

Resource Summary Report

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NEXTDB

RRID:SCR_004480

Type: Tool

Proper Citation

NEXTDB (RRID:SCR_004480)

Resource Information

URL: <http://nematode.lab.nig.ac.jp/>

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Description: Expression pattern map of the 100Mb genome of the nematode *Caenorhabditis elegans* through EST analysis and systematic whole mount in situ hybridization. NEXTDB is the database to integrate all information from their expression pattern project and to make the data available to the scientific community. Information available in the current version is as follows: * Map: Visual expression of the relationships among the cosmids, predicted genes and the cDNA clones. * Image: In situ hybridization images that are arranged by their developmental stages. * Sequence: Tag sequences of the cDNA clones are available. * Homology: Results of BLASTX search are available. Users of the data presented on our web pages should not publish the information without our permission and appropriate acknowledgment. Methods are available for: * In situ hybridization on whole mount embryos of *C.elegans* * Protocols for large scale in situ hybridization on *C.elegans* larvae

Abbreviations: NextDB

Synonyms: Nematode Expression Pattern DataBase

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

Keywords: rnai phenotype, homology, blast, fasta, chromosome map, cosmid, gene, cDNA clone, genome, in situ hybridization, expressed sequence tag, developmental stage, sequence, embryonic *Caenorhabditis elegans*, chromosome, phenotype, blastx, clone, sequence tag, yac, predicted gene, protein, development, larval *Caenorhabditis elegans*, image collection, experimental protocol, FASEB list

Funding: Core Research for Evolutional Science and Technology ;
Japan Science and Technology Corporation ;

Japanese Ministry of Education Culture Sports Science and Technology MEXT

Availability: Permission required, Acknowledgement required

Resource Name: NEXTDB

Resource ID: SCR_004480

Alternate IDs: nlx_46406

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260821T193725+0000

Ratings and Alerts

No rating or validation information has been found for NEXTDB.

No alerts have been found for NEXTDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Truong L, et al. (2023) Single-nucleus resolution mapping of the adult *C. elegans* and its application to elucidate inter- and trans-generational response to alcohol. *Cell reports*, 42(6), 112535.

Blanchette CR, et al. (2017) Functional Requirements for Heparan Sulfate Biosynthesis in Morphogenesis and Nervous System Development in *C. elegans*. *PLoS genetics*, 13(1), e1006525.

Tang H, et al. (2017) Fatty Acids Regulate Germline Sex Determination through ACS-4-Dependent Myristoylation. *Cell*, 169(3), 457.

Spiró Z, et al. (2015) Polarity-dependent asymmetric distribution and MEX-5/6-mediated translational activation of the Era-1 mRNA in *C. elegans* embryos. *PloS one*, 10(3), e0120984.

Praslicka B, et al. (2015) The *C. elegans* NR4A nuclear receptor gene *nhr-6* promotes cell cycle progression in the spermatheca lineage. *Developmental dynamics : an official publication of the American Association of Anatomists*, 244(3), 417.

Kim SH, et al. (2015) EZH2 protects glioma stem cells from radiation-induced cell death in a MELK/FOXM1-dependent manner. *Stem cell reports*, 4(2), 226.

George-Raizen JB, et al. (2014) Dynamically-expressed prion-like proteins form a cuticle in the pharynx of *Caenorhabditis elegans*. *Biology open*, 3(11), 1139.

Ortiz MA, et al. (2014) A new dataset of spermatogenic vs. oogenic transcriptomes in the nematode *Caenorhabditis elegans*. *G3 (Bethesda, Md.)*, 4(9), 1765.

Greer EL, et al. (2014) A histone methylation network regulates transgenerational epigenetic memory in *C. elegans*. *Cell reports*, 7(1), 113.

Mikoláš P, et al. (2013) GEI-8, a homologue of vertebrate nuclear receptor corepressor NCoR/SMRT, regulates gonad development and neuronal functions in *Caenorhabditis elegans*. *PloS one*, 8(3), e58462.

Pushpa K, et al. (2013) PUF-8 and TCER-1 are essential for normal levels of multiple mRNAs in the *C. elegans* germline. *Development (Cambridge, England)*, 140(6), 1312.

Ghai V, et al. (2012) Transcriptional regulation of HLH-6-independent and subtype-specific genes expressed in the *Caenorhabditis elegans* pharyngeal glands. *Mechanisms of development*, 129(9-12), 284.

Heustis RJ, et al. (2012) Pharyngeal polysaccharide deacetylases affect development in the nematode *C. elegans* and deacetylate chitin in vitro. *PloS one*, 7(7), e40426.

Mainpal R, et al. (2011) PUF-8 suppresses the somatic transcription factor PAL-1 expression in *C. elegans* germline stem cells. *Developmental biology*, 360(1), 195.

Raharjo WH, et al. (2011) Cell architecture: surrounding muscle cells shape gland cell morphology in the *Caenorhabditis elegans* pharynx. *Genetics*, 189(3), 885.

Waters K, et al. (2010) Genome-wide analysis of germ cell proliferation in *C. elegans* identifies VRK-1 as a key regulator of CEP-1/p53. *Developmental biology*, 344(2), 1011.

Furuhashi H, et al. (2010) Trans-generational epigenetic regulation of *C. elegans* primordial germ cells. *Epigenetics & chromatin*, 3(1), 15.

Sommermann EM, et al. (2010) Endoderm development in *Caenorhabditis elegans*: the synergistic action of ELT-2 and -7 mediates the specification?differentiation transition. *Developmental biology*, 347(1), 154.

Hench J, et al. (2009) Spatio-temporal reference model of *Caenorhabditis elegans* embryogenesis with cell contact maps. *Developmental biology*, 333(1), 1.

Hillwig MS, et al. (2009) Zebrafish RNase T2 genes and the evolution of secretory ribonucleases in animals. *BMC evolutionary biology*, 9, 170.