Poster Presentations

Sunday, September 15

Animal Models for Human Diseases

POS-01-001

Basic Analysis for Elucidation of the Mechanisms of Acute Effects Induced by Excessive Drinking

Yuki Iwahara[1], Kazuma Higashisaka[1], Akiyoshi Kunieda[1], Kota Tanaka[1], Shin-ichi Tsunoda[2,3], Shunji Oshima[4], Yasushi Kitagawa[4], Yasuo Yoshioka[1], Yasuo Tsutsumi[1,2,3]

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POS-01-002

Enrofloxacin Resistance of Uropathogenic Canine *Escherichia coli* Reveals Mechanism Involved in DNA Repair

Cristian Piras[1], Soggiu Alessio[1], Viviana Greco[2], Piera Anna Martino[1], Andrea Urbani[2,3], Jarlath Nally[4], Luigi Bonizzi[1], Paola Roncada[1,5]

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POS-01-003   ★Travel Award

Profiling of Thermostable Proteins in Diabetic Cardiovascular Rat Plasma

Thi Minh Phuong Nguyen, Viet Binh Doan, Kim Dung Nguyen, Thai Thuong Tran, Thi Bich Thao Le, Bich Nhi Nguyen, Dinh Minh Pham, Van Chi Phan

Vietnam Academy of Science & Technology, Vietnam

POS-01-004   PS25-05

Integrated Proteomics for the Study of Metastatic Human Tongue Cancer Development in a Heterogeneous Microenvironment

Masayo Wilson Morifuji, Akiko Niibori Nambu, Daiki Kobayashi, Norie Araki

Dept. Tumor Gen. Biol., Grad. Sch. Med. Sci., Kumamoto Univ., Japan

POS-01-005

Plasma Proteomic Pattern Analysis for Swine Partial Hepatectomy Model

Kohta Iguchi[1], Masaya Ikegawa[2], Etsuro Hatano[1], Tomohito Sakai[2], Kenya Yamanaka[1], Motohiko Sato[1], Gen Yamamoto[1], Tatsuya Okamoto[1], Yosuke Kasai[1], Satoru Seo[1], Kojiro Taura[1], Kei Tashiro[2], Shinji Uemoto[1]

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POS-01-006   PS25-02   ★Travel Award

Biomarkers of Diabetes in Plasma of NOD Mice

Juliana Almada Colucci[1], Juliana Perez[1], Maisa Mayumi Sakata[1], Regina Lucia Harumi Watanabe[3], Fernando Cesar Bizerra[2], Dulce Elena Casarini[1]

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POS-01-007

Aortic Stenosis in a Rabbit Model: Proteomic Analysis of Valve Tissue

Laura Mourino-Alvarez, Fernando de la Cuesta, Montserrat Baldan-Martin, Maria G. Barderas

Vascular Physiopathology Department, Hospital Nacional de Paraplejicos, Spain

POS-01-008   PS25-03

Proteomic Analysis of Left Ventricular Tissues in Dilated Cardiomyopathy Mouse Models

Mitsuhiro Nishigori[1], Hiroaki Yagi[1], Akikazu Mochizuki[1], Kazuki Sasaki[1], Yuko Iwata[2], Shigeo Wakabayashi[2], Naoto Minamino[1]

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POS-01-009   PS25-04

Plasma Proteomic Pattern Analysis for Murine Experimental Autoimmune Encephalomyelitis (EAE) Model

Tomohito Sakai[1], Takayuki Kondo[2], Takashi Nirasawa[3], Kazunori Yokoi[1], Kei Tashiro[4], Masaya Ikegawa[1,4]

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POS-01-010

Non-Genomic Regulation of Hyperactivation by Progesterone and Estradiol in Hamster Spermatozoa

Masakatsu Fujinoki

Department of Physiology, Dokkyo Medical University, Japan

POS-01-011

A Peptide Profile of Amniotic Fluid in a Fetal Lamb Model of Gastroschisis

Kei Ohyama[1,2], Toshiyuki Satou[1], Mitsumi Arito[1], Nobuko Iizuka[1], Kazuki Omoteyama[1], Manae S. Kurokawa[1], Kazuki Okamoto[1], Naoya Suematu[1], Hiroaki Kitagawa[2], Tomohiro Kato[1]

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POS-01-012

A Method for Simultaneous Quantitation of Underivatized Metabolites in the Rat Lens by LC-q-TOF-MS

Vadim V. Yanshole[1,2], Lyudmila V. Yanshole[1,2], Olga A. Snytnikova[1,2], Yuri P. Tsentalovich[1,2]

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POS-01-013

Phosphoproteome Dynamics of WHV/myc Transgenic Mouse Model During HCC Carcinogenesis

Chen Li, Hong Ni, Qing-run Li, Jing Gao, Zhen Xing, Mu-jun Zhao, Rong Zeng

Shanghai Institute for Biological Sciences, Chinese Academy of Sciences, China

POS-01-014

Protein Networks and Cellular Pathways Altered in Severe Cases of West Nile Virus Infection

Christophe Fraisier[1], Luc Camoin[2,3], Stéphanie Lim[4], Mahfoud Bakli[1], Maya Belghazi[5], Patrick Fourquet[2,3], Samuel Granjeaud[2,3], A.D.M.E. Osterhaus[4], Penelope Koraka[4], Byron Martina[4], Lionel Almeras[1,6]

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POS-01-015

Nutritional Proteomics for the Study of the Suppression of High Fat Diet-Induced Pre-Diabetes by Omega-3 Polyunsaturated Fatty Acids

Yusuke Kawashima[1,2], Yoshio Kodera[2,3], Hiroyuki Matsumoto[1]

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POS-01-017

Analysis of the Secretome of Cultured Cells with Antibody Microarray

Mohamed Saiel Saeed Alhamdani, Shakhawan Mustafa, Aseel Marzoq, Christina Hartl, Rico Uhler, Adem Yildirim, Joerg Hoheisel

Division of Functional Genome Analysis, Deutsches Krebsforschungszentrum (DKFZ), Germany

POS-01-018

Development of a MSIA UPLC-MS/MS Assay for the Analysis of Interleukins

Dayana Argoti[2], David Sarracino[1], Bryan Krastins[1], Maryann S Vogelsang[1], Gouri Vadali[1], Gregory Byram[1], Amol Prakash[1], Jennifer N Sutton[1], Scott Peterman[1], Patrick Bennett[2], Mary F Lopez[1]

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Antibody-Based Proteomics

POS-01-019

Establishment of Peptide Immunoaffinity Enrichment-Coupled Mass Spectrometric Assays for Oral Cancer Biomarker Validation in Body Fluids

Lang-Ming Chi[1,3], Kun-Yi Chien[2], Yung-Chin Hsiao[3], Yu-Sun Chang[3], Jau-Song Yu[2]

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POS-01-020

Structural Comparability of the Biosimilar and Innovator Version of a Recombinant Monoclonal Antibody

Andrew Michael Downey

University of Massachusetts-Lowell, USA

POS-01-021

Raising Monoclonal Antibody Against Cell Membrane Proteins Based on Flow Cytometry Screening and Protein Array Identification

Yangyang Liu[1], Xiaobo Yu[2], Junyi Jiang[1], Jing Liu[1], Joshua LaBaer[2], Ying Liu[1]
[1]State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, China, [2]Virginia G.Piper Center for Personalized Diagnostics, Biodesign Institute, Arizona State University, USA

POS-01-022

Classification of Cancer by Multiple Discriminant Analysis for Relationship between Cancer and Expression of Human Cellular Phosphoprotein

Yoko Motofuji[1], Asako Saitoh[1], Tomohito Ayabe[1], Morio Koike[1], Yoshio Kodera[2], Tadakazu Maeda[2], Hiroyoshi Komatsu[1]
[1]School of Health Science & Technology, Bunkyo Gakuin University, Japan, [2]Kitasato Univ., Sch. of Sci., Japan

POS-01-023

High-Throughput Production of Antibodies Within the Swedish Human Protein Atlas Project

Hanna Tegel, Holger Berling, Mathias Uhlen, Jenny Ottosson Takanen
Royal Institute of Technology, School of Biotechnology, Division of Proteomics

POS-01-024

Subcellular Localization of the Full Human Proteome Calls for a Selective Choice of Cells

Mikaela Wiking, Frida Danielsson, Mathias Uhlen, Emma Lundberg
Science for Life Laboratory, Royal Institute of Technology (KTH), Sweden

POS-01-025

Mgl-1 Regulated by Antagonistic Functions of STIP1 and DUB Enzyme USP-t

Kwang-Hyun Baek, Key-Hwan Lim, Jang-Joon Park, So-Ra Kim, Jin-Ock Kim, Lau Li
Department of Biomedical Science, CHA University, Bundang CHA Hospital, Korea

POS-01-026

Analysis of Differential Expression in a Four-Stage Human Cell Line Model for Malignant Transformation

Frida Danielsson[1], Marie Skogs[1], Mikael Huss[2], Elton Rexhepaj[1], Gillian O Hurley[3], Daniel Klevebring[1,4], Fredrik Ponten[3], Annica K. B. Gad[5], Mathias Uhlen[1], Emma Lundberg[1]
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POS-01-027

Detection and Clinical Validation of Circulating Autoantibodies as a Useful Sero-Diagnostic Markers for Non-Small Cell Lung Cancer

Makoto Kobayashi[1,2], Ryo Nagashio[1], Shinichiro Ryuge[3], Hiroyasu Nakashima[4], Kengo Yanagita[1], Benio Tsuchiya[1], Shi-Xu Jiang[5], Makoto Saegusa[5], Yukitoshi Satoh[4], Noriyuki Masuda[3], Yuichi Sato[1]
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POS-01-028

Detection of Tumor Associated Antigens in Culture Supernatant Using Autoantibodies in Sera from Patients with Bladder Cancer

Sho Minami[1,2], Kazumasa Matsumoto[3], Ryo Nagashio[1,2], Yuichi Sato[1,2]
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POS-01-029

Development of High-Throughput Screening System Using Autoantibody Library for Discovery of Scirrhous Gastric Cancer Biomarker

Satoshi Muraoka[1], Hideaki Kume[1], Hiromi Saitoh[1], Yurie Enomoto[2], Yuji Ito[2], Satoshi Nishizuka[3], Go Wakabayashi[3], Isamu Hoshino[4], Hisahiro Matsubara[4], Takeshi Tomonaga[1]
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POS-01-030

Diagnostic Significance of MUC5B and TTF-1 Expression in Resected Non-Small Cell Lung Cancer

Ryo Nagashio[1,2], Junpei Ueda[1], Sho Minami[1], Makoto Kobayashi[1], Kengo Yanagita[1], Shinichiro Ryuge[3], Ken Katono[3], Hiroyasu Nakashima[4], Shi-Xu Jiang[5], Yukitoshi Satoh[4], Noriyuki Masuda[3], Yoshiki Murakumo[5], Yuichi Sato[1,2]
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POS-01-031

Analysis of Autoantibodies Related to Tumor Progression in Sera from Patients with pT1G3 Bladder Cancer

Junpei Ueda[1,2], Sho Minami[1,2], Kazumasa Matsumoto[3], Ryo Nagashio[1,2], Yuichi Sato[1,2]
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POS-01-032

Towards Automated Enrichment and Quantitation of Insulin Using Immuno-MALDI

David Malmstrom[1], Robert Popp[1], Alex Camenzind[1], Daniel T. Holmes[2], Christoph Borchers[1,3]
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POS-01-033   PS02-04

Development of an Automated Immuno-MALDI Assay for the Clinical Measurement of Plasma Renin Activity

Robert Popp[1], David Malmstrom[1], Alexander G Camenzind[1], Daniel T Holmes[2], J Grace van der Gugten[2], Christoph H Borchers[1,3]
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POS-01-034

Antibody-Based Proteomics Using an Automated Tissue Microarray Quantification System

Kazufumi Honda, Mari Masuda, Masaya Ono, Tesshi Yamada

Division of Chemotherapy and Clinical Research, National Cancer Center Research Institute

POS-01-035

Study of Usefulness of Established Monoclonal Antibodies as a Sero Diagnostic Marker for Lung Cancer

Kengo Yanagita[1], Ryo Nagashio[1], Benio Tsuchiya[1], Shinichiro Ryuge[2], Shi-Xu Jiang[3], Makoto Saegusa[3], Yuichi Sato[1]

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POS-01-036

A Modified ELISA Strategy Using Graphene Oxide Sheets and Gold Nanoparticles Functionalised with Different Antibody Types

Hongjun Lin[1,2], Aihong Zhang[1,2], Fang Tian[1,2], Yun Cai[1,2], Yangjun Zhang[1,2], Xiaohong Qian[1,2]

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POS-01-037

Towards the Absolute Quantification of Therapeutic Proteins by Immunoaffinity Purification Mass Spectrometry

Wai Siang Law, Andrew Paul Warren, Peter Lloyd, Carsten Krantz

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POS-01-038

XIM Cross Species Immunoassays - Analyzing Proteins Across the Barrier

Oliver Poetz, Hannes Planatscher, Bart H.J. van den Berg, Frederik Weiss, Dieter Stoll, Markus F. Templin, Thomas O. Joos

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POS-01-039

DigiWest: High Content Western Blotting

Fridolin Treindl[1], Silke Schultz[2], Hans Neubauer[2], Markus F. Templin[1]

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POS-01-040

Identification of Altered Cell Signaling Pathways in B-Lymphocytic Chronic Leukemia (B-CLL) by Functional Proteomics Approaches

Manuel Fuentes[1], Raquel Bartolome[1], Martin Perez-Andres[1], Paula Diez[1], Noelia Dasilva[1], Jose Maria Sayagues[1], Laura Gutierrez[1], Maria Gonzalez-Gonzalez[1], Ana Nieto[1], Quentin Lecrevisse[1], Ignacio Criado[1], Marcos Gonzalez[1], Julia Almeida[1], Wei Wu[3], Holm Anders[3], Daniel LaRosa[3], Fridtjof Lund-Johansen[3], Alberto Orfao[1]

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POS-01-041

Signatures of Human Proteins in Plasma Discriminate Syndromes of Childhood Malaria

Jochen Schwenk[1,2], Julie Bachmann[1,2], Florence Burte[3], Setia Pramana[4], Olugbemiro Sodeinde[5], Yudi Pawitan[4], Mathias Uhlen[1,2], Mats Wahlgren[4], Delmiro Fernandez-Reyes[3,5], Peter Nilsson[1,2]

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POS-01-042

A Kinase Activity-Estimating Method Using LC-MS/MS

Maiko Nagano, Takahisa Kuga, Jun Adachi, Takeshi Tomonaga

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POS-01-043

Benefits of Fluorescent Detection for Quantitative Western Blotting

Susanne Grimsby[1], Christoffer Tamm[2], Karin Soderquist[1], Maria Winkvist[1]

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POS-01-044

Can We Detect Usually Undetectable Cytokines in Human Body Fluids?

Alamgir Khan

APAF, Macquarie University, Australia

POS-01-045

Intact Mass Analysis of Monoclonal Antibody (MAb) Charge Variants Separated Using Linear pH Gradient

Shanhua Lin, Laurent Rieux, Zhiqi Hao, Wim Decrop, Julia Baek, Andreas Huhmer, Remco Swart, Srinivasa Rao, Yury Agroskin, Chris Pohl

Thermo Fisher Scientific

Biomarker Discovery I: Cancer

POS-01-046

Secretome-Based Identification of Novel Serum Biomarkers for Ovarian Clear Cell Adenocarcinoma

Noriaki Arakawa[1], Etsuko Miyagi[1], Ayako Nomura[1], Erina Morita[1], Yusuke Masuishi[1], Yoko Ino[1], Norihisa Ohtake[2], Shohei Myoba[2], Yohei Miyagi[3], Fumiki Hirahara[1], Hisashi Hirano[1]

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POS-01-047

Search and Identification of Peptide Biomarkers of Colorectal Cancer in Sera

Igor Azarkin[1], Rustam Ziganshin[1], Georgy Arapidi[1], Sergey Kovalchuk[1,2], Victoria Shender[1], Olga Ivanova[1], Vadim Govorun[1,2], Vadim Ivanov[1]

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POS-01-048

Nuclear N-myc Downstream-Regulated Gene 1 Protein (NDRG1) as a Prognostic Biomarker in Renal Cell Carcinoma

Noriyuki Hosoya[1,2], Yuta Kurota[1,2], Vladimir Bilim[2], Yoshihiko Tomita[2], Tadashi Kondo[1]

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POS-01-049

Discovery of a Urinary Biomarker for Renal Cell Carcinoma Based on a Proteomic Analysis of Cyst Fluid

Shiho Kaneko[1], Satoru Minamida[1], Yusuke Kawashima[2,3], Kenichi Tabata[1], Kazumasa Matsumoto[1], Tetsuo Fujita[1], Takefumi Satoh[1], Tadakazu Maeda[3], Yoshio Kodera[2,3], Masatsugu Iwamura[1]

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POS-01-050

Revealing Annexin A4 as Potential Biomarker: New Order Towards Liver Cancer Therapy

Rizma Khan[1,2], Saadia Zahid[1], Yu Jui Yvonne[4], Jameson Forster[3], A. Bashar Abdul Karim[3], Atta M Nawabi[3], M.Atta Rahman[2], Nikhat Ahmed[1]

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POS-01-051

Discovery and Subsequent Validation of Biomarkers for Colorectal Cancer by Large-Scale Proteomic Analysis and Tissue Microarray Analysis

Hideaki Kume[1], Satoshi Muraoka[1], Yuuki Hashimoto[1], Shio Watanabe[1], Takeshi Masuda[2], Yasushi Ishihama[3], Junya Fukuoka[4], Yoshio Kodera[5], Kazuyuki Matsushita[6], Hisahiro Matsubara[7], Takeshi Tomonaga[1]

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POS-01-052

A Study of Protein and Glycoprotein Biomarker Discovery in Nipple Discharges from Breast Cancer by Nano-LC-ESI-Mass Spectrometry

Sadamu Kurono[1,2], Tomoyuki Nakajima[3], Norifumi Kobayashi[1,2], Shuji Matsuura[1], Nariaki Matsuura[4], Haruki Oishi[1,2]

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POS-01-053   PS07-04

Development of Novel Membrane Protein Marker for Lung Cancer Diagnosis and Therapy

Boram Lee, Jooyoung Chung, Hanyoung Chung, Taiyoun Rhim

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POS-01-054

Proteomics Identification of Novel Prognostic Biomarkers Associated with Relapse of Hepatocellular Carcinoma

Seow Chong Lee[1], Gek San Tan[1], Hwee Tong Tan[1], Teck Kwang Lim[2], Kiat Hon Lim[3], Han Chong Toh [4], Maxey Ching Ming Chung[1,2]

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POS-01-055

Low Expression of Chromatin Remodeling Gene *ARID1A* Induces Gastric Cancer Cell Proliferation and Migration

Hai-Bo Yan[1], Xue-Fei Wang[2], Qian Zhang[1], Zhao-Qing Tang[2], Ying-Hua Jiang[1], Yi-hong Sun[2], Peng-Yuan Yang[1], Feng Liu[1]

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POS-01-056

Identification of Plasma Membrane Proteins of Gastric Cancer Cells Reveals SYNJ2BP and C19ORF52 as the Pro-Proliferative Factors

Xiao-En Xu[1], Lei-Lei Xu[1], Sun-Xia Chen[1], Ying-Hua Jiang[1], Jun Yao[1], Peng-Yuan Yang[1,2], Feng Liu[1]

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POS-01-057

Quantitative Phosphoproteome Analysis of Cultured Stomach Cancer Cell Lines Aimed at Development of Biomarkers for Prediction of Drug Efficacy

Kazunari Hashiguchi, Satoshi Muraoka, Jun Adachi, Misako Sato, Takahisa Kuga, Ryosuke Watanabe, Takashi Shiromizu, Yuuki Hashimoto, Maiko Nagano, Marina Kishida, Takeshi Tomonaga

Lab. Proteome Res., Natl. Inst. Biomed. Innov., Japan

POS-01-058

Optimizing Techniques in Proteomics-Based Biomarker Discovery and Validation in Head and Neck Carcinoma

Ravi Raghavan[1], Anamika Basu[3], Rachel Conrad[1], Cliff Herrmann[2], Mia Perez[1], Laura Denham[1], Steve Lee[4], Carlos Casiano[3], Lawrence Sandberg[2]

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POS-01-059

Biomarker Proteins in Head and Neck Squamous Cell Carcinoma. A Brief Review

Rachel Conrad[1], Marnelli Bautista[1], Cliff Herrmann[2], Mia Perez[1], Lawrence Sandberg[2], Ravi Raghavan[1]

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POS-01-060

Proteome Analyses of Mammal Tumor Cells in Response to Treatment with Fibroblast Growth Factor 2

Carolina Santacruz-Perez, Julia Pinheiro Chagas da Cunha

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POS-01-061

Characterization of the Breast Cancer Marker Candidate LAG3 Protein in Human Plasma by Direct SPRi-MALDI-MS Analysis from Antibody Arrays

F. Remy-Martin[1,3], M. El Osta[2], G. Lucchi[2], R. Zeggari[1], T. Leblois[1], S. Bellon[3], E. Ly-Morin[3], C. Fryman[3], D. Suckau[4], P. Ducoroy[2], W. Boireau[1]

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POS-01-062

Proteomic Approach for Prognostic Biomarker in Myxoid Liposarcoma

Takashi Tajima[1,4], Kenta Mukaihara[1], Naofumi Asano[1], Akihiko Yoshoda[3], Takeshi Morii[4], Akira Kawai[2], Tadashi Kondo[1]

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POS-01-063   YI01-08   ★Travel Award

Secretome Analysis of Three-Dimensional *In Vitro* Model Cholangiocarcinoma

Phanthakarn Tit-oon[1], Phannee Sawangareetrakul[2], Daranee Chokchaichamnankit[2], Jisnuson Svasti[1,2], Chantragan Srisomsap[2]

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POS-01-064

Investigation into the Mechanisms of Prostate Cancer Androgen Independence Using Label-Free Data-Independent Quantitative LC-IM-DIA-MS and Pathway Analysis

B Morrisey[1], R Tonge[2], LA Gethings[2], Motoji Oshikata[2], S Pennington[1]

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POS-01-065

Bladder Cancer Proteome: A Multiplexing Approach Using Online 2D RP-RP Chromatography Coupled with Data Independent Ion Mobility

Quan Hui Wang[1], Lee A Gethings[2], Zhuowei Wang[3], Bo Wen[1], Ju Zhang[1], Quanhui Wang[1], Liang Lin[1], Chris Hughes[2], Johannes P.C. Vissers[2], James Langridge[2], Siqi Liu[1]

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POS-01-066

Proteomic Analysis Displays Overexpression of Lactoylglutathione (GLO1) is Associated with Tumor Progression in Murine Fibrosarcoma

Yufeng Wang[1], Yasuhiro Kuramitsu[1], Kazuhiro Tokuda[1], Tomio Ueno[2], Kazuyuki Nakamura[1], Nobuaki Suzuki[2], Shigefumi Yoshino[2], Norio Iizuka[2], Junko Akada[1], Masaaki Oka[2]

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POS-01-067

Proteomics Approach to Identify a Glycosylphosphoatidylinositol Specific Phospholipase D (GPLD-1) as a Lung Cancer Biomarker and Its Regulation in Lung Cancer

Yeon-Hee Yoon[1,2], Arul Narayanasamy[2], Jung-Mo Ahn[2], Je-Yoel Cho[2]

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POS-01-068

Up-Regulation of Type I Collagen During Tumorigenesis of Colorectal Cancer Revealed by Quantitative Proteomic Analysis

Xia Zou[1], Bo Feng[2], Taotao Dong[2], Binbin Tan[1], Hao Shen[1], Ao Huang[2], Xiu Zhang[1], Menghui Zhang[3], Minhua Zheng[2], Yan Zhang[1]

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POS-01-069

Treatment Efficacy of a Novel Polybisphosphonate on Soft Tissue Tumor Lesions

Ayodele Alaiya[1], Zakia Shinwari[1], Eman Barhoush[1], Steve Bobis[2], Goran Matic[2], Chaker Adra[1], Marcela Marquez[3], Sten Nilsson[3], Anders R Holmberg[3]
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POS-01-070

Analysis of Proteome Expression of Peripheral Blood Mononuclear Cells in Pancreatic Cancer Patients for Noval Biomarker Discovery

Xiaohui Liu
Institutes of Biomedical Sciences Fudan University, China

POS-01-071

Quantitation and Evaluation of Candidate Biomarkers of Pancreatic Cancer in Plasma Using Multiple Reaction of Monitoring (MRM) Method

Weimin Zheng
Institutes of Biomedical Sciences, Fudan University, China

POS-01-072

Differential Glycan Profiling of MY.1E12-positive MUC1 to Discover Serological Glyco-Biomarker for Cholangiocarcinoma Diagnosis

Atsushi Matsuda[1], Atsushi Kuno[1], Hideki Matsuzaki[1], Toru Kawamoto[2], Tatsuro Irimura[3], Yasuni Nakanuma[4], Masakazu Yamamoto[2], Nobuhiro Ohkohchi[5], Yuzuru Ikehara[1], Junichi Shoda[6], Jun Hirabayashi[1], Hisashi Narimatsu[1]
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POS-01-073

Novel Diagnostic Marker Candidates of Hepatocellular Carcinoma Revealed by Quantitative Proteomics

Dominik A. Megger[1], Thilo Bracht[1], Michael Kohl[1], Maike Ahrens[1], Carolin Puetter[2], Andre Scherag[2], Joerg F. Schlaak[2], Frank Weber[2], Andreas-Claudius Hoffmann[2], Helmut E. Meyer[1], Martin Eisenacher[1], Hideo A. Baba[2], Barbara Sitek[1]
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POS-01-074

Ratio of Glycochenodeoxycholate-3-Sulfate to Its Precursor as a Novel Biomarker of Small Hepatocellular Carcinoma

Yexiong Tan[1,2], Wenzhao Wang[2], Guowang Xu[2], Hongyang Wang[1]
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POS-01-075

Proteomic and Cytokine Plasma Biomarkers for Predicting Progression from Colorectal Adenoma to Carcinoma in Human Patients

Jung-Won Choi, Minji Choi, Jong Won Yun
Department of Biotechnology, Daegu University, Kyungsan, Korea

POS-01-076

Inhibition of Transketolase by Oxythiamine Altered Dynamics of Protein Signals in Pancreatic Cancer Cells

Gary Guishan Xiao

Genomics and Functional Proteomics Laboratories, Creighton University

POS-01-077

In-Depth Proteomic Characterization of the Secretome of Colorectal Cancer Metastatic Cells Identifies Key Proteins in Liver Metastasis

Ignacio Casal[1], Rodrigo Barderas[1], Marta L. Mendes[1], Sofia Torres[1], Ruben A. Bartolome[1], Roi Villar-Vazquez[1], Alberto Pelaez[1], Maria Lopez Lucendo[2], Felix Bonilla[3]

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POS-01-078

N-Linked Glycoprotein Profiling of Prostate Cancer Tissue by [18]O Labeling and High Resolution Mass Spectrometry

Caterina Gabriele[1], Marco Gaspari[1], Francesco Cantiello[2], Annalisa Nicastri[1], Giovanni Cuda[1], Rocco Damiano[2]

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POS-01-079

Nerve Growth Factor and Its Precursor as Cancer Biomarkers and Targets: Using Proteomics from Discovery to Validation

Severine Roselli[1], Jay Pundavela[1], Genevieve Choquet[2], Jordane Biarc[3], Jerome Lemoine[3], Ralph A. Bradshaw[4], Hubert Hondermarck[1]

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POS-01-080

Down-Regulation of the Tumor Suppressor Gene PML is a Novel Prognostic Biomarker in Gastrointestinal Stromal Tumor: Integrated Proteomic and Transcriptomic Approach

Hiroshi Ichikawa[1,4], Akihiko Yoshida[2], Tatsuo Kanda[3], Shin-ichi Kosugi[1], Takashi Ishikawa[1], Toshifumi Wakai[1], Tadashi Kondo[4]

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POS-01-081

Screening for Early Intestinal Metaplasia Biomarkers in Gastric Cardia Adenocarcinoma (GCA) by Navigated LCM and Proteomics

Cheng Yan, Jiang Jiong, Zhang Rong, Zhang Jun

Department of Gastroenterology, the Second Affiliated Hospital, Medical School of Xi'an Jiaotong University

POS-01-082

The Proteomic Study to Identify Proteins Specific to Invasion of Myxofibrosarcoma

Kazutaka Kikuta[1,2,3], Daisuke Kubota[1], Yoshihisa Suzuki[2], Hideo Morioka[3], Yoshiaki Toyama[3], Akihiko Yoshida[4], Fumihiko Nakatani[5], Akira Kawai[5], Hirokazu Chuuman[5], Tadashi Kondo[1]

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POS-01-083

Serum Metabolomics as a Screening Method for Pancreatic Cancer

Takashi Kobayashi[1], Shin Nishiumi[1], Masaru Yoshida[1,2,3], Takeshi Azuma[1]

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POS-01-084

Cancer Proteomics for Biomarker Development Toward Personalized Medicine

Tadashi Kondo, Takashi Mukaihara, Kenta Mukaihara, Naofumu Asano, Yuta Kurota

Division of Pharmacoproteomics, National Cancer Center Research Institute, Japan

POS-01-085

N-Linked Glycoprotein Profiling for Colorectal Cancer Biomarker Discovery Using High Resolution Quadrupole-Orbitrap Mass Spectrometry and ^{18}O Isotopic Labeling

Annalisa Nicastri[1], Laura Elia[2], Roberto Romano[2], Caterina Gabriele[1], Rosario Sacco[2], Giovanni Cuda[1], Marco Gaspari[1]

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POS-01-086

Analysis of Secretome and Quantitative Tissue Proteome Identified Fibulin-4 and Melanotransferrin as Serological Markers for Colorectal Cancer

Jihye Shin[1,2], Hye-Jung Kim[1,5], Gamin Kim[1,4], Meiying Song[4], Seung-Taek Lee[2], Hoguen Kim[4], Cheolju Lee[1,3]

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POS-01-087

Cancer-Specific Genome Changes Observed at Proteome Level in Colorectal Cancer

Sergei Moshkovskii, Alexei Chernobrovkin, Ksenia Kuznetsova, Mikhail Pyatnitsky, Victor Zgoda, Svetlana Novikova, Alexei Lupatov, Igor Vakhrushev, Andrei Lisitsa, Alexander Archakov

Institute of Biomedical Chemistry RAMS, Russia

POS-01-088   YI03-01   ★Travel Award

Differentially Glycosylated Circulating Protein Biomarker Discovery for Barretts Esophagus and Esophageal Adenocarcinoma

Alok Kishorkumar Shah[1], David Chen[2], Kim-Anh Le Cao[3], Eunju Choi[1], Derek Nancarrow[4], David Whiteman[4], Nicholas A. Saunders[1], Andrew Barbour[5], Michelle M. Hill[1]

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POS-01-089

Proteomic Analysis of Human Malignant Pleural Mesothelioma Cells Compared to Normal Mesotherial Cells

Yasuhiro Kuramitsu, Waka Tominaga, Byron Baron, Takao Kitagawa, Junko Akada, Kazuyuki Nakamura

Department of Biochemistry and Functional Proteomics, Yamaguchi University Graduate School of Medicine, Japan

POS-01-091

Search for Biomarker Proteins Related to Cisplatin-Susceptibility in Malignant Mesothelioma

Kazuya Nagano[1], Takuya Yamashita[1,2], Yuka Maeda[1,2], Kazuma Higashisaka[1,2], Yasuo Yoshioka[1,2,3], Masaki Inoue[1], Yasuhiro Abe[1], Yohei Mukai[1], Haruhiko Kamada[1,3], Yasuo Tsutsumi[1,2,3], Shin-ichi Tsunoda[1,3]

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POS-01-092

Autoantibody Biomarkers for the Detection of Early Stage Ovarian Cancer

Karina Martin[1], Carmela Ricciardelli[2], Martin K. Oehler[2], Peter Hoffmann[1]

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POS-01-093   ★Travel Award

Glioblastoma Cell Secretome Analysis and Relevance with Tumor Associated Pathways

Manoj Kumar Gupta[1], Ravindra Varma Polisetty[1], Anjali Shiras[2], Ravi Sirdeshmukh[1]

[1]Institute of Bioinformatics, India, [2]National Centre for Cell Science, India

POS-01-094

In-Depth Proteomic Characterization of Pancreatic Ductal Adenocarcinoma Subtypes

Laura Postolache[1,2,3], Wiebke Nadler[1,2,3], Alexander Kerner[1,2,3], Christian Eisen[2,4], Martin Sprick[2,4], Andreas Trumpp[2,4], Christoph Roesli[1,2]

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POS-01-095

Proteomics of High Grade Gliomas: New Molecular Insights

Ravindra Varma Polisetty[1], Poonam Gautam[2], Manoj Kumar Gupta[1], Rakesh Sharma[1], Megha S Uppin[3], Sundaram Challa[3], Praveen Ankathi[3], Aniruddh K Purohit[3], Durairaj Renu[5], Anjali Shiras[4], H C Harsha[1], Akhilesh Pandey[1], Ravi Sirdeshmukh[1]

[1]Institute of Bioinformatics, India, [2]National Institute of Pathology (ICMR), India, [3]Nizam's Institute of Medical Sciences, India, [4]National Centre for Cell Science, India, [5]Strand Life Sciences, India

POS-01-096

Towards the Mechanism of EGFR Inhibitor Resistance in Non-Small Lung Cancer Cells

Ryan Jacobs[2], Jason Fong[2], David Moravec[2], Greg Botting[2], Ryan Bomgarden[3], John Rogers[3], Michael Blank[1], Rosa Viner[1], Neelu Puri[2]

[1]Thermo Fisher Scientific (San Jose), USA, [2]University of Illinois College of Medicine, USA, [3]Thermo Fisher Scientific (Rockford), USA

POS-01-097

Proteomic Analysis of Tumor-Derived Exosomes Derived from Cultured Human Lung Cancer Cell as Tumor Biomarkers

Haruhiko Kamada[1,2,3], Takuya Yamashita[1], Masaki Inoue[1], Kazuya Nagano[1,3], Sumie Katayama[4], Yohei Mukai[1,3], Yasuo Yoshioka[2,3], Kazuma Higashisaka[3], Yasuo Tsutsumi[2,3], Shin-ichi Tsunoda[1,2,3,4]

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POS-01-098

The Role of 14-3-3 Protein in Cholangiocarcinoma

Amnart Khongmanee[1], Daranee Chokchaichamnankit[2], Jisnuson Svasti[1,2], Chantragan Srisomsap[2]

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POS-01-099

Search for New Urothelial Cancer Biomarkers

Tsutomu Fujimura[1], Hikari Taka[1], Saiko Kazuno[1], Reiko Mineki[1], Kimie Murayama[1], Takashi Ueno[1], Jun-ichi Furukawa[2], Yasuro Shinohara[2]

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POS-01-100

Oligosaccharide Structure Analysis of Acute Phase Protein in the Serum of the Prostate Cancer Patient

Tsutomu Fujimura[1], Saiko Kazuno[1], Kimie Murayama[1], Takashi Ueno[1], Jun-ichi Furukawa[2], Yasuro Shinohara[2]

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POS-01-101

Glycoproteomic Approaches Enable to Find Glycoproteins with Aberrant Glycans as Novel Biomarkers for Epithelial Ovarian Cancer

Maki Sogabe[1], Hirofumi Nozaki[1], Tomomi Kubota[1], Atsushi Kuno[1], Hiroyuki Kaji[1], Akira Togayachi[1], Hayao Nakanishi[2], Toru Nakanishi[3], Nao Suzuki[4], Kazushige Kiguchi[4], Mikio Mikami[5], Yuzuru Ikehara[1], Hisashi Narimatsu[1]

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POS-01-102

Substrates and Regulation Mechanisms for the SIRT5

Fang Wang[2], Leilei Xu[2], Hongxiu Yu[2], Pengyuan Yang[1,2]

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POS-01-103

Comparative and Targeted Proteomic Analyses of Urinary Exosomes/Microparticles from Bladder Cancer and Hernia Patients for Biomarker Discovery and Verification

Yi-Ting Chen[1], Chien-Lun Chen[2], Yue-Fan Lai[3], Petrus Tang[4], Jau-Song Yu[1,3], Cheng-Han Tsai[3], Hsiao-Wei Chen[1], Chih-Ching Wu[1,5], Yu-Sun Chang[1,3]

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POS-01-104

Differential Analysis of LG and HG pTa Bladder Tumors in Comparison to Controls for the Detection of Potential Biomarkers

Hanna C. Diehl[1], Kathrin Luedemann-Franke[1], Rena F. Oezdemir[2], Cordelia Geisler[2], Nadine T. Gaisa[2], Axel Heidenreich[3], Ruth Knuechel[2], Helmut E. Meyer[1], Corinna Henkel[1]

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POS-01-105

Targeted Proteomics for the Verification of Prostate Cancer Biomarkers in Clinically Stratified Expressed Prostatic Secretions and Urines

