

US HUPO NEWS

FALL/ WINTER 2011

Welcome to the third issue of US HUPO News. Our goal is to increase the visibility of US HUPO interests and activities and to provide a medium for communication among US HUPO members and the greater Proteomics community.

This issue includes the President's Corner, update on the US HUPO San Francisco conference, the HUPO World Congress in Boston, and 2012 membership renewal for US HUPO.

Please contact us with your feedback and ideas for topical items to include in the next newsletter.

Thank you.

US HUPO Newsletter Committee -

Laura Beretta, Scott Gerber, Brian Haab, Stan Hefta and Josh LaBaer

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President's Corner



Dear US HUPO Members and Friends—

This year has been a productive time for US HUPO. Our annual meeting in Raleigh NC in March was outstanding. Plans for the 4-7 March 2012 meeting in San Francisco are far advanced. The Organizing Committee of Karin Rodland (chair), Ralph Bradshaw, Susan Fisher, Josh LaBaer, and Joseph Loo has an excellent program of core proteomics work, speakers from cognate areas, and Sunday short courses. Check www.ushupo.org; please come/stimulate your students and colleagues to come. The theme is "The Future of Proteomics". The abstracts deadline: 9 January.

We hope you enjoy, value, and share the US HUPO Newsletter. We welcome your suggestions of topics for Talk tutorials on proteomics technology platforms. I encourage you to engage in the Wiki on the TechTalks (iTRAQ, Skyline so far). We hope you value your membership; please renew for the year starting 1 January, whether you come to the annual meeting or not.

USHUPO is the host organization for the HUPO World Congress of Proteomics in Boston 9-13 September 2012. The congress is held in the Western Hemisphere every third year. The organizing committee chaired by Mike Snyder includes Catherine Fenselau, Bill Hancock, and yours truly, plus others from the hemisphere. The program has 15 theme tracks for submitted presentations (www.hupo.org). We have kept registration quite modest to encourage maximal attendance.

Finally, we encourage you to consider becoming involved in the

HUPO-launched global Human Proteome Project (HPP) to detect and characterize proteins from all 20,300 protein-coding genes. You can contribute to the mass spectrometry, protein capture, and knowledgebase resource pillars for HPP or its complementary programs: the Chromosome-centric C-HPP chaired by Young-Ki Paik (15 chromosomes claimed by national groups so far) and the Biology and Disease-driven B/D-HPP chaired by Ruedi Aebersold, emphasizing biological networks. A detailed description appeared in July (Legrain et al, *Mol Cell Proteomics* 2011;10(7):M111.009993). Resources include the Human Protein Atlas v8, with tissue expression and intracellular localization images for 11,760 proteins; the Peptide Atlas, with re-analyzed combinations of datasets for organ and biofluid proteomes; and the rapidly emerging SRM Atlas, offering every investigator reference spectra and guidance to several commercially available heavy-labeled proteotypic peptides distinctive for each of the 20,300 protein products in humans. We have major progress on the way to the goals of the HPP.

We welcome your feedback. See you in San Francisco and Boston.



Gil Omenn
US HUPO President
(2010-2012)

Upcoming Events Save these dates!

**US HUPO 8th
Annual Conference**
March 4-7, 2012
Palace Hotel, San Francisco, CA

HUPO World Congress 2012
September 9-13, 2012
Hynes Convention Center
Boston, MA

Renew your membership for 2012.

Check out renewal / new membership form on the last page of this newsletter. Or, renew quickly online at www.ushupo.org.

Announcements for Student / Post-Docs

New for 2012 Membership. A \$75 unlimited multi-year membership for students and post-docs. Renew or join at the \$75 student / post-doc member rate and your membership remains valid for as long as you are a full-time student or post-doctoral fellow. The year following your \$75 unlimited multi-year dues you will receive a special renewal form asking for proof of your status as a student or post-doc. You will then be renewed for the new year at no charge.

Career Development Sessions at US HUPO 2012 Conference in San Francisco. Two concurrent sessions are dedicated to student, post-doc and junior faculty researchers. One session will focus on Applications (chaired by Cathy Costello) and the other on Technology (chaired by Fred Regnier). To make sure your abstract is considered for a talk in one of these sessions, respond 'yes' to the special career development session questions during abstract submission.

