

## Research

- 1176 **Changes in the Plasma Proteome of *Manduca sexta* Larvae in Relation to the Transcriptome Variations after an Immune Challenge: Evidence for High Molecular Weight Immune Complex Formation**  
[S] Yan He, Xiaolong Cao, Shuguang Zhang, Janet Rogers, Steve Hartson, and Haobo Jiang
- 1188 **Proteomic Analysis of *Rhizoctonia solani* Identifies Infection-specific, Redox Associated Proteins and Insight into Adaptation to Different Plant Hosts**  
[S] ✎ Jonathan P. Anderson, James K. Hane, Thomas Stoll, Nicholas Pain, Marcus L. Hastie, Parwinder Kaur, Christine Hoogland, Jeffrey J. Gorman, and Karam B. Singh
- 1204 **Proteome Dynamics: Tissue Variation in the Kinetics of Proteostasis in Intact Animals**  
[S] ✎ Dean E. Hammond, Amy J. Claydon, Deborah M. Simpson, Dominic Edward, Paula Stockley, Jane L. Hurst, and Robert J. Beynon
- 1220 **Application of Mass Spectrometry Profiling to Establish Brusatol as an Inhibitor of Global Protein Synthesis**  
[S] Steffan Vartanian, Taylur P. Ma, James Lee, Peter M. Haverty, Donald S. Kirkpatrick, Keping Yu, and David Stokoe
- 1232 **Proteome-wide Identification of Novel Ceramide-binding Proteins by Yeast Surface cDNA Display and Deep Sequencing**  
[S] Scott Bidlingmaier, Kevin Ha, Nam-Kyung Lee, Yang Su, and Bin Liu
- 1246 **High-resolution Antibody Array Analysis of Childhood Acute Leukemia Cells**  
[S] Veronika Kanderova, Daniela Kuzilkova, Jan Stuchly, Martina Vaskova, Tomas Brdicka, Karel Fiser, Ondrej Hrusak, Fridtjof Lund-Johansen, and Tomas Kalina
- 1262 **Predictions of Cleavability of Calpain Proteolysis by Quantitative Structure-Activity Relationship Analysis Using Newly Determined Cleavage Sites and Catalytic Efficiencies of an Oligopeptide Array**  
[S] ✎ Fumiko Shinkai-Ouchi, Suguru Koyama, Yasuko Ono, Shoji Hata, Koichi Ojima, Mayumi Shindo, David duVerle, Mika Ueno, Fujiko Kitamura, Naoko Doi, Ichigaku Takigawa, Hiroshi Mamitsuka, and Hiroyuki Sorimachi
- 1281 **Exosomes Secreted by Apoptosis-Resistant Acute Myeloid Leukemia (AML) Blasts Harbor Regulatory Network Proteins Potentially Involved in Antagonism of Apoptosis**  
[S] Anna Wojtuszkiewicz, Gerrit J. Schuurhuis, Floortje L. Kessler, Sander R. Piersma, Jaco C. Knol, Thang V. Pham, Gerrit Jansen, René J. P. Musters, Johan van Meerloo, Yehuda G. Assaraf, Gertjan J. L. Kaspers, Sonja Zweegman, Jacqueline Cloos, and Connie R. Jimenez
- 1299 **Proteomic Analysis Reveals a Novel Mutator S (MutS) Partner Involved in Mismatch Repair Pathway**  
[S] Zhen Chen, Mykim Tran, Mengfan Tang, Wenqi Wang, Zihua Gong, and Junjie Chen

On the cover: A novel technique for time-controlled digestion of monoclonal antibody (mAb) into peptides with desired medium size using an 8 M urea-compatible enzyme reactor. This technique combined with ETD, CAD, and ETD/ion-ion proton transfer mass spectrometry verified near complete mAb sequence, identified multiple post-translational modifications, and localized all the disulfide linkages. For details, see the article Lichao Zhang, *et al.*, pages 1479–1488.

