Resource Summary Report

Generated by RRID on May 13, 2025

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, storage service resource, data or information resource, service resource, database

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

Funding:

Resource Name: GenomeRNAi

Resource ID: SCR_013088

Alternate IDs: nif-0000-02901

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

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250513T061428+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 190 mentions in open access literature.

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

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.

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

Shi Y, et al. (2025) Acquired resistance to PD-L1 inhibition enhances a type I IFN-regulated secretory program in tumors. EMBO reports, 26(2), 521.

Shen L, et al. (2025) Marginal interaction test for detecting interactions between genetic marker sets and environment in genome-wide studies. G3 (Bethesda, Md.), 15(1).

Lee MK, et al. (2025) Genome scan reveals several loci associated with torus palatinus. Orthodontics & craniofacial research, 28(1), 159.

Pathak S, et al. (2025) Investigating the causal effects of childhood and adulthood adiposity on later life mental health outcome: a Mendelian randomization study. BMC medicine, 23(1), 4.

Konieczny MJ, et al. (2025) The genomic architecture of circulating cytokine levels points to drug targets for immune-related diseases. Communications biology, 8(1), 34.

Liu Y, et al. (2024) Variability in performance of genetic-enhanced DXA-BMD prediction models across diverse ethnic and geographic populations: A risk prediction study. PLoS

medicine, 21(8), e1004451.

Duan H, et al. (2024) Overweight as a Causal Factor Contributing to Better Survival at the Oldest Old Ages: A Mendelian Randomization Study. medRxiv : the preprint server for health sciences.

Fischer MA, et al. (2024) Decreased Left Atrial Cardiomyocyte Fibroblast Growth Factor 13 Expression Increases Vulnerability to Postoperative Atrial Fibrillation in Humans. Journal of the American Heart Association, 13(12), e034896.

Walker MT, et al. (2024) 5-HTP inhibits eosinophilia via intracellular endothelial 5-HTRs; SNPs in 5-HTRs associate with asthmatic lung function. Frontiers in allergy, 5, 1385168.

Liu W, et al. (2024) A Generalized Higher-order Correlation Analysis Framework for Multi-Omics Network Inference. bioRxiv : the preprint server for biology.

Suzuki T, et al. (2024) Ankle-Brachial Index and Risk of Sudden Cardiac Death in the Community: The ARIC Study. Journal of the American Heart Association, 13(6), e032008.

Schlam I, et al. (2024) Pharmacokinetics and pharmacogenomics of ribociclib in black patients with metastatic breast cancer the LEANORA study. NPJ breast cancer, 10(1), 84.

Claeys A, et al. (2024) MHC class II genotypes are independent predictors of anti-PD1 immunotherapy response in melanoma. Communications medicine, 4(1), 184.

Deng L, et al. (2024) Structure-adaptive canonical correlation analysis for microbiome multi-omics data. Frontiers in genetics, 15, 1489694.

Wang Z, et al. (2024) CancerPro: deciphering the pan-cancer prognostic landscape through combinatorial enrichment analysis and knowledge network insights. NAR genomics and bioinformatics, 6(4), lqae157.

Reyna J, et al. (2024) Loop Catalog: a comprehensive HiChIP database of human and mouse samples. bioRxiv : the preprint server for biology.

Zhou B, et al. (2024) An integrated strain-level analytic pipeline utilizing longitudinal metagenomic data. Microbiology spectrum, 12(11), e0143124.

Zhang W, et al. (2024) Understanding the Biological Basis of Polygenic Risk Scores and Disparities in Prostate Cancer: A Comprehensive Genomic Analysis. Cancer informatics, 23, 11769351241276319.