Resource Summary Report

Generated by NIF on May 16, 2025

PrognoScan

RRID:SCR_018740
Type: Tool

Proper Citation

ProgniScan (RRID:SCR_018740)

Resource Information

URL: http://www.prognoscan.org/

Proper Citation: ProgniScan (RRID:SCR_018740)

Description: Database for meta analysis of prognostic value of genes from server at Kyushu Institute of Technology. Collection of publicly available cancer microarray datasets with clinical annotation, as well as tool for assessing biological relationship between gene expression and prognosis. Provides platform for evaluating potential tumor markers and therapeutic targets.

Resource Type: service resource, production service resource, data or information resource, database, analysis service resource

Defining Citation: PMID:19393097

Keywords: Kyushu Institute of Technology, meta analysis, prognostic gene value, cancer microarray dataset, clinical annotation, gene expression, tumor marker, therapeutic target, bio.tools, FASEB list

Funding:

Availability: Free, Freely available

Resource Name: ProgniScan

Resource ID: SCR_018740

Alternate IDs: SCR_018741, biotools:prognoscan

Alternate URLs: http://dna00.bio.kyutech.ac.jp/PrognoScan/index.html, https://bio.tools/prognoscan

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250516T054209+0000

Ratings and Alerts

No rating or validation information has been found for PrognoScan.

No alerts have been found for PrognoScan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 333 mentions in open access literature.

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

Liang F, et al. (2025) Utilizing integrated bioinformatics and machine learning approaches to elucidate biomarkers linking sepsis to purine metabolism-associated genes. Scientific reports, 15(1), 353.

Tang Y, et al. (2025) FLT3 is associated with dendritic cell infiltration, tertiary lymphoid structure construction, and predict response to checkpoint inhibitors immunotherapy in solid cancers. Scientific reports, 15(1), 2477.

Li H, et al. (2025) Integrative bioinformatics and machine learning approach unveils potential biomarkers linking coronary atherosclerosis and fatty acid metabolism-associated gene. Journal of cardiothoracic surgery, 20(1), 70.

Lian Z, et al. (2025) Elucidating the expression and role of cGAS in pan-cancer using integrated bioinformatics and experimental approaches. BMC cancer, 25(1), 5.

Li J, et al. (2025) Elucidating the role of FBXW4 in osteoporosis: integrating bioinformatics and machine learning for advanced insight. BMC pharmacology & toxicology, 26(1), 20.

Sun K, et al. (2024) USP30 promotes the progression of breast cancer by stabilising Snail. Cancer gene therapy, 31(3), 472.

Bai Y, et al. (2024) Association analysis of FXYD5 with prognosis and immunological characteristics across pan-cancer. Heliyon, 10(9), e30727.

Wang Y, et al. (2024) Tubulin alpha-1b chain was identified as a prognosis and immune

biomarker in pan-cancer combing with experimental validation in breast cancer. Scientific reports, 14(1), 8201.

Dai F, et al. (2024) PDCD2 as a prognostic biomarker in glioma correlates with malignant phenotype. Genes & diseases, 11(5), 101106.

Soman A, et al. (2024) Decoding early-onset of colorectal cancer: Insights into SERPINA3 expression patterns. Heliyon, 10(22), e40119.

Qiu Z, et al. (2024) Low PPP2R2A expression promotes sensitivity to CHK1 inhibition in high-grade serous ovarian cancer. Theranostics, 14(19), 7450.

Wang DD, et al. (2024) Systematic characterization of the expression, prognosis and immune characteristics of PLOD family genes in breast cancer. Aging, 16(14), 11434.

Shen SH, et al. (2024) The GGCT and REST positive feedback loop promotes tumor growth in Glioma. Translational oncology, 49, 102083.

Guan L, et al. (2024) Pan-cancer analysis of the potential of PEA3 subfamily genes as tumor markers. Scientific reports, 14(1), 31518.

Wu Z, et al. (2024) Bioinformatic validation and machine learning-based exploration of purine metabolism-related gene signatures in the context of immunotherapeutic strategies for nonspecific orbital inflammation. Frontiers in immunology, 15, 1318316.

Bu F, et al. (2024) Unlocking potential biomarkers bridging coronary atherosclerosis and pyrimidine metabolism-associated genes through an integrated bioinformatics and machine learning approach. BMC cardiovascular disorders, 24(1), 148.

Fei Q, et al. (2024) A pan-cancer characterization of immune-related NFIL3 identifies potential predictive biomarker. Journal of Cancer, 15(5), 1271.

Liu R, et al. (2024) Annexin A2 combined with TTK accelerates esophageal cancer progression via the Akt/mTOR signaling pathway. Cell death & disease, 15(4), 291.

Xue X, et al. (2024) Comprehensive analysis of ALG3 in pan-cancer and validation of ALG3 as an onco-immunological biomarker in breast cancer. Aging, 16(3), 2320.

Wu Z, et al. (2024) The roles of IRF8 in nonspecific orbital inflammation: an integrated analysis by bioinformatics and machine learning. Journal of ophthalmic inflammation and infection, 14(1), 29.