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PRESIDENT'S MESSAGE



Mark S. Baker
HUPO President

Dear friends,
Welcome to HUPOST for 2016. I hope you and your families have a successful, productive and enjoyable year ahead.

We look forward to having a marvellous year in 2016 with our HUPO Congress being held in the Eastern region town of Taipei on the beautiful island of Taiwan. I encourage you all to submit your [HUPO 2016](#) abstracts and plan to

see this island in September – you won't be disappointed. HUPO continues its renewal and development of early career engagement and reinvigoration. We have now established a HUPO Marketing Committee under which the Publications, HUPOST, and Website & Social Media sub-committees are now operating. We hope to announce the Chair of this new committee soon. In the meantime, if you have any marketing materials (videos, photos or ideas) please send these through to [Chelsea](#) or offer your help on the committees.

One exciting change to note – I have asked Martin and the Awards Committee and the ECR group (part of the B/D HPP) to ensure from this year forward HUPO has formal awards for; (i) experienced scientists (as we currently have), (ii) early career postdoctoral/MD researchers, and (iii) current or under examination PhD students. I encourage you all to participate.

The HPP continues to build on past efforts with many new ideas now surfacing and becoming a reality. I encourage you to submit your data through [ProteomeX-change](#) and get involved in discussions about our flagship scientific project.

Finally – a big thank you to Christoph Borchers, Pierre Thibault, and their Vancouver team for a marvellous and financially successful HUPO2015. The congress was not only a very, very special scientific program packed with new topics, but also a fantastic social event where we had great fun.

I trust you will enjoy another of Emma's fantastic HUPOSTs and look forward to seeing you all in Taipei.

Best always,

Mark S. Baker, HUPO President

EDITOR'S MESSAGE



Emma K. Lundberg,
HUPOST Editor

Dear HUPO friends,

Welcome to the first HUPOST for 2016!

In line with the long-term strategy to improve the visibility of HUPO a Marketing Committee has been established. The HUPOST, Publications Committee, and the recently formed Website & Social Media Committee will all act as sub-committees of the HUPO Marketing Committee. Together we will feature important updates and reports to spread the knowledge of hot topics in proteomics and the HUPO organization.

In the quarterly HUPOST we will continue to present an HPP update where you can read all about the recent ad-

vancements and thrilling findings written by Gil Omenn, Chair of the HPP. Each issue also contains a highlight of News in Science, coordinated by Yu-Ju Chen as Chair of the Publications Committee. To synergize with regional and national proteomics societies, every issue features updates from a few national or regional societies as well as a calendar of upcoming events.

We are grateful for all your support and input to the content and redesign of this newsletter during 2015. I hope that 2016 will be an even more interactive year! As always, you are welcome to contact us if there is anything you would like us to highlight by sending an email to office@hupo.org.

I wish you all a wonderful year and hope to see you in Taipei, if not sooner.

All the best,
Emma Lundberg

HUPO 2016 AWARDS SUBMISSIONS OPEN!

Submit a candidate today for one of HUPO's annual Awards.

Science & Technology Sponsored by the <i>HUPO Industrial Advisory Board (IAB)</i>	\$3000
Translational Proteomics Sponsored by <i>Translational Proteomics (Published by Elsevier)</i>	\$3000
Discovery in Proteomic Sciences Sponsored by <i>HUPO</i>	\$3000
Distinguished Achievement in Proteomic Sciences Sponsored by the <i>Journal of Proteome Research (Published by ACS Publications)</i>	\$3000

Nominations are due on or before April 15, 2016.

[Click here](#) or visit www.hupo.org/about-hupo/awards for more information.

2016 HUPO COUNCIL UPDATES

2016 HUPO Executive Committee

Mark Baker 2015-2016, President
Mike Snyder 2016, President Elect
Rob Moritz 2016-2017, Vice President
György Marko-Varga 2015-2016, Secretary General
Bruno Domon 2014-2016, Treasurer
Yu-Ju Chen 2015-2016, Member-at-Large
Emma Lundberg 2015-2016, Member-at-Large

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. Welcome to our new Councilors, Welcome Back to our returning Councilors, and Thank You to all those who completed their terms at the end of 2015!

