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Nota di contenuto	HANDBOOK OF COMPARATIVE GENOMICS Principles and Methodology; CONTENTS; PREFACE; I GENOME FEATURES; 1 PROKARYOTES; 1.1 Introduction; 1.2 Morphology and Classification; 1.3 Genome Shape and Size; 1.4 Gene Content and Organization; 1.5 Base Composition; 1.6 Codon Use; 1.7 Replication and Expression; 2 EUKARYOTES; 2.1 Introduction; 2.2 Classification and Time Scale; 2.3 Genome Shape and Size; 2.4 Base Composition; 2.5 Replication, Repair, and Recombination; 2.6 Gene Expression; 2.6.1 Transcription and Posttranscriptional Regulation; 2.6.2 Genetic Code and Codon Use 2.6.3 Translation and Posttranslation Modifications2.7 Completely Sequenced Eukaryotic Genomes; 2.7.1 Saccharomyces cerevisiae Genome; 2.7.2 Schizosaccharomyces pombe Genome; 2.7.3 Caenorhabditis elegans Genome; 2.7.4 Drosophila melanogaster Genome; 2.7.5 Arabidopsis thaliana Genome; 2.7.6 Oryza sativa

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6.4.6 Statistical Significance of Alignment Scores

Sommario/riassunto

This comprehensive reference covers the comparative methodology involved in studying molecular evolution. Providing a practical introduction to the role of bioinformatics in comparative genomics, this publication further discusses the basic technology used in genome sequencing projects and provides an overview of genome storage databases currently in use. This timely and cutting-edge text also: Reviews the basic principles of genomics and gene expression analysis Discusses analytic methods in proteomics and transcriptomics Includes a comprehensive list of Web resource