

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 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, catalog, database

Defining Citation: [DOI:10.1101/2020.01.29.924266](https://doi.org/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: 20260815T182700+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.

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.

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*.

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).

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

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

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

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*.

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.

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

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.