Preface to the Series

From its inception, molecular biology has always been a discipline of rapid development. Despite this, we are presently experiencing a period of unprecedented proliferation of information in nucleic acid studies and molecular biology. These areas are intimately interwoven, so that each influences the other to their mutual benefit. This rapid growth in information leads to ever-increasing specialization, so that it becomes increasingly difficult for a scientist to keep abreast of developments in all the various aspects of the field, although an upto-date knowledge of the field as a whole is highly desirable.

With this background in mind, we have conceived the present series *Nucleic Acids and Molecular Biology*. It comprises focused review articles by active researchers, who report on the newest developments in their areas of particular interest. The reviews are not intended to be exhaustive, but rather to place the most recent data into context. This format will allow our colleagues of familiarize themselves with new developments in areas outside their own immediate speciality, thus facilitating a more global view of their own work. Moreover, we hope sincerely that this will convey some of the excitement of the interdisciplinary nature of the study of nucleic acids and molecular biology.

This series is planned to appear annually. This period will allow us to return to important topics with sufficient frequency to cover new developments as they emerge.

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Introduction to Volume 7

A substantial proportion of this volume has been devoted to the analysis of different aspects of nucleic acid-protein interactions. Following an initial chapter on the catalytic activity of *cis*-platinated DNA, the next three chapters address structural questions in prokaryotic proteins that interact with DNA. While most DNA binding proteins are based around sequence recognition by side chains from an α-helix (e.g. the 434 repressor and the restriction enzyme *Eco* RV), the MetJ repressor represents an important new class of proteins that are based on antiparallel β-sheet. An alternative use of the α-helix in sequence recognition is provided by the leucine zipper proteins, exemplified by the Fos-Jun heterodimer, where a coiled-coil plays an important role in mediating protein-protein interactions. Another very important class of DNA binding proteins is represented by the zinc fingers, yet these are also divisible into a number of distinct classes of proteins. The first to be identified contains TFIIIA as its archetypical member. The manner of the binding of this nine-finger transcription factor to its cognate binding site in the 5S rRNA gene is discussed in this volume. The steroid receptor proteins are structurally very different from the TFIIIA fingers, and are exemplified by the glucocorticoid and retinoic acid receptor proteins. We hope to cover additional zinc binding motifs in future volumes.

In addition to recognizing sequence, DNA binding proteins may also respond to, and indeed modify, the structure of DNA. *Eco* RV severely disrupts local DNA structure when bound to its target site, while the structure of the Fis protein suggests a major bending of DNA. Many of these proteins are involved in either repair or recombination. New insight has recently been gained into the enzymology of recombination in *Escherichia coli*, and in the mechanism of the site-specific recombination events that underlie DNA segregation in plasmids. Perhaps the histones may be thought of as the ultimate manipulators of DNA structure, wrapping DNA of random sequence into nucleosomes for packaging; however, this leaves the question of just how random this sequence can be, and how the nucleosomes may be positioned with respect to the DNA sequence. Further higher order structure of chromatin

and chromosomes appears to be genetically important, and the role of chromosomal attachment is considered.

RNA and its interactions are not neglected in this volume. The fundamentally single-stranded character of RNA molecules is extensively folded in secondary and tertiary structure, and an important structural element that is restricted to RNA is the pseudoknot. Still more interesting, RNA species that may be adapted to the binding of novel substrates may be selected using in vitro methods, potentially making the repertoire of RNA almost limitless. RNA-protein interactions, while not so extensively studied as those of DNA, are becoming better understood, as the studies of RNaseH and ribonucleoproteins indicate. Finally, perhaps the most complex functional RNA-protein apparatus in the cell is the ribosome, but even there we see significant progress.

We are grateful to all the authors of Volume 7 for maintaining the level of expertise, interest and clarity to which we have become accustomed in editing this series.

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