

Resource Summary Report

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Assemblosis

RRID:SCR_016571

Type: Tool

Proper Citation

Assemblosis (RRID:SCR_016571)

Resource Information

URL: <https://github.com/vetscience/Assemblosis>

Proper Citation: Assemblosis (RRID:SCR_016571)

Description: Software tool as a Common Workflow Language (CWL) based automated bioinformatics workflow to assemble haploid/diploid eukaryote genomes of non-model organisms using PacBio long-reads and Illumina short-reads.

Resource Type: training material, data processing software, software resource, data or information resource, software application, narrative resource, workflow

Keywords: common, workflow, language, automated, assemble, haploid, diploid, eukaryote, genome, longread, shortread, data

Availability: Free, Available for download, Freely available

Resource Name: Assemblosis

Resource ID: SCR_016571

License: BSD 3 Clause License

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260731T043002+0000

Ratings and Alerts

No rating or validation information has been found for Assemblosis.

No alerts have been found for Assemblosis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Korhonen PK, et al. (2019) Common workflow language (CWL)-based software pipeline for de novo genome assembly from long- and short-read data. GigaScience, 8(4).