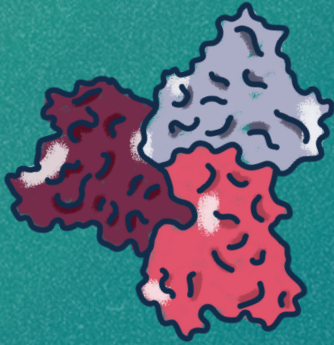


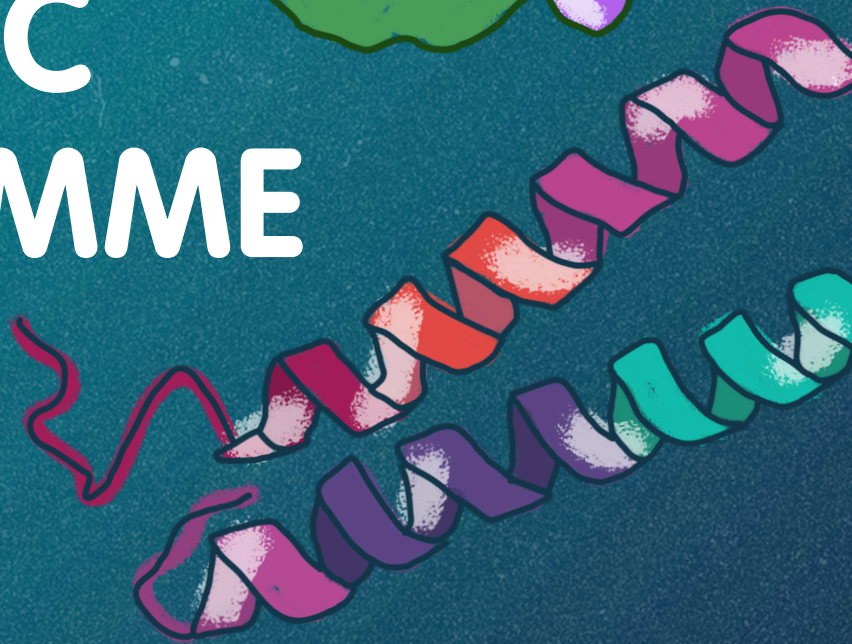
Proteo Vilamoura

6th Joint Meeting of Spanish,
French and Proteomics Societies

20-22 May 2026, Vilamoura, Portugal



SCIENTIFIC PROGRAMME



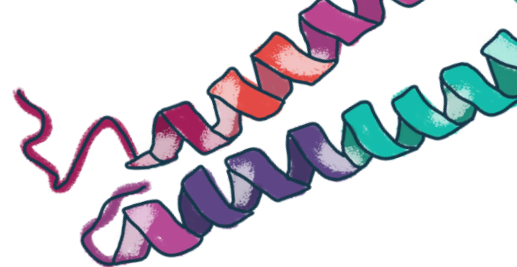
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May 20 Wednesday

9:30 - 12:00 (Pre-congress course optional)

Practical Introduction to Python Programming

Diego Mena Santos, Samuel Lozano Juárez

11:00 - 13:00

REGISTRATION

13:00 - 13:15

Welcoming Session

13:15 - 13:45

Nelson Soares Invited speaker

Proteomics profiling of Red Blood Cells (RBCs) combined with Deep Machine Learning analysis – reveals potential Diagnostic Biomarkers for Acute Venous Thromboembolism

Section 1 | Chairs: José Alexandre Ferreira, Hugo Osório

Proteomics in the Clinic: From Biomarkers to Precision Medicine #1

13:45 - 15:00

Oral Communications

Deep plasma EV proteomics by Data-Independent Acquisition reveals circulating signatures of cardiac tissue injury in a preclinical Atrial Fibrillation model, Estefanía Núñez

Expanding the knowledge on diagnostic autoantibodies in colorectal cancer through proteomics and immunosensing platforms, Javier Velázquez Gutiérrez

Sponsor

Thermo/Unicam: Orbitrap Astral Series MS - Bernard Delanghe

Mapping the circulating extracellular vesicle proteome in Marfan syndrome patients using minimal plasma volume, Diego Mena Santos

Methylthioadenosine: harnessing a natural metabolite to counteract cholestasis progression, Irene Blázquez García