- 1309 **Direct and Absolute Quantification of over 1800 Yeast Proteins via Selected Reaction Monitoring**  
 [S] ✎  
*Craig Lawless, Stephen W. Holman, Philip Brownridge, Karin Lanthaler, Victoria M. Harman, Rachel Watkins, Dean E. Hammond, Rebecca L. Miller, Paul F. G. Sims, Christopher M. Grant, Claire E. Evers, Robert J. Beynon, and Simon J. Hubbard*
- 1323 **Mapping the O-Mannose Glycoproteome in *Saccharomyces cerevisiae***  
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*Patrick Neubert, Adnan Halim, Martin Zauser, Andreas Essig, Hireen J. Joshi, Ewa Zatorska, Ida Signe Bohse Larsen, Martin Loibl, Joan Castells-Ballester, Markus Aebi, Henrik Clausen, and Sabine Strahl*
- 1338 **Phosphoproteomics Profiling of Tobacco Mature Pollen and Pollen Activated *in vitro***  
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- 1351 **Rapid Oligo-Galacturonide Induced Changes in Protein Phosphorylation in *Arabidopsis***  
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- 1360 **High-Density Peptide Microarray Analysis of IgG Autoantibody Reactivities in Serum and Cerebrospinal Fluid of Multiple Sclerosis Patients**  
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- 1397 **Comparative Study of Early Cold-Regulated Proteins by Two-Dimensional Difference Gel Electrophoresis Reveals a Key Role for Phospholipase D $\alpha$ 1 in Mediating Cold Acclimation Signaling Pathway in Rice**  
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- 1412 **Sampling From the Proteome to the Human Leukocyte Antigen-DR (HLA-DR) Ligandome Proceeds Via High Specificity**  
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*Geert P. M. Mommen, Fabio Marino, Hugo D. Meiring, Martien C. M. Poelen, Jacqueline A. M. van Gaans-van den Brink, Shabaz Mohammed, Albert J. R. Heck, and Cécile A. C. M. van Els*
- 1424 **Towards Understanding Male Infertility After Spinal Cord Injury Using Quantitative Proteomics**  
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*Barbara Ferreira da Silva, Chen Meng, Dominic Helm, Fiona Pachel, Jürgen Schiller, Emad Ibrahim, Charles M. Lynne, Nancy L. Brackett, Ricardo Pimenta Bertolla, and Bernhard Kuster*

## Technological Innovation and Resources

- 1435 **Glycomic Characterization of Induced Pluripotent Stem Cells Derived from a Patient Suffering from Phosphomannomutase 2 Congenital Disorder of Glycosylation (PMM2-CDG)**  
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*Christina T. Thiesler, Samanta Cajic, Dirk Hoffmann, Christian Thiel, Laura van Diepen, René Hennig, Malte Sgodda, Robert Weißmann, Udo Reichl, Doris Steinemann, Ulf Diekmann, Nicolas M. B. Huber, Astrid Oberbeck, Tobias Cantz, Andreas W. Kuss, Christian Körner, Axel Schambach, Erdmann Rapp, and Falk F. R. Buettner*
- 1453 **Simultaneous Metabolite, Protein, Lipid Extraction (SIMPLEX): A Combinatorial Multimolecular Omics Approach for Systems Biology**  
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*Cristina Coman, Fiorella Andrea Solari, Andreas Hentschel, Albert Sickmann, René Peiman Zahedi, and Robert Ahrends*

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**DeMix-Q: Quantification-Centered Data Processing Workflow**

*Bo Zhang, Lukas Käll, and Roman A. Zubarev*

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**Analysis of Monoclonal Antibody Sequence and Post-translational Modifications by Time-controlled Proteolysis and Tandem Mass Spectrometry**

*Lichao Zhang, A. Michelle English, Dina L. Bai, Scott A. Ugrin, Jeffrey Shabanowitz, Mark M. Ross, Donald F. Hunt, and Wei-Han Wang*

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