

POSTER PRESENTATIONS

All even numbered posters will be presented on Sunday and Monday
All odd numbered posters will be presented on Tuesday and Wednesday

Cellular Proteomics

Disease & Clinical Proteomics

Drug & Biopharmaceutical Proteomics

Precision & Personalised Proteomics

Methods, Systems & Bioinformatics

Human Proteome Project

Cellular Proteomics

A-001

Cell surface antigen-antibody microarray as a tool for detection macrophages polarization

Mohamed Saiel Saeed Alhamdani, Dkzf, Germany

A-002

The novel role of ADAM17 cytoplasmic domain in modulating redox state via Thioredoxin-1

Rute Alves Pereira E Costa, Brazilian Bioscience National Laboratory, Brazil

A-003

Thermal proteome profiling for drug discovery

Isabelle Becher, EMBL, Germany

A-004

Role of lipolysis in cancer

Ruth Birner-Gruenberger, Medical University Graz, Austria

A-005

Genetic wiring maps of single protein states reveal on off-switch for GPCR signaling

Onno Bleijerveld, The Netherlands Cancer Institute, Netherlands

A-006

Natural Polysaccharide Peptide (PSP) promotes an IFN and TLR4 induced anti-HIV response in human monocytes

Nawal Boukli, Universidad central del caribe, United States

A-007

Understanding GSK3 β function in cancer cells through precision knockout coupled to high resolution LC-MS/MS

Emily Bowler, University Of Southampton, United Kingdom

A-008

Proteome analysis of alveolar epithelial type II cells in response to pulmonary aspergillus fumigatus Infection

Thilo Bracht, Ruhr-Universität Bochum, Germany

A-009

Characterization of Data-Independent Acquisition (DIA) capabilities of a Q-TOF instrument for complex proteomics samples

Peter Brechlin, Bruker Daltonik GmbH, Germany

A-010

Global profiling of dehydration-induced mitochondrial dynamics and defense response in rice

Niranjan Chakraborty, National Institute Of Plant Genome Research, India

POSTER PRESENTATIONS

A-011

Proteomic analysis of Neutrophil Extracellular Traps (NETs) produced in response to PMA and A23187

Elinor Chapman, University Of Liverpool, United Kingdom

A-012

Retinoic acid induced specific changes in the Phosphoproteome of C17.2 Neural Stem Cells

Ping Chen, Hunan Normal University, China

A-013

Proteomics approach reveals the roles of mitochondria in NLRP3 inflammasome activation in Nasopharyngeal Carcinoma

I-Che Chung, Chang Gung University, Taiwan

A-014

Extracellular signaling in neuroblastoma through exosomes for novel drug targets discovery

Victor Corasolla Carregari, Fondazione Santa Lucia, Itália

A-015

Phosphoproteomic analysis of the neural progenitor to oligodendrocyte progenitor cell differentiation

Alireza Dehghani, University Of Bonn, Germany

A-016

A quantitative comparative proteomic approach to investigate Hülle cells from the filamentous fungus *Aspergillus nidulans*

Benedict Dirnberger, University Of Goettingen, Germany

A-017

Comparison of protocols for the processing of proteomics samples that are limited in quantity

Ute Distler, Institute for Immunology, UMC Mainz, Germany

A-018

Optimisation of sensitive and robust methods for characterisation of the PLK4-regulated phosphoproteome

Samantha Ferries, University Of Liverpool, United Kingdom

A-019

Regulation of peroxisomal matrix protein import by peroxin phosphorylation

Sven Fischer, Universität Freiburg, Germany

A-020

Proteome remodelling in senescent peritubular cells of human testis

Florian Flenkenthaler, LAFUGA, Gene Center, LMU Munich, Germany

A-021

Proteomic and phosphoproteomic analysis of cells lacking the catalytic activity of protein kinase CK2

Cinzia Franchin, University Of Padova, Italy

A-022

Impact of sulfation on SDF-1/receptor's extracellular domain interaction by affinity electrophoresis and mass spectrometry

Maud Fumex, Université-d'evry-val-d'essonne, France

A-023

Characterization of the signal transduction networks underlying the immunomodulation by the microbial metabolite trimethylamine.

Tariq Ganief, Pct, Germany

A-024

Lyn, a novel putative drug target for osteoporosis management

Shubhangi Gavali, National Institute For Research In Reproductive Health (icmr), India

A-025

Integrative proteo-metabolomic study illustrates role of nucleus in blast disease signaling and host-specific resistance

Sudip Ghosh, National Institute Of Plant Genome Research, India

A-026

Cell wall enrichment reveals further dysregulation in response to sub-MIC rifampicin stress

Alexander Giddey, University Of Cape Town, South Africa

A-027

Serologic profiling of the *Candida albicans* cell surface-associated proteome upon dimorphic transition in invasive candidiasis

Concha Gil, UCM, Spain

A-028

The signaling pathways of folliculin: a tumor suppressor in Birt-Hogg-Dubé syndrome

Iris Glykofridis, VUmc - CCA, Netherlands

POSTER PRESENTATIONS

A-029

New signaling pathways altered in restrictive cardiomyopathy revealed by tandem mass tag proteomics and phosphoproteomics

Aldrin Gomes, University Of California, Davis, United States

A-030

Phosphoproteomic analysis of acquired resistance to trastuzumab and dual HER2-blockade in HER2-positive breast cancer cells

Paula Gonzalez Alonso, Health Research Institute Fundacion Jimenez Diaz (IIS-FJD), Spain

A-031

Inactivation of endogenous tissue proteases by brief exposure to high hydrostatic pressure.

Vera Gross, Pressure Biosciences, Inc, United States

A-032

Analysis of human brain N-glycans by (PGC)-LC-ESI-MS using isotopically labeled standards

Clemens Grünwald-Gruber, University Of Natural Resources and Life Sciences, Austria

A-033

Complete proteomic description of ontogenic changes in haematopoietic stem and progenitor cells

Jenny Hansson, Lund University, Sweden

A-034

Evolutionary plasticity of neuroplastin basigin and embigin associated complexes with calcium and monocarboxylate transporters

Sebastian Henrich, University of Freiburg; Physiology Departement, Germany

A-035

Proteome variation related to thyroid regulation by iodide

Maha Hichri, Tiro CEA UNS, France

A-036

Analyzing the mechanisms of acquired resistance to MEK inhibitors in colorectal cancer using multi-proteomics approaches

Anna Jarzab, Technical University Of Munich, Germany

A-037

Protein iodination in thyroid function and regulation

Lun Jing, TIRO, France

A-038

Cell type-specific proteogenomics in the infarcted heart

Inmaculada Jorge, Centro Nacional De Investigaciones Cardiovasculares (cnic), Spain

A-039

Label-free differential phosphoproteomic analysis of recombinant chinese hamster ovary cells reveals growth related phosphoproteome modifications.

Prashant Kaushik, Dublin City University, Ireland

A-040

Serine palmitoyltransferase protein interaction landscape and structural characterisation

Van Kelly, University Of Edinburgh, United Kingdom

A-041

Somatic MED12 nonsense mutation escapes mRNA decay and reveals a motif required for nuclear entry

Salla Keskitalo, University Of Helsinki, Finland

A-042

Proteome and transcriptome analyses of phosphorylation site-specific mutants of BRG1, a chromatin remodeling component

Ayuko Kimura, Yokohama City University, Japan

A-043

Co-exposure of silver nanoparticles and Cd²⁺ induce disruption of the metabolic reprogramming in HepG2 cells

Frank Kjeldsen, University Of Southern Denmark, Denmark

A-044

Glycoproteomic and glycomic analysis of human induced pluripotent stem cells and stem cell-derived cardiomyocytes

Sarah Konze, Hannover Medical School, Germany

A-045

Quantitative interactome and phosphoproteome analysis identifies novel signaling components of parkinson's disease-associated kinase PINK1

Hidetaka Kosako, Tokushima University, Japan

POSTER PRESENTATIONS

A-046

Novel hypoxia-driven pro-angiogenic mechanisms unveiled by secretomics analysis of mammary CAFs

Fernanda Kugeratski, CRUK Beatson Institute, United Kingdom

A-047

Mechanistic insights into Ca²⁺ dependent regulation of cell cycle by label-free LC-MS/MS.

Anna Kwasnik, UCD, Ireland

A-048

Comprehensive analysis of human protein N-termini enables assessment of various protein forms

Cheolju Lee, Korea Institute of Science and Technology, Korea

A-049

Evaluation of dimethylated arginine containing peptides by LC-MS/MS with Electron Transfer Dissociation

Stephanie Lehman, University Of Virginia, United States

A-050

Proteome-wide identification of ADP-ribose acceptor sites in mammalian cells and mouse tissues

Mario Leutert, University Of Zurich, Switzerland

A-051

Comprehensive analysis of sulfonated cysteines in human peroxiredoxin 1 by Orbitrap Mass Spectrometry

Hong Li, Rutgers New Jersey Medical School, United States

A-052

Functional lipidomics: palmitic acid impairs hepatocellular carcinoma development by modulating membrane fluidity and glucose metabolism

Lyn Lin, Fudan University, China

A-053

Quantitative proteomics analysis of a primary bladder cell line treated with ketamine

Jo-chuan Liu, Chang Gung University, Taiwan

A-054

Impact of alternative splicing on the cellular proteome quantified by targeted proteomics

Yansheng Liu, Eth Zurich, Switzerland

A-055

Interactome analysis of the RLTPR protein reveals its essential role in T cells

Camoin Luc, Marseille Proteomics, France

A-056

Proteomics analysis of white blood cells in healthy humans

Alexey Lyashkov, National Institute On Aging, United States

A-057

Identification of cross-linked peptides in proteins subjected to photo-oxidation

Michele Mariotti, Technical University of Denmark, Denmark

A-058

Proteomic analysis of the impact of metabolic status and genetic predisposition on oviduct fluid composition

Katrin Meyer, LMU Munich, Germany

A-059

MRM and PRM assay development for a panel of >3,000 proteins from 20 mouse tissues

Sarah Michaud, Uvic Genome Bc Proteomics Centre, Canada

A-060

A draft proteome map of the Ginseng(Panax Ginseng C. A Meyer): mass spectrometry-based proteomic approach

Cheol Woo Min, Pusan National University, South Korea

A-061

Quantitative proteomic study of macrophage proteins interacting with candida albicans using an ATP affinity enrichment

Lucia Monteoliva, Complutense University of Madrid, Q28180141, Spain

A-062

Complete native SILAC of prototrophic yeast for proteome-wide quantification

Marcel Morgenstern, University Of Freiburg, Germany

A-063

Targeted proteomics of t helper cell transcription factors and lineage specific markers

Robert Moulder, University Of Turku, Finland

POSTER PRESENTATIONS

A-064

Expression and association of CDK10 with ETS2 proteins during human corneal epithelial wound healing

Shamim Mushtaq, Ziauddin University, Pakistan

A-065

A comprehensive analysis of glycome profiles on formalin-fixed paraffin-embedded mouse tissue sections

Chiaki Nagai-Okatani, National Institute of Advanced Industrial Science And Technology, Japan

A-066

Extracellular matrix function using integrated omics dissect cell wall mediated immune dynamics in wilt disease

Kanika Narula, National Institute Of Plant Genome Research, India

A-067

Global secretome analysis of human macrophages upon activation of innate immune response

Tuula Nyman, University Of Oslo, Norway

A-068

Phosphoproteomic analysis of murine synaptosome in sleep deprivation

Oliver Ozohanics, RCNS Hung. Acad. Sci., Hungary

A-069

Characterization of protein-protein interactions in the synapse by chemical cross-linking mass spectrometry

Iwan Parfentev, Max-Planck-Institute for Biophysical Chemistry, Germany

A-070

cIAPs as regulators of FALS-associated mutant SOD1

Byoung Chul, Park, KRIBB, South Korea

A-071

Membrane proteome of failing heart. Combined forces of trypsin and cyanogen bromide

Jiri Petrak, Biocev, First Faculty of Medicine, Czech Republic

A-072

Quantitative phosphoproteomic analysis reveals shared and specific targets of Arabidopsis MAPkinases MPK3, MPK4 and MPK6

Delphine Pflieger, CNRS, France

A-073

Radiation-induced endothelial inflammation is transferred via secretome to recipient cells in a STAT-driven process

Jos Philipp, Helmholtz Center Munich, Germany

A-074

The impact of protein thiol redox status on foetal and adult haematopoiesis

Kristyna Pimkova, Lund University, Sweden

A-075

Quantitative proteomic analysis of the interactome of mammalian S/MAR (scaffold/matrix attachment region) elements

Monika Puchalska, Max Planck Institute of Immunobiology and Epigenetics, Germany

A-076

A Lysis-free, vesiculation-based methodology to isolate high purity cell membranes for proteomics and lipidomics applications

Bini Ramachandran, National Centre For Biological Sciences (ncbs), India

A-077

Quantitative analysis of signaling pathways using 11plex TMT reagents and comprehensive phosphopeptide enrichment strategies

John Rogers, Thermo Fisher Scientific, United States

A-078

Proteomics analysis of heat shock proteins in glioblastoma cell lines induced by different drugs

Jose Cesar Rosa, Ribeirão Preto Medical School University Of São Paulo, Brazil

A-079

Analysis of mitochondrial protein interactome by in-organello chemical crosslinking and mass spectrometry

Elena Rudashevskaya, Leibniz-Institut für Analytische Wissenschaften-ISAS-e.V., Germany

A-080

Extent of growth-related and drug-induced proteome changes in cancer cells

Pierre Sabatier, Karolinska Institutet, Sweden

POSTER PRESENTATIONS

A-081

Triple extraction enables mass spectrometry-based proteomics and phospho-proteomics and is compatible with robust multi-omics analysis

Virginia Sanchez-quiles, Curie Institute, France

A-082

Investigations of LysN cleavage capability at biotinylated lysines

Peter Schein, Institute of Biochemistry and Molecular Biology, University of Bonn, Germany

