

Resource Summary Report

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Discover assembler

RRID:SCR_016755

Type: Tool

Proper Citation

Discover assembler (RRID:SCR_016755)

Resource Information

URL: <https://software.broadinstitute.org/software/discover/blog/>

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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: Discover

Synonyms: Discover de novo, Discover

Resource Type: data analysis software, data processing software, sequence analysis software, software application, 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: Discover assembler

Resource ID: SCR_016755

License: MIT

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260821T194057+0000

Ratings and Alerts

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

No alerts have been found for Discover 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 [dkNET](#) .

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

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

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.

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.

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.

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

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

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.

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).

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

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.

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.

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

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

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.