EuPA News

Summer 2017
Issue 2

In this issue

Message From The Editors

It is a pleasure for us to launch a new issue of the EuPA News. We would like to stress that the success of this publication is due to the effort, generosity and enthusiasm of the EuPa members. Many thanks to all contributors. You are more than welcome to contribute to the EuPA News content, please send your contribution by **December 15th 2017** to be included in the next issue.

Concha Gil and Natacha Turck
On behalf of the EuPA CCC

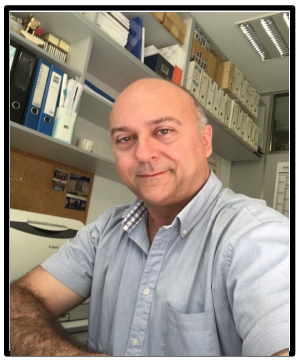
From the EUPA-Committees

News From The Conference and Communication Committee

It is with great pleasure that we announce the launch of the new EuPA portal (EuPA.org) on March 2017. Besides the traditional sections providing information about EuPA, EuPA national societies and the many EuPA activities, new sections are now offered to the reader under an updated format. It is our main objective to offer a platform where news, projects, educational and dissemination activities as well as new initiatives (affinity binder, standardization, biobanking, IMOP and EUBIC) are shared for the benefit of the proteomics community.

The EuPA web site aimed to become a place for sharing experiences and knowledge; we hope therefore to have the pleasure of receiving your inputs to enhance the coverage of the proteomics universe and to promote the interactions among the research community with special dedication to the active young proteomic investigators.

Prof. Fernando Corrales
Coordinator of the EuPA CCC
fcorrales@cnb.csic.es



Meeting reports

ISTANBUL MEETING, EUPA 2016

The X Annual Congress of EuPA was held in İstanbul at Acıbadem University Conference Center between 22-25 June, 2016. Over 300 participants and industry professionals got together in Istanbul against all odds and contributed to a very successful annual EuPA congress.

EuPA 2016 was a collaborative effort of TuPA - Turkish Proteomics Association and European Proteomics Society and the theme of this year was "Challenge Accepted: Standardization and Interpretation of Proteomics". Experts in the field presented new insights within the proteomics community, taking the historical evolution as well as the most important international standardization projects into account.

Participants from 27 countries spanning 5 continents met at Acıbadem University for a 3-and-a-half-day congress and a full EuPA Educational Day.

EuPA Educational day attracted 188 participants with Bioinformatics (entry and advanced level), standardization, cross-linking, LC/MS and biosimilars workshops. A Bioinfomatics Bazaar was also available during the congress where young researchers could find the opportunity to consult with the industry leaders.

Congress main program featured 2 keynote lectures from Prof. Samir Hanash from USA and Prof. Mathias Mann from Germany, as well as 6 plenary lectures and 24 invited speaker lectures.

44 oral and 62 poster abstracts were presented in Istanbul, congress abstract book including all accepted abstracts and invited speaker abstracts can be downloaded from: http://www.evronas.com/files/EuPA2016_Abstract_Book.pdf

Organizers are thankful to the industry who contributed greatly to EuPA 2016. The gold sponsors were Thermo Fisher Scientific and Waters, and 3 satellite symposia were organized by gold sponsors and Bruker. All exhibitors and sponsors are listed in the abstract book and available at the congress website.

The participants were offered a spectacular gala dinner on a cruise along the Bosphorus during sunset. The dinner offered the breathtaking beauty of Istanbul, experiencing both Europa and Asia on both sides of the Bosphorus strait.

TuPA thanks all contributors and participants of EuPA 2016 are looking forward to accommodate the EuPA community in the near future again, with a wider audience and vibrant social program.

Congress website will be available under the end of 2017 at www.eupa2016.com with all available information.

Prof. Aysel ÖZPINAR
Organizator of the EuPA congress 2016
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EuPA Conference and Communication Committee.

