

POSTERS

WP01- Proteogenomics

WO02-001

A proteogenomics approach to reveal molecular mechanisms of COPD

Peter Horvatovich, University of Groningen, UMCG, Department of Pathology and Medical Biology, Netherlands

WO02-002

Launch of MissingProteinPedia: Accelerating Discovery of the Human Proteome Project's "Missing Proteins"

Mark S Baker, Macquarie University, Australia

WO02-003

Proteogenomics of human cancer cell lines: coding variants identified by shotgun proteomics

Sergei Moshkovskii, Institute of Biomedical Chemistry, Russia

WO02-004

Proteogenomic profiling of neoantigens for personalized cancer immunotherapy

Koji Ueda, Japanese Foundation for Cancer Research, Japan

WO02-005

Missing genes and supplementary tissues in the Human Protein Atlas

Evelina Sjostedt, Kth - Royal Institute of Technology, Sweden

WP01-001

Identification of Proteomic and Proteogenomic Biomarkers of Prostate Cancer in Seminal Plasma

Andrei Drabovich, Department of Laboratory Medicine and Pathobiology, University of Toronto, Canada

WP01-002

Search Pipeline of Single Amino Acid Variants using neXtProt Database.

Heeyoun Hwang, Biomedical Omics Group, Korea Basic Science Institute, South Korea

WP01-003

Proteogenomic approaches to discovery of alternatively spliced proteins in hepatocellular carcinoma cell lines

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

WP01-004

Multiplexed Mass Spectrometric Screening of EGFR Mutation in Non-small-cell Lung Cancer

Chi-Ting Lai, Institute of Chemistry, Academia Sinica, Taipei, Taiwan

WP01-005

Protein expression landscape of mouse embryos during pre-implantation development

Lujian Liao, Ecnu, China

WP01-006

Have small proteins been overlooked? A proteogenomics approach using ribosome profiling, MS and bioinformatics

Volodimir Olexiouk, University of Ghent, Belgium

WP01-007

A comprehensive proteogenomic workflow reveals novel insights into leukemogenesis.

Jarrold Sandow, The Walter & Eliza Hall Institute, Australia

WP01-008

Proteogenomic Monitoring and Assessment of Increased Thermogenesis In response to β -Adrenergic Signaling

in Ahnak Deficiency

Jawon Seo, Seoul National University, South Korea

WP01-009**proBAMsuite: a bioinformatics framework for genome-based representation and analysis of proteomics data***Xiaojing Wang, Vanderbilt University Medical Center, United States***WP01-010****GAPP: a proteogenomic software for genome annotation and global profiling of posttranslational modifications in prokaryotes***Ming-Kun Yang, Institute of Hydrobiology, Chinese Academy of Sciences, China***WP01-011****Identification for protein-level evidence of genomic variants in cancer cells using new proteogenomic approach***Jeonghun Yeom, Department of Biological Chemistry, Korea University of Science and Technology, South Korea***WP01-012****Proteogenomic Monitoring and Assessment of Increased Thermogenesis In response to β -Adrenergic Signaling in Ahnak Deficiency***Junehyeong Yim, Department of Biochemistry, College of Veterinary Medicine, Research Institute for Veterinary Scienc, South Korea***WP01-013****A rigorous proteogenomics workflow to discover functional novel-coding loci and single amino acid variants***Yafeng Zhu, Karolinska Institutet, Sweden***WP02- Multiomics for Precision Medicine and Systems Biology****WP02-001****Human Personal Omics Profiling (hPOP)***Sara Ahadi, Stanford University, United States***WP02-002****Monitoring oxidative stress and progression to cell death: from secretome to blood diagnosis***Sandra I. Anjo, CNC - Center for Neuroscience and Cell Biology – University of Coimbra, Portugal***WP02-003****Meta-analysis of omics profiling to reveal translational regulation of chronic hypoxia stress in colon cancer cells***Jeng-Ting Chen, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan***WP02-004****Extracellular Vesicles - A novel class of biomarkers***Fouzi El Magraoui, Leibniz-Institut Für Analytische Wissenschaften – ISAS - e.V., Germany***WP02-005****Integrative Multi-Omic Analysis of a Single Immune Cell Type***Min-Sik Kim, Kyung Hee University, South Korea***WP02-006****The Dynamic Responses of Gene Expression in Meiosis I prophase of Mouse Spermatocytes***Qidan Li, BGI-SHENZHEN, China***WP02-007****Towards an in-depth overview about increasing arginine production in *C. glutamicum* by rational strain design using metabolomics and proteomics***Moon Liao, Bruker Daltonics, Taiwan***WP02-008****Quantitative Proteomics and Whole Transcriptomics Sequencing of Progeria-derived Cells Point to a Key Role of IGF Signaling Pathway in Premature Aging***Jesús Mateos, Cell Therapy and Reg Med Group, INIBIC- SERGAS. Medicine Dept UDC, A Coruña, Spain*

WP02-009**Transcriptomic and proteomic verification of predicted scheme of ATRA-induced HL60 cell line differentiation**

Svetlana Novikova, Institute of Biomedical Chemistry, Russia

WP02-010**THE RELATIONSHIP BETWEEN URINE PEPTIDOME AND PROTEIN MISFOLDING DURING PREECLAMPSIA**

Igor Popov, Moscow Institute of Physics and Technology, Russia

WP02-011**Diversity of HNF4A function in regulating growth and invasion of HCC**

Zhao-Yu Qin, Fudan University, China

WP02-012**Towards spatially resolved, multiplexed (up to 800 plex) digital characterization of protein and mRNA abundance in tissue**

