# **Resource Summary Report**

Generated by NIF on Apr 25, 2025

# fastqz

RRID:SCR 001006

Type: Tool

### **Proper Citation**

fastqz (RRID:SCR\_001006)

#### **Resource Information**

URL: http://www.mattmahoney.net/dc/fastqz/

**Proper Citation:** fastqz (RRID:SCR\_001006)

Description: Source code used to compress FASTQ files. FASTQ is DNA sequencing

machine output.

Resource Type: data management software, source code, software resource, software

application

**Defining Citation: PMID:23533605** 

Keywords: compress, source code, fastq output, fastq dna, fastq sequencing, fastq

compress, fastq compressor, fastq files, bio.tools

**Funding:** 

Availability: Free, Only available as source code, Available for download, libzpag is required

Resource Name: fastqz

Resource ID: SCR\_001006

Alternate IDs: OMICS\_00956, biotools:fastqz

Alternate URLs: https://bio.tools/fastqz

License: BSD 2 clause license

**Record Creation Time:** 20220129T080205+0000

Record Last Update: 20250424T064445+0000

## **Ratings and Alerts**

No rating or validation information has been found for fastqz.

No alerts have been found for fastqz.

## **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We have not found any literature mentions for this resource.