

IN THIS ISSUE

MESSAGE FROM THE EDITORS	2
MESSAGE FROM EUPA PRESIDENT	2
ACTIVITIES OF EC COMMITTEES	
CONFERENCE AND COMMUNICATION COMMITTEE	3
EDUCATION COMMITTEE	5
EUPA JOURNALS COMMITTEE	6
EUPA INITIATIVES COMMITTEE	7
UPDATE OF THE EUPA INITIATIVES.	
EuBIC	8
STANDARDIZATION	13
IMOP	15
COST ACTION CLININMARK	16
YPIC	20
MEETINGS REPORTS	24
EUPA 2018	24
NEXT-GENERATION PROTEIN ANALYSIS AND DETECTION (3RD EDITION)	26
ANNOUNCEMENTS AND COMMENTS ABOUT THE 23RD CHROMOSOMIC-CENTRIC HUMAN PROTEOME PROJECT SYMPOSIUM	29
ANNOUNCEMENTS AND COMMENTS ABOUT THE HUPO / EUPA 2020	31

MESSAGE FROM EDITORS

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.

Concha Gil (conchagil@ucm.es)

On behalf of the EuPA CCC

MESSAGE FROM THE EUPA PRESIDENT

CONFERENCE AND SYNERGISING WITH THE GENOMICS SUPREMACY

Dear Friends and Colleagues,

During the last months we have all been engaged in several discussions on the interest of the scientific community in the current and future developments of proteomics. Most of the comments I have collected are describing a new supremacy of nucleic acids technologies and in particular of genomics which is widely considered the “causative” agents of the reduction of investments and interest in proteomics investigations. I personally prefer to understand the fundamental reasons behind this vision and to possibly sketch a line of action to synergise with the genomics field.

Very often proteomics is considered a technique or at the best a technology based of protein molecules, the research methods papers are still between the most cited contributions within the scientific literature. Nevertheless, the many advancements in this area the basic instrumentations to performed proteomics technologies have been increasing their cost during the last 20 years. This cost profile is exactly opposite to what we have been observing in the field of genomics, in fact, if we considered the initial investment for the sequencing of the first human genome today we may forecast a reduction of 6 order of magnitude in its sequencing cost. Taking the same time span, proteomics investigations have been increasing their costs since the fundamental basic technologies, mass spectrometry, have increased the economic budget for the acquisition of instruments capable to respond to the current (A.D. 2020) protein annotation guidelines and challenges. In fact, instruments producers have been following a strategic line of action which has maximised the continuous development of new instrument release without effectively consolidating the technologies to a basic standard. Such a basic instrument standard can be easily defined as a LC-MS/MS apparatus capable to provide:

- 1) basic protein identification on 10 fmoles scale on prefractionated samples (e.g. SDS-PAGE),

- 2) basic capability for DDA experiment,
- 3) multiplex quantitative analysis overcoming the classical western blot technology,
- 4) providing MZxml data format of all the experimental data.
- 5) Openly accessible instrument acquisition parameters

We miss such an instrumental solution in order to engage the large life science community so as to significantly explore causative molecular relationships associated with the modulation of multiple proteins. A second consideration regarding the underdevelopment of the proteomics field arise from a meta-analysis on publicly available datasets under the (F)indable, (A)ccessible, (I)nteroperable, (R)eusable (FAIR) principles which was published last April 2019 from Perez-Riverol, Y., Zorin, A., Dass, G. et al. Quantifying the impact of public omics data. Nat Commun 10, 3512 (2019) doi:10.1038/s41467-019-11461-w. The snapshot provided in this paper per omics technology provided quite clear numbers: transcriptomics (125,891 datasets), genomics (309,961), proteomics (12,362), metabolomics (2411), multiomics (6578) and biological models (8651). If the proteomics community is finally engaging itself in the data deposition it is still more than 1 log below the current figures of the genomics and transcriptomics fields. This is still limiting the scientific impact of the associated publications which record a constant reduction of citation and consequently of the impact factors of the thematic proteomics journals. In this scenario an action to implement proteomics data into the NGS pipelines and molecular data modelling is most likely the best chance we have to gain a new momentum. I look forward the development of these initiatives which may well found a close translation into novel diagnostic products.

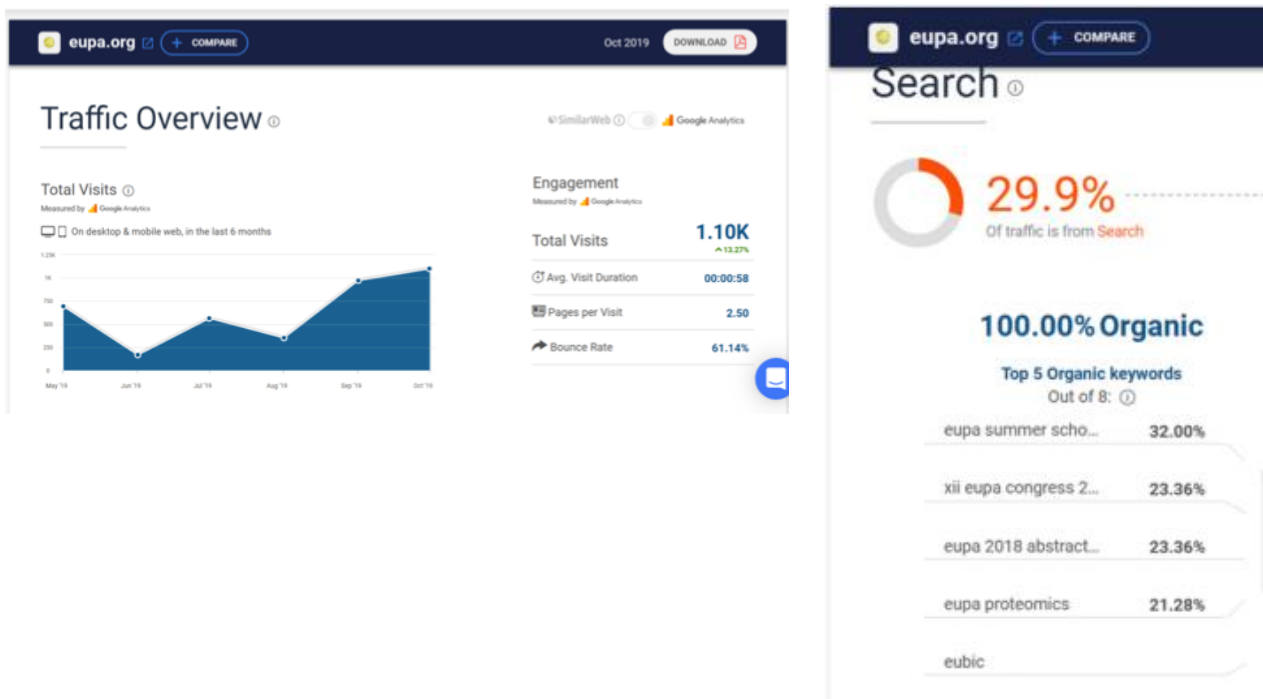
Andrea Urbani (andrea.urban@uniroma2.it)

ACTIVITIES OF EC COMMITTEES

CONFERENCE AND COMMUNICATION COMMITTEE

The aim of the EuPA CCC team is to provide EuPA structures and EuPA members with dissemination channels to ensure the visibility and impact of the programmed activities. To attend the increasing demand of our users, the EuPA web service has been reinforced by incorporating Adan Alpizar to the team, welcome Adan!!! We encourage all proteomics scientists to

share their reports, courses, seminars, and events through the EuPA web page; Martina and I will be more than happy to contribute to the dissemination and promotion of your outstanding activities. Some statistics relative to the EuPA web traffic are indicated in figure 1



