

# Resource Summary Report

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## PomBase

RRID:SCR\_006586

Type: Tool

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### Proper Citation

PomBase (RRID:SCR\_006586)

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### 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/](http://www.sanger.ac.uk/Projects/S_pombe/)

**Record Creation Time:** 20220129T080237+0000

**Record Last Update:** 20260919T195114+0000

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## Ratings and Alerts

No rating or validation information has been found for PomBase.

No alerts have been found for PomBase.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 396 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.

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

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

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

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<sup>Tyr</sup> 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).

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

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).

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

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.

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.

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

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

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

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.