On June 23rd 2016 at the EuPA meeting in Istanbul, a new European initiative was inaugurated that will bring together young European proteomics researchers. With a dedicated team of 17 nominated EuPA representatives (**Table**), this **Young Proteomics Investigator Club** or **YPIC** plans to become an established platform for young investigators.

Table: Nominated EuPA YPIC representatives.

Austria	Tamara Tomin
Belgium	Maarten Dhaenens (President)
Croatia	Dina Rešetar (Vice-President)
Denmark	Stefan Kempf (Communication)
France	David Gomez- Zepeda
	Margaux Benhaim (Secretary)
Germany	Christine von Toerne
Greece	Athanasios Anagnostopoulos
Ireland	Jane English (HUPO representative)
Italy	Maurizio Ronci
Netherlands	Meike de Wit (Treasurer)
Norway	Tina Rise Tuveng (Communication)
Portugal	Catarina Franco
Russia	Ekaterina Poverennaya
Serbia	Marija Pljesa-Ercegovac
Spain	Luis Valledor
Turkey	Zeynep Durer

Above all, the YPIC aims at helping young researchers to overcome the day-to-day issues holding them back to unfold their full potential. To find out what that is, YPIC members are asked to fill out **a survey** (https://goo.gl/forms/9gOhlR3JfcrGkBjt2) upon **free registration** (https://goo.gl/forms/FKza2CUC1Kr1YHPL2). Herein new members can reflect on what they would like the YPIC to address. Subjects can be as diverse as facilitating networking, organizing workshops on publishing and public presentations, creating an YPIC member CV database and brainstorming about the future of scientific practice and peer review. Through workshops, a **LinkedInn** group (https://www.linkedin.com/groups/12004091) and networking events, a buzzing community of open communication will help shape the future of Proteomics in Europe.

The one thing all these young scientists will have in common is their fascination for proteins and peptides. To consolidate this solidarity, the **YPIC challenge** will incite new members to engage in a dare that spans the whole of the continent. First, they will need to team up with complementary colleagues (mass spectrometrists, bioinformaticians, wet lab scientist...). When registered with this team, a mixture of synthetic peptides will be sent to them, which they have to analyze as they see fit (no restrictions) in order to decipher **the sentence formed by those peptides**. It is not so much about finding all the words encoded in these peptides, as it is about finding the book where this quotation comes from. Just as in biology, you never elucidate every little detail, but you need to make conclusions about the underlying biological process. As for any scientific challenge, the different teams will then present their methodologies and results in a short manuscript, according to the rules of publication. At the end of the ride, they will have experienced something that is very similar to everyday life: building collaborations, developing experimental designs, analyzing and reflecting on data and writing a scientific manuscript. In this way, YPIC can use their experiences to not only debrief on the outcome of the game but equally use it as a stepping stone for a discussion or workshop on real life in science at **HUPO 2017, September 17 – 20 in Dublin**. Everyone can exchange on their experience there, both in the game and IRL! And of course, the winning team will receive a prize and the eternal fame for having won the very first YPIC challenge.

Finally, the YPIC aims at getting together with other young researcher movements to learn from them and join forces. This interdisciplinarity can one day provide the fundament for building the next generation science. We aim for the stars...

Prof. Marten Dhaenens,

Maarten.Dhaenens@UGent.be

From the EUPA-Initiatives

EuBIC news – Update on the European Bioinformatics Community (EuBIC) Initiative

The European Bioinformatics Community (EuBIC) initiative, supported by EUPA, is an open community of both users and experts in bioinformatics with a special interest for computational mass spectrometry. We provide targeted training and support for every level of expertise (students, researchers, companies), defining guidelines for bioinformatics solutions, development and (re)usage of tools with coordination of software implementation efforts. Our ultimate goal is to make the field of bioinformatics more accessible in the proteomics and mass spectrometry community. In 2016, we have achieved progress on several fronts: (1) organization of bioinformatics hubs, (2) organization of educational workshops, (3) setup of an educational website, (4) creation of a wiki, (5) organization of a Q&A resource, and (6) organization of the EuBIC Winter School as follow-up to the 2015 Semmering meeting.

