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MESSAGE FROM THE EDITORS

Dear Colleagues and Members of the European Proteomic Society (EuPA),

Welcome to the October issue of the European Proteomic Society Newsletter!

We are excited to introduce this special intermediate issue, designed to bridge the gap between our regular editions and keep you updated with the latest proteomics news and forthcoming meetings. In this edition, you'll find updates on recent research breakthroughs that have emerged since our last issue, important announcements, and a curated list of upcoming meetings and conferences.

Our goal is to ensure that you remain at the forefront of the field, with timely insights and comprehensive coverage of advancements and events that shape our community and foster collaborations. We hope this newsletter will serve as a valuable resource, connecting you with the vibrant and dynamic world of proteomics.

Thank you for your continued engagement and support. We look forward to your feedback and contributions as we move forward together.

Best regards,

On behalf of the EuPA Conference and Communication Committee

the Editor of the EuPA Newsletter: Eleni Zografos, and

the Co-Editors of the EuPA Newsletter: Éva Csósz and Fernando Corrales

THE CHROMOSOME CENTRIC HUMAN PROTEOME PROJECT

ANNOTATING HUMAN PROTEINS AND PROTEOFORMS IN THEIR FUNCTIONAL SETTING

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The Chromosome Centric Human Proteome Project (C-HPP) was launched in Busan, Korea, during a meeting held in 2011, as one of the branches of the HPP, together with the Biology and Disease (B/D) HPP and the HPP technological pillars (www.hupo.org). The mission of the C-HPP was to map and annotate all the proteins encoded by each of the genes in the human genome. It was initially organized in a network configuration in which international teams adopted a chromosome with the aim of characterizing all the protein products encoded by its genes. Progress has been published annually since 2013 in thematic issues of the Journal of Proteome Research. They describe new versions of PeptideAtlas and neXtProt, progress in Missing Proteins (MPs, proteins lacking reliable detection in human cells) identification, new analysis methods and workflows, etc. In recent years, the objectives of the C-HPP have diversified to cover such interesting topics as the study of PTMs, splicing variants, SAPs (Single Amino acid Polymorphism), smORFs (small Open Reading Frame) or the functional annotation of proteins. All these aspects have a clear biological background, which promotes synergistic work with the B/D-HPP, something expected and already foreseen in the first HPP schemes. The C-HPP is currently chaired by Chris Overall, who chairs the C-HPP EC, of which the authors of this note are members. As one of the pillars of the recently launched flagship program of the Human Proteome Organization (HUPO), the HUPO Grand Challenge, the C-HPP has aligned its strategy to the overall objectives of this global initiative seeking for integration with the other partners in the project. Among other initiatives, the C-HPP work is organized into two major projects: the neXt-MP50 challenge, in which each chromosome team identifies and reports MPs and annotates the functional impact of proteoforms on protein function, and the neXt-CP50 project, in which each chromosome team adopts PE1 proteins (proteins with reliable evidence of detection in human cells) with unknown or predicted function and provides a specific function for each.

Mission

The C-HPP of the Human Proteome Organization (HUPO) aims to find high-stringency evidence for all proteins and their proteoforms encoded and non-encoded by the human genome, major splice forms, major protein post-translational modifications (PTMs), mature N- and C-termini, other proteoforms, their cell and tissue localization, and their protein-protein interactions accomplished by participating countries organized as Chromosome teams. In fulfilling this Mission, the C-HPP supports the HUPO Grand Challenge to functionalize every human protein.

Vision

To establish a fundamental basis for understanding human biological phenomena through experimental data on our proteome organized on a human chromosomal basis while emphasizing the value of proteomic research in exploring the biological complexity of humans and promoting research for a deeper understanding of human health and diseases.

Objectives

The global aim of the C-HPP is to participate in the HUPO Grand Challenge assuming the following specific goals:

- To produce mass spectrometric evidence for every protein in the human proteome that lacks MS evidence. Complete the annotation of the human proteome based on mass spectrometry identification for every protein, some of which remain identified only by non-MS validated biochemical methods.
- Explicitly determine the proteoforms of proteins as well as their major PTMs: phospho-, glyco-, methyl- and acetyl-forms.
- Find novel dark proteins at high stringency. Development of methods and tools to identify, quantify, and characterize 'dark proteins' that include novel splicing forms, smORF, lncRNA, circRNA, non-coded proteins, PE5 (predicted proteins from gene sequences), and the novel peptide forms in the immunopeptidome
- Define interactomes for each protein, which is essential to explain the phenomenological/mechanistic basis of a disease.

- Regularly update protein and function data for proteins in the human proteome in a new official repository of the HPP and Grand Challenge projects.
- Organization of 1-2 webinars/year.
- Organization of C-HPP workshops every year: (i) Annual 2 ½ day-workshop on the specifics of achieving our goals, (ii) Annual 0.5-day satellite meeting on the Saturday afternoon and evening immediately prior to the HUPO Congress.

