Preface

This is the second volume for a developing Jones and Bartlett Publishers series on methods in DNA sequencing technology. Similar to the first volume, *DNA Sequencing: Optimizing the Process and Analysis* (2005), *DNA Sequencing II: Optimizing Preparation and Cleanup* is devoted to techniques related to the analysis of DNA. Its primary goal is to assemble both overview and experimental articles into a single volume focused on various methods for extraction, cleanup, quantitation, and analysis of DNA.

This volume has four, distinct sections. The first and biggest theme includes eight chapters devoted to purification of DNA (and to a lesser degree RNA) from a variety of sources, each serving a different purpose. The choice of method varies when preparing difficult DNAs (Chapter 1), bacterial artificial chromosomes (BACs) (Chapter 2), DNA from animal (Chapter 3) or plants tissues (Chapter 4), DNAs for microarrays (Chapter 5), isolating DNA from preserved sources (Chapter 6), or amplifying whole genomes (Chapter 8). At least where DNA sequencing is concerned, TempliPhi methods to produce template DNAs are as good as other well-established, "classical" protocols for isolation of DNA (Chapter 7).

The second theme is the cleanup of DNA fragments used in specific applications. Chapter 9 describes the uses of magnetic beads for a variety of applications. Complementary to this topic is Chapter 10, which describes setup and operation of a high-throughput pipeline in one of the premiere DNA sequencing centers, Sanger Institute. Chapter 11 compares five protocols for cleanup of polymerase chain reaction (PCR) fragments suitable both for low- and high-throughput applications. Chapter 12 compares twenty different protocols, in four distinct categories, for cleaning of sequencing reactions before loading onto capillary electrophoresis instruments.

The third theme contains two chapters on short- (Chapter 14) and long-term (Chapter 15) storage of DNA under a variety of conditions.

Finally, the last section contains chapters on numerous ways to quantify DNA and RNA (Chapter 16) in which an interesting new parameter (Purity Quotient-PQ) is suggested as a measure of purity of nucleic acids. Chapter 13 describes new DNA polymerases with a range of unusual properties that may find broad applications in many molecular biology techniques. This volume ends with Chapter 17, which briefly touches upon many tools, mainly software programs that may be found in a typical modern biology laboratory.

The scope and content of articles presented in this volume are guided by the knowledge and experience of the contributing authors. Any omission of other methods, protocols, and analysis tools is unintentional. On the other hand, inclusion of any method, protocol, or software tool does not constitute their advertisement and represents the experiences and preferences of the contributing authors. As always, the reader is strongly encouraged to apply and test any method that is suitable for a particular environment and application. Although quite comprehensive, this by no means is an exhaustive or complete assembly of articles on DNA technologies. Notably, we did not include information devoted to extraction of DNA from hazardous and forensic sources. Future volumes will expand on the knowledge in this current text and will encompass many other methodologies (e.g., single nucleotide polymorphism [SNP] analysis, genotyping, high-content screening, etc.) and tools (e.g., primer design, automated fragment assembly and analysis, or gene annotation, etc.). Of course, your suggestions and recommendations would be greatly appreciated.

All of the figures in this volume have been reproduced in black and white. Some, for which color is critical, have been duplicated in color. Such figures are cited in the text as, for example, "Figure 9-11; color Plate 4." Figure legends also indicate if an image appears as a color plate. All color plates are gathered together in an insert near the middle of the book.

Acknowledgments

The production of any book, but a scientific one in particular, is a complex task and involves many people and groups of people. I like to thank everyone involved with this book for pulling together and making sure that all inquires were answered and deadlines met. Without your dedication and contributed chapters this book would be still in the "dream stage."

In particular, I thank the DNA sequencing staff and management at Biological Technologies Department, Wyeth Research in Cambridge for all the help and encouragement during the course of research and preparation of manuscripts; Stephen Weaver of Jones and Bartlett, Publishers,

the science editor of this volume, for superb editorial guidance; the entire editorial and production staff at Jones & Bartlett, including Lou Bruno, Dean DeChambeau, Rebecca Seastrong, Molly Steinbach, and Anne Spencer; and, lastly, my truly supporting wife Carla and children Alex, Kasia, and Michael.

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November 2005