

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/>

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: 20260805T044032+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 2273 mentions in open access literature.

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

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.

Langie J, et al. (2026) The impact of Indigenous American-like ancestry on the risk of acute lymphoblastic leukemia in Hispanic/Latino children. *HGG advances*, 7(1), 100534.

Sinke L, et al. (2026) DNA methylation of genes involved in lipid metabolism drives adiponectin levels and metabolic disease. *Diabetologia*, 69(1), 127.

Hafeez KS, et al. (2025) Integrating polygenic and methylation risk scores for pleural mesothelioma risk stratification. *International journal of cancer*.

Ochoa Tufiño V, et al. (2025) Arabidopsis thaliana Zn transporter genes ZIP3 and ZIP5 provide the main Zn uptake route and act redundantly to face Zn deficiency. *The Plant journal : for cell and molecular biology*, 121(3), e17251.

Ohshima N, et al. (2025) A variant in HMMR/HMMR-AS1 is associated with serum alanine aminotransferase levels in the Ryukyu population. *Scientific reports*, 15(1), 6494.

Chin D, et al. (2025) Genome-wide association study of Idiopathic Pulmonary Fibrosis susceptibility using clinically-curated European-ancestry datasets. *medRxiv : the preprint server for health sciences*.

Xu X, et al. (2025) Identification of potential susceptibility loci for non-small cell lung cancer through whole genome sequencing in circadian rhythm genes. *Scientific reports*, 15(1), 7825.

Toikumo S, et al. (2025) Gene discovery and pleiotropic architecture of Chronic Pain in a Genome-wide Association Study of >1.2 million Individuals. *medRxiv : the preprint server for health sciences*.

Gálvez-Montosa F, et al. (2025) Polymorphisms within autophagy-related genes as susceptibility biomarkers for pancreatic cancer: A meta-analysis of three large European cohorts and functional characterization. *International journal of cancer*, 156(2), 339.

Xu S, et al. (2025) Bidirectional causal relationships between the skin microbiome and psoriasis: Insights from Mendelian randomization analysis. *Medicine*, 104(10), e41736.

Lee MK, et al. (2025) Genome-Wide Scan of Fifth Finger Clinodactyly. *Molecular genetics & genomic medicine*, 13(3), e70090.

Özkaraca M?, et al. (2025) Divide and conquer approach for genome-wide association studies. *Genetics*, 229(4).

Euesden J, et al. (2025) Patient stratification by genetic risk in Alzheimer's disease is only effective in the presence of phenotypic heterogeneity. *PloS one*, 20(1), e0310977.

Tenopoulou M, et al. (2025) Fibrinogen post-translational modifications are biochemical determinants of fibrin clot properties and interactions. *The FEBS journal*, 292(1), 11.

Zhao SS, et al. (2025) Modifiable risk factors and inflammation-related proteins in polymyalgia rheumatica: genome-wide meta-analysis and Mendelian randomization. *Rheumatology (Oxford, England)*, 64(5), 3012.

McGrail C, et al. (2025) Genetic Discovery and Risk Prediction for Type 1 Diabetes in Individuals Without High-Risk HLA-DR3/DR4 Haplotypes. *Diabetes care*, 48(2), 202.

Roshandel D, et al. (2025) Genetics of C-Peptide and Age at Diagnosis in Type 1 Diabetes. *Diabetes*, 74(2), 223.

Oud M, et al. (2025) A planning approach for online adaptive proton therapy to cope with cone beam computed tomography inaccuracies. *Physics and imaging in radiation oncology*, 34, 100752.

Toikumo S, et al. (2025) Gene discovery and pleiotropic architecture of chronic pain in a genome-wide association study of >1.2 million individuals. *Research square*.