

Resource Summary Report

Generated by [NIF](#) on Apr 25, 2025

[BEETL-fastq](#)

RRID:SCR_002341

Type: Tool

Proper Citation

BEETL-fastq (RRID:SCR_002341)

Resource Information

URL: <https://github.com/BEETL/BEETL>

Proper Citation: BEETL-fastq (RRID:SCR_002341)

Description: Software tool that not only compresses FASTQ-formatted DNA reads more compactly than gzip but also permits rapid search for k-mer queries within the archived sequences. The full FASTQ record of each matching read or read pair is returned, allowing the search results to be piped directly to any of the many standard tools that accept FASTQ data as input. Searchable compressed archive for DNA reads.

Resource Type: software resource

Defining Citation: [PMID:24950811](#)

Keywords: Searchable compressed archive, DNA reads, compresses FASTQ-formatted DNA reads, bio.tools,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: BEETL-fastq

Resource ID: SCR_002341

Alternate IDs: OMICS_04900, biotools:beetl

Alternate URLs: <https://bio.tools/beetl>

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250420T014100+0000

Ratings and Alerts

No rating or validation information has been found for BEETL-fastq.

No alerts have been found for BEETL-fastq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.