Resource Summary Report

Generated by RRID on Apr 28, 2025

Rampart

RRID:SCR_016742
Type: Tool

Proper Citation

Rampart (RRID:SCR_016742)

Resource Information

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

Proper Citation: Rampart (RRID:SCR_016742)

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

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: 20250428T054017+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 RRID.

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).