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MESSAGE FROM THE EDITORS

There has been a long time since the last issue (number 5) appeared; more than one year ago. When the idea of the bulletin was conceived, we planned 6 issues per year, then moving to 3-4 per year, and in the way of none per year. This is, first, my fault as responsible, but I would like to share it with all of you, members of the EuPA, in general, and those with clear responsibility

as leaders of the EuPA (President, Vice-President, and coordinators of the different Committees), and of the different national societies, in particular. Despite the number of mails sent, no contribution was received during this 2012. I do not want to be insistent and I understand to persecute people is or should not be my job. I also understand that accepting responsibilities within EuPA or National Societies implicates, among other, to contribute to the bulletin. I am starting to think that no contribution means no need of the bulletin, am I wrong?. Apart for this, there have been changes in the direction of the EuPA and its committees, new policies have been discussed, new persons have been involved in the different tasks, and this also justifies this long silence. The last, but no the less, Christine Hoagland has made a change in her professional life, with no possibility of continuing as co-responsible of the bulletin edition. If we got the five previous issues was because of Christine: She has done a huge and incredible amount of very good work, not only with the bulletin, but also with the web page. Christine, thanks a lot, I will, and for sure the EuPA also, miss all your work and input. Fortunately, I am also sure you will be on the other side of the screen. From saying goodbye to hello and welcome, first to Natacha, the new co-responsible with me, and second to all the national representatives who accepted to be members of the “editorial board” with the compromise of contributing and distributing these bulletins and relevant news among their societies.

This is the working board group that I expect make this project a successful, realistic, and regular one:

Martina Marchetti-Deschmann (Austria), Marek Sebela (Czech Republic), Salla Kangas (Finland), Luc Camoin (France), Hans-Joachim Kraus (Germany), Tsangaris George (Greece), Alessandra Modesti (Italy), Connie R. Jiminez (Netherlands), Bernd Thiede (Norway), Angel Garcia Alonso (Spain), Gyorgy Marko-Varga (Sweden), Ozge Can (Turkey).

This is the right time to wish no just the best for the coming year, but, as Spanish, that the crisis does not bring us a worse year. This will be more than enough. It is not a matter of proteomics but just of sciences.

Merry Christmas,

Postscript. I EXPECT YOUR CONTRIBUTIONS FOR THE NEXT ISSUE.

Jesus V. Jorrin Novo

MESSAGE FROM THE PRESIDENT

Dear EuPA-Members,

It is with great pleasure and excitement that build the organisation with new initiatives and new member states. The EuPA bulletin is an important communication channel to reach out to each and every one.



We welcome Poland as a new member into EuPA and there expanding our organization. I would also draw your attention to our new homepage www.eupa.org, where we have improved and updated information and details related to Proteomics, including our courses, meetings and other engagements. The EuPA engagements in the EU-COST program (European Cooperation in the field of Scientific and Technical Research) on *Mass Spectrometry Imaging: New Tools for Healthcare Research*

We are very proud of the EuPA journal “Journal of Proteomics” that is developing strongly, publishing a lot of the science of EuPA member undertaken within our laboratories. At the executive meeting we had in Siena in August, we decided that we would start up a EupA electronic journal as a strong complement to “JOP”. We are happy to have Peter Verhaert as the Editor in charge; we feel a strong engagement from his side taking on this responsibility. Let’s all join in congratulating Peter, and support him in his new role by submitting proteomics developments and studies to the new journal. Christmas is closing up and we all will have some pace with family, children and friends so let me at the same time wish you all a peaceful holiday rest.

Best Wishes GYORGY

Gyorgy Marko- Varga

President of EuPA

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From the EUPA-Committees

NEWS FROM THE CONFERENCE AND COMMUNICATION COMMITTEE

The new Conference and Communication Committee was arranged at the end of 2011 and will be in charge for the next three years. It is currently composed by Luca Bini (Coordinator, Italy), Juan Calvete (Spain), Christine Hoogland (Switzerland/Australia), Jesus Jorin (Spain), Martina Marchetti-Deschmann (Austria), Deborah Penque (Portugal), Natacha Turck (Switzerland) and Peter Verhaert (Belgium/Netherlands). First of all we want to thank the previous committee coordinated by Concha Gil for its excellent work, having increased the visibility of EuPA all around the world. Our committee wants to continue the efforts to increase EuPA’s international recognition mainly through the coordination of EuPA congress organization and EuPA workshops, through the development and maintenance of the EuPA website and through modern communications media. Therefore, we are currently working on the following projects:

