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NEWSLETTER OF THE HUMAN PROTEOME ORGANIZATION

IN THIS ISSUE

EDITOR'S MESSAGE

Emma K. Lundberg,
HUPOST Editor

Dear HUPO friends,

Welcome to the Q3 edition of the 2016 HUPOST. It has been a busy year, with many accomplishments and innovations happening across the proteomics community.

As always, we encourage all HUPO members to share their proteomics events and news with us, for inclusion in the HUPOST, on social media, and the HUPO website.

I look forward to seeing many of you in Taipei at the upcoming HUPO 2016 congress, the organizers have put together a fantastic program. I invite all HUPO members to attend the annual HUPO General Assembly, which takes place in Taipei on Monday, September 19, from 18:15-19:15 in Room 101 AB at the TICC. The results of the 2016 HUPO Council Election will be announced at this meeting; if you are an active member I encourage you to cast your vote before September 18 and help to shape future HUPO governance. If you have any questions about voting please contact the HUPO office (office@hupo.org).

We highly recommend that attendees in Taipei participate in the Human Personal Omics Profiling Project (hPOP), offered by incoming HUPO President Mike Snyder. Visit the website to register.

In this issue we are also pleased to announce the finalists of the second annual ECR Manuscript Competition, and the recipients of the HPP Clinical Scientist Travel Grants. Congratulations to you all!

Best wishes,
Emma

HUPO 2016 CONGRESS UPDATES | WWW.HUPO2016.ORG

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

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.

HIGHLIGHTS FROM OUR PRE-CONGRESS SUNDAY WORKSHOP PROGRAM:

Click here to view the program of Pre-congress Courses.

- **Bioinformatics Hub** - *Click here* for more information

- **Clinical Day** - **Clinical Proteomics for Precision Medicine**
Speakers: Christoph Borchers, Michael X. Chen, Oliver Poetz, Albert Sickmann, Josh Labear, Tesshi Yamada, Chen-Yang Shen, Henry Rodriguez

- **Education Day** - **Refresher on Biology & Medicine**
Speakers: Bernd Bodenmiller, Arash Zandian, Jochen Schwenk, Chris Overall, Pengyuan Yang, Paola Roncada, Gerry W Hart, Loïc Dayon, Richard Semba

- **Mentoring Day**
Speakers: Ruedi Aebersold, Paola Roncada, Peipei Ping, Michael MacCoss, John Yates, Christine Miller, Christine Hunter, Ken Miller, Jennifer Van Eyk

- **Technology Day** - **Emerging Technologies**
Speakers: John Yates, Nicolle Packer, Bernd Bodenmiller, Ruedi Aebersold, LiHua Zhang, Roman Zubarev, Donald Hunt

- **HPP Investigator's Meeting**
To view the HPP Investigator's Meeting Program, please click **here**.

INDUSTRIAL ADVISORY BOARD (IAB) LUNCH SEMINARS AT HUPO 2016

Thermo SCIENTIFIC   SCIEX   BRUKER

Agilent Technologies   Waters THE SCIENCE OF WHAT'S POSSIBLE.

Monday, September 19 | 12:30 - 13:30

SCIEX: *Applications of Industrialized Quantitative Proteomics to Advance Precision Medicine*
Click here for more info and to register

Thermo Fisher: *High-Throughput Multiplexed Quantitative Proteomics for Personalized Medicine Applications*
Click here for more info and to register

Waters: *Novel Data Independent Acquisition and Processing Strategies for Quantitative Proteomics*
Click here for more info and to register

Thermo Fisher: *Sweet Revolution: Analytical Tools for the Characterization of Glycans and Glycoproteins*
Click here for more info and to register

Agilent: *Advances in Proteomics from Agilent Technologies*
Click here for more info and to register

Bruker: *Uncompromised Performance: Exploiting the Potential of UHR-Q-TOF for Discovery Proteomics*
Click here for more info and to register

Tuesday, September 20 | 12:30 - 13:30

SCIEX: *Innovations in Industrializing Quantitative Proteomics*
Click here for more info and to register

Bruker: *Answering the Proteoforms Challenge: Alternative Approaches for Biomarker Discovery*
Click here for more info and to register

