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: analysis service resource, data analysis service, data or information resource, database, production service resource, 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: 20260829T182741+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 38 mentions in open access literature.

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

Ishita Y, et al. (2026) Characterization of Heat Shock Protein Expression and Its Application to Temporal Gene Expression in the Nematode Pristionchus pacificus. Development, growth & differentiation, 68(2), e70045.

Wang Y, et al. (2026) Bacterial diet influences mutation rate in Pristionchus pacificus. G3 (Bethesda, Md.), 16(4).

Castro DL, et al. (2026) The rewiring of a terminal selector regulatory cascade generates convergent neuronal laterality. PLoS genetics, 22(2), e1011782.

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.

Nakayama K, et al. (2024) cGMP-dependent pathway and a GPCR kinase are required for photoresponse 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.

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

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).

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

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).

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

Athanasouli M, et al. (2022) Analysis of repeat elements in the Pristionchus pacificus genome reveals an ancient invasion by horizontally transferred transposons. BMC genomics, 23(1), 523.

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.

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.

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.