

Resource Summary Report

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[nematodes.org](http://www.nematodes.org)

RRID:SCR_003267

Type: Tool

Proper Citation

nematodes.org (RRID:SCR_003267)

Resource Information

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

Proper Citation: nematodes.org (RRID:SCR_003267)

Description: Nematode & Neglected Genomics (at) The Blaxter Lab is a nematode related portal including databases and services. Resources include genomic and transcriptomic databases for nematodes and other metazoan phyla and freely downloadable software tools for expressed sequence tag analysis, DNA barcode analysis and phylogenomics. Major categories include: * GenePool * 959 Nematode Genomes * Teaching * Research Projects * Bioinformatics Software Tools * Lab Personnel * Lab Wiki * Genomics Databases * NEMBASE4 * Tardigrada: *Hypsibius dujardini* * Earthworm: *Lumbricus rubellus* * MolluscDB * ArthropodDB * other Neglected Genomes

Abbreviations: nematodes.org

Synonyms: Nematode & Neglected Genomics (at) The Blaxter Lab, Blaxter Lab, Nematode and Neglected Genomics, nematodes.org Nematode & Neglected Genomics (at) The Blaxter Lab, Nematode & Neglected Genomics

Resource Type: topical portal, data or information resource, organism-related portal, portal

Keywords: nematode, genomics, genome, gene, database, transcriptome, analysis tool, bioinformatics, genomics databases, software, expressed sequence tag, analysis, dna barcode, phylogenomics, FASEB list

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: nematodes.org

Resource ID: SCR_003267

Alternate IDs: nif-0000-03187

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260801T190218+0000

Ratings and Alerts

No rating or validation information has been found for nematodes.org.

No alerts have been found for nematodes.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 [RRID](#) .

Papaleo S, et al. (2025) Nucleotide composition shapes gene expression in Wolbachia pipientis: a role for MidA methyltransferase? mSystems, 10(9), e0077925.

Chung M, et al. (2020) A Meta-Analysis of Wolbachia Transcriptomics Reveals a Stage-Specific Wolbachia Transcriptional Response Shared Across Different Hosts. G3 (Bethesda, Md.), 10(9), 3243.

Ibáñez-Shimabukuro M, et al. (2019) Structure and ligand binding of As-p18, an extracellular fatty acid binding protein from the eggs of a parasitic nematode. Bioscience reports, 39(7).

Fernández-Soto P, et al. (2016) Strong-LAMP: A LAMP Assay for Strongyloides spp. Detection in Stool and Urine Samples. Towards the Diagnosis of Human Strongyloidiasis Starting from a Rodent Model. PLoS neglected tropical diseases, 10(7), e0004836.

Campbell B, et al. (2016) Paramyosin of canine Onchocerca lupi: usefulness for the diagnosis of a neglected zoonotic disease. Parasites & vectors, 9(1), 493.

Morris CP, et al. (2015) A Proteomic Analysis of the Body Wall, Digestive Tract, and Reproductive Tract of Brugia malayi. PLoS neglected tropical diseases, 9(9), e0004054.

Zickmann F, et al. (2015) MProGene: integrative proteogenomics beyond six-frames and single nucleotide polymorphisms. Bioinformatics (Oxford, England), 31(12), i106.

Corsi AK, et al. (2015) A Transparent Window into Biology: A Primer on Caenorhabditis elegans. Genetics, 200(2), 387.

Zarowiecki M, et al. (2015) What helminth genomes have taught us about parasite evolution. Parasitology, 142 Suppl 1(Suppl 1), S85.

Nascimento FX, et al. (2014) New insights into 1-aminocyclopropane-1-carboxylate (ACC) deaminase phylogeny, evolution and ecological significance. PloS one, 9(6), e99168.

Kotze AC, et al. (2014) Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. International journal for parasitology. Drugs and drug resistance, 4(3), 164.

Iberkleid I, et al. (2013) Fatty acid-and retinol-binding protein, Mj-FAR-1 induces tomato host susceptibility to root-knot nematodes. PloS one, 8(5), e64586.

Buck AH, et al. (2013) Functional diversification of Argonautes in nematodes: an expanding universe. Biochemical Society transactions, 41(4), 881.

Weber KP, et al. (2012) Analysis of *C. elegans* NR2E nuclear receptors defines three conserved clades and ligand-independent functions. BMC evolutionary biology, 12, 81.

Millares P, et al. (2012) Proteomic profiling and protein identification by MALDI-TOF mass spectrometry in unsequenced parasitic nematodes. PloS one, 7(3), e33590.

Finn RD, et al. (2012) Making your database available through Wikipedia: the pros and cons. Nucleic acids research, 40(Database issue), D9.

Tyson T, et al. (2012) A molecular analysis of desiccation tolerance mechanisms in the anhydrobiotic nematode *Panagrolaimus superbus* using expressed sequenced tags. BMC research notes, 5, 68.

Yan C, et al. (2012) A method for rapid and simultaneous mapping of genetic loci and introgression sizes in nematode species. PloS one, 7(8), e43770.

Tarr DE, et al. (2012) Distribution and characteristics of ABFs, cecropins, nemapores, and lysozymes in nematodes. Developmental and comparative immunology, 36(3), 502.

Jones M, et al. (2011) jMOTU and Taxonerator: turning DNA Barcode sequences into annotated operational taxonomic units. PloS one, 6(4), e19259.