We encourage all HUPO members, not just Councilors, to become active in HUPO's many committees. If you are interested in serving on a HUPO committee we invite you to contact the HUPO office by email at office@hupo.org.

2015 Council Election Results

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

HUPO 2016 CONGRESS UPDATES | WWW.HUPO2016.ORG

IMPORTANT DATES

Online Submission Opens	February 29, 2016
Abstract Submission Deadline	May 25, 2016
Abstract Acceptance Notifications	June 19, 2016
Early Registration Deadline	July 17, 2016
Regular Registration Deadline	August 31, 2016
Congress!	September 18-22, 2016

MARK YOUR CALENDAR!

September 2016

Sun	Mon	Tues	Wed	Thurs	Fri	Sat
				1	2	3
4	5	6	7	8	9	10
11	12	13	14	15	16	17
18	19	20	21	22	23	24
25	26	27	28	29	30	

LOCATION



HUPO 2016:
Taipei International
Convention Center (TICC)

HPP Workshop Day:
Fleur de Chine Hotel, Sun Moon Lake



TOPICS OF INTEREST

- Antibodies & Protein Arrays
- Cancer, Clinical & Translational Proteomics
- Chemical Biology for Proteomics
- Cys Modifications & Redoxomics
- Drug Discovery & Pharmacoproteomics
- Extracellular & Membrane Proteomics
- Fractionation & Enrichment Technologies
- Glycomics & Glycosylation Diseases
- Glycosylation & Glycoproteomics
- Human Proteome Projects
- Immunity, Inflammation & Infectious Diseases
- Informatics for Mining Proteomic Datasets
- Integrated Omics & Systems Biology
- Interactomics & Protein Network
- Lys Modifications & PTM Crosstalks
- Metabolomics & Metabolic Disorders
- Microbial Proteomics
- Neurological Disorders & Brain Proteomics
- New Technology for Proteomics
- Peptide Centric MS-based Technical Innovation
- Phosphoproteomics & Signaling Network
- Plant Proteomics
- Proteogenomics
- Proteome Dynamics, Turnover & Secretomics
- Regenerative Medicine & Stem Cell Proteomics
- Single Cell Proteomics & Mass Cytometry
- Subcellular & Spatial Proteomics
- Topdown & Protein Complexes

HUPO 2016 CONGRESS UPDATES | WWW.HUPO2016.ORG

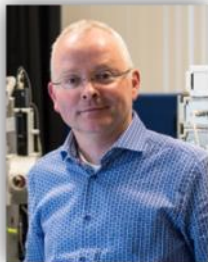
CONFIRMED PLENARY SPEAKERS



Ruedi Aebersold
*Institute of Molecular Systems
Biology - ETH
Switzerland*



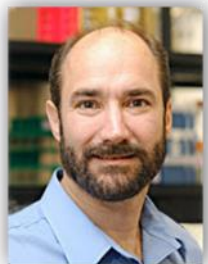
Henrik Clausen
*University of Copenhagen
Denmark*



Albert JR Heck
*Utrecht University and Netherlands
Proteomics Centre The
Netherlands*



Henry Rodriguez
*Office of Cancer Clinical Proteomics
Research - National Cancer Institute,
USA*



Michael Snyder
*Stanford University
USA*



Pan-Chyr Yang
*National Taiwan University
Taiwan*

HUPO 2019 | [REQUEST FOR PROPOSALS](#)

HUPO is still 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 for the application timeline and instructions. **The deadline to accept proposals is April 29, 2016.**

Human Proteome Project

Report from the Human Proteome Project

Gil Omenn

The HUPO Human Proteome Project (HPP) has enjoyed a sustained relationship with the Journal of Proteome Research. About 40 manuscripts each year have been selected from the Chromosome-centric HPP investigators and others in the proteomics community submitting for the C-HPP special issues in 2013, 2014, and 2015. JPR has just announced the Call for Papers for the 2016 special issue, with a submission deadline of 30 April and publication in September. The co-editors are Young-Ki Paik, Lydie Lane, Gilbert Omenn, Eric Deutsch, Bill Hancock, and Chris Overall. See <https://www.hupo.org/wp-content/uploads/2015/12/JPR-Special-Issue-Call-for-Papers.pdf>.

