

Resource Summary Report

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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 resource, software application

Defining Citation: [PMID:30016412](https://pubmed.ncbi.nlm.nih.gov/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: 20260803T040910+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 7 mentions in open access literature.

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

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).

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

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

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.