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## EDITOR'S NOTE



Emma K. Lundberg,  
HUPOST Editor

Dear HUPO friends,

It was a pleasure meeting many of you at the Vancouver Congress! The 14th HUPO World Congress in Vancouver was a great success and I would like to thank and congratulate the organizers for an outstanding job. Besides great science there was also plenty of fun. Read more on the Congress in this issue of the HUPOST (Page 12). If you have not already had a look at the photos from the Vancouver meeting, do so online in the [HUPO 2015 Dropbox Gallery](#).

The HUPO Council election results were announced during the General Assembly of Members on September 29. I would like to take the opportunity to welcome our newly elected HUPO council members and to congratulate Mike Snyder for being elected as the next President of HUPO. I would also like to thank all those who are completing their terms on the Council for their efforts on behalf of HUPO. See the full results of the HUPO 2015 Council Election on Page 3.

(Continued on page 2)

## EDITOR'S NOTE

(Continued from page 1)

The Human Proteome Project (HPP) held both a pre and post congress meeting. The interest was higher than ever and over 100 people were reviewing progress, discussing paths forward, and explored criteria for claims of detecting “missing proteins”. We are happy to see the increasing interest in the Human Proteome Project. Read more about the it in the HPP Presidents report in this newsletter.

The Early Career Researcher (ECR) initiative launched earlier this year arranged a much appreciated Mentoring Day and a manuscript competition in Vancouver. You can read our interviews with the three finalists of the manuscript competition and get to know them and their plans for the future better. See the interviews on Pages 18-22.

As always in HUPOST you can also find the News in Science section, read about events in proteomics and updates from regional societies. I would also like to direct our readers toward the HUPO website where we have included several papers that continue to bring international attention to proteomics.

‘[High Protein Research](#)’, written by Neil Savage and published in *Nature*, features an interview with HUPO President-Elect Mike Snyder. The study ‘[Priorities and trends in the study of proteins in eye research, 1924-2014](#)’ has been published in *PROTEOMICS – Clinical Applications*. Finally, read the November issue of *Journal of the American College of Cardiology* for the article, ‘[Prioritizing Proteomics Assay Development for Clinical Translation](#)’.

Again I would like to thank all of you that send us content for HUPOST – keep it coming! Help us make HUPO an even more active and vivid society. Stories, highlights, news, suggestions and announcements are gladly accepted for inclusion in the HUPOST. To contribute please email the HUPO Office at [office@hupo.org](mailto:office@hupo.org). And remember to follow us on social media, you can find us on [Facebook](#), [Twitter](#) and [LinkedIn](#).

Best wishes to all of you!

Emma

## PRESIDENT'S NOTE



Dear HUPO friends,

The Human Proteome Organization is an international community with many friends and colleagues in France. At this difficult time we send our thoughts and support to our HUPO family living in Paris and internationally.

Best always,

Mark Baker

HUPO President

## HUPO COUNCIL ELECTION RESULTS

Council Member election results were announced at the General Assembly of Members on September 29, 2015 in Vancouver during HUPO 2015. For terms commencing in 2016 there were 3 Council positions for the Eastern and Central regions. The Western region chose to have their two diversity appointments elected through the direct election process and therefore there were 5 Council positions for the Western region. Thank you to all who have served, continue to serve, and to those who are joining the HUPO Council!

### EASTERN Region (3)

**Fuchu He**  
China

**Tesshi Yamada**  
Japan

**Michelle Hill**  
Australia

### CENTRAL Region (3)

**Lennart Martens**  
Belgium

**Henning Hermjakob**  
UK

**Jean-Charles Sanchez**  
Switzerland

### WESTERN Region (5)

**Christoph Borchers**  
Canada

**Akhilesh Pandey**  
USA

**Donald F. Hunt**  
USA

**Robert Moritz**  
USA

**Hui Zhang**  
USA

## REGIONAL (DIVERSITY) APPOINTMENTS

### EASTERN Region

**Setsuko Komatsu**  
Japan

**Ping Xu**  
China

### CENTRAL Region

**Tamas Janaky**  
Hungary

**Tanja Cirkovic Velickovic**  
Serbia

## 2016 HUPO EXECUTIVE COMMITTEE

President

**Mark Baker** 2015-2016

President-Elect

**Mike Snyder** 2016 (President 2017-2018)

Vice President

**Rob Moritz** 2016-2017

Secretary General

**György Marko-Varga** 2015-2016

Treasurer

**Bruno Doman** 2014-2016

Member-at-Large

**Yu-Ju Chen** 2015-2016

Member-at-Large

**Emma Lundberg** 2015-2016

## NEWS IN SCIENCE

The HUPO Publications Committee, chaired by Dr. Yu-Ju Chen, coordinates the News in Science highlight for each HUPOST issue. If you have research you would like to share in the quarterly newsletter, please email your information to [office@hupo.org](mailto:office@hupo.org) for review by the Publications Committee.

By Chia-Feng Tsai & Yasushi Ishihama

Kyoto University

Dysregulation of cellular signaling based on protein phosphorylation is closely linked to pathogenesis of human diseases and therapeutic strategies to control the phospho-signaling have been accepted to develop molecular-targeting drugs for cancer. MS-based quantitative phosphoproteomic approaches have been widely used to quantify over 10,000 phosphorylation sites by utilizing strong cation exchange chromatography, hydrophilic interaction chromatography or basic-pH reversed-phase chromatography to fractionate the complex samples. However, such extensive fractionation approaches require longer LC-MS measurement time as well as tedious pretreatment steps, resulting in reduced throughput and low reproducibility. Besides, these approaches cannot be applied to primary cells of rare tissues or clinical biopsy samples due to the limited starting materials.

To address these issues, Humphrey et al. (from Matthias Mann's group) at Max Planck Institute of Biochemistry have developed a streamlined phosphoproteomics workflow called "EasyPhos" which has been designed as a high throughput and simplified workflow to study time-resolved phosphorylation alteration *in vivo* without any pre-fractionation strategy. They used trifluoroethanol for the digestion buffer which allows bypassing the peptide desalting step before phosphopeptide enrichment. This protocol can reduce the potential sample loss during the desalting process implemented in the conventional

protocols. Besides, this simplified procedure can be expanded to a 96-well plate format to increase the throughput of phosphopeptide enrichment. The combination of this workflow with Q Exactive benchtop Orbitrap mass spectrometer allows monitoring of more than 10,000 phosphorylation sites from a mouse cell line by single-shot LC-MS/MS analysis with 2hr gradient. The applicability of this parallelized EasyPhos workflow has been demonstrated on the analysis of liver phosphoproteomes at different time points (early and intermediate) in fasted mice under insulin exposure. Up to 31,605 phosphopeptides (25,507 phosphorylation sites belong to class 1) from 6,138 phosphoproteins were identified from 91 biologically distinct liver tissues by the high throughput 96-well EasyPhos assay. Importantly, at least six biological replicate analyses (separate mice) per sample for each time point provide a highly statistical power to illustrate time-resolved maps of insulin signaling. Moreover, these dynamics datasets illuminate not only the insulin-mediated signaling network but also the signaling cascade from cell surface to the nucleus within 1 min *in vivo*. This rapid and high throughput EasyPhos workflow will facilitate to accumulate the knowledges of cellular signaling dynamics under physiological or pathological regulation.

