

EUPA NEWSLETTER

APRIL 2023
ISSUE 4

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MESSAGE FROM THE EDITOR

Dear Colleagues and EuPA Members,

It is a real pleasure for me to launch the new issue of the EuPA Newsletter, and I would like to start by sincerely thanking all contributors!

In this fourth issue, you will find contributions from EuPA Initiatives. Please do not hesitate to contact me if you are interested in contributing to a future EuPA Newsletter (Core Facilities, Art & Science, *etc.*). Don't miss your chance to contribute to the literal story of EuPA!

In addition, the Newsletter team is looking for volunteers to help out in a variety of ways. Again, feel free to contact me if you are interested in contributing to making these Newsletters happen!

The EuPA Newsletter will be disseminated every quarter, and the next issue is planned for September 2023. So go ahead and contact me today, so we can make this next Newsletter together!!!

Enjoy reading.

Nicolas Desbenoit, EuPA Newsletter Editor (✉ n.desbenoit@cbmn.u-bordeaux.fr), on behalf of the EuPA Conference and Communication Committee.

Please find below some instructions:

Independent of the type of contribution, please provide the name of the author or authors, affiliations, e-mail address, and a picture of the main author. You can also include figures and legends, as well as references. Times New Roman will be used as font, with size 12 and interline at 1.5. Concerning the length of the contributions: Thesis abstract (½-1 pages), Students / ECRs overviews (3-5 pages), Invited EuPA speakers (½-1 page), European Core Facilities (1-2 pages), and Sponsors (1-2 pages).

Concerning the core facility section and following the instructions above, please, provide a short description (staff, website, equipment, bioinformatic tools, etc.), applications / main axis, national / European / international networks, involvement in education, and contact. Picture(s) would be appreciated. The idea is to promote European facilities which are members of EuPA and to disseminate to other learned societies interested in proteomic aspects.

EUPA INITIATIVES

The five EuPA Initiatives work towards common solutions for challenges in current proteomics. More specifically they focus on bioinformatics for mass spectrometry, metaproteomics, standardization, food and nutrition proteomics as well as proteomics in model organisms. As described in their respective articles, these vibrant scientific communities have developed an amazing portfolio of activities. They continuously recruit new motivated members at all career stages.

At the end of 2022, all Initiative leaders and committee members met in Paris in order to discuss their plans and needs for 2023 as well as possible new cross-cutting projects. We thank Mariette Matondo from the French national society for her very warm welcome at the Pasteur Institute. This retreat was very fruitful as several partnerships between initiatives could be launched or reinforced.

To push cooperation further, we discussed the possible initiation of a COST Action centred on the ambitious “Holobiont project” proposed by the iMOP initiative. Such a project would raise a number of experimental and bioinformatics challenges that would require an international and multidisciplinary effort. If you are interested to know more and/or be part of the team shaping the project please contact Frederique Lisacek (Initiatives committee member).

Lydie Lane, on behalf of the EuPA Initiatives Committee Chair (initiatives@eupa.org)

EUBIC-MS (EUROPEAN BIOINFORMATICS COMMUNITY FOR MASS SPECTROMETRY)



The European Bioinformatics Community for mass spectrometry (EuBIC-MS) is the EuPA initiative for mass spectrometry (MS)-related bioinformatics. It operates with a horizontal organizational structure, where two members officially represent the Initiative to EuPA, other stakeholders, and the public. Marie Locard-Paulet and David Bouyssié have taken this role since 2022. End of 2022, there are 92 members from 22 countries, who are free to positively contribute to the initiative activities.

EuBIC-MS aims to connect users with developers, and academics with industrial researchers, and to maximize the development of high-quality, sustainable and accessible bioinformatic solutions in computational mass spectrometry. The main activities of the initiative consist in organizing international meetings and educational workshops as well as providing online community platforms dedicated to computational mass spectrometry (proteomics-academy.org, qa.proteomics-academy.org). Additionally, EuBIC-MS also coordinates and participates in community-driven projects (e.g. Perez-Riverol et al. 2020).