A-083

Comprehensive, unbiased proteomic profiling of the cell-surface, exosomal, and secreted proteomes of senescent cells

Birgit Schilling, Buck Institute for Research on Aging, United States

A-084

Dissecting the subcellular secretory glycoproteome with SWATH

Ben Schulz, The University Of Queensland, Australia

A-085

Comparative, LFQ-based proteomic analysis of growth-phase dependent changes of Lactobacillus kunkeei isolates from honeybee

Christian Seeger, Uppsala University, Sweden

A-086

Quantitative profiling of post-translational modifications by labeling-based mass spectrometry approaches

Baozhen Shan, Bioinformatics Solutions, Inc., Canada

A-087

Understanding the molecular effects of antipsychotics on oligodendrocytes through phosphoproteomics and their relation with schizophrenia

Juliana Silva Cassoli, University Of Campinas (unicamp), Brazil

A-088

Effects of myristic acid on metabolism in hepg2 cells investigated by a proteomic approach

Giulia Speziali, University Of Verona, Italy

A-089

Quantitative map of beta-lactone induced virulence regulation

Matthias Stahl, TU München, Germany

A-090

GLP-1 analogues modulate MAPKs activity but not the heat shock response in human HepG2 cells

Ali Tiss, Dasman Diabetes Institute, Kuwait

A-091

A primary human cell line for down syndrome studies

George Tsangaris, Biomedical Research Foundation Of The Academy Of Athens, Greece

A-092

Proteomics analysis of skeletal muscle in healthy human

Ceereena Ubaida-Mohien, National Institute On Aging, United States

A-093

Proteomic insights into cancer-related extracellular proteolysis with cathepsin K

Matej Vizovišek, Jožef Stefan Institute, Slovenia

A-094

PhD abstract competition winner. Poster will be located by the innovation stage

Dynamics of the neuronal surface proteotype

Marc van Oostrum, ETH Zürich, Switzerland

A-095

Highly sensitive detection of adaptation in Staphylococcus aureus applying chemical tagging of newly synthesized proteins

Uwe Volker, University Medicine Greifswald, Germany

A-096

Characterization of NLRP3 inflammasome signaling pathway by proteomics

Jian Wang, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, China

A-097

Integrative organelle proteomics for deep characterization of the mitochondrial proteome

Bettina Warscheid, Uni Freiburg, Germany

POSTER PRESENTATIONS

A-098

Mining drug resistant targets from non-small cell lung cancer by phosphoproteomics

Shao-hsing Weng, Academia Sinica, Taiwan

A-099

Functional determination of a single methylation site in the human proteome using CRISPR/Cas9 and MS/MS

Marc Wilkins, University Of New South Wales, Australia

A-100

Secretome analysis of BSA-free cardiomyocyte differentiation

Hanna Wolling, Hannover Medical School, Germany

A-101

Quantitative proteomics reveals temporal changes of signal pathways in BV2 microglial cell activation

Jongmin Woo, Seoul National University, South Korea

A-102

EGFR interactome reveals multiple pathways and regulatory mechanism of drug-resistance in non-small cell lung cancer

Pei-Shan Wu, Academia Sinica, Taiwan

A-103

Myristoylation of human FMN2 protein causes individual localization pattern and function

Kayo Yamada, University of Dundee, United Kingdom

A-104

OST3 proteins link glycosylation and magnesium transport

Kent Yuen Benjamin, Yeo, School of Chemistry and Molecular Biosciences, University of Queensland, Brisbane, Australia, Australia

A-105

Elucidating the secondary cell wall cellulose synthase complex stoichiometry by multiple reaction monitoring

Xueyang Zhang, Umea University, Sweden

A-106

Ageing influence central carbon metabolism in a tissue specific manner

Rakesh Arya, International Center For Genetic Engineering And Biotechnology, New Delhi, India, India

A-107

Matrisome landscape of head and neck squamous cell carcinoma (HNSCC)-associated fibroblasts

Stéphane Audebert, Marseille Protéomique - Centre De Recherche En Cancérologie De Marseille, France

A-109

Environmental enrichment increases ribosomal, microtubule and metabolic proteins in pig hippocampus

Anna Bassols, Universitat Autònoma De Barcelona, Spain

A-110

Cardiotonic steroids reveal high interference on calcium-binding/dependent protein expression in H9c2 and Hek-293 cells

Cesar Batista, Ibt-unam, Mexico

A-111

A dynamic picture of the ubiquitinome upon proteasome inactivation.

Jeroen Demmers, Erasmus University Medical Center, Netherlands

A-113

Comparative study on skeletal muscle proteins from various vertebrate and invertebrate animals by agarose 2-DE

Masamichi Oishi, Kitasato University School Of Science, Japan

A-114

Social network architecture of human immune cells unveiled by quantitative proteomics

Jan Rieckmann, Max Planck Institute of Biochemistry, Germany

A-115

Investigation of cardiotoxicity in 3D human cardiac microtissue model

Parveen Sharma, University Of Liverpool, United Kingdom

A-116

Mass spectrometric analysis of complete cellular proteome via direct digestion of cells

Yun Xiong, Fudan University, China

A-117

Quantitative DUB interactomics to investigate the biology of DUBs

Jayaprakash Natarajan, University of Dundee, United Kingdom

POSTER PRESENTATIONS

Drug & Biopharmaceutical Proteomics

B-001

Phosphoproteomics of non-small-cell lung cancer cells treated with erlotinib reveals drug-resistant signatures and potential targets

Jun Adachi, National Institutes Of Biomedical Innovation, Health And Nutrition, Japan

B-002

Optimization of biotin enrichment protocols for the analysis of biotinylated proteins by LC-MS/MS

Shiva Ahmadi, University Of Bonn, Germany

B-003

Quantitative proteomic analysis of drug transporters in human blood brain barrier

Zubida Al-majdoub, The University Of Manchester, United Kingdom

B-004

Advanced data-acquisition methods for intact protein analyses by 21 Tesla FT-ICR mass spectrometry

Lissa Anderson, NHMFL-FSU, United States

B-005

Towards minute-made MS assays using surface acoustic wave nebulisation (SAWN)

Alina Astefanei, University Of Amsterdam, Netherlands

B-007

Next-generation positional proteomics - navigating substrate degradomes with quantitative digital terminome maps

Ulrich auf dem Keller, ETH Zurich, Switzerland

B-008

Identifying allergenic peptides presented class I major histocompatibility complex molecules on keratinocytes

Alistair Bailey, University Of Southampton, United Kingdom

B-009

Application of high-throughput serum proteomic strategy using DIA-MS

Ryotaro Ban, Yokohama City University, Japan

B-010

Parallel accumulation – serial fragmentation (PASEF) on a trapped ion mobility spectrometry QTOF instrument

Scarlet Beck, Bruker Daltonik GmbH, Germany

B-011

In-cell structural analysis of MeCP2 – a structural basis for (P225R) Rett syndrome?

Adam Belsom, The University of Edinburgh, United Kingdom

B-012

Deployment of DOSCAT technology to quantify proteins involved in paediatric pneumococcal meningitis pathogenesis

Richard Bennett, University Of Liverpool, United Kingdom

B-013

Robust high throughput dia plasma proteomics pipeline finds body mass index-associated increases in inflammatory pathways

Tue Bjerg Bennike, Harvard Medical School, Denmark

B-014

Multiplexed quantitative analysis using NeuCode SILAC metabolic labeling of signaling protein targets

Ryan Bomgardner, Thermo Fisher Scientific, United States

B-015

Biopharmaceutical characterization using size exclusion and cation exchange chromatography and high resolution native mass spectrometry

Jonathan Bones, National Institute For Bioprocessing Research And Training, Ireland

B-016

A novel FAIMS interface extend the sensitivity and depth of proteomic analyses

Eric Bonneil, IRIIC-Université de Montréal, Canada

B-017

Novel capillary-flow LC-MS platform for robust proteomics profiling of cell lysates and bio-fluids

Alexander Boychenko, Thermo Fisher Scientific, Germany

POSTER PRESENTATIONS

B-018

Uptake and distribution of the antidiabetic drug metformin into the perfused rat liver by MALDI-imaging

Giulio Calza, University Of Helsinki, Finland

B-019

HLA ligandomics drives the identification of targets for immunotherapeutics based on soluble T-cell receptors

Floriana Capuano, Immunocore Ltd, United Kingdom

B-020

Fast phosphoproteomics analysis of human jurkat T cells by HIFU-TiO₂-SCX-LC-MS/MS

Mónica Carrera, Spanish National Research Council (csic), Spain

B-021

Monitoring protein refolding process by disulfide linkage analysis of the intermediates using mass spectrometry

Sung-fang Chen, National Taiwan Normal University, Taiwan

B-022

Decoding site-specific alteration of Sialoglycoproteome in EGFR-subtype of non-small cell lung cancer towards precision medicine

Yi-Ju Chen, Academia Sinica, Taiwan

B-023

Combined top-down and bottom-up proteomics using capillary electrophoresis-mass spectrometry

Chien-hsun Chen, Thermo Fisher Scientific, United States

B-024

A new database search scoring method for better identification performance of endogenous small peptides

Yet-Ran Chen, Academia Sinica, Taiwan

B-025

Proteomic toolbox for understanding the interaction between nanodrugs and biomolecules

Susana Cristobal, Linköping University, Sweden

B-026

Universal solid-phase protein preparation (USP3) for bottom-up and top-down proteomics

Laura Dagley, The Walter and Eliza Hall Institute of Medical Research, Australia

B-027

SWATH® acquisition - a unique approach for untargeted metabolomics applications

Zuzana Demianova, Sciex, Germany

B-028

Robust, multiplexed ImmunoMRM assay for relative quantitation of phosphopeptides in DNA Damage Response (DDR) pathway

Joerg Dojahn, Sciex, Germany

B-029

Validation of antibodies using orthogonal methods

Fredrik Edfors, KTH, Sweden

B-030

Analysis of a super-sensitive in vitro diagnostic platform for Troponin I, a cardiovascular biomarker

Rachael Eineman, Stoller Biomarker Discovery Centre, United Kingdom

B-031

READYBEADS: A new tool to improve robustness and reliability in LC-MS analyses

Quentin Enjalbert, Anaquant, France

B-032

Cross-linking mass spectrometry database searches: perspectives and strategies for validation and error assessment

Michael Ewing, ETH Zürich, Switzerland

B-033

Fate of antigens encoded by self-amplifying RNA vaccines

Lucia Eleonora Fontana, Gsk Vaccines, Italy

B-034

All-inclusive proteoform profiling of serum proteins by hybrid mass spectrometry approaches

Vojtech Franc, Utrecht University, Netherlands

B-035

A dry method for preserving tear proteins

Youhe Gao, Beijing Normal University, China

POSTER PRESENTATIONS

B-036

Evaluation of KRASG12C cysteine-reactive inhibitors by proteomic cysteine profiling in living cells

Violette Gautier, Evotec, France

B-037

An organoruthenium anticancer agent shows unexpected target selectivity for plectin

Christopher Gerner, University Of Vienna, Faculty of Chemistry, Austria

B-038

Comparison of MALDI imaging sample preparation/DESI imaging for multimodal MSI of Pre-clinical breast cancer

Lee Gethings, Waters, United Kingdom

B-039

microDIA acquisition and software enables identification of peptides in pseudo-SRM MS/MS spectra from sequence databases

Michael Heaven, Vulcan Analytical, LLC, United States

B-040

Data independent versus data dependent acquisition mass spectrometry for proteomic classification of colorectal cancer subtypes

Alex Henneman, Netherlands Cancer Institute, Netherlands

B-041

The winning trio in Metaproteomic: 75 cm column, Orbitrap Fusion™ Lumos™ Tribrid™ and X!TandemPipeline

Celine Henry, Inra, France

B-042

Complex-centric proteome profiling by SEC-SWATH-MS reveals modularity and dynamics of the cellular proteome

Moritz Heusel, 1985, Switzerland

B-043

Optimization of SONAR collision energy ramps for different molecule classes

David Heywood, Waters, United Kingdom

B-044

Single amino acid resolution of glycosites using top-down UVPD of glycoproteins

Jenny Ho, ThermoFisher Scientific, United Kingdom

B-045

iST: a reproducible and universal sample preparation method for in-depth proteome discovery and interaction proteomics

Fabian Hosp, PreOmics GmbH, Germany

B-046

MRM mass spectrometry for quantification of histone H3 variants PTM marks in Arabidopsis Thaliana

Yajun Hu, Institutes of biomedical sciences, Fudan University, China

B-047

A TiO₂ based simultaneous multiple PTMomics enrichment strategy

Honggang Huang, Arla Foods Ingredients Group P/S, Denmark

B-048

Precise structural characterization of unsaturated lipids by 213 nm UV-Photodissociation MSn

Romain Huguet, Thermo Fisher Scientific, United States

B-049

Streamlined and sensitive sample preparation for phosphoproteomics using the EasyPhos workflow

Sean Humphrey, The University of Sydney, Australia

B-050

Assessing the selectivity of antibodies against various amyloid-beta species by an automated capillary based immunoassay

Melanie Hüttenrauch, University Medical Center Göttingen (UMG), Germany

B-051

Tracking subcellular localisation changes with Dynamic Organellar Maps using SILAC, TMT or LFQ

Daniel Itzhak, Max Planck Institute Of Biochemistry, Germany

B-052

Addressing the challenges of quantitative myelin proteomics

Olaf Jahn, Max-Planck-Institute of Experimental Medicine, Germany

POSTER PRESENTATIONS

B-053

A fast and sensitive LC-MS method for quantitation of a novel prodrug against Wilson's disease

Michel Jaquinod, CEA-Grenoble, France

B-054

Automated high-throughput sample preparation protocols for LC-MS/MS analysis of glyco-omics

Jongho Jeon, College Of Pharmacy, Gachon University, South Korea

B-055

EPIQ (Epic Protein Integrative Quantification): ultra-sensitive n-plexed isotopic labeling-based quantification by a model-based reconstruction method