Niroshan Ramachandran, Nanostring Technologies, United States

WP02-013**Proteomics e-learning and outreach initiatives: An effort from Indian proteomics community**

Panga Jaipal Reddy, Indian Institute of Technology Bombay, India

WP02-014**Proteome and transcriptome analysis of retinoic acid-induced differentiation of human leukemia HL-60 cells**

Olga Tikhonova, Institute of Biomedical Chemistry, Russia

WP02-015**A Systems Biology Approach to Dissect Acetylation-dependent Cancer Vulnerabilities**

Dijana Vitko, CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria

WP02-016**Lipidomic Analysis of Risk Factors for Chronic Total Occlusions after Percutaneous Coronary Intervention**

Zhenxin Wang, Institute of Biomedical Science, Fudan University, China

WP02-017**Systematic Identification of Arsenic-Binding Proteins Reveals that Hexokinase-2 is Inhibited by Arsenic**

Hainan Zhang, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University, China

WP02-018**Integrative systems biology investigation of Fabry disease**

Marco Fernandes, Institute of Cardiovascular and Medical Sciences, University of Glasgow, BHF Glasgow Cardiovascular Research Centre, 126 University Place, Glasgow, G12 8TA, UK, United Kingdom

WP03- Cysteine Modifications and Redoxomics**WO03-001****Quantitative proteomics depicts the landscape of cysteine redoxome for nitric oxide-mediated myocardial protection against ischemia-reperfusion injury**

Tzu-Ching Meng, Institute of Biological Chemistry, Academia Sinica, Taiwan

WO03-002**Proteomic analysis of S-sulfhydration by ultrafilter-assisted functional supramolecular polymer capture**

Huiming Yuan, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China

WO03-003**TRPC6-dependent S-nitrosylation in Duchenne Muscular Dystrophy**

Heaseung Sophia Chung, The Johns Hopkins Medical Institutions, United States

WO03-004**Proteomic and redox proteomic analyses reveal a dual ROS-regulation of glucose uptake in adipocytes**

Zhiduan Su, The University of Sydney, Australia

WO03-005**Identification of protein estrogenization as a redox post-translational modification by shot-gun proteomics and activity probe with dimethyl labeling**

Shu-Hui Chen, National Cheng Kung University, Taiwan

WP03-001**Multiplexed Isobaric IodoTMT-Switch Approach to Identify and Quantify the Changes in the Cardiac Redox-Environment**

Yi-Yun Chen, Institute of Biological Chemistry, Academia Sinica, Taiwan

WP03-002**Identification of Carbonylated Proteins Caused from Oxidative Stress in Hepatocyte line: Preliminary Study on Pathology of Fatty Liver Disease**

Peerut Chienwichai, Dept. of Social and Environmental Medicine, Faculty of Tropical Medicine, Mahidol University, Thailand

WP03-003**Thio-tag tip method by using zinc(II)-cyclen-attached agarose beads for enrichment of cysteine-containing biomolecules**

Hiroshi Kusamoto, Hiroshima University, Japan

WP03-004**Characterization of total thiol redox status in human fibroblasts using MS-based quantitative approach iodoTMT**

Kristyna Pimkova, Biomedical Research Center University Hospital Hradec Kralove, Czech Republic

WP04- Imaging Mass Spectrometry

TO04-001

Molecular Imaging of Protein in Tissues Using Ambient Ionization Top-Down Mass Spectrometry

Cheng-Chih Hsu, Department of Chemistry, National Taiwan University, Taiwan

TO04-002

3D MALDI imaging mass spectrometry using next generation technologies - Reconstruction of a molecular imaged epididymis

Charles Pineau, Protim - Inserm U1085 - Irset, 35042 Rennes, France

TO04-003

Localization and Identification of Peptides from Tissue using high-speed MALDI TOF/TOF mass spectrometry

Sabu Sahadevan, Bruker Daltonics, France

TO04-004

Monitoring ErbB1 and ErbB2 interaction and activation using engineered cell lines and Duolink proximity ligation assay by high-content imaging

Tracy Adair-Kirk, MilliporeSigma, United States

TO04-005

Molecular profile discrimination and mapping of skeletal muscle regeneration in rat crush model using MALDI im

Anne Denys, Université Paris 13; Sorbonne-Paris-Cité, UMR CNRS 7244, Bobigny, France

WP04-001

Identification Algorithm of Proteins in 2DE gel image Basing on Matlab Development Environment

Lijie Wu, Tongji University, China

WP04-002

A new Mass Spectrometry Imaging method for evaluation of drug distribution in the Central Nervous System

Kenichi Watanabe, Department of Biomedical Engineering, Clinical Protein Science & Imaging, Lund University, Swed

WP05- Subcellular, Spatial and Single Cell Proteomics

TO09-001

Quantitative proteome-wide profiling of the retromer cargo landscape

Christina Bell, Department of Cell Biology, Harvard Medical School, United States

TO09-002

Refining the details in the tissue-based map of the human proteome

Cecilia Lindskog, Science for Life Laboratory, Dept. of Immunology Genetics and Pathology, Uppsala University, Swed

TO09-003

Membrane localization of metabolic enzymes and metabolic modulation in a cell division mutant of *Escherichia coli* identified by omics approaches

Yu-Ling Shih, Academia Sinica, Taiwan

TO09-004

Determining post-translational modifications of nuclear proteins

Ryotaro Ban, Graduate School of Medical Life Science, Yokohama City University, Japan

TO09-005

Single-cell proteome profiling: Innovations in sample preparation

Masaki Wakabayashi, Kyoto University, Japan

WP05-001

Standardization of mitochondrial preparations for the Human Proteome Project.

