

## Research

- 1046 **Unconventional Secretion is a Major Contributor of Cancer Cell Line Secretomes**  
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- 1061 **Identification of Disease Specific Pathways Using *in Vivo* SILAC Proteomics in Dystrophin Deficient *mdx* Mouse**  
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- 1074 **Comprehensive Proteomics Analysis Reveals New Substrates and Regulators of the Fission Yeast Clp1/Cdc14 Phosphatase**  
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- 1115 **Protein Correlation Profiles Identify Lipid Droplet Proteins with High Confidence**  
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- 1144 **Integrative Proteomic and Transcriptomic Analyses Reveal Multiple Post-transcriptional Regulatory Mechanisms of Mouse Spermatogenesis**  
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- 1158 **Quantitative Phosphoproteomics after Auxin-stimulated Lateral Root Induction Identifies an SNX1 Protein Phosphorylation Site Required for Growth**  
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- 1170 **Urinary Angiostatin - A Novel Putative Marker of Renal Pathology Chronicity in Lupus Nephritis**  
*Tianfu Wu, Yong Du, Jie Han, Sandeep Singh, Chun Xie, Yuyuan Guo, Xin J. Zhou, Chul Ahn, Ramesh Saxena, and Chandra Mohan*

On the cover: Microarrays of SH2 and PTB domains were used to generate unbiased, quantitative interaction maps for most of the human Receptor Tyrosine Kinases, as well as upstream adaptor proteins. In addition to uncovering many previously unrecognized interactions, a systematic analysis of the data revealed a significant link between the connectivity of receptors and adaptor proteins and their intrinsic oncogenicity. For details, see article by Grigoriy Koytiger, *et al.*, pages 1204–1213.

- 1180 **Proteomic Profiling of *Mycobacterium tuberculosis* Identifies Nutrient-starvation-responsive Toxin–antitoxin Systems**  
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