## Sequencing and annotating multiple *Saccharomyces cerevisiae* strains at the *Saccharomyces* Genome Database

SGD

Edith D. Wong, Stacia R. Engel, Robert Nash, J. Michael Cherry, and The SGD Project Department of Genetics, Stanford University, Stanford, CA 94305, USA

With the recent release of the first major update to the S288C reference sequence, the Saccharomyces Genome Database (SGD; <u>http://www.yeastgenome.org</u>) continues to be the authoritative source for the Saccharomyces cerevisiae reference genome sequence and annotation. The systematic sequencing of a genome from a single yeast colony serves as the reference point to determine representative allellic variation among additional S288C-derived genomic sequences, as well as to expand upon SGD's annotation of additional *S. cerevisiae* strains. In collaboration with several groups, the complete genome sequences of a number of laboratory, industrial, and wild strains are being sequenced. In addition to making these genomes available as FASTQ and consensus sequences for researchers, SGD will annotate and provide comparative analyses of these sequences, correlating sequence changes with variations in strain phenotypes and protein function.

