Resource Summary Report

Generated by RRID on May 20, 2025

FastqSifter

RRID:SCR_017200
Type: Tool

Proper Citation

FastqSifter (RRID:SCR_017200)

Resource Information

URL: https://github.com/josephryan/FastqSifter

Proper Citation: FastqSifter (RRID:SCR_017200)

Description: Software tool to separate contaminating reads from FASTQ files.

Synonyms: FastqSifter v1.1.1

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

Keywords: FASTQ, genomics, separate, contaminating, read

Funding:

Availability: Free, Available for download, Freely available

Resource Name: FastqSifter

Resource ID: SCR_017200

License: GNU GPL v3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20250519T203950+0000

Ratings and Alerts

No rating or validation information has been found for FastqSifter.

No alerts have been found for FastqSifter.

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.

Ohdera A, et al. (2019) Box, stalked, and upside-down? Draft genomes from diverse jellyfish (Cnidaria, Acraspeda) lineages: Alatina alata (Cubozoa), Calvadosia cruxmelitensis (Staurozoa), and Cassiopea xamachana (Scyphozoa). GigaScience, 8(7).