

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 1Mbp.

Abbreviations: BWA

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

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

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: 20260905T132650+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 2638 mentions in open access literature.

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

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

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.

Kim N, et al. (2026) Performance Evaluation of Whole-Genome Amplification Platforms for Clinical Next-Generation Sequencing with Minimal Nucleic Acid Input. *Annals of laboratory medicine*, 46(4), 476.

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. *Cancer discovery*, 16(3), 497.

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.

Ma R, et al. (2026) Metagenomic next-generation sequencing for efficient detection of human parvovirus B19 in amniotic fluid: a case study of diagnosis and prenatal management of fetal infection. *BMC pregnancy and childbirth*, 26(1).

Conte B, et al. (2026) Pembrolizumab and Paclitaxel in Patients with HR+/HER2- Breast Cancer with HER2-Enriched or Basal-like Subtypes. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(7), 1246.

Naseem M, et al. (2026) Rapid Identification of Candidate SNPs and QTLs for *Capsicum annum* Chili Fruit Size and Capsaicin Content Using ddRAD-Sequencing and Bulk

Segregant Analysis. Current issues in molecular biology, 48(2).

Dai X, et al. (2026) Insights into antibiotic resistomes from gut metagenome-assembled genomes of the free-range pigs. Microbiology spectrum, 14(4), e0240725.

Ye H, et al. (2026) Early risperidone exposure impairs cognitive function by perturbation of the gut microbiome and bile acids/tyrosine-PTP1B axis. Microbiome, 14(1).

Mao K, et al. (2026) Rumen microbiota-associated stress alleviation by creatine pyruvate in newly received cattle: a multi-omics study. Microbiome, 14(1).

Huang Q, et al. (2026) Heat stress suppresses lactation through potential rumen-mammary communication mediated by extracellular vesicles: integrated analysis of microbiome, metabolome, and miRNA profiles. Microbiome, 14(1).

Guo J, et al. (2026) Metagenomics reveals gut microbial differences and ecological adaptation in plateau zokor (*Eospalax baileyi*) populations. BMC microbiology, 26(1).

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. Cancer research communications, 6(5), 1020.

Chen H, et al. (2026) Novel dual regulatory roles of RpoA in quorum sensing regulation and social behavior switching in *Pseudomonas aeruginosa*. mBio, 17(5), e0003226.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. GigaScience, 15.

Al Smadi MA, et al. (2026) Genetic alterations in poor-quality individually selected sperm highlight candidate biomarkers for male subfertility. Scientific reports, 16(1).

Huang Y, et al. (2026) Phage succession and putative mechanisms of microbial community regulation in Sichuan radish paocai (traditional Chinese fermented vegetable). Food chemistry: X, 36, 103997.

Gui Q, et al. (2026) RET fusion partners dictate oncogenic potential in undifferentiated spindle cell sarcomas. Cancer biology & therapy, 27(1), 2683190.

Li Y, et al. (2026) A novel prognostic biomarker combining TP53 loss-of-function and amplification of different combinations of nine genes in lung squamous cell carcinoma treated with chemotherapy. Oncology letters, 32(1), 289.