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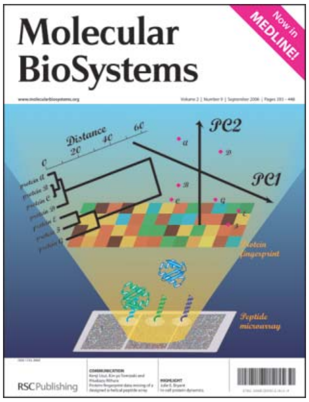

Cover
See Kenji Usui, Kin-ya Tomizaki and Hisakazu Mihara, page 417. The data generated from protein fingerprints (middle) with an α-helical peptide microarray (under) were analyzed using several statistical methods (upper) to discriminate target proteins. Image reproduced with permission of Hisakazu Mihara *et al.*, from *Mol. BioSyst.*, 2006, **2**, 417.

CHEMICAL BIOLOGY

B33

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
September 2006/Volume 1/Issue 9
www.rsc.org/chembiology

HOT OFF THE PRESS

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Hot off the Press

Topics highlighted in this month’s *Hot off the Press* include uncommon roles of HDAC1 in steroid receptor-mediated transcriptions, a novel post-translational protein modification mediated by nitrated fatty acids and targeting retroviral zinc finger–DNA interactions.

HOT OFF THE PRESS

OPINION

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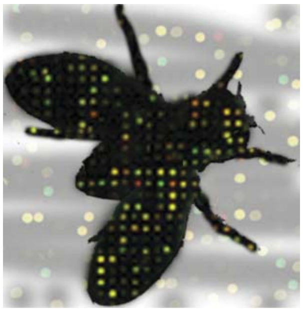

Learning to fly—getting the best out of microarrays

Steven Russell

Microarrays are becoming pervasive in biology and can offer unparalleled insights into biological processes. This article suggests that a more considered approach to the design of array probe sequences can substantially improve the technology.

HIGHLIGHTS

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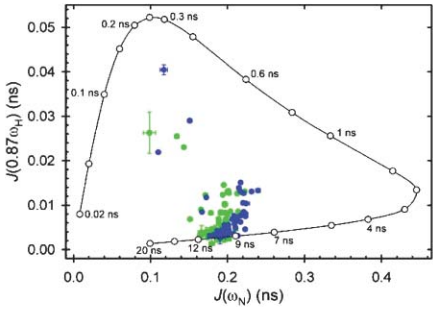

In-cell protein dynamics

Julie E. Bryant

Studies of structure, stability, and dynamics are frequently used to help explain how proteins function at the atomic level while intracellular studies of processes such as metabolism and the cell cycle are used to help explain biology. However, the connection between events in cells and atomic-level protein chemistry has yet to occur. In-cell NMR allows for the study of proteins in the crowded environment of living cells and, more specifically, yields quantitative information about protein backbone dynamics.

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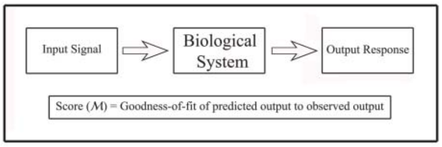

Is the future biology Shakespearean or Newtonian?

Ovidiu Lipan* and Wing H. Wong

"Cells do not care about mathematics" thus concluded a biologist friend after a discussion on the future of biology. And indeed, why should they care? But if we exchange the word "cell" with "rock", "Moon" or "electrons", do we have to change the sentence also? Starting from this line of thought, we review some recent developments in understanding the stochastic behavior of biological systems. We emphasize the importance of a molecular Signal Generator in the study of genetic networks.

COMMUNICATION

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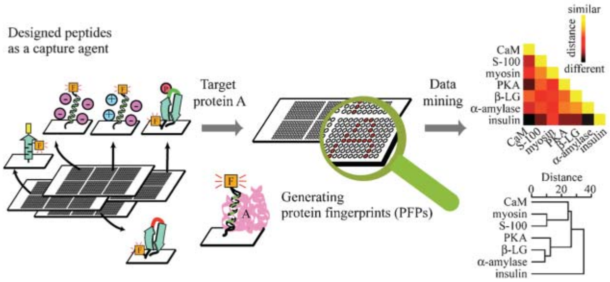

Protein-fingerprint data mining of a designed α-helical peptide array

Kenji Usui, Kin-ya Tomizaki and Hisakazu Mihara*

The data generated from protein fingerprints with an α-helical peptide array were analyzed using several statistical methods such as hierarchical clustering analysis and principal component analysis to discriminate target proteins.

PAPER

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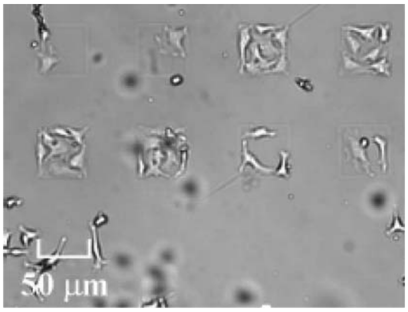
Whole genome expression profiling using DNA microarray for determining biocompatibility of polymeric surfaces

Michael Stangegaard, Z. Wang, J. P. Kutter, M. Dufva* and A. Wolff

Gene expression profiles can detect differences in cells grown on different surfaces that are not detected by other biocompatibility parameters such as growth, cell adhesion, morphology and hydrophobicity. HeLa cells grown on SU-8 patterned into biocompatible and bioincompatible areas.



BOOK CHAPTER

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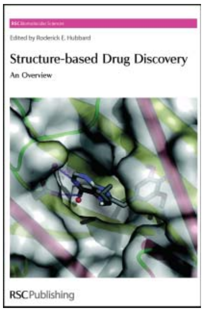
Fragment screening: an introduction

Andrew R. Leach, Michael M. Hann, Jeremy N. Burrows and Ed J. Griffen

This is Chapter 5 of the book *Structure-based Drug Discovery* which forms part of the RSC Biomolecular Sciences series. More information about this book and the whole series is available from www.rsc.org/biomolecularsciences or the RSC Sales team, email: sales@rsc.org.



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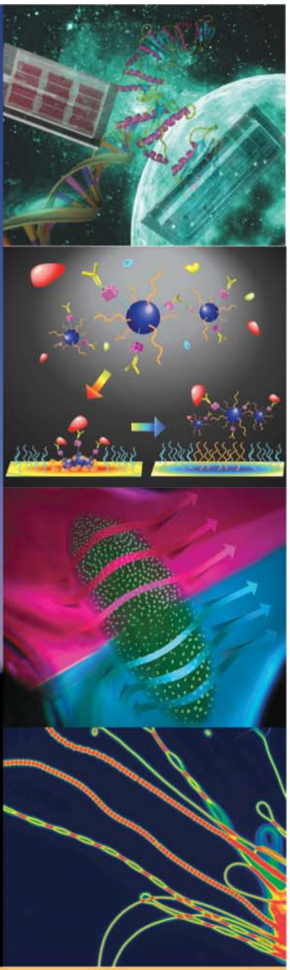

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