Resource Summary Report

Generated by NIF on May 18, 2025

is-rSNP

RRID:SCR_000387
Type: Tool

Proper Citation

is-rSNP (RRID:SCR_000387)

Resource Information

URL: http://bioinformatics.research.nicta.com.au/software/is-rsnp/

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Description: Software tool that predicts whether a single nucleotide polymorphism (SNP) is a regulatory SNP (rSNP). For a given SNP, and using a statistical framework, it can successfully predict the set of transcription factors (TFs) for which binding is affected. The algorithm provides the statistical power to scan large numbers of SNPs, making it suitable to use to screen all associated SNPs output by a typical genome-wide association studies (GWAS).

Abbreviations: is-rSNP

Synonyms: In silico regulatory SNP detection, is-rSNP: in silico regulatory SNP detection

Resource Type: software resource

Defining Citation: PMID:20823317

Keywords: genome-wide association study, single nucleotide polymorphism, transcription factor, regulatory single nucleotide polymorphism, in silico

Funding:

Availability: Registration requested

Resource Name: is-rSNP

Resource ID: SCR_000387

Alternate IDs: OMICS_01930

Record Creation Time: 20220129T080201+0000

Record Last Update: 20250420T013945+0000

Ratings and Alerts

No rating or validation information has been found for is-rSNP.

No alerts have been found for is-rSNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Li J, et al. (2015) Genetic Evidence for Possible Involvement of the Calcium Channel Gene CACNA1A in Autism Pathogenesis in Chinese Han Population. PloS one, 10(11), e0142887.