Resource Summary Report

Generated by T1D on Jul 29, 2026

SKAT

RRID:SCR_009396
Type: Tool

Proper Citation

SKAT (RRID:SCR_009396)

Resource Information

URL: https://www.hsph.harvard.edu/skat/

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Description: Software application that is a SNP-set (e.g., a gene or a region) level test for association between a set of rare (or common) variants and dichotomous or quantitative phenotypes. SKAT aggregates individual score test statistics of SNPs in a SNP set and efficiently computes SNP-set level p-values, e.g. a gene or a region level p-value, while adjusting for covariates, such as principal components to account for population stratification. SKAT also allows for power/sample size calculations for designing for sequence association studies. (entry from Genetic Analysis Software)

Synonyms: SNP-set (Sequence) Kernel Association Test

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, bio.tools

Resource Name: SKAT

Resource ID: SCR_009396

Alternate IDs: nlx_154634, biotools:skat

Alternate URLs: https://bio.tools/skat

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260727T040450+0000

Ratings and Alerts

No rating or validation information has been found for SKAT.

No alerts have been found for SKAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 273 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Shade LM, et al. (2025) Whole genome sequence association analysis of brain structural volume measures in the NHLBI TOPMed Program highlights novel loci in diverse participants. medRxiv : the preprint server for health sciences.

Galimberti M, et al. (2025) A contextual genomic perspective on physical activity and its relationship to health, well being and illness. Nature genetics, 57(8), 1860.

Chang JB, et al. (2025) A calcium-sensing receptor allelic series and underdiagnosis of genetically driven hypocalcemia. American journal of human genetics, 112(8), 1818.

Pardo-Seco J, et al. (2025) Whole-Genome Sequencing in Galicia Reveals Male-Biased Pre-Islamic North African Ancestry, Subtle Population Structure, and Microgeographic Patterns of Disease Risk. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(24), e71253.

Zhou D, et al. (2025) Non-coding genetic elements of lung cancer identified using whole genome sequencing in 13,722 Chinese. Nature communications, 16(1), 7365.

Jung S, et al. (2025) Rare Variants in Antisense lncRNA-Protein Coding Gene Overlap Regions Contribute to Obsessive-Compulsive Disorder. medRxiv : the preprint server for health sciences.

Tabata K, et al. (2025) Rare genetic variants involved in increased risk of paroxysmal atrial fibrillation in a Japanese population. Scientific reports, 15(1), 13216.

Cai Y, et al. (2025) Application of multigene panel testing for bleeding, thrombotic, and platelet disorders in patients and the general population in China. Molecular biomedicine, 6(1), 39.

Cao J, et al. (2025) Integrating rare pathogenic variant prioritization with gene-based association analysis to identify novel genes and relevant multimodal traits for Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(2), e14444.

Ishorst N, et al. (2025) Role of ZFHX4 in orofacial clefting based on human genetic data and zebrafish models. European journal of human genetics : EJHG, 33(5), 595.

Ali A, et al. (2025) Genetic variants associated with age-related episodic memory decline implicate distinct memory pathologies. Alzheimer's & dementia : the journal of the

Alzheimer's Association, 21(1), e14379.

Frydas A, et al. (2025) Investigation of the role of miRNA variants in neurodegenerative brain diseases. Frontiers in genetics, 16, 1506169.

Minikel EV, et al. (2025) Human genetic evidence enriched for side effects of approved drugs. PLoS genetics, 21(3), e1011638.

Zhu H, et al. (2025) Common cis-regulatory variation modifies the penetrance of pathogenic SHROOM3 variants in craniofacial microsomia. Genome research, 35(5), 1065.

Jing X, et al. (2025) Protein-truncating variants in UQCRC1 are associated with Parkinson's disease: evidence from half-million people. NPJ Parkinson's disease, 11(1), 120.

Lindholm ME, et al. (2025) Identification of candidate cardiomyopathy modifier genes through genome sequencing and RNA profiling. Frontiers in cardiovascular medicine, 12, 1546493.

Zheng D, et al. (2024) radioGWAS links radiome to genome to discover driver genes with somatic mutations for heterogeneous tumor image phenotype in pancreatic cancer. Scientific reports, 14(1), 12316.

Clarke B, et al. (2024) Integration of variant annotations using deep set networks boosts rare variant association testing. Nature genetics, 56(10), 2271.

Zhao Y, et al. (2024) Genetic analysis of transcription factors in dopaminergic neuronal development in Parkinson's disease. Chinese medical journal, 137(4), 450.

Leger BS, et al. (2024) Rare and Common Variants Associated with Alcohol Consumption Identify a Conserved Molecular Network. bioRxiv : the preprint server for biology.