



EuPA

EUROPEAN PROTEOMICS ASSOCIATION

EuPA NEWSLETTER

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Hope to see you in Leipzig!

PROTEOMIC FORUM | EuPA 2022
XIV Annual Congress of the European Proteomics Association
3–7 April 2022 | Leipzig/Germany | www.proteomic-forum.com

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 second issue, you will find details concerning our next event Proteomic Forum / EuPA 2022, activities of our young proteomicists (YPIC) at EuPA 2022, a new section named European Core Facilities open for any European platforms interested in promoting them, and finally another new section named “Art & Science” to be discovered. Regarding the latter two, please do not hesitate to contact me if you are interested in contributing to a future EuPA Newsletter. 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 July 2022. 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 (1/2-1 pages), Students / ECRs overviews (3-5 pages), Invited EuPA speakers (1/2-1 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.

YPIC AT EUPA2022 CONFERENCE

The XIV Annual Congress of the European Proteomics Association will take place from 3rd to 7th April 2022 in Leipzig, Germany. As usual, the Young Proteomics Investigators Club (YPIC) has organised quite a few events. Here is an overview of what the young scientists in proteomics can be excited about while attending the conference.

The Educational Day - 3rd April 2022 at 10:00-15:15

Together with the SoGS we are organising several sessions with scientific and non-scientific topics based on your feedback during our recent social media polls. The first session will start at 10 AM, we know so early for a Sunday morning, and will introduce you to **R for your proteomics data analysis**. If you want to come prepared so you can follow along on your own PC, look out for further details about this session in the next few weeks. Since there are so many interesting topics, the second session of the day will present you with some hard choices. Are planning to **work abroad** or **write a grant** and need some guidance? Or will you start working on **single-cell proteomics** or **PTM analysis** and want some tips? Afterwards, we hope you will join us in gaining insights on what to do with these long **protein lists** you worked so hard to obtain. Is there a **biological meaning**? And if so, how can we find it?

Career Session - 3rd April 2022 at 15:30-16:45

Do you feel ready for the switch from academia to industry? Do you prefer to stay in academia? Did you know that a conference is the perfect place to boost your career? In any case you should visit the **Career Session** at the end of the educational day, just before the Opening Ceremony, on Sunday, April 3rd, 2022.

The term “employability” refers to the attributes that make you able to gain and maintain employment. Employability has been one of the main goals since the creation of the European Higher Education Area (“Bologna process”). However, many universities neglect training their students’ skills in career planning, especially beyond academia. The Career Session can help to fill this gap. **Three well-known companies of the proteomics sector (Thermo Fisher, Waters, and Bruker)** will present their foci and inform about requested competences for candidates. Current job vacancies – if available – will be presented. In addition, the chances, obstacles, and necessary skills of **academic careers** will be addressed in one of the talks. One of the **highlights: EuPA president Lennart Martens** will tell you how to use this upcoming conference for career purposes.

The Meet-the-Experts session - 6th April 2022 at 17:15-18:15

Have you always wanted to pose a question to one of the experts in proteomics? No? Oh, you had more than one? Here is your chance! Join us for the **Meet-the-experts** session on April 6th. This session will give you the chance to participate in an **informal discussion** with two experts of your choice in a small round table setting. During this session we will have five tables with two experts each who are looking forward to engage in a lively discussion. Since **spaces are limited** you might want to register for the table you want to join. More information will follow in the next few weeks.

The moment you have all been waiting for... - 7th April 2022 at 11:30-13:15

Are you excited by MS-based proteomics and always on the lookout for a chance to prove your skills? Then stay tuned – we are excited to announce the **3rd YPIC challenge**, supported by PolyQuant. As with our [previous challenges](#), we invite you to crack the secret encoded in a peptide amino acid sequence. But this time, to allow broad participation also from those without MS access, we bring the data to you. At EuPA 2022 **during the Closing remarks**, we will open access to eight raw files of digested peptides, which you can use in any way you see fit to solve the challenge. **Will you be the first to decipher our hidden message?**

What is there to do in the evenings?

