EUPA 2018

XII EUPA CONGRESS

Translating genomes into biological functions

16-20 June 2018
Santiago de Compostela

JOINT MEETING WITH VII SEPROT CONGRESS
Dear colleagues,

It is for us a pleasure to welcome you to Santiago de Compostela for the celebration of the XII EuPA Congress, a joint meeting with the Spanish Proteomics Society (SEProt) and the Portuguese Proteomics Association (ProCura), both celebrating their 7th Congress. Santiago de Compostela is a historical UNESCO-protected city, famous for its pilgrims’ way and its 520 year old university. It is the capital of Galicia and is very close to North Portugal, which makes it an ideal location for this joint meeting.

We have prepared an interesting program for you that combines a variety of events, several of which are specially devoted to young researchers. Overall, we had close to 200 abstracts submitted, from which 69 have been selected for oral presentations distributed between the different topic sessions. In addition, we have 11 prestigious invited speakers who will be giving plenary lectures. Please check out our website (www.eupa2018.com) to download the complete program. We are especially pleased to have Prof. Ruedi Aebersold to give the Opening Lecture of the congress. Prof. Aebersold will be also named Honorary Member of SEProt for his outstanding contribution to the Proteomics field.

Besides the main scientific sessions, we will have various parallel activities. For instance, the EuPA Bioinformatics Community (EuBIC) initiative organizes a bioinformatics bazaar that will be available during the congress. In addition, the Young Proteomics Investigator Club (YPIC) is running a specific session on Sunday 17th early afternoon, before the Opening Session. Moreover, YPIC will also organize meet-the-expert breakfast sessions during the congress. We would like to encourage young researchers coming to the congress to participate actively in all these activities devoted to them. In line with the latter, we also have an exciting educational program that is taking place on Saturday 16th at the Faculty of Medicine, next to the congress venue. We have two workshops run in parallel: one organized by EuBIC, focused on bioinformatics, and a second one, organized by EuPA, focused on Cytoscape. We hope many of you decided to register for these events.
One of our priorities, as congress organizers, has been to facilitate young investigators to come to the meeting so we kept and even decreased the congress fees compared to previous years. Moreover, EuPA and SEProt awarded 20 travel grants (10 each) for young researchers. In addition, we have a Young Investigator Prize (YIP), selected among those presenting their application following the acceptance of an abstract. Prizes to the best posters will be also given during the closing ceremony. Talking about prizes, we have two important ones to be announced during the closing ceremony: the Juan Pablo Albar Proteome Pioneer Award 2018, sponsored by EuPA, and the SEProt-Juan Pablo Albar Prize, sponsored by Bruker. The former intends to honour a person involved in EuPA with a leading and long-standing involvement in the promotion of the principles of sharing and integrating resources for the development of excellent research in the Proteomics field. The SEProt prize acknowledges outstanding proteomic-related scientific activities by Spanish scientists carrying out their main work in Spain.

Finally, we cannot conclude without thanking the support of all our sponsors; without them, this congress would not be possible. Lunch seminars supported by these companies will take place during the congress so please check out the congress website for further information. As recognition, EuPA will award the company that best contributed to the scientific/technological advances in proteomics in the last year with the EuPA Industry Award, a ceremony taking place at the closing session of the congress.

We hope you will enjoy our congress and your time in Santiago de Compostela, a place to discover; do not miss the opportunity to walk the streets of the old city and enjoy the gastronomy and amiability of the composteláns. You will have time for science and much more.

Benvidos and have a great congress!!

Dr. Ángel García  
President of the Spanish Proteomics Society  
Email: angel.garcia@usc.es

Dr. Deborah Penque  
President of the Portuguese Proteomics Society  
Email: deborah.penque@insa.min-saude.pt
An official journal of

**EuPA**

**EUROPEAN PROTEOMICS ASSOCIATION**

**Editor-in-Chief: Juan J. Calvete**

Spanish Research Council (CSIC), PEDECIBA (Uruguay), Head of the Structural and Functional Venomics Laboratory, Instituto de Biomedicina de Valencia, Spain

Since 2008 *Journal of Proteomics* has been publishing fundamental and clinical research in diverse fields of proteomics research, aimed at protein scientists and analytical chemists.

