

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: image analysis software, alignment software, software application, software resource, data processing 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: 20260801T190621+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 [RRID](#) .

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.

Tulloch AJ, et al. (2025) Massively parallel reporter assay for mapping gene-specific regulatory regions at single nucleotide resolution. *bioRxiv : the preprint server for biology*.

Davison NJ, et al. (2025) The genome sequence of long-finned pilot whale, *Globicephala melas* (Traill, 1809). *Wellcome open research*, 10, 180.

Fanari O, et al. (2025) Pseudouridine reprogramming in the human T-cell epitranscriptome: from primary to immortalized states. *RNA* (New York, N.Y.), 31(9), 1320.

Zhang R, et al. (2025) Chromosome-level genome assembly of an Arctic fish species pale eelpout (*Lycodes pallidus*). *Scientific data*, 12(1), 1187.

Dong Z, et al. (2025) A rare, evolutionarily conserved venom protein benefits endoparasitism across parasitoids. *Cell genomics*, 5(8), 100920.

Clot CR, et al. (2025) Resolving a century-old enigma: potato 'Bolters' originate from instability of the *StCDF1.3* allele. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(10), 245.

Liang Y, et al. (2025) Splicing-dependent restriction of the HBZ gene by Tax underlies biphasic HTLV-1 infection. *PLoS pathogens*, 21(7), e1013381.

Li X, et al. (2025) Mitochondrial genome of *Quercus chenii*: genomic features and evolutionary implications. *BMC genomics*, 26(1), 701.

Ahn A, et al. (2025) Impact of Acute Endurance Exercise on Alternative Splicing in Skeletal Muscle. *FASEB bioAdvances*, 7(8), e70024.

Belchikov N, et al. (2025) A single-cell, long-read, isoform-resolved case-control study of FTD reveals cell-type-specific and broad splicing dysregulation in human brain. *Cell reports*, 44(9), 116198.

El Zowalaty ME, et al. (2025) Discovery, phylogenetic, and comparative genomic analysis of novel avian gammacoronaviruses identified in feral pigeons (*Columba livia domestica*). *Journal of virology*, 99(9), e0111225.

Bogaerts B, et al. (2025) Oxford Nanopore Technologies R10 sequencing enables accurate cgMLST-based bacterial outbreak investigation of *Neisseria meningitidis* and *Salmonella enterica* when accounting for methylation-related errors. *Journal of clinical microbiology*, 63(10), e0041025.

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

Boyes D, et al. (2025) The genome sequence of the Large Birch Bell moth, Large Birch Roller, *Epinotia brunnichana* (Linnaeus, 1767). *Wellcome open research*, 10, 101.

Grubben J, et al. (2025) CRISPR/Cas9-induced breaks are insufficient to break linkage drag surrounding the ToMV locus of *Solanum lycopersicum*. *G3 (Bethesda, Md.)*, 15(6).

Chen Z, et al. (2025) Biases from Oxford Nanopore library preparation kits and their effects on microbiome and genome analysis. *BMC genomics*, 26(1), 504.

Wang LY, et al. (2025) A chromosomal-level genome assembly of *Araneus marmoreus* Schenkel, 1953 (Araneae: Araneidae). *Scientific data*, 12(1), 859.