Thermo Fisher: *Defining biological phenotypes by quantifying small molecular changes*
Click here for more info and to register

Human Proteome Project

Update on the Human Proteome Project (HPP)

The HPP is poised for major activities in Taiwan as part of the main Congress scientific program, as well as the HPP Investigators meeting on Sunday, and the post-Congress HPP Workshop at beautiful Sun Moon Lake. We have extensive programming for early career researchers, including Mentoring Day and a ECR Manuscript Competition. The detailed program is available here (http://hupo2016.org/Program.html) and is open to Congress participants. The HPP offers consultations at the Bioinformatics Hub daily Mon-Wed, including instruction on the HPP Guidelines for Mass Spectrometry Data Interpretation v2.1, as applied in the 2016 C-HPP 4th annual special issue in the *Journal of Proteome Research*.

The HPP Metrics baseline for 2016 in neXtProt was 16,518 confidently identified PE1 proteins, with 2949 PE2+3+4 missing proteins. As highlighted by the Human Protein Atlas last year, testis, little studied, has by far the most tissue-specific transcripts and potentially expressed proteins. The most dramatic reports of the 19 manuscripts online for the November JPR special issue are the confirmed findings of 206 previously missing proteins from studies of spermatozoa by the Chromosome 2/Chromosome 14 consortium (Vandenbrouck et al) and 47 from studies of testis by a Chinese team (Wei et al). These same two groups had presented 89 and 166 previously missing proteins last year from sperm and testis. Duek et al then performed a highly informative analysis of the remaining 134 and 93 missing predicted proteins, respectively, from these two chromosomes, yielding a prioritized list of 25 for Chr 2 and 15 for Chr 14 as the most likely to be detectable by MS in spermatozoa and testis in the next cycle of research. We recommend that all investigators carefully study the Duek et al paper as a guide to organizing their priorities for finding missing predicted pro-

teins on their chromosome or highly informative proteins for biological and disease-oriented studies. There are many useful details in the workflow and tables.

The B/D-HPP has a particularly interesting paper from Lam et al on "popular proteins" prioritized for targeted SRM proteomic analysis after bibliometric evidence of the most studied proteins from six organ systems: cardiovascular, cerebral, hepatic, intestinal, pulmonary, and renal. The goal is to help the broad life sciences/biomedical research community to draw upon proteomics themselves, through collaborations, or through core labs. Meanwhile, the Moritz and Aebersold labs published in *Cell* (Kusebauch et al, 2016) the SRMAtlas, providing proteotypic peptides, synthetic peptides, MS transitions, and spectral libraries for nearly every predicted human protein. These resources will be valuable in seeking confirmation for missing protein candidates. The B/D-HPP has also initiated a newsletter, complementary to the C-HPP newsletters.

We welcome HUPO members and HUPO Congress attendees to learn more about the HPP, to become active in the 22 B/D teams, the 24 chromosome teams, and the 3 resource pillars (see www.thehpp.org). We will present the results of a survey of HUPO members about their interest in joining HPP teams and ideas about further development of the HPP.

Finally, we highly recommend that attendees in Taipei participate in the Human Personal Omics Profiling Project (hPOP) offered by our HUPO President-elect and HPP SAB Chair Mike Snyder that was piloted at the US HUPO meeting in March 2016. Mike will present pilot results in his keynote address Sunday evening. You can learn more and register for the study at www.hupo.org.

Gil Omenn, HPP Chair

JOIN OUR STUDY

Human Personal Omics Profiling

Sponsored By:
Stanford University

hPOP

The hPOP (Human Personalized Omics Profiling) project is designed to study the variance of molecular markers across a large number of participants. Recent advances in high throughput technologies allow profiling of thousands of analytes within a single experiment. These measurements could potentially be used to diagnose disease early, monitor treatment progression and stratify patient groups to ensure each individual obtains the treatment best suited to their needs. This personalized approach to medicine would include continuous monitoring of thousands of parameters over a whole lifetime. However, in order to be able to interpret such data, we need to have a better understanding of the underlying natural variation of these molecular parameters in health and disease. Only if we know the natural ranges of individual analytes, the expected responses to perturbations and the long-term trends in their levels, can we draw meaningful conclusions from comprehensive personalized profiling.