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<td><strong>Plenary Session II</strong></td>
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<td>11:00 – 13:00</td>
<td><strong>T. Session I: Cellular Proteomics</strong></td>
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<td>(A. Carlos V)</td>
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<td>19:30 – 20:30</td>
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<td><strong>Guided tour</strong></td>
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**PROGRAMME GENERAL OVERVIEW**
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<th>Time</th>
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<tr>
<td>08:30 – 10:00</td>
<td>Plenary Session IV</td>
<td>08:45 – 09:30 Plenary Session VI</td>
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<td>10:00 – 11:00</td>
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<tr>
<td>11:00 – 13:00</td>
<td>T. Session V: Disease Proteomics I (A. Carlos V)</td>
<td>09:30 – 10:15 T. Session IX: Top-down (C. Monumental)</td>
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<td>11:00 – 13:00</td>
<td>T. Sessión VI: Animal &amp; Plants (C.Monicnental)</td>
<td>10:15 – 11:00 T. Session X: Food &amp; Nutrition (C.Monicnental)</td>
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<td>Bruker Lunch Seminar (A. Carlos V) Lunch &amp; Posters</td>
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<td>15:00 – 16:30</td>
<td>Plenary Session V</td>
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<td>Break &amp; Posters</td>
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<td>16:45 – 18:45</td>
<td>T. Session VII: Standardization (A. Carlos V)</td>
<td>13:00 – 15:00 Biognosys Lunch Seminar Lunch &amp; Posters</td>
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<td>T. Session VIII: Disease Proteomics II (C. Monumental)</td>
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<td>18:35 – 18:50</td>
<td>Presentation EU-FT-ICR-MS Project</td>
<td>15:00 – 16:00 Plenary Session VII</td>
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<td>19:00 – 20:00</td>
<td>YPIC Challenge award</td>
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<tr>
<td>21:00</td>
<td>Gala Dinner at Hostal dos Reis Católicos</td>
<td>16:00 – 17:30 Awards &amp; Closing Remarks</td>
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SATURDAY 16TH JUNE

Pre-Congress Workshops & C-HPP Meeting
Venue: Faculty of Medicine; University of Santiago de Compostela, all day.
EuPA Educational Program: Cytoscape.
EuBIC workshop.
C-HPP meeting.
C-HPP and EuPA GC dinners

SUNDAY 17TH JUNE

09:00-13:00 C-HPP meeting
(Venue: Faculty of Medicine)
EuPA GC meeting
(Venue: Hotel Monumento San Francisco – Sala Columns)
13:00-17:30 YPIC session
(Hotel Monumento San Francisco – Sala Cimabue)

Registration opening
16:30 Hotel Monumento San Francisco

Plenary Session I: Opening Session & SEProt Honorary Member designation
Chairs: Deborah Penque, Ángel García.
18:30-19:30 The Proteotype: Integrator of Biological Information and Determinator of Phenotypes
Prof. Dr. Ruedi Aebersold
ETH Zurich. Inst. f. Molekulare Systembiologie. Switzerland

Welcome Reception
19:30 Hotel Monumento San Francisco

MONDAY 18TH JUNE

Meet the expert session
07:30-08:15 EUPA YPIC Meet the expert session

Plenary Session II: Proteomics in Cell Biology
Chairs: Montserrat Carrascal, Mercedes Pardo
08:30-09:15 Proteomics and data integration for unraveling the mysteries of spermatogenesis
Charles Pineau. Protim (Proteomics Core Facility Biogenouest). Irset – Inserm
U1085, Rennes, France

09:15-10:00 **OMICS TOOLS TO CHARACTERIZE PLATELET FUNCTION**
Albert Sickmann. Leibniz-Institut für Analytische Wissenschaften – ISAS – e.V. Dortmund, Germany

10:00-11:00 **Coffee Break & Posters**

**Topic Session I: Cellular Proteomics**
Chairs: Charles Pineau, Mercedes Pardo

11:00-11:20 **Searching for Ghost Proteins Interactome.**
Cardon Tristan. PRISM, France.

11:20-11:40 **Dissecting the Molecular Portrait of Ground State Pluripotency with Quantitative Proteomics**
Javier Muñoz. CNIO, Spain.

11:40-11:55 **The histone code studied by bottom-up label-free Mass Spectrometry: how comprehensive is the current picture?**
Maarten Dhaenens. Ghent University, Belgium.

