

Resource Summary Report

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RNAiDB

RRID:SCR_007900

Type: Tool

Proper Citation

RNAiDB (RRID:SCR_007900)

Resource Information

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

Proper Citation: RNAiDB (RRID:SCR_007900)

Description: It provides access to results from RNAi interference studies in *C. elegans*, including images, movies, phenotypes, and graphical maps. RNAiDB contains all published RNAi experiments in *C. elegans* that have been deposited in WormBase, including data from the literature and published large-scale RNAi studies. RNAi to gene mappings for all experiments have been re-analyzed using ePCR and/or a sliding n-mer window method to identify all genes in different genomic locations that may potentially be inhibited by each experiment. Gene maps showing canonical and putative alternate mappings are displayed graphically on RNAi Experiment and Gene/ORF card pages.

Synonyms: RNAiDB

Resource Type: database, data or information resource

Resource Name: RNAiDB

Resource ID: SCR_007900

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260725T191152+0000

Ratings and Alerts

No rating or validation information has been found for RNAiDB.

No alerts have been found for RNAiDB.

Data and Source Information

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Misra S, et al. (2017) RNA interference mediated knockdown of *Brugia malayi* UDP-Galactopyranose mutase severely affects parasite viability, embryogenesis and in vivo development of infective larvae. *Parasites & vectors*, 10(1), 34.

Lu CJ, et al. (2016) Nuclear receptor nhr-48 is required for pathogenicity of the second stage (J2) of the plant parasite *Meloidogyne incognita*. *Scientific reports*, 6, 34959.

Maia AF, et al. (2015) Genome-wide RNAi screen for synthetic lethal interactions with the *C. elegans* kinesin-5 homolog BMK-1. *Scientific data*, 2, 150020.

Lehmann S, et al. (2012) Using Multiple Phenotype Assays and Epistasis Testing to Enhance the Reliability of RNAi Screening and Identify Regulators of Muscle Protein Degradation. *Genes*, 3(4), 686.

Green RA, et al. (2011) A high-resolution *C. elegans* essential gene network based on phenotypic profiling of a complex tissue. *Cell*, 145(3), 470.

Markowetz F, et al. (2010) How to understand the cell by breaking it: network analysis of gene perturbation screens. *PLoS computational biology*, 6(2), e1000655.

Klink VP, et al. (2007) Developing a systems biology approach to study disease progression caused by *Heterodera glycines* in *Glycine max*. *Gene regulation and systems biology*, 1, 17.

Lall S, et al. (2006) A genome-wide map of conserved microRNA targets in *C. elegans*. *Current biology : CB*, 16(5), 460.

Leung RK, et al. (2005) RNA interference: from gene silencing to gene-specific therapeutics. *Pharmacology & therapeutics*, 107(2), 222.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.

Piano F, et al. (2002) Gene clustering based on RNAi phenotypes of ovary-enriched genes in *C. elegans*. *Current biology : CB*, 12(22), 1959.