

Resource Summary Report

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OncoDB

RRID:SCR_028340

Type: Tool

Proper Citation

OncoDB (RRID:SCR_028340)

Resource Information

URL: <https://oncodb.org/>

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Description: Database offers integrated multi-omic data for patients across 33 cancer types. It encompasses gene expression, DNA methylation, somatic mutations, proteomic profiles, and chromatin accessibility, drawing from TCGA, GTEx, and CPTAC projects. Users can compare gene expression, DNA methylation, and protein levels between tumor and normal tissues, identifying differentially expressed genes and proteins, and examining gene-to-gene correlations. Provides oncogene mutation profiles and allows for survival analysis based on gene expression and methylation, linked to clinical parameters. Facilitates exploration of multi-omic correlations, such as gene expression with DNA methylation, and their variations with mutation status. Extends its analytical capabilities to include six major oncoviruses, offering insights into their impact on gene expression, methylation, and patient survival.

Synonyms: OncoDB2.0

Resource Type: data or information resource, database

Defining Citation: [PMID:34718715](#), [PMID:40995640](#)

Keywords: cancer patients data, gene expression, DNA methylation, somatic mutations, proteomic profiles, chromatin accessibility,

Funding: NIDCR R01DE026471;
NIGMS R35GM141535;
NCI R01CA287778

Availability: Free, Freely available,

Resource Name: OncoDB

Resource ID: SCR_028340

Record Creation Time: 20260428T054601+0000

Record Last Update: 20260811T043838+0000

Ratings and Alerts

No rating or validation information has been found for OncoDB.

No alerts have been found for OncoDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Beamer P, et al. (2026) Multiscale domain identification for spatial transcriptomics via persistent homology. Cell reports methods, 6(5), 101376.

Jeong EA, et al. (2026) Integrative Multi-Omics Analysis Identifies NUP205 as a Candidate Prognostic Biomarker in Liver Hepatocellular Carcinoma. International journal of molecular sciences, 27(6).

Kousik SP, et al. (2026) A competing TMPO-AS1-let-7b-5p-kinesin superfamily RNA network predicts poor lung cancer patient survival. Reports of practical oncology and radiotherapy : journal of Greatpoland Cancer Center in Poznan and Polish Society of Radiation Oncology, 31(1), 1.

Rafi MSH, et al. (2026) Association of NUDT17 rs9286836 and rs2004659 variants with breast cancer risk in Bangladeshi Women. PloS one, 21(3), e0344584.

A UD, et al. (2026) Decoding the Oncogenic Role of USP22 Through Pan-Cancer Genomic and Epigenetic Analysis. Cancer reports (Hoboken, N.J.), 9(5), e70572.

Chen Y, et al. (2026) Effect of the G-Protein-Coupled Receptor T2R14 on Proliferation and Cell Population Growth in Oral Cancer Cells. Cells, 15(3).

Vasconcelos RI, et al. (2026) FOXK2 gene expression in cancer: Potential regulatory mechanisms and clinical implications. Genes & diseases, 13(4), 101951.

Ullah N, et al. (2026) Bacterial protein-oleate complexes induce ferroptosis-like cell death in colorectal cancer cells by disrupting cell membranes and inhibiting the β -catenin-GPX4 axis. Cell death discovery, 12(1).

Cho M, et al. (2026) OncoDB 2.0: a comprehensive platform for integrated pan-cancer omics analysis. *Nucleic acids research*, 54(D1), D1537.

Moon J, et al. (2026) Drug repositioning of regorafenib for renal cell carcinoma identifies DDR2-associated sensitivity in ACHN models. *The Korean journal of physiology & pharmacology : official journal of the Korean Physiological Society and the Korean Society of Pharmacology*, 30(1), 41.

Christou C, et al. (2026) Pharmacological Targeting of Midkine (MDK) Reveals Stiffness-Dependent Control of Hepatocellular Carcinoma Invasiveness. *International journal of molecular sciences*, 27(4).

Kumar S, et al. (2026) Pan-cancer analysis reveals differential PERK expression across tumour types and its potential as a therapeutic target. *Discover oncology*, 17(1).

Kashyap VK, et al. (2026) Bioinformatics analysis of TRPV1 expression and its role in hepatocellular carcinoma prognosis. *Discover oncology*, 17(1).

Yan P, et al. (2026) ADH4 deficiency activates the NRF2-CSF1 axis by increased lipid peroxidation in hepatocellular carcinoma. *Cancer cell international*, 26(1).

Huang YH, et al. (2026) BCL2-Associated Transcription Factor 1 Promotes SRC/Hypoxia-Inducible Factor 1 Subunit γ -Mediated Cancer Stemness in Radioresistant Triple-Negative Breast Cancer. *Oncology research*, 34(7), 19.

Tang G, et al. (2026) Pan-cancer analysis reveals molecular signatures for predicting matrix stiffness in solid tumors. *International journal of cancer*, 158(4), 1093.

Lee KS, et al. (2026) Epigenetic and ncRNA Regulation of CBX2 in Liver Hepatocellular Carcinoma: A Comprehensive Multi-Omics Analysis for Understanding Biological Significance. *Medicina (Kaunas, Lithuania)*, 62(5).

Zhao Z, et al. (2025) CDCA genes as prognostic and therapeutic targets in Colon adenocarcinoma. *Hereditas*, 162(1), 19.

Hui P, et al. (2025) Shared hub genes in membranous nephropathy and kidney renal clear cell carcinoma: investigating molecular overlap and tumor progression. *Discover oncology*, 16(1), 1035.

Appadurai MI, et al. (2025) ST6GalNAc-I regulates tumor cell sialylation via NECTIN2/MUC5AC-mediated immunosuppression and angiogenesis in non-small cell lung cancer. *The Journal of clinical investigation*, 135(10).