The EuPA Annual Conference is the principal event organized by EuPA, representing an excellent framework to share science from colleagues from EuPA Societies and all around the globe. Besides, it is the forum where the EuPA Societies meet and discuss relevant strategic issues. According to the integrative vision of our organisation, the idea of co-organising the Annual Conference has been always considered to harmonize the increasing number of activities in the proteomics domain. This has been the case for HUPO-EuPA Congresses (when the HUPO Congress is organised by an European Society: French, German, Netherlands, Swiss, Spanish, Irish) and in the last two editions, with National Societies including the Spanish Proteomics Society and REDE PROCURA from Portugal (Santiago de Compostela, 2018) as well as the German Proteomics Association (Postdam, 2019), whose reports are published in this EuPA News issue. In light of the success of these events, it was approved during the last General Council to maintain and extend the EuPA integrative policy and that the upcoming EuPA Congresses will be co-organized with the German Proteomics Society (Proteomics Forum) and with HUPO when its Annual Congress comes to Europe. This consensus among EuPA Societies still leaves some open dates for EuPA Conference organization in upcoming years (2022, 2024 and 2028), we do really hope to count on your enthusiasm to organise outstanding events, as it has been done in previous editions. Societies will receive all information to present their bids in due time.

The next EuPA Conference will be held in Stockholm and will be co-organized with HUPO (18-20 October, 2020, www.hupo2020.org). There will be an exciting program in which EuPA must have a principal role; it is time now to propose topics for sessions, speakers, courses, YPIC activities in liaison with the HUPO ECR team, etc. All your proposals will be welcomed and do not forget that we are looking forward to receiving your suggestions and information to make the EuPA web site and EuPA News our reference networking resources.

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EDUCATION COMMITTEE

EuPA Summer School on PTMs analysis, 24-28th June 2019 in Sète, France

After Split in Croatia in 2017 and Vienna in Austria in 2018, the French Proteomics Society together with the EuPA Education Committee organized the third edition of Summerschool end of June 2019 on the French Mediterranean coast, in the nice historic city of Sète. The school focused on post-translational modifications covering all aspects from sample preparation to mass spectrometry acquisition methods and dedicated data interpretation tools.

We had the pleasure to host a group of 54 participants coming over from 13 different countries, including PhD students but also engineers and post-docs.

We take this chance again to thank the renown experts in the field (Martin Larsen, Eduard Sabido, Evgenia Shishkova, Viktoria Dorfer, Marie Locard-Paulet) who accepted to join the group for their generosity and the time spent with us for fruitful scientific discussions and even more...

The program of the 4 days was dense and busy with alternation of courses, workshops on data processing tools, sponsors talks, open discussions and flash talk sessions during which participants took the chance to express their problems and to raise their questions to the experts present. After

deep concentration and hardworking, a refreshing jump in the see (beach was just next door☺) was highly appreciated by all attendees. Indeed, sun and heat turned up on time and contributed to the event's excellent all-round ambience. Lucky us, the meeting room was minimally air-conditioned!

Please find below a few extracts of the reports transmitted by our fellowship recipients and a few pictures.

To conclude, we have had a great time in Sète with a fantastic group of young and highly motivated people: attendance, environment, ambience, good mood and rich and exciting scientific exchanges were “au rendez-vous”!



Christine Carapito, for the French Proteomics Society (SFEAP) (ccarapito@unistra.fr)

Karl Mechtler, for the EuPA Education Committee (mechtler@imp.ac.at)

EUPA JOURNALS COMMITTEE

The EuPA Journals Committee has responsibility for overseeing the relationship between EuPA, the journal publisher Elsevier, the EuPA associated Journal of Proteomics (journals.elsevier.com/journal-of-proteomics), and the EuPA journal EuPA Open Proteomics (journals.elsevier.com/eupa-open-proteomics).

Each journals has its own editor in chief (EiC), who is independently responsible for the operation of the journal to ensure impartiality, but the EuPA journals Committee liaises with the EiCs and Elsevier to maximise the scientific presence of the journal and to promote EuPA and its activities. The EuPA Journals Committee also works with Elsevier to strengthen the links with EuPA and maximise the benefits for both partners.

The last couple of years has been a challenging time for publishing, with many new Journals entering the marketplace, the effects of PlanS and other reviews of the scientific publication system, such as reproducibility of data, impacting publishing, and a significant repositioning of Elsevier and its relationship with learned societies such as EuPA. During this time the Journal of Proteomics has maintained its position as one of the leading proteomics journals, and as a result EuPA has recently successfully renegotiated the relationship with Elsevier that generates income for EuPA and is important for supporting EuPA's training and education activities. EuPA has also been fortunate to have been able recently to appoint Dr Maarten Dhaenens, an active, young researcher leader in proteomics, as Managing Editor for EuPA Open, to work with the EiC to develop and grow this journal for the benefit of the proteomics community and EuPA.

Prof. Andrew R Pitt (a.r.pitt@aston.ac.uk)

EUPA INITIATIVES COMMITTEE

In the era of social media the principle “Unite and Win” works in all fields including science indeed. In Proteomics the synergy of scientific groups with clinics and bioinformatics tools developers is crucial and global approach of involving of more scientists from various institutes to certain project. Such way for the EuPA Initiatives was chosen enabling the progress not only of methodological projects as Standardization but also of more specific as EuBIC and Food and Nutrition, for example. Availability of social networks and increasing number of open access journals allow to make a project more known and reach and engage new members. In order to promote Initiatives activities the EuPA Initiatives Committee consider proposals and support organization of associated events like topic sessions and other events at annual EuPA/HUPO congresses, thematic workshops at National conferences, developers meetings and etc.

We always welcome 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.

See news from our active EuPA Initiatives below and support them by joining.

Chair of the EuPA Initiatives Committee

Oxana Trifonova, Ph.D. (oxana.trifonova@gmail.com)

Update of the EuPA initiatives.

EuBIC

EuBIC: the EuPA initiative for computational mass spectrometry

The European Bioinformatics Community (EuBIC) is the EuPA initiative for mass spectrometry (MS)-related bioinformatics. Its aim is to improve bioinformatics for MS-based research through the setup of community-driven dynamics, thereby improving collaboration, funding, publication, and training activities. Through its different activities EuBIC tries to raise awareness for the benefits of open science and continuously supported open software.

Mass spectrometry data analysis and integration requires proficiency in a combination of scientific fields, including bioinformatics and biostatistics. Despite being of critical importance, research groups often lack sufficient knowledge about these fields. One reason for this lies in the unavailability of adequate educational resources, help and support. We started the European Bioinformatics Community (EuBIC) initiative in November 2015 (Vaudel, 2016) to bring together the MS and bioinformatics communities in an open, collaborative and constructive environment. The initiative is carried enthusiastically by the bioinformatics community and welcomes everyone willing to help.

EuBIC organizes a dedicated yearly conference, bringing together researchers in the fields of mass spectrometry and bioinformatics, junior scientists and industry partners from across Europe. Every year, this conference alternates between a Winter School with keynote talks and workshops, and a Developers' Meeting consisting of collaborative project sessions with the participants (hackathons). Additionally, the EuBIC initiative actively contributes to bioinformatics hubs, and provides various workshops and presentations during international MS (e.g. annual conference of American Society of Mass Spectrometry) and proteomics (e.g. Human Proteome Organization congress, EuPA congress) conferences.

