

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

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

Keywords: FASTQ, genomics, separate, contaminating, read

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: 20260912T195849+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 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Ragosta MC, et al. (2026) The modulation of AUF1 regulates the R-loop resolution activating the immune response in DDR. *iScience*, 29(6), 115900.

Dur??n-Fuentes JA, et al. (2025) Repeatome diversity in sea anemone genomics (Cnidaria: Actiniaria) based on the Actiniaria-REPlib library. *BMC genomics*, 26(1), 473.

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).