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EDITOR'S NOTE

Dear HUPO friends,

Welcome to the Q3 HUPOST 2015, we have a lot in store for you this time. I would like to take the opportunity to thank all contributors to this HUPOST. They have all provided great pieces for you!

Firstly, I am proud to introduce the new HUPO tagline as a result of the recent tagline competition. Among many smart and funny contributions, Tiannan Guo suggested the winning tagline, "HUPO | translating the code of life". The tagline encapsulates everything that HUPO works on, from understanding single proteins to dynamic spatiotemporal networks, from

understanding a signaling pathway to studying human life!

On a less happy note, it is with great sorrow that we announce that Tom Fehniger recently passed away. Read the memorial written by György Marko-Varga.

The 14th HUPO World Congress in Vancouver is soon to start. The theme, 'Translating Proteomics and Allied -Omics to the Clinic', will underpin the need for collaboration and cooperation, and promises an interesting and fruitful event. You can read more in

the great congress update below. I am myself truly looking forward to the meeting in the city of the Canucks, and hope to see you all there!

A successful example of such a collaboration is the Human Proteome Project. The chair of HPP, Gil Omenn, has written an inspiring summary of the insights from the recent 3rd annual C-HPP Special Issue in JPR about putting the missing proteins in the spotlight.

In this issue we are pleased to highlight the 2015 HUPO Award Winners. Please join me in congratulating these outstanding scientists on their accomplishments. Awards will be presented at HUPO 2015, in Vancouver, and the winners will present talks during the Award Ceremony.

We have observed an increasing number of young researchers eager to participate in our community. PhD-students and postdocs now represent the largest group of members in HUPO. In line with this the newly started Early Career Initiative has arranged a mentoring day and a manuscript competition in Vancouver. The three finalists in the manuscript competition are revealed in this newsletter, make sure to support them on-site in Vancouver for their oral presentations too! We are glad to see such an increasing interest from young researchers and I am convinced that these new-to-the-field scientists will

be majorly involved in the future of HUPO and the shaping of proteomics.

I hope you will enjoy reading the newsletter.

Cheers and see you in Vancouver!

Emma



Emma K. Lundberg, HUPOST Editor

Stories, highlights, news, and announcements are gladly accepted for inclusion in the HUPOST. To contribute please email the HUPO Office at office@hupo.org.

WELCOME TO HUPO VANCOUVER 2015!



HUPO AWARDS 2015 | meet the winners

It is with great enthusiasm that we present the 2015 HUPO Award Winners! Please join us in congratulating these outstanding scientists on their accomplishments. The awards will be presented at HUPO 2015 in Vancouver, BC, and the winners will present a brief talk during the Congress award session.



Amanda Paulovich, *Fred Hutchinson Cancer Research Center, Seattle, Washington*

Distinguished Achievement in Proteomic Sciences Award

Sponsored by the *Journal of Proteome Research*

Dr. Amanda Paulovich is awarded the HUPO Achievement Award 2015 for her significant impact in advancing the accuracy/precision of clinical proteomic mass spectrometry. She has been in the forefront of developing targeted proteomic assays based on Multiple Reaction Monitoring mass spectrometry technology, which can be multiplexed, standardized, reproduced, and shared across laboratories and instrument platforms.

Science and Technology Award

Sponsored by the *HUPO Industrial Advisory Board*



The SISCAPA Team, from left to right: **Prof. Terry Pearson**, **Dr. Morty Razavi**, **Dr. Selena Larkin**, **Dr. N. Leigh Anderson**, **Matt Pope**

Leigh Anderson, Selena Larkin, and Morteza Razavi, *SISCAPA Assay Technologies, Inc., Washington, DC*

The SISCAPA team is collectively awarded the HUPO Science and Technology Award 2015 for the development of the SISCAPA (Stable Isotope Standards and Capture by Anti-Peptide Antibodies) technology. The SISCAPA assays enable targeted quantitation of proteins and peptides from complex biological samples. The SISCAPA process involves up-front trypsin digestion of the sample followed by immunocapture enrichment of proteotypic peptides that are surrogates for the proteins of interest. Stable isotope labeled peptides are spiked into each sample for relative quantitation of the target molecules via quantitative mass spectrometry (MS).

Distinguished Service Award

Prof. Catherine Costello is awarded the Distinguished HUPO Service Award for her long-term dedication to promote HUPO and HUPO activities.