1- **Bioinformatics Hubs**

The first "Bioinformatics Hub" was organized during the 14th Human Proteome Organization World Congress (HUPO 2015) in Vancouver. The idea was to provide a new space in conferences where participants and experts come together to freely, openly, and informally exchange ideas. This Hub received very positive feedback from the attendees, who unanimously recommended the generalization of the initiative. Only six months after the kick-off meeting of the EuBIC initiative (Dortmund, Germany), we organized a Bioinformatics Hub, the bioinformatics bazaar, during the 10th Annual Congress of the European Proteomics Association (EuPA 2016, Istanbul). We were also involved in the organization of the bioinformatics hubs at the ASMS and HUPO 2016. These events were a success and will most likely be repeated at future conferences including the joint HUPO-EuPA meeting in Dublin (2017) and the Proteomic Forum 2017 (DGPF2017).

2- **Educational Workshops**

Two workshops on proteomics bioinformatics were organized in parallel at the EUPA 2016 meeting in Istanbul, "Entry Level" and "Advanced". These were prepared and presented by five members of the EuBIC community working on different research areas and from different labs (Denmark, Austria, Norway, and France). The entry level covered peptide and protein identification, quality control and validation. The advanced workshop focused on label-free and label-based MS quantification followed by their statistical analysis. These one day events were a good opportunity for participants to discover new freely available tools presented by their developers and/or to discuss challenges in bioinformatics analysis of MS data. It gathered

students and researchers from multiple countries and will hopefully be repeated at future conferences including the joint HUPO-EuPA meeting in Dublin (2017).

3- **Educational Website**

Recently, in partnership with the EuPA Educational Committee (EC), we launched the Proteomics Academy web resource (proteomics-academy.org) as a central communication portal for the EuBIC and EC community's activities and services. The website contains updated information on the available conferences and courses in proteomics and bioinformatics. Its educational section contains videos and online teaching material. The website further integrates the EuBIC online resources like the educational wiki and the Q&A. More content can be added upon request.

4- **Wiki**

We have created a wiki-based system that will act as a central knowledgebase for proteomics bioinformatics (wiki.proteomics-academy.org). This system is, like Wikipedia, open to anyone to contribute and should serve as a central point for bioinformatics proteomics tutorials that are currently scattered throughout the internet and thereby often hard to find. Benefiting from the MediaWiki (www.mediawiki.org) infrastructure, it is easy to edit and enrich, without requirement for programming skills. We encourage the community to register and contribute!

5- **Q&A**

We have set up a central Questions and Answers board (qa.proteomics-academy.org) where we invite everyone to ask (bioinformatics for) proteomics related questions. The members of the EuBIC community will then answer these as quickly as possible. We envisage that this system will become a central point to exchange proteomics knowledge online. The Q&A is open for registration and moderated by EuBIC members.

6- **EuBIC Winter School**

Finally, we are currently organizing the EuBIC Winter School 2017 (January, 10th-13th) on Proteomics Bioinformatics in Semmering, Austria, which will bring together scientists in the field of proteomics and bioinformatics for proteomics (www.fh-ooe.at/eubic-ws17). Internationally renowned speakers, such as Nuno Bandeira, Dave Tabb, Lennart Martens, Oliver Kohlbacher, and Juergen Cox, will talk about current issues in the field of proteomics bioinformatics and will lead discussions on these topics. Afternoons are equipped with practical workshops covering the aspects of identification, quantification, result interpretation, and integration of MS proteomics data. Additionally, participants will have the opportunity to present their scientific work in poster sessions and selected flash talks. All participants will be housed together to encourage interaction and discussions throughout the whole conference. Registration is open until November, 30th (October, 15th for early bird rate). EuBIC is planning to establish a yearly Winter School in this format.

