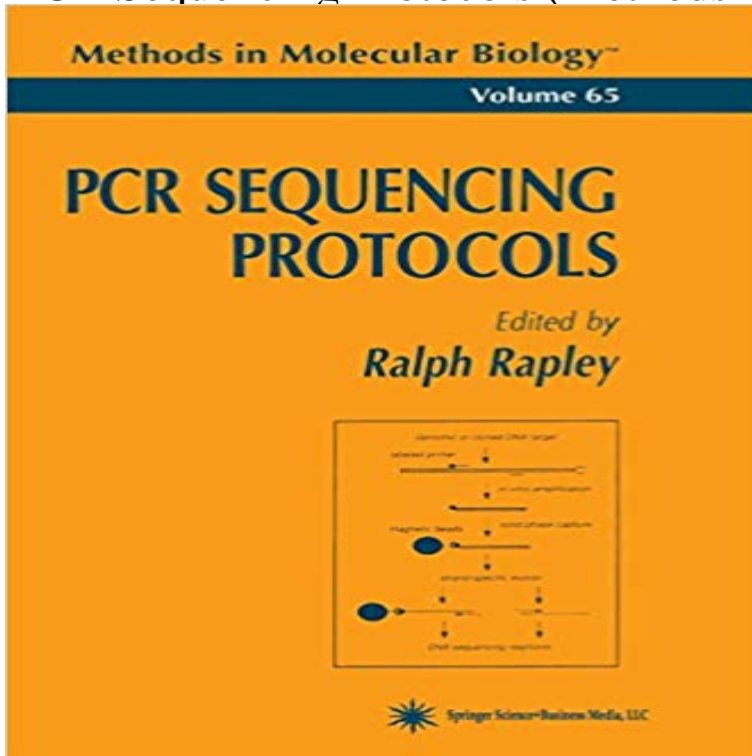


PCR Sequencing Protocols (Methods in Molecular Biology)



Advances in bioscience research usually arise as a result of the continuing refinement of existing technologies. However, there are a number of occasions where newly developed methodologies have a profound effect on nearly all areas of research. Frequently these are techniques that are elegantly simple in concept and require minimal technical manipulation. Two of these revolutionary techniques are the focus of PCR Sequencing Protocols. The first such technique is enzymatic chain termination sequencing developed by Sanger and his co-workers in Cambridge and reported in 1977. This essentially brought the possibility of deriving nucleotide sequence information in a very short time scale and has been widely accepted in many laboratories as a routine molecular biological research tool. Furthermore, it has not only led to the sequencing of many genes and gene fragments, but has also allowed the technical means of sequencing the human genome. The second technique that has found widespread acceptance in basic applied research and many routine applications is the polymerase chain reaction. This technique, first reported in 1985 by Mullis and his colleagues, provides the means to amplify nucleic acid sequence, which immediately proved invaluable in nearly all fields of biological laboratory research. Here, as with enzymatic DNA sequencing, is a very simple concept that relies on minimal information to prepare short oligonucleotide primers that direct the synthesis of a specified fragment of DNA in the presence of a thermostable DNA polymerase.

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