

TUESDAY POSTER PRESENTATION

TP01 - Cancer, Clinical and Translational Proteomics

MO01-001

Verification of colorectal cancer biomarker candidates in plasma/serum extracellular vesicles by targeted proteomics

Takeshi Tomonaga, Laboratory of Proteome Research, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

MO01-002

Proteomic Multimarker Panel Complements CA19-9 Insufficiency in the Diagnosis of Pancreatic Ductal Adenocarcinoma

Youngsoo Kim, Seoul National University College of Medicine, South Korea

MO01-003

Pathology-driven comprehensive proteomic profiling of the prostate cancer tumor microenvironment

Stephen Pennington, UCD Conway Institute of Biomolecular and Biomedical Research, Ireland

MO01-004

Tissue derived neo-antigens for T cell-based cancer immunotherapy

Michal Bassani, Unil/chuv, Switzerland

MO01-005

LinkedOmics: discovering associations between genomic, proteomic and clinical attributes in human cancer

Jing Wang, Vanderbilt University Medical Center, United States

TO05-004

Proteome analysis of microdissected tumor cells reveals Annexin A10 as biomarker candidate for differentiation of ICC and liver metastases of PDAC

Thilo Bracht, Medizinisches Proteom Center, Ruhr Universität Bochum, Germany

WO07-003

Quantitation and evaluation of candidate biomarkers of pancreatic cancer in plasma using multiple reaction of monitoring method

Weimin Zheng, Department of Chemistry, Fudan University, China

TP01-001

Clinically-Actionable Proteomic Biosignatures of Colorectal Cancer

Seong Beom Ahn, Department of Biomedical Sciences, Macquarie University, Australia

TP01-002

Integrative Analysis for the Discovery of Non-small Cell Lung Cancer Serological Markers and Validation by MRM-MS and ELISA

Hee-Sung Ahn, Department of Biological Chemistry, Korea University of Science and Technology, Daejeon, South Korea

TP01-003

Paradigm shift in accurate assessment of HER-2 in breast cancer patients by expression proteomics: Precision medicine and cost saving implications

Ayodele Alaiya, Proteomics Unit, King Faisal Specialist Hospital and Research Center, Saudi Arabia

TP01-004

Identification of new biomarkers for castration resistant prostate cancer by secretome analysis

Noriaki Arakawa, Graduate School of Medical Life Science, Yokohama City University, Japan

TP01-005

Muscadine Grape Skin Extract Induces an Unfolded Protein Response Mediated Autophagy in Prostate Cancer Cells

Nawal Boukli, Center for Cancer Research and Therapeutic Development, Dept Biological Sciences, Clark Atlanta Uni, United States

TP01-006

Biomarkers of Colorectal Carcinoma Liver metastasis in Urine

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

TP01-007

Targeted proteomics based clinical investigation of serum early detection biomarkers for malignant pleural mesothelioma cancer

Ferdinando Cerciello, James Thoracic Center, James Cancer Center, The Ohio State University Medical Center, Columbus, OH, United States

TP01-008

Development of a Multiplexed LC-MRM MS Method of Salivary Proteins for Evaluation of Oral Cancer Biomarkers

Yi-Ting Chen, Chang Gung University, Taiwan

TP01-009

Functional re-activation of mitochondria in the TGF- β 1 induced EMT of lung cancer A549 cells

Zhipeng Chen, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

TP01-010

Quantitative profiling of plasma proteome in Kawasaki disease

Yi-Hung Chen, Taipei Medical University/master Program for Clinical Pharmacogenomics and Pharmacoproteomics, Taiwan

TP01-011

Evaluation of biofluid biopsies by targeted proteome analysis for oral cancer biomarker discovery and verification

Lang-Ming Chi, Clinical Proteomics Core Laboratory, Chang Gung Memorial Hospital, Linkou, Taiwan

TP01-012

Identification of Salivary Biomarkers for Detecting Oral Cavity Squamous Cell Carcinoma by Quantitative Proteomics

Hao-Wei Chu, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

TP01-013

Variabilities of potential protein biomarkers level in saliva samples from healthy donor

Lichieh Chu, Molecular Medicine Research Center, Chang Gung University, Taiwan

TP01-014

Discovery and verification of blood biomarker for a diagnosis of acute graft-versus-host disease based on mass spectrometry and proteomics technology

Kisoon Dan, Proteomics Core Facility, Biomedical Research Institute, Seoul National University Hospital, South Korea

TP01-015

In-Depth Proteomic Analysis of Pancreatic Cyst Fluid in Intraductal Papillary Mucinous Neoplasm Dysplasia of the Pancreas

Misol Do, Department of Biomedical Sciences, Seoul National University College of Medicine, South Korea

TP01-016

Identification of protein and PTMs changes in gastric cancer patients from before to after surgery

Lylia Drici, University of Southern Denmark, Denmark

TP01-017

Immuno-MALDI for quantifying PI3K/AKT/mTOR signaling pathway activity in breast and colorectal cancer tumors

Björn Fröhlich, University of Victoria - Genome BC Proteomics Centre, Canada

TP01-018

Proteomic analysis identified heat shock protein 72 as a possible target of combination therapy with histone deacetylase inhibitor

Kazuyasu Fujii, Department of Dermatology, Kagoshima University Graduate School of Medical and Dental Sciences, Japan

TP01-019

Multi-dimensional Proteomics Reveals a Role of UHRF2 in the Regulation of Epithelial-Mesenchymal Transition (EMT)

Sai Ge, Beijing Proteome Research Center, China

TP01-020

A Set of Mass Spectrometry-derived Prognostic Biomarkers for Prostate Cancer Survival Prediction

Sandra Goetze, Swiss Federal Institute of Technology Zurich (ETH), Switzerland

TP01-021

Novel Risk Models for early detection and screening of Ovarian Cancer.