Catherine Costello, *Center for Biomedical Mass Spectrometry, Boston University School of Medicine*

HUPO AWARDS 2015 | meet the winners



From left: **Akhilesh Pandey**, *Institute of Genetic Medicine and Department of Biological Chemistry, Oncology and Pathology, John Hopkins University School of Medicine, Baltimore, USA*

Bernhard Kuster, *Technische Universitat Munchen, Germany*

Discovery in Proteomic Sciences Award

Professors Bernhard Kuster and Akhilesh Pandey are jointly awarded the 2015 HUPO Discovery Award for their independent large-scale mass spectrometry-based studies of the human proteome. They investigated a wide range of tissues and cell lines with advanced instruments and made their results, published in *Nature* in May 2014, publicly available through ProteomeXchange for reanalysis by others throughout the proteomics community. Their data were rapidly incorporated into the ongoing Human Proteome Project of HUPO and stimulated renewed interest in confirmation and validation of protein identifications.



Jennifer Van Eyk, *Cedars Sinai Medical Center, Los Angeles, CA*

Translational Proteomics Award

Sponsored by *Translational Proteomics (Elsevier)*

Dr. Jennifer Van Eyk is awarded the HUPO Translational Proteomics Award 2015 for her substantial contributions in translational medicine applying proteomics technology. She was one of the first to validate the concept that disease-induced modified protein biomarkers can add specificity to disease status and discovered the disease induced modifications of cardiac troponin I that revolutionized our understanding of the complexity of heart disease and improved our ability to diagnosis heart attacks. Based on this information she developed assays for the quantification of disease induced modified forms of cardiac troponin I that revolutionized the diagnosis of heart attacks.

HUPO 2015 | updates from our Vancouver organizers

Dear HUPO members,

We look forward to welcoming you and more than 1,200 delegates from over 55 countries to the [14th Human Proteome Organization World Congress \(HUPO 2015\)](#) from **September 27 – 30, 2015** at the Vancouver Convention Centre, East Building in beautiful Vancouver, British Columbia, Canada.

The HUPO Congress is pleased to present **over 1,000 abstracts** that will be presented in Oral, Mini Oral, and Poster presentations. All Oral and Mini Oral Presenters will have the chance to present a poster in addition to their oral presentations.

Be prepared to experience a world class scientific program like no other!

Plenary Sessions and Speakers:

- Ruedi Aebersold - Population Proteomics: Embracing Genomic Variability
- Aled Edwards - Opening Up New Areas of Drug Discovery with High Quality Research Tools
- Steven Carr - Quantitative Proteomics in Biology, Chemistry and Medicine
- Fuchu He - A New Chapter in Liver Physiology & Pathology Is Being Written with Big Data
- Ute Roessner - Metabolomics – An Important Piece in the 'Omics Puzzle
- John Yates - Using Mass Spectrometry to Understand Cystic Fibrosis as a Protein Misfolding Disease
- Emma Lundberg - Deciphering Functional Proteomes in the Human Protein Atlas – Organelles, Substructures and the Cell Cycle

There are more than 20 HPP Sessions and the Sunday Pre-Congress Workshops boast a diverse selection of workshops for all. [Click here for more details.](#)

Highlights from our Pre-Congress Sunday Workshop Program:

- Clinical Day - Includes a full day session from local speakers and moderators that will discuss various topics on clinical information. See the full program [here.](#)
- Education Day - Presentations on Peptide and Protein Atlas, Quantitative Targeted Proteomics – Technology & Applications. See the full program [here.](#)
- Mentoring Day - The first ever organized Mentoring Day will allow young scientists the opportunity to hear from world renowned scientists from a wide range of fields in science, technology and business. See the full program [here.](#)
- Technology Day - A new omics-based technology or the application of an existing technology from another field, applied to the field of genomics including proteomics, metabolomics, bioinformatics, etc., that is truly transformative in that it has the potential to either displace an existing technology, disrupt an existing market or create a new market
- HPP General Investigators' Meeting – The meeting will report on the progress of the Human Proteome Project.

HUPO 2015 | updates from our Vancouver organizers

Bioinformatics Hub

We are pleased to present the Bioinformatics Hub at HUPO 2015. The Bioinformatics Hub is organized by the Computational Mass Spectrometry initiative, a joint initiative of HUPO, ISCB and the Metabolomics Society. The group aims to develop and execute

original bioinformatics analyses on the publicly available human proteomics data during the conference and is open to everyone interested. Ask-The-Experts sessions will be held every day between 10:00 – 11:00.



