

# Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

## ArtificialFastqGenerator

RRID:SCR\_006880

Type: Tool

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### Proper Citation

ArtificialFastqGenerator (RRID:SCR\_006880)

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### Resource Information

**URL:** <http://sourceforge.net/projects/artfastqgen/>

**Proper Citation:** ArtificialFastqGenerator (RRID:SCR\_006880)

**Description:** Software to evaluate and improve the accuracy of sequencing error under different experimental conditions. It can identify which components of a system may be suboptimal and which regions of the genome may be problematic.

**Abbreviations:** ArtificialFastqGenerator

**Synonyms:** Artfastqgenerator - Ouputs artificial FASTQ files derived from a reference genome

**Resource Type:** software resource

**Defining Citation:** [PMID:23152858](#)

**Keywords:** matlab, java, Next Generation Sequencing, aligns reads, reference genome

**Availability:** GNU GPL v3

**Resource Name:** ArtificialFastqGenerator

**Resource ID:** SCR\_006880

**Alternate IDs:** OMICS\_00248, SCR\_015979

**Alternate URLs:** <https://sources.debian.org/src/artfastqgenerator/>

**Record Creation Time:** 20220129T080238+0000

**Record Last Update:** 20260801T190314+0000

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### Ratings and Alerts

No rating or validation information has been found for ArtificialFastqGenerator.

No alerts have been found for ArtificialFastqGenerator.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Shea J, et al. (2022) Novel Mycobacterium tuberculosis Complex Genotype Related to M. caprae. Emerging infectious diseases, 28(7), 1431.

Calderwood A, et al. (2021) Total FLC transcript dynamics from divergent paralogue expression explains flowering diversity in Brassica napus. The New phytologist, 229(6), 3534.

Vitali V, et al. (2021) Fifty Generations of Amitosis: Tracing Asymmetric Allele Segregation in Polyploid Cells with Single-Cell DNA Sequencing. Microorganisms, 9(9).

Southgate JA, et al. (2020) Influenza classification from short reads with VAPOR facilitates robust mapping pipelines and zoonotic strain detection for routine surveillance applications. Bioinformatics (Oxford, England), 36(6), 1681.

Sintsova A, et al. (2019) Genetically diverse uropathogenic Escherichia coli adopt a common transcriptional program in patients with UTIs. eLife, 8.

B??rlin CS, et al. (2019) A bioinformatic pipeline to analyze ChIP-exo datasets. Biology methods & protocols, 4(1), bpz011.

Rana S, et al. (2019) Loss of a chloroplast encoded function could influence species range in kelp. Ecology and evolution, 9(15), 8759.

Mahmoud M, et al. (2019) Efficiency of PacBio long read correction by 2nd generation Illumina sequencing. Genomics, 111(1), 43.

Pullan ST, et al. (2015) Whole-genome sequencing investigation of animal-skin-drum-associated UK anthrax cases reveals evidence of mixed populations and relatedness to a US case. Microbial genomics, 1(5), e000039.

Chou MT, et al. (2015) Tailor: a computational framework for detecting non-templated tailing of small silencing RNAs. Nucleic acids research, 43(17), e109.