Robert.L.J. Graham, Stoller Biomarker Discovery Centre, Institute of Cancer Sciences, University of Manchester, United Kingdom

TP01-022

Systems-wide analysis of protein expression in formalin-fixed paraffin-embedded Secretory Breast Carcinoma Tissues

Dohyun Han, Biomedical Research Institute, Seoul National University Hospital, South Korea

TP01-023

An in-depth proteomics investigation of the perturbed mechanisms underlying pemetrexed and paclitaxel treatments in non-small-cell lung cancer

Chia-Li Han, Mastor Program for Clinical Pharmacogenomics and Pharmacoproteomics, Taipei Medical University, Taiwan

TP01-024

Understanding male infertility after SCI through quantitative proteomics

Dominic Helm, Human Reproduction Section, Division of Urology, Department of Surgery, São Paulo Federal University, Brazil

TP01-025

Clinical application of plasma biomarkers for early detection of pancreatic cancer identified from proteomic profile

Kazufumi Honda, National Cancer Center Research Institute, Japan

TP01-026

Integration of SWATH and MRM for biomarker discovery of esophageal squamous cell carcinoma

Guixue Hou, BGI-SHENZHEN, China

TP01-027

Quantitative analysis of wild-type and V600E mutant BRAF proteins in colorectal carcinoma using immunoenrichment and targeted mass spectrometry

Yung-Chin Hsiao, Molecular Medicine Research Center, Chang Gung University, Taiwan

TP01-028

Quantitative tissue proteomics analysis of primary lung adenocarcinoma for potential biomarker discovery

Chiung-Hung Hsu, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

TP01-029

Identification of Potential Biomarker Related to EGFR Mutation by Functional Proteome Profiling in Primary Non-small Lung Cancer

Yuan-Ling Hsu, National Taiwan University, Taiwan

TP01-030

Proteomic Study on Pancreatic Cancer Patients with Long and Short Survivals with Samples from the South Swedish Biobank

Dingyuan Hu, Department of Surgery, Clinical Sciences Lund, Lund University, Sweden

TP01-031

Verification of new blood protein biomarkers for breast cancer

Yen-Chun Huang, Proteomics Research Center, National Yang-Ming University, Taiwan

TP01-032

Novel circulating peptide biomarkers for esophageal squamous cell carcinoma revealed by a magnetic bead-based MALDI-TOFMS assay

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

TP01-033

Investigating the Platelet-derived Growth Factor B regulation network in Gastric Cancer with a label free quantitative proteomics approach

Wenguo Jiang, Binzhou Medical University, China

TP01-034

Proteomic analysis of novel targets associated with simvastatin-induced cell death in DU145 human prostate cancer cells

Eun Joo Jung, Department of Biochemistry, Gyeongsang National University School of Medicine, South Korea

TP01-035

Verification of Prostate Cancer Genomics Biomarker Candidates at Protein Level Using SRM-MS

Jacob Kagan, National Cancer Institute, United States

TP01-036

PROTEOMICS IDENTIFIED THE PROTEINS ASSOCIATED WITH TUMOR INVASION IN MYXOFIBROSARCOMA

Kazutaka Kikuta, Division of Rare Cancer Research, National Cancer Center Research Institute, Japan

TP01-037

Development for Lung Cancer Diagnostic Meta-markers using Multiple Reaction Monitoring

Yong-In Kim, Seoul National University, South Korea

TP01-038

Phosphoproteomic analysis aimed at elucidating the mechanisms underlying the high malignancy of ovarian clear cell carcinoma

Ayuko Kimura, Yokohama City University, Advanced Medical Research Center, Japan

TP01-039

Potential diagnostic value of protein biomarkers in albumin-depleted pleural effusions for detection of NSCLC malignancy and EGFR mutation status

*Yee Jiun Kok, Bioprocessing Technology Institute, Agency for Science, Technology and Research (A*STAR), Singapore, Singapore*

TP01-040

Identification of cerebrospinal fluid markers for recurrent malignant brain tumor by quantitative proteomics.

Tomohiro Kouhata, Kumamoto University, Japan

TP01-041

Changes in Protein Expression between Primary Breast tumour and lymph node or distant metastases

Emila Kurbasic, Lund University, Sweden

TP01-042

2D Proteomic profile following Agrimonia Pilosa Ledeb roots extract treatment in oral squamous cell carcinoma

Yeon Ju Kwak, Department of Dental Pharmacology and Biophysics, School of Dentistry and Research Institute for Oral Biotechnology, Yangsan Campus of Pusan National University, South Korea

TP01-043

Anchorage-independency altered tubular phenotype of melanoma tumors through downregulation in ANPEP/SDC1/beta4-integrin axis

Shaochen Lee, Proteomics Laboratory, Cathay Medical Research Institute, Cathay General Hospital, Taiwan

TP01-044

The roles of AKR1C1 and AKR1C2 in ethyl-3, 4-dihydroxybenzoateinduced esophageal squamous cell carcinoma cell death

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

TP01-045

Identification of hypoxia-induced splicing variants in cancer cells using proteomics approach

Chia-Hung Li, National Taiwan Ocean University, Keelung/taiwan, Taiwan

TP01-046

Quantitative analysis of HER2 protein expression in multiple cancer indications

Wei-Li Liao, Nantomics, United States

TP01-047

Iron deprivation perturbs ribosome biogenesis on protein synthesis and cell growth in MCF-7 human breast cancer cells

Yih-Fong Liew, Fu Jen Catholic University Department of Nutritional Science, Taiwan

TP01-048

Quantitative Proteomics Investigation of Frataxin Over-Expression in Colorectal Cancer Cells

Justin Lim, Department of Biological Sciences, Faculty of Science, National University of Singapore, Singapore

TP01-049

Using SWATH to analysis Peripheral Blood Mononuclear Cells of Pancreatic cancer

Xiaohui Liu, Institute of Biomedical Science, Fudan University, China

TP01-050

Quantitative Proteomics Analysis of a Primary Bladder Cell line treated with Ketamine, a narcotics and anesthesia medicine