- Winter Schools and Developers' Meetings

The EuBIC Winter Schools on computational MS are sponsored by the European Proteomics Association (EuPA) and several MS companies. They bring together scientists from both academia and industry to present and discuss their research in workshops, keynote lectures, flash talks and poster presentations. We already hosted two Winter Schools, the first one in Semmering, Austria in 2017 (Willems et al., 2017) and the second in Zakopane, Poland in 2019 (Kopczynski et al., 2019).



Figure 1: picture of participants of the EuBIC Winter School 2019.

The Developers' Meetings is an event dedicated to computer scientists and developers, in the field of bioinformatics applied to MS, where they can discuss and work together in an open and constructive spirit. The program is split between keynote lectures and multiple hackathon sessions where the participants develop bioinformatics tools and resources that address outstanding needs in the bioinformatics community and among biologists using MS data. Our first Developers' Meeting took place in Ghent, Belgium in 2018 (Willems et al., 2018).

In total, our three conferences attracted about 250 participants from all over Europe and featured twenty-two different high class keynote speakers from the research area. The next Developers' Meeting will take place in January 2020 in Nyborg, Denmark. This event, like the previous ones, is expected to significantly contribute towards increasing the visibility of bioinformatics applications for analyzing MS proteomics data. Furthermore, as this EuBIC meeting will gather several established experts in the field of computational MS, it will provide the perfect opportunity to nurture fruitful international collaborations. Especially the hands-on sessions will stimulate the start of new collaborative projects. The registration to the Developers' Meeting 2020 has already opened (deadline December 23, 2019) and six collaborative projects - proposed by community members - were selected. More information is available on <https://eubic-ms.org/2020-dev-meeting>.

Recent EuBIC activities:

- Definition of guidelines for reproducible MS data analysis

The number of datasets published on public repositories is in constant increase (Deutsch et al., 2019; Perez-Riverol et al., 2019). This constitutes a highly valuable resource for meaningful biological data

in the form of scientific publications, as well as billions of mass spectra obtained from a wide range of biological samples that can be integrated or re-analysed in other biological contexts. While the quantity of available data is tremendous, there is a growing concern regarding the reproducibility of the associated bioinformatics analysis. The methods sections of research manuscripts, or supplementary files, often do not contain all the information necessary to interpret the analysis results and/or to reproduce them, such as complete and detailed experimental designs, or the correct parameters necessary to run the involved software tools. Therefore, it is necessary to increase the awareness of authors on providing truly reproducible procedures and results. EuBIC started to work on the definition of a new set of guidelines (<https://eubic.github.io/ReproducibleMSGuidelines>) as a support for authors to write complete material and methods sections, as well as editors and reviewers to evaluate data availability of submitted papers. This project is fully community-driven, and we encourage everybody to contribute in order to refine and extend the definitions of these guidelines.

- **New EuBIC website: eubic-ms.org**

In partnership with the EuPA Educational Committee (EC), the Proteomics Academy web resource (<https://www.proteomics-academy.org>) has become the central communication portal for EuBIC since its creation in 2015. To increase the visibility of EuBIC itself, we recently decided to set up a new website dedicated to the initiative at <https://eubic-ms.org>. There, people will find all information regarding past and upcoming EuBIC activities. The EuPA educational activities will remain on the Proteomics Academy. The job fair webpage (<http://jobs.proteomics-academy.org/>) developed in collaboration with the Young Proteomics Investigators Club (YPIC - eupa.org/ypic) remains accessible at the same location. The job platform has recorded several offers over the past months and statistics of November 2019 list 14 open job positions at different levels (PhD, post-doc, staff scientist and bioinformatician). We thus encourage all EuPA members and young scientists searching for a new position to visit this webpage.

- **How to get involved?**

The EuBIC community is open to everybody working in computational proteomics and mass spectrometry. You can join us by sending an email at info@eubic-ms.org or by using the contact form available from the eubic-ms.org website. We will then send you an invitation to join our Slack workspace (<http://eubic.slack.com>), which is our extensively used platform to interact with other EuBIC members. Additionally, you can follow and retweet our latest activities from our Twitter account ([@EuBIC_ms](https://twitter.com/EuBIC_ms)). By joining us, you will be part of a community effort, and thus contribute to the sustainability of these scientific activities, which we expect to foster the development of the computational MS field.

Acknowledgments

The EuBIC organizing committee would like to thank the European Proteomics Association for its support and funding since the creation of the initiative. We would also like to underscore the remarkable work accomplished by all organizers of the previous Winter Schools and Developers' Meetings.

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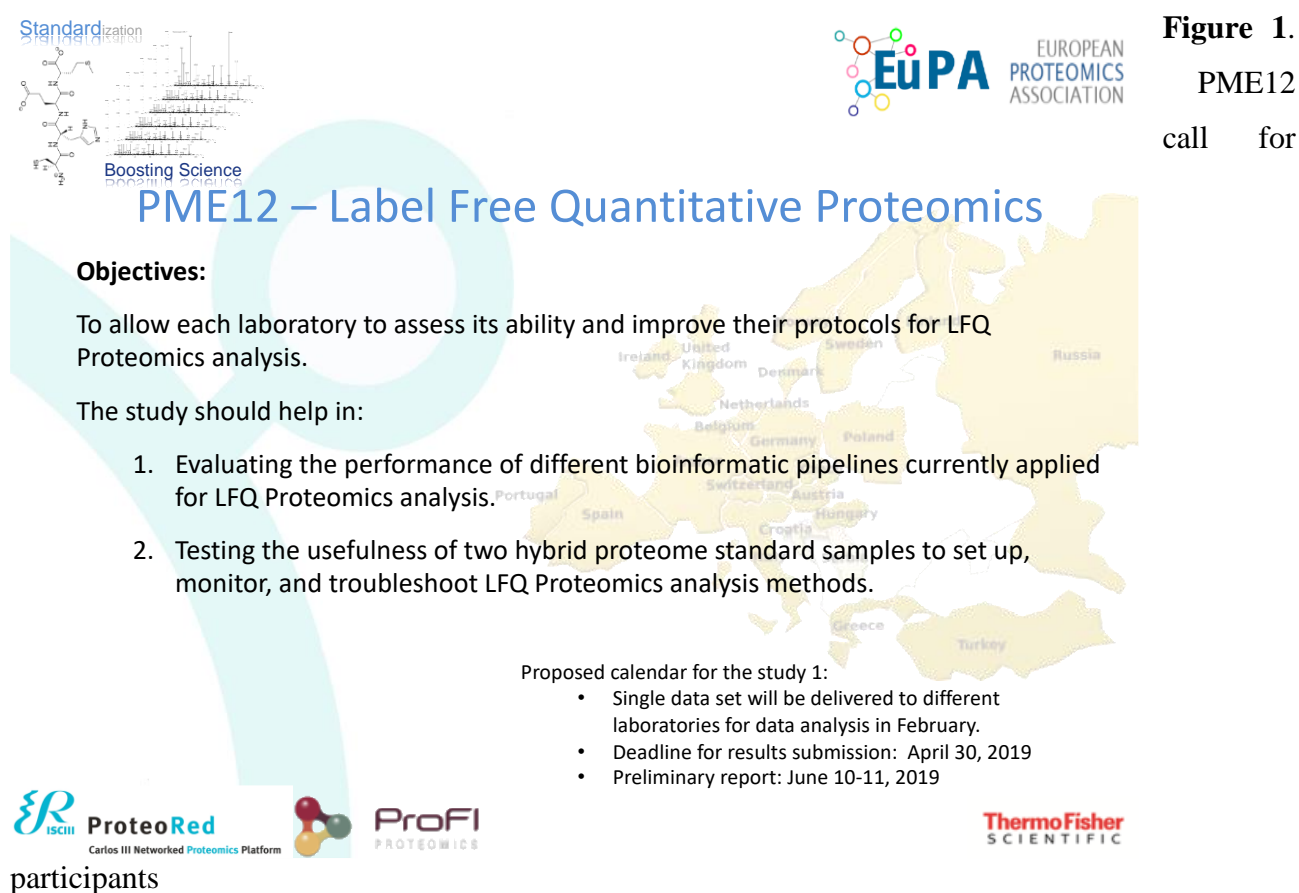
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STANDARDIZATION

EuPA Standardization Initiative. Proteomics Multicentric Experiment 12 (PME12)

PME12 was launched last April 2019 (figure 1) with the following aims:

1. To compare the performance of different label free quantification methods/pipelines on the analysis of an identical dataset
2. To check how robust is label free relative quantification methodology in proteomics
3. To assess the different factors that may affect in the final outcome for a proteomics nLC MS/MS based label free quantification experiment.



