

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

Rampart

RRID:SCR_016742

Type: Tool

Proper Citation

Rampart (RRID:SCR_016742)

Resource Information

URL: <https://github.com/TGAC/RAMPART>

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Description: Software for workflow management system for de novo genome assembly of DNA sequence data. Designed to exploit high performance computing environments, such as clusters and shared memory systems.

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

Defining Citation: [PMID:25637556](#)

Keywords: workflow, management, system, de novo, genome, assembly, DNA, sequence, data, high, performance, computing, environment, bio.tools

Funding: BBSRC

Availability: Free, Available for download, Freely available

Resource Name: Rampart

Resource ID: SCR_016742

Alternate IDs: biotools:rampart

Alternate URLs: <http://www.earlham.ac.uk/rampart/>, <https://bio.tools/rampart>

License: GPLv3

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260801T042801+0000

Ratings and Alerts

No rating or validation information has been found for Rampart.

No alerts have been found for Rampart.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Rantam FA, et al. (2021) Characterization of SARS-CoV-2 East Java isolate, Indonesia. F1000Research, 10, 480.

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