EuPA

EUROPEAN PROTEOMICS ASSOCIATION

EuPA NEWS

SPRING 2018
ISSUE 4

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MESSAGE FROM THE EDITOR

It is a pleasure for me to launch a new issue of the EuPA News. Many thanks to all contributors. You are more than welcome to contribute to the EuPA News content, please send your contribution by **November 2nd 2018** to be included in the next issue.

Concha Gil

On behalf of the EuPA CCC

MESSAGE FROM THE EUPA PRESIDENT

The proteomics scientific community is entering in a mature age getting a deeper awareness on appropriate **evaluation and conceptualization** of the experimental activities necessary to pursue a multivariate non-linear description of biological phenomena. While the **technological necessities** have been well described, we still significantly miss an active infrastructure to support the functional interaction of the data with the clinical and industrial applications. The many initiatives need a proper framework to assure the transferability of the concepts and fundamental evidences into practice. EuPA may well play a significant role in providing such a common framework for the integration of these actions. This should also include a **due diligence** program with political stakeholder on the industrialization capacity and sustainability of the EU H2020 financed actions. This is urgently needed in order to develop actual programs with clear milestones and deliverables, avoiding the spoiling of significant resources for the progressive and sustainable development of proteomics field. We should **dominate complexity and maintain focus on priorities** in the development of large scientific proposals. The development of a tight strategic & tactic agenda with **National programs** and scientific societies neighboring the field of proteomics needs to be a primary goal of the EuPA GC for the next years.

EuPA is also built on excellence scientists who have been and are currently involved different initiatives. Their ground breaking works are highlighting the roadmap for the next year actions. These are also providing a priority agenda for the next three years:

- Joined bioinformatics resources, EuBIC – EuPA Bioinformatic Club
- Data submission policy and open access promotion of scientific data
- Coordinated infrastructure program and standardization actions for opening the exploitation of proteomics to the biomedical community

In our **global society** formal educational institutions respond to the primary objective of producing science literate people, nevertheless there is a need for the population at large to appreciate aspects of advanced sciences and technologies. EuPA is committed with its resources to accomplish this fundamental task, providing the fundamental economic support to effectively engage young investigators, in the next years **competiveness and empathy** will be winning paradigms for attracting the early career researcher . This has been the leitmotiv for the development of the YPIC group which has proved its potentiality in the last global conference of Dublin in September 2017. Such a fundamental action will also provide **higher employability** of the young investigators engaged in proteomics research, thus ameliorating the recruiting of talented young scientists. Finally the engagement on the territory mediated and synergized by the National Societies will be further extended in order to provide the critical sustainability on this program.

Prof. Andrea Urbani, PhD.
President European Proteomics Association (EuPA)
Director of the Institute of Biochemistry and Clinical Biochemistry
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FROM THE EuPA COMMITTEES

NEWS FROM THE CONFERENCE AND COMMUNICATION COMMITTEE

The EuPA CCC team is glad to announce its commitment for a new term, with Martina Marchetti-Deschman as web manager and coordinator of EuPA social media with Deborah Penque, Concha Gil as editor of the EuPA News and Paola Roncada with Fernando Corrales coordinating the liaison between the EuPA EC and the EuPA Society Members for the organization of the EuPA Annual Conference.

In 2018 the Spanish and Protuguese Proteomics Societies have organised conjointly a fantastic program in Santiago de Compostela (www.eupa2018.org) amalgamating cutting edge technological and biomedical topics that will be presented by internationally recognised speakers. There is also a fantastic precongress program that includes the EUBIC workshop, the YPIC mentoring day, a Cytoscape course as part of the EuPA Educational Program, and the 19th Chromosome-Centric Human Proteome Project workshop. During the EuPA General Council the next EuPA Congress, hosted by the German Society for Proteome Research, will be presented. Finally, the 2020 edition (HUPO-EuPA Congress) to be hosted by the Swedish Proteomics Society in Stockholm will be announced.

The revamped web page (www.eupa.org) is maintaining an increasing activity in all its sections. Our young investigators (YPIC) have made an outstanding work updating and including new information in their dedicated section (www.eupa.org/ypic/) including the photo gallery, the next challenge, among others. We are looking forward to receiving your suggestions and information to make of the EuPA website a more efficient networking resource.

Prof. Fernando Corrales
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EDUCATION

The 2017 EuPA School on Practical Proteomics took place from the 8-12th October 2017 in the beautiful city of Split, Croatia. It was a workshop dedicated to young researchers (PhD students and Post-Docs) from diverse biological backgrounds with an interest in applying mass spectrometric methods in their projects.