In this project, we aim to use a multi-omics approach to study the genome, epigenome, transcriptome, proteome and metabolome of a large number of healthy volunteers. The hPOP project will be launched officially at the 2016 HUPO in Taipei where samples from several hundred people will be collected. The current protocol includes sampling of blood, urine and stool after overnight fasting. Additionally, a detailed questionnaire about food habits, personal health, physical activity and stress levels will be filled out by each participant. All data will be made available to the scientific community under public domain which will allow multiple research groups to use the generated data in their own studies and perform their own analysis of the data.

Mike Snyder's lab at Stanford is leading the hPOP project. If you have any questions please contact Sara Ahadi at sahadi@stanford.edu.
Information: http://med.stanford.edu/hpop.html

HPP Human Proteome Project

NEWSLETTER OF THE HUMAN PROTEOME ORGANIZATION

2016 HUPO AWARD WINNERS

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. 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
Award sponsored by the Journal of Proteome Research

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

Professor Ralph Bradshaw is awarded the HUPO Distinguished Achievement in Proteomic Sciences Award for his true dedication to promoting protein and proteomics science. He has been one of the strongest proponents of HUPO and protein science throughout his distinguished career. He has worked tirelessly with the US Government to support HUPO from the very beginning and has supported both HUPO and US-HUPO continuously through the years. Through his efforts as Associate Editor of the *Journal of Biological Chemistry* and Co-Editor of *Molecular and Cellular Proteomics*, he has guided protein and proteomics research to be published with the highest degree of confidence and has set standards to ensure results are properly analyzed and reported. His distinguished career in protein science has helped many within HUPO to achieve their best and he has been a mentor to so many scientists within proteomics.
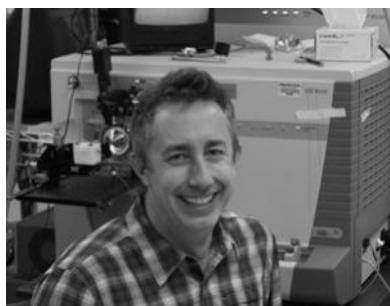
Discovery in Proteomic Sciences

Michael MacCoss
School of Medicine, University of Washington, USA

Professor Michael MacCoss is awarded the HUPO Discovery in Proteomic Sciences Award for his developments in methodology and software for the quantitative analysis of complex protein mixtures. Prof. MacCoss and his research team have developed the software program Skyline, an application with a remarkable impact within the proteomics community, which has placed him as a leader in the field of quantitative proteomics. The focus of his lab is the development of high-throughput quantitative proteomic methods and their application to model organisms. During his post-doc he developed RelEx, one of the first tools to quantify proteins from stable isotope labeling experiments. His lab at the University of Washington has developed several widely used tools for quantitative proteomic analysis including Skyline, a free software package for the design and interpretation of targeted proteomics experiments.

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Translational Proteomics Award
Award sponsored by Elsevier

Joshua LaBaer
Biodesign Institute, Arizona State University, USA

Professor Joshua LaBaer is awarded the HUPO Translational Proteomics Award for his significant contribution to biomarker discovery and the use of clinical proteomics in personalized medicine. His group has developed novel protein microarray technologies, including the Nucleic Acid Programmable Protein Array (NAPPA) platform, which has been used extensively in biomedical research and biomarker discovery (e.g. breast cancer and diabetes).

Science and Technology Award
Award sponsored by the HUPO Industrial Advisory Board

Bob Bateman and John Hoyes
*Waters Corporation, Wilmslow, UK*

The IAB felt the nomination of Bob Bateman and John Hoyes of Waters for the development of the Q-TOF mass spectrometer was outshining any other nomination for this year's HUPO Science and Technology Award. The history of the Q-TOF goes back to the mid 1990s, and Bateman and Hoyes played a key role in their development. The availability of a Q-TOF tandem MS instrument had tremendous influence on the development of proteomics in its early days, since this type of mass spectrometer coupled with a nanoLC provided unprecedented performance in analyzing a proteome. The Q-TOF design was subsequently adopted by other mass spectrometry companies and today a large variety of QTOF instruments exists.

Distinguished Service Award
The Distinguished Service Award is awarded every other year (2013, 2015, 2017).

