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: 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: GTEx eQTL Browser

Resource ID: SCR_001618

Alternate IDs: nlx_153884

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

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260821T193627+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 499 mentions in open access literature.

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

Pott J, et al. (2026) PCSK9 and Breast Cancer Survival: A Mendelian Randomization Study. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(6), 873.

Tjader NP, et al. (2026) Association of germline variants with KRAS-mutation status in colorectal cancer. Scientific reports, 16(1).

Wang X, et al. (2026) Pan-cancer analysis reveals HDAC1 as a key regulator of immune infiltration and T cell exhaustion. Discover oncology, 17(1).

Small AM, et al. (2026) Genomic and transcriptomic analyses of aortic stenosis enhance therapeutic target discovery and disease prediction. Nature genetics, 58(1), 57.

Spiga M, et al. (2026) TIGIT disruption rescues the antitumor activity of low avidity TCR-engineered T cells by increasing TCR signal strength. Nature communications, 17(1), 568.

Zhao C, et al. (2026) Ubenimex synergizes with the PD-L1 blockade in gastric cancer by competitively binding LAP3 with UBE3A. Cell death & disease, 17(1).

Kaushik A, et al. (2026) Comparative GWAS using global and Indian Reference Panels reveals non-coding drivers of COVID-19 severity and mortality. PLoS neglected tropical diseases, 20(3), e0014020.

Santos JLA, et al. (2026) CCorGsDB: a database for clock correlated genes in the mouse and human central nervous systems. Npj biological timing and sleep, 3(1).

Lin S, et al. (2026) Integrated single-cell and bulk RNA sequencing unravels neutrophil heterogeneity and validates SPP1 as a prognostic biomarker in cervical cancer. BMC cancer, 26(1).

Yie GE, et al. (2026) Discrepancy between Genetically Predicted and Observed Alcohol Intake and Its Impact on Gastric Cancer Susceptibility. Cancer research and treatment, 58(2), 563.

Campos M, et al. (2026) PFKM governs metabolic shifts throughout skeletal muscle differentiation. Nature metabolism, 8(2), 489.

Balde-Camara A, et al. (2026) A homozygous PIWIL1 frameshift variant triggers azoospermia and reveals a strong selective constraint on germline genome integrity. Journal of assisted reproduction and genetics, 43(4), 1309.

Zhang C, et al. (2026) Leveraging Deep Learning to Construct a Programmed Cell Death-Driven Prognostic Signature in Acute Myeloid Leukemia. Current issues in molecular biology, 48(4).

Lin S, et al. (2026) ADAMDEC1 predicts prognosis and immunotherapy response in a pan-cancer study with experimental validation. Discover oncology, 17(1).

Shi H, et al. (2026) Multi-Omics Analysis of TYMS as a Prognostic Biomarker and Therapeutic Target for Lung Adenocarcinoma. Cancer medicine, 15(4), e71814.

Agbektas T, et al. (2026) Evaluation of the Anticancer Effects of DODP on Gene Expression and Oxidative Stress in Gastric Cancer: An Integrated Docking, Bioinformatics, and Experimental Approach. Life (Basel, Switzerland), 16(4).

Liu QR, et al. (2026) Cell type-specific expression and subcellular localization of the human insulin upstream open reading frame (INSU) protein in pancreatic ?-cells. The Journal of biological chemistry, 302(7), 113209.

Spears E, et al. (2026) Pancreatic islet ? cell function and proliferation require the arginine transporter SLC7A2. The Journal of clinical investigation, 136(12).

Notini G, et al. (2026) Pan-cancer multi-omic integration of Trop2 reveals biological determinants and translational implications for ADC therapy. NPJ precision oncology, 10(1).

Lege BM, et al. (2026) Surface Marker Identification to Capture Live Circulating Tumor Cells in Metastatic Triple-Negative Breast Cancer. Cancer research communications, 6(1), 115.