生命科学(组学)专业英语

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English in Life Science (Omics)

哈爾濱工業大學出版社

内容提要

为了跟踪生命科学(组学)研究的最新进展,本书系统地介绍了"组学"研究领域的最新成果并加以中文注释。本书包括专业阅读、专业学术信息、专业词汇三部分内容。第一部分为主干内容,包括基因组、转录组、功能组、代谢组、蛋白组,以及与进化相关的比较组、进化组学的经典文献和有关内容,同时选取植物、动物、微生物中模式生物的"组学"研究成果加以介绍,为读者全面了解"组学"研究的原理、方法、方向以及意义搭建平台。本书最后介绍了"组学"研究中的伦理学问题,同时提供相关的高影响因子杂志名录及网址备查。

本书可作为大专院校生物工程、生物技术及生命科学专业的本科生、研究生的教材或教学参考书,并可供从事生命科学及其相关工作的科技工作者参考。

图书在版编目(CIP)数据

生命科学(组学)专业英语/刘丕钢,栾岩主编.—哈尔滨:哈尔滨工业大学出版社,2008.4

(21世纪专业英语系列丛书)

ISBN 978-7-5603-2661-0

Ⅰ.生… Ⅱ.①刘…②栾… Ⅲ.生命科学-英语-高等学校-教材 Ⅳ.H31

中国版本图书馆CIP数据核字(2008)第021686号

责任编辑 田新华 王勇钢
封面设计 卞秉利
出版发行 哈尔滨工业大学出版社
社 址 哈尔滨市南岗区复华四道街10号 邮编150006
传 真 0451-86414749
网 址 http://hitpress.hit.edu.cn
印 刷 哈尔滨工业大学印刷厂
开 本 880mm×1230mm 1/32 印张14.25 字数420千字
版 次 2008年4月第1版 2008年4月第1次印刷
书 号 ISBN 978-7-5603-2661-0
印 数 1~3 000册
定 价 29.80元

(如因印装质量问题影响阅读,我社负责调换)

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前　言

人类基因组计划的实施将生命科学从传统的单基因研究转向了对生物整个基因组结构和功能研究的新方向，将生命科学带入了“组学”研究的后基因组时代，对生命本质的探索真正进入到全面、系统、协同的新阶段。该书的编写，目的是使读者对“组学”研究的最新进展有一个全面的认识，为了解“组学”研究的新动向、新技术、新成果搭建一个基础平台。

全书包括专业阅读、专业学术信息、专业词汇三部分内容，第一部分为主干内容，共11章。第1章重点介绍了人类基因组计划实施及成果；第2章至第7章分别介绍了后基因组时代的转录组学、功能组学、代谢组学、蛋白组学以及比较组学、进化组学研究的策略及成果；并在第8章至第10章选取植物、动物以及微生物中的模式生物“组学”研究的经典文献及最新成果加以介绍。最后，在第11章中选取了“组学”研究中涉及的伦理学问题进行探讨。全书对文献中涉及的关键语句、关键结构以及关键词汇加以中文注释，为英文文章的撰写提供参考，同时为从事生命科学的本科生、研究生、科研工作者以及对生命科学感兴趣的读者提供“组学”研究的最新资料。

感谢杨谦教授及李钰教授在该书编写过程中在内容架构方面的建议；感谢杨力明博士在文献整理工作中付出的劳动；感谢王桂

芝教授在文献翻译、校对工作中所给予的大力支持。

本书在编写中参考了大量国外作者的研究成果,在此一并表示谢意。

“组学”研究方兴未艾,本书所介绍的许多内容甚至实验结论或许已有所改变,因此希望读者以本书为平台,及时关心“组学”研究的最新技术及成果,不必拘泥于已有的结论。同时,“组学”研究的成果远远非本书所能覆及,谨以此山之石,攻他山之玉,为读者提供科研新思维。翻译中涉及很多词汇,由于是“组学”研究中的全新说法,不当之处,共同商榷。

编 者

2007 年 12 月

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Preface

The Human Genome Project (HGP) is fulfilling its promise as the single most important project in biology and the biomedical sciences-one that will permanently change biology and medicine. With the recent completion of the genome sequences of several microorganisms, including *Escherichia coli* and *Saccharomyces cerevisiae*, and the imminent completion of the sequence of the metazoan *Caenorhabditis elegans*, the door has opened wide on the era of whole genome science. The ability to analyze entire genomes is accelerating gene discovery and revolutionizing the breadth and depth of biological questions that can be addressed in model organisms. These exciting successes confirm the view that acquisition of a comprehensive, high-quality human genome sequence will have unprecedented impact and long-lasting value for basic biology, biomedical research, biotechnology, and health care. The transition to sequence-based biology will spur continued progress in understanding gene-environment interactions and in development of highly accurate DNA-based medical diagnostics and therapeutics.