The School was organized by Karl Mechtler (IMP/IMBA Vienna), Jasna Peter-Katalinic (University of Rijeka), Boris Maček (University of Tuebingen), and Janoš Terzić (University of Split) and featured 68 participants coming from Universities of 14 different European countries. About 45 participants were students, while the rest were experts in the field of mass spectrometry and held lectures and/or were involved in the practical sessions of the workshop.
The workshop was evenly divided as: theoretical lecture sessions in the mornings, practical sessions in the afternoons and giving the participants a solid theoretical background in mass spectrometry and its applications (from MS basics, to proteomics, quantification and data evaluation) as well as hands-on experience in sample preparation and evaluation. In between the sessions, there was ample time for the participants to discuss their projects with each other, as well as with the experts in the field, during sunny coffee breaks and poster sessions with pizza, beer and a nice view of the sea. The background from which participants came were diverse, reflecting the range of topics that mass spectrometry can be applied to. Several student speakers were selected and their talks ranged from bacterial and eukaryotic proteomics, post-translational modifications to medical and ecological applications.

The lecture sessions started with the basics of mass spectrometry (Christian Kelstrup) and ventured on the different applications and specializations: Clinical Applications (Andrea Urbani), Human Proteomics (Jesper Velgaard Olsen), PTM Analysis and Interaction Proteomics (Michael Lund Nielsen), Glycomics and Glycoproteomics (Jasna Peter-Katalinić, Sergey Vakhrushev), Bacterial Proteomics (Boris Maček), Plant Proteomics (Karl Mechtler), Proteome Quantification (Kathryn Lilley) and Computational Proteomics and Data Analysis, Statistics and Visualisation (Jürgen Cox, Lennart Martens, Pablo Porras Millan).

While the lectures provided the theoretical background, the heart of the workshop lay with the practical application sessions, where lecturers prepared practical experiments themselves or in collaboration with companies. Different Immunoprecipitation techniques (commercial and self-made) were discussed and tested with the aid of ChromoTek, different tryptic digest/sample preparation protocols with PreOmics, and hands-on experience on the nano-HPLC with Thermo Fisher. The last was insofar remarkable, as Thermo Fisher flew in and set up a nano-HPLC at the University of Split just for the purpose of the Proteomics School. There, students could get their hands on this very sensitive equipment (that usually beginners are not allowed to touch) and try out the handling of the machine and especially learn different ways of preparing and connecting the nano-tubing. After that, the participants got an introduction into MaxQuant and could practice the evaluation of the data produced in the experiments.

Last (but definitely not least!) an extremely useful practical exercise was prepared by Kathryn Lilley: at the beginning of the workshop students were put into groups of four, assigned a research question and had time during the whole course to design an appropriate experiment (from sample generation to statistical evaluation and backup plans). The project plans were then presented at the end of the workshop and discussed and evaluated by their peers and the present experts. (This even included a competition between the groups for the best design – with a prize imported directly from the UK!)

One of the best things of the course, apart from the balanced mix of practical and theoretical sessions was the many opportunities to interact with the different experts, many of which were present during the whole course and always open for questions and discussions.

Also the social aspects of getting to know many people from different fields and exchanging ideas among students was easy in the setting of the course. Located at the Medical Faculty of the University of Split and which offered a superb location for such a summer school, it offered nice seminar and laboratory rooms, as well as coffee breaks with a view of the sea (and, even in October, the opportunity to sea-bathe during the lunchbreak). One evening was reserved for a tour of the historic city center of Split – which, despite an unlucky change in the weather which resulted in 2 hours of downpour exactly during our tour (the only occasion of rain in an otherwise super-sunny week), was a worthwhile experience followed by an even nicer Gala dinner.

In short, the EuPA Practical School of Proteomics provided a good theoretical basis for future mass spectrometrists who come from a biological background, and practical hands-on experience in sample preparation and evaluation. Excellent speakers, a superb setting (the sea view!), good food and excellent opportunity to discuss with experts and peers, made the whole school a success and I am sure that many participants left with many new ideas and good inputs on how to design and proceed with their projects.

For those interested stay tuned for the next course – the “2018 EuPA School of Advanced Practical Proteomics “which will provide a more in qualified experience on cutting-edge mass spectrometric techniques, sample quantification and also feature a focus on cross-linking mass spectrometry.

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EUPA INITIATIVES.

Despite the fact that all other the EuPA EC members have retained their seats, the Initiatives Committee has changed its guard at the last election in Dublin. Andrey Lisitsa, who headed the Committee for 2014-2017 years, has worked hard with the previous members of the Committee for development and maintenance of Initiatives, possessing a flavor of social science perspectives on proteomics. The new Committee is currently composed by Oxana Trifonova (Coordinator, Russia), Åsa Wheelock (Sweden), Garry Corthals (Netherlands), Myriam Ferro (France) and Veit Schwammle (Denmark). In order to continue fruitful work of the EuPA Initiatives Committee established with the goal to promote proteomics associated activities and achievements on a global scale, we are currently looking for new members from national proteomics societies and proposals for new projects. Please contact oxana.trifonova@gmail.com if you wish to join us or for more information.

