

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

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

Availability: Free, Available for download, Freely available

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: 20260829T182029+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 [NIF](#) .

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.