Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

GWAMA

RRID:SCR_006624
Type: Tool

Proper Citation

GWAMA (RRID:SCR_006624)

Resource Information

URL: http://www.geenivaramu.ee/en/tools/gwama

Proper Citation: GWAMA (RRID:SCR_006624)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software tool for meta analysis of whole genome association data.

Abbreviations: GWAMA

Synonyms: Genome-Wide Association Meta Analysis

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: PMID:20509871, DOI:10.1186/1471-2105-11-288

Keywords: meta, analysis, genome, association, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GWAMA

Resource ID: SCR_006624

Alternate IDs: biotools:gwama, OMICS_00235

Alternate URLs: https://bio.tools/gwama, https://sources.debian.org/src/gwama/

Old URLs: http://www.well.ox.ac.uk/GWAMA/

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260912T195642+0000

Ratings and Alerts

No rating or validation information has been found for GWAMA.

No alerts have been found for GWAMA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 177 mentions in open access literature.

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

Kamiza AB, et al. (2026) KidneyGenAfrica multi-cohort Genome-wide association study and polygenic prediction of kidney function in 110,000 Africans. Nature communications, 17(1).

Ma J, et al. (2026) Alcohol-Induced Metabolic Stress Sensed by m6A-Modified ChREBP Drives Immune Evasion in Esophageal Carcinogenesis. Cancer research.

Ajasa AA, et al. (2025) Genome-wide association analysis using multiple Atlantic salmon populations. Genetics, selection, evolution : GSE, 57(1), 9.

Marques IF, et al. (2025) Associations of maternal night shift work during pregnancy with DNA methylation in offspring: a meta-analysis in the PACE consortium. Clinical epigenetics, 17(1), 12.

Murrin O, et al. (2025) A systematic analysis of the contribution of genetics to multimorbidity and comparisons with primary care data. EBioMedicine, 113, 105584.

Zhang Y, et al. (2025) The causal relationship between steroid hormones and risk of stroke: evidence from a two-sample Mendelian randomization study. Molecular brain, 18(1), 6.

Downie CG, et al. (2025) Trans-ancestry genome-wide association study of childhood body mass index identifies novel loci and age-specific effects. HGG advances, 6(2), 100411.

Hrytsenko Y, et al. (2024) Obstructive sleep apnea mediates genetic risk of Diabetes Mellitus: The Hispanic Community Health Study/Study of Latinos. medRxiv : the preprint server for health sciences.

Munsch G, et al. (2024) Genomic Landscape of Thrombosis Recurrence Risk Across Venous Thromboembolism Subtypes. medRxiv : the preprint server for health sciences.

Wu XP, et al. (2024) Association between migraine and venous thromboembolism: a Mendelian randomization and genetic correlation study. Frontiers in genetics, 15, 1272599.

Schurz H, et al. (2024) Multi-ancestry meta-analysis of host genetic susceptibility to tuberculosis identifies shared genetic architecture. eLife, 13.

Burrows K, et al. (2024) A framework for conducting time-varying genome-wide association studies: An application to body mass index across childhood in six multiethnic cohorts. medRxiv : the preprint server for health sciences.

Eissman JM, et al. (2024) Sex-specific genetic architecture of late-life memory performance. Alzheimer's & dementia : the journal of the Alzheimer's Association, 20(2), 1250.

Quester J, et al. (2024) High SHBG and Low Bioavailable Testosterone are Strongly Causally Associated with Increased Forearm Fracture Risk in Women: An MR Study Leveraging Novel Female-Specific Data. Calcified tissue international, 115(5), 648.

Simmonds E, et al. (2024) Chromosome X-wide association study in case control studies of pathologically confirmed Alzheimer's disease in a European population. Translational psychiatry, 14(1), 358.

Keener R, et al. (2024) Validation of human telomere length multi-ancestry meta-analysis association signals identifies POP5 and KBTBD6 as human telomere length regulation genes. Nature communications, 15(1), 4417.

Rämö JT, et al. (2024) Rare genetic variation in VE-PTP is associated with central serous chorioretinopathy, venous dysfunction and glaucoma. medRxiv : the preprint server for health sciences.

Burrows K, et al. (2024) A framework for conducting GWAS using repeated measures data with an application to childhood BMI. Nature communications, 15(1), 10067.

Svyatova G, et al. (2024) Genetic Predisposition to Prediabetes in the Kazakh Population. Current issues in molecular biology, 46(10), 10913.

Pujol-Gualdo N, et al. (2024) Circulating anti-Müllerian hormone levels in pre-menopausal women: novel genetic insights from a genome-wide association meta-analysis. Human reproduction (Oxford, England), 39(7), 1564.