Saccharomyces Genome Database: How to find what you are looking for

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Everyone has experienced the frustration of being unable to find the information you want on a website because you have only a vague idea what you are looking for and don't know what search term(s) to use. Here we present several ways to find and explore data at SGD using new search methods. "Exact match" searches are effective and fast when it is already known that specific information exists. However, "exact match" searches do not allow browsing of all available data, and can sometimes obscure the context of the returned results, making it difficult to discover new connections and uncover novel relationships. To address these issues, the *Saccharomyces* Genome Database (SGD; http://www.yeastgenome.org) has recently implemented several new ways to find and explore yeast data. SGD's "exact match" search has been replaced with a new faceted search based on Elasticsearch, which allows filtering in multiple categories and speeds query performance. Faceted navigation provides immediate feedback and easy navigation so users can quickly refine and refocus their search based on the returned results. Other recent website additions include SGD's Variant Viewer, which employs a combination of data filters and visualizations to display novel sequence variants for open reading frames within a reference panel of 12 widely used *S. cerevisiae* genomes. Datasets are also now easier to find in SGD. Over 225 expression and other high-throughput datasets can now be filtered by curated metadata and displayed using JBrowse, a JavaScript- and HTLM5-based genome browser. This work is supported by a grant from the NHGRI (U41 HG001315).

Make new associations between data using Search

Looking for possible candidate yeast genes important in tyrosine metabolism, a factor in thyroid hormones involved in Graves disease

Filters as breadcrumbs

Auto complete search term

Switch views between a descriptive list and a wrapped name list

Download a gene name list for further analysis

Take the gene list and use YeastMine, Variant Viewer and JBrowse to find more information

Dendogram of S. cerevisiae strains for selected genes

Find genes enriched for molecular function

Finding variants easy since only differences displayed

Select tracks using curated metadata

Zero in on a variant coordinate