Resource Summary Report

Generated by dkNET on May 19, 2025

Opera

RRID:SCR_000665
Type: Tool

Proper Citation

Opera (RRID:SCR_000665)

Resource Information

URL: http://sourceforge.net/projects/operasf/

Proper Citation: Opera (RRID:SCR_000665)

Description: A sequence assembly software program that uses information from paired-end reads to optimally order and orient contigs assembled from shotgun-sequencing reads.

Synonyms: OPERA-LG, Optimal Paired-End Read Assembler

Resource Type: software resource

Defining Citation: PMID:27169502, PMID:21929371

Keywords: sequence assembly, paired-end, orient contigs, shotgun-sequencing, shotgun, software program, bio.tools

Funding:

Availability: Open Source

Resource Name: Opera

Resource ID: SCR_000665

Alternate IDs: biotools:opera, OMICS_00045

Alternate URLs: https://bio.tools/opera

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250420T014000+0000

Ratings and Alerts

No rating or validation information has been found for Opera.

No alerts have been found for Opera.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Gao S, et al. (2016) OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. Genome biology, 17, 102.

Young ND, et al. (2014) The Opisthorchis viverrini genome provides insights into life in the bile duct. Nature communications, 5, 4378.

El-Metwally S, et al. (2013) Next-generation sequence assembly: four stages of data processing and computational challenges. PLoS computational biology, 9(12), e1003345.