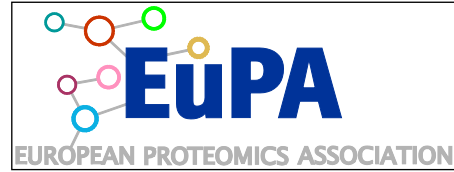


- **A new EuPA Logo**, realized in collaboration with a graphic designer and Deborah Penque from the CCC. The new logo is now available and represents EuPA's main mission which is to connect national Proteomics organizations and to facilitate collaborations and exchanges in the field of proteomics (colored circles with connections).
- **A new website**, built by a web designer under the supervision of Martina Marchetti-Deschmann and Christine Hoogland from the CCC. The new website was launched at the beginning of September and is accessible at www.eupa.org. It is designed to be simple, modern and easily accessible, with a new graphical design and all the important and essential information presented at a glance.
- **A new journal**, called **EuPA Open Proteomics**, was approved by the majority of the national societies during the last General Council in Glasgow. It is the official owned journal of EuPA and Elsevier is supporting the society as the publisher. The format is Open Access in accordance with modern demands. Peter Verhaert has accepted to be the editor in chief and is currently putting together the editorial board. The main scope of the journal is to publish high level scientific papers from young as well as senior scientists in all area of proteomics, but it is also the way to distribute news from our society, including the next issues of the bulletin. In order to increase the visibility of EuPA Open Proteomics, all EuPA members are kindly requested to submit articles.
- **EuPA Scientific Meeting**. The next three scientific meetings are already established as follow: 2013 Saint Malo (France), 2014 Madrid (Spain, joint meeting EuPA/HUPO), 2015 Milan (Italy). A new call for the 2016 will be open soon, to be voted during the next General Council in Saint Malo.
- **New EuPA Bulletin**: A new editorial board composed of representatives from all national societies has been created. This editorial board will work with the two editors from the CCC, Jesus Jorin and Natacha Turck, to realize next issues that will be probably published in EuPA Open Proteomics. If some national societies have not yet nominated a representative, please send the name to the two editors as soon as possible.

Luca Bini
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EuPA WEB SITE

THE KING'S NEW CLOTHES – REDESIGNING THE WEBSITE WWW.EUPA.ORG



After seven years the website definitely had to change. But independent from the field - redesigning is always critical.



For websites this means, one can like or dislike a webpage.

So a decision has to be made:

Choosing a mainstream layout the acceptance for a website will be very high, but it easily gets shallow and the recognition value is expected to be low.

Going for extraordinary designs, definitely catches the attention but as everyone is distracted by animations, colourful objects or breath-taking pictures, the visitor does not remember the actual content EuPA wants to distribute.

Already in April 2012 a workshop for the new EuPA website was held in Geneva. Christine Hoogland in her function as the administrator for the former website provided all her knowledge and experience necessary to set up a new concept. Half a day of brainstorming on the basic demands and content of the website lead to an agreement on general needs for the website:

- easy to look at
- up-to-date
- modern, simplified design
- better visualization of EuPA liaisons, educational activities and company interactions

Also the decision to stay with the established content management system of Joomla but to update it to the most recent version was made. It was also agreed upon the fact that the transfer of the old content to the new website has to be outsourced and the proposal from Christian Stephan (EGHOS GbR) was then accepted within the next month. Beside others this proposal was outstanding in terms of prize, availability and references (Christian Stephan



already built the website for the DGPF). The decision on the new EuPA logo was the starting point for the next changes.

In June 2012 the basis for the design in terms of colour and style was given Christian Stephan designed and structured the new website in close collaboration with Martina Marchetti-Deschmann.

In a pre-evaluation phase the result was presented to the Conference and Communication Committee and after streamlining all ideas and further suggestions from this step the new website was first presented at the General Council in Glasgow to the national EuPA representatives for approval. From that on the website was continuously improved and is now in an acceptable stage.

To keep the content up-to-date a student was hired to scrawl the internet for interesting events and news. It is also the responsibility of this person to update information on a monthly basis by contacting EuPA representatives, the EC coordinators and the EuPA secretary for GC and EC reports.

To keep our platform alive, EuPA asks you to contribute to the website. Please submit events and job announcements or suggest interesting topics for our educational activities.

Martina Marchetti-Deschmann
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EUPA OPEN PROTEOMICS: A NEW EUPA-OWNED JOURNAL

EuPA and Elsevier have a successful existing partnership since 2006 with the establishment of *Journal of Proteomics*. They now decided to continue this successful collaboration to launch a new title, *EuPA Open Proteomics*. This new EuPA society-owned journal will operate using the open access model. The journal will publish on all aspects of proteomics and cover the complete spectrum of proteomics, including bioinformatics and data processing. *EuPA Open Proteomics* will welcome manuscripts from plant, animal, microbial and human studies. *EuPA Open Proteomics* will also accept submissions from authors wishing to report on large data sets (submitted to raw data repositories) and descriptive studies. The journal will welcome short preliminary studies that warrant rapid publication. Manuscripts will be judged on scientific rigor, quality and novelty. The new journal will include original research papers, short communications, letters, meeting reports, technical reports, data records, etc. This will also automatically make the EuPA-owned journal the primary source of EuPA reports and publications and the platform for the publication of papers from young European scientists.

EuPA strongly felt that the journal would need a clear captain on the ship who acts as the main driver and initiator for developing new strategies, innovation (especially in new data formats) and acts as a EuPA voice. EuPA is really pleased to announce the appointment of **Peter**

Verhaert as the Editor in Chief. Peter is since 2005 full professor and group leader at the Faculty of Applied Sciences at Delft University of Technology (Netherlands). He has a long-standing experience in peptidomics and the characterization of biologically active peptides. He is also active in mass spectrometry imaging and analytical miniaturization. Peter will have the key mission of selecting very carefully a highly competent Editorial Board for the management of the conceived journal and bring this new Open Access journal towards success.