This study was reported in the journal of *Nature Biotechnology* on August 17, 2015.

<http://www.nature.com/nbt/journal/v33/n9/abs/nbt.3327.html>

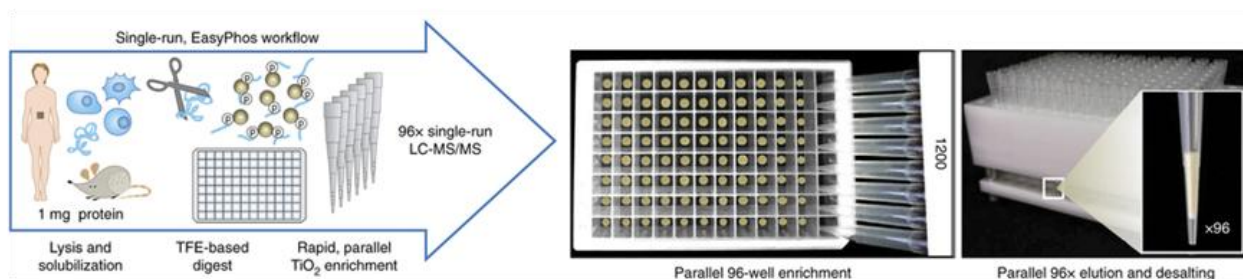


Figure reprinted with permission of the Nature Publishing Group.



## 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 this year!



Agilent Technologies

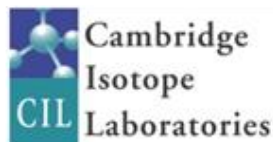


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## Human Proteome Project

### Human Proteome Project (HPP) Update from HUPO 2015

Gil Omenn, HPP Chair

The HPP played a major role in the 2015 HUPO Congress in Vancouver. Nearly 100 investigators met all day on Sunday to review progress and accelerate progress in each component of the HPP: the C-HPP (Paik), B/D-HPP and its program for Early Career Researchers (van Eyk), neXtProt with 16,793 PE1 and 2682 PE2-4 protein entries (Lane), PeptideAtlas and its Human PhosphoAtlas 2015-09 and Plasma Atlas 2015-09 (Deutsch), and the tissue-based Human Proteome and Human Protein Atlas v14 (Lundberg). neXtProt now offers [search.nextprot.org](http://search.nextprot.org) for complex queries and SPARQL for 100 pre-made queries.

Among the first 30 articles in the 3rd C-HPP special issue of the *J Proteome Research*, released on 4 September 2015 to be timely for the HUPO Congress, several were highlighted for their approaches to finding “missing proteins”: epigenetically-activated proteins (Lan), dental pulp proteome (Eckard), missing protein blocks along Chromosome 1 (Xu), and the *in vitro* transcription/translation/ MRM technology platform (Chr 5,10,15,16,19/Horvatovich). Those 30 articles are available at [www.thehpp.org](http://www.thehpp.org) and [www.c-hpp.org](http://www.c-hpp.org). An additional 12 articles will appear in November and December on-line in *JPR*. Given transcriptome evidence of large numbers of testis-specific (50X higher than any other tissue) or testis-enriched (5X) gene expression (Lindskog, HPA), we put a spotlight on the testis, spermatogenesis, and epididymis proteomes (Pineau, Chr 2 and 14), and proteogenomics (Liu). Some proteins (beta-defensin-126) migrate into sperm (without accompanying mRNA) from the epididymis. And we noted that a high proportion of missing proteins are membrane proteins, which present difficulties for both MS and antibody methods (Uhlen); membrane proteins are a high proportion in kidney and brain proteomes, intracellular proteins in heart and testis, and secreted proteins in pancreas and salivary glands. Extracellular vesicles/exosomes may be a good source of membrane proteins (Tomonaga).

The C-HPP sponsored a poster session and competition, a bioinformatics session, and a principal investigators council

meeting. The Biology- and Disease-driven (B/D) HPP and Resource Pillars presented 19 morning workshops, with a total of 650 participants: Cancer I and II, Plasma, Cardiovascular, Diabetes, Antibodies, EyeOME; Protein Standards, Glycoproteome, Toxicoproteome, Brain, PediOME; and Mitochondria, Liver, Multi-Organism, Extreme Conditions, Skeletal Muscle, Infectious Diseases, and Protein Misfolding & Aggregation Diseases. A Highlights publication is being prepared. Abstracts from the Congress workshops are available in [www.hupo2015.com](http://www.hupo2015.com). The B/D-HPP hosted a Mentoring Day for early career researchers and a manuscript competition, from which the three winners presented their papers in a well-attended Congress session: Olga Schubert on SWATH and functional analysis of the *M. tuberculosis* proteome; Justyna Fert-Bober on citrullinated proteins in heart failure; and Barcu Ayoglu on Anoctamin 2 as a biomarker in multiple sclerosis.

The HPP plenary session included Progress & Challenges of the HPP (Omenn), Mapping Missing Proteins in the C-HPP (Paik), Controlling False-Discovery Rates in Protein Identification (Cox), Effect of Trisomy 21 on the Quantitative Proteome (Li), a Testis-Epididymis Proteome Project (Pineau), and Combining RNA-Seq, MS, and Antibodies (Hahne). Bioinformatics specialists associated with the HPP held excellent daily consultative sessions open to all HUPO Congress participants, which were greatly appreciated and also facilitated discussion among the bioinformaticians.

During a full-day post-Congress Workshop, about 100 HPP investigators and other interested participants heard highlights from the Congress sessions and then explored criteria for claims of detecting “missing proteins” (the neXtProt PE2,3,4 predicted proteins) or “novel proteins” (potential translation products from lnc RNAs, small ORFs, or pseudogenes/neXtProt PE5 entries), with presentations by Michael Tress, Lydie Lane, Fernando Corrales, Ulrike Kusebauch, Alexey Nesvizhskii, Bill Hancock, Alexander Archakov, Yuju Chen, Elena Ponomarenko, Tadashi Yamamoto, Chris Overall, and Rob Moritz. Jennifer van Eyk addressed popular proteins for cardiovascular disorders, Tova Alm the affinity binder knockdown initiative, Juri Rappsilber computational mass spectrometry.

