Resource Summary Report

Generated by ASWG on Aug 4, 2026

RVTESTS

RRID:SCR_007639
Type: Tool

Proper Citation

RVTESTS (RRID:SCR_007639)

Resource Information

URL: http://genome.sph.umich.edu/wiki/RvTests

Proper Citation: RVTESTS (RRID:SCR_007639)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: RVTESTS

Synonyms: Rare Variants TESTS

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++

Resource Name: RVTESTS

Resource ID: SCR_007639

Alternate IDs: nlx_154603

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260801T191040+0000

Ratings and Alerts

No rating or validation information has been found for RVTESTS.

No alerts have been found for RVTESTS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Li R, et al. (2026) Whole-genome sequence-based association analysis of African American individuals with bipolar disorder and schizophrenia. HGG advances, 7(1), 100499.

Martín-Bórnez M, et al. (2025) Does COMT Play a Role in Parkinson's Disease Susceptibility across Diverse Ancestral Populations? Movement disorders : official journal of the Movement Disorder Society, 40(12), 2819.

Prijatelj V, et al. (2025) Genetic and epidemiologic assessment of mandibular cortical indices and bone mineral density in peripubertal children: the Generation R study. Clinical oral investigations, 29(12), 585.

Martín-Bórnez M, et al. (2025) Does COMT Play a Role in Parkinson's Disease Susceptibility Across Diverse Ancestral Populations? medRxiv : the preprint server for health sciences.

Wijnbergen D, et al. (2025) Multi-omics analysis in inclusion body myositis identifies mir-16 responsible for HLA overexpression. Orphanet journal of rare diseases, 20(1), 27.

Farashi S, et al. (2025) HTRA1/lncRNA HTRA1-AS1 dominates in age-related macular degeneration reticular pseudodrusen genetic risk with no complement involvement. Nature communications, 16(1), 10854.

Godrich D, et al. (2025) Genome-wide association studies of TDP-43 proteinopathy and hippocampal sclerosis reveal shared genetic associations with APOE and TMEM106B. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(11), e70760.

Sun W, et al. (2025) TMEM175, SCARB2 and CTSB associations with Parkinson's disease risk across populations. NPJ Parkinson's disease, 11(1), 348.

Lee MK, et al. (2025) Genome scan reveals several loci associated with torus palatinus. Orthodontics & craniofacial research, 28(1), 159.

Khani M, et al. (2025) Biobank-scale genetic characterization of Alzheimer's disease and related dementias across diverse ancestries. Nature communications, 16(1), 7554.

Zhong Y, et al. (2025) Common and rare variant analyses implicate late-infancy cerebellar development and immune genes in ADHD. Journal of neurodevelopmental disorders, 17(1), 34.

Haydar S, et al. (2025) A Genome-Wide Association Study of Taste Liking in the Danish Population. The Journal of nutrition, 155(8), 2591.

Sarnowski C, et al. (2024) Ancestrally diverse genome-wide association analysis highlights ancestry-specific differences in genetic regulation of plasma protein levels. medRxiv : the preprint server for health sciences.

Wang J, et al. (2024) Identification of eight genomic protective alleles for mitochondrial diabetes by Kinship-graph convolutional network. Journal of diabetes investigation, 15(1), 52.

Bayram E, et al. (2024) Genetic analysis of the X chromosome in people with Lewy body dementia nominates new risk loci. NPJ Parkinson's disease, 10(1), 39.

Haukka JK, et al. (2024) Whole-exome and whole-genome sequencing of 1064 individuals with type 1 diabetes reveals novel genes for diabetic kidney disease. Diabetologia, 67(11), 2494.

Tangtanatakul P, et al. (2024) Association of genetic variation on X chromosome with systemic lupus erythematosus in both Thai and Chinese populations. Lupus science & medicine, 11(1).

Ollila HM, et al. (2024) Nightmares share genetic risk factors with sleep and psychiatric traits. Translational psychiatry, 14(1), 123.

Wang Y, et al. (2024) NRDE2 deficiency impairs homologous recombination repair and sensitizes hepatocellular carcinoma to PARP inhibitors. Cell genomics, 4(5), 100550.

Luciano C, et al. (2024) Epigenetic patterns, accelerated biological aging, and enhanced epigenetic drift detected 6 months following COVID-19 infection: insights from a genome-wide DNA methylation study. Clinical epigenetics, 16(1), 112.