Due to the Corona pandemic, the 2021 Winter School was postponed to 2022, and finally took place on 21-24 March 2022 at the Instituto Gulbenkian de Ciência in Oeiras (Portugal): nine keynote speakers were invited to give lectures and hands-on sessions that completed the four entry-level workshops organized on the first day of each EuBIC-MS Winter School. In January 2023, EuBIC-MS organizes a Developers Meeting that will take place at the ETH meeting platform Congressi Stefano Franscini (CSF), in Monte Verità, Switzerland. 57 participants registered for this event: they will work for a week on seven projects that were proposed and selected by the community (see selected projects on the dedicated Github repository). The outputs of previous EuBIC-MS Developers Meetings can be found in the review Bittremieux et al. 2021, and the recently published Luo et al. 2022.

More information regarding EuBIC-MS can be found at eubic-ms.org. And finally, if you would like to join the initiative, this can be done in a minute, by filling out a very short form: eubic-ms.org/become-a-member. You can also follow us on twitter at twitter.com/EuBIC_ms.

On behalf of the EuBIC-MS fantastic community.



FOOD AND NUTRITION PROTEOMICS – FAN



Food and Nutrition Proteomics

FaN (~50 members) studies food, in all its aspects, and the microbiome and biomarkers of health status in relation to food and nutrition from a protein perspective, so as to build a new pillar of personalized medicine.

These studies involve many aspects, from animal health to food safety and nutrition by the perspective of the modern One-Health approach (i.e. the concept that the health of people, animals and ecosystems are interconnected). We are convinced that proteins are the true 'functional product of life', so the study is of enormous value in making food our main 'preventive medicine'.



Main projects EU: ImpARAS (Cost Action) FoodenTwin, BrucMedNet- National (just started IM-OH

Since 2016, we organized one event/year inside mainly the main congress of Italian proteomics Organization

We will organize next meeting in Padova at end of August 2023 during the joint international meeting- ItPA-SePA and HPS

This picture represents the Chair of the initiative, Prof. Paola Roncada, (Department of Health Sciences – University Magna Graecia of Catanzaro, Italy) at Foodomics Workshop organized in Analytica in June 2022, Munchen (DE).

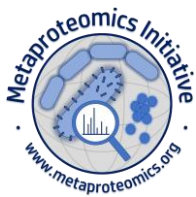
People can join the initiative email to the chair: roncada@unicz.it

You can also follow us on dedicated Facebook page: **@fanproteomics**

Chair: **Prof Paola Roncada** (University Magna Graecia of Catanzaro, Italy).

Co-Chairs: **Prof. Tanja Cirkovic Velickovic** (University of Belgrade, Republic of Serbia), and **Prof. George Tsangaris** (Biochemical Research Foundation Academy of Athens, Greece).

METAPROTEOMICS INITIATIVE



The Metaproteomics Initiative promotes the dissemination of metaproteomics fundamentals, advancements, and applications through collaborative networking in microbiome research. We aim 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. Currently, we have 176 members from 72 labs in 17 countries (twelve in Europe, Australia, Canada, China, India and the USA).

There are new CAMPI benchmark studies in the pipeline!

After finalizing and publishing the first community-driven, multi-lab benchmark study in metaproteomics (<https://www.nature.com/articles/s41467-021-27542-8>), the scientific committee has launched two new CAMPI benchmark studies!

CAMPI 2 will focus on sample handling, one of the main challenges in metaproteomics. Indeed, directly after sample collection, biological samples are shipped or stored at different temperatures, treated with preservation solutions or a direct protein extraction is performed. All these treatments can lead finally to a different proteome profile, which directly influences the biological interpretation of your study. The scope of CAMPI 2 therefore a comparative assessment of proteome sample stability after sample collection. Here, the most relevant issue is the sample treatment and the time spanning from sample collection to protein extraction (i.e., when microbiota composition and functions are challenged by short or long exposures to variations of temperature, humidity, pH, O₂, etc.). Different labs will participate by applying their methods to stabilize the samples to be subjected to a real world “stress-test”, that will include the shipment with no control over temperature conditions. The expected CAMPI 2 result is to provide a standard procedure for sample handling.