*(Continued on page 7)*

## H<sup>®</sup> Human Proteome Project

*(Continued from page 6)*

There was strong support for more specific Guidelines as proposed by Deutsch. These guidelines and a Checklist for authors and reviewers will be used for the 4th C-HPP special issue of JPR in 2016, with an April 30 deadline for submission of manuscripts. The details will be released in November in the JPR Call for Papers and at the HPP websites, with feedback welcomed.

The Guidelines will be recommended for broader use throughout the proteomics community. There is also a focus on identifying which predicted proteins are not amenable to detection with present preparative and analytical methods or have sequences indistinguishable from other (homologous) proteins.

Finally, future meetings. Led by Mike Snyder, the HPP will organize a Plasma Proteome Variation Project with extensive omics measurements of meeting participants at the March 2016 US HUPO meeting, as a pilot. The HUPO 2016 Congress in Taiwan will experiment with a linear track of HPP workshops instead of the simultaneous morning workshop schedule, with an offsite post-Congress workshop on 22 Sept in a beautiful rural setting. And steps were taken to have an HPP special conference in Rio de Janeiro in the 2nd week of December 2016 as part of the year-long 100th anniversary of the Brazilian Society of Biochemistry and Molecular Biology, hosted by Gilberto Domont, with emphasis on collaborations between C-HPP and B/D-HPP teams.



From left to right: Mark Baker, Gil Omenn, Pengyuan Yang, Fuchu He, Zihao Rao, Jun Qin, Yukui Zhang, Leroy Hood.

Photo from the October 14-16, 2015, Conference on Life Science in the Age of Big Data, hosted by Fuchu He for the National Center for Protein Sciences-Beijing and by Nick Campbell for the Nature Publishing Group.

## THE HUMAN PROTEIN ATLAS

### NEW VERSION OF THE HUMAN PROTEIN ATLAS

*The Human Protein Atlas launched a new version of the database on October 16, 2015. The major additions to version 14 are a new Mouse Brain Atlas and a new approach for antibody validation.*

STOCKHOLM, Sweden – 16 October, 2015

The Human Protein Atlas, a major multinational research project supported by the Knut and Alice Wallenberg Foundation, today launched a new version of the database. Since the release of Version 13 at the end of 2014, new data has been added and the atlas now holds data on more than 25,000 antibodies, covering over 17,000 of the human genes (approximately 86% of the human genome). Focus for this release has been to improve validation of the antibodies used to map the human proteome and the inclusion of a new atlas; the Mouse Brain Atlas, created by the Fluorescence Tissue Profiling facility at Science for Life Laboratory (SciLifeLab) in Stockholm.

The current version of the human protein atlas holds a comprehensive map of protein expression patterns in normal human tissues down to the single cell level. To assure the correct interpretation of the data, the RNA-seq data from transcriptomics has been evaluated against the gene/protein characterization data retrieved from antibody-based methods; antibody reliability, sub-optimal experimental procedures, and potential cross-reactivity has been assessed.

The result of the extensive evaluation is summarized in a data reliability description. Currently, almost 7500 genes have been updated with this knowledge-based annotation. In addition to this, co-localization of a fluorescent protein with the target protein has been introduced for antibody characterization, and complements the previously introduced gene silencing (siRNA) technique. In total, 104 genes have been analyzed using co-localization, 256 genes have been silenced and analyzed using immunocytochemistry, and 190 genes have been silenced and analyzed using western blot.

Many of the mouse proteins have extensive homology with the human counterpart and this forms the basis for

using the mouse brain as a model for the corresponding human brain to explore the expression and distribution of proteins in the various regions and cells of the brain. The new Mouse Brain Atlas, introduced in this version, includes additional brain regions and has additional information on cellular and sub cellular distribution of proteins in the brain. Currently, 88 genes and 129 brain regions are covered in the Mouse Brain Atlas.

“We believe this antibody-based data set is a valuable complement to our own human protein atlas and other international efforts that map the building-blocks of the brain, such as the Allen Brain Atlas and the Gensat effort.” says Dr Jan Mulder, head of the Mouse Brain Atlas effort at SciLifeLab.

The atlas is interactive, with the possibility of zooming in from a full brain section to single cells in a specific region of the brain.

#### About the Human Protein Atlas Project

The Human Protein Atlas project, funded by the Knut and Alice Wallenberg Foundation, has been set up to allow for a systematic exploration of the human proteome using antibody-based proteomics. This is accomplished by combining high-throughput generation of affinity-purified antibodies with protein profiling in a multitude of tissues and cells assembled in tissue microarrays. Confocal microscopy analysis using human cell lines is performed for more detailed protein localization. The program hosts the Human Protein Atlas portal with expression profiles of human proteins in tissues and cells. The main sites are located at AlbaNova and SciLifeLab, KTH - Royal Institute of Technology, Stockholm, Sweden, and the Rudbeck Laboratory, Uppsala University, Uppsala, Sweden. For more information on the Human Protein Atlas, visit our website at [www.proteinatlas.org](http://www.proteinatlas.org).



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## NATIONAL & REGIONAL SOCIETY UPDATES

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](mailto:office@hupo.org).

### 15<sup>TH</sup> HUMAN PROTEOME ORGANIZATION WORLD CONGRESS IN TAIPEI (HUPO 2016)

HUPO 2016, organized by the Taiwan Proteomics Society, will be held in Taipei from September 18th (Sunday) to September 22nd (Thursday), 2016!

For the past years, HUPO has been making a great evolution on advancing the science of proteome. To continue the object from the past congress, the HUPO 2016 in Taipei is focusing on “**Precision Proteomics for Precision Biology and Medicine**”. This unique platform is going to provide a great opportunity for proteomics scientists to stimulate and exchange the most up-to-date science knowledge.

Taipei is Taiwan's largest city as well as its economic, political, and cultural center. It is a modern cosmopolitan metropolis with a lively and diversified face, filled with exuberance. From the world's tallest building to the biggest collection of Chinese art, Taipei invites you into a world of fascinating contrasts—a mix of the modern and traditional, with a generous dash of energy and friendly smiles to make this one of your most memorable trips to Asia.

With open arms and warm regards, we look forward to welcoming you to Taipei in September, 2016. For more information please visit our [official website](#).



### THE U.S. HUMAN PROTEOME ORGANIZATION

Established in 2004, US HUPO continues to enhance its offerings and programs to the US-based community and beyond. The organization is led by officers Joshua LaBaer (President), David Muddiman (President-Elect), Ileana Cristea (Secretary), David Fenyo (Treasurer) and Natalie Ahn (Past President) along with Executive Committee members-at-large David Arnott, Lan Huang, Laurie Parker and Hanno Steen.

