

Resource Summary Report

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[Pristionchus.org](#)

RRID:SCR_003414

Type: Tool

Proper Citation

Pristionchus.org (RRID:SCR_003414)

Resource Information

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

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Description: This data resource is a genetic, molecular, and genomic toolkit that establishes one particular species, *Pristionchus pacificus*, as a major satellite system for evolutionary developmental biology. Users may download *Pristionchus* Sequences and use the *Pristionchus pacificus* genome browser where they may find gene or gene prediction data. Users can also use the BLAST feature, which allows users to search the assembly for position information of bacs, reads and contigs using the mapping tool. The center of the site's research is the evolutionary analysis of vulva formation. The general aim of the Department is to develop the nematode vulva as a suitable case study into the evolutionary alterations of developmental processes. By studying and comparing two distantly related species of the same phylum, such as *P. pacificus* and *C. elegans*, macroevolutionary alterations of developmental processes and mechanisms can be identified. The final goal of the Department is to achieve a comprehensive description of macro- and microevolutionary changes of developmental mechanisms at the molecular level in a phylogenetic and ecological context.

Synonyms: www.pristionchus.org

Resource Type: data analysis service, data or information resource, database, service resource, production service resource, analysis service resource

Defining Citation: [PMID:17062617](#)

Keywords: pristionchus, pristionchus pacificus, database, data analysis service, genetic toolkit, molecular toolkit, genomic toolkit

Availability: Free, Freely available

Resource Name: Pristionchus.org

Resource ID: SCR_003414

Alternate IDs: nif-0000-03339

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260801T042532+0000

Ratings and Alerts

No rating or validation information has been found for [Pristionchus.org](#).

No alerts have been found for [Pristionchus.org](#).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Piskobulu V, et al. (2025) High Nutritional Conditions Influence Feeding Plasticity in *Pristionchus pacificus* and Render Worms Non-Predatory. *Journal of experimental zoology. Part B, Molecular and developmental evolution*, 344(2), 94.

Levis NA, et al. (2025) Genomic parallelism defines repeated evolution of an inducible offense. *Science advances*, 11(42), eadw9964.

Zhang P, et al. (2025) Biosynthesis of modular signaling molecules requires functional diversification of carboxylesterases in *Pristionchus pacificus*. *Communications biology*, 8(1), 1213.

Wighard S, et al. (2024) Conserved switch genes that arose via whole-genome duplication regulate a cannibalistic nematode morph. *Science advances*, 10(15), eadk6062.

Theska T, et al. (2024) Starvation resistance in the nematode *Pristionchus pacificus* requires a conserved supplementary nuclear receptor. *Zoological letters*, 10(1), 7.

Nakayama K, et al. (2024) cGMP-dependent pathway and a GPCR kinase are required for photoreponse in the nematode *Pristionchus pacificus*. *PLoS genetics*, 20(11), e1011320.

Lo WS, et al. (2024) Microbiota succession influences nematode physiology in a beetle microcosm ecosystem. *Nature communications*, 15(1), 5137.

Kursel LE, et al. (2024) Skp1 is a conserved structural component of the meiotic synaptonemal complex. *bioRxiv : the preprint server for biology*.

Almeida AC, et al. (2024) An evolutionary perspective on the relationship between kinetochore size and CENP-E dependence for chromosome alignment. *Journal of cell science*, 137(24).

Ishita Y, et al. (2023) Co-option of an Astacin Metalloprotease Is Associated with an Evolutionarily Novel Feeding Morphology in a Predatory Nematode. *Molecular biology and evolution*, 40(12).

Lo WS, et al. (2022) Synergistic interaction of gut microbiota enhances the growth of nematode through neuroendocrine signaling. *Current biology : CB*, 32(9), 2037.

Han Z, et al. (2022) Horizontally Acquired Cellulases Assist the Expansion of Dietary Range in *Pristionchus* Nematodes. *Molecular biology and evolution*, 39(2).

Röseler W, et al. (2022) The improved genome of the nematode *Parapristionchus gibbindavisi* provides insights into lineage-specific gene family evolution. *G3 (Bethesda, Md.)*, 12(10).

Wenzel MA, et al. (2021) SLIDR and SLOPPR: flexible identification of spliced leader trans-splicing and prediction of eukaryotic operons from RNA-Seq data. *BMC bioinformatics*, 22(1), 140.

Rillo-Bohn R, et al. (2021) Analysis of meiosis in *Pristionchus pacificus* reveals plasticity in homolog pairing and synapsis in the nematode lineage. *eLife*, 10.

Sun S, et al. (2021) Single worm transcriptomics identifies a developmental core network of oscillating genes with deep conservation across nematodes. *Genome research*, 31(9), 1590.

Athanasouli M, et al. (2020) Comparative genomics and community curation further improve gene annotations in the nematode *Pristionchus pacificus*. *BMC genomics*, 21(1), 708.

Rödelsperger C, et al. (2019) Crowdsourcing and the feasibility of manual gene annotation: A pilot study in the nematode *Pristionchus pacificus*. *Scientific reports*, 9(1), 18789.

Prabh N, et al. (2019) De Novo, Divergence, and Mixed Origin Contribute to the Emergence of Orphan Genes in *Pristionchus* Nematodes. *G3 (Bethesda, Md.)*, 9(7), 2277.

Hong RL, et al. (2019) Evolution of neuronal anatomy and circuitry in two highly divergent nematode species. *eLife*, 8.