Resource Summary Report

Generated by dkNET on May 19, 2025

CloudAligner

RRID:SCR_012962
Type: Tool

Proper Citation

CloudAligner (RRID:SCR_012962)

Resource Information

URL: http://sourceforge.net/projects/cloudaligner/

Proper Citation: CloudAligner (RRID:SCR_012962)

Description: A map/reduce based application for mapping short reads generated by the next-generation sequencing machines.

Abbreviations: CloudAligner

Resource Type: software resource

Defining Citation: PMID:21645377

Keywords: matlab, mapreduce/hadoop, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: CloudAligner

Resource ID: SCR_012962

Alternate IDs: OMICS_00656, biotools:cloudaligner

Alternate URLs: https://bio.tools/cloudaligner

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250519T203746+0000

Ratings and Alerts

No rating or validation information has been found for CloudAligner.

No alerts have been found for CloudAligner.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Expósito RR, et al. (2018) HSRA: Hadoop-based spliced read aligner for RNA sequencing data. PloS one, 13(7), e0201483.

Soe S, et al. (2018) BiSpark: a Spark-based highly scalable aligner for bisulfite sequencing data. BMC bioinformatics, 19(1), 472.

Chen J, et al. (2013) Translational biomedical informatics in the cloud: present and future. BioMed research international, 2013, 658925.

Chen J, et al. (2013) Translational bioinformatics for diagnostic and prognostic prediction of prostate cancer in the next-generation sequencing era. BioMed research international, 2013, 901578.