In conclusion, despite its young age, the EuBIC initiative has yielded substantial progress thanks to active and motivated members. We hope that the community at large will join the effort and participate in the activities organized. We currently have active members from 12 EuPA societies, and are looking forward to welcoming new representatives. We are currently reaching out to include young researchers from yet not present countries. All bioinformaticians in Europe are welcome to join us, you can contact us via the proteomics-academy website. You will be part of an active group with a wide range of Europe-wide activities in computational proteomics. Having more active members will benefit the entire proteomics community, every support will therefore be appreciated!

A

B

Figure 1: (A) European countries represented in the EuBIC initiative (based on the affiliations of current active members). (B) Impressions of an Educational Workshop organized at the EUPA 2016 meeting in Istanbul.

	Name	Affiliation
1	Robert Ahrends	Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany
2	David Bouyssié	Institute of Pharmacology and Structural Biology (CNRS), France
3	Viktoria Dorfer	University of Applied Sciences Upper Austria (FH OÖ), Austria
4	Martin Eisenacher	Medizinisches Proteom-Center, Medizinische Bioinformatik, Ruhr-Universität Bochum, Germany
5	Christian Fufezan	Institute of Plant Biology and Biotechnology, University of Muenster, University of Muenster, Germany
6	Vladimir Gorshkov	Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark
7	Michael Kohl	Medizinisches Proteom-Center, Medizinische Bioinformatik, Ruhr-Universität Bochum, Germany
8	Dominik Kopczynski	Leibniz-Institut für Analytische Wissenschaften - ISAS - e.V., Germany
9	Chen Meng	Chair of Proteomics and Bioanalytics, Technische Universität München, Freising, Germany
10	Yasset Perez Riverol	The European Bioinformatics Institute (EMBL-EBI), U.K.
11	Hayley Price	University of Liverpool, U.K.
12	Maurizio Ronci	Mawson Institute, University of South Australia, Mawson Lakes, SA 5095, Australia Department of Medical, Oral and Biotechnological Sciences, University G. D'Annunzio, Chieti-Pescara, Italy
13	Timo Sachsenberg	Applied Bioinformatics Group, Universität Tübingen, Germany
14	Veit Schwämmle	Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark
15	Ugur Sezerman	Department of Biostatistics and Medical Informatics, Faculty of Medicine, Acıbadem University, Ataşehir, Istanbul
16	Alessio Soggiu	Dipartimento di Scienze Veterinarie e Sanità Pubblica (DIVET), Università degli studi di Milano, Milano, Italy
17	Stefka Tyanova	Max Planck Institute of Biochemistry, Germany
18	Julian Uszkoreit	Medizinisches Proteom-Center, Medizinische Bioinformatik, Ruhr-Universität Bochum, Germany
19	Marc Vaudel	Proteomics Unit, Department of Biomedicine, University of Bergen, Norway
20	Kenneth Verheggen	Department of Medical Protein Research, VIB, Belgium Department of Biochemistry, Ghent University, Belgium

Table 1: Participants of the first meeting of the EuPA Bioinformatics Community (EuBIC) initiative at the Leibniz-Institut für Analytische Wissenschaften – ISAS – e.V. (www.isas.de) in Dortmund, Germany ordered alphabetically.

Authors: D. Bouyssié (bouyssie@ipbs.fr)- V. Dorfer (Viktoria.Dorfer@fh-hagenberg.at)- J. Griss (johannes.griss@meduniwien.ac.at)- M. Locard-Paulet (marie.locard@ipbs.fr)- J. Uszkoreit (julian.uszkoreit@rub.de)- V. Gorshkov (vgor@bmb.sdu.dk)- H. Price (H.Price@liverpool.ac.uk)- M. Vaudel (marc.vaudel@uib.no)- V. Schwämmle (veits@bmb.sdu.dk).

