

# Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

## PurBayes

RRID:SCR\_002068

Type: Tool

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### Proper Citation

PurBayes (RRID:SCR\_002068)

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### 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:** 20260801T190207+0000

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### Ratings and Alerts

No rating or validation information has been found for PurBayes.

No alerts have been found for PurBayes.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

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.