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: data or information resource, database

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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NIAID AI019782;
American Heart Association 0830134N;
United States Department of Defense W81XHW-05-01-0227

Availability: Free, Available for download, Freely available

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

Record Last Update: 20260905T133120+0000

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 161 mentions in open access literature.

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

Garibaldi-R??os AF, et al. (2026) Regulatory Variants in the KRAS 3'UTR and Intron 2 Are Associated with Breast Cancer Susceptibility Through Independent and Combinatorial Effects in a Mexican Population. Biomedicines, 14(4).

Chen W, et al. (2026) ADIPOQ rs1063537 polymorphism correlates with diabetic kidney disease severity in southern Chinese Han patients with type 2 diabetes. Medicine, 105(11), e48028.

Alwabran AI, et al. (2026) Decoding the genetic basis of demyelination: Prediction of potential pathogenic coding and regulatory noncoding MBP SNPs in multiple sclerosis. PloS one, 21(5), e0347598.

Nila NN, et al. (2026) Comprehensive analysis of the deleterious nonsynonymous, non-coding SNPs and cancer variants of human aldo-keto reductase type 1 (AKR1C1) protein and their probable association with disease risk and progression: a computational study. Biochemistry and biophysics reports, 45, 102502.

Liu D, et al. (2026) Rs12516 A allele elevates the risk of colorectal cancer via functional CeRNA network of BDNF-AS, miR-4704-5p and BRCA1. BMC cancer, 26(1), 229.

Abdelazim AA, et al. (2026) Computational analysis and validation of UGT1A1/4 missense variants impacting tecovirimat metabolism in monkeypox patients. Frontiers in systems biology, 6, 1821230.

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.

Braicu C, et al. (2025) The Complex Role of the miR-17-92 Cluster in Stroke: Mechanistic Insights and Biomarker Potential. Genes, 16(6).

Ji G, et al. (2025) Genetic variants in m6A regulator genes confer susceptibility and progression of HCC in a Northern Chinese population. Discover oncology, 16(1), 526.

Ibrahim TAM, et al. (2025) Exome Sequencing of a Type 1 Diabetes Mellitus Family Exposes Both Common and Individualized Rare Variants Contributing to Pathogenesis. Journal of diabetes research, 2025, 3346256.

Kamal E, et al. (2025) In Silico Prioritization of STAT1 3' UTR SNPs Identifies rs190542524 as a miRNA-Linked Variant with Potential Oncogenic Impact. Non-coding RNA, 11(3).

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

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.

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.

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.

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

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.