Series Preface

The 2013 Nobel Prize in Chemistry was awarded for the "development of multiscale models for complex chemical systems." This prize was particularly special to the whole computational community as it was finally recognized the role computation has played since the pioneering works of Lifson, Warshel, Levitt, Karplus, and many others.

This SERIES IN COMPUTATIONAL BIOPHYSICS has been conceived to reflect the tremendous impact of computational tools in the study and practice of biophysics and biochemistry today. The goal is to offer a suite of books that will introduce the principles and methods for computer simulation and modeling of biologically important macromolecules. The titles cover both fundamental concepts and state-of-the-art approaches, with specific examples highlighted to illustrate cutting edge methodology. The series is designed to cover modeling approaches spanning multiple scales: atoms, molecules, cells, organs, organisms, and populations.

The series publishes advanced level textbooks, laboratory manuals, and reference handbooks that meet the needs of students, researchers, and practitioners working at the interface of biophysics/biochemistry and computer science. The most important methodological aspects of molecular modeling and simulations as well as actual biological problems that have been addressed using these methods are presented throughout the series. Prominent leaders have been invited to edit each of the books, and in turn those editors select contributions from a roster of outstanding scientists.

The SERIES IN COMPUTATIONAL BIOPHYSICS would not be possible without the drive and support of the Taylor & Francis Group series manager Luna Han. All the editors, authors, and I are greatly appreciative of her support and grateful for the success of the series.

Nikolay V. Dokholyan
Series Editor
Chapel Hill, NC