Mauro Fasano, University of Insubria, Italy

WP05-002

A Mouse Tissue Transcription Factors Atlas

Mingwei Liu, National Center for Protein Sciences, Beijing, China

WP05-003

Subcellular look at asthenozoospermia: Proteomic analysis of human sperm tail in asthenozoospermic patients

Tohid Rezaei Tobraggaleh, Department of Embryology, Reproductive Biomedicine Research Center, Royan Institute, ACECR, Iran

WP05-004

Major mitochondrial machineries are integral part of cell architecture comprising cytoskeleton and nuclear matri

Cheng Hsien Yang, Institute of Biochemistry & Molecular Biology, National Yang-Ming University, Taiwan

WP06- Membrane and Extracellular Proteomics

WO04-001

Analysis of plasma membrane proteomes of gastric cancer cells reveals that ASCT2 is involved in cancer metastasis by targeting WNT/b-catenin signaling

Feng Liu, Department of Medical Systems Biology, Fudan University, China

WO04-002

Tumour-dependent fibroblast activation: when a good neighbour turns bad

Wei Wu, Utrecht University, Netherlands

WO04-003

Analysis of proteoforms in membrane protein complexes by CID/ETD top-down proteomics

Pierre-Olivier Schmit, Bruker Daltonik, Bremen, Germany, France

WO04-004

In silico characterization of the human lipid raft proteome

Michelle Hill, The University of Queensland, Australia

WO04-005

Exosomal EphA2 transmits chemoresistance and predicts pancreatic cancer patient responses to therapy

Tony Hu, Houston Methodist Research Institute/weill Cornell Medical College of Cornell University, United States

WO04-006

Systemic perturbation of keratinocyte homeostasis by genetic loss of the extracellular matrix protein collagen VI

Kerstin Thriene, Department of Dermatology, Medical Center - University of Freiburg, Germany

WP06-001

Bio-inspired nanoparticles derived from immune cells: design, characterization, and understanding their cellular fate by proteomic tools

Claudia Corbo, Houston Methodist Research Institute, Houston, TX, United States

WP06-002

Label-free Proteomic Analysis of Exosomes Secreted by HBV-inducible HepAD38 Cell Line

Xiaofang Jia, Shanghai Public Health Clinical Center, Fudan University, Shanghai 201508, China, China

WP06-003

Mining biomarkers for gastric cancer diagnosis by personalized membrane proteomics and multiple reaction monitoring mass spectrometry

Tai-Du Lin, Institute of Chemistry, Academia Sinica, Taipei, Taiwan, Taiwan

WP06-004

Comprehensive membrane proteome analysis for discovery of novel potential therapeutic targets against HTLV-1 associated disease

Satoshi Muraoka, Cancer Proteomics Group, Genome Center, Japanese Foundation for Cancer Research, Tokyo, Japan

WP06-005

A novel TP53 pathway influences the colorectal cancer tumor microenvironment via exosomes

Yulin Sun, National Cancer Center/cancer Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China

WP06-006

Inflammatory signaling-derived exosome activate immune response in macrophages

Jian Wang, National Center for Protein Sciences (beijing), Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, China

WP06-007

Quantitative proteomics of fresh tissue-derived secretome reveal the molecular mechanisms of hepatocellular carcinoma tumorigenesis and development

Xiaohua Xing, Mengchao Hepatobiliary Hospital of Fujian Medical University, China

WP07- Stem Cell Proteomics

WP07-001

Functional integrated proteomics identified "glyco-niche" signalings as a regulator of the maintenance and differentiation of cancer stem cells

Norie Araki, Graduate School of Medical Sciences, Kumamoto University, Japan

WP07-002

Proteomic analysis of low folate-induced onco spheroid formations in human colonic adenocarcinoma cells

Wen-Yu Lan, Department of Nutritional Science, Fu Jen Catholic University, Taiwan

WP07-003

A Study on Effects of sRAGE Secreting Human UCB-MSC in Parkinson's disease Model

Jaesuk Lee, Lee Gil Ya Cancer and Diabetes Center, Gachon University, South Korea

WP07-004

Comprehensive N-glycoproteomics of neural stem cell differentiation

Da Kyeong Park, Korea Basic Science Institute, South Korea

WP07-005

Proteomics identifies cell surface marker for isolation of cardiac progenitors for cell-based therapy in cardiac infarction

Ghasem Hosseini Salekdeh, Royan Institute for Stem Cell Biology and Technology, ACECR, Tehran, Iran, Iran

WP07-006

Integrative omics reveals N-glycoproteome-wide alterations and their functional network in induced pluripotent stem cells

Putty-Reddy Sudhir, Genomics Research Center, Academia Sinica, Taiwan

WP08- Neurological Disorders and Neuroproteomics

WO08-001

Gene expression and proteomic analysis of cognitive dysfunction in people with remitted Major Depression

Klaus Oliver Schubert, The University of Adelaide, Australia

WO08-002

Proteomic dissection of AMPA receptor complexes identifies FRRS1 as a determinant for receptor biogenesis mutated in severe intellectual disability

Uwe Schulte, University of Freiburg, Institute for Physiology, Germany

WO08-003

Autoantibody response in meningioma patients reveals aberrations in signalling pathways

Shabarni Gupta, Indian Institute of Technology Bombay, India

WO08-004

Proteomic analysis of motor neurons from induced pluripotent stem cells: ALS

Victoria Dardov, Cedars Sinai Medical Center, United States

WO08-005

Analysis of the O-GlcNAcomic profiling of brain tissue in Alzheimer's disease

Wei-Wei Chang, Genomics Research Center, Academia Sinica, Taipei, Taiwan, Taiwan

WP08-001

Proteomics biomarkers from human cerebral cortex for molecular diagnostic and prognostic management of epilepsy patients