Hockey Night in Canada

Join us on **Tuesday, September 29, 2015** to experience an unforgettable Congress Night and uniquely Canadian pastime, "Hockey Night in Canada"! We encourage you to invite your friends and families to enjoy this wonderful night with us. Delegates will have the opportunity to skate on the large synthetic ice rink, or dance along with our amazing Canadian cover band, or sit back and relax while enjoying a casual Vancouver West Coast Style buffet in the lounge area.

Tickets are only 100 CAD and include skate rentals and commemorative photos with various hockey players.

HUPO GENERAL ASSEMBLY 2015 | the annual meeting of members

The **HUPO General Assembly** will take place in Vancouver, Canada at the 14th Human Proteome Organization World Congress (HUPO 2015) as follows:

Date: Tuesday, September 29, 2015

Time: 18:30 - 19:30

Location: Vancouver Convention Centre, East Building, Meeting Room 1

If you are attending the Congress we hope you will join us for this annual meeting of HUPO members. We look forward to seeing you in Vancouver!

HUPO IS NOW SOCIALLY CONNECTED | join the conversation



/humanproteomeorg



@hupo_org



Human Proteome Organization (HUPO)

The Human Proteome Organization (HUPO) is now socially connected – help us to spread the word! We invite you to connect with HUPO and participate in the proteomic conversation. We're excited for the upcoming HUPO World Congress and would love to hear from you. Be sure to use **#HUPO2015** in Vancouver!

HUPO 2015 | IAB activities in Vancouver

INDUSTRIAL ADVISORY BOARD SEMINARS

Our IAB members are active in HUPO and the Congress. Be sure to attend the IAB seminars (lunch will be provided) at HUPO 2015! Click on any company name for full program details and registration, or visit the overview page [here](#).

Monday, September 28 | 13:15-14:15

[Thermo Scientific](#) | From Markers to Assays: Accelerating Translational Proteomics

[Bruker](#) | New solutions in LC/MS based proteomics

[Waters](#) | Improving Multi-omic Workflows for the Discovery and Development of Novel Biomarkers

[Agilent Technologies](#) | Multi-omic analysis for Integrated Biology

Tuesday, September 29 | 13:15-14:15

[Thermo Scientific](#) | Pushing the Boundaries of Comprehensive Proteome Profiling

[SCIEX](#) | Testimonials in OneOmics™: Next-Generation Proteomics at Work

INDUSTRIAL ADVISORY BOARD EXHIBITORS

Visit our IAB members at their booths in the Exhibit Hall. For more information, click [here](#).

Booth 301

Thermo
SCIENTIFIC

Booth 213

BRUKER

Booth 201

Waters
THE SCIENCE OF
WHAT'S POSSIBLE.®

Booth 302

 **Agilent Technologies**

Booth 300

 **SCIEX**

Booth 212

 **Cambridge
Isotope
Laboratories**

ECR FINALISTS | the early career researcher initiative

The Early Career Researcher Initiative (ECR) is a new HUPO initiative with the intent to transmit the HUPO ideals to the future generations of proteomics leaders. For that, the ECR is engaged in providing opportunities for young proteomics researchers and help to guarantee a strong continuity between many generations of scientists. In this respect, the first activities organized by the ECR are i) the HUPO ECR Manuscript Competition and ii) the HUPO Mentoring Day which will have their début at the 14th World HUPO Congress in Vancouver. Thanks to their enthusiastic participation of exceptional group of mentors from academia, industry and funding agencies, the first HUPO Mentoring Day in Vancouver will be a unique opportunity to learn from and interact with many world proteomics leaders. See the full program [here](#).

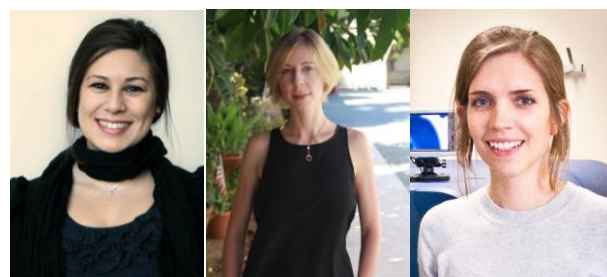
Regarding the first HUPO ECR Manuscript Competition, the underlying motivation was to offer a platform for early career scientists to highlight their recent scientific work. Participants were asked to present their research in the form of an original unpublished manuscript. Each manuscript was carefully reviewed by an ad hoc jury of senior scientists and members of the ECR committee. Review criteria focused on the career track of the applicant as well as scientific content, the quality of the presentation and finally the novelty and significance of the science. Participation to this first event was excellent: we received 14 applications and the quality of each application was extremely high! Congratulations to each of these amazing ECR participants on their amazing work.