Based on the experience reviewing hundreds of manuscripts and following extensive discussion at the Vancouver HUPO 2015 Congress HPP Workshop, the HPP has introduced Data Interpretation Guidelines with a checklist that must be completed by the authors. We expect that these guidelines will be very helpful to authors and streamline the review process. Editorial staff will screen the papers for compliance before sending them out for review. The checklist will also be an important assist for the reviewers, especially in considering whether protein matches to unusual peptides are truly newly-detected “missing proteins” (lacking protein evidence level 1 findings in neXtProt) or may be false-positives. In many cases, the latter match much better to known abundant proteins when a single amino acid substitution or an isobaric post-translational modification is considered. The same often applies strikingly to “extraordinary claims” that pseudogenes or non-coding RNAs have “novel pro-

teins” as protein translation products. Other suspicious claims are those attributed to coding transcripts not themselves expressed. A whole class of commonly misreported proteins is the GCPR family of olfactory receptors. The Guidelines and the Checklist are posted and discussed at the HUPO website: <https://www.hupo.org/2015/12/news/establishing-new-hpp-guidelines/> or HPP website: http://www.thehpp.org/guidelines/HPPDataGuidelines_2.0.1.pdf.

There are 9 general guidelines for mass spectrometry data and 8 special guidelines for extraordinary detection claims of missing proteins or novel coding elements. We are encouraged to specifically consider isobaric sequence/mass modification variants, all known SAAVs, even unknown SAAVs, and curated data in more than one data resource. Confident identifications should be based on two or more distinct uniquely-mapping peptide sequences of 9 or more amino acids in length. The core databases for the HPP are neXtProt and PeptideAtlas, both of which will release updated version in January and February 2016, as well as the Phospho-PeptideAtlas.

It is time for C-HPP, B/D-HPP, HPP resource pillar investigators and others interested in the human proteome to prepare abstract submissions for the Taipei HUPO 2016 Congress (18-21 Sept) and its HPP Workshop (22 Sept). Please note the Early Career Researchers manuscript competition and the special invitation and travel awards for clinician-investigators nominated by B/D team. We hope to see many of you at the U.S. HUPO meeting in Boston 13-16 March; C-HPP 14th Workshop in Shanghai 20-21 May; and the combined C-HPP and B/D-HPP Conference in Rio de Janeiro 10-12 December 2016, as well as the many national and regional proteomics meetings.

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 for review by the Publications Committee.

Capture All and then Release only the De-N-Glycosylated Peptides for Glycoproteomics

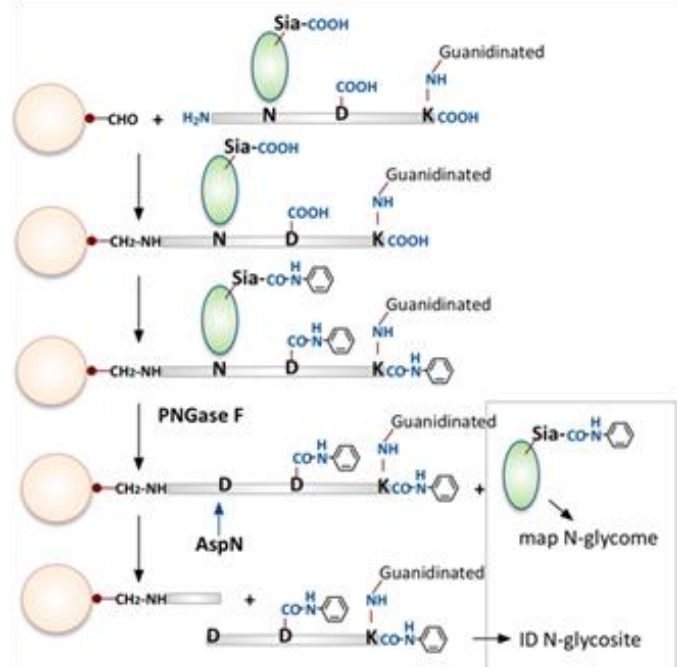
Dr. Kay-Hooi Khoo, Academia Sinica, Taiwan

Among the post-translational modifications, mass spectrometry (MS) analysis of protein glycosylation remains the most challenging due to the diversity in glycosylation. However, the glyco-savvy proteomic community continues to report major technical advances in all aspects of glycomics and glycoproteomics, from sample preparation, data acquisition to informatics associated with data analysis. It is particularly welcoming to see an increasing awareness and readiness to tackle analysis of intact N-glycopeptides instead of only defining the occupied N-glycosylation sites by the easier route of analyzing the de-N-glycosylated peptides.

