Resource Summary Report

Generated by RRID on Apr 8, 2025

SHEsis: Analysis Tools For Random Samples

RRID:SCR_002958
Type: Tool

Proper Citation

SHEsis: Analysis Tools For Random Samples (RRID:SCR_002958)

Resource Information

URL: http://analysis2.bio-x.cn/myAnalysis.php

Proper Citation: SHEsis: Analysis Tools For Random Samples (RRID:SCR_002958)

Description: A powerful web-based platform for analyses of linkage disequilibrium, haplotype construction, and genetic association at polymorphism loci.

Abbreviations: SHEsis

Resource Type: service resource, data analysis service, production service resource, analysis service resource

Defining Citation: PMID:19290020, PMID:15740637

Keywords: analysis, disequilibrium, haplotype, genetic, association, polymorphism, locus, linkage disequilibrium

Funding: Major State Basic Research Development program of China ;
National High Technology Research and Development Program of China

Availability: Acknowledgement requested

Resource Name: SHEsis: Analysis Tools For Random Samples

Resource ID: SCR_002958

Alternate IDs: nif-0000-30105

Old URLs: http://analysis.bio-x.cn/myAnalysis.php

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250407T215336+0000

Ratings and Alerts

No rating or validation information has been found for SHEsis: Analysis Tools For Random Samples.

No alerts have been found for SHEsis: Analysis Tools For Random Samples.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 77 mentions in open access literature.

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

Yan H, et al. (2024) Association between TIMP1 polymorphism and female neuromyelitis optica spectrum disorder in Chinese population. Heliyon, 10(17), e37091.

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.

Yan H, et al. (2021) Associations of IRAK1 Gene Polymorphisms and mRNA Expression With NMOSD Risk in the Northern Chinese Han Population. Frontiers in neurology, 12, 661791.

Fan G, et al. (2021) Association of TERT gene polymorphisms with clinical benign prostatic hyperplasia in a Chinese Han population of the Northwest region. Translational andrology and urology, 10(2), 692.

Chen W, et al. (2021) Association of Single-Nucleotide Polymorphisms of Gab1 Gene with Susceptibility to Meningioma in a Northern Chinese Han Population. Medical science monitor : international medical journal of experimental and clinical research, 27, e933444.

Zhao X, et al. (2020) Mutation screening of the UBE3A gene in Chinese Han population with autism. BMC psychiatry, 20(1), 589.

Sun CP, et al. (2020) Association of SOX11 Polymorphisms in distal 3'UTR with Susceptibility for Schizophrenia. Journal of clinical laboratory analysis, 34(8), e23306.

Lv Y, et al. (2020) Positive Association of Human SHC3 Gene with Schizophrenia in a Northeast Chinese Han Population. Psychiatry investigation, 17(9), 934.

Tan X, et al. (2020) Functional Genetic Polymorphisms in the IL1RL1-IL18R1 Region Confer Risk for Ocular Behçet's Disease in a Chinese Han Population. Frontiers in genetics, 11, 645.

Raza SHA, et al. (2020) Bioinformatics analysis and genetic polymorphisms in genomic region of the bovine SH2B2 gene and their associations with molecular breeding for body size traits in qinchuan beef cattle. Bioscience reports, 40(3).

Wu S, et al. (2019) Genetic variants and haplotype combination in the bovine CRTC3 affected conformation traits in two Chinese native cattle breeds (Bos Taurus). Genomics, 111(6), 1736.

Guo J, et al. (2018) Investigation of C1-complex regions reveals new C1Q variants associated with protection from systemic lupus erythematosus, and affect its transcript abundance. Scientific reports, 8(1), 8048.

Shen Y, et al. (2017) Association between TNFSF4 and BLK gene polymorphisms and susceptibility to allergic rhinitis. Molecular medicine reports, 16(3), 3224.

Long Z, et al. (2017) Polymorphism of the ABO gene associate with thrombosis risk in patients with paroxysmal nocturnal hemoglobinuria. Oncotarget, 8(54), 92411.

Li Y, et al. (2017) The association of six single nucleotide polymorphisms and their haplotypes in CDH13 with T2DM in a Han Chinese population. Medicine, 96(22), e7063.

Chen D, et al. (2016) Interaction between MLL3 genetic polymorphisms, smoking, and alcohol drinking in laryngeal cancer: a case-control study. Cancer medicine, 5(3), 527.

Wang Y, et al. (2016) Allele-specific expression of mutated in colorectal cancer (MCC) gene and alternative susceptibility to colorectal cancer in schizophrenia. Scientific reports, 6, 26688.

Yao Y, et al. (2016) Single Nucleotide Polymorphisms of the ERAP1 Gene and Risk of NSCLC: A Comparison of Genetically Distant Populations, Chinese and Caucasian. Archivum immunologiae et therapiae experimentalis, 64(Suppl 1), 117.

Luo JQ, et al. (2015) SLCO1B1 Variants and Angiotensin Converting Enzyme Inhibitor (Enalapril)-Induced Cough: a Pharmacogenetic Study. Scientific reports, 5, 17253.

Patente TA, et al. (2015) Linkage disequilibrium with HLA-DRB1-DQB1 haplotypes explains the association of TNF-308G>A variant with type 1 diabetes in a Brazilian cohort. Gene, 568(1), 50.