

1. Record Nr.	UNISA996465763703316
Titolo	Advances in bioinformatics and computational biology : second Brazilian Symposium on Bioinformatics, BSB 2007, Angra dos Reis, Brazil, August 29-31, 2007 proceedings // Marie-France Sagot; Maria Emilia M. T. Walter
Pubbl/distr/stampa	Berlin, Germany ; ; New York, New York : , : Springer, , [2007] 2007
ISBN	3-540-73731-6
Edizione	[1st ed. 2007.]
Descrizione fisica	1 online resource (185 p.)
Collana	Lecture Notes in Bioinformatics ; ; 4643
Disciplina	005.74
Soggetti	Computational biology Bioinformatics
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Selected Articles -- Automating Molecular Docking with Explicit Receptor Flexibility Using Scientific Workflows -- Gene Set Enrichment Analysis Using Non-parametric Scores -- Comparison of Simple Encoding Schemes in GA's for the Motif Finding Problem: Preliminary Results -- Multi-Objective Clustering Ensemble with Prior Knowledge -- Biological Sequence Comparison Application in Heterogeneous Environments with Dynamic Programming Algorithms -- New EST Trimming Procedure Applied to SUCEST Sequences -- A Method for Inferring Biological Functions Using Homologous Genes Among Three Genomes -- Validating Gene Clusterings by Selecting Informative Gene Ontology Terms with Mutual Information -- An Optimized Distance Function for Comparison of Protein Binding Sites -- Comparing RNA Structures: Towards an Intermediate Model Between the Edit and the Lapcs Problems -- Evolving Phylogenetic Trees: A Multiobjective Approach -- Comparing Several Approaches for Hierarchical Classification of Proteins with Decision Trees -- High Efficiency on Prediction of Translation Initiation Site (TIS) of RefSeq Sequences -- Extended Abstracts -- Outlining a Strategy for Screening Non-coding RNAs on a Transcriptome Through Support Vector Machines -- Mapping Contigs onto Reference Genomes -- Molecular Dynamics

Simulations of Cruzipains 1 and 2 at Different Temperatures -- Genetic Algorithm for Finding Multiple Low Energy Conformations of Poly Alanine Sequences Under an Atomistic Protein Model -- Cellular Fingerprints: A Novel Concept for the Integration of Experimental Data and Compound-Target-Pathway Relations (Extended Abstract) -- Identification of the Putative Class 3 R Genes in *Coffea arabica* from CafEST Database.