Zakia Zhinwari, King Faisal Specialist Hospital and Research Centre, Saudi Arabia

WP08-002

Full-length TDP-43 Forms Toxic Amyloid Oligomers in Frontotemporal Lobar Dementia-TDP Patients and Disturbs Amyloid- β Fibrillization

Yun-Ru (Ruby) Chen, Genomics Research Center, Academia Sinica, Taiwan

WP08-003

SCN phosphoproteomic analysis reveals GRK2 as an important modulator of neuronal structure and cytoskeleton organization

Cheng-Kang Chiang, Ottawa Institute of Systems Biology, University of Ottawa, Canada

WP08-004

Quantitative proteomics of the cytosolic fraction from orbitofrontal cortex of patients with schizophrenia

Gilberto Domont, Federal University of Rio De Janeiro, Brazil

WP08-005

CSF analysis for protein biomarkers identificatin in patients with CNS lymphoma

Manuel Fuentes, Cancer Research Center. University of Salamanca-csic, Spain

WP08-006

Proteomic analysis of vitamin D-regulated proteins in primary cultured OLGs

Jifang Gao, Institution of Biochemistry and Molecular Biology, School of Medicine, Shandong University, China

WP08-007

PROTEOMIC INVESTIGATION OF GLIOBLASTOMA MULTIFORME ON THE BASIS OF SVZ INVOLVEMENT

Saicharan Ghantasala, Indian Institute of Technology Bombay, India

WP08-008

An innovative HPLC quantitative method coupled with proteomics analysis to investigate hydrogen sulphide forms in cerebrospinal fluid

Viviana Greco, Santa Lucia Foundation, Rome, Italy, Italy

WP08-009

Chronic low-dose rate ionising radiation affects the hippocampal phosphoproteome in an ApoE^{-/-}-Alzheimer mouse

Stefan J. Kempf, Institute of Radiation Biology, Helmholtz Zentrum München, Munich, Germany

WP08-010

Proteomic analysis reveals metabolic alteration of substantia nigra in schizophrenic patients

Ayesha Khan, University of Karachi, Pakistan

WP08-011

Mapping of Gangliosides from Nine Regions of Mouse Brain by Negative Ion Mode Nano LC/MS

Sumin Kim, Chungnam National University, South Korea

WP08-012

Chronic exposure to low dose methylmercury induces various proteome changes in different regions of rat's brain

Hang-Kin Kong, The Hong Kong Polytechnic University, Hong Kong, China

WP08-013

Differential proteome changes in the brains of Arctic Ringed Seal induced by bioaccumulation of methylmercury

Samuel Chun-Lap Lo, The Hong Kong Polytechnic University, Hong Kong, China

WP08-014

A peptidomic profile of transgenic rat model for tauopathy: LC-MALDI/MS analysis of cerebrospinal fluid

Andrej Kovac, Institute of Neuroimmunology, Slovak Academy of Sciences, Slovakia

WP08-015

The mechanism research on GSN remission of MS/EAE: A proteome analysis

Shilian Liu, Institute of Biochemistry and Molecular Biology, School of Medicine, Shandong University, China

WP08-016

Human platelet lysate (HPL) proteome analysis by nanoLC-MS/MS mass spectrometry: new insights to understand HPL neuroprotective properties

Didier Lutomski, Université Paris 13; Sorbonne-Paris-Cité; UMR CNRS 7244, Bobigny, France

WP08-017

Estrogen partially reverses proteomic changes induced by excessive stretching of brain endothelial cells

Abidali Mohamedali, Macquarie University, Australia

WP08-018

A glimpse into the proteomic profile of Rasmussen's Encephalitis

Omesan Nair, Division of Chemical & Systems Biology, IIDMM, University of Cape Town, South Africa

WP08-019

Toxicoproteomics highlights the role of vimentin in neurotoxicity induced by fipronil

N. Monique Paricharttanakul, Environmental Toxicology, Chulabhorn Graduate Institute, Thailand

WP08-020

Amyloid beta activated human microglial cells through ER-resident proteins

Young Mok Park, Institute for Basic Science, South Korea

WP08-021

Differential protein expression in the cortex of mice exposed to the antipsychotic drugs haloperidol and clozapine

Cátia Santa, Center for Neuroscience and Cell Biology, Portugal

WP08-022

PROTEOMIC ANALYSIS OF MATURATION DEPENDENT ADVERSE EFFECTS OF PARAQUAT EXPOSURE IN 3D RAT BRAIN CELL CULTURES

Domitille Schwartz, University of Geneva, Switzerland

WP08-023

Beta-amyloid induces pathology-related patterns of tau hyperphosphorylation at synaptic terminals via CDK5 activation

Hwan-Ching Tai, Department of Chemistry, National Taiwan University, Taiwan

WP08-024

Investigation the roles of TDP-43 oligomers in neurodegenerative diseases

Tzu-Yu Weng, Academia Sinica, Taiwan

WP08-025

Chronic Exposure to Low Doses of Methylmercury Induced Proteome Changes on Polar Bear Brains

Yee-Man Melody Wong, The Hong Kong Polytechnic University, Hong Kong, China

WP08-026

Imaging Mass Spectrometry (IMS) for the proteomic studies of Experimental Autoimmune Encephalomyelitis (EAE) Mouse

Hiroki Yamashita, Doshisha University, Japan

WP09- Pharmacoproteomics and Drug Development

WO01-001

Proteome-wide drug dose-response of prostate cancer cell lines exposed to androgen receptor antagonists by microflow-LC SWATH MS analysis

Christie Hunter, Sciex, United States

WO01-002

Profiling changes in the phosphoproteome of hematopoietic cells in response to a novel class of anti-oncogenic compounds.

