

Resource Summary Report

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BWA

RRID:SCR_010910

Type: Tool

Proper Citation

BWA (RRID:SCR_010910)

Resource Information

URL: <http://bio-bwa.sourceforge.net/>

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Description: Software for aligning sequencing reads against large reference genome. Consists of three algorithms: BWA-backtrack, BWA-SW and BWA-MEM. First for sequence reads up to 100bp, and other two for longer sequences ranged from 70bp to 1Mbps.

Abbreviations: BWA

Synonyms: Burrows-Wheeler Aligner (BWA), Burrows-Wheeler Aligner

Resource Type: software resource, data processing software, sequence analysis software, alignment software, software application, data analysis software, image analysis software

Defining Citation: [PMID:19451168](#), [PMID:20080505](#), [DOI:10.1093/bioinformatics/btp324](#)

Keywords: sequence, alignment, reference, genome, human, short, long, read, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: BWA

Resource ID: SCR_010910

Alternate IDs: SCR_015853, biotools:bwa-sw, OMICS_00654

Alternate URLs: <https://sourceforge.net/projects/bio-bwa/files/>, <https://bio.tools/bwa-sw>, <https://sources.debian.org/src/bwa/>

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Record Creation Time: 20220129T080301+0000

Record Last Update: 20260803T040554+0000

Ratings and Alerts

No rating or validation information has been found for BWA.

No alerts have been found for BWA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2291 mentions in open access literature.

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

Browne IM, et al. (2026) The Prognostic and Predictive Impact of ctDNA Levels in Patients with Advanced Breast Cancer Enrolled on the plasmaMATCH Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(1), 148.

Chang LJ, et al. (2026) Assessment of Circulating Tumor DNA for Early Detection of Hepatocellular Carcinoma in Alpha-Fetoprotein-Negative Patients With Cirrhotic Nodules. JGH open : an open access journal of gastroenterology and hepatology, 10(1), e70331.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal Anaerostipes. Poultry science, 105(3), 106388.

Barajas JM, et al. (2026) Tandem Duplications in UBTF Create XPO1-Dependent Nuclear Export Signals that Reveal a Leukemic Therapeutic Dependency. Blood cancer discovery, 7(1), 51.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. EBioMedicine, 123, 106111.

Halim S, et al. (2026) Dominant-negative TP53 mutations potentiated by the HSF1-regulated proteostasis network. Molecular cell.

Morrissey RL, et al. (2026) Elucidating cooperative genetic events in DCIS progression in mutant p53-driven breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 123(2), e2526544123.

Chen Z, et al. (2025) Conditional lethality and suppressor analysis of plasmid-based temperature-sensitive fabZ expression in Pseudomonas aeruginosa. The Journal of biological chemistry, 301(6), 108553.

- Wolf M, et al. (2025) Ocean-Wide Conservation Genomics of Blue Whales Suggest New Northern Hemisphere Subspecies. *Molecular ecology*, 34(2), e17619.
- Bayam E, et al. (2025) Bi-allelic variants in WDR47 cause a complex neurodevelopmental syndrome. *EMBO molecular medicine*, 17(1), 129.
- Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.
- Wu Y, et al. (2025) Myocardial dysfunction caused by MyBPC3 P459fs mutation in hypertrophic cardiomyopathy: evidence from multi-omics approaches and super-resolution imaging. *Frontiers in cardiovascular medicine*, 12, 1529921.
- Pereira R, et al. (2025) The Spectrum of IDH- and H3-Wildtype High-Grade Glioma Subgroups Occurring across Teenage and Young Adult Patient Populations. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(15), 3259.
- Yang R, et al. (2025) Perturbations in the microbiota-gut-brain axis shaped by social status loss. *Communications biology*, 8(1), 401.
- Li Y, et al. (2025) Single-Cell Transcriptomic Landscape Deciphers Intratumoral Heterogeneity and Subtypes of Acral and Mucosal Melanomas. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(12), 2495.
- Proaño-Pérez E, et al. (2025) MITF regulates autophagy and extracellular vesicle cargo in gastrointestinal stromal tumors. *Molecular biomedicine*, 6(1), 92.
- Song Z, et al. (2025) Noncanonical target-strand cytosine base editing via engineered Un1Cas12f1 platform. *Nature communications*, 16(1), 9499.
- Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.
- Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.
- Yin HY, et al. (2025) CFAP300 loss-of-function variant causes primary ciliary dyskinesia and male infertility via disrupting sperm flagellar assembly and acrosome formation. *Asian journal of andrology*, 27(6), 743.