



# EuPA NEWSLETTER

2024

MAY

ISSUE 1

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## MESSAGE FROM THE EDITORS

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

We are delighted to announce the launch of the newest issue of the EuPA Newsletter, filled with updates and exciting developments in the field of proteomics.

In this edition, you will find a special message from the EuPA President, highlighting the latest advancements and initiatives within our society. Additionally, we are thrilled to present the activities of EuPA's Committees, showcasing the dedication and hard work of our members in advancing proteomic research. Furthermore, we bring you a comprehensive update on EuPA's Initiatives, outlining ongoing projects and future endeavors to foster collaboration and innovation in proteomics.

A highlight of this issue is the announcement of the highly anticipated HUPO-EuPA Congress, scheduled to take place in October 2024 in the scenic city of Dresden. Save the date for this landmark event, where leading experts and researchers will convene to exchange ideas and share groundbreaking discoveries in proteomics.

Moreover, we have included details on upcoming proteomics events in 2024, providing valuable opportunities for networking and professional development.

We also extend an invitation to all members who are interested in contributing to future EuPA Newsletters. Whether you have research insights to share, event announcements, or other relevant updates, we welcome your contributions. Please don't hesitate to reach out to the editors with your ideas and submissions.

Thank you for your continued support and participation in EuPA. We hope you enjoy reading this issue of the EuPA Newsletter and find it both informative and inspiring.

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

## MESSAGE FROM THE EUPA PRESIDENT

Dear EuPA Members and Colleagues in the Proteomics Field,

It is my pleasure to introduce to you in our first newsletter the recently elected EuPA Executive Committee. As a team, we have the goal of pursuing the development of EuPA as an engaged, inclusive, and transparent organisation to foster and support the proteomics community in Europe. Since its founding, EuPA has constantly evolved into an internationally recognizable research association, providing a European framework for national proteomics societies. We have set a motto for ourselves during the election phase which we would like to follow and fill with life: “EuPA – a European association with impact that feels like family.”

The upcoming period will require consolidation on the high level achieved by the recent EC team, led by Lennart Martens. Recently, a range of essential components were actively restructured, including integration of YPIC representation in the EC, changing the committee structure to represent the declining relationship with and funding by Elsevier, and reorganisation of the funding concept in general. Several high-workload issues were addressed and resolved, such as the relaunch of the website, changes in statutes, internal communication as well as means and frequency of communication with the national societies.

The new EC has held an internal retreat, and an impressive number of fresh ideas were launched to foster EuPA activities and initiatives, of which we will inform you step by step through this newsletter as well as during EuPA events.

With that I hope you enjoy the new issue of our newsletter!

Best regards,

On behalf of the EuPA Executive Committee: Klaus Kratochwill

### ***EuPA President***



Prof. Dr. Klaus Kratochwill –  
Medical University of Vienna,  
Austria

### ***EuPA Vice-President***



Prof. Dr. Connie R. Jimenez,  
Amsterdam University Medical  
Center, The Netherlands

### ***EuPA Conferences and Communication***



Prof. Dr. Éva Csósz, University  
of Debrecen, Hungary

### ***EuPA Education***



Dr. Maike Langini, Catapult  
Medicines Discovery, United  
Kingdom

***EuPA Industry***



Dr. Maarten Dhaenens, Ghent University, Belgium

***EuPA Funding***



Prof. Dr. Veit Schwämmle, University of Southern Denmark, Odense, Denmark

***EuPA Initiatives***



Dr. Franck Vandermoere, Institute for Functional Genomics, Montpellier, France

***YPIC***



Dr. Maurine Fucito, Evosep, Denmark

***EuPA Awards***



Dr. Marie Chion, University of Cambridge, United Kingdom

## ACTIVITIES OF EUPA'S COMMITTEES

### EUPA MENTORING COMMITTEE

**Current members:** Connie Jimenez (chair), Tamara Tomin, Maria Pavlou, Maïke Langini, Jochen Schwenk, Marie Chion



#### Goals:

- To support proteome scientists, early-stage researchers, to achieve their goals
- To set up a registry of mentors and couple mentees to the right mentor
- Host workshops to achieve the above

The EuPA Mentoring Committee was established in 2022. Past activities in 2023 and 2024 included organizing a zoom meeting to collect ideas, organizing several on-line events (a mentoring/mentee workshop, the active bystander training and a mental health workshop).



Our mentors aim to support the learning, progress, and development of a mentee by offering, advice, information and assistance in a way that empowers the mentee. A mentee is expected to set clear goals. We propose that the mentor-mentee relation lasts for one year in which a few on-line meetings are planned. A prospective mentee can fill out a short questionnaire so that we can make the most optimal match to a mentor in our database (we currently have 9 in various European countries).

**Feel free to reach out to us via the following email address: [mentoring@eupa.org](mailto:mentoring@eupa.org)**

Planned on-line/ in-person workshops will focus on effective communication (date tbd) and mental health (date tbd) so keep an eye on the EuPA website (<https://eupa.org/events/>) for more information.

## EUPA AWARDS COMMITTEE

The EuPA Awards Committee is responsible for the organisation of the EuPA Awards Campaign, including the evaluation of the applications. Our goal is to honour the members of the proteomics communities for their outstanding achievements.

The 2023 EuPA Awards campaign will be launched very soon, so stay tuned. Awardees will receive their award during the 2024 HuPO/EuPA conference in Dresden, Germany. We are looking forward to receiving your applications!

