

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Sickle

RRID:SCR_006800

Type: Tool

Proper Citation

Sickle (RRID:SCR_006800)

Resource Information

URL: <https://github.com/najoshi/sickle>

Proper Citation: Sickle (RRID:SCR_006800)

Description: Software tool for windowed adaptive trimming for fastq files using quality. Supports quality values like Illumina, Solexa, and Sanger. Takes the quality values and slides a window across them whose length is 0.1 times the length of the read.

Abbreviations: Sickle

Synonyms: sickle - A windowed adaptive trimming tool for FASTQ files using quality

Resource Type: data processing software, software application, software resource

Keywords: bio.tools, windowed, adaptive, trimming, FASTQ, quality, value, read

Availability: Free, Available for download, Freely available

Resource Name: Sickle

Resource ID: SCR_006800

Alternate IDs: OMICS_01077, biotools:sickle, SCR_016901

Alternate URLs: <https://bio.tools/sickle>, <https://sources.debian.org/src/sickle/>

License: MIT License

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260905T133042+0000

Ratings and Alerts

No rating or validation information has been found for Sickle.

No alerts have been found for Sickle.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1664 mentions in open access literature.

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

Withatanung P, et al. (2026) Genomic diversity and clade clustering of Burkholderia pseudomallei and B. thailandensis prophages with soil-derived phages. iScience, 29(2), 114658.

Kaur H, et al. (2026) Dynamicity of Topoisomerase 1 binding at super-enhancers regulates TLR-responsive gene expression program in macrophages. Cell reports, 45(7), 117604.

Choubey P, et al. (2026) Cohesin complex cooperates with PU.1 at super-enhancers to regulate the differentiation and identity of conventional dendritic cells. Cell reports, 45(5), 117331.

Steele SE, et al. (2026) Drought-associated genes exhibit high constitutive expression in Quercus douglasii, a drought-tolerant California oak. G3 (Bethesda, Md.), 16(2).

Matsubara K, et al. (2026) Composition and nutritional role of gut microbiota on growth performance of pigs at different growth stages. The British journal of nutrition, 135(4), 361.

Hayakawa R, et al. (2026) Globular garden beet represents a distinct lineage in the domestication of Beta vulgaris. BMC plant biology, 26(1), 216.

Vazquez-Munoz R, et al. (2026) Enterococcus faecalis induces H₂O₂-mediated epithelial cell death and enhances Candida albicans virulence in oropharyngeal candidiasis. mSphere, 11(1), e0082225.

Miyatake Y, et al. (2026) A single microRNA miR-195 rescues the arrested B cell development induced by EBF1 deficiency. eLife, 13.

Adachi K, et al. (2026) New insights into the feeding behaviour of the Japanese squid Todarodes pacificus paralarvae, and a combined analysis of metagenome and amino acid isotope ratios. PloS one, 21(3), e0340579.

Chen G, et al. (2026) Integrated Analysis of Transcriptome and Metabolome Reveals Metabolite Biosynthesis in Pigmented Potatoes. International journal of molecular sciences, 27(6).

Liang Q, et al. (2026) Effect of the antimicrobial peptide BmKn2-7 in inhibiting *Vibrio parahaemolyticus* and its role in improving microbiota, immunity and *Vibrio* resistance in *Litopenaeus vannamei*. BMC veterinary research, 22(1).

Tang W, et al. (2026) Transcriptome and metabolome profiling uncover phenotypic divergence of gigantic and dwarf mutant genotypes in induced Pakchoi autotetraploids. BMC plant biology, 26(1).

Peterse IF, et al. (2026) Robust ammonia oxidation by "Candidatus Nitrosacidococcus tergens" across a broad pH range. mBio, 17(5), e0297525.

Lepak A, et al. (2026) Evaluation of an in vivo pulmonary aspergillosis model for triazole susceptibility breakpoint development. Antimicrobial agents and chemotherapy, 70(3), e0164325.

Kurmangali D, et al. (2026) High-quality draft genome sequence data of *Levilactobacillus brevis* 3LB isolated from fermented milk koumiss. Data in brief, 67, 112985.

Begmatov S, et al. (2026) Plasmids of the multidrug-resistant *Citrobacter portucalensis* KOS1-1 strain isolated from a wastewater treatment plant harbor antibiotic resistance genes and gene clusters involved in carbon metabolism. Microbiology spectrum, 14(3), e0203825.

Cho AY, et al. (2026) Wild birds drive the introduction, maintenance, and spread of H5N1 clade 2.3.4.4b high pathogenicity avian influenza viruses in Spain, 2021-2022. Virus evolution, 12(1), veag006.

Beletsky AV, et al. (2026) Complete genome sequence of the wine strain *Saccharomyces cerevisiae* I-25 isolated from Cabernet Sauvignon sediment. Microbiology resource announcements, 15(2), e0122825.

Mkpuma N, et al. (2026) Molecular characterization and phylogeography of equine influenza virus H3N8 detected in donkeys in Nigeria 2022-2023. BMC veterinary research, 22(1).

Gumede NS, et al. (2026) Genomic Characterisation of Antibiotic-Resistant *Escherichia coli* from an Intensive Poultry Production System in the uMgungundlovu District, KwaZulu-Natal, South Africa: A Snapshot. Antibiotics (Basel, Switzerland), 15(2).