Peter Kubiniok, Department of Chemistry, University of Montreal, Canada

WO01-003

Cancer proteomics towards precision medicine by molecular targeting drug

Zhiwei Qiao, Division of Rare Cancer Research, National Cancer Center Research Institute, Japan

WO01-004

Drug Development by Linking Pathophysiology in Cancer to Proteomics

Marko-Varga György, Clinical Protein Science & Imaging Group, BioMedical Center, University of Lund, Lund, Sweden ; Dept. of Surgery, Tokyo Medical University, Tokyo, Japan, Sweden, Japan

WP09-001

A Study on the Intestinal Absorption and Functions of bioactive Peptide

Jing Chen, Shanghai Jiaotong University, China

WP09-002

Pharmacoproteomics reveals the pan-Aurora kinase inhibitor tozasertib as a potential therapeutic drug for *Mycn*-amplified neuroblastoma

Chiao-Hui Hsieh, Institute of Molecular and Cellular Biology, National Taiwan University, Taiwan

WP09-003

The Discovery and Potential Application of Bioactive Peptides from Fermented Milk and Probiotics

Wanru Li, Shanghai Jiao Tong University, China

WP09-004

Corosolic Acid, the Active Principle of *Actinide chinensis*, Inhibits Hepatocellular Carcinoma by Targeting the VEGFR2/Src/FAK Pathway

Hsuan-Yuan Lin, National Taiwan Normal University, Taiwan

WP09-005

Deciphering the molecular insights of phytoagent deoxyelephantopin against triple negative breast cancer using LC-MS based quantitative proteomics

Jeng-Yuan Shiau, Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

WP09-006

Identification of Novel HLA-A2 Restricted Phosphopeptide for Cancer Vaccine Development

Wang-Chou Sung, National Institute of Infectious Diseases and Vaccinology, NHRI, Taiwan

WP09-007

Cellular Thermal Shift Assay (CETSA) enables identification of drug targets of natural products

Peng Yu, Chair of Proteomics and Bioanalytics, Technische Universität München, Germany

WP09-008

The Discovery and Potential Application of Bioactive Peptides from Fermented Milk and Probiotics

Shao-Hui Zhang, School of Agriculture and Biology, SJTU, China

WO06-001

Target Identification in Living Cells via Mass Spectrometry-based Chemical Proteomics

*Xuezhi Bi, Bioprocessing Technology Institute, Agency for Science, Technology and Research (A*STAR), Singapore*

WO06-002

Comprehensive mass spectrometry analysis identifies a novel therapeutic target in the Wnt signaling pathway

Tesshi Yamada, National Cancer Center Research Institute, Japan

WO06-003

The Phosphoproteome of the NCI-60 Cell Line Panel Reveals Markers of Drug Sensitivity

Chen Meng, Lehrstuhl Für Proteomik Und Bioanalytik, Technische Universität Muenchen, Germany

WO06-004

Targeted proteomic profiling of enzymes that activate the prodrug PR-104A in human leukaemias

Yongchuan Gu, University of Auckland, New Zealand

WO06-005

Identification of TIFA as a novel therapeutic target in acute myeloid leukemia

Tong-You Wei, Academia Sinica, Taiwan

WP10-001

Drug Target Identification in Multiple Myeloma by Chemical Proteomics

Matthias Bach, University of Würzburg, Rudolf-Virchow-Center, Germany

WP10-002

Matrix Assisted Laser Desorption Ionization-Mass Spectrometry Imaging based analysis of distribution of anti-tumor agents on tissue

Sungmin Cho, Chemical Genomics Global Research Laboratory, Department of Biotechnology, College of Life Science & Biotechnology, Yonsei University, South Korea

WP10-003

Comparative Proteomic Analysis Reveals the Molecular Mechanisms of Mandibular Glands in Two Lines of

Honeybees (*Apis mellifera ligustica*)

Yue Hao, Institute of Apicultural Research, Chinese Academy of Agricultural Sciences, China

WP10-004

Anti-cancer Gold(III) Porphyrins Target Mitochondrial Chaperone Hsp60

Di Hu, State Key Laboratory of Synthetic Chemistry, Chemical Biology Center, The University of Hong Kong, Hong Kong, China

WP10-005

A novel platform for target identification of a natural small molecule and its target protein interaction on tissues using MALDI-MSI analysis

Yonghyo Kim, Chemical Genomics Global Research Laboratory, Department of Biotechnology, College of Life Science & Biotechnology, Yonsei University, South Korea

WP11- Metabolomics and Metabolic Disorders

MO04-001

GLOBAL DATA STANDARDIZATION ALGORITHM FOR APPLIED METABOLOMICS

Petr Lokhov, Institute of Biomedical Chemistry, Russia

MO04-002

Systemic proteomic and metabolomic analyses identify crucial roles of the polyol pathway in tumorigenesis

Anuli Uzozie, Institute of Molecular Systems Biology, Switzerland

MO04-003

Urine proteomics for evaluation of taking nano-mist sauna effects on the health

Yoshitoshi Hirao, Biofluid Biomarker Center, Niigata University, Japan

MO04-004

Mass spectrometry-based proteomic and metabolic analysis of different cell lines after perturbation of cellular cholesterol regulation

Peter Blattmann, ETH Zurich, Switzerland

MO04-005

imCorrect: New UHRMS Signal Handling Approach for More Accurate Elemental Composition Determination

Wei-Hung Chang, Academia Sinica, Taiwan

WP11-001

Investigations into the effect of fish oil on enzymes of lipid metabolism: a proteomics approach

Kk Asha, Icar-cift, India

WP11-002

Study the regulation of bioactive compounds and metabolome of *W. chinensis* under different plant hormone and stress treatment

Chih-Wei Chang, Academia Sinica, Taiwan

WP11-003

Monitoring phosphatidylcholine and sphingomyelin for concentration normalization in cellular lipidomics studies using FIA-ESI-MS/MS

Hsi-Chun Chao, School of Pharmacy, National Taiwan University, Taiwan

WP11-004

Development of the absolute quantification method for amino acids

Ya-Wen Chou, Academia Sinica, Taiwan

WP11-005

Epigenetic mechanism investigation in recessive neurometabolic disorder mice.