The awards currently endorsed by EuPA are:

- The **EuPA Best Doctoral Thesis Award** honours a young PhD who presented an outstanding thesis in the last two years. The 2022 recipient was Tim Van Den Bossche (VIB-UGent, Belgium).
- The **EuPA Bioinformatics for Mass Spectrometry Award** recognises a researcher for their outstanding contribution to bioinformatic developments for mass spectrometry. The 2022 recipient was Wout Bittremieux (University of Antwerp, Belgium).
- The **EuPA Breakthrough in Proteomics Award** rewards a discovery that has transformed the frontier of knowledge in proteomics and has a major impact on science, technology, and society. The 2022 recipient was Mikhail Savistki (EMBL Heidelberg, Germany).
- The **EuPA Juan-Pablo Albar Proteome Pioneer Award** honours a person with a leading and long-standing involvement in promoting the principles of sharing and integrating resources for the development of excellent research in the proteomics field. The 2022 recipient was Karl Mechtler (Research Institute of Molecular Pathology, Austria).
- The **EuPA Science Outreach Award** supports an individual or a group of individuals in the organisation of any event popularising any science topic to a lay audience. The 2022 recipient was PhD Pub Montpellier (France).
- The **EuPA Technology Award** is awarded to a private company for their outstanding contribution in commercialisation of a new proteomics technology. The 2022 awardee was Cellenion (France).
- The **EuPA Vision and Commitment Award** honours an early career researcher for their remarkable networking of young European scientists in Proteomics initiatives. The 2022 recipient was Marie Chion (University of Cambridge, United Kingdom).

All EuPA awardees receive a plate with name and recognition, as well as a free registration fee for the upcoming EuPA conference, sponsored by the conference organisation. The EuPA Best Doctoral Thesis, Bioinformatics for Mass Spectrometry

and Vision and Commitment awardees are invited to give a talk during an online event, organised by the EuPA Education Committee. The EuPA Breakthrough in Proteomics and Juan-Pablo Albar Proteome Pioneer awardees are invited to give a talk during the Awards ceremony at the upcoming EuPA conference. Finally, the EuPA Juan-Pablo Albar Proteome Pioneer awardee receives a prize of €5,000 and the EuPA Science Outreach awardee receives a prize of €1,000 to support any future outreach event.



The 2022 EuPA Awardees at the 2023 EuPA/BSPP conference

## EUPA CONFERENCES AND COMMUNICATION COMMITTEE

**Current members:** Éva Csősz (chair), Maria Bourganou, Tristan Cardon, Marie Chion, Fernando Corrales, Sandra Götze, Simon Daled, Swathy Krishna, Ana Obradović, Luisa Schmidt, Lilla Turiák and Eleni Zografos



### Goals:

- Increasing the visibility and accessibility of proteomics for scientists and clinicians from the scientific community (life science, clinical science, biostatistics, bioinformatics, etc.)
- Organization of crossover meetings with other scientific societies (ex. FEBS, EMBO, FEMS, ESCMID, etc.)
- Coordination between EuPA General Council, HUPO and National Societies for EuPA congress organization
- Development and facilitation of EuPA communication including official website, social media appearance, promotional material and EuPA Newsletter
- Encouraging and coordination of EuPA workshops
- Organization of webinars involving scientists (students, juniors, and seniors) from the National Societies
- Fostering communication among the National Societies

Throughout the years the Conferences and Communication Committee is involved in managing the EuPA Travel Grant applications, takes part in the Congress Organizing Committees of EuPA conferences, collects, and evaluates the bids for EuPA conferences, as well as working together with the Education Committee, helps the organization of the EuPA Job Fair and Student Exchange Event. Our committee is responsible for communicating with EuPA members through the Presidents of the National Societies and works on increasing the visibility of EuPA. The website, social media platforms and EuPA Newsletter are edited and maintained by the members of the Conferences and Communication Committee. Promo materials (logos, slides, promotional slides) are created and made available to help advertise EuPA and its mission.





***European association with  
impact that feels like family.***

## **Discover our events!**

### **Career development**

- EuPA Student Exchange Event
- EuPA Open Lab Day
- Mentoring sessions
- ECR Day
- Job fair

### **Community**

- Thematic meetings for National Societies
- Awards

### **Scientific events**

- Annual proteomics conference
- Summer school
- EuBiC Winter school
- Science Slam



***Engaged. Inclusive. Transparent.***

In case you need promotional material, feel free to ask us. We will be happy to share these with you.

If you know about an event organized by your National Society, or you have information about a webinar or scientific event which might be of interest for the broader community, let us know (send us the flyer or a picture in jpg format) and we can advertise it on the EuPA website and social media.

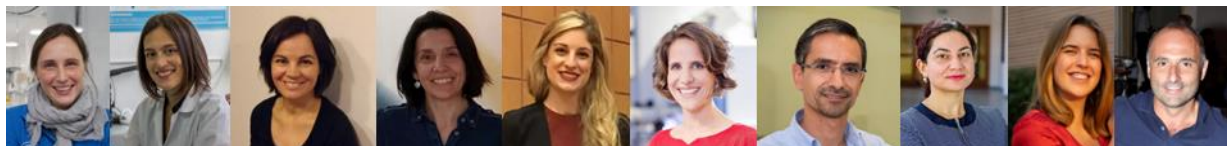
Please check out our website and social media sites (Facebook, X, LinkedIn) and let us know your opinion.

**Feel free to reach out to us via the following email addresses:**

**[communication@eupa.org](mailto:communication@eupa.org) or [conferences@eupa.org](mailto:conferences@eupa.org)**

## EUPA EDUCATION COMMITTEE

**Current members:** Maike Langini (chair), Tiziana Alberio, Christine Carapito, Montserrat Carrascal, Angeliki Katsafadou, Christina Ludwig, Bruno Manadas, Nurhan Özlü, Tine Claeys, Michalis Aivaliotis



### Goals:

- Organize European-wide workshops and courses to promote and enhance the quality of proteomics knowledge through the life sciences community, general public and governmental bodies.
- Setup and promote European-wide scientific exchange programs for young researchers to enhance their scientific career and promote cultural exchanges throughout Europe.

