

Resource Summary Report

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Minimap2

RRID:SCR_018550

Type: Tool

Proper Citation

Minimap2 (RRID:SCR_018550)

Resource Information

URL: <https://github.com/lh3/minimap2>

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Description: Software tool as pairwise alignment for nucleotide sequences. Alignment program to map DNA or long mRNA sequences against large reference database. Versatile pairwise aligner for genomic and spliced nucleotide sequences.

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

Defining Citation: [PMID:29750242](#)

Keywords: Pairwise alignment, nucleotide sequence, map DNA sequence, map mRNA sequence, reference database, spliced nucleotide sequence, bio.tools, FASEB list

Funding: NHGRI R01 HG010040

Availability: Free, Available for download, Freely available

Resource Name: Minimap2

Resource ID: SCR_018550

Alternate IDs: OMICS_31658, biotools:minimap2

Alternate URLs: <https://bio.tools/minimap2>, <https://sources.debian.org/src/libminimap2-dev/>

License: MIT License

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260829T182547+0000

Ratings and Alerts

No rating or validation information has been found for Minimap2.

No alerts have been found for Minimap2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1593 mentions in open access literature.

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

Sahoo RK, et al. (2026) Genome assembly and protein structure modeling reveal key molecular features of divergent wmk homologs in Wolbachia. Microbiology spectrum, 14(2), e0289325.

Mackey AI, et al. (2026) Temperature and genetic background drive mobilization of diverse transposable elements in a global human fungal pathogen. PLoS genetics, 22(1), e1011979.

Sedaghatkish A, et al. (2026) A contamination-reduced genome of Plasmodiophora brassicae with comprehensive functional annotation. BMC microbiology, 26(1), 118.

Zhuang Z, et al. (2026) A new integrated genetic and transcriptomic approach for investigating DUX4 and DUX4C. Journal of human genetics, 71(6), 373.

Hawkins JP, et al. (2026) Isolation and phylogenomic characterization of two novel, dissimilar orthoreoviruses from Northern Alaskan Sea otters (*Enhydra lutris kenyoni*). Scientific reports, 16(1), 3511.

Emerling CA, et al. (2026) Pseudogenes document protracted parallel regression of oral anatomy in myrmecophagous mammals. Molecular biology and evolution, 43(2).

Xue J, et al. (2026) Germline de novo mutation rate of the highly heterozygous amphioxus genome. Molecular biology and evolution, 43(2).

Zhang J, et al. (2026) A Set of Novel Venom Proteins Enables Parasitoid Wasps to Exploit Older Hosts and Coexist with Competitors. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(4), e12654.

Lizcano-Salas AF, et al. (2026) First genome assemblies of Neotropical Thoracobombus bumblebees *Bombus pauloensis* and *Bombus pullatus*. G3 (Bethesda, Md.), 16(3).

Stopa V, et al. (2026) Direct RNA sequencing identified solute carrier family 2 member 1 to improve neurological outcome prediction after cardiac arrest. Intensive care medicine experimental, 14(1), 3.

Tulloch AJ, et al. (2026) Massively parallel reporter assay for mapping gene-specific regulatory regions at single-nucleotide resolution. *eLife*, 14.

Schulz K, et al. (2026) African swine fever outbreaks in German pig holdings - experiences, epidemiological considerations and genome sequences. *Scientific reports*, 16(1), 4350.

Tao Y, et al. (2026) TENT5A Maintains MYC mRNA Stability to Enhance Osteosarcoma Stemness. *Cancer research*, 86(9), 2161.

Zhou C, et al. (2026) Chromosome-level genome assembly of the deep-sea solemyid bivalve *Acharax haimaensis*. *Scientific data*, 13(1).

Liang S, et al. (2026) Full-length haplotype reconstruction of CD36 by long-read sequencing: uncovers a novel structural variant. *BMC genomics*, 27(1).

Bourke BP, et al. (2026) Diverse novel and avian-associated viruses in the ileal viromes of Northern Mockingbird (*Mimus polyglottos*). *Archives of virology*, 171(4).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Washaya T, et al. (2026) Leveraging the Oxford Nanopore MinION sequencing platform for HIV-1 drug resistance surveillance in resource-limited settings: a post-COVID implementation opportunity. *Virology journal*, 23(1).

Thygesen VFDF, et al. (2026) The genomic history of *Streptococcus mutans* from the Mesolithic until modern times. *Genome biology*, 27(1).

Guo A, et al. (2026) Impaired bone matrix turnover with selective small bone fragility in a child with TENT5A-associated osteogenesis imperfecta. *JBMR plus*, 10(4), ziag029.