Resource Summary Report

Generated by RRID on Aug 4, 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 repository, data or information resource, database, storage service resource, 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: 20260804T043508+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 278 mentions in open access literature.

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

Showpnil IA, et al. (2026) De Novo Heterozygous ZFX Frameshift Variant in a Female With an X-Linked Neurodevelopmental Disorder. American journal of medical genetics. Part A, 200(2), 521.

Hu YM, et al. (2026) Elevated Tumor-Associated Androgen Receptor Activity Correlates with Poor Immune Infiltration and Immunotherapy Response across Cancer Types. Cancer research communications, 6(1), 17.

Zhi D, et al. (2025) Proxy panels enable privacy-aware outsourcing of genotype imputation. Genome research, 35(2), 326.

Unger M, et al. (2025) Deep Learning for Biomarker Discovery in Cancer Genomes. bioRxiv : the preprint server for biology.

McGrail C, et al. (2025) Genetic Discovery and Risk Prediction for Type 1 Diabetes in Individuals Without High-Risk HLA-DR3/DR4 Haplotypes. Diabetes care, 48(2), 202.

Wilson AM, et al. (2025) Transcriptional impacts of substance use disorder and HIV on human ventral midbrain neurons and microglia. bioRxiv : the preprint server for biology.

Kang Z, et al. (2025) Estimation of total mediation effect for a binary trait in a case-control study for high-dimensional omics mediators†. bioRxiv : the preprint server for biology.

Mazziotta F, et al. (2025) A phase I/II trial of WT1-specific TCR gene therapy for patients with acute myeloid leukemia and active disease post-allogeneic hematopoietic cell transplantation: skewing towards NK-like phenotype impairs T cell function and persistence. Nature communications, 16(1), 5214.

Mogire RM, et al. (2025) OSBPL11 is an African-specific locus associated with 25-hydroxyvitamin D concentrations and cardiometabolic health. medRxiv : the preprint server for health sciences.

Khvorykh G, et al. (2025) Determinant-based grouping of SNPs and its application for detecting disease-associated genomic loci. NAR genomics and bioinformatics, 7(1), lqaf024.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF-? Activity Driving Tumor Recurrence. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(24), 5211.

Heinsberg LW, et al. (2025) Study protocol for the Health Outcomes in Pregnancy and Early Childhood (HOPE) Study: A mother-infant study in American Samoa. PloS one, 20(9), e0326644.

Harigaya Y, et al. (2025) Probabilistic classification of gene-by-treatment interactions on molecular count phenotypes. PLoS genetics, 21(4), e1011561.

Genner R, et al. (2025) Assessing DNA methylation detection for primary human tissue using Nanopore sequencing. Genome research, 35(4), 632.

Solovyov A, et al. (2025) Pan-cancer multi-omic model of LINE-1 activity reveals locus heterogeneity of retrotransposition efficiency. Nature communications, 16(1), 2049.

Chen X, et al. (2025) Classification of schizophrenia, bipolar disorder and major depressive disorder with comorbid traits and deep learning algorithms. Schizophrenia (Heidelberg, Germany), 11(1), 14.

Oelsner EC, et al. (2025) Classifying COVID-19 hospitalizations in epidemiology cohort studies: The C4R study. PloS one, 20(2), e0316198.

Manduchi E, et al. (2025) Epigenetic adaptation of beta cells across lifespan and disease: age-related demethylation is advanced in type 2 diabetes. bioRxiv : the preprint server for biology.

Reho P, et al. (2025) Rare FN1 missense mutations indicate a protective role against Lewy body dementia in APOE?4 homozygous carriers. Acta neuropathologica, 150(1), 22.

Wilkinson S, et al. (2025) Localized high-risk prostate cancer harbors an androgen receptor activity-low subpopulation susceptible to HER2 inhibition. The Journal of clinical investigation, 135(22).