

Index

From: ISMB-00 Proceedings. Copyright © 2000, AAAI (www.aaai.org). All rights reserved.

- Abernethy, Neil, 239
Accelerating Protein Classification Using Suffix Trees, 128
Albermann, K., 152
Alignment of Flexible Protein Structures, 329
Altman, Russ B., 286
Analysis of Gene Expression Data with Pathway Scores, 407
Analysis of Gene Expression Microarrays for Phenotype Classification, 75
Analysis of Yeast's ORF Upstream Regions by Parallel Processing, Microarrays, and Computational Methods, 190
Andersen, Claus A. F., 25
- Bafna, Vineet, 3
Bailey-Kellogg, Chris, 13
Baldi, Pierre Baldi, 25, 190
Benton, David, 239
Biclustering of Expression Data, 93
Bischof, Horst, 46
Blanchette, Mathieu, 37
Bockhorst, Joseph, 116
Boguski, Mark, 317
Boland, Michael V., 251
Brändle, Norbert, 46
Brazma, Alvis, 384
Brown, Michael P. S., 57
Brunak, Søren, 25
Bruno, William J., 202
Buchanan, Bruce G., 171
Bussemaker, Harmen J., 67
- Califano, Andrea, 75
Cárdenas-García, Maura, 86
Casadio, Rita, 146
Chen, Horng-Yang, 46
Cheng, Yizong, 93
Church, George M., 93
CLICK: A Clustering Algorithm with Applications to Gene Expression Analysis, 307
Combinatorial Approaches to Finding Subtle Signals in DNA Sequences, 269
Computation and Visualization of Degenerate Repeats in Complete Genomes, 228
- Conserved Exon Method for Gene Finding, The, 3
Cosner, Mary E., 104
Craven, Mark, 116
- DeJongh, Matt, 239
Donald, Bruce Randall, 13
Dorohonceanu, Bogdan, 128
Dunbrack, Roland L., Jr., 296
- Edwards, Stephen, 317
Efficient Attractor Analysis Based on Self-Dependent Subsets of Elements—An Application to Signal Transduction Studies, 86
Eskin, Eleazar, 134
Evaluation of Ontology Exchange Languages for Bioinformatics, An, 239
Exact Algorithm to Identify Motifs in Orthologous Sequences from Multiple Species, An, 37
- Fariselli, Piero, 146
Fellenberg, M., 152
Finding Regulatory Elements Using Joint Likelihoods for Sequence and Expression Profile Data, 202
Fligelman, Zipora Y., 329
Friedberg, Iddo, 162
- Genes, Themes, and Microarrays: Using Information Retrieval for Large-Scale Gene Analysis, 317
Genomic Fold Assignment and Rational Modeling of Proteins of Biological Interest, 296
Giegerich, Robert, 228
Gish, Warren, 218
Glasner, Jeremy, 116
Glasscock, Jarret, 218
Glimmers in the Midnight Zone: Characterization of Aligned Identical Residues in Sequence-Dissimilar Proteins Sharing a Common Fold, 162
Godzik, Adam, 211
Gopalakrishnan, Vanathi, 171
Grundy, William Noble, 134
- Gusfield, Dan, 183
- Hampson, Steven, 190
Hani, J., 152
Hashimoto, Akihiro, 376
Helt, Gregg, 239
Hodnett, Dan, 239
Holmes, Ian, 202
Huson, Daniel H., 3
- Integrative Analysis of Protein Interaction Data, 152
Intelligent Aids for Parallel Experiment Planning and Macromolecular Crystallization, 171
- Jansen, Robert K., 104
Jaroszewski, Lukasz, 211
Jonassen, Inge, 384
Julliard, Laurent, 279
- Kan, Zhengyan, 218
Kaplan, Tommy, 162
Karp, Peter, 239
Kelley, John J. III, 13
Kent, Robert, 239
Kibler, Dennis, 190
Korneev, Nikolai, 86
Kosky, Anthony, 239
Küffner, Robert, 407
Kurtz, Stefan, 228
- Lagunez-Otero, Jaime, 86
Lapp, Hilmar, 46
Lengauer, Thomas, 407
Levitt, Michael, 395
Lewis, Suzanna, 239
Li, Hao, 67
Linear Modeling of Genetic Networks from Experimental Data, 355
Liu, Xuemin, 286
- Margalit, Hanah, 162
Matching Protein β -Sheet Partners by Feed-forward and Recurrent Neural Networks,