Yunee Kim[1], Vladimir Ignatchenko[1], Julius Nyalwidhe[2], Raymond Lance[2], Anthony Gramolini[3], Dean Troyer[2], O. John Semmes[2], Richard Drake[4], Neil Fleshner[1], Robert Bristow[1], Thomas Kislinger[1]

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POS-01-106

Serum Protein Biomarkers Discovery for Early Detection/Monitor Treatment Response of Epidermal Growth Factor Receptor Tyrosine Kinase Inhibitor in Non-Small Cell Lung Cancer

Chien-Wei Lee[1], Chih-Liang Wang[4], Yi-Wen Wang[3], Yi-Mei Wang[3], Jau-Song Yu[1,2,3], Yu-Sun Chang[1,3], Chia-Jung Yu[1,2,3]

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POS-01-107

Positive Regulation of Brain-Specific Serine Protease 4 by Thyroid Hormone Receptors Leads to Enhanced Tumor Motility in Human Hepatoma Cells

Cheng-Yi Chen, Kwang-Huei Lin

Chang-Gung University

POS-01-108   PS08-04

Label-Free Quantitative Personalized Tissue Membrane Proteomics and Targeted Membrane Glycoprotein Profiling for Gastric Cancer Biomarker

Tai-Du Lin[1,2], Chia-Li Han[1], Chih-Wei Chien[1], Pei-Mien Chen[1], Chi-Huey Wong[2,3], Yu-Ju Chen[1]

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POS-01-109

Proteomic Analysis of DLBCL Tumor Tissue Reveals Quantitative Differences in Regulators of Cytoskeletal Architecture between R-CHOP Responding and Non-Responding Patients

Ulla Ruetschi[1], Martin Stenson[2], Per-Ola Andersson[2]
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POS-01-110

Proteomic Analysis of Highly Invasive Colorectal Cancer Cells Established by Orthotopic Xenograft Mouse Model

Takashi Shiromizu[1], Jun Adachi[1], Shigeo Yagi[2], Robert M. Hoffman[2], Takeshi Tomonaga[1]
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POS-01-111

Proteomic Analysis of Saliva from Patients with Oral Cancer

Priya Sivadasan[1], Gajanan Sathe[2], Manoj Kumar Gupta[2], Amritha Suresh[1], Harsha H C[2], Ravi Sirdeshmukh[2], Moni Abraham Kuriakose[1]
[1]Head and Neck Oncology, Mazumdar Shaw Cancer Centre, Narayana Hrudayalaya, India, [2]Institute of Bioinformatics, India

POS-01-112

Discovery of Lung Cancer Biomarkers by Differential Proteomes Analysis from Six Types of Pleural Effusions

Pei-Jun Liu[1], Chi-De Chen[1], Chih-Liang Wang[5], Yu-Sun Chang[1,3], Jau-Song Yu[1,2,3], Chih-Ching Wu[3,4], Chia-Jung Yu[1,2,3]
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POS-01-113   YI03-07

An Improved Protocol for the Enrichment of Plasma Membrane Proteins Allows the Identification of Accessible Antibody Targets on Trastuzumab-Resistant Breast Cancer Cells

Yohei Mukai[1,2,3], Danilo Ritz[4], Dario Neri[1], Tim Fugmann[4]
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POS-01-114

Comprehensive Proteomics of Gastric Cancer for Biomarker and Drug Target Discovery

Yoon Pin Lim[1,2,3], Yixuan Yang[1], Poh Kuan Chong[1], Hassan Ashktorab[4], Khong Hee Lim[5], Bok Yan So[6], Boon Ooi Tan[7], Khay Guan Yeoh[8]
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POS-01-115   YI01-06

Basic Fetoprotein Is Homologous with G6PI/AMF/NLK/MF/PGI/PHI/SA-36 by the Identification of 99% AA Sequence for BFP Using MALDI-MS

Mutsumi Hosako, Hiroki Kuyama, Chihiro Nakajima, Shin-ichirou Kawabata, Koichi Tanaka

Koichi Tanaka Laboratory of Advanced Science and Technology, Shimadzu Corporation, Japan

Biomarker Discovery II: Liver, Kidney

POS-01-116

Renal Metabolic Profiling of Early Renal Injury and Renoprotective Effects of Poria Cocos Epidermis Using UPLC Q-TOF/HSMS/MS[E]

Yingyong Zhao[1], Xu Bai[2]

[1]The College of life sciences, northwest University, China, [2]Waters Technologies Shanghai Limited, China

POS-01-117

Using an Isolated Rat Kidney Model to Identify Kidney Origin Proteins in the Urine

Lulu Jia[1], Xundou Li[1], Chen Shao[1], Lilong Wei[1], Menglin Li[1], Zhengguang Guo[1], Zhihong Liu[2], Youhe Gao[1]

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POS-01-118

The Expression and Function of GP73 in Hepatocellular Carcinoma (HCC)

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POS-01-119

The PI3K Inhibitor, Wortmannin Ameliorates STZ-Induced Diabetic Nephropathy

Sang-Hoon Kim, Young-Woo Jang, Hyun-Jung Kim, Chan-Wha Kim

Korea University, Korea

POS-01-120

Serum Peptides, Represented by Complement 3f Des-Arginine, Are Useful for Prediction of the Response to Pegylated Interferon-α Plus Ribavirin in Patients with Chronic Hepatitis C

Yohei Noguchi[1], Manae S. Kurokawa[2], Chiaki Okuse[1], Nobuyuki Matsumoto[1], Kouhei Nagai[2], Toshiyuki Sato[2], Mitsumi Arito[2], Naoya Suematsu[2], Kazuki Okamoto[2], Michihiro Suzuki[1,3], Fumio Itoh[1], Tomohiro Kato[2]

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POS-01-121

Multi-Omic and Functional Network Analysis of Paediatric Urine from Patients Diagnosed with Idiopathic Nephrotic Syndrome

Motoji Oshikata[1], Lee A Gethings[1], Johannes PC Vissers[1], John Shockcor[2], Stephen McDonald[2], Sandra Kraljevic Pavelic[3], Mirela Sedic[3], Maja Lemac[4], Danica Batinic[4], James I Langridge[1], Olga Vasieva[5]

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POS-01-122

Proteomic Analysis of Non-Alcoholic Steatohepatitis in Mice

Masaaki Takamura[1], Bo Xu[2], Shuichiro Shimada[2], Satoshi Yamagiwa[1], Yasunobu Matsuda[3], Yutaka Yoshida[2], Minoru Nomoto[1], Tadashi Yamamoto[2], Yutaka Aoyagi[1]

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POS-01-123

Angiotensin-Converting Enzyme Inhibition Curbs Tyrosine Nitration of Mitochondrial Proteins in the Renal Cortex During the Early Stage of Diabetes Mellitus in Rats

Naohito Ishii[1,4], Pamela K. Carmines[2], Masanori Yokoba[1,4], Hideki Ikenaga[3], Tsuyoshi Ichikawa[4], Yuya Yamada[4], Yoshifumi Kurosaki[1,4], Tomoaki Tsukushi[5], Yoshio Kodera[6], Masamichi Oh-Ishi[6], Yoshikazu Aoki[7], Tadakazu Maeda[6], Takafumi Ichikawa[1,4], Tsuneo Takenaka[8], Masato Katagiri[1,4]

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POS-01-124

High Confident Human Glomerulus Proteome Identified Both by Mass Spectrometry- and Antibody-Based Proteomics

Masaaki Nameta, Yutaka Yoshida, Ying Zhang, Bo Xu, Sameh Magdeldin, Hidehiko Fujinaka, Eishin Yaoita, Mathias Uhlen, Tadashi Yamamoto

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POS-01-125

Phospho-Profiling of mTOR Inhibitor-Treated Renal Cell Carcinoma (RCC) Cell Line and Its Application to Drug Response-Efficacy Biomarkers

Ryosuke Watanabe, Yuki Hashimoto, Marina Kishida, Misako Matsubara, Jun Adachi, Takeshi Tomonaga

Proteome Research Project, National Institute of Biomedical Innovation

POS-01-126

Localization of Normal Human Glomerulus Proteins Detected by Mass Spectrometry and Immunohistochemistry in the Kidney

Tomizo Oyama, Masaaki Nameta, Masaki Taga, Fujio Nakamura, Toshikazu Ikoma, Yutaka Yoshida, Eishin Yaoita, Tadashi Yamamoto

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POS-01-127

Proteomes of Normal Human Glomerulus Identified by Mass Spectrometry (MS) and Immunohistochemistry: Origin of Proteins Identified Only by MS

Masaki Taga, Masaaki Nameta, Tomizo Oyama, Fujio Nakamura, Yutaka Yoshida, Eishin Yaoita, Tadashi Yamamoto

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POS-01-128

Is Urine a Better Biomarker Source Than Blood?

Youhe Gao

Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences

POS-01-129

Human Urine Proteome Changes Induced by Space Flight

Ludmila Kh Pastushkova[1], Kirill S. Kireev[2], Alexey S. Kononikhin[3,4], Igor V. Dobrokhotov[1], Igor A. Popov[3,4], Natalia L. Starodubtseva[3], Vladimir A. Ivanisenko[5], Pavel S. Demenkov[5], Evgeny S. Tiis[5], Nikolay A. Kolchanov[5], Irina M. Iarina[1], Evgeny N. Nikolaev[3,4]

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POS-01-130

Autosomal Dominant Polycystic Kidney Disease Patients Urine Proteome

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POS-01-131

Subtractive Proteomic Analysis Determines Lipid Droplet Associated Protein (LDP) and Unravels Differential Liver LDP Profiling in Fatty Liver Disease

Mingwei Liu[1,2], Chen Ding[1,2], Wanlin Liu[1,2], Gaigai Guo[1,2], Tianyi Fu[1,2], Sung Yun Jung[3], Bei Zhen[1,2], Yi Wang[3], Lawrence C. B. Chan[3], Jun Qin[1,2,3]

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POS-01-132

Urine Peptidomics and Exosome Profiling in Liver Diseases

Ibon Iloro[1], Esperanza Gonzalez[2], Eva Rodriguez-Suarez[1], Mikel Azkargorta[1], Virginia Gutierrez-de Juan[2], Jose M. Mato[2], Juan M. Falcon-Perez[3], Felix Elortza[1]

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POS-01-133

Changes of the *O*-GlcNAc Modification of Proteins Accompanied with Diabetic Nephropathy

Yoshihiro Akimoto[1], Yuri Miura[2], Tosifusa Toda[3], Toshiyuki Fukutomi[4], Daisuke Sugahara[1], Margreet A Wolfert[5], Lance Wells[5], Geert-Jan Boons[5], Gerald W Hart[6], Tamao Endo[2], Hayato Kawakami[1]

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POS-01-134

Application of Glycoproteomics for Development of Serum Biomarker of Liver Disease

Makoto Ocho[1], Akira Togayachi[1], Hiroyuki Kaji[1], Atsushi Kuno[1], Etsuko Iio[2], Maki Sogabe[1], Yasuhito Tanaka[2], Yuzuru Ikehara[1], Masashi Mizokami[3], Hisashi Narimatsu[1]

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Biomarker Discovery III: Brain, Heart, etc.

POS-01-135

Processed B-Type Natriuretic Peptide is a Biomarker of Post-Interventional Restenosis in Ischemic Heart Disease

Kenichi Aizawa[1,3], Toru Suzuki[1,3], Hirotaka Fujimoto[2], Daigo Sawaki[1,3], Junichi Ishida[1], Jiro Ando[1], Hideo Fujita[1], Issei Komuro[1], Ryozo Nagai[1]

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POS-01-136

Deciphering the Proteome and Secretome of Human Coronary Atherosclerotic Arteries

Fernando De la Cuesta[1], Irene Zubiri[2], Maria Posada[2], Aroa S. Maroto[2], Luis R. Padial[3], Fernando Vivanco[2], Gloria Alvarez-Llamas[2], Maria G. Barderas[3]

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POS-01-137

Proteomics and Metabolomics: New Tools to Study Albuminuria in Patients with Arterial Hypertension

Montserrat Baldan-Martin[1], Laura Mourino-Alvarez[1], Fernando de la Cuesta[1], Luis M. Ruilope[2], Luis R. Padial[3], Maria G. Barderas[1]

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POS-01-138

N-Glycan Profiling of Surfactant Protein D (SP-D) by MALDI Mass Spectrometry

Emi Ito[1], Ritsuko Oka[1], Ayako Kurimoto[1], Shinobu Kitazume[1], Shuichi Nakaya[2], Takeo Ishii[3], Kouzui Kida[3], Naoyuki Taniguchi[1]

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POS-01-139

Systematic Vascular Proteomics in Vascular Remodeling Model

Dong Hoon Kang[1], Soyoung Jang[2], Min young Lee[3], Doo Jae Lee[1], Jiran Kim[1], Daehee Hwang[3,4], Chulhee Choi[2], Snag Won Kang[1]

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POS-01-141

Discovery and Verification of Novel Biomarkers Predicting the Response of Antidepressants Using Mass Spectrometry-Based Proteomic Approach

Jisook Park[3], Hye In Woo[1], Jeong Soo Yang[2], Shinn-Won Lim[3], Doh Kwan Kim[4], Soo-Youn Lee[1,5]

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POS-01-142

Identification of Biomarkers Predictive of Chronic Lung Allograft Dysfunction (CLAD) After Lung Transplantation by Proteomic Technologies

Candice Trocme[1], Sandrine Bourgoin-Voillard[2,3], Izabel Berard[2], Helene Waret[2], Bertrand Toussaint[1], Karine Botturi[4], Antoine Magnan[4], Laurent Nicod[5], Christophe Pison[6], Michel Seve[2,3]

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POS-01-143

Proteome Profiling of Epidermal Differentiation

Hiroyuki Taguchi[1], Daishi Sakaguchi[1], Shigeru Moriwaki[1], Hisashi Hirano[2]

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POS-01-144

Direct Brain Omics-Study of Alzheimer's Disease Using UPLC-MS Assay for the Early Diagnosis

Haruhito Tsutsui[1], Koichi Inoue[1], Hiroyasu Akatsu[2,3], Yoshio Hashizume[2], Noriyuki Matsukawa[3], Takayuki Yamamoto[2], Toshimasa Toyo^oka[1]

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POS-01-145

Proteome Analysis of Aortic Aneurysm Based on Stage Classification Utilizing Protein Profiles

Hiroaki Yagi[1], Hiromitsu Nishigori[1], Tsukasa Osaki[1], Kazuki Sasaki[1], Sayaka Muto[1], Takayuki Morisaki[3], Yutaka Iba[4], Kenji Minatoya[4], Hatsue Ueda[2], Naoto Minamino[1]

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POS-01-146   ★Travel Award

Proteomic Analysis of Posttraumatic Stress Disorder Mouse Model Reveals Nucleus Accumbens Affected Pathways

Chi-Ya Kao, Kathrin Henes, Carsten T Wotjak, Christoph W Turck

Max Planck Institute of Psychiatry, Germany

POS-01-148

Establishing Apolipoprotein J as a Potential Candidate for Alzheimer's Disease Biomarker Panel: Australian Imaging, Biomarker and Lifestyle (AIBL) Flagship Study of Ageing

Veer Bala Gupta[1], Christopher Rowe[2], Cassandra Szoeke[3], David Ames[3], Lynne Cobiac[4], Ashley Bush[3], Kathryn Ellis[3], Lance Macaulay[3], Colin Masters[3], Ralph Martins[3]

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POS-01-149

Proteomic Analysis of Stratum Corneum of Human Scalp

Daishi Sakaguchi[1], Yoriko Nakagiri[1], Hiroyuki Taguchi[1], Shigeru Moriwaki[1], Hisashi Hirano[2]

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POS-01-150

Identification of Proteins Involved in Thoracic Aortic Aneurysm

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POS-01-151   PS12-05

Mass Spectrometry Methods for Surrogate Biomarker Discovery in Duchenne Muscular Dystrophy

Ramya L Marathi[1], Sree Rayavarapu[1], Kristy J Brown[1], Jenny Mac[1], Kanneboyina Nagaraju[1], Eric P Hoffman[1], Erik Henricson[2], Craig M. McDonald[2], Yetrib Hathout[1]

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POS-01-152

Relative Quantification of Endogenous Peptides in Cerebrospinal Fluid Using TMT 6-plex to Identify New Biomarkers for Alzheimer's Disease

Mikko Holtta[1], Lennart Minthon[4], Oskar Hansson[4], Ian Pike[2], Malcolm Ward[2], Karsten Kuhn[3], Henrik Zetterberg[1], Kaj Blennow[1], Johan Gobom[1]

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POS-01-153

Proteomics Biomarkers for Human African Trypanosomiasis

Natalia Tiberti[1], Veerle Lejon[2], Alexandre Hainard[1], Enock Matovu[3], John Charles Enyaru[4], Dieudonne Mumba Ngoyi[5], Joseph Ndung'u[6], Philippe Buscher[7], Jean-Charles Sanchez[1]

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POS-01-154

Comparative Proteomic Analysis of Neutrophils from Patients with Microscopic Polyangiitis and Granulomatosis with Polyangiitis

Teisuke Uchida[1,3], Kouhei Nagai[2], Toshiyuki Sato[1], Nobuko Iizuka[1], Mitsumi Arito[1], Yukiko Takakuwa[3], Hirosama Nakano[3], Seido Ooka[3], Manae Kurokawa[1], Noya Suematsu[1], Kazuki Okamoto[1], Shoichi Ozaki[3], Tomohiro Kato[1]

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POS-01-155

Proteomic and Transcriptomic Analysis of Triglyceride Deposit Cardiomyovasculopathy for Discovery of Novel Biomarkers

Yasuhiro Hara[1], Naoko Kawasaki[1], Kenichi Hirano[2], Yuki Hashimoto[1], Jun Adachi[1], Shio Watanabe[1], Takeshi Tomonaga[1]

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POS-01-156

Biomarker Discovery from Low Abundance Proteins in Bovine Serum; Proteomics for Developing Beef Production Systems

Haruka Ikegami[1], Kouhei Nagai[1], Atsushi Takemoto[2], Natsumi Shimizu[2], Kohtaro Morita[2], Chika Higuchi[2], Tamako Matsuhashi[3], Naohiko Kobayashi[4], Kazuya Matsumoto[1,2]

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POS-01-157

Identification of Proteins Related to Accumulation of Intramuscular Fat in Japanese Black by Proteomic Analysis

Atsushi Takemoto[1], Kouhei Nagai[2], Haruka Ikegami[2], Natsumi Shimizu[1], Kohtaro Morita[1], Chika Higuchi[1], Eiji Kobayashi[3], Kazuya Matsumoto[2]

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POS-01-158

The Regulatory Effects of the Tau Protein on Triose Phosphate Isomerase (TPI) in Brain Cells for the Normal and Diseased States are Different

Anastasia Aikins, Seung-Ah Park, Gi-Yeon Han, Chan-Wha Kim

Korea University, Korea

POS-01-159

Proteomic Analysis of Saliva Identifies Potential Biomarkers in Physiological State

Masako Mukai[1], Yuu Yamatani[1], Eri Hatano[1], Ayaka Saiki[1], Aki Harima[1], Yubo Cao[2], Toshio Kobayashi[2], Sachie Oda-Tamai[1]

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POS-01-160

Implications of Methylglyoxal Modification of Peroxiredoxin 6 for Impaired Healing in Diabetic Wound

Tomoko Oya-Ito[1], Yuji Naito[1], Tomohisa Takagi[1], Keisuke Shima[2], Yoshito Itoh[1], Toshikazu Yoshikawa[1]

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POS-01-161   PS12-04

Proteomic Study of Biomarkers for Amyotrophic Lateral Sclerosis in Human Muscle Biopsies

Konstantin Artemenko[1], Ganna Shevchenko[1], Kristin Elf[2], Hakan Askmark[2], Jonas Bergquist[1]

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POS-01-162

Proteomics and Biomarker Discovery in Bipolar Disorder

Jessica Holmen Larsson, Johan Gobom, Joel Jakobsson, Henrik Zetterberg, Kaj Blennow, Mikael Landen

Department of Psychiatry and Neurochemistry, Institute of Neuroscience and Physiology at Sahlgrenska Academy, University of Gothenburg

Proteomics of Axons During Presynapse Formation Using the Novel Culture Method "Neuron Ball Culture"

Yukio Sasaki[1,2], Akiyo Ishikawa[3], Takao Kawakami[3,4], Hisashi Hirano[3], Yoshio Goshima[1]
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Quantitative Mass Spectrometry for Proteomic Screening of Potential Biomarkers in Alzheimer's Disease

Ganna Shevchenko, Sravani Musunuri, Kim Kultima, Martin Ingelsson, Lars Lannfelt, Jonas Bergquist, Magnus Wetterhall[1]
Uppsala University, Sweden

Chemical Proteomics and Drug Discovery

YI01-02

ATP Accessibility Screening (AAS), A High-Throughput and High-Resolution Kinase Analysis Platform for Signaling Research

Jun Adachi[1], Daisuke Higo[2], Shio Watanabe[1], Masayoshi Kuwano[1], Yuki Hashimoto[1], Takeshi Tomonaga[1]
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Replenishment of Recombinant UQCRB Protein, A Terpestacin-Binding Mitochondrial Protein, Enhances Angiogenesis *In Vitro* and *In Vivo*

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Autophagonizer Induces Autophagy via Endocytosis Inhibition

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Phage Display-Based High Throughput Screening to Identify Cell-Internalizing Monoclonal Antibodies for Antibody-Drug Conjugates

Yohei Mukai[1,2], Mai Yoshikawa[2], Yoshiaki Okada[2], Yuki Tsumori[2], Shin-ichi Tsunoda[1], Yasuo Tsutsumi[2], William C. Aird[3], Yasuo Yoshioka[2], Naoki Okada[2], Takefumi Doi[2], Shinsaku Nakagawa[2]
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Target Identification of a Novel IL-12p40 Production Inhibitor by Chemical Proteomics

Naoto Nakamura, Masatoshi Yuri, Masashi Hiramoto, Masaomi Terajima, Yoko Kaneko, Kazuyuki Hattori, Hiroyuki Yokota
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POS-01-170

A Chemical Proteomics Strategy for the Discovery of Targets for Antibody-Based Therapy

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POS-01-171

Application of Proteomics to Drug Discovery Research

Naoto Nakamura, Tomohiro Yamauchi, Masashi Hiramoto, Masatoshi Yuri, Satoru Ujihara, Masanori Naito, Jun Takasaki, Hiroki Shirai, Hiroyuki Yokota

Astellas Pharma Inc., Japan

POS-01-172

Application of Various Types of Linkers for Photoaffinity Biotin-Tagged Chemical Probes to Identify Drug Targets

Masatoshi Yuri[1], Masashi Hiramoto[1], Satoru Ujihara[1], Naoto Nakamura[1], Tomohiro Yamauchi[1], Masanori Naitou[1], Miyuki Mabuchi[2], Akito Tanaka[2], Hiroyuki Yokota[1]

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POS-01-173

Proteomic Analysis of Two Lung Cancer Cell Lines Treated with Umbelliprenin

Narges Khaghanzadeh[1,2], Kazuyuki Nakamura[3], Takao Kitagawa[3], Zahra Mojtahedi[1], Mohammad Ramezani[4], Abbas Ghaderi[1,2]

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POS-01-174

Identification of Prostasin Serine Protease Against Hepatitis C Virus Replication

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POS-01-175

Functional Proteomics Approaches for High-Throughput Determination of Small Molecules Interactions on cKIT

Manuel Fuentes[1], Maria Jara-Acevedo[1], Ricardo Jara-Acevedo[4], Maria Gonzalez-Gonzalez[1], Luis Escribano[2], Joshua LaBaer[3], Alberto Orfao[1]

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POS-01-176 PS30-3

Target Identification of Novel Anti-Inflammatory Compound Using Chemical Proteomics Approach with Bait Compound

Takashi Yamamoto[1], Ayatoshi Andou[1], Nobuhiko Hayakawa[1], Masatsugu Noguchi[1], Sen Takeshita[1], Ryohei Yokoyama[1], Agung Eviryanti[1], Yukie Seki[1], Hikaru Nishio[1], Manami Shuto[1], Misato Noguchi[1], Yoichiro Shima[1], Kanna Kuribayashi[1], Shunsuke Kageyama[1], Hiroyuki Eda[1], Shun-ichiro Iemura[2], Tohru Natsume[2], Tomohisa Hatta[2], Masataka Shoji[1]

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POS-01-177

Andrographolide Analogue AL-1 Reciprocally Exerts Cytotoxic and Protective Effects on Cells by Inducing ROS Generation

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POS-01-178

Cell Permeable Conjugates for Identification of Small Molecule - Protein Interactions

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POS-01-179

Synthesis of Mannosylated Lipopeptides as Targets for the Mannose Receptor

Bita Sedaghat, Rachel Stephenson, Istvan Toth
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POS-01-180

Synthesis of Lipid LHRH Peptides for Targeted Drug Delivery

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Clinical Application of Proteomics

POS-01-181

Relative Quantification of Intact Hemoglobin A2 with an Ion Trap Mass Spectrometer

Adelina E Acosta Martin[1,2], Didia Coelho Graca[1], Lorella Clerici[2], Yury O Tsybin[3], Ralf Hartmer[4], Markus Meyer[4], Kaveh Samii[5], Denis Hochstrasser[1,2], Pierre Lescuyer[1,2], Alexander Scherl[1]
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POS-01-182

Analysis of PTH Variants by Immunocapture with High Affinity N and C Terminal Monoclonal Antibodies

Valdemir Melechco Carvalho[1], Gabriela Venturini da Silva[2], Karina Helena Morais Cardozo[1], Jose Gilberto Henriques Vieira[1,3]
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POS-01-183

Glycol Chitosan-Conjugated ApoA1 Protein Complex Regulation of Silica-Induced IPF

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POS-01-184

Proteomic Analysis on the Mechanism of LDL Apheresis Therapy in the Steroid-Resistant Nephrotic Syndrome

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POS-01-185

Discovery of New Therapeutic Targets in Epithelioid Sarcoma Using Proteomic Analysis

Kenta Mukaihara[1,2], Daisuke Kubota[2,3], Takashi Tajima[1], Naofumi Asano[1], Yoshiyuki Suehara[2], Akira Kawai[3], Kazuo Kaneko[2], Tadashi Kondo[1]

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POS-01-186

Comparative Proteomic Analysis of Extremely Low and Moderate Parasitemic Vivax Malaria for Identification of Potential Early Diagnostic and Prognostic Serum Biomarkers

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POS-01-187

Calcyclin Levels Determined by High-Throughput SRM in Serum Samples of Pre-Eclampsia Patients

Coskun Guzel[1], Maki Terasaki[2], Johannes PC Vissers[2], Lennard Dekker[1], Gerda G Zeeman[3], Eric AP Steegers[3], Theo M Luider[1]

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POS-01-188

Proteomic Study Discovering Talin 1 Fragment Related to HIV Infection

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POS-01-189

PlasmaQBaby: Quantification of Plasma Proteins in Preterm Infants Using Heavy Protein Standards and Peptide Group-Specific Immunoenrichment

Bart H.J. van den Berg[1], Benedikt Lang[1], Christopher J. Pynn[3], Dieter Stoll[3], Martin Gamer[2], Peter Schulz-Knappe[2], Thomas O. Joos[1], Oliver Poetz[1]

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POS-01-190

Production and Characterization of A Set of Mouse Monoclonal Anti-Peptide Antibodies Against Selected Oral Cancer Marker Candidates for SISCAPA-MRM and -MALDI Assay Development

Yung-Chin Hsiao[1], Lang-Ming Chi[1,2], Kun-Yi Chien[1,3], Yi-Ting Chen[1], Yu-Sun Chang[1,3], Jau-Song Yu[1,3]

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POS-01-191

Validation of Pancreatic Disease Markers in Secretin-Stimulated Duodenal Juice Using Selected Reaction Monitoring

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POS-01-192

A Proteomic Portrait of Colon Cancer-Associated Fibroblasts Identifies Novel Prognostic Markers

Sofia Torres[1], Ruben A. Bartolome[1], Marta L. Mendes[1], M. Jesus Fernandez-Acenero[2], Alberto Pelaez[1], Cristina Pena[3], Maria Lopez-Lucendo[4], Rodrigo Barderas[1], Antonio Garcia de Herreros[5], Felix Bonilla[4], J. Ignacio Casal[1]

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POS-01-193

Differences in Proteome Between Luminal A and Luminal B HER2 Negative Breast Cancers

Miki Hasegawa[1,2], Yutaka Yoshida[2], Yu Koyama[1], Takashi Shiromizu[3], Yasuhiro Hara[3], Akiko Kanagawa[3], Eiko Sakata[1], Kumiko Tatsuda[1], Chie Toshikawa[1], Naoko Manba[1], Mayuko Ikarashi[1], Eishin Yaoita[2], Takeshi Tomonaga[3], Toshifumi Wakai[1], Tadashi Yamamoto[2]

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POS-01-194

Quantitative Proteomics Characterization of Pancreatic Tumor Tissues: New Insights and Challenges

Sheng Pan, Ru Chen, Teresa Brentnall

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POS-01-195

Generation and Characterization of New Bispecific Antibodies to EphA10 and CD3 as Candidate Drugs Against Breast Cancer

Shintaro Taki[1,2], Haruhiko Kamada[1,3], Yuka Maeda[1,2], Kazuya Nagano[1], Yohei Mukai[1], Yasuo Tsutsumi[1,2,3], Shin-ichi Tsunoda[1,2,3]

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POS-01-196

Serum Fibrinogen Alpha C-chain 5.9 kDa Fragment (FIC 5.9) as a Biomarker for Early Detection of Hepatic Fibrosis Related to Hepatitis C Virus

Wataru Kikuchi[1,2], Kenta Noda[2], Kazuyuki Sogawa[1], Motoi Nishimura[1], Hideki Ishihara[2], Fumio Nomura[1]

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POS-01-197   YI03-06

A SILAC-Based Approach Defines an Angiotensin II- Regulated Proteome in Primary Human Kidney Cells

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POS-01-198

Efficient High Throughput Proteomic Workflow for Clinical Biopsy Samples

Bo Xu[1,2], Ying Zhang[1], Yansheng Liu[2], Ludovic Gillet[2], George Rosenberger[2], Sameh Magdaldin[1], Yutaka Yoshida[1], Eishin Yaoita[1], Ruedi Aebersold[2], Tadashi Yamamoto[1]

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POS-01-199

Potential Plasma Markers of Hypertrophic Cardiomyopathy - Targeted Proteomic Analysis of Soluble Fibronectin

Alena Fucikova[1], Jiri Dresler[2], Helena Rehulkova[3], Lenka Zidkova[3], Juraj Lenco[1], Jiri Stulik[1], Radek Pudil[4]

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POS-01-200

Biomarkers for Duchenne Muscle Dystrophy

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POS-01-201

Over-Expressed Calponin3 by Sub-Sonic Vibration Induces Neural Differentiation of hUC-MSCs by Regulating the Ionotropic Glutamate Receptor

Hyun-Jung Kim, Jin-Hee Kim, Chan-Wha Kim

Korea University, Korea

POS-01-202

Genome-Wide Protein Parts List of Human Placenta Tissues for the Chromosome-Centric Human Proteome Project

Hyoung-Joo Lee[1], Seul-Ki Jeong[1], Keun Na[1], Ja-Young Kwon[2], Hoguen Kim[2], Jong Shin Yoo[3], Young Mok Park[3], William S. Hancock[1,4], Young-Ki Paik[1]

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POS-01-203   YI01-06

Systematic Characterization of Human Platelets in Arterial Vascular Disorders by Quantitative Proteomics

Julia M. Burkhart[1], Marc Vaudel[1], Joerg Geiger[3], Kristin Becker[1], Stepan Gambaryan[2], Walter Ulrich[2], Lennart Martens[4], Rene P. Zahedi[1], Albert Sickmann[1]

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POS-01-204

Application of Quantitative Proteomic Analysis Using Tandem Mass Tags for Discovery and Identification of Novel Biomarkers in Periodontal Disease

Sachio Tsuchida[1,2], Mamoru Satoh[1,2,4], Yusuke Kawashima[3], Kazuyuki Sogawa[1,2], Sayaka Kado[4], Setsu Sawai[1,2], Motoi Nishimura[1,2], Mayumi Ogita[5], Yasuo Takeuchi[5], Hiroaki Kobyashi[5], Akira Aoki[5], Yoshio Kodera[2,3], Kazuyuki Matsushita[1,2], Yuichi Izumi[5], Fumio Nomura[1,2]

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POS-01-205

Analysis of Amniotic Fluid Proteome and Peptidome in PPROM Pregnancies with Inflammatory Complications

Marie Vajrychova[1], Vojtech Tambor[2], Miroslav Peterek[2], Marian Kacerovsky[2,3], Jiri Stulik[1], Juraj Lenco[1]

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POS-01-206

Proteomic Analysis of Cerebrospinal Fluid Gives Insight Into the Pain Relief Through Spinal Cord Stimulation

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POS-01-207

A Proteomics Approach to the Identification of Biomarkers for Psoriasis Utilising Keratome Biopsy

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POS-01-208

Discovery, Development, and Verification of Fatty Acid Binding Protein 5 as a Serological Marker of Crohns Disease

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POS-01-209

Separation of Mycobacterial Cell Wall Extracts Responsible for the Treatment of Bladder Tumor

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POS-01-210

Identification of Biomarkers Related to Capacetibine Response in Solid Tumors by Nucleic Acids Programmable Protein Arrays (NAPPA), iFISH, and SNPs Approaches

Manuel Fuentes[1], Maria Gonzalez-Gonzalez[1], Jose Maria Sayagues[1], Jacinto Garcia[3], Juan Antonio Alcazar[3], Oscar Bengoechea[4], Joshua LaBaer[2], Orfao Alberto[1]

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POS-01-211

Human Proteome Project in Cancer

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POS-01-212

Detection of Target Antigens for Anti-Endothelial Cell Antibodies in Patients with Kawasaki Disease

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POS-01-213

A Fast, Robust, and Reproducible Proteomic Solution to Convert Human Tissue Into a Digital Data Set for Targeted Data Analysis

Tiannan Guo[1], Petri Kouvonen[1], Chiek Koh Ching[1], Ludovic Gillet[1], Witold Wolski[1], Hannes Rost[1], George Rosenberger[1], Silke Gillessen[2], Markus Jorger[2], Ben Collins[1], Alexander Leitner[1], Ruedi Aebersold[1]

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POS-01-214

Towards the Use of Mass Spectrometric Immunoassay (MSIA) in Protein-Based Diagnostics

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POS-01-215

Protein C Inhibitor Proteotypic Peptide Quantitation by LC-Free SISCAPA-MALDI Mass Spectrometry Predicts Recurrence of Prostate Cancer After Radiotherapy

Morteza Razavi[1], N. Leigh Anderson[2], Terry Pearson[1], Lisa Johnson[3], Julian Lum[3], Gary Kruppa[4], Detlev Suckau[5]

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POS-01-216

A Platform for Multiplexed Quantitative Measurements of Low-Abundant Proteins in an Assay Format by Combining Recombinant Single-Chain Antibody Fragments (scFv) with LC-SRM-MS

Fredrika Carlsson, Anna Sall, Niclas Olsson, Christer Wingren, Mats Ohlin, Helena Persson, Sofia Waldemarson

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POS-01-217

Disease Proteomics Reveals Modulation of Cell Microenvironment Due to Loss of Collagen VII

Victoria Kuettner[1,2,3], Claudia Mack[3], Kristoffer TG Rigbolt[1,2], Johannes S Kern[3], Oliver Schilling[4], Hauke Busch[1,4], Leena Bruckner-Tuderman[1,3], Joern Dengjel[1,2]

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POS-01-218

Rapid Discrimination between Methicillin-Sensitive and Methicillin-Resistant Staphylococcus Aureus Using MALDI-TOF Mass Spectrometry

Kazuyuki Sogawa[1,2], Masaharu Watanabe[3], Kenta Noda[4], Fumie Iida[2], Syunsuke Segawa[3,4], Akiko Miyabe[3], Syota Murata[3], Tomoko Saito[3], Fumio Nomura[2,3,4]

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POS-01-219

Mechanisms of Virulence in MSSA/MRSA Staphylococcus Aureus Clinical Isolates

Paola Roncada[1,2], Alessio Soggiu[2], Cristian Piras[2], Monica Monaco[3], Annalisa Pantosti[3], Marco Tinelli[4], Andrea Urbani[5], Luigi Bonizzi[2]

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POS-01-220

Analysis of HER2 Graded Breast Cancer FFPE Tissue Samples with Reverse Phase Protein Arrays

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POS-01-221   JHP-03

Phosphoproteomics of Human Liver Cancer Analyzed by 2-Dimensional Image-Converted Analysis of Liquid Chromatography and Mass Spectrometry (2DICAL)

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POS-01-222   YI03-05

Synthesis of Galactose-Deficient IgA1 O-glycans by GalNAc-Transferases: Implications for the Pathogenesis of IgA Nephropathy

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POS-01-223

Population Based Omics ? Identification of Genetic Variants Influencing the Human Plasma Proteome

