Resource Summary Report

Generated by NIF on Apr 18, 2025

SNPTools

RRID:SCR_013052
Type: Tool

Proper Citation

SNPTools (RRID:SCR_013052)

Resource Information

URL: http://sourceforge.net/projects/snptools/

Proper Citation: SNPTools (RRID:SCR_013052)

Description: A suite of software tools that enables integrative SNP analysis in next generation sequencing data with large cohorts.

Abbreviations: SNPTools

Resource Type: software resource

Keywords: c++

Funding:

Resource Name: SNPTools

Resource ID: SCR_013052

Alternate IDs: OMICS_00075

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250410T070327+0000

Ratings and Alerts

No rating or validation information has been found for SNPTools.

No alerts have been found for SNPTools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Di Y, et al. (2024) Genetic association analysis of human median voice pitch identifies a common locus for tonal and non-tonal languages. Communications biology, 7(1), 540.

Chatzinakos C, et al. (2021) Increasing the resolution and precision of psychiatric genome-wide association studies by re-imputing summary statistics using a large, diverse reference panel. American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics, 186(1), 16.

Han X, et al. (2021) Targeted sequencing of NOTCH signaling pathway genes and association analysis of variants correlated with mandibular prognathism. Head & face medicine, 17(1), 17.

Binenbaum I, et al. (2020) Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. BMC genomics, 21(1), 761.

Xue C, et al. (2020) Reduced meiotic recombination in rhesus macaques and the origin of the human recombination landscape. PloS one, 15(8), e0236285.

Xiong X, et al. (2017) Targeted sequencing in FGF/FGFR genes and association analysis of variants for mandibular prognathism. Medicine, 96(25), e7240.

Rustagi N, et al. (2017) Extremely low-coverage whole genome sequencing in South Asians captures population genomics information. BMC genomics, 18(1), 396.

Li P, et al. (2017) A missense mutation in TCN2 is associated with decreased risk for congenital heart defects and may increase cellular uptake of vitamin B12 via Megalin. Oncotarget, 8(33), 55216.

Cai N, et al. (2017) 11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. Scientific data, 4, 170011.

Tyler AL, et al. (2017) Epistatic Networks Jointly Influence Phenotypes Related to Metabolic Disease and Gene Expression in Diversity Outbred Mice. Genetics, 206(2), 621.

Xue C, et al. (2016) The population genomics of rhesus macaques (Macaca mulatta) based on whole-genome sequences. Genome research, 26(12), 1651.

Huang Z, et al. (2016) A hybrid computational strategy to address WGS variant analysis in >5000 samples. BMC bioinformatics, 17(1), 361.

Docherty AR, et al. (2016) SNP-based heritability estimates of the personality dimensions and polygenic prediction of both neuroticism and major depression: findings from CONVERGE. Translational psychiatry, 6(10), e926.

Harris RA, et al. (2016) Genomic Variants Associated with Resistance to High Fat Diet Induced Obesity in a Primate Model. Scientific reports, 6, 36123.

Fulop D, et al. (2016) A New Advanced Backcross Tomato Population Enables High Resolution Leaf QTL Mapping and Gene Identification. G3 (Bethesda, Md.), 6(10), 3169.

, et al. (2015) Sparse whole-genome sequencing identifies two loci for major depressive disorder. Nature, 523(7562), 588.

Yu F, et al. (2015) Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. PloS one, 10(3), e0121644.

Delaneau O, et al. (2014) Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature communications, 5, 3934.

Mosedale M, et al. (2014) Dysregulation of protein degradation pathways may mediate the liver injury and phospholipidosis associated with a cationic amphiphilic antibiotic drug. Toxicology and applied pharmacology, 280(1), 21.