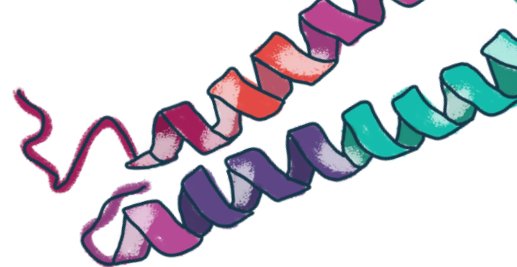
15:00 - 15:45

Coffee Break + Poster Session 1

15:45 - 16:15

Cherine Bechara Invited speaker

Structural Proteomics Reveals Chemokine Receptor Interactions and Dynamics



May 20 Wednesday

Section 2 | Chairs: Ana Varela Coelho, Felix Elortza
Next-Gen Proteomics: Single-Cell, Proteogenomics & Disruptive Technologies

16:15 - 17:15

Oral Communications

Integrative single-cell proteomics identifies pro-regenerative fingerprints in a sub-population of adult cardiomyocytes, Consuelo Marin-Vicente

Sponsor

Preomics: Advancing Plasma Proteomics Through a Next-Generation Enrichment Workflow for Deeper and More Quantitative Biomarker Discovery, Ann-Christine König

Benchmarking single-cell FACS-assisted strategies: effects on cellular component bias and post-translational modification detection, Samuel Lozano Juárez

Sponsor

Quilaban: Illumina Protein Prep: high-plex NGS-based proteomics designed to integrate with the Illumina Multiomics ecosystem, Álvaro Sánchez-Bernabéu

17:15 - 17:51

Flash presentations

In depth-analysis of Alzheimer's disease brain tissue reveals novel A β interactors, Ana Montero Calle

Proteomic and functional characterization of SLC8A1 in colorectal cancer development and metastasis, Sara Batuecas Domínguez

DIV Matters: Understanding Proteomic Shifts in Neuronal Maturation for Better Ischemic Modeling, Eva Ferro

In-depth serum glycoproteomics reveals stage-dependent α 2,6-sialylation and systemic prothrombotic signalling in gastric cancer, Lisandra Gabriela Fernandes Cruz

Comprehensive nucleolar proteome profiling reveals metastasis-associated remodeling in colorectal cancer, Elisa Carral Ibarra

When One is Enough: A Minimalistic "On-Pot" Proteomic Workflow for Global Profiling of Single Caenorhabditis elegans, Ibon Iloro Manzano

MALDI-MSI as a Platform for Spatial Multi-Omics in Glioblastoma Research, Cristina María López Vázquez

Beyond Acquisition: Turning Astral-Scale Data into Discovery: A Modular GUI for DIA Proteomics Analysis in a Core Facility Marta Isasa

Optimizing tissue disruption strategies to characterize in vivo subcellular proteome remodelling, María Cinta Picos Mora

18:00 - 18:45

Cocktail reception + Sci BINGO, organized by Young Investigators in Proteomics - SEPROT



May 21 Thursday

6:30-7:30

Sunrise Run/walk by the beach

8:30 - 9:00

Enrique Santamaria Invited speaker

Olfactory proteomics: Emerging mechanisms and translational opportunities in neurological disorders

Section 3 | Chairs: Avais Daulat, Deborah Penque

Proteomics in the Clinic: From Biomarkers to Precision Medicine #2

9:00 - 10:15

Oral Communications

Glycoproteomics uncovers a paucimannosylated proteome associated with tumour aggressiveness and poor clinical outcome in gastric cancer, Dylan Ferreira

Artificial intelligence-based clinical models predict plasma proteomic endotypes enabling precision medicine in knee osteoarthritis, Patricia Quaranta Díaz

Sponsor

Sciex Narrow-Window Scanning DIA: Redefining Selectivity and Quantitative Confidence in Proteomics with the SCIEX ZenoTOF 8600, Mário Armelão

Proteomic biomarkers predictive of response to antiangiogenic treatment: toward personalized medicine in neovascular age-related macular degeneration, Antonio Cañizo Outeiriño

Unravelling the proteome of human embryo implantation: new biomarkers and metabolic signatures, Girard Océane

