

# Resource Summary Report

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## SKAT

RRID:SCR\_009396

Type: Tool

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### Proper Citation

SKAT (RRID:SCR\_009396)

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### 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 resource, software application

**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:** 20260818T043340+0000

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### Ratings and Alerts

No rating or validation information has been found for SKAT.

No alerts have been found for SKAT.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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).

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.

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

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.

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.

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

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*.

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.