Resource Summary Report

Generated by dkNET on Aug 13, 2026

eQTL Catalogue

RRID:SCR_021700
Type: Tool

Proper Citation

eQTL Catalogue (RRID:SCR_021700)

Resource Information

URL: https://www.ebi.ac.uk/eqtl

Proper Citation: eQTL Catalogue (RRID:SCR_021700)

Description: Catalog provides uniformly processed gene expression and splicing QTLs from all available public studies on human. Expression and splicing QTLs recomputed from public datasets.

Resource Type: data or information resource, database, catalog

Defining Citation: DOI:10.1101/2020.01.29.924266

Keywords: Gene expression, splicing QTLs, public datasets, human data, public studies

Availability: Free, Freely available

Resource Name: eQTL Catalogue

Resource ID: SCR_021700

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260811T043658+0000

Ratings and Alerts

No rating or validation information has been found for eQTL Catalogue.

No alerts have been found for eQTL Catalogue.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Zhang S, et al. (2026) Single-cell polygenic risk scores dissect cellular and molecular heterogeneity of complex human diseases. Nature biotechnology, 44(5), 845.

Jesse M, et al. (2026) Ultra-fast genetic colocalisation across millions of association signals. PLoS genetics, 22(6), e1012209.

Yunusbayev B, et al. (2026) Psoriasis risk allele function in activated Th1/17 cells with "memory" to antigen exposure. PloS one, 21(3), e0344675.

Yu Z, et al. (2026) ChromBERT: A foundation model for learning interpretable representations for context-specific transcriptional regulatory networks. Cell genomics, 6(4), 101130.

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.

Xuekelati S, et al. (2026) Causal Implication of CD52-Driven Immune Dysregulation in Sarcopenic Obesity: Integrating Mendelian Randomization and Multiomics Profiling. Clinical interventions in aging, 21, 570497.

Chang X, et al. (2026) Genome-wide association study reveals a novel tuberculosis susceptibility locus in multiple East Asian and European populations. Genome medicine, 18(1).

Pottier C, et al. (2025) Deciphering distinct genetic risk factors for FTLD-TDP pathological subtypes via whole-genome sequencing. Nature communications, 16(1), 3914.

Oliva M, et al. (2025) Integration of GWAS, QTLs and keratinocyte functional assays reveals molecular mechanisms of atopic dermatitis. Nature communications, 16(1), 3101.

Linder J, et al. (2025) Predicting RNA-seq coverage from DNA sequence as a unifying model of gene regulation. Nature genetics, 57(4), 949.

Zhang ZE, et al. (2025) Efficient count-based models improve power and robustness for large-scale single-cell eQTL mapping. medRxiv : the preprint server for health sciences.

Wu AP, et al. (2025) Unveiling causal regulatory mechanisms through cell-state parallax. Nature communications, 16(1), 8096.

Ji L, et al. (2025) Identification of Schizophrenia-Risk Regulatory Variant rs1399178 in the Non-coding Region With Its Impact on NRF1 Binding. CNS neuroscience & therapeutics, 31(3), e70275.

Liao Y, et al. (2025) Genetic Analysis of the X Chromosome Associates Loci with Progression of Parkinson's Disease. Movement disorders : official journal of the Movement

Disorder Society, 40(9), 1908.

Antonatos C, et al. (2025) Transcriptome-wide analyses delineate the genetic architecture of expression variation in atopic dermatitis. HGG advances, 6(2), 100422.

Hingerl JC, et al. (2025) scooby: modeling multimodal genomic profiles from DNA sequence at single-cell resolution. Nature methods, 22(11), 2275.

Tambets R, et al. (2024) Extensive co-regulation of neighboring genes complicates the use of eQTLs in target gene prioritization. HGG advances, 5(4), 100348.

Bao C, et al. (2024) A cross-disease, pleiotropy-driven approach for therapeutic target prioritization and evaluation. Cell reports methods, 4(4), 100757.

Lessard S, et al. (2024) Leveraging large-scale multi-omics evidences to identify therapeutic targets from genome-wide association studies. BMC genomics, 25(1), 1111.

Guo J, et al. (2024) Phenome-wide association study in 25,639 pregnant Chinese women reveals loci associated with maternal comorbidities and child health. Cell genomics, 4(10), 100632.