

OPEN SOURCE SOLUTION TO SUPPORT PROTEOMICS RESEARCH

Client Profile:

A prominent Proteomics Research University whose focus is on the study of biomolecular interactions.

Technologies Used:

JBoss (Java J2EE), Apache AXIS (SOAP)

Project Summary:

The client manages an extensive database designed to store full descriptions of interactions, molecular complexes and pathways. The database stores variables such as small molecule biochemistry to signal transduction, which is abstracted in such a way that graph theory methods may be applied for data mining. The database is used to study networks of interactions, to map pathways across taxonomic branches and to generate information for kinetic simulations. A standard means of submitting data related to biomolecular interactions was vitally needed due to an anticipated large influx of interaction information from high-throughput proteomics efforts including detailed information about post-translational modifications from mass spectrometry. ASHVINS developed a custom open source solution that entailed web service API development. This involved creating independent application components and making them available for use across the Internet. Developers of Internet-based applications incorporate this service into their applications for the benefit of their end users in an unobtrusive and seamless implementation. This interface allows Integrated Development Environments (IDE) such as JBuilder and Delphi to generate a dynamic listing and access to the API utilizing the native SOAP services that are used to communicate and integrate with their internal applications. The API is made available to developers via a Web Service. The SOAP API provides a modular, more flexible, and higher-performing interface to increase the accessibility of the database.