

Resource Summary Report

Generated by [RRID](#) on Aug 5, 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 processing software, data analysis software, standalone software, software resource, sequence analysis software, software application

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: 20260805T044406+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 2 mentions in open access literature.

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

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).