

# Resource Summary Report

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## 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:** data processing software, software application, software resource

**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:** 20250428T054057+0000

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## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [NIF](#).

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).