzky*, S. P. Salas-Castillo, and A. L. Burlingame

- A.6 Enrichment and Characterization of Secreted Glycopeptides Bearing SA₁₋₆Gal β 1-3GalNAc α Structures**
Z. Darula and K. F. Medzihradzky*
- A.7 Enrichment of O-GlcNAc Modified Proteins by the Periodate Oxidation – Hydrazide Resin Capture Approach**
E. Klement, Z. Lipinszky, Z. Kupihar, A. Udvardy, and K. F. Medzihradzky*
- A.8 Proteome Survey Using Affinity Proteomics and Mass Spectrometry**
N. Olsson*, C. Wingren, M. Mattsson, P. James, F. Nilsson, and C. A. K. Borrebaeck
- A.9 Sampling the N-terminal Proteome of Human Serum and Plasma**
P. Wildes* and J. A. Wells
- A.10 Profiling Cell Surface and Secreted Glycoproteins Isolated from Human Thyroid Cancer Cell Lines**
T.-Y. Yen*, N. Haste, A. Castanieto, A. Arcinas, and B. Macher
- A.11 Chemical Cross-linking in Complex Mixtures**
M. J. Trnka* and A. L. Burlingame
- A.12 Rapid MRM Assay Development Strategies – Intelligent Software and Acquisition Strategies for Highest Productivity**
S. Mollah*, M. M. Champion, and C. L. Hunter
- A.13 Structural Proteins in the Complex Phage 201phi2-1**
S. Weintraub*, J. A. Thomas, K. Hakala, P. Serwer, and S. C. Hardies
- A.14 A Quick Method for Differential PTM Analysis of Hypermodified Proteins by FTICR/ECD/MS/MS and Bioinformatics**
F. Li*, S. Guan., F. Chu, R. Talroze, and A. L. Burlingame
- A.15 Improved Data Mining by Using TPP-based Analysis Workflows for Searching MS/MS Data**
A. Quandt*, L. Malstroem, H. Lam, D. Shteynberg, and R. Aebersold
- A.16 Microwave-assisted Phosphoproteomics**
P. Liu* and W. Sandoval
- A.17 Proteome Analysis of Apoplastic Proteins in Rice Shoot Respond to Salt Stress**
Y. Song, A. L. Burlingame, and Y. Guo*
- A.18 Investigation into the Use of Lys-N Combined with Electron Transfer Dissociation on a Quadrupole Time-of-Flight Mass Spectrometer for Peptide Sequencing**
J. Langridge*, J. Brown, S. Mohammed, N. Taouatas, I. D. G. Campuzano, and A. J. R. Heck

Tuesday, August 25

Session 3

Plenary Lecture

Chair: James Wells, University of California, San Francisco, CA, USA

Nikko Ballroom

8:30

a.m.

- 3.1** Quantitative Analysis of Proteome Localisation and Dynamics
Angus Lamond, Wellcome Trust Biocentre, University of Dundee, Scotland, United Kingdom

Chair: Nevan Krogan, University of California, San Francisco, CA, USA

- 9:30 **3.2** Post-Translational Adenosine Monophosphate (AMP) Modification of Proteins
Antonious Koller, Stony Brook University, Stony Brook, NY, USA
- 10:10** **Coffee Break**
- 10:30 **3.3** Dissecting the Structure of the Human Spliceosome by Looking at Its Pieces
Melissa Jurica, University of California, Santa Cruz, CA, USA
- 11:10 **3.4** Protein Complexes and Functional Pathways in *S. cerevisiae* and *E. coli*
Jack Greenblatt, University of Toronto, Ontario, Canada
- 11:50 **3.5** N-Terminomics: High Confidence, Broad Dynamic Range Coverage Utilizing Novel Polymers for Proteomics Reveals the Functional State of the Proteome
Christopher M. Overall, University of British Columbia, Vancouver, British Columbia, Canada
- 12:30**
p.m. **Lunch**

Session 4

Chair: Charles Craik, University of California, San Francisco, CA, USA

- 2:00 **4.1** Activity-based Proteomics: Applications for Enzyme and Inhibitor Discovery
Benjamin F. Cravatt III, The Scripps Research Institute, La Jolla, CA, USA
- 2:40 **4.2** Global Profiling of Proteolytic Cleavage Sites in Apoptosis
Sami Mahrus, University of California, San Francisco, CA, USA
- 3:20 **4.3** N-terminal & 'Genome free' Proteomics; *de novo* Sequence Analysis by a Combination of LysN Protein Digestion and Electron Transfer Dissociation
Albert J. R. Heck, Netherlands Proteomics Center, Utrecht, The Netherlands

