

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

2FAST2Q

RRID:SCR_025017

Type: Tool

Proper Citation

2FAST2Q (RRID:SCR_025017)

Resource Information

URL: <https://pypi.org/project/fast2q/>

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Description: Software package for general purpose sequence search and counting program for FASTQ files. Python3 program that counts sequence occurrences in raw FASTQ files. Used for CRISPRi-Seq, and for extracting and counting any kind of information from Illumina reads, such as barcodes.

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

Defining Citation: [PMID:36312750](#)

Keywords: Python3, count sequence occurrences, raw FASTQ files,

Funding: Swiss National Science Foundation

Availability: Free, Available for download, Freely available

Resource Name: 2FAST2Q

Resource ID: SCR_025017

Alternate URLs: <https://github.com/veeninglab/2FAST2Q>

License: GNU GPL

Record Creation Time: 20240221T003954+0000

Record Last Update: 20260815T042927+0000

Ratings and Alerts

No rating or validation information has been found for 2FAST2Q.

No alerts have been found for 2FAST2Q.

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 [RRID](#) .

Gil-Campillo C, et al. (2025) CRISPRi-seq in Haemophilus influenzae reveals genome-wide and medium-specific growth determinants. PLoS pathogens, 21(10), e1013650.