The principle “Divide and Rule” doesn’t work anymore; we live in an era of social media and we should “Unite and Win”!
See our active initiatives below and support them by joining.

Oxana Trifonova, Ph.D.

Chair of the EuPA Initiatives Committee

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FROM THE EUPA INITIATIVES

EUBIC NEWS – 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 (MS). We provide targeted training and support for the entire community (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. To achieve this, we collaboratively (*i*) organize bioinformatics hubs and educational workshops, (*ii*) develop and maintain online resources that now include a job fair and a page dedicated to grants, and (*iii*) organize international researchers/developers gatherings such as our EuBIC Winter School and developer's meetings.

1- Bioinformatics Hubs

Bioinformatics hubs provide a new platform in conferences where participants and experts come together to freely, openly, and informally exchange ideas. We organize Bioinformatics hubs at numerous conferences including EuPA, HUPO and ASMS. It allows to bring the community together, arrange discussions around specific topics, and provide educational activities. The setup varies from one conference to the other depending on the support of organizers. We continuously work on identifying the attendants' needs and improve the organization of the hubs. Importantly, it has become clear that having a reserved room and an advertised program is essential for the success of the hubs. In 2017, we participated to the HUPO bioinformatics hub and we co-organized the bioinformatics hub at the ASMS in Indianapolis, Indiana (github.com/CompMS/Overview/wiki/ASMS-2017). Each day had a certain topic assigned to, where people could meet and ask the experts. In 2018, we will organize/co-organize the Bioinformatics Hub at the EuPA and the ASMS meetings.

2- Educational Workshops

Together with the EuPA Young Proteomics Investigators Club (YPIC - eupa.org/ypic) and the HUPO Early Career Researcher Initiative (hupo.org/early-career-researcher-ecr-initiative), EuBIC organized the Mentoring Day that took place in Dublin in September before the HUPO meeting (hupo2017.ie). Very prominent speakers lectured about their vision with respect to time management, manuscript writing, grant writing, industrial collaborations / job opportunity, giving and receiving feedback, and work-life balance. At the annual scientific meeting "Clinical Proteomics. Postgenome Medicine" in Moscow (clinprot2017.org), a half-day workshop was held by two members of the EuBIC community. This concerned the topics of reusable workflows for reproducible analyses as well as advanced statistical and multivariate data analysis. We are currently organizing a one-day workshop for the EuPA 2018 meeting that will take place in Santiago de Compostela, Spain (eupa2018.com).

3- Proteomics-academy website

In partnership with the EuPA Educational Committee (EC), the Proteomics Academy web resource (proteomics-academy.org) has become the central communication portal for the EuBIC and EC community's activities and services. Together with YPIC we developed a new job portal for proteomics / bioinformatics jobs which was launched during HUPO 2017. It provides research groups with the possibility to post open positions, as well as researchers seeking jobs the opportunity to post their CV and gain visibility to future employers. Furthermore, with over 30 covered topics, the Proteomics Academy Q&A board has become an agile resource for proteomics bioinformatics knowledge.

4- EuBIC international meetings

Besides participating to the major MS-related congresses, we organize annual meetings dedicated to computational MS. These alternate between winter schools and smaller –more hands on– developer's meetings. The first EuBIC Winter School took place in Semmering (Austria), and has been a great success, with more than 110 attendants from 17 different countries [1]. In January 2018, we organized the inaugural EuBIC developer's meeting in Ghent, Belgium (uahost.uantwerpen.be/eubic18). It kicked off with an interactive keynote session during which several leading scientists in the field of proteomics illustrated outstanding issues in MS-based data analysis, and how bioinformatics plays a crucial role in solving these issues. The main focus of this meeting remained hackathon-style sessions during which the attendees split up into small groups to actively develop bioinformatics applications. The topics for the hackathon sessions were proposed by the community during an open review process and focused on three major topics: (*i*) quality control; (*ii*) workflows, protocols, and guidelines, and (*iii*) quantification. Despite the limited duration of the developer's meeting some very promising results were already achieved, which have sparked continuing international collaborations. A manuscript on the 2018 EuBIC developer's meeting in Ghent is in preparation. We are currently planning the next EuBIC Winter School that will be held in January 2019 in Zakopane, Poland. More information on this event will be announced soon.

Figure 1: Group picture of the EuBIC members at the developer's meeting 2018 (Ghent).

In conclusion, the EuBIC initiative has yielded substantial progress thanks to active and motivated members. We hope that the community at large will continue joining the efforts and participate in the activities organized. We would like to encourage researchers with interest in computational proteomics and mass spectrometry to join us. This can be done by subscription to our mailing list (groups.google.com/forum/#!forum/eupa-bioinfo) where larger tasks are discussed and joining our Slack platform (by contacting one of the EuBIC members) in case you are interested to actively participate in our scientific discussions and events organization. Everyone interested in bioinformatics is welcome to join us, and can get an overview of activities on proteomics-academy.org. By joining us, you will be part of an active group with a wide range of activities.