Kyowon Jeong, Seoul National University, South Korea

B-056

Development of site-specific glycome analysis method of complex glycoproteome

Hiroyuki Kaji, National Institute Of Advanced Industrial Science & Technology, Japan

B-057

Nobel protein interaction analysis method: MIK-MS (Molecular Interaction and Kinetics Mass Spectrometry)

Takeshi Kawamura, The University of Tokyo, Japan

B-058

A novel approach for tracing 15N tracer in proteins

Jasmeet Kaur Khanijou, National University Of Singapore, Singapore

B-059

Protein target identification of label-free bioactive small molecule

Tae Young Kim, Chemical Genomics Global Research Laboratory, Department of Biotechnology, Yonsei University, South Korea

B-060

Novel-platform for discovery of an angiogenesis inhibitor and identification of target on tissues using-MALDI-MSI analysis

Yonghyo Kim, Chemical Genomics Global Research Laboratory, Department of Biotechnology, Yonsei University, South Korea

B-061

Swedish national infrastructure for biological and medical mass spectrometry

Sven Kjellstrom, Lund University, Sweden

B-062

A multiplexed LC-MS/MS based assay for quantification of biomarkers of neurodegeneration in mouse brain homogenates

Apoorva Kotian, UCB Celltech, United Kingdom

B-063

Building ProteomeTools based on a complete synthetic human proteome

Bernhard Kuster, Technical University of Munich, Germany

B-064

Implementation of a novel scanning quadrupole DIA acquisition method for DESI imaging

James Langridge, Waters Corporation, United Kingdom

B-065

Multiplexed MRM-based protein quantitation using two different stable isotope labeled isotopologues peptides for calibration

André LeBlanc, McGill University - Lady Davis Institute, Canada

B-066

Development of online 2D-NCFC-RP/RPLC system for extensive and efficient proteomic analyses

Hangyeore Lee, Korea University, South Korea

B-067

Identification of citrullinated proteins in human tissues

Chien-Yun Lee, Chair of Proteomics and Bioanalytics, Technical University of Munich, Germany

B-068

A core facility approach to affinity purification-data independent analysis for interactome analysis

Christof Lenz, University Medical Center Goettingen, Germany

POSTER PRESENTATIONS

B-069

Proteome-wide analysis of cysteine oxidation reveals metabolic sensitivity to redox stress

Sergio Lilla, Cruk Beatson Institute, United Kingdom

B-070

High throughput sensitive microLC-MS/MS for peptide quantitation in highly targeted assays

Erika Lin, Sciex, United States

B-071

Proteomics analysis of single cells using a carrier-assisted targeted mass spectrometry approach

Tao Liu, Pacific Northwest National Laboratory, United States

B-072

Zwitterionically functionalized soluble nanopolymers used for efficient glycopeptides enrichment

Jialin Liu, Fudan University, China

B-073

Application of CE-MS for the quantification of mono-phosphorylated isobaric peptides

Stephen Lock, Sciex, United Kingdom

B-074

2D-precursor selection for trapped ion mobility with parallel accumulation - serial fragmentation (TIMS-PASEF)

Markus Lubeck, Bruker, Germany

B-075

Top-down proteomics identifies specific post-translational O-mycoloylations, which target outer membrane proteins to the mycomembrane

Julien Marcoux, Institute Of Pharmacology And Structural Biology, France

B-076

Site-specific N-glycosylation analysis of human IgA isotypes produced in glyco-engineered plants by LC-ESI-MS

Daniel Maresch, University of Natural Resources and Life Sciences, Austria

B-077

Mass spectrometry characterization of DOTA-Nimotuzumab as innovative β - tracer in radio-guided surgery

Claudia Martelli, Catholic University, Italy

B-078

Considerations for selecting the optimal stationary phases for proteomic trap-and-elute nanochromatography

Roy Martin, Waters, United States

B-079

Unbiased search of antibiotic targets by thermal proteome profiling

André Mateus, European Molecular Biology Laboratory, Germany

B-080

Which proteins are responsible for the selective neuronal vulnerability in Parkinson's disease?

Caroline May, Medical Proteom-Center, Ruhr-University Bochum, Germany

B-081

Maximizing proteome coverage on an Orbitrap Fusion Lumos with an advanced precursor determination algorithm

Graeme McAlister, Thermo Fisher Scientific, United States

B-082

Evaluation of Mitra microsampling device for multiple reaction monitoring based measurement of proteins in serum

Miriam Meier, UCD Conway Institute of Biomolecular and Biomedical Research University College Dublin, Ireland

B-083

A new workflow for deep proteome profiling of the human sperm

Valdemir Melechco Carvalho, Fleury Group, Brazil

B-084

Quantitative dot blot analysis (QDB) reveals the variation of housekeeping proteins at population level

Tingting Men, Binzhou Medical University, China

POSTER PRESENTATIONS

B-085

Unexpected covalent modification of protein histidine residues by drug metabolites in vitro and in vivo

Xiaoli Meng, University Of Liverpool, United Kingdom

B-086

Targeted detection of peptides in complex matrices combining the MIDAS™ Workflow with the Skyline software

Dietrich Merkel, Sciex, Germany

B-087

Quantitative dot blot analysis (QDB), a versatile high throughput immunoblot method for validating proteomics results

Jia Mi, Binzhou Medical University, China

B-088

Novel highly sensitive, selective and reproducible method for quantitative analysis of redox cysteine modifications

Ruzanna Mnatsakanyan, ISAS, Germany

B-089

Implementation of 213 nm Ultra Violet Photo Dissociation (UVPD) on a modified Orbitrap Fusion Lumos

Christopher Mullen, Thermo Fisher Scientific, United States

B-090

Optimization of phase transfer surfactant-aided in-solution digestion method for an automated large-scale sample preparation system

Ryohei Narumi, National Institutes Of Biomedical Innovation, Health And Nutrition, Japan

B-091

Proteome analysis of exhaled breath condensate before and after space flight

Evgeny Nikolaev, Skoltech, Russian Federation

B-092

Molecular Imprinted Polymers (MIPs) for the detection of low abundance proteins as biomarkers for NSCLC

Rachel Norman, University Of Leicester, United Kingdom

B-093

Structural proteomics uncovers the dynamic of DNA response element-transcription factor interaction

Petr Novak, Institute of Microbiology, Czech Republic

B-094

Highly sensitive quantitative phosphoproteomics and primary-sequence-based scoring reveals putative substrates of ERK

Kosuke Ogata, Graduate School of Pharmaceutical Sciences Kyoto University, Japan

B-095

Effect of intestinal flora on drugs, glucose and lipid metabolism in mouse

Sumio Ohtsuki, Kumamoto University, Japan

B-096

BioUb strategy: a key tool to study protein ubiquitination applied to investigate the Angelman Syndrome

Nerea Osinalde, University Of The Basque Country (upv/ehu), Spain

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Characterization of site-specific N-glycoproteins in DBS sample by LC-MS/MS with minimal sample preparation

Gun Wook Park, Korea Basic Science Institute, Korea

B-098

Screening of Mycobacterium tuberculosis 19kDa antigen proteoforms by top-down and bottom-up approaches

Julien Parra, CNRS IPBS, France

B-099

Capillary Electrophoresis – mass spectrometry for intact mass analysis of antibodies and antibody-drug-conjugates

Aran Paulus, Thermo Scientific, United States

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On-line immunoaffinity capillary electrophoresis-mass spectrometry using magnetic beads for protein biomarker analysis. Transthyretin in FAP-I

Roger Peró-Gascón, University of Barcelona (UB), Spain

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Rapid, rugged, and reliable screening methods for serum peptide degradomics profiling

Scott Peterman, Thermo Fisher Scientific, United States

B-102

Chemical and phosphoproteomics for mechanism of action analysis of AKT inhibitors in breast cancer

Svenja Petzoldt, Technical University of Munich, Germany

B-103

The loss-less and nano-flow SPIDER fractionator for high sensitivity, high coverage proteomics

Garwin Pichler, PreOmics GmbH,, Germany

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Comparison and optimization of global pSTY and pY-specific enrichment methods for mass spectrometry-based phosphoproteomics

Sander Piersma, Oncoproteomics Laboratory, VU University Medical Center, Netherlands

B-105

A mass spectrometry approach for the identification and localization of lysozyme modifications by acrolein

Andrew Pitt, Aston University, United Kingdom

B-106

Optimisation of methodologies for the in-solution preparation of human synovial fluid prior to SWATH-MS analysis.

Rachel Reed, Manchester University, United Kingdom

B-107

Prioritized iRT in spectral libraries generated from multiple sources for the targeted analysis of DIA

Lukas Reiter, Biognosys AG, Switzerland

B-108

An in vitro MS assay for sensitive determination of donor specific MHC class II immunopeptidomes

Ricardo Resende, Abzena, United Kingdom

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Increased efficiency for the preparation of complex proteomic samples

Michael Rosenblatt, Promega, United States

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Development of reference protein extraction protocols to quantify biotherapeutics in mice tissues by UPLC-sMRM

Blandine Rougemont, Ucb, United Kingdom

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Glycopeptide analysis to examine the role of chlamydial protease-like activity factor

Julian Saba, Thermo Fisher Scientific, Canada

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QCloud: An automated community cloud-based system for quality control in proteomics experiments

Eduard Sabidó, Centre De Regulació Genòmica, Spain

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Peptide-mediated 'miniprep' for high-throughput isolation of extracellular vesicles coupled to phosphoproteomics.

Tim Scheffhorst, Vumc, Netherlands

B-114

Displacement chromatography in two-dimensional liquid-chromatography for proteomics

Hartmut Schlueter, University Medical Center Hamburg-Eppendorf, Germany

B-115

Increasing dynamic range and sample insight for top-down proteoform profiling analysis.

Pierre-olivier Schmit, Bruker Daltonics, France

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Synthetic peptide reference standards for PTM proteomics

Karsten Schnatbaum, JPT Peptide Technologies GmbH, Germany

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Label-free microarrays for optimisation of protein and antibody binding

Julia Schuette, Biometrics Gmbh, Germany

B-118

Plasma-derived microparticle biomarkers of paracetamol-induced hepatotoxicity

Domitille Schwartz, University Of Geneva, Switzerland

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Automated proteolytic digestion for high precision peptide mapping and targeted bioanalysis

Alexander Schwahn, Thermo Fisher Scientific, Switzerland

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Simple, scalable and ultra-sensitive tip-based identification of protease substrates

Gerta Shema, Leibniz-institut Für Analytische Wissenschaften – Isas – E.v., Germany

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insSTAGE-diging: the in solution upgrade of STAGE-diging protocol for proteomic sample preparation

Paolo Soffientini, Cogentech S.c.a.r.l., Italy
PhD Abstract Competition Winner – posters are located by the innovation stage

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Understanding the protein corona of nanocarriers is a prerequisite for targeted drug delivery

Johanna Simon, Max Planck Institute For Polymer Research Mainz, Germany

B-123

Complementary tandem mass spectrometry approaches to distinguishing peptides containing amino acid isoforms

Elizaveta Solovyeva, Moscow Institute of Physics and Technology (State University), Russian Federation

B-124

DigiWest based focused proteomics of irradiated human embryonic stem cells and neuroepithelial cells

Dieter Stoll, Albstadt-Sigmaringen University Of Applied Sciences, Germany

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Automated, versatile and efficient sample clean-up using HILIC-functionalised magnetic microparticles

Stoyan Stoychev, CSIR, South Africa

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A feasibility study of pitavastatin distribution in liver tissue by MALDI-mass spectrometry imaging

Yutaka Sugihara, Lund University, Sweden

B-127

Quantitative assessment of the phosphoproteomes of kinase-deficient Escherichia coli strains

Abida Sultan, Novo Nordisk Foundation Center For Biosustainability, Technical University of Denmark, Denmark

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Impact Evaluation of Traditional Chinese medicine on Rat liver microsome P450s with mass spectrometry

Aihua Sun, Beijing Institute of Radiation Medicine; Beijing Proteome Research Center, China

B-129

In vitro characterisation of terbinafine protein adducts

Arun Tailor, University Of Liverpool, United Kingdom

B-130

Rapid production of virus protein microarray using protein microarray fabrication through gene synthesis (PAGES)

Sheng-ce Tao, Shanghai Jiao Tong University, China

B-131

Targeting single amino acid variants in melanoma cell lines by parallel reaction monitoring

Christoph Täumer, Herr, Germany

B-132

The forgotten proteome – approaches for the identification of short open reading frame encoded peptides

Andreas Tholey, Kiel University, Germany

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Characterisation and comparison of in-house produced Cetuximab with originator product

Anne Trappe, National Institute For Bioprocessing Research & Training, Ireland

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Relative protein quantification on model organisms

Christian Treitz, IEM, Kiel University, Germany

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Structural characterization of glycoconjugates by using functional carbon materials with hydrolysis reaction in MALDI-MS

Mei-Chun Tseng, Institute Of Chemistry, Academia Sinica, Taiwan

B-136

Monitoring kinase activity using customized substrate peptides

Kazuya Tsumagari, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

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Enrichment strategies for improvement of mass spec analysis of chemical cross-linked peptides

Rosa Viner, Thermo Fisher Scientific, United States

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A novel MS-cleavable tag for the analysis of redox-sensitive cysteines by shotgun proteomics

Sebastian Virreira Winter, Max Planck Institute Of Biochemistry, Germany

B-139

Definition of the intracellular flucloxacillin-haptenated proteins that may have involvement in iDILI

James Waddington, University Of Liverpool, United Kingdom

B-140

In-depth characterization of intact protein standards using top down mass spectrometry with multiple MSMS strategies

Hongqian (Anige) Yang, Thermo Fisher Scientific, Sweden

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Endoglycosidase-assisted high confident identification of intact glycopeptides

Wantao Ying, Beijing Institute Of Radiation Medicine, China

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Development of mass spectrometric-based assays for in situ target identification of covalent inhibitors