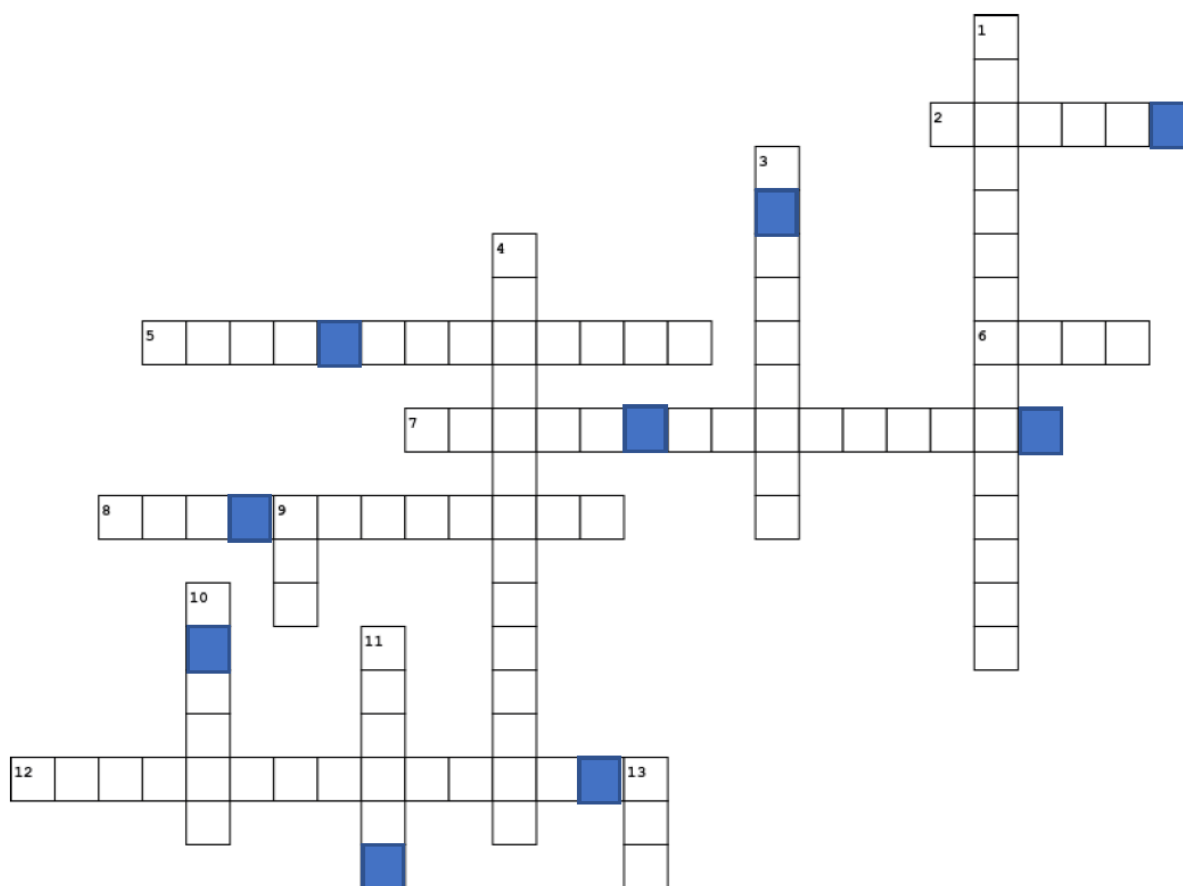
Are you attending the conference as the only one from your lab? Do you want to meet new people? Would you rather go for a drink with a bunch of proteomics enthusiasts than hang out alone in your hotel room? All of the above?

Why don't you join us for some networking in the evenings after the conference? More information will be available soon on social media.

You want to have some fun now...

How about solving the crosswords puzzle below? Who knows figuring out the phrase made up by the letters in the blue boxes might earn you a reward besides the satisfaction from solving a puzzle.

If you want to be the first to know about upcoming YPIC events as well as ECR related events, follow us on social media ([Facebook](#), [LinkedIn](#), and [Twitter](#)) and/or sign up to our [mailing list](#). You want to actively participate in organising future YPIC events, contact us via email to ypic@eupa.org.



Across

Down

- 2. In which German state did EuPA2022 take place?
- 5. Which country will host the 2023 EuPA meeting?
- 6. Which national society is hosting this year's congress?
- 7. Who is EuPA's proteome Pioneer award named after?
- 8. Where did the social evening take place?
- 12. Who is the winner of the Technology award?

