Resource Summary Report

Generated by NIF on Apr 8, 2025

Discovar assembler

RRID:SCR_016755
Type: Tool

Proper Citation

Discovar assembler (RRID:SCR_016755)

Resource Information

URL: https://software.broadinstitute.org/software/discovar/blog/

Proper Citation: Discovar assembler (RRID:SCR_016755)

Description: Software tool for variant calling with reference and de novo assembly of genomes. The heart of DISCOVAR is a de novo genome assembler which can generate de novo assemblies for both large and small genomes.

Abbreviations: Discovar

Synonyms: Discovar de novo, Discovar

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

Defining Citation: PMID:25326702

Keywords: variant, calling, reference, de novo, assembly, genome, genetic, human, sequence, analysis

Funding: NHGRI R01 HG003474;
NHGRI U54 HG003067;
NIAID HHSN272200900018C

Availability: Free, Available for download, Freely available

Resource Name: Discovar assembler

Resource ID: SCR_016755

License: MIT

Record Creation Time: 20220129T080332+0000

Record Last Update: 20250407T220341+0000

Ratings and Alerts

No rating or validation information has been found for Discovar assembler.

No alerts have been found for Discovar assembler.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Opulente DA, et al. (2023) Genomic and ecological factors shaping specialism and generalism across an entire subphylum. bioRxiv : the preprint server for biology.

Mathers TC, et al. (2023) Hybridisation has shaped a recent radiation of grass-feeding aphids. BMC biology, 21(1), 157.

Chen H, et al. (2023) Combined pangenomics and transcriptomics reveals core and redundant virulence processes in a rapidly evolving fungal plant pathogen. BMC biology, 21(1), 24.

Liedtke HC, et al. (2022) Chromosome-level assembly, annotation and phylome of Pelobates cultripes, the western spadefoot toad. DNA research : an international journal for rapid publication of reports on genes and genomes, 29(3).

Adolfi MC, et al. (2021) A duplicated copy of id2b is an unusual sex-determining candidate gene on the Y chromosome of arapaima (Arapaima gigas). Scientific reports, 11(1), 21544.

Nowak MD, et al. (2021) The genome of Draba nivalis shows signatures of adaptation to the extreme environmental stresses of the Arctic. Molecular ecology resources, 21(3), 661.

Bongaerts P, et al. (2021) Morphological stasis masks ecologically divergent coral species on tropical reefs. Current biology : CB, 31(11), 2286.

Duckett DJ, et al. (2021) Genomic Resources for the North American Water Vole (Microtus

richardsoni) and the Montane Vole (Microtus montanus). GigaByte (Hong Kong, China), 2021, gigabyte19.

Mathers TC, et al. (2020) Genome Sequence of the Banana Aphid, Pentalonia nigronervosa Coquerel (Hemiptera: Aphididae) and Its Symbionts. G3 (Bethesda, Md.), 10(12), 4315.

Wen M, et al. (2020) Sex chromosome and sex locus characterization in goldfish, Carassius auratus (Linnaeus, 1758). BMC genomics, 21(1), 552.

Zhou Q, et al. (2020) Haplotype-resolved genome analyses of a heterozygous diploid potato. Nature genetics, 52(10), 1018.

Etherington GJ, et al. (2020) Sequencing smart: De novo sequencing and assembly approaches for a non-model mammal. GigaScience, 9(5).

Fumero MV, et al. (2020) Fumonisin and Beauvericin Chemotypes and Genotypes of the Sister Species Fusarium subglutinans and Fusarium temperatum. Applied and environmental microbiology, 86(13).

Springer MS, et al. (2019) Odontogenic ameloblast-associated (ODAM) is inactivated in toothless/enamelless placental mammals and toothed whales. BMC evolutionary biology, 19(1), 31.

Paajanen P, et al. (2019) A critical comparison of technologies for a plant genome sequencing project. GigaScience, 8(3).

Du K, et al. (2019) The genome of the arapaima (Arapaima gigas) provides insights into gigantism, fast growth and chromosomal sex determination system. Scientific reports, 9(1), 5293.

Prabh N, et al. (2018) Deep taxon sampling reveals the evolutionary dynamics of novel gene families in Pristionchus nematodes. Genome research, 28(11), 1664.

Shen XX, et al. (2018) Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. Cell, 175(6), 1533.

Zhao X, et al. (2017) Complete mitochondrial genome of Bombus breviceps (Hymenoptera: Apidae). Mitochondrial DNA. Part B, Resources, 2(2), 604.

Zhao X, et al. (2017) Complete mitochondrial genome of Bombus consobrinus (Hymenoptera: Apidae). Mitochondrial DNA. Part B, Resources, 2(2), 770.