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## EDITOR'S MESSAGE



Emma K. Lundberg,  
HUPOST Editor

Dear HUPO friends,

In the spirit of the new HUPO tagline “Translating the code of life” we are proud to announce that HUPO has entered a biobanking collaboration agreement with ESBB with the aim to foster collaboration and benefit biobank patient cohorts. In the same spirit, a recent publication shed new light on the role of

proteins with essential amino acids in the diet of malnourished children in developing countries. Read all about it, and an interview with the author Prof. Richard Semba, in the *News in Science* section.

The HPP continues to make good progress on the Proteins Parts list. Read the update on the current protein

evidence for the human proteome and get inspired for the upcoming discussions at the HPP meeting in Sun Moon Lake. As the 15th HUPO World Congress in Taipei is closing in, we are proud to announce the winners of the prestigious HUPO awards as well as the candidates for council election.

Again I would like to thank all of you that provide content to HUPOST and our social media – keep it coming! Help us make HUPO an even more active and vibrant society. Stories, highlights, news, suggestions and announcements are gladly accepted. Simply email the HUPO Office at [office@hupo.org](mailto:office@hupo.org).

I hope to see you all in Taipei! Until then, you can find us on [Twitter](#), [Facebook](#), and [LinkedIn](#).

Best wishes,

Emma

## PROTEOMICS - TRANSLATING THE CODE OF LIFE

### New documentary “Proteomics - Translating the Code of Life” released

The completion of Human Genome Project was a major landmark achievement for the life sciences community. With genomics setting a foundation in the quest to uncover the mysteries of life and biology, what lies next? What are the prospects and challenges as we explore the post-genomic world?

Proteins and proteomics are central to connect genomes with phenotypes and biological function. Proteomics provides a veritable foundation to address whole systems, and uses a broad unbiased approach to decipher post-genomic biology.

This documentary portrays the journey of “Proteomics”, discusses its advancements, achievements and key issues that lay ahead. The first section of the documentary introduces the Post-genomic Era and establishes the necessity of proteomics. The second section focuses on development of various proteomic Technological Platforms and how persistent efforts of proteomics scientists have resulted in the First Draft of the Human Proteome.

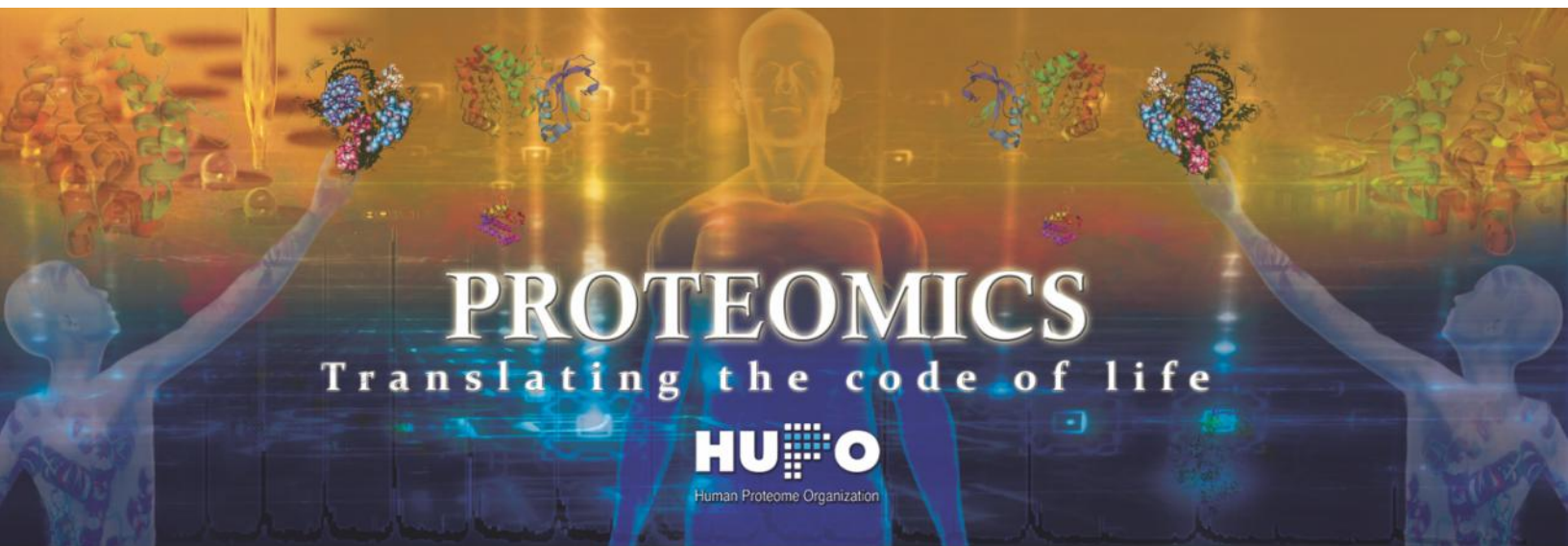
Next Generation Tools involving Trans-Proteomic Pipeline, SWATH-MS and Skyline have added to the arsenal of targeted proteomics. The proteomics community can contribute immensely to functional biology and offer innovative solutions in life sciences. Sustained and committed efforts from global proteomics communities like the Human Proteome Organization (HUPO) has helped proteomics establish an undeniable international presence. This has helped define the broader theme of research directions, thus, “Translating the Code of Life”.

