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message from the vice-president

Taking the European Proteomics Association (EuPA) into the Future-EuPA to Estoril and beyond - Shaping EuPA's future



CHANGING EuPA

EuPA held its Executive Council (EC), and the 7th Meeting of the General Council of the European Proteomics Association (EuPA) in Estoril Portugal 23-24 of October, 2010. The EC had worked out several areas for the GC to vote on that will change the EuPA as an organisation. The groundbreaking work from the EC has been made in order to meet the feedback and demands made throughout 2009-2010 from the member countries and representatives. Our goal was to take EuPA into the future by changing the organization as well as the committees and representations in these groups.

One major goal that we managed to get approved by the GC was to introduce a science development direction that EuPA already is taking. This is made by introducing a new EuPA committee, "EuPA developments". This new committee comprises three sections that address: i) Standardization, ii) Imaging mass spectrometry and iii) Biobanking. The aim of this new committee is to promote new research areas that will be important in the near future and that will give EuPA as an organization an operational role, based upon the activities within the three respective sections.

The responsibility and head of each section is, Juan Pablo Albar Ramirez (Standardization), Per Andrén (Imaging mass spectrometry), and Åsa Wheelock (Biobanking), respectively. PLEASE FEEL FREE TO TAKE CONTACT AND JOIN THESE NEW INITIATIVES.

The new organization of EuPA is presented in figure below.



The Funding of EuPA activities as well as future needs and prospects has been planned and discussed over the period. It has been realized that an extended funding committee will be needed in order to meet future demands of the organization. New members approved by the GC to strengthen the funding committee were: David O'Connor, Marius Ueffing and Peter Verhaert. They will together with Günter Thesseling as the head, work together and join the EC already at an upcoming meeting in Paris 9th December.

THE HUMAN PROTEOME PROJECT - HPP

Pierre Legrain, the Secretary General of HUPO, joined us at the GC meeting and gave an extensive presentation on the Human Proteome Project (HPP) developments. The official launch of HPP was made at the Annual HUPO Congress in Sydney, on September 23, 2010. The details and starting point of HPP is available on the HPP web page at the HUPO web site (<http://hupo.org/research/hpp/>).

A future outline for the Human Proteome Project (HPP), prepared by the Human Proteome Organization (HUPO) has been initiated, where the details and future role of EuPA will be decided on. There was a general consensus from the GC, that this initiative should be an important area for EuPA to be building on.

ELECTIONS

The representatives of the European National Proteomics Societies (GC) elected Jean-Charles Sanchez as the next EuPA Vice President, and György Marko-Varga as the next EuPA President. The EuPA GC also invited Russia as its 17th member. Alexander Archakov, the president of the Russian society gave a presentation of the Russian Proteomics organization and activities.

Additional decisions that were made were to propose Saint Malo for the 7th EuPA Congress in 2013. Madrid was elected as our candidate for the next HUPO/EuPA World Congress in 2014.

György Marko-Varga

Vice-President of EuPA

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euPA senior scientist 2011 award in proteomic sciences

EuPA Senior Scientist Award in Proteomic Sciences 2011

(Deadline 31 March, 2011)



The European Proteomics Association (EuPA) **invites nominations** for the EuPA Senior Scientist Award in Proteomics.

- This annual award is intended to acknowledge achievements in the field of proteomics in Europe.
- The Award will consist of a diploma and an honorarium of 5000 €.
- The winner will be announced at the EuPA meeting, where he/she will give a lecture. The registration fee will be waived.
- A biographical sketch of the winner will be published in the Journal of Proteomics and in other Proteomics Journals and will be posted on the EuPA website.
- Candidates must be a member of a national European proteomics society and nominated by any European proteomics society.
- The EuPA Award Panel will be composed of the EuPA executive committee.
- Nominations for the EuPA Senior Scientist Award in Proteomics should be sent to **Dr. Garry Corthals** (garry.corthals@btk.fi) by **31 March, 2011**.



