## **Resource Summary Report**

Generated by dkNET on May 18, 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:** 20250420T014626+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.