**MirSNP**

RRID:SCR_001629  
Type: Tool

**Proper Citation**  
MirSNP (RRID:SCR_001629)

**Resource Information**

**URL:**  [http://cmbi.bjmu.edu.cn/mirsnp](http://cmbi.bjmu.edu.cn/mirsnp)

**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.

**Resource Name:** MirSNP

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**Resource Type:** Resource, data or information resource, database

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

**Resource ID:** SCR_001629

**Parent Organization:** Peking University; Beijing; China

**Funding Agency:** International Science and Technology Cooperation Program of China, National High Technology Research and Development Program of China, National Natural Science Foundation of China

**References:** PMID:23173617
**Availability:** Acknowledgement requested, Public

**Website Status:** Last checked down

**Alternate IDs:** nlx_153896

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

**Abbreviations:** MirSNP

**Mentions Count:** 36

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**Ratings and Alerts**

No rating or validation information has been found for MirSNP.

No alerts have been found for MirSNP.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 36 mentions in open access literature.

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


Thabet K, et al. (2016) MBOAT7 rs641738 increases risk of liver inflammation and transition to fibrosis in chronic hepatitis C. Nature communications, 7, 12757.

Wang W, et al. (2016) A single-nucleotide polymorphism in the 3'-UTR region of the adipocyte fatty acid binding protein 4 gene is associated with prognosis of triple-negative
breast cancer. Oncotarget, 7(14), 18984-98.