11:55-12:10 **Quantitative proteomics and whole transcriptomics sequencing of Progeria-derived cells point to a key role of nucleotide metabolism in premature aging**
Maria del Carmen Arufe. UDC, Spain.

12:10-12:25 **Macrophages reactivation inside glioma microenvironments through PC1/3 inhibition associated with TLR3 activation**
Melanie Rose. PRISM, France.

12:25-12:40 **Role of exosomal Cx43 in melanoma progression**
Adrián Varela. INIBIC, Spain.

12:40-12:55 **Mechanisms of IL-33 activation through proteolytic maturation by environmental allergens analyzed by mass spectrometry**
Anne Gonzalez de Peredo. CRNS, France.

**Topic Session II: PTMs.**
Chairs: Albert Sickmann, Montserrat Carrascal

11:00–11:20 **A missing value-compatible algorithm to calculate absolute phosphorylation stoichiometry from LFQ-DIA, SILAC and TMT-based data.**
Alexander Hogrebe. NNF Center for Protein Research, Denmark.

11:20–11:40 **Histidine phosphorylation as another dimension of the phosphoproteome.**
Clement Potel. Utrecht University, The Netherlands.

11:40–12:00 **Comprehensive quantification of the modified proteome reveals oxidative heart damage in mitochondrial heteroplasmy.**
Jesús Vázquez. CNIC, Spain.

12:00–12:20 **Quantitative phosphoproteomics reveals novel phosphosites downstream Kappa-opioid receptor in human spermatozoa.**
12:20–12:40 **Quantitative proteomics reveals neuronal ubiquitination of Rngo/Ddi1 and several proteasomal subunits by Ube3a, accounting for the complexity of Angelman syndrome.**

_Ugo Mayor. University of the Basque Country, Spain._

12:40–13:00 **Application of thiol redox proteomics to clinical samples – valve heart disease and ischemic stroke.**

_Antonio Martínez-Ruiz. IIS-IP, Spain._

13:00-15:00 **Thermofisher Lunch Seminar**

_Expanding the Biomolecular Structural Analysis Capabilities using Orbitrap Technology._

_Sega Ndiaye, Thermo Fisher Scientific_  
_Fast, Sensitive and Quantitative Phosphoproteomics for Large-scale Cell Perturbation Analysis._

_Jesper Olsen, Novo Nordisk Foundation Center for Protein Research, Denmark_

**Lunch & Posters**

**Plenary Session III: Systems biology and quantitative proteomics**

15:00-15:45 **Dissecting EGF receptor signaling in-vivo by Quantitative Interaction Proteomics and Phosphoproteomics**

_Jesper Olsen. Novo Nordisk Foundation Center for Protein Research. University of Copenhagen. Denmark_

15:45-16:30 **Using a mass spectrometer as a microscope: a physical map of a human cell**

_Anne-Claude Gingras. The Lunenfeld-Tanenbaum Research Institute. Toronto. Canada._

16:30-16:45 **Break & Posters**

**Topic Session III: From Proteomics to integrated omics: data management and interpretation.**

_Chairs: Juan Antonio Vizcaíno and Cristina Ruiz-Romero_

16:45-17:05 **Creating a comprehensive functional map of the human phospho-proteome.**

_JA Vizcaíno. EMBL-EBI, UK._

17:05-17:25 **Proteogenomics of adenosine-to-inosine RNA editing in model organisms.**

_Sergei Moshkovskii. Institute of Biomedical Chemistry Moscow, Russia._

17:25-17:45 **Systems proteomics of gene expression.**

_Georg Kustatscher. Wellcome trust Edinburgh, UK._
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17:45-18:00 **ProteoRE, a Galaxy-based infrastructure for annotating and interpreting proteomics data.**
Yves Vandenbrouck. CEA, INSERM, France.

18:00-18:15 **VSClust: Feature-based variance-sensitive clustering of proteomics data.**
Veit Schwämmle. University of South Denmark, Denmark.

18:15-18:30 **Scop3P: the bridge between human phosphosites, protein structure and PRIDE data.**
Pathmanaban Ramasamy. VIB-UGent, Belgium.

