

Research

- 215 **Global Identification and Characterization of Both O-GlcNAcylation and Phosphorylation at the Murine Synapse**
[S] *Jonathan C. Trinidad, David T. Barkan, Brittany F. Gullledge, Agnes Thalhammer, Andrej Sali, Ralf Schoepfer, and Alma L. Burlingame*
- 230 **Characterization of Membrane-shed Microvesicles from Cytokine-stimulated β -Cells Using Proteomics Strategies**
[S] *Giuseppe Palmisano, Søren Skov Jensen, Marie-Catherine Le Bihan, Jeanne Lainé, James N. McGuire, Flemming Pociot, and Martin Røssel Larsen*
- 244 **Modulation of Neuronal Pentraxin 1 Expression in Rat Pancreatic β -Cells Submitted to Chronic Glucotoxic Stress**
[S] *Domitille Schwartz, Yohann Couté, Yannick Brunner, Claes B. Wollheim, and Jean-Charles Sanchez*
- 255 **Cells Lacking β -Actin are Genetically Reprogrammed and Maintain Conditional Migratory Capacity**
[S] *Davina Tondeleir, Anja Lambrechts, Matthias Müller, Veronique Jonckheere, Thierry Doll, Drieke Vandamme, Karima Bakkali, Davy Waterschoot, Marianne Lemaistre, Olivier Debeir, Christine Decaestecker, Boris Hinz, An Staes, Evy Timmerman, Niklaas Colaert, Kris Gevaert, Joël Vandekerckhove, and Christophe Ampe*
- 272 **Absolute Quantitation of Isoforms of Post-translationally Modified Proteins in Transgenic Organism**
[S] *Yaojun Li, Yiwei Shu, Changchao Peng, Lin Zhu, Guangyu Guo, and Ning Li*
- 286 **Proteomic Cornerstones of Hematopoietic Stem Cell Differentiation: Distinct Signatures of Multipotent Progenitors and Myeloid Committed Cells**
[S] *Daniel Klimmeck, Jenny Hansson, Simon Raffel, Sergey Y. Vakhrushev, Andreas Trumpp, and Jeroen Krijgsveld*
- 303 **A Cell Surfaceome Map for Immunophenotyping and Sorting Pluripotent Stem Cells**
[S] *Rebekah L. Gundry, Daniel R. Riordon, Yelena Tarasova, Sandra Chuppa, Subarna Bhattacharya, Ondrej Juhasz, Olena Wiedemeier, Samuel Milanovich, Fallon K. Noto, Irina Tchernyshyov, Kimberly Raginski, Damaris Bausch-Fluck, Hyun-Jin Tae, Shannon Marshall, Stephen A. Duncan, Bernd Wollscheid, Robert P. Wersto, Sridhar Rao, Jennifer E. Van Eyk, and Kenneth R. Boheler*
- 317 **Proteomic Study and Marker Protein Identification of *Caenorhabditis elegans* Lipid Droplets**
[S] *Peng Zhang, Huimin Na, Zhenglong Liu, Shuyan Zhang, Peng Xue, Yong Chen, Jing Pu, Gong Peng, Xun Huang, Fuquan Yang, Zhensheng Xie, Tao Xu, Pingyong Xu, Guangshuo Ou, Shaobing O. Zhang, and Pingsheng Liu*
- 329 **A Human Ubiquitin Conjugating Enzyme (E2)-HECT E3 Ligase Structure-function Screen**
[S] *Yi Sheng, Jenny H. Hong, Ryan Doherty, Tharan Srikumar, Jonathan Shloush, George V. Avvakumov, John R. Walker, Sheng Xue, Dante Neculai, Janet W. Wan, Sung K. Kim, Cheryl H. Arrowsmith, Brian Raught, and Sirano Dhe-Paganon*

On the cover: A structure-function analysis of ubiquitin (Ub) E2 conjugating proteins, consisting of the determination of fifteen new high resolution three-dimensional structures and autoubiquitylation assays against a panel of HECT E3 ligase domains, reveals properties associated with Ub chain building activity: (i) net positive/neutral charge; (ii) an "acidic trough" near the catalytic Cys, and; (iii) similarity to the UBE2L3(UbcH7) HECT binding signature. For details, see article by Yi Sheng *et al.*, pages 329–341.