EuPA Standardization Initiative: Multicentric Experiment 11 (PME11)

The PME11 was launched on March 2016 with the main goal of providing each laboratory with means to assess its ability and improve their protocols for phosphopeptide analysis. The study allowed for evaluating the performance and reproducibility of phosphopeptide enrichment procedures as well as testing the usefulness of phosphopeptide mixture standard to set up, monitor, and troubleshoot phosphopeptide analysis methods.

Upon optimization of the reference material, each participant received two aliquots of each of the three samples, containing:

- **PME11-A1**: 125 μg yeast tryptic digest plus 500 fmol of each of the 20 light Posphomix phosphopeptide standards (1.1L -1.10L, 2.1L-2-10L) per vial
- **PME11-A2**: 125 μg yeast tryptic digest, plus 250 fmol of each of the 20 light Posphomix phosphopeptide standards (1.1L -1.10L, 2.1L-2-10L) per vial
- **PME11-A3**: 125 μg yeast tryptic digest, plus 100 fmol of each of the 20 light Posphomix phosphopeptide standards (1.1L -1.10L, 2.1L-2-10L) per vial

One additional vial **PME11-B** was also distributed, containing 2 pmol of each of the corresponding isotopically labelled heavy Phosphomix standard peptides (1.1H-1.10H, 2.1H-2-10LH), in dried form.

In order to evaluate the performance and reproducibility of phosphopeptide enrichment, each laboratory carried on a phosphopeptide enrichment of the **PME11-A1, A2 and A3** mixtures. After enrichment, a known amount of the heavy phosphopeptide standard mixture was added to the enriched sample, before LC-MS analysis. This allowed assessing the recovery of the phosphopeptide standards in the enrichment procedure. Each laboratory performed the phosphopeptide enrichment procedure of his or her choice using the three PME11-A1, A2 and A3 samples, saving 1 mg of the sample pre-enrichment to analyze it also by LC-MS/MS.

The phosphopeptides-enriched samples were analyzed both by a shotgun LC-MS/MS method and by a targeted (SRM or PRM) method to monitor the Phosphomix standards. Shotgun analysis results were used to evaluate the general performance of the phosphopeptide enrichment and analysis procedure: number of phosphopeptides identified, mono- and poly-phosphates-containing peptides, and phosphosite assignment. Targeted analysis of the Phosphomix standard peptides was used to measure their overall recovery, and this provided an idea of the yield of the enrichment procedure. A table of putative transitions to be monitored for the standard peptides as well as a Skyline template were provided. Initial samples (pre-enrichment) were also analyzed by the shotgun LC-MS/MS method to check the ability of phosphopeptide identification without enrichment. It was also suggested to analyze the pre-enrichment samples by the targeted method, which can give a hint of the limits of detection for the Phosphomix peptides in a given LC-MS system.

Templates for data reporting were provided. In order to perform a centralized analysis of the shotgun results from all the laboratories, participants were also asked for submiting the mgf files corresponding to every analysis. It is expected that the results of the study should allow assessing and comparing both intra and inter-laboratory procedures or analysis:

- The comparative performance of the enrichment procedures used, measured by the number of yeast phosphopeptides identified, ant its intra-lab reproducibility, on the basis of the results of the triplicate analysis.
- The selectivity of the enrichment procedure, based on the number of mono-, poly- and non-phosphopeptides identified.
- The yield of the phosphopeptide enrichment, based on the quantification of the recovery of the Phosphomix standards spiked in the initial sample. The different concentrations present in samples PME11-A1, A2 and A3 could provide information on any influence of phosphopeptide concentration on enrichment efficacy or detection.
- The correlation of phosphopeptide enrichment yield and the overall performance in phosphopeptide identification.
- The ability of each lab to correctly assign phosphorylation sites, and its comparison to a centralized analysis.
- The ability of targeted quantification of isomeric phosphopeptides through the selection of isomer-specific transitions.