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POS-01-224   PS13-01

Quantitative Mass Spectrometry (SRM/MRM) to Amyloid Peptides, Tau Protein, and Apolipoprotein E in Human Cerebrospinal Fluid for Alzheimer Disease Diagnosis

Sylvain Lehmann[1], Nicolas Barthelemy[2], Jérôme Vialaret[1], Susanna Schraen-Maschke[3], Laurent Tiers[1], Constance Delaby[1], Christophe Junot[2], Jacques Touchon[1], Nicolas Sergent[3], Audrey Gabelle[1], François Becher[2], Christophe Hirtz[1]

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POS-01-225

Quantitative Target Proteomics-Based Personalized Molecular Target Chemotherapy for Recurrent Brain Tumor

Sumio Ohtsuki[1], Wataru Obuchi[2], Mitsuyoshi Nakada[3], Chiemi Ikeda[2], Akifumi Yoshikawa[2], Yutaka Hayashi[3], Yasunori Sato[3,4], Takuya Watanabe[3], Yosuke Kawahara[3], Takayuki Hasegawa[3], Amura Sabit[3], Daisuke Kita[3], Yasuhiko Hayashi[3], Jun-ichiro Hamada[3], Tetsuya Terasaki[2]

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POS-01-226

Absolute Quantitative Analysis of Human Tear Fluid Proteome Using Wheat Germ Cell-Free Protein Synthesis System and Quantitative Mass Spectrometry

Nobuaki Takemori[1], Atsushi Shiraishi[2], Ayako Takemori[1], Masahiko Yamaguchi[2], Tomoyuki Kamao[2], Xiaodong Zheng[2], Yasuhito Hayashi[2], Yuichi Ohashi[2]

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POS-01-227   PS13-03

Development of an LC-MRM Based Assay of Prostate Specific Antigen (PSA) in Blood Samples

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POS-01-228

Proteome Analysis of Exhaled Breath Condensate for Medical Diagnostics

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POS-01-229

Plasma Protein Quantification from Dried Blood Spots Using Stable Isotope Labelled Protein Standards

Benedikt Lang[1], Christopher J. Pynn[1], Hannes Planatscher[2], Bart H.J. van den Berg[2], Frederik T. Weiss[2], Cornelia Sommersdorf[2], Martin Gamer[3], Peter Schulz-Knappe[3], Thomas O. Joos[2], Oliver Poetz[2], Dieter Stoll[1,2]

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POS-01-230

Urine Profiling of Patients with Preeclampsia

Igor Popov[1,2,3,5], Natalia Starodubtseva[1,2], Alexey Kononikhin[1,2,3], Rustam Ziganshin[4], Eugene Nikolaev[2,3,5]

[1]Research Center for Obstetrics, Gynecology, Russia, [2]Institute for Energy Problems of Chemical Physics, Russia, [3]Emanuel Institute of Biochemical Physics, Russia, [4]Institute of Bioorganic Chemistry RAS, Russia, [5]Orekhovich Institute of Biomedical Chemistry, Russia

POS-01-231

An Integrated Proteomics for Extracting Molecular Target of Malignant Gliomas

Norie Araki[1], Takashi Morikawa[1], Souhei Mizuguchi[1], Daiki Kobayashi[1], Akiko Niibori Nambu[1], Uichi Midorikawa[1], Mio Hirayama[1], Masayo Morifuji Wilson[1], Shin Kawano[3], Hideo Nakamura[2], Junichi Kuratsu[2]

[1]Dept. Tumor Genetics and Biology, Graduate School of Medical Sciences, Kumamoto University, Japan, [2]Dept. Neurosurgery, Graduate School of Medical Sciences, Kumamoto University, Japan, [3]Database Center for Life Science, Research Organization of Information and Systems

Databases and Bioinformatics

POS-01-232

Comparative Study of Global Protein Turnover in Tissues and Cell Lines

Alexandre Podtelejnikov, Michael Andersen, Christian Ravnsborg

Thermo Fisher Scientific

POS-01-233

Shotgun Proteomics Data Analysis Using Personalized Protein Sequence Database Built from RNA-Seq Results from the Same Sample

Junwoo Bae[1], Soohan Ahn[1], Daehee Hwang[2], Sanghyuk Lee[3], Sangwon Lee[4], Heejin Park[5], Eunok Paek[5]

[1]Department of Electronics and Computer Engineering, Hanyang University, Korea, [2]Institute for Systems Biology, POSTECH, Republich of Korea, [3]Department of Life Sciences, Ewha Womans University, Korea, [4]Department of Chemistry and Center for Electro- & Photo-Responsive Molecules, Korea University, Korea, [5]Department of Computer Science and Engineering, Hanyang University, Korea

POS-01-234   ★Travel Award

Proteomic Quantitative Pathway Analysis Aided Potential Target Mining of Alkaloids from Herbal Medicine

Yi Man Eva Fung, Di Hu, Chi-Ming Che

Department of Chemistry, State Key Laboratory of Synthetic Chemistry, and Open Laboratory of Chemical Biology of the Institute of Molecular Technology for Drug Discovery and Synthesis, The University of Hong Kong, China

POS-01-235

Optimal FDR Threshold Surfaces for Combined Search Engine Identification Strategies

Alex A. Henneman, Magnus Palmblad, Paul J. Hensbergen, Yassene Mohammed, Andre M. Deelder

Center for Proteomics and Metabolomics, Leiden University Medical Center, The Netherlands

POS-01-236

A Novel Approach for Processing LC-Ion Mobility-MS Metabolomics Data

G Isaac[1], M Palmer[2], M Bennett[3], JI Langridge[2], JP Shockcor[1], A Borthwick[3], Lee Gethings[1]
[1]Waters Corporation, USA, [2]Waters Corporation, Manchester, UK, [3]Nonlinear Dynamics, UK

POS-01-237

iPEACH: Integrated Protein/Gene Expression Analysis CHart

Shin Kawano[1], Akiyasu C. Yoshizawa[2], Sohei Mizuguchi[3], Norie Araki[3]
[1]Database Center for Life Science, Research Organization of Information and Systems, [2]Bioinformatics Center, Institute for Chemical Research, Kyoto University, Japan, [3]Department of Tumor Genetics and Biology, Graduate school of Medical Sciences, Kumamoto University, Japan

POS-01-238

Finding Representatives in and for Protein Classes

Markus-Hermann Koch, Anna Kusnezowa, Martin Eisenacher, Lars I. Leichert, Helmut E. Meyer

Medizinisches Proteom-Center at the Ruhr-University Bochum, Germany

POS-01-239

CAPER 2.0: An Extensible, Configurable and Interactive Workflow-Based Platform to Mine the Knowledge from the Chromosome-Assembled Human Proteome

Dan Wang, Feifei Guo, Zhongyang Liu, Lihong Diao, Liang Lu, Ping Xu, Dong Li, Fuchu He
The State Key Laboratory of Proteomics, Beijing Proteome Research Center, National Center for Protein Sciences Beijing, National Engineering Research Center for Protein Drugs, Beijing Institute of Radiation Medicine, China

POS-01-240

New Functionality for the Trans-Proteomic Pipeline: Tools for the Analysis of Proteomics Data

Luis Mendoza[1], David Shteynberg[1], Joseph Slagel[1], Michael Hoopmann[1], Terry Farrah[1], Zhi Sun[1], Brian Pratt[2], Henry Lam[3], Jimmy K. Eng[4], Alexey I. Nesvizhskii[5], Eric W. Deutsch[1], Robert L. Moritz[1]
[1]Institute for Systems Biology, USA, [2]Insilicos, LLC, USA, [3]Hong Kong University of Science and Technology, Hong Kong SAR, China, [4]University of Washington, USA, [5]University of Michigan, USA

POS-01-241

Development of Web-Based Repository System for Mass Spectrometry Data and Equipment with Links to Chromosome-Centric Human Proteome Database

Hiraku Morisawa[1], Mikako Hirota[1,3], Machiko Iwamoto[1], Yuri Miura[1], Tosifusa Toda[1,2]
[1]Research Team for Mechanism of Aging, Tokyo Metropolitan Institute of Gerontology, Japan, [2]Advanced Medical Research Center, Yokohama City University, Japan, [3]Department of Pharmaceutical Sciences, Teikyo Heisei University, Japan

POS-01-242

PCDq and H-EPD: Human Protein Complex Database and Human Protein Sequence Database Developed to Research Uncharacterized Human Proteins

Katsuhiko Murakami[1], Yoko Nagai, Tadashi Imanishi[1,2]
[1]National Institute of Advanced Industrial Science and Technology, Japan, [2]Tokai University School of Medicine, Japan

POS-01-243

Integrating ENCODE in the Spanish Human Proteome Project: A Bioinformatics Approach

Daniel Tabas-Madrid[1], Victor Segura[2], Juan Pablo Albar[3], Fernando Corrales[2], Alberto Pascual-Montano[1]

[1]Functional Bioinformatics Group, National Center for Biotechnology (CNB-CSIC), Spain, [2]Unit of Proteomics, Genomics and Bioinformatics, Center for Applied Medical Research, CIMA, University of Navarra, Spain, [3]Proteomics Facility, Centro Nacional de Biotecnologia-Consejo Superior de Investigaciones Cientificas (CNB-CSIC), ProteoRed-ISCIII, Spain

POS-01-244

An Automated Workflow for Enterprise-Level High-Throughput Proteomics Analysis

Joe Slagel, Eric Deutsch, Robert L. Mortiz

Institute for Systems Biology, USA

POS-01-245

Development of "Proteome Tools" -A Web Application Suite for Proteomics Experiments

Tsuyoshi Tabata[1], Akiyasu C. Yoshizawa[2], Yuki Ohta[2], Maiko Kusano[2], Noboru Yamamoto[1], Ken Aoshima[1], Shigeki Kajihara[2], Yoshiya Oda[1], Koichi Tanaka[2]

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POS-01-246

Identification and Label-Free Quantitation of Mass Spectrometric Data Via Freely Available Plug-In Software, Mass++

Satoshi Tanaka[1], Yuichiro Fujita[1], Akiyasu C. Yoshizawa[1], Shin-ichi Utsunomiya[1], Shigeki Kajihara[1], Mitsuru Fukuda[2], Masayuki Ikawa[2], Kentaro Takahashi[2], Tsuyoshi Tabata[2], Ken Aoshima[2], Yoshiya Oda[2], Koichi Tanaka[2]

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POS-01-247

PRIDE-Q: Providing a Condensed and Quality-Scored View of Public MS Proteomics Data in the PRIDE Database

Joseph M. Foster[1], David Ovelleiro[1], Antonio Fabregat[1], Johannes Griss[1], Qing-Wei Xu[1,2], Javier Contell[1], Florian Reisinger[1], Henning Hermjakob[1], Juan Antonio Vizcaino[1]

[1]EMBL-European Bioinformatics Institute, Wellcome Trust Genome Campus, UK, [2]College of Computer, Hubei University of Education, China

POS-01-248

Unrestricted Modification Search in Formalin-Fixed Paraffin-Embedded Samples Using MS/MS Spectrum Library

Ying Zhang[1,2], Markus Muller[2], Bo Xu[1], Yutaka Yoshida[1], Sameh Magdeldin[1], Eishin Yaoita[1], Tadashi Yamamoto[1]

[1]Department of Structural Pathology, Institute of Nephrology, Graduate School of Medical and Dental Sciences, Niigata University, Japan, [2]Swiss Institute of Bioinformatics, Faculty of Medicine of University of Geneva, Switzerland

POS-01-249

Cross-Organism Comparison of the Uniqueness in Protein Terminal Region Sequences

Akiyasu C. Yoshizawa, Yuko Fukuyama, Shigeki Kajihara, Hiroki Kuyama, Koichi Tanaka

Koichi Tanaka Laboratory of Advanced Science and Technology, Shimadzu Corporation, Japan

POS-01-250

iProX: Integrated Proteome Resources

Jie Ma[1,2], Songfeng Wu[1,2], Tao Chen[1,2], Weimin Zhu[1,2], Yunping Zhu[1,2]

[1]State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, China, [2]National Engineering Research Center for Protein Drugs, China, [3]Taicang Institute for Life Sciences Information, China

POS-01-251

"Antibody Ranker" to Find Antibodies Used in Recent Publication

<u>Naohiko Kinoshita</u>, Masaaki Nameta, Yutaka Yoshida, Ying Zhang, Bo Xu,
Sameh Magdeldin, Hidehiko Fujinaka, Eishin Yaoita, Tadashi Yamamoto

Institute of Nephrology, Graduate School of Medical and Dental Sciences, Niigata University, Japan

POS-01-252

Identification of Short Terminal Motifs Enriched by Antibodies Using Peptide Mass Fingerprinting

<u>Hannes Planatscher</u>, Frederik Weiss, Bart H.J. Van Den Berg, David Eisen, Thomas Joos,
Oliver Poetz

Natural and Medical Sciences Institute at the University of Tuebingen

POS-01-253

Data Processing Within Multi '-OMICS' Projects

<u>Michael Kohl</u>[1], Dominik A. Megger[1], Martin Trippler[2], Hagen Meckel[1], Maike Ahrens[1],
Thilo Bracht[1], Frank Weber[3], Andreas-Claudius Hoffmann[4], Hideo A. Baba[5],
Barbara Sitek[1], Jörg F. Schlaak[2], Helmut E. Meyer[1], Christian Stephan[1,6],
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Transplantation Surgery, University Hospital of Essen, Germany, [4]Department of Medicine (Cancer
Research), Molecular Oncology Risk-Profile Evaluation, University Hospital of Essen, Germany,
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Universitaetsstrasse 136, D-44799 Bochum, Germany

POS-01-254

New 2-Dimensional Image-Converted Analysis of Liquid Chromatography and Mass Spectrometry (2DICAL) Optimized for High-Performance Mass Spectrometry

<u>Tomohiro Sakuma</u>[1], Miho Banno[1], Masahiro Kamita[2], Tesshi Yamada[2], Masaya Ono[2]

[1]Mitsui Knowledge Industry Co.,Ltd., Japan, [2]National Cancer Center Research Institute

POS-01-255

Development of a Tool for Label-Free Quantitation of Proteins Identified by Mass Spectrometry and Verification of the Results

<u>Toshikazu Ikoma</u>, Xu Bo, Naohiko Kinoshita, Tomizo Oyama, Tomoo Makiguchi,
Zhang Ying, Yutaka Yoshida, Eishin Yaoita, Tadashi Yamamoto

Department of Structural Pathology Institute of Nephrology Graduate School of Medical and Dental
Sciences Niigata University, Japan

POS-01-256

A Comparison of Two Different Library Construction Processes

<u>Wenyuan Lu</u>[1,2], Yang Zhang[2], Pengyuan Yang[1,2]

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Medical School, Fudan University, China

POS-01-257

'exKRT': Automated Extraction Analysis of Contamination in Proteomic

<u>Tomoo Makiguchi</u>, Bo Xu, Naohiko Kinoshita, Ying Zhang, Toshikazu Ikoma, Eishin Yaoita,
Yutaka Yoshida, Tadashi Yamamoto

Department of Structural Pathology Institute of Nephrology Graduate School of Medical and Dental
Sciences Niigata University, Japan

POS-01-258   PS21-03

Estimation of Protein Species Number for Mammalian, Bacteria, Insecta and Yeast

<u>Elena Ponomarenko</u>, Stanislav Naryzhny, Ekaterina Poverennaya, Mikhail Pyatnitskii,
Andrey Lisitsa, Alexander Archakov

Institute of Biomedical Chemistry of RAMS, Russia

POS-01-259

How to Submit MIAPE Compliant Data to ProteomeXchange Consortium

Salvador Martinez-Bartolome, J. Alberto Medina-Aunon, Miguel Angel Lopez-Garcia, Carmen Gonzalez-Tejedo, Severine I. Gharbi, Rosana Navajas, Juan Pablo Albar

Centro Nacional de Biotecnologia - CSIC, ProteoRed-ISCIII, Spain

POS-01-260

Update on the Transcriptomic and Proteomic Expression Data for the Placenta Within the GenomewidePDB

Seul-Ki Jeong[1], Hyoung-Joo Lee[1], Keun Na[1], William S. Hancock[2], Young-Ki Paik[1]

[1]Yonsei Proteome Research Center, Yonsei University, Korea, [2]Northeastern University, USA

POS-01-261

Novel Data Analysis Pipeline Based on Mass Spectrum Sequential Subtraction for High-Throughput Proteogenomics

Satomi Miyake, Mohamed Helmy, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

Kyoto University, Japan

POS-01-262

Benefits and Challenges of Combining Search Results from Multiple Algorithms

David Shteynberg, Eric Deutsch, Joseph Slagel, Luis Mendoza, Robert Moritz

Institute for Systems Biology, USA

POS-01-263

Solving the Bioinformatics Bottlenecks of Massive Storage & Data Distribution, Huge Computational Needs, and Flexible and Fast Reporting

Gautam Saxena[1], Rafael Dugarte[1], Christine Jellinek[3], Vidya Venkat[3], Jennifer Van Eyk[3], Scott Kuzdzal[2]

[1]Integrated Analysis, USA, [2]Shimadzu Scientific, Columbia, MD, [3]Johns Hopkins Medical School, MD

POS-01-264

A New Algorithm for Peptide *De Novo* Sequencing with Multiple Complementary Spectra

Mingjie Xie[1], Lian Yang[1], Bin Ma[2]

[1]Bioinformatics Solutions Inc., [2]University of Waterloo, Canada

POS-01-265

Peptide *De Novo* Sequencing Result Validation

Lian Yang[1], Baozhan Shan[1], Bin Ma[2]

[1]Bioinformatics Solutions Inc., [2]University of Waterloo, Canada

POS-01-266

PAA - A New R Package for Autoimmune Biomarker Discovery with Protein Microarrays

Michael Turewicz[1], Maike Ahrens[1], Caroline May[1], Dirk Woitalla[2], Beate Pesch[3], Swaantje Casjens[3], Helmut E. Meyer[1], Christian Stephan[1], Martin Eisenacher[1]

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POS-01-267

Computational Studies of Post-Translational Modifications

Zexian Liu[1], Jian Ren[2], Yu Xue[1]

[1]Huazhong University of Science and Technology, China, [2]Sun Yat-sen University, China

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POS-01-268

GlycoPepDecipher: Automated Identification of Intact *N*-Linked Glycopeptides

Chen-Chun Chen[1,4], Cheng-Wei Cheng[2], Ke-Shiuan Lynn[2], Wan-Chih Su[1,3], Chia-Ying Cheng[2], Wen-Lian Hsu[2], Chi-Huey Wong[1,4], Yu-Ju Chen[1,3], Ting-Yi Sung[2]

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POS-01-269

Bioinformatics Study for Elucidation of Lectin Recognition Patterns

Masae Hosoda, Yukie Akune, Kiyoko F. Aoki-Kinoshita

Graduate School of Engineering, Soka University, Japan

POS-01-270   PS23-04

Firmiana: An Integrated Platform for Mass Spectrometry-Based Proteomics Studies Based on Galaxy Framework

Jun Qin[2], Bingxin Lu[1], Peng Li[1], Ruichao Xue[1], Lihong Diao[2], Wei Zhang[2], Chen Ding[2], Jinwen Feng[1], Ruifang Cao[1], Juan Yang[1], Dong Li[2], Wanlin Liu[2], Cheng Chang[2], Naiqi Qiu[1], Yu Du[2], Tieliu Shi[1]

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POS-01-271

A Simple and Fast Label-Free Quantitation Algorithm for LC-MS

Ken Aoshima[1], Masayuki Ikawa[1], Takayuki Kimura[1], Mitsuru Fukuda[1], Kentaro Takahashi [1], Tsuyoshi Tabata [1], Satoshi Tanaka [2], Yuichiro Fujita[2], Akiyasu C. Yoshizawa[2], Shin-ichi Utsunomiya[2], Shigeki Kajihara[2], Koichi Tanaka[2], Yoshiya Oda[1]

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POS-01-272   PS21-04

Isobar: Making Sense Out of Protein and Modified Peptide iTRAQ/TMT Quantitative Data

Florian P. Breitwieser, Jacques Colinge

CeMM - Research Center for Molecular Medicine of the Austrain Academy of Sciences, Austria

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POS-01-273   PS21-05

"FindPairs" - The Protein Quantification Module of the PeakQuant Software Suite

Martin Eisenacher[1], Michael Kohl[1], Sebastian Wiese[2], Romano Hebeler[1,3], Helmut E. Meyer[1], Bettina Warscheid[2,4], Christian Stephan[1,5]

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POS-01-274

Approximative Statistical Approach for Absolute Quantification of the Human Chromosome 18 Proteins

Ekaterina V. Ilgisonis, Arthur T. Kopylov, Elena A. Ponomarenko, Andrey V. Lisitsa

Institute of Biomedical Chemistry

POS-01-275

Condenser: A Statistical Aggregation Tool for Multi-Sample Quantitative Proteomic Data

Anders Knudsen[1], Tue Bennike[1], Henrik Kjeldal[1], Svend Birkelund[1], Daniel Otzen[2], Allan Stensballe[1]

[1]Aalborg University, Denmark, [2]Aarhus University

Bioinformatic Workflow for Chr16 Characterization Using Proteomic Shotgun and Transcriptomic RNA-Seq Experiments

Elizabeth Guruceaga[1], Daniel Tabas-Madrid[2], Mariana B Monteiro[1], Salvador Martinez-Bartolome[3], Juan Pablo Albar[3], Fernando J Corrales[1], Alberto Pascual-Montano[2], Victor Segura[1]

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ProteomeXchange: Globally Coordinating Proteomics Data Dissemination

Henning Hermjakob[1], Juan Antonio Vizcaino[1], Eric W. Deutsch[2], The ProteomeXchange Consortium[1,2]

[1]EMBL-European Bioinformatics Institute, Wellcome Trust Genome Campus, UK, [2]Institute for Systems Biology, USA

Development of a Genome Annotation Pipeline of Protein-Coding Genes of the Liverwort, Marchantia paleacea var. diptera for *De Novo* RNA-Seq

Kazuo Ishii[1], Toshinori Kozaki[1], Tomomi Nakagawa[2]

[1]Tokyo University of Agriculture and Technology, Japan, [2]Meiji University, Japan

Improving the Efficiency in Obtaining True Protein IDs with Biological Significance in Protein Biomarker Discovery Platforms

Kyoko Kojima, Gregory J. Bowersock, James A. Mobley

University of Alabama at Birmingham, USA

Automatic Extraction of Correlation of Annotation Terms in Databases to Find Similar Concepts, Synonyms, and Multifunction

Katsuhiko Murakami[1], Tadashi Imanishi[2]

[1]National Institute of Advanced Industrial Science and Technology, Japan, [2]Tokai University, Japan

Electrophoresis-Based Proteomics

Proteome Analysis of Fenitrothion Exposed Adrenal and Pituitary Gland

Narumi Hirosawa[1], Takeshi Sakamoto[2], Yasushi Sakamoto[1]

[1]Biomedical Research Center, Saitama Medical University, Japan, [2]Faculty of Pharmaceutical Scieneces, Josai University, Japan

Proteomic Analysis of C14-Sphingosine-Triggered Germination of the Entomopathogenic Fungus, Nomuraea Rileyi

Tomofumi Nakajima[1], Takahiro Noda[2], Tomohiro Araki[1]

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POS-01-283

Global Protomap Profiling for Biomarker Discovery of Human Hepatocellular Carcinoma

Goro Terukina[1], Masato Taoka[1], Yoshio Yamauchi[1], Chiharu Fujita[1], Tadashi Kondo[2], Toshiaki Isobe[1]

[1]Department of Chemistry, Graduate School of Science and Engineering, Tokyo Metropolitan University, Japan, [2]Division of Pharmacoproteomics, National Cancer Center Research Institute, Japan

POS-01-284

Comparative Proteomic Analysis of Virulence Variations in *Xanthomonas campestris* pv. *campestris* Strain 17, 11A and P20H

Tao-Shan Chang, Chien-Chen Lai

Institute of Molecular Biology, National Chung-Hsing University, Taiwan

POS-01-285

Proteins Expression Clustering of Normal and Alzheimeric Rat Hippocampus Treated with Lavandula Angustifolia

Hakimeh Zali[1], Mostafa Rezaei Tavirani[2]

[1]Faculty of Paramedical Sciences, Shahid Beheshti University of Medical Sciences, Iran, [2]Proteomics Research Center, Faculty of Paramedical Sciences, Shahid Beheshti University of Medical Sciences, Iran

POS-01-286

Proteomic Analysis of the Cellular Signal Regulation Mechanism by Cholesterol Sulfation

Toshihiro Yoshimura[1], Katsuhisa Kurogi[1], Ming-Cheh Liu[2], Masahito Suiko[1], Yoichi Sakakibara[1]

[1]Department of Biochemistry and Applied Biosciences, Faculty of Agriculture, University of Miyazaki, Japan, [2]Department of Pharmacology, College of Pharmacy and Pharmaceutical Sciences, The University of Toledo, Spain

POS-01-287   ★Travel Award

Immunoproteomics Analysis of Antibody Response to Proteins of *Candida tropicalis*

Pey Yee Lee[1], Lay Harn Gam[2], Rozita Rosli[3], Pei Pei Chong[1]

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POS-01-288

Mechanistic Analysis on Potent Intermolecular Isomarase Activity of Protein Disulfide Isomerase-P5 with Down-Regulation in Sperm Maturation Highlighted by Electrophoresis-Based Proteomics

Miho Miyakawa[1], Shuntaro Shigihara[2], Gosuke Zukeran[1], Tetsutaro Tomioka[1], Akihiro Totsuka[2], Tasuku Yoshino[1], Mamoru Satoh[3], Sayaka Kado[6], Machiko Iwamoto[4], Yuri Miura[4], Kuniko Akama[1,5]

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POS-01-289

Proteomic Analysis of Cell Populations in Artificial and Clinical Peritoneal Dialysis Effluents

Anton Lichtenauer[1,2], Rebecca Herzog[2], Andreas Vychytil[1], Christoph Aufricht[1], Klaus Kratochwill[1,2]

[1]Medical University of Vienna, Austria, [2]Zytoprotec GmbH, Austria

POS-01-290

Basic Nuclear Proteins Alteration in Neurodegenerative Disorder

Beena Hasan[1,2], Nikhat Ahmed Siddiqui[1], Abid Azhar[2], Saadia Zahid[1]

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Monday, September 16

Imaging Mass Spectrometry and Mass Microscopy

POS-02-001

Bridging the Gap Between Imaging Mass Spectrometry and LC-MS/MS Identification

Ove Johan Ragnar Gustafsson[1], Stephan Meding[1], Karina Martin[1], James S Eddes[1], Sandra Hack[1], Tomas Koudelka[1], Martin K Oehler[2], Shaun R McColl[1], Peter Hoffmann[1]

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POS-02-002

Detection of Individual Cells in Tissue Using MALDI-TOF Imaging at $10\,\mu m$ Pixel Size

Eckhard Belau[1], Jane-Marie Kowalski[2], Janine Rattke[1], Alice Ly[3], Soeren-Oliver Deininger[1], Detlev Suckau[1], Axel Walch[3], Marius Ueffing[3], Toshiji Kudo[4], Michael Becker[1]

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POS-02-003

MALDI-FTICR Tissue Image Analysis of Rat Testis at $10\,\mu m$ Pixel Size and 200 k Mass Resolution - High Mass Resolution x High Spatial Resolution

Jens Fuchser[1], Eckhard Belau[1], Sören-Oliver Deininger[1], Michael Becker[1], Yoshihiko Morishita[2], Detlev Suckau[1]

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POS-02-004

Spatial Correlation Combined with Hierarchal Clustering Analysis for Reducing Complex Multi-Dimensional MALDI Imaging Dataset

K Nagase[1], M Towers[2], K Neeson[2], E Claude[2], T Paxton[1]

[1]Nihon Waters, Japan, [2]Waters Corporation, Manchester, UK

POS-02-005

Computational and Experimental Pipeline for MRI-Compatible Three-Dimensional MALDI Imaging Mass Spectrometry

Janina Oetjen[1,3], Michaela Aichler[4], Dennis Trede[1,2], Michael Becker[5], Jan Strehlow[6], Stefan Schiffler[1,2], Judith Berger[7], Stefan Heldmann[7], Stefan Wirtz[6], Klaus Steinhorst[1], Michael Gottschalk[8], Nicole Posorski[9], Jan Hendrik Kobarg[1,2], Andrey Dyatlov[2], Detlev Suckau[5], Takashi Nirasawa[10], Ferdinand von Eggeling[9], Axel Walch[4], Peter Maass[1,2], Theodore Alexandrov[1,2,3]

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POS-02-006

Investigation of Different Hierarchal Clustering Approaches for Protein Identification Directly from Tissue Section in a MALDI Imaging Experiment

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POS-02-007

ImageID: A New Spatially Resolved Proteomics Approach Providing Access to Disease Biomarker Proteoforms

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POS-02-008

A Study of Drug Distribution in Malignant Melanoma Tissue by MALDI Mass Spectrometry Imaging for Evaluation of Drug Efficacy

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POS-02-009   PS06-04

Peptide MALDI Imaging - How to Get Most Out of Your Sample?

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Immunoproteomics and Autoimmune Diseases

POS-02-010

Comparative Analyses of Peptidome and Proteome of CSF Samples from Patients with Guillain-Barre Syndrome and with Non-Neurological Diseases

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POS-02-011

Protein Profiles of Peripheral Blood Mononuclear Cells as a Biomarker for Behcet's Disease

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POS-02-012

Identification of Naturally Processed MHC Class I-Restricted HIV Epitopes Presented by Human HIV-Infected Cells

Marijana Rucevic[1], Georgio Kourjian[1], Majahonkhe Shabangu[2], Julie Boucau[1], Carl Kadie[1,3], Jonathan Carlson[3], David Heckerman[3], Bruce D. Walker[1,4], Sylvie LeGall[1]

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Immuno-Proteomics of *Helicobacter pylori* Antigens for IgG Antibodies in *H. pylori*-Positive Japanese Child Sera

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Proteomic Analysis of HLA Class I Binding Peptides from Prostate Cancer Cell Lines to Seek for Novel Cancer Vaccine and Cancer Biomarker

Yuko Kamata[1,2], Akiko Kuhara[1], Takeo Iwamoto[3], Takahiro Kimura[2], Kazumi Hayashi[1], Shigeo Koido[4], Shin Egawa[2], Sadamu Homma[1]

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Immune Complexome Analysis for Identifying the Immune Complex Antigens

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Shotgun Proteomic Analysis of Human Multiple Sclerosis Lesions

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Identification of Novel ACPA Targets in Rheumatoid Arthritis Synovial Tissues Using 2D Gel Electrophoresis and Mass Spectrometry

Elena Ossipova[1], Ganna Oliynyk[1,2], Catia Cerqueira[1], Susanne Becker[3], Jimmy Ytterberg[4], Gert Auer[3], Lars Klareskog[1], Per-Johan Jakobsson[1]

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Identification of Minor Antigens by Quantitative Proteomics and Its Impact on Next Generation Leukemia Immunotherapy

Pierre Thibault[1,2], Dev Sriranganadane[1], Diana Granados[1,3], Celine Laumont[1,3], Tariq Douada[1,4], Olivier Caron-Lizotte[1], Antoine Zieger[1,4], Sebastien Lemieux[1,5], Claude Perreault[1,3]

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POS-02-020

Extensive Phenotypically Characterization of Exosomes Derived from Activated, Non-Activated APCs and T-Cells Using an Extracellular Vesicle (EV) Array

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POS-02-021

Systems-Level Analysis of Proteolytic Events and Post-Translational N-Acetylation *In Vivo* in Increased Vascular Permeability and Complement Activation in Skin Inflammation Revealed by N-Terminomics Analyses

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POS-02-022

Comprehensive Analysis of Aberrantly Glycosylated Proteins in Rheumatoid Arthritis

Toshiyuki Sato[1], Mitsumi Arito[1], Manae S. Kurokawa[1], Yukiko Takakuwa[2], Seido Ooka[2], Kouhei Nagai[3], Hiroshi Nakamura[4], Nobuko Iizuka[1], Naoya Suematsu[1], Kazuki Okamoto[1], Tomohiro Kato[1]

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POS-02-023

Proteomic Analysis of Effects of Antirheumatic Drugs on Exosomes Derived from Synovial Sarcoma Cells

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POS-02-024

Ultra High-Density Peptide Microarrays Reveal a Receptor Domain as Novel Autoimmunity Target in Multiple Sclerosis

Peter Nilsson, Arash Zandian, Bjorn Forsstrom, Burcu Ayoglu, Anna Haggmark, Jochen M Schwenk, Mathias Uhlen

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POS-02-025

Differential Proteomic Analysis of Human Hippocampal Regions of Interest (CA1, CA2, CA3, fascia dentata) - Relevance for Alzheimer's Disease

Fouzi El Magraoui[1], Helmut Heinsen[2], Thomas Mastalski[1], Svenja Seger[1], Martin Eisenacher[1], Renata E. Leite[3], Lea T. Grinberg[4], Katja Kuhlmann[1], Helmut E. Meyer[1], Andreas Schroetter[1]

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POS-02-026

Global Quantitative Analysis of IL-2 and IL-15 Signaling Pathways

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LC-MS/MS-Based Large-scale Comprehensive Proteomics

POS-02-027

Improving Chr-16 Proteins Coverage with High Confidence and MIAPE Compliant MS Data

Manuel M. Sanchez del Pino[1], J. Alberto Medina-Aunon[2], Luz Valero[1], Severine I. Gharbi[2], Carmen Gónzalez-Tejedo[2], Kerman Eloria[3], Jesus M. Arizmendi[3], Felix Elortza[4], Mikel Azkargorta[4], Montserrat Carrascal[6], Joaquin Abian[6], Ignacio Casal[5], Eliandre Olivera[7], Nuria Colomé[8], Francesc Canals[8], Fernando J. Corrales[9], Juan P. Albar[2]

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POS-02-028

Dissecting Subcellular Compartments for Deep Proteome Coverage of Chromosome 16 in T Cells

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POS-02-029

First Draft of the Human Proteome

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POS-02-030

Identification and Characterization of Cow's Milk Proteins from the Rat Intestinal Lymph Using a Proteomic Strategy

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POS-02-031

LC Retention Behavior of Tryptic Peptides in Proteomics LC-MS

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POS-02-032

Maximizing Spectrum Identification Rate in Shotgun Proteomics on the Q Exactive Mass Spectrometer

Yue Xuan, Andreas Kuehn, Eugen Damoc, Markus Kellmann

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Proteomic Analysis of the *abi3* Deletion in *Physcomitrella patens*

Izumi Yotsui[1,2], Satoshi Serada[3], Tetsuji Naka[3], Masashi Saruhashi[2,5], Kenji Kuramoto[2], Teruaki Taji[2], Takahisa Hayashi[2], Ralph Quatrano[4], Yoichi Sakata[2]

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Proteomics Analysis of USP20 for Identifying Its Functions Through the Characterization of Putative Substrates

So-Ra Kim, Jang-Joon Park, Ji-Hyun Yun, Da-Yea Park, Kwang-Hyun Baek
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The Effects of 5-Fluorouracil on the Proteome of Colon Cancer Cells

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Targeting Cancer Metastasis Using Global, Quantitative and Integrative Network Biology

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Profiling and Annotation of Human Kidney Glomerulus Proteome

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Unraveling the Role of Progesterone in Cerebral Aneurysm Among Postmenopausal Women: Utilizing HBMECs

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Protein Profile of HaCaT Cells Under UV Radiation and Lipoic Acid Treatment

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Protein Profile of Human Plasma After Acrylamide Exposure

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POS-02-041

Comprehensive Peptide Searching Workflow to Maximize Protein Identifications

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POS-02-042

Comparative Proteogenomic Analysis of *Streptococcus suis* by High Resolution Mass Spectrometry

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POS-02-043

Analysis of the First Draft of the Human Proteome with ProteomicsDB

Mathias Wilhelm[1,2], Judith Schlegl[2], Amin Moghaddas Gholami[1], Hannes Hahne[1], Joos-Hendrik Boese[2], Marcus Lieberenz[2], Mikhail Savitski[3], Yuval Morad[2], Lars Butzmann[2], Emanuel Ziegler[2], Anton Niadzelka[2], Eyk Kny[2], Helmut Cossmann[2], Siegfried Gessulat[2], Marcus Bantscheff[3], Anja Gerstmair[2], Franz Faerber[2], Bernhard Kuster[1]

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POS-02-044

Molecular Signatures of Long-Lived Proteins: Autolytic Cleavage Adjacent to Serine Residues and Peptide Laddering

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POS-02-045

Proteomics Study of Serum from Patients with Acute Coronary Syndrome

Duc Dan Pham[1], Dinh Minh Pham[1], Thi Huyen Bui[1], Huu Chi Do[1], Thai Thuong Tran[1], Thi Dung Nguyen[1], Thi Bich Thao Le[1], Minh Hai Dang[2], Doan Loi Do[2], Bich Nhi Nguyen[1], Van Chi Phan[1]