Jean- Charles Sanchez (on behalf of the EuPA Executive Committee)
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THE HUMAN DIABETES PROTEOME PROJECT (HDPP). A NEW HUPO INITIATIVE LED BY EUPA SCIENTISTS



Diabetes prevalence has increased dramatically during recent years with rising numbers of individuals suffering from relative (type 2 diabetes mellitus, T2DM) and absolute (type 1 diabetes mellitus, T1DM) insulin deficiency. The majority of individuals with diabetes have T2DM, a disease now approaching epidemic proportions not in the least among young individuals. This rise is correlated with an increased prevalence of excess weight and obesity, with an incidence above 25% for those conditions in Europe and other regions. To slow down and ideally prevent this epidemic, deeper knowledge of the pathophysiological mechanisms responsible for impaired function of the multiple organs and cell types affected is required.

We propose to leverage a worldwide constellation of expertise into the Human Diabetes Proteome Project (HDPP) initiative to generate systems-level insights into diabetes-associated cellular changes. This will be achieved by gathering multivariate data sets over time from specialised cells and organs of healthy and diabetic individuals.

Diabetes is a complex condition encompassing genetic, environmental and lifestyle factors. Therefore, only a highly interdisciplinary international collaboration can deliver the multidimensional insights needed to understand the cellular pathways that are of particular relevance to diabetes and its associated complications. Systems biology data sets will be collected from fluids, organs and cells of human origin, as well as from tissues and cells of model systems of the disease. More specifically, the biological effects of chronically elevated glucose and lipid levels, reflecting the situation for individuals with T2DM and obesity, will be investigated. The research results obtained by the consortium will be shared among members of the group and made available to the wider research community through public repositories as well as in the neXtProt data integration platform.

The HDPP is expected not only to deliver comprehensive information on the disease mechanisms but also to identify proteins and isoforms associated with diabetic pathogenesis, thereby facilitating the development of better diagnostics, therapies and prevention strategies. The HDPP initiative was launched at the 2012 HUPO meeting in Boston with a dedicated workshop. A public website with information about the project and the partners is available (hdpp.info). As a short-term milestone, the consortium is building a list of proteins of interest to the field of diabetes. The list (with associated resources such as proteotypic peptides and affinity reagents) will be evolving and maturing over time and made available on the HDPP web site. A number of proteome databases dedicated to human islets, β -cells and glycosylated proteins detected in blood under different glycaemic conditions will also be deployed in 2013.

Finally, the opportunity for the HDPP to be part of the HPP initiative as a whole will generate favourable conditions for collaboration and information exchange across all C-HPP and B/D-HPP initiatives.

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CHROMOSOME CENTRIC HUMAN PROTEOME PROJECT - THE CHROMOSOME 5 CONSORTIUM

Sequencing of the human genome made raw information accessible that constitutes and governs the biochemical background of human life. In this enormous amount of information approximately 22000 human genes were identified, which comprises around 2% of



information stored in the complete human genome. Molecular products from approximately 7700 of these genes were never observed at the protein level and from approximately 6000 of genes only transcripts have been detected¹. One of the most



probable reasons for these missing proteins is the large dynamic concentration range of expressed proteins. In fact proteins cannot be amplified similarly to information stored in mRNA and DNA, and must be measured at concentrations present in the biological samples. Despite the considerable advance of mass spectrometry in the last decade, this technique still cannot cover the full dynamic concentration range of expressed proteins, which may be as large as 11 orders of magnitude in the case of human serum samples². Other

reasons could be related to the currently dominant database search peptide identification approach, which is based on similarity calculations of measured fragment mass spectra with *in-silico* generated mass spectra calculated from protein sequences stored in databases. In fact only 40-60% of the measured fragment mass spectra are generally identified, although an important part of non-identified spectra are of high quality. High quality non-identified spectra may belong to peptides modified with non-synonymous single nucleotide polymorphisms or by alternative splicing. In addition proteins may undergo chemical modifications after translation – posttranslational modification (PTM) – leading to several chemically different protein products from a single gene. This creates an enormous chemical space to discover, and despite intensive research in analytical methods such as the selective enrichment of peptides with specific modifications and in bioinformatics, most peptides with PTM remain unidentified.

The Human Proteome Organisation has started an ambitious project in 2010 – the Chromosome Centric Human Proteome Project (C-HPP), which has the goal to catalogue as many gene products as possible and link them to the chromosome and gene locations. C-HPP (Figure 1) consists of 25 consortia corresponding to 25 chromosomes (22 autosomal, X, Y and the mitochondrial chromosome)³. There is one or several biological projects included in each consortium providing biological material such as cell lines, tissues and body fluids, which tries to link protein identification to biological function. The diversity of biological projects covers many diverse protein expression events and PTM of proteins and will serve to identify the tissue and subcellular localisation of proteins. The main technological pillars supporting the C-HPP are knowledge based (bioinformatics), mass spectrometry and antibody based proteomics approaches.