Results were collected from 31 laboratories across Europe. Although the analysis of the data is still in progress, there are some preliminary outcomes:

- The reference material and the multi-centric experiment are useful resources that facilitate testing the performance of each lab.
- The reference material is qualified for intra-lab protocol benchmarking, indicating strengths, weaknesses, and guidance for optimization (Stage-Tip vs batch, glycolic acid vs DHB, sample/medium ratio).
- Overall comparisons are restricted by the use of different protocols and instruments, although improved selectivity of TiO_2 vs IMAC is suggested. Analysis of the actual peptides detected using either method is mandatory to define potential complementarity.

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The Affinity Binder Knockdown Initiative

The Affinity Binder Knockdown Initiative[1] was released at HUPO 2015 under the aegis of Antibodypedia in order to collect data that provide firm evidence on whether an antibody binds to its target protein in a specific manner.

With support from European Proteomics Association (EuPA) and Human Proteome Organization (HUPO), the Affinity Binder Knockdown Initiative was started as a response to numerous discussions in journals and the scientific community about antibody quality and validation procedures. A lot of knowledge on antibody performance resides in laboratory notebooks, and the initiative wanted to encourage scientists to share those data and make them publicly available. Antibody producers were asked to join the initiative and give rewards for positive data submitted. The initiative, which includes Atlas Antibodies, Aviva Systems Biology, Novus Biologicals, and R&D Systems, asks researchers to share validation data from experiments where gene-editing techniques (such as siRNA or CRISPR/Cas9) have been used to verify antibody binding.

Antibodypedia (www.antibodypedia.com), a database designed to allow comparisons and scoring of publicly available antibodies against human protein targets, has managed submissions to the initiative. Each submission has been reviewed, and accepted submissions have been given a score. The sum of scores for an antibody determines the rank. What is known about an antibody is the foundation of the scoring and ranking system in Antibodypedia. In total, researchers have uploaded 301 validations that are accepted and now publicly available in the database. The primary data resulted in validation of 244 antibodies, 57 of which have been validated both by Western blot analyses and by immunocytochemistry assays.

To continue this work, the Affinity Binder Knockdown Initiative expanded on September 30 to become the Antibodypedia Validation Initiative. The initiative currently includes the possibility to validate antibodies using a set of pillars that were proposed by the International Working Group on Antibody Validation (IWGAV). This ad hoc group has made an effort to standardize the best practice for validating antibodies, and resulted in a publication presenting guidelines, "A proposal for validation of antibodies" [2]. The pillars presented are directed to both users and producers of antibodies.

- **Genetic strategies.** The protein is knocked out using genetic methods.
- **Orthogonal strategies**. An antibody-independent method is used.

- **Independent antibody strategies**. Several antibodies are used.
- **Expression of tagged proteins**. The target protein is tagged and analyzed.
- **Mass spectrometry.** The target protein is captured by an antibody and analyzed.

In the new version of Antibodypedia the submission system is updated to allow both providers and users to upload data on the use of one or several of these strategies to validate their antibodies.

To identify good affinity reagents is the key to reproducibility and advancement of science. Most research is in one way or another relying on other scientific findings. A systematic exploration of affinity reagents to verify the quality will improve research outcome in all areas of proteomics. The initiative is grateful for the submitted data. We would like that more researchers contribute to building a user community where data are shared among scientists. Antibodypedia will continue to invite companies to participate in the Antibodypedia Validation Initiative in order to provide rewards for submitted data. Researchers are also encouraged to submit validation data to Antibodypedia for antibodies not included in the initiative with the aim of building a comprehensive knowledgebase of validated antibodies.

To find the right antibody for your research is not an easy task. The number of affinity binders available on the market is enormous. Antibodypedia (www.antibodypedia.com) currently lists more than 2.4 million antibodies. Considering the amount of money spent on research antibodies, estimated to be around $2 billion in 2014, and rising to about $3 billion by 2019, there is a great incentive to profile well-validated antibodies of high quality.

(1) Alm *et al,* Introducing the Affinity Binder Knockdown Initiative—A public–private partnership for validation of affinity reagents, *EuPA Open Proteomics*, **2016**

(2) Uhlen, M., *et al*. (2016). A proposal for validation of antibodies. Nature Methods, AOP.

