#### Stanford Saccharomyces Genome Database (SGD) Through the Years ▲ ◆ SGD

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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.

## 1994

25 Years of SGD

...and still your best bud!

2010

2015

2010-2014

tions; SGD on Facebook, Twitter

2011: YeastMine & SPELL tools +

2012: First research blog posting

YouTube channe

**SGD** Tutorials and Outreach

2013: Gene regulation + 2014:

ship and reach the broadest possible audience, content posted on one outreach platform is often publicized, announced or r rms. Colored arrows indicate the directions in which content is pushed from one platform to anoth

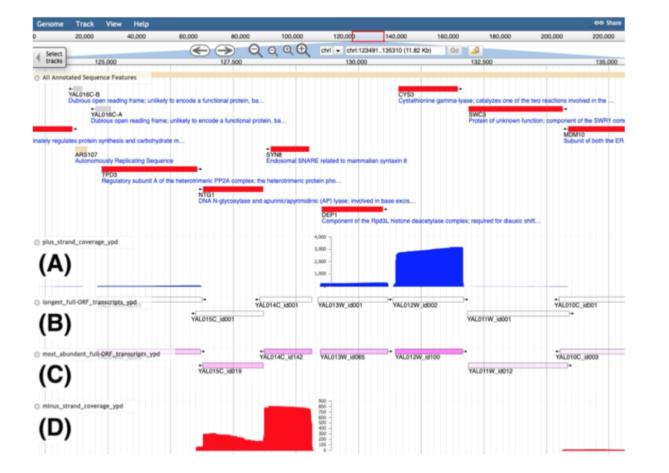
### First SGD Website and the Current 2019 Site for CDC6

SacchDB Server       Image: SacchDB Server         Image: SacchDB Server       Image: SacchDB Server     <	SGD Saco GENC	<i>haromyce</i> ME DATABA	es Analyze SE	- Sequence -	Function 👻	Literature 👻	Community 👻	Q search:	actin, kinase, glu		
Neighbours Link to other classes Bibliography	Summary	Sequence	Protein	Gene Ontology	Phenotype	Interactions	Regulation	Expression	Literature		
Class Locus cdc6 Name Description required for initiation of DWA replication Phenotype arrest at initiation of S phase Gene_class odc Type Gene		CL	CDC6 / YJL194W Overview								
			Standard Name:     CDC6 <sup>1</sup> / <sub>2</sub> Systematic Name:     YJL194W								
Type Gene Molecular_information Positive_clone <u>6822</u> <u>Hieter, P. (1994) Unpublished</u> <u>Hilger, F. (1985) Personal</u>	Sequence Protein		SGD ID:SGD:S000003730Feature Type:ORF , Verified								
Communication         5926       Hieter, P. (1994) Unpublished         Hilger, F. (1985) Personal	Gene Ontology	Desc	cription:	complex (pr	e-RC) which red	matin and is in to	ponent of the pre-replicativ n and is in turn required for				
Communication         4261       Hieter, P. (1994) Unpublished         Hilger, F. (1985) Personal       Communication         Communication       Kawasaki, G. (1979) Karyotypic         instability and carbon source       effects in cell cycle mutants of         Saccharomyces cerevisiae. Ph.D       Thesis         cseqX_11       Dietrich, F., et al. (1994)	Phenotype	Nam	ne Description	cytoplasm u	Mcm2-7p DNA association; homologous to S. pombe Cdc18p; relocalizes from nucleus to cytoplasm upon DNA replication stress; degraded in response to plasma membrane stress <sup>24</sup> Cell Division Cycle <sup>3</sup> Integrated model organism details available at the Alliance of Genome Resources website						
	Interaction Regulation		parative Info								
	Expression Summary	Sec	quence	)	Sequence Details						
	Paragraph Literature	E	Download (.fsa	-					View in: JBrows		
<u>Consensus sequence generated</u> <u>from GenBank by SGD</u> Sequence <u>YSCCDC6B (GB)</u>	History	С	CDC6 Location: Chromosome X 6933870879								
<u>VSCCDCAA (GB)</u>											

### 2019 **Transcriptome Visualization Paper**

Transcriptome visualization and data availability at the Saccharomyces Genome Database 👌 Patrick C Ng, Edith D Wong, Kevin A MacPherson, Suzi Aleksander, Joanna Argasinska, Barbara Dunn, Robert S Nash, Marek S Skrzypek, Felix Gondwe, Sagar Jha, Kalpana Karra, Shuai Weng, Stuart Miyasato, Matt Simison, Stacia R Engel, J Michael Cherry 🖂

Nucleic Acids Research, gkz892, https://doi.org/10.1093/nar/gkz892 Published: 15 October 2019 Article history v



