Title: A New Proteome Information Resource

Authors: P. Ulintz, J. Hartman*, P. Andrews
Affiliation: Dept. of Biological Chemistry, University of Michigan Medical School, Ann Arbor, MI 48109 and (*) Computational Biosciences, Inc., Ann Arbor, MI 48105
e-mail: pulintz@umich.edu

Abstract:

Recent advances in techniques for high-throughput proteome mapping and analysis have been accompanied by the development of new technologies for maintaining and publishing large, complex scientific databases via the World Wide Web (WWW). These synergistic revolutions in the collection, manipulation, and dissemination of genomic and proteomic information have already begun to make feasible the detailed study of the cell as a complex system.

We have constructed an object-relational database (based on Oracle 8i™) for the management of data in our laboratory associated with 2-D gel separations of cellular proteins. The database currently covers a hierarchy of data including experimental protocols and gel conditions, gel images, quantitative spot lists, and a variety of information on proteins and peptides that have been identified by sequencing and mass spectrometric fragment mapping.

The database functions as, and provides a framework for, a browser-based laboratory information management system that additionally facilitates the selective publication of data on the Web using embedded Java™ technologies (e.g., servlets, Enterprise Java Beans), and the Oracle 8i Database Server. The server currently generates pages in HTML, but will likely support XML directly in the future as relevant standards and available browsers evolve.