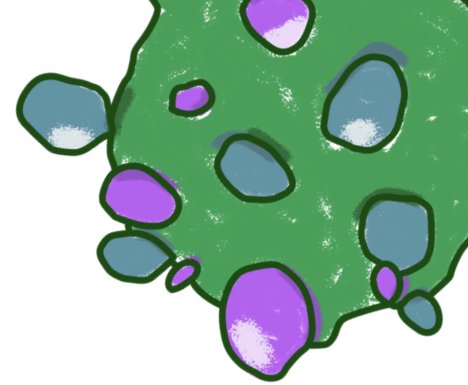
10:15 - 11:00

Coffee Break + Poster Session 2

11:00 - 11:30

Etienne Coyaud Invited speaker

Proximity labeling tools to investigate pathogenic protein networks



May 21 Thursday

Section 4 | Chairs: Eduardo Chicano-Galvez, Montserrat Carrascal
Networks in Action: Interactomes, Signalling & Bioinformatics Innovation

11:30 - 12:45

Oral Communications

Deciphering protein-protein interactions in live neurons using XL-MS, Hugo Gizardin-Fredon

Proteomic profiling of the interactome of phosphorylated Tau aggregates identifies modulators of Alzheimer's disease progression, Sofía Jiménez de Ocaña

Sponsor

Bruker: Harvesting the potential of 4D-omics approaches with the timsTOF product range, Pierre-Olivier Schmidt

Glycoavatars: bead-coated membrane models for studying the cancer-immune cells interactome, Andreia Rafaela Linhares Miranda

Orail facilitates angiogenesis after myocardial infarction through Notch1 signaling pathway, Isabel María Galeano Otero

12:45 - 14:30

Lunch Break

Sponsor

13:30 - 14:00

Sponsor Workshop : From Biosamples to Bioinsights - Bruker
Rafaelo Room (1st Floor)

Sponsor

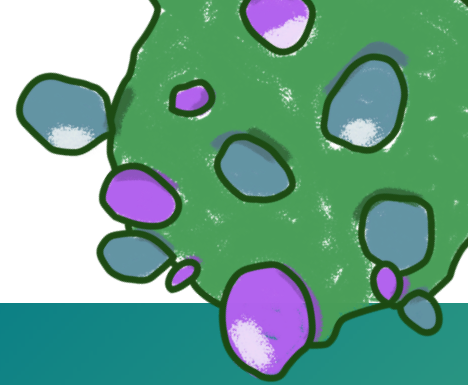
14:00 - 14:30

Sponsor Workshop - Thermo/Unicam - Rafaelo Room (1st Floor)

14:30 - 15:00

Ana Martinez del Val Invited speaker

Decoding Protein Function: How Proteomics Reveals Post-Translational Control in Cell Signalling and Disease



May 21 Thursday

Section 5 | Chairs: Hugo Osório, Avais Daulat
PTMs: Deciphering the dynamics of Protein Regulation

15:00 - 16:00

Oral Communications

Experimental design and multivariate analysis approaches for glycoproteomics, Estela Giménez López

Study of the links between the dysregulations of metabolism and epigenetics marks in Huntington's disease, Hisham Altoufaily

Phosphoproteomics as a tool to dissect the molecular mechanisms underlying a novel combinatorial therapeutic strategy in pseudomyxoma peritonei, Antonio Romero-Ruiz

Quantitative proteomic characterization of metastasis-associated succinylome in colorectal cancer, Raquel Rejas González

16:00 - 16:45

Coffee Break + Poster Session 3 + Group photo

16:45 - 17:15

Mélanie Blein-Nicolas Invited speaker

Proteomics as a cornerstone in deciphering the genotype-phenotype relationship in maize

Section 6 | Chairs: Monserrat Carrascal, Ana Varela Coelho
Proteomics Exploration in Non-Model Systems

17:15 - 18:30

Oral Communications

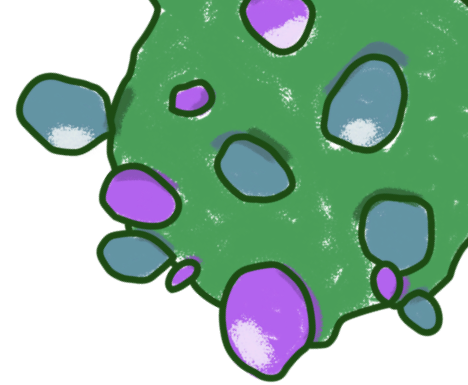
Geographical origin differentiation of tiger nut (*Cyperus Esculentus*) through liquid chromatography-high resolution mass spectrometry analysis, Enrique Sentandreu

Transforming Invasion into Innovation: Proteomics of *Rugulopteryx okamurae* for Monitoring, Degradation and Biomass Valorization, Almudena Escobar Niño