- 342 **Quantitative Proteomics Targeting Classes of Motif-containing Peptides Using Immunoaffinity-based Mass Spectrometry**
 [S] ✎ *Niclas Olsson, Peter James, Carl A. K. Borrebaeck, and Christer Wingren*
- 355 **Identification of Targets of c-Src Tyrosine Kinase by Chemical Complementation and Phosphoproteomics**
 [S] *Isabel Martinez Ferrando, Raghothama Chaerkady, Jun Zhong, Henrik Molina, Harrys K.C. Jacob, Katie Herbst-Robinson, Beverley M. Dancy, Vikram Katju, Ron Bose, Jin Zhang, Akhilesh Pandey, and Philip A. Cole*
- 370 **Urine Metabolomics Analysis for Biomarker Discovery and Detection of Jaundice Syndrome in Patients With Liver Disease**
 [S] *Xijun Wang, Aihua Zhang, Ying Han, Ping Wang, Hui Sun, Gaochen Song, Tianwei Dong, Ye Yuan, Xiaoxia Yuan, Miao Zhang, Ning Xie, He Zhang, Hui Dong, and Wei Dong*
- 381 **Quantitative Proteomics Profiling of Murine Mammary Gland Cells Unravels Impact of Annexin-1 on DNA Damage Response, Cell Adhesion, and Migration**
 [S] *Hannah L. F. Swa, Walter P. Blackstock, Lina H. K. Lim, and Jayantha Gunaratne*
- 394 **Development of a Pharmaceutical Hepatotoxicity Biomarker Panel Using a Discovery to Targeted Proteomics Approach**
 [S] *Ben C. Collins, Christine A. Miller, Alexandra Sposny, Phillip Hewitt, Martin Wells, William M. Gallagher, and Stephen R. Pennington*
- 411 **DNA Ends Alter the Molecular Composition and Localization of Ku Multicomponent Complexes**
 [S] *Guillaume Adelmant, Anne S. Calkins, Brijesh K. Garg, Joseph D. Card, Manor Askenazi, Alex Miron, Bijan Sobhian, Yi Zhang, Yoshihiro Nakatani, Pamela A. Silver, J. Dirk Iglehart, Jarrod A. Marto, and Jean-Bernard Lazaro*
- 422 **Quantitative Analysis of Energy Metabolic Pathways in MCF-7 Breast Cancer Cells by Selected Reaction Monitoring Assay**
 [S] *Andrei P. Drabovich, Maria P. Pavlou, Apostolos Dimitromanolakis, and Eleftherios P. Diamandis*
- 435 **Serum Proteomic Signature of Human Chagasic Patients for the Identification of Novel Potential Protein Biomarkers of Disease**
 [S] *Jian-Jun Wen, M. Paola Zago, Sonia Nuñez, Shivali Gupta, Federico Nuñez Burgos, and Nisha Jain Garg*
- 453 **Phosphoproteomic Analysis of Leukemia Cells under Basal and Drug-treated Conditions Identifies Markers of Kinase Pathway Activation and Mechanisms of Resistance**
 [S] *Maria P. Alcolea, Pedro Casado, Juan-Carlos Rodríguez-Prados, Bart Vanhaesebroeck, and Pedro R. Cutillas*
- 467 **Mapping of O-GlcNAc Sites of 20 S Proteasome Subunits and Hsp90 by a Novel Biotin-Cystamine Tag**
 [S] ✎ *Thorsten Overath, Ulrike Kuckelkorn, Petra Henklein, Britta Strehl, David Bonar, Alexander Kloss, Dagmar Siele, Peter-Michael Kloetzel, and Katharina Janek*

Technological Innovation and Resources

- 478 **Enhanced Peptide Identification by Electron Transfer Dissociation Using an Improved Mascot Percolator**
 [S] ✎ *James C. Wright, Mark O. Collins, Lu Yu, Lukas Käll, Markus Brosch, and Jyoti S. Choudhary*
- 492 **PaxDb, a Database of Protein Abundance Averages Across All Three Domains of Life**
 [S] ✎ *M. Wang, M. Weiss, M. Simonovic, G. Haertinger, S. P. Schrimpf, M. O. Hengartner, and C. von Mering*
- 501 **A Highly Efficient Multifunctional Tandem Affinity Purification Approach Applicable to Diverse Organisms**
 [S]

Hanhui Ma, Janel R. McLean, Lucy Fang-I Chao, Sebastian Mana-Capelli, Murugan Paramasivam, Kirsten A. Hagstrom, Kathleen L. Gould, and Dannel McCollum

512



Protein Turnover Quantification in a Multilabeling Approach: From Data Calculation to Evaluation

Christian Trötschel, Stefan P. Albaum, Daniel Wolff, Simon Schröder, Alexander Goesmann, Tim W. Nattkemper, and Ansgar Poetsch

527



Label-free Quantification and Shotgun Analysis of Complex Proteomes by One-dimensional SDS-PAGE/NanoLC-MS

EVALUATION FOR THE LARGE SCALE ANALYSIS OF INFLAMMATORY HUMAN ENDOTHELIAL CELLS

Violette Gautier, Emmanuelle Mouton-Barbosa, David Bouyssié, Nicolas Delcourt, Mathilde Beau, Jean-Philippe Girard, Corinne Cayrol, Odile Burlet-Schiltz, Bernard Monsarrat, and Anne Gonzalez de Peredo

540



A Computational Tool to Detect and Avoid Redundancy in Selected Reaction Monitoring

Hannes Röst, Lars Malmström, and Ruedi Aebersold