[1] S. Willems, D. Bouyssié, M. David, M. Locard-Paulet, K. Mechtler, V. Schwämmle, J. Uszkoreit, M. Vaudel, and V. Dorfer, "Proceedings of the EuBIC Winter School 2017," *J. Proteomics*, vol. 161, 2017.

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The PME11 aims to provide resources 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.

After the first PME11 study (manuscript in preparation), several participating groups several ideas were discussed in face to face meetings and conference calls, resulting in a proposal for some additional follow-up experiments. The main goal of this "PME11 Part II" study is to get a more thorough validation of the results concerning one of the main factors affecting the performance of phosphopeptide enrichment, the ratio of peptide sample to affinity resin used for enrichment. The study is designed to test this dependence, by assaying various ratios sample: affinity medium to enrich identical samples, on a multicentric setting. Different labs have been asked to conduct the experiment using either TiO2 or IMAC enrichment, following a standard protocol with the maximum adherence.

A second objective, also proposed on the discussions on PME11 is the comparison of TiO2 or IMAC beads in batch versus the corresponding magnetic beads. The proposal is assaying both formats for phosphopeptide enrichment in similar conditions (identical sample load, ratio sample/resin, analysis). This objective will be conducted at some additional labs that express their particular interest on this issue.

The results of these follow-up experiments should make a valuable contribution to benchmark the different methodological options under evaluation.

The samples to be analysed in the study **(PME11.2A)** consist of a tryptic digest of the human MCF7 breast cancer cell line (C-18 purified), spiked-in with a mixture of 20 human phosphopeptide standards (Phosphomix 1and 2 from Sigma-Aldrich, see attached specification file), containing light isotopes.

Each participant laboratory received 12 aliquots of this sample, containing:

PME11-2A: 125 µg cell digest, plus 200 fmol of each of the 20 light Posphomix phosphopeptide standards (1.1L -1.10L, 2.1L-2-10L) per vial. The samples were distributed in dry form, lyophilized from a water-acetonitrile mixture.

In the preliminary analysis, we have identified only three of the Phosphomix phosphopeptide standards as endogenous in the MCF7 digest. However, their abundance seems to be much lower than the spiked-in peptide standards. Therefore, they should not interfere in the analysis.

Additionally, one vial **PME11-2B** was distributed, containing 3 pmol of each of the corresponding isotopically labelled heavy Phosphomix standard peptides (1.1H-1.10H, 2.1H-2-10LH), in dried form.

SOPs and standardised data reporting formats were provided to the participants and data analysis is ongoing. Plans for future PMEs are currently under discussion, your ideas and proposals will be welcomed; just send them up through the Standardisation section on the EuPA web page (http://eupa.org/eupa-initiatives/standardization/).

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COST ACTION CLININMARK

CliniMark is the Cost Action CA16113 project dedicate to create a necessary guideline & standard platform for a biomarker validation and development to bring novel biomarkers from the bench to the bedside. To pursue this goal CliniMark engage commitment and collective efforts from various research institutions, clinical organizations and industry from about 30 European countries.


CliniMark Meeting, Cascais, Portugal, March 12-15, 2018

There is a broad recognition that increasing adoption of biomarkers in the clinical practice can significantly improve patient's survival and decrease health care costs. Biomarkers have the potential to expedite therapeutic drug development either as putative drug targets or surrogate endpoints in the multistep therapeutic drug development process. As a result, biomarker research has been recognized as a priority worldwide as exemplified by recent initiatives for extensive public and private funding in USA and Europe (1-3). In addition, regulatory and other authorities recognize the need to regulate and standardize biomarker development, as explained in several meetings and reports by the American Food Drug Administration (FDA), European Science Foundation and Organisation for Economic Co-operation and Development. Efforts are also being made to connect biobanks throughout Europe (BBMRI), and to coordinate biomarker validation studies for specific clinical needs (4-6).

Despite these efforts, only few diagnostic and prognostic biomarker assays enter the clinical practice. This is mainly due to the complex and time-consuming processes related to the discovery and validation studies to determine reliable biomarkers to engage regulatory accreditation or qualification for clinical use or drug development.

To address these key issues, CliniMark intends to establish a ‘Good Biomarker Practice’ to facilitate and significantly increase the number of clinically validated biomarkers with particular focus on protein biomarkers.

Proteins are very attractive as biomarkers since proteins are much closer to the clinical phenotypes and are the ones that best reflect a therapeutic response. Moreover, proteins are the main targets of therapeutic drugs. With the progress in development towards swift and high-throughput detection techniques like ELISA-assays, multi-plex immune-assays and mass spectrometry, protein as biomarkers hold a great promise for personalized medicine.

