

Resource Summary Report

Generated by [dkNET](#) on Sep 11, 2026

FASTQuick

RRID:SCR_019269

Type: Tool

Proper Citation

FASTQuick (RRID:SCR_019269)

Resource Information

URL: <https://github.com/Griffan/FASTQuick>

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Description: Software tool for rapid and comprehensive quality assessment of raw sequence reads. It generates comprehensive list of QC statistics, including ancestry and contamination estimation.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [DOI:10.1101/2020.06.10.143768](https://doi.org/10.1101/2020.06.10.143768)

Keywords: Sequenced genomes quality assessment, raw sequence reads, quality assessment, NGS sequencing fastq files, quality control,

Availability: Free, Available for download, Freely available

Resource Name: FASTQuick

Resource ID: SCR_019269

License: MIT

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260905T132848+0000

Ratings and Alerts

No rating or validation information has been found for FASTQuick.

No alerts have been found for FASTQuick.

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 [dkNET](#) .

Zhang F, et al. (2021) FASTQuick: rapid and comprehensive quality assessment of raw sequence reads. GigaScience, 10(2).