Kebing Yu, Genentech, United States

B-143

Oxidation of protein-bound methionine in Photofrin-photodynamic therapy-treated human tumor cells explored by quantitative proteomics approach

Jau-song Yu, Molecular Medicine Research Center, Chang Gung University, Taiwan

B-144

Middle-down analysis of monoclonal antibody with ETD and UVPD on an Orbitrap Fusion Lumos MS

Vlad Zabrouskov, ThermoFisher Scientific, United States

B-145

Mevalonate pathway inhibitors as potential therapeutic agents for Hepatocellular carcinoma: an in vitro study

Shamshad Zarina, National Center For Proteomics, University Of Karachi, Pakistan

B-146

Targeted mass spectrometry to determine the stoichiometry of phosphorylation sites in proteins

Lona Zeneyedpour, The Netherlands, Netherlands

B-147

Quantitative profiling of glycerophospholipids during mouse and human macrophage differentiation using targeted mass spectrometry

Cuiping Zhang, Guangxi Medical University, China

B-148

Toward a true quantitative protein atlas

Jiandi Zhang, Yantai Zestern Biotechnology Co. LTD, China

B-149

Molecular proteomic characterization of greek single-breed dairy products

Athanasios Anagnostopoulos, Biomedical Research Foundation Of The Academy Of Athens, Greece

B-150

Efficient micro-scale basic reverse phase peptide fractionation for global and targeted proteomics

Songyi Baek, Kbio, South Korea

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Improved top-down analysis on an Orbitrap Fusion Lumos with the advanced precursor determination algorithm

Helene Cardasis, Thermo Fisher Scientific, United States

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Multiplexed nucleic acid programmable protein arrays

Yang Lihui, National Center For Protein Sciences, China

B-153

Peptidomic analysis of rat plasma samples: effects of tranexamic acid against proteolysis in hemorrhagic shock

Elisa Maffioli, Università Degli Studi Di Milano, Italy

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A novel nanoflow LCMS limited sample proteomics approach using micro pillar array columns (μ PAC™)

Aran Paulus, Thermo Fisher, United States

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Beta amylin from the endophytic fungi Fusarium equiseti induce cell death in colon cancer cells

Thulasi Pillai, Indian Institute Of Technology Bombay, India

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Proteomics analysis of historical collagen glue retrieved from a Stradivari violin

Hwan-ching Tai, National Taiwan University, Taiwan

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Ultra-deep palmitoylomics enabled by a dithiodipyridine functionalized magnetic nanoparticles

Xiaoqin Zhang, Fudan university, China

Methods, Systems & Bioinformatics

C-001

Extracting peptide level quantification data from the PRIDE repository

Andrea, Argentini, VIB-UGent Center for Medical Biotechnology Department of Biochemistry, Faculty of Medicine, Ghent University, Belgium

C-002

Accurate LC retention time prediction for metabolites using calibrated predictions

Robbin, Bouwmeester, VIB-UGent, Belgium

C-003

An automated and integrated SWATH-MS informatics pipeline for clinical proteomics

Paul, Brack, University Of Manchester, United Kingdom

C-004

The Encyclopedia of Proteome Dynamics – A big data ecosystem for (prote)omics

Alejandro, Brenes, University Of Dundee, United Kingdom

C-005

Search engine score independent re-scoring of PSMs using predicted ion peak intensities

Ana S, C Silva, V.I.B. Universiteit Gent, Belgium

C-006

N-Glycome changes in CHO cells due to extractable and leachable exposure from single-use bioreactors

Sara, Carillo, Nibr, Ireland

C-007

Making Annotated Spectra Available when Standard Formats are not an Option

Robert, Chalkley, University Of California San Francisco, United States

C-008

SPECTRUM: A MATLAB toolbox for identifying proteins from top-down proteomics data

Safee, Chaudhary, Lahore University of Management Sciences, Pakistan

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Integrated omics analyses of oral cancer in Taiwan

Tingwen, Chen, Chang Gung University, China

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Accurate prediction of retention time shift for isotopic-labeling based protein quantification

Yeon, Choi, Seoul National University, South Korea

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Flexible data analysis for label-free time course proteomics experiments

Lieven, Clement, Ghent University, Belgium

C-012

Application of novel SILAC analysis software Proteolabels for large-scale meta-analysis of phospho-proteomes

Andrew, Collins, University Of Liverpool, United Kingdom

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'Omics' exploration of the human tears

Marianne, Dor, University Of Geneva, Switzerland

C-014

BayesProt: Robust iTRAQ and TMT protein-level quantification and statistical analysis with a Bayesian mixed-effects model

Andrew, Dowsey, University Of Bristol, United Kingdom

C-015

HD Proteome Base: A novel data repository for proteomics of a Huntington's disease mouse model

Sarah, Elschenbroich, Evotec (Muenchen) GmbH, Germany

C-016

Pathway analysis of altered kinases reveal gonadotropin hormone signaling in Glioblastoma

Poonam, Gautam, National Institute of Pathology ICMR, India

C-017

Integrated miRNA, mRNA and protein profiling of exosomes and their parental cells

Lucia, Geis-Asteggiante, University of Maryland College Park, United States

C-018

Efficient modelling of signalling networks derived from mass spectrometry phosphoproteomic data using Integer Linear Programming

Enio, Gjerga, Rwth Aachen University, Germany

C-019

A user-friendly spectrum clustering software for optimised proteomics data analysis

Johannes, Gris, Medical University Of Vienna, Austria

C-020

Label-free quantitative proteomic analysis to investigate the effect of heat stress on Panax ginseng leaves

Ravi, Gupta, Pusan National University, South Korea

C-021

The application of Commensal Computing for massively parallel analysis of proteomics data

John, Heap, Liverpool University, United Kingdom

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Reactome interactive pathway analysis

Henning, Hermjakob, Embl-ebi, United Kingdom

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Comparison of pipelines for differential analysis of label free quantification experiments

Véronique, Hourdel, Institut Pasteur, France

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Characterizing flame retardant-induced neurotoxicity in an hESC neural differentiation model using SWATH® Acquisition and RNA-Seq

Christie, Hunter, Sciex, United States

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UPS2 calibration set for biological matrix effect study

Ekaterina, Ilgisonis, Ibmc, Russian Federation

C-026

PSI standards compatible binary mass spectrometry data format for efficient read/write speed and storage requirements

Andris, Jankevics, University of Bristol, United Kingdom

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The PRIDE database: A proteomics data “gold mine” at your disposal

Andrew, Jarnuczak, European Bioinformatics Institute, United Kingdom

C-028

Proteogenomic approaches to identify alternatively splicing variants in pancreatic cancer cell lines

Seul-ki, Jeong, Yonsei Proteome Research Center, South Korea

C-029

OmicsDI RDF

Shin, Kawano, Database Center for Life Science, Research Organization of Information and Systems, Japan

C-030

Unveiling the translational consequences of fusion genes and isoforms present in cancer using proteogenomics approach

Chae-Yeon, Kim, Yonsei University, South Korea

C-031

Proteomic Cinderella: subtle analysis of bulky MS/MS data in one night

Olga, Kiseleva, Institute Of Biomedical Chemistry, Russian Federation

C-032

ADAR-mediated RNA editing in mouse brain proteome

Anna, Kliuchnikova, Institute Of Biomedical Chemistry, Russian Federation

C-033

Benchmarking data-independent acquisition workflows using hybrid proteome samples and LFQbench

Joerg, Kuharev, University Medical Center Of The Johannes Gutenberg University, Germany

C-034

Methionine-to-isothreonine conversion during sample preparation and its effects on proteomic data

Ksenia, Kuznetsova, Institute Of Biomedical Chemistry, Russian Federation

C-035

Label free quantitation: comparative analysis of XIC and SpCs based methods

Alfredo, Landolfi, University of Naples - "Federico II"; CEINGE - Biotechnologie Avanzate, Italy

C-036

Efficient proteomic and proteogenomic searches with IdentiPy

Lev, Levitsky, INEPCP RAS, Russian Federation

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UbiBrowser: an integrated bioinformatics platform for investigating human ubiquitin ligase (E3) - substrate interaction network

Dong, Li, No. 59, Middle Road of West 4th Ring Road, Beijing, China, China

C-038

Integrated data analysis pipeline for meta-omics

Sujun, Li, Indiana University, United States

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iProX: the integrated proteome resources in China

Mansheng, Li, Beijing Proteome Research Center, China

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The “Quantify then Identify” pipeline: a promising tool to minimize unexploited spectral information

Charlotte, Macron, Nestlé Institute of Health Sciences SA, Switzerland

C-041

IcmsWorld: A high-performance 3D software visualisation tool for LC/MS data

Antony, McCabe, University Of Liverpool, United Kingdom

C-042

SwathXtend modules to improve protein detection confidence using SWATH-MS with large peptide spectral reference libraries

Mark, Molloy, Australian Proteome Analysis Facility (APAF), Australia

C-043

Development of integrated proteomics database: jPOST

Yuki, Moriya, Database Center For Life Science, Research Organization Of Information And Systems, Japan

C-044

Proteogenomics of ADAR-mediated RNA editing in Drosophila melanogaster

Sergei, Moshkovskii, Institute Of Biomedical Chemistry, Russian Federation

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Protein- and Background- based ANOVA inference in proteomic analyses

Pedro, Navarro, Thermo Fisher Scientific (Bremen) GmbH, Germany

C-046

RiboZinB: Identifying the actively translated isoform. The case of the Zero-inflated model

Elvis, Ndah, University Of Gent, Belgium

C-047

jPOST provides a global public data repository for a wide variety of proteomics experiments

Shujiro, Okuda, Niigata University, Japan

C-048

Serving protein interaction data to the community – the HUPO-PSI Molecular Interaction Workgroup

Sandra, Orchard, European Bioinformatics Institute (EMBL-EBI), United Kingdom

C-049

Analytica: software for LC-MS omics data analysis and visualisation

Simon, Perkins, University Of Liverpool, United Kingdom

C-050

Advanced centroiding of low resolution MS/MS Spectra provides higher confidence identifications from proteomics datasets

Jeff, Peterson, Veritomyx, United States

C-051

Statistical analysis of ion intensities in label-free tandem mass spectrometry-based proteomics

Thang V, Pham, Vu University Medical Center, Netherlands

C-052

Proteomics space odyssey: strategy of proteoforms scouting

Ekaterina, Poverennaya, Ibmc, Russian Federation

C-053

Benchmarking statistical approaches for label-free quantitative proteomics

Hayley, Price, University Of Liverpool, United Kingdom

C-054

Serum degradation analysis by MALDI/ToF: a new method and tool

Aldo, Profumo, Ospedale Policlinico San Martino, Italy

C-055

Large scale integration of proteomics and genomics data to enhance rice genome annotation

Da, Qi, University of Liverpool, United Kingdom

C-056

Geena2 - a public tool for the automation of MALDI/ToF spectra pre-processing

Paolo, Romano, Ospedale Policlinico San Martino, Italy

C-057

A compendium of co-regulated protein complexes in breast cancer reveals collateral loss events

Colm J., Ryan, University College Dublin, Ireland

C-058

ProteomicsDB transforms into an interactive multi-omics platform

Patroklos, Samaras, Chair Of Proteomics And Bioanalytics, Germany

C-059

Quantitative analysis of protein, mRNA and miRNA response to hypoxia in primary hippocampal neurons

Christian, Schiffmann, Department of Psychiatry and Psychotherapy, University Medical Center Göttingen (UMG), Germany

C-060

ProteomicsDB enables custom spectral library and transition list generation

Tobias, Schmidt, Chair of Proteomics and Bioanalytics, Germany

C-061

COSS: Free, fast and powerful CompOmics spectral search tool

Genet Abay, Shiferaw, Ghent University, Belgium

C-062

Novel permutation scheme improves accuracy of permutation-based false discovery rate estimation in quantitative proteomics

Pavel, Sinitcyn, Max Planck Institute Of Biochemistry, Germany

C-063

mass-spectrometrists should search for all peptides, but assess only the ones they care about

Adriaan, Sticker, Vib-ugent, Belgium

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C-064

Integrating simulated spectral libraries into proteomics data analysis workflow for improved phosphosite identification

Veronika, Suni, Turku Centre For Biotechnology, University Of Turku and Åbo Akademi, Finland

C-065

Understanding the effect of Deisotoping MS/MS Spectra on protein identification

Aidan, Tay, University Of New South Wales, Australia

C-066

Fast and accurate protein false discovery rates on human proteome study scale with Percolator 3.0

Matthew, The, Kth Stockholm, Sweden

C-067

Colims: a distributed proteomics LIMS system

Demet, Turan, VIB, Belgium

C-068

ProteoRE, a Galaxy-based infrastructure for annotating and interpreting proteomics data

Yves Vandenbrouck, cea, Fundamental Research Division, BIG institute, France

C-069

Cross-linked peptide identification: a single answer from many tools?