Affinisep: High-Throughput SPE Membrane Approaches for Peptide Cleanup and Enrichment, Michel Artocarena

Proteomic characterization of baculovirus expression vector system (BEVS)-derived extracellular vesicles engineered for Gla-Rich Protein (GRP) γ -carboxylation reveals selective GRP incorporation and distinct vesicle populations, Carla Alexandra São Bento Viegas

Authentication of A2 bovine milk by routine LC-MS proteomic analysis, Lorea R. Beldarrain



May 21 Thursday

Section 6 | Chairs: Monserrat Carrascal, Ana Varela Coelho Proteomics Exploration in Non-Model Systems

18:30 - 19:02

Flash presentations

Phenotypic remodelling of smooth muscle cells in atherosclerosis: a low-input and single-cell proteomics approach, David del Rio Aledo

Multi-omics characterization of SIRT3 metabolism and its adaptation to the presence of amyloid-beta oligomers in nasal epithelial cells, Paz Cartas Cejudo

Extending Proteome Profiling to Red Blood Cells using an Aptamer Platform, Luis André Botelho de Carvalho

BiasTracker: a bioinformatics tool for quantifying physicochemical and functional biases in mass spectrometry-based proteomics, Gaelle Louffi

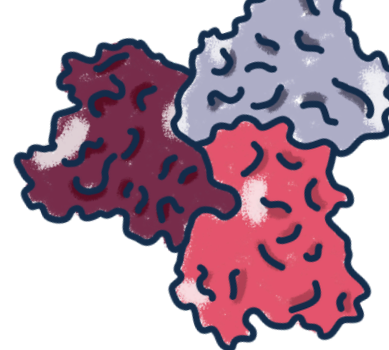
Comparative HLA-DR immunopeptidomics reveals disease- and genotype-associated signatures in rheumatoid arthritis, Jaxaira Maggi

Scaling-up low input spatial proteomics using Evosep Whisper Zoom on the timsTOF Ultra AIP, Beatriz Rocha Loureda

From Microbes to Ecosystems: Proteomic Insights into Agro-Environmental Interactions, Francisco Javier Fernandez Acero

20:30

Conference Dinner (optional, subject to registration and payment)



May 22 Friday

6:30-7:30

Sunrise Run/walk by the beach

8:30 - 9:00

Celso Reis Invited speaker

Glycomics and glycoproteomics in cancer: from oncogenic mechanisms to clinical applications

Section 7 | Chairs: Delphine Pflieger, Hugo Osório Quantitative and Computational Proteomics

9:00 - 10:15

Oral Communications

Global protein turnover dynamics in pluripotency, Orhi Barroso Gomila

Defining the Topology of Proteins in sEV Isolates by Protein Correlation Profiling,
Joanes Etxeberria Ugartemendia

Thermo/Unicam

Advanced applications for Orbitrap Astral Series MS - Bernard Delanghe

Are Your Replicates Independent? - Defining Experimental Units in Primary Neuron Proteomics, Miguel Maria Varandas Anão Rosado

Continuous telemetry-driven quality control for proactive LC-MS performance in proteomics core facilities, Daniel Lopez-Ferrer

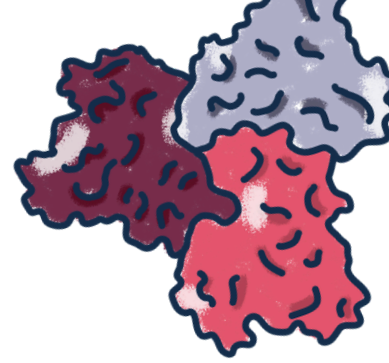
10:15 - 11:00

Coffee Break + Poster Session 4

11:00 - 11:30

Guadalupe Gómez Baena Invited speaker

Proteomics at the Service of Biodiversity Conservation



May 22 Friday

Section 8 | Chairs: Felix Elortza, Deborah Penque Beyond Proteins: Small Molecules, Peptides & Integrated Omics + 5. Environmental and Ecosystem Omics-Insights

11:30 - 12:30

Oral Communications

High-Throughput PISA-TMT Proteomics Enables Target Identification of Novel Antimicrobial Small Molecules, Gonçalo Raposo Matos