- 1. Who had a talk during the educational day and is a former YPIC president?
- 3. Which scientist gave the opening talk?
- 4. Who is the current president of EuPA?
- 9. How many experts were at the "meet the expert" session?
- 10. In which room did most of the educational day lectures take place?
- 11. Which colour t-shirt did the YPIC members wear on the Educational day?
- 13. How many YPIC team members are at EuPA2022?

Proteomic research is traditionally used in various clinical and biological sciences, including food technology and the discovery of biomarkers or drug targets. However, the study of proteins could be applied in many other research fields, such as the already highly interdisciplinary Heritage Science. In this field researchers from many different backgrounds come together to study cultural heritage collections, in order to understand more about the context in which an object was made, to identify different chemical components in an object, and to understand its conservation needs.

Since antiquity, protein-based materials have been used by artists to express themselves. For instance, one of the oldest painting techniques, before the emergence of oil paintings in the 15th century, was tempera (from Latin *temperare* meaning "to mix colours"), which is traditionally characterised by the use of egg (mostly yolk) as the *binder* in the paint. In a painted artwork, animal- or vegetable-based materials are used as binders to aid the cohesion and adhesion of fine particles of inorganic *pigments* or organic *dyes* to the support (usually wood, an easel or a stone wall), ensuring the formation of a homogeneous film. There are many famous examples of tempera paintings in Italian Renaissance art with the masterpieces of Sandro Botticelli, Michelangelo and Raphael. Eggs (mixed, or with yolk and white separated), casein from milk, and animal glues, manufactured from the boiling of bones or hides from mammals or fish, were used for various artistic purposes, including gildings' adhesives, writing supports (*i.e.* parchment), drawing sizing, and conservative coatings.

In the past two decades, mass spectrometry-based proteomic strategies have achieved remarkable results in cultural heritage studies, providing the reliable identification of proteins and the biological species of origin for many artefacts. The information achieved can be crucial for the comprehension of the artistic techniques and, sometimes, for the authentication of the artistic object and its historical, geographical, and cultural interpretation. Proteomics can also give a better understanding of the artworks' state of conservation, helping to define adequate preservation strategies (*i.e.*, restoration treatments, control of exposure and environmental parameters). Furthermore, undocumented details can be unveiled, sometimes resolving long-standing debates by confirming or refuting previous assessments.

For example, the pages in some 13th century pocket bibles were so thin that it was assumed that they had been made using the 'uterine vellum' technique, whereby aborted skins or unusual animals, such as rabbits and squirrels were used to make the pages, rather than more traditional animal hides. By using the MALDI-TOF based ZooMS (Zooarchaeology by Mass Spectrometry) peptide mass

fingerprinting strategy on 72 pocket bibles, Fiddymment et al. were able to identify collagen type I peptides diagnostic for three mammal species (calf, goat and sheep), thus dispelling the uterine vellum theory. Interestingly, some Bibles were composed of parchments of multiple species, in relation with the geographical availability of hides. The results suggested that ultrathin hides most likely resulted from a particular manufacturing process rather than from the hides of new-born animals.

A more recent nanoLC-MS/MS study provided the first evidence that milk-based fixatives were the secret behind Thomas Gainsborough's remarkably well-preserved drawings. The artist did not want to share the ruse with anyone other than a friend to whom he confided in a letter. The analysis on seven drawings of the English artist revealed the presence of numerous milk proteins, detected with high protein sequence coverage, including the most abundant caseins, whey proteins and minor proteins (*e.g.* milk fat globule membrane proteins). The identification of species-specific peptides allowed the attribution of the milk to the *Bos taurus* species (cattle). The strategy also provided the precise localisation of modifications on the proteins, principally induced by ageing and degradation processes, such as deamidation of asparagine and particularly glutamine, which is often used as a "molecular clock".

It is noteworthy that, in both referred studies, the analyses were successfully performed on micro-samples collected with minimally invasive techniques that guaranteed the preservation of the original integrity of the artwork. Indeed, reducing the sample collected is one of the challenges that has to be considered in the protein investigation of cultural heritage. Significant progress has been achieved on sample preparation and analysis methodologies to optimise the traditional proteomic protocol and investigate an analyte often embedded in a complex and heterogeneous matrix. The present challenge of proteomics in Heritage Science is to transcend the protein identification and pursue a higher understanding of the protein interactions within its matrix and their chemical and structural modifications induced during the ageing and degradation. We want to gain a greater understanding of the processes that are influenced by object storage conditions, environmental factors (*e.g.* temperature, relative humidity, light exposure), interactions between different chemical compounds in the objects, and invasive or unsuitable conservation conditions and restoration treatments.



