

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

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

Availability: Free, Available for download, Freely available

Resource Name: BayesPrism

Resource ID: SCR_027499

Record Creation Time: 20251003T062559+0000

Record Last Update: 20260801T042945+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 8 mentions in open access literature.

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

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.

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.

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

Santamaria-Martinez 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).