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POS-02-046

Preparation of Meter-Scale Monolithic Silica Capillary Column Modified with Urea Functional Group for Hydrophilic Interaction Chromatography and Its Application to One-Shot Proteomics Approach

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POS-02-047

Precise Column Temperature Control Enables Improved Protein Identifications in Proteomics Shot-Gun Sequencing Applications

Xiaoyue Jiang, Yi Zhang, Andreas FR Huhmer
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POS-02-048

Metaproteomic Analysis of Methanogens in the Thermophilic Reactor Treating Terephthalate at Different Loading

Yun-Chiao Chou, Hung-Jen Huang, Feng-Yau Wu, Jer-Horng Wu
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POS-02-049

Comprehensive Analysis of Downstream Targets of the Novel Protein E4TF-1 Binding Methyltransferase (EBM)

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POS-02-050

In-Depth Phosphoproteomic Analysis of Colorectal Cancer Stem Cells

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POS-02-051

Global Characterization of the Proteome and Phosphoproteome in Human Glioblastoma Initiating Cells by High-Resolution Mass Spectrometry

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POS-02-052

Dynamic Phosphoproteomic Profile of Brown Adipose Tissue Stimulated with Cold Temperation

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POS-02-053

Unveiling Phosphoproteome by pY-Enhanced Phosphopeptide Enrichment Coupled with High Resolution Capillary LC-MS

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POS-02-054

SILAC Based Quantitative Phosphoproteome Analysis of INS-1E Pancreatic Beta-Cells to Unravel the Mechanism of Insulin Secretion

Jia-Shu Tang, Qing-Run Li, Jia-Rui Wu, Rong Zeng
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POS-02-055

Establishment of LC/MS/MRM Assay for Glycopeptide Quantification of Human Serum Prostate Specific Antigen (PSA)

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POS-02-056

Enhanced Protein N-acetylation Analysis by SCX and Dimethyl Labeling and Its Application to Discrimination of Protein Isoforms

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POS-02-057

Elimination of the Last Valid Excuse for Not Testing Every Cellular Proteome Dataset for Viral Proteins

Alexey Chernobrovkin, Roman Zubarev
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POS-02-058 YI02-01

Applying SWATH-MS to Dissect the Variability and Heritability of the Human Plasma Proteome

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POS-02-059

Comparative Proteomics of *Thermococcus onnurineus* NA1: Insights Into the Sulfur Metabolism of a H2-Producing Hyperthermophilic Archaeon

Yoon-Jung Moon[1], Joseph Kwon[2], Sung-Ho Yun[1], Hye Li Lim[1], Sung Gyun Kang[3], Jung-Hyun Lee[3], Jong-Soon Choi[1], Seung Il Kim[1], Young-Ho Chung[1]
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POS-02-060

Proteomic Analysis of *Mycobacterium tuberculosis* Infection of Human Macrophages

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POS-02-061

Improvement of Rat Urinary Proteomics by a Differential Precipitation of Proteins

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POS-02-062

Towards Comprehensive Proteomic Characterization of Human Saliva and Investigation of Its Diagnostic Potential

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POS-02-063

Rapid and Deep Coverage in Single-Dimension Shotgun Human Proteomics

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POS-02-064

An Established One Dimensional LC-MS/MS Methods and Using It in Quantification Proteomics

Xuefei Yin[1], Xiaohui Liu[1,2], Yang Zhang[2], Huali Shen[1,2], Haojie Lu[1,2], Pengyuan Yang[1,2]

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Medicinal Plant and Agricultural Proteomics for Human Health

POS-02-065   PS33-07

Quantitative MS[E] Proteomics as a Tool for the Determination of Clinically Relevant Proteins in Wheat Grain

Lubica Uvackova[1], Ludovit Skultety[2,3], Slavka Bekesova[2], Scott McClain[4], Martin Hajduch[1]

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POS-02-066

Phosphoproteome Analysis of *Lotus japonicus* Seeds

Yoko Ino[1], Akiyo Ishikawa[1], Ayako Nomura[1], Hideyuki Kajiwara[2], Hisashi Hirano[1]

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POS-02-067

The Wheat Chloroplastic Proteome

Abu Hena Mostafa Kamal[1], Cho Kun[2], Jong-Soon Choi[3,4], Kwang-Hee Bae[1], Setsuko Komatsu[5], Nobuyuki Uozumi[6], Sun Hee Woo[7]

[1]Research Center for Integrative Cellulomics, Korea Research Institute of Bioscience and Biotechnology, Korea, [2]Division of Mass Spectrometry Research, Korea Basic Science Institute, Korea, [3]Division of Life Science, Korea Basic Science Institute, Korea, [4]Graduate School of Analytical Science and Technology, Chungnam National University, Korea, [5]National Institute of Crop Science, NARO, Japan, [6]Department of Biomolecular Engineering, Graduate School of Engineering, Tohoku University, Japan, [7]Department of Crop Science, Chungbuk National University, Korea

POS-02-068

Unraveling the Proteome of Sugarcane Leaves by Mass Spectrometric Analysis

Eduardo Shigueo Kitano[1], Andre Zelanis[1], Savio de Siqueira Ferreira[2], Milton Yutaka Nishiyama Junior[2], Glaucia Mendes Souza[2], Solange Maria de Toledo Serrano[1]

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POS-02-069

Quantitative Subcellular Proteomics Reveals that Phytohormone Mediated Mechanism Is Involved in the Flooding Tolerance of Soybean

Setsuko Komatsu, Yohei Nanjo

National Institute of Crop Science, National Agriculture and Food Research Organization

POS-02-070

Proteomic Analysis of the Seed Development in *Jatropha curcas*: From Carbon Flux to the Lipid Accumulation

Hui Liu[1], Setsuko Komatsu[2], Shihua Shen[1]

[1]Institute of Botany, the Chinese Academy of Sciences, China, [2]National Institute of Crop Science, Japan

POS-02-071

Mutation of Nucleotide Pyrophosphatase/Phosphodiesterase 1 Stimulates Accumulation of Starch in Rice Seedlings Under High CO_2 Concentration

Takahiro Masui[1,2], Takuya Inomata[2], Maiko Sasaki[2], Kentaro Kaneko[2], Toshiaki Mitsui[1]

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POS-02-072

Identification and Characterization of MARK, MAMP Responsive Phosphoprotein for Appropriated ROS Kinetics, in *Arabidopsis*

Hidenori Matsui, Yuko Nomura, Ken Shirasu, Hirofumi Nakagami

RIKEN Center for Sustainable Resource Science, Japan

POS-02-073

Analysis of Mechanism for Light Irradiation-Mediated Enhancement of Soybean Flooding Tolerance by Comparative Proteomics and Transcriptomics

Yohei Nanjo[1], Kyonoshin Maruyama[2], Setsuko Komatsu[1]

[1]NARO Institute of Crop Science, [2]Japan International Research Center for Agricultural Sciences, Japan

POS-02-074

Analysis of Flooding Stress Response Mechanism in Soybean Using Gel-Based and Gel-Free Proteomics Techniques

Rashid Hamid[1,2], Setsuko Komatsu[3], Katsumi Sakata[2]

[1]Department of Bioinformatics Muhammad Ali Jinnah University Islamabad, Pakistan, [2]Maebashi Institute of Technology, Japan, [3]National Institute of Crop Science, Japan

POS-02-075

Functional Proteomics Reveals Tanshinone IIA Induced Apoptosis of Activated Hepatic Stellate Cells

Tai-Long Pan

School of Traditional Chinese Medicine, Chang Gung University, Taiwan

POS-02-076

Comparative Proteome Analysis of Roots in Drought-Sensitive and Drought-Tolerant Rapeseed and Their Hybrid F1 Line Under Drought Stress

Payam Pour Mohammadi[1], Setsuko Komatsu[2]

[1]Ramin University of Agriculture and Natural Resources, Iran, [2]National Institute of Crop Science, Japan

POS-02-077

Differential Omics Approach on a Metabolic Network Outlined Flooding-Response Mechanisms in Soybean

Katsumi Sakata[1], Kentaro Ishige[1], Naoki Shirasaka[1], Setsuko Komatsu[2]

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POS-02-78

Investigation of Rice Proteomic Change in Response to Microgravity

Jing Pan, Ting Bi, Weining Sun

Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Science

POS-02-079

In-Depth Proteome Analysis of Developing Seeds of *Jatropha curcas*

Mohib U. Shah[1], Camila B. Pinheiro[1], Fabio C.S. Nogueira[2], Gabriel D.T. Araujo[2], Emanoella L. Soares[1], Paulo C. Carvalho[3], Magno Junqueira[2], Gilberto B. Domont[2], Francisco A.P. Campos[1]

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POS-02-080

Proteomic Analysis of the Japanese Crested Ibis

Toshiaki Mitsui[1], Kentaro Kaneko[2], Yoshinori Kaneko[3], Hideaki Yamashiro[4], Takahisa Yamada[4], Toshie Sugiyama[4], Maiko Sasaki[2], Yoichi Matsuda[5], Mitsuru Oyanagi[2,6,7]

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POS-02-081

Proteome Analysis of Roots of Wheat Seedlings Under Aluminum Stress

Sun Hee Woo[1], Myeong Won Oh[7], Abu Hena Mostofa Kamal[1], Swapan Kumar Roy[1], Kun Cho[3], Seong-Woo Cho[4], Chul-Soo Park[5], Jong-Soon Choi[6], Setsuko Komatsu[7]

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POS-02-082

Transcriptome and Quantitative Proteome Analyses Reveal Molecular Mechanism Associated with the Low Silk Production of Silkworm *Bombyx mori*

Shao-hua Wang[1], Zheng-ying You[1], Lu-peng Ye[1], Jiaqian Che[1], Qiujie Qian[1], Jianshe Liang[1], Ake Liu[1], Yohel Nanjo[2], Setsuko Komatsu[2,3], Bo-xiong Zhong[1,4]

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POS-02-083

Effects of Growth Hormone on the Salmon Pituitary Proteome

Yoichi Kurata[1,2], Yayoi Kimura[2], Yuko Yamanaka[2], Akiyo Ishikawa[2], Hiroyuki Okamoto[3], Tetsuji Masaoka[3], Hiroyuki Nagoya[3], Kazuo Araki[3], Shunsuke Moriyama[4], Akinobu Hamada[1], Tsukasa Mori[5], Hisashi Hirano[2]

[1]National Cancer Center Research Institute, Japan, [2]Yokohama City University, [3]National Research Institute of Aquaculture, [4]Kitasato University, [5]Nihon University

POS-02-084

Differential Protein Expression and Chemoprotection of Fenugreek Leaf Extract on Normal Rat Liver Cells Treated with Cadmium Chloride

Roy Lyles, Caroline Odewumi, Veera Badisa, Ramesh Katam, Lekan Latinwo

Department of Biological Sciences, College of Sciences and Technology, Florida A&M University, USA

S100P Up-Regulated in Hepatocellular Carcinoma Cell Line Treated with Thai Herbal Formula

Wanwisa Suksalak[2], Penchatr Diskul-Na-Ayudthaya[1], Daranee Chokchaichamnankit[1], Khajeelak Chiablaem[1], N. Monique Paricharttanakul[1], Jisnuson Svasti[1,2], Chantragan Srisomsap[1]

[1]Laboratory of Biochemistry, Chulabhorn Research Institute, Thailand, [2]Applied Biological Sciences, Chulabhorn Graduate Institute, Thailand

Proteomic Approach to Antioxidative Effects of Food Factors Using Fluorescence Labeled Difference Gel Electrophoresis

Yoichi Sakakibara, Takako Iwata, Katsuhisa Kurogi, Masao Yamasaki, Kazuo Nishiyama, Masahito Suiko

Depertment of Biochemistry and Applied Biosciences, Faculty of Agriculture, University of Miyazaki, Japan

Proteomic Analysis of Stress-Related Proteins Associated with Desiccation Tolerance in Developing Rice Seeds

Naoto Sano[1,2], Shunpei Masaki[1], Keiichi Izumikawa[3], Tetsuya Yamada[1], Motoki Kanekatsu[1]

[1]Department of Plant Production, United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology, Japan, [2]Research Fellow of the Japan Society for the Promotion of Science, Japan, [3]Department of Applied Life Science, Graduate School of Agriculture, Tokyo University of Agriculture and Technology, Japan

Analysis of Labor-Related Functions of the Cephalic and Thoracic Exocrine Glands of the European Honeybee by Using Large-Scale Proteomics

Toshiyuki Fujita[1], Hiroko Kozuka-Hata[2], Hiroko Ao-Kondo[2], Masaaki Oyama[2], Takeo Kubo[1]

[1]Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Japan, [2]Medical Proteomics Laboratory, Institute of Medical Science, The University of Tokyo, Japan

Characterization of Muscadine Berry Proteome Using Label and Label Free Mass Spectrometry Approaches

Ramesh Katam[1], Devaiah M Kambiranda[1], Katsumi Sakata[2], Tiratharaj Singh[4], Steve V Sluyter[3], Paul A Haynes[3], Mehboob B Sheikh[1], Lekan M Latinwo[1]

[1]Florida A&M University, USA, [2]Maebashi Institute of Technology, Japan, [3]Macquarie University, Australia, [4]Bioclues.org

Microbiota Profiling to Improve Quality and Safety of Dairy Products

Alessio Soggiu[1], Emøke Bendixen[2], Cristian Piras[1], Luigi Bonizzi[1], Paola Roncada[1,3]

[1]DIVET, Dipartimento di Scienze veterinarie e sanita pubblica, Universita degli Studi di Milano, Italy, [2]Department of Molecular Biology and Genetics - Aarhus University, Denmark, [3]Istituto Sperimentale Italiano "L. Spallanzani", Italy

Proteomic Characterization of Ascorbate Peroxidase in Soybean Under Abiotic Stress

Ghulam Muhammad Ali[1], Setsuko Komatsu[2]

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POS-02-092

Overexpression of Sucrose Synthase 1 (sus1) in Transgenic Canola Carrying AtDREB2A Transcription Factor

Alireza Shafeinia[1], Valiollah Mohammadi[2], Houshang Alizadeh[2], Afshin Salavati[1]
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POS-02-093

Two-Dimensional Gel Electrophoresis Analysis of Flavonoid Sulfate Effects on *A. thaliana* T87 Cells

Takuyu Hashiguchi[1,2], Yoichi Sakakibara[1,2], Takehiko Shimohira[1,2], Toshihiro Yoshimura[1,2], Katsuhisa Kurogi[1,2], Yosuke Hara[1], Ming-Cheh Liu[3], Masahito Suiko[1,2]
[1]Department of Biochemistry and Applied Biosciences, University of Miyazaki, Japan, [2]Interdisciplinary Graduate School of Agriculture and Engineering, University of Miyazaki, Japan, [3]Department of Pharmacology, College of Pharmacy and Pharmaceutical Sciences, The University of Toledo, USA

POS-02-094

Starch Glycomic and Proteomic Aspects of Grain Chalkness

Kentaro Kaneko[1], Maiko Sasaki[1], Tatsuya Maruyama[2], Takeshi Shiraya[3], Toshiaki Mitsui[1,2]
[1]Dept. Applied Biol. Chem., Niigata Univ., Japan, [2]Grad. Sch. Sci. & Tech., Niigata Univ., Japan, [3]Niigata Agricultural Research Institute, Japan

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POS-02-095

Proteomic Analysis of Soybean Root During Recovery After Flooding

Mudassar Khan[1,2], Yohei Nanjo[2], Katsumi Sakata[3], Setsuko Komatsu[1,2]
[1]University of Tsukuba, [2]National Institute of Crop Science, Japan, [3]Maebashi Institute of Technology, Japan

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POS-02-096

Label-Free Quantitative Proteomics of Nuclear Proteins in Soybean Under Flooding Stress

MyeongWon Oh[1,2], Yohei Nanjo[2], Setsuko Komatsu[1,2]
[1]University of Tsukuba, [2]National Institute of Crop Science, Japan

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POS-02-097

Acceleration of Germination of Rice Seeds by Soaking with Red Onion

Sumiko Nakamura[1], Kentaro Kaneko[2], Toshiaki Mitsui[1], Ken'ichi Ohtsubo[1]
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POS-02-098

Proteomic Analysis Applied to Meat Science: Characterizing Post Mortem Changes in Japanese Wild Deer Meat

Oka Eriko[1], Motoko Takaoka[1], Kyoko Suzuki[1], Minoru Yamanoue[2]
[1]Dept. of Biosphere Sciences, Kobe College, Japan, [2]Graduate School of Agricultural Science, Kobe Univ., Japan

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POS-02-099

Post-Translational Regulation of Nutrient Signaling and Metabolism Mediated by 14-3-3 Proteins in Plants

Takeo Sato[1], Shigetaka Yasuda[1], Shugo Maekawa[1], Yuko Nomura[2], Hirofumi Nakagami[2], Yoichiro Fukao[3], Junji Yamaguchi[1]
[1]Faculty of Science, Hokkaido University, Japan, [2]Plant Proteomics Research Unit, RIKEN CSRS, [3]Plant Global Education Project, NAIST

Comprehensive Identification of OsSUMO Binding Proteins in Rice Exposed to High Temperature Stress Condition

Takuya Kushioka[1], Hiroshi Ataka[1], Attia Kotb[2], Kentaro Kaneko[2], Toshiaki Mitsui[2], Kimiko Itoh[2]

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Development of an Inflammation-Specific MRM Assay for the Discovery of a Novel Pharmaceutical for the Treatment of Human Vascular Diseases from Derivatives of the Escin Chestnut Extract

Dominik Domanski[1], Anna Perzanowska[1], Oliwia Zegrocka-Stendel[2], Dorota Maciejko[2], Magdalena Kowalewska[2], Michal Dadlez[1], Katarzyna Koziak[2]

[1]Mass Spectrometry Laboratory, Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Poland, [2]Department of Immunology, Biochemistry and Nutrition. Medical University of Warsaw, Poland

Isotope Labeling-Based Quantitative Proteomics of Developing Seeds of Castor Bean (*Ricinus communis* L.)

Fabio CS Nogueira[1], Giuseppe Palmisano[2], Veit Schawmmle[2], Peter Roepstorff[2], Francisco AP Campos[3], Gilberto B Domont[1]

[1]Proteomics Unit, Institute of Chemistry, Universidade Federal do Rio de Janeiro, Brazil, [2]Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark, [3]Department of Biochemistry and Molecular Biology, Universidade Federal do Ceará, Brazil

Proteomic Identification of Diverse and Dynamic Metabolic Network Upon Reduction of Cellular Oxalate Level in Crop Plant

Sudip Ghosh, Kanika Narula, Niranjan Chakraborty, Subhra Chakraborty

National Institute of Plant Genome Research, India

Membrane and Organelle Proteomics

Proteomic Profiling of Ganglioside-Associated Microdomain in Malignant Melanomas

Noboru Hashimoto[1], Kazunori Hamamura[1], Norihiro Kotani[2], Yuki Ohkawa[1], Keiko Furukawa[3], Koichi Honke[2], Koichi Furukawa[3]

[1]Department of Biochemistry II, Nagoya University Graduate School of Medicine, Japan, [2]Department of Biochemistry, Kochi University School of Medicine, Japan, [3]Department of Biomedical Sciences, Chubu University College of Life and Health Sciences, Japan

Physiological and Proteomic Characterization of Outer Membrane Vesicle of *Pseudomonas putida* KT2440

Yeol Gyun Lee, Chi Won Choi, Sung Ho Yun, Young Ju Lee, Gun Hwa Kim, Yeon Hee Hong, Edmond Changkyun Park, Seung Il Kim

Division of Life Science, Korea Basic Science Institute, Korea

POS-02-106

2D-DIGE Analysis of Cell Surface Proteins Reveals Characteristic Proteome Profiles for Effects of Sulfasalazine in Human Synovial Sarcoma Cell Line, SW982

Kazuki Omoteyama, Mitsumi Arito, Toshiyuki Sato, Nobuko Iizuka, Manae S. Kurokawa, Kazuki Okamoto, Naoya Suematsu, Tomohiro Kato

St. Marianna Univ. Grad. Schl. Med., Japan

POS-02-107

Proteomic Analysis of Outer Membrane Vesicles (OMV) from Multidrug-Resistant *Acinetobacter baumannii* DU202

Sung Ho Yun, Yeol Gyun Lee, Chi Won Choi, Yong Ju Lee, Edmind Chang Kyun Park, Yeon Hee Hong, Gun Hwa Kim, Seung Il Kim

Division of Life Science, Korea Basic Science Institute, Korea

POS-02-108

Identification of Protein Complexes in the Golgi from Rat Liver by High Resolution Native Gel and nanoLC-ESI-Q-TOF

Yongqian Zhang[1,2], Yulin Deng[1], Tommy Nilsson[2]

[1]School of Life Science, Beijing Institute of Technology, China, [2]The Research Institute of the McGill University Health Centre, Department of Medicine, McGill University, Canada

POS-02-109   PS07-03

A Plasma Membrane Proteomic Analysis of Mouse and Human Cardiovascular Proteins

Parveen Sharma, Nicolas Bousette, Savo Lazic, Cynthia Abbasi, Nicole Dubois, Alex Ignatchenko, Vladimir Ignatchenko, Jie Liu, Allen Teng, Melissa Noronha, Robert Hamilton, Peter P Liu, Peter H Backx, Gordon Keller, Igor Stagljar, Ian C Scott, Thomas Kislinger, Anthony Gramolini

University of Toronto, Canada

POS-02-110

An Improved Subcellular Protein Atlas

Charlotte Stadler, Hammou Ait Blal, Frida Danielsson, Martin Hjelmare, Diana Mahdessian, Elton Rexhepaj, Rutger Schutten, Marie Skogs, Mikaela Wiking, Annica Abergh, Mathias Uhlen, Emma Lundberg

Royal Institute of Technology, Science for Life Laboratory, Sweden

POS-02-111

Proteome Analysis of Normal Human Circulating Microparticles

Ole Oestergaard[1], Christoffer T. Nielsen[1], Line V. Iversen[1], Soeren Jacobsen[2], Julia T. Tanassi[1], Niels H. H. Heegaard[1]

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POS-02-112

Subcellular Fractionation and Bottom-Up Proteomics for Proteome-Wide Protein Localization

Magnus Palmblad[1], Ekaterina Mostovenko[1], Suzanne van der Plas - Duivesteijn[1], Dana Ohana[1], Yassene Mohammed[1], Robert Passier[2], Andre M. Deelder[1]

[1]Center for Proteomics and Metabolomics, Leiden University Medical Center, The Netherlands, [2]Department of Anatomy and Embryology, Leiden University Medical Center, The Netherlands

POS-02-113

Proteome Analysis of *Gloeobacter violaceus* PCC7421: Fractionation of Total, Soluble and Insoluble Proteins

Soo Jung Kim[1,5], Jung Ha Choi[1], Yeol Gyun Lee[1], Kun Cho[2], Sang Oh Kweon[1], Joseph Kwon[3], Young Hwan Kim[2], Young Mok Park[2], Kwang Hwan Jung[4], Young-Ho Chung[1]

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POS-02-114

Proteomic Analysis Identifies CaFer1, A Dehydration-Responsive Ferritin in Chickpea (*Cicer arietinum* L.) Secretome, That Promotes Stress Tolerance

Shaista Parveen, Suchismita Dass, Subhra Chakraborty, Niranjan Chakraborty

National Institute of Plant Genome Research, India

POS-02-115

Profiling and Semi-Quantitative Analysis of Cell Surface Proteome in Human Mesenchymal Stem Cells

NamHyun Park[1,2], YoungMok Park[1,2]

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POS-02-116

Segment-Specific Membrane Protein Profiling of Human Colon

Sjoerd van der Post, Gunnar C. Hansson

Department of Medical Biochemistry and Cell Biology, University of Gothenburg, Sweden

POS-02-117

Membrane Proteomics Study of *Clostridium acetobutylicum*: Discovery of the Proteins Regulating the Transition from Acidogenic to Solventogenic Phase

Jingjing Zhao, Quanhui Wang, Xue Bai, Zhen Chen, Yao Sun, Siqi Liu

Beijing Institute of Genomics, Chinese Academy of Sciences, China

POS-02-118

Purification and Proteomic Profiling of Kidney Vascular Endothelial Cell Plasma Membrane Proteins

Zan Liu[1,2], Bo Xu[1], Masaaki Nameta[1], Ying Zhang[1], Sameh Magdeldin[1,3], Yutaka Yoshida[1], Keiko Yamamoto[1], Hidehiko Fujinaka[1,4], Eishin Yaoita[1], Masayuki Tasaki[2], Yuki Nakagawa[2], Kazuhide Saito[2], Kota Takahashi[2], Tadashi Yamamoto[1]

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POS-02-119

A Membrane Proteomics Signature Reveals Surface Factors Associated with Human Embryonic Stem Cell Pluripotency

Chia-Li Han[1], Wei-Ting Hsu[2], Chun-Neng Wang[3], Hsien-Jung Chen[1], Yi-Chuan Tsai[1], Hung-Chih Kuo[2], Yu-Ju Chen[1]

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Proteomic Profiling of Exosomes Reveal the Intercellular Transfer of Oncogenic Cargo

Suresh Mathivanan
Department of Biochemistry, La Trobe Institute for Molecular Science, La Trobe University, Australia

POS-02-121

Introducing the Mitochondrial Italian Human Proteome Project Initiative (mt-HPP)

Andrea Urbani[1,2,3], Luca Bini[3], Paola Roncada[3], Alessandra Modesti[3],
Anna Maria Timperio[3], Mauro Fasano[3], Massimo Castagnola[3]
[1]Dept. of Experimental Medicine and Surgery, Univeristy of Rome "Tor Vergata", Italy, [2]IRCCS-Fondazione Santa Lucia, Italy, [3]ItPA, Italian Proteomics Association (www.itpa.it), Italy

New Technologies in Proteomics

POS-02-122

Exploring the Capabilities and Specificities of CESI-MS for Bottom-Up Proteomics and Peptide Mapping of Proteins Through A Comparison to nanoLC

Jean-Marc Busnel[1], Anna Lou[1], Chitra Ratnayake[1], Sean Seymour[2], Christie Hunter[2]
[1]Beckman Coulter, USA, [2]AB Sciex, USA

POS-02-123

New Developments on a Benchtop Quadrupole-Orbitrap Mass Spectrometer

Jan-Peter Hauschild, Eduard Denisov, Amelia Peterson, Oliver Lange, Alexander Makarov, Eugen Damoc, Mathias Mueller, Andreas Wieghaus, Markus Kellmann
Thermo Fisher Scientific (Bremen), Germany

POS-02-124

Development of Methods for Information-Driven MS/MS (ID-MS/MS) for Increased Identification Rates in Bottom-Up Proteomics of Human Blood Serum

Peter Brechlin[1], Stuart Pengelley[1], Pierre-Olivier Schmit[2], Ow Sawyen[3], Haruo Hosoda[4], Dirk Wunderlich[1]
[1]Bruker Daltonik GmbH, Germany, [2]Bruker Daltonique S.A., France, [3]Bruker Daltonics Inc., China, [4]Bruker Daltonics K.K., Japan

POS-02-125

Development of High-Sensitivity nanoLC-MS/MS Systems Using Narrow-Bore Meter-Long Monolithic Silica Capillaries At Low Flow Rate

Suguru Ichihara, Mio Iwasaki, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama
Kyoto University, Japan

POS-02-126

Disease Model Cell System: A Novel Proteomics Tool to Elucidate Protein Networks with Spatio-Temporal Information

Fumi Kano[1,2], Daiki Nakatsu[1], Yoshiyuki Noguchi[1], Yuta Horiuchi[1], Masayuki Murata[1]
[1]Graduate School of Arts and Sciences, The University of Tokyo, Japan, [2]PRESTO, JST

POS-02-127

Travelling Wave Ion Mobility Assisted Duty Cycle Enhancements for Targeted and Non-Targeted Proteomics Experiments

CJ Hughes, JPC Vissers, JI Langridge
Waters Corporation, UK

POS-02-128

Sheathless Capillary Electrophoresis Mass Spectrometry as a Versatile and Powerful Tool for the Characterization of the Primary Sequence and Glycosylations of Monoclonal Antibodies

Anna Lou[1], Jean-Marc Busnel[1], Zhiqi Hao[2], Elsa Wagner[3], Hans Dewald[1], Alain Beck[3], Patrick Bennett[2]

[1]Beckman Coulter, USA, [2]Thermo Fisher, USA, [3]Centre d'immunologie Pierre Fabre, Saint-Julien en Genevois, France

POS-02-129

Improving Label-Free Quantitation of Plasma and Serum Proteins Using a High-Resolution Hybrid Orbitrap Mass Spectrometer

Maryann S. Vogelsang[1], Amol Prakash[1], David Sarracino[1], Scott Peterman[1], Bryan Krastins[1], Jennifer Sutton[1], Gregory Byram[1], Gouri Vadali[1], Shadab Ahmad[1], Bruno Darbouret[2], Mary F. Lopez[1]

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POS-02-130

Methodological Development of Gel-Filter for the Enrichment of Low-Molecular Weight Proteins from Serum and Comparative Study with Differential Solubilization Method

Lingsheng Chen[1,2], Linhui Zhai[1], Ning Li[1], Lingyan Ping[1], Lei Chang[1], Xiangping Li[2], Deshun Shi[2], Ping Xu[1]

[1]State Key Laboratory of Proteomics, Beijing Proteome Research Center, National Engineering Research Center for Protein Drugs, National Center for Protein Sciences Beijing, Beijing Institute of Radiation Medicine, Beijing, China, [2]State Key Laboratory for Conservation and Utilization of Subtropical Agro-Bioresources, Guangxi University, China

POS-02-131

Western Blot Quantification of GFAP in Organotypic Brain Slices Using Stain-Free Gel Technology or Housekeeping Proteins as Loading Control

Daniela Volke[1,2], Claudia Dietze[1], Agneta Mewes[1,2], Ralf Hoffmann[1,2], Ning Liu[3]

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POS-02-132

Stain Free Total Protein Quantitation - A Method for Greater Reliability in Western Blot Loading Controls

Ning Liu, Anton Posch, Matthew Hammond, Kenneth Oh, Jonathan Kohn

Bio-Rad Laboratories

POS-02-133

Higher Data Confidence in Western Blot Analysis - Stain-Free Technology as Novel Normalization Tool

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POS-02-134

Analysis of an Apidaecin 1b Resistant *E. coli* Strain Using Differential Gel Electrophoresis

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POS-02-135

Immuno-Sequencing (I-Seq): Digital and Sensitive Antibody Based Proteomics Using DNA Barcoding and Massively Parallel Sequencing

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POS-02-136   PS10-03

SOMAmer Capture Coupled to Mass Spectrometry for Plasma Protein Quantification

Thomas O. Joos[1], Frederik Weiss[1], Sheri Wilcox[3], Jeff Carter[3], Stephan Kraemer[3], Nick Saccomano[3], Larry Gold[3], Bart H.J. van den Berg[1], Martin Gamer[2], Peter Schulz-Knappe[2], Oliver Poetz
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POS-02-137

Affinity Probe Capillary Electrophoresis (APCE) of Insulin Using a Fluorescence Labeled Recombinant Fab as an Affinity Probe

Kiyohito Shimura, Ken-ichi Kasai
Fukushima Medical University, Japan

POS-02-138

Quantitative Screening of Aptamers via Particle Display

Jinpeng Wang, Qiang Gong, Nupur Maheshwari, Michael Eisenstein, H. Tom Soh
University of California Santa Barbara, USA

POS-02-139

Global Proteome Survey (GPS) Finds New Roads for Translational Biomarker Signatures in Breast Cancer

Sara Stahl[1], Niclas Olsson[1], Petter Carlsson[1], Peter James[1], Karin Hansson[1], Per Malmström[2], Mårten Fernö[2], Lisa Ryden[2], Sofia Waldemarson[1], Christer Wingren[1], Carl Borrebaeck[1]
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POS-02-140

Identification of Metastasis Related Membrane Glycoprotein in Triple Negative Breast Cancer Using a Lectin Microarray

Shu-Min Zhou[1,2,3], Li Cheng[1,2,3], Shu-Juan Guo[1,2,3], Sheng-ce Tao[1,2,3]
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POS-02-141

Preliminary Study on the Development of Novel Proteomic Analysis by Using Surface Enhanced Raman Scattering (SERS)

Hiroaki Ito[1], Haruhiro Inoue[1], Katsuyuki Hasegawa[2], Yuuki Hasegawa[2], Noriko Odaka[1], Norimasa Sando[1], Tohru Ohmori[3], Satoshi Kimura[4], Shin-ei Kudo[1]
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POS-02-142

A Quick Profiling System for Cancer Marker Proteins with Diverse Post-Translational Modifications by a Fully Automated 2DE Device, Auto-2D

<u>Munenori Nishimura</u>[1,2], Uichi Midorikawa[3], Megumi Nagayama[1], Daiki Kobayashi[1], Mio Hirayama[1], Yoji Murakami[4], Yoshihiro Wada[4], Takahisa Imamura[5], Yutaka Unuma[3], Norie Araki[1]

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POS-02-143

High-Resolution Separation for Western Blotting by Automated 2-DE and Blotting System

<u>Hiroshi Sakaya</u>[1], Yoshiyuki Ishida[2], Kimihiko Yabe[2], Shinichi Goto[2], Hideki Kinoshita[2], Yutaka Unuma[2], Makoto Nakamura[2]

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POS-02-144   YI02-02

Plasma Proteome Analysis Using LC-MS/MS with Travelling Wave Ion Mobility and an Alternative Computational Solution to Protein Quantitation

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POS-02-145

A Fast Workflow for Identification and Quantification of Proteomes

<u>Chen Ding</u>[1,2], Jing Jiang[1,2], Junying Wei[1,2], Wanlin Liu[1,2], Wei Zhang[1,2], Mingwei Liu[1,2], Tianyi Fu[1,2], Tianyuan Lu[1,2], Lei Song[1,2], Wantao Ying[1,2], Jie Ma[1,2], Yangjun Zhang[1,2], Lai Wei[1,2], Anna Malovannaya[3], Lijun Jia[4], Bei Zhen[1,2,4], Yi Wang[3], Fuchu He[1,2], Xiaohong Qian[1,2], Jun Qin[1,2,3]

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POS-02-146

DMSO Drastically Enhances Electrospray Response Boosting Sensitivity of Proteomic Experiments

<u>Hannes Hahne</u>[1], Fiona Pachl[1], Benjamin Ruprecht[1], Matthias Wilm[2], Stefan Maier[1], Susan Klaeger[1], Dominic Helm[1], Guillaume Medard[1], Simone Lemeer[1], Bernhard Kuster[1]

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POS-02-147

Increasing the Quality of Bottom-Up Proteomics Data by Computer-Assisted Liquid Chomatography Gradient Optimisation

<u>Chris Hodgkins</u>[1], Brad Patterson[1], Valentina Valova[2]

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POS-02-148

Metal-Chelate Methacylate Monolithic Support for Targeted Affinity Selection of Histidine-Peptides in High-Throughput Proteomics

<u>Rajasekar R. Prasanna</u>, Sidhik Sinash, Agamudi S Kamalanathan, Mookambeswaran A Vijayalakshmi

Centre for Bioseparation Technology, VIT University, India

POS-02-149

Improving MS^n Performance with a Multitasking Mass Spectrometer

Michael Senko, Philip Remes, Qingyu Song, Jesse Canterbury, Justin Blethrow, Vlad Zabrouskov, Oliver Lange, Alexander Makarov
Thermo Fisher Scientific

POS-02-150

Increased Throughput 2D Nanoscale LC Analysis of Human Placental Samples

M Stapels[1], K Fadgen[1], JW Thompson[2], MA Moseley[2], JI Langridge[1], Kenji Hirose[1]
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POS-02-151

Data Independent Acquisition (DIA) Analysis on the Q Exactive Mass Spectrometer

Yue Xuan[1], Reiko Kiyonami[3], Jarrett Egertson[2], Michael MacCoss[2], Andreas Kuehn[1], Andreas Huehmer[3], Markus Kellmann[1]
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POS-02-152

Missing Proteins in Chromosome 16-Spanish HPP

Manuel Fuentes[1], Noelia Dasilva[1], Felipe Clemente[2], Maria Luisa Hernaez[2], Paula Diez[1], Maria Gonzalez-Gonzalez[1], Alberto Orfao[1], Felix Elorzta[5], Fernando Corrales[4], Juan Pablo Albar[3], Concha Gil[2]
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POS-02-153

A Novel Chemical Tool for Proteomic Analysis of Tranlational Control

Kenichi Horisawa, Takaaki Miyazawa, Koji Ohkawa, Kotaro Oka, Nobuhide Doi
Graduate School of Science and Technology, Keio University, Japan

POS-02-154

Mass Spectrometry Based N- Terminal Sequence Determination with *De Novo* Sequencing Using CID and ETD

Jo Lene Lai, Chien-Chen Lai
Institute of Molecular Biology, National Chung Hsing University, Taiwan

POS-02-155

Application of a Peptide-Based Assay System to Study the Human Proteome

Igor Kozlov, Norihito Muranaka, Corey Dambacher, Petr Capek, Wayne Delport, Muskan Kukreja, Mark Chee
Prognosys Biosciences Inc.