Elien, Vandermarliere, Vib-ugent, Belgium

C-070

Large-scale discovery and quantitation of novel peptides using omics derived libraries

Vidya, Venkatraman, Cedars-Sinai Medical Center, United States

C-071

An integrative multi-omics approach for improved discovery of biomarkers related to prostate cancer progression

Sarah, Wagner, John Van Geest Cancer Research Centre, United Kingdom

C-072

Bringing proteomics data analysis into the cloud

Mathias, Walzer, EMBL-EBI, United Kingdom

C-073

P-Mart - Interactive online software to analysis and exploration from global proteomic datasets

Bobbie-Jo, Webb-Robertson, Pacific Northwest National Laboratory, United States

C-074

PepQuery: a peptide-centric search engine that makes proteomics data directly usable to the genomics community

Bo, Wen, Baylor College of Medicine, United States

C-075

MaxQuant Top-Down: a multifunctional software package for quantitative top-down proteomics

Christoph, Wichmann, Max-Planck Institute of Biochemistry, Germany

C-076

PMD: a resource for archiving and analyzing protein microarray data

Zhaowei, Xu, Shanghai Jiao Tong University, China

C-077

Improved detection sensitivity of quantitative changes for low-abundant proteins by data curation of PLGEM-STN p-values

San-Duk, Yang, Seoul National University, South Korea

C-078

Reducing false positive identifications for proteome datasets accumulated in jPOST repository

Akiyasu C., Yoshizawa, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

C-079

AAgAtlas 1.0: a human autoantigen database

Xiaobo, Yu, Beijing Proteome Research Center, China

C-080

Quality control of mass spectrometry proteomics data integration in neXtProt

Monique, Zahn, SIB Swiss Institute Of Bioinformatics, Switzerland

C-081

Integrated multi-omics characterization of neuroblastoma

Matthias, Ziehm, Max-Delbrück-Center For Molecular Medicine (MDC), Germany

C-082

Intelligent solution for mass spectrometry-based proteomics

Zhuoxin, Chen, Fudan University, China

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MS/MS-free protein identification in complex mixtures using multiple enzymes with complementary specificity

Mark, Ivanov, Moscow Institute of Physics and Technology, Russian Federation

C-084

Multiomics data integration using ontologies

Magnus, Palmblad, Leiden University Medical Center, Netherlands

C-085

A protocol for finding missing proteins

Shoba, Ranganathan, Macquarie University, Australia

C-086

Up to ~10,000x faster DIA processing using deepsearch: results during your coffee break

Gautam, Saxena, DeepDIA, United States

Disease & Clinical Proteomics

D-001

Comparative proteome analysis of long-term survivor and non-survivor patients with acute myeloid leukemia

Elise Aasebø, University Of Bergen, Norway

D-002

PhD abstract competition winner. Poster will be located by the innovation stage
Suppression of colorectal cancer proliferation and invasion by antagonising uPAR• α v β 6 interaction

Subash Adhikari, Macquarie University, Australia

D-003

Identification and localization of protein-pentanal adducts, a potential lipoxidation marker

Catarina Afonso, Aston University, United Kingdom

D-004

Detection of plasma colorectal cancer prognostic biomarkers

Seong Beom Ahn, Macquarie University, Australia

D-005

Identification of serum proteins that can delineate acute Hantavirus infection

Stuart Armstrong, University Of Liverpool, United Kingdom

D-006

The role of cardiac metabolism perturbation in radiation-induced human heart disease: a proteomics analysis

Omid Azimzaeh, Helmholtz Zentrum München, Radiation Proteomics, Germany

D-007

Quantitative proteome analysis of VEGF-induced vascular hyperpermeability in a mouse model by LC-MS/MS

Jingi Bae, Korea University, South Korea

D-008

Proteomic profiling of secretomes from M.tb-stimulated, PUFA-treated, ex vivo PBMCs in TB-IRIS

Marine Barnabe, University Of Cape Town, South Africa

D-009

Novel target identification in Alzheimer's disease brain by combined mass spectrometry imaging and subcellular proteomics

Joakim Bastrup, Aalborg University, Denmark

D-010

Differential proteomic analysis of metformin response in a preoperative window clinical trial for endometrial cancer

Nicholas Bateman, Gynecologic Cancer Center Of Excellence, United States

D-011

Biomarker search in prostate cancer by proteomic approach

Feyza Bayramoglu, Istanbul Medipol University, Turkey

D-012

Evaluation of synaptic proteins as cerebrospinal fluid stage biomarkers for Alzheimer's disease

Olivia Belbin, IIB-SantPau, Spain

D-013

Cytoskeleton and nuclear lamina affection in Osteogenesis imperfecta: a functional proteomics perspective.

Laura Bianchi, Siena University, Italy

POSTER PRESENTATIONS

D-014

Proteomics signature in early remodeling after myocardial ischemia/reperfusion and the effects of experimental treatments

Aleksandra Binek, Fundación Centro Nacional de Investigaciones Cardiovasculares Carlos III (CNIC), Spain

D-015

Identification of candidate prostate cancer biomarkers in urinary extracellular vesicle proteins by label-free LC-MS/MS-based proteomics.

Irene Bijnsdorp, Vu University Medical Center, Netherlands

D-016

Protein signature for endometrial cancer diagnosis in exosome-like vesicles of uterine aspirates

Eva Borrás, Center for Genomic Regulation, Spain

D-017

Response prediction for platinum-based treatment regimens in non-small cell lung cancer using a protein-based assay

Franziska Böttger, VU University Medical Center, Netherlands

D-018

Affinity MS identifies pre-synaptic proteins SNAP-25 and synaptotagmin-1 as novel CSF biomarkers for Alzheimer's disease

Ann Brinkmalm, University Of Gothenburg, Sweden

D-019

Novel CSF tau fragments as candidate biomarkers for Alzheimer's and other neurodegenerative diseases

Gunnar Brinkmalm, University Of Gothenburg, Sweden

D-020

Extracellular matrix proteomics reveals Aggrecan and Aggrecanases as novel contributors to vascular remodeling after stenting

Sean Burnap, King's College London, United Kingdom

D-021

Alterations to HDL protein composition in abdominal aortic aneurysm patients

Emilio Camafeita, CNIC, Spain

D-022

Proteomic characterization of new transcription factors associated with a more invasive phenotype in colorectal cancer

Ignacio Casal, Centro de Investigaciones Biológicas, Spain

D-023

Boiling produces hypoallergenic cashew nuts with potential to safely desensitize affected patients

Tim Chataway, Flinders University, Australia

D-024

Increased electronegativity of high density lipoproteins impairs its functional properties and increases risk of CAD

Chao-jung Chen, China Medical University, Taiwan

D-025

Proteomic analysis of plasma-derived extracellular vesicles in breast cancer PDX models

Jia-Xuan Chen, Cancer Research UK Cambridge Institute, United Kingdom

D-026

Phosphoproteomics analysis of plasma from Vietnamese type 2 diabetes patients

Phan Van Chi, Vietnam Academy Of Science & Technology, Viet Nam

D-027

Proteomic analysis of extracellular vesicles from clinically available volumes of CSF: application to Alzheimer's disease

Davide Chiasserini, VU University Medical Center, Nederland

D-028

Development of serum protein biomarkers for the recurrence in gastric cancers using multiple reaction monitoring

Byoung-kyu Cho, Seoul National University, South Korea

POSTER PRESENTATIONS

D-029

Phosphoproteomics study reveals the regulation of vasodilator-stimulated phosphoprotein upon stathmin-1 silencing in colorectal cancer metastasis

Maxey CM Chung, National University Of Singapore, Singapore

D-030

Identification, validation and characterisation of membrane protein tumour markers for pancreatic adenocarcinoma

Orla Coleman, Dublin City University, Ireland

D-031

The differential plasma proteome of obese and overweight individuals undergoing nutritional weight loss and maintenance

Ornella Cominetti, Nestle Institute Of Health Sciences, Switzerland

D-032

Use of MALDI imaging technology to predict the response to antiangiogenic therapy in colorectal cancer

Francisco Conde, Instituto Maimonides De Investigacion Biomedica De Cordoba, Spain

D-033

Investigating the potential of exosomes as biomarkers in Cystic Fibrosis

Judith Coppinger, Royal College Of Surgeons In Ireland, Ireland

D-034

Tear protein analysis in the different phases of wound healing following glaucoma surgery

Eva Csosz, University Of Debrecen, Hungary

D-035

Gut-brain axis in ageing: a proteomics approach

Alfonsina D'Amato, Quadram Institute Bioscience, United Kingdom

D-036

SDS vs urea: fast and sensitive non-mechanical conversion of tissues to peptides

Irena Dapic, Van't Hoff Institute For Molecular Sciences, Netherlands

D-037

MS/MS strategies to characterize the Proteoform landscape in human tears using top-down mass spectrometry

Claire Dauly, Thermo Fisher Scientific, France

D-038

Peptidomics: an innovative approach to study the "Auto-digestion" hypothesis in septic shock patients

Eliandre de Oliveira, Barcelona Science Park, Spain

D-039

Verification of saliva proteins candidates for OSCC markers and their correlation with prognosis

Tatiane De Rossi Mazo, Brazilian Biosciences National Laboratory (LNBio), Brazil

D-040

Novel stool-based protein biomarkers for improved colorectal cancer screening: a case-control study

Meike De Wit, The Netherlands Cancer Institute, Netherlands

D-041

Proteomics of the intestinal mucosal-luminal interface identifies biomarkers to improve pediatric inflammatory bowel disease diagnosis

Shelley Deeke, University Of Ottawa, Canada

D-042

Novel osteoporosis risk protein biomarkers suggested by a proteome study in Chinese elderly men

Fei-Yan Deng, Soochow University, China

D-043

Quantitative proteomics to investigate the effects of a pMRTP and smoking cessation on mouse lung

Sophie Dijon, PMI, Switzerland

D-044

Combinatorial mass spectrometry (MS) and artificial intelligence (AI) subclassification of diffuse glioma

Ugljesa Djuric, University Health Network, Canada

D-045

Affinity proteomic profiling of plasma for proteins associated to pancreatic cancer

Tea Dodig-crnkovic, Affinity Proteomics, Science For Life Laboratory, School Of Biotechnology, Royal Institute Of Technology (kth), Sweden

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In-depth quantitative mass spectrometry reveals the region and cell-type resolved proteome of the human heart

Sophia Doll, Max Planck Institute Of Biochemistry, Germany

D-047

Bridging the 'translation gap': a prospective study to validate biomarker panels predictive of prostate cancer

Will Dracup, Biosignatures, United Kingdom

D-048

Dynamic composition of the *Cryptococcus neoformans* proteome and secretome during dormancy phenomenon

Magalie Duchateau, Institut Pasteur, France

D-049

Adipocyte exosomes promote melanoma aggressiveness through fatty acid oxidation: novel mechanism linking obesity and cancer

Manuelle Ducoux-petit, IPBS/CNRS/UPS, France

D-050

Linking genotype to clinical phenotype through SWATH-MS analysis of chronic lymphocytic leukaemia trial samples

Gina Eagle, University Of Liverpool, United Kingdom

D-051

Comparative proteomic study of affected and non-affected tissues of clubfoot

Adam Eckhardt, Fgu AVČR, Czech Republic

D-052

Revealing histone variants by targeted proteomic analysis using the manually curated database MS_HistoneDB

Sara El Kennani, Cea, France

D-053

Proteomics analysis and lysine acetylation stoichiometry in cancer cells

Sergio Encarnacion-Guevara, Universidad Nacional Autónoma de México, México

D-054

HDMSE proteomic analysis of the mode of action of short chain fatty acids in colon

Caroline Evans, University Of Sheffield, United Kingdom

D-055

Protein biomarker discovery in Alzheimer's disease using SWATH MS analysis

Laura Farrell, Stoller Biomarker Discovery Centre, Uom, United Kingdom

D-056

Protein crossroads: Dementia vs. Alzheimer's Disease

Justyna Fert-Bober, Cedars-sinai Medical Center, United States

D-057

Establishment of the hnRNP C1/C2 role on schizophrenia through protein interaction network mapping

Mariana Fioramonte, University Of Campinas, Brazil

D-058

Social defeat stress: a plasma proteomic study to identify stress susceptible-associated and resilience-associated biomarkers

Melanie Focking, Royal College Of Surgeons In Ireland, Ireland

D-059

Quantification of PI3K/AKT/mTOR signalling pathway activity using immuno-MALDI mass spectrometry (iMALDI)

Bjorn Frohlich, University Of Victoria, Canada

D-060

Integrated investigation into characteristics of proteome, genome and transcriptome of rectal cancer with liver metastasis

Yanning Gao, National Cancer Center/cancer Hospital, Chinese Academy Of Medical Sciences, China

D-061

Changes of urinary proteins in a bacterial meningitis rat model

Youhe Gao, BEIJING NORMAL UNIVERSITY, China

D-062

Early detection in urinary proteome for effective treatment of bleomycin-induced pulmonary fibrosis in rat model

Youhe Gao, Beijing Normal University, China

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D-063

The analysis and identification of STAT3 interactions and modifications in the mitochondria of cancer cells

Daniel Garama, Hudson Institute Of Medical Research, Australia

D-064

First direct evidence of cross-linked A β dimers in the brains of Alzheimer's disease patients

Marina Gay, IRB Barcelona, BIST, Spain

D-065

Proteomics reveals associations between protein abundance and sepsis phenotypes

Manuela Gesell Salazar, Department Functional Genomics, University Medicine Greifswald, Germany

D-066

Online 2D-LC intact proteins separation for deeper shotgun proteomics of serum samples

Natalia Govorukhina, Rug, Netherlands

D-067

Combined biomarker panel shows improved sensitivity for the early detection of ovarian cancer

Ciaren, Graham, Manchester Metropolitan University United Kingdom

D-068

Proteomics of rare genetic diseases: impact of cystinosin mutations on protein stability and protein network

Ida Chiara Guerrero, Inserm, France

D-069

Discovery of the proteomic profile to predict the renal function decline in kidney disease

Reyna Gutierrez Rivera, The Stoller Biomarker Discovery Centre, United Kingdom

D-070

Landscape of proteomic alterations in cervical carcinomas through laser microdissection sampling

Coskun Guzel, Erasmus MC, Netherlands

D-071

MALDI-TOF mass spectrometry on the track of sand fly life cycle

Petr Halada, Institute of Microbiology, Czech Republic

D-072

OMICS based stratification of dilated cardiomyopathy patients

Elke Hammer, University Medicine Greifswald, Germany

D-073

In-depth proteome profiling of formalin-fixed paraffin-embedded urothelial carcinoma and benign disease tissues

Dohyun Han, Seoul National University Hospital, South Korea

D-074

Proteomic study on advanced glycation end-products treatment in kidney of mice

Eun Hee Han, Korea Basic Science Institute (kbsi), South Korea

D-075

To deplete or to equalize? Two pre-analytical strategies for human cerebrospinal fluid analysis

Karel Harant, Faculty Of Science Charles University In Prague, Czech Republic

D-076

Tissue specific secretomes, the hidden treasure for identification of disease related marker proteins

Sonja Hartwig, DDZ, Deutschland

D-077

Systematic development of sandwich immunoassays for the analysis of the secretome in plasma

Ragna S. Häussler, Science For Life Laboratory, Sweden

D-078

Applying a targeted proteoform profiling method for neurological disorder biomarker discovery

Romano Hebel, Bruker Daltonik GmbH, Germany

D-079

Early warning signals of aging in the hematopoietic stem cell niche

Marco L. Hennrich, Embl, Germany

D-080

Design of a targeted proteomics assay for the diagnosis of invasive candidiasis

María Luisa Hernaez, Complutense University, Spain

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D-081

Impact of peritoneal dialysis fluid on O-GlcNAcylation of the mesothelial cell proteome and cell survival

Rebecca Herzog, Medical University Of Vienna, Austria

D-082

Gender-enhanced alteration in airway epithelial proteome in COPD related to xenobiotic metabolism

Tina Heyder, Karolinska Institutet, Sweden

D-083

Glycosylation changes of cell membrane proteins in pancreatic cancer

Yoshimi Higashi, Hiroshima University, Japan

D-084

How can we effectively detect biomarker candidates by mass spectrometry?