Juo Chuan Liu, Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

TP01-051

Discovery of potential colorectal cancer serum biomarkers through quantitative proteomics of the tissue interstitial fluids from two mouse models

Xiaomin Lou, Beijing Institute of Genomics, Chinese Academy of Sciences, China

TP01-052

Targeted quantification of N-1-(carboxymethyl) valine and N-1-(carboxyethyl) valine peptides of β -hemoglobin for better diagnostics in diabetes

Jagadeeshaprasad M.G., Department of Diabetes and Endocrine Research, Chellaram Diabetes Institute, Pune, Maharashtra, Ind, India

TP01-053

Multicentric Study of the Effect of Pre-analytical Variables in the Quality of Plasma Samples Stored in Biobanks by Complementary Proteomic Methods

Nieves Domenech, Plataforma de Proteómica. Instituto de Investigación Biomédica (INIBIC), A Coruña, Spain

TP01-054

Tissue proteomic analysis to validate differentially expressed markers associated with meningioma pathobiology

Shuvolina Mukherjee, Indian Institute of Technology, Bombay, Department of Biosciences and Bioengineering, Mumbai 400076, India

TP01-055

Serum Proteomic Biomarkers of Hepatocellular Carcinoma Associated with Nonalcoholic Fatty Liver Diseases in Pigs

Naohiko Nakamura, Department of Surgery, Graduate School of Medicine, Kyoto University, Japan

TP01-056

A novel model system and approach for identification of biomarkers of response to heat shock protein 90 inhibitors in prostate cancer

Elizabeth Vi Nguyen, Monash University, Australia

TP01-057

Protein panel for monitoring the progression of Keratoconus- Clinical application of mass spectrometry

Krishnatej Nishtala, GROW Research Laboratory, Narayana Nethralaya Foundation, Bangalore, India

TP01-058

Proteomic profiling of serum exosomes to identify novel early detection biomarkers for gastric cancer

Naomi Ohnishi, Cancer Proteomics Group, Genome Center, Japanese Foundation for Cancer Research, Japan

TP01-059

Proteomic analysis of TGF- β -induced cancer metastasis

Akiko Okayama, Yokohama City University, Japan

TP01-060

Comparison of protein expression profiles between human crown and root dentins by label-free quantitative proteomics analysis

Pei-Jing Pai, Graduate Institute of Medicine, Kaohsiung Medical University, Taiwan

TP01-061

Data independent acquisition-based targeted proteomics for plasma analysis – in the context of cancer biomarker detection

Sheng Pan, University of Washington, United States

TP01-062

Ubiquitin specific protease 19 involved in transcriptional repression of retinoic acid receptor

Jung-Hyun Park, Department of Biomedical Science, Cha Universtiy, South Korea

TP01-063

Proteomic and bioinformatic analysis of overactive bladder in a rat model

Edmond Changkyun Park, Drug & Disease Target Team, Korea Basic Science Institute, Daejeon 34133, South Korea

TP01-064

The surveillance and early diagnosis of hepatocellular carcinoma using multiple reaction monitoring

Ji Young Park, Seoul National University College of Medicine, South Korea

TP01-065

Characterization of the discoid lateral meniscus tissues using mass spectrometry-based proteomics

Jisook Park, Samsung Medical Center, South Korea

TP01-066

Bioactive Dietary Compounds (BDCs)-mediated anti-cancer effects on colorectal cancer cells

Jung Eun Park, Nanyang Technological University, Singapore

TP01-067

Quantitative Analysis of AKT/mTOR Pathway using Multiplex-Immunoprecipitation and Targeted Mass Spectrometry

Bhavin Patel, Thermo Fisher Scientific, United States

TP01-068

A Serum Based Combinatorial Proteomic Biomarker Assay is Unaffected by the Density of Breast Tissue

David Reese, Provista Diagnostics, United States

TP01-069

Proteomic study of thyroid cancer metastasis using 3D culture system

Kittirat Saharat, Applied Biological Sciences, Chulabhorn Graduate Institute, Thailand

TP01-070

Plasticizer induced tumor migration by regulating of sialyltransferase expression in colon cancer cells

Pei-Chun Shih, Institute of Basic Medical Science, Taiwan

TP01-071

Proteomic analysis of the oral squamous cell carcinoma

Shuichiro Shimada, Biofluid Biomarker Center, Institute for Social Innovation and Promotion, Niigata University, Japan

TP01-072

Proteomic analysis of metastatic colorectal cancer cell and verification by SRM/MRM analysis.

Takashi Shiromizu, Laboratory of Proteome Research, National Institutes of Biomedical Innovation, Health and Nutrition, Japan

TP01-073

Salivary proteins from pre-malignant and malignant lesions of the oral cavity and their translational potential for early diagnosis

Priya Sivadadan, Institute of Bioinformatics, International Tech Park, Bangalore, India

TP01-074

Quantitative Analytical Method for Measuring the Levels of PIVKAI1 in Human Serum Using Multiple Reaction Monitoring-Mass Spectrometry

Areum Sohn, Department of Biomedical Engineering, Seoul National University College of Medicine, South Korea

TP01-075

Method Validation of the Protein Biomarkers Approved by FDA and LDT following CPTAC Assay Development Guidelines using Multiple Reaction Monitoring

Minsoo Son, Departments of Biomedical Engineering, Seoul National University College of Medicine, 28 Yongon-Dong, South Korea

TP01-076

Serum biomarker panels for the early detection of pancreatic cancer

Jin Song, Department of Pathology, Johns Hopkins Medical Institutions, Baltimore, MD, United States

TP01-077

Study on sputum cell proteomics for screening early detection biomarkers of lung cancer

Jie Song, State Key Laboratory of Molecular Oncology, Cancer Institute and Hospital, Chinese Academy of Medical Sciences, China

TP01-078

Effects of Apigenin on growth inhibition and apoptosis induction of human cholangiocarcinoma cell line

Chantragan Srisomsap, Laboratory of Biochemistry, Chulabhorn Research Institute, Thailand

TP01-079

Discovery of ARV induced kidney-injury related protein biomarkers in urine using SWATH-MS.