Poster Session B

Co-Chairs: Katalin Medzihradzky, University of California, San Francisco, CA, USA
Jonathan Trinidad, University of California, San Francisco, CA, USA

- 4:00 **Carmel and Monterey Rooms**
- B.1** **Elucidating Methyltransferase Target Amino Acid Residues and Downstream Modification Events by Quantitative Mass Spectrometry**
S. M. Eliuk*, F. Chu, B. Panning, and A. L. Burlingame

- B.2 Ecotoxicoproteomics to Study Microcystin-LR Effects in Medaka Fish**
M. Edery*, M. Malécot, K. Mezhoud, A. Marie, D. Praseuth, and S. Puiseux-Dao
- B.3 Analysis of the Death Inducing Signaling Complex (DISC) Using Mass Spectrometry**
V. Pham*, Z. Jin, R. Pitti, Y. Li, D. Lawrence, A. Ashkenazi, and J. Lill
- B.4 Proteome-scale Identification of Mitochondrial Transit Peptide Cleavage Sites**
E. Crawford* and J. A. Wells
- B.5 Enrichment and Analysis of Phosphopeptides Shaved from Membrane Fraction of Salt-stressed Arabidopsis**
I.-F. Chang*, J.-L. Hsu, L.-Y. Wang, and S.-Y. Wang
- B.6 Identification of Protein-Protein Interactions Using Chemical Cross-linking and CID and ETD Tandem Mass Spectrometry**
X. Du*, J. Rorie, S. Chowdhury, J. Adkins, G. Anderson, and R. Smith
- B.7 Quantitative 2D-Gel Analysis of Isotope Encoded Proteins Using SERRS Detection**
G. Knudsen*, B. M. Davis, S. K. Deb, Y. Loethen, R. Gudihal, P. Perera, D. BenAmotz, and V. J. Davisson
- B.8 Global Analysis of Caspase Proteolysis During Inflammation**
N. Agard* and J. A. Wells
- B.9 Two Mass Spectrometry Based Approaches for the Investigation of the Heparin Interactome**
A. Ori*, M. C Wilkinson, and D. G. Fernig
- B.10 Electron Transfer Dissociation Analysis of the Urinary Peptidome in Pregnancy**
S. Hart*, R. Blankley, and S. Guan
- B.11 Non-Targeted Characterization of Glycopeptides in Lysosomal Storage Disease Samples**
C. Dorschel*, R. R. Sprenger, J. M. F. G. Aerts, J. P. C. Vissers, and S. J. Geromanos
- B.12 A Novel Combinatorial Library/Mass Spectrometric Approach for Detection of Autoantibody Signatures to Cancer-Associated O-Glycoprotein Epitopes**
S. B. Lavery*, S. K. Kracun, O. Blixt, E. Clo, K. J. Jensen, and H. Clausen
- B.13 Peak Extraction and Deisotoping of Low-Level MSMS Spectra from Quadrupole/TOF Instruments**
J. Chen*, J. Trinidad, S. Guan, and A. L. Burlingame
- B.14 Network Analysis of Gcn5 HAT Complexes Refines the Organizational Makeup of the SAGA, SliK (SALSA) and ADA Complexes**
M. Sardu*, K. Lee, S. Swanson, J. Workman, L. Florens, and M. P. Washburn
- B.15 Quantitative Label-free Analysis of Complex Protein Mixtures through the MFPaQ Software**
E. Mouton Barbosa*, D. Bouyssié, A. Gonzalez de Peredo, F. Roux-Dalvai, O. Burlet-Schiltz, and B. Monsarrat
- B.16 Pigment Epithelium-derived Factor: A Biomarker of Preeclampsia with a Role in the Pathogenesis of the Syndrome**
K. Williams*, Y. Zhou, and S. Fisher
- B.17 Quantitative Comparison of 13-lined Ground Squirrel Kidney Proteins in Six Stages of Mammalian Hibernation**
N. M. Heidlebaugh, S. L. Martin, and L. E. Epperson*

