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# Preface

When I was asked to edit the second edition of *Protein NMR Techniques*, my first thought was that the time was ripe for a new edition. The past several years have seen a surge in the development of novel methods that are truly revolutionizing our ability to characterize biological macromolecules in terms of speed, accuracy, and size limitations. I was particularly excited at the prospect of making these techniques accessible to all NMR labs and for the opportunity to ask the experts to divulge their hints and tips and to write, practically, about the methods.

I commissioned 19 chapters with wide scope for *Protein NMR Techniques*, and the volume has been organized with numerous themes in mind. Chapters 1 and 2 deal with recombinant protein expression using two organisms, *E. coli* and *P. pastoris*, that can produce high yields of isotopically labeled protein at a reasonable cost. Staying with the idea of isotopic labeling, Chapter 3 describes methods for perdeuteration and site-specific protonation and is the first of several chapters in the book that is relevant to studies of higher molecular weight systems. A different, but equally powerful, method that uses molecular biology to “edit” the spectrum of a large molecule using segmental labeling is presented in Chapter 4. Having successfully produced a high molecular weight target for study, the next logical step is data acquisition. Hence, the final chapter on this theme, Chapter 5, describes TROSY methods for structural studies.

In Chapters 6–12 of *Protein NMR Techniques*, the focus shifts to studies of aligned molecules, beginning with Chapter 6, which describes different options for the preparation of an aligned sample. So many labs have contributed to the development of new media that I believe it will be particularly useful to have this information summarized in an easily digestible format. Residual dipolar coupling (RDC) data acquisition and incorporation into structure calculations are presented in an equally straightforward manner. Chapters 6 and 7 make it clear that RDCs, a powerful source of structural data that are complimentary to NOE-derived distance restraints, can be measured and used routinely. An exciting chapter on the use of RDCs to study protein dynamics highlights the range of information accessible using these methods and, also, their particular potential to inform on motions on a timescale that previously has not been accessible. Having opened the discussion on RDCs and relaxation, there is an elegant description of how the methods can be combined to yield insight into the properties of multimodule constructs.

Three chapters round out this section: Chapter 10 discusses the correct interpretation of relaxation data and the dangers of ignoring anisotropy; Chapter 11 introduces TROSY methods for the study of dynamics; and Chapter 12 provides a detailed and fascinating account of new methods for the characterization of intermediate timescale motions.

NMR studies often share common methodological features, and, in other features, they necessarily vary. Chapters 13–15, discussing studies of partially folded states and of protein–protein and protein–nucleic acid complexes, are designed to highlight three special areas of interest. A computational section focusing on the automation of both assignment and structure calculation methods follows. Having personally spent much time on these aspects of structure determination, I find these methods particularly exciting because of their potential to significantly expedite the process. Finally, Chapter 19 comprehensively reviews the application of solid state methods to the study of membrane proteins, a particularly important but difficult class of targets.

Editing *Protein NMR Techniques* has been more work than I had expected, but it was also even more rewarding than I anticipated. I hope that you will find it to be a valuable resource in your research.

***A. Kristina Downing***



<http://www.springer.com/978-1-58829-246-9>

Protein NMR Techniques

Downing, A.K. (Ed.)

2004, XIII, 487 p., Hardcover

ISBN: 978-1-58829-246-9

A product of Humana Press