

# Resource Summary Report

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## MAGMA

RRID:SCR\_005757

Type: Tool

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### Proper Citation

MAGMA (RRID:SCR\_005757)

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### 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 the ECJ evolutionary software package written by Sean Luke and includes the Strength Pareto Evolutionary 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 employs 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

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## Ratings and Alerts

No rating or validation information has been found for MAGMA.

No alerts have been found for MAGMA.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 456 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.

Wright SN, et al. (2025) Common and rare genetic variants show network convergence for a majority of human traits. *medRxiv : the preprint server for health sciences*.

Bai W, et al. (2025) Shared genetic architecture between stroke and blood lipids: a large-scale genome-wide cross-trait analysis. *Human genomics*, 19(1), 75.

Kim MS, et al. (2025) Genomics reveals eleven obesity endotypes with distinct biological and phenotypic signatures. *medRxiv : the preprint server for health sciences*.

Zhou F, et al. (2025) The shared genetic etiology of autoimmune disorders and interstitial lung disease: insights from large-scale genome-wide cross-trait analysis. *Clinical and experimental medicine*, 25(1), 305.

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.

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

Oliva M, et al. (2025) Integration of GWAS, QTLs and keratinocyte functional assays reveals molecular mechanisms of atopic dermatitis. *Nature communications*, 16(1), 3101.

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.

Lai Q, et al. (2025) Disentangling associations between complex traits and cell types with seismic. *Nature communications*, 16(1), 8744.

Wilhelm K, et al. (2025) Meta-evolutionary exome analysis identifies novel type 2 diabetes mellitus genes in the UK Biobank and all of us. *PLoS genetics*, 21(9), e1011889.

Antonyan L, et al. (2025) Polygenic Risk Scores for Pediatric Obsessive-Compulsive Symptoms and their Mediating Effect in Clinically Diagnosed Samples of Obsessive-Compulsive Disorder, Attention-Deficit/Hyperactivity Disorder, Anxiety, Depression, Autism and Tourette syndrome. *Research square*.

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

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

Liu SA, et al. (2025) Plume-induced emissions of deep methane linked to the end-Guadalupian mass extinction. *Nature communications*, 16(1), 5865.

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