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: biobank, material storage repository, data or information resource, data repository, storage service resource, portal, 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: 20260801T042713+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 T1D .

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.

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. Cell genomics, 5(3), 100775.

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.

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.

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

Wang J, et al. (2025) Assessment of lncRNA biomarkers based on NETs for prognosis and therapeutic response in ovarian cancer. Scientific reports, 15(1), 13042.

Toubia J, et al. (2025) TRanscriptome ANalysis of StratifiEd CohorTs (TRANSECT) enables automated assessment of global gene regulation linked to disparate expression in user defined genes and gene sets. NAR genomics and bioinformatics, 7(2), lqaf041.

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.

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

Mamun MAA, et al. (2025) Targeted degradation of extracellular proteins: state of the art and diversity of degrader designs. Journal of hematology & oncology, 18(1), 52.

He R, et al. (2025) Enhancing nonlinear transcriptome- and proteome-wide association studies via trait imputation with applications to Alzheimer's disease. PLoS genetics, 21(4), e1011659.

Bruno F, et al. (2025) Genetic variability in ADAM17/TACE is associated with sporadic Alzheimer's disease risk, neuropsychiatric symptoms and cognitive performance on the Rey Auditory Verbal Learning and Clock Drawing Tests. PloS one, 20(5), e0309631.

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

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.

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.

Liu Y, et al. (2025) Integrated pan-cancer analysis of ADM's role in prognosis, immune modulation and resistance. Frontiers in immunology, 16, 1573250.

Liu X, et al. (2025) Increasing Stemness Drives Prostate Cancer Progression, Plasticity, Therapy Resistance and Poor Patient Survival. bioRxiv : the preprint server for biology.