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

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

Record Creation Time: 20220129T080320+0000

Record Last Update: 20250426T060407+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 196 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhang S, et al. (2025) AL16431.1 is identified as a biomarker for bladder cancer progression and immunotherapy response. Scientific reports, 15(1), 1170.

Ye L, et al. (2025) Multi?omics identification of a novel signature for serous ovarian carcinoma in the context of 3P medicine and based on twelve programmed cell death patterns: a multi-cohort machine learning study. Molecular medicine (Cambridge, Mass.), 31(1), 5.

Chen Y, et al. (2025) Construction of a novel radioresistance-related signature for prediction of prognosis, immune microenvironment and anti-tumour drug sensitivity in non-small cell lung cancer. Annals of medicine, 57(1), 2447930.

Sun Z, et al. (2025) Predictive value of dendritic cell-related genes for prognosis and immunotherapy response in lung adenocarcinoma. Cancer cell international, 25(1), 13.

Zhao Y, et al. (2025) A novel machine learning-based immune prognostic signature for improving clinical outcomes and guiding therapy in colorectal cancer: an integrated bioinformatics and experimental study. BMC cancer, 25(1), 65.

Luan F, et al. (2025) Comprehensive pan-cancer analysis reveals NTN1 as an immune infiltrate risk factor and its potential prognostic value in SKCM. Scientific reports, 15(1), 3223.

Wang T, et al. (2024) Identification and validation of SLCO4C1 as a biological marker in hepatocellular carcinoma based on anoikis classification features. Aging, 16(2), 1440.

Ye L, et al. (2024) Identification of potential novel N6-methyladenosine effector-related lncRNA biomarkers for serous ovarian carcinoma: a machine learning-based exploration in the framework of 3P medicine. Frontiers in pharmacology, 15, 1351929.

Peng H, et al. (2024) Prediction of the survival status and tumor microenvironment in colorectal cancer through genotyping analysis based on toll-like receptors. Saudi journal of gastroenterology : official journal of the Saudi Gastroenterology Association, 30(4), 243.

Zhu X, et al. (2024) Increased co-expression of 4-1BB with PD-1 on CD8+ tumor-infiltrating lymphocytes is associated with improved prognosis and immunotherapy response in cervical cancer. Frontiers in oncology, 14, 1381381.

Liu X, et al. (2024) DIPAN: Detecting personalized intronic polyadenylation derived neoantigens from RNA sequencing data. Computational and structural biotechnology journal, 23, 2057.

Liu L, et al. (2024) A Novel RNA Methylation-Related Prognostic Signature and its Tumor Microenvironment Characterization in Hepatocellular Carcinoma. Technology in cancer research & treatment, 23, 15330338241276895.

Jia Y, et al. (2024) Comprehensive analysis of LD-related genes signature for predicting prognosis and immunotherapy response in clear cell renal cell carcinoma. BMC nephrology, 25(1), 298.

Zhou M, et al. (2024) Prognostic Significance and Immune Landscape of a Cuproptosis-Related LncRNA Signature in Ovarian Cancer. Biomedicines, 12(11).

Xin M, et al. (2024) Exploring the prognosis value, immune correlation, and drug responsiveness prediction of homeobox C6 (HOXC6) in lung adenocarcinoma. Discover oncology, 15(1), 393.

Zhang Z, et al. (2024) Comprehensive pan-cancer analysis of ACSS3 as a biomarker for prognosis and immunotherapy response. Heliyon, 10(15), e35231.

Li J, et al. (2024) Identification of immunotherapy-related subtypes, characterization of tumor microenvironment infiltration, and development of a prognostic signature in gastric carcinoma. Aging, 16(14), 11185.

Guo C, et al. (2024) Comprehensive analysis of tumor immune-related gene signature for predicting prognosis, immunotherapy, and drug sensitivity in bladder urothelial carcinoma. Translational cancer research, 13(12), 6732.

Li L, et al. (2024) Integration of machine learning and experimental validation to identify the prognostic signature related to diverse programmed cell deaths in breast cancer. Frontiers in oncology, 14, 1505934.

Huang Y, et al. (2024) Comprehensive analysis of cellular senescence and immune microenvironment in papillary thyroid carcinoma. Aging, 16(3), 2866.