

Resource Summary Report

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SeqKit

RRID:SCR_018926

Type: Tool

Proper Citation

SeqKit (RRID:SCR_018926)

Resource Information

URL: <https://bioinf.shenwei.me/seqkit/>

Proper Citation: SeqKit (RRID:SCR_018926)

Description: Software tool as cross platform and ultrafast toolkit for FASTA/Q file manipulation.

Resource Type: software toolkit, software resource

Defining Citation: [DOI:10.1371/journal.pone.0163962](https://doi.org/10.1371/journal.pone.0163962)

Keywords: FASTA file, Q file, file manipulation, fast toolkit

Availability: Free, Available for download, Freely available

Resource Name: SeqKit

Resource ID: SCR_018926

Alternate URLs: <https://github.com/shenwei356/seqkit>

License: MIT License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260815T183000+0000

Ratings and Alerts

No rating or validation information has been found for SeqKit.

No alerts have been found for SeqKit.

Data and Source Information

Usage and Citation Metrics

We found 210 mentions in open access literature.

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

Fan Z, et al. (2026) Deep Eutectic Solvent-Based Extraction Optimization, Structural Characterization, and Alleviating Effects of Tremella fuciformis Polysaccharides on Ulcerative Colitis. *Foods* (Basel, Switzerland), 15(12).

Sakdinan B, et al. (2026) Species-specific prophage induction by ciprofloxacin in human gut metagenomes. *bioRxiv : the preprint server for biology*.

Magallanes Alba ME, et al. (2026) Genome assembly and annotation of the olive grass mouse *Abrothrix olivacea* reveal transcriptomic and cellular adaptations across contrasting biomes. *BMC genomics*, 27(1).

Li K, et al. (2026) Centromere organization and epigenetic regulation in *Aristolochia fimbriata*. *Genome biology*, 27(1).

Suarez-Silva R, et al. (2026) Exploring the Algarrobo Decline in the Pómac Forest: Unraveling the Relationship between the Endomicrobiome of *Neltuma pallida* and *Enallodiplosis discordis*. *Microbial ecology*, 89(1).

Wang B, et al. (2026) Complete mitochondrial genomes of the two high-valued bromeliads: comparative genomics and evolutionary insights. *BMC genomics*, 27(1).

Bhalla N, et al. (2026) Large-scale cryptic proteome mining revealed potential phage-mediated host-pathogen genetic exchange in *Mycobacterium tuberculosis*. *PloS one*, 21(5), e0348602.

Rivera I, et al. (2026) Phylogenomic framework and virulence gene boundaries of emerging Shiga toxin-producing *Escherichia coli* O118 informed by the comprehensive profiling of 359 O118 genomes. *Virulence*, 17(1), 2672206.

Pamornchainavakul N, et al. (2026) QoALa: A comprehensive workflow for viral quasispecies diversity comparison using long-read sequencing data. *PLoS computational biology*, 22(4), e1014208.

Fakoya AO, et al. (2026) HapAsmbl: A reference-aided pipeline for assembling haplotypes in Nanopore amplicon sequence data of polymorphic populations. *Applications in plant sciences*, 14(3), e70062.

Dockman RL, et al. (2026) Improved chromosome-level genome assembly of the American cockroach, *Periplaneta americana*. *G3* (Bethesda, Md.), 16(1).

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Ji HJ, et al. (2026) Accurate serotype identification of *Streptococcus pneumoniae* using nanopore Cas9-targeted serotype identification (nCATSerotyping). *Journal of clinical microbiology*, 64(2), e0098425.

Dinana IA, et al. (2026) Reading Between the ABCs: Intrinsic Disorder and Evolutionary Dynamics of Non-Canonical Regions in ABC Transporters. *International journal of molecular sciences*, 27(11).

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. *Microbial genomics*, 12(2).

Kosushkin SA, et al. (2026) Genome sequencing uncovers the history of the Russian desman's gradual population decline and contributes to the evolutionary history of Talpidae. *BMC ecology and evolution*, 26(1), 12.

Deng X, et al. (2026) Comparative plastome analyses reveal life-form-associated selection signatures in Orchidaceae. *BMC plant biology*, 26(1).

Placide A, et al. (2026) The de novo transcriptome of the freshwater copepod *Cyclops abyssorum taticus* reveals high-elevation adaptation. *Scientific reports*, 16(1).

Biggel M, et al. (2026) Diversity and abundance of antimicrobial resistance genes in manure from pig farms with varying antibiotic use: a long-read metagenomic sequencing approach. *Porcine health management*, 12(1).

Ba?i? A, et al. (2026) Occurrence and molecular characterization of *Giardia duodenalis* in domestic and wild mesocarnivores in Bosnia and Herzegovina. *International journal for parasitology. Parasites and wildlife*, 29, 101197.