

Resource Summary Report

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The Cancer Immunome Database

RRID:SCR_014508

Type: Tool

Proper Citation

The Cancer Immunome Database (RRID:SCR_014508)

Resource Information

URL: <https://tcia.at/>

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Description: A database which provides results of comprehensive immunogenomic analyses of next generation sequencing data for 19 solid cancers from The Cancer Genome Atlas and other datasources. The database can be queried for the gene expression of specific immune-related gene sets, cellular composition of immune infiltrates (characterized using gene set enrichment analyses and deconvolution), neoantigens and cancer-germline antigens, HLA types, and tumor heterogeneity (estimated from cancer cell fractions). It also provides survival analyses for different types immunological parameters.

Abbreviations: TCIA

Synonyms: The Cancer Immunome Database (TCIA)

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1101/056101](https://doi.org/10.1101/056101)

Keywords: cancer, immunology, database, immunogenomic analysis, gene expression, FASEB list

Funding: European Union Horizon 2020 633592

Availability: Acknowledgement requested

Resource Name: The Cancer Immunome Database

Resource ID: SCR_014508

Alternate IDs: r3d100012052

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Record Creation Time: 20220129T080320+0000

Record Last Update: 20260820T054709+0000

Ratings and Alerts

No rating or validation information has been found for The Cancer Immunome Database.

No alerts have been found for The Cancer Immunome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 426 mentions in open access literature.

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

Ma Z, et al. (2026) Elevated PTK6 expression is associated with tumor immune microenvironment remodeling and predicts poor prognosis in endometrial carcinoma. *Frontiers in medicine*, 13, 1842564.

Pei Y, et al. (2026) Machine learning identifies disulfidptosis-related gene signature for pancreatic cancer prognosis and immune infiltration. *Discover oncology*, 17(1), 335.

Huang P, et al. (2026) Autophagy-related gene-based prognostic model for breast cancer. *Discover oncology*, 17(1).

Wei D, et al. (2026) Calcium-related genes predict prognosis, immune characteristics, and response to immunotherapy in LUAD patients. *Clinical proteomics*, 23(1).

Mu T, et al. (2026) Identification and external validation of a prognostic signature based on myeloid-derived suppressor cell-related lncRNAs for hepatocellular carcinoma. *Hereditas*, 163(1).

Chi J, et al. (2026) DCTPP1 drives immunosuppression and poor prognosis in breast cancer by promoting M2 macrophage polarization. *Scientific reports*, 16(1).

Lian X, et al. (2026) Identification and validation of a sphingolipid metabolism-related prognostic signature for predicting prognosis and immune microenvironment-related characteristics in ovarian cancer. *Translational cancer research*, 15(3), 153.

Weng J, et al. (2026) Comprehensive profiling of alternative splicing and immune landscapes in rectal cancer: implications for mRNA vaccine design and immune subtype stratification. *Frontiers in oncology*, 16, 1780631.

Wang Q, et al. (2026) Construction of taurine metabolism-related risk model and subtype identification in colorectal cancer to predict prognosis and immunological features. *Journal of gastrointestinal oncology*, 17(1), 7.

Ren T, et al. (2026) The Senescence-SASP Landscape in Colon Adenocarcinoma: Prognostic and Therapeutic Implications. *Current issues in molecular biology*, 48(1).

Sun J, et al. (2026) A Zinc Finger Protein-Based Prognostic Model in Lung Adenocarcinoma Identifies FGD3 as a Marker Associated with Lorlatinib Resistance. *Cancers*, 18(10).

Peng J, et al. (2026) Predictive analysis of BRAF V600E mutation and central lymph node metastasis in papillary thyroid carcinoma. *Oncology letters*, 31(1), 44.

Zhao X, et al. (2026) Establishment of an amino acid metabolism related signature for prognostic and therapeutic sensitivity prediction in breast cancer by machine learning. *PloS one*, 21(1), e0340586.

Mao C, et al. (2026) Integrating bulk and single-cell transcriptomic data to construct a risk model for histidine metabolism-related epithelial cell features in lung adenocarcinoma, predicting prognosis and immune landscape. *RNA biology*, 23(1), 1.

Wang S, et al. (2026) Multi-omics characterization of cachexia-related genes reveals prognostic signatures and immune landscape in breast cancer. *Clinical & translational oncology : official publication of the Federation of Spanish Oncology Societies and of the National Cancer Institute of Mexico*, 28(2), 557.

Chen Y, et al. (2026) Prognostic role of CDCA3 in lung adenocarcinoma with immune infiltration. *Scientific reports*, 16(1), 4153.

Bai G, et al. (2026) Comprehensive analysis reveals the molecular heterogeneity and the differences in prognosis and immunotherapy sensitivity in hypermutated colorectal cancer. *Medicine*, 105(2), e47073.

He DL, et al. (2026) Elevated DOCK4 expression correlates with favorable prognosis and immune infiltration in clear cell renal cell carcinoma. *Annals of medicine*, 58(1), 2642533.

Yang Y, et al. (2026) Loss of GGT6 promotes colorectal cancer progression and correlates with poor prognosis: a study based on multi-database mining and functional validation. *Translational cancer research*, 15(4), 322.

Shao Z, et al. (2026) Development and Validation of an m6A-Derived Prognostic Signature in Lung Adenocarcinoma. *Journal of Cancer*, 17(6), 1134.