Resource Summary Report

Generated by T1D on Sep 19, 2026

SNVrap

RRID:SCR_010512
Type: Tool

Proper Citation

SNVrap (RRID:SCR_010512)

Resource Information

URL: http://jjwanglab.org/snvrap

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Description: The web portal provides comprehensive local database of human genome variants with a user-friendly web page that provides a one-stop annotating and funtonal prediction service which is both convenient and up-to-date. A query can be accepted as either a dbSNP Id or a chromosomal location and our system will instantly provide all the annotation information in an interactive LD panel. The system can also simultaneously prioritize this variant based on additive effect mode by corresponding annotation information and evaluate the variant effect that is then displayed in a prioritization tree. Furthermore, cohort sequencing continuously produces lots of un-annotated variants such as rare variants or de novo variants, and our system can even fit this data by accepting genomic coordinates (hg19) to offer maximal annotations. Main Functions Over 40 up-to-date annotation items for human single nucleotide variations; Functional prediction for different types of variants; Dynamic LD panel for both HapMap and 1000 Genomes Project populations; Prioritization score and tree viewer based on variant functional model.

Resource Type: analysis service resource, data access protocol, data analysis service, data or information resource, data set, production service resource, service resource, software resource, web service

Defining Citation: PMID:25308971

Keywords: genetic variant, prioritize, genome, chromosome, functional prediction, transcription factor-binding site, mirna, mirna target site, prediction, target site, transcription factor, binding site, statistics, trait/disease-associated snp, single nucleotide polymorphism

Resource Name: SNVrap

Resource ID: SCR_010512

Alternate IDs: nlx_158733

Alternate URLs: http://jjwanglab.org/snvrap/snvrap/snvrap/quickrap

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260912T195720+0000

Ratings and Alerts

No rating or validation information has been found for SNVrap.

No alerts have been found for SNVrap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Sohn M, et al. (2018) Whole exome sequencing for the identification of CYP3A7 variants associated with tacrolimus concentrations in kidney transplant patients. Scientific reports, 8(1), 18064.

Huang D, et al. (2018) GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. Nucleic acids research, 46(W1), W114.

Li MJ, et al. (2017) Exploring genetic associations with ceRNA regulation in the human genome. Nucleic acids research, 45(10), 5653.

Li MJ, et al. (2017) mTCTScan: a comprehensive platform for annotation and prioritization of mutations affecting drug sensitivity in cancers. Nucleic acids research, 45(W1), W215.