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Cover

See Zuzana Demianova *et al.*, pp. 260–265.
A miniaturized PAGE device is shown which performs protein analysis in approximately 10 minutes. Image reproduced by permission of Zuzana Demianova, Eemeli Pöysä, Saara Ihalainen, Susanna Saura, Masahiko Shimmo, Sami Franssila and Marc Baumann from *Mol. BioSyst.*, 2008, **4**, 260.

CHEMICAL BIOLOGY

B17

Drawing together the 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

March 2008/Volume 3/Issue 3

www.rsc.org/chembiology

HOT OFF THE PRESS

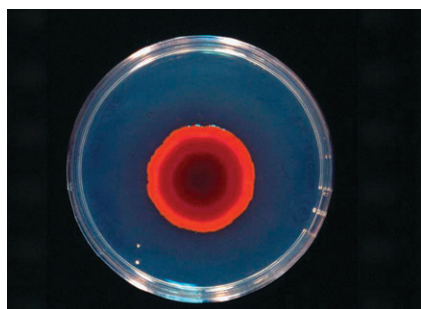
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Hot off the press

Hot off the Press highlights recently published work for the benefit of our readers. Our contributors this month have focused on the synthesis of the complete genome of bacterium *Mycoplasma genitalium*. 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

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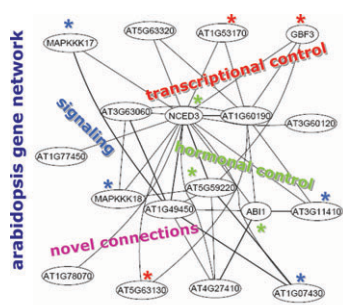


Spatial-temporal modelling of bacterial colony growth on solid media

Leonie Z. Pipe and Malcolm J. Grimson*

The study of bacterial colony growth dynamics is pivotal to microbial ecology and food technology. This review highlights the significant recent developments in the field that have led to a notable re-interpretation of the experimental data. (Concentric ring development in a *Serratia marcescens* colony exposed to periodic temperature changes.)

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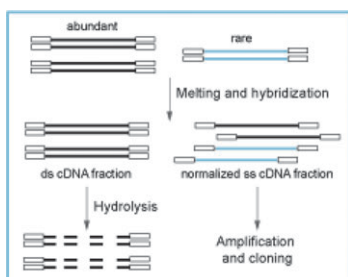


Gene networks in *Arabidopsis thaliana* for metabolic and environmental functions

Shisong Ma and Hans J. Bohnert*

Large datasets describing the dynamics of the *Arabidopsis* transcriptome are captured to construct a high-confidence GGM (Graphical Gaussian Model)-based gene network that identifies the dependency structure among more than 10,000 genes. The co-regulation pattern among > 22 000 genes in > 150 conditions are also analyzed using a fuzzy *k*-means clustering method.

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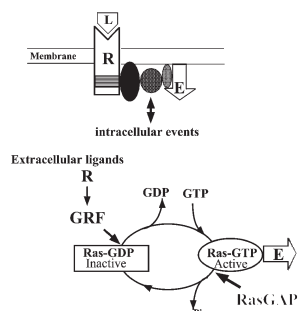


Normalization of full-length enriched cDNA

Ekaterina A. Bogdanova, Dmitry A. Shagin and Sergey A. Lukyanov*

Generation of equalized (normalized) cDNA libraries is essential for the discovery of rare messages. Highlighted in this article are the methods suitable for normalization of full-length-enriched cDNA and specifically a recently developed procedure based on the unique properties of duplex-specific nuclease from kamchatka crab.

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RasGAPs: a crucial regulator of extracellular stimuli for homeostasis of cellular functions

Shintaro Iwashita and Si-Young Song

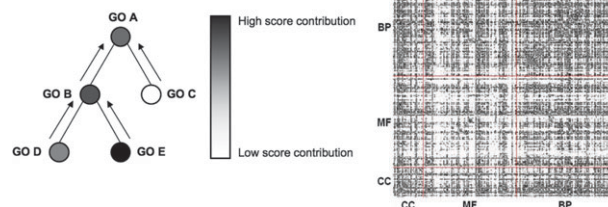
Cellular functions of RasGAPs and their signaling characteristics from the viewpoint of homeostasis are discussed.

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New paradigm in protein function prediction for large scale omics analysis

Troy Hawkins, Meghana Chitale and Daisuke Kihara

We review two recent approaches for function prediction for providing large coverage in function assignment, namely omics data driven approaches and a thorough data mining approach on homology search results.



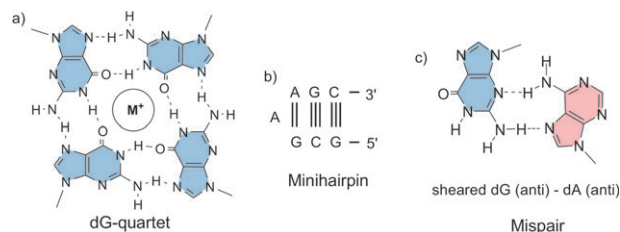
REVIEW ARTICLE

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Mismatch formation in solution and on DNA microarrays: how modified nucleosides can overcome shortcomings of imperfect hybridization caused by oligonucleotide composition and base pairing

Frank Seela* and Simone Budow

The review reports on stable mismatches (c) and unusual structures (a, b) formed in solution and on microarrays and discusses the use of modified nucleosides to reduce false positive read-outs.



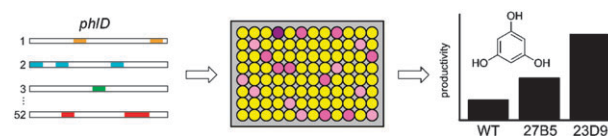
COMMUNICATION

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Exploiting genetic diversity by directed evolution: molecular breeding of type III polyketide synthases improves productivity

Wenjiao Zha, Sheryl B. Rubin-Pitel and Huimin Zhao*

Applying directed evolution to the phloroglucinol synthase PhlD from *Pseudomonas fluorescens* Pf-5 has provided the first example of engineering enhanced productivity in a type III polyketide synthase.



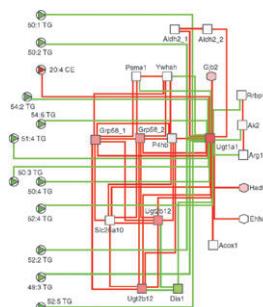
PAPERS

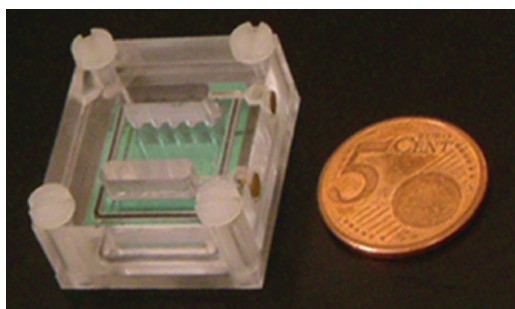
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Correlation network analysis for data integration and biomarker selection

Aram Adourian *et al.*

This work demonstrates the application of correlation networks to a systems-based investigation of drug-induced hepatotoxicity and the identification of specific and relevant biomarkers in this context.





Development and application of a miniaturized gel electrophoresis device for protein analysis

Zuzana Demianova,* Eemeli Pöysä, Saara Ihalainen, Susanna Saura, Masahiko Shimmo, Sami Franssila and Marc Baumann

We describe a miniaturized PAGE device which performs the analysis in approx. 10 min. This device was used for sub-sequent protein chemical analyses, *e.g.* peptide mass fingerprinting, Edman degradation and western blotting.