Educational Resources Hosted at the *Saccharomyces* Genome Database

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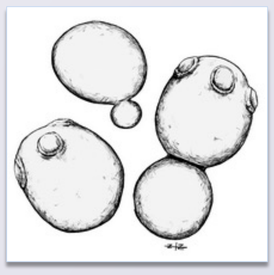
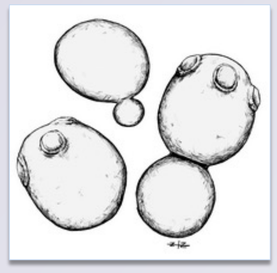
The *Saccharomyces* Genome Database (SGD; http://www.yeastgenome.org) is the leading community resource for the budding yeast *S. cerevisiae*. SGD provides high-quality, manually curated information on the yeast genome and offers a wide variety of tools and features that make it an indispensable resource for researchers. SGD engages in a variety of online training and educational outreach efforts to inform our user community about new developments, to improve user familiarity with SGD features and tools, and to increase public awareness of the importance of yeast not only for biological and biomedical research but also for instructional purposes. The SGD community wiki provides users with a venue for accessing and sharing information in areas that include educational resources. This includes information about associations and societies, general and yeast specific classroom materials (teaching modules and project-based courses), and some fun sites of general interest to the aspiring biologist. To inform the community about new features and tools, SGD creates and posts short videos to YouTube to both educate and address questions posed by users. This includes videos on how to use tools like: YeastMine, Variant Viewer, GO Term Finder, GO Slim Mapper and JBrowse, as well as videos to support users interested in navigating phenotypes, interactions, expression data, literature, homologs, human disease connections and functional complementation. SGD is also working with micropublications to promote the publication of brief, novel, technically sound research results and data that don't fit into full-length articles. This includes single high-quality research results as well as negative results that will accelerate scientific discovery and advance the scientific endeavor. This mechanism for publication is particularly attractive for students interested in rapidly publishing findings of general interest to the greater scientific community. Micropublications are indexed at PubMed, PubMed Central (PMC) and EuropePMC for greater visibility. We will continue to develop these services to provide access to educational resources and outreach for students, teachers and scientists to facilitate greater use and understanding of the resources made available by SGD. This work is supported by a grant from the NHGRI (U41HG001315).



Research Spotlights

https://www.yeastgenome.org/blog/category/research-spotlight

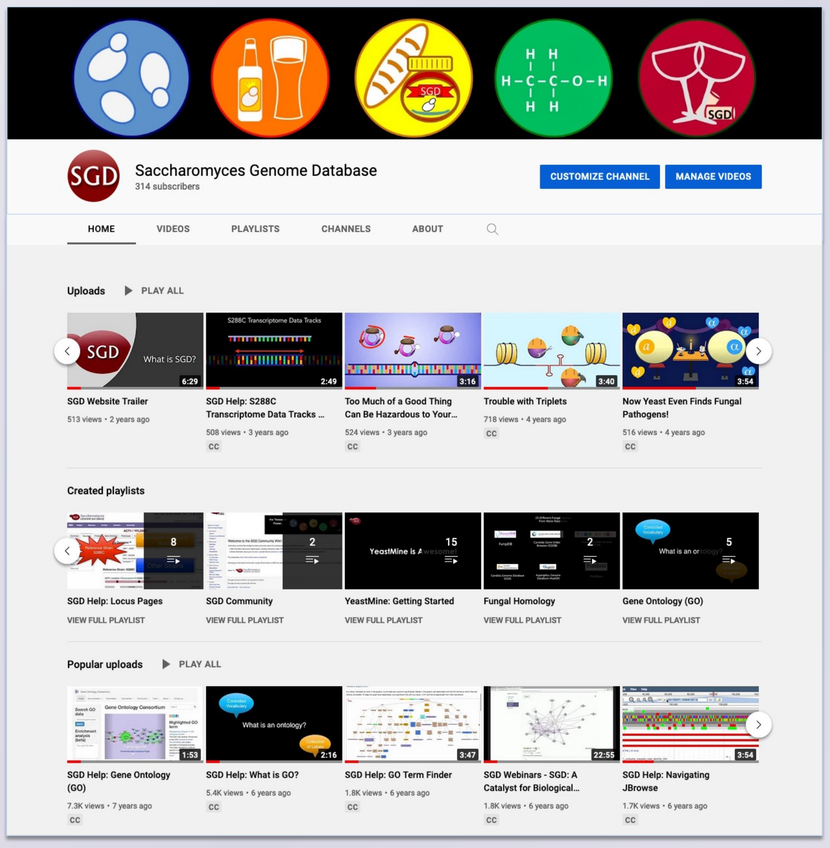
- Highlight interesting new work (ongoing stories, an unexpected twist, new technique or perspectives, disease-related)
- Written in a casual user-friendly style to reach a wide audience