Fiddymment, S., Holsinger, B., Ruzzier, C., Devine, A., Binois, A., Albarella, U., Fischer, R., Nichols, E., Curtis, A., Cheese, E. and Teasdale, M.D., 2015. Animal origin of 13th-century uterine vellum revealed using noninvasive peptide fingerprinting. *Proceedings of the National Academy of Sciences*, 112(49), pp.15066-15071.

Pozzi, F., Arslanoglu, J., Galluzzi, F., Tokarski, C. and Snyder, R., 2020. Mixing, dipping, and fixing: the experimental drawing techniques of Thomas Gainsborough. *Heritage Science*, 8(1), pp.1-14.

EUROPEAN CORE FACILITIES

PROTEOME CORE FACILITY – UNIVERSITY OF BORDEAUX (FRANCE)

Proteome is a mixed University of Bordeaux/CNRS (UMR 5248) platform headed by Prof. Caroline Tokarski and involving 20 people staff. The platform is offering service and R&D activities in omics (<https://proteome.cgfb.u-bordeaux.fr/en>). **Proteome** is certified ISO9001:2015 and NF X 50-900:2016 renewed for the period 2021-2024. The mission of **Proteome** is to provide researchers from academic and private or industrial communities with state-of-the-art scientific and technical support in omics. This requires a commitment to develop, implement, and optimise cutting-edge methodologies and instrumentation. Proteome is equipped with 8 mass spectrometers, including the latest generations of high-resolution instruments (*e.g.* Orbitrap Eclipse, Lumos), high mass instruments (*e.g.* MALDI-TOF/TOF equipped with high mass detector), imaging instruments (*e.g.* AP-SMALDI5 Orbitrap) and bioinformatics tools (9 servers, 11 data processing software).



The topics investigated by the platform are covering fields related to hospital and health (neurosciences, cancer, *etc.*), pharmaceuticals, the environment, the food industry, material sciences and cultural heritage. The scientific targets range from the identification of proteins, lipids, and polysaccharides (targeted and non-targeted analyses) to differential and quantitative analysis, structural characterization, trace analysis, and imaging. The following main axes have been developed:

- **Bottom up proteomic strategies**, for quantitative and differential analysis, as well as characterization of post-translational and chemical modifications (447 projects within the 3 last years including 30% projects for non-academics). Among examples that can be cited is the study of IgA N- and O-glycosylations (*e.g.* nephropathy), acetylation profiles as epigenetic markers (*e.g.* diagnosis), biological markers in sweat (*e.g.* Covid +/-), proteins partners (*e.g.* pulmonary hypertension), biofilms (*e.g.* study of the attachment phase) and specific proteomes (*e.g.* the *Arabiopsis thaliana* phagophore).

- **Top down proteomics methodologies**, including intact protein analysis and sequencing, addressing unsolved questions using more traditional approaches and targeting the study of protein isoforms/proteoforms and *in situ* breakdowns. A specific emphasis is given to medical/pharma (*e.g.* protein-based drugs), food (*e.g.* industrial milk production) and cultural heritage applications (*e.g.* the effects of preservation treatments).

- **Structural mass spectrometry methods**, including studies on protein conformation and dynamics, protein-protein and protein-ligand interactions, organization of protein complexes, using chemical cross-linking (XL-MS), hydrogen/deuterium isotopic exchange (HDX-MS), limited proteolysis (LiP-MS) and affinity-based protein profiling (ABPP). Applications that can be cited include studies involving natural compounds (*e.g.* cellular protein targets of wine polyphenols) and synthetic molecules (*e.g.* foldamers mimicking the structure of double-stranded B-DNA). Other examples are applications to health (*e.g.* oligomers' assemblies involved in targeted disease) and cultural heritage (crosslinked ancient proteins).

- **MALDI Mass Spectrometry Imaging (MALDI-MSI)**, to investigate qualitative and quantitative multi-omics distributions. Suited methodological developments are applied to address different questions focused on biomedical research including tuberculosis, cancer, respiratory disease, *etc.* In addition to this, multimodal imaging has been developed within **Proteome**, an emerging strategy based on MALDI-MSI combined with other modalities (vibrational spectroscopies, histological staining, MRI, MS, *etc.*) that is applied to biomedical research investigations. Multimodal imaging will enable us to simultaneously access more chemical information to understand in deeper detail the biomedical questions on which we work.