The three finalists for the competition are (in alphabetical order) Burcu Ayoglu, Justyna Fert-Bober and Olga Schubert. Dr. Ayoglu conducted her work at the School of Biotechnology of the KTH-Royal Institute of Technology in Stockholm, Sweden where she focused on development and utilization of protein and antibody microarrays for profiling autoantibodies and proteins in body fluids and biomarker discovery

within autoimmunity, as well as within neuro- and muscle-degenerative diseases such as multiple sclerosis and Duchenne muscular dystrophy. Dr. Fert-Bober is project scientist at Cedars-Sinai Medical Center, Los Angeles, CA, USA where she studies the role of protein deimination (citrullination) in heart diseases such as ischemic, dilated cardiomyopathy (and their animal models). Dr. Schubert performed her research at the Swiss Federal Institute of Technology (ETH) in Zurich, Switzerland, where she developed experimental resources and computational strategies for the comprehensive proteome quantification of the human pathogen *Mycobacterium Tuberculosis* using targeted proteomics technologies such as Selected Reaction Monitoring (SRM/MRM) and SWATH MS. The three finalists will present their work with an oral presentation during the ECR Manuscript Competition session at the 14th World HUPO Congress in Vancouver (Wednesday, September 30 from 10:15-11:00 in Meeting Room 1). Based on their presentations, a jury will select the winner and the two runner-ups! Please attend!

We wish Burcu, Justyna and Olga the best of luck and we are looking forward to learning more about their exciting work in Vancouver!

-ECR Committee



The three finalists of the inaugural HUPO Early Career Researcher Manuscript Competition in Vancouver 2015. From left to right, in alphabetic order: **Dr. Burcu Ayoglu**, **Dr. Justyna Fert-Bober**, and **Dr. Olga Schubert**.

IN MEMORIAM | Thomas Edward Fehniger, PhD (1948-2015)



Thomas Edward Fehniger, PhD (1948-2015)

It is with great sorrow that we announce that Tom Fehniger passed away on the 5th of July, 2015.

Tom was a highly respected scientist with a broad repertoire in biology and medicine with an absolute need to understand how things worked and how knowledge could be applied. Tom had a truly international perspective, travelling the world with me the last three years.

He graduated from Western Michigan University in 1970 and received his PhD in Microbiology and Immunology from the University of California at Los Angeles (UCLA), School of Medicine in 1985. Prior to gaining his PhD, Tom worked for two years at the NIH, followed by Staff Research positions in John Fahey's department at UCLA and Bob Cardiff's Pathology Department at UC Davis. Tom continued with an eight year period at UCLA. His investigation of the pathogenesis of human and experimental syphilis found Tom in Ethiopia where, together with scientists from the Karolinska Institute, he conducted field studies on cutaneous leishmaniasis and, latterly, on HIV/AIDS.

Significantly, Tom and his colleagues were responsible for the discovery of a unique strain of Ethiopian HIV-1 (C-clade), different from the HIV-1 clades prevalent in the western world. Tom was extremely excited about

this research field and followed the progresses and developments over decades.

Tom later spent eleven years at Stockholm University followed by nine years at the Karolinska Institute as head of Histology unit. In 1998 Tom made the transition from academia to industry. I met him when he joined Astra Draco in Lund, Sweden (later became AstraZeneca). He was heading up a research team as a senior scientist in drug discovery and development at their R&D site in Lund in 1998, specializing in respiratory pathology.

We made great developments together, and filed a whole bunch of patents. These patents we later bought back from AstraZeneca, and used them in Clinical developments in Academia. At AstraZeneca Tom established the Biobanking procedures and infrastructure that are used throughout all global studies in respiratory diseases.

In 2010 Tom left AstraZeneca and was appointed by the Estonian Science Foundation as Top Researcher in the EU sponsored Mobilitas Program, specializing in COPD and Lung Cancer pathology at the Tallinn Clinicum.

