

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 analysis software, data processing software, software application, sequence analysis software, 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: 20260810T040745+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 [NIF](#) .

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.

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.

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.

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).

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).

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

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.

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

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

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.

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).

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

Tretow K, et al. (2026) RNA G-quadruplexes mediate cooperativity in HNRNPH binding and splicing regulation. *bioRxiv : the preprint server for biology*.

Wu Y, et al. (2026) Tmn blocks phage spread via plasmolysis and triggers synergistic defence responses. *bioRxiv : the preprint server for biology*.

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.