

## **PIR Web-Based Tools and Databases for Genomic and Proteomic Research**

Barker, W.C., Chen, Y., Hu, Z., Huang, H., Lewis, K., Orcutt, B.C., Yeh, L.L., Wu, C.H.  
Protein Information Resource, National Biomedical Research Foundation,  
Georgetown University Medical Center, 3900 Reservoir Road, NW, Washington, DC  
20007-2195

We have recently expanded the Web site of the Protein Information Resource (PIR) with new web-based tools to facilitate data retrieval, sequence analysis and protein annotation. The PIR-International Protein Sequence Database (PIR-PSD) is a non-redundant, expertly annotated, fully classified, and extensively cross-referenced protein sequence database. The iProClass is an integrated resource that provides comprehensive family relationships and structural/functional classifications and features of proteins. The PIR Web site connects these useful databases and tools with a user-friendly navigation system and graphical interface. In addition to standard data retrieval and analysis tools, the following new tools have been implemented: 1) HMM (Hidden Markov Model) Domain/Motif Search Tool searches a query sequence against HMM profiles for PIR or Pfam domains or iProclass motifs. This search also allows users to build an HMM profile and search the profile against the PIR-PSD. 2) The Bibliography Submission Page provides a mechanism for the user community to submit literature information for building better protein databases with validated information. 3) The BLAST Similarity Search Tool searches a sequence against PIR-NR, a complete non-redundant protein sequence database currently containing more than 630,000 sequences. The search results, including links to all source databases, are displayed in a user-friendly graphical format. The newly enhanced PIR web-based tools and databases will better support genomic/proteomic research and scientific discovery. The PIR website is accessible at <http://pir.georgetown.edu>. This work is supported by NLM grant LM05798 and NSF grant DBI-9974855.

Presented at the 9th International Conference on Intelligent Systems for Molecular Biology (ISMB), Copenhagen, Denmark, 2001

[Back to Publications Page](#)