Postcards from...

Raleigh



US HUPO
2011 Raleigh
Conference
Organizers:
David Muddiman,
Joseph Loo, and
Adam Hawkridge.



Receptions are fun!

Geneva



The famous Geneva lake fountain at night.



HUPO Council President Cathy Costello 'clowning around'

US HUPO

from genes to function

8th Annual Conference

The Future of Proteomics

March 4 - 7, 2012

Palace Hotel • San Francisco, CA

SHORT COURSES

Sunday, March 4, 2012

See next page for course description

EVENING WORKSHOPS

- Data Repositories
- Moving Mass Spec into the Clinical Lab
- Pharma and Proteomics
- Targeted Proteomics

IMPORTANT DATES

January 9, 2012

Abstract Submission

Student and Post-Doc Travel Support

February 10

Hotel Reservations

February 15

Advance Conference and Short Course Registration

Conference Sessions

Talks from selected submitted abstracts will be included in each session.

- Bioinformatics at the Genome / Proteome Interface
- Biomarkers and Disease
- Engineering Proteins in the Plant World
- Frontiers in Mass Spectrometry Technologies
- Infectious Diseases
- Leveraging Genomics for Proteomics
- Metabolomics and Lipidomics
- Non-Traditional Proteomics
- Novel Applications
- Pan-PTMs -Beyond Phosphorylation
- Proteomic Data Repositories
- Signaling Pathways
- Career Development Sessions on Biotechnology and Applications featuring young researchers

Plenary Speakers

Ruedi Aebersold, *ETH Zurich*
Samir Hanash, *FHCRC*
Michael Snyder, *Stanford University*
Paul Spellman, *OHSU, NCI*
Keith Yamamoto, *UCSF*

Conference Organizers

Karin Rodland, *PNNL*
Ralph Bradshaw, *UCSF*
Joshua LaBaer, *Arizona State University*
Susan Fisher, *UCSF*
Joseph Loo, *UCLA*



SFCVB photo by Kerrick James



SFCVB photo by Phillip H. Coblenz

**Submit your abstract today!
Deadline is January 9, 2012**

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proteome
Research**

Visit www.ushupo.org for details

Short Courses - Sunday, March 4, 2012

Short courses are half and full-day as noted below. All courses will be at the Palace Hotel. There is no on-site registration for short courses. Tuition is \$100 for half-day courses and \$150 for full-day courses.

FULL-DAY COURSES

Quantitative Bottom-Up Proteomics: Discovery and Targeted Analysis (Full-day, 9 am – 4 pm)

Instructors: Sanford Markey, *Bethesda, MD*; Lisa Renee Olano, *Bethesda, MD*; Leesa Deterding, *RTP, NC*; Olga Vitek, *Purdue University*

Modern mass spectrometers provide a variety of platforms appropriate for the quantitative analyses of peptides from proteins. This 6-hour course will approach the resulting options broadly, covering topics from MS1 ion current quantification to the myriad of acronyms (ITRAQ, MS(E), SILAC, MRM, SISCAPA). We will present and discuss the many technical issues associated with quantitative analysis resulting from sample collection and preparation, protein digestion, and peptide chromatography; standards selection and use; MS1 data analysis (chromatographic run alignment, normalization); MS2 analysis (peak assignments, transition monitoring); statistical analyses of results; and study design.

Level: Intermediate (Intended for those doing or planning quantitative proteomics; familiarity with mass spectrometry assumed)

Targeted PTM Analysis (Full-day, 9 am – 4 pm)

Organized by Yingming Zhao, *University of Chicago*

Post-translational modifications (PTMs) represent a major vehicle to diversify a cellular proteome, the inventory of all protein species in an organism. Given the high abundance and diversities of PTMs, they are likely the most complex regulatory mechanisms in cells. Accordingly, systematic PTM analysis is critical to the understanding of cellular physiology and diseases.