18:30-18:45 **Benefits of rapid profile of modifications with SpecOMS**
Dominique Tessier. INRA, France.

**Topic Session IV: Microorganisms and microbiota**
Chairs: Concha Gil, Ana Varela-Coelho

16:45-17:00 **Rapid determination of host-pathogen quaternary protein structures in complex biological samples**
Johan Malmström. Lund University, Sweden.

17:00-17:15 **Absolute Quantification of Pseudomonas aeruginosa TonB-dependent Transporters Using PRM and SWATH-MS.**
Sandra Söderholm. University of Basel, Switzerland.

17:15-17:30 **Signatures of commensal and pathogenic Staphylococcus epidermidis: a genomic and proteomic approach**
Ana Varela-Coelho. ITQB NOVA, Portugal.

17:30-17:45 **Data-independent acquisition: high-throughput proteomic tool to monitor the response of Candida albicans to human macrophages.**
Ahinara Amador. UCM, Spain.

17:45-18:00 **Listeria monocytogenes planktonic and sessile cells adaptation to different temperatures seen through shotgun proteomics**
Tiago Santos. INRA, France.

18:00-18:15 **Candida albicans induces changes in human macrophage proteins involved in RNA-splicing, protein synthesis and apoptosis.**
Catarina Oliveira Vaz. UCM, Spain.

18:15-18:30 **An unbiased metaproteomic approach to describe the mucosal microbiome of HIV-exposed african infant cohort**
Suereta Fortuin. University of Cape Town, South Africa.

18:30-18:45 **Quantitative proteomics to study N and C metabolisms in the marine Cyanobacterium prochlorococcus**

18:45-19:30 **SEProt GC Meeting**
Guided tour:

TUESDAY 19TH

Meet the expert session
07:30-08:15 EUPA YPIC Meet the expert session

Plenary Session IV: Clinical Proteomics

SCIEX

Chairs: Ignacio Casal, Francisco Amado

08:30-09:15 MALT1 paracaspase activity and scaffolding regulation of linear ubiquitination, NFkB and therapeutic rescue
Chris Overall. University of British Columbia. Vancouver. Canada

09:15-10:00 (Phospho)Proteomics for marker and target discovery in cancer
Prof. Dr. Connie R. Jimenez. VU University Medical Center. Amsterdam. The Netherlands

10:00-11:00 Coffee Break & Posters

Topic Session V: Disease Proteomics I
Chairs: Ignacio Casal and Francisco Amado.

11:00-11:15 Cancer Moonshot Center Lund, Sweden
György Marko-Varga. Lund University, Sweden.

11:15-11:30 HMGB1 interactome analysis in epithelial cancer cells.
Aida Inés Barreiro-Alonso. UDC, Spain.

11:30-11:45 Parallel reaction monitoring-based strategy to validate colorectal cancer biomarkers in serum/plasma.
Consuelo Marin-Vicente. CIB-CSIC, Spain.

11:45-12:00 Serum extracellular vesicles contain protein biomarkers for primary sclerosing cholangitis and cholangiocarcinoma
Félix Elortza. CIC BioGUNE, Spain.

12:00-12:15 Early proteome dynamics of glioblastoma cells during the oncolytic adenovirus DNX-2401 infection
Andrea Gonzalez Morales. Navarrabiomed, Spain.

12:15-12:30 Investigating protein interactions of the long non-coding RNA MALAT-1 in brain tumors
Maike Langini. MPL – BMFZ, Düsseldorf, Germany

12:30-12:45 High-resolution quantitative proteomics applied to the discovery of biomarkers of innate immune response in tuberculosis.
Jesús Mateos. CSIC, Spain.
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12:45-13:00  **A MALDI-TOF MS Comparative Approach for Disclosing a Novel Peptide Biomarker Signature of Gingivitis**  
Chiara Villella. University “Magna Graecia”, Italy.

**Topic Session VI: Proteomics in Agriculture Biotechnology and Animal Proteomics**  
*Chair: Jesús Jorrín*

11:00-11:20 **Natural variation and pan-omics approach drove discovery of novel wood quality biomarkers in Pinus pinaster Aiton**  
Luis Valledor. University of Oviedo, Spain.

11:20-11:40 **ChloroKB: a web-application for the integration of knowledge related to chloroplast metabolic network**  
Myriam Ferro. CEA, France.