After Tom's return to Lund in 2013, I went to his house where I found him in the garage. He pointed out to me that he was "fixing things....." Usually we had a coffee together, and after several months I was wondering if these things perhaps might be fixed by now...Finally after numerous cups of coffee, Tom joined the Clinical Protein Science & Imaging division in 2013 where we together initiated the Centre of Excellence in Biological and Medical Mass Spectrometry (CEBMMS), Lund University. He then became the Director of CEBMMS, a position he held until his untimely death. As a Director he was highly respected by deans of faculties, PI's in the Center, colleagues and friends, simply because he was such a kind and supportive person, interested and happy in his life.

Tom had the ability to present and explain complicated science problems in such an elegant and straightforward way that even non experts and politicians could appreciate and take a stand for science developments, some even became experts after his lectures.

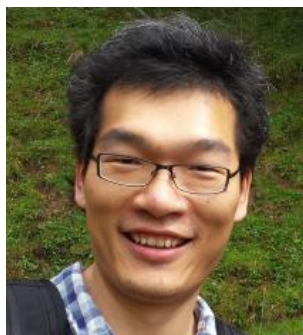
Our deepest sympathies are extended to Tom's wife Anne-Sophie, his children Carl and Emilia, and his relatives in America.

György Marko-Varga



In Santa Monica, where he once lived, June 2015.
We also visited UCLA, where it all began.

TAGLINE COMPETITION | translating the code of life



Tiannan Guo

*ETH Zürich
Institute of Molecular
Systems Biology*

The HUPO Executive Committee is pleased to announce the winner of the HUPO Tagline Competition, Dr. Tiannan Guo.

We wish to extend sincere thanks to everyone who participated in the competition. The EC was thrilled by the quantity, quality, and diversity of suggestions put forth by HUPO members. It was fantastic to see the members of HUPO, a truly international scientific community, engage in this competition.

One tagline in particular really captured HUPO's role in encouraging and facilitating the advancement of proteomic research. **The winning tagline, 'translating the code of life', was created by Tiannan Guo.** We believe this new tagline will play a vital role in the continued growth, visibility, and success of the Human Proteome Organization. Congratulations, Tiannan, and thank you!



translating
the code of life

NEWS IN SCIENCE

YuJu Chen, HUPO Publications Committee Chair

Discovery of unexplored potential of lipid-binding proteome for ligand/drug development

Niphakis, M.J. et al. *Cell* 161, 1668–1680 (18 June 2015)

Lipids are a class of hydrocarbon-containing natural molecules; important examples include some vitamins (A, D, E), hormones (estrogen, testosterone), neurotransmitters (endocannabinoids) and components of fat (triglycerides, cholesterol). Their biological functions to regulate cell physiology and disease are often mediated through interactions with proteins. Despite the fact that a substantial number of drug targets are lipid-binding proteins, it has been challenging to establish a global portrait of how lipids interact with proteins in cells.

Benjamin F. Cravatt's team at The Scripps Research Institute (TSRI) has devised a powerful chemical proteomic method to map the human lipid-binding proteome. In this study, Niphakis and colleagues described a set of fatty acid-based chemical probes combined with quantitative mass spectrometry to provide the first global portrait of lipid-protein interactions in human cells. Their results revealed a surprisingly large number of lipid-protein interactions from diverse functional classes, including some interactions which are already targeted by existing drugs and, most importantly, many novel lipid-binding proteins. The probes can also be used to identify the targets of drugs that disrupt lipid-protein interactions in cells, pointing to the broad potential of lipid-binding proteins for ligand/drug development.

"Traditionally, scientists have theorized fairly narrow limits for the types of proteins that can be targeted with small-molecule ligands, but our results suggest that those boundaries are much wider," said Cravatt (adapted from News Release of The Scripps Research Institute).

This study was reported in the journal of Cell on June 18, 2015.

Link: [http://www.cell.com/cell/abstract/S0092-8674\(15\)00635-2](http://www.cell.com/cell/abstract/S0092-8674(15)00635-2)

