

Preface

DNA sequence rearrangements are widespread in both prokaryotes and eukaryotes and are the subject of intense current research effort. Indeed the topic scope is now so large that it is impossible to review in any depth in a single book the recent discoveries which have been made in the field as a whole. An earlier volume in this series was devoted solely to the reorganization and expression of genes of the immune system. The present book extends this interest into several other related areas. Lex Van der Ploeg's chapter describes the molecular basis of antigenic variation in trypanosomes, covering DNA recombinational mechanisms in differential VSG gene expression in detail as well as other important expression events including discontinuous transcription and *trans*-splicing. In both the trypanosome and the immune system, DNA rearrangements are geared to providing a wide range of qualitative structural changes in the expressed gene product. In other circumstances it is the relative amount of a gene product which is the limiting factor, where the need for a particular product cannot be met by the maximal expression of the existing DNA sequences. Here DNA amplification is a solution to the problem. The chapter by George Stark, Michelle Debatisse, Geoffrey Wahl, and David Glover considers both developmentally programmed DNA amplification, particularly in dipteran flies where most progress has been made, and other increasingly important cases of amplification which occur as more isolated events such as the amplification of drug resistance genes and oncogenes in mammalian cells and the amplification of genes for resistance to toxic agents in whole organisms. Finally, every practising molecular biologist is all too aware that deletions, amplifications, inversions, insertions of foreign DNA, and translocations also occur in bacteria. We feel sure therefore that the chapter by Doug Berg, which examines the diverse mechanisms whereby these DNA rearrangements occur in prokaryotes, will be fascinating to a large cross-section of readers and not only to the specialists in this field. We thank each of the authors for their hard work and enthusiasm throughout this project and hope that their efforts will be as well-received by the readers as they were by the editors.

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