Throughout the year the education committee is involved in hosting various events such as the ECR day, the Proteomics Science Slam, Job Fairs, workshops, and the Student Exchange Event. In addition, most of these events give a chance to network with peers in Proteorealm, EuPA's very own gather town map.

The image displays three promotional posters for EUPA events. The first poster on the left is for the 'European Early Career Researchers in Proteomics' online event on 5 October 2023, featuring ECR award winners and a company job fair. The middle poster is for 'Science on Stage' on November 22nd, 2023, an educational webinar about connecting with an audience. The right poster is for the 'EuPA SEE - Student Exchange Event' on May 4th, 2023, a virtual event for students to meet host labs and sponsors.

Watch out for the official announcement of the next EuPA Job Fair and Student Exchange Event scheduled for the 18<sup>th</sup> of June from 3 to 5 PM CEST.

The next ECR day with a Proteomics Science Slam is planned for the end of this year. Keep an eye out for more information about upcoming events on social media, our homepage, through YPIC or your national society.

Feel free to reach out to us via the following email address: [education@eupa.org](mailto:education@eupa.org)

## EUPA INDUSTRY COMMITTEE

Throughout the course of the previous EuPA EC mandate under Lennart Martens' presidency, a gap was identified, and a new EuPA Committee was founded: the EuPA Industry Committee. This Committee is now chaired by Maarten Dhaenens (Belgium) and consists of four additional members, i.e. Maurine Fucito (Italy), Mehwish Kanwal (Italy), Christian Moritz (France) and Peter Blattmann (Switzerland).

As their first assignment, the Industry Committee defined their own set of core tasks. Essentially, everything revolved around facilitating the contact and communication between EuPA as a mainly academic interest group on the one hand and industry on the other. During the first brainstorm session, the "industry" was defined in two important groups:

- (i) **the industry whose business is focused on proteomics** (mass spectrometers, kits, software, offer analysis as service) and
- (ii) **industry partners that use proteomics as a tool** (e.g. for biomarker discovery and drug development).

The former group might be very interested to present their products or services e.g. as sponsors at EuPA events. Both groups are probably interested in learning and be part of the proteomic community. While not binary, this distinction helps to divide the different tasks of the Industry Committee.

For potential **industry partners whose business is focused on proteomics** and are looking for sponsorship deals, a set of packages are being developed to enable them to reach out to potential customers as much as possible. Briefly, EuPA has two kinds of activities: (i) all the digital events that overwhelmingly take place in Proteopolis, like the Job Fair, ECR events, Student Exchange Event (SEE) and the Open Lab Days and (ii) the physical events, which mainly is our annual EuPA conference, that alternately is organized with Proteomics Forum (in Leipzig in 2022), with HUPO (in Dresden this year) and independently with local proteomics associations (in Newcastle, UK, with BSPR in 2023 and in Saint-Malo, France, with the FPS in 2025).

What is entirely new, is that EuPA is also reaching out to **industrial users of proteomics technology**. This was facilitated through the **Proteomics in Industry Working Group ( $\pi$ WG)** that was established at EuPA Conference in Leipzig. Peter Blattmann is now connecting the Industry Committee and the  $\pi$ WG and jointly we have defined a few key goals for the upcoming months. Most prominently, EuPA will start mapping the proteomics expertise (industrial, academic, core facilities) all over Europe on a central platform that can help academic labs, CRO's and industrial partners to navigate the proteomics landscape in Europe and easily find the partnerships they are looking for. Additionally, by EuPA2025 in France in Saint-Malo, we aim to have a parallel track of

sessions devoted entirely to proteomics in industry. This will not only make this conference a more appealing networking hotspot for industrial researchers, but also provide a platform for career development and academic-industrial collaboration.

For the more distant future, we start dreaming of an even more profound cross-fertilization wherein for example EuPA could help develop documentation for e.g. GLP in proteomics and for example in clinical trials or clinical care. Moreover, with a strong emphasis on valorization in the European Funding landscape, joining forces can facilitate grant writing for specific calls. Irrespectively, whatever we manage to realize, we are convinced that this new Industry Committee can have impact on proteomics in Europe.

We are looking forward to embracing our goals.

**Do you have any questions? Don't hesitate to send an email to [industry@eupa.org](mailto:industry@eupa.org).**

## EUPA FUNDING COMMITTEE

**Current members:** Veit Schwämmle (chair), Pavel Bouchal, Peter Horvatovich, Mariette Mantondo, Markku Varjosalo



### Goals:

- Maintain formal processes and guidelines to ensure an appropriate day-to-day management of the EuPA finances.
- Investigate the European and international funding landscape for future participations of EuPA and its members.
- Contribute to ensure the future financial viability of the organization, in coordination with other stakeholders in the organization.

The Funding Committee oversees EuPA's financial operations and assesses the strategic financial direction of the organization. This includes the responsibility of inviting external reviewers to audit EuPA's finances, ensuring transparency and best practices.

Additionally, the committee will thoroughly review various income sources and discuss strategies to enhance industry engagement alongside the Industry Committee. We aim to explore new sponsorship opportunities and strengthen existing partnerships for sustaining our funding base.

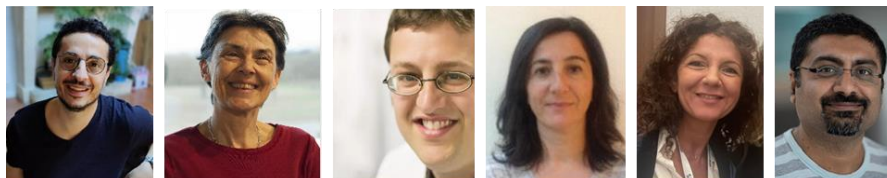
We will investigate opportunities for EuPA's active participation in the EU grant landscape to enhance funding for proteomics research. This includes involvement in COST actions and potentially responding to project calls within Horizon Europe, to increase the exposure and impact of proteomics research across the European continent.

