Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

RNAsnp

RRID:SCR_010837
Type: Tool

Proper Citation

RNAsnp (RRID:SCR_010837)

Resource Information

URL: http://rth.dk/resources/rnasnp/

Proper Citation: RNAsnp (RRID:SCR_010837)

Description: Software / Web Server to predict the effect of SNPs on local RNA secondary structure based on the RNA folding algorithms implemented in the Vienna RNA package.

Abbreviations: RNAsnp

Synonyms: RNAsnp Web Server, RNAsnp Web Server: Predicting SNP effects on local RNA secondary structure

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

Defining Citation: PMID:23630321

Resource Name: RNAsnp

Resource ID: SCR_010837

Alternate IDs: OMICS_00392

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260905T132648+0000

Ratings and Alerts

No rating or validation information has been found for RNAsnp.

No alerts have been found for RNAsnp.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Buslyk T, et al. (2026) Identification and bioinformatic functional analysis of novel and known polymorphisms in the myostatin gene of Ukrainian Carpathian Mountain sheep. Scientific reports, 16(1).

He J, et al. (2025) DNAJB13 polymorphisms and association with idiopathic asthenozoospermia in Sichuan, China. Basic and clinical andrology, 35(1), 49.

Jamalpour S, et al. (2025) Effects of rs3802177 G/A polymorphism on SLC30A8 mRNA and hsa-miR-183-5p in Malay women with gestational diabetes mellitus. Scientific reports, 15(1), 40327.

Kashani S, et al. (2025) A Preliminary Association Study of H19 Non-Coding Gene Variants With Risk of Non-Hodgkin Lymphoma: A Case-Control Study and Computational Analysis. Journal of clinical laboratory analysis, 39(11), e70024.

Han X, et al. (2025) Associating cancer-related RNA structure disrupting SNPs in LincRNAs to function. BMC genomics, 26(1), 1100.

Gholami M, et al. (2024) Genetic Variants and Haplotype Structures in the CASC Gene Family to Predict Cancer Risk: A Bioinformatics Study. Health science reports, 7(12), e70228.

He J, et al. (2024) The polymorphism analysis and therapy vaccine target epitopes screening of HPV-35 E6 E7 among the threaten ?-9 HPV in Sichuan area. Virology journal, 21(1), 213.

Peng XQ, et al. (2023) Association Between Transforming Growth Factor-?1 Polymorphisms and Ischemic Stroke Susceptibility: A Meta-Analysis. Clinical and applied thrombosis/hemostasis : official journal of the International Academy of Clinical and Applied Thrombosis/Hemostasis, 29, 10760296231166666.

He JY, et al. (2022) DEFB126 polymorphisms and association with idiopathic asthenozoospermia in China. Asian journal of andrology, 24(6), 607.

Pu L, et al. (2022) GPX2 Gene Affects Feed Efficiency of Pigs by Inhibiting Fat Deposition and Promoting Muscle Development. Animals : an open access journal from MDPI, 12(24).

Shahrokhi SZ, et al. (2021) The effect of A1298c polymorphism of the MTHFR gene on anti-Müllerian hormone levels: experimental and Web-based analysis. Journal of clinical laboratory analysis, 35(9), e23948.

Won SY, et al. (2021) The First Report of Genetic Polymorphisms of the Equine SPRN Gene in Outbred Horses, Jeju and Halla Horses. Animals : an open access journal from MDPI, 11(9).

Ansell BRE, et al. (2021) A survey of RNA editing at single-cell resolution links interneurons to schizophrenia and autism. RNA (New York, N.Y.), 27(12), 1482.

Kim JH, et al. (2021) The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. Scientific reports, 11(1), 2997.

Hosseini Rad Sm A, et al. (2020) Implications of SARS-CoV-2 Mutations for Genomic RNA Structure and Host microRNA Targeting. International journal of molecular sciences, 21(13).

Miladi M, et al. (2020) MutaRNA: analysis and visualization of mutation-induced changes in RNA structure. Nucleic acids research, 48(W1), W287.

Zhang D, et al. (2020) Somatic synonymous mutations in regulatory elements contribute to the genetic aetiology of melanoma. BMC medical genomics, 13(Suppl 5), 43.

Petkevicius V, et al. (2020) Association of Long Non-Coding RNA Polymorphisms with Gastric Cancer and Atrophic Gastritis. Genes, 11(12).

Basir A, et al. (2019) Methionine Synthase Reductase-A66G and -C524T Single Nucleotide Polymorphisms and Prostate Cancer: A Case-Control Trial. Asian Pacific journal of cancer prevention : APJCP, 20(5), 1445.

Ghaedi H, et al. (2018) Genetic variants in long noncoding RNA H19 and MEG3 confer risk of type 2 diabetes in an Iranian population. Gene, 675, 265.