Resource Summary Report

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MirSNP

RRID:SCR_001629
Type: Tool

Proper Citation

MirSNP (RRID:SCR_001629)

Resource Information

URL: http://cmbi.bjmu.edu.cn/mirsnp

Proper Citation: MirSNP (RRID:SCR_001629)

Description: Database of human SNPs in predicted miRNA-mRNA binding sites, based on information from dbSNP135 and mirBASE18. MirSNP is highly sensitive and covers most experiments confirmed SNPs that affect miRNA function. MirSNP may be combined with researchers' own GWAS or eQTL positive data sets to identify the putative miRNA-related SNPs from traits/diseases associated variants. They aim to update the MirSNP database as new versions of mirBASE and dbSNP database become available.

Abbreviations: MirSNP

Resource Type: data or information resource, database

Defining Citation: PMID:23173617

Keywords: single nucleotide polymorphism, mirna, genome-wide association study, expression quantitative trait locus, mirna-mrna binding site, trait, disease, variant, gene, mrna, FASEB list

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Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MirSNP

Resource ID: SCR_001629

Alternate IDs: nlx_153896

Alternate URLs: http://202.38.126.151/hmdd/mirsnp/search/

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260729T044021+0000

Ratings and Alerts

No rating or validation information has been found for MirSNP.

No alerts have been found for MirSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 73 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Weidhaas JB, et al. (2025) Germline microRNA-based signatures predict toxicity and response to anti-CTLA-4 therapy. Journal of translational medicine, 23(1), 848.

Zhai Z, et al. (2025) Identification of CircRNAs that promote cancer and their potential contribution to hepatocellular carcinoma (HCC) pathogenesis. Clinical and experimental medicine, 25(1), 60.

Causin RL, et al. (2024) EV-miRNAs from breast cancer patients of plasma as potential prognostic biomarkers of disease recurrence. Heliyon, 10(14), e33933.

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.

Yang WW, et al. (2024) Exosomal miR-155-5p promote the occurrence of carotid atherosclerosis. Journal of cellular and molecular medicine, 28(21), e70187.

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.

Zhang N, et al. (2022) Genome-Wide 3'-UTR Single Nucleotide Polymorphism Association Study Identifies Significant Prostate Cancer Risk-Associated Functional Loci at 8p21.2 in Chinese Population. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 9(23), e2201420.

De Mattia E, et al. (2022) Rare genetic variant burden in DPYD predicts severe fluoropyrimidine-related toxicity risk. Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie, 154, 113644.

Shen Y, et al. (2022) Genetic variant in miR-17-92 cluster binding sites is associated with esophageal squamous cell carcinoma risk in Chinese population. BMC cancer, 22(1), 1253.

Dominkuš PP, et al. (2022) PLK2 Single Nucleotide Variant in Gastric Cancer Patients Affects miR-23b-5p Binding. Journal of gastric cancer, 22(4), 348.

Martínez-Magaña JJ, et al. (2022) Association of FAAH p.Pro129Thr and COMT p.Ala72Ser with schizophrenia and comorbid substance use through next-generation sequencing: an exploratory analysis. Revista brasileira de psiquiatria (Sao Paulo, Brazil : 1999), 44(2), 164.

Mukherjee M, et al. (2022) Investigating the interference of single nucleotide polymorphisms with miRNA mediated gene regulation in pancreatic ductal adenocarcinoma: An in silico approach. Gene, 819, 146259.

Mokhtari MA, et al. (2022) Genetic Polymorphisms in miR-137 and Its Target Genes, TCF4 and CACNA1C, Contribute to the Risk of Bipolar Disorder: A Preliminary Case-Control Study and Bioinformatics Analysis. Disease markers, 2022, 1886658.

El-Huneidi W, et al. (2021) Single nucleotide polymorphisms in microRNA binding sites on the HOX genes regulate carcinogenesis: An in-silico approach. Biochemistry and biophysics reports, 27, 101083.

Wang Z, et al. (2021) Family-based association study identifies SNAP25 as a susceptibility gene for autism in the Han Chinese population. Progress in neuro-psychopharmacology & biological psychiatry, 105, 109985.

Dehghanzad R, et al. (2021) Prediction of Single-Nucleotide Polymorphisms within microRNAs Binding Sites of Neuronal Genes Related to Multiple Sclerosis: A Preliminary Study. Advanced biomedical research, 10, 8.

Deng F, et al. (2021) Increased hypospadias risk by GREM1 rs3743104[G] in the southern Han Chinese population. Aging, 13(10), 13898.

Yu W, et al. (2021) XPG is Modulated by miR-4715-3p and rs873601 Genotypes in Lung Cancer. Cancer management and research, 13, 3417.

Fan Z, et al. (2021) Identification of biomarkers associated with metabolic cardiovascular disease using mRNA-SNP-miRNA regulatory network analysis. BMC cardiovascular disorders, 21(1), 351.

Martínez-Gil N, et al. (2021) Genetics and Genomics of SOST: Functional Analysis of Variants and Genomic Regulation in Osteoblasts. International journal of molecular sciences, 22(2).