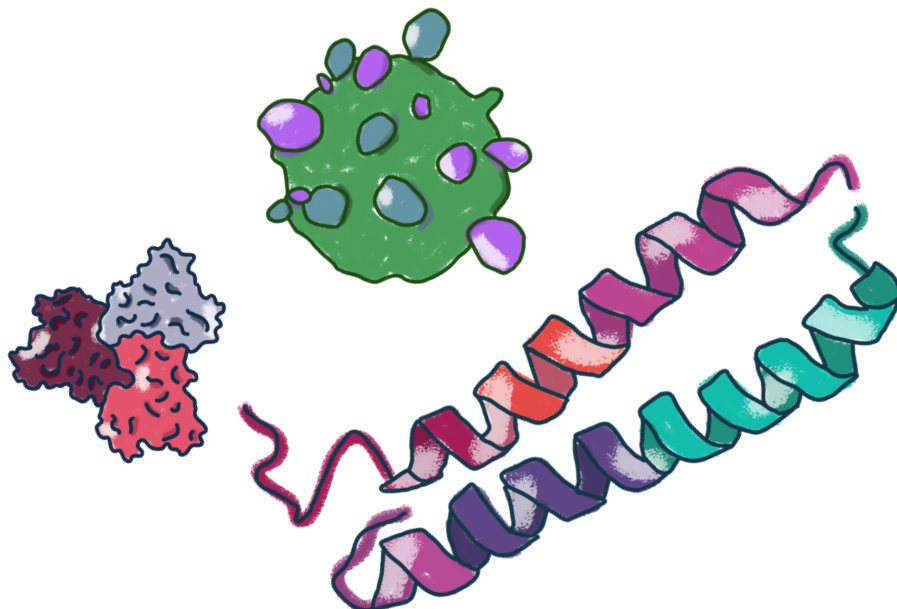
Molecular responses of Staphylococcus epidermidis to pH and endogenous antimicrobial fatty acids are strain-specific, Ana Maria Varela Coelho

Sewage protein information mining: A new frontier in community health and industrial surveillance, Montserrat Carrascal Perez

Seasonal dynamics of urinary protein profiles in the Iberian Lynx (Lynx pardinus), Beatriz Ortiz-Guisado

12:30

Closing Session/Awards



Session 1

| | | |
|-------|--|--|
| F1.01 | In depth-analysis of Alzheimer's disease brain tissue reveals novel A β interactors | Ana Montero Calle |
| F1.02 | Proteomic and functional characterization of SLC8A1 in colorectal cancer development and metastasis | Sara Batuecas Domínguez |
| F1.03 | DIV Matters: Understanding Proteomic Shifts in Neuronal Maturation for Better Ischemic Modeling | Eva Maria Ferro Abril Monteiro |
| F1.04 | In-depth serum glycoproteomics reveals stage-dependent α 2,6-sialylation and systemic prothrombotic signalling in gastric cancer | Lisandra Gabriela Fernandes Cruz |
| F1.05 | Comprehensive nucleolar proteome profiling reveals metastasis-associated remodeling in colorectal cancer | Elisa Carral Ibarra |
| F1.06 | When One is Enough: A Minimalistic "On-Pot" Proteomic Workflow for Global Profiling of Single <i>Caenorhabditis elegans</i> | Ibon Iloro Manzano |
| F1.07 | Scaling-up low input spatial proteomics using Evosep Whisper Zoom on the timsTOF Ultra AIP | Beatriz Rocha Loureda |
| 1.08 | Analysis of the involvement of GLG1 and BAIAP2 in colorectal cancer by functional proteomics | Ana García Romero |
| 1.09 | Proteomic differences between high- and low-grade medullary thyroid carcinomas | Alberto Peláez García |
| 1.10 | Functional proteomics characterization of neurochondrin in colorectal cancer | María Garranzo Asensio |
| 1.11 | Discovery of protein biomarkers for the diagnosis of Equine Metabolic Syndrome | Elisa M ^a Espinosa López |
| 1.12 | Molecular signatures of Macrophage-to-foam cell transition induced by dyslipidemic and atherosclerotic serum | Jorge Cabañas Penagos |
| 1.13 | Functional characterization of the mitochondrial protein NDUFAF4 and implications in cholestasis | Américo Cerqueira Mateo |
| 1.14 | Advancing Plasma Proteomics Through a Next-Generation Single-Particle Enrichment Workflow for Deeper and More Quantitative Biomarker Discovery | Karin Yeoh |
| 1.15 | Secretomic profiling of triple-negative breast cancer media using Mag-Net™ HP | Previn Naicker |
| 1.16 | QuickFit DualStream: A plug-and-play dual-column ion source for high-throughput proteomics | Adolfo Fernandez Gomez de Enterria |
| 1.17 | Spatial single-cell proteomics on routine Papanicolaou-stained liquid-based cervical cytology | Laura Cantero González-Salazar |

