

Resource Summary Report

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Genotype-Tissue Expression

RRID:SCR_013042

Type: Tool

Proper Citation

Genotype-Tissue Expression (RRID:SCR_013042)

Resource Information

URL: <http://commonfund.nih.gov/GTEX/>

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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, data repository, portal, biobank, storage service resource, service resource, material storage repository

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

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 545 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

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.

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.

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

Wang J, et al. (2025) A multi-omic approach implicates novel protein dysregulation in post-traumatic stress disorder. Genome medicine, 17(1), 43.

Ma S, et al. (2025) Integrated Omics and Multicohort Analyses Identify an Enhancer Variant Linking Ferroptosis to Precision Therapy in Prostate Cancer. Cancer research, 85(19), 3771.

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.

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.

Akiba K, et al. (2025) Intragenic duplication of PHEX in a girl with X-linked hypophosphatemia: a case report with review of literature. Endocrine journal, 72(4), 413.

Srivastava R, et al. (2025) Advancing precision oncology with AI-powered genomic analysis. *Frontiers in pharmacology*, 16, 1591696.

Sequera C, et al. (2025) The HDAC inhibitor romidepsin renders liver cancer vulnerable to RTK targeting and immunologically active. *Nature communications*, 16(1), 7919.

, et al. (2025) Multi-organ AI Endophenotypes Chart the Heterogeneity of Pan-disease in the Brain, Eye, and Heart. *medRxiv : the preprint server for health sciences*.

Beyene MB, et al. (2025) A genome-wide association study identified 10 novel genomic loci associated with intrinsic capacity. *The journals of gerontology. Series A, Biological sciences and medical sciences*, 80(11).

Bai G, et al. (2025) Leveraging diverse cell death patterns in osteosarcoma patients and identification of the function of FADS2 in osteosarcoma cells. *Scientific reports*, 15(1), 20831.

Cao Q, et al. (2025) Multomic analysis reveals the potential of LAG3 as a prognostic and immune biomarker and its validation in osteosarcoma. *Scientific reports*, 15(1), 25158.

Jain BK, et al. (2025) P4-ATPases control phosphoinositide membrane asymmetry and neomycin resistance. *Nature cell biology*, 27(7), 1114.

Li X, et al. (2025) SLC4A11 is a targetable marker correlated with therapeutic responses in ovarian cancer. *Journal of ovarian research*, 18(1), 167.

Guo X, et al. (2025) Neutrophil extracellular traps drive osteoporosis via NCF2-dependent signaling: integrated transcriptomics with mechanistic validation. *Redox report : communications in free radical research*, 30(1), 2534745.

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

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.