

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 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, data processing software, sequence analysis software, software application, software resource

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: 20260821T194153+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 1039 mentions in open access literature.

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

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

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

Sanz-Garcia E, et al. (2026) Investigating Early Kinetics in Plasma ctDNA and Peripheral T-cell Receptor Repertoire to Predict Treatment Outcomes to PD-1 Inhibitors in Head and Neck Squamous Cell Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(4), 735.

Carvalho AB, et al. (2026) Strong bias in long-read sequencing prevents assembly of *Drosophila melanogaster* Y-linked genes. *Genome research*, 36(1), 71.

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.

Rodriguez S, et al. (2026) Genomic plasticity and mobilome architecture of *Vibrio europaeus* reveal key mechanisms of evolutionary adaptation. *Microbial genomics*, 12(1).

Longmire P, et al. (2026) Human cytomegalovirus regulates host DNA repair machinery for viral genome integrity. *Nucleic acids research*, 54(2).

Toews DJ, et al. (2026) A genome assembly of Greene's tuctoria, *Tuctoria greenei*, an amphibious endemic and endangered California vernal pool grass. *The Journal of heredity*, 117(3), 526.

Martin JA, et al. (2026) High-quality de novo genome assembly for the Galápagos endemic lava gull using Oxford Nanopore Technologies. *G3 (Bethesda, Md.)*, 16(3).

Pennington LK, et al. (2026) A reference genome for Colusa grass, *Neostapfia colusana*, a threatened and endangered California vernal pool plant. *The Journal of heredity*, 117(3), 459.

Sessi IR, et al. (2026) First whole-genome assembly of the Galápagos Petrel (*Pterodroma phaeopygia*) using Oxford Nanopore sequencing to advance conservation genomics in a critically endangered seabird. *G3 (Bethesda, Md.)*, 16(3).

Labella-Ortega M, et al. (2026) Uncovering the genome evolutionary dynamics of the Mediterranean endemic palm *Chamaerops humilis*. BMC plant biology, 26(1).

Baril T, et al. (2026) MycoMobilome: a community-focused non-redundant database of transposable element consensus sequences for the fungal kingdom. NAR genomics and bioinformatics, 8(1), lqag026.

Ward AK, et al. (2026) Low-level contamination confounds population genomic analysis. G3 (Bethesda, Md.), 16(4).

Ge Q, et al. (2026) DNA diamond formulates a decomposable composite letter constellation model for DNA data storage. Nature communications, 17(1), 1704.

Zhang Z, et al. (2026) A methylome-derived m6-dAMP trigger assembles a PUA-Cal-HAD immune filament that depletes dNTPs to abort phage infection. bioRxiv : the preprint server for biology.

Hoang LH, et al. (2026) The emergence and spread of a novel sequence type of *Corynebacterium diphtheriae* in Vietnam. Scientific reports, 16(1).

Kislik G, et al. (2026) Inference of admixture in dogs from whole genome sequences. GigaByte (Hong Kong, China), 2026, gigabyte173.

Lin J, et al. (2026) Long-Read Whole-Transcriptome Sequencing and Selective Gene Panel Profiling Enable Sensitive Detection of Fusion Oncogenes in Pediatric B-Cell Acute Lymphoblastic Leukemia. The Journal of molecular diagnostics : JMD, 28(5), 406.

Escaffre O, et al. (2026) Efficacy of the nucleoside analog 4'-Fluorouridine against Nipah virus in the Syrian hamster model. PLoS pathogens, 22(4), e1014093.