

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

Gene-conservation-informed-contig-alignment

RRID:SCR_017617

Type: Tool

Proper Citation

Gene-conservation-informed-contig-alignment (RRID:SCR_017617)

Resource Information

URL: <https://github.com/asdcid/Gene-conservation-informed-contig-alignment>

Proper Citation: Gene-conservation-informed-contig-alignment (RRID:SCR_017617)

Description: Software tool for separation haplotigs from genome assembly. Method to separate haplotigs based on sequence similarity.

Abbreviations: GCICA

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

Keywords: Separation, haplotig, genome, assembly, sequence, similarity

Availability: Free, Available for download, Freely available

Resource Name: Gene-conservation-informed-contig-alignment

Resource ID: SCR_017617

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260912T200106+0000

Ratings and Alerts

No rating or validation information has been found for Gene-conservation-informed-contig-alignment.

No alerts have been found for Gene-conservation-informed-contig-alignment.

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 [Kravitz](#) .

Wang W, et al. (2020) The draft nuclear genome assembly of *Eucalyptus pauciflora*: a pipeline for comparing de novo assemblies. *GigaScience*, 9(1).