CAMPI3 will have a closer look at the taxonomic and functional annotation of metaproteomics data. Typically, acquired MS/MS data is searched against a protein sequence database to identify peptides, which are then used to infer a list of proteins in a metaproteome sample. Protein inference remains a major challenge for metaproteomics because of the many degenerate peptides shared among homologous proteins in different organisms. During this project, we’ll reach out to metaproteomics researchers with microbial datasets of low and high complexity and seek answers regarding the annotation of taxonomy, protein inference, and functional annotation.

Save the date! The 5th International Metaproteomics Symposium will take place in Avignon (France) from 25 to 27 April 2023, under the theme "Unlocking microbiome functions".

The symposium aims to bring together a growing international community of researchers and experts to advance the metaproteomics field and address its associated challenges. Please, visit the symposium website: <http://ims23.com/>

The program is designed to facilitate collaboration and community-led brainstorming, with six sessions on various metaproteomics application fields and aspects, two round tables, two additional sessions dedicated to collaborative projects and the Metaproteomic Initiative, and numerous opportunities for attendees to present their work. The breaks, poster sessions, and a social event are designed to encourage networking and interactions among the attendees. And that's not all! Two satellite workshops are also organized to provide training on metaproteomics analysis using the Galaxy platform and other informatics resources available for functional microbiome research (Tutorial 1) or a hands-on metaproteomics sample preparation and MS tips (Tutorial 2).

Don't miss out on this unique opportunity to learn from the leading experts in the field, share your work, and network with your peers. We look forward to welcoming you in Avignon for the 5th International Metaproteomics Symposium.



Group picture from the 4th International Metaproteomics Symposium (Luxemburg, September 2021, part in-person, part online due to COVID restrictions).

More information

Want to join the Metaproteomics Initiative? Becoming member is as easy as filling in the following Google form:

https://docs.google.com/forms/d/e/1FAIpQLSd0xfPtsn_eFNAXGL2uqEDhw9xAL3ZFBzhwVx9NiO25t87lkA/viewform?usp=sf_link

More information about the Initiative can be found on our website (www.metaproteomics.org) and in our commentary article in Microbiome:

<https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-021-01176-w>).

Contact: info@metaproteomics.org

Contact persons: Tim Van Den Bossche & Benoit Kunath (co-administrators); all members of the executive board can be found at <https://metaproteomics.org/about/>

Tim Van Den Bossche (VIB, Ghent University, Belgium).

EUPA STANDARDIZATION INITIATIVE

Rational purpose, and specific impacts of the Initiative

Proteomics methods including sample preparation, liquid chromatography, mass spectrometry and bioinformatics has experienced huge advances in the last decade increasing the accuracy and capacity of protein/peptide measurements in complex biological samples. The possibility of massive protein identification and quantification converts proteomics in one of the most valuable analytical resources to understand sophisticated cellular processes at the functional level. However, if proteomics has to deliver its resources and capabilities to the scientific community then, reliability, robustness and reproducibility must be ensured. To this end, it is mandatory to define quality control procedures and standardized protocols for the whole proteomics workflow, from sample collection and preparation to data computational analysis and exchange. Noteworthy, the translation of analytical results into relevant biological knowledge and practical applications is often hampered for the lack of standardized protocols that emerge, therefore, as an urgent need.

Goals of the initiative

The aim of this initiative is the organization of a multi-laboratory studies to:

- Allow to assess reproducibility and limitations of analytical methodologies
- Reinforce confidence in robustness of the methods
- Help to improve protocols / performance of laboratories

To this end, annual/biannual multi-centric studies will be programmed.

Relevance of the initiative for the EuPA community

This initiative is of utmost importance since standardization of proteomics workflows will promote the consolidation of a common space integrating proteomic strengths across Europe, based on the easy exchange of information generated under normalized protocols and data formats. Besides improving the efficiency within the proteomics environment, standardization is mandatory to increase the penetrance of proteomics in other scientific disciplines; it is worth mentioning that one of the main constrains to move from proteomics to the clinics is the difficulty to validate properly protein/peptide biomarkers as a result of the lack of standardized procedures on sample collection, storage and preparation, MS analysis, data processing and interpretation and common formats for an easy data sharing.

