Resource Summary Report

Generated by RRID on Aug 2, 2026

Ngmlr

RRID:SCR_017620
Type: Tool

Proper Citation

Ngmlr (RRID:SCR_017620)

Resource Information

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

Proper Citation: Ngmlr (RRID:SCR_017620)

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 RRID .

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.