Resource Summary Report

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SNPSTATS

RRID:SCR_002142
Type: Tool

Proper Citation

SNPSTATS (RRID:SCR_002142)

Resource Information

URL: http://bioinfo.iconcologia.net/snpstats/

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Description: A web-based application designed from a genetic epidemiology point of view to analyze association studies using single nucleotide polymorphisms (SNPs). For each selected SNP, you will receive: * Allele and genotype frequencies * Test for Hardy-Weinberg equilibrium * Analysis of association with a response variable based on linear or logistic regression * Multiple inheritance models: co-dominant, dominant, recessive, over-dominant and additive * Analysis of interactions (gene-gene or gene-environment) If multiple SNPs are selected: * Linkage disequilibrium statistics * Haplotype frequency estimation * Analysis of association of haplotypes with the response * Analysis of interactions (haplotypes-covariate)

Abbreviations: SNPStats

Synonyms: SNP STATisticS

Resource Type: software resource, data analysis service, source code, service resource, analysis service resource, production service resource

Defining Citation: PMID:16720584

Keywords: gene, genetic, genomic, single nucleotide polymorphism, association study, genetic, epidemiology, allele, frequency, genotype, allele frequency, genotype frequency, hardy-weinberg equilibrium, linkage disequilibrium, haplotype frequency, haplotype, interaction, haplotypes-covariate, association, linear regression, logistic regression, inheritance model, co-dominant, dominant, recessive, over-dominant, additive, gene-gene, gene-environment

Funding:

Availability: GNU General Public License

Resource Name: SNPSTATS

Resource ID: SCR_002142

Alternate IDs: nlx_154650

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250416T063256+0000

Ratings and Alerts

No rating or validation information has been found for SNPSTATS.

No alerts have been found for SNPSTATS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 593 mentions in open access literature.

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

Xu J, et al. (2025) Identification of genetic variants of the IL18R1 gene in association with COPD susceptibility. Annals of medicine, 57(1), 2446690.

Di Menna L, et al. (2025) Preclinical and clinical study on type 3 metabotropic glutamate receptors in Parkinson's disease. NPJ Parkinson's disease, 11(1), 9.

Al-Eitan L, et al. (2025) Effect of serotonin receptor gene variants on substance use disorders. Annals of medicine, 57(1), 2445779.

Chávez-Vélez E, et al. (2024) Single nucleotide variants in the CCL2, OAS1 and DPP9 genes and their association with the severity of COVID-19 in an Ecuadorian population. Frontiers in cellular and infection microbiology, 14, 1322882.

Kondkar AA, et al. (2024) Common Variants rs429358 and rs7412 in APOE Gene Are Not Associated with POAG in a Saudi Cohort. Biology, 13(1).

Ponce-de-León C, et al. (2024) Expression of Elafin and CD200 as Immune Checkpoint Molecules Involved in Celiac Disease. International journal of molecular sciences, 25(2).

Benmansour R, et al. (2024) TYK2, IFITM3, IFNAR2 and OAS3 single-nucleotide polymorphisms among severe COVID-19 ICU patients in Morocco. International journal of immunopathology and pharmacology, 38, 3946320241257241.

Angulo-Aguado M, et al. (2024) Next-generation sequencing of host genetics risk factors associated with COVID-19 severity and long-COVID in Colombian population. Scientific reports, 14(1), 8497.

Benmansour R, et al. (2024) Implication of IL-12A, IL-12B, IL-6, and TNF single-nucleotide polymorphisms in severity and susceptibility to COVID-19. International journal of immunopathology and pharmacology, 38, 3946320241279893.

Flore L, et al. (2024) Association of VDR Polymorphisms with Muscle Mass Development in Elite Young Soccer Players: A Pilot Study. Sports (Basel, Switzerland), 12(9).

Jab?o?ska A, et al. (2024) Polymorphisms in the genes encoding RLR and TLR3 and CMV DNAemia in subjects coinfected with human immunodeficiency virus and cytomegalovirus. Archives of virology, 169(10), 211.

Al-Eitan L, et al. (2024) Investigating CHRNA5, CHRNA3, and CHRNB4 variants in the genetic landscape of substance use disorder in Jordan. BMC psychiatry, 24(1), 436.

Xie Y, et al. (2024) CD147 TagSNP is associated with the vulnerability to lung cancer in the Chinese population: a case-control study. Discover oncology, 15(1), 281.

Ç???rta? R, et al. (2024) The ARK2N (C18ORF25) Genetic Variant Is Associated with Muscle Fiber Size and Strength Athlete Status. Metabolites, 14(12).

Zhong L, et al. (2024) Gene Interaction of Dopaminergic Synaptic Pathway Genes in Attention-Deficit Hyperactivity Disorder: a Case-Control Study in Chinese Children. Molecular neurobiology, 61(1), 42.

Shilenok I, et al. (2024) C11orf58 (Hero20) Gene Polymorphism: Contribution to Ischemic Stroke Risk and Interactions with Other Heat-Resistant Obscure Chaperones. Biomedicines, 12(11).

Sopori S, et al. (2024) CLOCK gene 3'UTR and exon 9 polymorphisms show a strong association with essential hypertension in a North Indian population. BMC medical genomics, 17(1), 289.

Bergez-Hernández F, et al. (2024) Deletion in a regulatory region is associated with underexpression of miR-148b?3p in patients with prostate cancer. Biomedical reports, 20(3), 52.

Zambrano-Román M, et al. (2024) PTCH1 Gene Variants, mRNA Expression, and

Bioinformatics Insights in Mexican Cutaneous Squamous Cell Carcinoma Patients. Biology, 13(3).

Gallego-Durán R, et al. (2024) Fibroblast growth factor 21 is a hepatokine involved in MASLD progression. United European gastroenterology journal, 12(8), 1056.