

Resource Summary Report

Generated by PRECISE-TBI on Jul 29, 2026

coloc

RRID:SCR_026041

Type: Tool

Proper Citation

coloc (RRID:SCR_026041)

Resource Information

URL: <https://github.com/chr1swallace/coloc>

Proper Citation: coloc (RRID:SCR_026041)

Description: Software package to perform genetic colocalisation analysis of two potentially related phenotypes, to ask whether they share common genetic causal variant(s) in a given region.Colocalisation Tests of Two Genetic Traits.

Synonyms: , coloc v5.2.3

Resource Type: source code, software toolkit, software resource

Keywords: Colocalisation tests, two genetic traits, genetic colocalisation analysis, genetic, colocalisation, two potentially related phenotypes, share common genetic causal variant,

Availability: Free, Available for download, Freely available,

Resource Name: coloc

Resource ID: SCR_026041

Alternate URLs: <https://CRAN.R-project.org/package=coloc>

License: GNU GPL v3

Record Creation Time: 20241114T053309+0000

Record Last Update: 20260729T044631+0000

Ratings and Alerts

No rating or validation information has been found for coloc.

No alerts have been found for coloc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 57 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Fan S, et al. (2025) Potential drug targets for systemic lupus erythematosus identified through Mendelian randomization analysis. *Medicine*, 104(7), e41439.

Wen S, et al. (2025) Association Analysis of the Circulating Proteome With Sarcopenia-Related Traits Reveals Potential Drug Targets for Sarcopenia. *Journal of cachexia, sarcopenia and muscle*, 16(1), e13720.

Qiu X, et al. (2025) Uncovering Novel Susceptible Genes and Therapeutic Targets of Prostate Cancer: a Multi-omics Study Integrating Summary-based Mendelian Randomization Analysis and Molecular Docking. *Biological procedures online*, 27(1), 40.

Song N, et al. (2025) Bridging pharmacovigilance and genetic insight: investigating drugs and indications for breast cancer risk in women with autoimmune diseases. *Journal of translational medicine*, 23(1), 1332.

Wang Z, et al. (2025) Prioritization of Lipid Metabolism Targets for the Diagnosis and Treatment of Cardiovascular Diseases. *Research (Washington, D.C.)*, 8, 0618.

Yang R, et al. (2025) PAQR5 drives the malignant progression and shapes the immunosuppressive microenvironment of hepatocellular carcinoma by activating the NF- κ B signaling. *Biomarker research*, 13(1), 70.

Rosoff DB, et al. (2025) Multiomic Mendelian Randomization Study Investigating the Impact of PCSK9 and HMGCR Inhibition on Type 2 Diabetes Across Five Populations. *Diabetes*, 74(1), 120.

Zhang X, et al. (2025) Association of glucagon-like peptide-1 receptor agonists with atrial fibrillation, cardiac arrest, and ventricular fibrillation: Casual evidence from a drug target Mendelian randomization. *Diabetology & metabolic syndrome*, 17(1), 179.

Zhu W, et al. (2025) Identifying genes and traits associated with pre-eclampsia using summary statistics. *PloS one*, 20(5), e0323683.

Yuan S, et al. (2025) Cross-population GWAS and proteomics improve risk prediction and reveal mechanisms in atrial fibrillation. *Nature communications*, 16(1), 6426.

Xiao X, et al. (2025) Single-cell transcriptomic profiling reveals cell type heterogeneity between HFpEF and HFrEF. *Communications biology*, 8(1), 1436.

Im C, et al. (2025) Genome-wide association study of childhood B-cell acute lymphoblastic leukemia reveals novel African ancestry-specific susceptibility loci. *Nature communications*, 16(1), 8974.

Jiang Y, et al. (2025) Comprehensive Genome-Wide Analysis of Shared Genetic Factors in Gastrointestinal and Neurodegenerative Diseases. *Brain and behavior*, 15(11), e71029.

Li X, et al. (2025) Integrating genetic regulation and schizophrenia-specific splicing quantitative expression with GWAS prioritizes novel risk genes for schizophrenia. *Translational psychiatry*, 15(1), 379.

Qiao J, et al. (2025) Contribution of leukocyte telomere length to cardiovascular disease onset from genome-wide cross-trait analysis. *Nature communications*, 16(1), 8677.

Bian L, et al. (2025) Single-cell eQTL mapping reveals cell-type-specific genes associated with the risk of gastric cancer. *Cell genomics*, 5(4), 100812.

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

Fu L, et al. (2025) Insights Into Causal Effects of Genetically Proxied Lipids and Lipid-Modifying Drug Targets on Cardiometabolic Diseases. *Journal of the American Heart Association*, 14(3), e038857.

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

Chu X, et al. (2025) Plasma proteins and different onset subtype of COPD: Proteome-wide Mendelian randomization study and co-localization analyses. *Medicine*, 104(19), e42409.