

Resource Summary Report

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Daligner

RRID:SCR_016066

Type: Tool

Proper Citation

Daligner (RRID:SCR_016066)

Resource Information

URL: <https://dazzlerblog.wordpress.com>

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Description: Software alignment tool to find all significant local alignments between long and noisy, up to 15% on average reads encoded in a Dazzler database. Used for DNA sequence assembly, specifically for next generation long-read sequencers such as the Pacbio RS II and Sequel sequencers.

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

Defining Citation: [DOI:10.1007/978-3-662-44753-6_5](https://doi.org/10.1007/978-3-662-44753-6_5)

Keywords: alignment, read, encode, dazzler, database, DNA, sequence, assembly, next, generation

Availability: Free, Available for download

Resource Name: Daligner

Resource ID: SCR_016066

Alternate URLs: <https://sources.debian.org/src/daligner/>

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260905T132803+0000

Ratings and Alerts

No rating or validation information has been found for Daligner.

No alerts have been found for Daligner.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Xu QZ, et al. (2025) Chromosome-level genome assembly and single-cell analysis unveil molecular mechanisms of arm regeneration in the ophiuroid *Ophiura sarsii vadicola*. *Genome biology*, 26(1), 82.

Yang S, et al. (2023) Genomic investigation of the Chinese alligator reveals wild-extinct genetic diversity and genomic consequences of their continuous decline. *Molecular ecology resources*, 23(1), 294.

Secomandi S, et al. (2023) A chromosome-level reference genome and pangenome for barn swallow population genomics. *Cell reports*, 42(1), 111992.

Hixson KK, et al. (2023) Annotated genome sequence of a fast-growing diploid clone of red alder (*Alnus rubra* Bong.). *G3 (Bethesda, Md.)*, 13(6).

Rhie A, et al. (2021) Towards complete and error-free genome assemblies of all vertebrate species. *Nature*, 592(7856), 737.

Somvanshi VS, et al. (2021) An improved draft genome assembly of *Meloidogyne graminicola* IARI strain using long-read sequencing. *Gene*, 793, 145748.

Liang Q, et al. (2019) The genome assembly and annotation of yellowhorn (*Xanthoceras sorbifolium* Bunge). *GigaScience*, 8(6).

Suzuki Y, et al. (2019) Long-read metagenomic exploration of extrachromosomal mobile genetic elements in the human gut. *Microbiome*, 7(1), 119.

Liu Q, et al. (2019) Sequencing of the black rockfish chromosomal genome provides insight into sperm storage in the female ovary. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 26(6), 453.

Wenger AM, et al. (2019) Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. *Nature biotechnology*, 37(10), 1155.

Butt SL, et al. (2018) Rapid virulence prediction and identification of Newcastle disease virus genotypes using third-generation sequencing. *Virology journal*, 15(1), 179.

Liechti N, et al. (2018) The genome of *Naegleria lovaniensis*, the basis for a comparative approach to unravel pathogenicity factors of the human pathogenic amoeba *N. fowleri*. *BMC genomics*, 19(1), 654.

Kamath GM, et al. (2017) HINGE: long-read assembly achieves optimal repeat resolution. *Genome research*, 27(5), 747.

Chu J, et al. (2017) Innovations and challenges in detecting long read overlaps: an evaluation of the state-of-the-art. *Bioinformatics (Oxford, England)*, 33(8), 1261.

Menegon M, et al. (2017) On site DNA barcoding by nanopore sequencing. *PloS one*, 12(10), e0184741.

Weissensteiner MH, et al. (2017) Combination of short-read, long-read, and optical mapping assemblies reveals large-scale tandem repeat arrays with population genetic implications. *Genome research*, 27(5), 697.

Schmid-Siegert E, et al. (2017) Mechanisms of Surface Antigenic Variation in the Human Pathogenic Fungus *Pneumocystis jirovecii*. *mBio*, 8(6).

Sovi?? I, et al. (2016) Fast and sensitive mapping of nanopore sequencing reads with GraphMap. *Nature communications*, 7, 11307.