Resource Summary Report

Generated by T1D on Jul 31, 2026

MAGMA

RRID:SCR_005757
Type: Tool

Proper Citation

MAGMA (RRID:SCR_005757)

Resource Information

URL: http://snp-magma.sourceforge.net

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Description: Software that utilizes a multiobjective evolutionary algorithm for genetic mapping. It is based on a the ECJ evolutionary software package written by Sean Luke and includes the Strength Pareto Evoluationary Algorithm Version 2 changes for multiobjective analysis. The code runs on any platform with Java Version 2. A genetic mapping project, typically implemented during a search for genes responsible for a disease, requires the acquisition of a set of data from each of a large number of individuals. This data set includes the values of multiple genetic markers. These genetic markers occur at discrete positions along the genome, which is a collection of one or more linear chromosomes. Typing the value of a marker in an individual carries a cost; one seeks to minimize the number of markers typed without excessively jeopardizing the probability of detecting an association between a marker and a disease phenotype. MAGMA is a project which employ"s a multiobjective evolutionary algorithm to solve this problem.

Abbreviations: MAGMA

Synonyms: Multiobjective Analyzer for Genetic Marker Acquisition, MAGMA: Multiobjective Analyzer for Genetic Marker Acquisition

Resource Type: software resource

Defining Citation: PMID:12875658

Keywords: gene, genetic mapping, algorithm, genomics, single nucleotide polymorphism, population study, haplotype-block elucidation, java

Funding: Juvenile Diabetes Research Foundation

Availability: Open unspecified license

Resource Name: MAGMA

Resource ID: SCR_005757

Alternate IDs: nlx_149220

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260725T190611+0000

Ratings and Alerts

No rating or validation information has been found for MAGMA.

No alerts have been found for MAGMA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 456 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Eising E, et al. (2026) De novo protein-coding gene variants in developmental stuttering. Molecular psychiatry, 31(1), 104.

Bj??rndal LD, et al. (2026) Prevalence, Characteristics, and Genetic Architecture of Avoidant/Restrictive Food Intake Phenotypes. JAMA pediatrics, 180(1), 45.

Zhou X, et al. (2026) Single-Cell RNA Sequencing of Thyroid Tissues Reveals Pathogenesis of Graves' Disease. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(1), e08449.

Mokhtari A, et al. (2025) Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study. EBioMedicine, 113, 105569.

Gaertner Z, et al. (2025) Molecular and spatial transcriptomic classification of midbrain dopamine neurons and their alterations in a LRRK2G2019S model of Parkinson's disease. eLife, 13.

Zhu T, et al. (2025) Mitochondrial FIS1 As a Novel Drug Target for the Treatment of Erectile Dysfunction: A Multi-Omic and Epigenomic Association Study. The world journal of men's health, 43(3), 669.

Willis C, et al. (2025) Gene expression differences associated with alcohol use disorder in human brain. Molecular psychiatry, 30(4), 1617.

Wang Y, et al. (2025) Genetic Links between Gastrointestinal Disorders and Kidney Stone Disease: Insights from a Genome-Wide Cross-Trait Analysis. Kidney360, 6(4), 616.

Cornelis MC, et al. (2025) Genetic Markers of Postmortem Brain Iron. Journal of neurochemistry, 169(2), e16309.

, et al. (2025) Trans-ancestry genome-wide study of depression identifies 697 associations implicating cell types and pharmacotherapies. Cell, 188(3), 640.

Nguyen PT, et al. (2025) Genome-wide association studies are enriched for interacting genes. BioData mining, 18(1), 3.

Yang F, et al. (2025) Elucidating shared genetic association between female body mass index and preeclampsia. Communications biology, 8(1), 322.

Tadros R, et al. (2025) Large-scale genome-wide association analyses identify novel genetic loci and mechanisms in hypertrophic cardiomyopathy. Nature genetics, 57(3), 530.

Valo E, et al. (2025) Genome-wide characterization of 54 urinary metabolites reveals molecular impact of kidney function. Nature communications, 16(1), 325.

Yamamoto Y, et al. (2025) Dissecting cross-population polygenic heterogeneity across respiratory and cardiometabolic diseases. Nature communications, 16(1), 3765.

Wu D, et al. (2025) Geochemical study on nitrogen isotope composition, speciation distribution, and influencing factors of vitrinite-rich coal seams during the Late Carboniferous. Scientific reports, 15(1), 19095.

Pottier C, et al. (2025) Deciphering distinct genetic risk factors for FTLD-TDP pathological subtypes via whole-genome sequencing. Nature communications, 16(1), 3914.

Wang R, et al. (2025) Neural Spectral Prediction for Structure Elucidation with Tandem Mass Spectrometry. bioRxiv : the preprint server for biology.

Newbury A, et al. (2025) Multi-domain rule-based phenotyping algorithms enable improved GWAS signal. NPJ digital medicine, 8(1), 499.

Cho S, et al. (2025) Genome-wide interaction study of physical activity and genetic susceptibility on colorectal cancer using UK biobank data. Scientific reports, 15(1), 30180.