Stoyan Stoychev, CSIR, South Africa

TP01-080

MDC1-SDTD repeats as a potential target to block DDR and promote radiosensitization in cancer cells

Hsiang-Chun Su, Academia Sinica, Taiwan

TP01-081

Novel hypoxia-driven oncogenic pathways are revealed by tandem quantitation of the tumor cell proteome, chromatome, and secretome.

Siu Kwan Sze, Nanyang Technological University, Singapore

TP01-082

Analysis of human high-grade serous ovarian carcinoma by mass spectrometry using data-dependent and data-independent acquisition

Stefani Thomas, Department of Pathology, Johns Hopkins University School of Medicine, United States

TP01-083

Quantitative proteomics of transgenic prostate cancer mice reveals that PDGF-B regulatory network plays a key role in prostate cancer progression

Geng Tian, Binzhou Medical University, China

TP01-084

Global proteome analysis of carcinoma associated fibroblasts and dystrophic epidermolysis bullosa fibroblasts in 3D cell culture

Regine Tölle, Department of Dermatology, University Medical Center, Freiburg, Germany

TP01-085

Integration of urine and tissue proteomes for biomarker verification of bladder cancer using targeted proteomics

Cheng-Han Tsai, Graduate Institute of Biomedical Sciences / Chang Gung University, Taiwan

TP01-086

The Effects of Dietary Polyunsaturated Fatty Acids on Prostate Cancer: Unbiased Proteomic and Phosphoproteomic Studies

Mu Wang, Indiana University, United States

TP01-087

Proteomic analysis of cell response to photon and particle irradiation

Uwe Warnken, German Cancer Research Center (DKFZ), Heidelberg, Germany

TP01-088

Phosphoproteome profiling of isogenic cholangiocarcinoma exosomes reveal differential expression of a key metastatic factor

Churat Weeraphan, Center for Genomics and Bioinformatics Research, Faculty of Science, Prince of Songkla University, Thailand

TP01-089

GLP-1 was identified as a potential therapy target for colorectal cancer through label-free quantitative proteomic analysis

Xiaodan Wei, Binzhou Medical University, China

TP01-090

Development of phage display-based platform for discovery of cancer biomarkers and targeting ligands

Chien-Hsun Wu, Institute of Cellular and Organismic Biology, Academia Sinica, Taiwan

TP01-091

Comprehensive proteome analysis of fine needle aspiration cystic fluid and cancer cell secretome for papillary thyroid cancer biomarker discovery

Chia-Chun Wu, Graduate Institute of Biomedical Sciences, College of Medicine, Chang Gung University, Taiwan

TP01-092

Uncovering the molecular mechanism of inhibitory activity of Taiwan local pomegranate against urinary bladder urothelial carcinoma cell

Ting-Feng Wu, Department of Biotechnology Southern Taiwan University of Science and Technology, Taiwan

TP01-093

Searching tumor-associated proteins for urinary bladder urothelial carcinoma in southwestern Taiwan using gel-based proteomics

Chia Cheng Su, Department of Biotechnology Southern Taiwan University of Science and Technology, Taiwan

TP01-094

Salivary proteome and extracellular vesicles for the detection of cancer

Hua Xiao, Shanghai Jiao Tong University, China

TP01-095

Metastatic colorectal cancer cell-derived exosomes directionally promote the translation and protein degradation of macrophages

Lijuan Yang, Institute of Life and Health Engineering, Jinan University, China

TP01-096

Predicting Ovarian Cancer Patients' Clinical Response to Platinum-based Chemotherapy by their Tumor Proteomic Signatures

Kun-Hsing Yu, Stanford University, United States

TP01-097

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

Victor Zgoda, Institute of Biomedical Chemistry, Russia

TP01-098

Multiple Post-translational Modifications Proteomes (PTMomes) Associated with TKIs in Non Small Cell Lung Cancer

Guolin Zhang, H.Lee Moffitt Cancer Center & Research Institute, United States

TP01-099

EBP50 suppresses the metastasis of breast cancer and HeLa cells by inhibiting matrix metalloproteinase-2 activity

Junfang Zheng, Capital Medical University, China

TP01-100

Osteoporosis Risk Protein Biomarkers Suggested by a Proteome Study in Chinese Males

Xu Zhou, School of Public Health, Soochow University, China

TP02 - Glycoproteomics, Glycomics and Glycosylation In Diseases

TO02-001

In-depth analysis of human plasma glycoproteins by a combination of high-resolution native mass spectrometry and middle-down proteom

Vojtech Franc, Biomolecular Mass Spectrometry and Proteomics, University of Utrecht, Netherlands

TO02-002

Confident, automated N-glycoproteomics profiling in enriched and unenriched cell samples

Scott Peterman, Optys Tech Corporation, United States

TO02-003

Identification of Intact Glycopeptides with In-Silico Deglycosylation Strategy for O-glycoproteomics Analysis

Hongqiang Qin, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, China

TO02-004

Glycoproteomic Analysis of Human Plasma using SWATH-MS

Chi-Hung Lin, Department of Chemistry and Biomolecular Sciences, Macquarie University, Australia

TO02-005

A suite of SWATH glycoproteomic approaches for easy global glycoprotein analysis

Ben Schulz, The University of Queensland, Australia

TO07-001

Identification of intact glycopeptides at a proteome scale

Mingqi Liu, Institute of Biomedical Sciences, Fudan University, China

TO07-002

Integrated glycoproteomics demonstrates fucosylated serum paraoxonase 1 alterations and functions in lung cancer