In general, the few key enabling steps in any MS-based glycoproteomic attempt to map the site-specific glycosylation pattern include 1) enrichment of the glycopeptides; 2) construction of glycan and glycosite-containing peptide library or database to allow identification of the intact glycopeptides by any of the currently available search algorithm; 3) generation of sufficiently good quality glycopeptide MS/MS data in the first place, which usually requires the presence of peptide core fragment ions, peptide core+HexNAc or the Y1 ion, and high resolution/accurate mass MS1 data of the glycopeptide precursors.

The main innovation introduced by Hui Zhang's group at Johns Hopkins University in a recent work published in the Jan 2016 issue of Nature Biotechnology is the way the N-glycan and N-glycosite containing peptide database was generated. Most other groups resorted to identifying

as many of the PNGaseF-de-N-glycosylated peptides from analysis of a separate aliquot of the enriched glycopeptide fractions and use a publicly available glycan library such as the GlycomeDB, or the default library option available in commercial software such as Byonic. The authors took a different approach by modifying their long established hydrazide chemistry-based glycopeptide-specific capture method. Solid phase immobilization was accomplished non-selectively instead by conjugation to aldehyde-functionalized solid support via reaction with the N-termini of all tryptic peptides and, after de-N-glycosylation by PNGase F, Asp-N was used to selectively



Key steps in solid phase extraction of N-glycans and N-glycosite containing peptides. Image adapted by Dr. Kay-Hooi Khoo

(Continued on page 8)

NEWS IN SCIENCE

(Continued from page 7)

cleave and release only glycosite-containing peptides with Asp at the initially N-glycosylated Asn site.

Thus only peptides carrying N-glycosites will be selectively recovered and identified. This is a very clever approach although many chemistry modification steps are involved including modifying sequentially the ϵ -amino group of Lys and free carboxylic groups of C-termini, Asp, Glu and sialic acids. The result is quite impressive and the authors showed that it led to many more N-glycosite-containing peptides identified. The authors also went on to profile the released glycans in order to construct their own sample-specific glycan library. This was performed by both MALDI- and LC-MS and facilitated by the sialic acids now being modified by aniline.

For actual analysis of the intact glycopeptides, HILIC enriched glycopeptides were subjected to LC-HCD MS/MS on a Q-Exactive instrument and the resulting spectra searched against the custom derived database using the precursor mass-matching option of their in-house developed GPQuest software. With filtering based on the presence of peptide+HexNAc and/or peptide ions, as well as ≥ 7 observed b and y ions (1% FDR), this resulted in positive assignment of 4,562 oxonium ion-containing spectra to 1,562 unique glycopeptides containing 518 glycosites and 81 glycans from OVCAR-3 cells.

Comprehensive analysis of protein glycosylation by solid-phase extraction of N-linked glycans and glycosite-containing peptides (2016) Sun S, Shah P, Eshghi ST, Yang W, Trikanad N, Yang S, Chen L, Aiyetan P, Hoti N, Zhang Z, Chan DW and Zhang H. Nat Biotechnol. 34, 84-88.

<http://www.nature.com/nbt/journal/v34/n1/abs/nbt.3403.html>

HUPO is socially connected. Join the conversation.



Human Proteome
Organization (HUPO)



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



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



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

Benefits of an IAB Membership

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

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

Genentech



SomaLogic



Waters
THE SCIENCE OF
WHAT'S POSSIBLE.®



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

KHUPO



KHUPO (www.khupo.org) was founded as the first national proteomics organization under HUPRO on June 24th, 2001.

Dr. Byoung Chul Park (KRIBB) was elected the president of KHUPO last year and will serve a two year term.