More information on the website <http://www.euPa.org/>

The Russian Human Proteome Organization (RHUPO) was founded in 2004. The members of RHUPO are research workers from 10 Russian Research Centers, including Institute of Biomedical Chemistry, Institute of Biomedical Problems, NT-MDT Company and others.

Its current priority aim is the consolidation of the efforts focused on 18th chromosome's proteins identification as part of the Human Proteome Project and nanotechnological complexes' development for specifying low-copied and ultralow-copied proteins. Other RHUPO tasks are to consolidate Russian scientists engaged in the proteomic researches to promote the scientific, innovative and educational activities in Russia to spread proteomic technologies and knowledge, to create the state support mechanisms of the proteomic researches and organize and coordinate the public proteome initiatives.

Among recent initiatives provided by RHUPO there are 2 scientific events dedicated to Human Proteome Project progression where the HPP Working Group and leading Russian and foreign scientists took part. Since our first conference in 2000, in 2010 the 5th International Conference "Genomics, Proteomics, Bioinformatics and Nanotechnologies for Medicine" was held with the assistance of RHUPO.

RHUPO also covers the Program "Proteomics in Medicine and Biotechnology" drawn up by the Russian Academy of Medical Sciences in 2007. In 2009 50 articles were published in the major journals on proteomics within the framework of this program and one patent was obtained.

Detailed information is available at <http://www.rhupo.ru/html/eng/facilities.htm> and <http://www.proteome.ru/>.

Prof. Alexander Archakov

Institute of Biomedical Chemistry, Russian Academy of Medical Sciences

4th EuPA scientific meeting, estoril 2010: a brief report

This year, the EuPA-Portuguese Proteomics Association Member - Rede ProCura - had the great honor and responsibility to host the **4th EuPA Scientific Meeting** jointly with the 6th ProCura Meeting in Estoril Congress Center, October 23-27, 2010.

Upon the theme - **2010: A Proteomics Odyssey Towards Next Decades** - approximately 350 participants, many of them from oversea (Brazil, Canada, United State, Mexico, Singapore, Russia,



2010
PROTEOMICS
ODYSSEY
TOWARDS NEXT DECADES

4th EuPA MEETING
6th ProCura MEETING
23 - 27 OCTOBER 2010
ESTORIL - PORTUGAL

Japan, Australia and South of Africa) joined the meeting and presented their scientific work (about 69 lectures and 277 posters presentations) in a warm, friendly and stimulating environment of the beautiful Estoril Coast.

The meeting covered ten different challenging Proteomics Topics. The main goal was to bring together scientists from multiple areas of proteomics to share and discuss their work and achievements, as well as their expectations and future challenges.

The opening welcome session started with the best four pre-selected candidate talks (MD Filiou, J Fisher, BL Parker and N Tiberti) for **EuPA-Young Investigator Award 2010**. The young investigator **Benjamim L Parker** that presented "Purification of O-GLcNac peptides using phosphate-based alkyne click chemistry, TiO₂ chromatography and MS" was the EuPA-YIP winner of this year.

The YIP session was followed by a Plenary Lecture – "Proteomics: where now, where next?"- given by the researcher who is credited with the concept of the proteome, Prof Marc R Wilkins. By joining young investigators with a recognizable name in proteomics science, the aim was to raise the awareness of proteomics and motivate new generations to the field.



We were also pleased to welcome the **2010 - EuPA Senior Scientist Award** in Proteomics Science, **Prof Joël Vandekerckhove**, which is recognized as a proteomics pioneer. His plenary lecture titled "Proteomics: from adolescence to adulthood" gave us an exciting and memorable proteomics historical journey.

Many of the sessions have shown the combination of molecular biology, biochemistry, genetics, informatics and physiological interpretation that 20 years ago we could hardly have dreamed about it. Two recognized scientists,

Giulio Superti-Furga and Pier G Righetti, gave the Closing lectures. PG Righetti, one of the most enthusiastic in the field surprised as always surprised the young audience with an original talk "The proteome buccaneers: how to unearth your treasure chest via combinatorial peptide ligand libraries".

All talks in the meeting, including the pre-meeting educational Workshops (see below) were audio-video recorded and all those that we have gotten author's permissions will be soon available on the EuPA website (www.eupa.org).