Jun Gao, Department of Chemistry & Institutes of Biomedical Sciences, Fudan University, China

WP11-006

IMS-DIA-MS Characterisation and IMS-MRM QconCAT Quantitation of the Lipidome and Apolipoprotein Complements of Obesity and Diabetes Cohorts

David Heywood, Waters, United Kingdom

WP11-007

Metabolomics Profiling of Paired OSCC Using Chemical Isotope Labeling LC-MS

Chia-Wei Hsu, Molecular Medicine Research Center, Chang Gung University, Taiwan

WP11-008

Quantitative Metabolome Analysis of Pleural Effusion with High-Performance Chemical Isotope-Labeling Liquid Chromatography-Mass Spectrometry

Pei-Chun Hsueh, Graduate Institute of Medical Biotechnology and Laboratory Science, Chang Gung University, Taiwan

WP11-009

Metabolomic profiling of subgrouping ischemic stroke

Tai-Ming Ko, Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan

WP11-010

Monte Carlo Simulation Reveals Reliable Molecular Formula Annotation of Metabolomic Data Obtained by Accurate Mass Spectrometry

Melody M. T. Lam, Proteomics Core, Faculty of Health Sciences, University of Macau, Macau, China

WP11-011

Urinary exposure marker discovery for toxicants using UPLC-LTQ-Orbitrap and three untargeted metabolomics approaches

Pal-Chi Liao, Department of Environmental and Occupational Health, National Cheng Kung University, Taiwan

WP11-012

Discovery of early-stage biomarkers for diabetic nephropathy using LC/MS-based metabolomics

Yu-Ning Lin, Proteomics Core Laboratory, Department of Medical Research, China Medical University, Taiwan

WP11-013

Defining the aberrant molecular profiles in liver and adipose tissues of ovariectomized rat model with different n-3 fatty acid interventions

Ming-Hsuan Lin, Master program for clinical pharmacogenomics and pharmacoproteomics, Taipei Medical University, Taiwan

WP11-014

Metabolomics investigation of voriconazole-induced hepatotoxicity

Shin-Lun Wu, School of Pharmacy, National Taiwan University, Taiwan

WP11-015

Using a Targeted Metabolomic Approach to Investigate Plasma Metabolites Associated With Risk of Diabetes Me

Yi-Hao Wu, School of Pharmacy, College of Medicine, National Taiwan University, Taiwan

WP11-016

Fragmentation Analysis of Amino acids by High Resolution Tandem MS and High-Energy Collision Dissociation

Pengwei Zhang, Pilot Laboratory, Faculty of Health Sciences, University of Macau, Macau, China

WP12- Plant Proteomics

WO09-001

Quantitative Proteomic Analysis of Flooding and Its Recovery in Soybean Exposed to Aluminum Oxide Nanoparticles
Setsuko Komatsu, National Institute of Crop Science, Japan

WO09-004

Integrated extracellular matrix proteome and organ specific transcriptome decipher cell wall mediated immunity in plant

Kanika Narula, National Institute of Plant Genome Research, India

WO09-005

Phosphoproteomic Analysis of Abscisic Acid Signaling Components in Arabidopsis seed

Anna Amagai, BASE, Tokyo University of Agriculture and Technology, Japan

WP12-001

Quantitation of tonoplast proteins simultaneously regulating inorganic phosphate(Pi) influx-efflux during varying Pi levels

Debayan Bose, Academia Sinica, Taiwan

WP12-002

The CAP Secretory Pathway is required for CAPE peptide production for the induction of SAR

Ying-Lan Chen, Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

WP12-003

Studying of Plant Novel Systemic Signaling and RNA Trafficking Proteins under Pi Deficiency Using Proteomics Approach

Yet-Ran Chen, Academia Sinica, Taiwan

WP12-004

Proteomic analysis of "Oriental Beauty" oolong tea leaves with different degrees of leafhopper infestation

Han-Ju Chien, Institute of Molecular Biology, National Chung Hsing University, Taiwan

WP12-005

Proteometabolomic study illustrates dual role of oxalic acid in anti-nutrient signaling and non-host resistance

Sudip Ghosh, National Institute of Plant Genome Research, India

WP12-006

Proteomic Analysis of Bee Pollen from a Natural Forest in Central Taiwan

Ya-Jin Jheng, Genomics Research Center, Academia Sinica, Taiwan

WP12-007

Quantitative Proteomics of *Phaeodactylum tricornutum* in Acidified Environment

Tai-Yi Jiang, National Taiwan Ocean University, Taiwan

WP12-008

Comparative Proteomics of *Chlorella* sp. FC2 IITG during Nitrogen-starvation using iTRAQ and MRM based Mass Spectrometry

Vineeta Rai, Indian Institute of Technology Bombay, India

WP12-009

Quantitative Proteomics of *Phaeodactylum tricornutum* in Phosphate Limited Environment

