

Resource Summary Report

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METAL

RRID:SCR_002013

Type: Tool

Proper Citation

METAL (RRID:SCR_002013)

Resource Information

URL: <http://csg.sph.umich.edu//abecasis/Metal/>

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Description: Software application designed to facilitate meta-analysis of large datasets (such as several whole genome scans) in a convenient, rapid and memory efficient manner. (entry from Genetic Analysis Software)

Synonyms: Metal - Meta Analysis Helper, METa AnaLysis Helper

Resource Type: software application, software resource

Defining Citation: [PMID:20616382](#)

Keywords: gene, genetic, genomic, whole genome

Resource Name: METAL

Resource ID: SCR_002013

Alternate IDs: nlx_154476, OMICS_00239

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260821T193634+0000

Ratings and Alerts

No rating or validation information has been found for METAL.

No alerts have been found for METAL.

Data and Source Information

Usage and Citation Metrics

We found 2413 mentions in open access literature.

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

Olafsson S, et al. (2026) A meta-analysis identifies driver genes and characterizes the molecular epidemiology of colorectal cancer. *Scientific reports*, 16(1).

Matías-García PR, et al. (2026) DNAm landscape up to 4 months post SARS-CoV-2 infection: insights from four population-based cohorts. *Clinical epigenetics*, 18(1).

Zhang Z, et al. (2026) Bidirectional Association between Atrial Fibrillation and Ovarian Cancer: Evidence from the UK Biobank and Mendelian Randomization. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(1), 144.

Jang HM, et al. (2026) SLC30A8 Rare Variant Modify Contribution of Common Genetic and Lifestyle Factors toward Type 2 Diabetes Mellitus. *Diabetes & metabolism journal*, 50(2), 385.

Tang W, et al. (2026) Novel Plasma Proteomic Markers and Risk of Venous Thromboembolism. *Circulation*, 153(11), 810.

Broberg M, et al. (2026) Genome-wide meta-analysis identifies genetic risk loci for mono- and polyneuropathies in 983 477 individuals. *Human molecular genetics*, 35(4).

Yang S, et al. (2026) Cell type resolved MR based on brain single cell eQTLs corroborated by single cell RNA sequencing uncovers neuroimmune and vascular programs in intracerebral hemorrhage. *Journal of translational medicine*, 24(1).

Lin Q, et al. (2026) Meta-GWAS of Pig Semen Quality Traits Reveals Conserved Genes Regulating Mammalian Fertility. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(16), e15203.

Lin SC, et al. (2026) Integrating multi-polygenic scores for enhanced prediction of antidepressant treatment outcomes in an East Asian population. *Neuropsychopharmacology : official publication of the American College of Neuropsychopharmacology*, 51(2), 422.

Ferrier K, et al. (2026) Epigenome-wide association study meta-analysis of BMI in African Americans. *HGG advances*, 7(1), 100552.

Vollenbrock CE, et al. (2026) Association of genetic variation with age at diagnosis in type 1 diabetes. *BMJ open diabetes research & care*, 14(1).

Feng Y, et al. (2026) Unraveling the genetic interplay and therapeutic potentials between major depressive disorder and metabolic syndrome: multi-ancestry and multi-trait genome-

wide association analyses. BMC psychiatry, 26(1), 153.

Geller F, et al. (2026) Central role of glycosylation processes in human genetic susceptibility to SARS-CoV-2 infections with Omicron variants. Nature genetics, 58(2), 299.

Yang Y, et al. (2026) Identifying pleiotropic genes for backfat thickness and semen traits in pigs using GWAS summary data. Journal of animal science, 104.

Ayalew W, et al. (2026) Mendelian randomization and colocalization reveal potential causal effects of average daily gain on carcass composition and reproductive traits in pigs. Journal of animal science and biotechnology, 17(1).

Dang X, et al. (2026) Investigating the shared genetic architecture between selective immunoglobulin A deficiency and autoimmune diseases. Human genetics, 145(1).

Wendland ZD, et al. (2026) A Genome-Wide Association Study of Hidradenitis Suppurativa from the VA's Million Veteran Program. Dermatology (Basel, Switzerland), 242(4), 418.

Xu Q, et al. (2026) Predicting rehabilitation outcomes of unilateral stroke after brain-computer interface training based on magnetic resonance imaging data. Medicine, 105(3), e46280.

Li YJ, et al. (2026) Leveraging genetic propensity to identify modifiable factors for the age at onset of Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(2), e71111.

Gill C, et al. (2026) Convergence and divergence of genes informed by common and rare variants of autism spectrum disorders in tissue-specific pathways and gene networks. Translational psychiatry, 16(1).