Experimental design

Commercially available HeLa, *Saccharomyces cerevisiae* and *Escherichia coli* tryptic digests were purchased, resuspended in milli Q water with 0.1% FA and sonicated for optimal recovery. Peptide extracts were then mixed in different proportions as described by Navarro *et al.* (Nature Biotech 2016) to obtain samples A and B.

	A	B	FOLD B/A
<i>E. coli</i>	20%	5%	0.25
<i>S. cerevisiae</i>	15%	30%	2
HeLa	65%	65%	1

Peptides were analyzed by LC-MS/MS in an Orbitrap LUMOS by quadruplicate where samples were injected in a randomized block way and having a blank run within every sample acquisition. Since provided aliquot was speed vacuumed, sample was resuspended in buffer A containing 3% ACN and 0.1% FA and further sonicated in a sonication bath for 5 minutes. LC-MS/MS acquisition details: 500 ng were loaded to a 300 $\mu\text{m} \times 5 \text{ mm}$ PepMap100, 5 μm , 100 \AA , C18 μ -precolumn (Thermo Scientific) at a flow rate of 15 $\mu\text{l}/\text{min}$ using a Thermo Scientific Dionex Ultimate 3000 chromatographic system (Thermo Scientific). Peptides were separated using a C18 analytical column NanoEase MZ HSS T3 column (75 $\mu\text{m} \times 250 \text{ mm}$, 1.8 μm , 100 \AA) (Waters) with a 120 minutes effective gradient was applied (3% to 35%); Data Dependent Acquisition in high/high mode was applied.

Participants received the database to be used and the raw files for the quadruplicates: Ax4 and Bx4. Each participant laboratory is asked to perform a double data analysis.

- A) Each laboratory was asked to use its own preferred Label Free quantification pipeline against the provided database. Free election of software, statistical parameters and tools.
- B) Each laboratory was asked to use the freely available MaxQuant software, and afterwards use Perseus as statistical tool trying to mimic the previously used own pipeline. In the case of no previous experience with this method, default parameters were recommended.

SOPs and standardised data reporting formats were provided to the participants. Twenty two laboratories participated in the study and submitted their results. Besides MaxQuant, Proteome Discoverer, Peaks, Progenesis, Proline and Proteobotics were used (figure 2), the last two were developed by PROFI and ProteoRed-ISCIII respectively. Data analysis is in process and a preliminary report will be presented for discussion in the ProteoRed meeting that will take place next November 29th in Zaragoza, Spain.

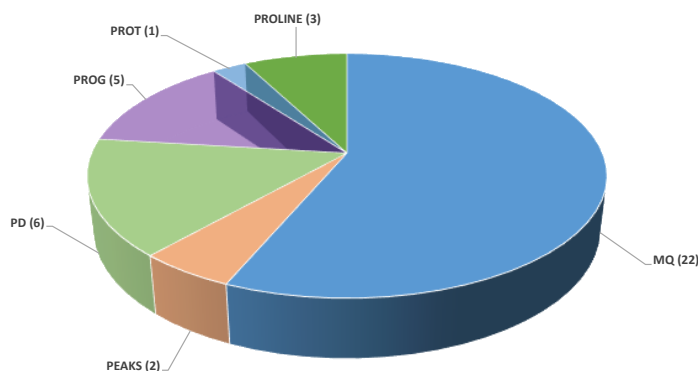


Figure 2. Software tools used by PME12 participating laboratories

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/>).

Data analysis is in process and a preliminary will be presented for discussion in the ProteoRed meeting that will take place next November 29th in Zaragoza, Spain.

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IMOP

iMOP news from HUPO-2019

The iMOP initiative aims to advance non-human proteome research within the HUPO frames. iMOP was launched on a recognition that understanding human biology and health is hampered by a

relatively slow and uncoordinated progress in proteome research on the many non-human species (e.g. food species (farm animals and plants), pathogens and commensal microbes on which all human life and health depends.

iMOP focus on harmonizing technologies across the species-oriented communities, implementing tools and approaches developed through HUPO, including data representation standards, analysis of mass spectrometry data (CompMS), public data repositories and tools that enables the direct integration of human and non-human proteomics data. This is crucial for e.g. areas including zoonosis, comparative biology and host-pathogen interaction studies.

HUPO 2019 held a parallel session on veterinary health, which attracted many new iMOP contributors. An informal post-session meet-up was arranged, and resulted in a common recognition of the need and opportunity to establish a cross-laboratory efforts to improve annotation of farm animal reference proteomes. We chose to undertake improving the current sheep reference proteome as a first step towards a sheep PeptideAtlas database. With a current reference proteome containing only 659 (UniProt), the sheep is by far the least well characterized of our common farm animals, despite its widespread importance in the growing sectors of low input organic farming and also the sheeps increasing importance for nature conservation and sustainable farming.

So far, this first sheep PeptideAtlas initiative includes Emøke Bendixen, Eric Deutsch, Jude Bond, Pawel Sadowski, Nana Satake, with consultancy from the EBI based bioinformatics communities of Sandra Orchard. This initiative is open to all who take interest in improving sheep proteome coverage, and in particular invites partners who can share sheep MS data.

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COST ACTION CLINIMARK

CliniMARK meetings in Greece, fall 2019

The CliniMARK COST action (CA16113) was established in 2017, to increase awareness of good biomarker practice. The action will endeavor to not only establish best practice guidelines for research in this field, but also disseminate said guidelines to the broader research community. As biomarker research gains more ground, the necessity of good practice for discovery, validation and implementation of biomarkers becomes evident.

The potential of biomarkers has been widely recognized for decades, and interest in the field has steadily increased. The implementation of biomarkers in the clinical setting improves the diagnosis and prognosis of diseases and paves the way for the development of new therapeutic approaches.

Thousands of studies are published claiming the discovery of biomarkers suitable for improving disease management. The stark reality, though, indicates that very few potential biomarkers are approved for clinical use. The application of omics approaches in biomarker discovery has contributed significantly to increasing the number of publications reporting initial findings that are not validated. This dire situation has been brought on by the difficulties in analytical validation of robust biomarker assays, flawed study designs, and the inability to exploit the full potential of high-throughput omics approaches. Thus, there is a waste of research resources, as these studies do not produce any tangible benefits to society. Moreover, many clinical needs are currently not addressed by the available biomarkers in diseases of high prevalence and of high financial and social cost such as cancer, cardiovascular disease, chronic kidney disease, and chronic obstructive pulmonary disease. These failures are partly due to a lack of education resources dedicated to omics studies in biomarker research. By establishing good practice guidelines for biomarker research and educating future research leaders on these practices, the CliniMARK action aims at increasing the number of biomarkers making it through the “valley of death” separating discovery from clinical application.