The 2016 the annual meeting will be in **Boston, Massachusetts, March 13-16, 2016**. Organized by Hanno Steen (Boston Children's Hospital), Natalie Agar (Brigham & Women's Hospital), Sasha Singh (Brigham & Women's Hospital), Judith Steen (Boston Children's Hospital), and Olga Vitek

(Northeastern University). Highlights include plenary lectures from Matthias Mann (Max-Planck) - Mass Spectrometry-based Proteomics, Sangeeta Bhatia (MIT) - Multiscale Regenerative Technologies, and Masanori Aikawa (Brigham & Women's Hospital, Harvard Medical School) – New Therapeutic Targets for Cardiometabolic Diseases. A hallmark of the US HUPO meeting is broad inclusion of **talks selected from submitted abstracts providing more than 60 opportunities** for attendees to present their work in the oral sessions. **Special focus is given to early career faculty, post-docs, and graduate students** providing a showcase, and platform, for the next generation of proteomics researchers. Travel stipends are available for both post-docs and graduate students. To be considered for a talk, submit your abstract by December 18, 2015.

*(Continued on page 10)*

## NATIONAL & REGIONAL SOCIETY UPDATES

*(continued from page 9)*

Each year **short courses** are offered in conjunction with the annual conference. These high quality, low cost courses provide instruction from top researchers in the areas of **protein-protein interactions** (Ileana Cristea and Alexey Nesvizhskii), **statistical methods** (Olga Vitek and Brendan MacLean), and new this year **cross-linking mass spectrometry** (Lan Huang).

A new addition to the 2016 conference is the introduction of the **Gilbert S. Omenn Computational Proteomics Award** (\$2,500 prize). This award will be offered annually along with the **Robert J. Cotter New Investigator Award** (\$1,000

prize). Recipients will give a featured plenary talk at the annual meeting. Learn how to apply at [www.ushupo.org](http://www.ushupo.org). Deadline is December 4, 2015.

To learn more about US HUPO's 2016 meeting and short courses in Boston and how you can benefit by participating, visit [www.ushupo.org](http://www.ushupo.org).



## THE DANISH PROTEOME SOCIETY | celebrating the 10<sup>th</sup> anniversary of DAPSOC!

The Danish Proteome Society (DAPSOC) was established in 2005, as an interest-group under the Danish Society of Biochemistry and Molecular Biology (DSBMB). DAPSOC aims to advance proteome research, education and training in Denmark, and to promote interactions across different research fields, academia, industry and technology providers. DAPSOC now has more than 100 registered members. Information about upcoming events and past activities can be found at [www.dapsoc.org](http://www.dapsoc.org).

DAPSOC serves as a national contact point to international proteome societies. DAPSOC members have been actively involved in forming the current HUPO and EuPA organisations since 2004.

DAPSOC's main annual event takes place as a full-day scientific meeting in the first week of December, usually at the Odense campus of SDU (University of Southern Denmark). This meeting serves as an important networking activity for Danish proteomics researchers and instrument vendors. The scientific program always highlights recent progress in Danish and international protein sciences and proteomics. Key-note speakers are selected among internationally recognized scientists. Moreover, this meeting provides an important training and education opportunity for young Danish scientists to present their research to a larger audience. At least four young researchers, typically at the end of their PhD studies, or early in their Post.Doc career, are invited to speak at the DAPSOC meeting, and all young researchers are en-

couraged to participate with posters.

DAPSOC's annual meetings are open to all, and welcoming international guests to join our meeting.

This year, DAPSOC celebrates our 10<sup>th</sup> anniversary. This coincides with the 40 year anniversary of protein mass spectrometry research at SDU at Odense. We have invited outstanding protein biochemists, proteomics and mass spectrometry researchers to present their latest research at the 2015 DAPSOC meeting on December 8, including Matthias Mann (MPI Biochemistry, Germany), Neil Kelleher (Northwestern Univ., USA) and Poul Nissen (Aarhus Univ., DK). Program details are found at [www.dapsoc.dk](http://www.dapsoc.dk).

### The DAPSOC steering Committee:

- Ole Nørregaard Jensen (President), Univ. Southern Denmark, [jenseno@mbm.sdu.dk](mailto:jenseno@mbm.sdu.dk)
- Emøke Bendixen, Aarhus University, [ebx@mbg.au.dk](mailto:ebx@mbg.au.dk)
- Allan Steensballe, Aalborg University, [as@hst.aau.dk](mailto:as@hst.aau.dk)
- Birte Svensson, Technical University of Denmark, [bis@biocentrum.dtu.dk](mailto:bis@biocentrum.dtu.dk)
- Rene Lametsch, Copenhagen University, [rla@ku.dk](mailto:rla@ku.dk)
- Jan Enghild, Aarhus University, [jje@mbg.au.dk](mailto:jje@mbg.au.dk)
- Niels Heegaard, Staten Serum Institut, [nhe@ssi.dk](mailto:nhe@ssi.dk)
- Steen Gammeltoft, Danish Biochemical Society, [gast@glo.regionh.dk](mailto:gast@glo.regionh.dk)

## EVENTS IN PROTEOMICS

### HUPO WORLD CONGRESSES

#### HUPO 2016 Taipei

September 18-22, 2016



#### HUPO 2017 Dublin

September 17-20, 2017



### REGIONAL & NATIONAL EVENTS

#### 5<sup>th</sup> Symposium on Structural Proteomics

November 19-20, 2015

Halle, Germany

<http://www.structuralproteomics.net/>

#### 7<sup>th</sup> Annual Meeting of Proteomics Society,

India 2015

December 3-6, 2015

Vellore, India

<http://www.psvellore2015.org/>

#### DAPSOC 2015 Symposium

December 8, 2015

Odense, Denmark

<http://www.dapsoc.org/?Events>

#### US HUPO Annual Conference

March 13-16, 2016

Boston, USA

<http://www.ushupo.org>

#### 6th International Conference on Bioinformatics

March 28-29, 2016

Valencia, Spain

<http://bioinformatics.conferenceseries.com/>

#### X Annual Congress of the European Proteomics Association

June 21-25, 2016

Istanbul, Turkey

<http://www.eupa2016.org>

#### British Society for Proteome Research 2016 Meeting

July 25-27, 2016

Glasgow, United Kingdom

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

## THANK YOU FOR ATTENDING HUPO 2015!

The 14th Annual HUPO World Congress took place in Vancouver from 27-30 September. On behalf of the Human Proteome Organization, thank you for attending HUPO 2015! From the beautiful venue and surrounding city, the fun social program, to the exceptional scientific program, we extend our sincere thanks and congratulations to the congress organizers. We wish to thank the Local Organizing Committee, the Scientific Organizing Committee, and the Advisory Committee for all of their incredible hard work in making this an exceptional congress.