EARLY CAREER RESEARCHER (ECR) MANUSCRIPT COMPETITION

We are pleased to announce the three finalists of the Early Career Researcher (ECR) Manuscript Competition. The winner of the competition will be determined during the ECR Manuscript Competition session at HUPO 2016 in Taipei. The session takes place on September 21, from 09:30-10:15, in Room 102.
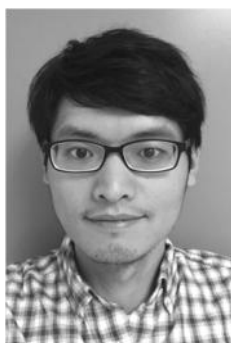
Cheng-Kang Chiang
Cheng-Kang Chiang is currently pursuing his postdoctoral training under Dr. Figeys supervision at University of Ottawa, Ottawa Institute of Systems Biology (OISB), Canada. He obtained his PhD from the Department of Chemistry, National Taiwan University with Dr. Huan-Tsung Chang. His current research interests include using quantitative mass spectrometric methodology to characterize and understand the cellular mechanisms of the circadian clock underlying environmental factors in metabolic processes, as well as deciphering key regulators between gut microbiota and host proteome at the mucosa-luminal interface of new-onset pediatric IBD patients.

Stefan J. Kempf
The aim of this study was to elucidate the effect of chronic low-dose-rate radiation exposure (1 mGy/day or 20 mGy/day – corresponding to doses of daily computed tomography (CT) scans) given over 300 days on the murine Apoe-/- hippocampus. Marked alteration in the phosphoproteome was found at both dose rates whereas changes in the unmodified and sialylated N-linked glycoproteins were scarce. The phosphoproteins were associated with control of synaptic plasticity, calcium-dependent signalling and brain metabolism. A reduced memory-related CREB signalling was found at both dose rates whereas synaptic morphology-related Rac1-Cofilin signalling was altered only at the lower dose rate. Adult neurogenesis, investigated by Ki67, GFAP and NeuN staining, and cell death (activated caspase-3) were not influenced at any dose or dose rate. This study shows that several molecular targets induced by chronic low-dose-rate radiation overlap with those of Alzheimer´s pathology that may suggest it as a contributing risk factor to this neurodegenerative disease.

Hannes Röst
I am a bioinformatics researcher interested in high-throughput technologies that allow us to study the molecular phenotype of a biological system comprehensively. I have worked on theoretical questions in targeted proteomics, contributed to the development of SWATH-MS and wrote the first software capable of targeted analysis of SWATH-MS data in high throughput. I studied at ETH Zurich, Switzerland, worked with Ruedi Aebersold during my PhD and I am now working with Mike Snyder at Stanford University to apply mass spectrometry in a personalized medicine context.

HPP Clinical Scientist Travel Grant Winners

Each year the Human Proteome Project supports six (6) clinical scientists with a travel grant to attend the HUPO World Congress. This year the congress takes place in Taipei from September 18-22, 2016.

Travel grant recipients 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.

Thank you to all those who applied! We appreciate the ongoing interest in the HPP and in the annual congress of the Human Proteome Organization.

Congratulations to the
2016 HPP Clinical Scientist Travel Grant winners!

Peter Bergsten, *Sweden*
Michael Chen, *Canada*
David Herrington, *USA*
Ana Konvalinka, *Canada*
Vinayak Nagaraja, *Australia*
Zhiwei Qiao, *Japan*

HUPO congratulates colleagues in the Moritz (Institute for Systems Biology) and the Aebersold (ETH Zurich) labs for their pivotal recent Cell paper "Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome" reported by Dr Ulrike Kusebauch

Dr. Ulrike Kusebauch
Institute for Systems Biology

In this remarkable work (click here for access), the authors describe how the SRMAtlas provides definitive verified high-resolution spectra and multiplexed SRM assay coordinates and chromatographic peaks that identify 166,174 proteotypic peptides providing multiple, independent assays to quantify any human protein and numerous spliced variants, non-synonymous mutations, and post-translational modifications.

