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558  Life and Death of Proteins: A Case Study of Glucose-starved Staphylococcus aureus
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571  N-glycosylation of Colorectal Cancer Tissues
A liquid chromatography and mass spectrometry-based investigation

586  Proteomics-based Dissection of Human Endoderm Progenitors by Differential Cell Capture on Antibody Array
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596  Direct Detection of Bacterial Protein Secretion Using Whole Colony Proteomics
Matthew M. Champion, Emily A. Williams, George M. Kennedy, and Patricia A. DiGiuseppe Champion

605  Morphine Produces Immunosuppressive Effects in Nonhuman Primates at the Proteomic and Cellular Levels

619  Precision, Proteome Coverage, and Dynamic Range of Arabidopsis Proteome Profiling Using 15N Metabolic Labeling and Label-free Approaches
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629  Chemical Visualization of Phosphoproteomes on Membrane
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640  Chemical Punch Packed in Venoms Makes Centipedes Excellent Predators
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651  Phosphosignature Predicts Dasatinib Response in Non-small Cell Lung Cancer
Martin Klammer, Marc Kaminski, Alexandra Zedler, Felix Oppermann, Stephanie Blencke, Sandra Marx, Stefan Müller, Andreas Tebbe, Klaus Godl, and Christoph Schaab

On the cover: This map ER chaperone interactions was assembled using an ER-localized yeast two-hybrid system, ER-specific affinity purifications, and FLAG-tagged co-IPs followed by mass spectrometry. The interaction between ERP72 and cyclophilin B (green edge) was further defined by NMR and mutagenesis (inset). Background: A live HeLa cell expressing GFP-tagged cyclophilin B. For details, see article by Gregor Jansen, et al., pages 710–723.

[S] Online version of this article contains supplemental material.  × Author’s Choice
Identification of New Autoantigens for Primary Biliary Cirrhosis Using Human Proteome Microarrays
Chao-Jun Hu, Guang Song, Wei Huang, Guo-Zhen Liu, Chui-Wen Deng, Hai-Pan Zeng, Li Wang, Feng-Chun Zhang, Xuan Zhang, Jun Seop Jeong, Seth Blackshaw, Li-Zhi Jiang, Heng Zhu, Lin Wu, and Yong-Zhe Li

Proteomic Profiling of the Planarian Schmidtea mediterranea and Its Mucous Reveals Similarities with Human Secretions and Those Predicted for Parasitic Flatworms
Donald G. Bocchinfuso, Paul Taylor, Eric Ross, Alex Ignatchenko, Vladimir Ignatchenko, Thomas Kislinger, Bret J. Pearson, and Michael F. Moran

Quantitative Proteomic Analysis of Type III Secretome of Enteropathogenic Escherichia coli Reveals an Expanded Effector Repertoire for Attaching/Effacing Bacterial Pathogens
Wanyin Deng, Hong B. Yu, Carmen L. de Hoog, Nikolay Stoynov, Yuling Li, Leonard J. Foster, and B. Brett Finlay

An Interaction Map of Endoplasmic Reticulum Chaperones and Foldases
Gregor Jansen, Pekka Määtätänen, Alexey Y. Denisov, Leslie Scarffe, Babette Schade, Haouaria Balghi, Kurt Dejgaard, Leanna Y. Chen, William J. Muller, Kalle Gehring, and David Y. Thomas

Rapid Phosphoproteomic and Transcriptomic Changes in the Rhizobia-legume Symbiosis
Christopher M. Rose, Muthusubramanian Venkateshwaran, Jeremy D. Volkening, Paul A. Grimsrud, Junko Maeda, Derek J. Bailey, Kwanghyun Park, Maegen Howes-Podoll, Désirée den Os, Li Huey Yeun, Michael S. Westphall, Michael R. Sussman, Jean-Michel Ané, and Joshua J. Coon

Use of Kinase Inhibitors to Correct ΔF508-CFTR Function
Agata M. Trzcińska-Daneluti, Leo Nguyen, Chong Jiang, Christopher Fladd, David Uehling, Michael Prakesch, Rima Al-awar, and Daniela Rotin

Isolation and Proteomic Characterization of the Mouse Sperm Acrosomal Matrix
Benoit Guyonnet, Masoud Zabet-Moghaddam, Susan SanFrancisco, and Gail A. Cornwall

Endo-β-N-acetylglucosaminidases from Infant Gut-associated Bifidobacteria Release Complex N-glycans from Human Milk Glycoproteins
Daniel Garrido, Charles Nwosu, Santiago Ruiz-Moyano, Danielle Aldredge, J. Bruce German, Carlito B. Lebrilla, and David A. Mills

Technological Innovation and Resources

Broad-spectrum Four-dimensional Orthogonal Electrophoresis: A Novel Comprehensively Feasible System for Protein Complexomics Investigation
Xiaodong Wang, Fenjie Li, Gaoguang Song, Shuai Guo, Hui Liu, Guoqiang Chen, and Zhili Li

A Novel Strategy for Global Analysis of the Dynamic Thiol Redox Proteome
Pablo Martínez-Acedo, Estefanía Núñez, Francisco J. Sánchez Gómez, Margoth Moreno, Elena Ramos, Alicia Izquierdo-Álvarez, Elisabet Miró-Casas, Raquel Mesa, Patricia Rodriguez, Antonio Martínez-Ruiz, David García Dorado, Santiago Lamas, and Jesús Vázquez

Peptide Production and Decay Rates Affect the Quantitative Accuracy of Protein Cleavage Isotope Dilution Mass Spectrometry (PC-IDMS)
Christopher M. Shuford, Ronald R. Sederoff, Vincent L. Chiang, and David C. Muddiman

A Mass Spectrometry Proteomics Data Management Platform
Vagisha Sharma, Jimmy K. Eng, Michael J. MacCoss, and Michael Riffle

Unbiased Selective Isolation of Protein N-terminal Peptides from Complex Proteome Samples Using Phospho Tagging (PTAG) and TiO₂-based Depletion
Geert P. M. Mommen, Bas van de Waterbeemd, Hugo D. Meiring, Gideon Kersten, Albert J. R. Heck, and Ad P. J. M. de Jong