POS-02-156

Toward Early Stage Detection of AD: Dynamic Binding and Unbinding of Kinesins during Collective Transport

Woochul Nam, Bogdan Epureanu
University of Michigan - Ann Arbor, USA

Comprehensive Mass Spectrometry-Based Characterization of Box H/ACA Small Nucleolar Ribonucleoprotein Complexes in Schizosaccharomyces Pombe

Masato Taoka[1], Yuko Nobe[1], Aiko Takeuchi[1], Masayuki Hori[1], Shunpei Masaki[1], Hiroshi Nakayama[2,4], Yoshio Yamauchi[3], Nobuhiro Takahashi[3,4], Toshiaki Isobe[1,4]

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Improving Throughput for Highly Multiplexed Targeted Quantification Methods Using Novel API-remote Instrument control and State-Model Data Acquisition Schemes

Amol Prakash[1], Scott Peterman[1], Barbara Frewen[1], Andreas Kuehn[2], Tara Schroeder[3], Lisa Vasicek[6], Brian Hood[6], Ryan Bomgarden[4], Bryan Krastins[1], David Sarracino[1], Gregory Bryam[1], Maryann Vogelsang[1], Shadab Ahmad[1], Jonathan Worboys[5], Claus Jorgensen[5], Thomas Conrads[6], Mary Lopez[1]

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In Vitro Phosphorylation-Assisted in Depth Human Serum Proteome Analysis

Shunsuke Takagi, Haruna Imamura, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

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Comprehensive Quantitative Phosphoproteomic Approach by MS/MS [ALL] with SWATH™ Acquisition

Ryo Yokoyama[1], Takeshi Shibata[1], Masato Aoshima[1], Masaki Matsumoto[2], Keiichi Nakayama[2], Naokazu Okamoto[1], Takuichi Tsubata[1], Sumie Ando[1]

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Large Scale Targeted Protein Quantification Using HR/AM Selected Ion Monitoring with MS/MS Confirmation on a Novel Hybrid, Q-OT-qIT Mass Spectrometer

Reiko Kiyonami[1], Michael Senko[1], Vlad Zabrouskov[1], Jarrett Egertson[2], Sonia Ting[2], Michael MacCoss[2], Andreas FR Huhmer[1]

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Quality Control Tool and Long-Term Performance of SRM Instruments

Johan Teleman, Johan Malmstroem, Fredrik Levander

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Facile Synthesis of Novel Magnetic Silica Nanoparticles Functionalized with Layer-by-Layer Detonation Nanodiamonds for Secretome Study of An Inducible Hepatitis B Virus Cell Line

Liming Wei[1], Muxing Guo[2], Huali Shen[1], Haojie Lu[1], Chao Zhao[2], Pengyuan Yang[1]

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POS-02-164

Urimem, A Simple Economical Urinary Protein Membrane, Will Facilitate Biomarker Research

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POS-02-165

A Comprehensive Analysis of the Interactions between *Streptococcus pyogenes* and Human Plasma Proteins

<u>Kristoffer Sjöholm</u>[1], Christofer Karlsson[1], Adam Linder[2], Lars Bjock[2], Johan Malmstrom[1]
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POS-02-166   PS03-04

Monitoring Protein Synthesis in Living Cells with Fluorescent Labeled tRNA FRET Pairs

<u>Zeev Smilansky</u>[1], Sima Barhoom[2], Ian Farrell[5], Dvir Dahary[1], Andrew Leask[3], Peter Vanderklish[4], Marcelo Ehrlich[2], Barry S. Cooperman[5], Ornal Elroy-Stein[2]
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POS-02-167

A Novel Method to Quantify Protein Conformational Changes in Complex Cellular Matrices

<u>Yuehan Feng</u>[1], Giorgia De Franceschi[2], Martin Soste[1], Abdullah Kahraman[1], Pedro Navarro[3], Patrizia Polverino de Laureto[2], Paola Picotti[1]
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POS-02-168

Intact Protein LC-MS, How to Overcome the Challenges?

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Pharmacoproteomics and Toxicoproteomics

POS-02-169

Data Independent LC-IM-MS Strategies for the Multi-Omic Scale Identification and Quantitation on Cytochrome P450 Transfected Hepatocytes

<u>K Hirose</u>[1], S Geenen[2], LA Gethings[3], C Cojocariu[3], G Isaac[4], R Tonge[3], JPC Vissers[3], JI Langridge[3], I Wilson[2]
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POS-02-170

Proteomic Analysis of Antidepressant-Like Effect of a Kampo (Japanese Herbal) Medicine "Kososan (Xiang-Su-San)" on Brain from Stress-Induced Depression-Like Model Mouse

Takayuki Nagai[1,2], Yoshio Kodera[3,4], Masamichi Oh-Ishi[4], Tadakazu Maeda[3], Naoki Ito[2], Toshihiko Hanawa[2], Haruki Yamada[1,2]
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POS-02-171

Proteomic Analysis of Cardiomyocetes after Inhibition of MMP-2 Gene Expression

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POS-02-172

Proteomic Analysis of Liver Microsomes in *X. tropicalis*

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POS-02-173

Monitoring Drug Metabolizing Enzymes and Transporters Using TXP Antibodies and Immunoaffinity MS

Frederik Weiss, Bart H.J. van den Berg, Hannes Planatscher, Helen S. Hammer, Thomas O. Joos, Oliver Poetz
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POS-02-174

Evaluation of Nanomaterial-Induced Biological Responses by Toxico-Proteomics Analysis

Kazuma Higashisaka[1], Akiyoshi Kunieda[1], Yuki Iwahara[1], Kota Tanaka[1], Shin-ichi Tsunoda[2,3], Yasuo Yoshioka[1], Yasuo Tsutsumi[1,2,3]
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POS-02-175

Discovering Novel Neurotoxins from Snake Venom by Using Mass-Spectrometry-Guided Purification Approach and Pharmacological Assays

Muhamad Rusdi Ahmad Rusmili[1,2], Wayne C. Hodgson[2], Mohd Rais Mustafa[3], Tee Ting Yee[2], Iekhsan Bin Othman[2]
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POS-02-176

Calcium Oxalate Crystals Induced Changes in Secretion of Proteins from Basolateral Compartment of Renal Tubular Cells That, in Turn, Enhanced Crystal Invasion

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POS-02-177

Temporal and Quantitative Proteomics Study Reveals Mitochondrial Dysfunction, Perturbed Secretory Pathway and ER Stress-Mediated Apoptosis as Anticancer Mechanisms of a Chalcone on A375 Melanoma Cells

Siew Li Lai[1], Pooi Fong Wong[1], Teck Kwang Lim[2], QingSong Lin[2], Rais Mustafa Mohammad[1]

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POS-02-178

New Insights Into the Cellular Response Triggered by Silver Nanoparticles Using Quantitative Proteomics

Thiago Verano-Braga[1], Rona Miethling-Graff[2], Katarzyna Wojdyla[1], Adelina Rogowska-Wrzesinska[1], Jonathan R. Brewer[1], Helmut Erdmann[2], Frank Kjeldsen[1]

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Protein Array and Chip Technology

POS-02-179

Protein-Protein Interaction Analysis Using Oligo-Cysteine Tagged Protein Chip. Detection of Tubulin from Mouse Brain Extract by Oligo-Cysteine Tagged Stathmin Chip

Hiroko Furumoto, Maoko Shimizu, Hisayuki Tanaka, Takao Kitagawa, Junko K. Akada, Kazuyuki Nakamura

Yamaguchi University, Japan

POS-02-180

Miniaturization of Multiplexed Planar Recombinant Antibody Nanoarrays for Serum Protein Profiling

Linn Petersson[1], Linda Dexlin-Mellby[1], Michael Coen[2], Navil Amro[2], Lennart Truedsson[3], Gunnar Sturfelt[4], Carl AK Borrebaeck[1], Christer Wingren[1]

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POS-02-181

Personalised Proteomics by Means of Individualised Protein Microarrays

Syafriza Yanti, Smiths Lueong, Joerg D. Hoheisel

Functional Genome Analysis, Deutsches Krebsforschungszentrum (DKFZ), Germany

POS-02-182   PS04-04

High Throughput Cell-Based Studies and Protein Microarrays for Biomarker and Target Discovery

Joshua LaBaer

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POS-02-183

Identification of B-Cell Lymphoma Subsets by Protein Profiling Using Recombinant Antibody Microarrays

Frida Pauly[1,2], Mats Jerkeman[3], Henrik Hjalgrim[5], Karin Ekstrom-Smedby[4], Carl AK Borrebaeck[1,2], Christer Wingren[1,2]

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POS-02-184

Protein Chip Methodology to Detect HSP70 Autoimmune Antibodies in the Sera of Hepatitis C Virus-Positive Hepatocellular Carcinoma Patients

Junko Akada[1], Shuichi Kamei[2], Akane Ito[2], Takao Kitagawa[1], Masaaki Oka[3], Yasuhiro Kuramitsu[1], Kazuyuki Nakamura[1]

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POS-02-185

Phenotyping of Various Membrane Markers on Plasma Exosomes from 80 Healthy Donors Using an Extracellular Vesicle (EV) Array

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POS-02-186   PS19-04

Extracellular Vesicle (EV) Array: Microarray Capturing of Exosomes and Other Extracellular Vesicles for Multiplexed Phenotyping

Malene Joergensen[1], Shona Pedersen[2], Rikke Baek[1], Evo Soendergaard[1], Soeren Risom Kristensen[2], Kim Varming[1]

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POS-02-187

Multiplexed Analysis of Target Protein and Its Lys Acetylation Using Antibody Microarray

Feina Yao[1,2], Ying Li[1,2], Pengyuan Yang[1,2], Yinkun Liu[3], Huizhi Fan[1]

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POS-02-188

Multiplexed Analysis of Target Protein and Lys Acetylation Using Antibody Microarray

Feina Yao[1,2], Ying Li[1,2], Pengyuan Yang[1,2], Yinkun Liu[3], Huizhi Fan[1]

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POS-02-189

DNA Methylation Presents Distinct Binding Sites for Human Transcription Factors

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Protein Interaction and Protein Complexes

POS-02-190

Structural Proteomics of the Human Nucleoporin 107 Complex

Alexander von Appen[1], Huy Khan Bui[1], Amanda DiGuilio[1,2], Joseph S Glavy[2], <u>Martin Beck</u>[1]

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POS-02-191   PS17-04

***In Vivo* Crosslinking Combined with Label-Free Quantitative Proteomics to Determine the Subcellular Distribution and Stoichiometry of Proteasome Complexes**

Bertrand Fabre, Thomas Lambour, Manuelle Ducoux-Petit, Luc Garrigues, Francois Amalric, Bernard Monsarrat, Marie-Pierre Bousquet-Dubouch, <u>Odile Burlet-Schiltz</u>

Institute of Pharmacology and Structural Biology (IPBS), CNRS, University of Toulouse, France

POS-02-192

Elucidating the Unfolded Protein Response in GPCR Expressing Yeast Host

<u>Hussain Dahodwala</u>, Anne S Robinson

Chemical and Biomolecular Engineering, Tulane University

POS-02-193

Molecular Mechanism Underlying IgSF11-Induced Cell Migration

Erika Hayashi[1], Hiroaki Akutsu[2], Hiroshi Funakoshi[2], Kenji Nakayama[3], <u>Yokichi Hayashi</u>[4]

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POS-02-194

Proteomics Approaches to Understand Molecular Basis of Mammalian Circadian Clock

<u>Kentaro Hirose</u>[1], Yasunori Sugiyama[2], Hikari Yoshitane[1], Yoshitaka Fukada[1]

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POS-02-195

Mapping the Dynamic Interactome Through the Human Cell Cycle

<u>Koshi Imami</u>, Hongbing Yu, Anders R Kristensen, Leonard J Foster

Centre for High-Throughput Biology, University of British Columbia, Canada

POS-02-196

A Novel Mechanism of Keratin Cytoskeleton Organization Through Casein Kinase I Alpha and FAM83H in Colorectal Cancer: Interactome Analysis of FAM83H

<u>Takahisa Kuga</u>[1], Hideaki Kume[1], Naoko Kawasaki[1], Misako Sato[1], Jun Adachi[1], Takashi Shiromizu[1], Isamu Hoshino[2], Hisahiro Matsubara[2], Takeshi Tomonaga[1]

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POS-02-197

Protease Resistant Soy Proteins Interact with the Cell Surface Proteins of an Intestinal Cell Line, Caco-2, and Change the Cell Signaling

<u>Jinkyu Lim</u>, Ju-Young Lee, You-Jin Youm

Kyungpook Univ., Korea

POS-02-198

Interactions between SAP155 and FUSE-binding Protein-Interacting Repressor Bridges c-Myc and P27Kip1 Expression Revealed by GeLC-MS Approach

<u>Kazuyuki Matsushita</u>[1], Mamoru Satoh[1], Takeshi Tomonaga[2], Hisahiro Matsubara[3], Hideaki Shimada[4], Fumio Nomura[1]

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POS-02-199

Dynamic Long-Range Chromatin Control of *Klf4* Transcription by IRF8 in Monocyte Differentiation

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POS-02-200

Analysis of Intact Macromolecular Assemblies on a Bench Top Orbitrap MS System

<u>Olaf Scheibner</u>, Eugen Damoc, Eduard Denisov, Alexander Makarov, Maciej Bromirski

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POS-02-201

The Monitoring of Protein Complex Dynamics in Response on Apoptosis Using PCP-SILAC

<u>Nichollas E Scott</u>, Anders R Kristensen, Leonard J Foster

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POS-02-202

Structural Analyses for the Effects of Ets1 Phosphorylation on Ets1-Containing TF-DNA Assemblies

<u>Masaaki Shiina</u>[1], Keisuke Hamada[1], Taiko Inoue-Bungo[1], Mariko Shimamura[1], Akiko Uchiyama[1], Shiho Baba[1], Ko Sato[1], Masaki Yamamoto[2], Tahir Tahirov[3], Kazuhiro Ogata[1]

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POS-02-203

Isolating, Characterizing, and Monitoring in Real Time Intracellular Epigenetic Protein Complexes

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POS-02-204

Molecular Dynamics Approach to Dynamical Protein Interaction

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POS-02-205

Identification of a Novel Binding Partner of the Cell Polarity-Regulating Kinase, PAR-1

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POS-02-206

System-Wide Characterization of Temporal Dynamics of Macromolecular Protein Complexes during Oncogene-Induced Cell Transformation

Britta Diedrich[1,2], Kristoffer T.G. Rigbolt[1,2], Joern Dengjel[1,2]
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POS-02-208

Charting Non-Sequence Specific Nucleic Acid-Protein Interactions in Human Cells

Gerhard Dürnberger, Tilmann Bürckstümmer, Kilian Huber, Roberto Giambruno, Andr Müller, Keiryn L. Bennett, Giulio Superti-Furga, Jacques Colinge
CeMM - Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria

POS-02-209

Obtaining Interactome Map by Sifting the Collection of MS-Data

Ekaterina V. Poverennaya, Alexey L. Chernobrovkin, Elena A. Ponomarenko, Andrey V. Lisitsa
Institute of Biomedical Chemistry

POS-02-210

A High-Resolution Quantitative BN-MS Approach for Comprehensive Analysis of Protein Complexes and Stoichiometries

Catrin Swantje Mueller[1], Wolfgang Bildl[1], Alexander Haupt[1], David Baehrens[1], Bernd Fakler[1,2], Uwe Schulte[1,2,3]
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POS-02-211

Structural Study of Proteins C3 and C3b by Time Resolved Hydroxyl Radical Footprinting

Anna Mlynarczyk[1], Florence Gonnet[1], Isabelle Salard[1], Serge Pin[2], Jean-Philippe Renault[2], Alexandre Giuliani[3], Pascal Mercere[3], Regis Daniel[1]
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POS-02-212

Human Cell Growth Regulator LYAR is Highly Expressed in Many Tumors and Accelerates Ribosome Biogenesis

Keiichi Izumikawa[1,2], Naoki Miyazawa[1], Harunori Yoshikawa[1,2], Hideaki Ishikawa[2,3], Goro Terukina[2,3], Yutaka Miura[1], Toshiya Hayano[4], Toshiaki Isobe[2,3], Akira Watanabe[5], Hiroyuki Aburatani[5], Nobuhiro Takahashi[1,2]
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POS-02-213   YI02-07

Defining the Structure of Mitotic Chromosomes Using Multi-Classifier Combinatorial Proteomics Together with DT40 Genetics

Shinya Ohta[1,2], Laura Wood[2], Itaru Samejima[2], Luis Fernando Montano[2], Juri Rappsilber[2], William C. Earnshaw[2]
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Trypanosome Proteome

Huoming Zhang[1], Anjelique Schulfer[2], Sung Hee Park[3], Rachel A Dalley[2], Atashi Anupama[2], Sami Alqarawi[1], Arthur Gunzl[3], Kenneth D Stuart[2], Aswini K Panigrahi[1]

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The Role of Nucleolar Protein Nop52 in the pre-rRNA Processing During Human Ribosome Biogenesis by Proteomic Approach

Harunori Yoshikawa[1,2,3], Hideaki Ishikawa[1,2], Keiichi Izumikawa[1,2], Toshiya Hayano[1,4], Yutaka Miura[1,2], Yoshio Yamauchi[3], Toshiaki Isobe[2,3], Nobuhiro Takahashi[1,2]

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A New Approach to Identify RNA-Protein Interactions Using a Conditional CRISPR Nuclease

Alex Apfel[1], Ho Young Lee[2], Rachel E. Haurwitz[2], Kaihong Zhou[2], Brian Smart[1], Craig D. Wenger[1], Steven Laderman[1], Laurakay Bruhn[1], Jennifer Doudna[2]

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Mapping of Cross-Links in Complex Protein Samples Introduced by Bis (Succinimidyl)-3-Azidomethyl Glutarate

Hansuk Buncherd[1], Winfried Roseboom[1], Behrad Ghavim[1], Weina Du[2], Martin Wanner[2], Jan H. van Maarseveen[2], Leo de Koning[1], Chris de Koster[1], Luitzen de Jong[1]

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Top-Down Proteomic Analysis of Enzymes and Complexes in *Trichoderma* Fungal Secretomes

Luis Henrique F. Do Vale[1,2], Adam Catherman[2], Ryan Tal Fellers[2], Paul Thomas[2], Edivaldo Ximenes F. Filho[3], Carlos Andre O. Ricart[1], Neil L. Kelleher[2], Marcelo Valle de Sousa[1]

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Structural Analysis of Histone Multimers and NCPs by Ion Mobility Mass Spectrometry

Kazumi Saikusa[1], Sotaro Fuchigami[1], Nanako Azegami[1], Aritaka Nagadoi[1], Hitoshi Kurumizaka[2], Yoshifumi Nishimura[1], Satoko Akashi[1]

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Genome-Wide Mass Spectrometry-Based RNA Analysis Reveals a Novel snRNA Metabolic Pathway in Human Cell

Hideaki Ishikawa[1,2,3], Keiichi Izumikawa[1,2], Harunori Yoshikawa[1,2,3], Yuko Nobe[3], Yoshio Yamauchi[3], Hiroshi Nakayama[2,4], Toshiaki Isobe[2,3], Nobuhiro Takahashi[1,2]

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POS-02-221

Proteomic Identification of Profilin1 as a Co-Repressor of Estrogen Receptor Alpha in MCF7 Breast Cancer Cells

Jitendra Kumar Kanaujiya, Savita Lochab, Isha Kapoor, Pooja Pal, Dipak Datta, Sabyasachi Sanyal, Arun Kumar Trivedi

CSIR-Central Drug Research Institute, India

POS-02-222

Analysis of Plk1-Bora Interaction Using the ProteoChip System

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POS-02-223

Current Status of the Human DREAM/Calsenilin/KChIP3 Interactome: Focus on ProtoArrays for the Screening of Novel Protein Interactions

Juan Casado-Vela[1], Manuel Fuentes[2], Joaquin Dopazo[1], Noelia Dasilva[2], Maria Gonzalez-Gonzalez[2], B Mellstrom[1], JR Naranjo[1]

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POS-02-224   PS32-04

Mapping the Human Methyltransferasome Reveals the Existence of a Posttranslational Modification Code That Targets Molecular Chaperones to Regulate Functional Organization of the Human Proteome

Philippe Cloutier[1], Anais Aulas[3], Mathieu Lavallee-Adam[2], Mathieu Blanchette[2], Christine VandeVelde[3], Benoit Coulombe[1]

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POS-02-225

Function Through Interaction: Identification and Characterisation of SOCS4 and 5 SH2 Domain Targets

Edmond M Linossi[1,2], Andrew I Webb[1,2], Lukasz Kedzierski[1,2], Thomas Nebl[1,2], Tatiana Kolesnik[1,2], Tracy A Wilson[1,2], Alex N Bullock[3], Jeffrey J Babon[1,2], Nicos A Nicola[1,2], Sandra E Nicholson[1,2]

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POS-02-226

Fill-in-the-Blanks on the List of Players in the Histone Code: Limitations of Conventional Pull-Down Proteomics and Efforts to Overcome the Difficulties

Kazuki Yamamoto, Gosuke Hayashi, Ryosuke Sakamoto, Takeshi Kawamura, Akimitsu Okamoto, Tatsuhiko Kodama

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POS-02-227

Proteomic Profiling of the IL-3 Receptor Complex and Signal Transduction in Leukemia

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POS-02-228

Cell-Type Specific Stoichiometries of the Human Nuclear Pore Complex

Alessandro Ori[1], Niccolo Banterle[1], Murat Iskar[1], Amparo Andres-Pons[1], Claudia Escher[2], Huy Khan Bui[1], Lenore Sparks[1], Victor Solis-Mezarino[1], Oliver Rinner[2], Peer Bork[1], Edward A Lemke[1], Martin Beck[1]

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POS-02-229   YI01-01

Role of CYLD Deubiquitinase in EGF Signaling Pathway

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POS-02-230

Interactome-Wide Analysis Identifies End-Binding Protein 1 as a Crucial Component for the Speck-Like Particle Formation of Activated AIM2 Inflammasomes

Chih-Ching Wu[1,2], Li-Jie Wang[1], Hao-Ping Liu[1], Yu-Sun Chang[1]

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POS-02-231   YI02-04

Investigation of Time Dependent Competitive Protein Adsorption to Surfaces Using Mass Spectrometry

Torgny Undin, Andreas Dahlin, Jonas Bergquist, Magnus Wetterhall

Uppsala University, Sweden

POS-02-232

An Efficient Affinity Purification Method for Interaction Proteomics in Mammalian Cells

Akio Yamashita[1], Hitomi Kurosawa[1], Hisashi Hirano[2], Shigeo Ohno[1]

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POS-02-233   YI02-03

Quantifying the Dynamics of a 14-3-3 Protein Interaction Network by Affinity Purification and SWATH Mass Spectrometry

Ben C. Collins[1], Ludovic C. Gillet[1], George Rosenberger[1,2], Hannes L. Rost[1,2], Matthias Gstaiger[1], Ruedi Aebersold[1,2,3,4]

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Proteomics on Aging and Geriatric Diseases

POS-02-234

Proteomic Analysis of Alpha Synuclein-Containing Inclusions in Neurodegenerative Disorders

Amelia McCormack[1], Fariba Chegini[2], Nusha Chegeni[1], Damien Keating[2], Weiping Gai[2], Tim Kennion Chataway[1]

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Serum Peptide Profiles as a Candidate Biomarker for Dementia with Lewy Bodies

Itsuku Suzuki[1], Manae S. Kurokawa[2], Miwa Noguchi[1], Toshiyuki Sato[2], Itaru Utagwa[1], Mitsumi Arito[2], Nobuko Iizuka[2], Kazuki Omoteyama[2], Naoya Suematsu[2], Kazuki Okamoto[2], Noboru Yamaguchi[1], Tomihiro Kato[2]

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★Travel Award

Proteomic Changes of Rat Lens During Cataractogenesis: Therapeutic Effect of Antioxidant SkQ1

Lyudmila V. Yanshole[1,2], Olga A. Snytnikova[1,2], Vadim V. Yanshole[1,2], Natalia G. Kolosova[3], Yury P. Tsentalovich[1,2]

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Proteomic and Functional Knockdown Study of the APP Binding Protein FE65 Shows a Down-Regulation of Proteins Involved in DNA Replication (Potential Relevance to Alzheimer's Disease)

Andreas Schroetter[1], Thomas Mastalski[1], Fabian M. Nensa[1], Martin Neumann[1], Christina Loosse[1], Kathy Pfeiffer[1], Fouzi El Magraoui[1,2], Harald W. Platta[2], Ralf Erdmann[2], Carsten Theiss[3], Julian Uszkoreit[1], Martin Eisenacher[1], Helmut E. Meyer[1], Katrin Marcus[1], Thorsten Mueller[1]

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Glycoproteomics Study of Plasma Glycoproteins in Japanese Semisuper Centenarians

Yuri Miura[1], Yoko Itakura[2], Yasumichi Arai[3], Machiko Iwamoto[1], Masashi Toyoda[2], Hideki Kinoshita[4], Yutaka Unuma[4], Tosifusa Toda[5], Nobuyoshi Hirose[3], Tamao Endo[1]

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Proteomic Analysis of Glycation and Glycosylation in a Diabetic Model Otsuka Long-Evans Tokushima Fatty (OLETF) Rat Using a Novel Boronate Affinity 2-DE

Yuichi Aikyo, Kenichi Nakazato, Masamichi Oh-Ishi

Department of Physics, Kitasato University School of Science, Japan

Label Free Quantitative Proteomic Analysis of Phosphoprotein and Glycoprotein of Aged Mouse Muscle Tissue

Na-Young Han[1], Jong-Moon Park[1], Sung-Chun Cho[3], Je-Hyun Baek[4], Sang-Chul Park[3], Hookeun Lee[1,2]

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Absolute Quantitation of Beta-Amyloid Peptide and Alpha-Synuclein Protein in Animal Models of Neurodegenerative Diseases Using Selected Reaction Monitoring

Adrien W. Schmid, Marc Moniatte

Proteomics Core Facility, Swiss Federal Institute of Technology, EPFL, Switzerland

PTM I: Phosphorylation, Acetylation, Methylation

POS-02-242

Acetylated Proteins Involved in Resistance to EGFR Tyrosine Kinase Inhibitors in Non-Small Cells Lung Cancer

Sylvia G. Lehmann[1,2,3], Laetitia Vanwonterghem[1,2], Amandine Hurbin[1,2], Michel Seve[1,2,3], Sandrine Bourgoin-Voillard[1,2,3]

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POS-02-243

Quantitative Analysis of the Phosphorylation State of a Hybrid Histidine Kinase in Bacterial Two-Component System by Using Phosphate-Affinity SDS-PAGE

Keisuke Edahiro, Akio Shiba, Emiko Kinoshita-Kikuta, Yuki Inoue, Eiji Kinoshita, Tohru Koike

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POS-02-244

Functional Proteomics Defines the Molecular Switch Underlying FGF Receptor Trafficking and Cellular Outputs

Chiara Francavilla[1], Kristoffer T.G. Rigbolt[2], Kristina B. Emdal[1], Gianni Carraro[3], Erik Vernet[1], Dorte B. Bekker-Jensen[1], Werner Streicher[1], Mats Wikstrom[1], Michael Sundstrom[1], Saverio Bellusci[3], Ugo Cavallaro[4], Blagoy Blagoev[2], Jesper V. Olsen[1]

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POS-02-245

Phos-Tag Biotin as an On-Demand Tool for Study on Protein Phosphorylome

Eiji Kinoshita, Emiko Kinoshita-Kikuta, Tohru Koike

Department of Functional Molecular Science, Institute of Biomedical & Health Sciences, Hiroshima University, Japan

POS-02-246

Phosphorylation Profiling of MAPK Signaling Cascade Proteins by Using Neutral Phos-tag SDS-PAGE

Emiko Kinoshita-Kikuta, Eiji Kinoshita, Tohru Koike

Department of Functional Molecular Science, Institute of Biomedical & Health Sciences, Hiroshima University, Japan

POS-02-247

A New Signaling Cascade in Breast Cancers with p53 Inducible Protein Phosphatase PPM1D Overexpression

Yuuki Kozakai, Yoshiro Chuman, Yuhei Kiyota, Toshiaki Imagawa, Kazuyasu Sakaguchi

Laboratory of Biological Chemistry, Department of Chemistry, Faculty of Science, Hokkaido University, Japan

POS-02-248

Old Tools in a New Jacket: Phosphopeptide Enrichment by TiO_2 and IMAC Columns

Simone Lemeer, Benjamin Ruprecht, Heiner Koch, Max Mundt, Bernhard Kuster

Chair of Proteomics and Bioanalytics, Technische Universitaet Muenchen, Germany

POS-02-249

Global Survey of Mouse Liver Protein Expression Using Off-Gel Isoelectric Focusing of Tryptic Peptides and LTQ-Orbitrap

Ying Li[1], Hong Liu[1], Siting Liu[1], Pengyuan Yang[1,2], Huizhi Fan[1]

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POS-02-250   PS09-03

Enhanced Phosphopeptide Identification in *Escherichia coli* by Stepwise Hydroxy Acid-Modified Metal Oxide Chromatography with Elevated Sample Loading Capacity

Miao-Hsia Lin, Shunsuke Takagi, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

POS-02-251

Mapping Global Histone Acetylation Patterns Using MALDI-TOF Mass Spectrometry

Gabriela Lochmanova[1], Iva Mitosinkova[2], Zbynek Zdrahal[1,2]

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POS-02-252

A Large Synthetic Phosphopeptide Library for Mass Spectrometry Based Proteomics

Harald Marx[1], Simone Lemeer[1], Jan Erik Schliep[1], Lucrece Matheron[2], Shabaz Mohammed[2], Juergen Cox[3], Matthias Mann[3], Albert Heck[2], Bernhard Kuster[1]

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POS-02-253

In Vivo Screening of Kinase-Specific Substrates by Phosphatase Inhibitor and Kinase Inhibitor Substrate Screening (PIKISS)

Tomoki Nishioka, Shinichi Nakamuta, Tomonari Hamaguchi, Mutsuki Amano, Kozo Kaibuchi

Department of Cell Pharmacology, Nagoya University Graduate School of Medicine, Japan

POS-02-254

Phosphoproteomic Analysis of Gamma-Irradiated Human Leukemic Cells

Barbora Salovska[1,2], Ales Tichy[1,2], Martina Rezacova[1], Jirina Vavrova[2]

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POS-02-255

Quantitative Analysis of Effects of pH on the Stability of His- and Asp-Phosphoproteins in Bacterial Two-Component System by Using Phosphate-Affinity SDS-PAGE

Akio Shiba, Keisuke Edahiro, Emiko Kinoshita-Kikuta, Eiji Kinoshita, Tohru Koike

Department of Functional Molecular Science, Graduate School of Biomedical & Health Sciences, Hiroshima University, Japan

POS-02-256 ★Travel Award

Sequential Phosphoproteomic Enrichment by Complementary Metal-Directed Immobilized Metal Ion Affinity Chromatography: Case Study on Kinase Substrate Mapping in Human Lung Cancer Tissue

<u>Chia-Feng Tsai</u>[1,2], Chuan-Chih Hsu[2], Jo-Nan Hung[1], Yi-Ting Wang[2,3,4], Pei-Yi Lin[2], Yu-Ju Chen[1,2,3,4]

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POS-02-257

Rapid and Selective Separation of Phosphorylated Biomolecules by Using a Phos-Tag-Based Magnetic-Bead Method

<u>Masaya Tsunehiro</u>, Yuma Meki, Emiko Kinoshita-Kikuta, Eiji Kinoshita, Tohru Koike

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POS-02-258

Proteomic Identification of the Posttranslational Modifications in TrkA-mediated Tyrosine Phosphorylation Signaling Network

<u>Eun Joo Jung</u>, Choong Won Kim

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POS-02-259 PS20-04

Identification of Dysregulated Kinase-Mediated Pathways in Hepatocellular Carcinoma by a Quantitative Phosphoproteome Approach

<u>Yu-Tsun Lin</u>[1], Kun-Yi Chien[1], Chau-Ting Yeh[1,2], Jau-Song Yu[1]

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POS-02-260

A Phospho-Peptide Spectrum Library for Improved Targeted Assays

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POS-02-261

Phosphoproteomics Approach Coupled with *In Vitro* Kinase Reaction to Construct Kinase-Substrate Network

<u>Haruna Imamura</u>, Naoyuki Sugiyama, Masaki Wakayashi, Yasushi Ishihama

Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

POS-02-262

Targeted Phosphoproteomics Analysis of Immunoaffinity Enriched Tyrosine Phosphorylation in Mouse Tissues

<u>Ravi K Krovvidi</u>[1], Jeffrey C Silva[2], Leo E Bonilla[3], Charles Farnsworth[2]

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POS-02-263 YI03-02

A Novel Titanium Dioxide Plate (TiO_2 plate) for Phosphopeptide Enrichment and On-Target MALDI-TOF Analysis

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China Medical University

POS-02-264

Novel Strategy for Lysine Acetylation Discovery Without Using Immunoprecipitation

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Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

POS-02-265

LC-MALDI-TOF-TOF Mass Spectrometry Distinguishing between Symmertric/Asymmetric Dimethylated Arginine3 of Histone H4 Peptide

Yoko Chikaoka[1], Matthew Openshaw[2], Yuzo Yamazaki[3], Omar Belgacem[2], Takeshi Kawamura[1], Tatsuhiko Kodama[1]

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POS-02-266

Deep Profiling of Molecular-Targeted Drugs by One-Shot Quantitative Phosphoproteomics

Yu Hayashi, Suguru Ichihara, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

POS-02-267

mTOR Complex 2 Phosphorylates Filamin A to Regulate Cell Migration

Tatsuhiro Sato, Yoshio Shibagaki, Seisuke Hattori

Kitasato University, School of Pharmacy, Division of Biochemistry, Japan

POS-02-268

Functional Analysis of Targeted Phosphorylation on Signaling Proteins

Ming-Quan Guo

Key Laboratory of Plant Germplasm Enhancement and Specialty Agriculture, Wuhan Botanical Garden, China

POS-02-269

Impact of High Glucose Concentration on ASA-Induced Acetylation of Human Serum Albumin: An in Vitro Study

Francesco Finamore[1], Feliciano Priego-Capote[2], Florent Gluck[1], Anne Zufferey[1], Pierre Fontana[3], Jean-Charles Sanchez[1]

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POS-02-270

Discovery of Novel Inhibitors for Human Sirtuins

Theresa Nowak[1], Claudia Roessler[2], Michael Scharfe[1], Clemens Steegborn[3], Wolfgang Sippl[1], Mike Schutkowski[2]

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POS-02-271

Quantitative Proteomic Analysis of Post Translational Modifications in Alzheimer's Disease Brain

Nikhat Ahmed

Neurochemistry Research Laboratory, Department of Biochemistry, University of Karachi, Pakistan

POS-02-272   ★Travel Award

Quantitative Phosphoproteome Analysis for Identification of Novel GSK-3 Substrates in HEK293 Cells

Jeng-Ting Chen

Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan

POS-02-273

Global In-Depth Quantitative Proteomic Analysis of HIV Infected Cells Using a Novel Q-OT-qIT Mass Spectrometer

Shannon Eliuk[1], Jeffrey Johnson[2], Vlad Zabrouskov[1], Nevan Krogan[2]
[1]Thermo Fisher Scientific, [2]University of California San Franciso, USA

POS-02-274

Phsophoproteomic Analysis of the Model *Cyanobacterium Synechococcus* sp. Strain PCC 7002

Feng Ge
Institute of Hydrobiology, Chinese Academy of Sciences

POS-02-275

Quantitative Phosphoproteomic Analysis of Calmodulin-Dependent Calcium Signaling

Atsushi Hatano[1], Masaki Matsumoto[2], Keiichi I. Nakayama[1]
[1]Department of Molecular and Cellular Biology, Medical Institute of Bioregulation, Kyushu University, Japan, [2]Department of Proteomics, Medical Institute of Bioregulation, Kyushu University, Japan

POS-02-276

Quantitative Variation of Protein Components and Their Phosphorylations in the SWI/SNF Chromatin Remodeling Complex Associated with High Malignancy of Ovarian Clear Cell Adenocarcinoma

Ayuko Kimura[1], Ayako Nomura[1], Takao Kawakami[1,2], Noriaki Arakawa[1], Hisashi Hirano[1]
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POS-02-277   PS13-04

Improved PhosphoTau SRM Assay Sensitivity Enables Multi-Site Tau Phosphorylation Quantitation in a Preclinical Model of AD Treated with Novel Small Molecule Inhibitors of Casein Kinase 1 Delta

Emma Louise Lahert, Claire Louise Russell, Ian Pike, Malcolm Ward
Proteome Sciences plc, UK

POS-02-279

Potent Lipolytic Action of Lactoferrin: Elucidation of the Lipolytic Action Mechanism in Mature Adipocytes, Using Proteomic Approach

