# Resource Summary Report

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## 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:** software resource, data processing software, software application, data analysis software

**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:** 20260804T043810+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 44 mentions in open access literature.

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


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.

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.

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.

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

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.

Liu S, et al. (2025) PRMT1-Mediated SWI/SNF Complex Recruitment via SMARCC1 Drives IGF2BP2 Transcription to Enhance Carboplatin Resistance in Head and Neck Squamous Cell Carcinoma. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(22), e2417460.

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.

Mau??s 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.

Zhang J, et al. (2025) Identification of molecular clusters and a risk prognosis model for diffuse large B-cell lymphoma based on lactate metabolism-related genes. Annals of hematology, 104(5), 2847.

Xia L, et al. (2025) Synergistic bioinformatics and sophisticated machine learning unveil ferroptosis-driven regulatory pathways and immunotherapy potential in breast carcinoma. Discover oncology, 16(1), 668.

Zhou S, et al. (2025) PTX3 as a diagnostic and prognostic biomarker in lung adenocarcinoma: a comprehensive analysis. Discover oncology, 16(1), 1158.

Wu X, et al. (2025) Single-cell analysis links DCUN1D5 to immune remodeling and cisplatin resistance in recurrent osteosarcoma. Communications biology, 8(1), 1019.

Ao S, et al. (2025) Identification and validation of an m5C-related lncRNA signature for predicting prognosis and immune response in clear cell renal cell carcinoma. Discover oncology, 16(1), 227.

Fan X, et al. (2025) A novel necroptosis related prognostic signature for skin cutaneous melanoma based on transcriptome and single cell sequencing analysis. Scientific reports, 15(1), 20650.

Zeng XX, et al. (2025) Identification of biomarkers associated with proliferation and differentiation of mesenchymal stem cells in pulmonary adenocarcinoma and establishment of prognostic models. Hereditas, 162(1), 118.

Zhang Z, et al. (2025) Identification of the clinical value and biological effects of TTN mutation in liver cancer. Molecular medicine reports, 31(6).

Wang Y, et al. (2025) Characterization of lactylation-based phenotypes and molecular biomarkers in sepsis-associated acute respiratory distress syndrome. Scientific reports, 15(1), 13831.