The congress program commenced on Sunday with the Bioinformatics Hub, HPP General Investigators' Meeting, Mentoring Day, Technology Day, Education Day, and Clinical Day. The Opening Plenary Session, delivered by Ruedi Aebersold and Aled Edwards, set the standard of excellence for the entire HUPO scientific program. Delegates were welcomed in the Opening Ceremonies by representatives of the Squamish Nation, who presented Congress Co-Chairs Christoph Borchers and Pierre Thibault with a Talking Stick. Following the ceremonies all attendees joined the Canadian Mounties and Lumberjacks for the Welcome Reception in the packed Exhibit Hall. The Congress continued until Wednesday, September 30. The scientific program was shaped by exceptional keynote speakers, more than 654 posters, and more than 900 presented abstracts. Starting with the morning HPP sessions, delegates could spend the day attending excellent sessions, learning about innovative technologies in the exhibit hall, attending an Industry-Sponsored lunch seminar, visiting the poster hall, and engaging in discussions with our wonderfully diverse array of delegates during networking breaks. More than 1100 delegates attended the Congress from over 40 different countries. The most notable social event was the HUPO Congress Night, Hockey Night in Canada, which took place on Tuesday, September 29 at the Convention Centre. Delegates competed in hockey challenges, tried Canadian cuisine, and danced the night away to the live band.

A number of awards and travel grants were presented in Vancouver to recognize the outstanding science in the proteomics community, both among the established researchers and early career researchers. The Human Proteome Project (HPP) presented individuals with the [HPP Clinical Scientist Travel Grant](#). The winners of the [2015 HUPO Awards](#) were presented with awards and shared their research with

us during their acceptance speeches. The HUPO Congress Travel Award, the BC Proteomics Network ([BCPN](#)) Travel Awards, and the Canadian National Proteomics Network ([CNPN](#)) Travel Awards were given during the Awards Ceremony. The HUPO Early Career Researcher (ECR) Award was also given during the Awards Ceremony. Read an interview with the finalists and the winner in this issue of the HUPOST.

On behalf of HUPO, thank you for attending and we look forward to seeing you all in Taipei for HUPO 2016!

We would like to thank the following companies for their support in making HUPO 2015 happen!

### Diamond Level



### Gold Level



### Silver Level



### Bronze Level



### Supporter Level



## HUPO 2019 | REQUEST FOR PROPOSALS

We are pleased to announce that HUPO is accepting applications to host the 18th HUPO World Congress in 2019. The Congress location rotates each year among three global regions: Eastern, Central, and Western. The 2019 Congress will take place in the Eastern Region (Asia-Oceania). If your national society would like to submit a proposal please email [Chelsea@hupo.org](mailto:Chelsea@hupo.org) for the application timeline and instructions. The deadline to accept proposals is April 30, 2016.

## IMAGES OF HUPO 2015

Photos from HUPO 2015 are now available online on the [HUPO 2015 Dropbox Gallery](#). Here are a few of our favourites!



**Above:** Representatives from the Squamish Nation welcome delegates to HUPO 2015 with a traditional dance and presentation of the talking stick.



**Above:** Congress Co-Chairs Christoph Borchers and Pierre Thibault welcome delegates to Vancouver.



**Left:** Presentations during Mentoring Day on Sunday.

## IMAGES OF HUPO 2015

Photos from HUPO 2015 are now available online on the [HUPO 2015 Dropbox Gallery](#). Here are a few of our favourites!



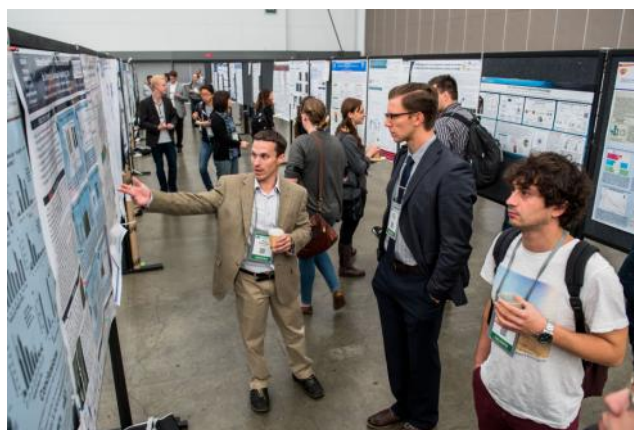
**Above:** Discussions at the HUPO Bioinformatics Hub.



**Above:** Presentations at the HUPO Clinical Day.



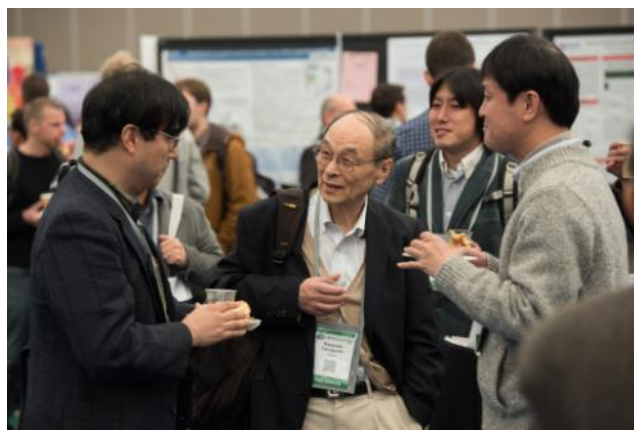
**Above:** A very busy Welcome Reception in the Exhibit Hall.



**Above:** Learning about one of over 600 posters at HUPO!



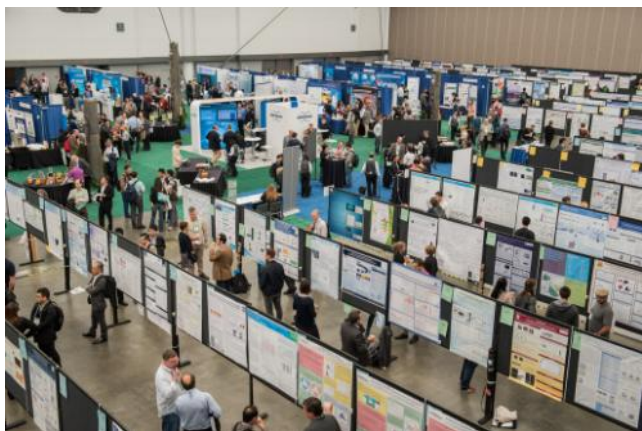
HUPO Executive Committee members in Vancouver. *From left to right:* Bruno Domon, Mike Snyder, Mark Baker, György Marko-Varga.



**Above:** Discussions during networking breaks took place in the Exhibit Hall.

## IMAGES OF HUPO 2015

Photos from HUPO 2015 are now available online on the [HUPO 2015 Dropbox Gallery](#). Here are a few of our favourites!



