Resource Summary Report

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SNP2TFBS

RRID:SCR_016885
Type: Tool

Proper Citation

SNP2TFBS (RRID:SCR_016885)

Resource Information

URL: http://ccg.vital-it.ch/snp2tfbs

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Description: Collection of text files providing specific annotations for human single nucleotide polymorphisms (SNPs), namely whether they are predicted to abolish, create or change the affinity of one or several transcription factor (TF) binding sites. Used to investigate the molecular mechanisms underlying regulatory variation in the human genome. SNP2TFBS is also accessible over a web interface, enabling users to view the information provided for an individual SNP, to extract SNPs based on various search criteria, to annotate uploaded sets of SNPs or to display statistics about the frequencies of binding sites affected by selected SNPs.

Abbreviations: SNP2TFBS

Synonyms: Single Nucleotide Polymorphisms 2 Transcription Factor Binding Site, SNP2TFBS

Resource Type: data access protocol, data or information resource, database, software resource, web service

Defining Citation: PMID:27899579

Keywords: collection, regulatory, single, polymorphism, SNP, affecting, predicted, transcription, factor, binding, site, affinity, data, human, nucleotide, genome

Funding: Swiss Institute of Bioinformatics ;
Swiss National Science Foundation

Availability: Free, Freely available

Resource Name: SNP2TFBS

Resource ID: SCR_016885

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T200019+0000

Ratings and Alerts

No rating or validation information has been found for SNP2TFBS.

No alerts have been found for SNP2TFBS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Schwarzerova J, et al. (2024) A perspective on genetic and polygenic risk scores-advances and limitations and overview of associated tools. Briefings in bioinformatics, 25(3).

Hara A, et al. (2024) Identification of an Allele-Specific Transcription Factor Binding Interaction that May Regulate PLA2G2A Gene Expression. Bioinformatics and biology insights, 18, 11779322241261427.

Islam MN, et al. (2022) In silico functional and pathway analysis of risk genes and SNPs for type 2 diabetes in Asian population. PloS one, 17(8), e0268826.

Moraghebi M, et al. (2021) In silico Analysis of Polymorphisms in microRNAs Deregulated in Alzheimer Disease. Frontiers in neuroscience, 15, 631852.

Ignatieva EV, et al. (2021) Disease-associated genetic variants in the regulatory regions of human genes: mechanisms of action on transcription and genomic resources for dissecting these mechanisms. Vavilovskii zhurnal genetiki i selektsii, 25(1), 18.

Xu C, et al. (2020) Annotation of susceptibility SNPs associated with atrial fibrillation. Aging, 12(17), 16981.

Sharma A, et al. (2019) Common genetic variants associated with Parkinson's disease display widespread signature of epigenetic plasticity. Scientific reports, 9(1), 18464.

Saucedo-Uribe E, et al. (2019) Differential effects on neurodevelopment of FTO variants in obesity and bipolar disorder suggested by in silico prediction of functional impact: An analysis in Mexican population. Brain and behavior, 9(6), e01249.