

Resource Summary Report

Generated by [T1D](#) on Sep 5, 2026

[InSilicoSeq](#)

RRID:SCR_024041

Type: Tool

Proper Citation

InSilicoSeq (RRID:SCR_024041)

Resource Information

URL: <https://github.com/HadrienG/InSilicoSeq>

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Description: Software tool as sequencing simulator producing realistic Illumina reads. Primarily intended for simulating metagenomic samples, it can also be used to produce sequencing data from a single genome.

Synonyms: insilicoseq, InSilicoSeq- A sequencing simulator

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:30016412](#)

Keywords: producing realistic Illumina reads, simulating metagenomic samples,

Availability: Free, Available for download, Freely available,

Resource Name: InSilicoSeq

Resource ID: SCR_024041

Alternate IDs: OMICS_31218

Alternate URLs: <https://sources.debian.org/src/insilicoseq/>,
<https://insilicoseq.readthedocs.io/en/latest/>

License: MIT License

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260903T235938+0000

Ratings and Alerts

No rating or validation information has been found for InSilicoSeq.

No alerts have been found for InSilicoSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Chilengue AFC, et al. (2026) Reference-free clustering as an epidemiological tool for Mycobacterium tuberculosis lineage typing. Microbial genomics, 12(6).

Fonseca EM, et al. (2025) Modeling Biases from Low-Pass Genome Sequencing to Enable Accurate Population Genetic Inferences. Molecular biology and evolution, 42(1).

Popov N, et al. (2025) AliMarko: A Pipeline for Virus Identification Using an Expert-Guided Approach. Viruses, 17(3).

Ghezzi H, et al. (2024) PUPpy: a primer design pipeline for substrain-level microbial detection and absolute quantification. mSphere, 9(7), e0036024.

Dylus D, et al. (2024) Inference of phylogenetic trees directly from raw sequencing reads using Read2Tree. Nature biotechnology, 42(1), 139.

Thomas Iv JC, et al. (2024) Emergence and evolution of mosaic penA-60 and penA-237 alleles in a Neisseria gonorrhoeae core genogroup that was historically susceptible to extended spectrum cephalosporins. Frontiers in microbiology, 15, 1401303.

Harmer CJ, et al. (2023) Acinetobacter baumannii GC2 Sublineage Carrying the aac(6')-Im Amikacin, Netilmicin, and Tobramycin Resistance Gene Cassette. Microbiology spectrum, 11(4), e0120423.

Berbel Caban A, et al. (2020) PathoSPOT genomic epidemiology reveals under-the-radar nosocomial outbreaks. Genome medicine, 12(1), 96.