

Support of ISMB Conference 2002 to be held in Edmonton

ROST, Burkhard Principal Investigator, from 7/01/02 through 6/30/03

The Intelligent Systems for Molecular Biology (ISMB) conference is the oldest and largest conference that specifically addresses bioinformatics and computational biology, i.e. interdisciplinary research that falls between computer science and biology. ISMB is distinguished from many other conferences in computational biology or artificial intelligence by an insistence that the researchers work with real molecular biology data, not theoretical examples; and from many other biological conferences by providing a forum for technical advances as they occur, which otherwise may be shunned until a firm experimental result is published. The resulting intellectual richness and cross-disciplinary diversity provides an important opportunity for both students and senior researchers. ISMB has become the premier conference series in this field with refereed, published proceedings, establishing an infrastructure to promote the growing body of research.

ISMB comprises five main types of presentations: tutorials, plenary presentations, poster presentations, topically focused satellite meetings and software demonstrations. These tutorials and fellows contribute to the development of human resources by allowing students and post-doctoral fellows to reach a state-of-the-art level rapidly, and to begin making contributions to the field. At ISMB 2002, 15 tutorials were held, 50 papers were presented, 498 posters were presented, 6 special interest group meetings were held, and 20 software demonstrations (both non-for-profit and corporate) were presented.

Of all the travel fellowships awarded for ISMB02 (funded by the NSF, NIH, and DOE); fellowships awarded to 40 women (39%) and 63 men (61%). In addition, 17 (16.5%) went to postdocs, 2 (1.9%) to early-stage scientists, 76 (73.8%) to graduate students, and 8 (7.8%) provided no answer as to their status.

The DOE funds provided for ISMB2002 funded travel for 24 individuals, listed below.

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### **DOE Grant for Travel - ISMB 2002, Edmonton, Canada**

**24 Fellowships awarded, general admin per person 1500.00**

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NAME	TITLE OF PAPER OR POSTER PRESENTED
Pierre-Francois Baisnée	89A. ICBS: A Database of Protein-protein Interactions Mediated by Interchain Beta-sheet Formation.
Henry Bigelow	226B. Transmembrane Beta-barrel Statistics and Prediction Approach.
Joseph Bockhorst	216B. Improving Regulatory Element Prediction with Weakly Labeled Training Data.
Michael Buck	86A. Structural Modeling for the Exploration of the Evolution of the Basic Helix-Loop-Helix Proteins.
Phil Carter	85B. The DSSPcont Database: Continuum Secondary Structure.

Yu Chen	239B. Computational Studies on Amino Acid Transport Pathway in Yeast.
Sam Chien	125B. Homophila: A Database of Human Disease Gene Cognates in Drosophila.
Jo Lan Chung	96B. Studying the Sequence-Structure Relationship across the Protein Kinase Family through Comparative Structural Analysis.
William Dirks	70B. An Exhaustive Study of the Notion of Functional Link based on Microarray Data, Protein-Protein Interactions and Pathways Information.
Blythe Durbin	226A. Learning Better Motif Discrimination using Generative Models.
Eleazar Eskin	80B. Predicting Protein Domains using Discriminative Margin Classifiers.
Rohan Fernandes	(paper) Discovering Statistically Significant Bioclusters in Gene Expression Data
Lynn Fink	34B. Elucidation of Genes Involved in HTLV-I-induced Transformation using the K-harmonic Means Algorithm to Cluster Microarray Data.
Debra Goldberg	233A. Using Small-World Topology to Refine Networks Derived via High-Throughput Methods.
Richard (Ed) Green	155B. Relationships between Alternative Splicing and Protein Structure.
Jenny Gu	33B. Microarray Analysis of the Developing Mouse Cerebellum.
Mayetri Gupta	188A. Discovery of Biological Sequence Motifs using a Stochastic Dictionary Model.
Amy Hauth	(paper) Beyond Tandem Repeats: Complex Pattern Structures and Distant Regions of Similarity
Steffen Heber	(paper) Splicing Graphs and EST Assembly Problem
Bo Kyeng Hou	219A. Predicting Microbial Metabolism: A Functional Group Approach.
Jonathan Jacobs	208A. Identification of -1 Programmed Ribosomal Frameshift Signals in <i>Saccharomyces cerevisiae</i> .
Yongmei Ji	223B. A New Approach to Identify Conserved RNA Secondary Structural Motifs in Homologous Sequences.
Rachel Karchin	216A. SAM_T02 Protein Structure Prediction Webserver.
Dipinder Keer	190A. A Bioinformatic Pipeline for In-Silico High-Throughput Discovery of Single Nucleotide Polymorphisms.

***SUM \$ spent 36,000.00***

**Overspent \$1000.00 Note: covered by other sources from ISMB budget**