**Above:** Delegates enjoying the poster hall and exhibits.



**Above:** High-stakes at the air hockey table.



**Above:** Expert goalie, Pierre Thibault, guarding the net.



**Above:** Delegates danced to live music at Hockey Night in Canada!



**Above:** Dr. Ming-Daw Tsai invites everyone to Taipei for HUPO 2016!



**Above, left to right:** Christoph Borchers, Grit Schoenherr, Natalie Glavas, Pierre Thibault. **Thank you for organizing a fantastic Congress!**

## #HUPO 2015 ONLINE

The 14th Annual Human Proteome Organization World Congress saw the successful launch of HUPO's new social media portals! There was lots of engagement with the Facebook, Twitter, and LinkedIn profiles. We invite all our HUPO members, associate members, and the entire proteomics community to continue the conversation online!

[/humanproteomeorg](http://humanproteomeorg)



[@hupo\\_org](https://twitter.com/hupo_org)



[Human Proteome Organization\(HUPO\)](https://www.linkedin.com/company/hupo)



**Atlas Antibodies** @atlasantibodies · Sep 24

Getting ready for #HUPO2015, Atlas Antibodies candy and Swedish toy-elks are now packed! Visit us in booth #204!



**Alexander Boichenko** @AlexBoichenko · Sep 27

Current state of Peptide Atlas 14070 canonical proteins with >2 peptides  $\geq 9$  AAs, but 3166 are still not detected, HPP Session #hupo2015



**Naveed Aziz** @DNAziz\_ · Sep 27

The holy grail of cancer therapy is early detection. Andre Marziali #HUPO2015



**Human Protein Atlas** @HumanProteome · Sep 27

More than 8000 proteins in the eyeOME. #HUPO2015




**Paola Roncada** @paolaroncada · Sep 27

@hupo\_org President Mark Baker welcome us#hupo2015



## #HUPO 2015 ONLINE

 Human Proteome @hupo\_org · Sep 28  
**#HUPO2015** youngest delegate meets our first dog exhibitor! Come visit Toby @ VICI Valco Instruments - Booth 109.



[/humanproteomeorg](https://www.facebook.com/humanproteomeorg)



[@hupo\\_org](https://twitter.com/hupo_org)



[Human Proteome Organization\(HUPO\)](https://www.linkedin.com/company/hupo)



Sara Feltesse @elssa78 · Sep 29  
Great presentation on **#sportomics** and how athletes can help understand the human metabolism **#HUPO2015**



The Overall Lab @OverallLabNews · Sep 30  
So proud of our 4 **#BCproteomics** travel award winners **#hupo2015**



Jason McDermott @BioDataGanache · Sep 30  
Really enjoyed **#HUPO2015**. What a great conference and a gorgeous location (the weather didn't hurt!)



Yasset Perez-Riverol @ypriverol · Oct 15  
HUPO-PSI now has their official [@github](https://github.com/HUPO-PSI) organisation  
[github.com/HUPO-PSI](https://github.com/HUPO-PSI) **#Proteomics** **#Standards** **#openscience**  
**#Ontologies** @hupo\_org

## ECR Manuscript Competition 2015

### *An interview with the three finalists of the inaugural HUPO ECR Manuscript Competition.*

The HUPO Early Career Researcher (ECR) initiative has launched this year the first HUPO ECR Manuscript Competition. The intent of this first competition was to provide young scientists with a platform to highlight their work. More than fourteen international young researchers have participated with manuscripts of very high quality. Three finalists were selected from a jury of senior scientists and members of the ECR committee to present their work with an oral presentation. The 14<sup>th</sup> World HUPO Congress in Vancouver hosted the final of this competition. It was outstanding to observe the large number of public attending this session! We are extremely thankful to the organizers of the congress for the exceptional support to this first event! The three finalists gave enthusiastic presentations of their excellent work and it has not been simple for the jury to determine the winner (Dr. Olga Schubert) and the two running up (Dr. Burcu Ayoglu and Dr. Justyna Fert-Bober).

We were interested to know a little bit more from our three finalists, as representative of the current generation of young promising researchers in proteomics. So, after the enthusiasm of Vancouver 2015, we have conducted an interview with Dr. Burcu Ayoglu (BA), Dr. Justyna Fert-Bober (JFB) and Dr. Olga Schubert (OS), sending them a short series of questions. In our interview we were interested in knowing more about their scientific work. But also, we wanted to learn in a spontaneous way, what are difficulties and happy moment in the work of a young researcher in proteomics! What are their dreams, their plans for the future, their challenges and how HUPO could help them! And finally, we wanted to learn about their vision of proteomics! Below, we report the questions from the ECR team and the answers from the three finalists. The interview resulted in a very interesting and fresh introspection in the ambitions of an early career researcher in proteomics. Many of the answers are a true inspiration... at least for the future work of the HUPO ECR initiative! But maybe the strongest underlying impression resulting from the interview is the genuine enthusiasm for proteomics!

Again, many congratulation to Burcu, Justyna and Olga and .... happy reading!

The ECR Team

**Question ECR Team: What was your position and affiliation when you conducted your project?**

**Answer Burcu Ayoglu – BA:** This project started as my main PhD project at KTH-Royal Institute of Technology in Stockholm, Sweden when I joined the Affinity Proteomics group directed by Prof. Peter Nilsson, which is also part of the Human Protein Atlas, directed by Prof. Mathias Uhlen. After receiving my PhD degree, I continued to work on this project for around a year as a postdoc in the group.

**Answer Justyna Fert-Bober – JFB:** Project Scientist at Cedars-Sinai Medical Center, Los Angeles, CA, USA.

**Answer Olga Schubert – OS:** PhD student in the lab of Prof. Ruedi Aebersold at the Institute of Molecular Systems Biology at ETH Zurich in Zurich, Switzerland.

**Q: What is your current position and affiliation?**

**A (BA):** In a week I will move to USA to start my postdoctoral fellowship at Stanford University School of Medicine, working in the group of Prof. PJ Utz at the Dept. of Immunology and Rheumatology. I was recently awarded a scholarship by the Knut & Alice Wallenberg Foundation for this fellowship.

**A (JFB):** Project Scientist at Cedars-Sinai Medical Center, Los Angeles, CA, USA.

**A (OS):** Postdoctoral fellow in the lab of Prof. Leonid Kruglyak at the Department of Human Genetics at University of California, Los Angeles (UCLA) in Los Angeles, USA.

**Q: In my project I did....**

**A (BA):** ... first the development of assay and data analysis workflows for autoantibody profiling in body fluids using various protein and peptide array formats. Then, using arrays with over 11,000 antigens, I screened plasma samples from around hundred multiple sclerosis (MS) patients and individuals with other neurological conditions. Following this, we got access to a much larger plasma sample collection of over 2,000 samples, which I profiled for autoantibody reactivity against the most interesting targets selected out of over 11,000. This revealed an interesting difference between MS cases and controls in plasma reactivity towards an ion channel protein called anoctamin 2. Then together with our collaborators we tried to further understand the increased autoimmune reactivity against this protein by e.g. immunofluorescence analysis on human brain tissue from MS patients.

