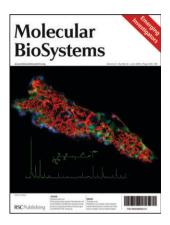
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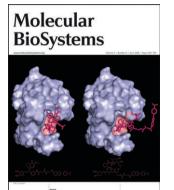
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IN THIS ISSUE

ISSN 1742-206X CODEN MBOIBW 4(6) 445-696 (2008)



Cover See E. Esquenazi et al., pp. 562–570. An epifluorescent (ex 590 nm) image of the marine sponge Dysidea herbacea overlaid with MALDI-TOF MS results showing the presence and localization of two different metabolite ions, depicted in blue and green. Image reproduced by permission of Eduardo Esquenazi, Cameron Coates, Luke Simmons, David Gonzalez, William H. Gerwick and Pieter C. Dorrestein from Molecular BioSystems, 2008, 4, 562.



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Inside cover

See P. S. Marinec *et al.*, pp. 571–578. Bifunctional Q1 molecules evade cytochrome P450 metabolism by forming protective complexes with FK506-binding protein. Image reproduced by permission of Paul S. Marinec, Jody K. Lancia and Jason E. Gestwicki from *Molecular BioSystems*, 2008, **4**, 571.

CHEMICAL BIOLOGY

B41

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

June 2008/Volume 3/Issue 6 www.rsc.org/chembiology

EDITORIAL

465

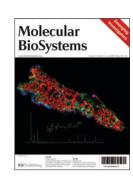
Emerging Investigators issue

The chair of the *Molecular BioSystems* Editorial Board, Professor Tom Kodadek, introduces the Emerging Investigators issue.



PROFILE

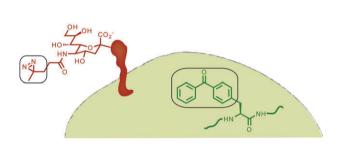
466



Contributors to the Emerging Investigators issue

Molecular BioSystems profiles the contributors to the Emerging Investigators issue.

REVIEW ARTICLES



Photocrosslinkers illuminate interactions in living cells

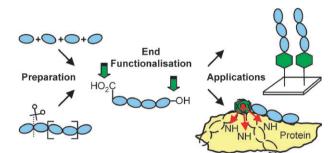
Yoshihito Tanaka, Michelle R. Bond and Jennifer J. Kohler*

This review highlights recent methodological developments that make it possible to introduce photocrosslinking groups into polypeptides or glycans as they are synthesized in cells and how these methods offer a non-invasive way to study macromolecular interactions in a native context.

481

496

473

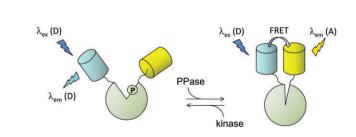


COMMUNICATIONS

Enabling methodology for the end functionalisation of glycosaminoglycan oligosaccharides

Emiliano Gemma, Odile Meyer, Dušan Uhrín and Alison N. Hulme*

We review methods for the preparation of end-functionalised glycosaminoglycan (GAG) oligosaccharides which may be used for a wide range of applications, including the study of GAG–protein complexes and the synthesis of GAG arrays.



Visualization of phosphatase activity in living cells with a FRET-based calcineurin activity sensor

Robert H. Newman and Jin Zhang*

We describe the first genetically-encodable phosphatase activity biosensor designed to specifically track calcineurin activity inside living cells. The successful design of a prototype phosphatase activity sensor lays a foundation for studying targeting and compartmentation of phosphatases.

COMMUNICATIONS

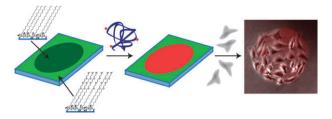
502

G

Direct printing of trichlorosilanes on glass for selective protein adsorption and cell growth

Dawn M. Yanker and Joshua A. Maurer*

Direct patterning of octadecyltrichlorosilane and backfilling with a glycol-terminated trichlorosilane on glass creates a surface on which protein adsorption and cell growth can be manipulated.



505

G

2-Methoxycyclopentyl analogues of a *Pseudomonas* aeruginosa quorum sensing modulator

Lydia Y. W. Lee, Timothy Hupfield, Rebecca L. Nicholson, James T. Hodgkinson, Xianbin Su, Gemma L. Thomas, George P. C. Salmond, Martin Welch and David R. Spring*

Cis- and *trans-2-*methoxycyclopentyl analogues of a quorum sensing molecule were synthesized and screened in *P. aeruginosa* and *Serratia* 39006 phenotypic assays. Both were agonists, but less active relative to a 2-oxocyclopentyl analogue and the cognate ligand.

