Resource Summary Report

Generated by T1D on Aug 1, 2026

RAREMETAL

RRID:SCR_003573
Type: Tool

Proper Citation

RAREMETAL (RRID:SCR_003573)

Resource Information

URL: http://genome.sph.umich.edu/wiki/RAREMETAL

Proper Citation: RAREMETAL (RRID:SCR_003573)

Description: A software program that facilitates the meta-analysis of rare variants from genotype arrays or sequencing.

Abbreviations: RAREMETAL

Resource Type: software resource

Defining Citation: PMID:24894501

Keywords: bio.tools

Resource Name: RAREMETAL

Resource ID: SCR_003573

Alternate IDs: biotools:raremetal, OMICS_00243

Alternate URLs: https://bio.tools/raremetal

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260725T190541+0000

Ratings and Alerts

No rating or validation information has been found for RAREMETAL.

No alerts have been found for RAREMETAL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Sandholm N, et al. (2022) Whole-exome sequencing identifies novel protein-altering variants associated with serum apolipoprotein and lipid concentrations. Genome medicine, 14(1), 132.

Bomba L, et al. (2022) Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American journal of human genetics, 109(6), 1038.

Irvin MR, et al. (2021) Whole-Exome Sequencing and hiPSC Cardiomyocyte Models Identify MYRIP, TRAPPC11, and SLC27A6 of Potential Importance to Left Ventricular Hypertrophy in an African Ancestry Population. Frontiers in genetics, 12, 588452.

Dauber A, et al. (2020) A Genome-Wide Pharmacogenetic Study of Growth Hormone Responsiveness. The Journal of clinical endocrinology and metabolism, 105(10), 3203.

Ratnapriya R, et al. (2020) Family-based exome sequencing identifies rare coding variants in age-related macular degeneration. Human molecular genetics, 29(12), 2022.

Erzurumluoglu AM, et al. (2020) Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular psychiatry, 25(10), 2392.

Jiang Y, et al. (2020) Association Analysis and Meta-Analysis of Multi-Allelic Variants for Large-Scale Sequence Data. Genes, 11(5).

Spracklen CN, et al. (2019) Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American journal of human genetics, 105(1), 15.

Justice AE, et al. (2019) Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature genetics, 51(3), 452.

Geng X, et al. (2019) An Exome-Wide Sequencing Study of the GOLDN Cohort Reveals Novel Associations of Coding Variants and Fasting Plasma Lipids. Frontiers in genetics, 10, 158.

Jackson VE, et al. (2018) Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome open research, 3, 4.

Marees AT, et al. (2018) Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. Drug and alcohol dependence, 188, 94.

Manning A, et al. (2017) A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 66(7), 2019.

Marouli E, et al. (2017) Rare and low-frequency coding variants alter human adult height. Nature, 542(7640), 186.

Hellwege JN, et al. (2017) Association of gene coding variation and resting metabolic rate in a multi-ethnic sample of children and adults. BMC obesity, 4, 12.

Sapkota Y, et al. (2017) Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific reports, 7(1), 11380.

Zhan X, et al. (2016) RVTESTS: an efficient and comprehensive tool for rare variant association analysis using sequence data. Bioinformatics (Oxford, England), 32(9), 1423.

Galesloot TE, et al. (2016) Meta-GWAS and Meta-Analysis of Exome Array Studies Do Not Reveal Genetic Determinants of Serum Hepcidin. PloS one, 11(11), e0166628.

Zhan X, et al. (2015) SEQMINER: An R-Package to Facilitate the Functional Interpretation of Sequence-Based Associations. Genetic epidemiology, 39(8), 619.

Tang CS, et al. (2015) Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. Nature communications, 6, 10206.