The pipeline from discovery of a protein biomarker to clinical implementation consists of four phases: (1) discovery, (2) selection and analytical validation of a research-grade biomarker detection test, (3) clinical validation of a biomarker, and (4) development and clinical validation of a clinical-grade biomarker assay. Significant hurdles lie within phases 2, and 3 , which explain the large number of identified protein candidate biomarkers and the low number of clinically validated ones. Therefore, the CliniMark will focus on removing hurdles in phases 2 and 3 to increase the number of clinically validated protein biomarkers, rather than increasing the number of protein biomarker discovery studies.

CliniMARK aims to achieve this goal by creating a good biomarker practice (GBP) guideline, which will provide guidance to:

1. Classify protein biomarkers according to their characteristics, anticipated clinical use, and their phase of development,
2. Select and validate appropriate research-grade protein biomarker detection tests,
3. Select appropriately designed studies and biological samples to reliably and reproducibly validate protein biomarkers clinically, and
4. Select and report on appropriate clinical data storage, protein biomarker data storage, data analysis protocols, privacy concerns, ethical issues, and statistical analysis methods.

To demonstrate the value of the generated GBP guidelines, Chronic Obstructive Pulmonary Disease (COPD) will be chosen as a demonstrator project. For COPD biomarkers, the CliniMARK network will compile and classify existing protein biomarker, and for these biomarkers select appropriate research-grade detection tests and design technical validation studies, select appropriate clinical validation study at multiple centres, and select and report on appropriate clinical data storage, biomarker data storage, and data analysis protocols.

Dissemination and implementation of GBP guidelines in protein biomarker research throughout Europe will greatly improve the protein biomarker research capacity by streamlining research initiatives. Therefore, CliniMARK will disseminate the results through channels such as scientific publications of guidelines, LinkedIn groups, conferences, flyers, and publication of reports, among others. An online 'webshop' will be also created where the expertise on biomarker detection technique, available biobanked material, study design experts, and data analysis experts will be compiled and classified. Within this webshop, scientists who are interested in clinically validating a biomarker can enter this biomarker in the webshop, classify the biomarker according to the GBP guidelines and receive an overview of experts in Europe that can provide the appropriate detection technique, biological samples, meta-data, study design, and data analysis tools for that specific biomarker.

CliniMark Action is coordinated by Dr Theo M. Luider, Univeristy and Dr Antonia Vlahou and operates through four working groups: WG1: 'Selection and analytical validation of biomarker detection techniques ' [chair: Dr Bojana Milutinovic , co-chair: Dr Marie Sammar]; WG2: 'Biomarker clinical validation study design' [chair: Dr Peter Groenen, co-chair: Harald Mischak]; WG3: 'Biomarker clinical validation study design' [chair: Dr Deborah Penque, co-Chair: Dr Rainer Bischoff] ; WG4: 'Capacity building' [chair: Ms Andrea Wutte, co-chair: Alain van Gool] that is complemented by an Educational Program (chair: Dr Makis Zoidakis) to coordinate short term scientific missions (STSMs) for the dissemination of "know-how" to young investigators and the promotion of collaborations between different research teams. For more information please visit the CliniMark website http://clinimark.eu/ or contact Theo M. Luider t.luider@erasmusmc.nl.

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FOOD AND NUTRITION PROTEOMICS

The Food and Nutrition Proteomics action was approved in 2017 as a new EuPA initiative. The main objective of this action is to bring together clinicians, veterinarians, food companies, regulatory agencies on the framework of the One Health approach.
In fact, the famous phrase 'we are what we eat' implies that the issues of nutrition and food safety and quality are at the heart of our all days life, and proteomics represents the tool to investigate the food and its effects to our health.

The need to carry out proteomic studies to ensure and improve knowledge of the whole food chain, -including human nutrition - and therefore with a view to non-communicable diseases, involved also the study of the microbiota of food (especially traditional food) together with the human gut microbiota. In this way, proteomics is an important tool for developing new strategies to ensure public health. Other topics, as antibiotic resistance, biotic and abiotic contaminants, strategies to counteract pathogens in food, allergies, outbreaks are at the core of the action.

The action has already begun in 2016 its activities within the Biology and Disease Human proteome Project, and continues with moments of scientific exchange. In Milan, from 22 to 23 March, it supported the 6th workshop of the COST program ’ Improving allergy risk assessment strategy for new food proteins’ where 50 European scientists discussed how to face emerging allergy risks in foods, creating proteomic analysis pipelines for the detection of new allergens.

In addition, the action will organize the meeting "Feeding the Proteome" at the opening of the congress of the Italian Society of Proteomics, in Como, Italy, September 5th,2018. This year's theme will focus on milk as the nutrient, from lactic bacteria to new rapid screening methods to ensure the food safety- and quality of this important product.

