## INVITED REVIEWS

- Identifying distantly related protein sequences
  - W.R. Pearson
- Linguistic approaches to biological sequences
  - D.B. Sears
- Sisyphus and prediction of protein structure
  - B. Rost and S. O'Donoghue

## ORIGINAL PAPERS

- Rapid protein fragment search using hash functions based on the Fourier transform
  - T. Akutsu, K. Onizuka and M. Ishikawa
- A method for identifying splice sites and translational start sites in eukaryotic mRNA
  - S. L. Salzberg
- The reversible Hill equation: how to incorporate cooperative enzymes into metabolic models
  - J.-H. S. Hofmeyr and A. Cornish-Bowden
- Introduction of a distance cut-off into structural alignment by the double dynamic programming algorithm
  - H. Toh
- Meta-MEME: Motif-based hidden Markov models of protein families
  - W. N. Grundy, T. L. Bailey, C. P. Elkan and M. E. Baker
- Visual BLAST and Visual FASTA: graphic workbenches for interactive analysis of full BLAST and FASTA outputs under Microsoft Windows 95/NT
  - P. Durand, L. Canard and J. P. Mornon
- Prediction of protein secondary structure using the 3D–1D compatibility algorithm
  - M. Ito, Y. Matsuo and K. Nishikawa
- Objectively judging the quality of a protein structure from a Ramachandran plot
  - R. W. W. Hooft, C. Sander and G. Vriend
- Micado—a network-oriented database for microbial genomes
  - V. Biaudet, F. Samson and P. Bessières
- A computer program for the analysis of protein complex formation
  - E. Lorenz, S. Leeton and R. J. Owen
- DISTREE: A tool for estimating genetic distances between aligned DNA sequences
  - J. Schäfer and M. Schöninger
- A new dynamic tool to perform assembly of Expressed Sequence Tags (ESTs)
- Predicting RNA H-type pseudoknots with the massively parallel genetic algorithm
  - B. A. Shapiro and J. C. Wu

## APPLICATIONS NOTES

- DSC: public domain protein secondary structure prediction
  - R. D. King, M. Saqi, R. Sayle and M. J. E. Sternberg
- JaMBW 1.1: Java-based Molecular Biologists' Workbench
  - L. I. G. Toldo
- EST_GENOME: a program to align spliced DNA sequences to unspliced genomic DNA
  - R. Mott
- Calculation of daylength
  - J. S. Amthor
- Sequence analysis of the Methanococcus jannaschii genome and the prediction of protein function
- A simple method for sizing large fragments of bacterial DNA separated by PFGE
  - E. Lorenz, S. Leeton and R. J. Owen

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