Resource Summary Report

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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

Resource Name: MAGMA

Resource ID: SCR_005757

Alternate IDs: nlx_149220

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260912T195631+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 495 mentions in open access literature.

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

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),

144.

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??rndal 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).

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

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

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

Werwath KE, et al. (2026) Trans-ancestry GWAS of hot flashes reveals potent treatment target and overlap with psychiatric disorders. Communications medicine, 6(1), 51.

Xu X, et al. (2026) sc-eQTL unveil immunogenetic architecture of polycystic ovary syndrome. Scientific reports, 16(1), 4462.