SRMAtlas data are freely accessible as a resources at http://www.srmatlas.org/ and the paper demonstrates the SRMAtlas' utility by examining protein network responses to (i) inhibition of cholesterol synthesis, and (ii) docetaxel sensitivity. HUPO applauds the SRMAtlas triumph as this supports proteome-wide quantification, as well as novel biology and disease hypothesis-driven research. The SRMAtlas demonstrates that the road to understanding the complete Human Proteome is progressing full-steam ahead, despite a few intricacies, challenges and blind alleys.

https://www.systemsbiology.org/research/quantitating-complete-human-proteome/

HUPO forecasts the completion of the Human Proteome Project (HPP) requires: (i) high-quality, publicly available evidence for every expressed protein from the human genome; (ii) analyses of the various forms these proteins take; (iii) spatiotemporal cellular and tissue localization; (iv) protein interaction and structural biology data; (v) an understanding of the biology of proteins and their many isoforms; and (vi) detailed information about their quantitation and roles in human wellness and disease. This journey must be based upon freely accessible resources containing high-quality, communally-verified "big data", so that we can navigate the proteome's complexity.

Revised 2016 Human Proteome Project metrics and guidelines are anticipated to be released soon. https://www.hupo.org/human-proteome-project/

- Mark Baker, HUPO President
All HUPO members are encouraged to contribute proteomics news and updates to HUPO, for inclusion in the newsletter, on social media, and the website.

HUPO PUBLICATIONS COMMITTEE

A) Mission of the Publications Committee

(from the HUPO Bylaws) :

The Publications Committee shall interact with the scientific journals and the scientists in the field of proteomics and shall establish and promote the vision of the corporation with respect to standards in publications related to proteomics and HUPO related activities. The Publications Committee shall oversee the Website and other electronic bases (e.g., Facebook, Twitter) established for sharing HUPO news and information with Members and the public.

B) Members:

Currently the Publications Committee is made up of the following members:

Jean-Charles Sanchez (Chair), Switzerland

Yu-Ju Chen (previous chair), Taiwan

Mark Baker, Australia

Charles Pineau, France

Yasushi Ishihama, Japan

Eric Deutsch, Canada

Visith Thongboonberd, Thailand

C) Committee Working Groups:

Working Group 1 (WG1): Define, draft, negotiate, and confirm agreements with Publishers including award opportunities. Evaluate the opportunities and pitfalls to establish an owned HUPO journal (leader: Jean-Charles Sanchez, Yu-Ju Chen, Mark Baker)

Working Group 2 (WG2): Oversee the website and social media activities related to proteomics journals, proteomic scientists, innovations in proteomics, and publication standards (leader: Charles Pineau)

Working Group 3 (WG3): Provide News in Science column in the quarterly HUPOST (leader: Yasushi Ishihama)

Working Group 4 (WG4): Establish and promote the vision of the corporation with respect to standards in publications related to proteomics (leader: Eric Deutsch)

Working Group 5 (WG5): Collect and promote HPP publications (leader: Visith Thongboonkerd)

Join the #proteomics conversation! Connect with HUPO online.

@hupo_org   Human Proteome Organization (HUPO)   @humanproteomeorg

NOMINATIONS & ELECTIONS COMMITTEE UPDATE

The governing body of HUPO is the **HUPO Council**, composed of 45 councilors elected by the HUPO membership. Following our call for nominations in the last HUPOST issue, we now have an excellent slate of candidates for the HUPO 2016 Council elections. As in previous years, the Council election will be conducted electronically; detailed information will be sent by email to all HUPO members.

The current affairs of HUPO are managed by the **HUPO Executive Committee** (EC), which consists of the President, immediate Past President, President-Elect, Vice President, Secretary, Treasurer and two Members-at-Large. All EC members are elected by vote of the HUPO Council for a term of two years. At the HUPO Council Meeting in Taipei, the Treasurer and two Members-At-Large are to be elected for the term beginning in January 2017. The Secretary General is appointed by the incoming President and the decision is ratified by Council vote at the HUPO Council Meeting. All candidates are listed below.

The HUPO NEC committee (Jonathan Blackburn, Catherine Fenselau Cotter, Henning Hermjakob (Chair), Peter Hoffmann, Jun Qin, Paola Roncada, Mathias Uhlen) would like to thank all nominees for their engagement in the HUPO governance process!