Shiang-Yu Tsai, National Taiwan Ocean University, Taiwan

WP12-010

Proteomic Analysis to Reveal the Calcium Function on Protein Glycosylation in Endoplasmic Reticulum of Soybean under Flooding and Drought Stresses

Xin Wang, University of Tsukuba, Japan

WP12-011

Proteomic and Transcriptomic Analyses to Reveal the Tolerance Mechanism in Soybean at Initial Flooding Stress

Xiaoqian Yin, University of Tsukuba, Japan

WP12-012

Comparative phosphoproteomic analysis of dormant and after-ripened seeds of barley

Shinnosuke Ishikawa, Tokyo University of Agriculture and Technology, Japan

WP13- Microbial Proteomics

TO10-005

Proteomics in Food safety: monitoring competition between *Listeria monocytogenes* and *Lactococcus lactis* by Imaging Mass Spectrometry

Isabella Alloggio, Dipartimento di Medicina Veterinaria, Università degli studi di Milano, Italy

WO09-002

Single-species proteomics, multi-species metaproteomics, trends and opportunities to read-across in environmental assessment

Susana Cristobal, Linköping University, Sweden

WO09-003

Gastric Bypass surgery clearly perturbs the community structure and the functional composition of the intestinal microbiota

Nico Jehmlich, Helmholtz-centre for Environmental Research - Ufz, Germany

WP13-001

The virulence mechanism mediated by a metalloprotein in *Streptococcus pneumoniae*

Kun Cao, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

WP13-002

Comparative proteomic analysis of virulence variations in *Xanthomonas campestris* pv. *campestris* strain 17, 11A and P20H

Tao-Shan Chang, Institute of Molecular Biology College of Life Science, National Chung Hsing University, Taiwan

WP13-003

Biodegradation of Crude Oil and Diesel by Novel Microorganism, *Arthrobacter* sp. MWB-30

Young-Ho Chung, Korea Basic Science Institute, South Korea

WP13-004

Isobaric Tagging-Based MS Quantification of HIV-1/gp120/tat in Astrocytoma: Implications for HIV-associated neurodegeneration

Luis Cubano, Biomedical Proteomics Facility, Dept of Microbiology and Immunology, Universidad Central del Caribe, United States

WP13-005

Novel characteristics of highly virulent ribotype 027 - Quantitative and qualitative proteomic analysis of *C. difficile* clinically relevant ribotypes

Jiri Dresler, Military Health Institute, Czech Republic

WP13-006

iTRAQ-Based Proteomics Revealed the Formation Mechanism of Drug-Resistant Bacteria

Gao Fei Du, Functional Protein Research of Guangdong Higher Education Institutes, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

WP13-007

A comprehensive proteomics analysis for *Streptococcus equi* subspecies *equi* Se071780 to antigen discovery and vaccine development

Hayoung Lee, Drug & Disease Target Team, Korea Basic Science Institute, Daejeon 34133, South Korea

WP13-008

Using multiple data analytical approaches to determine the metaproteome of the human gut

Andrew Nel, University of Cape Town, South Africa

WP13-009

Alkaline protease activity and alk protein level in clinical isolates of *A. flavus*

Mohammed Razeeth Shait Mohammed, Proteomics Department, Aravind Medical Research Foundation, Dr. G. Venkataswamy Eye Research Institute, India

WP13-010

Metalloproteome study on the iron transportation mechanism in bacteria.

Xiaoyan Yang, Jinan University, China

WP13-011

iTRAQ-Based Proteomics Revealed the Bactericidal Mechanism of Sodium New Houttuynonate (SNH) against *Streptococcus pneumoniae*

Xiao-Yan Yang, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

WP13-012

In-depth metaproteomic studies of human and mouse gut microbiota

Xu Zhang, University of Ottawa, Canada

WO05-001

The Benefits of Hybrid Fragmentation Technologies (EThcD) for Analysing the Immuno-peptidome

Albert J Heck, Utrecht University and Netherlands Proteomics Centre, The Netherlands

WO05-002

Digestomics of raw peanut and characterization of gastric-phase released peptides of peanut allergens

Tanja Cirkovic Velickovic, University of Belgrade - Faculty of Chemistry, Serbia

WO05-003

Ultra-Fast Analysis of Allergens using capillary electrophoresis coupled to mass spectrometry and Ultraviolet Photodissociation

Daniel Lopez-Ferrer, Thermo Fisher Scientific, United States

WO05-004

Characterisation of specificity of different commercial proteases for food hydrolysates

Cristian De Gobba, University of Copenhagen, Denmark

WO05-005

Characterization and Modulation of fish allergens

Pedro Rodrigues, Universidade do Algarve, Campus de Gambelas, Ed. 7, 8005-139 Faro, Portugal

WP14-001

Identification of 2-oxohistidine interacting proteins using E. coli proteome chips

Yun-Huan Chen, Department of Chemistry, National Taiwan University, Taiwan

WP14-002

Quantitative phosphoproteomic characterization of the effect of RN/HAL genotypes on post-mortem energy metabolism in pigs

Rene Lametsch, University of Copenhagen, Denmark

WP14-003

Proteomic analysis of antique glue on a Stradivari violin

Guo-Chien Li, Department of Chemistry, National Taiwan University, Taiwan

WP14-004

Rapid and Simultaneous Determination of γ -oryzanol, Vitamin E Isomers in Brown Rice sample by Ultra-Performance Liquid Chromatography Mass

Hung-Yu Lin, Institute of Molecular Biology College of Life Science, National Chung Hsing University, Taiwan

WP15- Kidney, Urine and Plasma: Opportunities for Early Diagnosis and Risk Assessment

WO10-001

Comparative proteomic analysis of kidney distal convoluted tubule and cortical collecting duct cells following long-term hormonal stimulation

Qi Wu, InterPrET Center, Department of Biomedicine, Aarhus University, Denmark

WO10-002

Targeted MS-based assay of circulating proteoforms related to aging in human plasma

Pingbo Zhang, Wilmer Eye Institute, Johns Hopkins University School of Medicine, Baltimore, MD, United States

WO10-003

Can proteomics contribute to solving the riddle of Diabetic Nephropathy?

