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 a.m. 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 a.m. MS.3 Decoding the Histone Code by Quantitative Proteomics
Benjamin A. Garcia, Princeton University, Princeton, NJ, USA

11:30 a.m. 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 p.m. 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 p.m. 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 p.m. 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. Medzihradszky*, S. P. Salas-Castillo, and A. L. Burlingame
A.6 Enrichment and Characterization of Secreted Glycopeptides Bearing SA$_{1-0}$Gal$_{1-3}$GalNAc$_x$ Structures
Z. Darula and K. F. Medzihradszky*

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. Medzihradszky*

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

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 Medzihradszky, 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

B.7 Quantitative 2D-Gel Analysis of Isotope Encoded Proteins Using SERRS Detection

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

B.12 A Novel Combinatorial Library/Mass Spectrometric Approach for Detection of Autoantibody Signatures to Cancer-Associated O-Glycoprotein Epitopes
S. B. Levery*, 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. Sardiu*, 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 Insitute, 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

C.4 Mass-Spectrometric Identification and Relative Quantification of N-linked Cell Surface Glycoproteins

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

C.8 Large Scale Multiplex Stable Isotope Dimethyl Labeling Applied to the Quantitative Analysis of Tyrosine Phosphorylation

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. Medzihradszky, 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. Sardiu, 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

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. Oses-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

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/EBPα 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 Dephoure, 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