<<基因X>>

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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.

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，尤其是基闪组结构和功能、表观遗传学，以及原核生物中非编码和小RNA的调控。

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书籍目录

章节摘录

Exons act as modules for building genes thaiare tried out in the course of evolution in various combinations （see Section 4.9, Some ExonCan Be Equated with Protein Functional Domains） At one extreme, an individual exon from onegene may be copied and used in another geneAt the other extreme, an entire gene, includingboth exons and introns, may be duplicated. Insuch a case, mutations can accumulate in onecopy without elimination by natural selectionas long as the other copy is under selection tcremain functional. The selectively neutral copymay then evolve to a new function, becomeexpressed at a different time or in a differenlcell type from the first copy, or become a nonfunctional pseudogene. FIGURE 8.19 summarizes our present view otthe rates at which these processes occur. Thereis a probability that a given gene will beincluded in a duplication in a period of onemillion years. After the gene has duplicated,differences evolve as the result of the occurrence of different mutations in each copy. Theseaccumulate at a rate of -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 deleteri ous mutation, and there will be no puri fying 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 mil lion 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 sequenceshows that -5% of the genome comprisesduplications of identifiable segments rangingin length from 10 to 300 kb. These duplicationshave arisen relatively recently; that is, there hasnot been sufficient time for divergence betweenthem for their homology to become obscured.They include a proportional share （-6%） of theexpressed exons, which shows that the duplications are occurring more or less irrespectiveof genetic content.

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