11:40-12:00 **Differentiation of the geographical origin of tiger nut (Cyperus esculentus) through a proteomic approach**  

12:00-12:15 **Immunoproteomic approaches to solve the proteomic profile of olive pollen and its complex allergogram**  
Pablo San Segundo Acosta. UCM, Spain.

12:15-12:30 **The alliance of proteogenomics & multiplexed targeted ecotoxico-proteomics for environmental monitoring of river water quality**  
Duarte Gouveia. CEA Marcoule, France.

12:30-12:45 **Study of myofibrillar proteome from pre-slaughter stressed animals using liquid isoelectric focusing and mass spectrometry.**  
Claudia Fuente García. IATA, Spain.

12:45-13:00 **Cultivation type makes a difference: the proteome of monolayers and spheroids of canine osteosarcoma cells.**  
Ingrid Miller. University of Veterinary Medicine, Austria.

13:00-15:00 **Bruker Lunch Seminar**

**Towards deeper, faster and more sensitive proteomics**  
Unleashing the power of QTOF technology for proteomics with TIMS and PASEF  
Pierre-Olivier Schmit, Bruker Daltonique, France

The Stable Isotope Labeling Kinetics (SILK) road: turnover, synthesis and breakdown of proteins in vivo  
Jérôme Vialarêt, University of Montpellier, LBPC-IRMB, CHU Montpellier, Montpellier, France

**Lunch & Posters**
Plenary Session V: Technology & Methodology Advances in Proteomics

Chairs: Félix Elortza, Jose Luis Capelo

15:00-15:45 The RNA binding proteome in time and space
Kathryn Lilley. Cambridge Centre for Proteomics. University of Cambridge, UK

15:45-16:30 Making use and sense of more data in mass spectrometry imaging
Benjamin Balluff. Maastricht University, Netherlands

16:30-16:45 Break & Posters

Topic Session VII: Standardization & Technological Innovation

Chairs: Félix Elortza, José Luis Capelo

16:45-17:00 Determination of site specific phosphorylation ratios in proteins with targeted mass spectrometry

17:00-17:15 Trapped ion mobility spectrometry with parallel accumulation – serial fragmentation (TIMS-PASEF): pushing the limits of shotgun proteomics analysis
Pierre-Olivier Schmit. Bruker SAS, France.

17:15-17:30 Targeted proteomics method comparison: SRM, PRM and SWATH-MS to quantify proteins in bovine muscle tissues
Joanna Bons. IPHC, France.

17:30-17:45 Towards absolute and generic top-down quantitative proteomics through combination of elemental and molecular mass spectrometry
Francisco Calderon. University of Oviedo, Spain.

17:45-18:00 Protein interaction screen on peptide matrices (PRISMA) dissect motif specific binding partners
Daniel Perez Hernandez. Max Delbruck Center, Berlin, Germany

18:00-18:15 The combination of protein, peptide and lipid MALDI-IMS analysis allows a deeper insight in Molecular Histology
Ibon Iloro. CIC BioGUNE, Spain.

18:15-18:30 Development of a novel LC concept for clinical proteomics
Alexandre Podtelejnikov. EVOSEP, Odense, Denmark

18:30-18:45 Suitability comparison of EDTA-plasma, heparin-plasma and serum for shotgun proteomics
Antonio Núñez Galindo. Nestle Institute of Health Sciences, Lausanne, Switzerland

Topic Session VIII: Disease Proteomics II

Chairs: Ángel García, Jesús Vázquez

16:45-17:10 An update on the Human Plasma Proteome
Jochen Schwenk. SciLifeLab (KTH), Sweden.

17:10-17:30 Protein aggregates enriched from blood as new and promising subproteome for biomarkers discovery in neurodegeneration
Rocco Adiutori. Queen Mary University of London, UK.
17:30-17:50 Deep-Dive in the Proteome of Human Cerebrospinal Fluid: A Comprehensive Database and Resource for the Discovery of Biomarkers and Missing Proteins
Charlotte Macron. Nestlé Institute of Health Sciences, Lausanne, Switzerland

17:50-18:05 Olfactory Proteomic Survey unveils a Stage-dependent Proteostasis Imbalance in Parkinson’s disease
Mercedes Lachén. Navarrabiomed, Spain.

