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: http://www.ncbi.nlm.nih.gov/gtex/GTEX2/gtex.cgi

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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: Public, Available to the research community

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: 20250525T032154+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 72 mentions in open access literature.

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

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.

Tan H, et al. (2025) Genetic predisposition to Behcet's disease mediated by a IL10RA enhancer polymorphism. Heliyon, 11(1), e41529.

Pandey RK, et al. (2024) Novel genetic association of the Furin gene polymorphism rs1981458 with COVID-19 severity among Indian populations. Scientific reports, 14(1), 7822.

Patel JN, et al. (2024) Pharmacogenetic and clinical risk factors for bevacizumab-related gastrointestinal hemorrhage in prostate cancer patients treated on CALGB 90401 (Alliance). The pharmacogenomics journal, 24(2), 6.

Funato N, et al. (2024) A regulatory variant impacting TBX1 expression contributes to basicranial morphology in Homo sapiens. American journal of human genetics, 111(5), 939.

Yang L, et al. (2024) Comprehensiveness cuproptosis related genes study for prognosis and medication sensitiveness across cancers, and validation in prostate cancer. Scientific reports, 14(1), 9570.

Wang S, et al. (2024) Integrative analysis of rs717620 polymorphism in therapeutic response to anti-seizure medications. Heliyon, 10(1), e23942.

Matsunami M, et al. (2024) Genome-wide association studies for pelvic organ prolapse in the Japanese population. Communications biology, 7(1), 1188.

Demir Eksi D, et al. (2024) The Role of WNT3A Protein and Gene Variants in Allergic Rhinitis: A Case-Control Study. Current issues in molecular biology, 46(9), 9523.

Zhang SS, et al. (2024) Discovery of RXFP2 genetic association in resistant hypertensive men and RXFP2 antagonists for the treatment of resistant hypertension. Scientific reports, 14(1), 13209.

Crocco P, et al. (2024) Evidence for a relationship between genetic polymorphisms of the L-DOPA transporter LAT2/4F2hc and risk of hypertension in the context of chronic kidney disease. BMC medical genomics, 17(1), 163.

Zhang W, et al. (2024) Whole exome sequencing identified a homozygous novel variant in DOP1A gene in the Pakistan family with neurodevelopmental disabilities: case report and literature review. Frontiers in genetics, 15, 1351710.

Shao L, et al. (2024) Active natural compounds perturb the melanoma risk-gene network. G3 (Bethesda, Md.), 14(2).

Tjader NP, et al. (2024) Association of ESR1 Germline Variants with TP53 Somatic Variants in Breast Tumors in a Genome-wide Study. Cancer research communications, 4(6), 1597.

Zhu Y, et al. (2024) A genome-wide association study based on the China Kadoorie Biobank identifies genetic associations between snoring and cardiometabolic traits. Communications biology, 7(1), 305.

Wahbeh MH, et al. (2024) A functional schizophrenia-associated genetic variant near the TSNARE1 and ADGRB1 genes. HGG advances, 5(3), 100303.

Pandey RK, et al. (2024) Author Correction: Novel genetic association of the Furin gene polymorphism rs1981458 with COVID-19 severity among Indian populations. Scientific reports, 14(1), 9523.

Pakha DN, et al. (2024) Investigation of missense mutation-related type 1 diabetes mellitus through integrating genomic databases and bioinformatic approach. Genomics & informatics, 22(1), 8.

Kerns S, et al. (2024) Genetic association with autoimmune diseases identifies molecular mechanisms of coronary artery disease. iScience, 27(9), 110715.

Ruisch IH, et al. (2024) Molecular landscape of the overlap between Alzheimer's disease and somatic insulin-related diseases. Alzheimer's research & therapy, 16(1), 239.