

<<基因X>>

图书基本信息

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前言

New data are acquired daily , and new insights into well-studied processes come on a scale measured in weeks or months rather than years. Its difficult to believe that the first complete organism genome sequence was obtained less than fifteen years ago. The structure and function of genes and genomes and their associated cellular processes are sometimes elegantly and deceptively simple but frequently amazingly complex , and no single book can do justice to the realities and diversities of natural genetic systems. This book is aimed at advanced students in molecular genetics and molecular biology. In order to provide the most current understanding of the rapidly-changing subjects in molecular biology , we have enlisted twenty-one scientists to provide revisions and content updates in their individual fields of expertise. Their expert knowledge has been incorporated throughout the text. Much of the revision and reorganization of this edition follows that of the second edition of Lewiss Essential GENES , but there are many updates and features that are new to this book. Most notably , there are two new chapters : Chapter3 ("Methods in Molecular Biology and Genetic Engineering") provides an introduction to the concepts and practice of laboratory techniques in molecular biology early on in the book , and Chapter 8 ("Genome Evolution") combines , expands , and updates material that had been scattered among various chapters in previous editions , as well as introducing a number of topics new to this book. This edition is generally up dated and reorganized for a more logical flow of topics , and many chapters have been renamed to better indicate their contents. In particular , discussion of chromatin organization and nucleosome structure now precedes the discussion of eukaryotic transcription , because chromosome organization is critical to all DNA transactions in the cell , and current research in the field of transcriptional regulation is heavily biased toward the study of the role of chromatin in this process. The discussion of transcriptional activation and chromatin remodeling has accordingly been combined into one chapter (Chapter 28) . Two chapters on transposons and retroposons have been combined into one (Chapter 17) . In addition , some chapters have been revised to contain extensive new material. The original intro ductory chapter on messenger RNA has been entirely rewritten to cover more advanced topics (Chapter 22 , "mRNA Stability and Localization") , and the regula tory RNA chapter has been dramatically expanded to include material on RNAi pathways (Chapter 30 , "Regulatory RNA") . Many new figures are included in this book , some reflecting new developments in the field , particularly in the topics of chromatin structure and function , epigenetics , and regulation by noncoding and micro RNAS in eukaryotes.

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内容概要

分子生物学与分子遗传学领域正经历着日新月异的变化，每天都会出现新的数据，那些热门的研究进程，过去每隔数年才会出现新的见解和看法，现在只要几周或几个月。

在过去几十年里，对广大教学者来说，Lewin的《基因》是一本十分优秀的教材，该书对分子生物学和分子遗传学进行了精彩的论述，内容涵盖了基因的结构、序列、组织和表达。