Je Yoel Cho, Seoul National University, South Korea

TO07-003

Decoding site-specific alteration of Sialo-glycoproteome in EGFR-subtype of non-small cell lung cancer

Yi-Ju Chen, Institute of Chemistry, Academia Sinica, Taiwan

TO07-004

Identifying Antibody and Lectin Recognition to HIV N-glycans through Native Mass Spectrometry and Glycoproteomic Analysis of Viral

Envelope Spikes

Weston Struwe, University of Oxford, United Kingdom

TO07-005

Dynamic mapping of human frontal cortex according to the developmental stage via neuroglycomic approach

Jua Lee, Asia Glycomics Reference Site, Chungnam National University, Daejeon, South Korea

TP02-001

In-depth LC-MS/MS Mapping of Sulfo-sialo-glycoproteome in B-chronic lymphocytic leukemia (CLL)

Merrina Anugraham, Institute of Biological Chemistry/ Academia Sinica, Taiwan

TP02-002

Improving confidence in glycan structure characterisation using alternative CID fragmentation

Christopher Ashwood, ARC Centre of Excellence in Nanoscale Biophotonics (CNBP), Macquarie University, North Ryde, Australia

TP02-003

Highly Selective Enrichment of Glycopeptides Based on Zwitterionically Functionalized Soluble Nanopolymers

Weiqian Cao, Institutes of Biomedical Sciences, Fudan University, China

TP02-004

Glycoproteomic analysis of O-GlcNAc-modified proteins in colorectal cancer

Voraratt Champattanachai, Chulabhorn Research Institute, Thailand

TP02-005

Glycoproteomic Analysis of Serum proteins for Oral Cancer

Shu-Chieh Chang, National Cheng Kung University, Taiwan

TP02-006

One-fraction nanoLC-MS²/MS³ analysis for high throughput glycome-wide precision mapping of glycotopes

Yen-Ying Chen, Institute of Biological Chemistry, Academia Sinica, Taiwan

TP02-007

Lectin Microarray: A Powerful Tool for Glycan-Based Biomarker Discovery

Li Cheng, Shanghai Jiao Tong University, China

TP02-008

Uncovering Target Glycoprotein Biosignatures using a One-Pot Dual Nanoprobe Mass Spectrometry Assay

Mira Anne Dela Rosa, Department of Chemistry, National Taiwan University, Taiwan

TP02-009

Integrated Proteomic and N-glycoproteomic Analyses of Alzheimer's Disease Mouse Brain Reveal the Precise Alterations in Protein N-glycosylation

Pan Fang, Institutes of Biomedical Sciences, Fudan University, China

TP02-010

Increased confidence for the identification of N-linked glycopeptides using an optimised collision energy workflow

Lee Gethings, Academia Sinica, Taiwan

TP02-011

GLYCOPROTEOMICS REVEALS DECORIN PEPTIDES WITH ANTI-MYOSTATIN ACTIVITY IN HUMAN ATRIAL FIBRILLATION

Eloi Haudebourg, King's College London, United Kingdom

TP02-012

Simplified Cell Strategy for Large Scale Identification of Mucin-type O-glycoproteins

Jiangming Huang, Department of Chemistry, Fudan University, China

TP02-013

INFLUENCE OF SIALYLATION ON INTRACELLULAR SIGNALLING PATHWAYS OF HeLa CELLS

María Ibañez-Vea, University of Southern Denmark, Denmark

TP02-014

Glycomic profiling of targeted serum haptoglobin for gastric cancer using nano LC/MS and LC/MS/MS

Seunghyup Jeong, Graduate School of Analytical Science and Technology, Chungnam National University, South Korea

TP02-015

Comparative Study of Fucosylation between Liver and Non-liver Secreted N-glycoproteins in Liver Cancer Plasma

Eun Sun Ji, Biomedical Omics Group, Korea Basic Science Institute, South Korea

TP02-016

In-depth N-glycoproteome Analysis of Human Metastatic Hepatocellular Carcinoma Cell Lines

Biyun Jiang, Institutes of Biomedical Sciences, Fudan University, China

TP02-017

Direct mapping of additional modifications on phosphorylated O-glycans of α -dystroglycan by mass spectrometry analysis

Chu-Wei Kuo, Academia Sinica, Taiwan

TP02-018

Identification and quantitation of site-specific N-glycoforms in biopharmaceutical glycoproteins using LC-MS/MS with glycoproteomic database search

Hyun Kyung Lee, Korea Basic Science Institute, O-chang Cheongju, South Korea

TP02-019

Characterization of site-specific N-glycopeptides of alpha-1-acid glycoprotein from Human Plasma by an interlaboratory study using LC-MS/MS

Ju Yeon Lee, Korea Basic Science Institute, South Korea

TP02-020

Smart polymer for saccharide discrimination and glycopeptide enrichment

Xiuling Li, Dalian Institute of Chemical Physics · chinese Academy of Sciences, China

TP02-021

Investigating the roles of glycosylation in plasticizer induced tumor migration in colon cancer cells

Tsung-Hsien Lin, National Cheng Kung University, Taiwan

TP02-022

Glycoproteome-wide identifications of novel GALNT14 substrates using tandem mass spectrometry

Yu-Hua Lin, Department of Chemistry, National Taiwan Normal University, Taiwan

TP02-023

Salivary Glycomic Approach for The Distinction of Human Constitutions

Hantae Moon, Graduate School of Analytical Science and Technology, Chungnam National University, South Korea

TP02-024

Neural glycomics and epigenetic regulation

Miyako Nakano, Graduate School of Advanced Sciences of Matter, Hiroshima University, Japan

TP02-025

Integrated GlycoProteome Analyzer (I-GPA) for Automatic Identification and Quantitation of Site-Specific N-Glycosylation in Human

Gun Wook Park, Biomedical Omics Group, Korea Basic Science Institute, South Korea

TP02-026

Glycomic Approach for Design of Humanized Mouse Model via Nano-LC/MS and LC/MS/MS

