Resource Summary Report

Generated by NIF on Aug 29, 2026

GenomeRNAi

RRID:SCR_013088
Type: Tool

Proper Citation

GenomeRNAi (RRID:SCR_013088)

Resource Information

URL: http://rnai.dkfz.de

Proper Citation: GenomeRNAi (RRID:SCR_013088)

Description: GenomeRNAi is a database of phenotypes from systematic RNA interference (RNAi) screens in cultured Drosophila cells. The phenotype database can be searched by keywords, RNAi identifiers or Drosophila gene sequences. Searches with homologous sequences from human or C. elegans are also possible. Integrated tools evaluate the specificity of long double-stranded RNAs (RNAi probes) by similarity searches against all predicted Drosophila transcripts. This site can also be used to identify pre-designed RNAi probes from available Drosophila RNAi libraries. Caenorhabditis elegans genome, human genome

Synonyms: GenomeRNAi, Genome RNAi

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Keywords: drosophila genome, caenorhabditis elegans, caenorhabditis elegans genome, c. elegans, drosophila, drosophila cells, human genome, rnai

Resource Name: GenomeRNAi

Resource ID: SCR_013088

Alternate IDs: nif-0000-02901, r3d100011089

Alternate URLs: https://www.ncbi.nlm.nih.gov/gap

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260829T182436+0000

Ratings and Alerts

No rating or validation information has been found for GenomeRNAi.

No alerts have been found for GenomeRNAi.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 385 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Webster R, et al. (2026) Neurocognitive impairment and substance use in adult survivors of childhood cancer: a cross-sectional analysis from the Childhood Cancer Survivor Study. EClinicalMedicine, 95, 103924.

Di Benedetto C, et al. (2026) An InDel Genomic Variant within a Bifunctional Super-Enhancer for LINC00636 and CD47 Regulation in Breast Cancer. Research square.

Onerup A, et al. (2026) Potential for risk reduction of chronic health conditions through lifestyle in childhood cancer survivors. Nature communications, 17(1).

Bethea M, et al. (2026) Activity of Cardiomyocyte Type 3 Deiodinase After Myocardial Infarction Influences Cardiac Recovery in Females. Endocrinology, 167(2).

Bouyssi-Kobar M, et al. (2026) Developmental trajectories of glutamate and the variable clinical course of ADHD in youth. Translational psychiatry, 16(1).

Piotrowski SL, et al. (2026) Herpesvirus genome integration in whole-genome sequences of dementia and control cohorts. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(3), e71047.

Li A, et al. (2026) Plasma Proteome Signature for Leukocyte Telomere Length and Its Link to Abdominal Aortic Aneurysm. Journal of cellular and molecular medicine, 30(3), e71047.

Duan H, et al. (2026) Towards personalized vaccine repurposing for Alzheimer's prevention: genotype-specific protective association of the shingles vaccine with odds of Alzheimer's disease in participants of two large cohort studies. BMC neurology, 26(1).

Manduchi E, et al. (2026) Epigenetic adaptation of beta cells across lifespan and disease. Nature metabolism, 8(4), 941.

Larrea-Sebal A, et al. (2026) Blood proteomics: insights from public data. Genome biology, 27(1).

Yadav A, et al. (2026) Tissue morphology predicts telomere shortening in human tissues. Cell reports methods, 6(3), 101336.

Stojkova O, et al. (2026) Identification of an ERCC2 mutation associated mutational signature of nucleotide excision repair deficiency in targeted panel sequencing data. bioRxiv : the preprint server for biology.

Horan MR, et al. (2026) Patient-reported symptoms in predicting the subsequent progression of chronic health conditions among childhood cancer survivors. Communications medicine, 6(1).

Yu K, et al. (2026) Aggregation of gene regulatory information and knowledge on FAIR principles enables discovery of pathogenic gene regulatory variants. Bioinformatics (Oxford, England), 42(3).

Priebe O, et al. (2026) Haplotype-aware segmentation with HapASeg increases accuracy of detecting homolog-specific somatic copy number alterations. Genome biology, 27(1).

Li C, et al. (2026) Molecular decoupling of lineage identity and morphology in aggressive variant prostate cancer. medRxiv : the preprint server for health sciences.

Li C, et al. (2026) Integrative molecular analyses of lineage identity and morphology in aggressive variant prostate cancer. NPJ precision oncology, 10(1).

Garside A, et al. (2026) Single-Cell Morphomechanics of Prostate Cancer-Associated Fibroblasts Identifies Distinct Features Associated with Patient Outcome. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(13), e22440.

Li Z, et al. (2026) Investigating the causal linkages between circulating inflammatory proteins and breast cancer risk and prognosis: Insights from a two-sample Mendelian randomization analysis. Medicine, 105(17), e48402.

Pan Y, et al. (2026) Cuproptosis as a novel predictor of immunotherapy response and shapes the immune landscape in pan-cancer analysis. Discover oncology, 17(1).