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Nota di contenuto	Full Papers -- Evolution of the Long Non-coding RNAs MALAT1 and MEN?? -- Granger Causality in Systems Biology: Modeling Gene Networks in Time Series Microarray Data Using Vector Autoregressive Models -- Semi-supervised Approach for Finding Cancer Sub-classes on Gene Expression Data -- Bounds on the Transposition Distance for Lonely Permutations -- Insights on Haplotype Inference on Large Genotype Datasets -- Extended Abstracts -- An SVM Model Based on

Physicochemical Properties to Predict Antimicrobial Activity from Protein Sequences with Cysteine Knot Motifs -- Enabling Annotation Provenance in Bioinformatics Workflow Applications -- BAT: A New Biclustering Analysis Toolbox -- Detection of Protein Domains in Eukaryotic Genome Sequences -- Discretization of Flexible-Receptor Docking Data.
