

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

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: 20260728T043705+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 [nidm-terms](#) .

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.