

Resource Summary Report

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FreeBayes

RRID:SCR_010761

Type: Tool

Proper Citation

FreeBayes (RRID:SCR_010761)

Resource Information

URL: <https://github.com/ekg/freebayes>

Proper Citation: FreeBayes (RRID:SCR_010761)

Description: A Bayesian genetic variant detector designed to find small polymorphisms, specifically SNPs, indels, MNPs, and complex events smaller than the length of a short-read sequencing alignment.

Abbreviations: FreeBayes

Resource Type: software resource

Defining Citation: [DOI:arXiv:1207.3907](https://doi.org/10.1101/051102)

Keywords: single-nucleotide polymorphism, indel, insertion, deletion, multi-nucleotide polymorphism, complex event, composite insertion, substitution event, bio.tools

Resource Name: FreeBayes

Resource ID: SCR_010761

Alternate IDs: OMICS_00059, biotools:freebayes

Alternate URLs: <https://bio.tools/freebayes>, <https://sources.debian.org/src/freebayes/>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190415+0000

Ratings and Alerts

No rating or validation information has been found for FreeBayes.

No alerts have been found for FreeBayes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1982 mentions in open access literature.

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

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. *Journal of virology*, 100(1), e0148725.

Niu T, et al. (2026) O⁺Island 28 encodes a type I secretion and RTX adhesion system regulated by RstA and required for early EHEC O157:H7 adherence. *Gut microbes*, 18(1), 2609461.

Clare SJ, et al. (2026) A high-recovery, high-density targeted genotyping platform for cranberry. *The plant genome*, 19(1), e70153.

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of *Candida glabrata* (*Nakaseomyces glabratus*) from across Canada, 2013-2020. *Microbiology spectrum*, 14(1), e0180325.

Khan N, et al. (2025) Human Papillomavirus Integration Induces Oncogenic Host Gene Fusions in Oropharyngeal Cancers. *Cancer discovery*, 15(9), 1927.

Meißner R, et al. (2025) Unraveling genome- and immunome-wide genetic diversity in modern and historical Jaguars. *Genome biology*, 26(1), 415.

Gui C, et al. (2025) The rare hemoglobin variants Hb O-Arab and Hb D-Punjab identified in population-based genetic screening throughout Guangxi, China. *Frontiers in genetics*, 16, 1622391.

Marques CI, et al. (2025) Physiological plasticity in zebra finch color varieties mitigates DNA damage under oxidative stress. *iScience*, 28(7), 112937.

Peng T, et al. (2025) Individualized patient tumor organoids faithfully preserve human brain tumor ecosystems and predict patient response to therapy. *Cell stem cell*, 32(4), 652.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. *GigaScience*, 14.

Ng NKL, et al. (2025) Mechanism of Initial Favorable Response to Decitabine in TP53-Mutated MDS/AML and Potential Mechanisms of Subsequent Relapse. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(14), 3048.

Lee LH, et al. (2025) Defining Non-small Cell Lung Cancer Tumor Microenvironment Changes at Primary and Acquired Immune Checkpoint Inhibitor Resistance Using Clinical and Real-World Data. *Cancer research communications*, 5(6), 1049.

Bayet M, et al. (2025) Modeling the PAX5P80R Mutation Reveals HIF2 α Activation as a Common Feature and Therapeutic Target in B-cell Acute Lymphoblastic Leukemia. *Cancer research*, 85(15), 2820.

Withers HG, et al. (2025) Intratumoral B cell and interferon signatures in newly diagnosed glioblastoma are associated with longer survival in patients treated with SurVaxM. *Cancer immunology, immunotherapy : CII*, 74(11), 332.

Suda K, et al. (2025) Low OLFM1 and BMP6 Expression Predicts Recurrence in Early-Stage Nonsquamous NSCLC with Pure Solid Tumor Appearance. *Cancer research communications*, 5(12), 2186.

Fiorica PN, et al. (2025) Germline Pathogenic DROSHA Variants Are Linked to Pineoblastoma and Wilms Tumor Predisposition. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(8), 1491.

Yang F, et al. (2025) Hierarchical architecture of neo-sex chromosomes and accelerated adaptive evolution in tortricid moths. *Genome research*, 35(1), 66.

Perlmutter JI, et al. (2025) Wolbachia enhances the survival of *Drosophila* infected with fungal pathogens. *BMC biology*, 23(1), 42.

Bergson S, et al. (2025) HMCN1 variants aggravate epidermolysis bullosa simplex phenotype. *The Journal of experimental medicine*, 222(5).

Owens GL, et al. (2025) Shared Selection and Genetic Architecture Drive Strikingly Repeatable Evolution in Long-Term Experimental Hybrid Populations. *Molecular biology and evolution*, 42(1).