Milestones and deliverables including project proposal submission

To design a multi-center study every 1-2 years

To prepare and distribute the reference sample

To analyze the results

To publish the outcomes

To create a repository of standardized protocols accessible from the EuPA web page.

The initiative is open to all EuPA-member groups. The participation of other external non-EuPA laboratories in EuPA PME will be also open by invitation or request. Participation will be limited to a certain number of laboratories (budgetary restrictions) on a first come first serves policy with priority to EuPA groups

Ideas for next PME

1. High sensitivity Proteomics. Towards single cell analysis. Expected launching March 2023
2. Xlinking-MS
3. Análisis de glycopeptides/glycoproteins.
4. Metaproteomics

Recent activity

PME11 has been conducted and the results (from 23 labs in 6 countries) have been submitted to the Journal of Proteomics:

Multi-laboratory experiment PME11 for the standardization of phosphoproteome analysis: Global analysis of protein phosphorylation by mass spectrometry proteomic techniques has emerged in the last decades as a powerful tool in biological and biomedical research. However, there are several factors that make the global study of the phosphoproteome more challenging than measuring non-modified proteins. The low stoichiometry of the phosphorylated species and the need to retrieve residue specific information require particular attention on sample preparation, data acquisition and processing to ensure reproducibility, qualitative and quantitative robustness and ample phosphoproteome coverage in phosphoproteomic workflows. Aiming to investigate the effect of different variables in the performance of proteome wide phosphoprotein analysis protocols, ProteoRed-ISCI and EuPA launched the Proteomics Multicentric Experiment 11 (PME11). A reference sample consisting of a yeast protein extract spiked in with different amounts of a phosphomix standard (Sigma/Merck) was distributed to 31 laboratories around the globe. Thirty-six

datasets from 23 laboratories were analyzed. Our results indicate the suitability of the PME11 reference sample to benchmark and optimize phosphoproteomics strategies, weighing the influence of different factors, as well as to rank intra and inter laboratory performance.

Multi-laboratory experiment PME11 for the standardization of phosphoproteome analysis. Colomé N, Abian J, Aloria K, Arizmendi JM, Barceló-Batllori S, Braga-Lagache S, Burlet-Schiltz O, Carrascal M, Casal JI, Chicano-Gálvez E, Chiva C, Clemente LF, Elortza F, Estanyol JM, Fernandez-Irigoyen J, Fernández-Puente P, Fidalgo MJ, Froment C, Fuentes M, Fuentes-Almagro C, Gay M, Hainard A, Heller M, Hernández ML, Ibarrola N, Iloro I, Kieselbach T, Lario A, Locard-Paulet M, Marina-Ramírez A, Martín L, Morato-López E, Muñoz J, Navajas R, Odena MA, Odriozola L, de Oliveira E, Paradela A, Pasquarello C, de Los Rios V, Ruiz-Romero C, Sabidó E, Sánchez Del Pino M, Sancho J, Santamaría E, Schaeffer-Reiss C, Schneider J, de la Torre C, Valero ML, Vilaseca M, Wu S, Wu L, Ximénez de Embún P, Canals F, Corrales FJ; ProteoRed-ISCIII; EuPA. *J Proteomics*. 2022 Jan 16;251:104409. doi: 10.1016/j.jprot.2021.104409. Epub 2021 Nov 7. PMID: 34758407.

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Members: To be recruited from EuPA scientists (announcement in social media and EuPA website). Members will participate in the selection, preparation and data analysis of PME experiments.

