

Resource Summary Report

Generated by T1D on Aug 1, 2026

Recognition of Errors in Assemblies using Paired Reads

RRID:SCR_017625

Type: Tool

Proper Citation

Recognition of Errors in Assemblies using Paired Reads (RRID:SCR_017625)

Resource Information

URL: <https://www.sanger.ac.uk/science/tools/reapr>

Proper Citation: Recognition of Errors in Assemblies using Paired Reads (RRID:SCR_017625)

Description: Software tool to identify errors in genome assemblies without need for reference sequence. Can be used in any stage of assembly pipeline to automatically break incorrect scaffolds and flag other errors in assembly for manual inspection. Reports mis-assemblies and other warnings, and produces new broken assembly based on error calls.

Abbreviations: REAPR

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

Defining Citation: [PMID:23710727](#)

Keywords: Identify, error, genome, assembly, without, reference, sequence, incorrect, scaffold, error

Funding: European Union ;
Wellcome Trust ;
JSPS KAKENHI

Availability: Free, Available for download, Freely available

Resource Name: Recognition of Errors in Assemblies using Paired Reads

Resource ID: SCR_017625

Alternate IDs: OMICS_04068

Alternate URLs: <https://sources.debian.org/src/reapr/>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260731T043012+0000

Ratings and Alerts

No rating or validation information has been found for Recognition of Errors in Assemblies using Paired Reads.

No alerts have been found for Recognition of Errors in Assemblies using Paired Reads.

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 [T1D](#) .

Etherington GJ, et al. (2020) Sequencing smart: De novo sequencing and assembly approaches for a non-model mammal. GigaScience, 9(5).

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