Resource Summary Report

Generated by RRID on Aug 4, 2026

SNPRelate

RRID:SCR_022719
Type: Tool

Proper Citation

SNPRelate (RRID:SCR_022719)

Resource Information

URL: https://bioconductor.org/packages/SNPRelate/

Proper Citation: SNPRelate (RRID:SCR_022719)

Description: Software R package as parallel computing toolset for relatedness and principal component analysis of SNP data.

Resource Type: software resource, data processing software, software application, data analysis software

Defining Citation: PMID:23060615

Keywords: parallel computing, relatedness and principal component analysis, SNP data analysis

Funding: NHGRI U01 HG 004446

Availability: Free, Available for download, Freely available

Resource Name: SNPRelate

Resource ID: SCR_022719

Alternate URLs: https://github.com/zhengxwen/SNPRelate

License: GPL v3

Record Creation Time: 20220902T050154+0000

Record Last Update: 20260804T043747+0000

Ratings and Alerts

No rating or validation information has been found for SNPRelate.

No alerts have been found for SNPRelate.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Stabler TC, et al. (2025) Regular Plasmodium falciparum importation onto Bioko Island, Equatorial Guinea, hampers malaria elimination from the island. PLOS global public health, 5(8), e0004999.

Akopyan M, et al. (2025) Reference genome choice compromises population genetic analyses. Cell.

Borda V, et al. (2024) Genetics of Latin American Diversity Project: Insights into population genetics and association studies in admixed groups in the Americas. Cell genomics, 4(11), 100692.

Hodonsky CJ, et al. (2024) Multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci. Cell genomics, 4(1), 100465.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.

Belleau P, et al. (2023) Genetic Ancestry Inference from Cancer-Derived Molecular Data across Genomic and Transcriptomic Platforms. Cancer research, 83(1), 49.

Schall PZ, et al. (2023) Genome-wide methylation patterns from canine nanopore assemblies. G3 (Bethesda, Md.), 13(11).

Saada OA, et al. (2022) Phased polyploid genomes provide deeper insight into the multiple origins of domesticated Saccharomyces cerevisiae beer yeasts. Current biology : CB, 32(6), 1350.

Dilliott AA, et al. (2021) Contribution of rare variant associations to neurodegenerative disease presentation. NPJ genomic medicine, 6(1), 80.

Fijarczyk A, et al. (2020) The Genome Sequence of the Jean-Talon Strain, an Archeological Beer Yeast from Québec, Reveals Traces of Adaptation to Specific Brewing Conditions. G3 (Bethesda, Md.), 10(9), 3087.

Jmel H, et al. (2018) Pharmacogenetic landscape of Metabolic Syndrome components drug response in Tunisia and comparison with worldwide populations. PloS one, 13(4),

e0194842.

Müller BSF, et al. (2017) Genomic prediction in contrast to a genome-wide association study in explaining heritable variation of complex growth traits in breeding populations of Eucalyptus. BMC genomics, 18(1), 524.