Resource Summary Report

Generated by dkNET on May 8, 2025

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 pombeGenome 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

Alternate URLs: https://bio.tools/pombase

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

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250508T065040+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 338 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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

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

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.

Liu L, et al. (2024) The absence of the ribosomal protein Rpl2702 elicits the MAPK-mTOR signaling to modulate mitochondrial morphology and functions. Redox biology, 73, 103174.

Lopez Maury L, et al. (2024) The Cdc14 phosphatase, Clp1, does not affect genome expression. microPublication biology, 2024.

Sun L, et al. (2024) Heat stress-induced activation of MAPK pathway attenuates Atf1-dependent epigenetic inheritance of heterochromatin in fission yeast. eLife, 13.

Encinar Del Dedo J, et al. (2024) The Greatwall-Endosulfine-PP2A/B55 pathway regulates entry into quiescence by enhancing translation of Elongator-tunable transcripts. Nature communications, 15(1), 10603.

Foltman M, et al. (2024) Central Role of the Actomyosin Ring in Coordinating Cytokinesis Steps in Budding Yeast. Journal of fungi (Basel, Switzerland), 10(9).

Pons C, et al. (2024) Meta-analysis of dispensable essential genes and their interactions with bypass suppressors. Life science alliance, 7(1).

Morozumi Y, et al. (2024) Rapamycin-sensitive mechanisms confine the growth of fission yeast below the temperatures detrimental to cell physiology. iScience, 27(1), 108777.

Cullati SN, et al. (2024) Substrate displacement of CK1 C-termini regulates kinase specificity. Science advances, 10(19), eadj5185.

Marešová A, et al. (2024) Cbf11 and Mga2 function together to activate transcription of lipid metabolism genes and promote mitotic fidelity in fission yeast. PLoS genetics, 20(12), e1011509.

Ohsawa S, et al. (2024) Nitrogen signaling factor triggers a respiration-like gene expression program in fission yeast. The EMBO journal, 43(20), 4604.

Muhammad A, et al. (2024) A systematic quantitative approach comprehensively defines domain-specific functional pathways linked to Schizosaccharomyces pombe heterochromatin regulation. Nucleic acids research, 52(22), 13665.

Schwer B, et al. (2024) Suppression of inositol pyrophosphate toxicosis and hyper-repression of the fission yeast PHO regulon by loss-of-function mutations in chromatin remodelers Snf22 and Sol1. mBio, 15(7), e0125224.

Wang J, et al. (2024) Churros: a Docker-based pipeline for large-scale epigenomic analysis. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(1).

Wang Y, et al. (2024) Natural Transposable Element Insertions Contribute to Host Fitness in Model Yeasts. Genome biology and evolution, 16(9).

Anver S, et al. (2024) Ageing-associated long non-coding RNA extends lifespan and reduces translation in non-dividing cells. EMBO reports, 25(11), 4921.

Bednor L, et al. (2024) Genetic suppressor screen identifies Tgp1 (glycerophosphocholine transporter), Kcs1 (IP6 kinase), and Plc1 (phospholipase C) as determinants of inositol

pyrophosphate toxicosis in fission yeast. mBio, 15(2), e0306223.