Collaboration between chromosome consortia implies the establishment of standard operation procedures for sample acquisition, sample storage in biobanks, analytical measurements, data processing and interpretation as well as data and sample quality control. Chromosome consortium members will share biological samples, analytical measurement capacities, analytical protocols, and reagents such as antibodies or synthetic peptides, bioinformatics expertise and acquired data. Bioinformatics is a key point for the C-HPP project and contribute extensively to organise data sharing, and data dissemination through the proteomeXchange portal⁴. Consortium members are developing several bioinformatics tools to explore the observed proteome linked to chromosomes and genes, to integrate mass spectrometry and antibody based proteomics data with transcriptomics data and work out novel peptide identification methods. The acquired data will be not only shared between chromosome consortia but also deposited in public databases, such as for fragment ion spectra in PeptideAtlas⁵ and GPMDB⁶, MRM data in the PASSEL database⁷, status on protein evidence in NextProt⁸, UniProt⁹ and multiple protein information in chromosome based protein browsers such as CAPE¹⁰ or TPB¹¹ to mention a few examples.

The C-HPP project was launched in 2010 at the HUPO meeting in Sydney and all C-HPP consortia were finalized in 2012 in HUPO meeting in Boston. The Chromosome 5 team was among the last consortia to be formed and is one of six consortia having their base in Europe. Rainer Bischoff and Péter Horvátovich at the University of Groningen lead the consortium. When it comes to Biology, we collaborate with the research group of Professor Dirkje Postma

studying the development of COPD, asthma and lung cancer at the University Medical Center Groningen. Postma's research group is an international leader in lung research and disposes of a rich source of lung related cell lines, human tissue and large transcriptomics datasets that were acquired during the differentiation of bronchial epithelial cells studying lung cancer and asthma development. This research group recently identified protocadherin-1 as a susceptibility gene for asthma development, a gene that is located on chromosome 5¹². We believe that characterisation of the product of this gene will provide additional insight into asthma development and will provide tangible impact for human health. The consortium is further supported by the research groups of Professor Manfred Wuhrer at the University of Leiden Medical Center and VU University Amsterdam providing access to advanced glycopeptide analysis methods using CID and ETD fragmentation, and by the research group of Dr. Henry Lam at the Hong Kong University of Science and Technology developing spectral libraries and automated identification tools for mass spectrometry data acquired for glycopeptides. Our consortium will work closely together with five consortia having their base in Europe (Chromosome 2, Pierre-Alain Binz, Switzerland; Chromosome 14, Jérôme Garin and Charles Pineau, France; Chromosome 16, Juan Pablo Albar, Spain; Chromosome 19, Gyorgy Marko Varga, Sweden; mitochondrial chromosome, Andrea Urbani, Italy) for example by developing and assessing common data acquisition and processing pipelines and sharing efficiently tasks between partners.

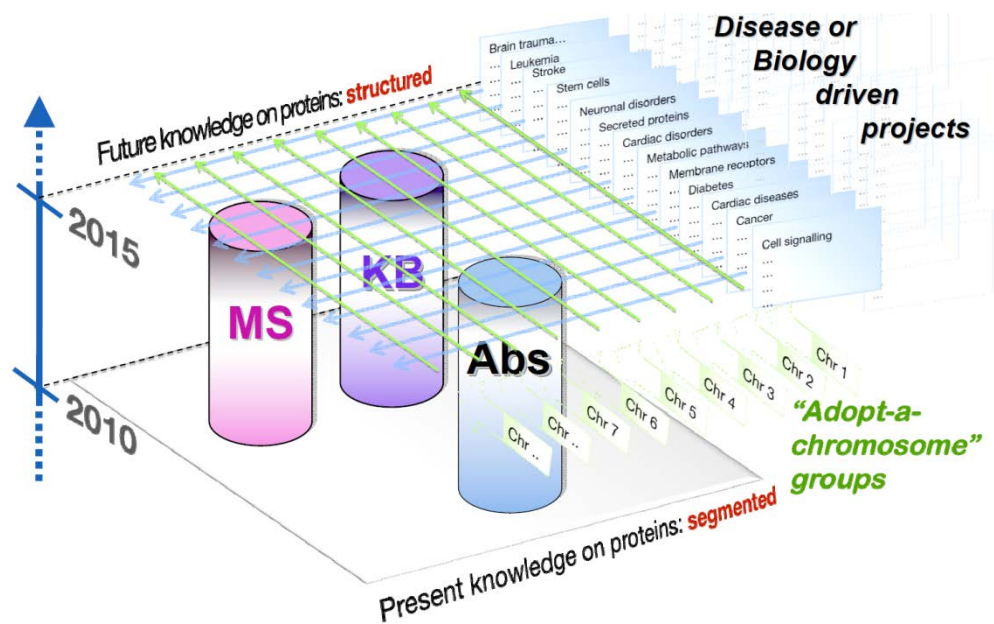


Figure 1. Organisation of the C-HPP project. Each consortium includes one or multiple biological projects, which provide biological material and enable the consortium to study missing proteins and multiple protein forms. The C-HPP project is based on 3 main technological pillars related to mass spectrometry, knowledge based (bioinformatics) and the use of antibody techniques.

