Preface

This book aims to highlight recent advances in characterizing biomacromolecules using a range of state-of-the-art NMR approaches. The role of NMR spectroscopy in solving biomolecular structures to atomic resolution is well-established. Novel methods now allow the extension of these studies to larger molecules and complexes. In addition, it is perhaps the ability to tailor NMR experiments to answer a broad range of specific questions at the atomic level that sets NMR apart from other techniques.

The first NMR-based structure determination of a protein was published in 1984 by the Wüthrich group. X-ray crystallographic and NMR structure determination methods were shown to arrive at similar conclusions, though by vastly different approaches. However, as the resolution and capabilities of each technique has grown, so have the distinctions. The recent extension of NMR techniques to larger biomolecules and complexes has revealed that interdomain and intermolecular contacts can be exquisitely sensitive to differences in environment, including the difference between a crystalline and solution environment. The importance of NMR in probing dynamics and folding has also continued to be evident. In addition, we now know that most proteins contain at least one region of intrinsic disorder, a state that can much more effectively be examined by NMR than by crystallography. Thus, as we enter the second decade of the 21st century, it seems clear that the complementary techniques of NMR and X-ray crystallography, with increasing cooperation from other biophysical techniques such as SAXS/SANS and computational approaches, will continue to serve hand-in-hand toward the tasks of structural biology.

The following chapters are organized into four sections. The overexpression of isotopically-enriched proteins for NMR study has become routine. Therefore, the first section entitled "Sample Preparation" focuses on the less well-established preparation of isotopically-enriched nucleic acids and on the option of cell-free protein synthesis. Section two focuses on the structure and dynamics of proteins, including large proteins, complexes and disordered states, in solution, in the solid state and in cells. The chapters in section three examine the challenges and rewards of NMR-based nucleic acid structure and dynamics studies. Finally, recent advances to speed NMR data acquisition and structural analysis, along with procedures that efficiently combine NMR data with data from complementary techniques, are discussed in section four.

We are grateful to all authors for their contributions to this volume, which includes both the writing and formatting of their chapters. We would also like to thank Parvez Haris for his ongoing support and guidance in the preparation of the book, and the publisher, Peter Brown from IOS Press, for his assistance with our queries. The permission from various publishers to reproduce figures from original publications is kindly acknowledged.

Andrew J. Dingley and Steven M. Pascal