The C-HPP is a global project that aims to achieve equal representation of ECR and female scientists in Chromosome Team activities and leadership. It is open to all HUPO investigators with projects that follow the C-HPP mission. We look forward to receiving your proposals (Peter Horvatovich: p.l.horvatovich@rug.nl).

The 28th C-HPP Workshop was held in Madrid on 24-26th April. In addition to reports from several teams, there was a fruitful discussion on the criteria for categorizing the level of functional evidence of proteins. A first draft of guidelines has been produced and work is underway to consolidate the basis for the next steps.

As the Grand Challenge moves forward and to support its objectives, the HPP is consolidating 3 complementary actions:

- while neXtProt no longer exists, continue to publish the Protein Evidence (PE) metrics every year. Release of annual PE numbers is now carried out by UniProt.
- to better formalize what we mean by protein function, set up a Function Evidence (FE) scoring system. A FE Scoring working group has been set up to further draw up guidelines.
- Set up a new repository that will be the new gateway to the HPP Grand Challenge. The HPP Portal is under construction and will be presented at HUPO-EuPA 2024.

Upcoming C-HPP Workshops for 2024 and 2025:

- 26th Chromosome-Centric Human Proteome Project Workshop: (0.5 days), Dresden, Sunday 20th October 2024, 9:00 AM – 14:00 PM (before HUPO Congress).

- 27th Chromosome-Centric Human Proteome Project Workshop on the new Human Proteome Project Portal, Guangzhou LEDY Life and Health City, China, November 28 & 29th 2024.
- 28th Chromosome-Centric Human Proteome Project Workshop: The HPP Grand Challenge, Saint-Malo, France, June 13-15, 2025 (before EUPA).

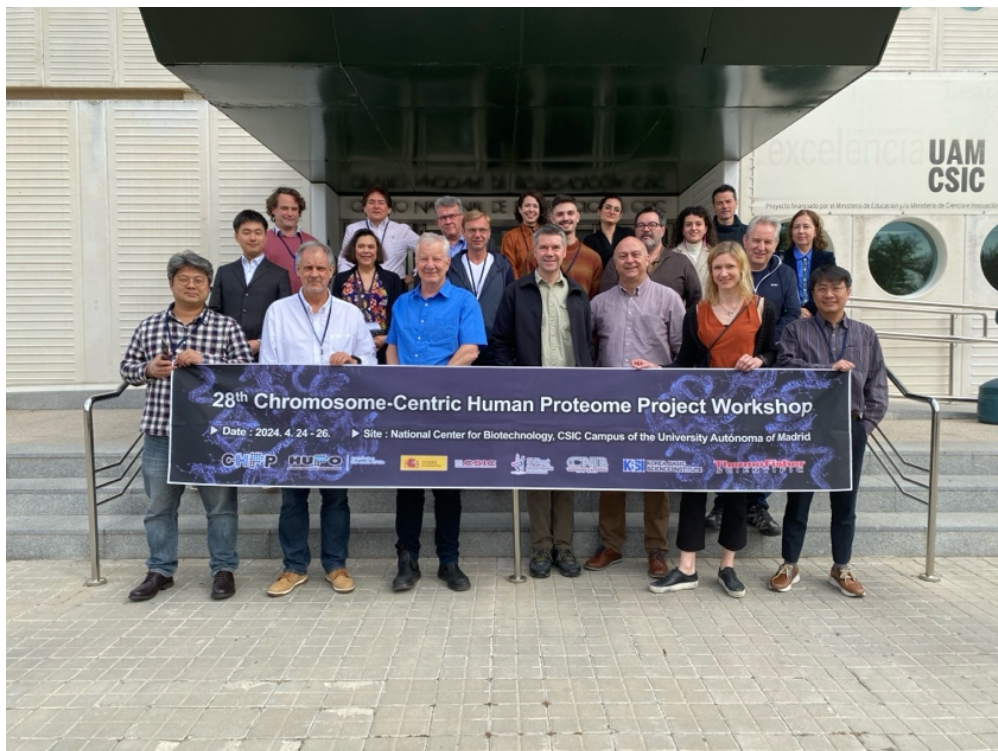


Figure 1. C-HPP participants of the 28th C-HPP meeting that took place at the National Center for Biotechnology in Madrid, Spain

Submitted by:

Fernando Corrales
National Center for Biotechnology, CSIC, Madrid, Spain

CELEBRATING MILESTONES

CELEBRATING 50 YEARS OF PROTEIN RESEARCH AT THE UNIVERSITY OF SOUTHERN DENMARK



This year marks the 50th anniversary of Protein Research Group at the University of Southern Denmark (SDU). Founded in 1974 by Professor Peter Roepstorff, the group has been a pioneer in the field of biological mass spectrometry, pushing the boundaries of what this technology can achieve in understanding proteins and their roles in biology, biomedicine and beyond.

