

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

WormBase

RRID:SCR_003098

Type: Tool

Proper Citation

WormBase (RRID:SCR_003098)

Resource Information

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

Proper Citation: WormBase (RRID:SCR_003098)

Description: Central data repository for nematode biology including complete genomic sequence, gene predictions and orthology assignments from range of related nematodes. Data concerning genetics, genomics and biology of *C. elegans* and related nematodes. Derived from initial ACeDB database of *C. elegans* genetic and sequence information, WormBase includes genomic, anatomical and functional information of *C. elegans*, other *Caenorhabditis* species and other nematodes. Maintains public FTP site where researchers can find many commonly requested files and datasets, WormBase software and prepackaged databases.

Abbreviations: WB, WB REF, WP

Synonyms: , WB, Worm Base, WB REF, WP

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

Defining Citation: [PMID:24194605](#), [PMID:19910365](#), [PMID:17991679](#), [PMID:15608221](#)

Keywords: RIN, Resource Information Network, catalog, database, blast, genomic sequence, gene prediction, orthology assignment, gene function, ortholog, roundworm, geneotype, phenotype, gene mapping, genomics, gene expression, transposon family, *c elegans*, wormmart, FASEB list, RRID Community Authority

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Resource Name: WormBase

Resource ID: SCR_003098

Alternate IDs: nif-0000-00053, OMICS_01664, r3d100010424

Alternate URLs: <http://www.wormbase.org/#01-23-6>, <https://doi.org/10.17616/R3089Z>

License: CC0, CC BY 4.0

License URLs: <https://wormbase.org/about/policies#23--10>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132458+0000

Ratings and Alerts

No rating or validation information has been found for WormBase.

No alerts have been found for WormBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1911 mentions in open access literature.

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

Qu X, et al. (2026) Investigation of epilepsy-related genes in a Drosophila model. Neural regeneration research, 21(1), 195.

Collington EL, et al. (2026) Widespread gene fusion artifacts in helminth genome annotations. BMC genomics, 27(1).

Ajmera S, et al. (2026) Curation of the Fasciola hepatica kinome as a resource for drug target discovery. BMC genomics, 27(1), 98.

Schaveling AS, et al. (2026) The potato cyst nematode Globodera pallida overcomes major potato resistance through selection on standing variation at a single locus. The New phytologist, 249(6), 3039.

Panagiotidis K, et al. (2026) Mapping molluscan endocrinology: a systematic and critical appraisal. Biological reviews of the Cambridge Philosophical Society, 101(2), 970.

Huynh L, et al. (2026) Canonical and noncanonical Hippo signaling in C. elegans. Genetics, 233(1).

Klapproth C, et al. (2026) Computational Analysis of Telomerase RNA Evolution in *Caenorhabditis* Species. *Non-coding RNA*, 12(1).

Chawla B, et al. (2026) Condensin IDC has a functional ATPase that is required for X-Chromosome dosage compensation in *C. elegans*. *Genetics*, 233(1).

DiNardo AL, et al. (2026) *Caenorhabditis elegans* form sexually dimorphic and dynamic germ granules throughout meiotic prophase I progression. *bioRxiv : the preprint server for biology*.

Elaswad MT, et al. (2026) Targeted RNAi screen reveals novel regulators of RNA-binding protein phase transitions in *Caenorhabditis elegans* oocytes. *G3 (Bethesda, Md.)*, 16(1).

Lou A, et al. (2026) Cell atlases and the developmental foundations of the phenotype. *PLoS computational biology*, 22(2), e1013944.

Huang R, et al. (2026) p38 MAPK orchestrates cross-tissue potassium homeostasis for survival. *Nature communications*, 17(1).

Niu L, et al. (2026) A scaffold attachment factor PHM-2 regulates synaptic transmission through SLO-2 potassium channel in *C. elegans*. *PLoS genetics*, 22(3), e1011962.

Freire CF, et al. (2026) Comprehensive *Schistosoma mansoni* Hierarchical Transcriptome Assembly Points to Novel lncRNAs Associated with Sexual Dimorphism. *Non-coding RNA*, 12(2).

Vajs V, et al. (2026) Integrated transcriptomic and proteomic analysis of cancer-suppressive *Mesocostoides corti* larvae. *Parasites & vectors*, 19(1).

Roca M, et al. (2026) Evolution of sensory systems underlies the emergence of predatory feeding behaviors in nematodes. *Proceedings of the National Academy of Sciences of the United States of America*, 123(5), e2514172123.

Gürhanl? A, et al. (2026) rbpCNN: a biophysics-informed deep learning model for predicting piRNA and mRNA interactions. *Scientific reports*, 16(1).

Bell AD, et al. (2026) Allelic Variation at tRNA Genes in Three Nematode Species Indicates Mutation Load Despite Strong Purifying Selection. *Genome biology and evolution*, 18(3).

Li DZ, et al. (2026) An antifungal effector from a plant-parasitic nematode modulates host fungal community composition and supports ecological fitness. *NPJ biofilms and microbiomes*, 12(1).

Langleib M, et al. (2026) Transcriptome profiling of intra-snail stages of the liver fluke *Fasciola hepatica* reveals key mediators underlying parasite development and interaction with the host. *BMC genomics*, 27(1).