**A (JFB):** Discovery of citrullination in major sarcomeric pro-

*(Continued on page 19)*

teins and prove that this PTM have a negative inotropic effect on myocardial contractility. Furthermore our group presented a strategy; create a bioinformatics pipeline for verifying citrullinated sites in complex biological samples.

**A (OS):** In my project, we implemented a label-free method to estimate absolute cellular protein concentrations on a genome-wide scale based on SWATH MS data. We applied this method to study the human pathogen *Mycobacterium tuberculosis*, which remains a health concern due to its ability to enter a non-replicative dormant state linked to drug resistance. We reproducibly quantified over 2000 *M. tuberculosis* proteins during the transition into and out of dormancy, providing unprecedented insights into proteome composition and dynamics. Specifically, by relating absolute abundances of metabolic enzymes to corresponding metabolites using a genome-scale metabolic model, we could determine the biomass investment of the cell into specific compartments of metabolism and infer the fluxes through metabolic pathways.

**Q: My project is great, because ...**

**A (BA):** ... it is one of the largest efforts to characterize the plasma autoantibody repertoire within multiple sclerosis, where our approach has been based on an entirely unbiased and large-scale exploration of the autoantibody repertoire in MS. This approach paid off by allowing us to identify a novel protein which seems to be the targets of autoantibodies in multiple sclerosis patients and which has not been impli-

cated in the context of MS before.

**A (JFB):** Citrullination has been associated with several diseases, and autoantibodies against citrullinated proteins are today used as an important clinical diagnostic biomarker for characterizing rheumatoid arthritis (RA). The exact physiological role of citrullination in relation to diseases is incomplete, and specific analyses are needed to expand upon current knowledge. My finding offers the potential for extensive further investigations attempting to sort out the complex modifications that occur in sarcomeric proteins in heart failure and other various diseases and what they mean. Created citrullinated pipeline is going to help future proteomics studies identify citrullinated peptides in complex biological samples which will result in more reliable, more sensitive and faster disease diagnostics.

**A (OS):** My project is great, because it highlights the importance of absolute quantification in quantitative biology and mathematical modeling, by integrating protein and metabolite data based on a genome-scale metabolic model. The data provide an unprecedented picture of proteomic adaptation and cellular biochemistry of *M. tuberculosis* under clinically relevant stress conditions. The exemplary analysis of key enzymes in glycolysis and TCA cycle, and the conceptual analysis on a more global scale, beautifully illustrate the importance of absolute cellular protein concentrations for a truly quantitative understanding of an organism's metabolism.

*(Continued on page 20)*



The award ceremony of the inaugural HUPO ECR Manuscript Competition at the 14<sup>th</sup> HUPO World Congress.

From left to right: Prof. Mark Baker (HUPO President), Dr. Burcu Ayoglu (runner-up of the ECR Manuscript Competition), Dr. Justyna Fert-Bober (runner-up of the ECR Manuscript Competition), Dr. Olga Schubert (winner of the ECR Manuscript Competition), Prof. Jennifer Van Eyk (ECR chair).

**Q: My project will change the world, because....**

**A (BA):** ... our findings suggest that it is possible to identify a subgroup of multiple sclerosis patients who have a positive autoimmune reactivity towards the protein we identified. This information has a great potential to contribute, directly or indirectly, to the development of diagnostic algorithms to characterize a subgroup of MS patients.

**A (JFB):** I believe that my research will make a direct impact on people quality of life. Protein citrullination has been implicated in several physiological and pathological processes, including rheumatoid arthritis, multiple sclerosis, Alzheimer's disease and cancer. Understanding the role of citrullination in these processes will help to development of novel therapeutic approaches and more sensitive and specific diagnostic tools.

**A (OS):** The resulting molecular inventory of cellular protein concentrations for over 2000 M. tuberculosis proteins under clinically highly relevant growth states is complementary to existing proteomic and transcriptomic data sets and can serve as a reference for further quantitative analyses and mathematical modeling. Furthermore, knowledge of absolute concentrations of proteins in M. tuberculosis might assist in the development of treatments and preventive measures to fight tuberculosis. The discovery of highly upregulated and abundant proteins can support the identification of important pathways and processes and indicate where the system might be vulnerable to drug interventions as well as facilitate identification of appropriate antigens for rational design of future multi-stage vaccines.

**Q: What I loved during my work is....**

**A (BA):** ... that as a new PhD student in a relatively small group, I started with the very basics such as generating antigen arrays and developing assay protocols from scratch, and after fine-tuning all these strategies both for labwork and for data analysis over a long while, I analyzed over 2,000 samples, and then like finding a grain of sand in a desert, we find this interesting protein among 11,000 others! In that sense the outcome of this project was like cooking a nice dish with your family by using the different ingredients you have been patiently producing in your house and by working on different parts of your recipe for several months. This work taught me that hard work is what keeps the ship moving and there is no other substitute for it.

**A (JFB):** Generating questions from biological research and bringing new technologies that can be applied to biology.

The mix of two opens the ability to see a completely new and different picture of what's going on in biological systems. This is what I love generally in the science. This particular project gave me the opportunity to learn about this amazing posttranslational modification disturbs across many cellular organelles and effecting cellular processes, impacting both physiological and pathological pathways. Now I have more questions to answer than before.

**A (OS):** I enjoyed the constructive collaboration with colleagues in our group and our institute as well as with tuberculosis experts from Germany. It was great to see our joint expertise resulting in new insights into the molecular reorganization of M. tuberculosis during clinically relevant states. This project also gave me the opportunity to learn how omics data can be integrated using a metabolic model to reveal novel aspects of regulation and interplay among molecules in cellular networks.

**Q: And what I hated during my work is...**

**A (BA):** ... nothing I'd say I "hated" but there are various challenges and impracticalities which might happen in large-scale projects involving clinical samples. Such as you might receive thousands of samples in a plate format not suited for your liquid handling equipment and you have to manually transfer all samples into a different type of plates; or when you think you are almost finished with the analysis of your data, you might receive an email with a subject "Updated sample info". My take-home message has been that we should not make assumptions on the quality and characteristics of samples and sample information and as proteomics "end-users" we have to increase awareness and propose relevant sample delivery, quality and data transfer requirements to be adhered when receiving samples from clinical collaborators.

**A (JFB):** I think we are fortunate to work with the leading edge instrumentations. However proteomics field is still unexplored in many fields and the mandate of proteomics should be much broader than is frequently recognized. For me the biggest obstacle was to find a good detection and verification method for citrullinated peptides. This modification is low abundance with the same mass shift as deamination of N and Q so even if you have super sensitive instrument you still come across the problem from which residue the +0.984 Da shift comes from. Fortunately for me, in my lab we have a great group of people with different expertise so we came up with the bioinformatics pipeline that auto-

*(Continued on page 21)*

matically verify the citrullinated peptides by searching for RT difference, position of the modified residue etc.

