Resource Summary Report

Generated by Kravitz on Sep 10, 2026

QTLbase

RRID:SCR_021649
Type: Tool

Proper Citation

QTLbase (RRID:SCR_021649)

Resource Information

URL: http://mulinlab.org/qtlbase/index.html

Proper Citation: QTLbase (RRID:SCR_021649)

Description: Curates and compiles genome wide QTL summary statistics for many human molecular traits across tissues and cell types. Comprises tens of millions significant genotype molecular trait associations under different conditions. Users can visualize QTL results in phenome wide and tissue wide levels, and annotate their biological functions through comprehensive genomic features and functional evidence. QTLbase provides one stop shop of QTLs retrieval and comparison across multiple tissues and multiple layers of molecular complexity, and it will greatly help researchers interrogate biological mechanism of causal variants and guide direction of functional validation.

Resource Type: data or information resource, database

Keywords: Genome wide QTL summary statistics, genome wide QTL, genotype molecular trait associations, QTLs retrieval, QTLs comparison

Availability: Free, Freely available

Resource Name: QTLbase

Resource ID: SCR_021649

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260905T133217+0000

Ratings and Alerts

No rating or validation information has been found for QTLbase.

No alerts have been found for QTLbase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Maiti AK, et al. (2025) In Silico Analysis of Post-COVID-19 Condition (PCC) Associated SNP rs9367106 Predicts the Molecular Basis of Abnormalities in the Lungs and Brain Functions. International journal of molecular sciences, 26(14).

Ramachandran D, et al. (2025) GWAS meta-analysis identifies five susceptibility loci for endometrial cancer. EBioMedicine, 118, 105830.

Gong Z, et al. (2025) Exploring the Causal Association Between 91 Circulating Inflammatory Proteins and Neurodegenerative Diseases: A Bidirectional Two-Sample Mendelian Randomization and Bioinformatics Analysis. Brain and behavior, 15(6), e70586.

Lei H, et al. (2024) Exploration of the causality of frailty index on psoriasis: A Mendelian randomization study. Skin research and technology : official journal of International Society for Bioengineering and the Skin (ISBS) [and] International Society for Digital Imaging of Skin (ISDIS) [and] International Society for Skin Imaging (ISSI), 30(3), e13641.

Lagattuta KA, et al. (2024) The genetic basis of autoimmunity seen through the lens of T cell functional traits. Nature communications, 15(1), 1204.

Xu X, et al. (2024) Investigating causal associations among gut microbiota, metabolites, and psoriatic arthritis: a Mendelian randomization study. Frontiers in microbiology, 15, 1287637.

Shilenok I, et al. (2023) SERPINE1 mRNA Binding Protein 1 Is Associated with Ischemic Stroke Risk: A Comprehensive Molecular-Genetic and Bioinformatics Analysis of SERBP1 SNPs. International journal of molecular sciences, 24(10).

Huang D, et al. (2023) QTLbase2: an enhanced catalog of human quantitative trait loci on extensive molecular phenotypes. Nucleic acids research, 51(D1), D1122.

Kobzeva KA, et al. (2023) Association between HSPA8 Gene Variants and Ischemic Stroke: A Pilot Study Providing Additional Evidence for the Role of Heat Shock Proteins in Disease Pathogenesis. Genes, 14(6).

Buchynskyi M, et al. (2023) Genetic Predictors of Comorbid Course of COVID-19 and MAFLD: A Comprehensive Analysis. Viruses, 15(8).

Zhabin S, et al. (2023) The Joint Link of the rs1051730 and rs1902341 Polymorphisms and Cigarette Smoking to Peripheral Artery Disease and Atherosclerotic Lesions of Different Arterial Beds. Life (Basel, Switzerland), 13(2).

Dai Y, et al. (2023) Disentangling accelerated cognitive decline from the normal aging process and unraveling its genetic components: A neuroimaging-based deep learning approach. Research square.

Yu S, et al. (2023) Association study for the role of MMP8 gene polymorphisms in Colorectal cancer susceptibility. BMC cancer, 23(1), 1169.

Kim MH, et al. (2022) Association of genetic variants of oxidative stress responsive kinase 1 (OXSR1) with asthma exacerbations in non-smoking asthmatics. BMC pulmonary medicine, 22(1), 3.

Caron B, et al. (2022) Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes. Genome medicine, 14(1), 28.

Zhang C, et al. (2022) Association of CYP19A1 rs28757157 polymorphism with lung cancer risk in the Chinese Han population. World journal of surgical oncology, 20(1), 400.

Song K, et al. (2022) Genome-wide association study of SNP- and gene-based approaches to identify susceptibility candidates for lupus nephritis in the Han Chinese population. Frontiers in immunology, 13, 908851.

Xavier J, et al. (2022) Interaction between COMT Val158 Met polymorphism and childhood trauma predicts risk for depression in men. International journal of developmental neuroscience : the official journal of the International Society for Developmental Neuroscience, 82(5), 385.

Camerini L, et al. (2022) Genetic Variations in Elements of the Oxytocinergic Pathway are Associated with Attention/Hyperactivity Problems and Anxiety Problems in Childhood. Child psychiatry and human development.

Zinski AL, et al. (2021) Genome-to-phenome research in rats: progress and perspectives. International journal of biological sciences, 17(1), 119.