Session 2

| | | |
|-------|--|----------------------------------|
| F2.18 | Beyond Acquisition: Turning Astral-Scale Data into Discovery: A modular GUI for DIA Proteomics Analysis in a Core Facility | Marta Isasa |
| F2.19 | Optimizing tissue disruption strategies to characterize in vivo subcellular proteome remodelling | María Cinta Picos Mora |
| 2.20 | Plasma proteomic biomarkers of Hutchinson–Gilford progeria syndrome: evidence from a mouse model | Inés Perales Sánchez |
| 2.21 | Exploring the molecular link between aortic stenosis and chronic kidney disease through DIA-PASEF-based plasma proteomics | Laura Mourino-Alvarez |
| 2.22 | Unique high-throughput workflow for deeper plasma/serum proteome coverage enables discovery of potential biomarkers | Ann-Christine König |
| 2.23 | Integrated serum proteomics and autoantibody profiling reveal a protein signature predictive of flare in rheumatoid arthritis during biologic tapering | Cristina Ruiz-Romero |
| 2.24 | CSF proteomic profiling for biomarker identification in patients with MCI | Daniela Araújo |
| 2.25 | Proteomic pathway alterations in mouse hippocampus and prefrontal cortex following chronic citalopram treatment | Verônica Techmeier Morato |
| 2.26 | Organ-specific proteomic response to semaglutide treatment in healthy mice | Lucía Beltrán Camacho |
| 2.27 | ML-Driven Clinical-Proteomics Identifies a 6-Protein Signature for Precise Atherosclerosis Stratification | M ^a Carmen Durán Ruiz |
| 2.28 | Proteomic landscape of the PBMCs from diabetic patients with and without diabetic complications: preliminary results | Josefa Benítez Camacho |
| 2.29 | Analysis of Plasma Depleted Samples for Chronic Diseases' Biomarker Discovery with the Orbitrap Astral Mass Spectrometer | Rodrigo Barderas |
| 2.30 | Phenotypic characterization of breast cancer cells using stochastic proteomic profiling | Kamami Sarah |
| 2.31 | Novel Insights into Red Blood Cell Dysregulation in Obstructive Sleep Apnea: a multi-omic approach | Sofia Maria Sentieiro Neves |
| 2.32 | Pathophysiological subtypes of mild cognitive impairment due to Alzheimer's disease identified by CSF proteomics | Bruno Manadas |
| 2.33 | Changes at salivary proteomic level elicited by exposure to food odorants | Carla Sofia da Silva Simões |
| 2.34 | Proteome-Informed Therapeutic Prioritisation for Patient-Specific Prescriptomics in Muscle-Invasive Bladder | João de Matos Reis Aleixo Montes |

Session 3

| | | |
|-------|---|----------------------------------|
| F3.35 | Multi-omics characterization of SIRT3 metabolism and its adaptation to the presence of amyloid-beta oligomers in nasal epithelial cells | Paz Cartas Cejudo |
| F3.36 | Phenotypic remodelling of smooth muscle cells in atherosclerosis: a low-input and single-cell proteomics approach | David del Rio Aledo |
| F3.37 | From Microbes to Ecosystems: Proteomic Insights into Agro-Environmental Interactions | Francisco Javier Fernandez Acero |
| 3.38 | High-sensitivity N-glycopeptide identification in human plasma using electron-activated dissociation | Javier Lago Nuñez |
| 3.30 | Fast and robust phosphoproteomics sample prep with AttractSPE® Disks C18 Tips for high phosphopeptide recovery and identification | Michel Arotcarena |
| 3.40 | Small-molecule post-translational modification in <i>Chlamydomonas reinhardtii</i> | Víctor García-Riaño Domínguez |
| 3.41 | Comparison of Strategies for Global Glycoprotein Profiling by LC-MS | Javier Beaskoetxea Lejarzegi |
| 3.42 | Sequential analysis of differential protein abundance, glycosylation and phosphorylation in WNT7A overexpressing MDA231 cells | Mikel Azkargorta |
| 3.43 | Exploring glycosylation alterations during atherosclerosis progression | Emilio Camafeita |
| 3.44 | Preconditioning therapy prevents site-specific oxidation of Trp/Cys redox sensors in contractile and metabolic cardiac proteins | Inmaculada Jorge Cerrudo |
| 3.45 | VPS4A validation as a Parkin substrate | Ainhoa Atxa Espiga |
| 3.46 | Metaproteomics in an Archaeological Environment: A Pipeline for Deciphering Ancient Remains | María Luz Valero Rustarazo |
| 3.47 | Seasonal protein variations of wild boar meat | Miguel Angel Sentandreu |
| 3.48 | Tracking 10 Stages of a Fruit Fly's Life Cycle with High-Throughput Proteomics | Iraide Escobés Corcuera |
| 3.49 | Secretome analysis to understand the intracellular traffic networks in fungi | Silvia Rodríguez Pires |

