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Cathy H. Wu received her B.S. in Plant Pathology from National Taiwan University and M.S. and Ph.D. from Purdue University. She conducted postdoctoral research in Molecular Biology and later obtained a second M.S. degree in Computer Science. With background and experience in both biology and computer science, Dr. Wu has conducted bioinformatics and computational biology research for 20 years. Since 1999 she has led the development of PIR as a major public bioinformatics resource. Dr. Wu has served on several advisory boards, including the NIGMS/NIH Protein Structure Initiative Advisory Committee, NSF TeraGrid User Advisory Committee, NRC Board on Research Data and Information, US HUPO (Human Proteome Organization) and Protein Data Bank (PDB). She has also served on numerous program committees for international bioinformatics and proteomics conferences and workshops. She has published about 140 peer-reviewed papers and three books, and given more than 100 invited lectures. Her research interests include protein evolution-structure-function relationships, biomedical text mining, biomedical ontology, proteomic bioinformatics, computational systems biology, and bioinformatics cyberinfrastructure.

“Bioinformatics and Systems Biology”

Systems integration is becoming the driving force for 21st century biology. Researchers are systematically tackling gene functions and complex regulatory processes by studying organisms at different levels of organization, from genomes, transcriptomes and proteomes to metabolomes and interactomes. To fully realize the value of such high-throughput data requires advanced bioinformatics for integration, mining, comparative analysis, and functional interpretation. We are developing a bioinformatics research infrastructure that links text mining with data mining and network analysis in the systems biology context for biological network discovery. The integrative approach will reveal hidden interrelationships among the various components of the biological systems, allowing researchers to ask complex biological questions and gain better understanding of biological and disease processes, thereby facilitating target discovery.

About the Protein Information Resource (PIR)
(http://ProteinInformationResource.org)

A scientific leader in protein bioinformatics for more than four decades, PIR provides integrated databases and bioinformatics tools to support genomics, proteomics and systems biology research. PIR is a member of the UniProt Consortium that provides the central international resource on protein sequence and function. The PIR web sites are accessible by researchers worldwide with over 4 million hits per month from over 100,000 unique sites.