

# Molecular BioSystems

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## IN THIS ISSUE

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### Cover

See Diane M. Ramos and Antónia Monteiro, p. 530. A mosaic of artificially colored images that represent a new technical advance in controlled spatial and temporal expression of genes on a developing butterfly wing. Image reproduced by permission of Diane M. Ramos and Antónia Monteiro from *Mol. BioSyst.*, 2007, 8, 530.

## CHEMICAL BIOLOGY

B57

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

August 2007/Volume 2/Issue 8

[www.rsc.org/chembiology](http://www.rsc.org/chembiology)

## HOT OFF THE PRESS

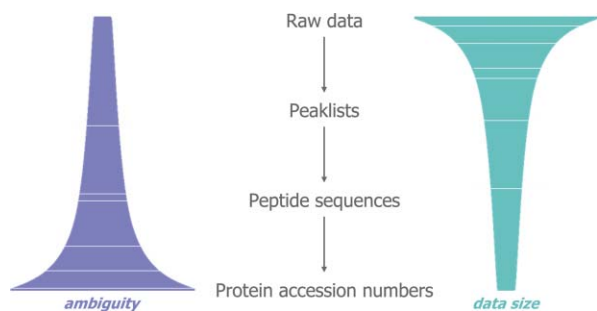
516

### 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 a semi-synthetic approach to identify kinase substrates. New contributors are always welcome. If you are interested please contact [molbiosyst@rsc.org](mailto:molbiosyst@rsc.org) for more information, we'd like to hear from you.

# HOT OFF THE PRESS

518

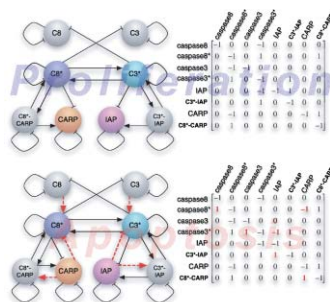


### Proteomics data validation: why all must provide data

Lennart Martens\* and Henning Hermjakob

The field of proteomics has become a large-scale producer of data. The derived results sometimes remain contested, however. This opinion outlines the causes for this situation, and suggests some guidelines to allow validation of results reported in proteomics papers.

523

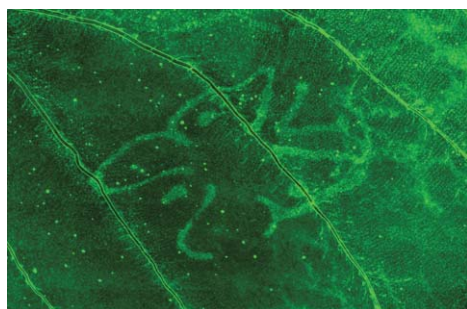


### Deduction of intracellular sub-systems from a topological description of the network

Torbjörn E. M. Nordling,\* Noriko Hiroi, Akira Funahashi and Hiroaki Kitano

Identification of functional modules is difficult; since they only exist in the mode of their biological function while biochemical network graphs commonly contain interactions active in different dynamic modes.

530

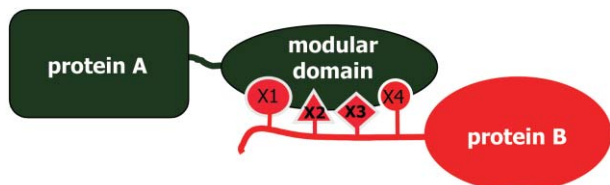


### Transgenic approaches to study wing color pattern development in Lepidoptera

Diane M. Ramos and Antónia Monteiro\*

Butterflies and moths are emerging as exceptional model organisms to study the evolution of development. Here we review new functional genetic tools for the Lepidoptera that will allow genes and developmental mechanisms underlying their diverse wing color patterns to be studied in detail.

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### Reverse interactomics: decoding protein–protein interactions with combinatorial peptide libraries

Dehua Pei\* and Anne-Sophie Wavreille

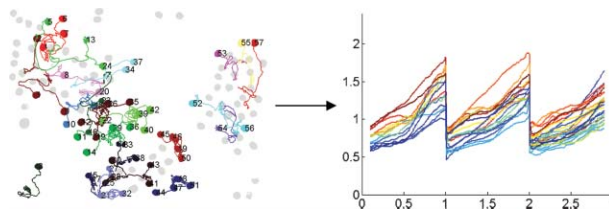
A method combining chemical, bioinformatics and cell biology tools is applied to determine the optimal peptide motifs and *in vivo* protein partners/substrates of a variety of modular domains and enzymes.

542

### Dynamic proteomics in mammalian cells: capabilities and challenges

Ron Milo

A review of a method for dynamic proteomics incorporating random endogenous gene tagging, high-throughput time-lapse microscopy, and automated image analysis resulting in quantitative data for thousands of single cells at a temporal resolution of minutes over several cell cycles.



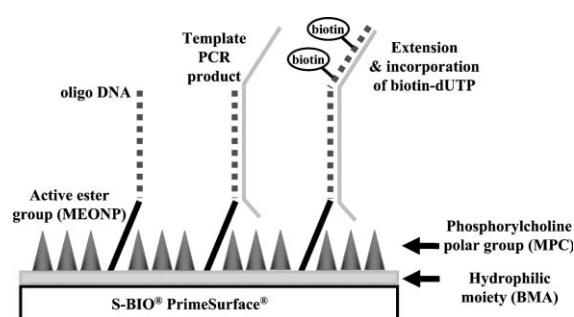
## METHOD

547

### A novel SNP detection technique utilizing a multiple primer extension (MPEX) on a phospholipid polymer-coated surface

Kazuhide Imai, Yasukazu Ogai, Daisuke Nishizawa, Shinya Kasai, Kazutaka Ikeda and Hisashi Koga\*

A novel SNP technique utilizing multiple primer extension is presented. The technique is successfully tested by analyzing representative SNPs on 4 LD blocks of the  $\mu$  opioid receptor gene.



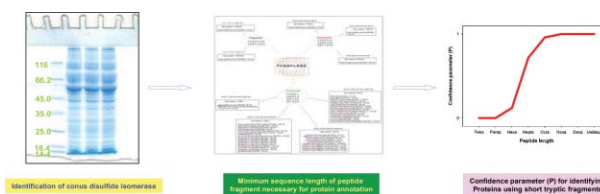
## PAPER

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### Identification of *Conus amadis* disulfide isomerase: minimum sequence length of peptide fragments necessary for protein annotation

Konkallu Hanumae Gowd, K. S. Krishnan and Padmanabhan Balaram\*

The disulfide isomerase of *Conus amadis* has been identified by 'de novo' mass spectrometric sequencing. Unambiguous protein identification requires a peptide sequence length of at least nine residues.





# 30 years

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