

# 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:** 20260815T182318+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 495 mentions in open access literature.

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

Khan Y, et al. (2026) Transdiagnostic and Disorder-Level Genome-Wide Association Studies Enhance Precision of Substance Use and Psychiatric Genetic Risk Profiles in African and European Ancestries. *Biological psychiatry*, 99(1), 68.

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

Bright U, et al. (2026) The genetics of cannabis lifetime use. *Neuropsychopharmacology* : official publication of the American College of Neuropsychopharmacology, 51(3), 554.

Jiang H, et al. (2026) Decoding Human Placental Cellular and Molecular Responses to Obesity and Fetal Growth. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(17), e09691.

Liu A, et al. (2026) Concordance of cortical morphological anomalies with genetic predisposition to multisite chronic pain in females. *The Korean journal of pain*, 39(2), 260.

Nakao T, et al. (2026) Genomic, phenomic and geographic associations of leukocyte telomere length in the United States. *Nature genetics*, 58(4), 831.

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),

Suresh V, et al. (2026) Molecular dynamics of Brodmann Area 22 in development and autism. *bioRxiv : the preprint server for biology*.

Zheng H, et al. (2026) A single-cell spatiotemporal transcriptomic atlas of mouse prefrontal cortex maps dynamics of intratelencephalic neurons during postnatal development. *PLoS biology*, 24(1), e3003594.

Yu ZM, et al. (2026) scVMAP: a comprehensive platform for integrating single-cell chromatin accessibility regions with causal variants. *Nucleic acids research*, 54(D1), D1270.

Westerman KE, et al. (2026) Polygenic scores capture genetic modification of the adiposity-cardiometabolic risk factor relationship. *Cell genomics*, 6(3), 101075.

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

Li X, et al. (2026) Genomic structural equation modeling reveals shared genetic structure of cardiac function and structure-function association studies of CLCNKA mutations. *Scientific reports*, 16(1), 4283.

Kim MJ, et al. (2026) In-Depth characterization of the shared genetic architecture of suicide attempts with other major psychiatric disorders. *Translational psychiatry*, 16(1).

Pan L, et al. (2026) Large-Scale Plasma Proteomics and Genetic Integration Uncover Novel Biological Pathways in Male Pattern Baldness. *International journal of molecular sciences*, 27(4).

Fu L, et al. (2026) Genetic insights and mechanistic parallels in gestational diabetes mellitus and type 2 diabetes. *Nature communications*, 17(1), 660.

Spence JP, et al. (2026) Specificity, length and luck drive gene rankings in association studies. *Nature*, 649(8098), 918.

Mushunuri A, et al. (2026) Genetic risk factor identification for common epilepsies guided by integrative omics data analysis. *Epilepsia*, 67(3), 1406.

Wang Y, et al. (2026) Organ-specific proteomic aging clocks predict disease and longevity across diverse populations. *Nature aging*, 6(1), 162.

Ming M, et al. (2026) Drivers of systemic male-female allele frequency divergence in humans. *bioRxiv : the preprint server for biology*.