Paola Roncada

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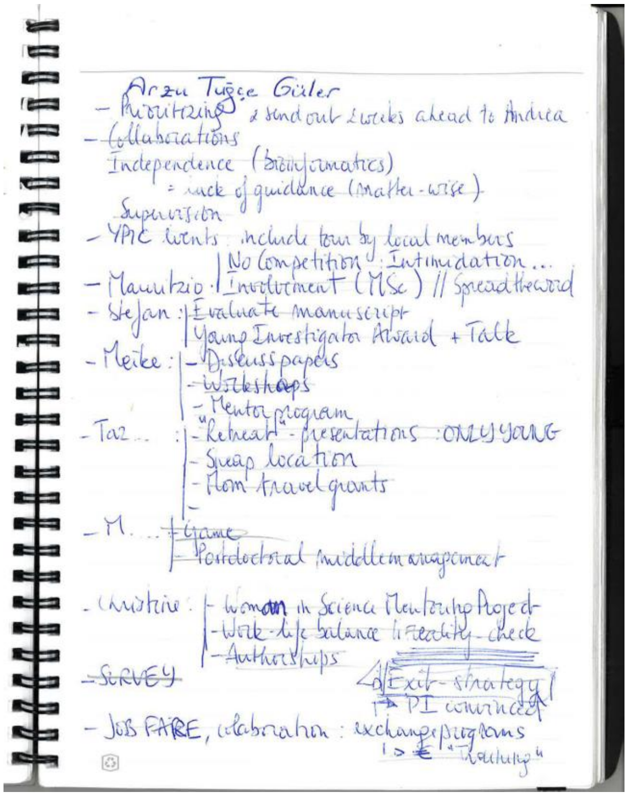
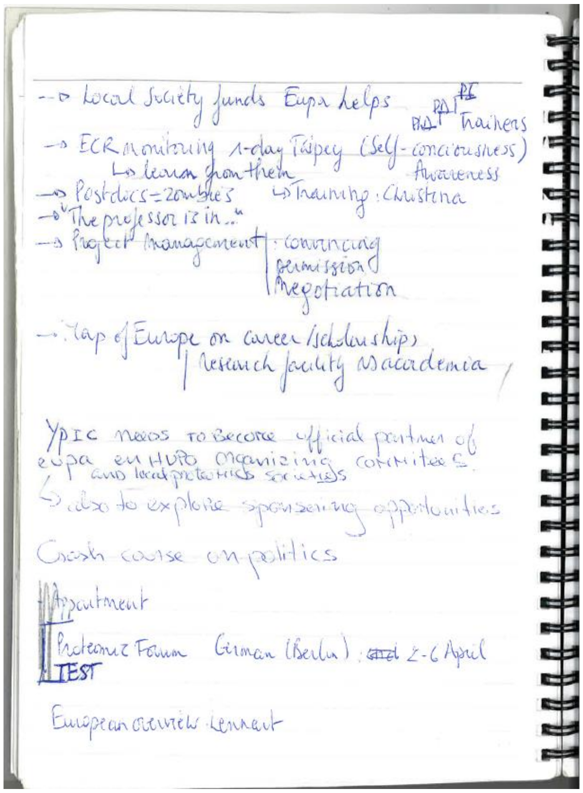
YPIC

In Istanbul, June 2016, EuPA gathered over a dozen young proteomics investigators from just as much different nationalities to inaugurate the Young Proteomics Investigators Club, YPIC for short. Our mission statement was as clear as it was open: help young proteomics scientists throughout Europe to develop their full potential… Following the election of the board, we decided that dinner was pertinent because nobody actually knew what we were supposed to do. Fortunately, apart from delicious, it was also very inspiring. The notes that were scribbled down into a little sketchbook became the foundation for our very first manifest:



Arzu Tuğçe Güler
- Prioritizing & send out 2 weeks ahead to Andrea
- ~~Collaborations~~
Independence (bioinformatics)
= lack of guidance (matter-wise)
Supervision
- YPIC events : include tour by local members
| No Competition : Intimidation…
- Maurizio : Involvement (MSc) // Spread the word
- Stefan : ~~Evaluate manuscript~~
| Young Investigator Award + Talk
- Meike : - Discuss papers
- ~~Workshops~~
- Mentor program
- Taz… : - "Retreat" - presentations : ONLY YOUNG
- Swap location
- Hom travel grants
-
- M… : ~~Game~~
- Postdoctoral middlemanagement
- Christine : - Woman in Science Mentorship Project
- Work-life balance / reality-check
- Authorships
~~SURVEY~~
↳ Exit-strategy!
↳ PI convinced
- JOB FAIRE, celebration : exchange programs
↳ € "Training"



--> Local Society funds EuPA helps
~~PAI~~ ~~PhD~~ PI Trainers
-> ECR monitoring 1-day Taipei (Self-consciousness) Awareness
↳ learn from them
-> Postdocs = zombies ↳ Training : Christina
-> "The professor is in…"
-> Project management : convincing
permission
negotiation
-> Map of Europe on career/scholarships
| research faculty vs academia
YPIC needs to become official partner of eupa en HUPO organizing committees
and local proteomics societies
↳ also to explore sponsoring opportunities
Crash course on politics
Appointment
Proteomic Forum German (Berlin) : ~~and~~ 2-6 April
TEST
European overview Lennart

Admittedly, the president had a hard time understanding and spelling all the names (who is "Taz…"?!) and as the wine kicked in, postdocs turned into "zombies" and nobody could remember what "The professor is in…". But hey, here we are, two years later and having realized nearly everything we wanted!

