

Resource Summary Report

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GTEEx eQTL Browser

RRID:SCR_001618

Type: Tool

Proper Citation

GTEEx 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: data or information resource, database

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: GTEEx 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 [PRECISE-TBI](#) .

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 $\alpha 5$, associated with immune infiltration and therapeutic response in ovarian cancer utilizing online resources. *European journal of medical research*, 30(1), 1125.