

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

## Minimap2

RRID:SCR\_018550

Type: Tool

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### Proper Citation

Minimap2 (RRID:SCR\_018550)

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### Resource Information

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

**Proper Citation:** Minimap2 (RRID:SCR\_018550)

**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:** 20260905T132838+0000

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## Ratings and Alerts

No rating or validation information has been found for Minimap2.

No alerts have been found for Minimap2.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1593 mentions in open access literature.

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

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-N<sub>2</sub>-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).