Resource Summary Report

Generated by dkNET on Apr 24, 2025

Genotype-Tissue Expression

RRID:SCR_013042
Type: Tool

Proper Citation

Genotype-Tissue Expression (RRID:SCR_013042)

Resource Information

URL: http://commonfund.nih.gov/GTEx/

Proper Citation: Genotype-Tissue Expression (RRID:SCR_013042)

Description: Project to study human gene expression and regulation in multiple tissues, providing valuable insights into mechanisms of gene regulation and its disease related perturbations. Genetic variation between individuals will be examined for correlation with differences in gene expression level to identify regions of the genome that influence whether and how much a gene is expressed. Includes initiatives: Novel Statistical Methods for Human Gene Expression Quantitative Trait Loci (eQTL) Analysis ,Laboratory, Data Analysis, and Coordinating Center (LDACC), caHUB Acquisition of Normal Tissues in Support of GTEx Project.

Abbreviations: GTEx

Synonyms: GTEx, Genotype-Tissue Expression, Genotype-Tissue Expression (GTEx)

Resource Type: portal, service resource, data repository, biobank, material storage repository, data or information resource, storage service resource

Keywords: gene expression, regulation, genetic variation, genotype, tissue, tissue bank, database, genome, disease, inherited disease, FASEB list

Funding: NIH Common Fund

Resource Name: Genotype-Tissue Expression

Resource ID: SCR_013042

Alternate IDs: OMICS_00271

Alternate URLs: https://gtexportal.org/home/

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250424T065220+0000

Ratings and Alerts

No rating or validation information has been found for Genotype-Tissue Expression.

No alerts have been found for Genotype-Tissue Expression.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 411 mentions in open access literature.

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

Dupuy M, et al. (2025) Chimeric protein EWS::FLI1 drives cell proliferation in Ewing Sarcoma via aberrant expression of KCNN1/SK1 and dysregulation of calcium signaling. Oncogene, 44(2), 79.

Smith TB, et al. (2025) Bi-allelic variants in DAP3 result in reduced assembly of the mitoribosomal small subunit with altered apoptosis and a Perrault-syndrome-spectrum phenotype. American journal of human genetics, 112(1), 59.

Scherer N, et al. (2025) Coupling metabolomics and exome sequencing reveals graded effects of rare damaging heterozygous variants on gene function and human traits. Nature genetics, 57(1), 193.

Smith JR, et al. (2025) Standardized pipelines support and facilitate integration of diverse datasets at the Rat Genome Database. Database : the journal of biological databases and curation, 2025.

Bueckle A, et al. (2025) Construction, Deployment, and Usage of the Human Reference Atlas Knowledge Graph for Linked Open Data. bioRxiv : the preprint server for biology.

Zhou Y, et al. (2025) Chromosome-level echidna genome illuminates evolution of multiple sex chromosome system in monotremes. GigaScience, 14.

Baldari S, et al. (2025) Expression pattern and prognostic significance of aldehyde dehydrogenase 2 in lung adenocarcinoma as a potential predictor of immunotherapy efficacy. Cancer innovation, 4(1), e149.

Xu J, et al. (2025) Identification of genetic variants of the IL18R1 gene in association with COPD susceptibility. Annals of medicine, 57(1), 2446690.

Zou X, et al. (2025) Impact of rare non-coding variants on human diseases through alternative polyadenylation outliers. Nature communications, 16(1), 682.

Wills C, et al. (2025) Relationship between inherited genetic variation and survival from colorectal cancer stratified by tumour location. Scientific reports, 15(1), 2423.

Lei Q, et al. (2025) NOL-7 serves as a potential prognostic-related biomarker for hepatocellular carcinoma. Discover oncology, 16(1), 69.

Sun Y, et al. (2025) MYBBP1A?mediated IGFBP4 promoter methylation promotes epithelial?mesenchymal transition and metastasis through activation of NOTCH pathway in liver cancer. International journal of oncology, 66(1).

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

Angelats L, et al. (2025) Linking tumor immune infiltration to enhanced longevity in recurrence-free breast cancer. ESMO open, 10(1), 104109.

Harada K, et al. (2025) Intestinal butyric acid-mediated disruption of gut hormone secretion and lipid metabolism in vasopressin receptor-deficient mice. Molecular metabolism, 91, 102072.

Gálvez-Montosa F, et al. (2025) Polymorphisms within autophagy-related genes as susceptibility biomarkers for pancreatic cancer: A meta-analysis of three large European cohorts and functional characterization. International journal of cancer, 156(2), 339.

Scuderi G, et al. (2025) Comprehensive Analysis of TSPAN32 Regulatory Networks and Their Role in Immune Cell Biology. Biomolecules, 15(1).

Guo Q, et al. (2025) Identification of GBN5 as a molecular biomarker of pan-cancer species by integrated multi-omics analysis. Discover oncology, 16(1), 85.

Ding H, et al. (2025) Integrating genetics and transcriptomics to characterize shared mechanisms in digestive diseases and psychiatric disorders. Communications biology, 8(1), 47.

Zhu Y, et al. (2025) NIPAL1 as a prognostic biomarker associated with pancreatic adenocarcinoma progression and immune infiltration. BMC cancer, 25(1), 165.