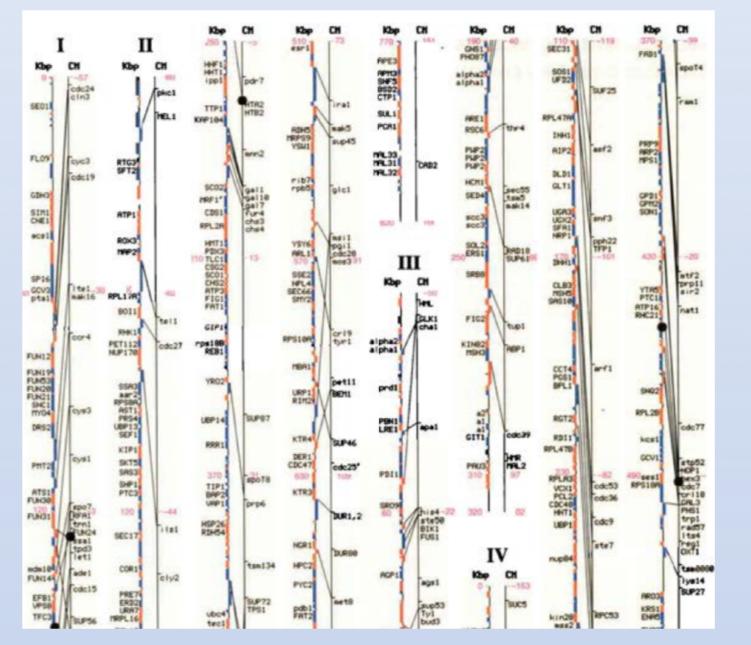
#### David Botstein and J. Michael Cherry 1997 Proc. Natl. Acad. Sci.

#### y © Hans Hillewaert, CC BY-SA 4.0, https://commons.wikimedia.org/w/index.php?curid=315392

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. genetic maps, nomenclature and cerevisiae 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 was based on this complete genomic data sequence. 1997

## Alignment of Genetic and **Physical Map**





1993

1993-2001

1993: SGD initiated with AceD8+

aps and nomenclature + 1996;

ce + 2000: Oracle data

ng yeast genome



2018

2015-2018

lariant Viewer + 2016: W

member of Alliance of Gen

Resources + 2018: 25th a

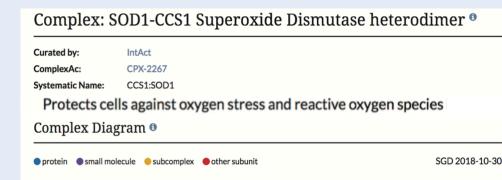
ry database and search;

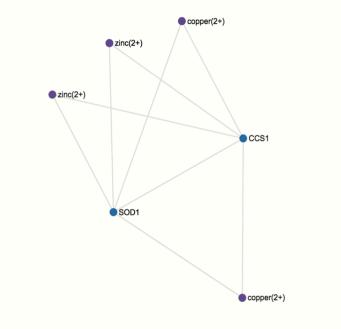
versary of SGDI

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

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

#### ☆ 🕵 🛆 🔶 🚺 🕻 **Video Tutorials** GD has created short video tutorials that describe specific aspects of tools and features at SGD. Click on the name of a tool or feature below t find associated video tutorials describing its use Basic Navigatio Biochemical Pathway Genome Brows

2002

2002-2009

2002: GO Term Mapper, Synteny

Functional annotations for all ORFs:

