*i*ProClass: An Integrated Protein Classification Database for Proteomics

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Advanced databases are essential for gaining insight into protein structure and function from the voluminous, heterogeneous, and distributed molecular data. Protein family classification is now well recognized as an effective means for large-scale functional characterization of genes. The iProClass database [1] is an integrated resource that provides comprehensive family relationships at both global (whole protein) and local (domain and motif/site) levels, as well as structural/functional classifications and features of proteins. The PIR superfamily/family organization allows complete and non-overlapping clustering of all proteins. The iProClass consists of more than 266,000 non-redundant PIR and Swiss-Prot proteins organized with more than 30,000 superfamilies, 100,000 families, 2600 domains, 1300 motifs, 280 post-translational modification sites, and links to over 40 databases of protein families, structures, functions, genes, genomes, literature, and taxonomy. Protein and superfamily summary reports provide rich annotations, including membership information with length, taxonomy, and keyword statistics, comprehensive enzyme and PDB cross-references, and graphical feature display. The database facilitates classification-driven annotation for protein sequences and complete genomes, and supports proteomics research. The iProClass is implemented in Oracle 8i object-relational system and available for sequence/text search and report retrieval at http://pir.georgetown.edu/iproclass/.

References

1 Wu, C. H., Xiao, C., Hou, Z., Huang, H., and Barker, W. C. (2001). iProClass: An integrated and comprehensive protein classification database. *Nucleic Acids Research*, 29, 52-54, 2001. .

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