

Preface

The activities associated with the genome center around the readout, processing, maintenance and transfer of the information encoded in the DNA sequence. In eukaryotes, the corresponding processes like gene expression and RNA processing, as well as DNA repair, replication, recombination and genome segregation take place in the environment of the nucleus. It provides a complex dynamic organization that serves to establish two apparently contradicting functions: On the one hand the genome has to be protected from uncontrolled modifications that would compromise its function, and it has to be reliably replicated and segregated during cell division and meiosis. On the other hand it has to be remarkably plastic to allow for a dynamic (re)organization so that the cell is able to adopt different functional states.

To understand how this is accomplished, findings from research in genomics, chromatin, epigenetics and nuclear organization have to be integrated. This need is addressed in the present book by combining complementary and interconnected contributions from renowned experts in these different fields of research. Issues that are directly related to DNA sequence and epigenetic information are discussed in Chapters 1, 2, 4 and 15. Chromatin organization and dynamics are covered from the scale of a single nucleosome to that of whole chromosomes in Chapters 2–6, 8, 9, 15, 17–20. The architecture of the nucleus and its subcompartments are discussed in relation to genome function in Chapters 7–10, 12 and 17. Within this framework, the central genome activities are treated in dedicated chapters for transcription, RNA processing and non-coding RNAs (Chapters 10–14), DNA replication and repair (Chapters 15, 16) as well as genome segregation and recombination during cell division and meiosis (Chapters 18, 19). Finally, using two exemplary cases, protein complex assembly during DNA repair and chromatin folding, it is discussed how quantitative models are applied to describe and predict functional genome features (Chapter 20).

Bringing together results from these different research areas in one book has been a highly rewarding experience for me. It has provided me with new insight on how the genome structure and its nuclear environment are interconnected with its functions, and hopefully the readers of the book will share this view. I am most

grateful to all authors for their excellent contributions, and I wish to thank my colleagues from the DKFZ and BioQuant, the members of my laboratory and the editorial staff from Wiley-VCH for their advice and help in preparing this book.

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