Resource Summary Report

Generated by RRID on Sep 10, 2026

CTDatabase

RRID:SCR_007614
Type: Tool

Proper Citation

CTDatabase (RRID:SCR_007614)

Resource Information

URL: http://www.cta.lncc.br/

Proper Citation: CTDatabase (RRID:SCR_007614)

Description: A database of information about each Cancer-Testis (CT) gene, its gene products and the immune response induced in cancer patients by these proteins. CT antigens are proteins normally expressed only in the human germ line but that are also present in a significant subset of malignant tumors. The practical importance of these proteins is that due to their restricted expression pattern they are frequently recognized by the immune system of cancer patients. Moreover, this antigenicity has raised the possibility of their being used as vaccines to actively stimulate immune responses in order to combat tumor growth. As a result worldwide research into many aspects of CT antigens is rapidly growing prompting the construction of this database as a resource for investigators involved in this area.

Synonyms: CTDatabase

Resource Type: data or information resource, database

Keywords: data set, FASEB list

Related Condition: Cancer

Resource Name: CTDatabase

Resource ID: SCR_007614

Alternate IDs: nif-0000-02704

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133141+0000

Ratings and Alerts

No rating or validation information has been found for CTDatabase.

No alerts have been found for CTDatabase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 109 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Jensen JL, et al. (2026) Shared PRAME epitopes are T-cell targets in NUT carcinoma. Journal for immunotherapy of cancer, 14(2).

Kert ??, et al. (2026) Identification and prioritisation of tumour antigen candidates from 79 glioblastoma transcriptomes. Cancer immunology, immunotherapy : CII, 75(5).

Zhuo S, et al. (2026) Druggable target ATAD2 enhances the malignant progression and cooperates with E2F1 to up-regulate PDK1 expression in glioma. Genes & diseases, 13(1), 101810.

Huang A, et al. (2026) Integrative Proteogenomic Characterization of Left-Sided and Right-Sided Colorectal Cancer. MedComm, 7(6), e70806.

Chen A, et al. (2025) Expression of Cancer-Testis Antigens MAGE-A1, MAGE-A4, NY-ESO-1 and PRAME in Bone and Soft Tissue Sarcomas: The Experience From a Single Center in China. Cancer medicine, 14(7), e70750.

Pandey K, et al. (2025) Multiple Classes of Antigen Contribute to the Antigenic Landscape of Mesothelioma. Molecular & cellular proteomics : MCP, 24(3), 100925.

Alip M, et al. (2025) A cancer-testis antigen signature for predicting prognosis and response to immunotherapy in acute myeloid leukemia. Medicine, 104(50), e46374.

Qiu Z, et al. (2025) Screening colorectal cancer associated autoantigens through multi-omics analysis and diagnostic performance evaluation of corresponding autoantibodies. BMC cancer, 25(1), 713.

Lemke S, et al. (2025) PCI-DB: a novel primary tissue immunopeptidome database to guide next-generation peptide-based immunotherapy development. Journal for immunotherapy of cancer, 13(4).

Azimi P, et al. (2025) Cancer/testis antigens FBXO39 and CEP55 expression correlates with survival in GBM patients. PloS one, 20(6), e0326054.

Verma S, et al. (2024) Melanoma Antigen Family A (MAGE A) as Promising Biomarkers and Therapeutic Targets in Bladder Cancer. Cancers, 16(2).

Beckabir W, et al. (2024) Immune features are associated with response to neoadjuvant chemo-immunotherapy for muscle-invasive bladder cancer. Nature communications, 15(1), 4448.

Almutairi MH, et al. (2024) Differential expression and regulation of ADAD1, DMRTC2, PRSS54, SYCE1, SYCP1, TEX101, TEX48, and TMPRSS12 gene profiles in colon cancer tissues and their in vitro response to epigenetic drugs. PloS one, 19(8), e0307724.

Yi X, et al. (2024) Tumor-associated antigen prediction using a single-sample gene expression state inference algorithm. Cell reports methods, 4(11), 100906.

Almutairi MH, et al. (2024) Increased MAGE-C Family Gene Expression Levels as a Biomarker of Colon Cancer Through the Demethylation Mechanism. Pharmaceuticals (Basel, Switzerland), 17(11).

Kortleve D, et al. (2024) TCR-Engineered T Cells Directed against Ropporin-1 Constitute a Safe and Effective Treatment for Triple-Negative Breast Cancer. Cancer discovery, 14(12), 2450.

Meijer DM, et al. (2024) Enhanced immune responses are accompanied by increased MAGEA expression in osteosarcoma metastases. BMJ oncology, 3(1), e000472.

Garcia-Marquez MA, et al. (2024) Germline homozygosity and allelic imbalance of HLA-I are common in esophagogastric adenocarcinoma and impair the repertoire of immunogenic peptides. Journal for immunotherapy of cancer, 12(4).

Karlow JA, et al. (2023) Non-small Cell Lung Cancer Epigenomes Exhibit Altered DNA Methylation in Smokers and Never-smokers. Genomics, proteomics & bioinformatics, 21(5), 991.

Qin C, et al. (2023) Development and validation of a DNA damage repair-related gene-based prediction model for the prognosis of lung adenocarcinoma. Journal of thoracic disease, 15(12), 6928.