

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

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

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

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: 20260801T190606+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 827 mentions in open access literature.

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

Xu Y, et al. (2026) From degraded to deciphered: Applying ATAC-seq to forensic molecular diagnosis under degradation conditions. *Forensic science international*, 379, 112789.

Dekker RJ, et al. (2026) Evaluation of RNA extraction and rRNA depletion protocols for RNA-Seq in eleven edible seaweed species from brown, red, and green algae. *PloS one*, 21(1), e0339896.

Payne CY, et al. (2026) A genome assembly for Lahontan Cutthroat Trout, *Oncorhynchus clarkii henshawi*. *The Journal of heredity*, 117(1), 159.

Dur??n-Fuentes JA, et al. (2025) Repeatome diversity in sea anemone genomics (Cnidaria: Actiniaria) based on the Actiniaria-REPlib library. *BMC genomics*, 26(1), 473.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. *GigaByte (Hong Kong, China)*, 2025, gigabyte154.

Boyes D, et al. (2025) The genome sequence of Red Underwing, *Catocala nupta* Linnaeus, 1767. *Wellcome open research*, 10, 36.

Trivedi M, et al. (2025) Historical Demography and Species Distribution Models Shed Light on Speciation in Primates of Northeast India. *Ecology and evolution*, 15(2), e70968.

Power D, et al. (2025) The genome sequence of Greek sea-spurrey, *Spergularia bocconeii* (Scheele) Graebn. (Caryophyllaceae). *Wellcome open research*, 10, 34.

Barclay MVL, et al. (2025) The genome sequence of a longhorn beetle, *Rhagium mordax* (Degeer, 1775). *Wellcome open research*, 10, 51.

Adkins P, et al. (2025) The genome sequence of the amphioxus, *Branchiostoma lanceolatum* (Pallas, 1774). *Wellcome open research*, 10, 95.

Bird E, et al. (2025) BALROG-MON: a high-throughput pipeline for Bacterial Antimicrobial Resistance annOtation of Genomes-Metagenomic Oxford Nanopore. *microPublication biology*, 2025.

Booth R, et al. (2025) The genome sequence of a leaf beetle, *Galerucella nymphaeae* (Linnaeus, 1758). *Wellcome open research*, 10, 57.

Barclay MVL, et al. (2025) The genome sequence of a pallopterid fly, *Toxonevra muliebris* (Harris, 1780). *Wellcome open research*, 10, 55.

Dotto-Maurel A, et al. (2025) Evaluation of long-read sequencing for Ostreid herpesvirus type 1 genome characterization from *Magallana gigas* infected tissues. *Microbiology spectrum*, 13(3), e0208224.

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.

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.

Broad GR, et al. (2025) The genome sequence of the Straw-barred Pearl moth, *Pyrausta despicata* Scopoli, 1763. *Wellcome open research*, 10, 151.

Morrison J, et al. (2025) Synthbar: A Lightweight Tool for Adding Synthetic Barcodes to Sequencing Reads. *bioRxiv : the preprint server for biology*.

Kinoshita Y, et al. (2025) Minimal disruption of equine gut microbiota by intravenous cephalothin treatment. *The Journal of veterinary medical science*, 87(6), 690.

Davison NJ, et al. (2025) The genome sequence of long-finned pilot whale, *Globicephala melas* (Traill, 1809). *Wellcome open research*, 10, 180.