Positions Available:
Secretary General Position
Treasurer Position
2 x Member-at-Large Positions

HUPO Executive Committee (EC) Nominees 2016:

Position	Nominee	Institution (Affiliation):	Country:
The Secretary General is appointed by the incoming President; the decision is ratified by Council vote at the Council Meeting.			
Secretary General	**Emma Lundberg**	SciLifeLab (Royal Institute of Technology)	Sweden
The Treasurer and two Members-At-Large are to be elected, by vote of the Council, for the term beginning in January 2017.			
Member at Large	**Lennart Martens**	VIB	Belgium
Member at Large	**Christopher Overall**	University of British Columbia	Canada
Member at Large	**Sanjeeva Srivastava**	Indian Institute of Technology Bombay	India
Member at Large	**Hui Zhang**	Johns Hopkins University	USA
Member at Large	**Pengyuan Yang**	Fudan University	China
Treasurer	**Peter Hoffmann**	Adelaide Proteomics Centre, University of Adelaide	Australia
Treasurer	**Paola Roncada**	Istituto Sperimentale Italiano L. Spallanzani	Italy

HUPO COUNCIL ELECTION 2016 | EASTERN REGION CANDIDATES

In the Eastern Region, there are six (6) candidates and three (3) open council positions.
Further details of the 2016 HUPO Council Election may be found at www.hupo.org/elections-2016/.

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

NEWSLETTER OF THE HUMAN PROTEOME ORGANIZATION

ELECTION 2016 | CENTRAL REGION CANDIDATES

In the Central Region, there are nine (9) candidates and three (3) open council positions.
Further details of the 2016 HUPO Council Election may be found at www.hupo.org/elections-2016/.

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 Professorr
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.

Further details of the 2016 HUPO Council Election may be found at www.hupo.org/elections-2016/.

Cristea, Ileana
Professor
Princeton University

Nita-Lazar, Aleksandra
Investigator
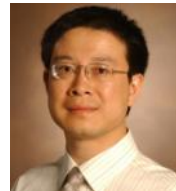Laboratory of Systems Biology

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

HU PO

Dublin Ireland

17 – 20 September 2017

16th Human Proteome Organisation World Congress

We are delighted to announce our Speakers for HUPO 2017 in Dublin, Ireland!

CONFIRMED SPEAKERS

- Ruedi Aebersold
- Jonathan Bones
- Christoph Borchers
- William Gallagher
- Albert Heck
- Matthias Mann
- Lennart Martens
- Andrew Percy
- Andrea Urbani
- Alain van Gool

PROVISIONAL SPEAKERS

- Ben Cravatt
- Thomas Joos
- Hanson Langen
- Joshua Labaer
- Rob Moritz
- Pauline Rudd
- Mike Snyder
- Matthias Uhlen

Visit us at Stand 33 at HUPO 2016 to learn more about next year's HUPO conference taking place in Dublin, 2017!

Visit our website

www.hupo2017.ie

BSPR

EuPA

EUROPEAN PROTEOMICS ASSOCIATION

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?

Contact the HUPO Office 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!
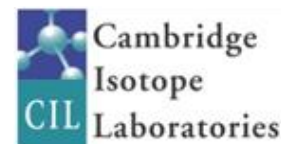
EVENTS IN PROTEOMICS

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 please email office@hupo.org.

HUPO WORLD CONGRESSES

HUPO 2016 Taipei
September 18-22, 2016
www.hupo2016.org

HUPO 2017 Dublin
September 17-20, 2017
www.hupo2017.ie

HUPO 2018 Orlando

REGIONAL & NATIONAL EVENTS

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

10th Central and Eastern European Proteomics Conference
October 11-14, 2016
http://www.szki.ttk.mta.hu/ms/10thceepc/

Symposium: Proteomic Applications in Oncology
November 7-9, 2016
http://www.cruk.cam.ac.uk/

16th C-HPP Workshop
December 10-14, 2016
https://www.hupo.org/events/16th-c-hpp-workshop/

The 15th Swedish Proteomics Society Symposium & SMSS Annual Meeting
November 20-21, 2016
http://www.malmokongressbyra.se/spssmss

II-Caparica Christmas Conference on Sample Treatment
December 5-7, 2016
http://www.sampletreatment2016.com