

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 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: 20260903T234833+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 396 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Gálvez-Merchán C, et al. (2026) Fission yeast Whi5 represses MBF-dependent transcription in quiescent cells. *iScience*, 29(2), 114576.

Durán L, et al. (2026) Sequence bias in chromatin fragmentation leads to misinterpretation of protein-DNA interactions in vivo. *Genome biology*, 27(1).

Laffitte A, et al. (2026) The LINC complex component Kms1 and CENP-B protein Cbp1 cooperate to enforce faithful homology-directed DNA repair at the nuclear periphery in *S. pombe*. *Genes & development*, 40(7-8), 456.

Kamei KF, et al. (2026) Revealing global stoichiometry conservation architecture in cells from Raman spectral patterns. *eLife*, 14.

Patel BI, et al. (2026) Evaluation of Dorado v5.2.0 de novo basecalling models for the detection of tRNA modifications using RNA004 chemistry. *BMC genomics*, 27(1).

Sun Y, et al. (2026) Defective queuosine and i6A/ms2i6A modification of tRNA^{Tyr} cause frameshifting and protein aggregation. *Nucleic acids research*, 54(12).

Bhatt B, et al. (2026) Stress controls heterochromatin inheritance via histone H3 ubiquitylation. *Nature*, 650(8102), 768.

Besson D, et al. (2026) Interplay between cohesin and TORC1 links chromosome segregation and gene expression to environmental changes. *eLife*, 14.

Finkel JM, et al. (2026) Humanization of the *rpb9* Locus in Fission Yeast Reveals Conserved and Divergent Roles of *rpb9* and Human POLR2I. *Genes*, 17(6).

Nirmal MB, et al. (2026) Deletion of Elongator Protein 1 (Elp1) relieves heterochromatin defects in a Pol II mutant of *Schizosaccharomyces pombe*. *Genetics*, 232(2).

Vasilevsky NA, et al. (2026) Mondo: integrating disease terminology across communities. *Genetics*, 232(4).

Carme P, et al. (2026) PomBase in 2026: expanding knowledge, modeling connections. *Genetics*, 232(4).

N'Guessan A, et al. (2026) Parallel but distinct adaptive routes in the budding and fission yeasts after 10,000 generations of experimental evolution. *Nature ecology & evolution*, 10(4), 765.

Kováč B, et al. (2026) Genetic and environmental determinants of multicellular-like phenotypes in fission yeast. *Genetics*, 233(1).

Ghanegolmohammadi F, et al. (2026) Synonymous codon usage defines functional gene families. *BMC biology*, 24(1), 44.

Shi F, et al. (2026) HDGS-Net: nucleosome occupancy prediction based on a hybrid dilated gated separable convolutional neural network. *BMC genomics*, 27(1), 209.

Liu G, et al. (2026) Contributions of DNA mechanics and trans-regulation to nucleosome positioning in *Schizosaccharomyces pombe* and its role in co-transcriptional splicing. *Epigenetics & chromatin*, 19(1).

Giordano G, et al. (2026) Uncoupling the TFIIF Core and Kinase Modules leads to misregulated RNA polymerase II CTD Serine 5 phosphorylation. *eLife*, 15.

Akikusa Y, et al. (2026) Thermosensitivity of cellular translation restricts the growth of fission yeast at high temperatures. *Communications biology*, 9(1).

Mazumder A, et al. (2025) Discrete Subdomains Establish Epigenetic Diversity in Subtelomeric Heterochromatin. *bioRxiv : the preprint server for biology*.