Prof. Frida Henningson Johnson, Tove Alm, Emma Lundberg and Mathias Uhlen.

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Forthcoming Meeting

THE 2018 EuPA CONGRESS AT SANTIAGO DE COMPOSTELA

"TRANSLATING GENOMES INTO BIOLOGICAL FUNCTIONS"

Dear EuPA colleagues:
During the EuPA General Council meeting that took place in Istanbul last June, it was approved that the 2018 EuPA Congress will take place in Santiago de Compostela (Spain). This was a joint proposal by the Spanish Proteomics Society (SEProt) and the Portuguese Proteomics Association (ProCura) to organize the XII EuPA Annual Congress, where Dr Deborah Penque –president of ProCura– and I will be co-chairs. Both societies have recent experience in organizing major proteomic congresses: the 2010 EuPA Congress, celebrated in Estoril, and the 2014 HUPO Congress, celebrated in Madrid, respectively. After those successful meetings, we will put together our best efforts to organize the 2018 EuPA congress offering an exciting scientific program complemented by attractive social activities. The event will take place from 16-20th June at *Hotel Monumento San Francisco*, an UNESCO protected monumental hotel located in the heart of the old city, which used to be a Franciscan convent and now works as a congress venue (http://www.sanfranciscohm.com/2015).

The driving topic of the Congress will be "Translating genomes into biological functions". Together with workshops and educational activities, the congress official opening will be preceded by the EuPA Young Investigator Club (YIC) session on Sunday 17th of June. During the three following days, the congress will be structured in several non-parallel sessions where all major proteomic topics will be covered, with a major emphasis in proteomics-related mass spectrometry analytical advances and their influence on learning protein biological functions and impact on diseases. Plenary and topic sessions will be combined to make an attractive program where relevant figures in the field will give key lectures together with talks by young scientists submitting their work to each topic session. At lunch breaks we will have specialized symposiums and round tables favouring scientific interactions between all participants. The poster area will be in the cloister, next to the lecture theatres and commercial area. In addition, it is for me a pleasure to confirm that the event will be preceded by the 19th C-HPP workshop, a HUPO activity devoted to present the most recent advances in the Chromosome-centric Human Proteome Project. This latter event will take place on Saturday 16th of June at the Faculty of Medicine of the Universidad de Santiago de Compostela, next to San Francisco Hotel.

I believe this congress will be a perfect opportunity for proteomic scientists around Europe and worldwide to share their experiences and learn about the latest advances in proteomics research. In this regard, the C-HPP and YIC pre-meetings should work as additional attracting poles to guarantee an interesting and successful congress from the first day. We are planning to maintain reasonable fees, in line with recent congresses, making available travel grants for students from EuPA and SEProt/ProCura.

Santiago de Compostela is a historical UNESCO-protected city, capital of Galicia and very close to North Portugal. Famous for its 500 years old university and its pilgrim way, the old city is built around the cathedral. Compostela is a reference city for scientific meetings. It has got an international airport with good connections with Europe, and a good hotel capacity. It is a city used to welcoming people from all around the world and an excellent place to celebrate scientific events. We are sure that the city, the congress venue, and the scientific program will be convincing enough by themselves to make the XII EuPA Annual Congress an attractive event where all of you will find your place.

We hope to see you in Santiago de Compostela in June 2018!

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About the EuPA News

This bulletin is the official newsletter of the European Proteomics Association. It will be on line published (http://www.eupa.org/), being edited by the EuPA Conference and Communication Committee. It will also be distributed by e-mail through the national societies. Depending on the number of contributions received, at least two issues per year are planned. Through short articles it aims at being the vehicle for the dissemination of the EuPA and the different Proteomics National Society activities and initiatives, its committees, and representatives. It also expects to be a platform/forum for discussion and ideas exchange on all areas of proteomics. It may contain information on "who is who in proteomics" (research groups, scientists), books, papers, databases, and announcements of meetings, courses, thesis and job offers. Also brief notes on key methodological or biological issues, complementary approaches, recent relevant literature are very appreciated.

