

Center for Eukaryotic Structural Genomics

Technology Dissemination Report

CESG Tech Report No.	001
Title	Sesame Laboratory Information Management for Structural Genomics
Research Unit	Sesame
Authors	Zolnai, Z. and Markley, J.L.
Primary Contact	zsolt@nmrfam.wisc.edu or markley@nmrfam.wisc.edu

Sesame © 1999-2007, Zsolt Zolnai, and the University of Wisconsin-Madison.



Sesame



Summary

The Sesame laboratory information management system (LIMS) [1] consists of a series of web-based Java applet-applications designed to organize data generated by projects in structural genomics, structural biology, metabolomics, and shared laboratory resources. Sesame allows collaborators on a given project to enter, process, view, and extract relevant data, regardless of location, so long as web access is available. Sesame is a multi-tier system, with data residing in a relational database. As its associated relational database management system (RDMS), Sesame supports Oracle 8.1.7+, Microsoft SQL Server 2005, and PostgreSQL 8+ (an advanced open-source RDMS). Full details concerning the Sesame project can be found at <http://www.sesame.wisc.edu>. Sesame is Java SE Development Kit (JDK) 1.4.2 compliant.

The Madison implementation of Sesame is used by the Center for Eukaryotic Structural Genomics (CESG), the National Magnetic Resonance Facility at Madison (NMRFAM), and by structural biology projects at the University of Wisconsin-Madison and the Medical College of Wisconsin. Centers that wish to have free-standing versions of Sesame support these on their own servers with their own relational database management system. Such free-standing versions of Sesame are now operational at the New York Consortium on Membrane Protein Structure (NYCOMPS); the Bio21 Molecular Science and Biotechnology Institute, University of Melbourne, Australia; and the Promega Corporation in Madison, Wisconsin.

Sesame is easily configurable by laboratory scientists with minimal programming knowledge to tailor the software to the organizational structure, research environment, and physical layout of the laboratory or center (single site or multiple locations). Sesame can be configured to interact with instrumentation (Crystallization Robots, Y2H screening robotics, spectrophotometers, NMR spectrometers, etc.) and it has the capability of printing and reading barcodes. Information is easily uploaded from external databases (e.g. GenBank, UniProt, PubChem).

A multi-window environment, called the Board, allows users to display many records in a drag-and-drop environment. These windows can be cascaded, tiled, minimized, and maximized, much like a standard windows environment. Users can attach files (gel scans, images of spectra, text files, etc.) or URL identifiers to most every Sesame Item defined within the system. The attached images and files can and viewed, manipulated, downloaded, and printed. Sesame has extensive searching and reporting capabilities. Sesame has the capability of exporting information in the form of XML files. CESG uses these files to gather the full range of information required for deposition in the TargetDB and PepcDB.

Publication:

- [1] Zolnai, Z. Lee, P.T., Li, J., Chapman, M.R., Newman, C.S., Phillips, G.N., Jr., Rayment, I., Ulrich, E.L., Volkman, B.F., Markley J.L. (2003) Project management system for structural and functional proteomics: Sesame. *JSFG* 4(1):11-23.

Acquiring the Technology	http://www.sesame.wisc.edu
Other Acknowledgements	Support from NIH grants P41 RR02301 and 1R01 GM 077139-01.
Center for Eukaryotic Structural Genomics (CESG), University of Wisconsin-Madison Biochemistry Department, 433 Babcock Drive, Madison, WI 53706-1549; phone: 608.263.2183; fax: 608.890.1942; email: cesginfo@biochem.wisc.edu ; website: http://www.uwstructuralgenomics.org . This research funded by NIH / NIGMS Protein Structure Initiative grants U54 GM074901 and P50 GM064598.	