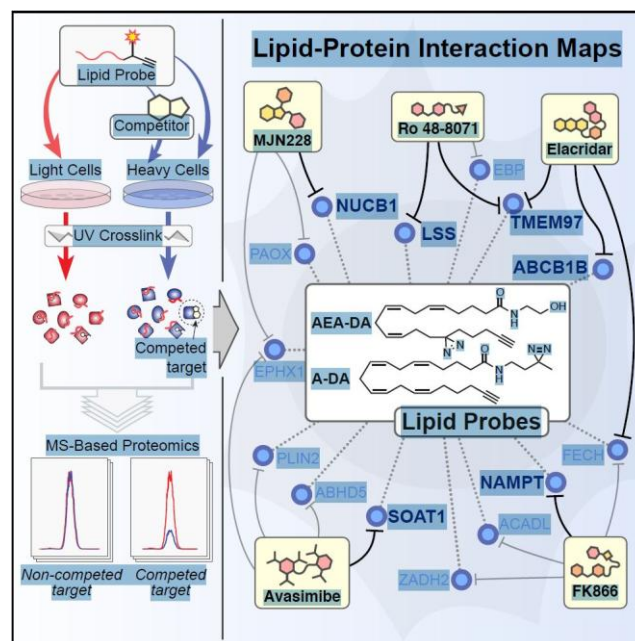


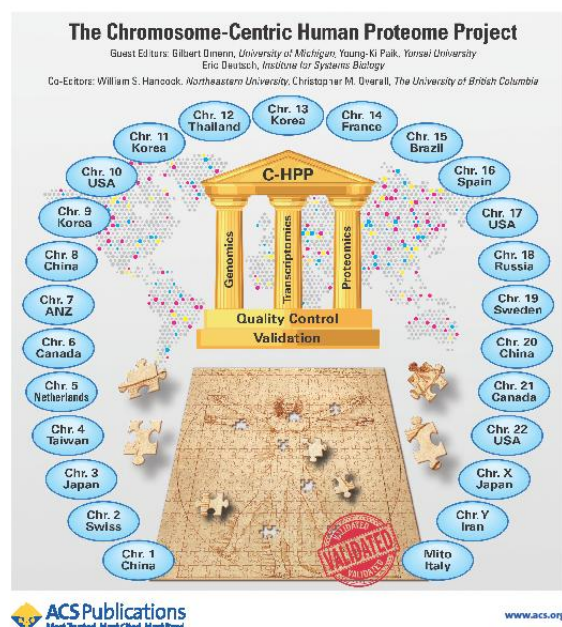
Figure provided by Benjamin F. Cravatt

HPP UPDATE

Journal of
proteome
research

September 2015

Volume 14 Number 9 pubs.acs.org/jpr



The 3rd annual C-HPP Special Issue of Journal of Proteome Research: Missing Proteins in the Spotlight

Gil Omenn, HPP Chair

The Human Proteome Project continues on a very active course. Over the past 3 years the number of highly confident protein identifications in neXtProt (PE level 1) grew from 13 664 in Dec 2012 to 16 491 in October 2014, the baseline for the 2015 cycle of C-HPP publications. The September issue of the *Journal of Proteome Research* (JPR) has 30 articles from HPP investigators, and about 12 others will appear in the December JPR issue¹.

The emphasis is on making credible identifications of the 2948 neXtProt entries lacking any or sufficient protein-level evidence and on recognizing the reasons why some substantial number of products from

protein-coding genes may not be detectable at the protein level, or at least by current specimen preparation and mass spectrometry methods. Increasingly we have realized that even excellent mass spectra and peptides confirmed with synthetic peptides and MRM/SWATH may be challenging to match to the missing proteins due to alternative matches to known proteins. These include additional reference genomes, sequence variants, and isobaric post-translational modifications. These alternative explanations apply also to “novel proteins”, inferred as potential translation products from long non-coding RNAs or pseudogenes.

The JPR articles are organized as follows: (a) 9 articles on genome complexity, proteogenomics, integrated analysis of transcriptomics and proteomics, and functional studies of splice variant proteins; (b) 7 articles on the choice of little-studied biological or clinical specimens to identify and characterize tissue-specific or tissue-enriched low-abundance missing proteins, guided by evidence of transcript expression (PE level 2); (c) 6 articles on development of improved analytical techniques and related experimental methods to solubilize, capture, and characterize proteins that are difficult to measure, especially membrane proteins; and (d) 8 articles on upgrading bioinformatics knowledge and related informatics tools to enable credible identification and validation of new protein observations.

Certain papers provide a thorough examination of the challenges of claiming, confirming, and validating peptide findings and protein matches^{2,3}. Such quality assurance will be subjected to open discussion at the HUPO 2015 Congress in Vancouver. These papers guide investigators to use of the valuable data in neXtProt, PeptideAtlas, GPMDB, and Human Protein Atlas.