Satoru Morishita[1], Keiko Ikoma[1], Ayako Nomura[2], Kanae Taki[1], Tomoji Ono[1,2], Michiaki Murakoshi[1,3], Keikichi Sugiyama[1,4], Hisashi Hirano[2], Hoyoku Nishino[3,4]
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POS-02-280

SILAC-Based Quantitative Phosphoproteome Analysis of Glioblastoma Stem Cell Differentiation by High-Resolution nanoLC-MS/MS

Yuta Narushima[1], Hiroko Kozuka-Hata[1], Yumi Goto[1], Tomoko Hiroki[1], Ryo Koyama-Nasu[2], Kouhei Tsumoto[1], Tetsu Akiyama[2], Masaaki Oyama[1]
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POS-02-281

Phosphoproteomics of the Cellular Response to MAPK Blockade in V600EBRAF Mutant Cells

Robert Parker[1], Mark Molloy[1], Roderick Clifton-Bligh[2]
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POS-02-282

Acetyl-Phosphate Links Metabolism to Global Acetylation Dynamics in *E. coli*

Brian Tate Weinert[1], Vytautas Iesmantavicius[1], Sebastian A. Wagner[1], Bertil Gummesson[2], Thomas Nystrom[2], Chunaram Choudhary[1]

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POS-02-283

MRM-Based Absolute Quantitation of Metabolic Enzymes Acetylation

Leilei Xu[1], Fang Wang[1], Hongxiu Yu[2], Pengyuan Yang[1,2]

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POS-02-284

Quantitative Phosphoproteome Analysis in Differentiation of Human Promyelocytic Leukemia Hl-60 Cells

Mitsuaki Yanagida, Masako Miura, Kenji Takamori

Institute for Environmental and Gender Specific Medicine, Juntendo University Graduate School of Medicine, Japan

POS-02-285

Optimization of Enrichment Conditions on TiO$_2$-affinity Chromatography for Phosphoproteomic Analysis

Isao Fukuda, Yoshino Hirabayashi-Ishioka, Ikue Sakikawa, Takeshi Ota, Mari Yokoyama, Takaoki Uchiumi, Atsushi Morita

Shionogi Pharmaceutical Research Center, Shionogi & Co. Ltd., Japan

POS-02-286

Identification of Novel p38 MAP Kinase Substrates Using *In Vitro* Phosphorylation

Naoyuki Iida[1], Masayuki Fujita[1], Kohtaro Miyazawa[1], Michimoto Kobayashi[2], Seisuke Hattori[1]

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POS-02-287

Multidimensional Phosphoproteomic Characterization of Human Embryonic Stem Cells SILAC Labelled Using a Chemically Defined Medium

Albert R. Liberski[1], Muna N. Al-Noubi[1], Najeeb M. Halabi[1], Jeremie A. R. Tabrizi[2], Kasper Engholm-Keller[3,4,5], Roopesh Krishnankutty[1], Hisham Ben Hamidane[1], Pankaj Kumar[1], Marcella N. Melo-Braga[3], Melanie Schulz[3], Martin R. Larsen[3], Rasha Mismar[1], Johannes Graumann[1]

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POS-02-288   PS09-04

Unravelling Cell Signaling Events with Sub-Minute Temporal Resolution

Evgeny Kanshin[1,4], Louis-Philippe Sandoval-Bergeron[1], Pierre Thibault[1,2,4], Stephen Michnick[1,3]

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PTM II: Glycosylation, Glycation, Oxidation

POS-03-001

Abrogated Expression and Identification of O-GlcNAcylated Proteins in Colorectal Cancer Cells

Parunya Chaiyawat[1], Voraratt Champattanachai[1,2], Kriengsak Lirdprapamongkol[2], Chantragan Srisomsap[2], Jisnuson Svasti[1,2]
[1]Chulabhorn Graduate Institute, [2]Chulabhorn Research Institue

POS-03-002

Alcoholic Liver Disease Alters the Glycosylation of Membrane Proteins

Maja N. Christiansen[1], Wil M.H. d'Avigdor[2], Aimei Lee[2], Nicholas Shackel[2], Nicolle H. Packer[1]
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POS-03-003

Large-Scale Identification of Mouse and Human N-Glycoproteins and Data Sharing Through an Experimental-Based Glycoprotein Database, GlycoProtDB

Mika Fujita, Hiroyuki Kaji, Atsushi Kuno, Toshihide Shikanai, Yoshinori Suzuki, Hiromichi Sawaki, Hisashi Narimatsu
Research Center for Medical Glycoscience, AIST, Japan

POS-03-004

Milk Protein Modifications Associated with Processing Treatments

Jessica Gathercole, Stefan Clerens, Rex Humphrey, Paul Harris, Mariza Gomes Reis, Jolon Dyer, Brendan Haigh
AgResearch Ltd., New Zealand

POS-03-005

Multi-Acquisition Ion Mobility Strategies Utilizing LC/MS and MALDI for the Characterization of Enriched Glycopeptides

Lee A Gethings[1], Mark W Towers[1], Chen Chun Chen[2], Pei Yi Lin[2], Yu Ju Chen[2]
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POS-03-006

Advanced nano-LC-MALDI Spotting System for the Detection of Low-Abundance Glycopeptides from Complex Samples

Yusaku Hioki, Ritsuko Tanimura, Koichi Tanaka
Koichi Tanaka Laboratory of Advanced Science and Technology, Shimadzu Corporation, Japan

POS-03-007

In-Depth Characterization of Glycopeptides by Combination of CID and ETD Fragmentation After Charge State Enhancement

Andreas Brekenfeld[1], Kristina Marx[1], Andrea Kiehne[1], Noriyuki Iwasaki[2], Markus Meyer[1]
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POS-03-009

Identification of Ectonucleotide Pyrophosphatase/Phosphodiesterase 3 (ENPP3) as a New Modifier of Glycan Biosynthesis

Hiroaki Korekane[1,2], Jong Yi Park[2], Akio Matsumoto[2], Kazuki Nakajima[2], Shinji Takamatsu[2], Kazuaki Ohtsubo[1,2], Yasuhide Miyamoto[3], Naoyuki Taniguchi[1,2]
[1]Systems Glycobiology Research Group, RIKEN-MAX Planck Joint Research Center, RIKEN Global Research Cluster, [2]Department of Disease Glycomics, Alliance Laboratory, ISIR, Osaka University, Japan, [3]Department of Immunology, Osaka Medical Center for Cancer and Cardiovascular Diseases, Japan

POS-03-010

Application of the Lectin Microarray System to Glycome Mapping of Mouse FFPE Tissue Sections

Atsushi Kuno[1], Atsushi Matsuda[1], Binbin Tan[2], Yan Zhang[2], Takashi Sato[1], Hiroyuki Kaji[1], Hisashi Narimatsu[1]

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POS-03-011

Off-Line Hydrophilic Interaction Liquid Chromatography Enrichment of Glycopeptides Coupled with LC/MS Analysis

Ju Yeon Lee[1,2], Hyun Kyoung Lee[1,3], Gun Wook Park[1,3], Heeyoung Hwang[1], Myeong Hee Moon[2], Jin Young Kim[1], Jong Shin Yoo[1,3]

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POS-03-012

Comprehensive Characterization of the Phosphorylation and Glycosylation of OPN Using Integrated Mass Spectrometry-Based Approaches

Hong Li[2], Guoquan Yan[1], Mingqi Liu[1], Lei Zhang[1], Pengyuan Yang[1,2]

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POS-03-013

LC-MS Ion Trap Workflows for Glycan and Glycopeptide Analysis Using CID and ETD Fragmentation

Kristina Marx[1], Andrea Kiehne[1], Yumiko Matsuyama[2], Ullrike Schweiger-Hufnagel[1]

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POS-03-014   ★Travel Award

Proteomic Analysis of O-Glcnacylated Proteins Associated to Cancer Metastasis in Breast Cancer Cells

Pukkavadee Netsirisawan[1], Voraratt Champattanachai[1,2], Kriengsak Lirdprapamongkol[2], Chantragan Srisomsap[2], Jisnuson Svasti[1,2]

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POS-03-015

Comprehensive Glycome/Glycoproteome Analysis in α1,3-Fucosyltransferase-9 Knockout Mice

Erika Noro[1,2], Akira Togayachi[1], Takashi Sato[1], Nami Suzuki[1], Atsushi Matsuda[1], Atsushi Kuno[1], Hiroyuki Kaji[1], Hisashi Narimatsu[1]

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POS-03-016   YI03-03

Site-Specific N-Linked Glycosylation Analysis by nano-LC Tandem Mass Spectrometry Coupled with a Spectral Library Searching Approach

Pei-Jing Pai, Yingwei Hu, Henry Lam

Department of Chemical and Biomolcular Engineering, The Hong Kong University of Science and Technology, HK

POS-03-017

Large-Scale Identification of Glycoproteins Having LDN Glycans for Mechanism Elucidation in Protein-Specific Glycosylation

Takashi Sato, Hiroyuki Kaji, Hisashi Narimatsu

Research Center for Medical Glycoscience (RCMG), National Institute of Advanced Industrial Science and Technology (AIST), Japan

POS-03-018

Comprehensive Study of O-Linked Glycans of Erythropoietin

Ulrike Schweiger-Hufnagel[1], Kristina Marx[1], Stephanie Kaspar[1], Pierre-Olivier Schmit[2], Anja Resemann[1]

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POS-03-019

Qualitative and Quantitative Investigation of Glyco-Proteoforms from Prostate-Specific Antigen (PSA) in Healthy and Cancer Samples

Ulrike Schweiger-Hufnagel, Kristina Marx, Wolfgang Jabs, Anja Resemann, Detlev Suckau

Bruker Daltonik GmbH, Germany

POS-03-020

Enhancement of the Search Function in JCGGDB

Toshihide Shikanai, Noriaki Fujita, Yoshinori Suzuki, Masako Maeda, Hongling Wen, Madoka Ishizaki, Elena Solovieva, Daisuke Shinmachi, Hideyo Yasuda, Hiromichi Sawaki, Hiroyuki Kaji, Hisashi Narimatsu

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POS-03-021

An LC/MS-based Glycoproteomic Approach for Systematic Identification of *In Vivo* Target Proteins Specific for a Glycosyltransferase Isozyme

Daisuke Sugahara[1,3], Hiroyuki Kaji[1], Kazushi Sugihara[2], Masahide Asano[2], Hisashi Narimatsu[1]

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POS-03-022

Inhibition of N-Glycan Biosynthesis Reveals Site-Specific Glycan Types by a Glycoproteome Approach

Huanhuan Han, Jing Jiang, Bo Peng, Wantao Ying, Xiaohong Qian

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POS-03-023

Glycan Changes of GP73 in Hepatocellular Carcinoma Cell Lines

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POS-03-024

A Complete Workflow Solution for Monoclonal Antibody Glycoform Characterization Combining a Novel Glycan Column Technology and Bench-Top Orbitrap LC-MS/MS

Zhiqi Hao[1], Udayanath Aich[2], Julian Saba[2], Rosa Viner[1], Xiaodong Liu[2], Srinivasa Rao[2], Chris Pohl[2], Andreas Huhmer[1], Patrick Bennett[1]

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POS-03-025

Aberrant Expression of *O*-GlcNAcylated Proteins Associated with Primary Breast Cancer

Voraratt Champattanachai[1,2], Pukkavadee Netsirisawan[2], Parunya Chaiyawat[2], Phaibul Punyarit[3], Chantragan Srisomsap[1], Jisnuson Svasti[1,2]
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POS-03-026

Biomarker Discovery of N-glycopeptide of Immunoprecipitated Vitronectin from Human Cancer Plasma by High Resolution Mass Spectrometry

Heeyoun Hwang[1], Hyun Kyoung Lee[1,2], Ju Yeon Lee[1,3], Gun Wook Park[1,2], Jong Shin Yoo[1,2], Jin Young Kim[1]
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POS-03-027

GlycoProtein Analysis (GPA): High-Throughput MS Platform for Automated N-linked Glycoproteome Analysis and Its Application to Human Plasma for Biomarker Discovery

Jin Young Kim[1], Gun Wook Park[1,2], Ju Yeon Lee[1,3], Hyun Kyoung Lee[1,2], Heeyoun Hwang[1], Yeong Hee Ahn[1], Hyun Joo An[2], Jae-Han Kim[4], Jong Shin Yoo[1,2]
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POS-03-028   PS24-04

Breast Cancer Tumour Transformation from Primary Tumour to Secondary Site

Emila Kurbasic[1], Sofia Waldemarson[1], Peter James[1], Emma Nimeus Malmstrom[2]
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POS-03-029

Site-Specific Analyses of N-Glycans on Haptoglobin in Sera of Patients with Various Kinds of Cancers: A Possible Implication of Differential Diagnosis for Cancer

Miyako Nakano[1], Shiro Takahashi[1], Eiji Miyoshi[2]
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POS-03-030   ★Travel Award

Comparison of Single, Serial and Multiple Lectin Affinity Chromatography Using Secreted Proteins from Colorectal Cancer Cell Lines

Manveen K Sethi[1], Nicolle H Packer[1], Mark S Baker[1], Susan Fanayan[1], William S Hancock[2]
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POS-03-031

Acquired Drug Resistance by Alteration of Glycan Structure on Leukemia Cell-Membrane Glycoproteins

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POS-03-032

Improvement of Lectin Microarray-Based Tissue Glycan Profiling with Lectin-Assisted Fractionation for Glyco-Biomarker Discovery

Binbin Tan[1,2], Atsushi Matsuda[1], Atsushi Kuno[1], Yan Zhang[2], Hisashi Narimatsu[1,2]
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POS-03-033

Extensive Characterization of Glycoconjugates in Nanobioparticles in Blood - Analysis of HDL and Other Lipoproteins

Carlito Lebrilla
University of California, USA

POS-03-034

Significance of Glycosylation-Focused Proteome Strategy for Discovery of the Biomarker of Heart Failure

Chiaki Nagai, Naoto Minamino
Department of Molecular Pharmacology, National Cerebral and Cardiovascular Center Research Institute

POS-03-035

Direct Proteomics Analysis of Protein Oxidation in Blood Plasma of Alzheimer's Disease Patients

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POS-03-036

Glycomic Approach for Identification of Diagnostic Markers of the Acquisition of Drug Resistance Against Microtubule-Targeting Drugs

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POS-03-037

Resolving Double Disulfide Bond Patterns in SNAP25B Using Liquid Chromatography-Ion Trap Mass Spectrometry

Nozomi Ogawa[1], Ryan Taylor[2], Dixon Woodbury[1], John Prince[2]
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POS-03-038

UniCarbKB: Connecting Proteomics with Glycomics

Nicolle H. Packer[1], Matthew P. Campbell[1], Frederique Lisacek[2]
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POS-03-039

DJ-1 Isoforms are Altered in Mouse Hypothalamus Upon High-Fat Diet

Gereon Poschmann[1], Katrin Seyfarth[2], Helmut E. Meyer[3], Martin Klingenspor[2], Stuehler Kai[1]
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POS-03-040

Recent Advances in Glycoprotein Analysis by Mass Spectrometry

Marshall Bern[1], Christopher Becker[1], Wilfred Tang[1], Yong J. Kil[1], Xiaoke Yin[2], Manuel Mayr[2], K.-H. Khoo[3], Rosa Viner[4]
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POS-03-041

Cell Surface Proteome Profiling to Discover Therapeutic Targets for Adult T-Cell Leukemia

Koji Ueda[1], Makoto Ishihara[1], Natsumi Araya[2], Tomoo Sato[2], Ayako Tatsuguchi[1], Naomi Saichi[1], Atae Utsunomiya[3], Yoshihisa Yamano[2], Hidewaki Nakagawa[1]
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POS-03-043

Glycan Structural Elucidation on a Novel Quadrupole Dual Cell Linear Ion Trap Orbitrap Hybrid Mass Spectrometer

Julian Saba[1], Katie Southwick[1], Shannon Eliuk[1], Sergei Snovida[2], Vlad Zabrouskov[1], Daisuke Higo[3]
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POS-03-044   YI03-08

Mass Isotopomer Analysis of Metabolically Labeled Nucleotide Sugars and N- and O-Glycans for Tracing Nucleotide Sugar Metabolisms

Kazuki Nakajima
Systems Glycobiology Research Group, RIKEN

POS-03-046

Modulation of the Intracellular Phosphorylation-Dependent Signaling Upon Sialoglycoconjugates Remodeling in Cancer

Giuseppe Palmisano, Martin Rossel Larsen
University of Southern Denmark, Denmark

POS-03-047

Age- and Sex-Associated Differences in the Glycopatterns of Human Salivary Glycoproteins and Their Roles Against Influenza A Virus

Yannan Qin[1], Yaogang Zhong[1], Minzhi Zhu[1], Liuyi Dang[1], Hanjie Yu[1], Zhuo Chen[1], Wentian Chen[1], Xiurong Wang[2], Hua Zhang[3], Zheng Li[1]
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POS-03-048

Global Substrate Profiling of the UDP-GalNAc: Polypeptide *N*-Acetylgalactosaminyltransferase Using A Human Proteome Microarray

Xing Li, Wenxian Xie, Zhijue Xu, Jing Wang, Shu-min Zhou, Li Cheng, Sheng-ce Tao, Yan Zhang
Ministry of Education Key Laboratory of Systems Biomedicine, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University, China

POS-03-049

Glycosylation of Human Plasma Clusterin Yields Novel Biomarkers of Alzheimer's Disease

Malcolm Ward[1], Hui-Chung Liang[1], Claire Russell[1], Ray Chung[2], Abdul Hye[2], Chantal Bazenet[2], Simon Lovestone[2], Ian Pike[1], Emma Lahert

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POS-03-050

N-Linked Global Glycan Profiling from Human Gastric Cancer Tissue Using High Performance Liquid Chromatography on a Microfluidic Chip and Time-of-Flight Mass Spectrometry

Jong-Moon Park[1], Na-Young Han[1], Su-Jin Kim[3], Seung Ho Choi[4], Hark Kyun Kim[4], Sang-Won Lee[3], Hookeun Lee[1,2]

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POS-03-051

Novel Glycan Column Technology for the LC-MS Analysis of Labeled and Native N-Linked Glycans

Julian Saba[1], Udayanath Aich[2], Xiaodong Liu[2], Srinivasa Rao[2], Yury Agroskin[2], Chris Pohl[2]

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POS-03-052

Quantitative Mapping of Glycoprotein Micro- and Macro- Heterogeneity: An Evaluation of Mass Spectrometry Signal Strengths Using Synthetic Peptides and Glycopeptides

Kathrin Stavenhagen[1,2], Hannes Hinneburg[1], Morten Thaysen-Andersen[3], Laura Hartmann[1], Daniel Varón Silva[1], Jens Fuchser[4], Stephanie Kasper[4], Detlev Suckau[4], Erdmann Rapp[2], Peter H. Seeberger[1,5], Daniel Kolarich[1]

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POS-03-053

From Qualitative to Quantitative: The Evolution of Glycoproteomics

Michael Blank[1], David Horn[1], Marshall Bern[2], Michael Athanas[1], Amol Prakash[1], Scott Peterman[1], Julian Saba[1], Rosa Viner[1]

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POS-03-054

In-Depth Structural Characterization of Glycopeptides Using Complete Derivatization for Carboxyl Groups Followed by Tandem Mass Spectrometry

Takashi Nishikaze, Shin-ichirou Kawabata, Koichi Tanaka

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POS-03-055

Glycomic Analysis Using Glycoprotein Immobilization for Glycan Extraction

Shuang Yang, Yan Li, Punit Shah, Hui Zhang

Department of Pathology, Johns Hopkins University, USA

PTM III: All other PTMs

POS-03-056

Impaired Tryptic Proteolytic Activity at Citrullinated Amino Acids

Tue Bennike[1], Kasper B. Lauritsen[1], Vibeke Andersen[2], Svend Birkelund[1], Allan Stensballe[1]
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POS-03-057

Crystal Structure of Tyrosylprotein Sulfotransferase: The Reaction Mechanism of Post-Translational Tyrosine Sulfation

Takamasa Teramoto[1,2], Katsuhisa Kurogi[3], Yoichi Sakakibara[3], Ming-Cheh Liu[4], Masahito Suiko[3], Makoto Kimura[1,2], Yoshimitsu Kakuta[1,2]

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POS-03-058

Mass Spectrometric Identification of Glycosylphosphatidylinositol-Anchored Peptides

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POS-03-059

Functional Studies of Post-Translational Modification by Tyrosine Sulfation: Knockdown Analysis of Three Kinds of Zebrafish Tyrosylprotein Sulfotransferases

Emi Mishiro-Sato[1,2], Tomomi Kondo[1], Naoya Kenmochi[3], Tamayo Uechi[3], Katsuhisa Kurogi[1], Ming-Cheh Liu[4], Masahito Suiko[1], Yoichi Sakakibara[1]

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POS-03-060

A Proteomics Strategy for Identification of FAT10 Modified Proteins and Specific Sites by Mass Spectrometry

Ling Leng[1], Changming Xu[2], Jiyang Zhang[2], Boya Liu[1], Jie Ma[1], Ning Li[1], Weijie Qin[1], Wanjun Zhang[1], Chengpu Zhang[1], Xiaohua Xing[1], Linhui Zhai[1], Fan Yang[1], Mansheng Li[1], Chaozhi Jin[1], Yanzhi Yuan[1], Ping Xu[1], Jun Qin[1], Hongwei Xie[2], Fuchu He[1], Jian Wang[1]
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POS-03-061

Nitroproteomics Analyses of Pituitary Adenomas

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POS-03-062

USP-t Elongates Telomerase Activity by Stabilizing Human Telomerase Reverse Transcriptase (hTERT)

Key-Hwan Lim, Jang-Joon Park, Jin-Ock Kim, Bon-Hee Gu, Kwang-Hyun Baek
Department of Biomedical Science, CHA University, Bundang CHA General Hospital, Korea

POS-03-063

The Roles of HAUSP/USP7 Deubiquitinating Enzyme in Human Cancer and Apoptosis

Jang-Joon Park, Key-Hwan Lim, Bon-Hee Gu, So-Ra Kim, Kwang-Hyun Baek
Department of Biomedical Science, CHA University

POS-03-064

Identification of Novel Human N-myristoylated Proteins Using cDNA Resource and Cell-Free Protein Synthesis System

Toshihiko Utsumi[1], Emi Takamitsu[1], Takashi Suzuki[2], Koko Moriya[1]
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POS-03-065

Quantitative Analysis of Deamidation and Isomerization in β2-Microglobulin by ^{18}O Labeling

Masafumi Fukuda, Toshifumi Takao
Institute for Protein Research, Osaka University, Japan

POS-03-066

USPJ is Critical for Regulating 14-3-3 in Cell Proliferation

Jin-Ock Kim, Key-Hwan Lim, Lan Li, Jun-Hyun Kim, Eun-Hea Kim, Kwang-Hyun Baek
Department of Biomedical Science, CHA University

POS-03-067

N-Terminal Modification of Proteasome Subunit Rpt1 in Yeast

Yayoi Kimura, Yoichi Kurata, Akiyo Ishikawa, Akiko Okayama, Masahiro Kamita, Hisashi Hirano
Yokohama City University, Japan

POS-03-068

Second Generation Electron Transfer Dissociation (ETD) on a Novel Hybrid Instrument with Improved Functionality, Increased Speed, and Robustness of Data

Christopher Mullen[1], Lee Earley[1], Jean-Jacques Dunyach[1], John E.P. Syka[1], Philip Daniel Compton[3], Jeffrey Shabanowitz[2], Donald F. Hunt[2]
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POS-03-069

Systems-Wide Analysis of Protein Ubiquitylation in Response to DNA Damage

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POS-03-070   YI03-04

Proteome-Wide Identification of Poly (ADP-ribosyl)ation Targets in Different Genotoxic Stress Responses

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POS-03-071

Analysis of Post-Translational Modifications in Human Transthyretin Associated with Familial Amyloidotic Polyneuropathy by Targeted LC/MS and Intact Protein MS

Marta Vilà[1], Núria Colomé[1], Antoni Planas[1], <u>Stephanie Kaspar</u>[3], Pierre-Olivier Schmit[4], Carsten Baessmann[3], Francesc Canals[2]

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POS-03-072

Site-Specific Quantitative Analysis of Protein Ubiquitylation in Cellular Signaling

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POS-03-073

Identification of Differentially S-Nitrosylated Proteins in Alzheimer's Disease Brain

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Quantitative and Differential Proteomics

POS-03-074

Comparative Secretomics Reveals Wound Environment Acidification-Associated Secretome and Novel Microbial Virulence Factors for Group A *Streptococcus pyogenes* Infection

Yao-Tseng Wen[1], Jie-Siou Wang[1], Sue-Han Tsai[1], Jiunn-Jong Wu[2], <u>Pao-Chi Liao</u>[1]

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POS-03-075

Multiplexed Quantitative Analysis of 51 Proteins in Human Tears Using High Resolution Multiple Reaction Monitoring (HR-MRM) Mass Spectrometry

<u>Roger W Beuerman</u>[1,2,3], Louis Tong[1,4], Siew Kwan Koh[1], Lei Zhou[1,2,3]

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POS-03-076   YI01-04

Targeted Proteomics to Validate and Quantify One-Hit Wonders Proteins in Human Liver

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POS-03-077

The Human Embryonic Secretome

<u>Thomas F. Dyrlund</u>[1], Ebbe T. Poulsen[1], Kirstine K. Kirkegaard[2], Jakob Ingerslev[2], Jan J. Enghild[1]

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POS-03-078

Hepatocyte Pathway Alterations in Response to in Vitro Crimean Congo Hemorrhagic Fever Virus Infection

Christophe Fraisier[1,2], Raquel Rodrigues[3], Vinh Vu Hai[1,2], Luc Camoin[4,5], Maya Belghazi[6], Stephanie Bourdon[1], Patrick Fourquet[4,5], Glaucia Paranhos-Baccala[3], Lionel Almeras[1,2], Christophe Nicolas Peyrefitte[3,7]

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POS-03-079   YI02-08

Targeted Analysis of *Salmonella* Effector Proteins Using Multiple Reaction Monitoring

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POS-03-080

Fibroblast Activation Protein (FAP) Degradomics

Elizabeth Hamson[1], Stefan Tholen[2], Maria Koczorowska[2], Charles Bailey[1], Fiona Keane[1], Oliver Schilling[2], Mark Gorrell[1]

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POS-03-081

Honeybee Worker (*Apis mellifera ligustica*) Larvae Have a More Diverse Hemolymph Proteome Than Pupae

Bin Han, Dereje Woltedji, Jianke Li, Yu Fang, Mao Feng

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POS-03-082

Absolute Quantitation of Yeast Kinases by Means of LC-MS/MS Using QconCat and SRM Technologies

Y Haramaki[1], PJ Brownridge[2], V Harman[2], S Cubbon[3], JPC Vissers[3], C Lawless[4], SJ Hubbard[4], RJ Beynon[2]

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POS-03-083

The Profiling of the Effects of Adenomatous Polyposis Coli (APC) Mutation on the Cellular Proteome in Colorectal Cancer Cells

Yasuhiro Irino[1], Akiyo Koshiyama[2], Tomoko Ichibangase[2], Kazuhiro Imai[2], Masaru Yoshida[1,3]

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POS-03-084

Proteomic Analysis of Oil Metabolic Pathway in Arthrobacter Nicotinovorans MWB-30

Jonghyun Kim[1], Soo Jung Kim[1], Hyung-Yeel Kahng[2], Seung Il Kim[1], Young-Ho Chung[1]

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POS-03-085

Comparative Proteomics for Yeast Interspecies Differences in Metabolic Pathway and Regulation of Protein Expression

Mihoko Ohnishi, Haruka Ito, Takehiro Nohara, <u>Keiji Kito</u>
Department of Life Science, School of Agriculture, Meiji University, Japan

POS-03-086

Improved Throughput and Reproducibility for Targeted Protein Quantification Using a New High Performance Triple Quadrupole Mass Spectrometer

<u>Reiko Kiyonami</u>, Mary Blackburn, Andreas FR Humer
Thermo Fisher Scientific (San Jose), USA

POS-03-087

Integrated Proteomics Identified Novel Activation of Dynein IC2-GR-COX-1 Signaling by Suppression of NF1 Tumor Suppressor Gene Product, Neurofibromin, in Neuronal Cells

<u>Daiki Kobayashi</u>[1], Mio Hirayama[1], Souhei Mizuguchi[1], Takashi Morikawa[1], Megumi Nagayama[1], Uichi Midorikawa[1], Masayo Wilson-Morifuji[1], Akiko Nambu-Niibori[1], Akiyasu Yoshizawa C.[2], Shin Kawano[3], Norie Araki[1]
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POS-03-088

Altered Protein Expression of Rat Prefrontal Cortex Following Perinatal Asphyxia: Implications of Schizophrenia and Autism

<u>Sylvia Lam</u>[1], Tomoyasu Wakuda[2], Qi Li[1], Ran Wei[1], Xiaofan Zhang[1], Jana Leung[1], Siew Eng Chua[1,3], Pak Sham[1,3], Nori Takei[4], Grainne McAlonan[3,5]
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POS-03-089

Novel Aspects in the Understanding of Honeybee (*Apis mellifera*) Venom from Electrical Stimulation and Manual Extraction from the Venom Gland: A Proteomic Study

<u>Jianke Li</u>, Rongli Li, Yu Fang, Bin Han, Mao Feng
Institute of Apicultural Research/Key Laboratory of Pollinating Insect Biology, Ministry of Agriculture, Chinese Academy of Agricultural Science

POS-03-090

Quantitative Proteomics Applied to Biobank Samples from Patients with Acute Myocardial Infarction Enrolled in SWEDEHEART, The Swedish Cardiac Registry

Melinda Rezeli[1], Akos Vegvari[1], Karin Sjodin[1], Olof Gidlof[2], Gustav Smith[2], Pontus Andell[2], David Erlinge[2], <u>Gyorgy Marko-Varga</u>[1]
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POS-03-091

A Qualitative and Quantitative Ion Mobility Enabled Data Independent SILAC Workflow

<u>T Paxton</u>[1], AJK Williamson[2], S Ciavarini[3], SJ Geromanos[3], A Tudo[4], B Dyson[3], LA Gethings[4], K McMahon[4], R Tonge[4], JI Langridge[4], AD Whetton[2], JPC Vissers[4]
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POS-03-092

Proteomics Profiling of Fuchs Corneal Endothelial Dystrophy (FECD)

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POS-03-093

Analysis of Proteins in the Brain Cortex Tissues of as Alzheimer's Disease Transgenic Mouse (TG)

Bernardo Ramos Raymundo, Gi-Yeon Han, Chan-Wha Kim

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POS-03-094

Changes in Protein Expression Profiles of Brain Tissue during Cervical Cancer Development

Maria Elena Mitzy Rios de Anda, Alberto Checa Rojas, Luis Fernando Delgadillo Silva, Sergio Manuel Encarnacion Guevara

National Autonomous University of Mexico, Mexico

POS-03-095

Serine Protease HtrA1 Accumulates in Corneal Transforming Growth Factor Beta Induced Protein (TGFBIp) Amyloid Deposits

Kasper Runager[1], Henrik Karring[2], Ebbe Toftgaard Poulsen[1], Ida B. Thoegersen[1], Gordon K. Klintworth[3], Peter Hoejrup[4], Jan J. Enghild[1]

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POS-03-096   YI02-05

Establishment and Application of a High-Quality Comparative Analysis Strategy of Low-Abundance Biomarker Peptide in Serum Based on Optimized Novel Peptide Extraction Method

Tatsuya Saito[1], Kawashima Yusuke[1,2], Minamida Satoru[3], Kazumasa Matsumoto[3], Takashi Matsui[4], Mamoru Satoh[5], Fumio Nomura[5,6], Masatsugu Iwamura[3], Tadakazu Maeda[1,2], Shiro Baba[3], Yoshio Kodera[1,2,5]

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POS-03-097

Quantitative Proteome Analysis with Isotope Dimethyl Labeling to Identify TGF-beta-mediated Tumor Proteins Using the Metastatic Mouse Breast Cancer Model

Misako Sato, Jun Adachi, Takeshi Tomonaga

Center National Institute of Biomedical Innovation

iTRAQ-Based Quantitation and Validation by Multiple Reaction Monitoring to Identify Diabetes-Related Biomarkers in Sera from KK-A[y] Diabetes Mice

Eri Takahashi[1,2], Hiroyuki Unoki-Kubota[1], Akinori Okumura[1], Hisashi Hirano[2], Yasushi Kaburagi[1]

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Elucidating the Functional Role of Frataxin (FXN) Over-Expression in HCT116 by a Quantitative Proteomics Approach

Xing Fei Tan, Teck Kwang Lim, Qingsong Lin

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Identification and Quantification of a Novel Prostate Specific Antigen Proteoform (SNP Leu132Ile) in Clinical Samples by Multiple Reaction Monitoring

Akos Vegvari[1], Karin Sjodin[1], Melinda Rezeli[1], Johan Malm[2], Hans Lilja[2], Thomas Laurell[1], Gyorgy Marko-Varga[1,3]

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Stathmin-1 (STMN1) Silencing Restricts Metastatic Processes, Induces Chemosensitisation, and Potentially Inhibits EMT in CRC

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Dynamic Proteomic Survey on the Colon Tissue Interstitial Fluids (TIFs) During Tumorigenesis Process of APC[Min] Mouse Model

Yingying Xie[1], Qiang Shan[1], Lechuang Chen[2], Xiaomin Lou[1], Ju Zhang[1], Yinghui Zhu[1], Yang Wang[1], Ningzhi Xu[2], Siqi Liu[1]

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Confirming Different Roles of Embryo and Endosperm During Rice Seed Germination Though Proteomic Strategy

Chao Han[1,2], Pingfang Yang[1]

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Targeted Protein Quantitation for Plasma Samples by Scheduled MRM-HR Using a TripleTOF Mass Spectrometer

Thiri Zaw, Xiaomin Song, Mark P Molloy

Australian Proteome Analysis Facility, Macquarie University, Australia

POS-03-105   PS13-02

High Resolution MRM Quantification of 300 Tear Proteins Using MS/MS[ALL] with SWATH[TM] Acquisition and Its Application to Biomarker Discovery

Lei Zhou[1,2,3], Louis Tong[1,4], Tina Wong[1,4], Jocelyn Chua[4], Siew Kwan Koh[1], Justin Lim[5], Jason Neo[5], Roger W Beuerman[1,2,3]

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POS-03-106

SILVER: An Efficient Tool for Stable Isotope Labeling LC-MS Data Quantitative Analysis with Quality Control Methods

Cheng Chang[1], Jiyang Zhang[2], Mingfei Han[1], Jie Ma[1], Songfeng Wu[1], Wei Zhang[2], Hongwei Xie[2], Fuchu He[1,3], Yunping Zhu[1]

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POS-03-107

The Comparative Proteomic Study on Ana-1 and Ana-1-Derived Tumor Associated Macrophages

Yinghui Zhu[1], Ju Zhang[1], Yingying Xie[1], Ningzhi Xu[2], Xiaomin Lou[1], Siqi Liu[1]

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POS-03-108

Fast Stable Isotope Labeling of the Murine Intestinal Tract

Liisa Arike, Sjoerd van der Post, Ana Maria Rodriguez Pinero, Anna Ermund, Andre Schutte, George Birchenough, Malin E.V. Johansson, Gunnar C. Hansson

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POS-03-109

Quantitative Proteomic Analysis of the Hippocampus in the 5XFAD Mouse Model at Early Stages of Alzheimer's Disease Pathology

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POS-03-110

Application of Nano-LC Tandem Mass Spectrometry for Screening the Differential Vitreous Protein Expressions in the Lens-Induced Myopic Chicks

Chuen Lam, Fengjuan Yu, King Kit Li, Chi ho To

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POS-03-111

Proteomics Analysis of Endogenous Nuclear Receptor Proteins in Diet Induced Obesity Mouse Liver

Qiongming Liu[1,2], Chen Ding[1,2], Wanlin Liu[1,2], Mingwei Liu[1,2], Lei Song[1,2], Lei Lei[1,2], Bei Zhen[1,2], Yi Wang[3], Jun Qin[1,2,3]

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POS-03-112

Comparison of Cuprizone and Experimental Autoimmune Encephalomyelitis Multiple Sclerosis Models Using TMT and Label-Free Quantitative Proteomics and Translation to Patients

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POS-03-113

Quantitative Proteomic Techniques: Exploring Protein Pathways and Potential Biomarkers in Dorsal Region of Rat Spinal Cord Associated with Neuropathic Pain

Ping Sui[1], Hiroyuki Watanabe[2], Jonas Bergquist[1], Georgy Bakalkin[2], Konstantin Artemenko[1]

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POS-03-114

Combination of a Discovery LC-MS/MS Analysis and a Label-Free Quantification for the Epithelial-Mesenchymal Transition Signature Characterization

Jordane Biarc[1,3], Ivan Mikaelian[2,3], Philippe Gonzalo[2,3], Laurent Fattet[2,3], Pierre-Germain Gillet[2,3], Ruth Rimokh[2,3], Jerome Lemoine[1,3]