In addition to the scientific talks, the meeting includes for the first time, luncheon **thematic Round-Tables** joining experts and young investigators to discuss particular proteomics issues as follow:

R1-experimental design in disease biomarkers discovery (moderator: Peter James)



R2-sample collection/preparation/biobanking for biomarker discovery (moderators: Jean-Charles Sanchez & Pier Giorgio Righetti)
R3-labeling vs label-free quantitative proteomics (moderator: Juergen Cox)
R4-imaging MS on cryo vs FFPE preserved tissues (moderator: Ron Heeren)
R5-protein post-translational modifications (moderator: Nicholas Morrice)
R6-peptidomics and bioinformatic tools (moderator: Eugene Kolker)
R7-databases, data management and data mining (moderator: Frederick Levander)
R8-interactomes, networks and pathways analysis (moderator : Roman Zubarev)
R9-SRM/MRM challenging (moderator: Paola Picotti)
R10-translational proteomics: from the lab to the clinic (moderator: Christoph W Turck).
R11-translational plant proteomics: from the lab to the field/table (moderator: Jesus J Novo).

The summary of their thoughts/conclusions will be soon expressed in a special Journal of Proteomics (JPROT) issue dedicated to the meeting.

This year we were also happy to have an interesting **EuPA-Educational Program**, which was organized as a pre-meeting one-day course covering an important proteomics concern in nowadays - Proteomics Experimental Design – by Peter James. To complement the educational program, two exciting workshops also took place: Workshop I - Pathway Analysis (Roman Zubarev, Mikhail Savitski and Holger Karas) and Workshop II - Phospho- and ADP-ribo-protein sequencing (David Goodlett, Nick Morrice and Garry Corthals).

Also, the **1st Contest in Proteomics Photo-Graphic Art** was promoted by EuPA jointly with Rede-PROCURA and the Portuguese Association Viver a Ciência (VAC). The aim was to capture the general public attention to the Proteomics importance in this post-genomic era. About 48 images were submitted to this Contest. The best 21 images were pre-selected by a jury composed by Joana Barros (Scientist and VAC representative), Mike Dunn and Juan Calvete (Scientists and EuPA and JPROT representatives, respectively) and Dina Cereja



and Marta Agostinho (Art Designers) taking in consideration the three main aspects of the images: aesthetic value, clarity of the description and the significance of the scientific subject. The 21 images were exhibited on the meeting website and at Estoril Congress Center during the meeting for online voting.

The final Contest count showed about 600 votes. The winner (with 34% of the votes) was Image 9 "Freedom" submitted by Fátima Vaz from INSA-Lisboa, Portugal, who received 1000€ of prize and will get her image published on the cover of the JPROT-Elsevier special issue dedicated to Meeting. We believe that this contest will be the first among many others, encouraging creativity and responsibility of scientists to stimulate and disseminate proteomics science into public.

The 4th EuPA Meeting Estoril 2010 was sponsored by Thermo Fisher Scientific (Gold Sponsor), AB/Sciex, Bruker/Dionex/Dias de Sousa, Bio-Rad (Silver Sponsors), Agilent Technologies, Decodon, Denator, Caprotec, MedicWabeb AB, Integrated

Analysis, Integromics, Serva Electrophoresis, Sigma, Swedish Academy of Pharmaceutical Sciences, Waters, FCUL, INSA, Estoril & Sintra Convention Bureau, EuPA, VAC and Rede-ProCura.

We hope that the 4th EuPA Meeting Estoril 2010 helped researchers to achieve new knowledge and opportunities to open up new avenues of exploration in their works.

We also encourage all EuPA members to support and provide constructive input for the upcoming EuPA scientific meetings in Geneva 2011 as well in Glasgow 2012.

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a flavor of the HUPO 2010 meeting in sydney

This short text will not pretend to give a detailed report on the Sydney meeting. As all the HUPO meetings, there are many parallel sessions, so that it is impossible to attend everything. Thus, it will rather be limited to picking some highlights of the meeting.

