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Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 3695
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Soggetti	Life sciences Information storage and retrieval systems Medical informatics Database management Application software Proteins Life Sciences Information Storage and Retrieval Health Informatics Database Management Computer and Information Systems Applications Protein Biochemistry
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Nota di contenuto	Systems Biology -- Structural Protein Interactions Predict Kinase-Inhibitor Interactions in Upregulated Pancreas Tumour Genes Expression Data -- Biochemical Pathway Analysis via Signature Mining -- Recurrent Neuro-fuzzy Network Models for Reverse Engineering Gene Regulatory Interactions -- Data Analysis and Integration -- Some Applications of Dummy Point Scatterers for Phasing in Macromolecular X-Ray Crystallography -- BioRegistry: A Structured Metadata Repository for Bioinformatic Databases -- Robust Perron Cluster Analysis for

Various Applications in Computational Life Science -- Structural Biology -- Multiple Alignment of Protein Structures in Three Dimensions -- Protein Annotation by Secondary Structure Based Alignments (PASSTA) -- MAPPIS: Multiple 3D Alignment of Protein-Protein Interfaces -- Genomics -- Frequent Itemsets for Genomic Profiling -- Gene Selection Through Sensitivity Analysis of Support Vector Machines -- The Breakpoint Graph in Ciliates -- Computational Proteomics -- ProSpect: An R Package for Analyzing SELDI Measurements Identifying Protein Biomarkers -- Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples -- Detection of Protein Assemblies in Crystals -- Molecular Informatics -- Molecular Similarity Searching Using COSMO Screening Charges (COSMO/3PP) -- Increasing Diversity in In-silico Screening with Target Flexibility -- Multiple Semi-flexible 3D Superposition of Drug-Sized Molecules -- Molecular Structure Determination and Simulation -- Efficiency Considerations in Solving Smoluchowski Equations for Rough Potentials -- Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization -- Visual Analysis of Molecular Conformations by Means of a Dynamic Density Mixture Model -- Distributed Data Mining -- Distributed BLAST in a Grid Computing Context -- Parallel Tuning of Support Vector Machine Learning Parameters for Large and Unbalanced Data Sets -- The Architecture of a Proteomic Network in the Yeast.
