

# Resource Summary Report

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## NEMBASE

RRID:SCR\_006070

Type: Tool

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### Proper Citation

NEMBASE (RRID:SCR\_006070)

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### Resource Information

**URL:** <http://www.nematodes.org/nembase4/>

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**Description:** NEMBASE is a comprehensive Nematode Transcriptome Database including 63 nematode species, over 600,000 ESTs and over 250,000 proteins. Nematode parasites are of major importance in human health and agriculture, and free-living species deliver essential ecosystem services. The genomics revolution has resulted in the production of many datasets of expressed sequence tags (ESTs) from a phylogenetically wide range of nematode species, but these are not easily compared. NEMBASE4 presents a single portal into extensively functionally annotated, EST-derived transcriptomes from over 60 species of nematodes, including plant and animal parasites and free-living taxa. Using the PartiGene suite of tools, we have assembled the publicly available ESTs for each species into a high-quality set of putative transcripts. These transcripts have been translated to produce a protein sequence resource and each is annotated with functional information derived from comparison with well-studied nematode species such as *Caenorhabditis elegans* and other non-nematode resources. By cross-comparing the sequences within NEMBASE4, we have also generated a protein family assignment for each translation. The data are presented in an openly accessible, interactive database. An example of the utility of NEMBASE4 is that it can examine the uniqueness of the transcriptomes of major clades of parasitic nematodes, identifying lineage-restricted genes that may underpin particular parasitic phenotypes, possible viral pathogens of nematodes, and nematode-unique protein families that may be developed as drug targets.

**Abbreviations:** NEMBASE

**Synonyms:** NEMBASE4, NEMBASE4 - Nematode Transcriptome Analyses

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

**Defining Citation:** [PMID:21550347](#), [PMID:14681449](#)

**Keywords:** nematode, transcriptome, expressed sequence tag, protein, cluster, library, sequence, peptide prediction, functional annotation, gene family, gene, annotation, pathway, genome, partigene, bio.tools

**Funding:** Wellcome Trust ;  
Hospital for Sick Children ;  
BBSRC ;  
MRC ;  
NERC

**Availability:** Public

**Resource Name:** NEMBASE

**Resource ID:** SCR\_006070

**Alternate IDs:** nlx\_151476, biotools:nembase4

**Alternate URLs:** <https://bio.tools/nembase4>

**Record Creation Time:** 20220129T080234+0000

**Record Last Update:** 20260804T043259+0000

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## Ratings and Alerts

No rating or validation information has been found for NEMBASE.

No alerts have been found for NEMBASE.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Pietrow RE, et al. (2025) Wb5, a novel biomarker for monitoring efficacy and success of mass drug administration programs for *Wuchereria bancrofti* elimination. PLoS neglected tropical diseases, 19(5), e0013146.

Elashry AM, et al. (2020) Transcriptome and Parasitome Analysis of Beet Cyst Nematode *Heterodera schachtii*. Scientific reports, 10(1), 3315.

Bogale M, et al. (2020) Nematode Identification Techniques and Recent Advances. Plants (Basel, Switzerland), 9(10).

Umair S, et al. (2020) Characterisation and structural analysis of glyoxylate cycle enzymes of *Teladorsagia circumcincta*. *Molecular and biochemical parasitology*, 240, 111335.

Vicente CSL, et al. (2019) Identification and characterization of the first pectin methylesterase gene discovered in the root lesion nematode *Pratylenchus penetrans*. *PloS one*, 14(2), e0212540.

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).

Roderick H, et al. (2018) Rational design of biosafe crop resistance to a range of nematodes using RNA interference. *Plant biotechnology journal*, 16(2), 520.

Mani T, et al. (2018) G-protein-coupled receptor genes of *Dirofilaria immitis*. *Molecular and biochemical parasitology*, 222, 6.

Mani T, et al. (2017) Polymorphism in ABC transporter genes of *Dirofilaria immitis*. *International journal for parasitology. Drugs and drug resistance*, 7(2), 227.

Yang D, et al. (2017) Comparative analysis of pre- and post-parasitic transcriptomes and mining pioneer effectors of *Heterodera avenae*. *Cell & bioscience*, 7, 11.

Stoltzfus JD, et al. (2017) Perusal of parasitic nematode 'omics in the post-genomic era. *Molecular and biochemical parasitology*, 215, 11.

Somvanshi VS, et al. (2016) A transcriptomic insight into the infective juvenile stage of the insect parasitic nematode, *Heterorhabditis indica*. *BMC genomics*, 17, 166.

Mani T, et al. (2016) Polymorphism in ion channel genes of *Dirofilaria immitis*: Relevant knowledge for future anthelmintic drug design. *International journal for parasitology. Drugs and drug resistance*, 6(3), 343.

Tzelos T, et al. (2016) A preliminary proteomic characterisation of extracellular vesicles released by the ovine parasitic nematode, *Teladorsagia circumcincta*. *Veterinary parasitology*, 221, 84.

Hernández-Vargas MJ, et al. (2016) An Insight into the Triabin Protein Family of American Hematophagous Reduviids: Functional, Structural and Phylogenetic Analysis. *Toxins*, 8(2), 44.

Vieira P, et al. (2015) The *Pratylenchus penetrans* Transcriptome as a Source for the Development of Alternative Control Strategies: Mining for Putative Genes Involved in Parasitism and Evaluation of in planta RNAi. *PloS one*, 10(12), e0144674.

Eves-van den Akker S, et al. (2014) The transcriptome of *Nacobbus aberrans* reveals insights into the evolution of sedentary endoparasitism in plant-parasitic nematodes. *Genome biology and evolution*, 6(9), 2181.

Kumar M, et al. (2014) De novo transcriptome sequencing and analysis of the cereal cyst nematode, *Heterodera avenae*. *PloS one*, 9(5), e96311.

McNeilly TN, et al. (2014) Immune modulation by helminth parasites of ruminants: implications for vaccine development and host immune competence. *Parasite* (Paris, France), 21, 51.

Bouchery T, et al. (2012) The chemokine CXCL12 is essential for the clearance of the filaria *Litomosoides sigmodontis* in resistant mice. *PloS one*, 7(4), e34971.