- **Trace and ultra-trace analysis**, specifically in the field of cultural heritage using miniaturized workflows targeting proteins, lipids and polysaccharides, including the study of unsequenced biological species and macromolecules with unknown or unreferenced structures. These

developments are applied to questions ranging from identification of ancient biomolecules trapped within complex matrixes (*e.g.* artworks, archaeological ceramics, and bones) to the study of molecular networks and assemblies. Among studied questions are: the composition of artworks, how this changes over time, improvement of conservation strategies, authentication; information related to human habits and commercial exchanges from the past; information on extinct species and phylogenetic links, ancient pathologies and pathogens.

Proteome is involved as leading platform in national, European, and international structures and infrastructures through the coordination of the CNRS GdR-MSI (Mass Spectrometry Imaging), the coordination of the HS_OMICS platform within the European Infrastructure IPERION HS (<https://www.iperionhs.eu/tool/165/>) and the coordination of the CNRS International Laboratory ARCHE (<https://arche.cnrs.fr/>).

Proteome has also a strong commitment to educating researchers from academic and non-academic communities through the organization and involvements in international schools (*e.g.* <https://bss-appliedchemistry.u-bordeaux.fr/en/>) and organization of theoretical and practical courses.

Core Facility Contact: Prof. Caroline Tokarski (c.tokarski@cbmn.u-bordeaux.fr), & Dr. Stéphane Claverol (stephane.claverol@u-bordeaux.fr).

Proteo Vilamoura

May 11-13, 2022, Portugal

2nd Joint Meeting of Spanish, French
and Portuguese Proteomics Societies

[Registration and abstract submissions are OPEN in proteo-vilamoura.sci-meet.net](https://proteo-vilamoura.sci-meet.net)

Website: proteo-vilamoura.sci-meet.net | **Contact:** info@procuraomics.pt

Chairwoman – Dina Simes (PROCURA, University of Algarve, Portugal)

ProteoVilamoura 2022 will be the 2nd Joint Meeting of Spanish, French and Portuguese Proteomics Societies. The meeting was assembled to grant a broad view at the diverse perspectives and applications of proteomics and its related fields focusing on new developments and scientific advances.

The meeting program is organised into 4 main sessions that integrate technical and methodological aspects, their various applications, complementarity with other areas and methodologies (MixOmics), together with up to date state-of-the-art research. Reference invited speakers were carefully chosen to share and discuss from the most fundamental aspects to new subjects. Conditions were put in place to allow and promote science sharing by all participants. Plenary lectures, small talks, flash talks, poster sessions, and relaxed social events are programmed so that everyone can interact, discuss and promote their projects in a great ambience.

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14TH EUROPEAN SUMMER SCHOOL
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ADVANCED PROTEOMICS

31. Juli – 6. AUGUST 2022
BRIXEN, ITALY

ORGANIZERS:

Bernhard Kuster, Technical University of Munich, Germany
Britta Eggers, Ruhr University Bochum, Germany
Caroline May, Ruhr University Bochum, Germany
Katrin Marcus, Ruhr University Bochum, Germany
Shabaz Mohammed, University of Oxford, United Kingdom
Simone Lemeer, Utrecht University, The Netherlands

REGISTRATION DEADLINE:

31.5.2022

CONFIRMED SPEAKERS:

BEATRIX UEBERHEIDE, New York University, USA
BEN COLLINS, Queen's University Belfast, Ireland
CHRISTIAN HUBER, University of Salzburg, Austria
CONNIE JIMENEZ, Amsterdam University, The Netherlands
DANIEL MOLINA, Pelago Biosciences, Sweden
EDUARD SABIDO, Centre for Genomic Regulation, Spain
FABIA SIMONA, Biognosys, Switzerland
NAGARJUNA NAGARAJ, Bruker, Germany
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JESPER OLSEN, University of Copenhagen, Denmark
JONAS LOHSE, Omicscouts, Germany
KAI SCHEFFLER, Thermo Fisher Scientific, Germany
KATHRYN LILLEY, University of Cambridge, United Kingdom
MEENA CHOI, Genentech, USA
NICK MORRICE, Sciex, United Kingdom
NICOLE ZITZMANN, University of Oxford, United Kingdom
TEJAS GANDHI, Biognosys, Switzerland
THIERRY RABILLOU, CNRS Grenoble, France