The HUPO 2010 meeting took place in Sydney Sept. 19 to 23. The first day was devoted to the education day, well attended with 200 participants.



The main meeting began on Monday Sept 20, and extended to Thursday Sept 23, with 4 plenary sessions, 32 parallel sessions and 2 sessions devoted to young investigators (PhD and early postdocs), and close to 1500 attendees. The sessions covered a rather wide spectrum within proteomics. Although it is always true that disease-oriented had the lion's share, as usual for a HUPO meeting, Purely disease-oriented sessions represented "only" 13 of the 32 parallel sessions, 6 being devoted to proteomic technologies (e.g. protein arrays, SRM, tissue imaging), 4 to general biology subjects (e.g. organelles), 4 to post-translational modifications, 3 to databases and 2 to protein interactions and networks. In these more general sessions, a few communications were devoted to plant biology. While this is in progress over previous HUPO meetings, there is still a strong under-representation of plant proteomics, not to speak about non-model microbiological or animal proteomics.

Among this huge amount of proteomic science, there were some hotspots that deserve further mention. One of these is the use of bacteria typing by MALDI profiling, and using profile correlation to achieve typing. Another one was the discovery of a new post-translational modification occurring on serines, O-GlcNAc phosphate. This means that serines can bear at least three modifications, phosphate, GlcNAc and O-GlcNAc phosphate, resulting in steric and surface charge modulations that can alter protein-protein interactions in a very subtle way.

However, the big event in this HUPO meeting was the official launch of the Human Proteome Project. A working group had been built by HUPO fall 2009, and has worked a lot on the definition of a human proteome project. The scheme that

was exposed in Sydney was the following:

- The human proteome project will be gene-centric. It aims at providing tools and knowledge on each of the products of the 21,000 human genes, to be used by the proteomics community but also by the biology community at large

-There will be three major components of the Human Proteome Project. The two analytical ones will be based on antibodies and on SRM. The third one will be the construction of a knowledge base.

-In order to split the task into non-redundant chunks, a chromosome-based organization has been proposed. This means that consortia will be built, each consortium being in charge of the annotation of the knowledge obtained on each protein coded by its assigned chromosome, but each consortium will also produce knowledge (by antibodies or SRM) on this chromosome. However, it is stressed with great strength that these consortia are not the alpha and omega of the Human Proteome Project. The real project is the intertwined work of these consortia and of all the various laboratories around the world carrying out biology-driven proteomics studies. Should these laboratories find new data on a given protein, they can provide to the adequate consortium these new annotations (e.g. subcellular localization, disease implication etc...). In return, if the consortium has in store an analytical reagent for this protein (antibody or SRM peptides) it will benefit the biology lab for the validation studies.

-All of the above raises the problem of error propagation and of quality control of the data. This means that one of the big challenges that the Human Proteome Project working group will have to tackle very soon will be the definition of quality metrics, so that only high quality data will be deposited in the Human Proteome Project knowledge base.

To illustrate the three pillars of the Human Proteome Project, there were conferences as to the degree of advancement of the analytical tools. As to the antibodies, there are now 11,000 validated antibodies targeting 8500 human gene products, with subcellular localization data for half of them, and the total collection is expected within the next 5 years. As to the SRM tools, more than 100,000 proteotypic peptides are now tested, with the goal of having 5 testable SRM per human gene product. Here again, the complete test should be finished within the next 5 years, and both resources will be publicly available.

To get further insights on the Human Proteome Project, The EuPA-HUPO liaison committee invited Pierre Legrain, head of the Human Proteome Project working group, to give a talk at the EuPA General Council in Estoril (Oct 23-24). This allowed to get further details, and the national delegates within the EuPA General Council should be able to give more details to the interested scientists. Moreover, the EuPA-HUPO liaison committee will try to set in place wider communication initiatives, so that all interested European scientists will be able to have a better grasp of the Human Proteome Project.

