

Resource Summary Report

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TIDE

RRID:SCR_026350

Type: Tool

Proper Citation

TIDE (RRID:SCR_026350)

Resource Information

URL: <http://tide.dfci.harvard.edu/login/>

Proper Citation: TIDE (RRID:SCR_026350)

Description: Web platform for large-scale public data reuse to model immunotherapy response and resistance. Provides integrated large-scale omics data and biomarkers on published ICB trials, non-immunotherapy tumor profiles, and CRISPR screens.

Synonyms: Tumor Immune Dysfunction and Exclusion

Resource Type: data or information resource, web application, software resource

Defining Citation: [PMID:32102694](#)

Keywords: public data reuse, model immunotherapy, response and resistance, integrated large-scale omics data and biomarkers,

Availability: Restricted

Resource Name: TIDE

Resource ID: SCR_026350

Record Creation Time: 20250129T053338+0000

Record Last Update: 20260811T043806+0000

Ratings and Alerts

No rating or validation information has been found for TIDE.

No alerts have been found for TIDE.

Data and Source Information

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Lai Z, et al. (2026) Neuroendocrine prostate cancer (NEPC)-associated CEP55 promotes cisplatin resistance in prostate cancer by regulating CDK1 phosphorylation. *Cancer pathogenesis and therapy*, 4(1), 51.

Ma P, et al. (2026) Transcriptional activation of LINGO1 facilitates proliferation and immune escape in colorectal cancer. *Scientific reports*, 16(1).

Shang J, et al. (2026) High COMP expression promotes tumor cell proliferation and migration of rectal cancer, contributing to unfavorable prognosis and suppressive immune microenvironment. *Discover oncology*, 17(1).

Han YX, et al. (2026) ??Integrating machine learning and spatial transcriptomics uncovers shared immunomodulatory deubiquitinases in MAFLD and HCC. *Human genetics*, 145(1).

Wang W, et al. (2026) A putative prognostic model for lung adenocarcinoma based on crotonylation-related genes by bioinformatics and experimental verification. *Frontiers in cell and developmental biology*, 14, 1639773.

Zhang W, et al. (2026) United multi-omics and machine learning refine regulatory T cell-defined hepatocellular carcinoma subtypes. *iScience*, 29(1), 114328.

Zhang C, et al. (2026) Integrative analyses of metastatic cancer transcriptome reveal clinically distinct cellular States and ecosystems. *Scientific reports*, 16(1).

Liu T, et al. (2026) Prognostic prediction and immune correlation analysis of anoikis- and epithelial-mesenchymal transition-related genes in lung adenocarcinoma. *Translational cancer research*, 15(2), 100.

Yang C, et al. (2025) ERCC3 serves as a prognostic biomarker for hepatocellular carcinoma and positively regulates cell proliferation and migration. *Discover oncology*, 16(1), 419.

Freitas-Cortez MA, et al. (2025) Cancer cells avoid ferroptosis induced by immune cells via fatty acid binding proteins. *Molecular cancer*, 24(1), 40.

Xing C, et al. (2025) NOS2 as a prognostic biomarker for early-onset colorectal cancer based on public data and clinical validation analysis. *Scientific reports*, 15(1), 4300.

Yu Z, et al. (2025) NETosis-based prognostic model reveals immune modulation in clear cell renal cell carcinoma using single-cell and bulk RNA sequencing. *Scientific reports*, 15(1), 27156.

Liu L, et al. (2025) Ferroptosis-related gene analysis revealing novel biomarkers and therapeutic targets in diffuse large B-cell lymphoma. *Scientific reports*, 15(1), 38613.

Yang X, et al. (2025) Identification and external validation of a prognostic signature based on N6-methyladenosine- and tertiary lymphoid structures-related genes to evaluate survival prognosis and treatment efficacy in lung adenocarcinoma. *Discover oncology*, 16(1), 2265.

Zhao G, et al. (2025) Integrative Analysis of Immune- and Metabolism-Related Genes Identifies Robust Prognostic Signature and PYCR1 as a Carcinogenic Regulator in Clear Cell Renal Cell Carcinoma. *International journal of molecular sciences*, 26(10).

Li S, et al. (2025) Different neutrophil extracellular trap related Ewing sarcoma subtypes exhibit distinct prognosis, and immune microenvironment characteristics. *Scientific reports*, 15(1), 24523.

Zhao H, et al. (2025) Influence of migrasome-associated long noncoding RNAs on the immune microenvironment and prognosis in lung adenocarcinoma. *Discover oncology*, 16(1), 1168.

Hu H, et al. (2025) High expression of GRB14 is associated with cancer progression and poor prognosis in gastric cancer. *Discover oncology*, 16(1), 2117.

Chen X, et al. (2025) Deciphering lactate/lactylation networks in AML: integrated scRNA-seq and transcriptomics reveal functions and prognostic model. *BMC cancer*, 25(1), 1647.

Cui K, et al. (2025) Transcriptome-wide Mendelian randomization and single-cell analysis during CD4+ T cell activation deciphers immunotherapeutic targets for colorectal cancer. *NPJ precision oncology*, 10(1), 32.