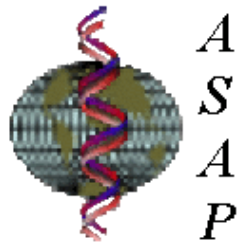


ASAP Overview

A Systematic Annotation Package for Community Analysis of Genomes



About ASAP

Developments in genome-wide approaches to biological research have yielded greatly increased quantities of data, necessitating the cooperation of communities of scientists focusing on shared sets of data. ASAP leverages the internet and database technologies to meet these needs. ASAP is designed to organize the data associated with a genome from the early stages of sequence annotation through genetic and biochemical characterization, providing a vehicle for ongoing updates of the annotation and a repository for genome-scale experimental data. Development was motivated by the need to more directly involve a greater community of researchers, with their collective expertise, in keeping the genome annotation current and to provide a synergistic link between up-to-date annotation and functional genomic data. The system is continually under development at the Genome Evolution Lab with the stable, in-use, publicly available University of Wisconsin installation updated regularly.

Software development on ASAP began in early 2002, and ASAP has been continually improved up until the present day. A longstanding goal of the ASAP project was to make the source code of ASAP available so that other installations of ASAP could be implemented. As future ASAP installations come to pass, ASAP will be further extended to be inter-operable between sites.

Downloading ASAP

ASAP is distributed free of charge under the GPL. It requires PHP 4 and MySQL 4.

Click [here](#) to download the latest packaged version of ASAP. Packaged releases of ASAP are not built regularly and may not be the same code that is present on the [live site](#). To request a more up-to-date release of the source, contact Michael Rusch.