As part of these efforts two meetings recently took place in Greece: 1) the CliniMARK Athens meeting 21-22/09/19; 2) the CliniMARK training school in Spetses on approaches for biomarker discovery and validation 23-27/09/19.

The CliniMARK Athens meeting presented unique opportunities for international collaborations on the dissemination of biomarker practice. During the meeting, participants agreed on a specific plan for writing several publications. Amongst them was a review on analytical techniques for protein biomarker validation focusing on multiplex detection of soluble biomarkers with clinical applications, which should be submitted by the end of 2019. Further, a white paper concerning the necessary alignments between academic biomarker research and the requirements of regulatory organizations, clinical laboratories, and the industry was proposed. Submission of the paper is expected in the spring of 2020. Ideas for other publications, e.g. concerning the role of extracellular matrix remodeling in chronic obstructive pulmonary disease, were discussed. The meeting minutes and above-mentioned publications are available on the COST CliniMARK website (<https://clinimark.eu/>).

Directly following the Athens meeting the CliniMARK school on approaches for biomarker discovery and validation took place in Spetses. A unique feature of the training school was the focus on problems associated with omics biomarker studies and training a new generation of scientists to

be able to fix the flawed biomarker discovery and implementation paradigm. The learning outcomes for the students were to obtain a global view of omics approaches and the biomarker life cycle from discovery to clinical implementation, as well as to acquire skills relevant for biomarker data analysis. Lastly, particular emphasis was placed on the development of student critical thinking by thorough evaluation of published biomarker studies, and on the improvement of writing and presentation skills. The school included an introduction to the different biomarker types and the different omics approaches and their application in the context of biomarker research. Particular emphasis was put on the importance of defining the biomarker context of use in the clinical setting before initiating a research protocol on biomarker discovery and validation. During the course, biomarkers were discussed in the context of academia, industry and clinical applications. The students were introduced to omics approaches in general, and to the specifics of proteomics, metabolomics and genomics in biomarker discovery and validation. Additionally, several talks focused on different methods for biomarker detection and the analytical pitfalls within each technique. Special focus was put on a plethora of mass-spectrometry and immunoassay detection techniques. Particular emphasis was also put on pre-analytical conditions, quality control and the importance of planning for particular implementation contexts. Finally, several examples of current studies on biomarker validation and implementation were given. These examples ranged from biomarkers for obstructive sleep apnea, anxiety and psychiatric disorders to human aging and oxidative stress.

The training school also provided excellent opportunities for interaction between the trainees and the lecturers. Each student gave a short presentation of his or her work, which culminated in several poster sessions and provided many occasions for discussion. The high ratio of lecturers to trainees (24:34) afforded the students several opportunities for fruitful consultation with experts in the field. Indeed, the training school resulted in multiple collaborations; not only between students and lecturers but amongst the attendees as a whole. During the closing ceremony, awards were given for excellence in poster presentations to Joana Pinto and Eda Aydindogan, and for outstanding academic writing to Tenna Vesterman Henriksen. All the presentations and relevant information regarding the training school are available at the CliniMARK website (<https://clinimark.eu/>).

In conclusion, the CliniMARK meetings and training school resulted in multiple international collaborations across different fields of scientific research. The world of biomarker research can look forward to several publications bridging the gap between biomarker discovery and clinical implementation. The planned publications, the established collaborations, and the courses from the training school indicate that the future of biomarker research is bright. Brilliant new scientists enter the field every day, and with proper guidance, they can contribute significantly to the implementation of biomarkers in the clinical setting.



Figure 1: CliniMARK Athens meeting participants



Figure 2: CliniMARK training school participants

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Activities of the Young Proteomics Investigators Club



The Young Proteomics Investigators Club, or YPIC for short, was initiated by the EUPA General Council in 2015 and officially launched as a “blank paper” in 2016 (1). Now, three years later YPIC proudly fights for early career researchers (ECR) within EuPA with the second garniture of elected Executive Committee (EC) members (figure 1). Moreover, through several long-term activities, which

together form the “YPIC pillars” (figure 1), the YPIC board promotes the exchange of knowledge, discussions, network growth and collaboration among ECRs on a world-wide scale. Here, I invite you to a time travel through a third year in the life of YPIC (figure 1).

Personally, I feel the most important characteristic of current YPIC board members is **listening**. Through casual networking and other face-to-face occasions, we have carefully listened to various problems which **young researchers in the field of proteomics** encounter in their working environments. Despite our different origins, cultural, sociological and working backgrounds, several problems were frequently addressed. For example, it was clear that many senior researchers do not fully realize the impact mentoring can have, both on the career development of others as well as their own. Therefore, we started anonymous **surveys on the junior/senior professional relationships** in October 2018 (figure 1). The survey is still ongoing and we expect it to be completed until the end of 2019. However, even though its preliminary results paint a good picture of junior/senior professional relationships, confessions made by a few young colleagues shockingly reveal instances of power abuse, intimidation and sexual harassment behavior at workplace. As I have mentioned, the survey is still ongoing and I therefore invite all our young colleagues to complete the questionnaire and thereby state their own view (2). **Every voice counts and together we have the power to make a difference!** Lastly, to allow the other party to express their opinion on the same subject, a survey intended for senior researchers (mentors) was recently initiated (figure 1). It needs to be mentioned that without the additional effort of YPIC board members **Yasemin Ucal** and **Francisco J. Colina** these surveys would not have seen daylight so soon.

To keep the minds of ECRs sharp and bright, the YPIC Challenge, a proteomic game firstly initiated in 2017, experienced a second edition in 2018. **The Challenge no. 2** was initiated by **Maarten Dhaenens**, the first YPIC president, in collaboration with Polyquant and was heavily advertised online, including the Nonlinear dynamics (a Waters Company) blog (3) and Planet Orbitrap. For the 2nd challenge, a protein, comprising of known sequence of amino acids, was expressed in *Escherichia coli* and the researchers could choose from a variety of experimental approaches.

Depending on the researchers' preferences, they were allowed to choose among several categories: 1. Answer *E. coli*'s question; 2. Three-dimensional grammar (find out how the protein folds); 3. Bioinformazing (develop the coolest bio-informatics approach to decipher amino acid sequence); 4. Protein punctuation (PTMs left by *E. coli*); 5. Bioactivity. As always, to make it more enjoyable for participants the amino acid sequence of expressed protein was actually a (slightly modified) English sentence:

Have You Ever Wondered What The Most Fundamental Limitations In Life Are

Is There A Structure To Respect When It Comes To What You Can Produce In A Cell

In total out of 8 registered teams, two teams survived the complete selection process and made it to the finals. These teams were **Team Fun** – represented by researcher Lili Niu (Clinical proteomics, Novo Nordisk Foundation Center for Protein Research, Copenhagen University) and **Team IgNobels** – represented by researchers Lindsey K. Pino, Andy Lin and Wout Bittremieux (University of Washington, Department of Genome Sciences). In the finals, which took place as part of the official program of EUPA Congress 2019, Lili Niu and Lindsay Pino both presented their struggles while trying to complete the Challenge projects. Finally, after careful consideration and vivid discussion, a panel comprised of four YPIC board members announced that the **winner of the YPIC Challenge no. 2 is Lili Niu** (figure 1). Her effort was awarded during the YPIC challenge award ceremony with a timeless cup, a certificate and a free registration to any EuPA supported congresses or workshops organized in the near future. I use this opportunity to acknowledge the effort of the whole YPIC team for reviewing manuscripts, and especially **Simon Daled**, for sending vials, **Joanna Bons**, for leading email communication with the participants, and **Florian Wiesenhofer**, for technical support at the EUPA 2019 Congress.

