

# Anatomy of the PomBase Main page

PomBase ([www.PomBase.org](http://www.PomBase.org), funded by the Wellcome Trust) is the model organism database for the fission yeast *Schizosaccharomyces pombe*. Its primary goal is to support exploratory and hypothesis-driven research and to promote and support the use of fission yeast as a model eukaryotic system. PomBase integrates the *S. pombe* genome sequence with genetic, molecular and cell biological data, and provides tools to interrogate these data. A longer term goal of PomBase is to provide a detailed and comprehensive networked model of a eukaryotic cell.

The front page of PomBase showcases fission yeast research (research spotlight and community curation), and other news of interest to the community. The frontpage provides access to all areas of PomBase as indicated by the numbers in the image below.

The screenshot shows the PomBase homepage with the following elements and callouts:

- 1**: Search bar at the top right.
- 2**: Navigation menu at the top including Search, Submit, Genome status, Downloads, Community, About, and Help.
- 3**: Links for About, Advanced search, and GO process overview.
- 4**: Examples: Gene, Term, and Publication.
- 5**: Archive link in the Explore PomBase: Help! section.

**Welcome to PomBase**  
PomBase is a comprehensive database for the fission yeast *Schizosaccharomyces pombe*, providing structural and functional annotation, literature curation and access to large-scale data sets

**Research spotlight: Bestul AJ et al., 2017**  
Molecular model of fission yeast centrosome assembly determined by superresolution imaging. Originally published in JCB.  
Publication record in PomBase ...  
Archive ...

**Recent community curation**  
Lingering single-strand breaks trigger Rad51-independent homology-directed ...  
RNase H eliminates R-loops that disrupt DNA replication but is ...  
Inhibition of Ras activity coordinates cell fusion with cell-cell ...  
Atg20- and Atg24-family proteins promote organelle autophagy ...  
All community curation ...

**Explore PomBase: Help!**  
PomBase provides extensive documentation and answers many questions in the FAQ. For any information you can't find there, please contact the helpdesk .  
Archive ...

**Recent news**  
PomBase releases JBrowse 2018-04-16  
PomBase has now implemented JBrowse, from the GMOD project, as its genome browser. The new browser offers a number of improvements over

**1** - the 'simple search' box. Search for:

- *S. pombe* gene names, or genes orthologous to human or *S. cerevisiae* genes by ortholog name
- Annotations from specific publications by searching for the PubMed ID
- Annotations to specific terms in ontologies (e.g. the Gene Ontology GO, or the fission yeast phenotype ontology FYPO)

**2** - The website navigation menu. Comprised of the following sections:

- Search  
Links to the advanced search (query builder), peptide motif search and genome browser
- Submit  
Links to instructions for contributing data to PomBase
- Genome status  
Links to a gene annotation overview (the GO slim overview) and curation statistics, genome relevant information (sequence status, updates, statistics and coordinate changes), and a list of 'priority unstudied genes' (genes with orthologs in vertebrates not characterized in any species)
- Downloads  
Datasets (e.g. annotation, protein sequences, orthologs), posters and presentations
- Community  
The community hub. Instructions how to subscribe to the fission yeast mailinglist, external links, the news archive, and information about our community curation project
- About  
About PomBase: contact details, how to cite the website, terms of use, etc
- Help  
FAQ and documentation

**3** - Quick links to the about page, advanced search (query builder) and gene annotation overview

**4** - Links to an example gene page, GO term page, and publication page

**5** - Explore PomBase - rotating help articles, click the 'archive' link to access all help articles