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Altri autori (Persone)	BertholdM (Michael)
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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.

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