最新版的Lewin本书，拥有一支崭新的知识渊博的作者队伍，21位科学家根据各自的专业研究特长，对书中内容进行了修订和更新，以保证本书是本领域最新颖全面的教材。

本书在内容上增加了一些新的章节，结构也进行了一些调整，使得全书各个主题在排列上更加富有逻辑性。

另外许多章节也重新命名，和内容更加相符。

新版中还包含了一些新的教学特色，便于学生在阅读本书过程中更好地学习；增加一个在线学习导航，学生可以使用它对关键内容进行自我测试。

新版特色 · 全新的第3章——分子生物学和基因工程方法，详细介绍了分子生物学实验技术的概念和实践。

· 新插入的第8章——基因组进化，对于早期版本分散在各章节中的相关材料做了整合、扩展和更新，并介绍了一些新进展。

· 第22章——mRNA的稳定性和定位，完全更新并重写，以包含更多的前沿内容。

· 第30章——调控RNA和小RNA，特别引入了RNAi通路的相关内容。

· 大量崭新的精美插图反映了相关领域的新进展，尤其是基因组结构和功能、表观遗传学，以及原核生物中非编码和小RNA的调控。

书籍目录

Contents	Preface	Part 1. GENES AND CHROMOSOMES	1	Chapter 1. Genes Are DNA	2	Chapter 2.	
	Genes Code for Proteins	26		Edited by Esther Siegfried, Pennsylvania State University, Altoona		Chapter 3.	
	Methods in Molecular Biology and Genetic Engineering	42		Edited by John Brunstein, University of British Columbia		Chapter 4. The Interrupted Gene	79
				Edited by Donald Forsdyke, Queens University		Chapter 5. The Content of the Genome	98
				Chapter 6. Genome Sequences and Gene Numbers	118	Chapter 7. Clusters and Repeats	139
				Chapter 8. Genome Evolution	159	Chapter 9. Chromosomes	189
				Edited by Hank W. Bass, Florida State University		Chapter 10. Chromatin	220
		Part 2. DNA REPLICATION AND RECOMBINATION	262				
		Chapter 11. The Replicon	263	Edited by Stephen D. Bell, Oxford University		Chapter 12. Extrachromosomal Replicons	282
				Edited by Sgren Johannes Serensen & Iars Hestbjerg Hansen, University of Copenhagen		Chapter 13. Bacterial Replication Is Connected to the Cell Cycle	299
				Edited by Barbara Funnell, University of Toronto		Chapter 14. DNA Replication	320
				Edited by Peter Burgers, Washington University Medical School		Chapter 15. Homologous and Site-Specific Recombination	348
				Edited by Hannah L. Klein & Samantha Hoot, New York University Langone Medical Center		Chapter 16. Repair Systems	391
				Chapter 17. Transposable Elements and Retroviruses	419	Edited by Damon Lisch, University of California, Berkeley	
				Chapter 18. Somatic Recombination and Hypermutation in the Immune System	458	Edited by Paolo Casali, Institute for Immunology, University of California, Irvine	
		Part 3. TRANSCRIPTION AND POSTTRANSCRIPTIONAL MECHANISMS	503			Chapter 19. Prokaryotic Transcription	504
				Edited by Richard Gourse, University of Wisconsin, Madison		Chapter 20. Eukaryotic Transcription	546
				Chapter 21. RNA Splicing and Processing	573	Edited by Xiang-Dong Fu, University of California, San Diego, School of Medicine	
				Chapter 22. mRNA Stability and Localization	618	Edited by Ellen Baker, University of Nevada, Reno	
				Chapter 23. Catalytic RNA	642	Edited by Douglas, J. Briant, University of Victoria	
				Chapter 24. Translation	665	Edited by Cheryl Keller Capone, Pennsylvania State University	
				Chapter 25. Using the Genetic Code	704	Edited by John Perona, University of California, Santa Barbara	
		Part 4. GENE REGULATION	734			Chapter 26. The Operon	735
				Edited by Liskin Swint-Kruse, University of Kansas School of Medicine		Chapter 27. Phage Strategies	767
				Chapter 28. Eukaryotic Transcription Regulation	795		
				Chapter 29. Epigenetic Effects Are Inherited	828	Edited by Trygve Tøufsbøl, University of Alabama, Birmingham	
				Chapter 30. Regulatory RNA	861	Glossary	881
				Index	905		

章节摘录

Exons act as modules for building genes that are tried out in the course of evolution in various combinations (see Section 4.9, Some Exons Can Be Equated with Protein Functional Domains) At one extreme, an individual exon from one gene may be copied and used in another gene. At the other extreme, an entire gene, including both exons and introns, may be duplicated. In such a case, mutations can accumulate in one copy without elimination by natural selection as long as the other copy is under selection to remain functional. The selectively neutral copy may then evolve to a new function, become expressed at a different time or in a different cell type from the first copy, or become a nonfunctional pseudogene. FIGURE 8.19 summarizes our present view of the rates at which these processes occur. There is a probability that a given gene will be included in a duplication in a period of one million years. After the gene has duplicated, differences evolve as the result of the occurrence of different mutations in each copy. These accumulate at a rate of $\sim 0.1\%$ per million years (see Section 8.4, A Constant Rate of Sequence Divergence Is a Molecular Clock) . If this does not happen, one of the genes is likely to become a pseudogene because it will by chance gain a deleterious mutation, and there will be no purifying selection to eliminate this copy so by genetic drift the mutant version may increase in frequency and fix in the species.

Typically this takes ~ 4 million years for globin genes; in general, the time to fixation of a neutral mutant depends on the generation time and the effective population size, with genetic drift being a stronger force in smaller populations. In such a situation, it is purely a matter of chance which of the two copies becomes inactive. (This can contribute to incompatibility between different individuals, and ultimately to speciation, if different copies become inactive in different populations.) Analysis of the human genome sequence shows that $\sim 5\%$ of the genome comprises duplications of identifiable segments ranging in length from 10 to 300 kb. These duplications have arisen relatively recently; that is, there has not been sufficient time for divergence between them for their homology to become obscured. They include a proportional share ($\sim 6\%$) of the expressed exons, which shows that the duplications are occurring more or less irrespective of genetic content.

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