18:05-18:20 A two-step PRM strategy identifies a new biomarker signature in cerebrospinal fluid for multiple sclerosis prognosis
Marin Philippe. University of Montpellier, CNRS INSERM, France.

18:20-18:35 Cardiovascular risk stratification in young population: application of thiol redox proteomics
Nerea Corbacho Alonso. HNP, Spain.

Presentation of the EU-FT-ICR-MS Project
18:35-18:50 Presentation of the EU-FT-ICR-MS Project

YPIC challenge award
19:00-20:00 YPIC challenge award

Gala Dinner
21:00 Hostal dos Reis Católicos

WEDNESDAY 20TH

Plenary Session VI: Top-down proteomics
Chair: Juan J Calvete

08:45-09:30 The Increasingly Important Role of Top-Down Proteomics and the Proteoform in Human Health and Disease
Neil Kelleher. Northwestern University, Evanston, USA

Topic Session IX: Top-down and Chemical Proteomics

09:30-09:45 A systematic map of protein-metabolite interactions reveals principles of chemical communication
Ilaria Piazza. ETH Zurich, Switzerland.

09:45-10:00 Structural elucidation of proteoforms from Actinobacteria by Top-down MS
Julien Parra. CNRS IPBS, France.

10:00-10:15 An integrated workflow for cross-linking/mass spectrometry
Marta Mendes. Technische Universität Berlin, Germany.
**Topic Session X: Food & Nutrition Proteomics**  
*Chairs: Paola Roncada, Miguel Ángel Sentandreu*

10:15-10:30 **Optimisation of protein extraction for in-depth profiling of the cereal grain proteome**  
*Utpal Bose. C CSIRO, Queensland, Australia*

10:30-10:45 **Characterization of short digestion-resistant peptides of cow’s milk allergens by digestomics approach**  
*Tanja Cirkovic Velickovic. Ghent University Global Campus, South Korea*

10:45-11:00 **Differentiation between fresh and frozen–thawed curled octopus using two-dimensional gel and shotgun proteomics**  
*Chiara Guglielmetti. Istituto Zooprofilattico Sperimentale del Piemonte, Italy.*

11:00-11:30 **Coffee Break & Posters**

**Topic Session XI: Disease Proteomics III**  
*Chairs: Fernando Corrales, Bruno Manadas*

11:30-11:45 **Multi-omics and functional investigations in hepatic and skeletal muscle mitochondria of pre-diabetic mice**  
*Lisa Kappler. University Hospital of Tübingen, Germany.*

11:45-12:00 **Exosomes as new players in dedifferentiation and cartilage remodelling in osteoarthritis**  
*Marta Varela Eirín. INIBIC, Spain.*

12:00-12:15 **An optimized protocol for the analysis of laser microdissected muscle tissue samples for mass spectrometry**  
*Britta Eggers. Ruhr-University Bochum, Germany.*

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12:15-12:30 Verification of rheumatoid arthritis activity biomarkers by targeted proteomics.  
Lucía González Rodríguez. INIBIC, Spain.

12:30-12:45 Integrating Serum Proteomics, Metabolomics and Lipidomics to Study the Effect of Sport Activity  
Marcello Manfredi. University of Piemonte Orientale, Italy.

12:45-13:00 Unravelling a knee Osteoarthritis-associated Autoantibody profile for early diagnosis: Data from the Osteoarthritis Initiative  
Maria Camacho Encina. INIBIC, Spain.

Biognosys Lunch Seminar

13:00-15:00 Longitudinal Plasma Profiling with stable isotope standards and data-independent acquisition analysis  
Sebastian Müller, Biognosys

Use of a novel DIA acquisition for enhanced throughput analysis with an exploratory targeted reagent strategy in Clinical Proteomics Research  
David Heywood, Waters Corporation

Lunch & Posters

Plenary Session VII: Closing Session  
Chairs: Deborah Penque, Ángel García

15:00-16:00 A proteomic map of the target landscape of clinical kinase inhibitors  
Bernhard Küster. Technische Universität München, Germany

16:00-16:45 Juan Pablo Albar EuPA and SEProt Awards ceremony.
16:45-17:15 Young Investigator Prize, Industry Award, and poster prizes.
17:15-17:30 Closing remarks
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