

Resource Summary Report

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GraphMap2

RRID:SCR_024035

Type: Tool

Proper Citation

GraphMap2 (RRID:SCR_024035)

Resource Information

URL: <https://github.com/lbcb-sci/graphmap2>

Proper Citation: GraphMap2 (RRID:SCR_024035)

Description: Software tool as splice aware RNA-seq mapper for long reads produced by Pacific Biosciences and Oxford Nanopore devices

Synonyms: graphmap2

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

Defining Citation: [PMID:27079541](#)

Keywords: splice aware RNA-seq mapper, long reads, Pacific Biosciences, Oxford Nanopore,

Availability: Free, Available for download, Freely available,

Resource Name: GraphMap2

Resource ID: SCR_024035

Old URLs: <https://sources.debian.org/src/graphmap2/>

License: MIT License

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260731T043135+0000

Ratings and Alerts

No rating or validation information has been found for GraphMap2.

No alerts have been found for GraphMap2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Ndiaye M, et al. (2025) Phage diversity mirrors bacterial strain diversity in the honey bee gut microbiota. *Nature communications*, 16(1), 9738.

Heged  s B, et al. (2025) Morphogenesis, starvation, and light responses in a mushroom-forming fungus revealed by long-read sequencing and extensive expression profiling. *Cell genomics*, 5(6), 100853.

Diensthuber G, et al. (2024) Enhanced detection of RNA modifications and read mapping with high-accuracy nanopore RNA basecalling models. *Genome research*, 34(11), 1865.

Bergin S, et al. (2024) Analysis of clinical *Candida parapsilosis* isolates reveals copy number variation in key fluconazole resistance genes. *Antimicrobial agents and chemotherapy*, 68(6), e0161923.

LoTempio J, et al. (2023) Benchmarking long-read genome sequence alignment tools for human genomics applications. *PeerJ*, 11, e16515.

Bergin S, et al. (2023) Analysis of clinical *Candida parapsilosis* isolates reveals copy number variation in key fluconazole resistance genes. *bioRxiv : the preprint server for biology*.

Mikheenko A, et al. (2022) Sequencing of individual barcoded cDNAs using Pacific Biosciences and Oxford Nanopore Technologies reveals platform-specific error patterns. *Genome research*, 32(4), 726.

Cao Y, et al. (2021) Discriminating Clonotypes of Influenza A Virus Genes by Nanopore Sequencing. *International journal of molecular sciences*, 22(18).

Oguchi Y, et al. (2021) NanoSINC-seq dissects the isoform diversity in subcellular compartments of single cells. *Science advances*, 7(15).

Riaz N, et al. (2021) Adaptation of Oxford Nanopore technology for hepatitis C whole genome sequencing and identification of within-host viral variants. *BMC genomics*, 22(1), 148.

Prawer YDJ, et al. (2020) Major SCP/TAPS protein expansion in *Lucilia cuprina* is associated with novel tandem array organisation and domain architecture. *Parasites & vectors*, 13(1), 598.

Liu X, et al. (2020) Pathogenic Adaptations Revealed by Comparative Genome Analyses of Two *Colletotrichum* spp., the Causal Agent of Anthracnose in Rubber Tree. *Frontiers in microbiology*, 11, 1484.

Deng X, et al. (2020) Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance. *Nature microbiology*, 5(3), 443.

Bokma J, et al. (2020) Phylogenomic analysis of *Mycoplasma bovis* from Belgian veal, dairy and beef herds. *Veterinary research*, 51(1), 121.

Reis AC, et al. (2019) Comparative genomics reveals a novel genetic organization of the sad cluster in the sulfonamide-degrader 'Candidatus *Leucobacter sulfamidivorax*' strain GP. *BMC genomics*, 20(1), 885.

Stjelja S, et al. (2019) The architecture of the *Plasmodiophora brassicae* nuclear and mitochondrial genomes. *Scientific reports*, 9(1), 15753.

Winand R, et al. (2019) TARGETING THE 16S RRNA GENE FOR BACTERIAL IDENTIFICATION IN COMPLEX MIXED SAMPLES: COMPARATIVE EVALUATION OF SECOND (ILLUMINA) AND THIRD (OXFORD NANOPORE TECHNOLOGIES) GENERATION SEQUENCING TECHNOLOGIES. *International journal of molecular sciences*, 21(1).

Schmid M, et al. (2018) Pushing the limits of de novo genome assembly for complex prokaryotic genomes harboring very long, near identical repeats. *Nucleic acids research*, 46(17), 8953.

Jenjaroenpun P, et al. (2018) Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of *Saccharomyces cerevisiae* CEN.PK113-7D. *Nucleic acids research*, 46(7), e38.

Castro-Wallace SL, et al. (2017) Nanopore DNA Sequencing and Genome Assembly on the International Space Station. *Scientific reports*, 7(1), 18022.