

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 15, 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: 20260912T195642+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 [SPARC SAWG](#) .

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*.