508

Light-activated deoxyguanosine: photochemical regulation of peroxidase activity

Hrvoje Lusic, Mark O. Lively and Alexander Deiters*

A novel photocaged deoxyguanosine phosphoramidite was synthesized and incorporated into DNA. Peroxidase deoxyribozymes carrying the caged dG were catalytically inactive due to inhibition of structural organization. Brief UV irradiation efficiently restored the formation of a G-quadruplex wire and peroxidase activity.

512

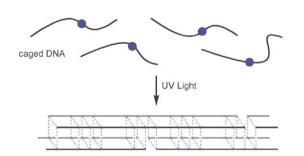
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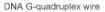
Toward autonomously operating molecular machines driven by transition-metal catalyst

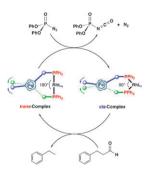
Kenichi Tanaka and Kazushi Kinbara*

A Vaska-type complex carrying a ferrocene-appended diphosphine ligand was developed as a prototype of autonomous molecular machines that is able to undergo continuous scissoring motion in the presence of diphenylphosphoryl azide and aldehyde.

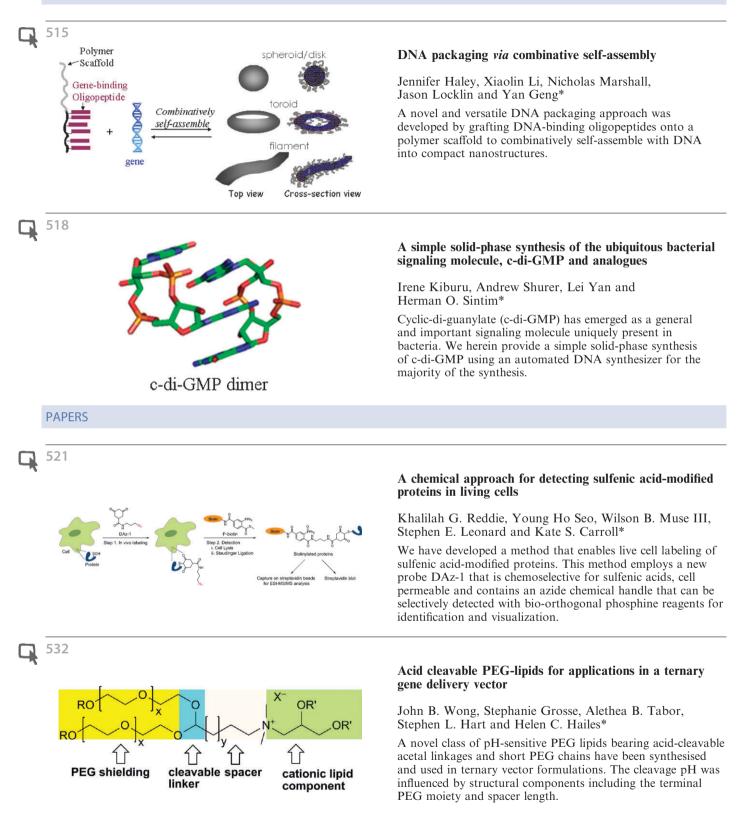








COMMUNICATIONS



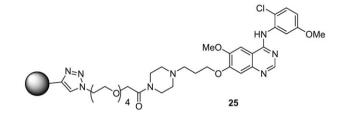
542

G

Design, synthesis and characterization of "clickable" 4-anilinoquinazoline kinase inhibitors

B. Gayani K. Perera and Dustin J. Maly*

A versatile method for the generation of "clickable" 4-anilinoquinazoline kinase inhibitors is reported. This methodology was used to generate potent and selective inhibitors of Aurora A, p38 and Src that can be modified *via* the Huisgen 1,3-dipolar cycloaddition.



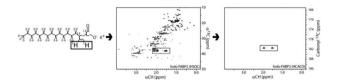
551

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Design, synthesis, and evaluation of an isotopic labeling strategy for studying fatty acid-protein binding by NMR

Yong Han, Timothy E. Alexander and Gregory P. Tochtrop*

We illustrate the utility of a fatty acid isotopic labeling strategy to study protein ligand binding using FABP2 as proof of principle.



