

## Research

- 1397 **The Vac14-interaction Network Is Linked to Regulators of the Endolysosomal and Autophagic Pathway**  
[S] *Ulf Schulze, Beate Vollenbröcker, Daniela A. Braun, Truc Van Le, Daniel Granado, Joachim Kremerskothen, Benjamin Fränzel, Rafael Klosowski, Johannes Barth, Christian Fufezan, Dirk A. Wolters, Hermann Pavenstädt, and Thomas Weide*
- 1412 **Sialylation of Outer Membrane Porin Protein D: A Mechanistic Basis of Antibiotic Uptake in *Pseudomonas aeruginosa***  
[S] *Biswajit Khatua, Jeremy Van Vleet, Biswa Pronab Choudhury, Rama Chaudhry, and Chitra Mandal*
- 1429 **Alternative Mammalian Target of Rapamycin (mTOR) Signal Activation in Sorafenib-resistant Hepatocellular Carcinoma Cells Revealed by Array-based Pathway Profiling**  
[S] *Mari Masuda, Wei-Yu Chen, Akihiko Miyanaaga, Yuka Nakamura, Kumiko Kawasaki, Tomohiro Sakuma, Masaya Ono, Chi-Long Chen, Kazufumi Honda, and Tesshi Yamada*
- 1439 **Structural and Functional Analysis of Novel Human Cytochrome c Targets in Apoptosis**  
[S] *Jonathan Martínez-Fábregas, Irene Díaz-Moreno, Katuska González-Arzoła, Simon Janocha, José A. Navarro, Manuel Hervás, Rita Bernhardt, Adrián Velázquez-Campoy, Antonio Díaz-Quintana, and Miguel A. De la Rosa*
- 1457 **Cross-species Proteomics Reveals Specific Modulation of Signaling in Cancer and Stromal Cells by Phosphoinositide 3-kinase (PI3K) Inhibitors**  
[S] *Vinothini Rajeeve, Iolanda Vendrell, Edmund Wilkes, Neil Torbett, and Pedro R. Cutillas*
- 1471 **Discovery of Colorectal Cancer Biomarker Candidates by Membrane Proteomic Analysis and Subsequent Verification using Selected Reaction Monitoring (SRM) and Tissue Microarray (TMA) Analysis**  
[S] *Hideaki Kume, Satoshi Muraoka, Takahisa Kuga, Jun Adachi, Ryohei Narumi, Shio Watanabe, Masayoshi Kuwano, Yoshio Kodaera, Kazuyuki Matsushita, Junya Fukuoka, Takeshi Masuda, Yasushi Ishihama, Hisahiro Matsubara, Fumio Nomura, and Takeshi Tomonaga*
- 1485 **Identification of Bacterial Factors Involved in Type 1 Fimbria Expression using an *Escherichia coli* K12 Proteome Chip**  
*Yi-Wen Chen, Ching-Hao Teng, Yu-Hsuan Ho, Tien Yu Jessica Ho, Wen-Chun Huang, Masayuki Hashimoto, I-Yuan Chiang, and Chien-Sheng Chen*
- 1495 **Quantitative Chemical Proteomics Identifies Novel Targets of the Anti-cancer Multi-kinase Inhibitor E-3810**  
[S] ✂ *Mara Colzani, Roberta Noberini, Mauro Romanenghi, Gennaro Colella, Maurizio Pasi, Daniele Fancelli, Mario Varasi, Saverio Minucci, and Tiziana Bonaldi*
- 1510 **Controlling for Gene Expression Changes in Transcription Factor Protein Networks**  
[S] *Charles A. S. Banks, Zachary T. Lee, Gina Boanca, Mahadevan Lakshminarasimhan, Brad D. Groppe, Zhihui Wen, Gaye L. Hattem, Chris W. Seidel, Laurence Florens, and Michael P. Washburn*

On the cover: “**Beadfection**”. Protein is attached covalently to the shell of fluorescently-labelled core-shell microspheres by rapid, generic chemistry. Transit of loaded microspheres across the cell membrane via passive diffusion, takes up to 24 hours. Inside the cells, within 12 hours, the reducing environment of the cytoplasm cleaves the disulfide linker on the microspheres, thereby releasing the protein cargo. For details, see the article by David Nagel *et al.*, pages 1543–1551.

- 1523 **Protein Abundance Changes and Ubiquitylation Targets Identified after Inhibition of the Proteasome with Syringolin A**  
[S] *Julia Svozil, Matthias Hirsch-Hoffmann, Robert Dudler, Wilhelm Gruissem, and Katja Baerenfaller*

## Technological Innovation and Resources

- 1537 **Numerical Compression Schemes for Proteomics Mass Spectrometry Data**  
*Johan Teleman, Andrew W. Dowsey, Faviel F. Gonzalez-Galarza, Simon Perkins, Brian Pratt, Hannes L. Röst, Lars Malmström, Johan Malmström, Andrew R. Jones, Eric W. Deutsch, and Fredrik Levander*
- 1543 **Polymeric Microspheres as Protein Transduction Reagents**  
[S] ✂ *David Nagel, Jonathan M. Behrendt, Gwen F. Chimonides, Elizabeth E. Torr, Andrew Devitt, Andrew J. Sutherland, and Anna V. Hine*
- 1552 **SpliceVista, a Tool for Splice Variant Identification and Visualization in Shotgun Proteomics Data**  
[S] *Yafeng Zhu, Lina Hultin-Rosenberg, Jenny Forshed, Rui M. M. Branca, Lukas M. Orre, and Janne Lehtiö*
- 1563 **A Universal Chemical Enrichment Method for Mapping the Yeast N-glycoproteome by Mass Spectrometry (MS)**  
[S] *Weixuan Chen, Johanna M. Smeeckens, and Ronghu Wu*
- 1573 **Confetti: A Multiprotease Map of the HeLa Proteome for Comprehensive Proteomics**  
[S] *Xiaofeng Guo, David C. Trudgian, Andrew Lemoff, Sivaramakrishna Yadavalli, and Hamid Mirzaei*
- 1585 **Proteome-wide Epitope Mapping of Antibodies Using Ultra-dense Peptide Arrays**  
[S] *Björn Forsström, Barbara Bislawska Axnäs, Klaus-Peter Stengele, Jochen Bühler, Thomas J. Albert, Todd A. Richmond, Francis Jingxin Hu, Peter Nilsson, Elton P. Hudson, Johan Rockberg, and Mathias Uhlen*
- 1598 **Comparative Performance of Four Methods for High-throughput Glycosylation Analysis of Immunoglobulin G in Genetic and Epidemiological Research**  
[S] ✂ *Jennifer E. Huffman, Maja Pučić-Baković, Lucija Klarić, René Hennig, Maurice H. J. Selman, Frano Vučković, Mislav Novokmet, Jasminka Krištić, Matthias Borowiak, Thilo Muth, Ozren Polašek, Genadij Razdorov, Olga Gornik, Rosina Plomp, Evropi Theodoratou, Alan F. Wright, Igor Rudan, Caroline Hayward, Harry Campbell, André M. Deelder, Udo Reichl, Yurii S. Aulchenko, Erdmann Rapp, Manfred Wuhler, and Gordan Lauc*
- 1611 **Immunoproteomics Using Polyclonal Antibodies and Stable Isotope-labeled Affinity-purified Recombinant Proteins**  
[S] *Fredrik Edfors, Tove Boström, Björn Forsström, Marlis Zeiler, Henrik Johansson, Emma Lundberg, Sophia Hober, Janne Lehtiö, Matthias Mann, and Mathias Uhlen*

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