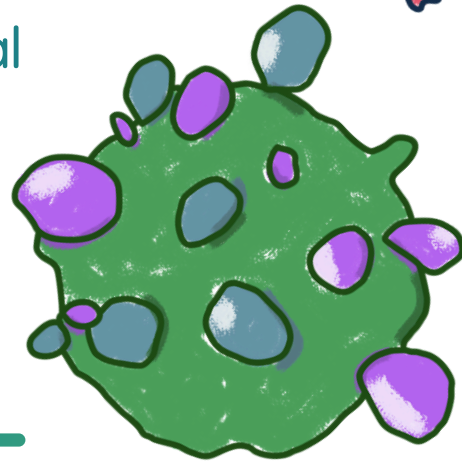
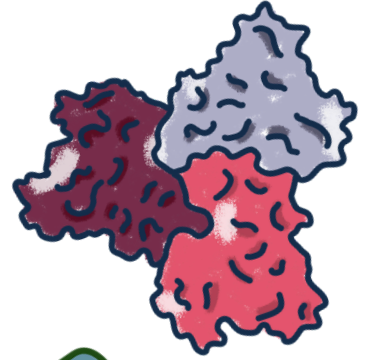
Session 4

| | | |
|-------|---|--|
| F4.50 | Extending Proteome Profiling to Red Blood Cells using an Aptamer Platform | Luis André Botelho de Carvalho |
| F4.51 | BiasTracker: a bioinformatics tool for quantifying physicochemical and functional biases in mass spectrometry-based proteomics | Gaelle Loutfi |
| F4.52 | Comparative HLA-DR immunopeptidomics reveals disease- and genotype-associated signatures in rheumatoid arthritis | Jaxaira Maggi |
| F4.53 | MALDI-MSI as a Platform for Spatial Multi-Omics in Glioblastoma Research | Cristina María López Vázquez |
| 4.54 | Plasma Proteome Equalization Uncovers Dysregulated Proteostasis and Amyloidogenic Pathways in Multiple Myeloma | Inês de Freitas Domingos |
| 4.55 | Towards the Development of a Liquid Chromatography Free Workflow for Measurement of Clinically Important Proteins | Pierre-Olivier Schmit |
| 4.56 | Universal pipeline unlocking inter taxonomic differential abundance analyses: Brain matrisome characterization across mouse, ferret and human | Gianluca Arauz Garofalo |
| 4.57 | Proteomic Signatures Rescued by Two Candidate Molecules in a Zebrafish Model of CDKL5 Deficiency Disorder | Márcio Alexandre Filipe Simão |
| 4.58 | Label Free Quantitative Proteomics reveals MAM remodeling and immunometabolic adaptation in LPS-activated Microglia | Vivian de los Ríos Benítez |
| 4.59 | Quantitative DIA-PASEF proteomic profiling reveals molecular alterations in a murine model of retinopathy of prematurity | Viviane de Almeida Bastos |
| 4.60 | Kuiper enables effective, fast and reliable library-free analysis of DIA Immunopeptidomics data | Jorge Peinado-Izaguerra |
| 4.61 | Ultrasound-Assisted Dental Peptidomics Reveals Integrated Host, Dietary, and Microbial Signatures | Raquel Inês Oliveira Lourenço da Fonseca |
| 4.62 | Exploring the proteomics capabilities of a new Trapped Ion Mobility Q-TOF designed for enhanced metabolomics performances | Pedro Cano |
| 4.63 | Red blood cell modulation in response to COVID-19 vaccination – A multiomics study | Joana Saraiva |

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