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IN THIS ISSUE

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Cover

See Igor L. Medintz, Gary J. Vora, Amir M. Rahbar and Dzung C. Thach, p. 623. Transcript/proteomic analysis of wild-type and glucose sensing mutant Baker's yeast (Saccharomyces cerevisiae) strains suggest carbon source sensing contributes to pseudohyphal differentiation as part of glycolysis. This novel transduction pathway may help elucidate this complex multicomponent pathway which is used as a model system for understanding aspects of pathogen virulence and invasive behavior. Image reproduced by permission of Igor L. Medintz, Gary J. Vora, Amir M. Rahbar and Dzung C. Thach from Mol. BioSyst., 2007, 9, 623.

CHEMICAL BIOLOGY

B65

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.



September 2007/Volume 2/Issue 9

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HOT OFF THE PRESS

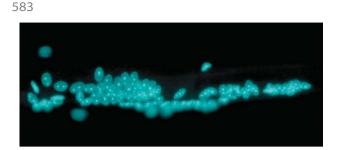
579

Hot off the press

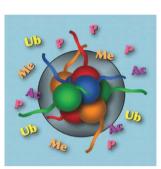
Hot off the Press highlights recently published work for the benefit of our readers. Our contributors this month have focused on the imaging of cell surface glycans, ubiquitin's dual role in the regulation of SRC-3 functional life time and the X-ray crystallisation of recombinant rhodopsin. New contributors are always welcome. If you are interested please contact molbiosyst@rsc.org for more information, we'd like to hear from you.



HIGHLIGHTS



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Communication between the cytoskeleton and the nuclear envelope to position the nucleus

Daniel A. Starr

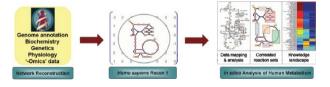
Nuclear positioning is essential in many cellular processes and diseases. Microtubules, actin filaments and intermediate filaments function together to control nuclear positioning. Forces from the cytoskeleton are transferred across the nuclear envelope through KASH and SUN proteins.

Moving marks: Dynamic histone modifications in yeast

Jocelyn E. Krebs

In order to control the access to DNA by factors necessary for the dynamic processes of transcription, repair, and replication, both the addition and removal of covalent post-translational modifications of histones must be similarly dynamic.

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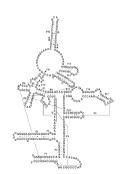


A genome-scale, constraint-based approach to systems biology of human metabolism

Monica L. Mo, Neema Jamshidi and Bernhard Ø. Palsson*

Homo sapiens Recon 1, a functionally tested, genome-scale reconstruction of human cellular metabolism, can be used for the understanding of physiological and disease metabolic states.

604



A view of RNase P

Sidney Altman

Recent progress in crystallography and catalysis of the RNA components of RNase P holoenzymes is summarised. Amongst others, the search for the catalytic centre and the differing activity of eukaryotic and bacterial RNAs are discussed. The term "RNA–protein world" is suggested to describe our world.

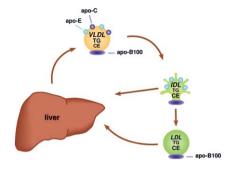
REVIEW

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The physiological and molecular regulation of lipoprotein assembly and secretion

Daniel A. Blasiole, Roger A. Davis and Alan D. Attie*

The cellular assembly of triglyceride-rich lipoproteins requires the synthesis, translocation, and association of their lipid and protein components. In this critical review, we focus on the machinery involved in regulating this process.



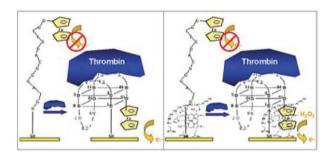
COMMUNICATION

620

Aptamers as elements of bioelectronic devices

Mònica Mir and Ioanis Katakis*

A ferrocene labelled aptamer is used as a redox partner of co-immobilised microperoxidase demonstrating a reversible amperometric biomolecular device that could respond to external stimuli in real time.



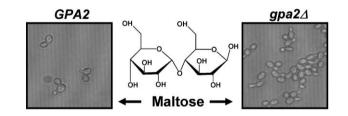
PAPER

623

Transcript and proteomic analyses of wild-type and gpa2 mutant Saccharomyces cerevisiae strains suggest a role for glycolytic carbon source sensing in pseudohyphal differentiation

Igor L. Medintz,* Gary J. Vora, Amir M. Rahbar and Dzung C. Thach

Transcript/proteomic analysis of wild-type and glucose sensing mutant *S. cerevisiae* suggest carbon source sensing contributes to pseudohyphal differentiation as part of glycolysis. This complex multi-component pathway is used as a model system for understanding aspects of pathogen virulence and invasive behavior.



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