

Resource Summary Report

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Ngmlr

RRID:SCR_017620

Type: Tool

Proper Citation

Ngmlr (RRID:SCR_017620)

Resource Information

URL: <https://github.com/philres/ngmlr>

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Description: Software tool as long read mapper designed to align PacBio or Oxford Nanopore reads to reference genome and optimized for structural variation detection.

Abbreviations: NGMLR

Synonyms: coNvex Gap-cost alignMent for Long Reads

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

Defining Citation: [PMID:29713083](#)

Keywords: Long, read, mapper, align, PacBio, Oxford Nanopore, read, reference, genome, structural, variantion, detection, bio.tools

Funding: National Science Foundation ;
NHGRI R01 HG006677;
NHGRI UM1 HG008898

Availability: Free, Available for download, Freely available

Resource Name: Ngmlr

Resource ID: SCR_017620

Alternate IDs: biotools:ngmlr

Alternate URLs: <https://bio.tools/ngmlr>

License: MIT License

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260801T190551+0000

Ratings and Alerts

No rating or validation information has been found for Ngmlr.

No alerts have been found for Ngmlr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Parida P, et al. (2025) Precise identification of viral-host integration events in HPV-positive cervical cancers by targeted long-read sequencing. *Tumour virus research*, 20, 200325.

Su X, et al. (2025) The promising role of nanopore sequencing in cancer diagnostics and treatment. *Cell insight*, 4(2), 100229.

Liang X, et al. (2024) Genome comparisons reveal accessory genes crucial for the evolution of apple Glomerella leaf spot pathogenicity in Colletotrichum fungi. *Molecular plant pathology*, 25(4), e13454.

Low EL, et al. (2024) Chromosome-scale Elaeis guineensis and E. oleifera assemblies: comparative genomics of oil palm and other Arecaceae. *G3 (Bethesda, Md.)*, 14(9).

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. *Cell genomics*, 4(2), 100484.

Helal AA, et al. (2024) Benchmarking long-read aligners and SV callers for structural variation detection in Oxford nanopore sequencing data. *Scientific reports*, 14(1), 6160.

Wang C, et al. (2024) High-depth whole-genome sequencing identifies structure variants, copy number variants and short tandem repeats associated with Parkinson's disease. *NPJ Parkinson's disease*, 10(1), 134.

Romagnoli S, et al. (2023) Resolving complex structural variants via nanopore sequencing. *Frontiers in genetics*, 14, 1213917.

- Higuera A, et al. (2023) Draft genomes of Blastocystis subtypes from human samples of Colombia. *Parasites & vectors*, 16(1), 52.
- Sedeek K, et al. (2023) Multi-omics resources for targeted agronomic improvement of pigmented rice. *Nature food*, 4(5), 366.
- Feng L, et al. (2022) The highly continuous reference genome of a leaf-chimeric red pineapple (*Ananas comosus* var. *bracteatus* f. *tricolor*) provides insights into elaboration of leaf color. *G3 (Bethesda, Md.)*, 12(2).
- Du Y, et al. (2022) Dynamic Interplay between Structural Variations and 3D Genome Organization in Pancreatic Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 9(18), e2200818.
- van der Lee M, et al. (2022) Application of long-read sequencing to elucidate complex pharmacogenomic regions: a proof of principle. *The pharmacogenomics journal*, 22(1), 75.
- Xiao C, et al. (2022) Personalized genome assembly for accurate cancer somatic mutation discovery using tumor-normal paired reference samples. *Genome biology*, 23(1), 237.
- Liu H, et al. (2022) Assessment of two-pool multiplex long-amplicon nanopore sequencing of SARS-CoV-2. *Journal of medical virology*, 94(1), 327.
- Walker K, et al. (2022) The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. *F1000Research*, 11, 530.
- Lou H, et al. (2022) Haplotype-resolved de novo assembly of a Tujia genome suggests the necessity for high-quality population-specific genome references. *Cell systems*, 13(4), 321.
- Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. *Genome biology*, 22(1), 249.
- Chawla HS, et al. (2021) Long-read sequencing reveals widespread intragenic structural variants in a recent allopolyploid crop plant. *Plant biotechnology journal*, 19(2), 240.