Availability of the human genome sequence presents unique scientific opportunities, chief among them the study of natural genetic variation in humans. Genetic or DNA sequence variation is the fundamental raw material for evolution. Importantly, it is also the basis for variations in risk among individuals for numerous medically important, genetically complex human diseases. An understanding of the relationship between

genetic variation and disease risk promises to change significantly the future prevention and treatment of illness. The new focus on genetic variation, as well as other applications of the human genome sequence, raises additional ethical, legal, and social issues that need to be anticipated, considered, and resolved.

The HGP has made genome research a central underpinning of biomedical research. It is essential that it continue to play a lead role in catalyzing large-scale studies of the structure and function of genes, particularly in functional analysis of the genome as a whole. However, full implementation of such methods is a much broader challenge and will ultimately be the responsibility of the entire biomedical research and funding communities.

Editor

Dec, 2007

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PART ONE ACADEMIC READING
第一部分 专业阅读

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PART ONE
ACADEMIC READING

第一部分 专业阅读

1

Overview of Human Genome Project
人类基因组总述

【本章导读】 本章重点地介绍了人类基因组计划。第一节介绍人类基因组计划的产生及技术支持，以及人们对人类基因数量的猜测。第二节重点从遗传学角度探讨人类基因的数量问题，从基因组计划中判定人类基因的数量远远少于人们的预期，这与人类的复杂性不相匹配。第三节探讨人类基因组计划对社会伦理的影响，以及人类对自身的再认识。

1.1 The Human Genome Project
人类基因组计划

Many of you will have heard of the Human Genome Project (HGP)—some of you may be familiar with most of its objectives and will have followed its progress. There will be those amongst you who have questioned its usefulness, but there is no-one who will be ultimately unaffected, either personally or professionally, by the description of the human genomic DNA sequence, the ultimate reductionist biologist's and physical anthropologist's template. There is an inevitability in the realization of the HGP which may not have been apparent to the early pioneers of molecular genetics, but which followed as a simple consequence of human curiosity. When Watson and Crick published their

model for the structure of DNA, when Sanger and, separately, Maxam and Gilbert first sequenced it, when Berg created the first recombinant DNA molecule, when Boyer and Cohen generated the first recombinant organism, the logical consequence was the description of the linear sequence of the human DNA code, organized as it is into two sex chromosomes and 22 non-sex chromosomes (autosomes). Although those who fought hard to secure the vision of a co-ordinated, funded effort to map and sequence the human genome may take issue with this thought as a trivialization, it is not intended as such.① It is merely a recognition of the human tendency to classify and record, to attempt to understand where we have come from (the human genome sequence is the ultimate anthropological tool) and what we are made of. The current estimated date of completion of the human genome sequence is 2005, 52 years after the description of the structure of the double helix. Perhaps a technical innovation or increase in funding will permit the completion celebration to coincide with this important anniversary.

The genetic and physical mapping, and eventual sequencing, of three thousand million nucleotide bases of DNA has brought "Big Science" to biology and allows the discipline to hold up its head in the company of the more mature sciences such as particle physics, and bears comparison with areas of technological achievement like the Soviet and US space initiatives.② The pace with which the project has progressed has been remarkable. As with the space race, which thrived on and drove the development of computer, rocket and materials technology, the rapid progress of the HGP reflects the development of a number of key enabling technologies and resources. Several essential stages have preceded the megabase sequencing. The first of these has been the construction of an integrated genetic and physical map which has provided a framework upon which to hang the sequence and the means to connect the linear DNA code of each chromosome.③ Genetic mapping involves recording the

relationship between an extensive set of genetic markers, most recently segments of DNA, which vary in configuration between individuals. If pairs of the various forms of markers are inherited together in families more than 50% of the time, markers are said to be genetically linked. By making multiple comparisons of this type with a large set of DNA based genetic markers, it has been possible to put together a genetic linkage map of the human genome. The value of this map is the ability to carry out examinations of linkage between sets of markers and putative disease loci which segregate in families. Increasingly, as the density of markers on the map improves, the nature of developing genotyping technologies will allow throughput to be raised by several orders of magnitude. It will then be possible to carry out large-scale whole-genome association analysis which will supersede linkage studies.

The second key element has been the development of DNA host/vector systems capable of accommodating large clones of genomic DNA, most notably yeast artificial chromosomes (YACs) in 1987 and subsequently bacterial artificial chromosomes (BACs). Together with radiation hybrid cell lines, these have enabled a physical map of the human genome to be assembled by providing a resource upon which sequence tagged sites (STSs) can be placed. STSs are essentially polymerase chain reaction (PCR)-based signposts which relate long overlapping stretches of human cloned DNA. The integration of the physical map with the genetic map has been a key event which has already paid off in terms of the positional cloning of a number of disease genes. It is anticipated that such early success in uncovering the genetic basis of simple yet relatively rare Mendelian diseases will be extended to components of relatively common polygenic diseases such as insulin-dependent diabetes mellitus, rheumatoid arthritis, ankylosing spondylitis, cancers and cardiovascular diseases. This remains the single most justifiable element of the HGP in our increasingly utilitarian world.

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