The future EuPA will be key to further enhance EuPA's visibility and facilitate outreach for both industry and academic collaborations, as to provide a comprehensive overview of proteomics labs across Europe, and to showcase the extensive network and sophisticated capabilities within our community.

**Feel free to reach out to us via the following email address: [funding@eupa.org](mailto:funding@eupa.org)**

## EUPA INITIATIVE COMMITTEE

**Current members:** Franck Vandermoere (chair, FR), Maria Hernandez-Valladares (N), Frédérique Lisacek (CH), Oxana Trifonova (R), Richard Unwin (UK), Viviana Greco (ITA), Shabaz Mohammed (UK)



### Goals:

- support existing European proteomics initiatives by providing funding and infrastructure and promoting their scientific and educational activities in a fair and transparent way.
- encourage the creation of new initiatives that value scientific excellence, equality, inclusion, and diversity.
- foster links between initiatives and stimulate interdisciplinary exchanges to favor scientific innovation.

### Current EuPA initiatives:

- European Bioinformatics Community (EuBIC), **new chairs** Marie Locard-Paulet (FR) and Ralf Gabriels (B)
- Food and Nutrition Initiative (FNI), chair Paola Roncada (IT)
- Initiative for Model Organisms Proteomics (iMOP), **new chair** Fabrice Bertile (FR)
- Metaproteomics Initiative, chair Tim Van Den Bossche (B)
- Standardization Initiative, chair Fernando Corrales (E)

### Upcoming Initiatives events:

- Gathering of EuPA Initiatives, EuPA/HUPO Dresden, Oct 21, 2024
- iMOP pregress symposium, EuPA/HUPO Dresden, Oct 21, 2024.
- iMOP webinar on “Integrating new model organisms and unravelling the mysteries of unknown proteins”, May 21, 2024. [Zoom link](#)
- Metaproteomics online webinar, June 11, 2024. <https://metaproteomics.org/symposia/webinar-2024/>
- International Metaproteomics Symposium, Oslo, Norway, January 13 - 15, 2025. <https://metaproteomics.org/symposia/sixth/>

Feel free to reach out to us via the following email address: [initiatives@eupa.org](mailto:initiatives@eupa.org)

### EUPA STANDARDIZATION INITIATIVE

#### **Proteomics Multi-laboratory Experiment 13 (PME13)**

##### **Coordination Team:**

Marina Gay (IRBB)

Félix Elortza (CIC bioGUNE-BRTA)

Fernando Corrales (CNB-CSIC)

Odile Buret-Schiltz (Université de Toulouse, CNRS)

Sarah Cianferani (Université de Strasbourg, CNRS)

Ferdinando Cerciello (University of Bern)

##### **Introduction**

High sensitivity proteomics (HSP) has emerged in the last few years as a powerful tool in the field. Nowadays, mass spectrometry (MS) is sensitive enough to identify proteins at the single-cell level. On the other hand, MS sensitivity is approximately at attomole level ( $10^{-18}$  moles), which involves hundred thousand ions. Since the median of protein copies in mammalian cells is around 18k copies per cell, MS is sensitive enough to analyze single cell samples. Indeed, most advanced studies provide more than 5000 protein identifications per cell. In this journey towards HSP, sample preparation remains one of the most crucial steps. Handling a low amount of material and transferring it into a mass spectrometer is still a challenge in proteomics.

Within the EuPA standardization initiative, we are launching a Proteomics Multicentric Experiment (PME13) focused on HSP. This multicentric study will provide a unique opportunity to assess the performance and reproducibility of HSP experiments (from sample preparation to data analysis) within a specific lab and across multiple labs, platforms and sample preparation methodologies.

The reference samples used in the study consist of a serial dilution of *E. coli* protein extract and peptide digest from 100 to 1 ng. The use of standard *E. coli* samples will allow not only to monitor the number of identified proteins from *E. coli* but also to track potential human protein contaminants during sample preparation, which is one of the drawbacks/pitfalls of the whole procedure. The final aim of the study is to test the performance and reproducibility of HSP protocols and assess the usefulness of the *E. coli* standard to set up and troubleshoot HSP workflows.

## Objectives

The main goal of PME13 is to benchmark protocols for HSP analysis and to provide tools to facilitate HSP implementation and to assess laboratory performance on HSP analyses. Specifically:

1. To assess the robustness and reproducibility of different HSP protocols.
2. To deliver references to assess performance on HSP analysis.
3. To provide a reference sample for HSP protocol standardization.
4. To provide a data analysis workflow.

## Study design

There were two sample sets: **protein** and **peptide**.

- **Protein:** *E. coli* protein extract (BioRad: *E.coli* Protein Sample -- [163-2110](#)) at different amounts: 100, 10, 1 ng. For each protein concentration 4 replicates were provided (4x3 = 12 samples)
- **Peptide:** Tryptic digest of *E.coli* protein extract (BioRad: *E.coli* Protein Sample -- [163-2110](#)) at different amounts: 100, 10, 1 ng. For each peptide concentration 4 replicates were provided (4x3 = 12 samples).

Participants have processed protein samples and analyzed the 24 samples provided (protein and peptide) by LC-MS. They run the samples by data dependent acquisition (DDA) and, optionally, they could also opt for data independent acquisition (DIA) mode.