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PROTEOMICS JOURNALS

TRANSLATIONAL PROTEOMICS



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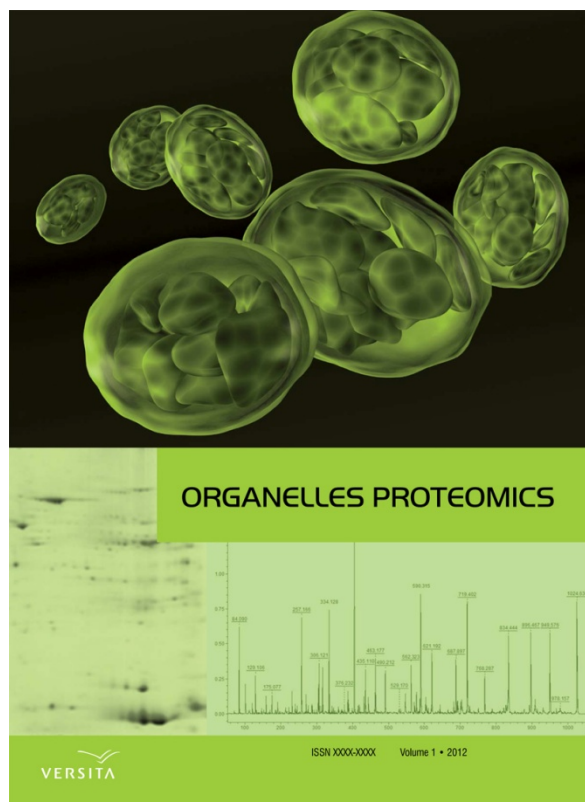
 

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ORGANELLES PROTEOMICS

Dear Colleagues from Proteomic Community

I would like to kindly invite you to know a new Open Access journal *Organelles Proteomics*, launched recently by Versita (<http://www.versita.com/op/>). Currently, we are starting up a new journal covering an important topic that have emerged in the recent years, is growing fast, and has generated a considerable number of papers, yet not having a dedicated journal. This remarkable topic is the sub-cellular and organelles proteomics including also other omics sciences, including genomics and transcriptomics as well bioinformatics. This journal could be a natural publishing option for authors from different part of the world writing on proteomics and transcriptomics at sub-cellular levels, and a hub integrating the relevant research community. *Organelles Proteomics* is published in Open Access model and at the moment the papers are completely free of charge. Furthermore our peer-review process is modern, and papers are published fast. Finally we also provide free language editing for individuals for whom English is not a first language. In summary, please come to know this new journal and enjoy it.



Octavio Luiz Franco
Journal Editor, *Organelles Proteomics*

PROTEOMES A NEW PROTEOMIC JOURNAL

Proteomic technologies are becoming one of the most desired tools in biology and medicine. Considering the rapidly growing number of publications that focus on development, optimization, and application proteomic technologies in diverse research areas MDPI launches a new proteomic journal—*Proteomes*. The journal is an open access and peer reviewed one publishing articles covering variety of aspects of proteome science. Publication in *Proteomes*

offers the presentation of methods, technical details, data, and theoretical results in as much detail as possible, because we do not set any limits in the length of the published articles. During the first two years, 2013 and 2014, publication of articles will be free of charge.

Proteomes Editor-in-Chief Prof. Dr. Jacek R. Wiśniewski

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Jacek R. Wiśniewski

MEETING REPORTS

III BIENNIAL MEETING OF YOUNG PROTEOMIC RESEARCHERS, SANTIAGO DE COMPOSTELA 2012, SPAIN.

The Biennial Meeting of Young Proteomic Researchers (*Jornadas Bienales de Jóvenes Investigadores en Proteómica*) is an event promoted by the Spanish Proteomics Society (SEProt) with the aim of bringing together young researchers from all over Spain so they can share their scientific experiences in the field of proteomics. The target audience includes PhD students and postdocs in the early stages of their career. Most participants are in their late 20s or early 30s.

The meeting is organized into different sessions and the idea is not to reproduce a typical congress format but to prioritize discussions among participants. Thus, each section has one or two chairmen/chairwomen with freedom to organize their section in agreement with the meeting organizers. Typical formats include short oral presentations, with a big discussion among speakers and with the audience at the end, or round tables. Besides presenting their research, speakers are encouraged to bring up questions related to scientific/methodological problems they find in their research. The idea is to answer these questions during the discussion section with the help of all participants. The overall format is very dynamic, with no parallel sections so everybody can attend the whole meeting and participate at any time. Besides oral presentations, a short number of communications are selected for poster presentation. Posters can be viewed during coffee breaks and at lunch time.

This year we organized the third edition of the meeting, which took place at Santiago de Compostela (Spain) on the 9th and 10th of February. The capital of Galicia welcomed almost 200 participants who enjoyed two days of proteomic discussions at the Faculty of Chemistry of the Universidade de Santiago de Compostela. The meeting was distributed into six sessions covering the following topics: quantitative proteomics; post-translational modifications; protein arrays, data analysis and systems biology; biomedical proteomics; parasites and microorganisms; and plant and animal proteomics. Sponsored prizes were given to the best session, and also to the best poster and oral presentation.