Several issues were identified as drivers for the coming years of the C-HPP: (1) We will build consensus on what is sufficient evidence for publishing claims of detection of missing proteins. (2)

We can improve methodological approaches, select optimal biological samples, and recommend stringent informatics protocols for the characterization of challenging protein families, such as the olfactory receptors. (3) We should expand the focus on identifying missing proteins to recognizing the huge space of protein proteoforms, including splice isoforms, PTMs, and sequence variants. (4) As technology and methodology continue to advance, we can integrate bioinformatics tools and

experimental methods and perform cross-over analyses with mass spectrometry and antibody profiling. (5) We have reached a point where it is strategic to enhance the capabilities and deliverables of the C-HPP teams through forming clusters of teams with overlapping interests, sharing data collected from whole proteomes, focusing on amplicons and other cis-regulatory features of chromosomes, and welcoming investigators with fresh ideas and new methods.

¹ Paik et al, Recent advances in the chromosome-centric Human Proteome Project: Missing proteins in the spotlight. JPR 2015, DOI: 10.1021/acs.jproteome.5b00785.

² Omenn et al: Metrics for the Human Proteome Project 2015: progress on the human proteome and guidelines for high-confidence protein identification. JPR 2015, DOI: 10.1021/acs.jproteome.5b00499.

³ Deutsch et al: State of the human proteome in 2014/2015 as viewed through PeptideAtlas: enhancing accuracy and coverage through the AtlasProphet. JPR 2015, DOI: 10.1021/acs.jproteome.5b00500.



Members of the HPP Executive Committee, from left: Young-Ki Paik, William Hancock, Lydie Lane, Michael Snyder, Amos Bairoch, Jennifer van Eyk, Gil Omenn, Emma Lundberg, Ruedi Aebersold, Fuchu He, Tadashi Yamamoto, and Eric Deutsch

HPP Clinical Scientist Travel Grant Winners

The HUPO Human Proteome Project (HPP) Executive Committee is pleased to announce the winners of the HPP Clinical Scientist Travel Grants. These grants are provided to a select number of scientists working in a clinically relevant field. Congratulations to the recipients, we look forward to seeing you in Vancouver!

Hyewon Chung, *Republic of Korea*
Andrei Drabovich, *Canada*
Johannes Griss, *Austria*
Kurt Højlund, *Denmark*

Heeyoun Hwang, *Republic of Korea*
Ryan Ratts, *United States of America*
Irene van den Broek, *Netherlands*

NATIONAL & REGIONAL SOCIETY HIGHLIGHTS

The Human Proteome Organization encourages the formation of national and regional human proteome-related societies. For a comprehensive list of proteomics societies, please visit <https://www.hupo.org/national-and-regional-societies/>.

In each HUPOST issue one society from each region is featured. If you wish for your society to be featured in a particular quarterly issue of the HUPOST, please email office@hupo.org.



Asia Oceania Human Proteome Organisation (AOHUPO) was conceived at the Pacific-Rim International Proteome and Proteomics Conference in 1999. At that time there were no proteomics societies in the Asian-oceanic region. In 2001, the AOHUPO was founded by four co-founding members: the late Dr. Akira Tsugita (Japan), Richard Simpson (Australia), Kazuyuki Nakamura (Japan) and Young-Ki Paik (Korea). The organization affiliates with HUPO, and represents the community of over 2000 proteomics scientists from 15 societies/countries in the Asia Oceania region. Currently, Dr. Fuchu He is President of AOHUPO (China), and Dr. Bill Jordan (New Zealand) and Dr. Ho Jeong Kwon (Korea) are the Vice-Presidents. AOHUPO has been actively promoting proteomics collaboration between research groups and education in the region. AOHUPO organizes a biennial international proteomics conference. The first AOHUPO congress was held in Seoul in 2002. Subsequent AOHUPO congresses have been held in Taipei (2004), Singapore (2006), Cairns (2008), Hyderabad (2010), Beijing (2012) and Bangkok (2014).

The upcoming 8th AOHUPO congress will be held in Taipei in September 2016. AOHUPO also organizes research and education workshops, for example the 1st AOHUPO XML workshop (Tsukuba, 2002) and PPS-AOHUPO-HEC Education Workshop on “Tools in Quantitative Proteomics” (Karachi, 2012). Moreover, AOHUPO has been fostering proteomics initiatives in the region, including Membrane Protein Initiative, Embryonic Stem Cell Membrane Proteome Initiative, Nuclear Proteome Initiative and Chemical Proteomics Initiative.