The SGD YouTube Channel

https://www.youtube.com/SaccharomycesGenomeDatabase

- Many help videos on various topics at SGD
- Organized playlists arrange tutorials from basic to advanced
- Easy-to-follow tutorials: helpful examples and animations
- SGD fans subscribe-are you subscribed, too?



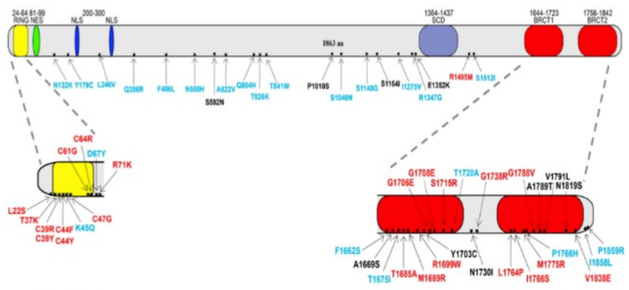
New & Noteworthy

New Yeast-Based Assay for Classifying BRCA1 Variants

May 13, 2022

Like 0 Tweet

Lifetime risk of developing ovarian or breast cancer is increased by germline mutations in the BRCA1 gene. While specific pathogenic variants have been well studied, new sequencing technologies continue to identify variants of uncertain significance (VUS). These variants are comparatively rare and cannot easily be studied in humans. Thus, a recent study in the *International Journal of Molecular Sciences* by Bellè et al. demonstrates a means to assess pathogenicity of a given variant in a cell-based assay in yeast. The new technique complements previous techniques (one in yeast, others computational) to improve the accuracy and sensitivity of assessing pathogenicity for the numerous variants of BRCA1.



From Bellè et al., 2022; red pathogenic, turquoise benign, black uncertain

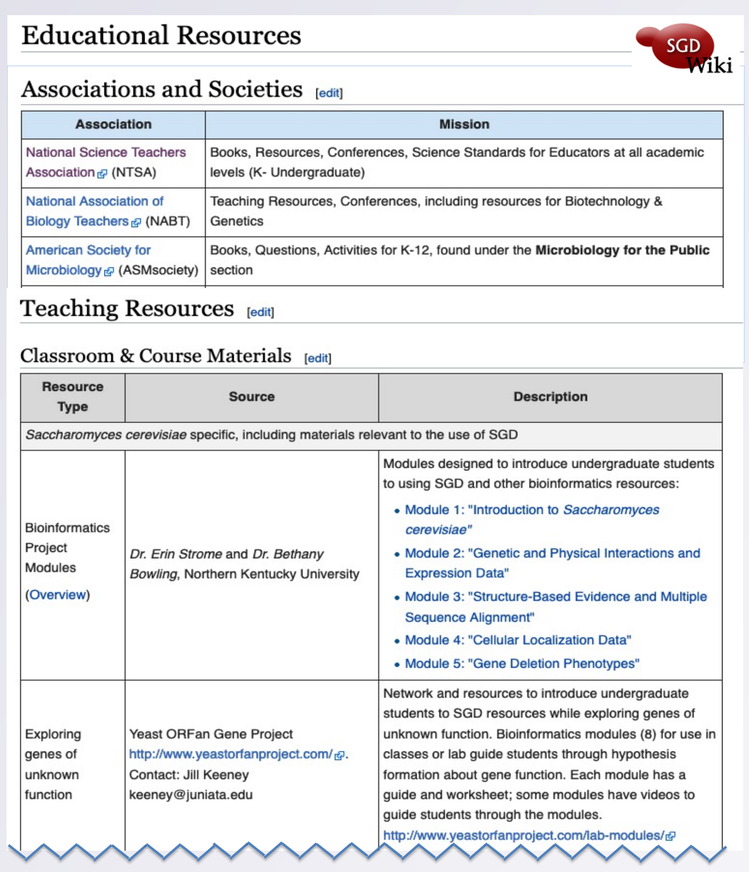
Belle et al. approached their study by noting that BRCA1 mainly affects DNA repair and genome stability, and that yeast has a full toolbox for studying these processes. The team previously demonstrated that pathogenic BRCA1 variants increase the rates of intra- and interchromosomal homologous recombination (HR) and also gene reversion (GR) in yeast.

