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IN THIS ISSUE

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Cover

See Hendrik Luesch, page 609. Genome-scale analysis has been extended from gene expression profiling to parallel cell-based functional profiling, allowing the characterization of gene function and small molecule actions in yeast and in mammalian cells. Image reproduced with permission of Hendrik Luesch, from *Mol. BioSyst.*, 2006, **2**, 609.

CHEMICAL BIOLOGY

EDITORIAL

HOT OFF THE PRESS

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Hot off the Press

Topics highlighted in this month's *Hot off the Press* include X-ray structures of a bacterial drug-resistance transporter, a new method for the exploration of intra- and interchromosomal interactions and some items published recently in the RSC's journals.

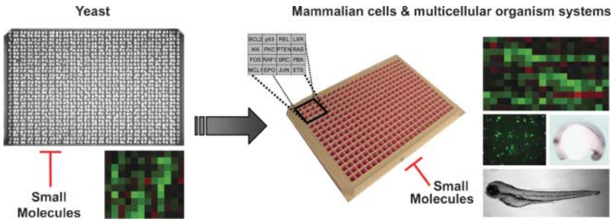
HIGHLIGHTS

609

Towards high-throughput characterization of small molecule mechanisms of action

Hendrik Luesch*

Genome-wide studies in yeast can infer the targets of bioactive small molecules. These approaches are systematically transferred into mammalian systems and multicellular model organism systems to interrogate more complex pathways.

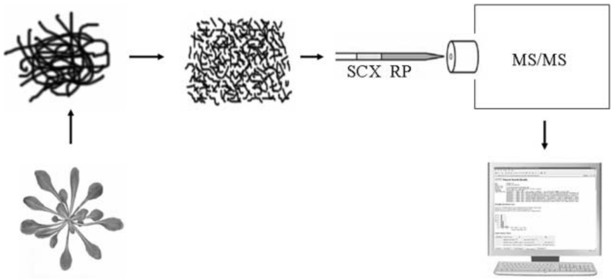


621

Alternative workflows for plant proteomic analysis

Joohyun Lee and Bret Cooper*

By using alternative sample processing and protein separation strategies biologists can improve their proteomics research and gain new information about the proteins that define plant cells.



PAPERS

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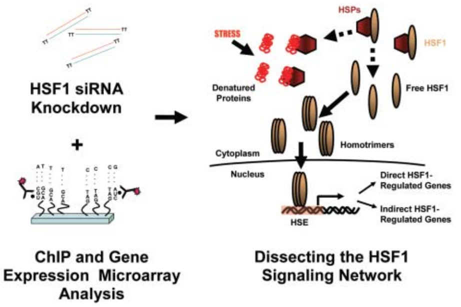
Genome-wide analysis of human HSF1 signaling reveals a transcriptional program linked to cellular adaptation and survival

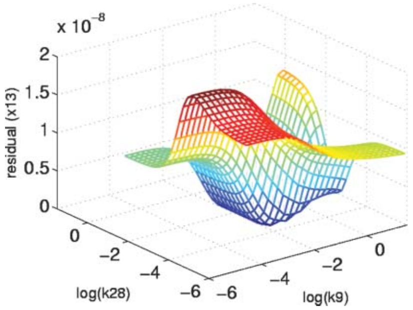
Todd J. Page, Devanjan Sikder, Longlong Yang, Linda Pluta, Russell D. Wolfinger, Thomas Kodadek and Russell S. Thomas*

Through a combination of chromatin immunoprecipitation microarray analysis and time course gene expression microarray analysis with and without siRNA-mediated inhibition of HSF1, genes directly and indirectly regulated by HSF1 under heat shock and non-heat shock conditions were identified.



PAPERS

640



Insights into the behaviour of systems biology models from dynamic sensitivity and identifiability analysis: a case study of an NF-κB signalling pathway

Hong Yue,* Martin Brown, Joshua Knowles, Hong Wang, David S. Broomhead and Douglas B. Kell

Mathematical modelling offers a variety of useful techniques to help in understanding the intrinsic behaviour of complex signal transduction networks; we describe a whole analysis scheme for complex cell networks.

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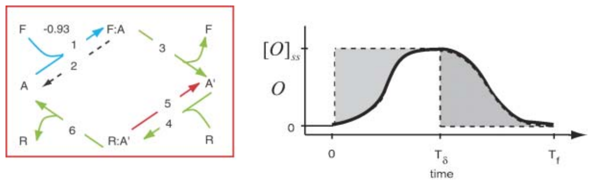

Biological network design strategies: discovery through dynamic optimization

Bambang S. Adiwijaya, Paul I. Barton* and Bruce Tidor*

Analysis of structure–function relationships in simple biochemical networks reveals that a single network topology encodes multiple strategies based on parameterization. This flexibility may endow biological networks with enhanced performance across variable circumstances.

BOOK CHAPTER

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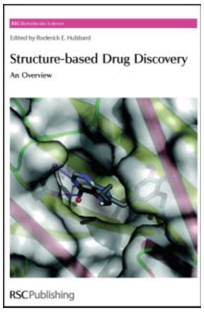

Molecular Modelling

Xavier Barril and Robert Soliva

This is chapter 3 of the book Structure Based Drug Discovery (Edited by Roderick E. Hubbard) which forms part of the RSC Biomolecular Sciences series. More information about this book and the whole series is available from www.rsc.org/biomolecularsciences or the RSC Sales team, email: sales@rsc.org.