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# Preface

There can be no doubt that some of the most spectacular advances made in science over the past few decades have been in the isolation, analysis, and manipulation of nucleic acids. This has led to a much greater understanding of mechanisms and processes across many fields of bioscience, such as biochemistry, microbiology, physiology, pharmacology, and the medical sciences to name a few. It has also led to the growth of the biotechnology industry, which seeks to develop and commercialize many of these important processes and methods. Much of this has come about because of the development of numerous molecular biology and genetic manipulation techniques. The discovery of restriction enzymes and the development of cloning vectors in the early 1970s opened the door to ways of isolating and manipulating nucleic acids that had never been thought possible. Gene probe labeling and hybridization were developed and refined to provide powerful methods of analysis. These—together with the development of DNA sequencing methods, protein engineering techniques, and PCR—have all continued to contribute substantially to the understanding of biological processes at the molecular level. The protocols for these important methods are the focus of *The Nucleic Acid Protocols Handbook*, whose aim is to provide a comprehensive set of techniques in one volume that will enable the isolation, analysis, and manipulation of nucleic acids to be readily undertaken.

*The Nucleic Acid Protocols Handbook* is divided into 10 parts; within each there are approximately 10 chapters. The first four parts follow one another logically: nucleic acid extraction (Part I), basic separation and analysis of DNA (II), through probe design and labeling (III), and RNA analysis techniques (IV). The following three sections deal with gene library construction and screening (V), DNA sequencing (VI), and the polymerase chain reaction (VII). Part VIII deals with the analysis of genes, mutations, and protein interactions and is followed by Part IX, on mutagenesis, transcription, and translation *in vitro*. This is followed finally by Part X, on gene localization and mapping *in situ*. In compiling this volume a number of techniques have been drawn and updated from versions appearing in earlier volumes of Humana Press' *Methods in Molecular Biology* series. These highly successful books have provided numerous laboratories with the techniques needed to undertake modern laboratory molecular biology successfully. As such, their format has been followed in *The Nucleic Acid Protocols Handbook*. Thus a short introduction to the basic theory of the technique is followed by a complete listing of all materials and reagents needed before a particular protocol is presented. Step-by-step instructions are then provided in the Methods section. In addition, Notes are cited throughout the Methods and appear at the end of the chapter, providing valuable and highly useful information not found in traditional scientific literature. This essential

information in many cases may mean the difference between the success or failure of a particular technique and is one of the recognized key points of the *Humana Methods in Molecular Biology* series.

It is inevitable that a degree of overlap occurs between some of the chapters. Indeed, the use of the polymerase chain reaction is now so widespread that it is a key element of many of the protocols. These have been cross referenced where possible, although most of the protocols are self-contained and can be attempted without the need to read further chapters. For those new or unfamiliar to laboratory molecular biology, the compilation of protocols in *The Nucleic Acid Protocols Handbook* also provides the ability to attempt protocols confidently. The intent was not to list all protocols in molecular biology (within one volume, this is an impossible task), and certainly more advanced protocols may be found in a number of excellent texts including many in the *Humana Methods in Molecular Biology* series. It was, however, the aim to provide the most commonly used protocols and alternatives in one volume at a level accessible to most laboratories, which we believe has been achieved. In such a large compilation, much credit must go to the authors, who have devoted valuable time and effort to write and update these protocols; to Prof. John M. Walker, the series editor, for his helpful advice and guidance; and to the staff at Humana Press for their substantial efforts in the production of the volume.

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