Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

MicroSNiPer

RRID:SCR_009880
Type: Tool

Proper Citation

MicroSNiPer (RRID:SCR_009880)

Resource Information

URL: http://cbdb.nimh.nih.gov/microsniper/

Proper Citation: MicroSNiPer (RRID:SCR_009880)

Description: A web-based application which predicts the impact of a SNP on putative microRNA targets.

Abbreviations: MicroSNiPer

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: PMID:20809528

Keywords: bio.tools

Resource Name: MicroSNiPer

Resource ID: SCR_009880

Alternate IDs: biotools:microsniper, OMICS_00388

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

Record Creation Time: 20220129T080255+0000

Record Last Update: 20260905T133156+0000

Ratings and Alerts

No rating or validation information has been found for MicroSNiPer.

No alerts have been found for MicroSNiPer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

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

Grasso C, et al. (2022) Association Study between Polymorphisms in DNA Methylation-Related Genes and Testicular Germ Cell Tumor Risk. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 31(9), 1769.

Bug DS, et al. (2021) Evaluating the Effect of 3'-UTR Variants in DICER1 and DROSHA on Their Tissue-Specific Expression by miRNA Target Prediction. Current issues in molecular biology, 43(2), 605.

Medina-Trillo C, et al. (2019) Role of FOXC2 and PITX2 rare variants associated with mild functional alterations as modifier factors in congenital glaucoma. PloS one, 14(1), e0211029.

Zhang R, et al. (2019) SNP rs4937333 in the miRNA-5003-Binding Site of the ETS1 3'-UTR Decreases ETS1 Expression. Frontiers in genetics, 10, 581.

Espinoza JL, et al. (2016) A functional polymorphism in the NKG2D gene modulates NK-cell cytotoxicity and is associated with susceptibility to Human Papilloma Virus-related cancers. Scientific reports, 6, 39231.

Naccarati A, et al. (2016) Double-strand break repair and colorectal cancer: gene variants within 3' UTRs and microRNAs binding as modulators of cancer risk and clinical outcome. Oncotarget, 7(17), 23156.

Marouf C, et al. (2016) Analysis of functional germline variants in APOBEC3 and driver genes on breast cancer risk in Moroccan study population. BMC cancer, 16, 165.

Medrano LM, et al. (2016) Relationship of TRIM5 and TRIM22 polymorphisms with liver disease and HCV clearance after antiviral therapy in HIV/HCV coinfected patients. Journal of translational medicine, 14(1), 257.

Puim??ge L, et al. (2015) Glucocorticoid-induced microRNA-511 protects against TNF by down-regulating TNFR1. EMBO molecular medicine, 7(8), 1004.

Maxwell EK, et al. (2015) SubmiRine: assessing variants in microRNA targets using clinical genomic data sets. Nucleic acids research, 43(8), 3886.

Kalyani A, et al. (2015) Post-Transcriptional Regulation of Renalase Gene by miR-29 and miR-146 MicroRNAs: Implications for Cardiometabolic Disorders. Journal of molecular biology, 427(16), 2629.

Sethupathy P, et al. (2013) Illuminating microRNA Transcription from the Epigenome. Current genomics, 14(1), 68.

Bianco AM, et al. (2013) Database tools in genetic diseases research. Genomics, 101(2), 75.

Paolicchi E, et al. (2013) A single nucleotide polymorphism in EZH2 predicts overall survival rate in patients with cholangiocarcinoma. Oncology letters, 6(5), 1487.

Sabina S, et al. (2013) Germline hereditary, somatic mutations and microRNAs targeting-SNPs in congenital heart defects. Journal of molecular and cellular cardiology, 60, 84.

Wei R, et al. (2012) Impact of the Interaction between 3'-UTR SNPs and microRNA on the Expression of Human Xenobiotic Metabolism Enzyme and Transporter Genes. Frontiers in genetics, 3, 248.

Cunha C, et al. (2011) Genetically-determined hyperfunction of the S100B/RAGE axis is a risk factor for aspergillosis in stem cell transplant recipients. PloS one, 6(11), e27962.