While looking back through a third year in the life of YPIC, our main focus was organizing YPIC activities for the **XIII. Annual Congress of the EUPA** held during March, 2019 in Potsdam, Germany (figure 1). This joint effort together with the Deutsche Gesellschaft für Proteomforschung – ECR section (Prof. Dr. Kai Stühler and Nina Schmidt) was met by roughly 250 participants in total, spread through several days and activities. YPIC pre-opened the congress with the dedicated **YPIC Educational (mentoring) Day**, featuring presentations dedicated to ECRs given by renowned experts in various fields of proteomics. Our program continued with the **Meet the expert session**. Here, at round-table discussions, young and curious researchers could ask questions and discuss ideas and directions of their proteomic research with expert pioneers in the proteomics field, all in an informal and relaxing environment. All the experts who have supported our activities at EUPA 2019 Congress by presenting and/or discussing with ECRs deserve to be mentioned here: Dr. Charles

Pineau, Dr. Andrea Sinz, Dr. Marcus Bantscheff, Dr. Kathryn Lilley, Dr. Matthias Selbach, Dr. Lennart Martens, Dr. Mohan Babu, Dr. Stephen Pennington, Dr. John Yates and Dr. Jenny Van Eyk.

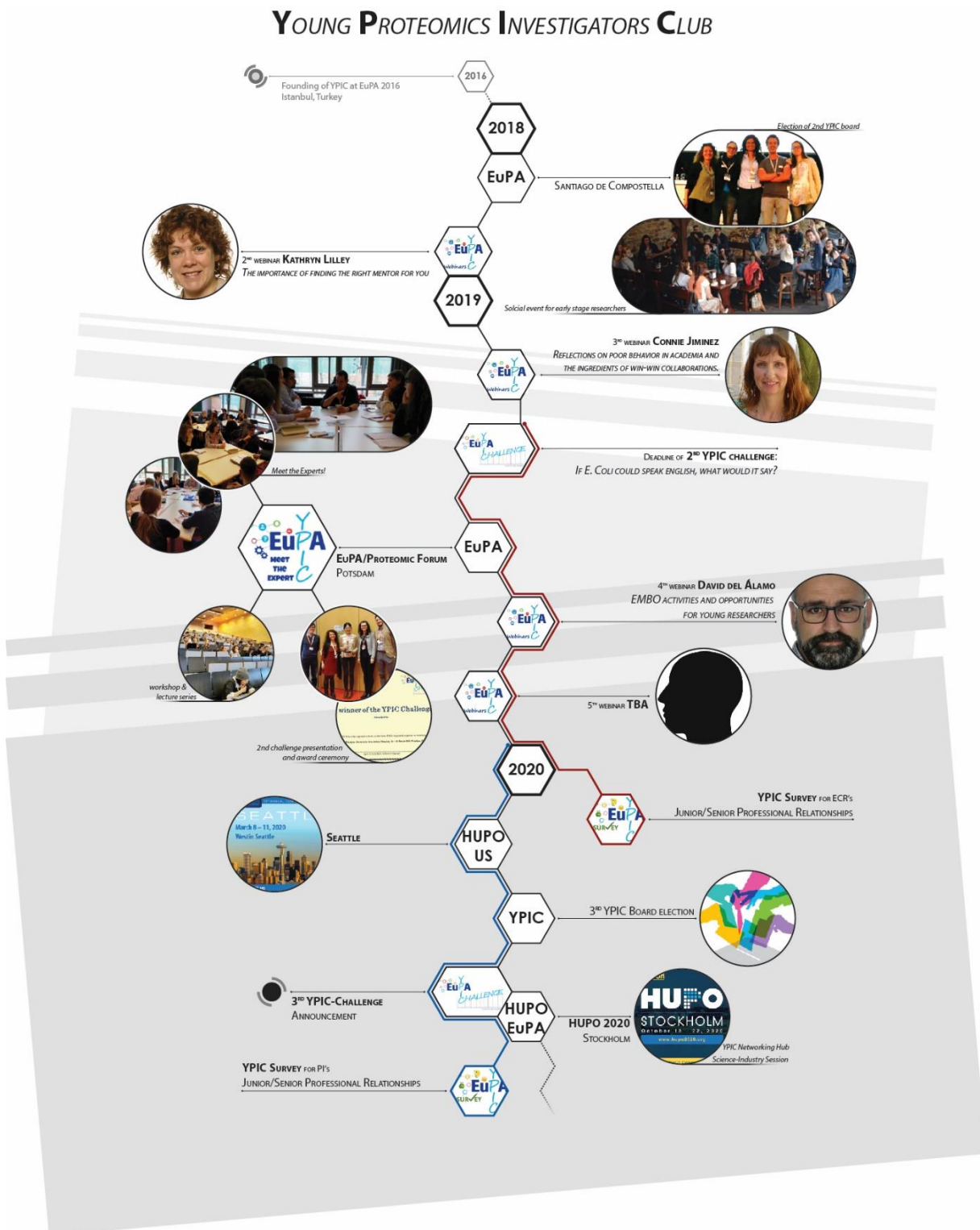


Figure 1. Time travel through a third year in the life of YPIC. Author: **Florian Wiesenhofer** (CD Laboratory of Molecular Stress Research in Peritoneal Dialysis, Medical University of Vienna, Austria)

Moreover, several experts have given their permission for sharing presentations among ECRs, therefore, if interested **do not hesitate to contact us** (ypic16@gmail.com). Finally, for the first time under the umbrella of YPIC activities, YPIC co-hosted **Career sessions** with the aim of training ECRs in skills needed in career planning within and beyond academia. For this occasion, several industry representatives shared their experience and advice with the ECRs: Tobias Börsig (Thermo Fisher Scientific), Dr. Barbara Müller (SERVA Electrophoresis + Decodon), Dr. Christian Scherling (TECAN), Dr. Markus Macht (MS Vision and Dr. Petra Blankenstein (SCIEX). Also, Jörg Scherer (EURICE) and Dr. Matthias Selbach (Max Delbrück Center for Molecular Medicine) joined these sessions. Interestingly, Career sessions were followed with increased attention also by an audience with more experience in their careers, which highlights the added value and importance of the activity. Without the **team spirit** present on-site, successful organization would not have been possible. Therefore, I acknowledge my EUPA 2019 team for their dedication and professionalism: **Alexander Högbe, Florian Wiesenhofer** and **Amir Banaei Esfahani** for chairing sessions, and an especially big THANK YOU goes to the main organizers, **Christian Moritz**, for Career sessions and **Maike Langini**, for Mentoring Day and Meet the experts sessions. Also, thanks to the organizers of EUPA 2019, Dr. Uwe Völker, Dr. Albert Sickmann and EUPA president Dr. Andrea Urbani, who have given us the opportunity to shine again.

