Resource Summary Report

Generated by NIF on May 16, 2025

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

Defining Citation: PMID:19451168, PMID:20080505, DOI:10.1093/bioinformatics/btp324

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

Funding:

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: 20250516T053952+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 2095 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

Ji N, et al. (2025) Binding of zebrafish lipovitellin and L1?ORF2 increases the accessibility of L1?ORF2 via interference with histone wrapping. International journal of molecular medicine, 55(1).

Funasaki S, et al. (2025) Protocol for transcriptomic and epigenomic analyses of tip-like endothelial cells using scRNA-seq and ChIP-seq. STAR protocols, 6(1), 103326.

Liu M, et al. (2025) Sex disparities in the association between rare earth elements exposure and genetic mutation frequencies in lung cancer patients. Scientific reports, 15(1), 2185.

Fan X, et al. (2025) Genotype-phenotype correlations for 17 Chinese families with inherited retinal dystrophies due to homozygous variants. Scientific reports, 15(1), 3043.

Kubota T, et al. (2025) Hydrops fetalis due to loss of function of hNav1.4 channel via

compound heterozygous variants. Journal of human genetics, 70(1), 3.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. Molecular cell, 85(1), 24.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, Protosalanx chinensis. GigaScience, 14.

Felicelli C, et al. (2025) Genomic characterization and histologic analysis of uterine leiomyosarcoma arising from leiomyoma with bizarre nuclei. The Journal of pathology, 265(2), 211.

Xie H, et al. (2025) Application of metagenomic next-generation sequencing (mNGS) to describe the microbial characteristics of diabetic foot ulcers at a tertiary medical center in South China. BMC endocrine disorders, 25(1), 18.

Skystad Kvernebo M, et al. (2025) Genetic Variants in the SCN9A Gene are Detected in a Minority of Erythromelalgia Patients. Acta dermato-venereologica, 105, adv42022.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant Stylosanthes angustifolia: insights into genome evolution and drought adaptation. GigaScience, 14.

Zeng J, et al. (2025) Protocol for genetic analysis of population-scale ultra-low-depth sequencing data. STAR protocols, 6(1), 103579.

Rekhtman N, et al. (2025) Chromothripsis-Mediated Small Cell Lung Carcinoma. Cancer discovery, 15(1), 83.

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Liu Y, et al. (2025) Reference genome provide insights into sex determination of silver aworana (Osteoglossum bicirrhosum). BMC biology, 23(1), 29.

Allman A, et al. (2025) Splenic fibroblasts control marginal zone B cell movement and function via two distinct Notch2-dependent regulatory programs. Immunity, 58(1), 143.