From its early days, when mass spectrometry of proteins was novel and exotic, research at SDU has grown into a leading centre, now integrating its activities with modern proteomics research in the wet and the dry lab. The work spans a wide range of applications, including studying the composition, structure, and function of proteins, nucleic acids, metabolites, and a large diversity of post-translational modifications. Their research plays a critical role in revealing the molecular mechanisms that drive biological processes with applications ranging from translational research to archaeology.

Today, 14 principal investigators form the section for [Biomedical Mass Spectrometry and Systems Biology](#) of the [Department of Biochemistry and Molecular Biology](#) at SDU in Odense. With a team of over 80 researchers, staff, and students, the section continues to innovate, collaborating with national and international research consortia, as well as with partners in the pharmaceutical and biotech industries. The section is also dedicated to training the next generation of scientists, ensuring the continuation of high standards in proteomics research.

To commemorate this milestone, we are hosting the international [CelebrateMS conference](#) on advances in mass spectrometry, bringing together world-leading experts to share knowledge, discuss the latest developments, and explore the future of this essential technology. This conference will not only highlight past

achievements but also set the stage for future innovations in mass spectrometry, continuing the legacy of excellence established 50 years ago.

As we celebrate this significant anniversary, we reflect on the impact of our and international colleagues' contributions to science and look forward to the continued advancement of proteomics research. Our vision remains to contribute to the elucidation of molecular mechanisms that maintain and sustain life, and to foster collaboration, openness, and the sharing of knowledge in pursuit of novel biomedical and biological discoveries.

We are proud of our history and look forward to continuing our contributions to the fields of biological mass spectrometry, protein science and multi-omics research.



Submitted by:

Veit Schwämmle

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SPOTLIGHT ON RECENT CONFERENCES AND EVENTS

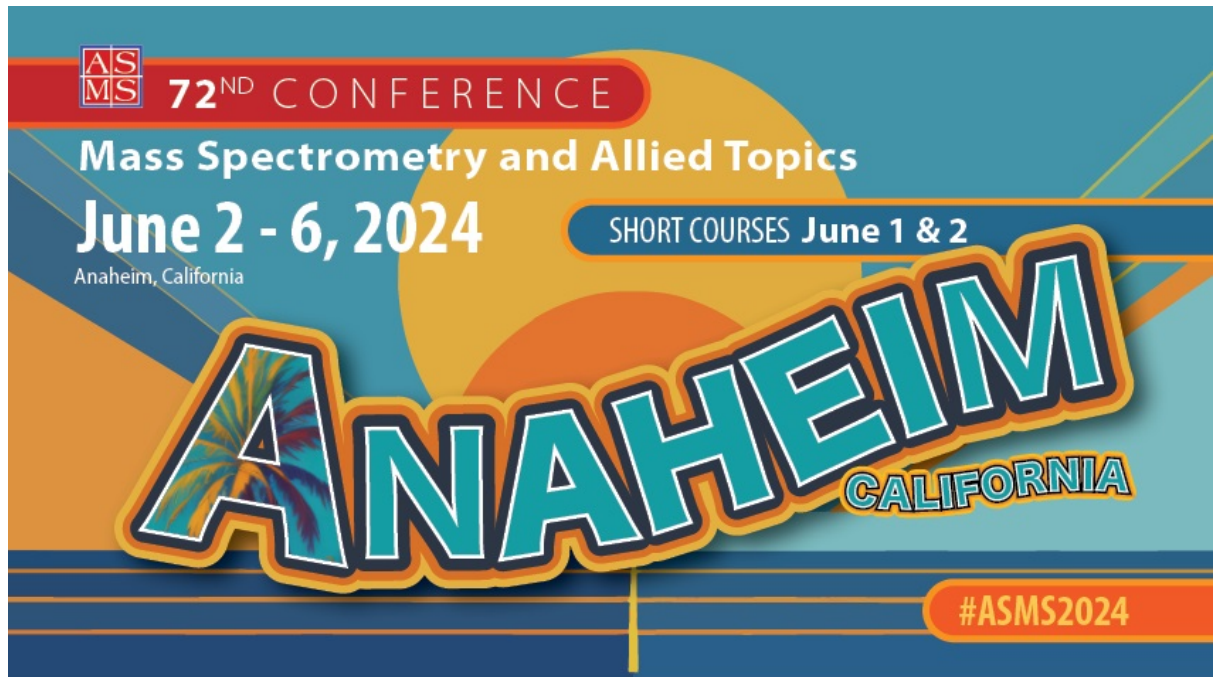
HIGHLIGHTS FROM ASMS 2024

The 72nd ASMS Conference on Mass Spectrometry and Allied Topics was held June 2-6 at the Anaheim Convention Center in California. This year's meeting attracted nearly 7000 scientists and over 500 exhibitors. The venue covered a wide range of cutting-edge science and technology around mass spectrometry presented in 384 oral sessions. The poster sessions, as always at ASMS, were great, allowing space and time for intense discussion among the attendees. What also stood out at this year's ASMS was the large number of interactive workshops on topics such as chemoproteomics, data-independent acquisition, breakthroughs & challenges in de novo peptide sequencing, and many more. Together with a panel of experts, the audience was able to discuss current challenges and exchange opinions and thoughts.

