

Resource Summary Report

Generated by [NIF](#) on May 25, 2025

oncoPredict

RRID:SCR_023872

Type: Tool

Proper Citation

oncoPredict (RRID:SCR_023872)

Resource Information

URL: <https://CRAN.R-project.org/package=oncoPredict>

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Description: Software tool bridges in vitro drug screening with in vivo drug and biomarker discovery. Predicts in vivo or cancer patient drug response and biomarkers to enrich for response from cell line screening data. Builds model using ridge regression, and enables biomarker discovery by imputing drug response in large cancer molecular datasets. Enables drug specific biomarker identification by correcting for general level of drug sensitivity shared among the population.

Resource Type: data processing software, software resource, data analysis software, software application

Defining Citation: [PMID:34260682](#)

Keywords: drug specific biomarker identification, drug screening, drug and biomarker discovery, cancer molecular datasets, drug response,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: oncoPredict

Resource ID: SCR_023872

Record Creation Time: 20230725T050218+0000

Record Last Update: 20250525T032008+0000

Ratings and Alerts

No rating or validation information has been found for oncoPredict.

No alerts have been found for oncoPredict.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Wei G, et al. (2025) An integrated machine learning framework for developing and validating a prognostic risk model of gastric cancer based on endoplasmic reticulum stress-associated genes. *Biochemistry and biophysics reports*, 41, 101891.

Peng J, et al. (2025) Integrative multi-omics analysis reveals the role of toll-like receptor signaling in pancreatic cancer. *Scientific reports*, 15(1), 52.

Wu M, et al. (2024) Connections Between Endoplasmic Reticulum Stress and Prognosis of Hepatocarcinoma. *Bioengineering (Basel, Switzerland)*, 11(11).

Li H, et al. (2024) Construction and validation of a prognostic signature based on microvascular invasion and immune-related genes in hepatocellular carcinoma. *Scientific reports*, 14(1), 26994.

Li Y, et al. (2024) MFG-E8 promotes M2 polarization of macrophages and is associated with poor prognosis in patients with gastric cancer. *Heliyon*, 10(1), e23917.

Lei C, et al. (2024) Unraveling breast cancer prognosis: a novel model based on coagulation-related genes. *Frontiers in molecular biosciences*, 11, 1394585.

Wang Z, et al. (2024) Characterize molecular signatures and establish a prognostic signature of gastric cancer by integrating single-cell RNA sequencing and bulk RNA sequencing. *Discover oncology*, 15(1), 301.

Li D, et al. (2024) Identification of Clinical Value and Biological Effects of XIRP2 Mutation in Hepatocellular Carcinoma. *Biology*, 13(8).

Ji Q, et al. (2024) Unveiling divergent treatment prognoses in IDHwt-GBM subtypes through multiomics clustering: a swift dual MRI-mRNA model for precise subtype prediction. *Journal of translational medicine*, 22(1), 578.

Wang SY, et al. (2024) Construction of a gene model related to the prognosis of patients with gastric cancer receiving immunotherapy and exploration of COX7A1 gene function. *European journal of medical research*, 29(1), 180.

Wang KL, et al. (2024) Predicting colorectal cancer prognosis based on long noncoding RNAs of disulfidptosis genes. *World journal of clinical oncology*, 15(1), 89.

Li Y, et al. (2024) Identification of prognostic risk model based on plasma cell markers in hepatocellular carcinoma through single-cell sequencing analysis. *Frontiers in genetics*, 15, 1363197.

Cao W, et al. (2024) Predicting the prognosis of glioma patients with TERT promoter mutations and guiding the specific immune profile of immune checkpoint blockade therapy. *Aging*, 16(6), 5618.

Wu X, et al. (2024) Spatiotemporal evolutionary process of osteosarcoma immune microenvironment remodeling and C1QBP-driven drug resistance deciphered through single-cell multi-dimensional analysis. *Bioengineering & translational medicine*, 9(5), e10654.

Linazi G, et al. (2024) Prognostic value of anoikis-related genes revealed using multi-omics analysis and machine learning based on lower-grade glioma features and tumor immune microenvironment. *Heliyon*, 10(17), e36989.

Han L, et al. (2024) Prognostic model based on disulfidptosis-related lncRNAs for predicting survival and therapeutic response in bladder cancer. *Frontiers in immunology*, 15, 1512203.

Li L, et al. (2024) Oxidative stress gene signature construction to identify subtypes and prognosis of patients with lung adenocarcinoma. *Heliyon*, 10(20), e38306.

Liao Z, et al. (2023) Comprehensive analysis of angiogenesis pattern and related immune landscape for individual treatment in osteosarcoma. *NPJ precision oncology*, 7(1), 62.

Wu X, et al. (2023) Spatiotemporal evolution of AML immune microenvironment remodeling and RNF149-driven drug resistance through single-cell multidimensional analysis. *Journal of translational medicine*, 21(1), 760.

Cao W, et al. (2023) An immune signature to predict the prognosis of ATRX-wildtype glioma patients and guide immune checkpoint blockade therapy. *Aging*, 15(19), 10453.