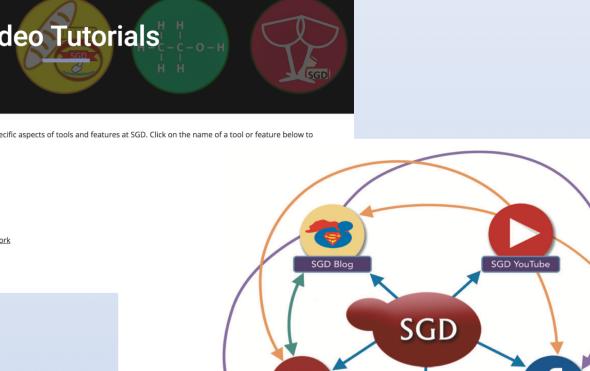
30 million hits + 2004: Genome

ion data + 2005; Exp

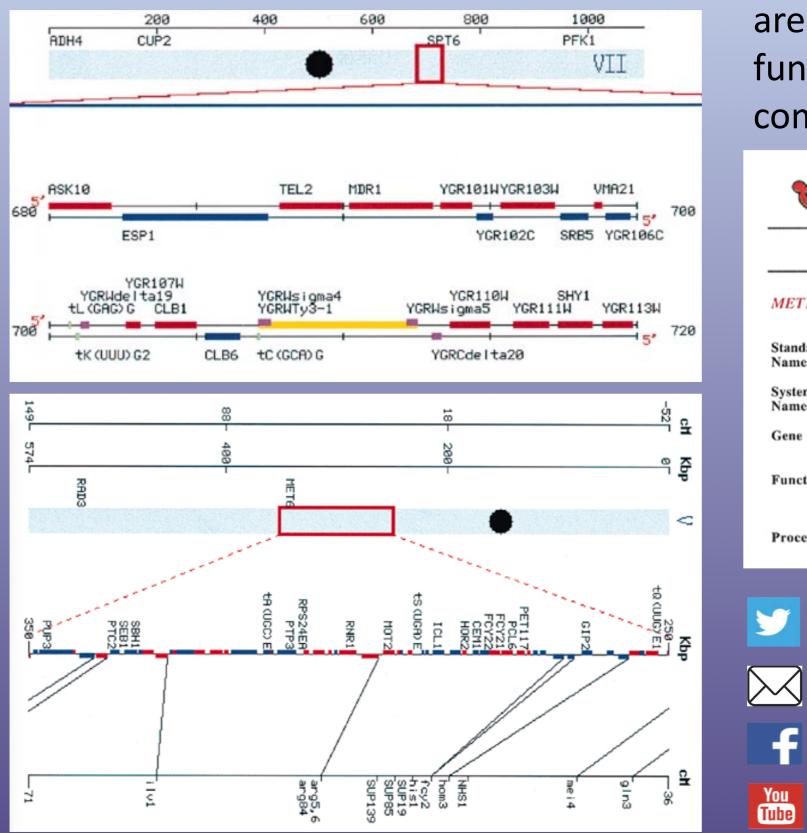
nt = 2008:

/iewer, Fungal Alignments • 2003:

<u>YeastMine</u>

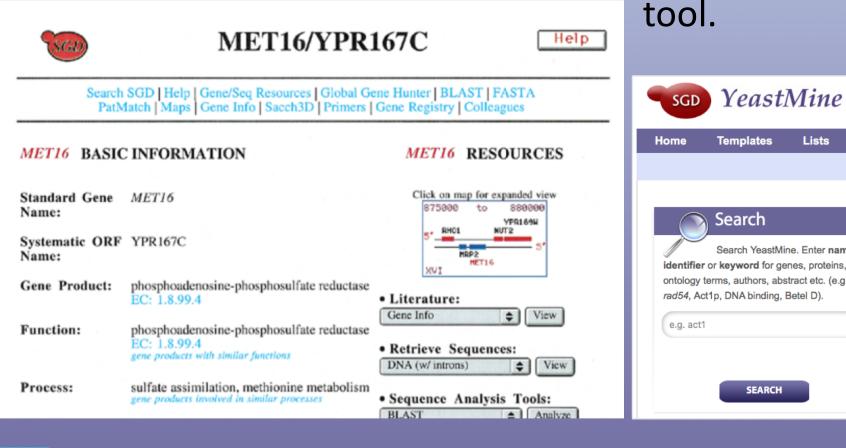


### 1998 **First Clickable Features Map** and Clickable Combined Physical and Genetic Map



### 2000 **Introducing Gene Ontology** (GO) Terms

mutant phenotypes was developed integrated to genes with similar retrieval searches for phenotypes. Three new descriptions YeastMine on the are added function, process and component.



## 2012 YeastMine Advanced Query

A controlled vocabulary to describe The InterMine platform was to the create facilitate quick and accurate multifaceted search and YeastMine tool enables querying locus page: across multiple data sources, cellular navigating between data types and managing data all in one

#### Enter a list of identifi ntifier or keyword for genes, protein ntology terms, authors, abstract etc. (e.g rad54, Act1p, DNA binding, Betel D). e.g. act1 57; spo11; dmc1; rad17; rad9; rad24 ANALYSE SEARCH

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**





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 use ot and experimental results, the genomes for IRIP00000000 which we have the most curated SEY6210 IRIW00000000 Lab strain IRIO0000000 Lab strain NCLS0000000 Lab strain phenotype data and for which we aim <sup>w303</sup> x2180-1A Lab strain IRIU00000000 IRIX00000000 Lab strain Lab strain IRIF00000000 specific functional curate to

strain	Provenance	Accession
CEN.PK	Lab strain	JRIV00000000
D273-10B	Lab strain	JRIY00000000
FL100	Lab strain	JRIT00000000
K9-3d	Lab strain	IRIZ00000000

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@yeastgenome

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

https://www.youtube.com/SaccharomycesGenomeDatabase

