Research

1453
Enhanced Interferon Signaling Pathway in Oral Cancer Revealed by Quantitative Proteome Analysis of Microdissected Specimens Using $^{16}O/^{18}O$ Labeling and Integrated Two-dimensional LC-ESI-MALDI Tandem MS
Lang-Ming Chi, Chien-Wei Lee, Kai-Ping Chang, Sheng-Po Hao, Hang-Mao Lee, Ying Liang, Chuen Hsueh, Chia-Jung Yu, I-Neng Lee, Yin-Ju Chang, Shih-Ying Lee, Yuan-Ming Yeh, Yu-Sun Chang, Kun-Yi Chien, and Jau-Song Yu

1475
Mechanical Injury and Cytokines Cause Loss of Cartilage Integrity and Upregulate Proteins Associated with Catabolism, Immunity, Inflammation, and Repair
Anna L. Stevens, John S. Wishnok, Forest M. White, Alan J. Grodzinsky, and Steven R. Tannenbaum

1490
Evaluation of Blastomere Biopsy Using a Mouse Model Indicates the Potential High Risk of Neurodegenerative Disorders in the Offspring
Yang Yu, Jindao Wu, Yong Fan, Zhuo Lv, Xuejiang Guo, Chun Zhao, Rong Zhou, Zhuo Zhang, Fuqiang Wang, Min Xiao, Ling Chen, Hui Zhu, Wen Chen, Min Lin, Jiayin Liu, Zuomin Zhou, Liu Wang, Ran Huo, Qi Zhou, and Jiahao Sha

1501
Protein Profiling of Plasma Membranes Defines Aberrant Signaling Pathways in Mantle Cell Lymphoma
Robert S. Boyd, Rebekah Jukes-Jones, Renata Walewska, David Brown, Martin J. S. Dyer, and Kelvin Cain

1516
Multiple Motif Scanning to Identify Methyltransferases from the Yeast Proteome
Tanya C. Petrossian and Steven G. Clarke

1527
The Phosphoproteome of Bloodstream Form Trypanosoma brucei, Causative Agent of African Sleeping Sickness
Isabelle R. E. Nett, David M. A. Martin, Diego Miranda-Saavedra, Douglas Lamont, Jonathan D. Barber, Angela Mehler, and Michael A. J. Ferguson

1539
Identification of Novel SHPS-1-associated Proteins and Their Roles in Regulation of Insulin-like Growth Factor-dependent Responses in Vascular Smooth Muscle Cells
Xinchun Shen, Gang Xi, Yashwanth Radhakrishnan, and David R. Clemmons

1552
Parvulin (Par14), a Peptidyl-Prolyl cis-trans Isomerase, Is a Novel rRNA Processing Factor That Evolved in the Metazoan Lineage
Sally Fujiiyama-Nakamura, Harunori Yoshikawa, Keiichi Homma, Toshiya Hayano, Teruko Tsujimura-Takahashi, Keiichi Izumikawa, Hideaki Ishikawa, Naoki Miyazawa, Mitsuaki Yanagida, Yutaka Miura, Takashi Shinkawa, Yoshio Yamauchi, Toshiaki Isobe, and Nobuhiro Takahashi

On the cover: The study procedure of influence of blastomere biopsy was described. Mouse was used as animal model to evaluate the potential risk of blastomere biopsy. Our study suggested that the mouse behavior, especially in memory, could be sensitive to blastomere biopsy procedures besides some physiology index and indicated an increased relative risk of neurodegenerative disorders in the offspring generated following blastomere biopsy. For details, see the article by Yu et al., pages 1490–1500.