Finally, one of the longest ongoing YPIC pillars is the YPIC webinars, so far, with more than 500 live participants and viewers in total. With limited funding preventing ECRs to participate in YPIC activities at international/world conferences, **free YPIC webinars** keep them informed and allow discussions on mostly non-proteomic, but highly relevant topics in academia. Through webinars, ECRs learned about fellowship programs in Europe, the important difference between PI, mentor and a supervisor, how a good mentor can make their professional life easier and which qualities to look for when choosing a good supervisor/PI/collaborator and much more. Most importantly, even when working in academia can be hard, **we have learned to never give up!** Indeed, the YPIC board members strongly believe that for an ECR it is especially important to meet the right people, who are good in giving advices and sharing personal experience, both good and bad. Addressing this crucial step, **Dr. Kathryn Lilley** gave an inspiring talk entitled "The importance of finding the right mentor for you" (figure 1). Following up, **Dr. Connie R. Jimenez** presented on "Reflections on poor behavior in academia and the ingredients of win-win collaborations" (figure 1), which further included preliminary results from the above-mentioned YPIC survey (2). More recently, **Dr. David del Álamo**, the head of the EMBO Fellowship Programme which has funded thousands of early career researchers since 1966, gave an overview of funding opportunities for ECRs as part of 4th webinar entitled "EMBO activities and opportunities for young researchers" (figure 1). We are aware that planning

time for webinars during a workday is sometimes difficult. Therefore, all webinars are freely available on our YPIC YouTube channel (4) and a complete overview can be seen on the webinar page (5). Next to experts, several YPIC board members have significantly contributed to YPIC webinar serial by organizing, hosting and editing, specifically: **Maarten Dhaenens, Florian Wiesenhofer, Simon Daled and Viviana Greco.**

In the end, I would like to show my appreciation to the active YPIC board members. Personally, during the last year I enjoyed coordinating a talented, bright and most of all motivated group of colleagues. Sometimes we were struggling with finding breath between different activities; however, as a reward we have learned a lot about each other and from each other as well as from our experts. I hope that personal growth, common goals and friendship will keep motivating us to contribute further.

To you, dear reader, I hopefully have shown how **EUPA YPIC is all about team spirit and selfless helping, driven entirely by a desire to show to the scientific world that ECRs matter.** The YPIC team already brainstorms and prepares upcoming exciting activities and opportunities for ECRs throughout 2020 (figure 1). To keep these operations going, YPIC is continuously looking for new board members, participants and followers. Therefore, if you see yourself reflected in YPIC, contact us (ypic16@gmail.com), subscribe as a member (1) and follow YPIC on social media platforms (Facebook, LinkedIn, Twitter).

Dina Rešetar Maslov (University of Rijeka, Department of Biotechnology, Rijeka, Croatia)

Alexander Hogrebe (University of Washington, Department of Genome Sciences, Seattle, USA)

(1) How to become a member: <https://eupa.org/ypic/>

(2) Survey intended for junior researchers:

<https://docs.google.com/forms/d/e/1FAIpQLSfkVW4dsWMSzmM6eU6NI1mDmHwo5xjklne1uF-caYol5IrcuA/viewform?c=0&w=1>

(3) YPIC Challenge no 2. on Nonlinear dynamics blog: <http://blog.nonlinear.com/2018/03/19/ypic-challenge/>

(4) YPIC YouTube Channel: <https://www.youtube.com/channel/UCgJ5yXiKIFCZ0kNxMrlRcMw>

(5) EUPA YPIC webinar page: <https://eupa.org/ypic/webinar/>

Meetings Reports

EuPA 2018

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

In June 2018 we hosted in Santiago de Compostela the XII EuPA Congress. As President of the Spanish Proteomics Society (SEProt) it was for me a pleasure to chair the congress together with my colleague Deborah Penque, President of the Portuguese Proteomics Association (ProCura). The Congress took place at San Francisco Hotel Monumento, right in Santiago de Compostela's historic city centre. The number of participants was just over 250, and the number of abstracts close to 190, from which 69 were selected for oral presentations distributed in the following 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 had 11 prestigious invited speakers who gave lectures distributed between the different plenary sessions. Of special relevance was the presence of Prof. Ruedi Aebersold who gave the Opening Lecture of the congress and was named Honorary Member of SEProt for his outstanding contribution to the Proteomics field.

Besides the main scientific sessions, the congress had various parallel activities. The EuPA Bioinformatics Community (EuBIC) initiative organized a bioinformatics bazaar that was available during the congress. In addition, the EuPA Young Proteomics Investigator Club (YPIC) organized a “mentoring day” on Sunday 17th early afternoon, before the Opening Session. This specific session had the active participation of Prof. R. Aebersold, and the invited speakers A Sickmann, K Lilley, B. Küster, and C Jimenez. Moreover, the YPIC also organized meet-the-expert breakfast sessions during the congress. These sessions were very well received, especially by the youngest participants. I would like to thank both the EuBIC and YPIC colleagues for their enthusiasm and active involvement in the congress; we got a very positive feedback regarding the activities they organized; activities that led to open and informal discussions between the participants. This is for sure the kind of activities to keep in future congresses.

In addition to the above parallel events, we also had a very interesting educational program that took place on Saturday 16th, just before the congress started, at the Faculty of Medicine, next to the congress venue. Two workshops were run in parallel: one organized by EuBIC, focused on

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

One of our priorities, as congress organizers, was to facilitate young investigators to come to the meeting. In that sense, EuPA and SEProt awarded 10 travel grants each for young researchers. In addition, the Young Investigator Prize (YIP) and prizes to the best oral and poster presentations were awarded by both EuPA and SEProt. More precisely, the YIP was for Dr. Ilaria Piazza (Institute of Molecular Systems Biology, ETH Zurich). In addition, two important awards were 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 awardee was Prof. Paula Picotti, from the Institute of Molecular Systems Biology, ETH Zurich. The SEProt prize acknowledges outstanding proteomic-related scientific activities developed in the previous two years by Spanish scientists carrying out their main work in Spain. In this case, the prize was for Dr. Enrique Calvo (Centro Nacional de Investigaciones Cardiovasculares (CNIC), for his work *Mechanism of super-assembly of respiratory complexes III and IV*, published in *Nature* in 2016.

Finally, it is fair to say that the congress could not have taken place without the valuable contribution of all the sponsors, some of which also participated actively in the meeting giving lunch seminars. Indeed, it is worth mentioning that the EuPA Industry Award was also announced during the closing session of the meeting, acknowledging outstanding technological developments during the previous year. The awardee in this case was Thermo Fisher Scientific.

In resume, the 2018 EuPA Congress was a total success in terms of participants, scientific contributions, sponsors...and also socially. During that week all the attendees could enjoy the beauty of Santiago de Compostela, its food and social life. The Congress dinner, which took place in *the Comedor Real del Hostal de los Reyes Católicos*, a beautiful historic building, just by the cathedral, was a good example of it. As organizers, this congress was a lot of work, but we really enjoyed both socially and scientifically. Hope to see you back in Compostela soon!!

Dr. Ángel García (angel.garcia@usc.es)

President of the Spanish Proteomics Society (2015-2019), Head of the Platelet Proteomics Lab,

Center for Research in Molecular Medicine and Chronic Diseases (CIMUS), Universidade de Santiago de Compostela (Galicia, Spain).

NEXT-GENERATION PROTEIN ANALYSIS AND DETECTION (3RD EDITION)

Looking back at NGAPA19

Facts & figures:

On 2 & 3 December 2019, VIB welcomed 270 people for the third edition of **Next-Generation Protein analysis and Detection**. This VIB Tools & technologies conference took place in the Aula, Ghent. A mix of academic and company speakers presented their novel technologies in plenary and parallel sessions focused on: Analytical and Clinical Proteomics, Biosensing and Molecular Diagnostics, Recombinant Antibody Tools, Single Cell and Single Protein Analysis, Interactomics and Post Translational Modifications (<https://www.vibconferences.be/events/next-generation-protein-analysis-and-detection-3rd-edition#oc>)



Our conference reporter *An Staes* (VIB Center for Medical Biotechnology) about NGAPA19

When one thinks of protein sequencing, mass spectrometry is the first thing that comes in mind. At the third Next-Generation Protein Analysis and Detection meeting that took place at the beginning of December in wintery Ghent, some skilled speakers showed that other players are arising. By adapting the method for DNA sequencing, it is not only possible to sequence proteins, but also to detect and analyze them on a single molecule level. The technology for protein analysis on this single molecule level is what is still very preliminary in mass spectrometry driven proteomics. Keeping in mind the

fact that tumors contain quite some different cell types, single molecule detection will show more differences that matter compared to healthy tissue. Will this development shift the technology to analyze the proteome away from mass spectrometry in the future? Or will both fields merge and new technologies like mass photometry will take over, which was shown in this meeting to be quite powerful.