Within the EuPA CCC, the following persons are in charge of the preparation of the EuPA News:

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Instructions to authors

Manuscripts to be published in the EuPA News must be short (no more than four A4 pages, 2 cm margin, 1,5 space between lines in the original submission, that can be no more than two pages in the printed version of the bulletin). Use Times New Roman 12 pt font, except for the title (14 pt, bold type). The authors and e-mail will be located at the end. A photograph of the contributor(s) can be included.

In special cases, and in agreement with the editors, longer contributions can be admitted.

Hands-on workshop on MRM/PRM for multiplexed protein quantitation

MS instruments: Q-Exactive HF™ (Thermo), TSQ Vantage™ (Thermo), Xevo TQD™ (Waters), Triple Quad 6500+ System™ (Sciex)
Data analysis: Skyline

In individual groups (group size max. 5 attendees) participants will learn:

- sample preparation,
- development and optimization of the MRM/PRM approach,
- data acquisition and analysis using different LC/MS systems and software

The hands-on training will be accompanied by in-depth tutorials and lectures.

Key Note Speaker: John R. Yates

Lecturers: Sebastien Gallien & Christoph Borchers

advancing analytics

Registration

Please register under http://isas-events.de

Contact

Events & Services Office

Heike Schweda
E-mail: events@isas.de
Phone: +49 231 1392 102
Fax: +49 231 1392 200

Workshop costs

(3-day workshop, including catering and social program)

EuPA/HUPO Members

Student:	500,- Euros
Academia:	900,- Euros
Industry:	1250,- Euros

Non EuPA/HUPO Members

Student:	750,- Euros
Academia:	1350,- Euros
Industry:	1875,- Euros

All prices including VAT (19%), if applicable

MRM Proteomics

Cambridge Isotope Laboratories, Inc. isotope.com

ThermoFisher SCIENTIFIC

HUPO

SERVIZO GALEGO de SAÚDE | Complexo Hospitalario Universitario A Coruña

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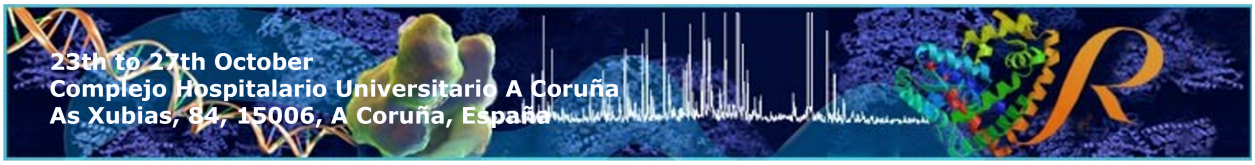
ISCIII ProteoRed



I Clinical Proteomics Course

Maximum number of attendees:
15 (in groups of 3 per rotation area)

Course overview:
This course aims to show:
1) the clinical applications of proteomics technologies to residents in medicine
2) the analytical routines that take place in a hospital to PhD students in proteomics.
The attendees will be incorporated during the morning into the daily working routines of different areas in the hospital, while the afternoons will consist in theoretical lessons on the clinical applications of proteomics technologies and the discussion of their link to what has been seen in the morning.

Hospital rotation platforms:
Histomorphology, Biobank,
Clinical Analyses, Microbiology, Pharmacy.

Registration:
Send a brief CV to
coordinacion@proteored.org

Contact:
ProteoRed Coordination Unit
Centro Nacional de Biotecnología, CSIC
C/ Darwin, 3
28049, Madrid
Spain

e-mail:
coordinacion@proteored.org

Phone:
+34915854668

Audience:
Clinical residents and students in clinical proteomics.

Course costs:
5 days course, including lunch

HUPO Members
200€

Non HUPO Members
300€

All prices including VAT, if applicable

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