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significant growth of proteomics and the start of metabolomics in central and eastern europe - 4th central and eastern european proteomic conference welcomes international metabolomics austria

The popularity of proteomics for the study of biological systems relates not only to promising developments for the identification of potential new drug targets for the treatment of various diseases, but also to the understanding of the structure and function of each protein and the complexities of protein-protein interactions. Such studies are critical for developing novel tools using specific protein biomarkers for diagnosis as well as prognosis purposes as well as monitoring a plethora of diseases which currently plague mankind.

The meeting entitled 'The 4th Central and Eastern European Proteomics Conference (CEEPC) meets International Metabolomics Austria (IMA)', was held in Vienna, Austria, from the



29th August to 3rd September 2010 at the Vienna University of Technology organized by G. Allmaier, M. Marchetti-Deschmann and W. Weckwerth (<http://www.cta.tuwien.ac.at/ceepc-ima/>). The meeting was the fourth in a series of proteomic conferences to be held in this region of Central Europe (Prague, Jena, Budapest and Vienna) with the key aim of strengthening links between scientists from Central, Eastern Europe as well as International groups world-wide. It was attended by more than 130 delegates and many proteomic topics including biomarkers discovery, quantitative proteomics, clinical proteomics, metabolomics as well as novel proteomic technologies which may facilitate future progress were discussed over the five days. The wider aim was to bring together scientists from the field of proteomics, peptidomics and metabolomics because a lot of tools applied in these fields are very similar and absolutely vital to the progress moving forward.

Evening prior to commencement of the conference was dedicated to a lecture on the splendors of Vienna by Manfred Schreiner from the Academy of Fine Arts, Vienna who delighted everyone with a lecture on the 'analysis of art through the art of analysis.

The Conference commenced with a presentation from Friedrich Lottspeich (Max Planck Institute of Biochemistry, Martinsried, Germany) on "Development of quantitative proteomics" which discussed several exciting strategies for quantitative proteomics and with a view to obtaining reliable and accurate results. Florian P. Breitwieser (CeMM - Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna) highlighted statistical models for quantitative proteomics using isobaric tags followed by Wolfgang Hoehenwarter (Department of

Molecular Systems Biology, University of Vienna, Faculty of Life Sciences, Vienna) who delivered an excellent talk about a new method for comparative proteome analysis called Mass Accuracy Precursor Alignment (MAPA). Johannes Stadlmann (University of Natural Resources and Life Sciences (BOKU), Vienna) presented an interesting talk on the characterization of heme-protein linkages by CID – where CID fragmentation behavior of peptides, covalently linked to heme groups was investigated. Snake venomomics may send shivers down one's spine, but on this occasion, it was a great pleasure listening to Martina Marchetti-Deschmann (Institute of Chemical Technologies and Analytics, Vienna University of Technology, Vienna) talking about proteomics and peptidomics of *Bothrops moojeni* - a species with little known about its venom. Goran Mitulović (Medical University of Vienna, Vienna) followed with a talk on 'The role of HPLC in Proteomics' where there are significant challenges involved in the proteomics analytical workflow with conventional methodologies currently used. With a title like 'Aiming Shotgun at the Heart' with reference to 'Proteomics of a Failing Pump', Jiri Petrak (Institute of Pathological Physiology, Charles University and Institute of Hematology and Blood Transfusion, Prague, Czech Republic) showed differential expression of many proteins that have not been connected with heart remodeling and failure previously. The presentation from Tamas Janaky (NeuroProteomics Laboratory, University of Szeged, Szeged, Hungary) questioned the dependence of the brain proteome on genetic background.

The second day started with a talk from Dominic Desiderio (University of Tennessee Health Science Center, Memphis, TN, USA) who presented a study of 'The Nitroproteome of the Human Pituitary' with a much focused approach at signaling pathway networks associated with human pituitary adenomas. The safety driven presentation was delivered by Klaus Kratochwill (Department of Pediatrics, Medical University of Vienna, Vienna) identifying biological processes leading to mesothelial cells