For the current study, they developed a diploid strain that allows simultaneous assessment of intra- and interchromosomal HR by use of two mutated markers, one that repairs by intrachromosomal exchange and the other by interchromosomal exchange. When they induced BRCA1 variants from a plasmid, they were able to compare rates of HR (compared to the WT BRCA1 gene) by the simple use of plate assays.

Community Wiki: Educational Resources

https://wiki.yeastgenome.org/index.php/Educational_Resources

- Associations and Societies
- Teaching Resources (Classroom & Course Materials, Courses, Fun Sites)
- General Learning (Books, Dedicated sites, Tutorials & Presentations



Educational Resources

SGD Wiki

Associations and Societies [edit]

Association	Mission
National Science Teachers Association (NTSA)	Books, Resources, Conferences, Science Standards for Educators at all academic levels (K- Undergraduate)
National Association of Biology Teachers (NABT)	Teaching Resources, Conferences, including resources for Biotechnology & Genetics
American Society for Microbiology (ASMsociety)	Books, Questions, Activities for K-12, found under the **Microbiology for the Public** section

Teaching Resources [edit]

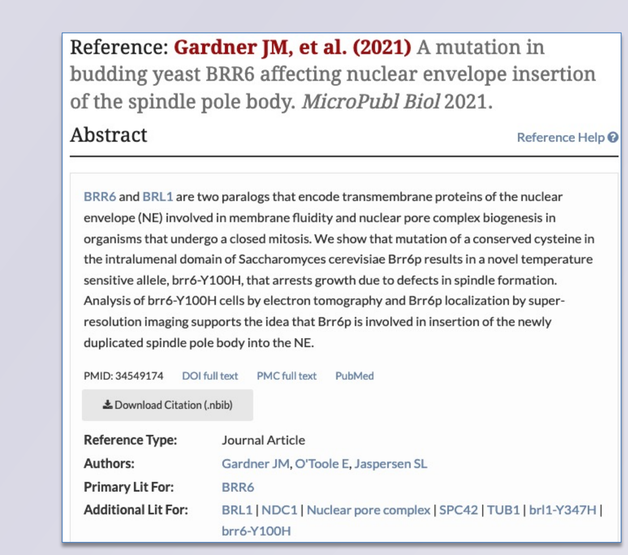
Classroom & Course Materials [edit]

Resource Type	Source	Description
Saccharomyces cerevisiae specific, including materials relevant to the use of SGD		
Bioinformatics Project Modules (Overview)	*Dr. Erin Strome* and *Dr. Bethany Bowling*, Northern Kentucky University	Modules designed to introduce undergraduate students to using SGD and other bioinformatics resources: • Module 1: "Introduction to *Saccharomyces cerevisiae*" • Module 2: "Genetic and Physical Interactions and Expression Data" • Module 3: "Structure-Based Evidence and Multiple Sequence Alignment" • Module 4: "Cellular Localization Data" • Module 5: "Gene Deletion Phenotypes"
Exploring genes of unknown function	Yeast ORFan Gene Project http://www.yeastorfanproject.com/. Contact: Jill Keeney keeney@juniata.edu	Network and resources to introduce undergraduate students to SGD resources while exploring genes of unknown function. Bioinformatics modules (8) for use in classes or lab guide students through hypothesis formation about gene function. Each module has a guide and worksheet; some modules have videos to guide students through the modules. http://www.yeastorfanproject.com/lab-modules/