*Dr. Sanjeeva Srivastava and IIT Bombay Team.*

<http://www.bio.iitb.ac.in/~sanjeeva/documentary/>

### **WATCH THE DOCUMENTARY HERE:**

<https://www.youtube.com/watch?v=m4U9bcnGtg4&feature=youtu.be>



## Human Proteome Project

### Update from the Human Proteome Project

*Gil Omenn, Chair*

The HUPO [Human Proteome Project \(HPP\)](#) continues to make very good progress on the Protein Parts List for the Human Proteome and on creating reagents, databases, and SRM capabilities for integrating proteomics into many other biomedical studies.

The current versions of [PeptideAtlas](#) 2016-01 and [neXtProt](#) 2016-02 are the benchmarks for the HPP community and others who submitted manuscripts for the 4<sup>th</sup> annual special issue of the Journal of Proteome Research led by the C-HPP, which will be released in time for the HUPO2016 Congress in Taiwan. A total of 120 articles were published in the three previous JPR special issues.

All authors are required to utilize the HPP Data Interpretation Guidelines v2.0 (see <http://www.thehpp.org/guidelines/>) and to submit a completed checklist along with the manuscript. This checklist is helpful to authors and to reviewers. For anyone not familiar with these guidelines, we encourage you to examine them and consider their use in your own work and in your evaluation of others' work.

There are now 16,518 Protein Existence Level 1 (PE1) proteins in neXtProt, even after 485 proteins that would have qualified as PE1 under the previous guidelines (one peptide of 9 aa or two peptides of  $\geq 7$ aa) were excluded by the new guidelines, specifically by the requirement for two uniquely-mapping peptides of at least 9 aa in length, to reduce false-positives. Of those 485, 432 are now PE2, 40 PE3, and 7 PE4. Of the 16,518, 14,658 are based on PeptideAtlas analyzed MS data, while 1860 are validated as PE1 based on multiple types of non-MS evidence. The PE 2+3+4 "missing

proteins" now number 2949, including the 485 excluded under the new Guidelines from PE1; thus, the missing proteins represent only 15% of the PE 1-4 predicted proteins.

PeptideAtlas 2016-01 has 14,629 canonical, 1187 uncertain, 1755 redundant, and 2484 not-observed protein entries. The canonical figure dropped from 14 928 in 2015 to 14 070 when the more stringent guidelines were adopted. In 2016 a major increment is from the new Phosphoproteome PeptideAtlas (2015-09), which captured 128 000 phosphopeptides assigned to ~10 000 canonical proteins from 143 samples enriched for phosphopeptides using PTMProphet, including 81 new canonical entries.

GPMDb now has 16,190 "good" protein IDs (EC4/green). Its numbers exceed those of PeptideAtlas canonical by 1581, primarily because there are more datasets and no parsimony rule is applied to high-quality peptide-to-protein matches; more than one match can be included, whereas PeptideAtlas excludes all redundant or ambiguous matches from the canonical list.

The HPP and these databases are putting emphasis on PTMs, sequence variants, splice isoforms, and modified N- and C-termini, long a part of the stated goal for the protein parts list. GPMDb has launched g2pDB, mapping protein PTMs to protein modification acceptor sites and then to genomic coordinates.

Finally, the [Human Protein Atlas](#) has mounted a major validation effort for the specificity of its antibodies in identifying and localizing protein expression in 44 tissue types. HPP investigators in Europe and China have identified many previously missing proteins in testis and sperm, shown to have the highest number of highly enriched tissue-specific proteins.

## HPP CLINICAL SCIENTIST TRAVEL GRANTS | CALL FOR APPLICATIONS

The HPP is reaching out to clinical scientists or clinicians who are using or consider using proteomics for their research projects. The HPP is supporting six (6) clinical scientists with a travel grant to attend the 2016 HUPO World Congress in Taipei, that will take place from September 18-22, 2016.

