



Nucleic Acids Hybridization

Anton Buzdin, Sergey Lukyanov

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Watson–Crick hybridization of complementary sequences in nucleic acids is one of the most important processes necessary for molecular recognition *in vivo*, as well as nucleic acid identification and isolation. This book is devoted to a large family of *in vitro* DNA hybridization-based experimental techniques. A wide spectrum of experimental tasks covered by these approaches includes finding differential sequences in both genomic DNAs and mRNAs, genome walking, multiplex PCR, cDNA library construction starting from minute amount of total RNA, rapid amplification of cDNA 5' and 3' ends, effective smoothing of the concentrations of rare and abundant transcripts in cDNA libraries, recovery of promoter active repeats and differentially methylated genomic DNA, identification of common sequences in genomic or cDNA sources, new gene mapping, finding evolutionary conserved DNA and both single-nucleotide and extended mutation discovery or large-scale monitoring. Several approaches, such as microarray hybridization, have become extremely popular tools for specialists in biochemistry and in biomedicine, whereas the potential of many other advantageous techniques seems to be underestimated now. The international team of the authors of this book has tried both to elucidate the current state-of-art in hybridization techniques and to help the readers in choosing an appropriate method for performing an experiment in the most efficient way. Enclosed experimental protocols along with both comprehensive and detailed method descriptions make this truly universal book useful to all those interested in the modern life science methodologies.

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