

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

PurBayes

RRID:SCR_002068

Type: Tool

Proper Citation

PurBayes (RRID:SCR_002068)

Resource Information

URL: <https://cran.r-project.org/src/contrib/Archive/PurBayes/>

Proper Citation: PurBayes (RRID:SCR_002068)

Description: An MCMC-based algorithm that uses next-generation sequencing data to estimate tumor purity and clonality for paired tumor-normal data.

Synonyms: PurBayes: Bayesian Estimation of Tumor Purity and Clonality

Resource Type: software resource

Defining Citation: [PMID:23749958](#)

Keywords: software package, unix/linux, mac os x, windows, r, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: PurBayes

Resource ID: SCR_002068

Alternate IDs: biotools:purbayes, OMICS_03561

Alternate URLs: <https://bio.tools/purbayes>

Old URLs: <http://cran.r-project.org/web/packages/PurBayes/>

License: GNU General Public License, v2

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260725T190519+0000

Ratings and Alerts

No rating or validation information has been found for PurBayes.

No alerts have been found for PurBayes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Prip F, et al. (2025) Comprehensive genomic characterization of early-stage bladder cancer. *Nature genetics*, 57(1), 115.

Anurag M, et al. (2024) Multiomics profiling of urothelial carcinoma in situ reveals CIS-specific gene signature and immune characteristics. *iScience*, 27(3), 109179.

Revkov E, et al. (2023) PUREE: accurate pan-cancer tumor purity estimation from gene expression data. *Communications biology*, 6(1), 394.

Tang J, et al. (2021) Single-cell exome sequencing reveals multiple subclones in metastatic colorectal carcinoma. *Genome medicine*, 13(1), 148.

Zhu G, et al. (2021) Tissue-specific cell-free DNA degradation quantifies circulating tumor DNA burden. *Nature communications*, 12(1), 2229.

Li X, et al. (2021) Whole-genome sequencing of phenotypically distinct inflammatory breast cancers reveals similar genomic alterations to non-inflammatory breast cancers. *Genome medicine*, 13(1), 70.

Kobayashi H, et al. (2020) Characterization of tumour mutation burden in patients with non-small cell lung cancer and interstitial lung disease. *Respirology (Carlton, Vic.)*, 25(8), 850.

Hatakeyama K, et al. (2019) Mutational burden and signatures in 4000 Japanese cancers provide insights into tumorigenesis and response to therapy. *Cancer science*, 110(8), 2620.

Árnadóttir SS, et al. (2018) Characterization of genetic intratumor heterogeneity in colorectal cancer and matching patient-derived spheroid cultures. *Molecular oncology*, 12(1), 132.

Kohli M, et al. (2015) Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. *PloS one*, 10(12), e0145176.