Travel grant recipients will receive USD \$1,000 to offset travel and hotel costs in addition to complimentary congress registration. The recipients are expected to actively participate in the HUPO congress, particularly in the activities and discussions related to the HPP.

### APPLICATION PROCESS

1. Download and complete the [application form](#) (found here <https://www.hupo.org/about-hupo/awards/hpp-clinical-scientist-travel-grants>)
2. In a separate document, write a brief description of your area of research, its relation to proteomics and the HPP, and detailed plans of how you will enhance your research with proteomics technologies (two pages maximum).
3. Submit both items via email to [office@hupo.org](mailto:office@hupo.org) by Thursday, June 30, 2016.

## ESBB-HUPO BIOBANKING AGREEMENT

*György Marko-Varga, HUPO Secretary General*

The HUPO Biobanking team has worked out a strategic link with the European, Middle Eastern & African Society for Biopreservation and Biobanking ([esbb.org](http://esbb.org)), to build and manage the distribution of biobank samples with global access from a number of biobank repositories that can be accessed by the C-HPP and BD-HPP research teams.

ESBB is a forum that addresses harmonization of scientific, technical, legal, and ethical issues relevant to repositories of biological and environmental specimens. Developing and sharing innovations and best practice in biobanking.

Together, HUPO & ESBB have the opportunity to promote best practices that cut across the broad range of repositories and biobanks.

This initiative is intended to strengthen the quality and global collaborative win-win efforts, as most proteomics researchers are not deeply involved in the sample collection processes.

In order to further build and improve proteomics research, our goal is to collaborate with ESBB and to benefit biobank patient cohorts.



HUPO and ESBB in biobanking collaboration. From left: Mark Baker, HUPO President; György Marko-Varga, HUPO Secretary General; Erik Steinfeld, ESBB President

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## 2016 HUPO AWARD WINNERS

The Human Proteome Organization presents a number of distinguished awards annually at the World Congress. HUPO gratefully acknowledges the support of the Industrial Advisory Board, the Journal of Proteome Research (ACS Publications), and Elsevier as sponsors of three of these awards. The HUPO Executive Committee and the Awards Committee would like to thank all those who submitted nominations for the 2016 awards.

It is with great enthusiasm that we present the 2016 HUPO Award Winners! Please join us in congratulating these outstanding scientists on their accomplishments and contributions to the field of proteomics. The awards will be presented at HUPO 2016 in Taipei and the winners will present a talk during the congress award session.

**Distinguished Achievement in Proteomic Sciences** (sponsored by the Journal of Proteome Research)

**Ralph Bradshaw**, *College of Medicine, University of California, Irvine, USA*

**Discovery in Proteomic Sciences**

**Michael MacCoss**, *School of Medicine, University of Washington, USA*

**Science and Technology Award** (sponsored by the Industrial Advisory Board)

**Bob Bateman**, *Waters Corporation, Wilmslow, UK*

**John Hoyes**, *Waters Corporation, Wilmslow, UK*

**Translational Proteomics Award** (sponsored by Elsevier)

**Joshua LaBaer**, *Biodesign Institute, Arizona State University, USA*

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## CALL FOR NOMINATIONS | HUPO Executive Committee Positions

The Executive Committee (EC) of the Human Proteome Organization consists of the President, immediate Past President, President-Elect, Vice President, Secretary General, Treasurer, and two Members-at-Large to be elected by a vote of the HUPO Council. A person who is not currently a member of the Council and is elected to an EC position shall serve as *ex officio* on the Council. All officers must be active members of HUPO and shall serve a two-year term, except as may be designated by the Council.

The following EC positions are to be filled by Council vote at the HUPO World Congress in Taipei, for the term beginning January 2017:

- HUPO Treasurer
- 2 x Member at Large positions

For further information, or to submit your candidacy (before 19 August, 2016), please email [office@hupo.org](mailto:office@hupo.org).

HUPO Congress: September 18-21  
HPP workshop day: September 22

Precision Proteomics  
for Precision  
Biology and Medicine

## HUPO 2016 CONGRESS UPDATES | [WWW.HUPO2016.ORG](http://WWW.HUPO2016.ORG)

### SCOPE OF CONGRESS

7 Plenary Lectures

30 Keynote Sessions

10 Luncheon Symposia

Sunday Pre-Congress Courses:

Clinical Day / Education Day / Mentoring Day / Technology Day / HPP Leadership Meeting