DNA sequencing technology has evolved to the stage where it can be applied in the field, and is not bound anymore to the lab environment. Transposing the technology to protein sequencing would inevitably mean taking protein sequencing to the field as well using very small devices. Opposed to the more high-end proteomics which is still very lab restricted.

Nevertheless, quite some nice biological questions were addressed and exploited by the use of novel and clever mass spectrometry-based technologies. Looking into the matter from a different angle such as digging into the waste bin of the cell aka the proteasome or the surfaceome instead of the regular cytosolic shotgun proteome, discovers quite some new insights. Moreover, resulting conclusions can be more easily implemented for treatments and diagnostics.

Concluding from quite some work presented here, mass spectrometry is still evolving quite extensively, and new technologies are ahead that shift proteomics by mass spectrometry to another level.

Not only a shift in analysis was proposed, even moving away from the very well-established use of antibodies for diagnostic tools was addressed. Furthermore, on the level of detection, bioluminescence was proposed as a very powerful alternative for fluorescence, again a well-established and widely used technique. Since bioluminescence does not have a background problem in plasma as fluorescence has, it is of high interest for diagnostic tools.

Last but not least, artificial intelligence is also taking its first steps in the world of proteomics, showing insights and tendencies in the data that no human brain could ever cover. Using the already extensive data that is present, a lot is to be learned by machine learning that can be used to create data of higher quality by the use of better and more classifications.



The Next-Generation Protein Analysis and Detection meeting opened the world and the mind of both genomics and proteomics people to look passed the borders of their field and join forces in the battle against diseases evolving into a next-generation of omics people.

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Announcements and comments about the 23rd Chromosome-Centric Human Proteome Project Symposium

Dear Friends and Colleagues,

The 23rd Chromosome-Centric Human Proteome Project Symposium (C-HPP2020) "FROM CHROMOSOME-CENTRIC PROJECT TO THE HUMAN PROTEOME" will be held in Russia from 15 to 18 May, 2020, aboard a ship traveling from Saint Petersburg to Valaam Island and back to Saint Petersburg. The Symposium will address the main challenges associated with the development of bioinformatic methods for the transition from chromosome-centric project to the human proteome of separate organs and tissues, taking into account individual and population transcriptoproteomic data, followed by the application of these data in medicine. The application of nanotechnology for the analysis of individual molecules and sensitivity assessment of methods for determining the depth and width of the proteome will be discussed. There will also be discussed the impact of OMICs on medicine.

The scientific part of the symposium will be composed of the following scientific topics:

1. Status update from Chromosome and neXt-50 teams
2. Bioinformatics Tools Development –from C-HPP to HP
3. Transcriptoproteomics – the way from Genome to Proteome
4. Proteomics Technology Innovations
5. Proteomics and other OMICs - Impact on Medicine
6. Missing proteins in rare tissues and diseases (with B/D-HPP)

The Symposium will be held on a river-class cruise ship, traveling along the rivers and lakes, at the same time visiting numerous attracting places between sessions. Such way of conducting the Symposium gives an opportunity for many informal and fruitful discussions between participants combining the high level of the scientific program with the visiting of some cultural and historic places of Russia.

We look forward to seeing you soon.

Prof. Alexander Archakov, Chair (c-hpp2020@ibmc.msk.ru)



23rd Chromosome-Centric Human Proteome Project Symposium



FROM CHROMOSOME-CENTRIC PROJECT TO THE HUMAN PROTEOME
10th Anniversary of the C-HPP Initiative

15-18 May, 2020

Saint Petersburg – Valaam Island – Saint Petersburg, Russia



The Symposium will be in Honor of Prof. Alexander Archakov's 80th Birthday and 75th Anniversary of the Institute of Biomedical Chemistry (Moscow, Russia).

SCIENTIFIC TOPICS:

- Status update from chromosome and neXt-50 teams
- Bioinformatics tools development - from C-HPP to HP
- Transcriptoproteomics - the way from genome to proteome
- Proteomics technology innovations
- Proteomics and other OMICs - impact on medicine
- Missing proteins in rare tissues and diseases (with B/D-HPP)

For more information about registration and abstract submission
please visit the official website.

Email: c-hpp2020@ibmc.msk.ru

Website: c-hpp2020.ibmc.msk.ru



Announcements and comments about the HUPO / EuPA 2020

CELEBRATE LAUNCHING THE HUPO DECADAL HUMAN PROTEOME PROJECT BLUEPRINT AT HUPO 2020 IN STOCKHOLM

Dear Colleagues,

The 19th Human Proteome Organization World Congress will take place at the stunning Waterfront Congress Center in Stockholm, Sweden. Under the theme of '*Clinical Proteomics for the Benefit of Patients*', the HUPO 2020 World Congress will bring together biopharma and biotech drug developers. For the first time, we also hope to have the pharmaceutical industry actively participating in a HUPO Congress.

Proteomics advances will be theme of this Congress with dedicated sessions for systems biology, and disease areas like oncology, cardiovascular diseases, pulmonary diseases, neurodegenerative diseases and infection/immunology. These are areas of great importance that show tremendous impact in the quest for new directions in treatments, early indication of disease, as well as biomarkers and diagnostics that can aid in optimal drug selection and use for the patient benefit.

In addition, the Human Proteome Project (HPP) will celebrate a milestone decadal birthday by releasing the first community-endorsed high-stringency blueprint draft of the human proteome. It was only two decades ago that a company (Celera Genomics) and public competition called the Human Genome Project jointly assembled the draft human genome. This draft contained far fewer protein-coding genes than was ever anticipated and was jam-packed with gaps and ambiguities. Recent data suggests that the human genome only codes for ~20,000 proteins. Armed with the draft genome, HUPO's first challenge was to assemble a parts-list blueprint of the human proteome. This initial phase involved an unparalleled collaborative enterprise, this time involving research scientists assembled from over 100 countries around the globe – each with different skill sets, and all freely uploading and communally analyzing and integrating this proteomics data. This collaborative approach now culminates in the production of a high-precision human proteome knowledgebase. Some researchers sought to find the elusive missing proteins that dodged discovery whilst others sought to appreciate how the proteome knowledgebase could be harnessed to better diagnose and treat cancer, Alzheimer's disease, heart attacks, diabetes and other diseases.

Join us in Stockholm, Sweden from October 18 – 22, 2020 to celebrate the launch of the collaborative Human Proteome Project blueprint.

Important Dates

Abstract Submission Opens	February 2020
Registration & Housing Opens	February 2020
Abstract Submission Deadline	May 22, 2020
Scholarship Submission Deadline	May 22, 2020
Abstract Notifications	July 3, 2020
Early Registration Deadline	July 15, 2020
Regular Registration Deadline	September 2, 2020
Congress	October 18 – 22, 2020

Sincerely,



Gyorgy Marko-Varga (gyorgy.marko-varga@bme.lth.se), HUPO 2020
World Congress Chair, hupo2020@icsevents.com , www.hupo2020.org

HUPO | **STOCKHOLM**
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19th Human Proteome Organization World Congress