3rd - 6th July

2022 BSPR Annual Scientific Meeting

NEXT GENERATION PROTEOMICS

St Anne's College

Oxford

Invited Speakers

Sir Peter Ratcliffe | University of Oxford

Perdi Barran | University of Manchester

Evangelia Petsalaki | EMBL-EBI

Manuel Mayr | Kings College London

Sabine Flitsch | Manchester Institute of Biotechnology

Christopher Tape | University College London

Matthew Collins | University of Cambridge

Anne-Claude Gingras | University of Toronto

Mike Gilette | Broad Institute of MIT and Harvard

Melanie Bailey | University of Surrey

Claire Eyers | University of Liverpool

Alfredo Castello | University of Glasgow

Hagan Bayley | University of Oxford

Pre-conference Workshop

Protein-protein interactions (PPI) and networks

Instructors: **Ed Huttlin** (Harvard Medical School) | **Sandra Orchard** (EMBL-EBI)

MORE INFORMATION TO FOLLOW

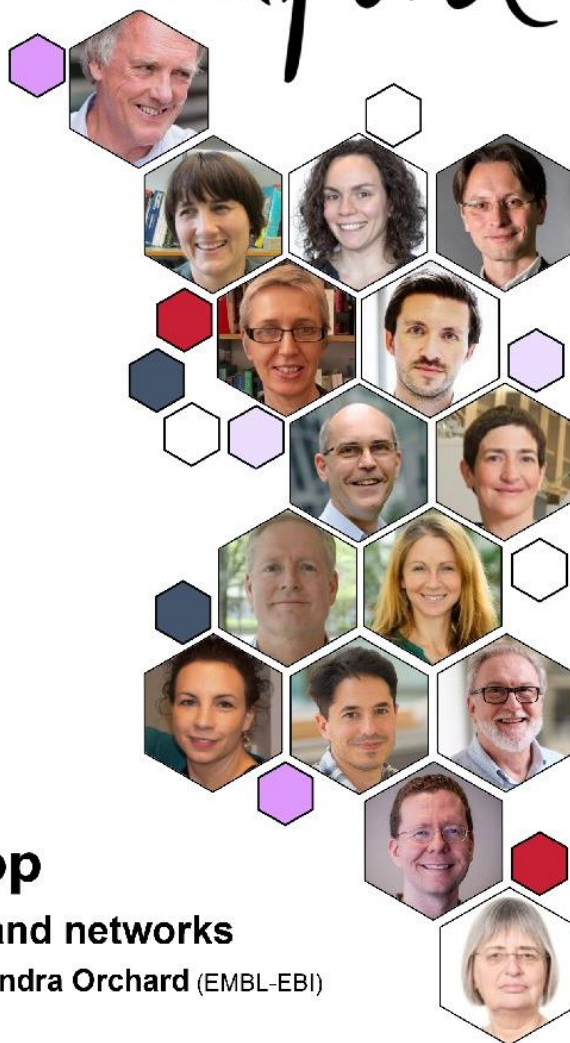
Native/Structural Proteomics | Systems Biology/Networks | Towards P5 Medicine | Chemical Biology |
Bioinformatics | Imaging and Spatial Proteomics | One Health Research | Next Generation Technology

