

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

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: 20260821T194122+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 36 mentions in open access literature.

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

Wu SX, et al. (2026) Dynamic regulation of spermatogenesis and hybrid sterility revealed by single-cell analysis in yak and cattle. *Molecular biology and evolution*, 43(2).

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

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 W, et al. (2025) Deconvolution of the On-Target Activity of Plasmepsin V Peptidomimetics in *Plasmodium falciparum* Parasites. *ACS infectious diseases*, 11(12), 3581.

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.

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.

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.

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).

Zhou L, et al. (2022) Long-read sequencing unveils high-resolution HPV integration and its oncogenic progression in cervical cancer. *Nature communications*, 13(1), 2563.

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.

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.

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.

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.