

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

oncoPredict

RRID:SCR_023872

Type: Tool

Proper Citation

oncoPredict (RRID:SCR_023872)

Resource Information

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

Proper Citation: oncoPredict (RRID:SCR_023872)

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 analysis software, data processing software, software application, software resource

Defining Citation: [PMID:34260682](#)

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

Availability: Free, Available for download, Freely available

Resource Name: oncoPredict

Resource ID: SCR_023872

Record Creation Time: 20230725T050218+0000

Record Last Update: 20260903T235930+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 57 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Shao Z, et al. (2026) Development and Validation of an m6A-Derived Prognostic Signature in Lung Adenocarcinoma. *Journal of Cancer*, 17(6), 1134.

Li N, et al. (2026) Exploration of m7G-related immune genes and construction of a prognostic risk model in gastric cancer. *Scientific reports*, 16(1).

Yang L, et al. (2026) A prognostic model utilizing disulfidptosis-related long noncoding RNAs to differentiate pathological grades in hepatocellular carcinoma: functional analysis of AL031985.3. *World journal of surgical oncology*, 24(1).

Li G, et al. (2026) Integrated Proteogenomic Characterization Identifies Breast Cancer Immune Subgroups and Subtype-Specific Therapeutic Strategies. *Research (Washington, D.C.)*, 9, 1271.

Cui H, et al. (2026) The consensus molecular subtypes of esophageal squamous cell carcinoma. *Signal transduction and targeted therapy*, 11(1), 65.

Liu YW, et al. (2026) Integrative Analysis of Glycosylation-Related Genes Reveals Prognostic Subtypes, Immune Evasion, and Therapeutic Vulnerabilities in Lung Adenocarcinoma. *Oncology research*, 34(7), 18.

Liu J, et al. (2026) Single-cell mapping of neutrophil extracellular trap signatures in lung adenocarcinoma reveals immune landscapes, prognostic potential, and therapeutic targets. *Translational oncology*, 64, 102651.

Tao Y, et al. (2026) TENT5A Maintains MYC mRNA Stability to Enhance Osteosarcoma Stemness. *Cancer research*, 86(9), 2161.

Sun W, et al. (2026) Reconstruction of T cell infiltration in an osteosarcoma PDX-organoid interactive biobank for personalized immunotherapy. *Cell reports. Medicine*, 7(3), 102644.

Deng J, et al. (2026) Construction of immune related genes predictive models of elderly rectal cancer patients based on machine learning. *Discover oncology*, 17(1).

Huang HH, et al. (2026) Drug repurposing targeting miRNA-mRNA networks to mitigate areca nut-induced head and neck cancer. *Biomedical journal*, 49(2), 100886.

Chen Y, et al. (2025) SAE1 May Play a Pro-Carcinogenic Role in Pancreatic Adenocarcinoma: A Comprehensive Study Integrating Multiple Pieces of Evidence. *IET systems biology*, 19(1), e70017.

Yijia Z, et al. (2025) Identification of intratumoral microbiome-driven immune modulation and therapeutic implications in diffuse large B-cell lymphoma. *Cancer immunology, immunotherapy* : CII, 74(4), 131.

Shen K, et al. (2025) Bioinformatics-based identification of key genes for Olaparib resistance in breast cancer: prognostic implications and therapeutic relevance. *Discover oncology*, 16(1), 1144.

Li G, et al. (2025) Discovery and validation of proliferative exhausted T cells as a favorable prognostic biomarker in esophageal squamous cell carcinoma. *Scientific reports*, 15(1), 41619.

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.

Xia JQ, et al. (2025) Lactate dehydrogenase a is a crucial biomarker that affects the prognosis, chemotherapy effect, and immune infiltration of breast cancer. *BMC women's health*, 25(1), 497.

Maués JHDS, et al. (2025) Integrated Genomic and Transcriptomic Profiling of Isolated Trisomies in AML Reveals Cell Cycle Dysregulation and Therapeutic Vulnerabilities. *Journal of cellular and molecular medicine*, 29(22), e70941.

Wang W, et al. (2025) Integrated Analysis to Reveal Heterogeneity of Tumor-Associated Neutrophils in Glioma. *Cancer medicine*, 14(5), e70745.

Lin GT, et al. (2025) Combining Apatinib and Oxaliplatin Remodels the Immunosuppressive Tumor Microenvironment and Sensitizes Desert-Type Gastric Cancer to Immunotherapy. *Cancer research*, 85(11), 2117.