

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/10.1101/054122)

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: 20260905T132646+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 2118 mentions in open access literature.

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

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.

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(12), 2413.

Chen J, et al. (2026) A Genomically Tailored Multiagent Precision Medicine Clinical Trial for Adults with Recurrent Glioblastoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1652.

Katko A, et al. (2026) Gene regulatory network determinants of rapid recall in human memory CD4+ T cells. *Cell reports*, 45(4), 117103.

López-Girona E, et al. (2026) Fine-mapping, candidate gene identification, and marker development for the apple scab resistance gene Rvi2. *Journal of experimental botany*, 77(6), 1647.

Xia S, et al. (2026) Genomic prediction in insects: a case study on wing morphology traits in the jewel wasp *Nasonia vitripennis*. *G3 (Bethesda, Md.)*, 16(2).

Nazki S, et al. (2026) Evaluating how infectious bursal disease virus (IBDV) infection influences influenza H3N8 challenge in chickens. *The Journal of general virology*, 107(3).

Manat Y, et al. (2026) Population genomics of *Drosophila pseudoobscura*. *bioRxiv : the preprint server for biology*.

Xu H, et al. (2026) Determinants of pancreatic tropism in metastatic renal cell carcinoma. *JCI insight*, 11(5).

Krishnamachari K, et al. (2026) Improved tumor-only variant calling and mutation burden estimation with VarNet-T. *Nature communications*, 17(1).

Niu T, et al. (2026) O₁₅₇ 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.

Romero-Magaña A, et al. (2026) Pathogenicity of Brucella sp. ST27 Kogia sima Isolates in Murine and Cell Models. Tropical medicine and infectious disease, 11(4).

Castledine M, et al. (2026) Short-term antagonism between bacteriophages and macrophages decreases with bacteria-phage coevolution. The ISME journal, 20(1).

Courcelles M, et al. (2026) Noncanonical Transcription and Splicing Shape the Colorectal Cancer Immunopeptidome in MSI and MSS Tumors. Molecular & cellular proteomics : MCP, 25(6), 101581.

Flores-Saavedra M, et al. (2026) Water stress tolerance, genomic selection and identification of genomic regions in a MAGIC population of eggplant. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(6).

Dlamini N, et al. (2026) Whole-genome sequences of 240 indigenous African cattle from Egypt, Uganda, and South Africa. Scientific data, 13(1).

Zhou H, et al. (2026) One Health genomics reveals niche-specific lineage replacement in Salmonella Enteritidis. National science review, 13(11), nwag275.

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

Qu M, et al. (2026) Impairment of the Uroporphyrinogen Decarboxylase 2 Gene Induces Lesion Mimicry and Downregulates Tetrapyrrole Biosynthesis Pathway Genes in Rice. Rice (New York, N.Y.), 19(1).