Resource Summary Report

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PolymiRTS

RRID:SCR_003389
Type: Tool

Proper Citation

PolymiRTS (RRID:SCR_003389)

Resource Information

URL: http://compbio.uthsc.edu/miRSNP/

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Description: Database of naturally occurring DNA variations in microRNA (miRNA) seed regions and miRNA target sites. MicroRNAs pair to the transcripts of protein-coding genes and cause translational repression or mRNA destabilization. SNPs and INDELs in miRNAs and their target sites may affect miRNA-mRNA interaction, and hence affect miRNA-mediated gene repression. The PolymiRTS database was created by scanning 3'UTRs of mRNAs in human and mouse for SNPs and INDELs in miRNA target sites. Then, the potential downstream effects of these polymorphisms on gene expression and higher-order phenotypes are identified. Specifically, genes containing PolymiRTSs, cis-acting expression QTLs, and physiological QTLs in mouse and the results of genome-wide association studies (GWAS) of human traits and diseases are linked in the database. The PolymiRTS database also includes polymorphisms in target sites that have been supported by a variety of experimental methods and polymorphisms in miRNA seed regions.

Abbreviations: PolymiRTS

Synonyms: Polymorphism in microRNA Target Site, PolymiRTS Database, Polymorphism in microRNAs and their TargetSites

Resource Type: database, data or information resource

Defining Citation: PMID:24163105, PMID:22080514

Keywords: polymorphism, microrna, human, disease, trait, snp, indel, pathway, genetic variant, gene expression, phenotype, chromosome, chromosome location, bio.tools, FASEB list

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Availability: Acknowledgement requested

Resource Name: PolymiRTS

Resource ID: SCR_003389

Alternate IDs: nif-0000-03324, biotools:polymirts, OMICS_00391

Alternate URLs: https://bio.tools/polymirts

Old URLs: http://compbio.utmem.edu/miRSNP/

Record Creation Time: 20220129T080218+0000

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Ratings and Alerts

No rating or validation information has been found for PolymiRTS.

No alerts have been found for PolymiRTS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 146 mentions in open access literature.

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

Tedja MS, et al. (2025) A genome-wide scan of non-coding RNAs and enhancers for refractive error and myopia. Human genetics, 144(1), 67.

Paniri A, et al. (2024) Genetic variations in IKZF3, LET7-a2, and CDKN2B-AS1: Exploring associations with metabolic syndrome susceptibility and clinical manifestations. Journal of clinical laboratory analysis, 38(1-2), e24999.

Garibaldi-Ríos AF, et al. (2024) In Silico Identification of Dysregulated miRNAs Targeting KRAS Gene in Pancreatic Cancer. Diseases (Basel, Switzerland), 12(7).

Chen M, et al. (2024) miRSNP rs188493331: A key player in genetic control of microRNA-induced pathway activation in hypertrophic scars and keloids. Skin research and technology : official journal of International Society for Bioengineering and the Skin (ISBS) [and] International Society for Digital Imaging of Skin (ISDIS) [and] International Society for Skin Imaging (ISSI), 30(5), e13686.

Tanshee RR, et al. (2024) A comprehensive in silico investigation into the pathogenic SNPs in the RTEL1 gene and their biological consequences. PloS one, 19(9), e0309713.

Sarkar B, et al. (2024) Comprehensive characterization of high-risk coding and non-coding single nucleotide polymorphisms of human CXCR4 gene. PloS one, 19(12), e0312733.

Yalaev B, et al. (2024) MicroRNA binding site variants-new potential markers of primary osteoporosis in men and women. Frontiers in genetics, 15, 1470310.

Sultana T, et al. (2024) Computational exploration of SLC14A1 genetic variants through structure modeling, protein-ligand docking, and molecular dynamics simulation. Biochemistry and biophysics reports, 38, 101703.

Cavalleri E, et al. (2024) An ontology-based knowledge graph for representing interactions involving RNA molecules. Scientific data, 11(1), 906.

Mustafa A, et al. (2024) Genetic polymorphism in untranslated regions of PRKCZ influences mRNA structure, stability and binding sites. BMC cancer, 24(1), 1147.

Uddin MN, et al. (2024) Variations in Furin SNPs, a Major Concern of SARS-CoV-2 Susceptibility Among Different Populations: An In-Silico Approach. Bioinformatics and biology insights, 18, 11779322241306388.

Hassan MM, et al. (2023) In Silico Analysis: HLA-DRB1 Gene's Variants and Their Clinical Impact. Cell transplantation, 32, 9636897231184473.

Liu L, et al. (2023) DHT inhibits REDOX damage and neuroinflammation to reduce PND occurrence in aged mice via mmu_circ_0001442/miR-125a-3p/NUFIP2 axis. Brain and behavior, 13(10), e3180.

Gallegos-Arreola MP, et al. (2023) Association of the rs8720 and rs12587 KRAS Gene Variants with Colorectal Cancer in a Mexican Population and Their Analysis In Silico. Cells, 12(15).

Özkan Oktay E, et al. (2023) In Silico Prediction and Molecular Docking of SNPs in NRP1 Gene Associated with SARS-COV-2. Biochemical genetics, 1.

Fashina IA, et al. (2023) In silico prioritisation of microRNA-associated common variants in multiple sclerosis. Human genomics, 17(1), 31.

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. Functional & integrative genomics, 23(1), 33.

Chu YJ, et al. (2023) HBV genotype-dependent association of HLA variants with the serodecline of HBsAg in chronic hepatitis B patients. Scientific reports, 13(1), 359.

Mohammadi M, et al. (2022) The miR526b-5p-Related Single Nucleotide Polymorphisms, rs72618599, Located in 3'-UTR of TCF3 Gene, is Associated with the Risk of Breast and Gastric Cancers. Iranian biomedical journal, 26(1), 53.

Giovannetti A, et al. (2022) MiRLog and dbmiR: Prioritization and functional annotation tools to study human microRNA sequence variants. Human mutation, 43(9), 1201.