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IN THIS ISSUE

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Cover

See J.-L. Plouhinec and E. M. De Robertis, p. 454.

Systems biology of embryonic patterning in *Xenopus*.

The cover shows a frog embryo stained for the expression of dorsal (top) and ventral (bottom) genes. The dorsal gene is Chordin, an inhibitor of Bone Morphogenetic proteins (BMPs). The ventral gene is Sizzled, an inhibitor of Tolloid metalloproteinases that digest Chordin. The circular structure is the blastopore, which later on will close to form the anus. Image reproduced by permission of J.-L. Plouhinec and E. M. De Robertis from *Mol. BioSyst.*, 2007, **7**, 454.

CHEMICAL BIOLOGY

B49

Drawing together research highlights and news from all RSC publications, *Chemical Biology* provides a 'snapshot' of the latest developments in chemical biology, showcasing newsworthy articles and significant scientific advances.

Chemical Biology

July 2007/Volume 2/Issue 7

www.rsc.org/chembiology

HOT OFF THE PRESS

450

Hot off the press

Hot off the Press highlights recently published work for the benefit of our readers. Our contributors this month have focused on peptide beacons for targeting antibodies, peptide ligation using gold nanoparticles and a new method for fabricating probe-bearing particles. New contributors are always welcome. If you are interested please contact molbiosyst@rsc.org for more information, we'd like to hear from you.

HOT OFF THE PRESS

OPINION

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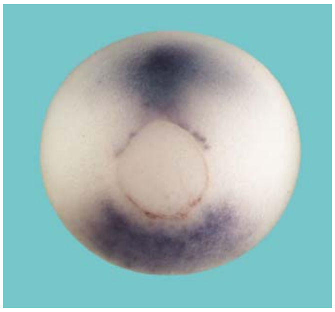

Systems biology of embryonic morphogens

Jean-Louis Plouhinec and E. M. De Robertis*

A network of secreted proteins that interact with each other in the extracellular space regulates embryonic morphogenesis. Mathematical modeling offers an excellent opportunity to understand how morphogens signal and self-regenerate pattern.

HIGHLIGHTS

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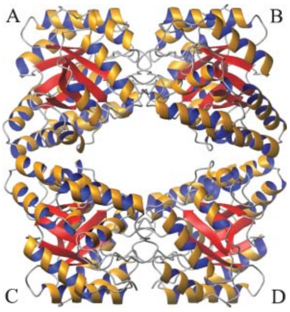

Inhibition of lysine biosynthesis: an evolving antibiotic strategy

Craig A. Hutton,* Matthew A. Perugini and Juliet A. Gerrard

Recent studies of the lysine biosynthetic pathway have validated several enzymes as antibiotic targets and provided structural information for the design of inhibitors of these enzymes, in the first steps toward the development of novel antibiotics.

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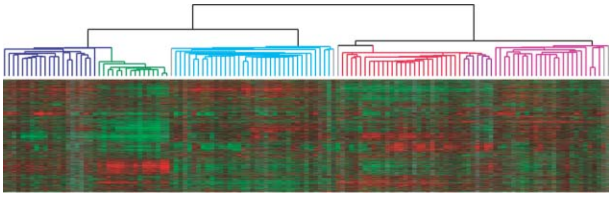

Transcriptomic signatures in breast cancer

Jianjiang Fu and Stefanie S. Jeffrey*

Expression profiling in breast cancer heralds a new approach to predicting outcome, survival, response to treatment, and identification of novel therapeutic targets. We summarize this ever-expanding field, including limitations and prospects.

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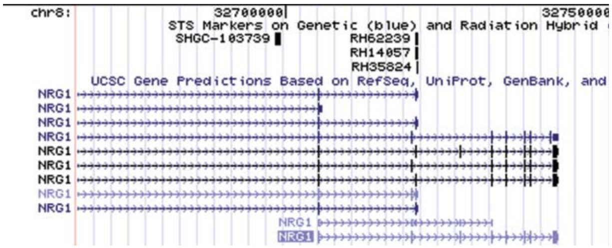

Alternative splicing: a bioinformatics perspective

Elisa Napolitano Ferreira, Pedro A. F. Galante, Dirce Maria Carraro and Sandro José de Souza*

The degree of diversity at the transcriptome and proteome levels generated by alternative splicing is astonishing, several issues related to alternative splicing are discussed.

HIGHLIGHTS

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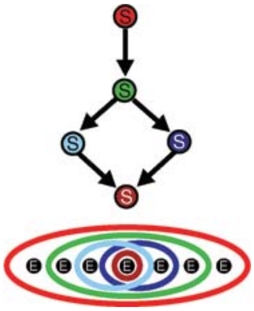
Computational identification of cellular networks and pathways

Florian Markowetz and Olga G. Troyanskaya*

Recent developments in computational functional genomics to identify networks of functionally related genes and proteins based on diverse sources of genomic data are highlighted, with specific focus on statistical methods to identify genetic networks.



REVIEW

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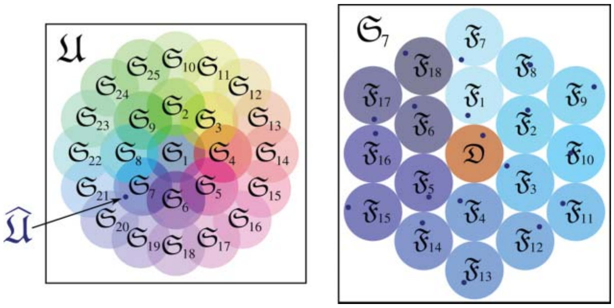
Set theory formulation of the model-free problem and the diffusion seeded model-free paradigm

Edward J. d'Auvergne and Paul R. Gooley

The model-free dynamic analysis of NMR relaxation data investigates molecular motions at the atomic level. Using set notation to encapsulate the entirety of the complex problem, the important developments which have occurred in the field, are reviewed.



PAPER

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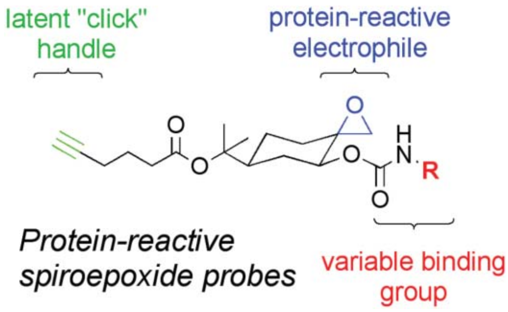
Mechanistic and structural requirements for active site labeling of phosphoglycerate mutase by spiroepoxides

Michael J. Evans, Garrett M. Morris, Jane Wu,
Arthur J. Olson, Erik J. Sorensen and
Benjamin F. Cravatt*

An anti-proliferative agent originating from a library of protein-reactive spiroepoxides is found to act as a covalent inactivator of phosphoglycerate mutase.



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* Indicates the author for correspondence: see article for details.

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