

Research

- 1435 **Functional Proteomic Analysis of Repressive Histone Methyltransferase Complexes Reveals ZNF518B as a G9A Regulator**
[S] *Verena K. Maier, Caitlin M. Feeney, Jordan E. Taylor, Amanda L. Creech, Jana W. Qiao, Attila Szanto, Partha P. Das, Nicholas Chevrier, Catherine Cifuentes-Rojas, Stuart H. Orkin, Steven A. Carr, Jacob D. Jaffe, Philipp Mertins, and Jeannie T. Lee*
- 1447 **Quantitative Proteomics Analysis Reveals Novel Insights into Mechanisms of Action of Long Noncoding RNA Hox Transcript Antisense Intergenic RNA (HOTAIR) in HeLa Cells**
[S] *Peng Zheng, Qian Xiong, Ying Wu, Ying Chen, Zhuo Chen, Joy Fleming, Ding Gao, Lijun Bi, and Feng Ge*
- 1464 **Identification of O-Glycan Structures from Chicken Intestinal Mucins Provides Insight into *Campylobacter jejuni* Pathogenicity**
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- 1478 **The *Drosophila* Helicase Maleless (MLE) is Implicated in Functions Distinct From its Role in Dosage Compensation**
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- 1489 **High-Resolution Metabolomics with Acyl-CoA Profiling Reveals Widespread Remodeling in Response to Diet**
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- 1501 **Label-free Quantitative Proteomics Reveals a Role for the *Mycobacterium tuberculosis* SecA2 Pathway in Exporting Solute Binding Proteins and Mce Transporters to the Cell Wall**
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- 1517 **Immunocapture-Selected Reaction Monitoring Screening Facilitates the Development of ELISA for the Measurement of Native TEX101 in Biological Fluids**
[S] *Dimitrios Korbakis, Davor Brinc, Christina Schiza, Antoninus Soosaipillai, Keith Jarvi, Andrei P. Drabovich, and Eleftherios P. Diamandis*
- 1527 **Integrated Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Isobaric Tags for Relative and Absolute Quantitation (iTRAQ) Quantitative Proteomic Analysis Identifies Galectin-1 as a Potential Biomarker for Predicting Sorafenib Resistance in Liver Cancer**
[S] *Chao-Chi Yeh, Chih-Hung Hsu, Yu-Yun Shao, Wen-Ching Ho, Mong-Hsun Tsai, Wen-Chi Feng, and Lu-Ping Chow*
- 1546 **Gamma-Carboxylation and Fragmentation of Osteocalcin in Human Serum Defined by Mass Spectrometry**
[S] *Douglas S. Rehder, Caren M. Gundberg, Sarah L. Booth, and Chad R. Borges*

On the cover: Integrated workflow for target isolation and proteomic profiling of limited amounts of rare cells from biological fluids. A combination of the immunoaffinity microfluidic magnetophoretic cell isolation, focused ultrasonication-assisted cell lysis, reduction, alkylation and digestion, followed by 1D PLOT-nLC-MS profiling and advanced data processing resulted in the identification of approximately 4,000 proteins from the injection of only 100–200 cells per analysis. For details, see the article by Siyang Li, *et al.*, pages 1672–1683.

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