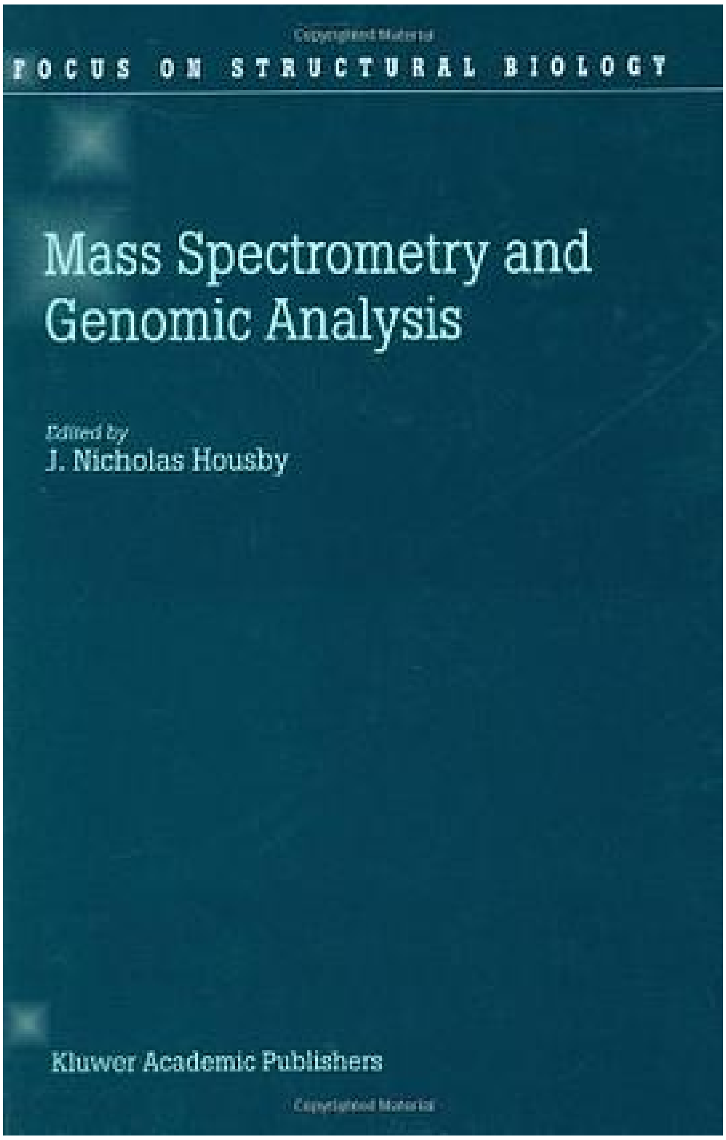
Mass Spectrometry and Genomic Analysis



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出版者:Kluwer Academic Pub

出版时间:2001-10

装帧:HRD

isbn:9780792371731

The human genome project is set to revolutionise health care and medicine in the near future. The genetic make up of each individual gives clues as to the genetic factors that predispose one to a particular genetic disease. Single Nucleotide Polymorphisms (SNPs), single base changes in the nucleotide DNA sequence of individuals, are thought to be the main cause of genetic variation. By comparing patterns of SNP allele frequencies between disease affected and control populations, disease associated SNPs can be identified and potential disease gene(s) located. These types of study necessitate genotyping of thousands of SNPs which requires the use of powerful, high throughput, systems of analysis. Mass spectrometry is fast becoming the preferred technology for this type of high throughput analysis. This book contains a collection of descriptions of some of the most outstanding advances in the field of mass spectrometry from which, I hope, the reader will be able to learn both the principles and the most up to date methods for its use in genomic analysis. It covers the general principles of the technologies and more in depth detailed descriptions for more academic reading and information. Audience: Whether you are a student, a post-doctoral researcher or experienced MS user, this book will be a stimulating addition to the analytical arena of mass spectrometry and genomic analysis.

作者介绍:

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标签

评论

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