KHUPO holds an international conference (research paper presentation, exhibition, and poster presentation, etc) every year, and makes contribution to the spreading of education and information exchange through the summer symposium.

KHUPO will hold 'the 16th Annual International Proteomics Conference' which consist of four plenary speeches and six symposium sessions. An additional oral session from Young Scientists is also held to find talented young scientists.

Dr. Byoung Chul Park President Byoung Chul Park spoke about the 16th conference as follows: "As KHUPO is already entering its 16th year, we have matured greatly. I hope all the efforts and activities of KHUPO will serve as the main core for the human health by exploring the translational relevancy of all proteins and their variants to human biology and disease. I also welcome you all and hope that the 16th Annual International Conference of KHUPO serves as a major scientific forum for the concerted research among proteome scientists and clinicians, linking between Korea and the rest of the world."

KHUPO 16th Annual International Proteomics Conference



Date : March 28 – 29, 2016

Venue : Daejeon Convention Center, Daejeon, Korea

Theme : Proteomics as a melting pot of omic technologies

PLs : Aldons J. Lusic (UCLA, USA), Kong-Joo Lee (Ewha Womans University, Korea), Jin-Soo Kim (Seoul National University, Korea)

Symposia:

- Proteomics for overcoming metabolic diseases
- Proteomics for understanding brain functions
- New innovations in proteomics
- Proteomics in multi-disciplinary approaches
- Proteomics for precision medicine
- Proteomics for stem cell medicine

NATIONAL & REGIONAL SOCIETY UPDATES



16TH C-HPP Workshop - Translating the Code of Life into Proteins and Diseases



Welcome to the 16th C-HPP and B/D Workshop,

We have the pleasure to announce and invite all colleagues to the 16th Chromosome-centric Human Proteome Workshop of the Human Proteome Organization in Rio de Janeiro, Brazil.

The 16th Workshop, an event of the Brazilian Proteomics Society, will be independent but held at the same time and venue as the VI Congress of the Brazilian Society on Mass Spectrometry, December 10-14, 2016.

What does the 16th Workshop want to achieve?

- Celebrate the 100 years of The Brazilian Academy of Sciences during 2016. The workshop is already incorporated as an official scientific event of the Centennial Anniversary.
- Jointly discuss and integrate the Chromosome-centric Human Proteome and the Human Biology Diseases Projects. We hope that all groups will share their ideas on the benefits of the integrated studies of these two Human Proteome Projects.
- Present cutting-edge science on disease proteomics

and mass spectrometry with impact on diseases and targeted medicine. Plans to invite frontier scientists are under way.

- Assessment and evaluation of the first Human Proteome Map. Is time ripe for publication of the first complete draft of the Human Proteome? How should it be structured, what information should be included as well as other important issues have to be immediately discussed during the next HUPO Congress. If not, begin the discussion at the Meeting in Rio; if yes, continue discussion in the workshop.
- Other goals of the C-HPP 1st Phase not yet fully addressed are the pursuit of systematic ways for identification of proteoforms & complexes as well as cell & tissue localization
- Ask whether is there the need of a distinct data deposition for human proteoforms & complexes?
- Begin discussion of phase 2: validation. What actually does this mean? For instance, are we already validating protein existence as gene products when target techniques are used to identify missing proteins?
- Science has a strong impact on Society. We propose an open discussion with fellow scientists as well as lay citizens and media on the impact of the Human Proteome Project in our daily life.

DETAILED PROGRAM COMING SOON!

For further information, please contact:
Gilberto B. Domont: [gilberto\(at\)iq.ufrjlbr](mailto:gilberto(at)iq.ufrjlbr)

NATIONAL & REGIONAL SOCIETY UPDATES



TPWIS Reflections: Thank you!

Dear All,

Wishing you all a Happy New Year-2016!

It brings us great pleasure to announce that the Targeted Proteomics Workshop and International Symposium (TPWIS-2015) followed by GIAN proteomics course ended on a high note. Overall 7 parallel events were conducted at IIT Bombay from Dec 10 - 19, 2015 with a unique set of participants at each event.

