

<<基因X>>

图书基本信息

书名：<<基因X>>

13位ISBN编号：9787040269611

10位ISBN编号：7040269619

出版时间：2010-1

出版时间：高等教育出版社

作者：Krebs

页数：930

版权说明：本站所提供下载的PDF图书仅提供预览和简介，请支持正版图书。

更多资源请访问：<http://www.tushu007.com>

## 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 Lewis 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.

## &lt;&lt;基因X&gt;&gt;

## 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  $\sim 4$  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.

<<基因X>>

编辑推荐

《基因X》由教育部高等教育司推荐，是国外优秀生命科学教学用书。

#### 版权说明

本站所提供下载的PDF图书仅提供预览和简介，请支持正版图书。

更多资源请访问:<http://www.tushu007.com>