Hisashi Hirano, Yokohama City University, Japan

D-085

Analysis of an amyloid aggregation conformational conversion of TDP-43 in neurodegenerative diseases

Yi-Chi Ho, Institute Of Chemistry, Academia Sinica, Taiwan

D-086

Proteome-wide study of cerebrospinal fluid biomarkers for bipolar disorder and other neuropsychiatric disorders

Jessica Holmén Larsson, University of Gothenburg, Sweden

D-087

The power of multiplexing- combining TMT discovery and targeted label free quantitation for biomarker analysis

Andreas Huhmer, Thermo Fisher Scientific, United States

D-088

Dissecting the TRIM8 role in the pathogenesis of glioblastoma

Iaria Iacobucci, University of Naples "Federico II", Ceinge Advanced Biothecnology, Italy

D-089

Phosphoproteome and sialome of cells modelling tumour infiltrating myeloid populations

Maria Ibáñez-Vea, Navarrabiomed Biomedical Research Centre, Navarra Institute for Health Research (IdiSNA), Spain

D-090

Investigation of the lymphatic malformation cystic fluid and plasma proteomes

Vera Ignjatovic, Murdoch Children's Research Institute, Australia

D-091

Unraveling amyloid beta-pathology in Alzheimer's disease with MALDI imaging mass spectrometry

Masaya Ikegawa, Doshisha University, Japan

D-092

Extraction and analysis of A β fractions of the peptidome from human blood components

Maria Indeykina, IBCP RAS, Russian Federation

D-093

Identification of candidate diagnostic serum biomarkers for Kawasaki disease using proteomic analysis

Yoko Ino, Yokohama City University, Japan

D-094

Lacrimal proteome: possible source of biomarkers?

Tamas Janaky, Department of Medical Chemistry, University of Szeged, Hungary

D-095

Plasma proteins associated with advanced liver fibrosis in patients with nonalcoholic fatty liver disease

Michael Janech, Medical University of South Carolina, United States

D-096

The human neutrophil: improved proteome coverage and clinical insights

Peypier Janique, University of Cape Town, South Africa

D-097

In-depth proteome-profiling to evaluate a novel combinatory metronomic treatment for therapy-resistant multiple myeloma patients

Lukas Janker, University Of Vienna - Department Of Analytical Chemistry, Austria

D-098

Integrative analysis of transcriptomic and proteomic data from testicular tissues of Liver-X receptor knockout mice

Sheba Jarvis, Imperial College, United Kingdom

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Plasma membrane proteomic analysis of host protein expression in response to Enterovirus 71 infection

Xiaofang Jia, Shanghai Public Health Clinical Center, China

D-100

Development of a nonglycopeptide-based MRM strategy for screening of differential glycoproteins in hepatocellular carcinoma

Biyun Jiang, Fudan University, China

D-101

Serum fragment of TSP1 as a biomarker for metastasis and poor prognosis of ESCC

Zongpan Jing, National Cancer Center. The State Key Laboratory of Molecular Oncology., China

D-102

Annexin A3 as potential biomarker in first-onset psychosis

Helena Joaquim, Neuroscience Laboratory - Fmusp, Brazil

D-103

Autoantibody profiling in schizophrenia affected brain tissues

David Just, Science for Life Laboratory, School of Biotechnology - KTH, Royal Institute of Technology, Sweden

D-104

Protein modification and the immune system; a ménage a trois gone wrong in Multiple Sclerosis

Kenneth Kastaniegaard, Aalborg University, Denmark

D-105

DCBLD2 is a novel biomarker of myxofibrosarcoma invasion identified by global protein expression profiling

Kazutaka Kikuta, Department Of Orthopedic Surgery, Keio University School Of Medicine, Japan

D-106

Oxidized methionine levels in serum proteins as potential clinical biomarkers to assess oxidative stress status

Yoshio Kodera, Kitasato University, Japan

D-107

Proteomics for rare cancer: Lesson learned from Sarcoma biomarker research

Tadashi Kondo, National Cancer Center, Japan

D-108

Immunomodulatory effects of peritoneal alanyl-glutamine in clinical peritoneal dialysis detected by a multi-omics biomarker approach

Klaus Kratochwill, Medical University Of Vienna, Austria

D-109

The quantitative proteomic study of human saliva samples obtained from caries-free and caries-susceptible people

Lucie Kulhavá, Charles University, Czech Republic

D-110

Phosphoproteomic profiling of heart tissue: from mouse model to patient samples

Uros Kuzmanov, University Of Toronto, Canada

D-111

Imaging mass spectrometry of kidney from type 2 Diabetes (T2D) rat model

Yuki Kuzuhara, Doshisha University, Japan

D-112

Proteomics investigation of Wilson's disease pathophysiology in the ATP7B-/- murine model

Maud Lacombe, CEA Grenoble, France

D-113

Biomarkers to differentiate between CT-positive and CT-negative patients with mild traumatic brain injury

Linnea Lagerstedt, University Of Geneva, Switzerland

D-114

Functional analysis in pulmonary systemic sclerosis

Claudia Landi, University Of Siena, Italy

D-115

Quantitative phosphoproteomics reveals T cell signaling drives HIV-1 spread

Alice Len, University College London, United Kingdom

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Super-SILAC mix coupled with SIM/AIMS assays for targeted verification of phosphopeptides discovered in hepatocellular carcinoma

Yu-Tsun Lin, Molecular Medicine Research Center, Chang Gung University, Taiwan

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Chronic administration of methylmercury induces differential proteome changes in different regions of mammalian brains

Samuel CL Lo, Hong Kong Polytechnic University, Hong Kong

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Glycosylation analysis of prostate specific antigen – towards improved diagnosis of prostate cancer

Stephen Lock, Sciex, United Kingdom

D-119

Vascular niche E-selectin plays a key role in leukemia chemo-resistance

Dorothy Loo Oey, Translational Research Institute, Australia

D-120

Identification of nephropathy predictive markers in urine from children affected by type-1 diabetes

Cinzia Magagnotti, San Raffaele Scientific Institute, Italy

D-122

Plasma protein targets for early detection and monitoring of sinusoidal obstruction syndrome

Pavel Majek, Institute Of Hematology And Blood Transfusion, Czech Republic

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14-3-3 σ /Stratifin as candidate biomarker for smokeless tobacco associated Oral Squamous Cell Carcinoma in Pakistan

Uzma Urooj Malik, National Center For Proteomics, University Of Karachi, Pakistan

D-124

Temporally- & spatially-resolved microproteomics and MALDI MSI lipidomic analysis for traumatic brain injury biomarker identification

Khalil Mallah, Laboratoire Protéomique, Réponse Inflammatoire Et Spectrométrie De Masse (prism) Inserm U1192- Université Lille 1, France

D-125

Monitoring oxidative stress and progression to cell death: are we closer to Parkinson's disease diagnosis?

Bruno Manadas, Center For Neuroscience And Cell Biology - University Of Coimbra, Portugal

D-126

μ ZIC-HILIC-MS/MS methodology for the characterization of N-glycan isomers

Montserrat Mancera Arteu, University of Barcelona, Spain

D-127

Old dog with new tricks: Tear proteome changes associated with renoucement of contact lenses

Caroline Manicam, Department Of Ophthalmology, University Medical Centre of the Johannes Gutenberg University Mainz, Germany

D-128

Proteomic characterization of neuromelanin granules isolated from human substantia nigra by laser-microdissection

Katrin Marcus, Medizinisches Proteom-center, Ruhr-university Bochum, Germany

D-129

Identification of signaling pathways involved in colorectal adenoma-to-carcinoma progression

Sanne Martens-de Kemp, VU University Medical Center, Netherlands

D-130

A proteomics approach to subclinical atherosclerosis

Diego Martínez López, FIS-Fundación Jiménez Díaz-Universidad Autónoma, Spain

D-131

Glycan profiling for exploring relationship of MUC1 O-glycoform with tumor-characteristic by lectin microarray

Atsushi Matsuda, Department Of Biochemistry, Keio University, Japan

D-132

Combined proteomics and metabolomics approach for the investigation of metabolic deregulations in chronic lymphocytic leukemia

Rupert Mayer, University Of Vienna, Department Of Analytical Chemistry, Austria

D-133

Revealing the systemic disorders underlying environmental enteropathy using in vivo proteomics of SILAC-mice, and metabolomics

James McCoy, University Of British Columbia, Canada

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Epidermal barrier improvement after Excipial application in atopic xerosis is revealed by non-invasive proteome analysis.

Bruno Mehul, Nestle Skin Health / Galderma, France

D-135

Human neocortex proteome profiling during progression of tau pathology in Alzheimer's disease

Clarissa Mendonça, Federal University Of Rio De Janeiro, Brazil

D-136

Proteomic analysis of glomerular extracellular matrix proteomes differentiates FSGS variants

Michael Merchant, University Of Louisville, United States

D-137

Quantitative determination of specific serum IgG; diagnosis of Staphylococcus aureus bloodstream infection as an example

Stephan Michalik, University Medicine Greifswald, Germany

D-138

Phosphoproteome profiling of different clinical phases in multiple myeloma

Juho Miettinen, Institute for Molecular Medicine Finland (fimm), University of Helsinki, Finland

D-139

Affinity proteomics identifies proteins associated with asthma severity

Maria Mikus, SciLifeLab, KTH - Royal Institute of Technology, Sweden

D-140

PhD abstract competition winner. Poster will be located by the innovation stage

Tissue proteomics unravel EIF3D as a potential candidate associated with bladder cancer invasion

Marika Mokou, Biomedical Research Foundation Academy Of Athens, Greece

D-141

Multi-omics analysis of esophageal adenocarcinoma: how lipid metabolism affects cancer progression

Jeffrey Molendijk, University Of Queensland, Australia

D-142

Identification of new early biomarkers of Diabetic Nephropathy using proteomic approaches

Laurence MOLINA, CNRS UMR 9005, France

D-143

ProLiPALS: Proteomics of Lymphocytes from Parkinson's disease and Amyotrophic Lateral Sclerosis patients.

Chiara Monti, University Of Insubria, Italy

D-144

Standardising and harmonising multiple TripleTOF® systems for proteomics using a dedicated SWATH® acquisition performance kit

Nicholas Morrice, Sciex, United Kingdom

D-145

Securitized production of stromal stem cells for therapy: Proteomic investigation on genetic stability and senescence

Emmanuelle Mouton Barbosa, Ipbs Cnrs, France

D-146

Characterization and identification of dityrosine cross-linked peptides using tandem mass spectrometry

Soumya Mukherjee, The Florey Institute of Neuroscience and Mental Health, Australia

D-147

Reproducible in-depth proteome analysis of formalin-fixed paraffin-embedded tissues by data independent acquisition method

Jan Muntel, Biognosys AG, Switzerland

D-148

Proteomic identification of elevated serum haptoglobin levels in dystrophinopathy

Sandra Murphy, Maynooth University, Ireland

D-149

Potential biomarkers in the urine of babies with ROP

Krishna Murthy, Vittala International Institute Of Ophthalmology, India

D-150

Proteomic assessment of HIV-Tat Treated human neurons: towards a molecular model for HIV-associated neurocognitive disorders

Brandon Murugan, University of Cape Town, South Africa

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Analyses of glycans on haptoglobin in sera of patients with various types of cancer

Miyako Nakano, Hiroshima University, Japan

D-152

Comparative proteomic analysis of mouse kidney with systemic lupus erythematosus

Orthodoxia Nicolaou, Cyprus Institute Of Neurology & Genetics, Cyprus

D-153

Plasma proteome analysis enables accurate quantification of liver-secreted proteins

Lili Niu, Novo Nordisk Foundation Center For Protein Research , University Of Copenhagen, Denmark

D-154

MS-based epigenetic profiling of breast cancer samples for patient stratification and discovery of novel targets

Roberta Noberini, Fondazione Istituto Italiano Di Tecnologia, Italy

D-155

iTRAQ labeling and label-free quantitative proteome analysis of synaptosome from schizophrenic patients

Fábio Nogueira, Ufrj, Brazil

D-156

Proteomics as part of systems toxicological assessment of a mentholated candidate modified risk tobacco product

Catherine Nury, Philip Morris International, Switzerland

D-157

MRM of synucleins in CSF reveals alterations in Alzheimer's and Creutzfeldt-Jakob disease but not synucleinopathies

Patrick Oeckl, Ulm University Hospital, Department Of Neurology, Germany

D-158

Quantitative proteomic analysis of vitreous humor from idiopathic epiretinal membrane and macular hole patients

