# Resource Summary Report

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## MENDEL

RRID:SCR_009288
Type: Tool

### Proper Citation

MENDEL (RRID:SCR_009288)

### Resource Information

**URL:** http://www.genetics.ucla.edu/software/

**Proper Citation:** MENDEL (RRID:SCR_009288)

**Description:** Software application for genetic analysis of human pedigree data under models involving a small number of loci. MENDEL is useful for segregation analysis, linkage calculations, genetic counseling, allele frequency estimation, and related kinds of problems. (entry from Genetic Analysis Software)

**Abbreviations:** MENDEL

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic, fortran77

**Resource Name:** MENDEL

**Resource ID:** SCR_009288

**Alternate IDs:** nlx_154473

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260829T183058+0000

### Ratings and Alerts

No rating or validation information has been found for MENDEL.

No alerts have been found for MENDEL.

### Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 569 mentions in open access literature.

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


Tang R, et al. (2026) Mendelian randomization study: investigating the causal impact of Covid-19 on adverse pregnancy outcomes. Virology journal, 23(1).

Jade E, et al. (2026) An Increase in Male Recombination Rate With Age in Dairy Cattle Is Heritable and Polygenic. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 143(1), 35.

Hao J, et al. (2026) gSV: a general structural variant detector using the third-generation sequencing data. Briefings in bioinformatics, 27(3).

Jiang Y, et al. (2026) PROVGEN: A Privacy-Preserving Approach for Outcome Validation in Genomic Research. Proceedings on Privacy Enhancing Technologies. Privacy Enhancing Technologies Symposium, 2026(2), 642.

Morse L, et al. (2026) Distinct Symptom Profiles in Younger and Older Patients With Cancer Receiving Chemotherapy. Cancer medicine, 15(2), e71652.

Vincze K, et al. (2026) Genetic variation in antidiabetic drug targets: associations with Parkinson's disease risk and age at onset. NPJ Parkinson's disease, 12(1).

Boscaini S, et al. (2026) Habitual coffee intake shapes the gut microbiome and modifies host physiology and cognition. Nature communications, 17(1).

Wang C, et al. (2026) Key genes of Taohong Siwu decoction in treating coronary heart disease based on network pharmacology and Mendelian randomization. Medicine, 105(1), e46856.

McClelland P, et al. (2026) A multi-ancestry genetic reference for the Quebec population. Nature communications, 17(1), 1319.

Li J, et al. (2026) Potential causal role of mitochondrial biological effects in COVID-19: Evidence from Mendelian randomization study. Medicine, 105(19), e48654.

Pan X, et al. (2025) Effects of fourteen essential minerals and vitamins on acute and chronic tubulointerstitial nephritis: a multivariate Mendelian randomization study. Hereditas, 162(1), 63.

Sun M, et al. (2025) Transcriptome combined with Mendelian randomization to identify key genes related to polyamine metabolism in childhood obesity and elucidate their molecular regulatory mechanisms. Scientific reports, 15(1), 17799.

Devite FT, et al. (2025) Performance of Valencia sweet orange grafted onto dwarfing citrandarins. Frontiers in plant science, 16, 1530396.

Zu Y, et al. (2025) Endometriosis Severity and Risk of Preeclampsia: A Combined Mendelian Randomization and Observational Study. International journal of women's health, 17, 923.

Du H, et al. (2025) An integrated platform for concurrent structural and single-nucleotide variants improves copy-number detection and reveals pathogenic alleles in undiagnosed Mendelian families. Genome medicine, 18(1), 16.

Picchetta L, et al. (2025) Maternal age and genome-wide failure of meiotic recombination are associated with triploid conceptions in humans. American journal of human genetics, 112(11), 2665.

Shah A, et al. (2025) Systematic evaluation of de novo mutation calling tools using whole genome sequencing data. Briefings in bioinformatics, 26(6).

Lai C, et al. (2025) Relationship between Tic disorders and 41 inflammatory factors in circulating blood: a two-sample Mendelian randomization study. Clinics (Sao Paulo, Brazil), 80, 100649.

Kamps A, et al. (2025) Bidirectional causal relationship between obesity and osteoarthritis: Insights from a two-sample Mendelian randomization study. Osteoarthritis and cartilage open, 7(3), 100636.

Zhang L, et al. (2025) Universal noninvasive prenatal diagnosis for monogenic disorders using cell-free plasma DNA. Genome medicine, 18(1), 4.