- TPW - Targeted Proteomics Workshop (10-14 Dec)
- TPP - Trans-Proteomic Pipeline Workshop (10-14 Dec)
- HR-LC-MS Workshop (10-12 Dec)
- Targeted Proteomics International Symposium (13-14 Dec)
- Education Day (12 Dec)
- Innovative Seminars (10-12 Dec)
- GIAN Proteomics - Global Initiative of Academic Networks (10 - 19 Dec)

We take this opportunity to thank all the distinguished speakers and invited guests for providing their valuable perspectives to the audience. This ambitious effort



of organising dedicated workshops and symposium heavily benefitted large numbers of participants. We wish to extend our appreciation to all delegates for their active participation in this multi-faceted event.

Event photographs are now available online:
<http://www.bio.iitb.ac.in/~sanjeeva/itpws/award-winners/>.

We are humbled by the support you all have provided us and made it a very stimulating, enjoyable and one of the very unique international events of 2015. We hope that TPWIS-2015 has been as memorable to you, as it has been for us. The attached "Reflections" booklet (click here: [TPWIS-2015 Reflections](#)) is a memoir of the TPWIS-2015 and we wish that these remembrances and experience would last you a lifetime.

Warm regards,

Sanjeeva

Dr. Sanjeeva Srivastava
Convener, TPWIS-2015

NATIONAL & REGIONAL SOCIETY UPDATES



New Initiatives from the European Proteomics Association (EuPA)

Dear Colleagues,

The next [EuPA2016](#) conference will be held in Istanbul between June 22nd – 25th under the wise organisation of Prof. Aysel Ozpinar and the whole local team who have made impressive progress and are well on track. This long ago taken decision may now sound questionable given the days we all are living in Europe. We are facing events that are giving us all a strong demonstration that from Madrid to London and from Paris to Istanbul we are European. Not only for geographic reasons but also in the vision of an open democratic discussion of ideas for the development of science and society it is based our definition of Europe.

In the last months EuPA has been in the process of launching of a number of new initiatives. This process is ongoing and it is currently centered on the promotion of an active and direct role from the National Societies. The main activities of this effort is based on the support and active engagement of young investigators.

The initiatives include:

1. EuPA Young Proteomics Investigators Club (YPIC). *(Odile Burlet-Schiltz)*

The creation of the EuPA Young Proteomics Investigators Club (YPIC) was agreed on and voted for at the last EuPA GC meeting held in Milano in June 2015. This initiative has been motivated by the positive experience of some National Societies where young scientists already play an active role in activities of these Societies. The main objective of the YPIC is to promote networking among young European scientists with a common interest in proteomics and who constitute the next generation of scientists in our community. Having opportunities to interact with each other from the very beginning of their career will be an important step forward and

a unique opportunity to initiate collaborative work and to plan future actions in Europe. Another objective is to organize scientific meetings, itself an important training opportunity to learn how to plan an event, find sponsors and construct a scientific program etc. In this way and by engaging with their international counterparts, the YPIC will thus contribute to increasing the visibility of EuPA worldwide.

The current board of YPIC is composed of:

Tamara Tomin, Austria
Maarten Dhaenens, Belgium
Dina Rešetar, Croatia
Stefan Kempf, Denmark
David Gomez-Zepeda, France
Christine von Toerne, Germany
Athanasios Anagnostopoulos, Greece
Maurizio Ronci, Italy
Meike de Wit, Netherlands
Tina Rise Tuveng, Norway
Catarina Franco, Portugal
Ekaterina Poverennaya, Russia
Marija Pljesa-Ercegovac, Serbia
Luis Valledor, Spain
Zeynep Durer, Turkey

2. EuPA Bioinformatics Community (EuBIC) initiative - eupa-bioinfo.github.io. *(Marc Vaudel)*

This initiative will pursue three main goals. (1) Funding: establishment of new funding paradigms for user-oriented bioinformatic tools; (2) publications: creation of guidelines and novel publication means to reward the efforts of bioinformaticians in providing user friendly and well-maintained tools; and (3) cooperation: setting up community dynamics, including the organization of events and retreats, both scientific and educational. The initiative is carried by an open group of young investigators representing the individual EuPA societies, attempting to balance between national societies, research groups, and genders. You can join us on GitHub (github.com/eupa-bioinfo/EuBIC), contact us at eupa-bioinfo@googlegroups.com, and follow us on social media ([EuBicEupa](#)). In the end of 2015, a kick-off meeting took place at the Leibniz-Institut für Analytische Wissenschaften – ISAS – e.V. (www.isas.de) in Dortmund, Germany.