**Post Congress Workshop:** HPP workshop day (Sep 22) at Sun Moon Lake, Nantou

**Joint Events:** Proteomics Informatics Course (Sep 13-16) / AO HUPO 2016 (Sep 22-23)



### Plenary Speakers



Ruedi Aebersold  
Switzerland



Henrik Clausen  
Denmark



Jennifer Van Eyk  
USA



Albert JR Heck  
The Netherlands



Henry Rodriguez  
USA



Michael Synder  
USA



Pan-Chyr Yang  
Taiwan

### KEYNOTE SESSIONS

Keynote sessions cover a wide range of topics including innovative MS techniques, informatics & computational proteomics, various PTMomics & their cross talks, imaging & spatial proteomics, antibodies & protein arrays, interactomics, proteogenomics, chemical & pharmacoproteomics, metabolomics, plant & microbial proteomics, and applications to cancer, immunity, neurological and other diseases.

### CONFIRMED KEYNOTE SPEAKERS

Per E. Andr�n	Joshua Heazlewood	Lennart Martens	Igor Stagljari
Nuno Bandeira	Peter Hoffmann	Daniel Martins-de-Souza	Michael Sussman
Bernd Bodenmiller	Donald Hunt	Tsutomu Masujima	Andy Tao
Christoph Borchers	Daehee Hwang	Katalin Medzihradzky	Morten Thaysen-Andersen
Etienne Caron	Yasushi Ishihama	Peter Nilsson	Alice Ting
Peng Chen	Hiroyuki Kaji	Jesper Olsen	Mathias Uhl�n
Chuna Choudhary	Neil Kelleher	Christopher Overall	Andrea Urbani
Stuart Cordwell	Donald Kirkpatrick	Akhilesh Pandey	Bernd Wollscheid
Fernando Corrales	Bernhard Kuster	Junmin Peng	Tadashi Yamamoto
Ileana Cristea	Maggie Lam	Oliver Poetz	Pengyuan Yang
Henrik Daub	Martin Larsen	Jun Qin	JauSong Yu
Lo�c Dayon	Kong-Joo Lee	Paola Roncada	Hui Zhang
Eric Deutsch	Kathryn Lilley	Mikhail Savitski	Yingming Zhao
Frank Gonzalez	Emma Lundberg	Jochen Schwenk	Heng Zhu
Gerald Hart	Michael MacCoss	Richard Semba	Wei Min Zhu

Clinical Day / Education Day /  
Mentoring Day / Technology Day /  
HPP Leadership Meeting

**SUNDAY  
SESSION**

Date: 2016/09/18 (Sun.)

Time: 09:00 am - 15:30 pm

Location: Taipei International Convention Center (TICC), Taipei



**Post congress workshop -  
HPP workshop day**

Date: September 22, 2016

Location: Fleur De Chin Hotel, Sun Moon Lake



HPP workshop day

**Free Boat Tour**

Welcome to Sun Moon Lake



## NEWS IN SCIENCE

### Proteins with essential amino acids may be key to eliminating child malnutrition in developing countries

Yu-Ju Chen, Academia Sinica, Taiwan

While proteins are widely recognized as playing key roles in nearly all processes in living organisms, an odd debate arose about the role of protein in the diet of malnourished children in developing countries.

Stunting affects about one-quarter of children under five years of age worldwide; the World Health Organization estimates that 156 million children were stunted in 2015, nearly all of whom live in low-income countries. Stunted growth is closely linked with impaired brain and organ growth and higher risks for obesity, diabetes and other chronic diseases later in adulthood. In the 1950s and 1960s, protein-rich food mixtures were the main focus of study as a treatment for malnutrition in children in developing countries. In 1974, a paper "The Great Protein Fiasco" published in *The Lancet* cast doubt upon the central role of protein in childhood malnutrition. The focus in the international nutrition community shifted from proteins to micronutrient malnutrition, that is, lack of vitamins and minerals for the following four decades.

A recent study of essential amino acids and child stunting challenged the widespread belief that children in developing countries receive adequate dietary protein. The work led by Richard Semba from Johns Hopkins University was published in the April 2016 issue of the journal *EBioMedicine*. Semba and colleagues applied a targeted MRM-mass spectrometry-based metabolomics approach to measure serum levels of amino acids, as well as other essential compounds including glycerophospholipids, sphingolipids and other metabolites in blood samples from a community-based study of more than 300 children ages 1 to 5 years, more than 60 percent of whom had stunted growth, from six villages in rural southern Malawi. Participants' height and weight were recorded by trained field workers. The main finding is that children with stunting had lower serum concentrations of all nine essential amino acids (tryptophan, isoleucine, leucine, valine, methionine, threonine, histidine, phenylalanine, lysine) compared with nonstunted children. In addition, stunted children had 10 to 40 percent lower concentrations of other nutritional markers, such as conditionally essential amino acids (arginine, glycine, glutamine), nonessential amino acids (asparagine, glutamate, serine) and six different

sphingolipids, which are essential ingredients for development of the brain. Stunting was also associated with alterations in serum glycerophospholipid concentrations.