Fuchu He (left), current president of AOHUPO (2014-2016) with **Kazuyuki Nakamura** (right), past AOHUPO president (2011-2013).

NATIONAL & REGIONAL SOCIETY HIGHLIGHTS



6th Symposium of Proteomics

The 6th Symposium on Mass Spectrometry, Molecular, and Cellular Proteomics, organized by **the Mexican Proteomics Society**, will be held in Puerto Vallarta Mexico, November 9 – 12, 2015. Our goal is to provide a forum to exchange information on proteomics, metabolomics, lipidomics, and other omics technologies while promoting opportunities to meet renowned scientists from all over the world. For more information please visit [our website](#).

Puerto Vallarta is a beautiful Mexican beach resort situated on the Pacific Ocean, located on the same latitude as Hawaii, and it has a subtropical weather with an average temperature of 25 degrees C.

The program includes plenary sessions, individual papers presentation and two days pre-congress bioinformatic courses that provide participants with unmatched opportunities to exchange scientific ideas while enjoying the magical Puerto Vallarta. The organizing committee has also placed a special social program to celebrate the ten year anniversary of the Mexican proteomics society. Join us on this special event.

We look forward to seeing you at the 6th Symposium on Mass Spectrometry, Molecular, and Cellular Proteomics.



Prof. Lennart Martens awarded with the Juan Pablo Albar Protein Pioneer Award by EuPA President Prof. Andrea Urbani during the Annual Conference of the British Society for Proteome Research (BSPR) in Reading, July 20th, 2015.

The European Proteomics Association is the federation of European national proteomics societies. It has been established to coordinate, support and integrate national initiatives within the proteomics field. EuPA pursues its objectives by strengthening the national and European proteomics organizations in their efforts through a bottom-up approach. This includes coordinating and providing educational programs; promoting the networking of scientists through meetings, workshops and student exchange; advanced training in proteomics technologies and applications. The new EC for the year 2015-2017 is composed by: Andrea Urbani (President, IT), Emøke Bendixen (Vice-President, DK), Karl Mechtler (Education Committee, AU), Albert Sickmann (Funding, DE), Andy Pitt (Journals, UK), Andrey Lisitsa (EuPA Initiatives, RU) and Fernando Corrales (Communication and Conferences, ES).

EuPA has currently active programs to support student participation in National Educational Initiatives and for the scientific exchange throughout the EU National Conferences, for more information contact eupa.information@gmail.com.

EVENTS IN PROTEOMICS

If you would like to include your meetings in the HUPOST or on the [HUPO website](http://hupo.org), please email the details to office@hupo.org.

FUTURE HUPO ANNUAL WORLD CONGRESSES

- [HUPO 2015 Vancouver](#)

September 27-30, 2015



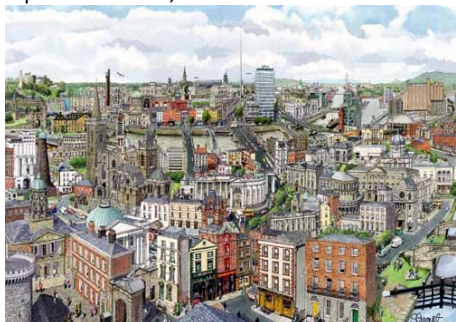
- [HUPO 2016 Taipei](#)

September 18-22, 2016



- [HUPO 2017 Dublin](#)

September 17-20, 2017



REGIONAL & NATIONAL PROTEOMICS SOCIETY EVENTS

- [6th Symposium on Mass Spectrometry, Molecular, and Cellular Proteomics](#)
November 9-12, 2015
Puerto Vallarta, Mexico
<http://espectrometriademexas.mx/>
- [Joint EMBL-EBI/Wellcome Trust Course: Proteomics Bioinformatics](#)
November 11-15, 2015
Cambridge, United Kingdom
<http://www.ebi.ac.uk/>
- [5th Symposium on Structural Proteomics](#)
November 19-20, 2015
Halle, Germany
<http://www.structuralproteomics.net/>
- [7th Annual Meeting of Proteomics Society, India 2015](#)
December 3-6, 2015
Vellore, India
<http://www.psivellore2015.org/>
- [DAPSOC 2015 Symposium](#)
December 8, 2015
Odense, Denmark
<http://www.dapsoc.org/?Events>
- [British Society for Proteome Research 2016 Meeting](#)
July 25-27, 2016
Glasgow, United Kingdom
<http://www.bspr.org/event/bspr-meeting-2016>