

1. Record Nr.	UNISA996466144303316
Titolo	Comparative Genomics [[electronic resource]] : RECOMB 2006 International Workshop, RECOMB-CG 2006, Montreal, Canada, September 24-26, 2006, Proceedings // edited by Guillaume Bourque, Nadja El' Mabrouk
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2006
ISBN	3-540-44530-7
Edizione	[1st ed. 2006.]
Descrizione fisica	1 online resource (X, 231 p.)
Collana	Lecture Notes in Bioinformatics ; ; 4205
Disciplina	572
Soggetti	Biochemistry Algorithms Computer science—Mathematics Data structures (Computer science) Database management Bioinformatics Biochemistry, general Algorithm Analysis and Problem Complexity Discrete Mathematics in Computer Science Data Structures Database Management
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Reconstructing Domain Compositions of Ancestral Multi-domain Proteins -- Domain Architecture in Homolog Identification -- Inferring Positional Homologs with Common Intervals of Sequences -- On Genome Evolution with Accumulated Change and Innovation -- Paths and Cycles in Breakpoint Graphs of Random Multichromosomal Genomes -- Common Intervals and Symmetric Difference in a Model-Free Phylogenomics, with an Application to Streptophyte Evolution -- How Pseudo-boolean Programming Can Help Genome Rearrangement Distance Computation -- Sorting by Translocations Via Reversals Theory -- Inferring Gene Orders from Gene Maps Using the Breakpoint

Distance -- Ordering Partially Assembled Genomes Using Gene Arrangements -- Evolution of Tandemly Repeated Sequences Through Duplication and Inversion -- A PQ Framework for Reconstructions of Common Ancestors and Phylogeny -- Intron Loss Dynamics in Mammals -- Finding Maximum Likelihood Indel Scenarios -- Conservation Patterns in *cis*-Elements Reveal Compensatory Mutations -- Transcription Factor Centric Discovery of Regulatory Elements in Mammalian Genomes Using Alignment-Independent Conservation Maps -- Identifiability Issues in Phylogeny-Based Detection of Horizontal Gene Transfer.
