Resource Summary Report

Generated by NIF on Apr 28, 2025

Seqtk

RRID:SCR_018927
Type: Tool

Proper Citation

Seqtk (RRID:SCR_018927)

Resource Information

URL: https://github.com/lh3/seqtk

Proper Citation: Seqtk (RRID:SCR_018927)

Description: Software fast and lightweight tool for processing sequences in FASTA or FASTQ format.

Synonyms: SEQTK

Resource Type: data processing software, sequence analysis software, software resource, data analysis software, software application

Keywords: Sequence processing, FASTA format, FASTQ format, data processing, bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Seqtk

Resource ID: SCR_018927

Alternate IDs: OMICS_09736, biotools:seqtk

Alternate URLs: https://bio.tools/seqtk, https://sources.debian.org/src/seqtk/

Record Creation Time: 20220129T080342+0000

Record Last Update: 20250428T054149+0000

Ratings and Alerts

No rating or validation information has been found for Seqtk.

No alerts have been found for Seqtk.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 652 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Yang J, et al. (2025) MARTRE family proteins negatively regulate CCR4-NOT activity to protect poly(A) tail length and promote translation of maternal mRNA. Nature communications, 16(1), 248.

Kunz L, et al. (2025) Avirulence depletion assay: Combining R gene-mediated selection with bulk sequencing for rapid avirulence gene identification in wheat powdery mildew. PLoS pathogens, 21(1), e1012799.

De Simone M, et al. (2025) A comprehensive analysis framework for evaluating commercial single-cell RNA sequencing technologies. Nucleic acids research, 53(2).

Petroll R, et al. (2025) Enhanced sensitivity of TAPscan v4 enables comprehensive analysis of streptophyte transcription factor evolution. The Plant journal : for cell and molecular biology, 121(1), e17184.

Bogaerts B, et al. (2025) Galaxy @Sciensano: a comprehensive bioinformatics portal for genomics-based microbial typing, characterization, and outbreak detection. BMC genomics, 26(1), 20.

Zeng J, et al. (2025) Protocol for genetic analysis of population-scale ultra-low-depth sequencing data. STAR protocols, 6(1), 103579.

Hebert PDN, et al. (2025) Barcode 100K Specimens: In a Single Nanopore Run. Molecular ecology resources, 25(1), e14028.

Gadila SKG, et al. (2025) Comparison of transcriptomic profiles between intracellular and extracellular Bartonella henselae. Communications biology, 8(1), 143.

Brcko IC, et al. (2025) Comprehensive molecular epidemiology of influenza viruses in Brazil: insights from a nationwide analysis. Virus evolution, 11(1), veae102.

Zhou M, et al. (2025) A copy number variation detection method based on OCSVM algorithm using multi strategies integration. Scientific reports, 15(1), 3526.

Mimoso CA, et al. (2025) Restrictor slows early transcription elongation to render RNA polymerase II susceptible to termination at non-coding RNA loci. bioRxiv : the preprint server for biology.

Magossi G, et al. (2025) Genomic and metabolic characterization of Trueperella pyogenes isolated from domestic and wild animals. Applied and environmental microbiology, 91(1), e0172524.

Chen J, et al. (2025) Horizontal Transfer and Recombination Fuel Ty4 Retrotransposon Evolution in Saccharomyces. Genome biology and evolution, 17(1).

Longmire P, et al. (2025) Complex roles for proliferating cell nuclear antigen in restricting human cytomegalovirus replication. bioRxiv : the preprint server for biology.

Fowler K, et al. (2025) The genome sequence of a leafhopper, Allygus modestus Scott, 1876. Wellcome open research, 10, 9.

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish Entelurus aequoreus (Syngnathiformes: Syngnathidae). GigaByte (Hong Kong, China), 2024, gigabyte105.

Ly?ka M, et al. (2024) TeloBase: a community-curated database of telomere sequences across the tree of life. Nucleic acids research, 52(D1), D311.

Hiralal A, et al. (2024) Closing the genome of unculturable cable bacteria using a combined metagenomic assembly of long and short sequencing reads. Microbial genomics, 10(2).

Hoelzel AR, et al. (2024) Genomics of post-bottleneck recovery in the northern elephant seal. Nature ecology & evolution, 8(4), 686.

Yang L, et al. (2024) Evolutionary insights from profiling LINE-1 activity at allelic resolution in a single human genome. The EMBO journal, 43(1), 112.