

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 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: software application, software resource, data processing software, data analysis software

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: 20260728T043236+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 175 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

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

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.

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.

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.

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.

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.

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.

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.

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.

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*.

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.

Uddin MM, et al. (2024) Long-term longitudinal analysis of 4,187 participants reveals insights into determinants of clonal hematopoiesis. *Nature communications*, 15(1), 7858.

Wang Z, et al. (2024) Analysis of C-reactive protein omics-measures associates methylation risk score with sleep health and related health outcomes. *medRxiv : the preprint server for health sciences*.

Landvreugd A, et al. (2024) Using Polygenic Scores for Circadian Rhythms to Predict Wellbeing, Depressive Symptoms, Chronotype, and Health. *Journal of biological rhythms*, 39(3), 270.

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.