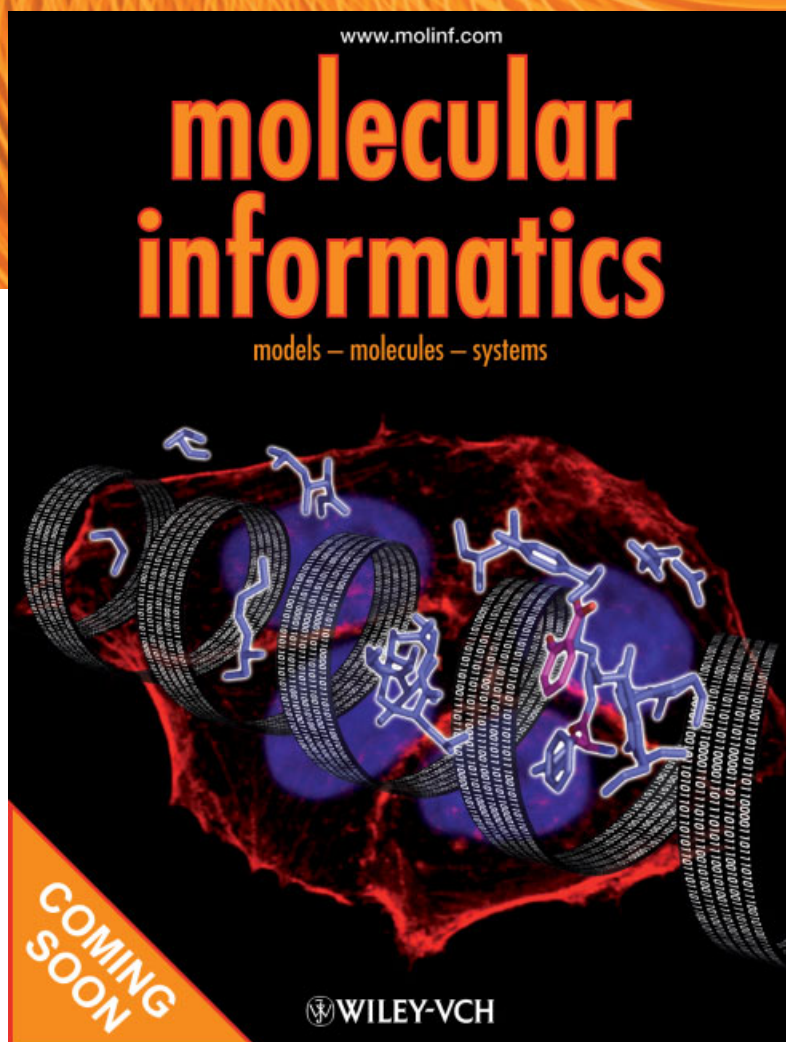


Where Design Meets Experiment



Succeeding *QSAR & Combinatorial Science*
from 2010

ISSN (print) 1868-1743 · ISSN (online) 1868-1751
2010 · Volume 29 · 12 issues

www.molinf.com

Submit Now ← ← ←
CALL FOR PAPERS

Editors

Knut Baumann
Braunschweig University of Technology
Germany
k.baumann@tu-braunschweig.de



Gerhard Ecker
University of Vienna
Austria
gerhard.f.ecker@univie.ac.at



Jordi Mestres
Municipal Institute of Medical Research
Spain
jmestres@imim.es



Gisbert Schneider
University of Frankfurt
Germany
gisbert@modlab.net



Editorial Advisory Board

Dimitris K. Agrafiotis (USA) · Karl-Heinz Baringhaus (Germany) ·
Scott Boyer (Sweden) · Mark T. Cronin (UK) · Peter Ertl (Switzerland) ·
Kimito Funatsu (Japan) · Robert Glen (UK) · Andrew C. Good (USA) ·
Paola Gramatica (Italy) · Wolfgang Guba (Switzerland) · Philip J.
Hadjuk (USA) · Donald Hilvert (Switzerland) · Andrew L. Hopkins
(UK) · Ad P. IJzerman (The Netherlands) · Hualiang Jiang (China) ·
Muthukumarasamy Karthikeyan (India) · Dimitry A. Konovalov (Austra-
lia) · David Lloyd (Ireland) · David Manallack (Australia) · Jonathan S.
Mason (Denmark) · Stefano Moro (Italy) · Ingo Mügge (USA) · Tudor
I. Oprea (USA) · John P. Overington (UK) · Stephen D. Pickett (UK) ·
Brian K. Shoichet (USA) · Sung-Sau So (USA) · Michael J. E. Sternberg
(UK) · Igor V. Tetko (Germany) · Alexander Tropsha (USA) · Alexandre
Varnek (France) · Patrick Walters (USA) · Renxiao Wang (China) · Tanja
Weil (Singapore) · Jianhua Yao (China)

 **WILEY-VCH**



Molecular Informatics...

Topics

- Cheminformatics
- Bioinformatics
- Pharmacoinformatics
- Drug design
- Virtual screening
- Molecular modeling
- QSAR
- Protein modeling
- Protein engineering
- Nucleic acid engineering
- Pharmacogenomics
- Chemogenomics
- Systems biology
- Small molecules
- Macromolecular complexes
- Molecular networks
- Protein-protein interactions

Author Benefits

- **High visibility** through wide circulation
- Easy and convenient web-based online submission and reviewing system
- Prompt peer-review process and **rapid publication**
- Online publication of individual articles ahead of the print edition
- **Open-access option** for authors who wish to pay to make their article freely available online (Online Open)
- Reproduction of essential color figures **free of charge**
- Presentation of your personal **Cover Artwork**

Readership

- Computational chemists and biologists
- Medicinal, pharmaceutical, organic and biochemists
- Chemical and molecular biologists
- Pharmacists and pharmacologists
- Drug designers
- Researchers in the fields of bio/cheminformatics

Submit your next excellent manuscript at

<http://mc.manuscriptcentral.com/minf>

For enquiries or further information, please e-mail us at

STM-Journals@wiley-vch.de

...will be a peer-reviewed, international forum for publication of high-quality, interdisciplinary research on all molecular aspects of bio/cheminformatics and computer-assisted molecular design.

Molecular Informatics presents **methodological innovations** that will lead to a deeper understanding of ligand-receptor interactions, macromolecular complexes, molecular networks, design concepts and processes that demonstrate how ideas and design concepts lead to molecules with a desired structure or function, preferably including experimental validation.

The journal's scope includes but is not limited to the fields of drug discovery and chemical biology, protein and nucleic acid engineering and design, the design of nanomolecular structures, strategies for modeling of macromolecular assemblies, molecular networks and systems, pharmaco- and chemogenomics, computer-assisted screening strategies, as well as novel technologies for the de novo design of biologically active molecules.

As a unique feature *Molecular Informatics* will publish so-called "**Methods Corner**" review-type articles which will feature important technological concepts and advances within the scope of the journal.

...will publish

- "Methods Corner" Reviews
- Reviews
- Communications
- Full Papers



WILEY-VCH

