Resource Summary Report

Generated by NIF on Aug 19, 2026

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

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: 20260819T044345+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 608 mentions in open access literature.

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

Liang J, et al. (2026) Comprehensive Pan-Cancer Analysis Reveals RNF20 as a Candidate Prognostic and Diagnostic Biomarker. Bioinformatics and biology insights, 20, 11779322261427126.

Pang C, et al. (2026) Translating transcriptomics analysis into diagnostic workflows: clinical variant identification and interpretation in hypothesis-driven and hypothesis-free approaches. EBioMedicine, 128, 106313.

Wang Y, et al. (2026) CRISPR activation screens identify oncogenic lncRNAs that are susceptible to CDK4/6 inhibitor treatment. Nature communications, 17(1).

Hu YM, et al. (2026) Elevated Tumor-Associated Androgen Receptor Activity Correlates with Poor Immune Infiltration and Immunotherapy Response across Cancer Types. Cancer research communications, 6(1), 17.

Ren T, et al. (2026) scSurvival: Single-Cell Survival Analysis of Clinical Cancer Cohort Data at Cellular Resolution. Cancer discovery, 16(5), 931.

Spalato Ceruso M, et al. (2026) Adenosine A2B Receptor Promotes Tumor Progression and Metastases in Undifferentiated Pleomorphic Sarcoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1887.

Shen R, et al. (2026) Integrating Single-Cell and RNA Sequencing to Predict Glioma Prognosis Through Lactylation. International journal of molecular sciences, 27(4).

Martínez-Bosch N, et al. (2026) PARP2 deficiency impairs pancreatic cancer progression by promoting genomic instability and antitumor immunity. Science advances, 12(19), eadu8849.

Li Y, et al. (2026) The contribution of short tandem repeats to splicing variation in the human cortex. bioRxiv : the preprint server for biology.

Prélot L, et al. (2026) ImmunoPepper: extracting personalized peptides from complex splicing graphs. Bioinformatics (Oxford, England), 42(1).

Fu T, et al. (2026) Comprehensive pan-cancer analysis of AARS1, a newly identified lactyltransferase in human cancers. Cancer cell international, 26(1).

Luan R, et al. (2026) Pan-cancer multi-omics reveals DCAF7 as an immune-modulating prognostic driver and Wnt/?-catenin activator in hepatocellular carcinoma. Clinical and translational medicine, 16(1), e70572.

Tankka AT, et al. (2026) Integrative CRISPR Screening and RNA Analyses Discover an Essential Role for PUF60 Interactions with 3' Splice Sites in Cancer Progression. Cancer research, 86(7), 1586.

Yogo A, et al. (2026) Spatial Transcriptomics Reveals Location-Specific Tumor Cell Subtypes and Signaling within Multifocal Small Intestinal Neuroendocrine Tumors. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(10), 2098.

Lawrence KA, et al. (2026) Focus on single-gene effects limits discovery and interpretation of complex-trait-associated variants. American journal of human genetics, 113(4), 842.

Wang Y, et al. (2026) Identification of CADM1 as an Immunotherapeutic Target and Evaluation of a Novel CADM1-Targeting Antibody-Drug Conjugate in Preclinical Osteosarcoma Models. Molecular cancer therapeutics, 25(6), 881.

Zhao C, et al. (2026) Progranulin promotes glioma progression via interaction with cathepsin D and serves as a diagnostic and prognostic biomarker. Discover oncology, 17(1), 336.

Gao L, et al. (2026) COL10A1 overexpression potentially contributes to poor outcomes in breast cancer via autophagy and vasculogenic mimicry. Translational cancer research, 15(5), 392.

Mogi M, et al. (2026) Pan-cancer analysis of RNA expression signatures associated with cancer tissue architecture. British journal of cancer, 134(1), 141.

Ma B, et al. (2026) MYC-Mediated USP39 Upregulation Stabilizes SRSF1 in Pancreatic Cancer. Molecular cancer research : MCR.