

# Computational Methods for Macromolecules: Challenges and Applications

*Proceedings of the 3rd International  
Workshop on Algorithms for Macromolecular  
Modeling, New York, October 12-14, 2000*

**Tamar Schlick** and **Hin H. Gan**, both, New York University,  
New York (Eds.)

This special volume collects invited articles by participants of the Third International Workshop on Methods for Macromolecular Modeling, Courant Institute of Mathematical Sciences, Oct. 12-14, 2000. Leading developers of methods for biomolecular simulations review advances in Monte Carlo and molecular dynamics methods, free energy computational methods, fast electrostatics (particle-mesh Ewald and

fast multipole methods), mathematics, and molecular neurobiology, nucleic acid simulations, enzyme reactions, and other essential applications in biomolecular simulations. A Perspectives article by the editors assesses the directions and impact of macromolecular modeling research, including genomics and proteomics. These reviews and original papers by applied mathematicians, theoretical chemists, biomedical researchers, and physicists are of interest to interdisciplinary research students, developers and users of biomolecular methods in academia and industry.

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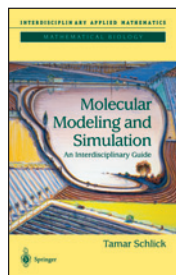


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# Molecular Modeling and Simulation

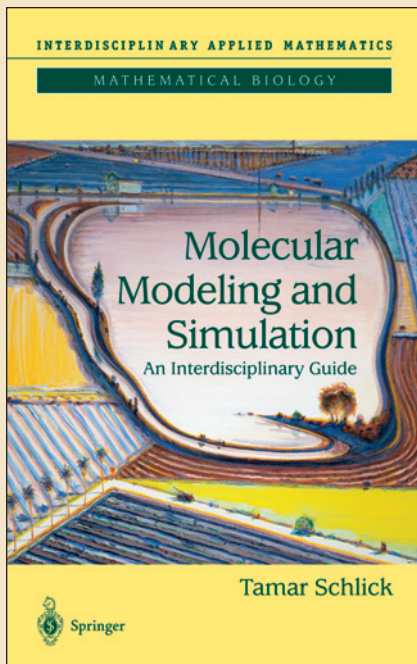
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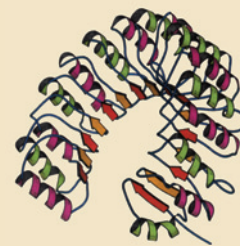
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# Molecular Modeling and Simulation

## An Interdisciplinary Guide

Tamar Schlick, New York University, New York, NY



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**-J. Andrew McCammon, Howard Hughes Medical Institute, University of California at San Diego**

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*I am also often approached by my colleagues in computational biology to recommend a solid textbook for a graduate course in the area. Tamar Schlick has written the book that I will be recommending to both groups. Tamar has done an amazing job in writing a book that is both suitably accessible for beginners, and suitably rigorous for experts."*

**-J.J. Collins, Co-Director, Professor of Biomedical Engineering, Boston University**

This book evolved from an interdisciplinary graduate course entitled Molecular Modeling developed at New York University. Its primary goal is to stimulate excitement for molecular modeling research while introducing readers to the wide range of biomolecular problems being solved by computational techniques and to those computational tools. The book is intended for beginning graduate students in medical schools and scientific fields such as biology, chemistry, physics, mathematics, and computer science. Other scientists who wish to enter, or become familiar, with the field of biomolecular modeling and simulation may also benefit from the broad coverage of problems and approaches.

The book surveys three broad areas: biomolecular structure and modeling: current problems and state of computations; molecular mechanics: force field origin, composition, and evaluation techniques; and simulation methods: geometry optimization, Monte Carlo, and molecular dynamics approaches. Appendices featuring homework assignments, reading lists, and other information useful for teaching molecular modeling complement the material in the main text. Extensive use of world wide web resources is encouraged, and additional course and text information may be found on a supplementary website.

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