

# Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

## METAL

RRID:SCR\_002013

Type: Tool

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### Proper Citation

METAL (RRID:SCR\_002013)

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### Resource Information

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

**Proper Citation:** METAL (RRID:SCR\_002013)

**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:** 20260829T183046+0000

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### Ratings and Alerts

No rating or validation information has been found for METAL.

No alerts have been found for METAL.

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### 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).