

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

ClipKIT

RRID:SCR_026411

Type: Tool

Proper Citation

ClipKIT (RRID:SCR_026411)

Resource Information

URL: <https://github.com/JLSteenwyk/ClipKIT>

Proper Citation: ClipKIT (RRID:SCR_026411)

Description: Software fast and flexible alignment trimming tool that keeps phylogenetically informative sites and removes others. Multiple sequence alignment-trimming algorithm for accurate phylogenomic inference.

Resource Type: software resource, software application, source code

Defining Citation: [PMID:33264284](#)

Keywords: multiple sequence, alignment trimming, accurate phylogenomic inference,

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National Science Foundation ;
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Fundamental Research Funds for the Central Universities

Availability: Free, Available for download, Freely available

Resource Name: ClipKIT

Resource ID: SCR_026411

License: MIT license

Record Creation Time: 20250212T060343+0000

Record Last Update: 20260808T190745+0000

Ratings and Alerts

No rating or validation information has been found for ClipKIT.

No alerts have been found for ClipKIT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Hoff SNK, et al. (2026) Rapid genome modifications including chromosomal fusions and large-scale inversions are key features in Arctic codfish species. *Genome biology*, 27(1).

Hernández-Roco D, et al. (2026) Chromosome-level genome assembly of the common tenrec, *Tenrec ecaudatus* (Schreber, 1778), a new model for early placental mammal evolution. *BMC genomics*, 27(1).

Ordoñez JF, et al. (2026) Early nervous system development in the chaetognath *Spadella cephaloptera* exhibits conserved bilaterian patterning features. *Frontiers in cell and developmental biology*, 14, 1819435.

Ohkura S, et al. (2026) Study of retroviral restrictions in a *Tadarida* bat cell line enlightens specific early blocks and TRIM5 locus multiplication. *Journal of virology*, 100(4), e0192725.

Boisramé A, et al. (2026) Genomic and transcriptomic insights into *Trichomonascus vanleenenianus*, a xylan-degrading yeast isolated from saproxylic insect larvae. *BMC genomics*, 27(1).

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Huang YT, et al. (2026) Genome diversification of symbiotic fungi in beetle-fungus mutualistic symbioses. *The ISME journal*, 20(1).

Bianchini G, et al. (2026) AliFilter: a machine learning approach to alignment filtering. *Molecular biology and evolution*, 43(4).

Rose AE, et al. (2026) Rational engineering of facultative anaerobiosis enables commensal survival in the oxygenated gut. *bioRxiv : the preprint server for biology*.

Beals DG, et al. (2026) Genomic signatures in *Variovorax* enabling colonization of the *Populus* endosphere. *mSystems*, 11(2), e0160525.

Rosenqvist T, et al. (2026) Detecting "invisible" Phytophthora lineages in publicly available sequencing data. ISME communications, 6(1), ycag019.

Tsai CH, et al. (2026) Phyling: phylogenetic inference from annotated genomes. G3 (Bethesda, Md.), 16(5).

Madhuprakash J, et al. (2026) A potato late blight pathogen effector interacts with ENTH-domain protein TOL9a and an activated helper NLR to suppress immunity. Science advances, 12(23), eaea4500.

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).

Kato K, et al. (2025) Structure of a photosystem I supercomplex from Galdieria sulphuraria close to an ancestral red alga. Science advances, 11(20), eadv7488.

Abou-Kandil A, et al. (2025) The proteomic response of Aspergillus fumigatus to amphotericin B (AmB) reveals the involvement of the RTA-like protein RtaA in AmB resistance. microLife, 6, uqae024.

Zhao T, et al. (2025) Mitonuclear Discordance of Beetles Shaped by Incomplete Lineage Sorting and Introgression Under Loose Interaction Mechanism. Molecular biology and evolution, 42(11).

Barrera Grijalba CC, et al. (2025) Molluscan Shells, Spicules, and Gladii Are Evolutionarily Deeply Conserved. Journal of experimental zoology. Part B, Molecular and developmental evolution, 344(4), 198.

Cantu Morin LM, et al. (2025) The accessory protein CvnF8 modulates histidine kinase activity in an Actinobacterial G protein system in Streptomyces coelicolor. bioRxiv : the preprint server for biology.

Acosta DJ, et al. (2025) Plastic degradation by enzymes from uncultured deep sea microorganisms. The ISME journal, 19(1).