In terms of innovations in mass spectrometry instrumentation, Bruker introduced its new timsTOF Ultra 2 with enhanced performance. Thermo Fisher Scientific introduced a new instrument for highly multiplexed targeted quantification, the Stellar MS. Waters introduced the new Xevo MRT benchtop MS, which combines the power and resolution speed of multi-reflector time-of-flight (MRT) and hybrid quadrupole time-of-flight (QToF) technologies.

This year's ASMS award recipients were Jennifer Brodbelt, who received the John B. Fenn Award, and Gary J. Patti, who received the Biemann Medal. Jennifer S. Brodbelt received the John B. Fenn Award for the development and application of UltraViolet PhotoDissociation (UVPD) as a powerful ion fragmentation method for structural elucidation of biomolecules in mass spectrometry. Gary J. Patti received the 2024 ASMS Biemann Medal for his pioneering work in metabolomics using stable isotope labeling to understand the dynamic role of metabolism in biology.

Finally, the 72nd ASMS ended with a bit of magic with Parag Mallick's closing plenary. He literally performed a series of tricks and experiments on stage. His conclusion was that modern science is actually derived from what was once thought to be magic, i.e., alchemy, necromancy, and more. The audience was invited to find inspiration in magic, to be open-minded, and to accept the biases and gaps in understanding and perception - allowing the mind to perceive more and create more ideas to combat the problems of today's world - a rather nice take-home message.



Submitted by:

Sandra Goetze
ETH Zürich, Switzerland

UPCOMING EVENTS

HUPO-EuPA Congress, October 20th-24th, 2024, Dresden, Germany

The congress will provide a unique opportunity to present and discuss progress in the interdisciplinary field of proteome research from application of new technologies to advancement of biological knowledge, global health, and wellness in a variety of workshops, sessions, training courses and poster sessions. You are cordially invited by the Human Proteome Organisation (HUPO), the European Proteomics Association (EuPA), and the German Society of Proteome Research (DGPF).

Full details are available on the website: <https://2024.hupo.org>



XVIII ItPA Congress, November 27th-29th, 2024, Rome, Italy

The XVIIIth congress of the Italian Society of Proteomics, joint with the Hellenic and Serbian Proteomics Association, will have an international scope again this year. The congress will take place in Rome, at the House of the Knights of Rhodes, located in the Forum of Augustus from November 27 to November 29, 2024.

All information regarding scientific program, registration and abstract submission will be available soon at www.itpa.it



Belgian Proteomics Association Conference, December 5th-6th, 2024, Ghent, Belgium

The Belgian Proteomics Association is hosting its conference in the medieval city of Ghent this year. Join them for a cozy two-day conference with lots of interesting talks and plenty of time to network.

Early-bird registration for the conference is available until November 15th. The abstract submission deadline is October 31st.

Register here: <https://belgianproteomics.be/events/bepac/>

Belgian Proteomics Association Conference
#BePAc24
December 5-6, 2024 – Ghent
Register here:

BePA kvcv

Noemi Procopio
Eduard Sabido
Roman Fischer
Bryan Gonzales
Maria Wahle
Magnus Palmblad
Julia Chamot-Rooke

FUNDING OPPORTUNITIES

There is a **new proteomics funding opportunity** proposed by YPIC: **the student proteomics fund** (SPF).

SPF will allow a student's research project to come to reality by awarding 5000 EUR to be spent in proteomics analysis. SPF is open to BSc., MSc. And PhD students who are carrying out research in a European university. No previous proteomics experience is required, just a well designed scientific project which would benefit from the use of proteomics approaches to gain valuable insights that may help answering a relevant research question. Laboratories within YPIC's network will be available to carry out the analysis as well as provide guidance on technical details and data processing. Additionally, SPF will allow young scientists to engage directly with the YPIC community and receive feedback on their project proposals. Following the evaluation of SPF applications, the three young scientists with the highest project's score will be invited to the 2nd YPIC Annual Proteomics Gathering which will be held in Athens on the 20th of March 2025. Travel and accommodation expenses will be covered and candidates will be expected to present their project idea in front of the audience. The recipient of the fund will be announced at the end of the event.

Applications should be sent by email to ypic@eupa.org before **24th November at 23:00 CEST** time.

Funding call opening!!!