More than a hundred abstracts were presented at the meeting along the different sessions, 36 as oral communications and 68 as poster presentations. The first part of the meeting was devoted to quantitative proteomics technologies. This session allowed the discussion of different quantitative strategies. The advantages and specific problems of quantitative shotgun approaches, based either on stable isotope labelling (SILAC, iTRAQ, ¹⁸O...) and label-free strategies, were described. Furthermore, the session also focused on targeted proteomics techniques (SRM) and the new challenges inherent to the absolute quantification of proteins.

Subsequently, a session centred in the analysis of post-translational modifications (PTMs) took part, which discussed the particularities of this kind of analyses, paying special attention to phosphorylation, oxidation and ubiquitination. This session won the prize to the best session, as its chairwomen encouraged and favoured a very exciting discussion on PTM topics. Next, a third session involving research performed on protein microarrays, data analysis and systems biology closed the first morning of the meeting.

Then, the whole afternoon was dedicated to the most represented session (in terms of abstract quantities), biomedical proteomics. This subject included the presentation of strategies for the discovery of novel protein biomarkers with potential clinical use in different human diseases. Several types of biological samples were studied, such as bronchoalveolar lavages, urine exosomes or synovial fluid. Additionally, the session also debated the use of proteomics for pathogenesis studies on medical areas like cardiovascular disease, endocrinology or mental disorders. Furthermore, technological/methodological innovations in biomedical proteomics were also discussed. These comprised, for example, the use of MALDI imaging as a strategy to obtain a molecular histology profile of the tissue, or procedures for the extraction of proteins from formalin-fixed paraffin-embedded (FFPE) tissues stored in clinical bio-banks.

Finally, the last part of the meeting was committed to proteomics of microorganisms, parasites, animals and plants. A large amount of presentations were devoted to these topics, especially in the case of plant proteomics, reflecting the high activity of Spanish research in this area. A talk describing the identification of those proteins involved in the resistance of *C. glutamicum* to dicarboxylic acids won the prize to the best oral communication.

Altogether, the meeting was a good opportunity for young proteomic researchers to share their scientific interests and establish new collaborations. After three successful editions, we can say this is already a well-established proteomics meeting in Spain; a very dynamic and affordable event that brings together young proteomic scientists in Spain every two years to share their experiences in the field.

Ángel García¹, María Pardo² and Cristina Ruiz-Romero³

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³Rheumatology Division, Proteomics Group - ProteoRed/ISCIII, INIBIC-Complejo Hospitalario Universitario de A Coruña, A Coruña, Spain.

SPECIAL FOCUS ON FUNCTIONAL PROTEOMICS AT THE APRS 2012, AUSTRIA

With increasing numbers of sequenced genomes there is a concomitant raise in the number of identified proteins with unknown function. Functional proteomics constitutes an emerging research area in the proteomic field whose approaches are addressed towards the elucidation of the biological function of unknown proteins and of cellular mechanisms at the molecular level.

The 10th Austrian Proteomic Research Symposium (APRS 2012), held for the first time in Graz, had a special focus on this important topic. The meeting assembled more than 100 students, post-doctoral fellows and senior scientists from across Austria and international guests at the Graz University of Technology-campus from September 24-26th, 2012.

The symposium was jointly organised by the Austrian Proteomics Association (AuPA), the Medical University of Graz, the Graz University of Technology, the University of Graz, the PhD program "Metabolic and Cardiovascular disease" (DK-MCD) and the Austrian Center of Industrial Biotechnology (ACIB). The conference organising committee consisting of Ruth Birner-Grünberger, Bernd Gesslbauer, Jürgen Hartler, Andreas Kungl and Gerhard G. Thallinger, aimed to provide a scientifically excellent and challenging program covering recent advances in functional proteomics. Scientific sessions covered specific thematic areas in functional proteomics. Each session included a key note lecture presented by world leading experts in the field and short presentations selected from submitted abstracts. In addition, in two poster sessions, the latest results from the participating laboratories were shown. The latest products in proteomic technologies were presented in an industrial exhibition by market leading companies (Serva, Bruker, Waters, ABSciex, Thermo Scientific, Li-cor, Bio-Rad, Shimadzu, Decodon, NHDyeAgnostics, THP, Sigma-Aldrich and GE-Healthcare).



The first session on functional proteomics was opened in the late afternoon on Monday, September 24th, by a fascinating keynote lecture of Daniel K. Nomura, University of California, Berkeley, USA, on the annotation of dysregulated metabolic pathways that drive cancer progression by functional proteomics and metabolomics. Matthias Schittmayer, Medical University of Graz, talked about his latest results on functional mapping of CGI-58/ABHD5 protein, an activator of adipose triglyceride lipase (ATGL), which is a key lipase involved in mobilisation of intracellular lipid stores. Novel activity-based probes for

flavin-dependent oxidases were presented by Rolf Breinbauer, Graz University of Technology. Keiryn L. Bennett, Center of Molecular Medicine in Vienna, gave a lecture on miniaturisation of chemical proteomics to profile clinically-relevant kinase inhibitors in tumour needle biopsies. The session was concluded by a presentation of Anita Sahu, Medical University of Graz, on the investigation of the protein coat of lipid droplets in the absence of perilipins, known protein regulators of intracellular lipid mobilisation. In the evening the participants got together for food and drinks and delightful discussions.

