TOPSAN: a dynamic web database for structural genomics

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ABSTRACT

The Open Protein Structure Annotation Network (TOPSAN) is a web-based collaboration platform for exploring and annotating structures determined by structural genomics efforts. Characterization of those structures presents a challenge since the majority of the proteins themselves have not yet been characterized. Responding to this challenge, the TOPSAN platform facilitates collaborative annotation and investigation via a user-friendly web-based interface pre-populated with automatically generated information. Semantic web technologies expand and enrich TOPSAN’s content through links to larger sets of related databases, and thus, enable data integration from disparate sources and data mining via conventional query languages. TOPSAN can be found at http://www.topsan.org.

INTRODUCTION

Over the past decade, structural genomics (SG) efforts in the USA alone have determined the structures of more than 3000 previously uncharacterized proteins at a sustained rate of over 500 novel structure depositions per year to the Protein Databank (PDB) (1). Through the discovery of numerous new folds and an even greater number of variants of known folds (2), SG structures provide key input for innovative research into protein evolution and function. One of the main challenges presented by such high-throughput research involves the timely annotation and integration of the resulting data to provide direct input into ongoing research within the greater biological community. Traditional mechanisms for publication are simply too slow to keep pace with the speed of structure determination. Thus, currently over 90% of SG deposited structures are not yet described in literature. The rate and volume of protein structures being produced requires novel mechanisms to ensure that the knowledge gained by these structures is disseminated in a timely manner.

Several new protein structure annotation platforms, using wiki-based methods, have been described (3–5). However, their content is largely static and derived from peer-reviewed publications, aspects that do not easily lend themselves to exploring new knowledge about structures. We developed The Open Protein Structure Annotation Network (TOPSAN) to serve both as an annotation and a communication platform with the goal of facilitating and accelerating research relevant to SG structures. TOPSAN integrates a wide range of information about SG proteins, from different high-throughput experiments to literature, evolutionary analysis and even functional predictions. Through the implementation of a semantic web layer in the current version, TOPSAN enables database-like searches through its entire content and thus promotes further integration between its content and mainstream biology.

THE DATABASE

Content and interface

TOPSAN currently contains annotations for over 7250 structures from SG efforts from around the world. Prominent among these are several hundred structures that represent the first experimentally characterized members of their respective families, as well as many proteins for which there is extensive interest within the research community. Traditional mechanisms for publication are simply too slow to keep pace with the speed of structure determination. Thus, currently over 90% of SG deposited structures are not yet described in literature.
in different stages of development. An overview of the database interface is given in Figure 1.

Implementation

Implementation of the TOPSAN platform has been described in detail elsewhere (6). In brief, TOPSAN was developed using MindTouch, an enterprise open source collaboration and integration platform, which provides tools and scripting capabilities that were used to develop a dynamic website. At the backend, data are collected from a variety of different sources, using multiple tools that have been integrated into the MindTouch platform. An application called TopsanApp is used to retrieve

Figure 1. Screenshot of a TOPSAN entry [PDB id: 3kk7 (9)]. Automatically generated data (data from external sources) are combined with human input (WYSIWYG editor, tagging, discussion page) and analyses (tools). Authorship and version tracking enable accountability and quality control. Semantic web technologies enable easy import and export of this data. Details of the data specifications can be found on the website.
TOPSAN additionally utilizes a semantic web-based data import system that enables rapid integration of new data. Semantic web is an architectural layer built on top of existing web pages that consists of hidden embedded tags that employ standardized ontology, allowing searches normally associated with structured databases to be carried out across unstructured data collections (7,8). For our purposes, the semantic web provides a unified framework for integration of data automatically imported from external sources and human-curated annotations. In this environment, scripting calls made from the Dekiscript environment build requests to access and convert XML formatted data available on the web into a semantic web compatible format. Data from compatible sites that provide all records in a semantic web compatible format can be imported directly with no manual conversion. Thus, semantic web data can be automatically imported to TOPSAN from Pfam, UniProt, KEGG Pathway database and PDB. Other sources of data can be imported with a variety of modular, easily adapted plug-ins. Once imported, the data can be queried and utilized in the same web-based Dekiscript environment that was used for the import. Data export is handled by a variety of modular tools that make data available in formats including standard HTML, stripped-down XML, RDF/XML and RDFa. In addition to individual protein annotations, bulk compilations of the entire site format can be imported directly with no manual conversion.

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