

BIRD 2008 - Accepted Papers

1. #8: A discriminative method for protein remote homology detection based on N-nary profiles
Authors : (Bin Liu, Lei Lin, Xiaolong Wang, Qiwen Dong, Xuan Wang,)
2. #10: A Novel Adaptive Multiple Imputation Algorithm
Authors : (Veselka Boeva, Elena Tsiporkova,)
3. #22: Motif Location Prediction by Divide and Conquer
Authors : (Reda Alhadj,)
4. #25: Families of FPGA-Based Accelerators for BLAST Algorithm with Multi-seeds Detection and Parallel Extension
Authors : (Fei Xia, Yong Dou,)
5. #29: GENOME STRUCTURE AND CHARACTERIZATION OF AN ENDOGENOUS RETROVIRUS FROM THE ZEBRAFISH GENOME PROJECT DATABASE.
Authors : (Roziyah kambol, M. Faris Abtholuddin,)
6. #32: Use Artificial Neural Network to Align Biological Ontologies
Authors : (Jingshan Huang, Jiangbo Dang, Michael Huhns, Jim Zheng,)
7. #35: Clustering in a Fixed Manifold to Detect Groups of Genes with Similar Expression Patterns
Authors : (Phuong Nguyen, Tuan Hoang,)
8. #38: Multi-functional Protein Clustering in PPI Networks
Authors : (Clara Pizzuti, Simona Rombo,)
9. #39: A Tree Index to Support Clustering Based Exploratory Data Analysis
Authors : (Christian Martin, Tim W. Nattkemper,)
10. #42: Fast Structured Motif Search in DNA Sequences
Authors : (Mihail Halachev, Nematollaah Shiri,)
11. #43: Identifying Subcellular Locations from Images of Unknown Resolution
Authors : (Luis Pedro Coelho, Robert Murphy,)
12. #45: Finding Frequent Subgraphs in Biological Networks via Maximal Item Sets
Authors : (Hans Zantema, Stefan Wagemans, Dragan Bosnacki,)
13. #52: Matching Spatial Regions with Combinations of Interacting Gene Expression Patterns
Authors : (Jano van Hemert, Richard Baldock,)
14. #54: Bayesian phylogeny on Grid
Authors : (Richard van der Wath, Elizabeth van der Wath, Antonio Carapelli, Francesco Nardi, Francesco Frati, Pietro Lio,)
15. #55: Combining Molecular and Physiological Data of Complex Disorders
Authors : (Emanuel Schwarz, F.Markus Leweke, Sabine Bahn, Pietro Lio,)

16. #56: Combining PPI network and sequence attributes for predicting hypertension related proteins
Authors : (Richard JB Dobson, Patricia B Munroe, Charles A Mein, Mark J Caulfield, Mansoor AS Saqi,)
17. #58: A robust class of stable proteins in the 2D HPC model
Authors : (Alireza Hadj Khodabakhshi, Jan Manuch, Arash Rafiey, Arvind Gupta,)
18. #60: EXPLORATION OF EVOLUTIONARY RELATIONS BETWEEN PROTEIN STRUCTURES
Authors : (Natalja Kurbatova, Juris Viksna,)
19. #62: E-BioFlow: Different Perspectives on Scientific Workflows
Authors : (Ingo Wassink, Paul van der Vet, Han Rauwerda, Anton Nijholt, Timo Breit,)
20. #69: Protein-protein interaction network querying by a "focus and zoom" approach.
Authors : (Valeria Fionda, Luigi Palopoli, Simona Panni, Simona E. Rombo,)
21. #71: Nested q-Partial Graphs for Genetic Network Inference from "Small n, Large p" Microarray Data
Authors : (Kevin Kontos, Gianluca Bontempi,)
22. #73: A computational method for reconstructing gapless metabolic networks
Authors : (Esa Pitkänen, Ari Rantanen, Juho Rousu, Esko Ukkonen,)
23. #74: A Symmetry-free Subspace for Ab initio Protein Folding Simulations
Authors : (Xiangchao Gan, Kathleen Steinhofel, Leonidas Kapsokalivas,)
24. #76: Topological metrics in Blast data mining: plasmid and nitrogen-fixing proteins case studies
Authors : (Pietro Liò, Matteo Brilli, Renato Fani,)
25. #77: Translational Control by RNA-RNA Interaction
Authors : (Ulrike Mueckstein, Hakim Tafer, Stephan Bernhart, Joerg Vogel, Peter F. Stadler, Ivo Hofacker, Maribel Hernandez-Rosales,)
26. #78: Two local Search Methods for Protein Folding Simulation in the HP and MJ Lattice Models
Authors : (Leonidas Kapsokalivas, Xiangchao Gan, Andreas Albrecht, Kathleen Steinhofel,)
27. #79: Searching for Supermaximal Repeats in Large DNA Sequences
Authors : (Chen Na Lian, Mihail Halachev, Nematollaah Shiri,)
28. #80: Gene Expression Mining for Cohesive Pattern Discovery
Authors : (Ramkishore Bhattacharyya, Balaram Bhattacharyya,)
29. #81: XMAS: An Experiential Approach for Visualization, Analysis, and Exploration of Time Series Microarray Data
Authors : (Ben Dalziel, Hui Yang, Rahul Singh, Matthew Gormley, Susan J. Fisher,)

30. #82: Comparative Analysis of Disulfide Bond Determination Using Computational-Predictive Methods and Mass Spectrometry-based Algorithm

Authors : (Timothy Lee, Rahul Singh,)

31. #84: Knowledge Acquisition Focused Cooperative Development of Bio-Ontologies - A Case Study with BIO2Me

Authors : (Dominic Mainz, Ingo Paulsen, Indra Mainz, Katrin Weller, Arndt von Haeseler,)