

Resource Summary Report

Generated by PRECISE-TBI on Aug 4, 2026

Qudaich

RRID:SCR_006775

Type: Tool

Proper Citation

Qudaich (RRID:SCR_006775)

Resource Information

URL: <http://sourceforge.net/projects/qudaich/>

Proper Citation: Qudaich (RRID:SCR_006775)

Description: A software package for local sequence alignment for next-generation sequencing (NGS) data. It generates the pairwise local alignments between a query dataset against a database. The main design purpose of qudaich is to focus on datasets from next generation sequencing. These the datasets generally have hundreds of thousand sequences or more, and so, the input database should contain large number of sequences. Qudaich is flexible and its algorithmic structure imposes no restriction on the absolute limit of the acceptable read length, but the current version of qudaich allow read length 2000 bp. Qudaich can be used to align DNA, translated DNA and protein sequences.

Abbreviations: Qudaich

Synonyms: Queries and unique database alignment inferred by clustering homologs

Resource Type: software resource

Keywords: next-generation sequencing, alignment

Resource Name: Qudaich

Resource ID: SCR_006775

Alternate IDs: OMICS_00678

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260801T190312+0000

Ratings and Alerts

No rating or validation information has been found for Qudaich.

No alerts have been found for Qudaich.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.