Resource Summary Report

Generated by <u>dkNET</u> on Apr 29, 2025

Fastahack

RRID:SCR_016090 Type: Tool

Proper Citation

Fastahack (RRID:SCR_016090)

Resource Information

URL: https://github.com/ekg/fastahack

Proper Citation: Fastahack (RRID:SCR_016090)

Description: Software application for indexing and extracting sequences and subsequences from FASTA files. It will only generate indexes for FASTA files in which the sequences have self-consistent line lengths.

Resource Type: software resource, software application

Keywords: extract, quickly, subsequence, sequence, FASTA, files, generate, index

Funding:

Availability: Free, Available for download

Resource Name: Fastahack

Resource ID: SCR_016090

Alternate IDs: OMICS_20516

Alternate URLs: https://packages.debian.org/stretch/fastahack, https://sources.debian.org/src/fastahack/

License: MIT license

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250429T055805+0000

Ratings and Alerts

No rating or validation information has been found for Fastahack.

No alerts have been found for Fastahack.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Vromman M, et al. (2022) CIRCprimerXL: Convenient and High-Throughput PCR Primer Design for Circular RNA Quantification. Frontiers in bioinformatics, 2, 834655.