- 25
- Matsuda, Hideo, 376
- McEntire, Robin, 239
- Mewes, H. W., 152
- Mining for Putative Regulatory Elements in the Yeast Genome Using Gene Expression Data, 384
- Moret, Bernard M. E., 104
- Multiple Alignment Algorithm for Metabolic Pathway Analysis Using Enzyme Hierarchy, A, 376
- Murphy, Robert F., 251
- Nevill-Manning, C. G., 128
- Neumann, Eric, 239
- New Fast Heuristic for Computing the Breakpoint Phylogeny and Experimental Phylogenetic Analyses of Real and Synthetic Data, A, 104
- Nussinov, Ruth, 329
- Ohlebusch, Enno, 228
- Oken, Frank, 239
- Page, David, 116
- Pathak, Dhiraj, 239
- Pattern Recognition of Genomic Features with Microarrays: Site Typing of *Mycobacterium tuberculosis* Strains, 286
- Pe'er, I., 260
- Pevzner, Pavel A., 269
- Pollastri, Gianluca, 25
- Practical Algorithm for Optimal Inference of Haplotypes from Diploid Populations, A, 183
- Pragmatic Information Extraction Strategy for Gathering Data on Genetic Interactions, A, 279
- Prediction of the Number of Residue Contacts in Proteins, 146
- Probabilistic Learning Approach to Whole-Genome Operon Prediction, A, 116
- Protein Family Classification Using Sparse Markov Transducers, 134
- Proux, Denys, 279
- Raubeson, Linda A., 104
- Raychaudhuri, Soumya, 286
- Rechenmann, François, 279
- Reducing Mass Degeneracy in SAR by MS by Stable Isotopic Labeling, 13
- Regulatory Element Detection Using a Probabilistic Segmentation Model, 67
- Rehmsmeier, Marc, 367
- Reinders, M. J. T., 355
- Robinson, Alan, 384
- Robust Parametric and Semi-Parametric Spot Fitting for Spot Array Images, 46
- Rosenberg, John M., 171
- Rouchka, Eric, 218
- Sandmeyer, Suzanne B., 190
- Sauder, J. Michael, 296
- Schleiermacher, Chris, 228
- Schwikowski, Benno, 37
- Search for a New Description of Protein Topology and Local Structure, 211
- Sequence Database Search Using Jumping Alignments, 367
- Shamir, R., 260
- Shamir, Ron, 307
- Sharan, Roded, 307
- Shatkay, Hagit, 317
- Shatsky, Maxim, 329
- Shavlik, Jude, 116
- Siggia, Eric D., 67
- Sinha, Saurabh, 344
- Singer, Yoram, 134
- Small Subunit Ribosomal RNA Modeling Using Stochastic Context-Free Grammars, 57
- Small, Peter M., 286
- Spang, Rainer, 367
- Spectrum Alignment: Efficient Resequencing by Hybridization, 260
- States, David, 218
- Statistical Method for Finding Transcription Factor Binding Sites, A, 344
- Stein, Cliff, 13
- Stolovitzky, Gustavo, 75
- Stoye, Jens, 228, 367
- Stuart, Joshua M., 286
- Sze, Sing-Hoi, 269
- Tarczy-Hornoch, Peter, 239
- Tohsato, Yukako, 376
- Toldo, Luca, 239
- Tompa, Martin, 37, 344
- Topaloglou, Thodoros, 239
- Towards a Complete Map of the Protein Space Based on a Unified Sequence and Structure Analysis of All Known Proteins, 395
- Towards a Systematics for Protein Subcellular Location: Quantitative Description of Protein Localization Patterns and Automated Analysis of Fluorescence Microscope Images, 251
- Tu, Yuhai, 75
- Ukkonen, Esko, 384
- UTR Reconstruction and Analysis Using Genomically Aligned EST Sequences, 218
- van Someren, E. P., 355
- Velliste, Meel, 251
- Vilo, Jaak, 384
- Wang, Li-San, 104
- Warnow, Tandy, 104
- Wessels, L. F. A., 355
- Wilbur, W. John, 317
- Wolfson, Haim J., 329
- Wyman, Stacia, 104
- Yona, Golan, 395
- Zien, Alexander, 407
- Zimmer, Ralf, 407
- Zollner, A., 152