Resource Summary Report

Generated by NIF on Apr 22, 2025

SNPper

RRID:SCR_001963
Type: Tool

Proper Citation

SNPper (RRID:SCR_001963)

Resource Information

URL: http://snpper.chip.org/

Proper Citation: SNPper (RRID:SCR_001963)

Description: Retrieve known single-nucleotide polymorphisms (SNPs) by position or by association with a gene; save, filter, analyze, display or export SNP sets; explore known genes using names or chromosome positions.

Abbreviations: SNPper

Resource Type: software resource

Defining Citation: PMID:12490454

Keywords: single-nucleotide polymorphism, gene, chromosome

Funding:

Availability: Free, Non-commercial, Registration requested

Resource Name: SNPper

Resource ID: SCR_001963

Alternate IDs: OMICS_01926

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250420T014046+0000

Ratings and Alerts

No rating or validation information has been found for SNPper.

No alerts have been found for SNPper.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Firdaus R, et al. (2021) Multiple Mutations in Exon-2 of Med-12 Identified in Uterine Leiomyomata. Journal of reproduction & infertility, 22(3), 201.

Ornelas AMM, et al. (2019) Association between MBL2 haplotypes and dengue severity in children from Rio de Janeiro, Brazil. Memorias do Instituto Oswaldo Cruz, 114, e190004.

Hu VW, et al. (2019) ASD Phenotype-Genotype Associations in Concordant and Discordant Monozygotic and Dizygotic Twins Stratified by Severity of Autistic Traits. International journal of molecular sciences, 20(15).

Lundbäck V, et al. (2018) FAM13A and POM121C are candidate genes for fasting insulin: functional follow-up analysis of a genome-wide association study. Diabetologia, 61(5), 1112.

Pahlevan Kakhki M, et al. (2018) HOTAIR but not ANRIL long non-coding RNA contributes to the pathogenesis of multiple sclerosis. Immunology, 153(4), 479.

Ghali RM, et al. (2018) Differential association of ESR1 and ESR2 gene variants with the risk of breast cancer and associated features: A case-control study. Gene, 651, 194.

Nadeali Z, et al. (2017) UGT1A1 gene linkage analysis: application of polymorphic markers rs4148326/rs4124874 in the Iranian population. Iranian journal of basic medical sciences, 20(8), 880.

Molina-Guzman G, et al. (2017) Gender differences in the association between HTR2C gene variants and suicidal behavior in a Mexican population: a case-control study. Neuropsychiatric disease and treatment, 13, 559.

Yoosefee S, et al. (2016) ? Association Between Neuregulin-1 Gene Variant ??(rs2439272) and Schizophrenia and Its Negative ?Symptoms in an Iranian Population. Iranian journal of psychiatry, 11(3), 147.

Arruda MB, et al. (2016) Single Nucleotide Polymorphisms in Cellular Drug Transporters Are Associated with Intolerance to Antiretroviral Therapy in Brazilian HIV-1 Positive Individuals. PloS one, 11(9), e0163170.

Keshari PK, et al. (2016) Allelic imbalance of multiple sclerosis susceptibility genes IKZF3 and IQGAP1 in human peripheral blood. BMC genetics, 17, 59.

Berge T, et al. (2016) The multiple sclerosis susceptibility genes TAGAP and IL2RA are regulated by vitamin D in CD4+ T cells. Genes and immunity, 17(2), 118.

Schieck M, et al. (2016) Doublesex and mab-3 related transcription factor 1 (DMRT1) is a sex-specific genetic determinant of childhood-onset asthma and is expressed in testis and macrophages. The Journal of allergy and clinical immunology, 138(2), 421.

DePriest AD, et al. (2016) Regulators of Androgen Action Resource: a one-stop shop for the comprehensive study of androgen receptor action. Database : the journal of biological databases and curation, 2016.

Torres-Poveda K, et al. (2016) Risk allelic load in Th2 and Th3 cytokines genes as biomarker of susceptibility to HPV-16 positive cervical cancer: a case control study. BMC cancer, 16, 330.

Lokki AI, et al. (2015) Genetic analysis of membrane cofactor protein (CD46) of the complement system in women with and without preeclamptic pregnancies. PloS one, 10(2), e0117840.

Stevenson M, et al. (2015) Burden of disease variants in participants of the Long Life Family Study. Aging, 7(2), 123.

Sampaio AS, et al. (2015) COMT and MAO-A polymorphisms and obsessive-compulsive disorder: a family-based association study. PloS one, 10(3), e0119592.

Paszkowska-Szczur K, et al. (2015) Polymorphisms in nucleotide excision repair genes and susceptibility to colorectal cancer in the Polish population. Molecular biology reports, 42(3), 755.

Lardo M, et al. (2015) MDR1/ABCB1 gene polymorphisms in patients with chronic myeloid leukemia. Blood research, 50(3), 154.