Essential amino acids cannot be synthesized by the body. The richest sources of essential amino acids are animal-source foods, such as milk, eggs, and meat, and also soybeans. This study suggested that children need quality protein in their diet for normal growth. These results are stimulating new recommendations and approaches to child malnutrition. Semba and his colleagues hope that this research will prompt a broader discussion on how to address child malnutrition.

"Providing high-quality protein with sufficient levels of essential amino acids in developing countries will be a major challenge and will require substantial investment in the agricultural sector," says Semba (quoted from press release of Johns Hopkins University, February 23, 2016).

This study challenges a long held paradigm about dietary protein for children in developing countries. Future studies are needed to address how lack of essential amino acids affects biological pathways and contributes to the pathogenesis of child stunting. Let's look forwards to more discoveries from the proteomic community.

Child Stunting is Associated with Low Circulating Essential Amino Acids (2016). *EBioMedicine* 6, 246–252. <http://www.ebiomedicine.com/article/S2352-3964%2816%2930069-X/fulltext>



Dr. Lacey LaGrone and Malawi health workers measuring the length of a child at a rural health center.

Photo credit: Indi Trehan



## The -omics approach reveals a key to the problem of child malnutrition

An interview with Professor Richard D. Semba, Johns Hopkins University

*Interview conducted by Marta González-Freire, Ph.D., Visiting Fellow, National Institute on Aging, and early career scientist working on skeletal muscle proteomics with Dr. Luigi Ferrucci, Scientific Director of the National Institute on Aging.*

**GONZÁLEZ-FREIRE:** You have been a faculty member at the Johns Hopkins School of Medicine for your entire career. Your lab group was mostly focused on nutrition and immunology but you recently made a mid-career transition to proteomics and metabolomics. What happened?

**SEMBA:** My lab was doing conventional immunology and nutritional biochemistry using conventional platforms such as ELISA, HPLC, and atomic absorption spectrometry. I would call this “normal science”, which by nature, is largely corroborative. The research was mostly validation of single biomarkers in large study cohorts of older adults. I became restless. Normal science offered little in terms of discovery and generating new hypotheses. Recent advances in proteomics, metabolomics, and mass spectrometry certainly caught my attention.

**GONZÁLEZ-FREIRE:** How did you get started in proteomics?

**SEMBA:** Your mentor, Dr. Ferrucci, introduced me to Jennifer Van Eyk. He urged me to try something different. I soon found myself back at the bench in Jenny’s lab to learn sample preparation for proteomics. Jenny’s enthusiasm, teaching, and guidance were a life-changing experience. She recommended that I take the intensive summer course in proteomics at Cold Spring Harbor Laboratories. This influential course, run by Ileana Cristea and her colleagues, has launched the careers of many scientists in proteomics. And now Ileana has become a dear friend and collaborator.

**GONZÁLEZ-FREIRE:** Did the promise of the field meet your expectations?

**SEMBA:** Wow, maybe way beyond my expectations.

**GONZÁLEZ-FREIRE:** Were there any surprises?

**SEMBA:** Dealing with the sheer amount of data is a daunting challenge. The buzz in the field seems to center around detecting more and more proteins, but making sense of the biology compels one to read hundreds of papers. That is the bottleneck of the process.

**GONZÁLEZ-FREIRE:** I notice your research interests include eye research, aging, nutrition in developing countries, and history of medicine. How did you end up working so broadly?

**SEMBA:** I have academic attention deficit syndrome [laughing]. Somehow it all seems related to me. After my residency in ophthalmology, I worked in Indonesia on vitamin A deficiency, the leading cause of blindness in children. That links eye research with nutrition. Then I got interested in the relationship of micronutrient malnutrition with HIV/AIDS, so I worked many years in Malawi and Uganda doing clinical trials. In the meantime, I built up a nutritional biochemistry lab at Hopkins. I wanted to do more hypothesis-generating work, so I closed my work in Africa and started working on aging. The history of medicine relates to everything. I think scientists working in proteomics need to know J. J. Thomson, Francis Aston, and Dorothy Hodgkin.

**GONZÁLEZ-FREIRE:** What are your big projects right now?

**SEMBA:** We are using selected reaction monitoring (SRM) to characterize the relationship of the systemic complement pathway with age-related macular degeneration. Another application of SRM is to understand circulating proteoforms that are purportedly associated with aging, such as GDF8 and GDF11 and their circulating inhibitors. SRM should clarify the issue, since antibody and aptamer-based studies have yielded conflicting data.

