

BIRD 2008 Accepted Posters:

1. Precise and Statistically Sound Protein Quantification in Mass Spectrometry Based Proteomics Using iTRAQ

Authors : (Andreas M. Boehm, Daniela Altenhöfer, Stephanie Pütz,)

2. Cognitive Inference in Structure Modelling and Interpretation of Medical Images

Authors : (Lidia Ogiela, Ryszard Tadeusiewicz, Marek Ogiela,)

3. Identification of Structural Stability of Mutated Hepatitis B Virus Capsid Proteins by Nanoenvironmental Energetics Measurements

Authors : (Harish Chandra Soundararajan, Muthukumaran Sivanandam,)

4. Software Development of a Web-based Computing Tool for Improving Estimation of In Vitro HIV-1 Virus Fitness

Authors : (Jingming Ma, Carrie Dykes, Yangxin Huang, Lisa Demeter, Hulin Wu,)

5. MOLECULAR EVOLUTION OF LASSA VIRUS GLYCOPROTEIN

Authors : (Lawrence Okoror, Hillary Alaiya, Paul Aliga, Keneth Imarenezor,)

6. Context Analysis of Differential Gene Expression Data

Authors : (Paul Perco, Andreas Bernthaler, Irmgard Mühlberger, Martin Haiduk, Raul Fecete, Claus Stadler, Rainer Oberbauer, Arno Lukas, Bernd Mayer,)

7. AN AGE-STRUCTURED STOCHASTIC MODEL OF INTRAPATIENT HIV EVOLUTION

Authors : (Elena Giorgi, Bette Korber, Brandon Keele, George Shaw, Alan Perelson, Tanmoy Bhattacharya,)

8. Single nucleotide polymorphism in exon 17 of the insulin receptor gene is associated with polycystic ovary syndrome in Saudi fem

Authors : (Mazin Daghestani, Maha Daghestani, Ahmed Al-Himaidi, Pinar Ozand, Ali Al-Odaib, Nadia El-Eisa,)

9. Discriminating protein hetro -oligomeric state from amino acid sequences

Authors : (Suresh Kumar, Oliviero Carugo,)

10. Association of polymorphisms in the Beta2-adrenergic receptor gene with obesity, hypertriglyceridemia and hyperleptinemia in Sau

Authors : (Maha Daghestani, Gamal Eldin Mohamed ,)

11. Three dimensional structural model for human TCR-collagenII-MHC complex: protein-protein docking and molecular dynamics study

Authors : (Maria Cristina De Rosa, Francesco Ria, Davide Pirolli, Bruno Giardina, Gianfranco Ferraccioli, Cristiana Carelli Alinovi,)

12. Effect of mutations in p53 “extreme” C-terminal domain on the interactions with S100B($\beta\beta$) and CBP: a molecular dynamics simulati

Authors : (Cristiana Carelli Alinovi, Davide Pirolli, Bruno Giardina, Ettore Capoluongo, Maria Cristina De Rosa,)

13. Normalisation of 2D DIGE Data – On the way to a Standard Operating Procedure

Authors : (Daniela Albrecht, Olaf Kniemeyer, Reinhard Guthke, Axel Brakhage,)

14. Two-dimensional modularization of gene expression regulation using sequential pattern mining

Authors : (Mingoo Kim, Hyungjung Shin, Tae Su Chung, Ju Han Kim,)

15. EST2uni: an open tool for parallel, automated EST analysis and database creation, with a powerful data mining tool

Authors : (Javier Forment, Francisco Gilabert, Antonio Robles, Vicente Conejero, Fernando Nuez, Jose Blanca,)

16. CO-EXPRESSION ANALYSIS OF GENES INVOLVED IN THE RESPIRATORY CHAIN IN MICROARRAYS STUDIES

Authors : (Susanna Márquez, Tatiana Sukhomlin, Vitali Selivanov, Marta Cascante, Josep Roca, Susana G. Kalko,)

17. INTEGRATION OF TRANSCRIPTOMICS DATA IN SYSTEMS BIOLOGY MODELING IN THE BIOBRIDGE PORTAL

Authors : (Àlex Gómez, Susanna Márquez, Miguel Hernández, Jordi Villà-Freixa, Susana G. Kalko,)

18. Proline-induced distortions of alpha-helices

Authors : (Julien Rey, Julie Devillé, Marie Chabbert,)

19. The role of duplication in the origin of biological networks and topological features of nodes in the yeast protein-protein inte

Authors : (Mohammad Sharif Tabe Bordbar, Leila Pirhaji, Mehdi Kargar,)

20. Pearson's Chi-square Test: A Method for Finding Gene Signals Correspond to Conditional Cell Responses

Authors : (Leila Pirhaji , Mehdi Kargar , Hadi Poormohammadi, Mohammad Sharif Tabe Bordbar,)

21. Improved control of fuzzy C-means clustering of high-dimensional data based on the optimization of the fuzziness parameter

Authors : (Ulrich Möller,)

22. Sequence analysis and potential action of eukaryotic type protein kinase from *Streptomyces coelicolor* A3(2)

Authors : (Daisy Roy, Sathees Chandra,)

23. Similarities and Differences; A Statistic for Evaluating Clinical Hypotheses on High-Throughput RNA Expression Data

Authors : (Thomas Hardcastle,)

24. Phylogenetic Quality Assessment for Campus Grids

Authors : (Hannes Schabauer, Joachim Zottl, Arndt von Haeseler, Wilfried Gansterer, Heiko A. Schmidt,)

25. Towards more reliable analysis of cytosine methylation sites for plant and animal bisulfite sequence data with CyMATEads

Authors : (Christoph Müllner, Jennifer Hetzl,)

26. Methods for robust class discovery in gene expression profiles of tissue samples
Authors : (Ulrich Möller,)
27. Exact Methods and Metaheuristic Approaches for Deriving High Quality Fully Resolved Consensus Trees
Authors : (Sandro Pirkwieser, Günther Raidl, Rubén Ruiz-Torrubiano,)
28. New method for inferring ancient migration rates, using genetics variation, applied to prehistoric human migration.
Authors : (Yosef E. Maruvka, John Wakeley, Yaneer Bar-Yam, Nadav N. Shnerb,)
29. Protein Functional Annotation with the Conserved Domain Database (CDD)
Authors : (Gabriele Marchler, Aron Marchler-Bauer, John Anderson, Myra Derbyshire, Carol DeWeese-Scott, Steve Bryant,)
30. Modeling Protein Domain Evolution with CDTree/Cn3D
Authors : (Aron Marchler-Bauer, David Hurwitz, Christopher Lanczycki, Chunlei Liu, Paul Thiessen, Stephen Bryant,)
31. Molecular Dynamics simulation of membrane bound state of bacteriocin AS-48
Authors : (Victor Cruz, Javier Ramos, Maria Jose Sanchez-Barrena, Armando Albert, Javier Martinez-Salazar,)
32. The Virtual R Workbench, towards an open platform for R based e-Science
Authors : (karim chine,)
33. GABOS/GAFEP - A Sequence retrieval and primer Management System
Authors : (Keith Satterley,)