

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 resource, software application

Keywords: gene, genetic, genomic, fortran77

Resource Name: MENDEL

Resource ID: SCR_009288

Alternate IDs: nlx_154473

Ratings and Alerts

No rating or validation information has been found for MENDEL.

No alerts have been found for MENDEL.

Data and Source Information

Usage and Citation Metrics

We found 464 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Viinikainen J, et al. (2024) Effect of weight on depression using multiple genetic instruments. PloS one, 19(2), e0297594.

Dujak C, et al. (2024) Genomic analysis of fruit size and shape traits in apple: unveiling candidate genes through GWAS analysis. Horticulture research, 11(2), uhad270.

Chen Y, et al. (2024) Genetic causal association between frozen shoulder and carpal tunnel syndrome: a two-sample mendelian randomization. BMC musculoskeletal disorders, 25(1), 58.

Hayeck TJ, et al. (2024) The Impact of Patterns in Linkage Disequilibrium and Sequencing Quality on the Imprint of Balancing Selection. Genome biology and evolution, 16(2).

Zhu J, et al. (2024) Causal relationship between particulate matter and COVID-19 risk: A mendelian randomization study. Heliyon, 10(5), e27083.

Xia L, et al. (2024) PMSeeker: A Scheme Based on the Greedy Algorithm and the Exhaustive Algorithm to Screen Low-Redundancy Marker Sets for Large-Scale Parentage Assignment with Full Parental Genotyping. Biology, 13(2).

Huang Y, et al. (2024) A survey on puncture models and path planning algorithms of bevel-tipped flexible needles. Heliyon, 10(3), e25002.

Ho WK, et al. (2024) Age-specific breast and ovarian cancer risks associated with germline BRCA1 or BRCA2 pathogenic variants - an Asian study of 572 families. The Lancet regional health. Western Pacific, 44, 101017.

Qin P, et al. (2024) The role of mitochondrial DNA copy number in cardiometabolic disease: a bidirectional two-sample mendelian randomization study. Cardiovascular diabetology, 23(1), 45.

Zhang Z, et al. (2024) Kled: an ultra-fast and sensitive structural variant detection tool for long-read sequencing data. Briefings in bioinformatics, 25(2).

Wu Y, et al. (2024) Shared genetic architecture and causal relationship between sleep behaviors and lifespan. Translational psychiatry, 14(1), 108.

Nyberg T, et al. (2023) CanRisk-Prostate: A Comprehensive, Externally Validated Risk Model for the Prediction of Future Prostate Cancer. Journal of clinical oncology : official

journal of the American Society of Clinical Oncology, 41(5), 1092.

Deschenes NM, et al. (2023) Characterization of a phenotypically severe animal model for human AB-Variant GM2 gangliosidosis. *Frontiers in molecular neuroscience*, 16, 1242814.

Ma L, et al. (2023) Genome-wide identification of RNA recognition motif (RRM1) in *Brassica rapa* and functional analysis of RNA-binding protein (BrRBP) under low-temperature stress. *BMC plant biology*, 23(1), 621.

Li J, et al. (2023) Harnessing *Wolbachia* cytoplasmic incompatibility alleles for confined gene drive: A modeling study. *PLoS genetics*, 19(1), e1010591.

Montembault E, et al. (2023) Two RhoGEF isoforms with distinct localisation control furrow position during asymmetric cell division. *Nature communications*, 14(1), 3209.

Weeden NF, et al. (2023) A hypervariable intron of the STAYGREEN locus provides excellent discrimination among *Pisum fulvum* accessions and reveals evidence for a relatively recent hybridization event with *Pisum sativum*. *Frontiers in plant science*, 14, 1233280.

Guyatt A, et al. (2023) Mendelian randomisation of eosinophils and other cell types in relation to lung function and disease. *Thorax*, 78(5), 496.

Hashim KN, et al. (2023) The Mechanism of Kelulut Honey in Reversing Metabolic Changes in Rats Fed with High-Carbohydrate High-Fat Diet. *Molecules (Basel, Switzerland)*, 28(6).

Wu H, et al. (2023) NAKED ENDOSPERM1, NAKED ENDOSPERM2, and OPAQUE2 interact to regulate gene networks in maize endosperm development. *The Plant cell*, 36(1), 19.