Dan Bi Park, Chungnam National University, South Korea

TP02-027

Building a high confidence, quantitative O-glycopeptide profile for IgA

Amol Prakash, Optys Tech Corporation, United States

TP02-028

Performance Evaluation of First and Second Generation Quadrupole Dual Cell Linear Ion Trap Orbitrap Hybrid MS for Glycopeptide

Julian Saba, Thermo Fisher Scientific, Canada

TP02-029

Role of CD52 glycosylation in immunosuppression

Abdulrahman Shathili, Macquarie University, Australia

TP02-030

Ligand-independence of the Colony Stimulating Factor 3 Receptor (CSF3R) results from loss of sialylation which leads to increased

David Spicariach, Departments of Chemistry, University of California, Berkeley, California 94720, United States, United States

TP02-031

Glycoproteomic Alterations in Drug-resistance Lung Cancer Cell Lines Revealed by Lectin Magnetic Nanoprobe-based Affinity Mass Spectrometry

Juanilita Waniwan, Institute of Chemistry, Academia Sinica, Taiwan

TP02-032

Preference of the universal enrichment methods for N-glycopeptides with particular glycoforms

Yu Xue, Institute of Chemistry, Fudan University, China

TP02-033

Integrating Glycoproteomics in the Multi-Omics Analysis of Type II Diabetes Onset

Christine Yiwen Yeh, Stanford University School of Medicine, United States

TP02-034

Ion Mobility and High-Resolution Native Mass Spectrometry Reveals Glycan-Specific Modulation of Glycoprotein Stability

Hsin-Yung Yen, Department of Chemistry, Oxford University, United Kingdom

TP02-035

Preparative purification of N-linked glycopeptides by using two-dimensional chromatography for the structural characterization

Long Yu, Dalian Institute of Chemical Physics, China

TP02-036

New glycoproteomic tools to study N-glycosylation and to uncover novel glycophenotypes in human diseases

Lucia Zacchi, The University of Queensland, Australia

TP03 - Lysine Modifications and PTM Crosstalks

TO03-001

Unravelling crosstalks between SUMOylation and other protein modifications in human cells using dynamic proteomics

Pierre Thibault, Institute for Research in Immunology and Cancer, Université de Montréal, Canada

TO03-002

Towards Comprehensive Analysis of Protein ADP-ribosylation

Yonghao Yu, Ut Southwestern Medical Center, United States

TO03-003

Acetylome analysis reveals carbon metabolism as a key factor enhancing thermogenesis in white adipocytes

Hsin-Yi Chang, Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

TO03-005

Efficient Enrichment of SUMOylated Peptides from Alpha-lytic Protease Digest Using K-ε -GG Remnant Immuno-affinity Purification

Hongbo Gu, Cell Signaling Technology, United States

TP03-001

Apoptotic protein Bax is regulated by multiple deubiquitinating enzymes in response to DNA damage

Kwang-Hyun Baek, CHA University, South Korea

TP03-002

Investigating the significance of Methyltransferase-like (METTL)-family lysine methylation enzymes on Heat Shock Proteins and their role in cancer

Byron Baron, Centre for Molecular Medicine and Biobanking, Faculty of Medicine and Surgery, University of Malta, Malta

TP03-003

Lysine propionylation is a widespread post-translational modification involved in regulation of photosynthesis and metabolism in cyanobacteria

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

TP03-004

PIAS1-mediated SUMOylation of BAF57 is a critical regulator of cell growth and drug sensitivity in ovarian cancer cells

Chongyang Li, Institute for Research in Immunology and Cancer, Canada

TP03-005

A novel post-translational modification: lysine propionylation was identified in bacterial species

Hiroki Okanishi, Kumamoto University, Japan

TP03-006

Acetyl proteomics using a novel enrichment strategy for lysine acetylated peptides

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

TP03-007

Comprehensive Analysis of Proteome and Lysine Acetylome in Human Esophageal Carcinoma Cells

Kai Zhang, Tianjin Key Laboratory of Medical Epigenetics, Tianjin Medical University, China

TP04 - Other PTMomics and Crosstalks

TO03-004

Effects of co-/post-translational modifications on protein function

Hisashi Hirano, Yokohama City University, Japan

TP04-001

Quantification of ADP-ribosylated peptides during oxidative stress using a label-free PRM approach

Vera Bilan, Department of Molecular Mechanisms of Disease, University of Zurich, Switzerland

TP04-002

Characterization of ribosomal protein modifications in response to glucose starvation

Hsin-Lian Lin, Institute of Biochemistry and Molecular Biology, NYMU, Taiwan

TP04-003

Identification of Glycosylphosphatidylinositol-anchored Proteins Profile in Organs

Yusuke Masuishi, Graduate School of Medical Life Science, Yokohama City University, Japan

TP04-004

A HPLC coupled mass spectrometry approach to analyze modified ribonucleosides from RNA

Selene Swanson, Stowers Institute for Medical Research, United States

TP04-005

Rapid identification and quantification of amino acid isomers occurring in peptides under physiological conditions: a targeted proteomics approach.

Atsuhiko Toyama, Shimadzu Corporation Mass Spectrometry Business Unit, Japan

TP04-006

Global identification of free protein N-termini and protease substrates by chemical modification of N-termini

Hao Zhang, Xi'an Jiaotong-Liverpool University (XJTLU), China

TO08-001

Copy number alteration programmed protein turnover quantified by pSILAC and SWATH mass spectrometry

Yansheng Liu, Department of Biology, Institute of Molecular Systems Biology, ETH Zurich, Zurich, Switzerland

TO08-002

High Resolution Mass Spectrometry Cellular Thermal Shift Assay (HR-MS-CETSA) - post-translational modifications impact on protein

*Radoslaw Sobota, Institute of Molecular and Cell Biology, Agency for Science, Technology and Research (A*STAR), Singapore*

TO08-003

A dynamic picture of the proteome and ubiquitinome upon proteasome inactivation.