UPCOMING EVENTS IN PROTEOMICS

5TH INTERNATIONAL METAPROTEOMICS SYMPOSIUM

<https://ims23.com/>

April 25th – 27th, 2023, Avignon, France

And Workshop 1 “Integrative Multiomics in Galaxy”, April 24th, 2023, Avignon, France

Workshop 2 “Hands on Metaproteomics Mass Spectrometry”, April 28th, 2023, Avignon, France

The image shows a screenshot of the website for the 5th International Metaproteomics Symposium. The top navigation bar includes links for HOME, PROGRAMME, VENUE & ACCOMMODATIONS, TRAVEL GRANTS, and CONTACT US. The main banner features an aerial view of Avignon, France, with the text "5th International Metaproteomics Symposium" and "25-27 April 2023 Avignon, France". Below the banner are two buttons: "REGISTER" and "SUBMIT AN ABSTRACT".

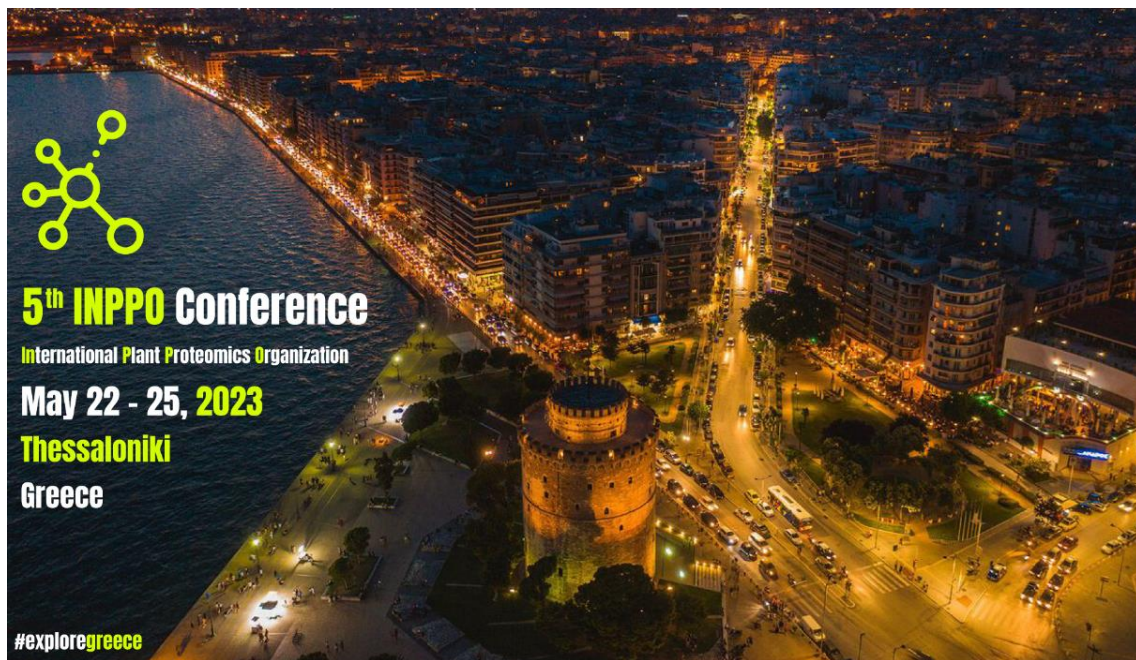
Below the main banner are two workshop promotional graphics:

- Workshop 1: INTEGRATIVE MULTIOMICS IN GALAXY**
Date: 24 APRIL, 2023
Time: 9:00 AM-17:00 PM
Speakers: PERATI K. JAGTAP, VALERIE SCHIML, ROBERT HEYER, MAGNUS ARNTZEN
Topic: Introduction to Microbiome Research and Metaproteomics
- Workshop 2: HANDS ON: METAPROTEOMICS MASS SPECTROMETRY**
Date: 28 APRIL, 2023
Time: 9:00 AM-17:00 PM
Speakers: JEAN ARMENGAUD, LUCIA GRENGA, THIBAUT DUMAS, CLEMENT LOZANO
Topic: Introduction to mass spectrometry of proteins and peptides

