Molecular BioSystems

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IN THIS ISSUE

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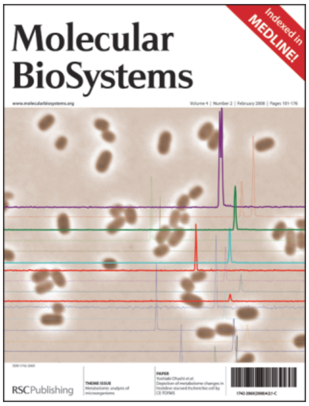

Cover
See Yoshiaki Ohashi, Akiyoshi Hirayama, Takamasa Ishikawa, Seira Nakamura, Kaori Shimizu, Yuki Ueno, Masaru Tomita and Tomoyoshi Soga, pp. 135–147. Depiction of metabolome changes in histidine-starved *Escherichia coli* by CE-TOFMS. Image reproduced by permission of Yoshiaki Ohashi, Akiyoshi Hirayama, Takamasa Ishikawa, Seira Nakamura, Kaori Shimizu, Yuki Ueno, Masaru Tomita and Tomoyoshi Soga from *Mol. BioSyst.*, 2008, **4**, 135.

CHEMICAL BIOLOGY

B9

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
February 2008/Volume 3/Issue 2
www.rsc.org/chembiology

EDITORIAL

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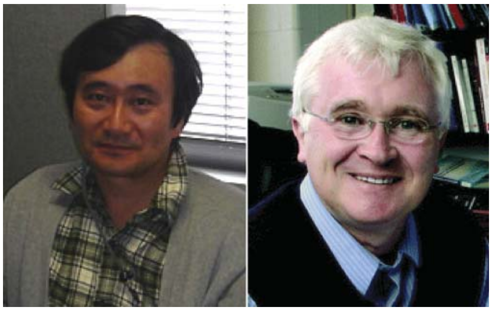
Metabolomic analysis of microorganisms

Molecular BioSystems Editorial Board members Hirotada Mori and Tadhg Begley introduce this theme issue on the field of metabolomic analysis in bacteria and its future direction.



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 protein labelling of DNA and RNAi affecting a behavioral change in fruit flies. If you are interested please contact molbiosyst@rsc.org for more information, we'd like to hear from you.

HIGHLIGHTS

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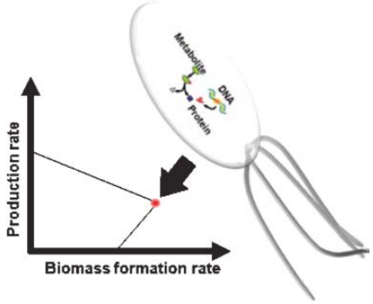

Metabolic flux analysis and metabolic engineering of microorganisms

Hyun Uk Kim, Tae Yong Kim and Sang Yup Lee*

Recent advances in metabolic flux analysis are reviewed with special emphasis on genome-scale constraints-based flux analysis. Computational aspects of flux analysis, several algorithms that allow identification of target genes for metabolic engineering, and successful examples of metabolic engineering based on *in silico* simulation are reviewed. Finally, current limitations that need to be overcome are discussed.

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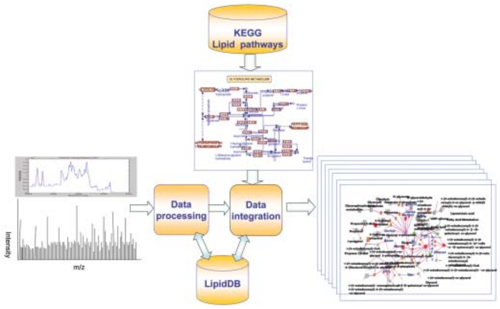

Informatics and computational strategies for the study of lipids

Laxman Yetukuri, Kim Ekroos, Antonio Vidal-Puig and Matej Orešič*

One of the major bottlenecks in pursuing lipidomics research is the processing and interpretation of the complex lipidome data. The present report is an update on a young but rapidly emerging field of lipid bioinformatics.

