

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: 20260912T195902+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 [SPARC SAWG](#) .

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

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

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.

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

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.

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).

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.

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

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.

Mao X, et al. (2026) Sex chromosome evolution mediated by a large inversion and a possible switch of the sex determination gene. *Genome biology*, 27(1).

Susanto FA, et al. (2026) Cyanoglobule lipid droplet accumulation as a stress response to nitrogen starvation in a non-N₂-fixing mutant strain of *Anabaena* sp. PCC 7120. *PloS one*, 21(2), e0343220.

Ramirez AL, et al. (2026) Metagenomic analysis of the human gut virome reveals functional signatures and viral stability across hospitalized and non-hospitalized diarrheal and non-diarrheal individuals. *Gut pathogens*, 18(1).

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).

Xu B, et al. (2026) The Mitochondrial Genome of *Curcuma longa*: A Large and Structurally Complex Genome with Extensive Intracellular DNA Transfer. *Genes*, 17(2).

Zhao Z, et al. (2026) Evolutionary and Modification Features of Two Monkeypox Virus Strains: Insights from Integrated Genomic and Epigenomic Analyses. *Viruses*, 18(2).

Wang Y, et al. (2026) A chromosome level genome, as well as transcriptomes and metabolomes, insights into genome evolution and the biosynthesis of kaempferol and kaempferol derivatives in *Impatiens balsamina* (Balsaminaceae). *Frontiers in plant science*, 17, 1725789.

Debler JW, et al. (2026) Comparative genome analysis identifies necrosis-inducing effectors in the lentil pathogen *Ascochyta lentis* in isolates with distinct virulence profiles. *BMC genomics*, 27(1).