558

Chemical site-selective prenylation of proteins

David P. Gamblin, Sander van Kasteren, Gonçalo J. L. Bernardes, Justin M. Chalker, Neil J. Oldham, Antony J. Fairbanks and Benjamin G. Davis*

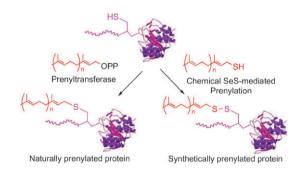
A direct thionation procedure allows conversion of allylic alcohols into the corresponding thiols, the products of which are immediately compatible with one-pot site-selective selenenyl sulfide mediated protein conjugation.

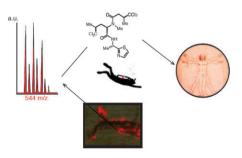
562

Visualizing the spatial distribution of secondary metabolites produced by marine cyanobacteria and sponges *via* MALDI-TOF imaging

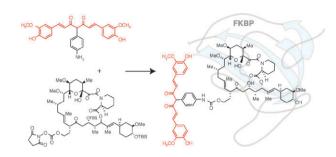
Eduardo Esquenazi, Cameron Coates, Luke Simmons, David Gonzalez, William H. Gerwick and Pieter C. Dorrestein*

MALDI-TOF imaging is a promising tool in marine natural products research: it gives us the ability to visualize the presence and distribution of bioactive compounds in both simple and complex assemblages of intact marine organisms.

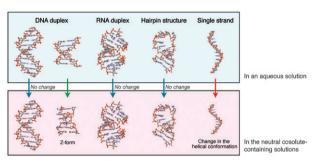




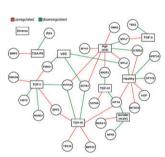
571



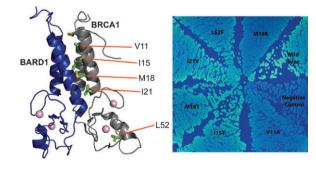
579



589



599



Bifunctional molecules evade cytochrome P_{450} metabolism by forming protective complexes with FK506-binding protein

Paul S. Marinec, Jody K. Lancia and Jason E. Gestwicki*

FK506 has a surprisingly good pharmacology, despite its high molecular weight. We modified unrelated compounds, such that they also acquire affinity for FKBP. Strikingly, these derivatives become resistant to metabolism *in vitro*. These findings suggest one mechanism that is responsible for FK506's long half-life *in vivo*.

Conformation and the sodium ion condensation on DNA and RNA structures in the presence of a neutral cosolute as a mimic of the intracellular media

Shu-ichi Nakano,* Lei Wu, Hirohito Oka, Hisae Tateishi Karimata, Toshimasa Kirihata, Yuichi Sato, Satoshi Fujii, Hiroshi Sakai, Masayuki Kuwahara, Hiroaki Sawai and Naoki Sugimoto*

Comprehensive studies of the conformations and the thermal stabilities of DNA and RNA structures in cosolute-containing solutions implicated the significance of the intracellular environment on nucleotide structures in a cell.

Prediction of cardiac transcription networks based on molecular data and complex clinical phenotypes

Martje Toenjes, Markus Schueler, Stefanie Hammer, Utz J. Pape, Jenny J. Fischer, Felix Berger, Martin Vingron and Silke Sperling*

An integrative approach to identifying cardiac transcription networks based on correlated gene expression and optimized prediction of transcription factor binding sites can enable explanation of gene expression profiles observed for congenital heart disease.

Re-engineering a split-GFP reassembly screen to examine RING-domain interactions between BARD1 and BRCA1 mutants observed in cancer patients

Mohosin Sarkar and Thomas J. Magliery*

We re-engineered the split-GFP system for fast reassembly and bright fluorescence with whole protein domains. The improved system was used to study interactions of BARD1 with cancer-associated mutants of the tumor suppressor BRCA1.

606

G

Estimating P-coverage of biosynthetic pathways in DNA libraries and screening by genetic selection: biotin biosynthesis in the marine microorganism *chromohalobacter*

Eun Jin Kim, Scott Angell, Jeff Janes and Coran M. H. Watanabe*

An algorism called BPC is put forth to estimate the size of a library necessary to achieve proper coverage of biosynthetic pathways housed within microbial genomes. Genetic selection is demonstrated as a method to identify and localize biosynthetic gene clusters within metagenomic DNA libraries.



