1. Record Nr. UNISA996465499603316

Titolo	Research in Computational Molecular Biology [[electronic resource]] : 12th Annual International Conference, RECOMB 2008, Singapore, March 30 - April 2, 2008, Proceedings / / edited by Martin Vingron, Limsoon Wong
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2008
ISBN	3-540-78839-5
Edizione	[1st ed. 2008.]
Descrizione fisica	1 online resource (XVI, 480 p.)
Collana	Lecture Notes in Bioinformatics ; ; 4955
Disciplina	572.80285
Soggetti	Algorithms Data structures (Computer science) Computer science—Mathematics Database management Artificial intelligence Bioinformatics Algorithm Analysis and Problem Complexity Data Structures Discrete Mathematics in Computer Science Database Management Artificial Intelligence Computational Biology/Bioinformatics
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	Computational Biology: Its Challenges Past, Present, and Future -- Bootstrapping the Interactome: Unsupervised Identification of Protein Complexes in Yeast -- CompostBin: A DNA Composition-Based Algorithm for Binning Environmental Shotgun Reads -- Reconstructing the Evolutionary History of Complex Human Gene Clusters -- Ab Initio Whole Genome Shotgun Assembly with Mated Short Reads -- Orchestration of DNA Methylation -- BayCis: A Bayesian Hierarchical HMM for Cis-Regulatory Module Decoding in Metazoan Genomes -- A

Combined Expression-Interaction Model for Inferring the Temporal Activity of Transcription Factors -- A Fast, Alignment-Free, Conservation-Based Method for Transcription Factor Binding Site Discovery -- The Statistical Power of Phylogenetic Motif Models -- Transcriptional Regulation and Cancer Genomics -- Automatic Recognition of Cells (ARC) for 3D Images of C. elegans -- Spectrum Fusion: Using Multiple Mass Spectra for De Novo Peptide Sequencing -- A Fragmentation Event Model for Peptide Identification by Mass Spectrometry -- A Bayesian Approach to Protein Inference Problem in Shotgun Proteomics -- De Novo Sequencing of Nonribosomal Peptides -- Systems Metabolic Engineering -- Protein Function Prediction Based on Patterns in Biological Networks -- Automatic Parameter Learning for Multiple Network Alignment -- An Integrative Network Approach to Map the Transcriptome to the Phenome -- Fast and Accurate Alignment of Multiple Protein Networks -- High-Resolution Modeling of Cellular Signaling Networks -- At the Origin of Life: How Did Folded Proteins Evolve? -- Locating Multiple Gene Duplications through Reconciled Trees -- Rapid and Accurate Protein Side Chain Prediction with Local Backbone Information -- Algorithms for Joint Optimization of Stability and Diversity in Planning Combinatorial Libraries of Chimeric Proteins -- DLIGHT – Lateral Gene Transfer Detection Using Pairwise Evolutionary Distances in a Statistical Framework -- Computation of Median Gene Clusters -- BCL-2: From Translocation to Therapy -- Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles -- Constructing Treatment Portfolios Using Affinity Propagation -- Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs -- More Efficient Algorithms for Closest String and Substring Problems -- Disruption of a Transcriptional Regulatory Pathway Contributes to Phenotypes in Carriers of Ataxia Telangiectasia -- Accounting for Non-genetic Factors Improves the Power of eQTL Studies -- Effects of Genetic Divergence in Identifying Ancestral Origin Using HAPAA -- On the Inference of Ancestries in Admixed Populations -- Increasing Power in Association Studies by Using Linkage Disequilibrium Structure and Molecular Function as Prior Information -- Panel Construction for Mapping in Admixed Populations Via Expected Mutual Information -- Constructing Level-2 Phylogenetic Networks from Triplets -- Accurate Computation of Likelihoods in the Coalescent with Recombination Via Parsimony.