Jeroen Demmers, Erasmus University Medical Center Rotterdam, Netherlands

TO08-004

Proteome Turnover analysis reveals substrates and physiological role of membrane proteases

Ansgar Poetsch, IIB-CONICET-UNMdP Mar del Plata, Argentina

TO08-005

A Novel Function of CRL2 Ubiquitin Ligase in Protein Quality Control

Hsiu-Chuan Lin, Institute of Molecular Biology, Academia Sinica, Taiwan

TP05-001

Identification of HTRA1 Substrates in the Context of Age-Related Macular Degeneration

Chia-Yi Chen, Institute of Molecular Medicine and Cell Research, University of Freiburg, Germany

TP05-002

Old-age proteins asymmetrically inherited in mother cells of budding yeast

Keiji Kito, School of Agriculture, Meiji University, Japan

TP05-003

A novel ubiquitin ligase complex regulates gastric cancer proliferation by modulating biosynthesis of guanine nucleotides

J. Eugene Lee, Korea Research Institute of Standards and Science, South Korea

TP05-004

Proteome-wide analysis of protein stability in *E. coli* using pulse proteolysis

Liang Zhao, Max Planck Institute of Biochemistry, Germany

TP06- Interactomics and Protein Network

TO01-001

The Regulatory Role of Methylation and Methylation–Phosphorylation Crosstalk in Protein Interaction Networks

Marc Wilkins, University of New South Wales, Australia

TO01-002

Network analysis reveals a dominant role of protein-level regulation in coordinating gene functions

Bing Zhang, Vanderbilt University Medical Center, United States

TO01-003

Profiling the phosphotyrosine interactome of receptor tyrosine kinases

Runsheng Zheng, Chair of Proteomics and Bioanalytics, Technische Universitaet Muenchen, Freising, Germany

TO01-004

Phylointeractomics reconstructs functional evolution of protein binding

Dennis Kappel, Cancer Science Institute of Singapore, Singapore

TP06-001

Systematic protein interactome analysis of glycosaminoglycans revealed YcbS as a novel bacterial virulence factor

Shih-Hsiang Hsiao, Department of Biomedical Science and Engineering, National Central University, Taiwan

TP06-002

Metastatic hepatocellular carcinoma cells enrich translation regulatory proteins in exosomes

Zhang Jing, Jinan University, China

TP06-003

Unraveling the dynamic signaling network capacity of HBx in HBV host infection

Emanuela Milani, Institute of Molecular Systems Biology, Dep. of Health Sciences and Technology, ETH Zürich, Switzerland

TP06-004

Tête-à-TET: Elucidating the Interactome of Tet1 and Tet3

Andrea Kuenzel, Ludwig-Maximilians Universität München, Germany

TP06-005

Identification of HAX1 interacting proteins by BioID system

Byoung Chul Park, Kribb, South Korea

TP06-006

Discovery of Parasite-Host Interaction Contributing Changing of Host-Lipid Metabolism for Malaria Liver Stage Development

Supachai Topanurak, Dept. of Molecular Tropical Medicine and Genetics, Faculty of Tropical Medicine, Mahidol University, Thailand

TP06-007

Characterization of the EGFR Interactome in Non-Small Cell Lung Cancer Cells

Pei-Shan Wu, Institute of Chemistry, Academia Sinica, Taiwan

TP06-008

Proteomic Analysis Reveals a Role for PKM2 in modulating DNA damage response

Li Xia, Shanghai Jiao Tong University School of Medicine, China

TP06-009

Interactome analysis reveals a critical role of DDX3-hnRNP interaction in the hnRNP-mediated apoptosis

Jen-Hao Yang, Department of Life Sciences and Institute of Genome Sciences, National Yang-Ming University, Taiwan

TP06-010

PTPLAD1 suppresses colorectal cancer metastasis through interacting with PHB

Jie Yang, Key Laboratory of Functional Protein Research of Guangdong Higher Education Institutes, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

TP06-011

Proteomic exploration of invasiveness-associated KPNA2 (importin α 1) interactome and its upstream signaling in lung cancer

Chia-Jung Yu, Molecular Medicine Research Center, Chang Gung University, Taiwan

TP06-012

Unfolded protein and preeclampsia: a proteomics investigation

Wanling Zhang, Institute of Life and Health Engineering, College of Life Science and Technology, Jinan University, China

TP07- Protein Complexes and Structural Proteomics

TO01-005

Determining network topology, distance restraints and activation markers from endogenous protein complexes

Marco Faini, Eth Zurich, Switzerland

TP07-001

Optimization of crosslinked peptide analysis on an Orbitrap Fusion Lumos mass spectrometer

Ryan Bomgardner, Thermo Fisher Scientific, United States

TP07-002

Characterization of EV71 replicative mechanisms targeted by anti-EV71 cocktail therapy

Yen Chiu Chang, Department of Biotechnology and Laboratory Science in Medicine, National Yang-Ming University, Taiwan

TP07-003

Examination of Aptamer-Protein Complex Structure by Mass Spectrometry

Guo-Ming Hung, National Taiwan Ocean University, Taiwan

TP07-004

Interactome analysis identified the specific interaction of TCTP and EF1A2 in Neurofibromatosis type 1 (NF1)-associated tumors

Daiki Kobayashi, Graduate School of Medical Sciences, Kumamoto University, Japan

TP07-005

Establishment of an APEX-based procedure that effectively helps analyze protein quaternary structures

Li-Hua Li, Department of Pathology and Laboratory Medicine, Taipei Veterans General Hospital, Taiwan

TP07-006

Effect of Different Lipid Membranes on the Structural Dynamics of Aquaporin Z

Qingsong Lin, Department of Biological Sciences, National University of Singapore, Singapore

