

Resource Summary Report

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[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: data analysis service, service resource, production service resource, analysis 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: 20260801T190959+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 [RRID](#) .

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.

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

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.

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.

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

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

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.