Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

MetaSKAT

RRID:SCR_003489
Type: Tool

Proper Citation

MetaSKAT (RRID:SCR_003489)

Resource Information

URL: http://www.hsph.harvard.edu/skat/metaskat/

Proper Citation: MetaSKAT (RRID:SCR_003489)

Description: A R package for multiple marker meta-analysis.

Abbreviations: MetaSKAT

Resource Type: software resource

Defining Citation: PMID:23768515

Availability: Free

Resource Name: MetaSKAT

Resource ID: SCR_003489

Alternate IDs: OMICS_00241

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260912T195559+0000

Ratings and Alerts

No rating or validation information has been found for MetaSKAT.

No alerts have been found for MetaSKAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Chifamba LV, et al. (2026) Lack of association between G6PD variants and Parkinson disease. HGG advances, 7(1), 100555.

Wan J, et al. (2026) The genetic spectrum of LRRK2 variants in Parkinson's disease: findings from a large Chinese cohort. NPJ Parkinson's disease, 12(1).

Dering R, et al. (2026) Investigating the Genetic Relationship Between Vitamin B12 Metabolism and Parkinson Disease. Neurology. Genetics, 12(2), e200350.

Senkevich K, et al. (2026) Rare-variant burden across lysosomal genes implicates sialylation and ganglioside metabolism in Parkinson's disease. medRxiv : the preprint server for health sciences.

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.

Vuori N, et al. (2025) Exome and Genome Sequencing Reveals Novel Variants for Severe Diabetic Retinopathy in Type 1 Diabetes. Investigative ophthalmology & visual science, 66(13), 36.

Sonehara K, et al. (2025) Whole-genome sequencing reveals rare and structural variants contributing to psoriasis and identifies CERCAM as a risk gene. Cell genomics, 100978.

Senkevich K, et al. (2024) Lack of genetic evidence for NLRP3 inflammasome involvement in Parkinson's disease pathogenesis. NPJ Parkinson's disease, 10(1), 145.

Senkevich K, et al. (2024) Are rare heterozygous SYNJ1 variants associated with Parkinson's disease? NPJ Parkinson's disease, 10(1), 201.

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.

Dorion MF, et al. (2024) MerTK is a mediator of alpha-synuclein fibril uptake by human microglia. Brain : a journal of neurology, 147(2), 427.

Senkevich K, et al. (2024) Are rare heterozygous SYNJ1 variants associated with Parkinson's disease? medRxiv : the preprint server for health sciences.

Antikainen AA, et al. (2024) Whole-genome sequencing identifies variants in ANK1, LRRN1, HAS1, and other genes and regulatory regions for stroke in type 1 diabetes. Scientific reports, 14(1), 13453.

Senkevich K, et al. (2023) Genetics of NLRP3 suggests lack of involvement and inefficient druggability in Parkinson's disease. medRxiv : the preprint server for health sciences.

Jones-Tabah J, et al. (2023) The Parkinson's disease risk gene cathepsin B promotes fibrillar alpha-synuclein clearance, lysosomal function and glucocerebrosidase activity in dopaminergic neurons. bioRxiv : the preprint server for biology.

Senkevich K, et al. (2023) GALC variants affect galactosylceramidase enzymatic activity and risk of Parkinson's disease. Brain : a journal of neurology, 146(5), 1859.

Senkevich K, et al. (2023) Association of rare variants in ARSA with Parkinson's disease. medRxiv : the preprint server for health sciences.

Neumann A, et al. (2022) Rare variants in IFFO1, DTNB, NLRC3 and SLC22A10 associate with Alzheimer's disease CSF profile of neuronal injury and inflammation. Molecular psychiatry, 27(4), 1990.

Kim YJ, et al. (2021) The burden of rare damaging variants in hereditary atypical parkinsonism genes is increased in patients with Parkinson's disease. Neurobiology of aging, 100, 118.e5.

van Walree ES, et al. (2021) Germline variants in HEY2 functional domains lead to congenital heart defects and thoracic aortic aneurysms. Genetics in medicine : official journal of the American College of Medical Genetics, 23(1), 103.