

Resource Summary Report

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BWA-MEM2

RRID:SCR_022192

Type: Tool

Proper Citation

BWA-MEM2 (RRID:SCR_022192)

Resource Information

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

Proper Citation: BWA-MEM2 (RRID:SCR_022192)

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 analysis software, software application, software resource, sequence analysis software, data processing software

Defining Citation: [DOI:10.1109/IPDPS.2019.00041](https://doi.org/10.1109/IPDPS.2019.00041)

Keywords: Intel Corporation, sequence mapping, aligning sequencing reads, large reference genome, Burrows-Wheeler Aligner,

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: 20260801T042848+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 4822 mentions in open access literature.

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

Vlachos G, et al. (2026) Functional footprints of homologous recombination deficiency in prostate cancer revealed by ctDNA fragmentation and transcription factor accessibility. British journal of cancer.

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. Journal of virology, 100(1), e0148725.

Jarrell AF, et al. (2026) Building genomic resources to facilitate the study and use of *Solanum microdontum*, a wild relative of cultivated potato. G3 (Bethesda, Md.), 16(1).

Lim KHJ, et al. (2026) Cross-presentation of dead cell-associated antigens shapes the neoantigenic landscape of tumor immunity. Nature immunology, 27(1), 72.

Johns J, et al. (2026) A near chromosome-level assembly of the serpentine endemic columbine, *Aquilegia eximia*. The Journal of heredity, 117(1), 85.

Richmond JQ, et al. (2026) A chromosome-level reference genome assembly for Gilbert's skink *Plestiodon gilberti*. The Journal of heredity, 117(1), 115.

Carlson BJ, et al. (2026) A reference genome assembly for the pink volcano barnacle, *Tetraclita rubescens*, Nilsson-Cantell, 1931. The Journal of heredity, 117(1), 173.

Gazzah A, et al. (2026) Biomarker analysis from a Phase 1/1b study of tusamitamab ravtansine in patients with advanced non-small cell lung cancer. Translational oncology, 63, 102615.

Kim CY, et al. (2026) Integrative multi-omics of matched primary and liver metastatic colorectal cancer organoids identifies putative molecular targets. Translational oncology, 63, 102592.

Yuan ML, et al. (2026) Demographic expansion and panmixia in a St. Martin endemic, *Anolis pogus*, coincides with the decline of a competitor. The Journal of heredity, 117(1), 1.

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.

James DQ, et al. (2026) Optimized ChIP-exo for mammalian cells and patterned sequencing flow cells. G3 (Bethesda, Md.), 16(1).

Han P, et al. (2025) Extrachromosomal circular miRNA-gene amplifications contribute to the renal cancer phenotype. *Cell reports*, 44(12), 116660.

Laplante P, et al. (2025) Effect of MisMatch repair deficiency on metastasis occurrence in a syngeneic mouse model. *Neoplasia (New York, N.Y.)*, 62, 101145.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. *Cancer discovery*, 15(4), 717.

Mirahmadi M, et al. (2025) Genetic Heterogeneity of Autism Spectrum Disorder: Identification of Five Novel Mutations (RIMS2, FOXG1, AUTS2, ZCCHC17, and SPTBN5) in Iranian Families via Whole-Exome and Whole-Genome Sequencing. *Biochemical genetics*.

Garsmeur O, et al. (2025) The genomic footprints of wild *Saccharum* species trace domestication, diversification, and modern breeding of sugarcane. *Cell*, 188(25), 7252.

Li YR, et al. (2025) Long-Term Latency of Highly Mutated Cells in Normal Mouse Skin Is Reversed by Exposure to Tumor Promoters and Chronic Tissue Damage. *Cancer discovery*, 15(6), 1115.

Xu X, et al. (2025) Genomic Analyses Reveal the Evolving Characteristics of Intestinal Metaplasia and Gastric Cancer. *Cancer research*, 85(16), 3123.

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).