Tiina Öhman, Institute Of Biotechnology, University Of Helsinki, Finland

D-159

Proteomics of post-translational lysine acetylation in glioma-derived stem cells

Hiroki Okanishi, Kumamoto University, Japan

D-160

Proteomics as a tool in revealing the biology of thyroid eye disease

Garrett Ong, Singapore General Hospital, Singapore

D-161

Methylglyoxal-modified peroxiredoxin 6 as a biomarker for diabetic complications

Tomoko Oya-ito, Shubun University, Japan

D-162

Lung cancer biomarker discovery using integrated transcriptomics and proteomics approach

Jisook Park, Samsung Medical Center, South Korea

D-163

Correlation of histopathologic characteristics to protein expression and function in malignant melanoma

Krzysztof Pawlowski, Lund University, Sweden

D-164

Proteome changes of extracellular vesicles isolated from the plasma of myelodysplastic syndrome patients

Klara Pecankova, Institute Of Hematology And Blood Transfusion, Czech Republic

D-165

Thermal profiling of breast cancer cells reveals proteasomal activation by CDK4/6 inhibitor palbociclib

Julien Peltier, Institute For Cell And Molecular Biosciences (icamb), United Kingdom

D-166

Proteofoms of transthyretin - candidate biomarkers in diagnosis of obstructive sleep apnea

Deborah Penque, Instituto Nacional de Saude dr Ricardo Jorge, Portugal

D-167

Identification of tear fluid biomarkers in dry eye and glaucoma patients using targeted proteomics strategy

Natarajan Perumal, University Medical Center Of The Johannes Gutenberg University Mainz, Germany

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Toxins of Clostridium difficile reorganize the proteome of target cells

Andreas Pich, Hannover Medical School, Germany

D-169

Proteomic insights in extracellular microvesicles from CSF and tears of multiple sclerosis patients

Damiana Pieragostino, University "G. d'annunzio" Of Chieti- Pescara, Italy

D-170

Proteomic investigation supporting behavioural characterization of recovery upon DHA treatment of Spinal Cord Injury (SCI)

Luisa Pieroni, IRCCS Fondazione S.Lucia, Italia

D-171

Differential protein expression related to testosterone deficiency in healthy men. a quantitative proteomics study

Indira Plá, Lund University/BMC, Sweden

D-172

MRM based absolute quantification of myeloid derived growth factor

Felix Polten, Medical School Hannover, Germany

D-173

Proteomics identified predictive biomarkers for response to treatment with pazopanib in sarcoma

Zhiwei Qiao, National Cancer Center Research Institute, Japan, Japan

D-174

Proteomic Analysis of Staphylococcus aureus Planktonic and Hydrated Biofilms using TMT-based Mass Spectrometry

Md. Arifur Rahman, Macquarie University, Australia

D-175

Deregulation of immunological pathway in chronic schizophrenia analysed by quantitative proteomics

Ravikumar Raju, National Institute Of Mental Health And Neuro Sciences, India

D-176

HIV Latency: deep-proteome coverage reveals the extent of cellular awareness of HIV and immunotherapy targets

Sri, Ramarathinam, Monash University, Australia

D-177

Understanding differential signaling via toll like receptor-2 by multipronged quantitative proteomics

Nagender Rao Rameshwaram, Centre For DNA Fingerprinting & Diagnostics, India

D-178

Role of posttranslational modifications on potential blood-based protein biomarkers in Alzheimer's disease

Chaminda Ranasinghe, Edith Cowan University (ECU), Australia

D-179

Post-translational modifications (PTMs) of huntingtin protein in Huntington's disease

Tamara Ratovitski, Johns Hopkins University, United States

D-180

Studying mechanisms using omics-based approaches in ischemia reperfusion injury associated with kidney transplant

Shelby Reid, University Of Toronto, Canada

D-181

Profiling basement membrane proteins in plasma and cerebrospinal fluid within ALS and FTD

Julia Remnestål, Royal Institute Of Technology, Sweden

D-182

Novel plasma proteomic risk markers for malignant ventricular arrhythmias and sudden cardiac death

Ben Richards, University Of Leicester, United Kingdom

D-183

Biomarker validation using quantitative LC-MS combined with automated processing of human CSF and blood samples.

Anne Roberts, Florey Institute Of Neuroscience And Mental Health, Australia

D-184

Post-translationally modified alpha-1-microglobulin as a plasma biomarker for the early diagnosis of Parkinson's disease.

Blaine Roberts, Florey Inst. Neuroscience, U. of Melbourne, Australia

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Identification and validation of protein biomarkers for homologous recombination deficiency in breast cancer

Frank Rolfs, OncoProteomics Laboratory, Dept. Medical Oncology, Cancer Center Amsterdam, VU University Medical Center, Amsterdam, Netherlands

D-186

New tools to improve serodiagnosis of Brucellosis

Paola Roncada, Istituto Sperimentale Italiano Lazzaro Spallanzani, Italy

D-187

Molecular pathways impairment in Zika virus-infected neural stem cells revealed by proteomic approach

Livia Rosa-fernandes, SDU, Denmark

D-188

Identification of cartilage endogenous peptides differentially released in the serum of osteoarthritic and healthy patients

Cristina Ruiz Romero, Iinibic, Spain

D-189

Plasma Proteomic Analysis of Intravenous Omega-3 Fatty Acid and Gemcitabine in Advanced Pancreatic Adenocarcinoma

Franscois Runau, University Of Leicester, United Kingdom

D-190

Proteomic biomarkers for urothelial carcinoma diagnosis in liquid-based cytology via cross validation with FFPE samples

Han Suk Ryu, Seoul National University Hospital, South Korea

D-191

MitoModules as cancer biomarkers: A technique to identify context-based protein biomarkers in mouse liver cancer

Tatjana Sajic, Ethz, Switzerland

D-192

In vivo SILAC-based proteomics identifies a novel potential target in castration resistant prostate cancer

Mark Salji, Cruk Beatson Institute, United Kingdom

D-193

Whole proteome sequence map of early stage human ovarian follicular fluid

Aniel Sánchez, Lund University/BMC, Sweden

D-194

Characterization of proteome of vitreous humor in retinal detachment using different experimental setups

Fátima Milhano Santos, University of Beira Interior, Portugal

D-195

A pathogenic Escherichia coli virulence factor manipulates the host ubiquitin-modified proteome during infection

Andrew Santos, University of British Columbia, Canada

D-196

Role of biomarkers in predicting healing of chronic venous ulcers: a proteomic approach

Lucilene Delazari dos Santos, Unesp, Brazil

D-197

Deciphering interconnected activities of matrix metalloproteinases in the healing skin wound by targeted degradomics

Simonas Savickas, ETH Zurich, Switzerland

D-198

Discovery and targeted MS-based strategies for the identification of glaucoma-related IgG V domain peptides.

Carsten Schmelter, Medical Center Mainz, Germany

D-199

A proteomics approach to decipher pneumococcal adaptation during CSF infection

Frank Schmidt, University Medicine Greifswald, Germany

D-200

Integration of targeted proteomics into systems-toxicology approach: candidate modified-risk tobacco product assessment using nasal cultures

Thomas Schneider, Philip Morris International Research & Development, Switzerland

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Stratifying asthma disease in the U-BIOPRED project: large-scale MSE and TDA to define sub-phenotypes

James Schofield, University Of Southampton, United Kingdom

D-202

Decoding the role of human cardiac stem cells in acute myocardial infarction using proteomic tools

Maria Sebastião, Ibet/itqb, Portugal

D-203

Combined targeted and shotgun proteomics analysis in saliva for verification of markers of aggressive periodontitis

Nathalie Selevsek, Eth Zurich, Switzerland

D-204

Proteomic analysis of serum from patient with alcoholic pancreatitis to compare disease with treated status

AeEun Seok, Eulji University, South Korea

D-205

The nipple aspirate fluid in health and disease

Sadr-ul Shaheed, University Of Bradford UK, United Kingdom

D-206

Identification of non-invasive urinary novel biomarkers in urothelial carcinoma of bladder: a Proteomic approach

Alpana Sharma, Aiims, New Delhi, India

D-207

Early-stage blood-based proteomic diagnosis of colorectal cancer

Samridhi Sharma, Macquarie University, Australia

D-208

Temporal quantitative phosphoproteomics of ADP stimulation reveals novel central nodes in platelet activation and inhibition

Albert Sickmann, ISAS, Germany

D-209

Proteomics evidence for commonality in altered energy and apoptotic pathways in Alzheimer's Disease and Schizophrenia

Nikhath Ahmed, Siddiqui, Barrett Hodgson University, Pakhistan

D-210

Impact of obesity-induced diet on mice brain phospho-proteome

Valentina Siino, Lund University, Sweden

D-211

Identification of protein targets in cerebral endothelial cells for brain arteriovenous malformation (AVMs) molecular therapies

Margaret Simonian, UCLA, United States

D-212

Quantitative phosphoproteomic profiling to identify new drug targets to treat chronic obstructive pulmonary disease

David Skerrett-Byrne, University Of Newcastle, Australia

D-213

Multiple myeloma associated bone marrow fibroblasts characterized by multi-omics analyses including proteomics, metabolomics and eicosadomics

Astrid Slany, University Of Vienna, Department of Analytical Chemistry, Austria

D-214

Ultrasensitive Glycoproteomics pairing LP-IEF with UPLC-MSE to identify site-specific N-Glycosylation changes in Gastric Adenocarcinoma

Josh Smith, NIBRT, Ireland

D-215

A quantitative analytical method using multiple reaction monitoring-mass spectrometry for early diagnosis of hepatocellular carcinoma

Areum Sohn, Seoul National university, Korea, Republic of

D-216

Optimization of quantitative proteomic analysis of clots generated from plasma of patients with venous thromboembolism

Aneta Stachowicz, Jagiellonian University Medical College, Poland

D-217

Pediatric inflammatory bowel disease characterization by proteomics of pre- and post-therapy colon biopsies

Amanda Starr, University Of Ottawa, Canada

D-218

Protein biomarkers of metastatic propensity in prostate cancer

Pascal Steffen, University Medical Center Hamburg-Eppendorf, Germany

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Development of an apoE-isoform specific PRM assay aiming early prediction of Alzheimer's disease.

Christoph Stingl, Erasmus Medical Center Rotterdam, Netherlands

D-220

Comparing the CSF proteome of neuromyelitis optica patients to multiple sclerosis patients and control subjects

Marcel Stoop, Erasmus MC, Netherlands

D-221

Quantitative proteomics reveals a crucial role of the allergen context during activation of dendritic cells

Lisa Strasser, University Of Salzburg, Austria

D-222

MHC peptide ligands from influenza virus differ in their kinetics of presentation

Theo Sturm, Biomolecular Mass Spectrometry and Proteomics, Utrecht University, Netherlands

D-223

Identification of urinary biomarkers for metastatic colorectal cancer

Yulin, Sun, State Key Laboratory of Molecular Oncology, National Cancer Center/cancer Hospital, Chinese Academy Of Medical Sciences, China

D-224

Assessment of the activation of macrophages by quantitative secretome analysis

Maciej Suski, Jagiellonian University Medical College, Poland

D-225

Investigation of 5-fluorouracil resistance in colorectal cancer

Chris Sutton, University Of Bradford, United Kingdom

D-226

Comprehensive high-throughput analysis of IgA1 O-glycoforms by a sequential deglycosylation protocol

Kazuo Takahashi, Fujita Health University School of Medicine, Japan

D-227

Role of α 2,6-Sialylation in inhibiting adipogenesis

Naoyuki Taniguchi, Riken, Japan

D-228

Innovative mass spectrometry to assess the clinical value of proinsulin as early biomarker for diabetes

Roel Tans, Radboudumc, Nijmegen, Netherlands

D-229

Reproducible quantitative proteomics of extracellular vesicles released from stimulated brain tumour cells

Lorne Taylor, RI-MUHC, Canada

D-230

Combatting drug resistance in multiple myeloma

Ciara Tierney, Maynooth University, Ireland

D-231

Quantitation of putative colorectal cancer biomarker candidates in serum extracellular vesicles by targeted proteomics

Takeshi Tomonaga, National Institutes of Biomedical Innovation, Health And Nutrition, Japan

D-232

Proteomic characterization of microneedle-extracted human dermal interstitial fluid

Bao Tran, Excet Incorporated / Edgwood Chemical Biological Center, United States

D-233

Platelet proteome reveals novel pathways of platelet activation and platelet-mediated immunoregulation in dengue.

Monique Trugilho, Fiocruz, Brazil

D-234

Lacrimal protein biomarkers for thyroid associated orbitopathy (TAO)

Natacha Turck, University Of Geneva, Switzerland

D-235

Proteome-wide profiling of exosomes revealed exosome-driven intercellular communications in gastric cancer

microenvironment and macroenvironment
Koji Ueda, Japanese Foundation For Cancer Research, Japan

D-236

Proteomics of rat hippocampus reveals proteins related to operant learning

Marcelo Valle de Sousa, University of Brasilia, Brazil

POSTER PRESENTATIONS

D-237

Differential excretion of uromodulin peptides indicates early changes in the diabetic kidney

Julie Van, University of Toronto, Canada

D-238

PRDX2- redox-oligomeric state in Obstructive Sleep Apnea patients with diabetes mellitus

Fátima Vaz Rodrigues, Institut Ricardo Jorge, Portugal

D-239

Apolipoprotein E status determination in human saliva using LC-MRM: In Saliva Veritas?

