

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/>

Proper Citation: BWA (RRID:SCR_010910)

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 1Mbp.

Abbreviations: BWA

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

Resource Type: sequence analysis software, data analysis software, image analysis software, software resource, software application, data processing software, alignment 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: 20260728T043350+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 [nidm-terms](#) .

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.

Bando H, et al. (2025) Atezolizumab following definitive chemoradiotherapy in patients with unresectable locally advanced esophageal squamous cell carcinoma - a multicenter phase 2 trial (EPOC1802). Nature cancer, 6(3), 445.

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.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. *GigaScience*, 14.

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.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. *Cell genomics*, 5(3), 100775.

Yang R, et al. (2025) Perturbations in the microbiota-gut-brain axis shaped by social status loss. *Communications biology*, 8(1), 401.

Zhou Y, et al. (2025) Chromosome-level echidna genome illuminates evolution of multiple sex chromosome system in monotremes. *GigaScience*, 14.

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.

Li Z, et al. (2025) Phased high-quality genome of the gymnosperm Himalayan Yew assists in paclitaxel pathway exploration. *GigaScience*, 14.

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.

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.