# Resource Summary Report

Generated by NIF on Apr 21, 2025

# FastqSifter

RRID:SCR_017200
Type: Tool

## Proper Citation

FastqSifter (RRID:SCR_017200)

## Resource Information

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

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

**Synonyms:** FastqSifter v1.1.1

**Resource Type:** sequence analysis software, data analysis software, software application, software resource, data processing software, 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:** 20250420T014829+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 NIF.

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).