injury and their possible occurrence in glucose-based peritoneal dialysis in clinical practice. An excellent presentation by Pavel Rehulka (Institute of Molecular Pathology, University of Defence, Hradec Králové, Czech Republic) focused on a simple micro-gradient device producing an S-shaped gradient of strong mobile phase for analyte separation using RP capillary column. Hana Kovarova (Institute of Animal Physiology and Genetics, Czech Academy of Sciences v.v.i., Libechov, Czech Republic) presented a study with the clear aim to study small molecule inhibitors of Aurora kinase with focus on drug resistance in colorectal cancer. Suresh Jivan Gadher (Institute of Animal Physiology and Genetics, AS CR, v.v.i., Libechov, Czech Republic and Millipore Bioscience, St. Charles, MO, USA) presented a study where paired samples of follicular fluid and plasma obtained from women undergoing in vitro fertilization were extensively analyzed and a crucial role of complement cascade and angiogenesis was highlighted in the reproductive process. György Marko-Varga (Div. Clinical Protein Science & Imaging of Biomedical Center, Lund University, Lund, Sweden) discussed dedicated protein biomarker diagnosis technologies that allow multiple reaction monitoring with MS.

The third day commenced with Giulio Superti-Furga (CeMM - Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna) who started with an excellent presentation on integrated interaction proteomics approaches. This was followed by a fascinating talk on the proteomics profiling with microarray based on monoclonal antibodies generated against natural plasma proteome by István Kurucz (Biosystems International, Debrecen, Hungary). 'Lipolytic proteomics' has its rightful place in proteomics and Ruth Birner-Grünberger (Medical University of Graz, Graz, Austria) discussed the regulation of enzymes involved in lipid metabolism. The day's fascinating sessions were concluded by the presentation from Peter Verhaert (Netherlands Proteomics Center, Delft University of Technology, Delft, The Netherlands) entitled 'Peptidomics: in between proteomics and metabolomics'.

The following morning brought 'Proteomics' face to face with 'Metabolomics' as the metabolomics sessions kicked off with a presentation by Oliver Fiehn (UC Davis Genome Center, Davis, CA, USA). Fiehn discussed the novel perspectives of metabolomics and personalized medicine with reference to platforms, data processing algorithms, metabolites and essential advantages that come with metabolomics. Rainer Schuhmacher (IFA, University of Natural Resources and Life Sciences Vienna, Tulln, Austria) presented an overview of the approaches together with firsthand experience gained during the establishment of the metabolomics platform for the study of interactions between microorganisms and plants using an MS/MS. Arvand Haschemi (Clinical Institute of Laboratory Medicine, Medical University of Vienna, Vienna) discussed the screening of approximately half of the human kinome in macrophages for unknown key players involved in immune regulation. Age Smilde (Biosystems Data Analysis, Swammerdam Institute for Life Sciences, University of Amsterdam, Amsterdam, The Netherlands), Christian Zuehlke (LECO Instrument) and Xiaoliang Sun (Department of Molecular Systems Biology, University of Vienna, Vienna) continued with the presentations on analysis of metabolomic data with reference to functional genomic, yet more exciting technologies and novel ways to infer perturbation sites in a metabolic network directly from the experimental data using mathematical framework. The final half day session once again focused on different aspects of metabolomics such as computational frameworks for the study of large-scale evolutionary investigations of different networks (Christoph Flamm, Institute for Theoretical Chemistry, University of Vienna, Vienna) to computational identification of obligatory autocatalytic replicators (Ádám Kun - Department of Plant Taxonomy and Ecology, Eötvös University, Budapest, Hungary). Stefanie Wienkoop (Department of Molecular Systems Biology, University of Vienna, Vienna) and Georg Weingart (IFA, University of Natural Resources and Life Sciences, Tulln, Austria) brought the conference to a close with sessions on plant system biology looking at integration of metabolomics and proteomics.

The conference was a great success and this success was enhanced by the much appreciated attendance and support of commercial companies with a focus on medical and scientific instruments, reagents and softwares. Already, interest has turned to the 5th Central and Eastern European Proteomics Conference which will take place in Prague, Czech Republic in the middle of September 2011. It is envisaged that many participants will gather together in the vibrant capital city to not only savor the bohemian hospitality but also to share the fascination of proteomics and any 'Omics' that you may wish to think of.

