

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

TCGAbiolinks

RRID:SCR_017683

Type: Tool

Proper Citation

TCGAbiolinks (RRID:SCR_017683)

Resource Information

URL: <https://bioconductor.org/packages/TCGAbiolinks/>

Proper Citation: TCGAbiolinks (RRID:SCR_017683)

Description: Software R Bioconductor package for integrative analysis with TCGA data. TCGAbiolinks is able to access National Cancer Institute Genomic Data Commons thorough its GDC Application Programming Interface to search, download and prepare relevant data for analysis in R.

Synonyms: Cancer Genome Atlas (TCGA) biolinks

Resource Type: data processing software, data analysis software, software application, software resource

Defining Citation: [PMID:26704973](#), [DOI:10.12688/f1000research.8923.2](#)

Keywords: Integrative, analysis, TCGA data, cancer, genome, atlas, genomic, analysis, expression, methylated, region, survival plot, phenotype, tumor, epigenomic, alteration, clinical, molecular, retrival

Funding: BridgeIRIS ;
INNOVIRIS ;
Region de Bruxelles Capitale ;
Brussels ;
Belgium ;
GENGISCAN ;
S??o Paulo Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: TCGAbiolinks

Resource ID: SCR_017683

Alternate URLs: <https://github.com/BioinformaticsFMRP/TCGAbiolinks>

License: GPLv3

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260801T042823+0000

Ratings and Alerts

No rating or validation information has been found for TCGAbiolinks.

No alerts have been found for TCGAbiolinks.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 93 mentions in open access literature.

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

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.

Nibeyro G, et al. (2025) Evaluating Gene Fusions as Prognostic Biomarkers and Therapeutic Targets in Immune Checkpoint Blockade-Treated Advanced Melanoma: A Retrospective Analysis. Cancer research communications, 5(8), 1332.

Liu F, et al. (2025) Integrated analysis of single-cell and bulk transcriptomics reveals cellular subtypes and molecular features associated with osteosarcoma prognosis. BMC cancer, 25(1), 280.

Petroni G, et al. (2025) Th17-like cells and immunosuppressive macrophages infiltrate tertiary lymphoid structures with distinct maturation status in soft-tissue sarcoma. Cell death & disease, 16(1), 917.

Jin N, et al. (2025) Epigenetic Modulation, Intratumoral Microbiome, and Immunity in Early-Onset Colorectal Cancer. Cancer research communications, 5(11), 1985.

Withers HG, et al. (2025) Intratumoral B cell and interferon signatures in newly diagnosed glioblastoma are associated with longer survival in patients treated with SurVaxM. Cancer immunology, immunotherapy : CII, 74(11), 332.

Su D, et al. (2025) Molecular Subtyping and Genomic Profiling Expand Precision Medicine in KRAS Wild-Type Pancreatic Cancer. Cancer science, 116(4), 1094.

Rohan P, et al. (2025) High expression of THY1 is a prognostic marker for gastric Cancer: Deciphering its transcriptional regulation as a component of the Epithelial-mesenchymal transition. *Biochemistry and biophysics reports*, 42, 102050.

Fu X, et al. (2025) Spatial gene expression at single-cell resolution from histology using deep learning with GHIST. *Nature methods*, 22(9), 1900.

Zhao B, et al. (2025) A spatial transcriptomics study of MES-like and mono/macro cells in gliomas. *Scientific reports*, 15(1), 12730.

Zhao S, et al. (2025) FuSViz-visualization and interpretation of structural variation using cancer genomics and transcriptomics data. *Nucleic acids research*, 53(4).

Tang K, et al. (2025) Construction of a prognostic model and identification of key genes in liver hepatocellular carcinoma based on multi-omics data. *Scientific reports*, 15(1), 13393.

Wang C, et al. (2025) Benchmarking the translational potential of spatial gene expression prediction from histology. *Nature communications*, 16(1), 1544.

Wang Y, et al. (2025) Homeodomain protein PRRX1 anchors the Ku heterodimers at DNA double-strand breaks to promote nonhomologous end-joining. *Nucleic acids research*, 53(6).

Dumut DC, et al. (2025) Diethyldithiocarbamate-copper complex ignites the tumor microenvironment through NKG2D-NKG2DL axis. *Frontiers in immunology*, 16, 1491450.

Pane K, et al. (2025) Feature Selection and Network-Driven Analyses to Unveil Common RNA Signatures in Colon and Pancreatic KRAS-Mutant Cancers. *Cancer medicine*, 14(5), e70468.

Lakbir S, et al. (2025) Tumor break load quantitates structural variant-associated genomic instability with biological and clinical relevance across cancers. *NPJ precision oncology*, 9(1), 140.

Lu H, et al. (2025) Epithelial-Mesenchymal Transition is Associated with Altered Immune Composition and Cytotoxic Function in Triple-Negative Breast Cancer. *bioRxiv : the preprint server for biology*.

Loriot A, et al. (2025) A survey of human cancer-germline genes: Linking X chromosome localization, DNA methylation and sex-biased expression in early embryos. *PLoS genetics*, 21(10), e1011734.

Li X, et al. (2025) The Dynamically Evolving Cell States and Ecosystem from Benign Nevi to Melanoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(12), 2478.