Resource Summary Report

Generated by dkNET on Sep 19, 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 resource, software toolkit, source code

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: 20260919T200040+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 85 mentions in open access literature.

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

Wang H, et al. (2026) Potential Risk Factors and Therapeutic Targets for Dilated Cardiomyopathy Identified Through Mendelian Randomization Analysis. Journal of the American Heart Association, 15(1), e038088.

Yi P, et al. (2026) Genetic link between metabolic syndrome and coronary artery disease: Insights from genome-wide cross-trait analysis. Global medical genetics, 13(1), 100092.

Nicholls HL, et al. (2026) Genome-wide analysis of cardiac ventricular phenotypes reveals novel loci and therapeutic targets for heart failure. Nature communications, 17(1).

Yao W, et al. (2026) Cross-ancestry genome-wide association studies of liver function biomarkers uncover pleiotropic variants, systemic disease links and therapeutic targets. Genome medicine, 18(1).

Haapaniemi H, et al. (2026) The genetic basis of dermatophytosis skin infection susceptibility. Nature communications, 17(1).

Moreno E, et al. (2026) Genome-wide association meta-analyses over one million individuals identify 54 loci associated with urinary incontinence and its subtypes. medRxiv : the preprint server for health sciences.

Zhao R, et al. (2026) Independent association of leg-height ratio with 15 cardiometabolic diseases. Cardiovascular diabetology, 25(1), 41.

Belbasis L, et al. (2026) Integrative proteogenomic analyses identify plasma proteins that impact the risk of ischemic stroke. Communications medicine, 6(1).

Xiao L, et al. (2026) Shared genetic architecture of obesity and gastroesophageal reflux disease. Medicine, 105(6), e47404.

Chaudhary S, et al. (2026) HistoGWAS: an AI-enabled framework for automated genetic analysis of tissue phenotypes in histology cohorts. Genome biology, 27(1).

Kraft J, et al. (2026) Identifying drug targets for schizophrenia through gene prioritization. Translational psychiatry, 16(1).

Xiao X, et al. (2026) Mendelian Randomization Uncovers Potential Repurposable Medications for Neuropsychiatric Disorders. Current neuropharmacology, 24(2), 241.

, et al. (2026) MRI-based multi-organ clocks for healthy aging and disease assessment. Nature medicine, 32(1), 82.

Maravall-L??pez J, et al. (2026) Ancient DNA reveals that natural selection has upregulated the immune system over the last 10,000 years. bioRxiv : the preprint server for biology.

Xiao Z, et al. (2026) Advancing PCOS drug development: multi-omics discovery of key targets and repurposable compounds. Naunyn-Schmiedeberg's archives of pharmacology.

Zhang HL, et al. (2025) Candida albicans and colorectal cancer: A paradoxical role revealed through metabolite profiling and prognostic modeling. World journal of clinical oncology, 16(4), 104182.

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.

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.