**GONZÁLEZ-FREIRE:** How do you think proteomics and metabolomics can contribute to global health?

**SEMBA:** The work we just did on essential amino acids and child stunting overturned the widespread belief that children in developing countries receive adequate dietary protein. Children need quality protein in their diet, such as animal source foods. These results are already having an impact on approaches to child malnutrition.

**GONZÁLEZ-FREIRE:** How do you think we can use proteomics to understand aging?

**SEMBA:** Your GESTALT project at the National Institute on Aging is really important. You and Luigi are characterizing normative data on the proteome of many tissues, including skeletal muscle, across a wide age range of healthy individu-

*(Continued on page 10)*

## The -omics approach reveals a key to the problem of child malnutrition

An interview with Professor Richard D. Semba, Johns Hopkins University

(Continued from page 9)

als. This study will likely become the benchmark for proteomics in aging research.

**GONZÁLEZ-FREIRE:** Who have been the most influential people in your career?

**SEMBA:** The evolutionary biologist Charles Sibley played an important role in forming my own perspective on science. He had an ambitious project to construct the global phylogeny of birds using DNA. I worked for him as an undergraduate, helping him prepare a book. Then he sent me out to do fieldwork for a year in the Amazon in Peru and in the rainforests of Borneo – it was a rare experience. Our field team discovered three new species of birds to science: a hummingbird, a flycatcher, and a new genus of owl. The other influential scientist was Linda Fried, the expert on frailty and aging. We worked together for several years until she left to become dean at Columbia.

**GONZÁLEZ-FREIRE:** What do you view as the ideal laboratory?

**SEMBA:** Perhaps there is no such thing as the ideal laboratory. It depends on what you want to accomplish. My main focus is on the research, as I don't have a large training program with dozens of graduate students and post-docs. I think clearly delineated research goals, a realistic lab schedule, clear communication, emphasis on papers and productivity, and investment in the career development of the people in your lab are paramount.

**GONZÁLEZ-FREIRE:** What do you do to relax?

**SEMBA:** I enjoy cooking for my friends. Food is sharing, sensory, symbolic, rich in social meaning, and forms the bond and social glue of our existence. I enjoy sharing meals and

my cooking with friends from all walks of life. I swim about an hour every day. One of my biggest joys is classical piano. My favorites are Bach, Mozart, and Brahms.

**GONZÁLEZ-FREIRE:** What kind of advice would you give to younger scientists that are forming their careers?

**SEMBA:** Develop writing skills, a love of writing, and set ambitious goals to write and publish as many papers as possible. No paper is ever perfect, so don't let perceived imperfection slow you down. Don't procrastinate. Communicate clearly with your colleagues and mentors. Be responsive. Understand the history of your subject, as scientific disciplines and topics have their own trajectories. Luckily for you, the fields of proteomics and metabolomics are on the ascending trajectory, which promises a stimulating and productive career ahead of you.



Professor Richard D. Semba and Marta González-Freire, Ph.D.

Join the #proteomics conversation! Connect with HUPO online.

@hupo\_org

Human Proteome Organization (HUPO)

@humanproteome



## EVENTS IN PROTEOMICS

HUPO is pleased to post meeting announcements for HUPO-related national and regional societies and for proteomics workshops and symposia. If you have an announcement to share, please email [office@hupo.org](mailto:office@hupo.org).

### HUPO WORLD CONGRESSES

[HUPO 2016 Taipei](#)

September 18-22, 2016

[www.hupo2016.org](http://www.hupo2016.org)



[HUPO 2017 Dublin](#)

September 17-20, 2017

[www.hupo2017.ie](http://www.hupo2017.ie)



### REGIONAL & NATIONAL EVENTS

[British Society for Proteome Research 2016 Meeting](#)

July 25-27, 2016

<http://www.bspr.org/event/bspr-meeting-2016>

[JProS 2016 \(14th JHUPO Conference\)](#)

July 28-29

[http://www.cnpn.ca/events/sym8/pdf/CNPN\\_2016\\_program.pdf](http://www.cnpn.ca/events/sym8/pdf/CNPN_2016_program.pdf)

[FEBS 2016](#)

September 3-8, 2016

<https://www.febs2016.org>

[EMBL—Wellcome Genome Campus Conference](#)

September 14-17, 2016

<http://www.embl.de/training/events/2016/PRO16-02>

[16th C-HPP Workshop](#)

