

## Minireview

- 706 **Protein Footprinting Comes of Age: Mass Spectrometry for Biophysical Structure Assessment**  
[S] *Liwen Wang and Mark R. Chance*

## Research

- 717 **Proteome-wide Mapping of Endogenous SUMOylation Sites in Mouse Testis**  
[S] ✎ *Lili Cai, Jun Tu, Lei Song, Zihua Gao, Kai Li, Yunzhi Wang, Yang Liu, Fan Zhong, Rui Ge, Jun Qin, Chen Ding, and Fuchu He*
- 728 **Quantitative Proteomic Approach Identifies Vpr Binding Protein as Novel Host Factor Supporting Influenza A Virus Infections in Human Cells**  
[S] *Anne Sadewasser, Katharina Paki, Katrin Eichelbaum, Boris Bogdanow, Sandra Saenger, Matthias Budt, Markus Lesch, Klaus-Peter Hinz, Andreas Herrmann, Thomas F. Meyer, Alexander Karlas, Matthias Selbach, and Thorsten Wolff*
- 743 **Structural Diversity of Human Gastric Mucin Glycans**  
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- 759 **Accurate Quantification of Site-specific Acetylation Stoichiometry Reveals the Impact of Sirtuin Deacetylase CobB on the *E. coli* Acetylome**  
[S] *Brian Tate Weinert, Shankha Satpathy, Bogi Karbech Hansen, David Lyon, Lars Juhl Jensen, and Chunaram Choudhary*
- 770 **Monitoring Cell-surface N-Glycoproteome Dynamics by Quantitative Proteomics Reveals Mechanistic Insights into Macrophage Differentiation**  
[S] *Mathias Kalxdorf, Stephan Gade, H. Christian Eberl, and Marcus Bantscheff*
- 786 **Machine Learning of Global Phosphoproteomic Profiles Enables Discrimination of Direct versus Indirect Kinase Substrates**  
[S] *Evgeny Kanshin, Sébastien Giguère, Cheng Jing, Mike Tyers, and Pierre Thibault*
- 799 **Development of a Multiplexed Liquid Chromatography Multiple-Reaction-Monitoring Mass Spectrometry (LC-MRM/MS) Method for Evaluation of Salivary Proteins as Oral Cancer Biomarkers**  
[S] *Yi-Ting Chen, Hsiao-Wei Chen, Chun-Feng Wu, Lichieh Julie Chu, Wei-Fang Chiang, Chih-Ching Wu, Jau-Song Yu, Cheng-Han Tsai, Kung-Hao Liang, Yu-Sun Chang, Maureen Wu, and Wei-Ting Ou Yang*

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On the cover: DSSO-based *in vivo* and *in vitro* cross-linking mass spectrometry (XL-MS) strategies represent new analytical workflows to study protein-protein interactions of large protein assemblies in cells. In combination with EM maps and computational modeling, the architecture of the human 26S proteasome was determined to infer its structural dynamics and regulation. For details, see the article by Xiaorong Wang, *et al.*, pages 840–854.

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- 812 **Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex**  
 [S] *Eric Cox, Woochang Hwang, Ijeoma Uzoma, Jianfei Hu, Catherine M. Guzzo, Junseop Jeong, Michael J. Matunis, Jiang Qian, Heng Zhu, and Seth Blackshaw*
- 824 **Human Immunoglobulin Heavy Gamma Chain Polymorphisms: Molecular Confirmation of Proteomic Assessment**  
 [S] *Magalie Dambrun, Célia Dechavanne, Alexandra Emmanuel, Florentin Aussenac, Marjorie Leduc, Chiara Giangrande, Joëlle Vinh, Jean-Michel Dugoujon, Marie-Paule Lefranc, François Guillonneau, and Florence Migot-Nabias*
- 840 **Molecular Details Underlying Dynamic Structures and Regulation of the Human 26S Proteasome**  
 [S] *Xiaorong Wang, Peter Cimermancic, Clinton Yu, Andreas Schweitzer, Nikita Chopra, James L. Engel, Charles Greenberg, Alexander S. Huszagh, Florian Beck, Eri Sakata, Yingying Yang, Eric J. Novitsky, Alexander Leitner, Paolo Nanni, Abdullah Kahraman, Xing Guo, Jack E. Dixon, Scott D. Rychnovsky, Ruedi Aebersold, Wolfgang Baumeister, Andrej Sali, and Lan Huang*
- 855 **Deciphering the Acute Cellular Phosphoproteome Response to Irradiation with X-rays, Protons and Carbon Ions**  
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- 873 **Extended Multiplexing of Tandem Mass Tags (TMT) Labeling Reveals Age and High Fat Diet Specific Proteome Changes in Mouse Epididymal Adipose Tissue**  
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- 891 **Quantitative Tyrosine Phosphoproteomics of Epidermal Growth Factor Receptor (EGFR) Tyrosine Kinase Inhibitor-treated Lung Adenocarcinoma Cells Reveals Potential Novel Biomarkers of Therapeutic Response**  
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- 911 **Differential Protein Expression Marks the Transition From Infection With *Opisthorchis viverrini* to Cholangiocarcinoma**  
 [S] *Jarinya Khoontawad, Chawalit Pairojkul, Rucksak Rucksaken, Porntip Pinlaor, Chaisiri Wongkham, Puangrat Yongvanit, Ake Pugkhem, Alun Jones, Jordan Plieskatt, Jeremy Potriquet, Jeffery Bethony, Somchai Pinlaor, and Jason Mulvenna*
- 924 **Quantitative Age-specific Variability of Plasma Proteins in Healthy Neonates, Children and Adults**  
 [S] *Stefan Bjelosevic, Dana Pascovici, Hui Ping, Vasiliki Karlaftis, Thiri Zaw, Xiaomin Song, Mark P. Molloy, Paul Monagle, and Vera Ignjatovic*

## Technological Innovation and Resources

- 936 **Covariation of Peptide Abundances Accurately Reflects Protein Concentration Differences**  
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- 949 **New Quantitative Mass Spectrometry Approaches Reveal Different ADP-ribosylation Phases Dependent On the Levels of Oxidative Stress**  
 [S] *Vera Bilan, Nathalie Selevsek, Hans A. V. Kistemaker, Jeannette Abplanalp, Roxane Feurer, Dmitri V. Filippov, and Michael O. Hottiger*

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