

Resource Summary Report

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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, software application, data analysis software, sequence analysis software, software resource

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: 20250421T054259+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 [FDI Lab - SciCrunch.org](#).

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.

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.

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.

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

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.
- Chen J, et al. (2025) Horizontal Transfer and Recombination Fuel Ty4 Retrotransposon Evolution in *Saccharomyces*. *Genome biology and evolution*, 17(1).
- 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.
- 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*.
- 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.
- Miao Z, et al. (2024) *Bifidobacterium animalis* subsp. *lactis* Probio-M8 alleviates abnormal behavior and regulates gut microbiota in a mouse model suffering from autism. *mSystems*, 9(1), e0101323.
- Lossouarn J, et al. (2024) The virtue of training: extending phage host spectra against vancomycin-resistant *Enterococcus faecium* strains using the Appelmans method. *Antimicrobial agents and chemotherapy*, 68(5), e0143923.
- Zhong Y, et al. (2024) Systematic identification and characterization of exon-intron circRNAs. *Genome research*, 34(3), 376.
- Liu X, et al. (2024) Introgression and disruption of migration routes have shaped the genetic integrity of wildebeest populations. *Nature communications*, 15(1), 2921.