Molecular Informatics is 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 publishes so-called “Methods Corner” review-type articles which feature important technological concepts and advances.

Most of the articles in this issue have already appeared online in Wiley OnlineLibrary. See www.molinf.com under EarlyView®.

Special Issue:
19th European Symposium on Quantitative Structure-Activity Relationships

Cover Picture

Molecular Informatics publishes research that will deepen our understanding about information storage and processing on the molecular level, signaling and regulation of biological and chemical systems including cellular systems and macromolecular assemblies, modeling of molecular interactions and networks, and the design of molecular modulators that exhibit desired biochemical and pharmacological effects. Various aspects of this transdisciplinary scientific area are depicted on the cover: Cells with their nuclei and membranes (image courtesy of Dr. A. Schreiner and E. Resch), models of receptor-ligand interactions, and an artistic representation of “biological information” as multiple bit-codes presented on a right-handed helix.

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