

《分子生物学》

图书基本信息

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作者：特罗普

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前言

在上个世纪，1953年DNA双螺旋结构的解析和1956年中心法则的成形宣告着分子生物学时代的到来。分子生物学凭其影响力的自然渗透和许多科学家几十年的辛勤耕耘成为生命科学的基石学科。52年后的今天，定义遗传物质流动方向的中心法则仍然是分子生物学的框架，即遗传物质通过DNA复制来实现传代，通过转录合成RNA，再通过翻译从mRNA合成蛋白质。当然，现代分子生物学教材都会加入基因表达的调控和分子生物学方法的相关内容。另外，有许多分子生物学教材会以介绍生物活性大分子蛋白质和核酸的结构为开胃菜，这两类大分子是所有分子生物学事件的主要执行者。《分子生物学——从基因到蛋白质》前两版书名是《分子生物学》，分别在1983年和1987年出版，由先后在Brandeis大学和加州大学圣地亚哥分校教授生物化学和分子生物学课程的David Freifelder教授编写并修订的。《分子生物学——从基因到蛋白质》第3版是由纽约城市大学皇后学院的Burton E. Tropp教授编写的，具有以下4个主要特色：1. 基础性强。翔实全面。该书共包括六部分20章。第一到第三部分共8章是引导性基础知识：包括蛋白质的结构和功能；核酸结构、核酸技术和染色体结构；遗传分析及病毒对分子生物学的贡献和地位。第四到第六部分共12章是分子生物学的核心内容：包括DNA代谢（DNA复制，DNA损伤和修复，DNA重组和转座），RNA的合成和加工（细菌内的转录和基因表达调控，真核细胞内mRNA转录、调控和转录后加工，核糖体RNA、转运RNA和细胞器RNA的合成），以及蛋白质的合成（转运RNA和遗传密码，核糖体和翻译过程）。该书对所涉及内容的描述非常全面翔实，并具有一定的前沿性，非常适用于初学者。

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内容概要

《分子生物学:从基因到蛋白质(第3版)(影印版)》前两版书名是《分子生物学》，分别在1983年和1987年出版，由先后在Brandeis大学和加州大学圣地亚哥分校教授生物化学和分子生物学课程的DavidFreifelder教授编写并修订的。

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These nucleases, which were called restriction endonucleases because they blocked or restricted viral replication, act only on DNA with specific recognition sequences and only when the recognition sequences are not modified. Host DNA is protected because it has methyl groups attached to specific bases within the recognition sequence. Three major types of restriction modification systems have been studied (Table S.2). Type I restriction modification systems consist of five polypeptide subunits: two identical restriction endonuclease subunits (R), two identical modification subunits (M), and a specificity subunit (S). If the sequence that is recognized by the specificity subunit does not have a methyl group, then one of two things will happen. The modification subunits will methylate the sequence and the DNA will be protected, or the restriction subunits will cleave the DNA at a nonspecific site, often 1 kb or more from the recognition sequence, and the DNA will be degraded. Type II restriction modification systems are made of two independent enzymes, a homodimeric restriction endonuclease and a monomeric methyl transferase (methylase). Type II restriction modification enzymes recognize sequences that are 4 to 8 bp long. Type II methylases transfer methyl groups to bases within the recognition sequence and type II endonucleases cleave DNA within the recognition sequence. Type III restriction modification systems consist of two subunits, a modification subunit and a restriction subunit. Modification occurs within the recognition sequence but cleavage takes place about 25 bp away from this site. The discussion that follows is limited to the type II endonucleases because they are the only one of the three types that has been widely used to manipulate DNA.

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