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POS-03-115

Quantitative Proteomic Analysis of Serum Proteins in Patients with Gastric Carcinoma Using an Isobaric Tag for Relative and Absolute Quantification Labeling, 2DLC-MS/MS

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POS-03-116

Biomarker Verification: Assessment of the Performances of LFABP as New CRC Marker on 4 Independent Cohorts of 798 Patients, Using ELISA, MRM and MRM3. Detection of CRC Early Stages and Adenomas

Jerome Lemoine[1], Tanguy Fortin[1], Jean-Philippe Charrier[2], Gaspard Gervasi[2], Frederique Steinbrugger[2], Elodie Charmette[2], Corinne Beaulieu[2], Arnaud Salvador[1], Come Lepage[3], Jean Faivre[3], Genevieve Choquet-Kastylevsky[2]

[1]Institut des Sciences Analytiques, UMR 5280 CNRS. Universite Lyon 1, France, [2]bioMerieux, Marcy l'Etoile, France, [3]CHU du Bocage, Dijon (University Hospital), France

POS-03-117   ★Travel Award

Identification of Novel Biomarkers for Prostate Cancer Radioresistance Using the Label-Free LC-MS/MS Approach

Lei Chang[1,2], Valerie Wasinger[3], Peter Graham[1,2], Jingli Hao[1,2], Jie Ni[1,2], Julia Beretov[1,2], Joseph Bucci[1,2], Paul Cozzi[2,4], John Kearsley[1,2], Yong Li[1,2]

[1]Cancer Care Centre, St George Hospital, Australia, [2]St George Clinical School, Faculty of Medicine, UNSW, Australia, [3]Bioanalytical Mass Spectrometry facility, Mark Wainwright Analytical Centre, UNSW, Australia, [4]Department of Surgery, St George Hospital, Australia

POS-03-118

Quantitative Analysis of Colorectal Cancer Secretomes Using MS/MSALL with SWATH? Acquisition

Qifeng Lin[1], Hannah Soo Rei Lim[2], Hui Ling Lin[2], Hwee Tong Tan[1], Teck Kwang Lim[2], Justin Wee Eng Lim[3], Jason Chun Hong Neo[3], Maxey Ching Ming Chung[1,2]

[1]Department of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore, Singapore, [2]Department of Biological Sciences, Faculty of Science, National University of Singapore, Singapore, [3]AB SCIEX, Singapore

POS-03-119

Proteomic Analysis for Discovering Therapeutic Targets and Prognostic Markers for Early-Stage Lung Adenocarcinoma

Akiko Okayama[1], Yohei Miyagi[2], Fumihiro Oshita[2], Mayuko Nishi[1], Yayoi Kimura[1], Yoji Nagashima[1], Akihide Ryo[1], Hisashi Hirano[1]

[1]Yokohama City University, Japan, [2]Kanagawa Cancer Center, Japan

POS-03-120

Gel-Based and Gel-Free Quantitative Proteomic Analysis in Oral Malignant Transformation

Sijia Zhao, Xiaobing Chen, Kai Su, Peixi Liao, Da Ma, Zhi Wang

Guanghua School Stomatology, Hospital of Stomatology, Sun Yat-sen University; Guangdong Provincial Key Laboratory of Stomatology, China

POS-03-121

Protein Dynamics of Human Cancer/Tumour Inducible Model Cell Lines Analysed by Next Generation Proteomics

Kayo Yamada[1], Motoharu Ono[1], Neil D. Perkins[2], Sonia Rocha[1], Angus I. Lamond[1]

[1]Centre for Gene Regulation and Expression, College of Life Sciences, University of Dundee, UK, [2]Institute for Cell and Molecular Biosciences, Medical School, Newcastle University, UK

POS-03-122

Laser Capture Microdissection-based Quantitative Proteomics Analysis of Stromal Differentially Expressed Proteins in the Colon Carcinomas

Xianquan Zhan, Yibing Mu, Guiying Zhang, Zhuchu Chen

Xiangya Hospital, Central South University, China

POS-03-123

Quantative Proteomic Analysis of RIP3 Mediated Cisplatin Sensitivity in ESCC Cells

Shouzhi Ma[1], Linhui Zhai[2], Heng Zhang[2], YuLin Sun[1], Yang Xu[1], Ning Li[2], Chengpu Zhang[2], Tao Zhang[2], Ping Xu[2], Xiaohang Zhao[1,3]

[1]State Key Laboratory of Molecular Oncology, Cancer Institute & Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College, China, [2]State Key Laboratory of Proteomics, Beijing Proteome Research Center, National Engineering Research Center for Protein Drugs, National Center for Protein Sciences Beijing, Beijing Institute of Radiation Medicine, China, [3]Center for Basic Medical Science, Navy General Hospital, China

POS-03-124

Serum Proteome Analysis During Metastatic Processes of Hepatocellular Carcinoma and Function of Transaldolase and Secretory Clusterin

Yinkun Liu[1,2], Cun Wang[1,2], Kai Jiang[2]

[1]Liver Cancer Institute, Zhongshan Hospital, Fudan University, China, [2]Institutes of Biomedical Sciences, Fudan University, China

POS-03-125

Comprehensive and Comparative Proteomics Reveals Alterations of Metabolomics between Monolayer and Three-Dimensional Cell Cultures

Shushi Nagamori[1], Hideki Aizaki[2], Yoshihiro Matsumoto[2], Noriyoshi Isozumi[1], Pattama Wiriyasermkul[1], Tomokazu Matsuura[3], Yoshikatsu Kanai[1]

[1]Bio-system Pharmacology, Osaka University Graduate School of Medicine, [2]Department of Virology II, National Institute of Infectious Diseases, [3]Department of Laboratory Medicine, Jikei University School of Medicine, Japan

POS-03-126 ★Travel Award

A Proteomic Investigation into the Molecular Mechanism of HIV Tat Induced Neuronal Apoptosis

Tariq Ganief[1,2], Shaun Garnett[1], Putuma Gqamana[1], Salomie Smit[2], Jonathan Blackburn[1]

[1]Institute of infectious disease and molecular medicine (IIDMM), University of Cape Town, South Africa, [2]Central Analytical Facilities, Stellenbosch University, South Africa

POS-03-127

Screening for Protein Biomarkers in Alzheimer's Disease Using Multiplex Quantitative Mass Spectrometry

Sravani Musunuri, Magnus Wetterhall, Martin Ingelsson, Lars Lannfelt, Jonas Bergquist, Ganna Shevchenko

Uppsala University, Sweden

POS-03-128

Proteome Analysis of a Hepatocyte-Specific BIRC5-Knockout Mouse Model during Liver Regeneration

Thilo Bracht[1], Marius Loscha[1], Sascha Hagemann[2], Dominik A. Megger[1], Juliet Padden[1], Stephanie Tautges[1], Martin Eisenacher[1], Katja Kuhlmann[1], Helmut E. Meyer[1], Hideo A. Baba[2], Barbara Sitek[1]

[1]Medizinisches Proteom-Center, Ruhr-Universitaet Bochum, Germany, [2]Institut fuer Pathologie, Universitaetsklinikum Essen, Germany

POS-03-129

A Proteomic Analysis of Radio-Resistance in Breast Cancer Cell Lines

Paolo Cifani, Peter James

Protein Technology, Department of Immunotechnology, CREATE Health, Lund University, Sweden

POS-03-130

Quantitative Proteome Analysis of Cervical Cancer Tissues Using a iTRAQ Approach

Alberto Carlos Ramirez-Torres[1], Jeovanis Gil-Valdes[1], Sandra Contreras-Martinez[1], Alejandro Garcia-Carranca[2], Sergio Encarnacion-Guevara[1]

[1]Centro de Ciencias Genomicas. Universidad Nacional Autonoma de Mexico, Mexico, [2]Instituto de Investigaciones Biomedicas. Universidad Nacional Autonoma de Mexico, Mexico

POS-03-131

Label Free Quantitative Proteome Analysis on Cerebrospinal Fluid to Discover Severity Grade Markers for Human T-cell Leukemia Virus Type 1 Associated Myelopathy/Tropic Spastic Paraparesis (HAM/TSP)

Makoto Ishihara[1], Natsumi Araya[2], Sato Tomoo[2], Hidewaki Nakagawa[1], Yoshihisa Yamano[2], Koji Ueda[1]

[1]Laboratory for Biomarker Development, Center of Genomic Medicine, RIKEN, Japan, [2]Department of Molecular Medical Science, Institute of Medical Science, St. Marianna University School of Medicine, Japan

Performance of the Label-Free Differential LC-MS/MS Incorporating Peptide Identification Items to Associate Peptide Detection Signals Among Measurements

Takao Kawakami[1,2], Makiko Otsuji[1], Keiko Nagasaka[1]
[1]Research and Development Division, Medical Proteoscope Company, [2]Advanced Medical Research Center, Yokohama City University, Japan

Quantitative Mass Spectrometric Immunoassay of Clusterin

Makoto Nogami[1,2], Jason W. Jarvis[1], Paul E. Oran[1], Nisha D. Sherma[1], Chad R. Borges[1], Randall W. Nelson[1]
[1]Molecular Biomarkers, The Biodesign Institute at Arizona State University, USA, [2]Research and Development Division, Hitachi High-Technologies Corporation, Japan

Absolute Quantitation of Plasma Biomarker Peptides APL1β for Alzheimer Disease at fmol/ml Level Using SRM

Seizo Sano[1], Shinji Tagami[2], Kumiko Yoshizawa-Kumagaye[3], Masahiko Tsunemi[3], Masayasu Okochi[2], Takeshi Tomonaga[1]
[1]Laboratory of Proteome Research, National Institute of Biomedical Innovation, Japan, [2]Psychiatry, Department of Integrated Medicine, Division of Internal Medicine, Osaka University Graduate School of Medicine, Japan, [3]Peptide Institute, Inc.

Metabolomics Data Normalization Improves Correlation with NMR and Physiology Data

Yuliya Karpievitch[1], Lindsay Edwards[3], Sonja Nikolic[2], James Sharman[2]
[1]School of Mathematics and Physics, University of Tasmania, Australia, [2]Menzies Research Institute Tasmania, Australia, [3]School of Biological Sciences, University of Essex, UK

Deconvolution of Overlapping Peptide Isotopic Clusters with EM Algorithm for Label-free Quantification

Lei Xin[1], Ziaur Rahman[1], Weiwu Chen[1], Zefeng Zhang[1], Mingjie Xie[1], Bin Ma[2]
[1]Bioinformatics Solutions Inc., Canada, [2]University of Waterloo, Canada

Comparative Proteomic Analysis of Early Salt Stress-Responsive Proteins in Roots and Leaves of Rice

Chien-Chen Lai, Chih-Wei Liu, Yu-Kai Hsu
Institute of Molecular Biology, National Chung-Hsing University, Taiwan

Novel Aspects of Understanding Molecular Working Mechanisms of Salivary Glands of Worker Honeybees (*Apis mellifera*) Investigated by Proteomics and Phosphoproteomics

Mao Feng, Yu Fang, Bin Han, Lan Zhang, Xiaoshan Lu, Jianke Li
Institute of Apicultural Research/Key Laboratory of Pollinating Insect Biology, Ministry of Agriculture, Chinese Academy of Agricultural Science, China

High Resolution LC-MS/MS versus SOMAscan Proteomics Platform: An In-Depth Comparison of Two Quantitative Proteomic Technologies

Anja M. Billing, Shaima S. Dib, Hisham Ben Hamidane, Muna N. Al-Noubi, Albert R. Liberski, Johannes Graumann
Proteomics Core, Weill Cornell Medical College in Qatar, Qatar

POS-03-140

Urinary Proteome Variability Assessment of Normal Monozygotic Twins

Young Ah Goo[1], Claire Yang[2], David Goodlett[1]
[1]University of Maryland, USA, [2]University of Washington, USA

POS-03-141

Proteome Analysis of Ginseng Extract, Ginsenoside F2 and Ginsenoside Rg2 Treated Neuronal Cell

Jeong-ju Ha
Department of Physiology, Kyung Hee University School of Medicine, Korea

POS-03-142

Quantitative Proteomics to Study Neuromuscular Disorders

Laxmikanth Kollipara[1], Stephan Buchkremer[2], Andreas Roos[2], René Zahedi[1]
[1]Leibniz-Institut fuer Analytische Wissenschaften - ISAS - e.V., Germany, [2]Institute of Neuropathology, University Hospital RWTH, Germany

POS-03-143   YI01-03

Hidden Proteome: Multiplex Quantitation of Low- and Ultralow-Copy Number Proteins in HepG2 Cells and Human Plasma

Arthur T. Kopylov, Zgoda G. Victor, Lisitsa V. Andrei, Elena Ponomarenko, Ekaterina Poverennaya, Ekaterina Ilgisonis, Alexander A. Moisa, Alexey D. Filimonov, Alexander I. Archakov
Orekhovich Institute of Biomedical Chemistry of the Russian Academy of Medical Sciences, Russia

POS-03-145

Label Free Mass Spectrometry Proteome Quantification of Human Embryonic Kidney Cells Following 24 Hours of Sialic Acid Overproduction

Ville Ilmari Parviainen, Sakari Joenvaara, Niina Johanna Tohmola, Risto Olavi Renkonen
Haartman Institute, University of Helsinki & HUSLAB, Helsinki University Central Hospital, Finland

POS-03-146

Integrating Approach of Proteomics and Metabolomics in EAM Rat Model

Jong Bok Seo, Soo Young Kim, Joo Hee Chung
Korea Basic Science Institute, Korea

POS-03-147

Proteomic Analysis of Human Obesity Reveals Differential Expression of the Epigenetic Factor HDAC4 and Role of Physical Exercise in Correcting Its Expression

Ali Tiss[1], Mohamed Abu-Farha[1], Jehad Abubaker[1], Fahad Al-Ghimlas[2], Irina Al-Khairi[1], Preethi Cherian[1], Naser Elkum[3], Jeena John[1], Sina Kavalakatt[1], Abdelkrim Khadir[1], Samia Warsame[1], Kazem Behbehani[1,2,3], Said Dermime[1], Mohammed Dehbi[1]
[1]Biomedical Research Department, Dasman Diabetes Institute, Kuwait, [2]Fitness and Rehabilitation Centre, Dasman Diabetes Institute, Kuwait, [3]Biostatistics and Epidemiology Department, Dasman Diabetes Institute, Kuwait

POS-03-148

Membrane Proteomic Analysis of the Effect of Lysophosphatidic Acid on Platelet-Monocyte Interaction in the Context of Atherosclerosis

Jiqing Huang, Juergen Kast
The Biomedical Research Centre, University of British Columbia, Canada

Towards the Identification of Yeast Endoplasmic Reticulum Phospholipid Flippase Using Quantitative Proteomics Approach

Roopesh Krishnankutty[1], Madhavan Chalat[2], Anja Billing[1], Hisham Ben Hamidane[1], Albert Liberski[1], Shaima Salah Dib[1], Muna N. Al-Noubi[1], Anant K. Menon[2], Johannes Graumann[1]

[1]Proteomics Core, Weill Cornell Medical College in Qatar, Research Division, Qatar Foundation, Qatar, [2]Department of Biochemistry, Weill Cornell Medical College, USA

Improving Throughput of Relative Protein Quantitation Using 10 Plex Isobaric Tags

Rosa Viner[1], Ryan Bomgarden[2], Michael Blank[1], John Rogers[2], Masayuki Kubota[3]

[1]Thermo Fisher Scientific (San Jose), USA, [2]Thermo Fisher Scientific (Rockford), USA, [3]Thermo Fisher Scientific, Japan

A Six-Plex Proteome Quantification Strategy Reveals the Dynamics of Protein Turnover

Kai Cheng, Fangjun Wang, Xiaoluan Wei, Hanfa Zou

Key Lab of Separation Science for Analytical Chemistry, National Chromatography R&A Center, Dalian Institute of Chemical Physics, the Chinese Academy of Science, China

Quantification of Peptides in Clinical Samples Based on High-Resolution Mass Measurements

Bruno Domon, Sebastien Gallien, Antoine Lesur, Marie-Aline Pierrard, Yeoun-Jin Kim, Guy Berchem

Luxembourg Clinical Proteomics Center, CRP-Sante, Luxembourg

Liver Mitochondria Proteomics Employing High Resolution MS Technology

Jenny T.C Ho[1], Loic Dayon[2], John Corthesy[2], Umberto de Marchi[2], Antonio Nunez[2], Andreas Wiederkehr[2], Rosa Viner[3], Michael Blank[3], Steve Danielson[3], Madalina Oppermann[1], Martin Hornshaw[1], Martin Kussmann[2,4,5]

[1]ThermoFisher Scientific, UK, [2]Nestle Institute of Health Sciences, Switzerland, [3]Thermo Fisher Scientific (San Jose), USA, [4]Faculty of Life Sciences, Ecole Polytechnique Federale Lausanne (EPFL), Switzerland, [5]Faculty of Sciences, Aarhus University, Denmark

Quantitative CID Cleavable Crosslink Strategy on a Benchtop Instrument Using All-Ion-Fragmentation and SILAC

Richard Alexander Scheltema, Herbert Schiller, Matthias Mann

Max Planck Institute for Biochemistry, Germany

Compared Performances of Different Targeted Proteomics Approaches on a Benchtop UHR-Q-TOF

Stephanie Kaspar[1], Wolfgang Jabs[1], Andrew Percy[2], Carsten Baessmann[1], Pierre-Olivier Schmit[4], Jouji Seta[3], Christoph Borchers[2]

[1]Bruker Daltonik GmbH, Germany, [2]University of Victoria, Genome BC Proteomics Centre, Canada, [3]Bruker Daltonics K.K., Japan, [4]Bruker Daltonique S.A., France

POS-03-156   ★Travel Award

Global *In Vivo* Terminal Amino Acid Labeling for Exploring Dialyzed Serum Cultivation Induced Proteins Differential Expression in SILAC Studies

Li-Qi Xie[1,2], Ai-Ying Nie[1], Chao Zhao[2], Lei Zhang[1], Peng-Yuan Yang[1,2], Hao-Jie Lu[1,2]

[1]Shanghai Cancer Center and Department of Chemistry, Fudan University, China, [2]Key Laboratory of Medical Molecular Virology and Institutes of Biomedical Sciences, Shanghai Medical College, Fudan University,China

POS-03-157

Quantitative Proteomics Analysis Reveals the Significant Changes on the Cell Shape and Energy Shift After IPTG Inducing Via SILAC Approach on *Escherichia coli*

Heng Zhang[1], Lingyan Ping[1], Duc M. Duong[1,3], Eric B. Dammer[1,3], Linhui Zhai[1], Lei Chang[1], Junzhu Wu[2], Ping Xu[1]

[1]State Key Laboratory of Proteomics, Beijing Proteome Research Center, National Engineering Research Center for Protein Drugs, National Center for Protein Sciences Beijing, Beijing Institute of Radiation Medicine, China, [2]Wuhan University, China, [3]Emory University, USA

POS-03-158

A Hybrid Multiple Reaction Monitoring Method Using mTRAQ/iTRAQ Labeling for Multiplex Absolute Quantification and Validation of Human Colorectal Cancer Biomarker

Hong-Rui Yin[1,2], Lei Zhang[1], Li-Qi Xie[1], Li-Yong Huang[1], Ye Xu[1], San-Jun Cai[1], Peng-Yuan Yang[1,2], Hao-Jie Lu[1,2]

[1]Shanghai Cancer Center and Institutes of Biomedical Sciences, Fudan University, China, [2]Department of Chemistry, Fudan University, China

POS-03-159

Increasing the Breadth and Depth of Multi-Notch MS3-based TMT Quantitation Using a Hybrid Q-OT-qIT Mass Spectrometer

Graeme Mcalister[1], Edward Huttlin[1], Mark Jedrychowski[1], Martin Wuehr[1], Ramin Rad[1], David Nusinow[1], Philip Remes[2], Jesse Canterbury[2], Vlad Zabrouskov[2], Justin Blethrow[2], Shannon Eliuk[2], Mike Senko[2], Julian Saba[2], Wilhelm Haas[1], Steven Gygi[1]

[1]Harvard Medical School, USA, [2]Thermo Fisher Scientific (San Jose), USA

POS-03-160

Development of SRM Methods for the Detection and Quantification of Chromosome 16 Proteins

Maria I Mora[1], Nuria Colome[2], Francesc Canals[2], Felipe Clemente[3], Concha Gil[3], Patricia Fernandez[4], Cristina Ruiz[4], Irene Orera[5], Silvia Barcel[6], Miguel Marcilla[7], Juan Pablo Albar[1,7], Fernando J. Corrales[1]

[1]ProteoRed-ISCIII, Center for Applied Medical Research (CIMA), University of Navarra. Spain, [2]ProteoRed-ISCIII. Proteomics Laboratory Vall d Hebron University Hospital Research Institute, Spain, [3]ProteoRed-ISCIII, Departamento de Microbiologia II, Facultad de Farmacia, Universidad Complutense de Madrid, Spain, [4]ProteoRed-ISCIII, Osteoarticular and Aging Research Lab, Proteomics Unit, Rheumatology Division, INIBIC-CHU A Coruna, Spain, [5]Instituto Aragon de Ciencias de la Salud, Spain, [6]Institut D'Investigacio Biomedica de Bellvitge (IDIBELL), Barcelona, Spain, [7]ProteoRed-ISCIII, Centro Nacional de Biotecnologia - CSIC, Spain

POS-03-161

Proteomic Analysis of Whole Glomeruli in Patients with IgA Nephropathy Using Micro-Sieving

Shigeki Kojima[1,2], Kenichiro Koitabashi[2], Nobuko Iizuka[1], Kazuki Okamoto[1], Mitsumi Arito[1], Toshiyuki Sato[1], Manae (S) Kurokawa[1], Naoya Suematsu[1], Takashi Yasuda[2], Kenjiro Kimura[2], Tomohiro Kato[1]

[1]Clinical Proteomics and Molecular Medicine, St. Marianna University Graduate School of Medicine, Japan, [2]Division of Nephrology and Hypertension, Department of Internal Medicine, St. Marianna University School of Medicine, Japan

POS-03-162

Whole Cell Proteome Quantification and Cell Shaving Analyses of the *Staphylococcus aureus* Response to Oxacillin

Nestor Solis[1], Stephen Kwong[3], Neville Firth[3], Mark Graham[4], Stuart J Cordwell[1,2]

[1]School of Molecular Bioscience, The University of Sydney, Australia, [2]Discipline of Pathology, School of Medical Sciences, The University of Sydney, Australia, [3]School of Biological Sciences, The University of Sydney, Australia, [4]Cell Signalling Unit, Children's Medical Research Instititue

POS-03-163

Proteome-Wide Dysregulation by G6PD Reveals a Novel Protective Role for G6PD in Aflatoxin B1-Mediated Cytotoxicity

Hao-Ping Liu[1], Hsin-Ru Lin[2,3], Daniel Tsun-Yee Chiu[2,3], Chih-Ching Wu[1,2,3]

[1]Molecular Medicine Research Center, Chang Gung University, Taiwan, [2]Department of Medical Biotechnology and Laboratory Science, College of Medicine, Chang Gung University, [3]Graduate Institute of Biomedical Science, College of Medicine, Chang Gung University, Taiwan

POS-03-164   YI02-06

Quantitative Proteomic Approach to Identify Proteins

Nurul Farhana Jufri[1,2], Mark Baker[1], Jian Tu[1]

[1]Macquarie University, [2]National University of Malaysia, Malaysia

POS-03-165

Advanced SILAC Proteomic Analysis of Human Protein Replacement Stable Cell Lines Established Using snoMEN-PR Vector

Motoharu Ono[1], Kayo Yamada[1], Akinori Endo[1], Fabio Avolio[2], Angus I. Lamond[1]

[1]Centre for Gene Regulation and Expression, College of Life Sciences, University of Dundee, UK, [2]Diabetes Genetics Team, Université de Nice Sophia-Antipolis (UNS), Institut de Biologie Valrose, France

POS-03-166

Quantification and Mathematical Modeling of the CD95 Death Inducing Signaling Complex

Uwe Warnken[1], Kolja Schleich[2], Inna Lavrik[3], Martina Schnoelzer[1]

[1]Functional Proteome Analysis, German Cancer Research Center (DKFZ), Germany, [2]Division of Immunogenetics, German Cancer Research Center (DKFZ), Germay, [3]Department of Translational Inflammation Research, Institute of Experimental Internal Medicine, Otto von Guericke University, Germany

POS-03-167

Further Exploration of Plasma Biomarkers for Alzheimers Disease Using Isotopic Tandem Mass Tags and a Combined Targeted /Non-Targeted LC/MS/MS Method

Christopher Lossner[1], Stephan Jung[1], Emma Lahert[2], Ian Pike[2], Hans-Dieter Zucht[1], Malcolm Ward[2]

[1]Proteome Sciences R&D GmbH & Co. KG, Germany, [2]Proteome Sciences plc, UK

POS-03-168

Phosphoproteomic Analysis of ABA Signaling Pathways in Physcomitrella Patens

Yoshimasa Honda[1], Naoyuki Sugiyama[2], Mayuri Kuwamura[3], Ryosuke Terao[1], Kozue Ishizuka[1], Yoichi Sakata[3], Daisuke Takezawa[4], Kazuo Shinozaki[5], Yasushi Ishihara[2], Taishi Umezawa[1]

[1]Tokyo University of Agriculture and Technology, Japan, [2]Kyoto University, Japan, [3]Tokyo University of Agriculture, Japan, [4]Saitama University, Japan, [5]RIKEN Center for Sustainable Resource Science

POS-03-169

Detection of Cellular Response to an in Vitro Challenge with Bacterial Gram-Negative Lipopolysaccharides (LPS) in Peripheral Blood Mononuclear Cells (PBMCs)

David A Sarracino, Jennifer Sutton, Maryann S Vogelsang, Bryan Krastins, Gregory Byram, Amol Prakash, Dayana Argoti, Scott Peterman, Mary Lopez

BRIMS, Thermo Fisher Scientific, USA

POS-03-170

Integrating Genetics and Phosphoproteomics Reveals a Protein Phosphorylation Network in the Abscisic Acid Signaling Pathway in *Arabidopsis*

Taishi Umezawa[1], Naoyuki Sugiyama[2,3], Fuminori Takahashi[4], Jeffrey C. Anderson[5], Ryosuke Terao[1], Kozue Ishizuka[1], Yasushi Ishihama[2,3], Scott Peck[5], Kazuo Shinozaki[4]
[1]Tokyo University of Agriculture and Technology, Japan, [2]Keio University, Japan, [3]Kyoto University, Japan, [4]RIKEN Center for Sustainable Resource Science, [5]University of Missouri, USA

POS-03-171

Comprehensive Study of Redox Proteomics in THP-1 Cells Using a Modified Biotin-Switch Assay

Ru Li, Juergen Kast
University of British Columbia, Canada

POS-03-172   PS32-05

A Proteomic Investigation of Proteasome Malfunctioning

Karen A Sap, Karel Bezstarosti, Dick HW Dekkers, Olaf Voets, Erikjan Rijkers, C Peter Verrijzer, Jeroen AA Demmers
Erasmus University Medical Center, The Netherlands

POS-03-173

Variability of Signature Peptide Production in Bottom-Up Proteomics

Siri Valen Egeland, Leon Reubsaet, Trine Gronhaug Halvorsen
Department of Pharmaceutical Chemistry, School of Pharmacy, University of Oslo, Norway

POS-03-174

Discovery of Subnanomolar Serum/Plasma Biomarkers Inclusive of Albumin-Bound Molecules by Novel Sample Pretreatment and High Quality Comparative Analysis

Yoshio Kodera[1,2,3], Yuya Hidoh[2], Tatsuya Saito[2], Yusuke Kawashima[1,2], Kazuyuki Sogawa[3,4], Satoru Minamida[5], Kazumasa Matsumoto[5], Masatsugu Iwamura[5], Shiro Baba[5], Tadakazu Maeda[1], Takeshi Tomonaga[3,6], Fumio Nomura[3,7]
[1]Center for Disease Proteomics, Kitasato University School of Science, Japan, [2]Laboratory of Biomolecular Dynamics, Department of Physics, Kitasato University School of Science, Japan, [3]Clinical Proteomics Research Center, Chiba University Hospital, [4]Department of Food Biochemistry, School of Life and Environmental Science, Azabu University, Japan, [5]Department of Urology, Kitasato University School of Medicine, Japan, [6]Proteome Research Center National Institute of Biomedical Innovation, [7]Department of Molecular Diagnosis, Graduate School of Medicine, Chiba University, Japan

POS-03-175   ★Travel Award

Revealing the Membrane Proteome, Phosphoproteome and Sialiome of Human Embryonic and Neural Stem Cells

Marcella N Melo-Braga[1], Melanie Schulz[1], Qiuyue Liu[2], Andrzej Swistowski[2], Giuseppe Palmisano[1], Kasper Engholm-Keller[1], Lene Jakobsen[1], Xianmin Zeng[2], Martin R Larsen[1]
[1]Biochemistry and Molecular Biology, University of Southern Denmark, Denmark, [2]Buck Institute for Age Research, USA

POS-03-176

Quantitative Phosphoproteomics Studies Reveal Different Signaling Events for Cultured Distal Convoluted Tubular Cells Upon Vasopressin or Angiotensin II Stimulation

Lei Cheng, Trairak Pisitkun, Robert Fenton
Department of Biomedicine, Aarhus University, Denmark

POS-03-177

A Proteomics-Based Study to Reveal Profilin1-Induced Molecular Changes in Breast Cancer Cells

Joelle Victorine Coumans[1], David Gau[2], Anne Poljak[3], Valerie Wasinger[3], Partha Roy[2], Pierre Moens[1]

[1]University of New England, Australia, [2]University of Pittsburgh, USA, [3]University of New South Wales, Australia

POS-03-178

Using 2D-PAGE and iTRAQ Proteomics Approaches to Investigate the Effect of Cigarette Smoke Fraction Exposure on Primary Normal Human Bronchial Epithelial (NHBE) Cells

Ashraf Elamin, Thomas Schneider, Sophie Dijon, Fabio Talamo, Sandra Wagner, Ulrike Kogel, Caole Mathis, Julia Hoeng, Patrick Vanscheeuwijck, Manuel Peitsch

Philip Morris Products S.A.

POS-03-179

Protein Expression Analysis of Soft-Tissue Sarcomas

Ufuk Kirik[1], Fredrik Levander[1], Peter James[1], Ana Carneiro[2,3]

[1]Lund University, Department of Immunotechnology, Sweden, [2]Lund University, Department of Oncology, Sweden, [3]Skane University Hospital, Institute of Clinical Sciences

POS-03-180

Mechanism Survey on Cell Senescence Induced by the Knockdown of Cathepsin D Through Quantitative Proteomic Approach

Siyuan Su[1], Ju Zhang[1], Huiying Sun[1], Xu Zhu[1], Ningzhi Xu[2], Siqi Liu[1], Xiaomin Lou[1]

[1]Beijing Institute of Genomics, Chinese Academy of Sciences, China, [2]Cancer Institute, Chinese Academy of Medical Sciences, China

Sample Preparation and Preprocessing

POS-03-181

Why Less is More When Generating Tryptic Peptides for Bottom-Up Proteomics

Siri Hildonen, Trine Gronhaug Halvorsen, Leon Reubsaet

Department of Pharmaceutical Chemistry, School of Pharmacy, University of Oslo, Norway

POS-03-182

Rapid and Simple Method of Tamm-Horsfall Protein Removal for Urinary Exosomal Protein Identification

Aki Nakayama[1], Yuki Arai[2], Akira Katayama[3], Hidenori Suzuki[4], Kiyoko Shiba[2], Shiro Iijima[1,2]

[1]Faculty of Health Science Technology, Bunkyo Gakuin University, Japan, [2]Graduate School of Health Care Science, Bunkyo Gakuin University, Japan, [3]Department of Biochemistry and Molecular Biology, Nippon Medical School, Japan, [4]Department of Pharmacology, Nippon Medical School, Japan

POS-03-183

Depletion of Abundant Plasma Proteins by Irreversible Trapping in Poly-*N*-Isopropylacrylamide-Acrylic Acid Hydrogel Particles

Gerard Such-Sanmartin, Estela Ventura-Espejo, Ole Norregaard Jensen

Protein Research Group, Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark

POS-03-184

Selective Preparation of Faecal Material for Parasite Proteome and Biomarker Identification

Francesca M. Jones[1], Richard Lipscombe[2], R.C. Andrew Thompson[1]

[1]Murdoch University, Australia, [2]Proteomics International, Australia

POS-03-185

Quantitative Analysis of Whole Proteome Using Denator in Two Human Cancer Cell Lines Treated with Doxorubicin

Albert-Baskar Arul[1], Na-Young Han[1], Young-Su Jang[2], Hwan-Mook Kim[2], Hookeun Lee[1,2]

[1]Lee Gil Ya Cancer and Diabetes Institute, College of Pharmacy, Gachon University, Korea, [2]College of Pharmacy, Gachon University, Korea

POS-03-186

Electrostatic Repulsion-Hydrophilic Interaction Chromatography for Profiling of Human Urine Shotgun Proteome

Michiko Takakura, Hiroyuki Unoki-Kubota, Yasushi Kaburagi

Department of Diabetic Complications, Diabetes Research Center, Research Institute, National Center for Global Health and Medicine, Japan

POS-03-187

Middle-Down Proteomic Analysis of Embryonic Proteins Secreted Prior to Implantation

Unige A. Laskay[1], Kristina Srzentic[1], Tanja Panic-Jankovic[2], Michel Monod[3], Goran Mitulovic[2], Yury O. Tsybin

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POS-03-188   PS20-03

Development of Universal Protocols for Clinical Tissue Phosphoproteomics Optimized for Formalin-Fixed Paraffin-Embedded Specimens

Mayu Ogura, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

Kyoto University, Japan

POS-03-189

Differential Solublization Method to Extract Low-Molecular-Weight Proteins/Peptides for Successful Serum SRM Analyses

Mamoru Satoh[1,2,4], Yusuke Kawashima[3], Tatsuya Saito[3], Masumi Ishibashi[1], Kazuyuki Sogawa[1,2], Sayaka Kado[4], Yoshio Kodera[1,3], Fumio Nomura[1,2]

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POS-03-190

Selective Analysis of Cell Surface-Associated Proteins: Characterization of Intracellular Proteins that are Released from Damaged Cells and Interact with the Surface of Human Monocytic Cell Line U937

Tomonori Izumi, Katsumi Yokoyama, Isao Sakaida

Center for Reparative Medicine, Yamaguchi University Graduate School of Medicine, Japan

POS-03-191

Evaluation of OFF Gel- Based Prefractionation Approach in Combination with In-Solution or Ultra Filtration Protein Digestion

Sameh Magdeldin, Keiko Yamamoto, Yutaka Yoshida, Bo Xu, Ying Zhang, Shymaa Enany, Eishin Yaoita, Tadashi Yamamoto

Department of Structural Pathology, Institute of Nephrology, Niigata University, Japan

POS-03-192

Method Development for Metaproteomic Analyses of Biofilms from Methanogenic Consortia Degrading Terephthalate

Hung-Jen Huang, Jer-Horng Wu

Department of Environmental Engineering, National Cheng Kung University, Taiwan

POS-03-193

Application of Group Specific Anti-Peptide Antibodies for Immunoaffinity Enrichment of Signature Peptides of Allergens from Food Samples

Kerstin Pohl[1], Christopher J. Pynn[1], Silvia Panther[1], Sven Hellwig[1], Hannes Planatscher[2], Bart H.J. van den Berg[2], Frederik T. Weiss[2], Cornelia Sommersdorf[2], Thomas O. Joos[2], Oliver Poetz[2], Joerg Bergemann[1], Dieter Stoll[1,2]

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POS-03-195

Boronate Affinity Materials for the Selective Enrichment of Glycoproteins for Proteomic Analysis

Zhen Liu

State Key Laboratory of Analytical Chemistry for Life Science, School of Chemistry and Chemical Engineering, Nanjing University, Taiwan

POS-03-196

A Graphene Based Soft Material Platform for Facile One-Step Glycan Enrichment and Derivatization for MALDI-TOF-MS Analysis

Haihong Bai, Wanjun Zhang, Weijie Qin, Xiaohong Qian

State Key Lab of Proteomics, Beijing Proteome Research Center, National Engineering Research Center for Protein Drugs, National Center for Protein Sciences Beijing, Beijing Institute of Radiation Medicine, China

POS-03-197

Accurate Quantification of Peptides for Mass Specrtometric Analysis: A Modified Micro-Scale Bicinchoninic Acid Assay

Yutaka Yoshida[1], Miki Hasegawa[1,2], Lim Lay Cheng[3], Takashi Shiromizu[4], Yasuhiro Hara[4], Akiko Kanagawa[4], Yu Koyama[2], Eishin Yaoita[1], Toshifumi Wakai[2], Takeshi Tomonaga[4], Tadashi Yamamoto[1]

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Stem Cell Biology: ES, iPS, Cancer Stem Cells

POS-03-198

iTRAQ Proteome Analysis of Inner Cell Mass Derived Versus Epiblast Derived Murine Embryonic Stem Cells

