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"The human genome project has spawned a vigorous new science called genomics. The model organisms were to serve as the "Rosetta Stone" that would allow us to understand the human genome sequence. The rise of genomics and bio-informatics has had another consequence: the increasing dependence of all biology on results available only in electronic form. Most of the useful genomic data, notably genetic maps, physical maps, as well as DNA and protein sequences, are available only on the Worldwide Web. As a result, databases of genomic information for a variety of organisms have been organized."

David Botstein and J. Michael Cherry 1997  
Proc. Natl. Acad. Sci.

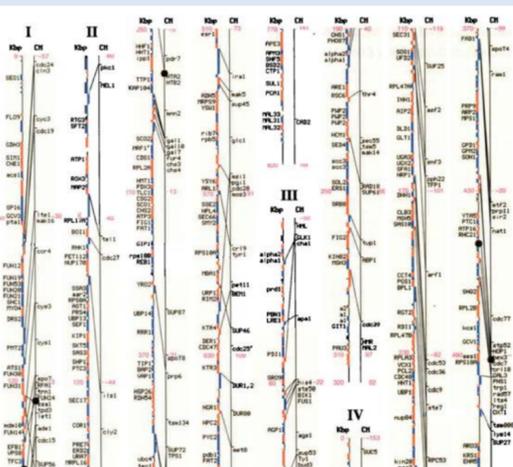
By © Hans Hillewaert, CC BY-SA 4.0, <https://commons.wikimedia.org/w/index.php?curid=3153928>

The *S. cerevisiae* database was created in 1993 using the AceDB software created by R. Durbin for visualization of the *C. elegans* genome. SacchDB website was launched in 1994 featuring *S. cerevisiae* genetic maps, nomenclature and curated literature. The genetic maps were the result of 40 years of genetic analysis.

In 1996 the complete sequence of the first eukaryote, *Saccharomyces cerevisiae*, appeared on the World Wide Web and the physical mapping data was based on this complete genomic sequence.

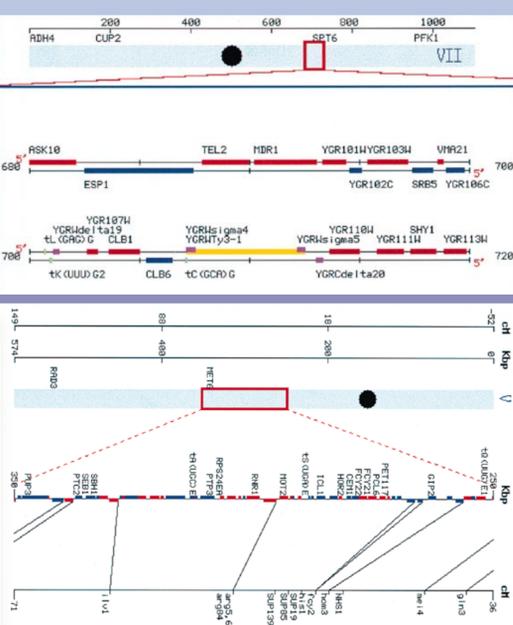
1997

### Alignment of Genetic and Physical Map



1998

### First Clickable Features Map and Clickable Combined Physical and Genetic Map



## 1994 First SGD Website and the Current 2019 Site for CDC6

2019

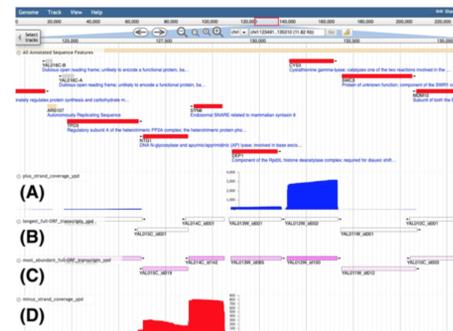
## Transcriptome Visualization Paper

Transcriptome visualization and data availability at the *Saccharomyces* Genome Database

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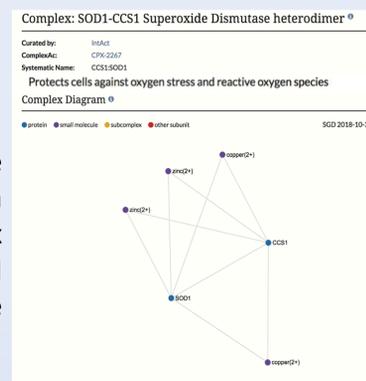


Representative tracks for transcript isoforms and coverage in glucose containing media. (A) Plus-strand transcript coverage in blue. (B) Longest transcript isoform for each ORF. (C) Most abundant transcript isoform for each ORF. (D) Minus-strand transcript coverage in red.

2019

## Yeast Macromolecular Complexome

SGD collaborates with the Molecular Interactions team that provides the Complex Portal database at EMBL-EBI to manually curate the complete yeast complexome.



2018

## Yeast-Human Complementation Data: a tool to understand human genes and a bridge between biological kingdoms

A human gene can successfully replace the function of a yeast gene, and/or vice versa. Using YeastMine, a human gene, or list of genes, can be entered to retrieve information on yeast genes that can be complemented by the human gene and vice versa.

## Founding member of Alliance of Genome Resources



SGD, along with the five other major model organism database (MOD) projects (Mouse Genome Database (MGD), Rat Genome Database (RGD), Zebrafish Information Network (ZFIN), WormBase, and FlyBase) and the Gene Ontology (GO) Consortium founded the Alliance of Genome Resources, a new platform that aims to integrate, develop and maintain genome information resources in order to facilitate the use of a variety of model organisms to understand the genetic bases of human biology and disease.

2016

## Multi-genome Reference Panel

Strains were selected based on a substantial history of use and experimental results, the genomes for which we have the most curated phenotype data and for which we aim to curate specific functional information.

Strain	Provenance	Accession
CEN.PK	Lab strain	JR100000000
D273-10B	Lab strain	JR100000000
R1100	Lab strain	JR100000000
JK9-3d	Lab strain	JR100000000
RM11-1a	Vineyard	JR100000000
SEY6210	Lab strain	JR100000000
Sigma1279b	Lab strain	JR100000000
SK1	Lab strain	NCL300000000
W303	Lab strain	JR100000000
X2189-1A	Lab strain	JR100000000
Y55	Lab strain	JR100000000



## SGD Tutorials and Outreach

2000

## Introducing Gene Ontology (GO) Terms

A controlled vocabulary to describe mutant phenotypes was developed to facilitate quick and accurate searches for genes with similar phenotypes. Three new descriptions are added on the locus page: function, process and cellular component.

2012

## YeastMine Advanced Query

The InterMine platform was integrated to create the multifaceted search and retrieval tool YeastMine. YeastMine enables querying across multiple data sources, navigating between data types and managing data all in one tool.

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<https://www.facebook.com/yeastgenome/>

<https://www.youtube.com/SaccharomycesGenomeDatabase>