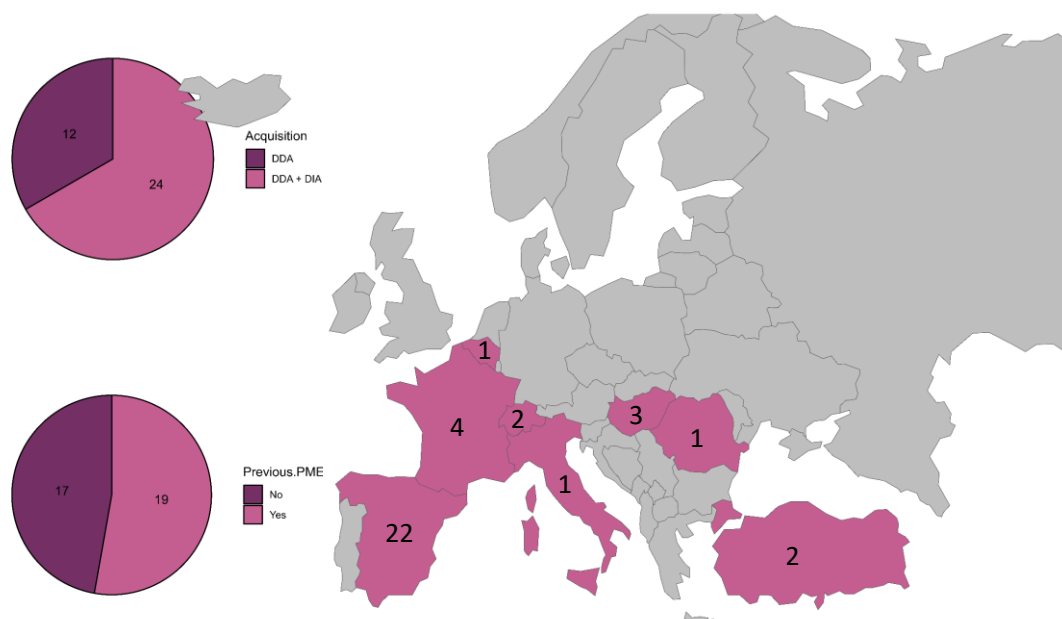
In addition, participants have provided detailed information regarding the most relevant sample preparation conditions (reduction, alkylation, tube transference, digestion enzyme and buffer, etc) and the LC-MS instrumentation used to generate the MS data (HPLC, gradient, MS instrument, MS2 detector, etc). This metadata will be key for downstream data analysis.

## Participation

Thirty-six labs from eight different countries requested PME13 samples, being Spain the one with the highest number of participants. Almost half of the labs (17 out of 36) had not participated in previous PMEs. Two thirds of the labs (23 out of 36) asked for the 48 samples to perform DDA and DIA analysis.



To date we received the DDA results from 28 out of 36 labs (78 %) and DIA results from 16 out of 23 labs (70 %).

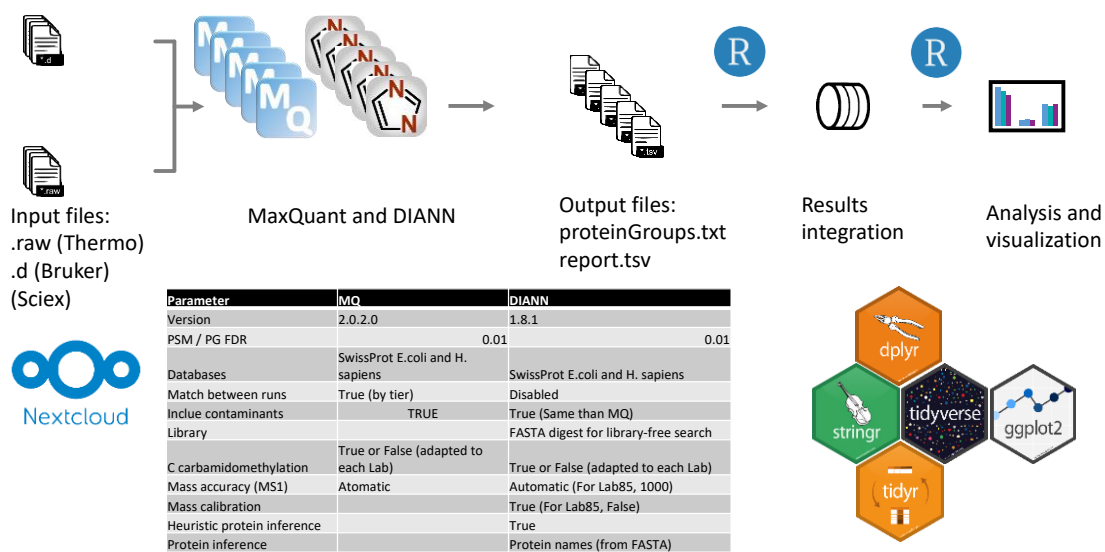


**Figure 1:** (Right) Map showing the number of participants per country. (top left) Pie chart with the number of participants that used DDA or DDA + DIA to generate their data. (Bottom left) Pie chart with the number of participants that participated in previous PMEs editions or not.

### Data processing

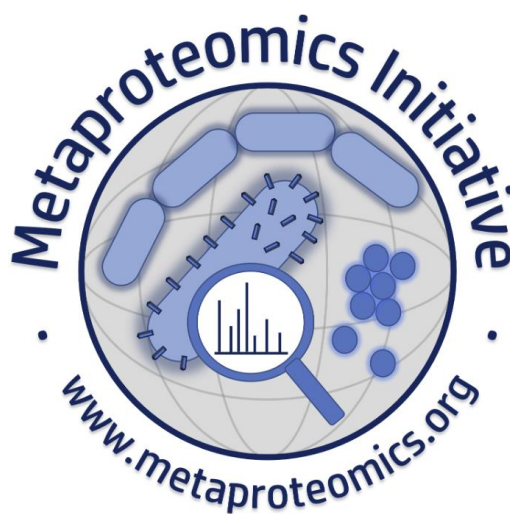
We collected all data via NextCloud and received 28 DDA sets and 16 DIA sets. We centralized all the database searches to homogenize all the search parameters. We used MaxQuant v2.0.2.0 with *E. coli*, *H. sapiens* and default MQ contaminants databases. All the proteinGroups.txt output files were integrated, visualized and analyzed using R programming language. We mainly used default parameters and performed match between runs within the same tier and sample (i.e. within protein samples of 1 ng). We selected FDR 1 % at peptide and protein levels.