TP07-007

Characterizing folding and misfolding properties of human serum amyloid A1

Jin-Lin Wu, Ph.D. Program for Cancer Biology and Drug Discovery, China Medical University and Academia Sinica, Taiwan

TP08- Antibodies and Protein Arrays

TO06-001

Status of the Affinity Binder Knockdown Initiative

Tove Alm, Science for Life Laboratory, KTH Royal Institute of Technology, Sweden

TO06-002

Heterogeneous Ribonucleoprotein K (hnRNP K) binds the 5' terminal sequence of the hepatitis C virus RNA and mature miR-122

Chien-Sheng Chen, Department of Biomedical Science and Engineering, National Central University, Taiwan

TO06-003

A High-Content Functional Mycobacterium Tuberculosis Proteome Microarray and Its Applications

Yang Li, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University, China

TO06-004

Utilizing protein microarray to monitor blood-brain barrier disruption and active inflammation in plasma samples from multiple sclerosis patients

Malene Moeller Joergensen, Department of Clinical Immunology, Aalborg University Hospital, Denmark

TO06-005

Mapping Transcription Factor Interactome Networks using HaloTag Protein Arrays

Junshi Yazaki, Riken, Japan

TP08-001

Molecular design of scFv antibodies for site-specific photochemistry-based applications in affinity proteomics

Mattias Brofelth, Dept. of Immunotechnology, Lund University, Sweden

TP08-002

Deciphering systemic lupus erythematosus associated serum biomarkers reflecting apoptosis and disease activity

Payam Delfani, Dept. of Immunotechnology and CREATE Health, Lund University, Medicon Village, Lund, Sweden

TP08-003

Quantitative Analysis of Acetylated Protein and Its Modification Level based on UCNPs

Fan Huizhi, Fudan University, China

TP08-004

Development of lung cancer diagnostic method using exosomal protein DDOST.

Jisu Lee, Department of Bioengineering, College of Engineering, Hanyang Univ., South Korea

TP08-005

Development of humanized antibody against EpCAM for cancer and cancer stem cell theranostics

Ruei-Min Lu, Institute of Cellular and Organismic Biology, Academia Sinica, Taiwan

TP08-006

Subpopulations of Hepatocellular Carcinoma with High MAPK and mTOR Signaling Activity Revealed by Reverse-Phase Protein Array Analysis

Mari Masuda, National Cancer Center Research Institute, Japan

TP08-007

Autoantibody profiling in healthy heavy smokers at risk for COPD

Maria Mikus, Affinity proteomics, SciLifeLab, KTH-Royal Institute of Technology, Stockholm, Sweden

TP08-008

Generation and purification of highly phosphorylated site specific antibodies for human N1ICD

Yunshan Ning, Biotherapy Institute, School of Biotechnology, Southern Medical University, China

TP08-009

Autoimmunity screening and antibody validation using high-density protein microarrays

Ulrika Qundos, Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden

TP08-010

PEAKS AB – A software tool for monoclonal antibody sequencing and characterization with LC-MS

Baozhen Shan, Bioinformatics Solutions Inc, Canada

TP08-011

Harnessing Translational Research with Protein Microarrays

Xiaobo Yu, Beijing Proteome Research Center, China

TP08-012

Autoantibody Profiling Using Ultra-Dense Peptide Microarrays

Arash Zandian, SciLifeLab - KTH (Royal Institute of Technology), Sweden

TP09- Liver and Toxicoproteomics: Metabolism, Drug Transformation and Toxicity

TO05-001

Personalized proteomic characterization of hepatitis B virus-associated hepatocellular carcinomas

Ying Jiang, National Center for Protein Science . Beijing, China

TO05-002

In vitro investigation of an adverse outcome pathway of cholestatic liver injury using quantitative phosphoproteomics

René Zahedi, Isas, Germany

TO05-003

Differential proteomic analysis of cholangiocarcinoma cells and cell-derived extracellular vesicles by label free mass spectrometry

Felix Elortza, CIC bioGUNE, Proteomics Platform, CIBERehd, ProteoRed-ISCIII, Spain

TP09-001

Relative quantitation for expression evaluation of drug metabolizing enzymes using surrogate peptide approach by Quadrupole Time of Fig

Christine Miller, Agilent Technologies, India

TP09-002

Hepatic proteome analysis of dioxin-sensitive and -resistant mice exposed to 2,3,7,8-tetrabromodibenzo-p-dioxin

Thanh Hoa Nguyen, Center for Marine Environmental Studies (cmes), Ehime University, Japan

TP09-003

Simultaneous quantification of drug transporters, CYP enzymes, and UGTs in human liver microsomes by high-microflow LC-MS/MS.

Sumio Ohtsuki, Faculty of Life Sciences, Kumamoto University, Japan

TP10- Protein Standards and Model Organisms: Expanding Our Horizons

TO10-001

The ProteomeXchange Consortium: 2016 update

Juan Antonio Vizcaino, EMBL-European Bioinformatics Institute, United Kingdom

TO10-002

proBAMconvert: organizing MS identifications in a genome-centric fashion enables proteogenomics and proteomics integration.

Gerben Menschaert, University of Ghent, Belgium

TO10-004

Adipose tissue pathways in obesity: Iberian pig as large animal model of metabolic disorders

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

TO10-006

Proteome alterations in the porcine endometrium during embryo implantation.

Thomas Fröhlich, Laboratory for Functional Genome Analysis, Gene Center, LMU-Munich, Germany

TP10-001

A QPrEST Resource for Targeted Plasma Analysis

Fredrik Edfors, Science For Life Laboratory, Sweden

TP10-003

High-throughput production of heavy isotope-labeled Protein Epitope Signature Tags to use as internal standards in Mass Spectrometry

Anne-Sophie Svensson, Human Protein Atlas, Sweden

TP10-004

Development of an all-recombinant intact protein standard for LC MS application development and system suitability testing

Rosa I Viner, Thermo Fisher Scientific, United States