Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 21, 2025

TwoSampleMR

RRID:SCR_019010
Type: Tool

Proper Citation

TwoSampleMR (RRID:SCR_019010)

Resource Information

URL: https://github.com/MRCIEU/TwoSampleMR

Proper Citation: TwoSampleMR (RRID:SCR_019010)

Description: Software R package for performing Mendelian randomization using genome wide association study summary data.

Resource Type: data analysis software, software resource, software application, data processing software

Defining Citation: PMID:29846171

Keywords: GWAS data, genome wide associated study data, genome data, Mendelian randomization, analysis

Funding:

Availability: Free, Available for download, Freely available

Resource Name: TwoSampleMR

Resource ID: SCR_019010

License: MIT license

Record Creation Time: 20220129T080343+0000

Record Last Update: 20250421T054303+0000

Ratings and Alerts

No rating or validation information has been found for TwoSampleMR.

No alerts have been found for TwoSampleMR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 393 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhao F, et al. (2025) Exploring the causal impact of body mass index on metabolic biomarkers and cholelithiasis risk: a Mendelian randomization analysis. Scientific reports, 15(1), 415.

Hu Y, et al. (2025) The relationship between smoking and recurrent aphthous stomatitis: A Mendelian randomization study. Tobacco induced diseases, 23.

Zeng J, et al. (2025) Protocol for genetic analysis of population-scale ultra-low-depth sequencing data. STAR protocols, 6(1), 103579.

Roshandel D, et al. (2025) Genetics of C-Peptide and Age at Diagnosis in Type 1 Diabetes. Diabetes, 74(2), 223.

Jia M, et al. (2025) Integrative bioinformatics approach identifies novel drug targets for hyperaldosteronism, with a focus on SHMT1 as a promising therapeutic candidate. Scientific reports, 15(1), 1690.

Kachuri L, et al. (2025) Genetic predisposition to altered blood cell homeostasis is associated with glioma risk and survival. Nature communications, 16(1), 658.

Xu L, et al. (2025) Plasma Proteomes and Genome-Wide Association Data for Causal Protein Identification in Stroke. Molecular neurobiology, 62(2), 2450.

Li J, et al. (2025) Elucidating the role of FBXW4 in osteoporosis: integrating bioinformatics and machine learning for advanced insight. BMC pharmacology & toxicology, 26(1), 20.

Shi W, et al. (2025) Smoking may be a risk factor for carpal tunnel syndrome: Insights from Mendelian randomization analysis. Tobacco induced diseases, 23.

Pan J, et al. (2025) Gastroesophageal reflux disease increases predisposition to severe COVID-19: Insights from integrated Mendelian randomization and genetic analysis. Annals of human genetics, 89(1), 54.

Valo E, et al. (2025) Genome-wide characterization of 54 urinary metabolites reveals molecular impact of kidney function. Nature communications, 16(1), 325.

Xu Y, et al. (2025) Exploring potential drug targets for SLE through Mendelian randomization and network pharmacology. PloS one, 20(1), e0316481.

Su Y, et al. (2025) Association between wide-ranging food intake and Parkinson's disease: a comprehensive mendelian randomization study. Scientific reports, 15(1), 2374.

Yu S, et al. (2025) Serum Urate and Atrial Fibrillation: A Bidirectional Mendelian Randomization Study. Clinical cardiology, 48(1), e70089.

Chen X, et al. (2025) Potential drug targets for asthma identified through mendelian randomization analysis. Respiratory research, 26(1), 16.

Lu T, et al. (2024) Entertainment activities and the risk of Alzheimer's disease: a Mendelian randomization analysis. Frontiers in aging neuroscience, 16, 1419317.

Shang Z, et al. (2024) Single-cell transcriptomics and Mendelian randomization reveal LUCAT1's role in right-sided colorectal cancer risk. Frontiers in genetics, 15, 1357704.

Venkatesh SS, et al. (2024) Genome-wide analyses identify 21 infertility loci and over 400 reproductive hormone loci across the allele frequency spectrum. medRxiv : the preprint server for health sciences.

Dziedzic M, et al. (2024) Interplay Between Plasma Glycine and Branched-Chain Amino Acids Contributes to the Development of Hypertension and Coronary Heart Disease. Hypertension (Dallas, Tex. : 1979), 81(6), 1320.

Cai S, et al. (2024) Causal Relationship Between Branched-Chain Amino Acids and Hypertension: A Mendelian Randomization Study. Journal of the American Heart Association, 13(5), e032084.