Jerome Vialaret, Montpellier Hospital, France

D-240

Sirtuin 5 is probably a potential functional regulator of amino acid metabolism

Ke Wang, Institutes of Biomedical Sciences, Fudan University, China

D-241

New targets for inhibition of the PDL1 – PD1 immune checkpoint

James Williamson, University Of Cambridge, United Kingdom

D-242

Towards a fit-for-purpose selection of sample preparation strategies for mass spectrometry-based proteomics

Justina Clarinda Wolters, University Medical Center Groningen, Netherlands

D-243

Quantitative evaluation towards the Glutathione S-transferases in human plasma using affinity coupling with LC-MS/MS

Feng Xian, BGI-shenzhen, China

D-244

Saliva-specific differential protein signatures for non-invasive detection of cervical carcinoma

Savita Yadav, AIIMS, India

D-245

In situ characterization of infiltrated immune cells of murine EAE by MALDI imaging mass spectrometry

Hiroki Yamashita, Doshisha University, Japan

D-246

PhD abstract competition winner. Poster will be located by the innovation stage

Uncovering the molecular underpinnings of NGLY1 disease through personalized proteomics and glycoproteomics profiling

Christine Yeh, Stanford University, United States

D-247

A high-throughput quantitatively platform for serum stathmin detection in esophageal cancer

Lu Yan, Chinese Academy of Medical Sciences and Peking Union Medical College, China

D-248

Reprogramming of the acute transcriptome and total proteome underlies oncogene-induced stress adaptability

Hai Feng Zhang, University Of British Columbia, Canada

D-249

Identification of differential expression proteins in renal cell carcinoma by label-free quantitative proteomics analysis

Haili Zhang, Binzhou Medical Universitydong, China., China

D-250

iTRAQ based plasma membrane proteomic study discovered CAPG related to HIV latency

Lijun Zhang, Shanghai Public Health Clinical Center, Fudan University, China, China

D-251

Identification of serum autoantibodies for esophageal squamous cell carcinoma using human proteome microarrays

Xiaohang Zhao, National Cancer Centre/Cancer Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

D-252

Abnormal tear proteomic profile in patients with traumatic vegetative state

Lei Zhou, Singapore Eye Research Institute, Singapore

D-253

Discovering proteome alterations in PARK2-mutated Parkinson's disease patients.

Mara Zilocchi, University Of Insubria, Italy

POSTER PRESENTATIONS

D-254

Tissue proteomic alterations of colon adenocarcinoma

Apurva Atak, Indian Institute Of Technology Bombay, India

D-255

Identification of biomarkers for Proliferative Diabetic Retinopathy (PDR) in the human vitreous humor

Keshava Datta, Yu-iob Center For Systems Biology And Molecular Medicine, Yenepoya University, India

D-256

Long Noncoding RNA HOTAIR Promotes Hepatocellular Carcinoma Cell Proliferation by regulating opioid growth factor receptor

Feng Ge, Institute Of Hydrobiology, Chinese Academy Of Sciences, China

D-257

Cervical mucus proteome in endometriosis

Giuseppe Grande, International Scientific Institute "paul VI", Italy

D-258

Development of a selected reaction monitoring mass-spectrometry assay to detect TSG-6 in human synovial fluid

Oliver Gray, University Of Manchester, United Kingdom

D-259

Mutations in HIV GAG peptides and their effect on cellular immune response in Pakistani patients

Saeed Khan, Dow University Of Health Sciences, Pakistan

D-260

Exposure to metals during pregnancy and adverse birth outcomes: mechanistic insights from the MIREC study

Premkumari Kumarathan, Health Canada, Canada

D-261

Identification of proteomic biomarkers of arsenic toxicity and evaluation of dietary curcumin supplementation for mitigation

Bimal Mohanty, Icar-Central Inland Fisheries Research Institute, India

D-262

Identification of candidate serum biomarkers of pediatric Growth Hormone deficiency using SWATH-MS and feature selection

Ignacio Ortea, Imibic, Spain

D-263

Secretome analysis of U937 DC-SIGN cell line after dengue infection

Victoria Pando-robles, Instituto Nacional De Salud Publica, Mexico

D-264

Comparative proteomic study of CD34 hematopoietic stem cells from HbE/beta thalassaemia

Saranyoo Ponnikorn, Chulabhorn International College Of Medicine, Thammasat University, Thailand

D-265

Detection of novel types of protein carbonylations in human plasma.

Adelina Rogowska-Wrzesinska, University Of Southern Denmark, Denmark

D-266

Proteome Profiles of Malignant and Non-malignant Human Colon

Saira Saleem, Shaukat Khanum Memorial Cancer Hospital And Research Centre, Pakistan

D-267

Shedding new light on Spinal Cord injury

Michel Salzet, Laboratoire Prism, U1192 Inserm, France

D-268

Integration of "omics" strategies for the elucidation of molecular mechanisms underlying Brugada Syndrome

Domenica Scumaci, Magna Graecia University Of Catanzaro, Italy

D-269

Airway proteome signature associated with second-hand smoke exposure

Sofia Sentieiro, Insa Lisbon, Portugal

D-270

Aggregation as a consequence of glycation: insight into the pathogenesis of arthritis.

Anas Shamsi, Aligarh Muslim University, India

POSTER PRESENTATIONS

D-271

Global Proteomics of Tauopathy Brains to Identify Tauopathy-differentiating Disease Pathways

Hendrik Wesseling, Boston Children's Hospital/ Harvard Medical School, United States

D-272

Proteomic Approaches to Identify the Mechanism of rapid progression of Alzheimer's Disease

Saima Zafar, Clinical Dementia Center And Dzne, University Medical Center Goettingen (umg), Goettingen, Germany

Precision & Personalised Proteomics

E-001

Contribution of combined limited proteolysis and LC-MS/MS to emerin self-assembly characterization

Beatrice Alpha-bazin, French Alternative Energies and Atomic Energy Commission, France

E-002

Breast cancer classification based on proteotypes obtained by SWATH-MS

Pavel Bouchal, Masaryk University, Faculty of Science, Czech Republic

E-003

Development of an enzyme-assisted targeted glycopeptide quantification method for early detection of liver diseases

Chen-Chun Chen, Academia Sinica, Taiwan

E-004

Proteomic analysis of single cell clusters using laser capture microdissection

Simon Davis, University Of Oxford, United Kingdom

E-005

Systems pharmacology and quantitative proteomics for developing targeted triple therapy

H. Alexander Ehardt, University College Dublin / Systems Biology Ireland, Ireland

E-006

Towards comprehensive signaling pathway monitoring using advanced PRM methods

Sebastien Gallien, Thermo Fisher Scientific, France

E-007

There are still proteins in rat urine after 7-day starvation

Youhe Gao, Beijing Normal University, China

E-008

Early protein biomarker discovery in urine of Walker 256 subcutaneous rat model

Youhe Gao, Beijing Normal University, China

E-009

The discovery of kidney injury-related protein biomarkers associated with first-line antiretroviral treatment in South Africa

Ireshyn Govender, Council for Scientific and Industrial Research South Africa, South Africa

E-010

Use of Andrew liquid handling robot for protein digestion of serum for quantitative proteomic workflows

Darren Greene, Ucd, Ireland

E-011

Membrane proteome profiling of peripheral immune cells in non-small-cell lung cancer patients with PEM/CIS chemotherapy

Chia-Li Han, Master Program For Clinical Pharmacogenomics And Pharmacoproteomics, Taipei Medical University, Taiwan

E-012

Identification of a novel therapeutic target for tongue cancer by antibody-based proteomics

Onidani Kaoru, National Cancer Center Research Institute Division of Early Detection for Cancer, Japan

E-013

Novel LC-MS assay unveils an acute decrease in serum sRAGE levels after cigarette smoking

Frank Klont, University of Groningen, Netherlands

E-014

Profiling Of proteoforms in human tears using chip-based capillary electrophoresis coupled to mass spectrometry

Daniel Lopez-ferrer, Thermo Fisher Scientific, United States

E-015

Proteomic identification of vitreous biomarkers for retinal degeneration

Vinit Mahajan, University Of Iowa, United States

POSTER PRESENTATIONS

E-016

Towards an understanding of neoantigen presentation by Human Leukocyte Antigen (HLA) class I

Geert Mommen, Immunocore, United Kingdom

E-017

Individualised proteogenomics in analysis of single amino acid variants in cancer

Nicolas Nalpas, Proteom Centrum Tübingen, Germany

E-018

Revolutionary proteome profiling and quantitation without compromising speed, sensitivity, and selectivity

Sega NDIAYE, Thermo Fisher Scientific, France

E-019

Absolute quantification of a membrane-localized chemosensory protein network

Ansgar Poetsch, Plymouth University, United Kingdom

E-020

Phenotyping of rheumatoid arthritis patients by citrulline specific immunome protein arrays

Thomas B.G. Poulsen, Aalborg University, Denmark

E-021

Co-stimulatory inhibition with abatacept and the effect on the complement system in rheumatoid arthritis

Allan Stensballe, Aalborg University, Denmark

E-022

Identification of functional protein biomarkers from cancer patient serum with PEP technology

Xing Wang, Array Bridge Inc, United States

E-023

Strategies for identification of organ-specific biomarkers of exposure to ionizing radiation

Julian Whitelegge, Ucla, United States

E-024

In-depth quantitative proteomic profiling of rat heart

Juanjuan Xie, Institute Of Biomedical Science, Fudan University, China

E-025

Impact of AssayMap Bravo Liquid handling Platform on high throughput protein digestion for quantitative proteomics

Alison Doody, Ucd, Ireland

E-026

Comprehensive tissue proteomic analysis of human gliomas

Kishore Gollapalli, Indian Institute Of Technology Bombay, India

Human Proteome Project

F-001

Profiling biochemical individuality: human personal omics profiling (hPOP)

Sara Ahadi, Stanford, United States

F-002

Towards the standardization of mitochondrial proteomics: the Italian mt-HPP initiative

Tiziana Alberio, University of Insubria, Italy

F-003

Sensitivity, specificity and accuracy of the targeted and shotgun mass-spectrometry approaches

Alexander Archakov, Institute Of Biomedical Chemistry, Russian Federation

F-004

Discovery of new proteins and modifications with community-scale proteomics big data

Nuno Bandeira, University of California, San Diego, United States

F-005

The iMOP initiative and its roles in a biology and disease driven human proteome project

Emoke Bendixen, AARHUS - Department of Molecular Biology and Genetics, Denmark

F-006

Development of an analytic interface for multiple peptide library search and label-free comparative proteomic analysis

Jin-young Cho, Yonsei University, South Korea

F-007

Evaluation of NCI-7 cell line panel as new CPTAC CompRef material

David Clark, The Johns Hopkins University, United States

POSTER PRESENTATIONS

F-008

Zika virus signature in fetal brains with microcephaly

Gilberto Domont, Universidade Federal do Rio de Janeiro, Brazil

F-009

comprehensive bioinformatics workflow for analysis and identification of human missing proteins

Amr Elguoshy, Biofluid And Biomarker Center-Niigata University, Japan

F-010

Terminal Amine Isotopic Labeling of Substrates (TAILS) approach to study mitochondrial proteases in Parkinson's disease

Mauro Fasano, University Of Insubria, Italy

F-011

CSF analysis for protein biomarker identification and validation in patients with CNS Lymphoma

Manuel Fuentes, Cancer Research Center, Spain

F-012

Impairment of Protein Mitochondrial Quality Control (PMQC) in Amyotrophic Lateral Sclerosis

Viviana Greco, Fondazione Santa Lucia IRCCS, Italy

F-013

Native peptidomics: Workflow of discovering biomarker for disease from human body fluids

Yoshitoshi Hirao, Niigata University, Japan

F-014

Taking up the "neXt50 challenge" using human sperm

Lydie Lane, Sib-swiss Institute Of Bioinformatics, Switzerland

F-015

Determination of the RNA / protein ratio in human cells

Gianluca Maddalo, Kth, Sweden

F-017

MissingProteinPedia (MPP), a platform to uncover the human 'Missing proteins' (www.missingproteins.org)

Abidali Mohamedali, Macquarie University, Australia

F-018

Detection of low abundant HPV16-derived HLA-A2 epitopes on the tumor cell surface by mass spectrometry

Nitya Mohan, Deutsches Krebsforschungszentrum, Germany

F-019

Protocol optimization for deep analysis of Major Histocompatibility Complex (MHC) Immunopeptidomes

Annalisa Nicastrì, University Of Oxford, United Kingdom

F-020

Protein array enabled profiling of autoantibody repertoires in ALS, ALS-FTD and FTD

Peter Nilsson, SciLifeLab, KTH - Royal Institute of Technology, Sweden

F-021

Insights into human brain development; a proteomics perspective

Sureyya Ozcan, University Of Cambridge, United Kingdom

F-022

The human proteome discovery via diseased testis tissues in search of missing proteins

Hyoung Min Park, Seoul National University, South Korea

F-023

Peptidomics characterization of allergenic and non allergenic tropomyosin orthologs

Cristian Piras, University of Milan, Department of Veterinary Medicine DIMEVET, Italy

F-024

Digging more missing proteins using a depletion approach with ProteoMiner

Yan Ren, Bgi-shenzhen, China

F-025

Effects of amino acid supplementation on the performance of gilthead seabream using 2D-DIGE

Denise Schrama, Centre Of Marine Sciences, Portugal

F-026

Enhanced proteome coverage of MCF7 cells using an integrative search engine approach

Victor Segura, Fima, Spain

POSTER PRESENTATIONS

F-027

A method for selecting a representative protein of the highest protein evidence from non-unique proteins.

Hiromasa Tojo, Translational Medicine Informatics, St. Marianna University School Of Medicine, Japan

F-028

Regional variation and novel pathogenesis in the human Alzheimer's disease brain

Richard Unwin, The University Of Manchester, United Kingdom

F-029

Multi-protease strategy identifies more membrane-associated missing proteins in human testis tissue

Ping Xu, Beijing Proteome Research Center, China

F-030

Proteomics of Urine AQP2-bearing Exosome

Keiko Yamamoto, Biofluid Biomarker Center, Niigata University, Japan

F-031

Next-generation Proteomic Pipeline (NextPP) for Chromosome-based Proteomic Research Using GENCODE and neXtProt Databases

Jong Shin Yoo, Korea Basic Science Institute, South Korea

F-032

Quantitation of phosphorylated myelin basic protein in brain tumor tissues using pSRM

Maria Zavalova, Institute of biomedical chemistry, Russian Federation

F-033

Targeted quantitative screening of Chromosome 18 encoded proteome in plasma samples of astronaut candidates

Victor Zgoda, Institute Of Biomedical Chemistry, Russian Federation