In summary,

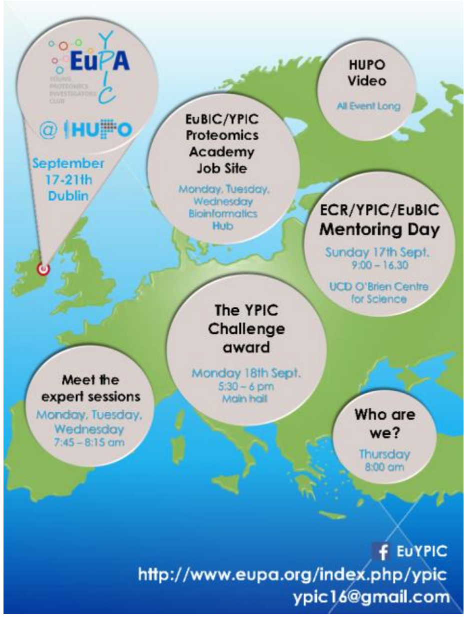
- We started with the obvious efforts **online**: Facebook (Facebook/EuYPIC) and LinkedInn (www.linkedin.com/groups/12004091), a website (eupa.org/ypic) and an e-mail address with google account (ypic16@gmail.com).
- Once in place, we surveyed our (future) members for their interests. The new **survey** is still open for your input btw!
- In the meantime, we needed a way to pop out, to attract attention, to show who we are, to do something unique for our members... The **YPIC challenge** was born.

  The one thing all the young scientists have in common is their fascination for proteins and peptides. To consolidate this solidarity, the first edition of the YPIC challenge incited the members to team up with complementary colleagues (mass spectrometrists, bioinformaticians, wet lab scientist...). When registered, a mixture of synthetic peptides was sent to them, which they had to analyze (no restrictions) in order to decipher the sentence formed by those peptides… It was not so much about finding all the words encoded in these peptides, as it was 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. Seven out of the nineteen teams could crack the code and they presented their methodologies and results in a short manuscript, according to the instructions of publication. At HUPO 2017 in Dublin, the winning team was announced in a special session in the main hall, following the plenary talk of Dr. Albert Heck. The winning team, AxlRose was awarded the very first YPIC challenge award and their PI (Jesper Olsen) proudly accepted the quadrupole! Check our website for details!

- **The second edition is currently ongoing** and open for registration (http://eupa.org/ypic/the-challenge). It goes without saying that we took it up a notch. This time, we expressed the first-ever English sentence in E. coli, with the help of PolyQuant! We have five separate challenges now, each requiring a different expertise. And this time it has become a dare that spans the entire planet! Check it out here: http://eupa.org/ypic/the-challenge. Are you the one who wins the “Three-dimensional Grammar”, “Bioinformazing”, “Protein Punctuation”, “#Bioreactivity” or “Best manuscript”, the main prize? Even the vendors are actively looking for customers who want to take part in this challenge! Check out PlanetOrbitrap and the Nonlinear Dynamics Blog. And if we gather enough teams, we know of a journal that would be willing to attribute a special issue to the first English sentence ever expressed in E. coli and studied by an international team of young scientists! So, the more teams enlisting, the bigger the chance of getting a full-blown publication on your CV! The Award Ceremony will be held at the EuBIC2019 Winter School (online soon!) and broadcasted live, so that every participant can join us!

- That’s all fun and games (and so much more), but a lot of our members also indicated in our survey last year that they wanted us to help them in their next career move. So we joined forces with EuBIC and created a **proteomics job fair,** where employers and employees from industry and academia can meet. Young researchers can even post their CV there! Have a more detailed look at our Poster that we made for the launch at HUPO2017.
- Each year, we have one **conference** where we focus all our efforts on creating an environment where young researchers grow as we try to address their answers from the

survey. Last year, at HUPO2017, we got a lot of gratitude from the people who attended one of our many activities.



- This year, we choose **EuPA2018** in Santiago de Compostella as our hub. You can still register if you want to join us (deadline is June 1st)! Over 50 participants are already coming to one or more of the following activities:
    - The Mentoring Day on Sunday June 17th, 12 am. Some confirmed speakers are Rudi Aebersold, Albert Sickmann, Kathryn Lilley, Bernhard Kuster….
    - Breakfast meet-the-expert sessions
    - Our YPIC Network Hub, to have a drink at night.
    - Our own YPIC session on Tuesday, 19th, just before the Gala Dinner.
- Attending a conference is however not an easy thing to do for young scientists. So, this year we also kicked off a **bi-monthly webinar series**, wherein mentors present an attribute of the scientific career that is rarely discussed. You can check out our first edition with Lennart Martens on YouTube: “*A peek behind the curtain: what happens to your manuscript and to your grant after you've submitted it?*”

So here we are, two years later, reading our statutes that state that “no function can be held for more than two consecutive years”. And thus, we will hold elections at EuPA2018 to create a new board and pass the torch on to a new generation. **Everybody who is a member of YPIC can also apply for the board and make YPIC an influential organization that represents the young generation in proteomics for decades to come.**

We can’t wait to welcome you all!

