# **Resource Summary Report**

Generated by NIF on Apr 29, 2025

# **BWA-MEM2**

RRID:SCR\_022192

Type: Tool

### **Proper Citation**

BWA-MEM2 (RRID:SCR\_022192)

#### **Resource Information**

URL: https://github.com/bwa-mem2/bwa-mem2

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**Description:** Software tool for sequence mapping. The next version of BWA-MEM. Used for

aligning sequencing reads against large reference genome.

Synonyms: BWA-MEM

Resource Type: data processing software, sequence analysis software, data analysis

software, software resource, software application

Defining Citation: DOI:10.1109/IPDPS.2019.00041

**Keywords:** Intel Corporation, sequence mapping, aligning sequencing reads, large

reference genome, Burrows-Wheeler Aligner,

**Funding:** 

Availability: Free, Available for download, Freely available

Resource Name: BWA-MEM2

Resource ID: SCR 022192

License: MIT License

**Record Creation Time:** 20220427T191217+0000

Record Last Update: 20250429T060141+0000

### **Ratings and Alerts**

No rating or validation information has been found for BWA-MEM2.

No alerts have been found for BWA-MEM2.

#### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 3853 mentions in open access literature.

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

Tan Q, et al. (2025) Microbiological aspects and clinical impact of lower lung field tuberculosis: An observational cohort study in Peru. International journal of infectious diseases: IJID: official publication of the International Society for Infectious Diseases, 150, 107284.

Pegoraro FB, et al. (2025) Application of Principal Component Analysis as a Prediction Model for Feline Sporotrichosis. Veterinary sciences, 12(1).

Del Olmo V, et al. (2025) Insights into the origin, hybridisation and adaptation of Candida metapsilosis hybrid pathogens. PLoS pathogens, 21(1), e1012864.

Schwarz JM, et al. (2025) Somatic DNA Variants in Epilepsy Surgery Brain Samples from Patients with Lesional Epilepsy. International journal of molecular sciences, 26(2).

Subramanian DN, et al. (2025) Assessment of candidate high-grade serous ovarian carcinoma predisposition genes through integrated germline and tumour sequencing. NPJ genomic medicine, 10(1), 1.

Paulo DF, et al. (2025) Functional genomics implicates ebony in the black pupae phenotype of tephritid fruit flies. Communications biology, 8(1), 60.

Tavallaee G, et al. (2025) Mapping the 3D genome architecture. Computational and structural biotechnology journal, 27, 89.

Fu M, et al. (2025) The Role of de novo and Ultra-Rare Variants in Hirschsprung Disease (HSCR): Extended Gene Discovery for Risk Profiling of Patients. medRxiv: the preprint server for health sciences.

Jiang X, et al. (2025) The whole-genome dissection of root system architecture provides new insights for the genetic improvement of alfalfa (Medicago sativa L.). Horticulture research, 12(1), uhae271.

Manullang C, et al. (2025) Slight thermal stress exerts genetic diversity selection at coral (Acropora digitifera) larval stages. BMC genomics, 26(1), 36.

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.

Zhang X, et al. (2025) Prevalence of Transcription Factor 4 Gene Triplet Repeat Expansion Associated with Fuchs' Endothelial Corneal Dystrophy in the United States and Global Populations. Ophthalmology science, 5(1), 100611.

Ren Q, et al. (2025) Clinical features and search for genetic determinants of postprandial hypoglycaemia. Endocrine connections, 14(1).

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.

Zhao Q, et al. (2025) Near telomere-to-telomere genome assemblies of Silkie Gallus gallus and Mallard Anas platyrhynchos restored the structure of chromosomes and "missing" genes in birds. Journal of animal science and biotechnology, 16(1), 9.

Ni M, et al. (2025) Epigenetic phase variation in the gut microbiome enhances bacterial adaptation. bioRxiv: the preprint server for biology.

Liu P, et al. (2025) Long-read sequencing revealed complex biallelic pentanucleotide repeat expansions in RFC1-related Parkinson's disease. NPJ Parkinson's disease, 11(1), 21.

Wang L, et al. (2025) Novel loci for triglyceride/HDL-C ratio longitudinal change among subjects without T2D. Journal of lipid research, 66(1), 100702.

Chen YC, et al. (2025) Multiomics Analysis Reveals Molecular Changes during Early Progression of Precancerous Lesions to Lung Adenocarcinoma in Never-Smokers. Cancer research, 85(3), 602.

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: Phoxinus phoxinus) provide evidence of haplotype diversity. GigaScience, 14.