December 10-14, 2016

<https://www.hupo.org/events/16th-c-hpp-workshop/>

## 8th Annual CNPN Symposium



The 8th Annual Canadian National Proteomics Network (CNPN) Symposium, “Proteomic Advances in Health and Diseases”, was held in Montreal on April 12-13, 2016. The focus of this symposium was on the use and applications of proteomics to unveil important molecular mechanisms and protein biomarkers of importance in cancer and disease development. Six thematic sessions (e.g. biomarkers, chemical and structural proteomics, protein modifications, protein interactions, bioinformatics and technology developments) are directly related to cancer research. Through major breakthroughs in mass spectrometry and affinity purification strategies, proteomics has provided novel insights in cell biology, and different oral and poster presentations featured emerging technological developments in these fields. The symposium also acknowledged the scientific contributions and leadership of Mike Tyers, recipient of the 2016 Tony Pawson Proteomics Award. While international in breadth and impact, this symposium provided an excellent opportunity for researchers to engage in active discussions in a stimulating environment and to foster collaborations in proteomics research.

The program of the symposium can be obtained at [http://www.cnpn.ca/events/sym8/pdf/CNPN\\_2016\\_program.pdf](http://www.cnpn.ca/events/sym8/pdf/CNPN_2016_program.pdf).



# HUPO

Dublin Ireland

17 - 20 September 2017



16th Human Proteome Organisation World Congress



**11th January 2017**  
Opening of  
registration



**11th January 2017**  
Call for  
abstracts



**5th April 2017**  
Close of  
abstracts



**31st May 2017**  
Notifications of  
acceptance



**14th June 2017**  
End of Early  
Registration



**16th August 2017**  
End of Regular  
registration

Visit our website



[www.hupo2017.ie](http://www.hupo2017.ie)

Email us at: [hupo2017@conferencepartners.com](mailto:hupo2017@conferencepartners.com)

Call us on: +353 1 296 8688

## HUPO NOMINATIONS & ELECTIONS COMMITTEE

The HUPO Nominations & Election Committee (NEC) plays a central role in ensuring a fair, transparent, and democratic representation of its membership in all HUPO activities. Based on nominations from the HUPO membership, the NEC develops the slate of eligible candidates for the HUPO council elections.

In practice, this means going out to the HUPO membership and encouraging candidates to stand for election to the HUPO council. In recent years, we have been successful in recruiting a sufficient number of candidates in all three HUPO regions to ensure competitive elections. However, the committee depends on candidacies to ensure a balanced representation of regions, gender, level of seniority, and research field in the candidate list. To mitigate the strong bias towards high profile, senior scientists on the HUPO council, two of the five new council positions per year and region are reserved for "Diversity Candidates", nominated

directly by the regional HUPO societies.

We would like to strongly encourage HUPO members to put themselves or esteemed colleagues forward as candidates for council election, in particular those from currently underrepresented groups. The HUPO council is the central decision-making assembly of HUPO, and HUPO depends on a broad council participation of its membership to ensure its continued innovative, dynamic, and balanced representation of the field.

### **2016 Nominations and Elections Committee:**

Jonathan Blackburn  
Catherine Fenselau Cotter  
Henning Hermjakob (Chair)  
Peter Hoffmann  
Jun Qin  
Paola Roncada  
Mathias Uhlen

## HUPO COUNCIL ELECTION 2016

The Nominations and Elections Committee of the Human Proteome Organization is pleased to announce the official slate of candidates for the HUPO Board of Directions (HUPO Council) election. HUPO wishes to express thanks to those candidates who are willing to stand for council election for a three-year term beginning in 2017 (2017-2019).

The election period for HUPO Council is August 26-September 18. Again this year, the vote is conducted online. All active HUPO members will receive an email containing a secure election ID code. Electors simply click on the link provided and cast their anonymous votes.

### **Diversity Candidates**

Each Regional (Eastern, Central, Western) HUPO organization is asked to nominate two (2) candidates to be considered for 'diversity' positions on the HUPO Council. 'Diversity' candidates are nominated by the national/regional proteomics societies with the understanding that the selections should increase the diversity of the Council from each region (examples: less represented countries as defined by HUPO membership fees, gender balance, young scientists, agricultural and micro-organism proteomic, industry). There is a block vote for diversity candidates with "accept" or "not accept" as part of the global HUPO election process.

The Western Region submitted 1 diversity candidate for the 2016 election whereas the Central and Eastern regions submitted 2 diversity candidates each. Therefore there is an additional council position that will be filled, via direct election, by a candidate from the Western Region.

## HUPO COUNCIL ELECTION 2016 | EASTERN REGION CANDIDATES

In the Eastern Region, there are six (6) candidates and three (3) open council positions.