Micropublications

https://www.micropublication.org/

- Publish brief, novel findings, technically sound research results
- Peer reviewed, assigned a DOI and indexed in PMC, PubMed, EuropePMC
- Curated, deposited to and integrated in community databases like SGD
- Rapidly publish findings of interest to the greater scientific community



Reference: **Gardner JM, et al. (2021)** A mutation in budding yeast BRR6 affecting nuclear envelope insertion of the spindle pole body. *MicroPubl Biol* 2021.

Abstract

Reference Help

BRR6 and BRL1 are two paralogs that encode transmembrane proteins of the nuclear envelope (NE) involved in membrane fluidity and nuclear pore complex biogenesis in organisms that undergo a closed mitosis. We show that mutation of a conserved cysteine in the intralumenal domain of Saccharomyces cerevisiae Brr6p results in a novel temperature sensitive allele, brr6-Y100H, that arrests growth due to defects in spindle formation. Analysis of brr6-Y100H cells by electron tomography and Brr6p localization by super-resolution imaging supports the idea that Brr6p is involved in insertion of the newly duplicated spindle pole body into the NE.

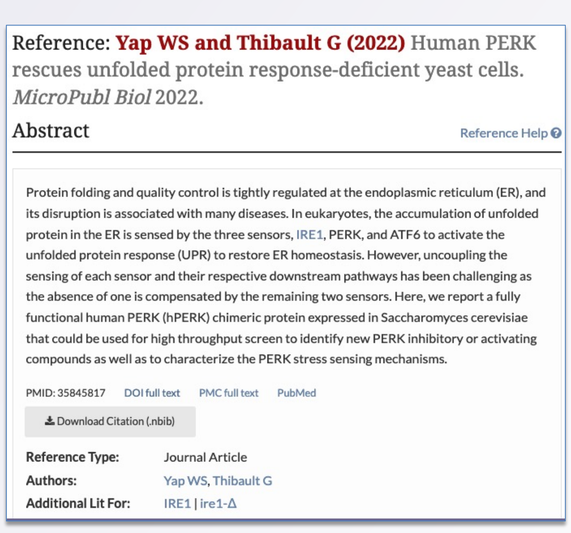
PMID: 34549174 DOI full text PMC full text PubMed

Download Citation (.nbib)

Reference Type: Journal Article
Authors: Gardner JM, O'Toole E, Jaspersen SL
Primary Lit For: BRR6
Additional Lit For: BRL1 | NDC1 | Nuclear pore complex | SPC42 | TUB1 | brl1-Y347H | brr6-Y100H

μP microPublication Biology

get your data out, be cited



Reference: **Yap WS and Thibault G (2022)** Human PERK rescues unfolded protein response-deficient yeast cells. *MicroPubl Biol* 2022.

Abstract

Reference Help

Protein folding and quality control is tightly regulated at the endoplasmic reticulum (ER), and its disruption is associated with many diseases. In eukaryotes, the accumulation of unfolded protein in the ER is sensed by the three sensors, IRE1, PERK, and ATF6 to activate the unfolded protein response (UPR) to restore ER homeostasis. However, uncoupling the sensing of each sensor and their respective downstream pathways has been challenging as the absence of one is compensated by the remaining two sensors. Here, we report a fully functional human PERK (hPERK) chimeric protein expressed in Saccharomyces cerevisiae that could be used for high throughput screen to identify new PERK inhibitory or activating compounds as well as to characterize the PERK stress sensing mechanisms.

PMID: 35845817 DOI full text PMC full text PubMed

Download Citation (.nbib)

Reference Type: Journal Article
Authors: Yap WS, Thibault G
Additional Lit For: IRE1 | ire1-Δ

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