



# PREFACE

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There have been some significant changes in our understanding of genetics since the second edition. Genome sequencing is no longer a frontier project, but the data produced is driving most aspects of research. The human genome has only 20,000 genes identified, with an upper estimate of 25,000, putting us firmly in with most other multicellular organisms, far below earlier guesses. We appear to have fewer genes than a cabbage. Genome comparisons have also revealed between 67 and 83 genes that remain active in chimps, but are now inactive pseudogenes in humans due to mutations in the course of human evolution. A further surprise is that some parts of the human genome differ much more than others from chimpanzees. This implies a long period with some genetic exchange between the ancestral populations as they diverged into the two species.

Another new development is discovery of the role of RNA in the control of chromatin architecture, and the importance of covalent modifications to the N-terminal tails of histones in regulating chromatin structure. Some histone modifications (e.g. site specific methylation) promote tight nucleosome compaction and result in densely compacted chromatin which restricts access by the transcription machinery and restricts gene expression. Double-stranded RNA has a role in targeting specific DNA sequences for this modification, which is associated with histone deacetylation, while cytosines in CpG sequences (or CpNpG in plants) are methylated. The so-called "histone code" will become clearer as more monoclonal antibodies are produced to identify increasing numbers of specific histone modifications.

To reflect these changes, we have reduced the coverage of techniques used for genome sequencing, and moved the topic of epigenetics to Section A, Molecular Genetics, because that seemed appropriate. Human evolution has been given its own section. The geography of human colonization of the world is becoming clearer, and the molecular differences between humans and the other great apes are just beginning to appear as the apes' genomes become available.

We are grateful to the many reviewers who commented on the previous edition and the proposed changes. We have tried to respond to their suggestions where practicable and reasonable within the scope of a text of this type. We hope that some of the reviewers may be satisfied by some of the changes.