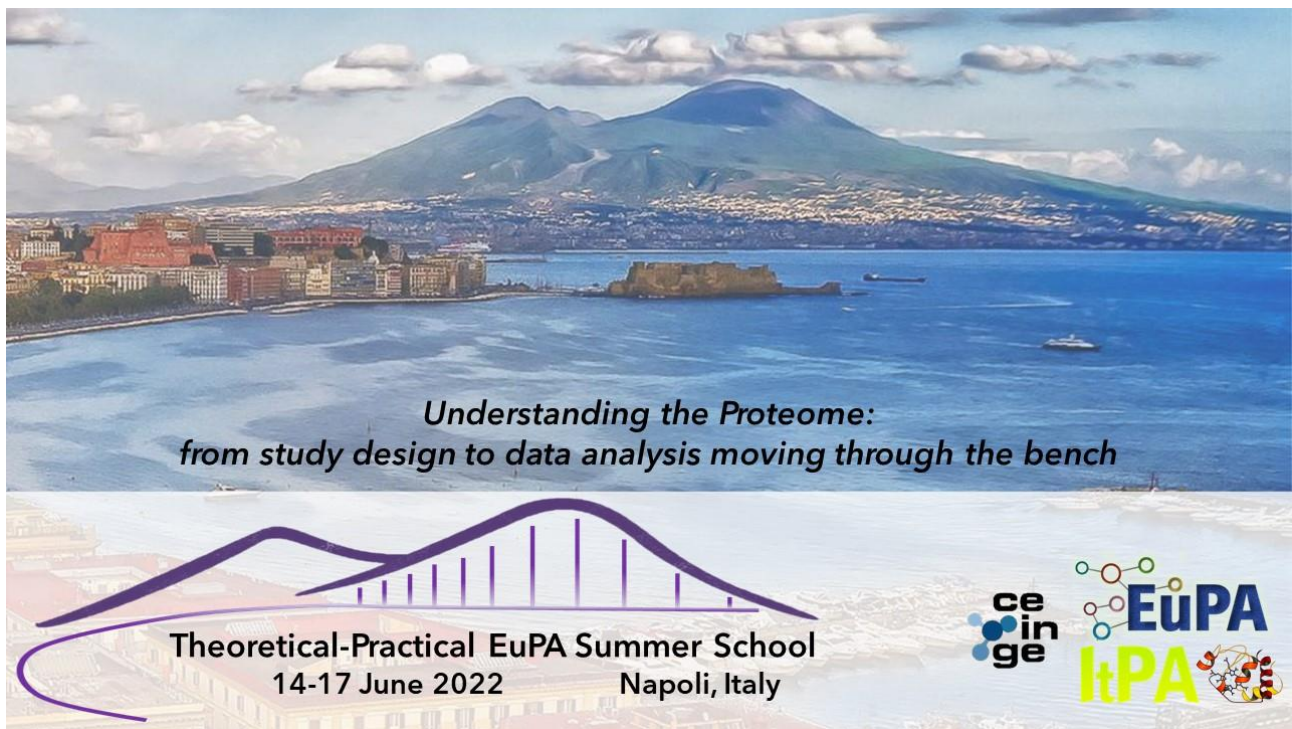


www.bspr.org
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St Anne's College
University of Oxford





You can find more information on the website: <https://itpa.it/index.php/news/eupa-summer-school-dal-14-17-giugno-2022-ceinge-napoli/>

SHORT NEWS

FEBRUARY 11, 2022 – THE INTERNATIONAL DAY OF WOMEN AND GIRL IN SCIENCE

For the celebration of the International day of Women and Girls in Science, the EuPA Education Committee has collected pictures from women working in proteomics field. From the pictures sent by female scientists from all across Europe, a photomosaic was created and posted on the EuPA Website (http://eupa.org/wp-content/uploads/2022/02/We-are-Eupa_VF.jpg).

Due to the high interest, more pictures arrived after posting the photomosaic, so from the previously arrived and new pictures the mosaic was updated and a banner was created, which will be visible during the Proteomic Forum/EuPA 2022 conference in Leipzig.

HELP US TO SHAPE THE EUPA WEBSITE

The EuPA Conferences and Communication Committee is working on the renewal of the EuPA website. If you are a user of the website, please fill out the following questionnaire regarding the website.

<https://docs.google.com/forms/d/1A229oLipETG0XhSVLN2AhqHNzuOf7B7ruMkmJyY8Fys/edit>

A small contribution, can make a big change, as the questionnaire takes only a few minutes but can give us valuable information and can help generating a user-friendly website.

ECR DAY 28TH OF JUNE, 2022 – BOOK THE DATE

The ECR Day will be organized this year as well. It will be held online, in Proteopolis at 28th of June, 2022. More details are coming soon. Hope meeting you there.

CONTRIBUTORS FOR THE CURRENT ISSUE

- *Dr. Nicolas Desbenoit as editor, & Dr. Eva Csoz as co-editor.*
- *Maike Langini & the YPIC team as contributors for “YPIC at EuPA 2022”.*
- *Dr. Francesca Galluzzi as contributor for “Art & Science”.*
- *Prof. Caroline Tokarski & Dr. Stéphane Claverol as contributors for “European Core Facilities”.*
- *Catherine Gilbert & Michael David Tuck as proofreaders.*