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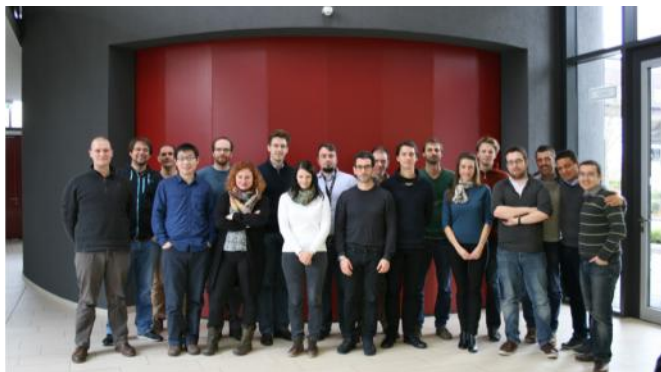


Fig 2. The Movember Foundation – Global Collaborators.
Taken from Movember website (www.movember.com)

3. EuPACa: EuPA Prostate Cancer Proteomics Initiatives (Corinna Henkel, Steve Pennington)

How quickly the months wizz by? Not so long ago we were in the month of November – known by some by its ‘proper’ name Movember. Movember marks an important time when many men - and a few very brave women – grow moustaches (or in the case of women draw them on their upper lip!) to raise awareness and raise money for men’s healthcare research. The Movember Foundation (www.movember.com), which initiated this hugely successful campaign, focused its initial efforts on distributing the funds raised to Prostate Cancer research. In its early stages the funding was delivered through national cancer research agencies. Subsequently, in an effort to promote international collaboration the Movember organisation introduced an on-going series of Global Action Plans (GAPS) to complement national funding efforts. There are currently 5 GAPS and a number of European proteomics scientists play a part in these collaborative projects to identify and evaluate protein biomarkers in tissue, blood, urine, exosomes and circulating tumor cells. The proteomics part of these programmes is undertaken in an interdisciplinary approach alongside genomic, epigenetic and other strategies. EuPA is ideally placed to promote, co-ordinate and contribute to global prostate cancer research efforts including those of the Movember Foundation.

The overlap between EuPA’s aims and the objectives for the GAP initiatives of Movember (see Fig 2) which seek to promote the sharing of knowledge, avoid duplication and create collaborations to accelerate translation of this knowledge to improve health outcomes, is obvious.

EuPA is ideally placed to co-ordinate the Prostate Cancer proteomics efforts of European researchers by:

- Creating an active network and database of EU Prostate Cancer proteomics scientists and their on-going research projects and interactions between them;
- Promoting the dissemination and raising awareness of the fundamental knowledge of new proteomic strategies for combatting Prostate Cancer; and
- Contributing to the education and training of young cancer proteomics researchers.

For such an effort to be successful it will need to be inclusive, forward-looking and develop the credibility and ‘authority’ for it to make an impact. This impact should include promoting the funding of proteomics activities that have the potential to impact on Prostate Cancer research and Prostate Cancer patients themselves. We invite all those interested in this initiative to join us in discussion (Linkedin Group: <https://www.linkedin.com/groups/8460418>) and to meet for a workshop session at the next EuPA meeting in 2016.

One of the major goals in this initiative – shall we call it EuPACa? (pronounced: upacca) - is the connection of researchers in different proteomic fields to gain the most beneficial output out from their combined research efforts for the development of new proteomic approaches for the diagnosis and treatment of Prostate Cancer (see Box).

We encourage all who are interested in this initiative to sign into the Linkedin group as soon as possible and so enable us

(Continued on page 15)

(Continued from page 14)



to establish a community of Prostate Cancer researchers who will be ready for the next Movember grant calls (February 2017) and other European initiatives. Additionally, we hope that the participation of clinicians in the EuPACA group and the ability to link to patient sample biobanks coordinated through Movember will be of inestimable value for the proteomics community and accelerate research goals and outcomes to improve the lives of the many men diagnosed with Prostate Cancer.

