**Sickle**

**RRID:** SCR_006800  
**Type:** Tool

**Proper Citation**

Sickle (RRID:SCR_006800)

**Resource Information**

**URL:** https://github.com/najoshi/sickle

**Description:** Software tool that uses sliding windows along with quality and length thresholds to determine when quality is sufficiently low to trim the 3''-end of reads and also determines when the quality is sufficiently high enough to trim the 5''-end of reads. It will also discard reads based upon the length threshold. It takes the quality values and slides a window across them whose length is 0.1 times the length of the read. If this length is less than 1, then the window is set to be equal to the length of the read. Otherwise, the window slides along the quality values until the average quality in the window rises above the threshold, at which point the algorithm determines where within the window the rise occurs and cuts the read and quality there for the 5''-end cut. Then when the average quality in the window drops below the threshold, the algorithm determines where in the window the drop occurs and cuts both the read and quality strings there for the 3''-end cut. However, if the length of the remaining sequence is less than the minimum length threshold, then the read is discarded entirely. 5''-end trimming can be disabled. Sickle also has an option to discard reads with any Ns in them. Sickle supports three types of quality values: Illumina, Solexa, and Sanger. Note that the Solexa quality setting is an approximation (the actual conversion is a non-linear transformation). The end approximation is close. Illumina quality refers to qualities encoded with the CASAVA pipeline between versions 1.3 and 1.7. Illumina quality using CASAVA >= 1.8 is Sanger encoded. Note that Sickle will remove the 2nd fastq record header (on the + line) and replace it with simply a +. This is the default format for CASAVA >= 1.8. Sickle also supports gzipped file inputs. There is also a sickle.xml file included in the package that can be used to add sickle to your local Galaxy server.

**Resource Name:** Sickle

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Resource Type: Resource, software resource

Resource ID: SCR_006800

Website Status: Last checked up

Alternate IDs: OMICS_01077

Abbreviations: Sickle

Mentions Count: 504

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 504 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.

Geoghegan IA, et al. (2020) Weak Acid Resistance A (WarA), a Novel Transcription Factor Required for Regulation of Weak-Acid Resistance and Spore-Spore Heterogeneity in Aspergillus niger. mSphere, 5(1).


