Resource Summary Report

Generated by RRID on Aug 15, 2026

SMR

RRID:SCR_026042
Type: Tool

Proper Citation

SMR (RRID:SCR_026042)

Resource Information

URL: https://yanglab.westlake.edu.cn/software/smr/

Proper Citation: SMR (RRID:SCR_026042)

Description: Software tool to test for pleiotropic association between expression level of gene and complex trait of interest using summary-level data from GWAS and expression quantitative trait loci eQTL studies. Used to prioritize genes underlying GWAS hits for follow up functional studies.

Abbreviations: SMR

Synonyms: , Summary-data-based Mendelian Randomization, SMR v1.3.1

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

Keywords: pleiotropic association, expression level of gene, complex trait, prioritize genes underlying GWAS hits, follow up functional studies,

Resource Name: SMR

Resource ID: SCR_026042

Record Creation Time: 20241114T053309+0000

Record Last Update: 20260815T042910+0000

Ratings and Alerts

No rating or validation information has been found for SMR.

No alerts have been found for SMR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

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

Dai H, et al. (2026) Integrating machine learning and multi-omics analysis to explore Treg-associated programmed cell death features in clear cell renal cell carcinoma. Cancer cell international, 26(1), 15.

Wu L, et al. (2026) Integrative SMR prioritizes oxidative stress-related regulatory genes for Alzheimer's disease with brain-tissue validation. The journal of prevention of Alzheimer's disease, 13(5), 100535.

Li Z, et al. (2026) Potential of SP1 as a prognostic marker and therapeutic target in acute myocardial infarction: a bioinformatics, Mendelian randomization and experimental validation study. Frontiers in immunology, 17, 1742618.

Chen Y, et al. (2026) Programmed cell death and risk of diabetic retinopathy: a Mendelian randomization study. Journal of translational medicine, 24(1).

Guo A, et al. (2026) Multi-omics analysis suggests ZDHHC18 as a potential risk factor for clear cell renal cell carcinoma linked to myeloid DC morphology. Discover oncology, 17(1).

Zhang C, et al. (2026) 6PPD-quinone exposure and Alzheimer's disease: insights from integrative network pharmacology, transcriptomics, machine learning, and molecular docking. Open medicine (Warsaw, Poland), 21(1), 20261477.

Chen Y, et al. (2026) Genetic architecture of primary sclerosing cholangitis: shared pathways with inflammatory bowel disease and gut-liver axis mediation. International journal of surgery (London, England), 112(1), 629.

Liu R, et al. (2026) Genetic regulation of methylation across East Asian and European populations. Nature communications, 17(1).

Wang Y, et al. (2026) Mendelian Randomization Identified SLC2A9 as a Novel cis-eQTL-Mediated Susceptibility Gene in Suppressing Renal Cancer and Its Related Metabolic Mechanisms. Mediators of inflammation, 2026(1), e5817314.

Wang Y, et al. (2026) Mitochondrial dysfunction in the pathogenesis of intervertebral disc herniation: a mitochondrial related genome-wide Mendelian randomization analysis. Journal of translational medicine, 24(1).

He J, et al. (2026) Interferon signaling gene expression, and DNA methylation interactions in Sjögren's disease via mendelian randomization. iScience, 29(3), 114950.

Zhang ZH, et al. (2026) Multiomics analysis reveals that senescent CXCL16+ macrophages promote lung adenocarcinoma progression through TGF-? signalling. Journal of translational medicine, 24(1).

Hong T, et al. (2026) Causal inference of glucocorticoid signaling in non-small cell lung cancer: integrating Mendelian randomization, single-cell transcriptomics, and imaging data. NPJ precision oncology, 10(1).

Yi E, et al. (2026) Multiomics Mendelian randomization identifies serpin family G member 1 as a chronic obstructive pulmonary disease modulator. Signal transduction and targeted therapy, 11(1), 34.

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

Shen J, et al. (2025) Shared genetic architecture of posttraumatic stress disorder with cardiovascular imaging, risk, and diagnoses. Nature communications, 16(1), 5631.

Wang Z, et al. (2025) Multi-omics analysis of bidirectional liquid-liquid phase separation signatures reveals immunotherapy response and prognosis in renal cell carcinoma. BMC cancer, 25(1), 1314.

Zhao X, et al. (2025) Synergistic blood-based diagnostic value of AP3B1 and BMPR2 in Parkinson's disease. NPJ Parkinson's disease, 11(1), 310.

Cheng S, et al. (2025) Druggable genome-wide Mendelian randomization integrating GWAS and eQTL/pQTL data identifies targets for lung squamous cell carcinoma. Scientific reports, 15(1), 30116.

Li B, et al. (2025) Increased TSPO alleviates neuropathic pain by preventing pyroptosis via the AMPK-PGC-1? pathway. The journal of headache and pain, 26(1), 16.