[Online version of this article contains supplemental material. Author’s Choice]
In Vivo Stable Isotope Labeling of Fruit Flies Reveals Post-transcriptional Regulation in the Maternal-to-zygotic Transition
Joost W. Gouw, Martijn W. H. Pinkse, Harmjan R. Vos, Yuri Moshkin, C. Peter Verrijzer, Albert J. R. Heck, and Jeroen Krijgsveld

Dehydration-responsive Nuclear Proteome of Rice (Oryza sativa L.) Illustrates Protein Network, Novel Regulators of Cellular Adaptation, and Evolutionary Perspective
Mani Kant Choudhary, Debarati Basu, Asis Datta, Niranjan Chakraborty, and Subhra Chakraborty

Identification and Quantitation of Newly Synthesized Proteins in Escherichia coli by Enrichment of Azidohomoalanine-labeled Peptides with Diagonal Chromatography

Tissue Profiling of the Mammalian Central Nervous System Using Human Antibody-based Proteomics
Jan Mulder, Erik Björling, Kalle Jonasson, Henrik Wernérus, Sophia Hober, Tomas Hökfelt, and Mathias Uhlen

Identification of Cellular Proteome Modifications in Response to West Nile Virus Infection
Boris Pastorino, Eodie Boucomont-Chapeaublanc, Christophe N. Peyrefitte, Maya Belghazi, Thierry Fusaï, Christophe Rogier, Hugues J. Tolou, and Lionel Almeras

Snapshot Peptidomics of the Regulated Secretory Pathway
Kazuki Sasaki, Yoshinori Satomi, Toshifumi Takao, and Naoto Minamino

An In-solution Ultrasonication-assisted Digestion Method for Improved Extracellular Matrix Proteome Coverage
Kirk C. Hansen, Lauren Kiemele, Ori Maller, Jenean O’Brien, Aarthi Shankar, Jaime Fornetti, and Pepper Schedin

Application of Label-free Quantitative Peptidomics for the Identification of Urinary Biomarkers of Kidney Chronic Allograft Dysfunction
Luis F. Quintana, Josep M. Campistol, Maria P. Alcolea, Elisenda Bañon-Maneus, Amanda Solé-González, and Pedro R. Cutilias

Elucidation of Thioredoxin Target Protein Networks in Mouse
Cexiong Fu, Changgong Wu, Tong Liu, Tetsuro Ago, Peiyong Zhai, Junichi Sadoshima, and Hong Li

Immunocapture and Identification of Cell Membrane Protein Antigenic Targets of Serum Autoantibodies
Edward Littleton, Mathias Dreger, Jackie Palace, and Angela Vincent

The Prevalence and Nature of Glycan Alterations on Specific Proteins in Pancreatic Cancer Patients Revealed Using Antibody-Lectin Sandwich Arrays
Tingting Yue, Irwin J. Goldstein, Michael A. Hollingsworth, Karen Kaul, Randall E. Brand, and Brian B. Haab

Mass Spectrometry-based Protein Profiling to Determine the Cause of Lysosomal Storage Diseases of Unknown Etiology
David E. Sleat, Lin Ding, Shudan Wang, Caifeng Zhao, Yanhong Wang, Winnie Xin, Haiyan Zheng, Dirk F. Moore, Katherine B. Sims, and Peter Lobel

A Label-free Quantitative Proteomics Strategy to Identify E3 Ubiquitin Ligase Substrates Targeted to Proteasome Degradation

Surfome Analysis as a Fast Track to Vaccine Discovery: Identification of a Novel Protective Antigen for Group B Streptococcus Hypervirulent Strain COH1
Francesco Doro, Sabrina Liberatori, Manuel J. Rodríguez-Ortega, Cira D. Rinaudo, Roberto Rosini, Marirosa Mora, Maria Scarselli, Emrah Altindis, Romina D’Aurizio, Maria Stella, Immaculada Margarit, Domenico Maione, John L. Telford, Nathalie Norais, and Guido Grandi
SLP-65 Phosphorylation Dynamics Reveals a Functional Basis for Signal Integration by Receptor-proximal Adaptor Proteins

Thomas Oellerich, Mads Grønborg, Konstantin Neumann, He-Hsuan Hsiao, Henning Urlaub, and Jürgen Wienands

Large-scale Proteomics Analysis of the Human Kinome

Felix S. Oppermann, Florian Gnad, Jesper V. Olsen, Renate Hornberger, Zoltán Greff, György Kéri, Matthias Mann, and Henrik Daub