This course is designed for both mass spectrometrists and biologists who want to understand more about the fundamental and practical aspects of systematic PTM analysis using mass spectrometry. Topics that will be discussed include: (i) an introduction to PTMs; (ii) sample preparation for PTM analysis; (iii) HPLC/MS/MS analysis and manual verification of PTM peptides; (iv) Full-spectrum PTM analysis using non-restrictive sequence alignment algorithms; (v) proteomics analysis of PTMs: phosphorylation, ubiquitination, glycosylation, and lysine acetylation as case studies. Examples of troubles and challenges in performing these experiments will be chosen from the instructors' personal experience. Ample time will be provided for general discussion of the topics presented and other current topics in PTM analysis.

Level: Intermediate (intended for those who have some background on mass spectrometry or PTMs, and want to advance their knowledge and skills).



SFCVB photo by Phillip H. Coblenz



SFCVB photo by Kerrick James



SFCVB photo

Half-Day Short Courses - Sunday, March 4, 2012

Manual Interpretation of Electron Transfer Dissociation (ETD) Mass Spectra of Peptides

(Half-day, 9 am - 12 pm)

Instructor: Donald F. Hunt, *University of Virginia*

Electron transfer dissociation mass spectrometry is a break-through technology for sequencing post-translationally modified peptides and proteins. In this technique, radical anions of polyaromatic hydrocarbons (fluoranthene and azulene) are employed to transfer electrons to the carbonyl group in the polyamide backbone of multiply charged peptides generated by electrospray ionization. Capture of an electron into the peptide backbone reduces the positive charge on the ion by one, and forms a carbonyl radical anion that then abstracts a proton from a nearby protonated amino group. The resulting carbonyl radical triggers cleavage of the adjacent nitrogen-carbon bond to produce fragments of type c' and z .

The purpose of the workshop is to provide instruction on how to manually interpret peptide ETD mass spectra. In the morning session (9 am to 12 pm) we will begin with an overview of the technique and present examples that illustrate how superior this approach is to classical collision activated dissociation MS/MS. Following a lengthy tutorial about ion structures, fragmentation pathways, predictable changes in fragment ion isotope patterns, etc., we will outline a general approach for the manual interpretation of peptide ETD spectra and solve the sequence of several post-translationally modified peptides. Homework problems will be assigned for the afternoon session from 12:00 pm - 4:15 pm. We will then reconvene, go over the assigned problems, and hopefully tackle interpretation of several spectra recorded on more highly charged (and larger) peptides (+4 and +5).

A packet of lecture notes and handouts will be provided. Attendees should bring an inexpensive calculator, pad of paper, and a small ruler.

Level: Intermediate to advanced.



Palace Hotel,
San Francisco

Stable and Transient Protein-Protein Interactions: Discovery, Quantification and Validation

(Half-day, 1 - 4 pm)

Organizer: Ileana M. Cristea, *Princeton University*

Dynamic protein interactions carry out the majority of the processes within a cell, including cellular responses to environmental stimuli and pathogens. Isolation of protein complexes and characterization of protein-protein interactions provide critical insights into their biological functions. An ideal isolation would maintain the protein-protein interaction or the protein assembly as close as possible to the original state in the cell. Therefore, proteomic-based methodologies that can access stable and transient interactions are invaluable for diverse studies, such as those of cell cycle or pathogen infection that require characterization of temporal and spatial protein interactions. This course will cover fundamental and practical aspects of studying protein interactions. Topics discussed will include: 1) protein function considerations for workflow design, 2) cell lysis methods for efficient protein extraction, 3) critical choices for optimizing an immunoaffinity purification experiment, including resin type and speed of isolation, 4) denaturing and non-denaturing methods of eluting captured protein complexes, 5) assessing the specificity of interactions using bioinformatics approaches, metabolic labeling with stable isotopes, or peptide labeling with isobaric tags, 6) challenges for assessing direct or indirect interactions, and 7) aspects of data analysis and generation of interaction networks. Detailed protocols will be provided, and enough time will be set aside for discussing these topics from either a mass spectrometry or biology perspective.

Level: Beginner to advanced.