Thomas Frohlich[1], Miwako Kosters[1], Alexander Graf[1], Eckhard Wolf[1], Julianna Kobolak[2], Vincent Brochard[4], Andras Dinnyes[2,3], Alice Jouneau[4], Georg J. Arnold[1]

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POS-03-199

Proteome Dynamics During Reprogramming of Fibroblasts to the Pluripotent State

Jenny Hansson[1], Mahmoud Reza Rafiee[1], Sonja Reiland[1], Jose M. Polo[2], Konrad Hochedlinger[2], <u>Jeroen Krijgsveld</u>[1]
[1]European Molecular Biology Laboratory, Germany, [2]Harvard Stem Cell Institute, USA

POS-03-200

Sox2, Oct4 and Nanog, Key Stem Cell Transcriptional Factors, Contribute to Different Aspects of Cancer Stem-Like Properties of HCC

<u>Yan Li</u>[1], Chun Sun[2], Lu Sun[2], Yin Kun Liu[1,2]
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POS-03-201

Transgelin Regulates Metastatic Ability of Cancer Stem Cells

<u>Won-Yong Jeong</u>, Eun-Kyung Lee, Gi-Yeon Han, Yeo-Ju Song , Chan-Wha Kim
Korea University, Korea

POS-03-202　　★Travel Award

Generating a Proteomic Profile on Neurogenesis, Throught the Comparision of Differentiating Human Foetal Neural Stem Cells

<u>Shaun Garnett</u>[1], Jignesh Tailor[2], Austin Smith[2], Kathryn Lilley[2], Susan Kidson[1], Jonathan Blackburn[1]
[1]University of Cape Town, South Africa, [2]University of Cambridge, UK

POS-03-203

Comparative Nuclear Proteomic Analysis of Spermatogonial Stem Cells and Differentiating Spermatogonia Induced by Retinoic Acid

<u>Kazue Kakiuchi</u>, Kiyohiko Takagishi, Hiroshi Kubota
Lab. of Cell and Mol. Biol. Sch. of Vet. Med., Kitasato Univ., Japan

POS-03-204

Integrated Proteomics Identified the Differentiation Niche Induced by Glioma Stem Cells

<u>Akiko Niibori Nambu</u>[1], Uichi Midorikawa[1], Souhei Mizuguchi[1], Takuichiro Hide[2], Minako Nagai[1], Yoshihiro Komohara[3], Megumi Nagayama[1], Mio Hirayama[1], Daiki Kobayashi[1], Hideo Nakamura[2], Motohiro Takeya[3], Jyunichi Kuratsu[2], Norie Araki[1]
[1]Department of Tumor Genetics and Biology, Graduae School of Medical Sciences, Kumamoto University, Japan, [2]Department of Neurosurgery, Graduate School of Medical Sciences, [3]Department of Cell Pathology, Graduate School of Medical Sciences

POS-03-205

High-Resolution Accurate Mass (HRAM) and Intelligent Acquisition-Enabled Global Discovery and Quantification of Histones, Histone PTMs and Histone Modification Enzymes in Mesenchymal Stem Cells

<u>Amol Prakash</u>[1], Maryann S Vogelsang[1], David Sarracino[1], Scott Peterman[1], Victoria V Lunyak[2], Benny Blackwell[2], James R Tollervey[2], Shadab Ahmad[1], Gregory Byram[1], Bryan Krastins[1], Mary F Lopez[1]
[1]BRIMS, Thermo Fisher Scientific, USA, [2]Buck Institute for Age Research, USA

POS-03-206

Marked Expression of MSY Genes During Differentiation of Human Embryonic Stem Cells Into Dopaminergic Precursor Cells

<u>Mehdi Sharifi Tabar</u>[1], Ali Fathi[2], Haghighat Vakilian[1], Mehdi Alikhani[2], Hossein Baharvand[2], Ghasem Hosseini Salekdeh[1]
[1]Molecular Systems Biology Group of Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Iran, [2]Stem Cells and Developmental Biology Group of Cell Science Research Center, Royan Institute for Stem Cell Biology and Technology, ACECR, Iran

Systems Biology

POS-03-207

Investigating the Group A *Streptococcus* Surface Proteome Dynamic Using a Combination of Mass Spectrometry Techniques

Ola Kilsgard, Christofer Karlsson, Johan Malmstrom
Department of Immuntechnology, Sweden

POS-03-208

Comparative Analyses of Cellular Responses to Different Aggregation-Prone Proteins

Andre Melnik[1], Martin Soste[1], Dan Tardiff[2], Kent Matlack[2], Alexander Schmidt[3], Susan Lindquist[2], Paola Picotti[1]
[1]ETH Zurich, Switzerland, [2]Whitehead Institute of Biomedical Research, USA, [3]Biocentre, University of Basel, Switzerland

POS-03-209

An Integrative Systems Analysis of Glioma and Medulloblastoma for the Identification of Diagnostic and Therapeutic Targets

Rekha Jain, Sanjeeva Srivastava
Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, India

POS-03-210

Expanding the Known Substrate Degradome of Snake Venom Metalloproteinases by Mass Spectrometric Analysis Using PICS and TAILS

Andre Zelanis[1], Pitter F. Huesgen[2], Anna Prudova[2], Lindsay Rogers[2], Philipp Lange[2], Ana Karina Oliveira[1], Alexandre K. Tashima[1,3], Christopher M. Overall[2], Solange M. T. Serrano[1]
[1]Laboratorio Especial de Toxinologia Aplicada, Instituto Butantan, Brazil, [2]Centre for Blood Research, Department of Oral Biological and Medical Sciences, University of British Columbia, Canada, [3]Departamento de Ciencias Exatas e da Terra, Universidade Federal de Sao Paulo, Brazil

POS-03-211

Integrative Transcriptomic and Proteomic Data Analysis to Identify OSCC-Relevant Protein Targets

Li-Chieh Julie Chu[1], Chia-Wei Hsu[2], Shu-Jen Chen[1,2], Chih-Ching Wu[1,3], Jau-Song Yu[1,2]
[1]Molecular Medicine Research Center, Chang Gung University, Taiwan, [2]Graduate Institute of Biomedical Sciences, Chang Gung University, [3]Department of Medical Biotechnology and Laboratory Science, Chang Gung University

POS-03-212

Multi-parameter Systematic Strategy Opinion that Predicts, Prevents and Personalized Treats a Cancer

Xianquan Zhan, Xiaowei Wang, Rong Hu
Xiangya Hospital, Central South University, China

POS-03-213 PS21-04

An Integrated View on the Exploitation of Affinity Purification-Mass Spectrometry Data

Jacques Colinge[1], Alexey Stukalov[1], Roberto Sacco[1], Andreas Pichlmair[2], Keiryn L. Bennett[1], Giulio Superti-Furga[1]
[1]CeMM - Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria, [2]Innate Immunity laboratory, Max-Planck Institute for Biochemistry Am Klopferspitz, Germany

Prediction of Phosphorylated Residues Based on Machine Learning Technique and Large Scale Phosphoproteomics Experiment

Satoshi Tamaki[1], Haruna Imamura[2], Masaru Tomita[1], Naoyuki Sugiyama[2], Yasushi Ishihama[2]

[1]Institute for Advanced Biosciences, Keio University, Japan, [2]Graduate School and Faculty of Pharmaceutical Sciences, Kyoto University, Japan

Integration of 'omics and Phenotypic Data to Elucidate Mechanisms of Social Immunity

M. Marta Guarna[1], Matthew Bundala[1], Kyung-Mee Moon[1], Rick White[1], Robert Parker[1,4], Elizabeth Huxter[2], Andony P Melathopoulus[3], Stephen F Pernal[3], Leonard J Foster[1]

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Proteogenomics Framework to Elucidate TGFB Induced Epithelial to Mesenchymal Transition (EMT)

Shivashankar H Nagaraj[1], Magdalene Michael[2], Nicola Waddell[1], Alun Jones[2], Katia Nones[1], David Miller [1], John V Pearson[1], Alpha S. Yap[2], Sean M Grimmond[1]

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Hemorrhagic Activity of HF3, A Snake Venom Metalloproteinase: Insights from the Peptidomic Analysis of Muscle Cells

Milene Cristina Menezes, Andre Zelanis, Ana Karina Oliveira, Eduardo Shigueo Kitano, Amanda Francine Asega, Solange Maria de Toledo Serrano

Laboratorio Especial de Toxinologia Aplicada, Instituto Butantan, Brazil

Comparative Analysis of Platelets Stimulated with Thrombin, TRAP and PA-BJ: A Proteomics Approach

Ana K. Oliveira[1], Andre Zelanis[1], Aline S. Lopes[2], Eduardo S. Kitano[1], Marcelo L. Santoro[3], Solange M. T. Serrano[1]

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Assessment of the Activation Profile of Multiple Small GTPase Isoforms Using Targeted Proteomics

Chengcheng Zhang, Juergen Kast

The Biomedical Research Centre, University of British Columbia, Canada

Sentinel Protein Assays Take System-Wide Snapshots of Alpha-Synuclein Induced Cytotoxicity

Martin Soste[1], Stefanie Wanka[2], Andre Melnik[1], Timon Wernas[1], Alexander Schmidt[3], Christian Von Mering[2], Paola Picotti[1]

[1]Institute of Biochemistry, ETH Zurich, Switzerland, [2]Institute of Molecular Life Sciences, University of Zurich, Switzerland, [3]Biozentrum, University of Basel, Switzerland

The Methylproteome Network of *Saccharomyces cerevisiae*

Marc R. Wilkins

University of New South Wales, Australia

POS-03-222

Protein Quantitative Trait Locus (pQTL) Analysis in Mouse by Targeted Proteomics

Yibo Wu[1], Evan G. Williams[2], Johan Auwerx[2], Ruedi Aebersold[1]

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POS-03-223

Platelet Secretory Granules Proteome Characterization: Association with Platelet Reactivity in Stable Cardiovascular Patients Treated with Aspiri

Anne Zufferey[1,2], Mark Ibberson[3], Domitille Schvartz[2], Severine Nolli[1,2], Jean-Luc Reny[4], Ioannis Xenarios[3], Jean-Charles Sanchez[2], Pierre Fontana[1,2]

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Top-Down Proteomics

POS-03-224

Top-Down Analysis of Intact Antibodies Using Orbitrap Mass Spectrometry

Eugen Damoc, Eduard Denisov, Alexander Makarov

Thermo Fisher Scientific (Bremen), Germany

POS-03-225   PS05-03

Top-Down and Flexible Analysis of Protein Using MALDI In-Source Decay

Mitsuo Takayama

Yokohama City University, Japan

Other Topics in Proteomics

POS-03-226

Global Proteomic Analysis of Intracellular and Extracellular Amastigote Forms of _Trypanosoma cruzi_ Reveals Key Differences in Morphologically Similar Parasites

Igor C. Almeida[1], Alexandre F. Marques[1], Tiago J.P. Sobreira[2], Clemente Aguilar-Bonavides[1], Alexey I. Nesvizhskii[3], Hyungwon Choi[4], Ariel M. Silber[5], Ernesto S. Nakayasu[1]

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POS-03-227

Investigation of Effects of Angiotensin II (ATII) on Human Articular Chondrocytes by Proteomic Approach

Wataru Endo[1], Mitsumi Arito[1], Toshiyuki Sato[1], Manae S. Kurokawa[1], Kazuki Okamoto[1], Naoya Suematsu[1], Kazuki Omoteyama[1], Moroe Beppu[2], Tomohiro Kato[1]

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POS-03-228

Investigation of Effects of Edaravone on Human Brain Microvascular Endothelial Cells

Hidetaka Onodera[1,2], Mitsumi Arito[1], Toshiyuki Sato[1], Manae S. Kurokawa[1], Kazuki Okamoto[1], Naoya Suematsu[1], Yuichiro Tanaka[2], Takuo Hashimoto[2], Tomohiro Kato[1]
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POS-03-229

Production and Characterization of Monoclonal Antibodies to Hepatitis B Virus X (HBx) Protein

Shun-ichi Asano, Satoko Matsunaga, Akihide Ryo
Department of Microbiology, Yokohama City University School of Medicine, Japan

POS-03-230

Lipidomic Profiling Using a Prototype Microfluidic MS Platform

G Astarita[1], A Doneanu[1], W Thompson[2], SA Cohen[1], G Isaac[1], J Johnson[1], MA Moseley[2], J Murphy[1], JI Langridge[3], Yukari Haramaki[1]
[1]Waters Corporation, USA, [2]Duke Proteomics Core Facility, USA, [3]Waters Corporation, UK

POS-03-231

The Anticancer Curcumin Induces the Unfolded Protein Response in Prostate Cancer Cells

Yanilda Ramos[1], Ricardo Carrero[1], Jin Zou[2], Luis Cubano[1], Shafiq Khan[2], Nawal Boukli[1]
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POS-03-232

Use Specific Proteins of Taiwan Tea as Biomarkers for the Certification of Origin

Han-ju Chien, Chien-chen Lai
Institute of Molecular Biology, National Chung Hsing University, Taiwan

POS-03-233

Moss Proteomics and Peptidomics. Peptides in the Stress Adaptation Process

Igor Fesenko[1], Dmitry Alexeev[2], Alexander Scripnikov[1], Vadim Govorun[1,2], Vadim Ivanov[1]
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POS-03-234

Analysis of p53 Transcriptional Activity Toward the Promoters of Target Genes in Living Cells

Takayoshi Higashi, Toshiaki Imagawa, Aya Tanaka, Yoshiro Chuman, Kazuyasu Sakaguchi
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POS-03-235

Phosphoproteomic Analysis of *Rhodopseudomonas palustris* Reveals the Role of Pyruvate Phosphate Dikinase Phosphorylation in Lipid Production

Chia-Wei Hu[1], Miao-Hsia Lin[2], Hsuan-Cheng Huang[3], Wei-Chi Ku[4], Tsun-Hsuan Yi[1], Chia-Feng Tsai[5], Yu-Ju Chen[5], Naoyuki Sugiyama[4], Yasushi Ishihama[4], Hsueh-Fen Juan[1,7], Shih-Hsiung Wu[2]
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POS-03-236

Y Chromosome-Located Gene, Lysine-Specific Demethylase 5D, Associated with Prostate Cancer Progression

<u>Zohreh Jangravi</u>[1], Haghighat Vakilian[1], Pouria Parsamatin[1], Paul A Haynes[2], Ann K Goodchild[3], Mehdi Mirzaei[3], Ghasem Hosseini Salekdeh[1]

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POS-03-237

Generation and Utilization of Full-Length Recombinant Proteins of Human T-cell Leukemia Virus Type 1

<u>Satoko Matsunaga</u>, Akihide Ryo

Department of Microbiology, Yokohama City University School of Medicine, Japan

POS-03-238

Wheat Germ Cell-Free Protein Production of Human Immunodeficiency Virus Accessory Protein Vif

<u>Mayu Miyamoto</u>, Satoko Matsunaga, Kei Miyakawa, Akihide Ryo

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POS-03-239

Influence of Arginine, Lysine, Phenylalanine Residues and Phosphorylation on the Positive- and Negative-Ion Yields of Peptides in ESI-MS

<u>Issey Osaka</u>, Mitsuo Takayama

Yokohama City University, Japan

POS-03-240

Bioinformatics Analysis of Protein Dynamics in Urine of Healthy Volunteers Exposed 105-Day Isolation

<u>Ludmila Pastushkova</u>[1], Hans Binder[2], Evgeny Tiys[3], Vladimir Ivanisenko[3], Irina Larina[1], Evgeny Nikolaev[4]

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POS-03-241

Process Optimization for Shake Flask Bio-Treatment of Disperse Yellow 9 Textile Dye with White-Rot Fungi and Their Enzymes

<u>Muhammad Ramzan</u>[1], Muhammad Asgher[1], Raymond Legge[2]

[1]University of Agriculture Faisalabad Pakistan, [2]University of Waterloo, Canada

POS-03-242

Identification of *HAMP* Transcript Variant Coding for an Abnormal Polypeptide in Human Hepatoma-Derived Cell Line HLF

<u>Katsunori Sasaki</u>[1], Katsuya Ikuta[2], Hiroki Tanaka[1], Takaaki Ohtake[2], Yoshihiro Torimoto[3], Mikihiro Fujiya[2], Yutaka Kohgo[2]

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POS-03-243

Venom Proteomics of the Brazilian Spider *Acanthoscurria gomesiana*

Bianca Naomi Sumitomo[1], Andre Zelanis[2], Eduardo Shigueo Kitano[2], Pedro Ismael Silva Junior[2], Solange Maria de Toledo Serrano[2], Alexandre Keiji Tashima[1,2]
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POS-03-244

Proteomic Analysis of Two Transcriptional Start Sites of the *argC* Gene and Its Implication on the *Sinorhizobium meliloti* Physiology

Maria del Carmen Vargas-Lagunas, Angel Gabriel Martinez, Rafael Diaz, Emmanuel Salazar, Yolanda Mora, Sergio Encarnacion, Jaime Mora
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POS-03-245

Proteomic Analysis of Hepatocarcinoma Cell Line SMMC7721 in Response to Over Expression of the RING Finger Protein, HSPC238

Suihai Wang, Xiaobo Wang, Ming Li
School of Biotechnology, Southern Medical University, China

POS-03-246

Biomarkers of Social Immunity in Honey Bees: Real-World Application of Biomarkers in a Marker-Assisted Selective Breeding Program

M Marta Guarna[1], Kyung-Mee Moon[1], Rick White[1], Derek Smith[2], Elizabeth Huxter[3], Heather Higo[1], Shelley Hoover[4], Abdullah Ibrahim[4], Robert Currie[5], Christoph Borchers[2], Stephen F Pernal[4], Leonard J Foster[1]
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POS-03-247

Depth and Width of Human Proteome

Alexander Archakov, Victor Zgoda, Andrey Lisitsa, Elena Ponomarenko
Institute of Biomedical Chemistry of RAMS, Russia

POS-03-248

The Utility of ETD in Peptidomics for Endogenous Secretory Peptides

Kazuki Sasaki[1], Tsukasa Osaki[2], Naoto Minamino[1]
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POS-03-249

Pyrococcus Furiosus: The Perfect Standard for Proteomics?

Julia M. Burkhart[1], Marc Vaudel[1], Lennart Martens[2], Albert Sickmann[1,3], Rene P. Zahedi[1]
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POS-03-250

Alcohol Induced ER Stress Markers in Human Microglia Cells

Ricardo Carrero[1], Yanilda Ramos[1], Sheila Lopez[1], Hiram Escobales[1], Madeline Rodriguez[1], Janaina Alves[1], Luis Cubano[1], Shilpa Buch[2], Nawal Boukli[1]
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POS-03-251

Identification of Cell Polarity Target Phospho-Protein by Using Inducible Gene Knock-Out Strategy

Masa-aki Nakaya
Yokohama City University School of Medicine, Japan

POS-03-252

Analysis of Structural Changes in Erythropoietin by LC/MS Induced by Different pH Conditions

In-Rok Oh, Dong-Ho Ha, Hyun-Jung Kim, Chan-Wha Kim
Korea University, Korea

POS-03-LB-001

On-Line Chip-Based Strategy for 2D Fractionation - Comparing Peptides Found between 1D and 2D Proteomic Analysis

Tina Settineri[1], Christie Hunter[2], Jenny Albanes[2], Xiang Zhu[1], Remco van Soest[1]
[1]Eksigent, part of AB SCIEX, [2]AB SCIEX

POS-03-LB-002

Shedding Light on Placental Infection and Inflammation in Preterm Birth by Terminomics - A Comprehensive Protein Termini Orientated Genome Wide Analysis of Human Placental Tissue

Ulrich Eckhard, Pitter F Huesgen, Philipp F Lange, Karen Nguyen, Reinhild Kappellhoff, Christopher M Overall[1]
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POS-03-LB-003

Glycosylation Profiling of Cancer Biomarkers by a Nanoprobe-Based Strategy Combined with Lectin-Based Enrichment

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POS-03-LB-004

The Role of Collapsin Response Mediator Protein 2 in Amyloid-β 25-35 Induces Impairment of Cognitive Function and Long-Term Potentiation

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POS-03-LB-005

Insights into UV-A & Dark Incubation Induced Paclitaxel in *Taxus chinensis* by Genomic and Proteomic Analysis

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POS-03-LB-006

Enzymatic Approach to Reduce the Complexity of Proteome Samples by Depleting Glutamine-Containing Peptides

Yanbo Pan, Mingliang Ye, Hanfa Zou

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POS-03-LB-007

Systematic Evaluation of Ultrahigh Resolution MS Instrument Parameter to Optimize Topdown Analysis

Martin Zeller[1], Mathias Mueller[1], Eugen Damoc[1], Eduard Denisov[1], Alexander Makarov[1], Dirk Nolting[1], Shannon Eliuk[2], Justin Blethrow[2], August Specht[2], Thomas Moehring[1], Vlad Zabrouskov[2]

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POS-03-LB-008

Characterization of Monoclonal Antibodies with LC-MS by Integration of *De Novo* Sequencing and Database Search

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POS-03-LB-009

Proteomic Investigation of Breast Cancer Biomarkers Using Human Plasma and Serum Samples

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POS-03-LB-010

Ero1alpha and PDIs Constitute a Hierarchical Electron Transfer Network of Endoplasmic Reticulum Oxidoreductases

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POS-03-LB-011

Zebrafish Scube1 [Signal Peptide-CUB (Complement Protein C1r/C1s, Uegf, and Bmp1)-EGF Domain-Containing Protein 1] Is Involved in Primitive Hematopoiesis

Ku-Chi Tsao[1], Cheng-Fen Tu[1], Shyh-Jye Lee[2], Ruey-Bing Yang[1]

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POS-03-LB-012

Serum *N*-Glycans Profiling for the Discovery of Potential Oral Cancer Tumor Markers

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POS-03-LB-013 ★Travel Award

Proteomic Alterations of *Plasmodium falciparum* by Dihydroartemisinin, Mefloquine and Chloroquine

<u>Patcharee Isarankura-Na-Ayudhya</u>[1,2,3], Suthidarak Chaijan[1], Jarunee Vanichtanankul[1], Chairat Uthaipibull[1], Phantip Vattanaviboon[2], Yongyuth Yuthavong[1], Sumalee Kamchonwongpaisan[1]

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POS-03-LB-014

Proteomic Analysis of Urine from HIV Co-Infected Tuberculosis Patients

<u>Pichapat Piamrojanaphat</u>[1], Rodjana Suyayai[1], Pacharee Kantipong[2], Supalert Nedsuwan[2], Norio Yamada[3], Sittiruk Roytrakul[4]

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POS-03-LB-015

Targeted Quantification of TMPRSS2-ERG Fusion Protein Products in Prostate Cancer Cell Lines and Tumors Using an Antibody-Independent PRISM-SRM Approach

Jintang He[1], Xuefei Sun[1], Tujin Shi[1], Athena A Schepmoes[1], Thomas L. Fillmore[2], Vladislav A. Petyuk[1], Fang Xie[1], Naoki Kitabayashi[3], Sung-Suk Chae, Mark A. Rubin[3], Javed Siddiqui[4,5], John T. Wei[4], Arul M. Chinnaiyan[5], <u>Wei-Jun Qian</u>[1], Richard D. Smith[1], Jacob Kagan[6], Sudhir Srivastava[6], Karin D. Rodland[1], Tao Liu[1], David G. Camp II[1]

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POS-03-LB-016

An Experimental Platform for the Analysis of Mammalian Protein Interaction Networks and Ligand Receptor Interactions

<u>Thomas Uhlmann</u>, Björn Wienke, Daniel Auerbach

Dualsystems Biotech AG

POS-03-LB-017

Bottom-Up Mass Spectrometry Reveals Biomarker Candidate Proteins in Cerebrospinal Fluid of Patients Treated with Electric Spinal Cord Stimulation for Severe Chronic Pain

<u>Anne-Li Lind</u>[1,2], Marcus Sjodin[2], Lenka Katila[1], Magnus Wetterhall[2], Torsten Gordh[1]

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POS-03-LB-018

Analysis of the Liver Non-Parenchymal Cells Proteome in Response to Ethanol: Novel Molecular Targets of Disease

Xiaofang Jia, <u>Lijun Zhang</u>

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POS-03-LB-019

Dissection of the Human GalNAc *O*-Glycoproteome: Mapping Specific Functions of Individual Polypeptide GalNAc-Transferase Isoforms by Zinc-Finger Gene Engineering of Human Cells

Katrine ter-Borch Gram Schjoldager, Sergey Vakhrusjev, Yun Kong, Hiren Joshi, Eric Bennett, Ulla Mandel, Hans Wandall, Henrik Clausen

Center for Glycomics, Department of Cellular and Molecular Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark

POS-03-LB-020

Approaching Nanoflow Level Sensitivity Using Microflow Rates for Peptide Quantitation

Christie L Hunter

AB SCIEX, USA

POS-03-LB-021

Using Variable Widths in Q1 Selection Windows to Improve Data Quality in Data Independent Acquisition

Christie L Hunter

AB SCIEX, USA

POS-03-LB-022

Phosphoproteomic Analysis of Pancreatic Cancer Signaling Identifies Drug Targets for Individualized Patient Treatment

David James Britton[1], Yoh Zen[2], Stefan Selzer[1], Alberto Quaglia[2], Christopher Loessner[1], Stephan Jung[1], Vikram Mitra[1], Julia Gee[4], Robert Nicholson[4], Malcolm Ward[1], Leandro Castellano[3], Justin Stebbing[3], Hans Dieter Zucht[1], Nigel Heaton[2], Ian Pike[1]

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POS-03-LB-023

EDEM2 and OS-9 are Required for the ER-Associated Degradation of Nonglycosylated Sonic Hedgehog Proteins

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POS-03-LB-024

Derlin2 Facilitates HRD1-Mediated Retro-Translocation of Sonic Hedgehog at the Endoplasmic Reticulum

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POS-03-LB-025

AGSY: Automatic Glycopeptide Sequencing by Y1 Ion

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POS-03-LB-026

Quantitative Proteomic Analysis of Human Lung Tumor Xenografts Treated with the Ectopic ATP Synthase Inhibitor Citreoviridin

Yi-Hsuan Wu, <u>Chia-Wei Hu</u>, Chih-Wei Chien, Yu-Ju Chen, Hsuan-Cheng Huang, Hsueh-Fen Juan

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POS-03-LB-027

Application of Survival Analysis Methodology to the Quantitative Analysis of LC-MS Proteomics Data

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POS-03-LB-028

Y Chromosome Genes Expression Profiling During Differentiation of NT2 Cells to Dopaminergic Neurons Under Androgen Treatments

<u>Haghighat Vakilian</u>[1], Mehdi Sharifi Tabar[1], Lida Habibi Rezei[1], Babak Arefnejad[1], Mehdi Alikhani[1], Zohreh Jangravi, Shahab Mirshahvaladi[1], Hossein Baharvand[2], Ghasem Hosseini Salekdeh[1]

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POS-03-LB-029

Towards the Proteome Profiling and Signature of Glioblastoma

<u>Stanislav Naryzhny</u>, Natalia Ronzhina, Tatiana Shtam, Vladimir Burdakov, Michail Filatov
Petersburg Nuclear Physics Institute, Russia

POS-03-LB-030

Two Dimensional Electrophoresis (2DE) Based Approach for Detecting of Numbers of Protein Species in Cell

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POS-03-LB-031

Prognostic Biomarkers for Predicting Metastatic Relapse versus Non-Relapse Hepatocellular Carcinoma

Gek San Tan[1], Kiat Hon Lim[3], Hwee Tong Tan[1], Avery Khoo[3], Sze Huey Tan[4], Han Chong Toh[5], <u>Maxey C.M. Chung</u>[1,2]

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POS-03-LB-032

A Novel Oncogenic Gene, L-FABP, Promotes Cancer Cell Migration and Invasion by Inducing the Expression of VEGF-A and MMP-2

<u>Chung-Yu Ku</u>[1], Jung-Yaw Lin[2]

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POS-03-LB-033

iPhos: A Tool Kit to Streamline the Label-Free LC-MS-Based Tyrosine Phosphoproteome Investigation

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Academia Sinica, Taiwan

POS-03-LB-034

Impact of Human Blood Specimen Collection, Manipulation, and Storage on Protein Integrity and Implications for Use in Clinical Research

Geun-Cheol Gil, Bich Nguyen, Yiyong Zhou, Yuliya Karpievitch, Xiaolei Xie,
Daniel Lopez-Ferrer, Michael Schirm, Paul Drogaris, Rene Allard, Julie Lamontagne,
Howard Schulman, Daniel Chelsky, Sushmita Mimi Roy
Caprion Proteomics US LLC, USA

POS-03-LB-035

Utilized Mass Spectrometry-Based Protein Profiling System to Identify Potential Biomarkers of Hepatocellular Carcinoma

Ming-Hui Yang, Hung Su, Yu-Chang Tyan
Kaohsiung Medical University, Taiwan

POS-03-LB-036

Is NAP an Additional Neuroprotection in Alzheimer's Disease?

Ming-Hui Yang, Yu-Chang Tyan
Kaohsiung Medical University, Taiwan

POS-03-LB-037

Identification of Specific Epitopes for West Nile Virus Diagnostics

Stefan Chabierski[1], Luisa Barzon[2], Petra Fiebig[3], Uwe G. Liebert[3], Anna Papa[4],
Michael S. Diamond[5], Giorgio Palu[2], Sebastian Ulbert[1]
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School of Medicine, USA

POS-03-LB-038

Elucidation of Structure-Activity Relationship of Recombinant Human Kinases by Quantitative Phosphoproteomics

Ayaka Sato, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama
Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

POS-03-LB-039

Antibodypedia - How to Find the Right Antibody for the Right Application

Tove Lovisa Alm, Kalle von Feilitzen
Royal Institute of Technology, Sweden

POS-03-LB-040

Membrane Phosphoproteomics Profiling for the Elucidation of Molecular Dynamics during Sperm Capacitation

Pei-Hsuan Hsieh[1], Ting-Wei Lin[1,2], Ben-Hang Lai[1,2], Yet-Ran Chen[1,2]
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National Taiwan University, Taiwan

POS-03-LB-041

One-Shot Human Proteome Analysis by nanoLC-MS/MS with Meter-Scale Monolithic Silica Capillary Columns

Takeo Kamakura, Suguru Ichihara, Mio Iwasaki, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

Kyoto University, Japan

POS-03-LB-042

On-Line Chip-Based Strategy for 2D Fractionation - Comparing Peptides Found between 1D and 2D Proteomic Analysis

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POS-03-LB-043

Proteomic Analysis of Proteins Involved in Apoptosis during Leukaemic Cells Treatment with HDACI BML-210

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POS-03-LB-044

In-Depth 2-DE Reference Map of a Medically Important Fungus, *Aspergillus fumigatus*, and Proteomic Profiling on Exposure to Itraconazole

Poonam Gautam[1,2,3], Dolly Mushahary[1], Wazid Hassan[2,9], Santosh Kumar Upadhyay[2,7], Taruna Madan[2,4], Ravi Sirdeshmukh[1,8], Curam Sreenivasacharlu Sundaram[1], Wasudev Namdev Gade [5], Puranam Usha Sarma[2,6]

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POS-03-LB-045

Glycopeptide and Glycan Analysis of Monoclonal Antibodies Using Capillary Electrophoresis Electrospray Ionization Mass Spectrometry

Suresh Babu CV[1], Ravindra Gudihal[1], Ravi Krovvidi[1], Ning Tang[2], Martin Greiner[3]

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POS-03-LB-046

Novel Proteomic Biomarkers in the Evaluation of Childhood Asthma

Honghua Lu, Liping Peng, Dan Li, Li Liu, Shucheng Hua

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POS-03-LB-047

Enrichment of Protein N-Terminal Peptides for Shotgun Proteogenomics

Michiko Kimura, Takayuki Hashimoto, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

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POS-03-LB-048

Dynamics of Protein Expression Measured by SRM Reveals Direct Targets and Secondary Messengers of Estrogen Receptor in MCF-7 Breast Cancer Cells

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POS-03-LB-049

Proteome Profiling and Identification of *In Vivo* Substrates of Cysteine Cathepsins in a Murine Model of Pancreatic Cancer

Anna Prudova[1], Vasilena Gocheva[2], Ulrich auf dem Keller[1], Oakley Olson[2], Johanna Joyce[2], Christopher Overall[1]

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POS-03-LB-050

PrESTs as Reagents for Proteomics

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POS-03-LB-051

Deep Proteome Characterization as a Tool for Identification of Novel Intraamniotic Infection and Inflammation Biomarkers in Preterm Birth Patients

Vojtech Tambor[1], Juraj Lenco[1,2], Ramkumar Menon[3], Marian Kacerovsky[1,4], Marek Link[2], Jiri Stulik[2]

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POS-03-LB-052

Characterization of the Host and Microbiota Proteomes in Pediatric IBD

Cheng-Kang Chiang[1], Shelley Deeke[1], Walid Mottawea[1], Alain Stintzi[1], Daniel Figeys[1], Dave Mack[2]

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POS-03-LB-053

Targeted Phosphoproteomics to Analyze Kinase-Mediated Signaling Pathway

Tatsuya Yazaki, Shunsuke Takagi, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Isihama

Kyoto University, Japan

POS-03-LB-054

iTRAQ-Based Plasma Protein Profiling of Mild Cognitive Impairment Across Two Independent Cohorts

Julia Muenchhoff[1], Fei Song[1], Anne Poljak[2], Nicole A. Kochan[1], Henry Brodaty[1], George A. Smythe[3], John Attia[4], Peter W. Schofield[4,5], Perminder S. Sachdev[1,3]

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POS-03-LB-055

Mapping the Chromosome 10 Proteome: Objectives and Progress

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Improved Enrichment of S-Nitrosylated Peptides Using Iodoacetyl Tandem Mass Tag Reagents, Immbolized anti-TMT Antibody Resin and TMT Elution Buffer

Ryan Bomgarden[1], Zhe Qu[3], Eric Hommema[1], Rosa Viner[2], Zezong Gu[3], Navid Haghdoost[1], John C. Rogers[1]

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Customized Real-Time Control of Benchtop Orbitrap MS

Andreas Kuehn[1], Florian Grosse-Coosmann[1], Thomas Rietpietsch[1], Jan-Peter Hauschild[1], Katja Tham[1], Tim Stratton[2], Derek Bailey[1], Robert Malek[1], Markus Kellmann[1], Christoph Henrich[1], Oliver Lange[1], Andreas Wieghaus[1], Stevan Horning[1], Alexander Makarov[1]

[1]Thermo Fisher Scientific (Bremen), Germany, [2]Thermo Fisher Scientific (San Jose), USA

Preliminary Verification of Lung Cancer Plasma-based Stratification Markers for Chemotherapy

Konstantinos Petritis[4], Tony Tegeler[4], Regine Schoenherr[1], Haizhen Zhang[1], Patrick Pirrotte[4], Michael Syring[4], Jeffrey R. Whiteaker[1], Chenwei Lin[1], Ping Yan[1], Yeounjin Kim[2], Helen J. Ross[3], Guy Berchem[2], Bruno Domon[2], Amanda G. Paulovich[1]

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Proteomic Analysis of Salivary Proteins in Patients with Oral Precancerous Lesions

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Deep Subcellular Proteome Profiling of Human Induced Pluripotent Stem Cell by One-shot nanoLC-MS/MS Analyses with Meter-scale Monolithic Silica Columns

Mio Iwasaki[1], Masato Nakagawa[1], Yasushi Ishihama[2], Shinya Yamanaka[1,3]

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Changes in the Protein Profiles of *Beta vulgaris* Leaf Apoplastic Fluid with Iron Deficiency and Iron Resupply

Elain Gutierrez-Carbonell, Giuseppe Lattanzio, Anunciación Abadía, Javier Abadía, Ana Flor López-Millán

Plant Nutrition Department, Aula Dei Experimental Station, Spain

Integrated -omic Analysis Uncovers a Fundamental Hypoxia-driven Mechanism of Breast Cancer Progression

Safia Thaminy[1,2], Heiko Blaser[3], Timothy Clough[4], Yong Zhou[2], Berend Snijder[5], Ching-Yun Chang[4], Danni Yu[4], Carey Sheu[2], Lucas Pelkmans[5], Tak W. Mak[3], Mi-Youn Brusniak[2], Julian D. Watts[2], Olga Vitek[4], Ruedi Aebersold[1,2,6]

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Quantitative Proteomic Analysis of Oyster Larvae to Study the Effect of Multiple Climate Change Stressors by 8-plex iTRAQ Labeling

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Targeted Proteomic Absolute Quantification on Transporters of Human Pancreatic Cancer Cells with Gemcitabine-resistance

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Deciphering Human-Microbe Proteome Interactions using an E. coli Proteome Chip

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Comparative Proteomics of Wild Type, Mutant and Overexpressing Strains of Diazotrophic Anabaena PCC7120 Unviels the Role of ahpC in Abiotic Stress Management

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Diagnosis of Male Reproductive System Disorders with Proteomic Biomarkers Measured in Seminal Plasma

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Scalable Multiplexed and Sensitive Immunoassays by the Proximity Extension Assay

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