

Minireview

- 2525 **Omics Profiling in Precision Oncology**
Kun-Hsing Yu and Michael Snyder

Research

- 2537 **The Clathrin-dependent Spindle Proteome**
[S] *Sushma R. Rao, Neftali Flores-Rodriguez, Scott L. Page, Chin Wong, Phillip J. Robinson, and Megan Chircop*
- 2554 **Stage-specific Proteomes from *Onchocerca ochengi*, Sister Species of the Human River Blindness Parasite, Uncover Adaptations to a Nodular Lifestyle**
[S] ✎ *Stuart D. Armstrong, Dong Xia, Germanus S. Bah, Ritesh Krishna, Henrietta F. Ngangyung, E. James LaCourse, Henry J. McSorley, Jonas A. Kengne-Ouafo, Patrick W. Chounna-Ndongmo, Samuel Wanji, Peter A. Enyong, David W. Taylor, Mark L. Blaxter, Jonathan M. Wastling, Vincent N. Tanya, and Benjamin L. Makepeace*
- 2576 **Using the Ubiquitin-modified Proteome to Monitor Distinct and Spatially Restricted Protein Homeostasis Dysfunction**
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- 2594 **Systematic Protein-Protein Interaction Analysis Reveals Intersubcomplex Contacts in the Nuclear Pore Complex**
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- 2607 **Urinary Proteomics Yield Pathological Insights for Ureteropelvic Junction Obstruction**
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- 2616 **Identification of Maturation-Specific Proteins by Single-Cell Proteomics of Human Oocytes**
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- 2628 **Plasma-derived Extracellular Vesicles Contain Predictive Biomarkers and Potential Therapeutic Targets for Myocardial Ischemic (MI) Injury**
[S] *Esther Sok Hwee Cheow, Woo Chin Cheng, Chuen Neng Lee, Dominique de Kleijn, Vitaly Sorokin, and Siu Kwan Sze*
- 2641 **Proteomic Analysis of the Spatio-temporal Based Molecular Kinetics of Acute Spinal Cord Injury Identifies a Time- and Segment-specific Window for Effective Tissue Repair**
[S] *Stephanie Devaux, Dasa Cizkova, Jusai Quanico, Julien Franck, Serge Nataf, Laurent Pays, Lena Hauberg-Lotte, Peter Maass, Jan H. Kobarg, Firas Kobeissy, Céline Mériaux, Maxence Wisztorski, Lucia Slovinska, Juraj Blasko, Viera Cigankova, Isabelle Fournier, and Michel Salzet*

On the cover: This work develops label-free quantification for single embryonic cells to ask how cell heterogeneity is established in the developing vertebrate embryo. Proteins are digested from individual cells from 16-cell frog (*Xenopus laevis*) embryos, separated by microanalytical capillary electrophoresis, ionized by electrospray ionization, and sequenced by high-resolution mass spectrometry. The results reveal appreciable translational differences between cells of similar tissue fates. For details, see the article by Camille Lombard-Banek, *et al.*, pages 2756–2768

- 2671 **Resolution of Novel Pancreatic Ductal Adenocarcinoma Subtypes by Global Phosphotyrosine Profiling**
 [S] *Emily S. Humphrey, Shih-Ping Su, Adnan M. Nagrial, Falko Hochgräfe, Marina Pajic, Gillian M. Lehrbach, Robert G. Parton, Alpha S. Yap, Lisa G. Horvath, David K. Chang, Andrew V. Biankin, Jianmin Wu, and Roger J. Daly*
- 2686 **Autoimmune Regulator (AIRE) Is Expressed in Spermatogenic Cells, and It Altered the Expression of Several Nucleic-Acid-Binding and Cytoskeletal Proteins in Germ Cell 1 Spermatogonial (GC1-spg) Cells**
 [S] *Karthika Radhakrishnan, Kongattu P. Bhagya, Anil Kumar TR, Anandavalli N. Devi, Jeeva Sengottaiyan, and Pradeep G. Kumar*
- 2699 **Identification of RNA-binding Proteins in Macrophages by Interactome Capture**
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- 2730 **Structure of Complement C3(H₂O) Revealed By Quantitative Cross-Linking/Mass Spectrometry And Modeling**
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- 2756 **Label-free Quantification of Proteins in Single Embryonic Cells with Neural Fate in the Cleavage-Stage Frog (*Xenopus laevis*) Embryo using Capillary Electrophoresis Electrospray Ionization High-Resolution Mass Spectrometry (CE-ESI-HRMS)**
 [S] *Camille Lombard-Banek, Sushma Reddy, Sally A. Moody, and Peter Nemes*

Technological Innovation and Resources

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- 2802 **Proteomics Analysis with a Nano Random Forest Approach Reveals Novel Functional Interactions Regulated by SMC Complexes on Mitotic Chromosomes**
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Peptide Biosynthesis with Stable Isotope Labeling from a Cell-free Expression System for Targeted Proteomics with Absolute Quantification

Feng Xian, Jin Zi, Quanhui Wang, Xiaomin Lou, Haidan Sun, Liang Lin, Guixue Hou, Weiqiao Rao, Changcheng Yin, Lin Wu, Shuwei Li, and Siqi Liu

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PyQuant: A Versatile Framework for Analysis of Quantitative Mass Spectrometry Data

Christopher J. Mitchell, Min-Sik Kim, Chan Hyun Na, and Akhilesh Pandey

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