All the metadata regarding sample preparation and LCMS instrumentation have been unified and harmonized.



**Figure 2.** Schematic pipeline used for the DDA data analysis.

Analyses are programmed to be finished by the end of July 2024 and the results will be presented and discussed in a session that will take place as a satellite activity before the upcoming HUPO-EuPA congress in Dresden on 20-24 October 2024.



The Metaproteomics Initiative, founded in 2021 as a EuPA Initiative, aims to promote the dissemination of metaproteomics fundamentals, advancements, and applications through collaborative networking in microbiome research. This Initiative aims to be the central information hub and open meeting place where newcomers and experts interact to communicate, standardize, and accelerate experimental and bioinformatic methodologies in this field [[doi: 10.1186/s40168-021-01176-w](https://doi.org/10.1186/s40168-021-01176-w)]. Our efforts are concentrated across three different pillars.

The first pillar of the Metaproteomics Initiative, Communication and Collaboration, is focused on sharing technological advancements in metaproteomics research, connecting researchers within the field, and conducting a series of Critical Assessment of MetaProteome Investigation (CAMPI) studies. The first CAMPI study, the very first community-driven, multi-laboratory benchmark study in the field, emphasized metaproteomics as a reliable way for examining functional interactions within microbial communities [[10.1038/s41467-021-27542-8](https://doi.org/10.1038/s41467-021-27542-8)]. Although many metaproteomic workflows exist, the influence of methodological choices on results had been unclear. This comparison evaluated the impact of sample preparation, mass spectrometry, and bioinformatic analysis. Utilizing both a simplified, laboratory-assembled human intestinal model and a human fecal sample, findings indicated that while variability at the peptide level primarily arose from sample processing workflows, differences largely diminished at the protein group level. Notably, despite observed discrepancies in predicted community composition, functional profiles remained consistent across workflows. The CAMPI study thus demonstrated the robustness of current metaproteomics research, serving as a template for future multi-laboratory studies and offering publicly accessible datasets for benchmarking. Building on this, the ongoing second CAMPI study (CAMPI2) focuses on the comparative assessment of proteome sample stability post-collection. The main

challenge addressed is the variability in sample handling, such as differences in storage temperatures, the use of preservation solutions, or immediate protein extraction, all of which significantly affect the proteome profile and hence the biological interpretation of studies. CAMPI2 includes a real-world "stress-test" involving uncontrolled shipment conditions, aiming to standardize procedures for sample handling to ensure reliable and reproducible results. In parallel, we are also performing a third CAMPI study (CAMPI3). This study aims to identify strengths and limitations of bioinformatic workflows used in protein assignment and peptide spectral matching. It assesses the impact of key decision points commonly encountered across various bioinformatic methods on taxonomic and functional annotation. This study targets enhancing the understanding of how different levels of expertise and experience in the field of metaproteomics affect the outcomes of bioinformatic analyses. Through these studies, the Communication and Collaboration pillar not only advances the field of metaproteomics but also fosters a collaborative environment that bridges gaps between researchers, enhancing both methodological rigour and community-wide standards. In addition to the CAMPI series, we actively encourage our members to disseminate their research by submitting manuscripts for inclusion in our newsletters. We are also forging strategic collaborations with other organizations, including the Human Proteome Organization (HUPO) [<https://www.hupo.org/Metaproteomics>] and the ELIXIR Microbiome Community [[doi: 10.12688/f1000research.144515.1](https://doi.org/10.12688/f1000research.144515.1)], to enhance our network and impact. Furthermore, we host the International Metaproteomics Symposium biennially. The latest event, held in April 2023 in Avignon, France, attracted over 100 researchers from around the world. Preparations are well underway for the next symposium, scheduled for 13-15 January 2025 in Oslo, Norway. For those eager for the latest developments in the metaproteomics field before the symposium, we are organizing a webinar on June 11 with mainly talks from our ECR members [<https://metaproteomics.org/symposia/webinar-2024/>].

The second pillar, Education, is dedicated to improving understanding within the microbiome community about the potential of metaproteomics. We achieve this by organizing educational workshops at international conferences, such as the American Society for Mass Spectrometry (ASMS), and by co-organizing specialized workshops like the Applied Metaproteomics workshop at the University of Magdeburg and the Lorentz Center workshop on "Deciphering Microbiome Functions" [<https://www.lorentzcenter.nl/deciphering-microbiome-functions.html>]. These events provide valuable opportunities for attendees to engage directly with leading experts in the field. Furthermore, to make metaproteomics more accessible, particularly for those new to the field, we are in the process of developing an extensive review about metaproteomics for beginners. This review will be specifically designed for single-species proteomics researchers and microbiome researchers who are eager

to explore metaproteomics, offering them a foundational understanding and practical insights into this dynamic area of study.

The third pillar, Standardization, is committed to establishing uniform reporting data and metadata standards. To this end, we are currently drafting a white paper that highlights the unique aspects of metaproteomics as distinct from single-species proteomics and other meta-omics approaches. This document will describe the need for field-specific guidelines, the standardization of metaproteomics metadata, and the enhancement of open data practices - while ensuring as much as possible overlap with existing standards. By clarifying these distinctions, we aim to facilitate more consistent and reproducible research outcomes across the metaproteomics community.