The team of the Research Group Bio- and Polymer Analysis of the Institute of Chemical Technologies and Analytics (TU Wien) in the back helping to make the conference running smoothly.



**Suresh Jivan Gadher^{1,2}, Martina Marchetti-Deschmann³, Günter Allmaier³,
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breaking news

- The international proteomics tutorial programme

The most critical functions of the various Proteomics organisations are the training of young scientists and the dissemination of information to the general scientific community. An International Tutorial Programme is therefore being launched to meet these needs. It is a cooperation between selected journal publishers in the field of proteomics on the one hand, and HUPO and its affiliated regional and national organisations.

The overall level is aimed at Masters/PhD level students with good basic training in biology, biochemistry and mathematics / statistics.

The tutorials, which will be published in the following Journals: Journal of Proteome Research, Journal of Proteomics, Molecular and Cellular Proteomics, and Proteomics, will consist of a review/teaching article with an accompanying talk slide presentation for classroom teaching.

The tutorial program will cover core techniques and basics as an introduction to scientists new to the field. A second series of more advanced topics focussing on the application of proteomics techniques to biological problem solving will be launched at a later date after the basic series is completed.

The entire series of articles and slides will be made freely available for teaching use at the Journals and Organisations home-pages.

More information at:

http://www.proteomicstutorials.org/Proteomics_Tutorials/Welcome.html

breaking news

- Journal of Proteomics - first official IF: 3.851

We are happy to announce that *Journal of Proteomics* has achieved an outstanding result by receiving a first impact factor of 3.851.

2009 Journal Citation Reports® Science Edition (Thomson Reuters, 2010)

The journal has now appeared in the JCI reload with the following metrics:

Journal Impact Factor	3.851
5 Year Impact Factor	3.894
Immediacy Index	0.977

Based on the number of citations already in SCOPUS and extrapolating this for the full year, we can already predict the citation ratio to be over 4.2 in the next release. The editors work hard to continue this trend and acknowledge the role of the reviewers in establishing this high standard.

The Publisher congratulates the Authors, Editors and the European Proteomics Association with this excellent start.

Adriaan Klinkenberg
Publisher, Life Sciences
Elsevier BV

upcoming events

April 3-7, 2011 – Berlin, Germany
Proteomic forum 2011
<http://www.ctw-congress.de/ProteomicForum2011/>



April 6-13, 2011 – Odense, Denmark
EMBO practical course: Mass Spectrometry and Proteomics
<http://cwp.embo.org/pc11-04/>



June 14-26, 2011 – Odense, Denmark
HUPO Education and Training programs: Bioinformatics in Mass Spectrometry Based Proteome Analysis
http://www.hupo.org/educational/courses/details.asp?course_id=msspcp_02



June 20-23, 2011 – Dublin, Ireland
Cancer Proteomics 2011 - Systems Biology, Developmental Models & Data Integration
<http://cwp.embo.org/cfs2-11-03/>





8th BSPR-EBI Meeting

From the visible to the hidden proteome

12th - 14th July 2011

Wellcome Trust Conference Centre, Cambridge, UK



More information at: <http://www.bspr.org/>

next eupa events

September 3-7, 2011 – Geneva, Switzerland
10th HUP0 World Congress – 5th EuPA Annual
Scientific Meeting – 8th SPS scientific
meeting
<http://www.hupo2011.com/>

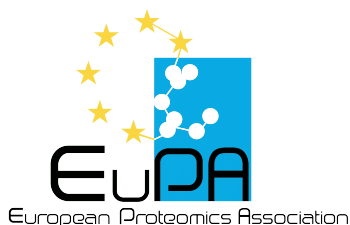


June 3-6, 2012 – Glasgow, Scotland
6th EuPA Annual Scientific Meeting – 9th
Annual BSPR meeting
<http://www.bspr.org/>



about this bulletin

This bulletin is the official newsletter of the European Proteomics Association. A quarterly online publication edited by the EuPA Conference and Communication Committee. 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 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. You are more than welcome to contribute to this bulletin content, please send your contribution by **April 15th** to be included in the next issue.



<http://www.eupa.org/>

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