# Resource Summary Report

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## 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:** 20260829T183101+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 287 mentions in open access literature.

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


Badia M, et al. (2026) Massively parallel quantification of mutational impact on IAPP amyloid formation. Nature communications, 17(1).

Zhu J, et al. (2026) Leveraging ancestral recombination graphs for scalable mixed-model analysis of complex traits. Cell genomics, 6(2), 101072.

Menon S, et al. (2026) Massive-scale single-nucleus multi-omics identifies novel rare noncoding drivers of Parkinson's disease. bioRxiv : the preprint server for biology.

Nelson M, et al. (2026) Genetic determinants of childhood onset systemic lupus erythematosus. Lupus science & medicine, 13(1).

Sun X, et al. (2026) ASSOCIATION ANALYSIS OF MITOCHONDRIAL HETEROPLASMIC VARIANTS AND CARDIOMETABOLIC TRAITS. medRxiv : the preprint server for health sciences.

Bu R, et al. (2026) Exome-Wide Association Analysis Identifies Rare Germline Susceptibility Variants in Early-Onset Breast Cancer Among Saudi Women. International journal of molecular sciences, 27(4).

Yehia L, et al. (2026) Genomic modifiers of malignant and neurodevelopmental phenotypes in individuals with PTEN hamartoma tumor syndrome. NPJ genomic medicine, 11(1).

Sun Y, et al. (2026) Distinctive genetic architecture of infantile epileptic spasms syndrome compared to self-limited infantile epilepsy by trios whole-exome sequencing. Epilepsia open, 11(1), 280.

Shi X, et al. (2026) Statistical methods to harmonize electronic health record data across healthcare systems: case study and lessons learned. Bioinformatics (Oxford, England), 42(3).

Ishigami D, et al. (2026) Delineating the Genetic Basis of RNF213-related vasculopathies: The association of PKHD1 variants with bilateral cerebral vasculopathy. European journal of human genetics : EJHG, 34(6), 788.

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.

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.

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.

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.

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.

McCaw ZR, et al. (2025) A scalable framework for identifying allelic series from summary statistics. American journal of human genetics, 112(11), 2772.

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.

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.

Chen C, et al. (2025) A Novel, Variance Component-Based Method for Detecting Brain-Behavior Associations in Neuroimaging Data. Statistics and data science in imaging, 2(1).

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.