

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

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: 20260803T040758+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 1325 mentions in open access literature.

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

Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3* (Bethesda, Md.), 16(1).

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Jeon JY, et al. (2026) Short-Read Pangenomes and Their Potential Utility in Population and Conservation Genomics. *Molecular ecology resources*, 26(1), e70060.

Schneberg Y, et al. (2025) Three Novel Spider Genomes Unveil Spidroin Diversification and Hox Cluster Architecture: *Ryuthela nishihirai* (Liphistiidae), *Uloborus plumipes* (Uloboridae) and *Cheiracanthium punctorium* (Cheiracanthiidae). *Molecular ecology resources*, 25(1), e14038.

Dong Z, et al. (2025) Chromosome-level genome sequencing and assembly of the parasitoid wasp *Leptopilina myrica*. *Scientific data*, 12(1), 235.

Fu Y, et al. (2025) Evidence for evolution of a new sex chromosome within the haploid-dominant Marchantiales plant lineage. *Journal of integrative plant biology*, 67(6), 1533.

Bangratz M, et al. (2025) Deciphering mixed infections by plant RNA virus and reconstructing complete genomes simultaneously present within-host. *PloS one*, 20(1), e0311555.

Mormile BW, et al. (2025) Activation of three targets by a TAL effector confers susceptibility to bacterial blight of cotton. *Nature communications*, 16(1), 644.

Landis JB, et al. (2025) Reference genome of *Calochortus tolmiei* Hook. & Arn. (Liliaceae), a cat's ear mariposa lily. *G3* (Bethesda, Md.), 15(3).

Cheng L, et al. (2025) Leveraging a phased pangenome for haplotype design of hybrid potato. *Nature*, 640(8058), 408.

Sargent DJ, et al. (2025) A CACTA-like transposon in the Anthocyanidin synthase 1 (Ans-1) gene is responsible for apricot fruit colour in the raspberry (*Rubus idaeus*) cultivar 'Varnes'. *PloS one*, 20(2), e0318692.

Hunt JMT, et al. (2025) Enhanced HDR-mediated correction of heterozygous COL7A1 mutations for recessive dystrophic epidermolysis bullosa. *Molecular therapy. Nucleic acids*, 36(1), 102472.

Yong Y, et al. (2025) The organelle genomes of the endangered seagrass *Zostera caespitosa* reveal sequence divergences, massive gene transfer, and uncommon RNA editing types. *Frontiers in plant science*, 16, 1550467.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Yu S, et al. (2025) Nanopore sequencing for precise detection of *Mycobacterium tuberculosis* and drug resistance: a retrospective multicenter study in China. *Journal of clinical microbiology*, 63(4), e0181324.

Sun M, et al. (2025) The Genomic Characteristics of Potential Probiotics: Two *Streptococcus salivarius* Isolates from a Healthy Individual in China. *Microorganisms*, 13(3).

Bird E, et al. (2025) BALROG-MON: a high-throughput pipeline for Bacterial Antimicrobial Resistance annotation of Genomes-Metagenomic Oxford Nanopore. *microPublication biology*, 2025.

Dotto-Maurel A, et al. (2025) Evaluation of long-read sequencing for Ostreid herpesvirus type 1 genome characterization from *Magallana gigas* infected tissues. *Microbiology spectrum*, 13(3), e0208224.

Hart LN, et al. (2025) Metagenomics reveals spatial variation in cyanobacterial composition, function, and biosynthetic potential in the Winam Gulf, Lake Victoria, Kenya. *Applied and environmental microbiology*, 91(2), e0150724.

Mariz J, et al. (2025) Exploring Environmental Microfungal Diversity Through Serial Single Cell Screening. *Molecular ecology resources*, 25(3), e14055.