## Table of Contents

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### Research

1. Improved Validation of Peptide MS/MS Assignments Using Spectral Intensity Prediction  

18. Secretome of Primary Cultures of Human Adipose-derived Stem Cells: Modulation of Serpins by Adipogenesis  
   Sanjin Zvonic, Michael Lefevre, Gail Kilroy, Z. Elizabeth Floyd, James P. DeLany, Indu Kheterpal, Amy Gravois, Ryan Dow, Angie White, Xiying Wu, and Jeffrey M. Gimble

29. Morphine Administration Alters the Profile of Hippocampal Postsynaptic Density-associated Proteins: A Proteomics Study Focusing on Endocytic Proteins  
   José A. Morón, Noura S. Abul-Husn, Raphael Rozenfeld, Georgia Dolios, Rong Wang, and Lakshmi A. Devi

43. A Serum Glycomics Approach to Breast Cancer Biomarkers  
   Crystal Kirmiz, Bensheng Li, Hyun Joo An, Brian H. Clowers, Helen K. Chew, Kit S. Lam, Anthony Ferrige, Robert Alecio, Alexander D. Borowsky, Shola Sulaimon, Carlito B. Lebrilla, and Suzanne Miyamoto

56. Proteomic Identification of Macrophage Migration-inhibitory Factor upon Exposure to TiO₂ Particles  
   Myung-Hwa Cha, TaiYoun Rhim, Kyung Hun Kim, An-Soo Jang, Young-Ki Paik, and Choon-Sik Park

64. Mass Spectrometric Detection of Tissue Proteins in Plasma  
   Hui Zhang, Alvin Y. Liu, Paul Loriaux, Bernd Wollscheid, Yong Zhou, Julian D. Watts, and Ruedi Aebersold

72. Mass Spectrometric Mapping of Linker Histone H1 Variants Reveals Multiple Acetylations, Methyllations, and Phosphorylation as Well as Differences between Cell Culture and Tissue  
   Jacek R. Wiśniewski, Alexandre Zougman, Sonja Krüger, and Matthias Mann

88. A Proteomics Screen Implicates HSP83 and a Small Kinetoplastid Calpain-related Protein in Drug Resistance in *Leishmania donovani* Clinical Field Isolates by Modulating Drug-induced Programmed Cell Death  
   Baptiste Vergnes, Benjamin Gourbal, Isabelle Girard, Shyam Sundar, Jolyne Drummelsmith, and Marc Ouellette

102. Distorted Relation between mRNA Copy Number and Corresponding Major Histocompatibility Complex Ligand Density on the Cell Surface  
   Andreas O. Weinzierl, Claudia Lemmel, Oliver Schoor, Margret Müller, Tobias Krüger, Dorothee Wernet, Jörg Hennenlotter, Arnulf Stenzl, Karin Klingel, Hans-Georg Rammensee, and Stefan Stevanović

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On the cover, an approach for a quantitative comparison of the MHC ligandome and the transcriptome is shown. From pairs of tumor and autologous normal tissues, both MHC ligands and mRNA were isolated and quantified. Using the differential N-terminal isotope coding (dNIC) strategy for modification of MHC bound peptides, several hundred peptide ratios and sequences were identified. RNA levels were assessed by gene chip analysis and correlated with their respective peptide presentation ratios. For details, see the article by Weinzierl et al., pages 102–113.

[S] Online version of this article contains supplemental material.
Proteomics Exploration Reveals That Actin Is a Signaling Target of the Kinase Akt
Franck Vandermoere, Ikram El Yazidi-Belkoura, Yohann Demont, Christian Slomianny, Johann Antol, Jérôme Lemoine, and Hubert Hondermarck

Technology

Determination of Binding Specificities in Highly Multiplexed Bead-based Assays for Antibody Proteomics
Jochen M. Schwenk, Johan Lindberg, Mårten Sundberg, Mathias Uhlén, and Peter Nilsson

On-chip Complement Activation Adds an Extra Dimension to Antigen Microarrays
Krisztián Papp, Zsuzsanna Szekeres, Nóra Terényi, Andrea Isák, Anna Erdei, and József Prechtl

Shotgun Glycopeptide Capture Approach Coupled with Mass Spectrometry for Comprehensive Glycoproteomics
Bingyun Sun, Jeffrey A. Ranish, Angelita G. Utleg, James T. White, Xiaowei Yan, Biaoyang Lin, and Leroy Hood

Dataset

Multivariable Difference Gel Electrophoresis and Mass Spectrometry: A Case Study on Transforming Growth Factor-β and ErbB2 Signaling
David B. Friedman, Shizhen E. Wang, Corbin W. Whitwell, Richard M. Caprioli, and Carlos L. Arteaga

Information

Calendar
Instructions to Authors