Leena Kerstin Maria Liljedahl, Immunotechnology, Lund University, Sweden

WO10-004

Quantification of Angiotensin II-Regulated Proteins in Urine of Patients with Polycystic and Chronic Kidney Diseases by Selected Reaction Monitoring

Ana Konvalinka, Division of Nephrology, University Health Network, University of Toronto, Toronto, Canada

WO10-005

Analysis of the HDL Proteome - Myths and Legends and Reality

Manfred Raida, National University of Singapore, Microbiology and Immunology, Singapore

WP15-001

Proteomic insight reveals elevated levels of albumin in circulating immune complexes in diabetic plasma.

Shweta Bhat, Proteomics Facility, Division of Biochemical Sciences, CSIR-National Chemical Laboratory, Pune, India

WP15-002

Profiling of plasma for proteomic signatures of mammographic density

Sanna Byström, Science for Life Laboratory, School of Biotechnology, KTH – Royal Institute of Technology, Stockholm, Sweden

WP15-003

Novel proteomics-based pipeline for identifying predictive Biomarkers of chemotherapy-induced toxicity

Emily Chen, Herbert Irving Comprehensive Cancer Center at Columbia University Medical Center, United States

WP15-004

Human native Peptidome database for Peptidomics studies

Amr Elguashy, Niigata University, Japan

WP15-005

Urimem, a membrane that can store urinary proteins simply and economically, makes the large-scale storage of clinical samples possible

Youhe Gao, Beijing Normal University, China

WP15-006

Rapid and high-throughput identification of acute hepatic porphyria by SALDI-TOF MS analysis

Han-Chih Ke, Institute of Molecular Biology, National Chung Hsing University, Taiwan

WP15-007

Developing a strategy to identify low-abundance native peptides in plasma

Yoshio Kodera, Center for Disease Proteomics, Kitasato University School of Science, Japan

WP15-008

Preliminary study into the quantitative impact of long-duration space travel on the cosmonaut plasma proteome

Irina Larina, Institution for Biomedical Problems, RAS, Moscow, Russia

WP15-009

Proteomics Analysis Of Rat Kidney Under Maleic Acid Treatment By SWATH-MS Technology

Chao-Yi Lee, Institute of Molecular Biology, National Chung Hsing University, Taiwan

WP15-010

The discovery of HDL-associated protein biomarkers to predict stroke

Hsin-Yi Liao, College of Medicine, China Medical University, Taichung, Taiwan, Taiwan

WP15-011

EVALUATION OF CARDIOVASCULAR SYSTEM STATE BY URINE PROTEOME AFTER MANNED SPACE FLIGHT

Liudmila Pastushkova, Institute for Biomedical Problems – Russian Federation State Scientific Research Center RAS, Russia

WP15-012

Human plasma proteome analysis using meter-long monolithic silica columns with match-between-runs

Yi-Ting Wang, Center for Genomic Medicine, Kyoto University, Japan

WP15-013

Comparative Proteomic Analysis of Human Calcium Oxalate and Calcium Phosphate Kidney Stone Matrices

Frank Witzmann, Indiana University School of Medicine, United States

WP15-014

Proteomics of urine from healthy volunteers by SWATH-MS

Bo Xu, Niigata University Biofluid Biomarker Center (BB-C), Japan

WP15-015

Proteomics of Diabetic Nephropathy Glomerulus

Keiko Yamamoto, Biofluid Biomarker Center/ Niigata University, Japan

WP15-016

Application of High Throughput Urinary Proteomic Strategy in the Diagnosis of Acute Appendicitis with Confusable Acute Abdomens

Yinghua Zhao, National Center for Protein Sciences - Beijing, China

WP16- Late Breaking Abstracts

WP16-001

Biological characteristic of human enterovirus species A in human nucleolin transgenic mice

Yi-Chen Lin, Department of Medical Laboratory Science and Biotechnology, College of Medicine, National Cheng Kung University, Taiwan

WP16-002

Zika virus is not alone: proteomics associates a bovine-like viral diarrhea virus to microcephaly

Federal University of Rio de Janeiro, Rio de Janeiro, Brazil

WP16-003

Lymph node metastasis of primary endometrial cancers: associated proteins revealed by maldi imaging

Parul Mittal, The University of Adelaide, Australia

WP16-004

Human SRMATlas: A resource of targeted assays to quantify the complete human proteome

Ulrike Kusebauch, Institute for Systems Biology, Seattle, United States

WP16-005

Low microgram amount protein samples coupled with novel polymers for TAILS terminomics yield efficient enrichments utilizing precipitation with organic solvents

Nestor Solis, Centre for Blood Research, 2350 Health Sciences Mall Life Sciences Centre, University of British Columbia, Vancouver, Canada

WP16-006

Identification of Cofilin-1 Induces G0/G1 Arrest and Autophagy in Angiotensin-(1-7)-treated Human Aortic Endothelial Cells from iTRAQ Quantitative Proteomics

Wan-Yu Lo, Cardiovascular & Translational Medicine Laboratory, Department of Biotechnology, Hung Kuang University