Since its establishment in 2021, the Metaproteomics Initiative has gathered over 300 members from 85 labs in 22 countries, and significantly influenced the field of metaproteomics through dedicated efforts in communication and collaboration, education, and standardization. By maintaining these efforts, we aim to stay at the cutting edge of scientific research, pushing forward both experimental and bioinformatic innovations. Ultimately, these activities support researchers in gaining a deeper understanding of microbiomes.

For more information about this community, please have a look at our white paper [doi: [10.1186/s40168-021-01176-w](https://doi.org/10.1186/s40168-021-01176-w)], our website ([www.metaproteomics.org](http://www.metaproteomics.org)), X ([https://twitter.com/MetaP\\_Init](https://twitter.com/MetaP_Init)) and become a member via this link [<https://forms.gle/zAqJDPZNvf7vSoNi9>].



Group picture from the last Metaproteomics Conference in Avignon (April 2023).

## IMOP (INITIATIVE FOR MODEL ORGANISM PROTEOMICS)

At the forefront of evolutionary biology, medicine, environmental proteomics, and ecotoxicology, iMOP uses comparative proteomics, proteogenomics, (eco) toxicoproteomics and bioinformatics resources. This makes it possible to decipher new fundamental molecular mechanisms, particularly those that are difficult to study directly in humans, to identify new coding sequences and characterize the function of coded proteins, to identify and characterize the therapeutic potential of new biological products, and to monitor the environment in terms of the fate of pathogens and the impact of environmental quality on living organisms.

With the main aim to advance knowledge of proteins important for human health and disease, and more generally for the environment, as part of the "One-Health" concept, iMOP proposes to rethink the concept of model organisms. While few historically well-established organisms, such as laboratory rodents, have led to significant scientific breakthroughs, embracing a multitude of new model organisms, such as holobiont systems, is essential to capture the intricacies of biological principles across the breadth of biodiversity. By fostering collaboration between biology and omics communities, we can collectively adopt new models, unraveling their molecular functioning, and uncovering fundamental mechanisms. This concerted effort will undoubtedly enhance human health, environmental quality, and biodiversity conservation.

The vision of iMOP and how the post-genomic era promises new and essential knowledge for human and animal health has been published recently (Communications Biology 2023. doi: [10.1038/s42003-023-05458-x](https://doi.org/10.1038/s42003-023-05458-x)).

In 2024, iMOP actions include a webinar (May 21) and a satellite workshop/symposium at HUPO Dresden (October 20-24) on the theme "Delving into biodiversity's depths: integrating new model organisms and unravelling the mysteries of unknown proteins". For any further information, contact Fabrice Bertile ([fbertile@unistra.fr](mailto:fbertile@unistra.fr); +33 368 852681)

Currently, iMOP is driven with 5 people: Susana Cristobal (Linköping University, Sweden), Sabine Matallana-Surget (University of Stirling, UK), Jean Armengaud (Paris-Saclay University, CEA, France), Andreas Tholey (Kiel University, Germany), Tristan Cardon (Inserm, University of Lille, France), and Fabrice Bertile (CNRS/University of Strasbourg, France).

Anyone interested to become a member of iMOP, please contact the chair or any of the co-chairs.

## UPCOMING EVENTS

- **HUPO-EuPA Congress, October 20<sup>th</sup>-24<sup>th</sup>, 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>

***\*\*EuPA is providing six Travel Grants to support and encourage the participation of students and early career researchers from Europe in the HUPO-EuPA 2024 Congress in Dresden. Submit your application via the Google form below by May 31st, 2024.***

[https://docs.google.com/forms/d/e/1FAIpQLSd4D27KPZAYcgsJR72ILOGQXpM-qDjzwlqA0tUKBJ21o4oy\\_A/viewform](https://docs.google.com/forms/d/e/1FAIpQLSd4D27KPZAYcgsJR72ILOGQXpM-qDjzwlqA0tUKBJ21o4oy_A/viewform)



- **5th International Conference on Post-Translational Modifications in Bacteria (PTMBact) 2024**, May 29<sup>th</sup>-30<sup>th</sup>, 2024, Rouen, France

The meeting topics will cover all known bacterial PTMs, including protein phosphorylation, acetylation, glycosylation, pupylation, RiPP, targeted degradation and other modifications, as well as the methods used to study them.

Full details are available on the website: <https://ptmbact2024.sciencesconf.org>





- **EuPA Job Fair and Student Exchange Event**, June 18<sup>th</sup>, 2024, 15:00-17.00 (CEST), Online Event

This online event is a unique opportunity for students and early career researchers to learn more about exchange opportunities with other laboratories in other countries and potential job opportunities.

Registration is mandatory: <https://forms.gle/TY8WeG8U2YfuGUQQ7>



- **Held online & Free (registration mandatory)**
- **Connects:**
  - ▷ **students seeking exchange opportunities with potential hosting labs and funding agencies**
  - ▷ **ECRs with companies seeking to recruit new talent**
  - ▷ **students and ECRs with Organizations like FEBS, EMBO, or Erasmus that provide fellowships for mobility**
- **EuPA aims to broaden the scope of exchange programs and increase ECR participation**
- **Providing a platform for ECRs, Labs, and companies to connect**

**EuPA Job Fair & Student Exchange Event**  
June 18th, 2024,  
15:00-17:00 (CEST)



**EuPA**  
EUROPEAN PROTEOMICS ASSOCIATION

- **Congress of Mass Spectrometry and Proteomic Analysis (SMAP 2024)**, September 16<sup>th</sup>-19<sup>th</sup>, 2024, Lille, France

The next conference on Mass Spectrometry and Proteomic Analysis (SMAP) will be held in Lille at the Grand Palais from September 16 to 19, 2024. This interdisciplinary event bringing together the world of mass spectrometry analysis and proteomics is organized by the French Society of Mass Spectrometry (SFSM) and the French Proteomics Society (FPS).

