

Resource Summary Report

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GTEX eQTL Browser

RRID:SCR_001618

Type: Tool

Proper Citation

GTEX eQTL Browser (RRID:SCR_001618)

Resource Information

URL: <https://gtexportal.org/home/>

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Description: Database and browser that provides a central resource to archive and display association between genetic variation and high-throughput molecular-level phenotypes. This effort originated with the NIH GTEx roadmap project: however the scope of this resource will be extended to include any available genotype/molecular phenotype datasets.

Synonyms: NCBI GTEx eQTL Browser, Genotype-Tissue Expression eQTL Browser, GTEx (Genotype-Tissue Expression) eQTL Browser, NCBI GTeX eQTL Browser

Resource Type: database, data or information resource

Keywords: genetic variation, high-throughput, phenotype, genotype, molecular, molecule, gene, gene expression, snp, trait, expression, quantitative trait locus, expression quantitative trait locus, genome, probe, sequence, statistics, p-value, rna-seq, array, lymphoblastoid, liver, cerebellum, frontal cortex, temporal cortex, pons, gene regulation, tissue, mrna, data set

Funding: NIH Common Fund 268201000029C-4-0-2

Availability: Free, Freely available

Resource Name: GTEX eQTL Browser

Resource ID: SCR_001618

Alternate IDs: nlx_153884

Alternate URLs: <http://www.gtexportal.org/home/>

Record Creation Time: 20220129T080208+0000

Ratings and Alerts

No rating or validation information has been found for GTEx eQTL Browser.

No alerts have been found for GTEx eQTL Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 111 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Vinogradov-Talyah E, et al. (2026) Human clearance systems have a layered architecture across tissues and cell types that supports varied proteome compositions. *Autophagy*, 22(1), 145.

Drost M, et al. (2026) Routine RNA-based analysis of potential splicing variants facilitates genomic diagnostics and reveals limitations of in silico prediction tools. *HGG advances*, 7(1), 100521.

Arcego DM, et al. (2026) Sex-specific interaction effects of Syntaxin 1A coexpression network and childhood trauma on adult depressive symptoms. *EBioMedicine*, 123, 106062.

Niu Q, et al. (2025) Multidimensional analysis reveals the potential of ACSL3 as a cancer biomarker: from pan-cancer exploration to functional validation in hepatocellular carcinoma. *Clinical and experimental medicine*, 25(1), 351.

Yu S, et al. (2025) The role and prognostic value of mitochondria-related gene PARK7 in breast cancer. *Breast cancer research : BCR*, 27(1), 200.

Parag RR, et al. (2025) Novel Isoforms of Adhesion G Protein-Coupled Receptor B1 (ADGRB1/BAI1) Generated from an Alternative Promoter in Intron 17. *Molecular neurobiology*, 62(1), 900.

Jiang W, et al. (2025) The health impacts and genetic architecture of food liking in cardio-metabolic diseases. *Nature communications*, 16(1), 4810.

Lv Y, et al. (2025) Comprehensive pan-cancer analysis of KRT6A as a prognostic and immune biomarker. *Scientific reports*, 15(1), 35728.

Dong X, et al. (2025) Tissue-specific co-expression patterns of BAF complex genes across human endocrine and non-endocrine tissues. *Endocrine connections*, 14(10).

Durao P, et al. (2025) Systemic immunosuppression from ultraviolet radiation exposure inhibits cancer immunotherapy. *Journal for immunotherapy of cancer*, 13(10).

Dacey R, et al. (2025) Alzheimer's disease multi-ancestry genome-wide interaction and stratified study with smoking. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(11), e70922.

Zheng L, et al. (2025) A pan-cancer analysis of CTSC as a candidate prognostic and immune-related biomarker. *Discover oncology*, 16(1), 2258.

Abudusalam K, et al. (2025) WSCD2 Expression: Its Relevance to Tumor-Infiltrating Immune Cells and Glioma Prognosis. *Current medicinal chemistry*, 32(24), 5043.

Chen Z, et al. (2025) Comprehensive pan-cancer evaluation of NUP85 prognosis, immune infiltration response, and validation in prostate cancer. *Discover oncology*, 16(1), 1953.

Bai G, et al. (2025) Construction of a lipid metabolism-based prognostic gene signature in cervical squamous cell carcinoma and validation of LIPG's oncogenic role. *Cancer cell international*, 25(1), 349.

Ullah N, et al. (2025) Identification of missense DMC1 variants in males with non-obstructive azoospermia. *Journal of assisted reproduction and genetics*, 42(11), 3723.

Wang M, et al. (2025) Metabolic reprogramming and prognostic insights in molecular landscapes driven by glycolysis in ovarian cancer. *Scientific reports*, 15(1), 26956.

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. *Cell genomics*, 5(3), 100775.

Wang T, et al. (2025) Predictive and therapeutic value of the ferroptosis gene C1SD1 in non-small cell lung cancer. *Oncology letters*, 29(5), 235.

Wang Y, et al. (2025) Development of a novel prognostic model based on laminin $\gamma 5$, associated with immune infiltration and therapeutic response in ovarian cancer utilizing online resources. *European journal of medical research*, 30(1), 1125.