On the next morning, the focus shifted to computational proteomics and Lennart Martens, Ghent University, Belgium, gave an inspiring keynote lecture on bioinformatics approaches handling the challenging analysis of metaproteomic and proteomic data of non-model organisms. Jacques Colinge, Center of Molecular Medicine in Vienna, presented the largest dataset of its kind for global mapping of host biological processes hit and perturbed upon viral infection. This was followed by a talk from Johannes Stadlmann, Institute of Molecular Pathology in Vienna, who reported on the *in silico* construction of a human N-glycan database based on the catalytic properties of glycosylation enzymes. The session was concluded by Oana A. Tomescu, ACIB and Graz University of Technology, with a presentation on integration of transcriptome and proteome data by generalised singular value decomposition.

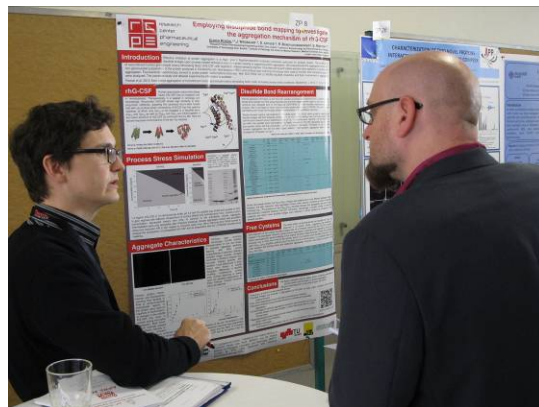
After a coffee break sponsored by ABSciex, Christian Baumann, presented the SWATH acquisition workflow on the ABSciex TripleTOF 5600 creating a digital image of any sample in the MS² space.

Another highlight of the meeting were two one hour poster sessions, one before lunch and one in the afternoon on Tuesday, with the presentation of in total 39 posters covering recent research in the Austrian and their collaborating proteomic laboratories, as well as in the laboratories of international guests.

The early afternoon session was focused on clinical proteomics. Martin Kussmann, Nestlé Institute of Health Sciences, Lausanne, Switzerland, gave a highly pertinent keynote lecture on nutrigenomic studies addressing nutritionally actionable health conditions and searching for biomarkers and bioactives.

A search for marker proteins induced by tumor-stroma interactions in the progression of multiple myeloma was presented by Andrea Bileck, University of Vienna. Peter Valentin Tomazic, Medical University of Graz, held a talk on proteomic changes of the nasal mucus in allergic rhinitis in dependence of the season. The session was closed by Rudolf Öhler reporting on the identification of non-HLA antigens targeted by alloreactive antibodies in patients undergoing chronic hemodialysis.

After a coffee break sponsored by Serva, Reiner Westermeier presented improved tools for gel-based proteomics based on flatbed 2D electrophoresis of thin-layer pre-cast gels on plastic backing. Monika Ehling-Schultz, University of Veterinary Medicine in Vienna, talked about integration of plasmid and chromosomal signals in toxigenic *Bacillus cereus*. Glycan profiles of





the 27 N-glycosylation sites of an HIV envelope protein were presented by Friedrich Altmann, University of Natural Resource and Life Sciences in Vienna.

In the evening, participants enjoyed the outdoor party with fine food and drinks by candle light and smooth jazz music.

The Wednesday morning session was focussed on interactomics and post translational modifications and opened by the fascinating keynote lecture of Matthias Gstaiger, ETH Zurich, Switzerland, on his recent approaches to chart the protein interaction landscape of mammalian signalling systems.

Taras Stasyk, University of Innsbruck, reported on interactome analysis of MAP kinase signalling scaffold complexes. A quantitative proteomic search for substrates of DNA damage kinases ATM and ATR was presented by Elisabeth Roitinger, Institute of Molecular Pathology in Vienna. Finally, Dijana Vitko, provided a glimpse on her planned study on histone deacetylation in T-cell differentiation.

Two company talks concluded the morning session: Michaela Scigelova, Thermo Fisher Scientific, compared high resolution/ accurate mass- and single reaction monitoring-based approaches in targeted peptide quantitation. Ion mobility was introduced by Matthew Kennedy, Waters, as useful tool in diverse applications, such as MALDI imaging, protein identification and hydrogen deuterium exchange.

In the final scientific session after the AuPA general assembly on early Wednesday afternoon, Christoph Jüschke, reported on their iTRAQ study of post-transcriptional gene regulation in *Drosophila*. Martin Samonig, University of Salzburg, presented a top-down



proteomic method to characterize allergens. The session was closed by the inspiring keynote lecture of Wilhelm Haas, Harvard Medical School, Boston, USA, who showed latest results on driving quantitative multiplexing proteomics to the limits.

