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, service resource, database, analysis service resource, data or information resource, production service resource

Defining Citation: PMID:17062617

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

Funding:

Availability: Available to the research community, Results are available for download

Resource Name: Pristionchus.org

Resource ID: SCR_003414

Alternate IDs: nif-0000-03339

Record Creation Time: 20220129T080218+0000

Record Last Update: 20250430T055220+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 30 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

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

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

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.

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 giblindavisi provides insights into lineage-specific gene family evolution. G3 (Bethesda, Md.), 12(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.

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.

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

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.

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

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.

Falcke JM, et al. (2018) Linking Genomic and Metabolomic Natural Variation Uncovers Nematode Pheromone Biosynthesis. Cell chemical biology, 25(6), 787.

Bui LT, et al. (2018) A sulfotransferase dosage-dependently regulates mouthpart polyphenism in the nematode Pristionchus pacificus. Nature communications, 9(1), 4119.

Sieriebriennikov B, et al. (2017) The Role of DAF-21/Hsp90 in Mouth-Form Plasticity in Pristionchus pacificus. Molecular biology and evolution, 34(7), 1644.

Moreno E, et al. (2017) Regulation of hyperoxia-induced social behaviour in Pristionchus pacificus nematodes requires a novel cilia-mediated environmental input. Scientific reports, 7(1), 17550.