

Resource Summary Report

Generated by [T1D](#) on Aug 1, 2026

PomBase

RRID:SCR_006586

Type: Tool

Proper Citation

PomBase (RRID:SCR_006586)

Resource Information

URL: <http://www.pombase.org/>

Proper Citation: PomBase (RRID:SCR_006586)

Description: Model organism database that provides organization of and access to scientific data for the fission yeast *Schizosaccharomyces pombe*. PomBase supports genomic sequence and features, genome-wide datasets and manual literature curation. PomBase also provides a community hub for researchers, providing genome statistics, a community curation interface, news, events, documentation, mailing lists, and welcomes data submissions.

Abbreviations: PomBase

Synonyms: Schizosaccharomyces pombe Genome Sequencing Project

Resource Type: data or information resource, database, service resource

Defining Citation: [PMID:22039153](#)

Keywords: fission yeast, gene ontology, genome sequence, schizosaccharomyces pombe (4896), schizosaccharomyces pombe, dna, protein, cosmic assembly, intron, go, chromosome, telomere, centromere, mating region, data mapping, model organism, genome, bio.tools, FASEB list

Funding: Wellcome Trust WT090548MA

Availability: Public, Acknowledgement requested

Resource Name: PomBase

Resource ID: SCR_006586

Alternate IDs: biotools:pombase, nlx_144356, r3d100011478

Alternate URLs: <https://bio.tools/pombase>, <https://doi.org/10.17616/R3NS78>

Old URLs: http://www.sanger.ac.uk/Projects/S_pombe/

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260731T042725+0000

Ratings and Alerts

No rating or validation information has been found for PomBase.

No alerts have been found for PomBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 362 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Jiménez-Martín A, et al. (2025) Centromere positioning orchestrates telomere bouquet formation and the initiation of meiotic differentiation. *Nature communications*, 16(1), 837.

Cheng T, et al. (2025) Transcription-replication conflict resolution by nuclear RNA interference. *Molecular cell*, 85(21), 3930.

Hooks MA, et al. (2025) Golgi_traff phylogeny reveals ancient eukaryotic genes with recent surprises: replication and diversification of HID1 domain-containing protein unique to *Schizosaccharomyces*. *FEMS microbiology letters*, 372.

Zhang H, et al. (2025) Fission yeast Caprin protein is required for efficient heterochromatin establishment. *PLoS genetics*, 21(3), e1011620.

Berraquero M, et al. (2025) Ltc1 localization by EMC regulates cell membrane fluidity to facilitate membrane protein biogenesis. *iScience*, 28(3), 112096.

Tan C, et al. (2025) Intracellular diffusion in the cytoplasm increases with cell size in fission yeast. *Molecular biology of the cell*, 36(4), ar51.

Mohamed HABE, et al. (2025) A novel method for telomere length detection in fission yeast. *FEMS yeast research*, 25.

Wei Q, et al. (2025) Site-to-site mutational dissection of fission yeast cohesin reveals its dynamics. *G3 (Bethesda, Md.)*, 15(7).

Schwer B, et al. (2025) Tandem inactivation of inositol pyrophosphatases Asp1, Siw14, and Aps1 illuminates functional redundancies in inositol pyrophosphate catabolism in

fission yeast. *mBio*, 16(5), e0038925.

Papp LA, et al. (2025) Transcriptome changes of fission yeast cells exposed to fumonisin B1 or co-cultured with *Fusarium verticillioides*. *Applied microbiology and biotechnology*, 109(1), 211.

Pathak S, et al. (2025) Differential gene expression drives cell-cycle-dependent transition from monopolar to bipolar growth in fission yeast. *bioRxiv : the preprint server for biology*.

Zeisner TU, et al. (2025) Phosphatase specificity influences phosphorylation timing of CDK substrates during the cell cycle. *Nature communications*, 16(1), 11604.

Zhang S, et al. (2025) The Ync13-Rga7-Rng10 complex selectively coordinates secretory vesicle trafficking and secondary septum formation during cytokinesis. *PLoS biology*, 23(10), e3003466.

Li Y, et al. (2025) Transcriptomic and proteomic effects of gene deletion are not evolutionarily conserved. *Genome research*, 35(3), 512.

Ku? K, et al. (2025) DSIF factor Spt5 coordinates transcription, maturation and exoribonucleolysis of RNA polymerase II transcripts. *Nature communications*, 16(1), 10.

Takeuchi M, et al. (2025) Combinatorial Analyses of Pre-mRNA Splicing-Defective Mutants Reveal Differential Quantitative Requirements for Shelterin in Distinct Telomere Functions. *Genes to cells : devoted to molecular & cellular mechanisms*, 30(6), e70064.

Ren L, et al. (2025) Oligomerization and exocyst coupling underlie Spa2-mediated focusing of polarized growth in fission yeast. *Journal of cell science*, 138(17).

Glauninger H, et al. (2025) Transcriptome-wide mRNP condensation precedes stress granule formation and excludes new mRNAs. *Molecular cell*, 85(23), 4393.

Roche B, et al. (2025) RiboCop surveils pre-rRNA processing by Dicer in cellular quiescence. *bioRxiv : the preprint server for biology*.

Srivastav MK, et al. (2025) PhpCNF-Y transcription factor infiltrates heterochromatin to generate cryptic intron-containing transcripts crucial for small RNA production. *Nature communications*, 16(1), 268.