Finally, Martina Marchetti-Deschmann, University of Technology Vienna, gave an overview of AuPA in the context of the European Proteomics Association (EuPA). The meeting was closed by the best presentation award ceremony to honour two young scientists for their excellent contributions. Ulrich Rössl, Research Center

Pharmaceutical Engineering (RCPE) and Graz University of Technology, was awarded the price for the best APRS 2012 poster for his presentation on disulphide bond mapping for investigation of the aggregation mechanism of recombinant human granulocyte-colony stimulating factor (rhG-CSF).

Elisabeth Roitinger, Institute of Molecular Pathology in Vienna, was awarded the price for the best oral presentation of the meeting for her talk on a quantitative proteomic search for substrates of DNA damage kinases. After closing remarks by the organising committee and Karl Mechtler, AuPA's president, it was announced that next year the AuPA members will assemble in Innsbruck for the APRS 2013.

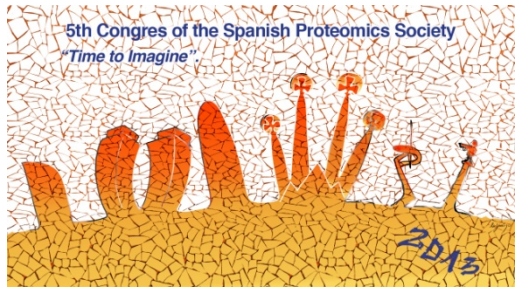
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FORTHCOMING MEETINGS

EUPA 2013 SCIENTIFIC MEETING

The next EuPA Scientific meeting will be organized from the 14th to the 17th of October, 2013 in Saint Malo (France). More information will be available soon in the EuPA website (www.eupa.org).

SEPROT MEETING

	<p>5th Congress of the Spanish Proteomics Society Time to Imagine 5-8 February 2013 Barcelona, Spain www.seprot2013.org</p>
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Barcelona, September 2012

Dear colleagues,

We are happy to announce the 5th Congress of the Spanish Proteomics Society (SEProt) that will be celebrated next February in Barcelona. The congress, which will take place at the AXA Auditorium Center on the 5th-8th of February 2013, will gather the most relevant contributions of the Spanish proteomics groups, as well as lectures delivered by relevant national and

international speakers, covering topics such as Quantitative Proteomics, Posttranslational Modifications, Disease Proteomics, Network/Protein-Protein Interactions, Bioinformatics and Emerging Technologies.

This year Professor Richard M. Caprioli (Stanford Moore Chair in Biochemistry, Director of the Mass Spectrometry Research Center, VICC Member) will be awarded an honorary membership.

All information regarding the event, including registration forms and abstract submission instructions, is available at the website <http://www.seprot2013.org>. We look forward to meeting you in Barcelona.

Best regards,

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8th Meeting of the Norwegian Proteomics Society

March 4th - 5th, 2013, Forskningsparken, Oslo



<http://norwegian-proteomics-society.uio.no>

UiO : Universitetet i Oslo



WORKSHOP ON FARM ANIMAL AND FOOD PROTEOMICS

(Sponsored by COST Action FA1002; <http://www.cost-faproteomics.org/>)

Barcelona, February 5th 2013, 9:00 pnd-1 – 16:30

Residència d'investigadors del CSIC. C/Hospital, 64 - 08001 Barcelona

Coordinators: Anna Bassols (U niversitat Autònoma de Barcelona), Miguel Ángel Sentandreu (IATA, Instituto de Agroquímica y Tecnología de Alimentos, Valencia)

List of speakers:

- 9:00-10:00 **André de Almeida** (Instituto de Investigação Científica Tropical, Lisboa, Portugal)
"Proteomics a novel
expnd0 tool for Animal science: advantages and drawbacks"
Presentation of COST FA1002.
- 10:00-11:00 - **Ingrid Miller** (Department -13 for Biomedical Sciences, University of Veterinary Medicine, Vienna, Austria)
"The proteomic toolbox: 2-DE gels and more"
- ult11:00-11:30 *Coffee break*
- 11:30-12:30 - **Emøke Bendixen** (Department of Molecular Biology and Genetics, University of Aarhus, xpndtw0 Denmark)
"The proteomic toolbox: targeted mass spectrometry"
- 12:30-13:30 - **M^a Ángeles Álava** (Departamento de Bioquímica y Biología

dMolecular y Celular, Universidad de Zaragoza)
"Proteomics and inflammation: an open door in the study of farm animal diseases"
- 13:30 -14:30 *Lunch*
- 14:30-15:30 - **Paola Roncada** (ISILS-Department of Veterinary Science and Public Health University, Mila dtw-2 no, Italia)
"Unraveling the milk proteome: perspective in human nutrition and animal

production”
15:30-16:30 - **Brigitte Picard pnd0** (INRA, UR1213, Unité de Recherches sur les Herbivores, Centre de Clermont-Ferrand/Theix, France.)
“Biomarkers of beef sensory qualities: from proteomics to phenotyping w0 tools”

REGISTRATION IS FREE!

ABOUT THE EUPA BULLETIN

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 bulletin:

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Instructions to authors

Manuscripts to be published in the EuPA bulletin 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, affiliation and e-mail will be located at the end. A photograph of the contributor(s) will be included.

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

Contributions must be submitted at least 15 days before the release of the issue, by May 30th and November 30th.