**A (OS):** Because we used measurement techniques and analysis tools that were still in their infancy, we had to invest considerable amounts of time in manual assessment of the data combined with extensive testing of different analysis strategies and various software tools and parameters. This was very time consuming work and I completely underestimated the time needed to obtain the final data set. The slow progress during this stage of the project was at times quite frustrating.

**Q: You close your eyes and you dream a little bit about your professional and personal future...and...**

**...where will you be in January 2016, and doing what?**

**A (BA):** I see myself surrounded by my new colleagues at Stanford and meeting many more new researchers, clinicians, PhD students and postdocs in several other groups at Stanford. We will be working in new, cool projects some of which involving the development of new strategies and proteomics approaches for discovery and analysis of autoantibodies and for study of cellular signaling pathways in autoimmune conditions. As you can tell by my excessive use of “new” here, I’m expecting January 2016 the start of a new personal and professional development stage and the beginning of an important networking and intensive learning phase. And when not in lab, I will probably be finding out more about the Silicon Valley spirit and discovering California!

**A (JFB):** At work, writing a grant proposal.

**A (OS):** In January 2016 I will be working on a project aimed at understanding the genetic basis of protein abundance regulation in the lab of Prof. Leonid Kruglyak at UCLA, which I joined few months ago. I am currently going through a steep learning curve regarding various aspects of genetics and genomics and I hope that by January 2016 I will have gained a deeper and more complete understanding of these fields. Regarding my research project, I hope to have completed the pilot experiments and to be ready to move on to larger scale analyses.

**...where will you be in January 2021, and doing what?**

**A (BA):** In five years, I see myself having made a good synthesis of the experience I gained during PhD and postdoc years, being equipped with several academic and professional skills, having built a very diverse research network and

having a much more enriched research perspective. I imagine myself having worked for a track record well-suited for an academic position as an independent group leader, where I define truly exciting and clinically meaningful research questions within autoimmunity research and where we set up, apply and combine cutting-edge methods at a unique intersection of technology development, immunology and medicine. When not traveling for conferences and sitting in front of my laptop and writing grant applications (yes, grant applications are inevitable even in dreams...), I see myself enjoying the simple moments with my small family.

**A (JFB):** At work, writing a grant proposal.

**A (OS):** By January 2021, in my dreams, my work has revealed significant new insights into the genetic architecture underlying protein abundance variation in microbes as well as mammalian cells. With all the knowledge, skills and expertise acquired during my doctoral and postdoctoral studies, I hope to be ready to take up a position as an independent group leader. It will be exciting to work on the integration of genomic and proteomic data, making sense of the flood of data, which will be acquired with the ever-increasing coverage, sensitivity and throughput of the relevant measurement technologies. Proteomics will be an important layer of information to better understand how genomic variation in organisms manifests in different phenotypes, such as, for example, virulence or drug resistance in bacteria or disease-susceptibility in humans.

**...where will you be in January 2026, and doing what?**

**A (BA):** In ten years, I hope my work will have revealed valuable insights into the role and study of autoantibodies, both in health and in disease. By then I hope I will have created a nurturing environment for a small but diverse group of junior researchers and I hope I would have become a good role model and an inspiring research mentor for them. In parallel to working on establishing my research within translational proteomics in autoimmunity, by that time I can also see myself at academic leadership positions where I actively work on the subject of how to promote and embed diversity and gender balance in academic research. As a female and internationally mobile researcher with several years of studying, living and working experience in countries else than my home country, I find this subject very important.

**A (JFB):** At work, writing a grant proposal.

*(Continued on page 22)*

**A (OS):** Spinning my dreams further, one scenario could be that I will have successfully established my research at the intersection of genomics and proteomics, using a combination of experimental and computational strategies. My aspiration for my professional future is, however, not necessarily to hold a specific position, such as a professorship, but to have an inspiring and fulfilling occupation.

**...and how do you think HUPO can help you realizing your dreams?**

**A (BA):** For early-career proteomics researchers as myself, HUPO and HUPO events have a very important function to serve as an interaction platform, where we can build our own international research network by finding the right collaboration partners complementing our own expertise, whether it is technology-oriented or clinically-oriented. In that sense, continuous opportunities to present our research and research interest are of course extremely valuable. In addition to this, possibilities to get more active roles within HUPO and at HUPO events at an early career stage are very important as such responsibilities can truly help to broaden your vision about the field and to be always up-to-date.

**A (JFB):** HUPO is a great way to networking new ideas and new technological/methodological innovation. I think HUPO organizers should keep each event memorabilia by inviting reputed scientists, follow trends of new methodology and technology and concentrate to improve networking between younger and more professional members.

**A (OS):** Due to the rapidly increasing scale of research projects (both, in terms of coverage and samples/subjects) in combination with the increasing complexity of instrumentation and analysis strategies, it will become more difficult for an isolated research group to conduct competitive research and collaborations will become more important. HUPO will be important for me and others to continue its role in forming a platform where researchers from around the globe meet to discuss scientific advances and new ideas, and to coordinate efforts in addressing major open questions in the field of proteomics. HUPO can help realizing my dreams by promoting early career researchers as myself, giving them the opportunity to present their work to an international audience in order to gain visibility and facilitate scientific interactions.

**Q: And finally, why do you think that the study of the proteome and proteomics is important?**

**A (BA):** Part of the answer is hidden in the origin of the term protein, namely “proteios”, meaning “primary”, “first rank” in Greek. Proteins are the primary molecules involved in every structure and process of life, so our interest in proteins is truly intuitive but through proteomics we are of course aiming at something more ambitious and complex than studying one protein at a time. Using continuously maturing proteomics technologies, we are building larger and larger bodies of experimental evidence for protein expression and its changes in various aspects to characterize biological processes, such as a disease process. A small piece of such information hidden in the large datasets we generate at a quite corner of a proteomics lab might eventually make a change in the diagnosis process, life quality or life expectancy of a patient, who might be a family member or a close friend. For me, this very humane aspiration at the intersection between medicine and proteomics is what makes proteomics so important.

**A (JFB):** The study of proteomics is important because proteins are responsible for both the structure and the functions of all living things. Genes are simply the instructions for making proteins. It is proteins that make life. I think proteomics is likely to be a part of standard medical diagnostics in the future. Many diseases will soon be treated with efficacious drugs developed through rational design with the aid of proteomics. We are in the right pathway to personalize medicine; we just need to continue to make headway in understanding how the proteome relates to function.

**A (OS):** Proteins are responsible for most functions of a cell. To understand how information encoded in the genome is translated into a phenotype and how a cell responds to different stimuli, there is no way around analyzing the protein content of a cell. Proteins, furthermore, provide attractive intervention points for drugs or can be used as biomarkers. In conclusion, proteomics is indispensable for basic as well as applied research.