

Resource Summary Report

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pRRophetic

RRID:SCR_024417

Type: Tool

Proper Citation

pRRophetic (RRID:SCR_024417)

Resource Information

URL: <https://github.com/paulgeeleher/pRRophetic>

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Description: Software R package for prediction of clinical chemotherapeutic response from tumor gene expression levels. Used to predict phenotypes from gene expression microarray data, gene expression microarray data,

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:25229481](#)

Keywords: clinical chemotherapeutic response prediction, tumor gene expression levels, predict phenotypes,

Funding: U01GM61393 ;
GM089941 ;
CA139278 ;
University of Chicago ;
UL1RR024999

Availability: Free, Available for download, Freely available

Resource Name: pRRophetic

Resource ID: SCR_024417

Record Creation Time: 20230913T050234+0000

Record Last Update: 20260905T133030+0000

Ratings and Alerts

No rating or validation information has been found for pRRophetic.

No alerts have been found for pRRophetic.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Du J, et al. (2026) Novel fatty acid metabolism-related molecular subtyping and prognostic signature for breast cancer. *Translational cancer research*, 15(1), 29.

Liu Y, et al. (2025) The role of TMEM119 in gastric adenocarcinoma and its specific effects on immunity. *The Journal of international medical research*, 53(4), 3000605241306668.

Ling L, et al. (2025) Metabolism-associated marker gene-based predictive model for prognosis, targeted therapy, and immune landscape in ovarian cancer: an integrative analysis of single-cell and bulk RNA sequencing with spatial transcriptomics. *BMC women's health*, 25(1), 233.

Ma Z, et al. (2025) Identification of prognostic biomarker of non-small cell lung cancer based on mitochondrial permeability transition-driven necrosis-related genes and determination of anti-tumor effect of ARL14. *Hereditas*, 162(1), 16.

Ge X, et al. (2025) A Golgi apparatus-related signature for predicting prognosis and evaluating the tumor immune microenvironment of uveal melanoma. *Medicine*, 104(25), e42909.

Ding Z, et al. (2025) A novel signature predicts prognosis in pancreatic cancer based on tumor membrane-associated genes. *Heliyon*, 11(4), e42791.

Zhang H, et al. (2025) UBC9: a novel therapeutic target in papillary thyroid carcinoma. *Journal of endocrinological investigation*, 48(5), 1101.

Ying L, et al. (2025) Predicting immunotherapy prognosis and targeted therapy sensitivity of colon cancer based on a CAF-related molecular signature. *Scientific reports*, 15(1), 6387.

Huang F, et al. (2025) Identification of three subtypes of thyroid cancer based on IFN- γ -related genes to reveal their prognostic characteristics. *Langenbeck's archives of surgery*, 410(1), 69.

Tu B, et al. (2025) A novel cancer-associated membrane signature predicts prognosis and therapeutic response for lung adenocarcinoma. *Scientific reports*, 15(1), 25482.

Sun D, et al. (2025) Construction of T-Cell-Related Prognostic Risk Models and Prediction of Tumor Immune Microenvironment Regulation in Pancreatic Adenocarcinoma via Integrated Analysis of Single-Cell RNA-Seq and Bulk RNA-Seq. *International journal of molecular sciences*, 26(6).

Lei Y, et al. (2025) Disulfidptosis in pediatric AML: a multi-omics approach to risk stratification and potential therapeutic strategy. *Cancer cell international*, 25(1), 199.

Bian T, et al. (2025) Comprehensive analysis indicates DDX46 as a novel biomarker for the prognosis of lung adenocarcinoma. *Oncology letters*, 29(6), 292.

Chen G, et al. (2025) Tumor innervation in cervical cancer: Prognostic insights from myelin-associated risk signatures. *FASEB bioAdvances*, 7(5), e70004.

Qin F, et al. (2025) Analysis of immune cell infiltration in the tumor microenvironment of cervical cancer and its impact on immunotherapy. *Frontiers in oncology*, 15, 1608597.

Su Q, et al. (2025) Mechanistic insights into SLAMF8-mediated prostate cancer metastasis via the TLR4-NF- κ B pathway. *Journal of translational medicine*, 23(1), 1189.

Li MT, et al. (2024) Identification of immune cell-related prognostic genes characterized by a distinct microenvironment in hepatocellular carcinoma. *World journal of clinical oncology*, 15(2), 243.

Bao N, et al. (2024) A scoring model based on bacterial lipopolysaccharide-related genes to predict prognosis in NSCLC. *Frontiers in genetics*, 15, 1408000.

Zhu M, et al. (2024) Predicting lymphoma prognosis using machine learning-based genes associated with lactylation. *Translational oncology*, 49, 102102.

Shi Y, et al. (2024) A prognostic and immune related risk model based on zinc homeostasis in hepatocellular carcinoma. *iScience*, 27(4), 109389.