

Resource Summary Report

Generated by [RRID](#) 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 [RRID](#) .

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.

Durán-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.

Li X, et al. (2025) Microbiome Single Cell Atlases Generated with a Commercial Instrument. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(27), e2409338.

Eibner-Gebhardt MW, et al. (2025) A historical Hawaiian Avipoxvirus genome reconstructed from an 1898 museum specimen. *iScience*, 28(4), 112153.

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.

Guerrero Garzón JF, et al. (2025) Genome mining of *Streptomyces bambergiensis* AC-800 unravels the biosynthetic gene cluster for inhibitors of prolyl hydroxylase fibrostatins. *Scientific reports*, 15(1), 32142.

Carmola LR, et al. (2025) Viral and host factors associated with SARS-CoV-2 disease severity in Georgia, USA. *PloS one*, 20(4), e0317972.

Boyes D, et al. (2025) The genome sequence of the Large Birch Bell moth, Large Birch Roller, *Epinotia brunnichana* (Linnaeus, 1767). *Wellcome open research*, 10, 101.

Grubben J, et al. (2025) CRISPR/Cas9-induced breaks are insufficient to break linkage drag surrounding the ToMV locus of *Solanum lycopersicum*. *G3* (Bethesda, Md.), 15(6).

Salman M, et al. (2025) Evolutionary dynamics of repetitive elements and genome size in Tetrigidae (Orthoptera: Caelifera). *Scientific reports*, 15(1), 34509.

Queiroz C, et al. (2025) Similar patterns of benzimidazole resistance alleles in ovine gastrointestinal nematodes from Western Canada and Eastern United States supports their shared origins and subsequent spread. *International journal for parasitology. Drugs and drug resistance*, 29, 100620.

Hajjar J, et al. (2025) Gut dysbiosis patterns in CVID patients with noninfectious complications observed in a germ-free mouse model through fecal microbiota transplantation. *Journal of human immunity*, 1(1).

Yessembekova G, et al. (2025) Prevalence and Genetic Diversity of Torque teno felis virus (FctTV) in Domestic Cats from Kazakhstan. *Viruses*, 17(9).

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

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.