Wednesday, August 26

Session 5

Chair: Jonathan Trinidad, University of California, San Francisco, CA, USA

Nikko Ballroom

8:30

a.m. **5.1** Characterization of the Velos, an Enhanced LTQ Orbitrap, for Proteomics
Jesper Velgaard Olsen, University of Copenhagen, NNF Center for Protein Research, Copenhagen, Denmark

9:10 **5.2** Analysis of the Yeast Kinase-Substrate Networks by Quantitative Phosphoproteomics
Bernd Bodenmiller, ETH - Swiss Federal Institute of Technology, Zurich, Switzerland

9:50 **5.3** Quantitative Phosphoproteomics to Define Kinase-Substrate Relationships in Cell Division
Judit Villén, Harvard Medical School, Boston, MA, USA

10:30 Coffee Break

Plenary Lecture

Chair: John Stults, Genentech, Inc., South San Francisco, CA, USA

10:50 **5.4** Global Analysis of Cdk1 Substrate Phosphorylation Sites *in vivo*
David O. Morgan, University of California, San Francisco, CA, USA

11:50

a.m. **Lunch**

Session 6

Chair: Ilena Cristea, Princeton University, Princeton, NJ, USA

1:20

p.m. **6.1** Characterization and Quantification of Phosphosites in the Proteome of Human Primary T-Lymphocytes
Emilio Gelpi, Instituto Investigaciones Biomedicas, Barcelona, Spain

2:00 **6.2** Analysis of Ubiquitin Chain Editing by Quantitative Mass Spectrometry
Donald S. Kirkpatrick, Genentech, Inc., South San Francisco, CA, USA

2:40 **6.3** Age Determination in the Adult Human Brain and Body Using Bomb-Carbon
Kirsty L. Spalding, Karolinska Institute, Stockholm, Sweden

Poster Session C

Co-Chairs: Robert Chalkley, University of California, San Francisco, CA, USA
Nicholas Hertz, University of California, San Francisco, CA, USA

3:20 Carmel and Monterey Rooms

- C.1 Epitope Tagging of Endogenous Proteins in Human Cells for Discovery of Novel Protein/Protein Interactions**
T. Waldman*, J.-S. Kim, W. Lane, and F. Bunz
- C.2 Quantitative Analysis of the Phosphoproteome of Resting and Activated Human Primary T Cells**
P. Ruperez*, J. A. Oses-Prieto, Ana Gago, and A. L. Burlingame
- C.3 ATAQS Computational Software Tool for High Throughput Transition Optimization and Validation for SRM**
M.-Y. Brusniak*, D. Campbell, J. Chen, M. Christiansen, E. Deutsch, C. Kwok, S. Letarte, H. Ramos, P. Picotti, L. Reiter, J. Watts, and R. Aebersold
- C.4 Mass-Spectrometric Identification and Relative Quantification of N-linked Cell Surface Glycoproteins**
B. Wollscheid*, D. Bausch-Fluck, C. Henderson, R. O'Brien, M. Bibel, R. Schiess, R. Aebersold, and J. D. Watts
- C.5 Chronic Ethanol Feeding Affects Proteasome Interacting Proteins**
M. P. Bousquet-Dubouch*, S. Nguen, D. Bouyssié, O. Burlet-Schiltz, S. W. French, B. Monsarrat, and F. Bardag-Gorce
- C.6 Phosphorylation Dynamics at Synapses in the Central Nervous System**
J. C. Trinidad*, A. Thalhammer, R. Schoepfer, and A. L. Burlingame
- C.7 Linaclotide, a Novel Peptide Therapeutic Agent in Clinical Development for the Treatment of IBS-C and Chronic Constipation is Digested in the Mouse and Human Small Intestine to Small Peptides**
M. Kessler*, R. W. Busby, J. D. Wakefield, W. P. Bartolini, P. Germano, A. P. Bryant, C. B. Kurtz, and M. G. Currie
- C.8 Large Scale Multiplex Stable Isotope Dimethyl Labeling Applied to the Quantitative Analysis of Tyrosine Phosphorylation**
P. Boersema*, L. Y. Foong, V. Ding, S. Lemeer, S. Mohammed, R. Raijmakers, B. van Breukelen, J. Boekhorst, A. B. H. Choo, and A. J. R. Heck
- C.9 Structural Characterization of Novel Components from the Venom of the Mexican Scorpion *Vaejovis mexicanus smithi* by Electron Capture Dissociation and Electron Transfer Dissociation**
S. P. Salas-Castillo*, K. F. Medzihradzsky, S. Guan, and A. L. Burlingame
- C.10 Proteomics Analysis Reveals a New Player Involved in DNA Repair and/or Replication**
J. M. Gilmore*, M. E. Sardu, S. Venkatesh, B. Stutzman, and M. P. Washburn
- C.11 Quantitative Comparison of the *Shigella dysenteriae* Proteome Assessed by Two Label-Free Global Profiling Methods, APEX and 2D Gels**
S. Kuntumalla*, J. C. Braisted, S.-T. Huang, P. P. Parmar, D. J. Clark, H. Alami, Q. Zhang, A. Donohue-Rolfe, S. Tzipori, R. D. Fleischmann, S. N. Peterson, and R. Pieper
- C.12 Characterization of Protein Kinase C-catalyzed CYP3A4 Phosphorylation by LC Tandem Mass Spectrometry**
Y. Q. Wang*, S. Guan, A. L. Burlingame, and M. A. Correia

