

# Resource Summary Report

Generated by [RRID](#) on Sep 10, 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:** 20260905T132600+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.