Resource Summary Report

Generated by RRID on Aug 6, 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: software toolkit, source code, 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: 20260806T054826+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 RRID .

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.

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

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.

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.

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.

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

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

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

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

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

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.

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.