Registrations End Early Bird: 12 July 2024

Abstract Submissions Close: 14 June 2024

Full details available at the website: <https://www.smap2024.inviteo.fr/en/welcome/4>

**SMAP 2024 Lille** **SEPTEMBER 16-19 2024** **LILLE / FRANCE** **CONGRESS OF MASS SPECTROMETRY AND PROTEOMIC ANALYSIS**

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- Artificial Intelligence and Bioinformatics
- Spatial OMICs and MS Imaging
- Top-Down and Structural analysis
- Proteogenomics and metaproteomics
- New topics in OMICs
- Plant and Food OMICs
- Lipidomics, Metabolomics, and Small molecules
- Quantification
- Ion mobility spectrometry
- Instrumental development
- Environmental analysis
- Complex mixtures - polymers - microplastics
- Forensic and cultural heritage
- Health and biological sciences
- PTM (Post-Translational Modifications)
- Interatomic

**Abstract submissions**  
Close: 14 June 2024

**Registrations**  
End Early bird: 12 July 2024

**Meet our plenary speakers**

- Alexander Makarov**, Frontiers of high-resolution accurate mass
- Sarah Cianferani**, My journey into structural mass spectrometry methods
- Karl Mechtler**, 5300 protein per single-cell
- Maarten Dhaenens**, The metabolic projection hypothesis
- Leila Birolo**, Challenge of identification of ancient proteins
- Sebastian Böcker**, Turning tandem mass spectra into metabolite structure

SFSM, fps, ProFI, Université de Lille, GDR, Université de Strasbourg, Lille

## UPCOMING COURSES

- Initiative for Model Organism Proteomics WEBINAR on “Integrating new model organisms and unravelling the mysteries of unknown proteins”, May 21<sup>st</sup>, 2024, ZOOM MEETING



### Initiative for Model Organism Proteomics

an initiative within  
**HUPO** (Human Proteome Organization)  
and **EuPa** (European Proteomics Association)

#### WEBINAR

##### THEME

Integrating new model organisms  
and unravelling the mysteries of unknown proteins

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<b>Date</b>	May 21, 2024
<b>Time</b>	3:00pm – 5:00pm CET

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##### SPEAKERS

Dr **Fabrice BERTILE**

CNRS, University of Strasbourg, FR

" Introducing iMOP: initiative for Model Organism Proteomics "

Prof. **Xavier ROUCOU**

Sherbrooke University, CA

" Strategies and challenges for the identification of multicoding genes "

Prof. **Marc-André SELOSSE**

Muséum national d'Histoire naturelle, FR

"We are not individuals, and organismic homeostasis belongs to ecology "

##### JOIN THE WEBINAR

<https://cnrs.zoom.us/j/91878642574?pwd=N3RMemdIMlUwVWlWRGEwVXYrRnZhUT09>

ID de réunion: 918 7864 2574

Code secret: cfpYq9

- **Proteomics Summer School, July 28<sup>th</sup> - August 3<sup>rd</sup>, 2024, Brixen, Italy**

The Brixen Summerschool is a mixture of basic and advanced lectures as well as workshops ranging from sample preparation and mass spectrometry. It also includes lectures for experimental design, data analysis as well as career advice.

It is aimed at graduate students and early career researchers; hence, it has had over the years a variety of attendees from many scientific backgrounds. The course also includes a great social program that gives plenty of time for networking. The organizers have assembled an impressive lineup of speakers and are eagerly anticipating the participation of many new faces.

For more information: <https://www.brixenproteomics.org/>

To register: <https://www.brixenproteomics.org/application/>

The deadline for registrations is May 20<sup>th</sup>, 2024.

**BRIXEN PROTEOMICS SUMMERSCHOOL**  
28<sup>th</sup> July - 3<sup>rd</sup> August 2024, Brixen, Italy

**Speakers**  
HELEN COOPER, University of Birmingham, UK  
BERNHARD KUSTER, Technical University Munich, Germany  
MIKE MACCOSS, University of Washington, USA  
THIERRY RABILLOU, CNRS, France  
MARKUS RALSER, Charite - Medical University Berlin, Germany  
KELLY STECKER, Utrecht University, The Netherlands  
JUDIT VILLEN, University of Washington, USA  
OLGA VITEK, Northeastern University, USA  
MICHAEL WASHBURN, University of Kansas Medical Center, USA  
MATHIAS WILHELM, Technical University Munich, Germany

More to be confirmed....

Registration Deadline  
20<sup>th</sup> May 2024

**Organisers**  
BRITTA EGGERS, Bochum, Germany  
KATHRYN LILLEY, Cambridge, UK  
CHRISTINA LUDWIG, Freising, Germany  
CAROLINE MAY, Bochum, Germany  
SHABAZ MOHAMMED, Oxford, UK  
JESPER V. OLSEN, Copenhagen, Denmark

Logos at the bottom: Bruker, EVOSEP, Bruker, ThermoFisher, RUH, University of Copenhagen, University of Oxford, University of Cambridge, TUM, EuPA.

- **2nd International School on Mass Spectrometry**, September 9<sup>th</sup>-14<sup>th</sup>, 2024, Erice, Italy

The International School on Mass Spectrometry (IntSMS) is a six-day full immersion school aimed to give advanced and higher education in mass spectrometry to graduate, PhD, post-doc students, and all those working in different areas of science, ranging from physics, chemistry, biosciences, food, environment, omics sciences to medicine, interested to improve their knowledge and culture in mass spectrometry.

The 2nd Course is devoted to “ION MOBILITY MASS SPECTROMETRY: Fundamentals, Advances, and Applications”.

The school joins together participants from academia, public and private research centers, and industry, and it is a useful occasion for allowing meeting of students and tutors coming from different countries and for creating new links and networking.

For more information: <https://www.spettrometriadimassa.it/intsms2024/>

The deadline for registrations is June 15th, 2024.