- C.13 Analysis of H5N1 Influenza Hemagglutinin Glycosylation by LC/MS/MS Utilizing Hydrazide Capture SPE and HILIC Separation of Intact Glycopeptides**
T. A. Blake*, T. L. Williams, J. L. Pirkle, and J. R. Barr
- C.14 Mapping the Chromatin Structure Controlling Life Cycle Progression of the Human Malaria Parasite**
A. Saraf*, S. Cervantes, L. Florens, and K. Le Roch
- C.15 Developing Optimized Sensitivity for Proteomic Characterization of Minimal Numbers**
J. A. Osés-Prieto*, D. Maltby, and A. L. Burlingame
- C.16 A Proteomics Approach to Overcoming Bacterial Drug Resistance: The Ribosomal QconCAT**
J. Barber, Z. Al-majdoub*, and S. Gaskell
- C.17 Proteomic Analysis of the Venom from the Mexican Scorpion *Centruroides limpidus limpidus***
C. V. Ferreira Batista*, O. Villa-Hernández, L. Hernández Orihuela, V. Pando, and L. D. Possani

6:00 **Reception**

Julia Morgan Ballroom

7:00 **Conference Dinner**
Julia Morgan Ballroom

Thursday, August 27

Session 7

Chair: Emilio Gelpi, Instituto de Investigaciones Biomedica, Barcelona, Spain

Nikko Ballroom

- 8:30
a.m. **7.1** Signaling to Transcription Networks in Nerve Injury Response
Michael Fainzilber, Weizmann Institute of Science, Rehovot, Israel
- 9:10 **7.2** Regulation of Neuronal Protein Levels at Subcellular Sites Distant from the Cell Body
Jeffery L. Twiss, A.I. duPont Hospital for Children, Wilmington, DE, USA
- 9:50 **7.3** Organelle Proteomics: Linking Axonal Transport to Nerve Regeneration
Valeria Cavalli, Hope Center for Neurological Diseases, Washington University, St. Louis, MO, USA
- 10:30** **Coffee Break**
- 11:00 **7.4** Quantitative Phosphoproteomics Identifies Sites in K-Cl Co-Transporters that Regulate Cell Volume and Neuronal Excitation
Jesse J. Rinehart, Yale University, New Haven, CT, USA
- 11:40**
a.m. **Lunch**

Session 8

Chair: Pete Wildes, University of California, San Francisco, CA, USA

- 1:40
p.m. **8.1** A Proteomics Approach to Overcoming Bacterial Drug Resistance: The Ribosomal QconCAT
Jill Barber, University of Manchester, Manchester, United Kingdom
- 2:20 **8.2** Quantitative Proteomics Analysis of C/EBP α Transcription Factor Complexes in Leukemia
Jarrod A. Marto, Dana-Farber Cancer Institute, Harvard Medical Center, Boston, MA, USA
- 3:00 **8.3** Rapid, Near Proteome-wide, Quantitative Analysis of Aneuploid Budding Yeast
Noah Dephore, Harvard Medical School, Boston, MA, USA

Plenary Lecture

Chair: A. L. Burlingame, University of California, San Francisco, CA, USA

- 3:40 **8.4** Advancing Epigenetics Research by Proteomics: Technologies, Applications and Perspectives.
Ole Nørregaard Jensen, University of Southern Denmark, Odense, Denmark
- 4:40 **Closing Remarks**
- 5:00 **Adjourn**