

Resource Summary Report

Generated by [dkNET](#) on May 1, 2025

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 resource, software application

Defining Citation: [PMID:20509871](#), [DOI:10.1186/1471-2105-11-288](#)

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

Funding:

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: 20250429T055105+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 172 mentions in open access literature.

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

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.

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

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*.

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.

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.

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.

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.

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

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.

Koel M, et al. (2023) GWAS meta-analyses clarify the genetics of cervical phenotypes and inform risk stratification for cervical cancer. *Human molecular genetics*, 32(12), 2103.

Lagou V, et al. (2023) GWAS of random glucose in 476,326 individuals provide insights into diabetes pathophysiology, complications and treatment stratification. *Nature genetics*, 55(9), 1448.