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ISMB 2002 SGI Awards

- President's Letter ISCB is pleased to announce the winners of this year's ISMB Best Paper and Best Poster Awards by SGI.
- ISMB 2002 Overview Pier Luigi Martelli took home best paper honors for "A sequence profile based HMM for predicting and discriminating beta barrel membrane proteins." Co-authors included: Piero Fariselli, Anders Krogh, and Rita Casadio.
- Overton Prize Prior to ISMB, Martelli was selected as one of three finalists in the best paper category. It was determined-by a subset of the senior review committee-that Martelli should receive the award for best paper based on his written paper and oral presentation at ISMB.
- New Board Members
- 2003 ISCB Membership Registration Now Open Ten posters-from a pool of over 500-were selected to receive Best Poster honors. ISMB delegates selected the best poster winners. The winners selected were:
- ISCB Members' Meeting
- Application Deadline to Host ISMB 2004 or 2005
- ISMB Goes Down Under
- SGI Awards Best Paper and Best Poster Awards at ISMB 2002
- CAPRI and ECCB Travel Fellowship Recipients
- Bourne Receives Sun Convergence Lifetime Achievement Award
- McKay: Executive Officer
- Events and Opportunities
- *Using Structure and Sequence Information for Predicting Transcription Factor Binding Sites.* Tommy Kaplan, Nir Friedman and Hanah Margalit. The Hebrew University, Jerusalem.
 - *Automatic Classification of Protein Structures Using Gauss Integrals.* Peter Røgen and Boris Fain. Department of Mathematics, Technical University of Denmark, Denmark and Department of Structural Biology, Stanford University.
 - *Mauve: Multiple Genome Alignments.* Aaron Darling, Bob Mau, Frederick R. Blattner and Nicole T. Perna. Departments of Computer Science, Animal Health, Biomedical Sciences, Oncology and Genetics, University of Wisconsin-Madison. The first two authors contributed equally to this work.
 - *Finding Biological Themes in z-derived Gene Lists with EASE: the Expression Analysis Systematic Explorer.* Douglas A. Hosack and Richard A. Lempicki. Laboratory of Immunopathogenesis and Bioinformatics, SAIC Frederick.
 - *From RegulonDB to a Multigenomic Microbial Database of Operon Organization and Gene Regulation.* Salgado H, Sanchez-Solano F, Diaz-Peredo E, Gama-Castro S, Garcia-Alonso D, Perez-Rueda E, Jimenez-Jacinto V, Medrano-Soto A, Moreno-Hagelsieb G and Collado-Vides J. Nitrogen Fixation Research Center, Av. Universidad, Cuernavaca, Morelos.
 - *Modeling Genetic Regulatory Networks Using Dynamic Bayesian Networks.* Y. Zeng, R. Khan, J. Garcia-Frias and G. Gao. Department of Electrical and Computer Engineering, University of

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Delaware.

- *Expert-system based annotation strategies using GenDB, an open source genome annotation system.* Alice McHardy, Jan Kleinluetzum and Folker Meyer. Center for Genome Research, Bielefeld University
- *G-language Genome Analysis Environment.* Kazuharu Arakawa, Koya Mori, and Masaru Tomita. Institute for Advanced Biosciences, Keio University, Department of Environmental Information and Graduate School of Media and Governance.
- *A High Throughput Pipeline for Validating Novel Splice Variants Discovered Using Whole-Genome Junction Arrays.* Patrick Loerch, Chris Armour, Phil-Garrett-Engel, Ralph Santos, Zhengyan Kan, Jason Johnson and Daniel Shoemaker. Rosetta Inpharmatics.
- *Atomic Reconstruction of Metabolism.* Masanori Arita. Computational Biology Research Center, Koto-ku Aomi, Tokyo.

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