The YPIC Team

FORTHCOMING MEETINGS

XII EuPA Congress – “Translating genomes into biological functions” Santiago de Compostela, Spain, 16-20 June 2018

Every year EuPA organizes a congress to gather together scientists from all around Europe with interests in the proteomics field. This is good opportunity to present recent proteomics research data, share experience and set up collaborations. This year, the congress will take place in Santiago de Compostela (Galicia, Spain) on the 16-20 June (www.eupa2018.com). This will be a joint meeting with the Spanish Proteomics Society (SEProt) – celebrating our 7th Congress - and the Portuguese Proteomics Association (ProCura), which makes it something special, more than a regular EuPA congress. The Congress will take place at San Francisco Hotel Monumento, right in Santiago de Compostela’s historic city center. Santiago de Compostela is a historical UNESCO-protected city, famous for its pilgrims’ way and its 520-year-old university. It is the capital of Galicia and is very close to North Portugal, which makes it an ideal location for this joint meeting.

We are pleased that just one month ahead of the congress we have guaranteed 250 participants and still expect the number to increase since the early registration deadline ends on the 1st of June, and that same day also ends the late poster abstracts call. Overall, the number of abstracts will be close to 190, among these paper, 69 have been selected for oral presentations distributed between different topic sessions: cellular proteomics, PTMs, data management and interpretation, microorganisms and microbiota, disease proteomics, proteomics in agriculture biotechnology and animal proteomics, standardization and technological innovation, top-down and chemical proteomics, food and nutrition proteomics. In addition, we will have 11 prestigious invited speakers who will be giving lectures distributed between the different plenary sessions. We are especially pleased to have Prof. Ruedi Aebersold to give the Opening Lecture of the congress. Prof. Aebersold will be also named Honorary Member of SEProt for his outstanding contribution to the Proteomics field.

Besides the main scientific sessions, the congress will have various parallel activities. The EuPA Bioinformatics Community (EuBIC) initiative will organize a bioinformatics bazaar that will be available during the congress. In addition, the Young Proteomics Investigator Club (YPIC) will organize a specific session on Sunday 17th early afternoon, before the Opening Session. Moreover, YPIC will also organize meet-the-expert breakfast sessions during the congress. I would like to encourage young researchers to come to the congress and participate actively in all these activities devoted to them. In line with the latter, we also have a very interesting educational program that will take place on Saturday 16th at the Faculty of Medicine, next to the congress venue. We will have two workshops run in parallel: one organized by EuBIC, focused on bioinformatics, and a second one, organized by EuPA, focused on Cytoscape. Those interested in attending these events can still register through the congress website.

In addition to the EuPA-educational courses, a Chromosome-based Human Proteome Project (C-HPP) Meeting - promoted by HUPO - will take place on Saturday 16th and Sunday 17th at the Faculty of Medicine, bringing additional scientific value to our congress.

One of our priorities, as congress organizers, has been to facilitate young investigators to come to the meeting. We are aware the recent economic crisis had a dramatic impact in many labs and so we kept and even decreased the congress fees compared to previous years. Moreover, EuPA is awarding 10 travel grants for young researchers, and SEProt already awarded another 10. In addition, we will have a Young Investigator Prize (YIP), selected among those presenting their application following the acceptance of an abstract. Prizes to the best posters will be also given during the closing ceremony. Talking about prizes, we have two important ones to be announced during the closing ceremony: the Juan Pablo Albar Proteome Pioneer Award 2018, sponsored by EuPA, and the SEProt-Juan Pablo Albar Prize, sponsored by Bruker. The former intends to honour a person involved in EuPA with a leading and long-standing involvement in the promotion of the principles of sharing and integrating resources for the development of excellent research in the Proteomics field. The SEProt prize acknowledges outstanding proteomic-related scientific activities by Spanish scientists carrying out their main work in Spain.

Finally, I cannot conclude this report without thanking the support of all our sponsors; without them, this congress would not be possible. They will be also organizing parallel activities, such as lunch seminars; please check out the congress website for further information.

In conclusion, as chair of the congress, and on behalf of my co-chair, Dr. Deborah Penque, I hope you can join us for this exciting meeting that I am sure will be a reference event for the Proteomics field in 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:

Manuscripts must be sent at conchagil@ucm.es

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 placed 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.