Control of bacterial biofilms with marine alkaloid derivatives

Robert W. Huigens III, Luyan Ma, Christopher Gambino, Peter D. R. Moeller, Anne Basso, John Cavanagh, Daniel J. Wozniak and Christian Melander*

Bacterial biofilms are responsible for a plethora of medical problems. Herein we report the identification of bicyclic 2-aminoimidazole derivatives that inhibit and disperse bacterial biofilms.

622

Characterization of TioF, a tryptophan 2,3-dioxygenase involved in 3-hydroxyquinaldic acid formation during thiocoraline biosynthesis

Anita Sheoran, Andrew King, Ana Velasco, Jessica M. Pero and Sylvie Garneau-Tsodikova*

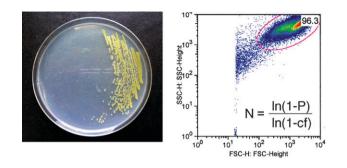
TioF, a new member of the family of tryptophan 2,3-dioxygenases with broader substrate specificity than other TDOs, is involved in the formation of the marine anticancer agent thiocoraline.

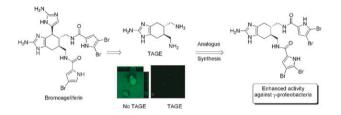
629

Targeting telomerase and telomeres: a click chemistry approach towards highly selective G-quadruplex ligands

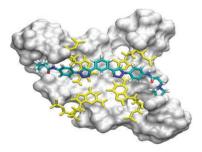
Adam D. Moorhouse, Shozeb Haider, Mekala Gunaratnam, Deeksha Munnur, Stephen Neidle* and John E. Moses*

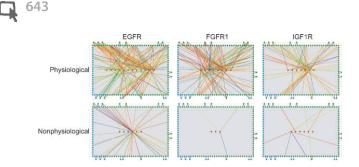
A library of new telomerase inhibitors have been discovered utilizing the Cu(1) catalyzed 'Click' reaction between a azides and terminal alkynes. These 'click' ligands show promising activity and selectivity *in vivo* against telomerase.

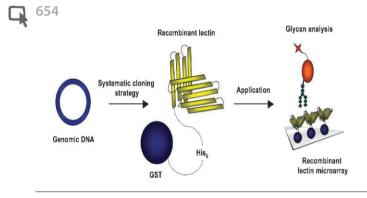












663



A quantitative study of the recruitment potential of all intracellular tyrosine residues on EGFR, FGFR1 and IGF1R

Alexis Kaushansky, Andrew Gordus, Bryan Chang, John Rush and Gavin MacBeath*

This paper reports quantitative interaction maps for EGFR, FGFR1 and IGF1R, obtained by probing protein microarrays comprising human SH2 and PTB domains with phosphopeptides representing every intracellular tyrosine residue on each of the three receptors.

A simple strategy for the creation of a recombinant lectin microarray

Ku-Lung Hsu, Jeffrey C. Gildersleeve and Lara K. Mahal*

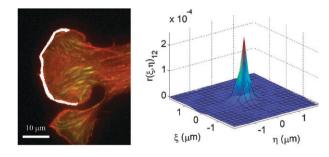
We describe an efficient strategy for the systematic creation of bacterially-derived recombinant lectins for use in lectin microarray technology. We demonstrate that a recombinant lectin microarray is capable of distinguishing glycopatterns of protein and tumor cell samples.

The unusual macrocycle forming thioesterase of mycolactone

Jordan L. Meier, Tiffany Barrows-Yano, Timothy L. Foley, Candice L. Wike and Michael D. Burkart*

The putative macrocycle forming thioesterase MLSA2 TE was cloned, expressed and biochemically characterized. The findings suggest that the enzyme utilizes a unique biochemical mechanism for macrocycle formation.

672



Accurate measurements of protein interactions in cells *via* improved spatial image cross-correlation spectroscopy

Jonathan W. D. Comeau, David L. Kolin and Paul W. Wiseman*

New strategies to overcome some of the limitations of spatial image cross-correlation spectroscopy promise to significantly improve the dynamic range and practical usage of an accurate method for measuring molecular interactions *via* analysis of fluorescence microscopy images.

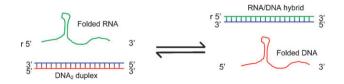
686

G

Thermodynamic prediction of RNA–DNA duplex-forming regions in the human genome

Julian L. Huppert*

The energetic contributions of both duplex formation and single-strand folding are considered and used to search the entire human genome for regions predicted to form RNA–DNA hybrids, confirming previous experiments.





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