**Hondermarck, Hubert**  
Professor  
University of Newcastle



**Nice, Edouard**  
Professor  
Monash University



**Ishihama, Yasushi**  
Professor  
Kyoto University



**Poon, Chuen Wai Terence**  
Associate Professor,  
Director of Proteomics  
University of Macau



**Lu, Haojie**  
Professor  
Fudan University



**Purcell, Anthony**  
Professor  
Monash University

### Eastern Region Diversity Candidates



**Srivastava, Sanjeeva**  
Associate Professor  
Indian Institute of Technology Bombay  
India



**Yoo, Jong Shin**  
Professor, Graduate School of Analytical  
Science & Technology  
Korea

## ELECTION 2016 | CENTRAL REGION CANDIDATES

In the Central Region, there are nine (9) candidates and three (3) open council positions.



**Cristobal, Susana**  
Professor  
Linköping University



**Pennington, Stephen**  
Professor  
University College Dublin



**Larsen, Martin**  
Professor  
University of Southern Denmark



**Pineau, Charles**  
Research Director  
Inserm Unit 1085 & Protim Core Facility



**Lundberg, Emma**  
Assistant Professor  
Royal Institute of Technology (KTH)



**Tsangaris, George**  
Professor  
Biomedical Research Foundation of the  
Academy of Athens



**Nikolaev, Evgeny**  
Professor, Institute of Biochemical  
Physics Russian Academy of Science



**Wollscheid, Bernd**  
Professor, ETH Zurich



**Ozpinar, Aysel**  
Professor  
Acibadem University

### Central Region Diversity Candidates



**Birner-Grünberger, Ruth**  
Professor, Doctor  
Medical University of Graz  
Austria



**Urbani, Andrea**  
Professor  
Catholic University  
Italy

## ELECTION 2016 | WESTERN REGION CANDIDATES

In the Western Region, there are eight (8) candidates and four (4) open council positions. The Western Region submitted one (1) diversity candidate for the 2016 election whereas the Central and Eastern regions submitted two (2) diversity candidates each. Therefore there is an additional council position that may be filled by direct election by a candidate from the Western Region.



**Cristea, Ileana**  
Professor  
Princeton University



**Nita-Lazar, Aleksandra**  
Investigator  
Laboratory of Systems Biology



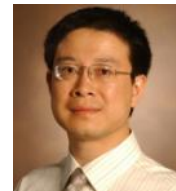
**Garcia, Benjamin**  
Presidential Associate Professor  
University of Pennsylvania



**Weintraub, Susan**  
Professor  
UT Health Science Center at San Antonio



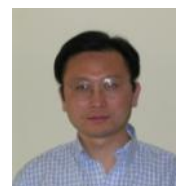
**Hathout, Yetrib**  
Associate Professor  
Children's National Health System



**Zhang, Bing**  
Associate Professor  
Vanderbilt University Medical Center



**Ivanov, Alexander**  
Research Associate Professor  
Northeastern University



**Zhao, Yingming**  
Professor  
University of Chicago

### Western Region Diversity Candidate



**Domont, Gilberto**  
Emeritus Professor  
Federal University of Rio de Janeiro  
Brazil



## HUPO INDUSTRIAL ADVISORY BOARD

Created in 2006, the HUPO Industrial Advisory Board (IAB) facilitates communication and input from industry partners to support the proteomics community and to recognize these partners as HUPO affiliates. HUPO supports industry allies active in the development of innovative technologies and appropriate standards that are responsive to the constant changes in the scientific proteomics environment.

### The IAB Mission

To provide HUPO leadership (the Executive Committee) valuable input on technology and product innovation for the benefit of members and to identify industry trends that will position HUPO to meet the future challenges of its partners and organization.

### Interested in joining HUPO as an IAB member?

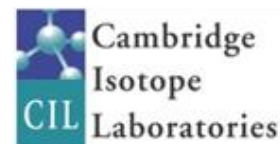
Complete the [IAB Membership Sign-Up Form](#) or

Contact the HUPO Office [office@hupo.org](mailto:office@hupo.org)

### Benefits of an IAB Membership

- Two complimentary individual HUPO memberships available for company employees (value \$200).
- Involvement in Human Proteome Project (HPP) with regular updates from project leadership.
- Direct connection with HUPO Executive Committee and Congress Organizers via monthly IAB calls.
- IAB sponsored Science and Technology Award, established in 2011, awarded to an industrial scientist. IAB representatives solicit and vet nominees. Award recipient presents a talk at the annual HUPO Congress.
- Selection of abstracts for the New Technological Advances in Proteomics presentations at the annual HUPO Congress.

The Human Proteome Organization wishes to thank the following IAB members for their participation!



Genentech

