

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 [PRECISE-TBI](#) .

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.

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

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

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