

Resource Summary Report

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BayesPrism

RRID:SCR_027499

Type: Tool

Proper Citation

BayesPrism (RRID:SCR_027499)

Resource Information

URL: <https://github.com/Danko-Lab/BayesPrism>

Proper Citation: BayesPrism (RRID:SCR_027499)

Description: Software R package for fully Bayesian inference of tumor microenvironment composition and gene expression deconvolution. Used to analyze bulk RNA-seq data and estimate cell type-specific expression profiles.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:35469013](#)

Keywords: tumor microenvironment composition, gene expression deconvolution, analyze bulk RNA-seq data, estimate cell type-specific expression profiles,

Funding: NCI U2C CA288284;
NCI U54 CA209975;
NHGRI R01 HG009309

Availability: Free, Available for download, Freely available

Resource Name: BayesPrism

Resource ID: SCR_027499

Record Creation Time: 20251003T062559+0000

Record Last Update: 20260912T200528+0000

Ratings and Alerts

No rating or validation information has been found for BayesPrism.

No alerts have been found for BayesPrism.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Li M, et al. (2026) Evaluating deconvolution methods using real bulk RNA-expression data for robust prognostic insights across cancer types. *Genome biology*, 27(1), 38.

Li B, et al. (2026) scPER: A Rigorous Computational Approach to Determine Cellular Subtypes in Tumors Aligned With Cancer Phenotypes From Total RNA Sequencing. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(8), e14502.

Dietrich A, et al. (2026) omnideconv: a unifying framework for using and benchmarking single-cell-informed deconvolution of bulk RNA-seq data. *Genome biology*, 27(1), 6.

Roger E, et al. (2026) ATM Deficiency Induces TGF β -Mediated Stromal Programming in Pancreatic Cancer. *Cancer research*, 86(14), 3412.

Huang S, et al. (2025) A Multi-Omics-Based Exploration of the Predictive Role of MSMB in Prostate Cancer Recurrence: A Study Using Bayesian Inverse Convolution and 10 Machine Learning Combinations. *Biomedicines*, 13(2).

Traeuble K, et al. (2025) Integrated single-cell atlas of human atherosclerotic plaques. *Nature communications*, 16(1), 8255.

Sun J, et al. (2025) MOADE: a multimodal autoencoder for dissociating bulk multi-omics data. *Genome biology*, 26(1), 325.

Chen J, et al. (2025) CD146⁺ CAFs mediate immunosuppression in gastric cancer via COL4A1: potential therapeutic targets. *Journal for immunotherapy of cancer*, 13(12).

Peng T, et al. (2025) Single-cell integration analysis reveals molecular signatures of the tumor microenvironment in early-onset colorectal cancer. *NPJ precision oncology*, 9(1), 360.

Zhang Y, et al. (2025) PMAIP1-mediated glucose metabolism and its impact on the tumor microenvironment in breast cancer: Integration of multi-omics analysis and experimental validation. *Translational oncology*, 52, 102267.

Zhao C, et al. (2025) Molecular landscape, subtypes, and therapeutic vulnerabilities of central nervous system solitary fibrous tumors. *Nature communications*, 16(1), 7870.

Huuki-Myers LA, et al. (2025) Benchmark of cellular deconvolution methods using a multi-assay dataset from postmortem human prefrontal cortex. *Genome biology*, 26(1), 88.

Santamaria-Martínez A, et al. (2024) Development of patient-derived lymphomoids with preserved tumor architecture for lymphoma therapy screening. *Nature communications*, 15(1), 10650.

Li L, et al. (2024) Comparative Transcriptomic Analysis Revealing the Potential Mechanisms of Erythritol-Caused Mortality and Oviposition Inhibition in *Drosophila melanogaster*. *International journal of molecular sciences*, 25(7).