

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

ArtificialFastqGenerator

RRID:SCR_006880

Type: Tool

Proper Citation

ArtificialFastqGenerator (RRID:SCR_006880)

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: 20260725T190630+0000

Ratings and Alerts

No rating or validation information has been found for ArtificialFastqGenerator.

No alerts have been found for ArtificialFastqGenerator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

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.