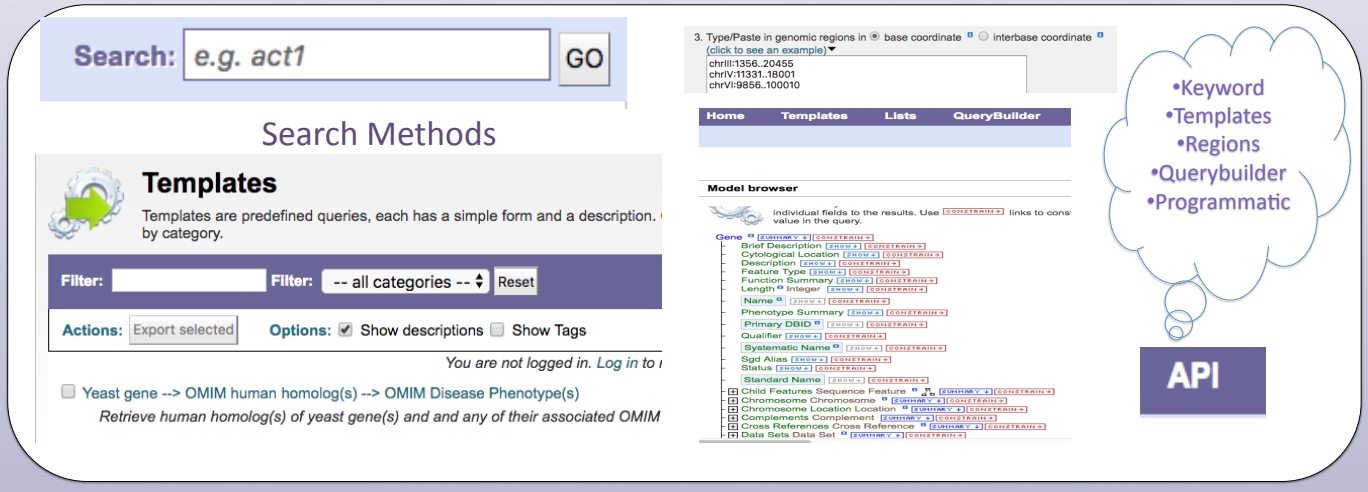
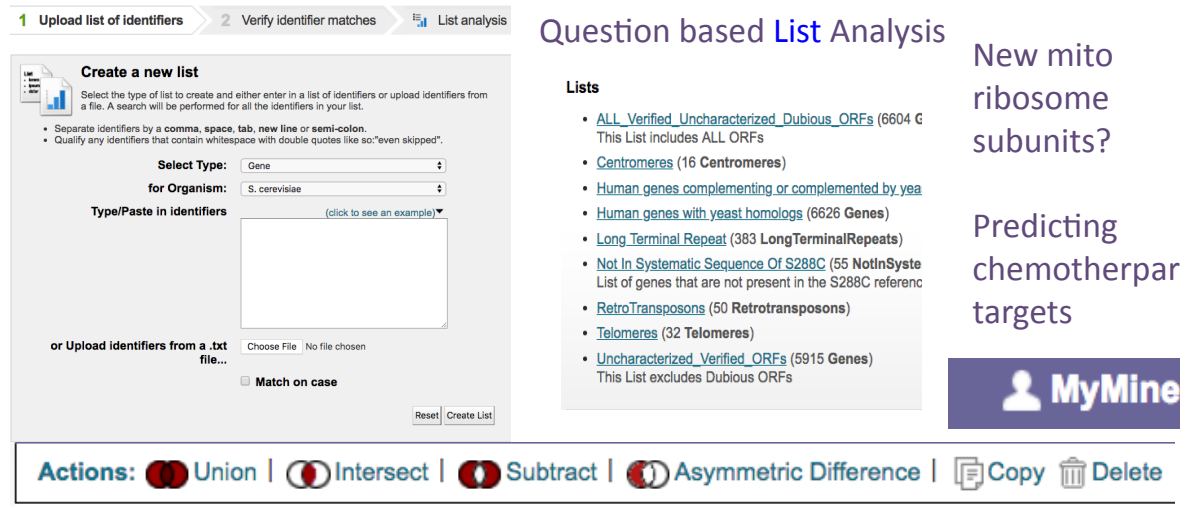
YeastMine: An Advanced Search and Analysis Tool for SGD Data

Kalpana Karra[1], Robert Nash[1], Kevin MacPherson[1], Gail Binkley[1], J. Michael Cherry[1] and the SGD Project[1]

[1]Stanford University, School of Medicine, Department of Genetics, Stanford, CA

The Saccharomyces Genome Database (SGD; http://www.yeastgenome.org/) provides high-quality curated genomic, genetic, and molecular information on the genes and gene products of the budding yeast Saccharomyces cerevisiae. YeastMine provides a sophisticated tool for searching SGD data with a list of genes, GO terms and other data types. Pre-made queries called templates can be used to get results for most commonly asked questions. For more complex questions, one can use multiple templates, intermediate steps and list operations to get answers. Registered users can store their queries and results in MyMine. Regulatory relationships, human homolog and disease connections, and protein complex data are the most recent data types loaded into YeastMine. YeastMine is built using the open source software InterMine (http://www.intermine.org), a data warehouse solution for biological data.





sgd-helpdesk@lists.stanford.edu
@yeastgenome
https://www.facebook.com/yeastgenome/
https://www.youtube.com/SaccharomycesGenomeDatabase

ALLIANCE of GENOME RESOURCES FOUNDING MEMBER