

Resource Summary Report

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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 [RRID](#) .

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.

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? *Movement disorders : official journal of the Movement Disorder Society*, 40(12), 2819.

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.

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

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.

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

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.

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.

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.

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.

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.

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