HUPO

Boston 2012

11th World Congress
September 9 – 13, 2012

Hynes Convention Center
Boston, Massachusetts

IMPORTANT DATES

January 14

Registration and Abstract
Submission open

February 28

Early Bird Registration
deadline

May 4

Abstract submission
deadline

June 15

Regular Registration
deadline

August 15

Hotel Reservation
deadline



KEYNOTE SPEAKERS

Neil L. Kelleher

Northwestern University



Susan Lindquist

*Whitehead Institute for Biomedical Research
Massachusetts Institute of Technology*



Stuart L. Schreiber

*Broad Institute of Harvard and MIT
Harvard University*

PLENARY SPEAKERS

Natalie Ahn, *University of Colorado at Boulder*

Wolfgang Baumeister, *Max Planck Institute for
Biochemistry*

Anne-Claude Gingras, *Samuel Lunenfeld Research
Institute*

Samir Hanash, *Fred Hutchinson Cancer Research Center*

Hanno Langen, *Roche Molecular Laboratories*

Ulf Landegren, *Uppsala University*

Jeremy Nicholson, *Imperial College London*

Jun Wang, *Beijing Genomics Institute*

ORGANIZERS

Michael P. Snyder, *Chair, Stanford University*

Catherine C. Fenselau, *University of Maryland*

William Hancock, *Northeastern University*

Gilbert S. Omenn, *University of Michigan*

**INITIATIVES WORKSHOPS
POSTERS • EXHIBITION
INDUSTRY LUNCH SEMINARS**

ORAL SESSIONS

Data Galore: Bioinformatics and Databases

*The Business of Biology: BioPharma /
Biotherapeutics and Toxicology*

Beyond Genomics: Proteomics of Cancers

Clinical Insights: Disease Proteomics

*A World Unseen: Microbes & Infectious
Diseases*

Personal Proteomics: Diagnostics and Targets

*Charging it up: Post-Translational
Modifications I*

A Degrading Experience: Post-Translational II

Creating the Future: Emerging Technologies

Express Your Phenotypes: Epigenetics

*Searching Within: Membranes and
Organelles*

*Small Connections: Metabolomics / Protein
Small Molecule Interactions*

*Seeing the Whole Picture: Cell Signaling /
Systems Biology*

*Staying Connected: Regulatory Networks /
Protein-Protein Interactions*

*Catch and Display: Protein Capture
Agents + Arrays*



WWW.HUPO2012.COM

2012 Membership Form for Renewals or New Members

Complete the form below or go to [Online Membership Form](#).

Member Benefits

- \$200 discount on conference registration fees;
- Support the new "US HUPO News" newsletter and participate in the TechTalk discussion wiki online;
- Option to purchase online subscription for Molecular and Cellular Proteomics (MCP) at discounted rate of \$70;
 - Access to online Employment Center;
- Opportunity for involvement in US HUPO-sponsored initiatives;
 - Student travel stipends to attend the annual conference.
 - Short courses at annual conference.
- Support of U.S.-based proteomics community.

Name Affiliation

Address

City, State, Zip or Postal Code, and Country

Phone Email

Membership Dues. Membership is based on the calendar year, January 1 - December 31. US HUPO is pleased to offer multi-year membership savings for regular memberships (see rates below). Student/Post-Doc membership is offered on a one-year basis only. Student/Post-Doc membership is available to full-time students or post-doctoral fellows.

New! Student and Post-Doc Membership is now Multi-Year Unlimited for a \$75 one-time dues payment. After you join or renew at the new Student / Post-Doc rate of \$75 your membership is valid for as long as you are a student or post-doctoral fellow. You will receive a special renewal form in 2013 that will ask for proof of your status as a full-time student or post-doc.

Regular 1-year Membership (Jan 1 - Dec 31, 2012)	\$100
Regular 2-year Membership (Jan 1, 2012 - Dec 31, 2013)	\$175
Regular 3-year Membership (Jan 1, 2012 - Dec 31, 2014)	\$250
Student/Post-Doc Membership Multi-Year Unlimited	\$75

Select Membership Type: Regular 1-yr, \$100 Regular 2-yr, \$175 Regular 3-yr, \$250 Student/Post-Doc*, \$75

*Applies to full-time students and post-doctoral fellows. Please email or fax a copy of student ID or letter from advisor with this form as proof of status.

MCP Subscription Options: \$70, Online subscription

Payment:

- Check payable to US HUPO. Must be payable in U.S. dollars through a U.S. bank.
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