We hope you will join us in these efforts and we promise that there will be no obligation to grow or draw a moustache next November – sorry – that should read ‘Movember’. Who knows maybe you could be sponsored NOT to grow one? The evidence presented in Fig 3 suggests that some European Proteomic researchers might possibly have significantly greater success with the latter strategy?

A ‘random’ selection of EuPA Movember moustache growers 2015!



If you are interested in joining us to form a pan-Europe MOVEMBER Team to raise funds in 2016 let us know via the LinkedIn Group

Prostate Cancer

Prostate Cancer (PCa) is currently the third most common cancer diagnosed in Europe. For diagnosis and treatment decisions, blood PSA levels, digital rectal examination and histological findings based on needle biopsy material are the clinical standard but do not support accurate prediction for tumour progression, aggressiveness and PCa related death.

PSA is widely acknowledged to have benefits and limitations – see infographic.

It is recognized that most men die with the slow growing tumour rather than because of it. As a result there is significant over-treatment of the disease.

But once PCa is metastatic the currently used treatments will delay but not prevent tumour growth and the disease is fatal. New therapeutic strategies and agents are needed because resistance against hormone or chemotherapy often occurs.

There is huge need for better tools for diagnosis, risk assessment of PCa progression as well as new treatments and proteomics has an important role in the development of both.

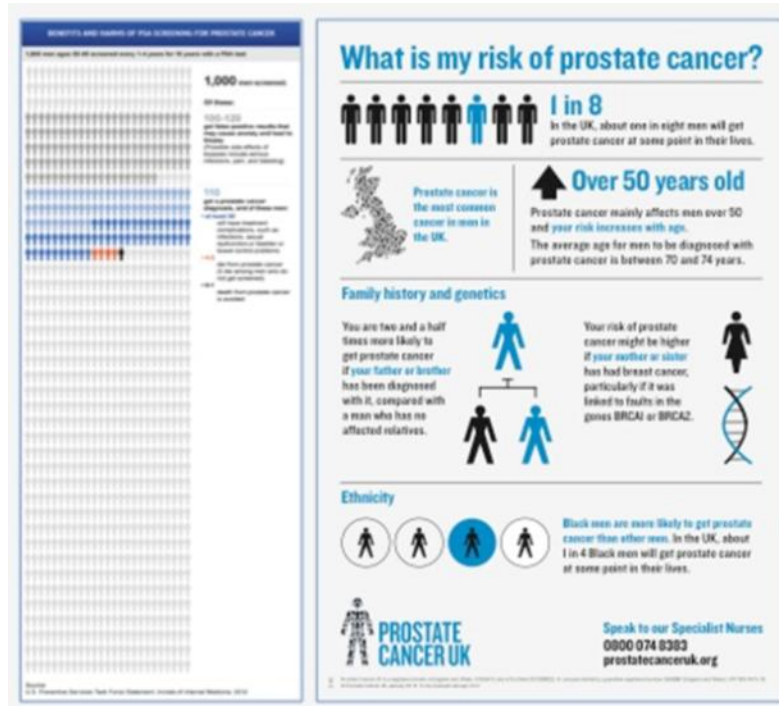


Fig 3. Infographic (see <http://prostatecanceruk.org>)

EVENTS IN PROTEOMICS

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

HUPO WORLD CONGRESSES

[HUPO 2016 Taipei](#)
September 18-22, 2016
hupo2016.org



[HUPO 2017 Dublin](#)
September 17-20, 2017
hupo2017.ie



REGIONAL & NATIONAL EVENTS

[27th MassSpec Forum Vienna](#)
February 23-24, 2016
Vienna, Austria
<http://mass-spec-forum-vienna.conf.tuwien.ac.at/>

[US HUPO Annual Conference](#)
March 13-16, 2016
Boston, USA
<http://www.ushupo.org>

[KHUPO 16th Annual International Proteomics Conference](#)
March 28-29, 2016
Daejeon, Korea
<http://www.khupo.org/>

[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>

[16th C-HPP Workshop](#)
December 10-14, 2016
Rio de Janeiro, Brazil
<https://www.hupo.org/events/16th-c-hpp-workshop/>