5TH INPPO CONFERENCE

<https://thessinppo2023.com/>

May 22th – 25th, 2023, Thessaloniki, Greece



3RD JOINT PROTEOMICS CONGRESS: PROTEOAIX

<https://proteoaix2023.sciencesconf.org/>

June 20th – 23th, 2023, Aix-en-Provence, France

PROCURA OMICS PT

fps
40 years

SEProt
Sociedad Española de Proteómica

@2023ProteoAix

3rd joint Proteomics congress

ProteoAix

en Provence

Congress Center of Aix-en-Provence
20-23 June 2023

CONFIRMED SPEAKERS

Ana Varela Coelho | New University of Lisbon
Julien Marcoux | CNRS Toulouse
Charles Pineau | Inserm Rennes
Ana Martinez del Val | Novo Nordisk Foundation
Vadim Demichev | Universitätsmedizin Berlin
Albert Heck | Utrecht University
Juri Rappsilber | Technische Universität Berlin
Javier Muñoz Peralta | Biocruces Bizkaia Health Research Institute

<http://proteoaix2023.sciencesconf.org>

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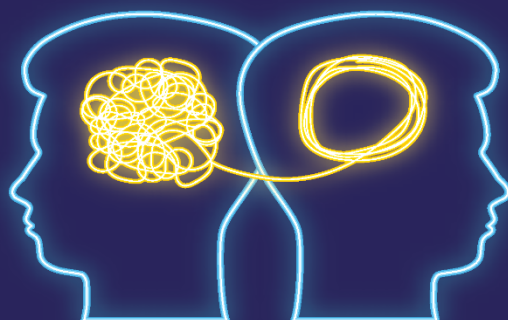
Bronze Sponsor: **Cell Signaling**

Partners: **ProFi**, **BIOBOSYS**, **GENE RECORDS**

EUPA ACTIVE BYSTANDER TRAINING

July 14th, 2023, Online

EuPA Active Bystander Training



Wed July 14th | 4.30pm CET

Training developed by award-winning Scott Solder



**Strategies to call out bad behaviour in academia
and create a safe, pleasant and productive workplace**



Scan to register



 EuropeanProteomicsAssociation

 EuPAProteomics

 eupa.org

BSPR & EUPA ANNUAL MEETING 2023

<https://conferences.ncl.ac.uk/bspr-eupa2023/>

July 17th – 20th, 2023, Newcastle upon Tyne, UK



Once Upon a Tyne ...



Newcastle
BSPR-EuPA 2023

BSPR/EuPA2023

- YPIC Event Schedule

Date	Time	Session Title
16th July	Evening	Networking Session
17th July	09:15-10:45	Intro to Bioinformatic Tools
	11:00-11:45	Intro to Metaproteomics
	11:30-12:45	Mental Health Lunch Seminar
	12:50-14:20	Proteomics 101 Session
	12:50-14:20	Advanced Proteomics
	14:30-16:00	Career Session
18th July	during lunch break	Discussion Over Lunch: Expert Insights
	Evening	Networking Session
19th July	8:00-9:00	Meet-the-Experts Breakfast
	during lunch break	Discussion Over Lunch: Expert Insights

HUPO BUSAN 2023

<https://2023.hupo.org/>

September 17th – 21st, 2023, Busan, South Korea



Together Through Proteomics



SAVE THE DATE

SEPTEMBER 17–21, 2023
BEXCO, Busan, Korea

 [LEARN MORE](#)



2023.hupo.org



[#HUPO2023](#)

SHORT NEWS

EUPA MERCHSHOP

EuPA launched the Merch Shop where you can buy various clothes and items with EuPA or YPIC logo.



For the full list of items and color varieties, please visit the EuPA Merch Shop site:
<https://eupashop.myspreadshop.net/>

CONTRIBUTORS FOR THE CURRENT ISSUE

- *Dr. Nicolas Desbenoit as editor, & Dr. Éva Csősz as co-editor.*
- *The EuPA Initiatives: Lydie Lane, EuBIC, Paola Roncada, Tim Van Den Bossche, & Fernando Corrales.*
- *Michael David Tuck as proofreaders.*