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Autore	Dardel Frederic
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Nota di contenuto	Cover; Contents; Preface to the French edition; Preface to the English edition; 1: Genome sequencing; 1.1 Automatic sequencing; 1.2 Sequencing strategies; 1.3 Fragmentation strategies; 1.4 Sequence assembly; 1.5 Filling gaps; 1.6 Obstacles to reconstruction; 1.7 Utilizing a complementary 'large'1 clone library; 1.8 The first large-scale sequencing project: The Haemophilus influenzae genome; 1.9 cDNA and EST; 2: Sequence comparisons; 2.1 Introduction: Comparison as a sequence prediction method; 2.2 A sample molecule: the human androsterone receptor
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| Sommario/riassunto | This book is an excellent introductory text describing the use of bioinformatics to analyze genomic and post-genomic data. It has been translated from the original popular French edition, which was based on a course taught at the well-respected Ecole Polytechnique in Palaiseau. This edition has been fully revised and updated by the authors. After a brief introduction to gene structure and sequence determination, it describes the techniques used to identify genes, their protein-coding sequences and regulatory regions. The book discusses the methodology of comparative genomics, using informati |