PAPERS

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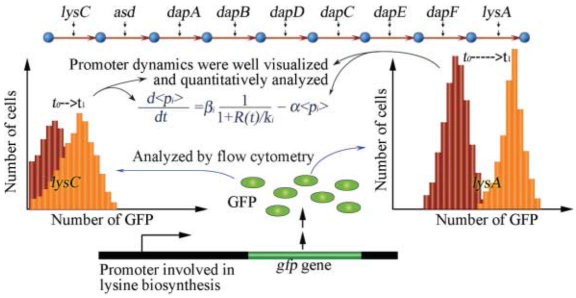

Dynamic change in promoter activation during lysine biosynthesis in *Escherichia coli* cells

Jianhong Ou, Tadashi Yamada, Keisuke Nagahisa, Takashi Hirasawa, Chikara Furusawa, Tetsuya Yomo and Hiroshi Shimizu*

The dynamics of gene promoters involved in lysine biosynthesis in *Escherichia coli* cells in response to changes in lysine concentration were investigated. The results provide a better quantitative understanding of the expression dynamics in the lysine biosynthesis pathway.

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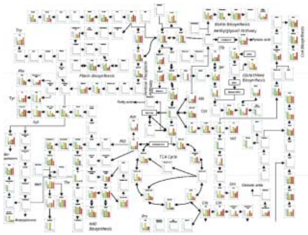
Depiction of metabolome changes in histidine-starved *Escherichia coli* by CE-TOFMS

Yoshiaki Ohashi, Akiyoshi Hirayama,
Takamasa Ishikawa, Seira Nakamura, Kaori Shimizu,
Yuki Ueno, Masaru Tomita and Tomoyoshi Soga*

Over 300 primary metabolites in histidine-starved *E. coli* were analysed using capillary electrophoresis time-of-flight mass spectrometry (CE-TOFMS), unveiling global metabolome changes induced by amino acid starvation in bacteria.



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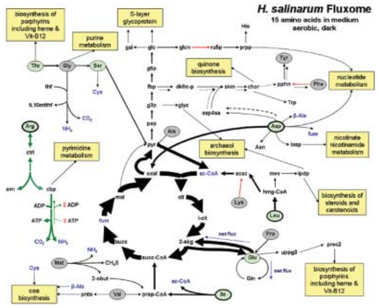
Reconstruction, modeling & analysis of *Halobacterium salinarum* R-1 metabolism

Orland Gonzalez,* Susanne Gronau, Michaela Falb,
Friedhelm Pfeiffer, Eduardo Mendoza, Ralf Zimmer and
Dieter Oesterhelt

A genome-scale metabolic reconstruction for the extreme halophile *Halobacterium salinarum* is presented. We used the network for computational analysis and studied the aerobic growth of the organism. Systems level behaviors of the network model, such as nutrient utilization, are described.



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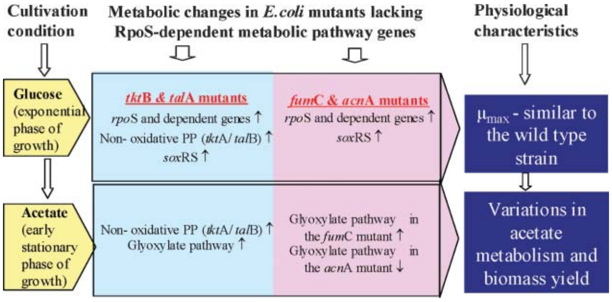
Altered acetate metabolism and biomass production in several *Escherichia coli* mutants lacking *rpoS*-dependent metabolic pathway genes

Mahbuba Rahman and Kazuyuki Shimizu*

Metabolic changes were observed in four *E. coli* mutants lacking the RpoS-dependent pentose phosphate pathway and TCA cycle genes in batch fermentation. Mutations affected acetate metabolism and biomass yield suggesting a broader role of RpoS associated with the physiological changes.



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Poly-*N*-acetylglucosamine and poly(glycerol phosphate) teichoic acid identification from staphylococcal biofilm extracts using excitation sculptured TOCSY NMR

Jane L. Wagstaff, Irina Sadovskaya, Evgeny Vinogradov,
Saïd Jabbouri and Mark J. Howard*

Selective excitation sculptured TOCSY NMR identifies the simultaneous presence of key carbohydrate biopolymers in crude biofilm extracts from *Staphylococcus epidermidis* without the need for laborious purification or component separation.