

Resource Summary Report

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Consed

RRID:SCR_005650

Type: Tool

Proper Citation

Consed (RRID:SCR_005650)

Resource Information

URL: <http://www.phrap.org/consed/consed.html>

Proper Citation: Consed (RRID:SCR_005650)

Description: A graphical tool for sequence finishing (BAM File Viewer, Assembly Editor, Autofinish, Autoreport, Autoedit, and Align Reads To Reference Sequence)

Abbreviations: Consed

Resource Type: software resource

Defining Citation: [PMID:23995391](#), [PMID:9521923](#)

Keywords: next-generation sequencing, graphical editor, linux, macosx, solaris, c++

Funding: NIH ;
NHGRI R01HG005710

Availability: Free for academic use, Free for non-profit use, Commercial license

Resource Name: Consed

Resource ID: SCR_005650

Alternate IDs: OMICS_00879

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260801T190256+0000

Ratings and Alerts

No rating or validation information has been found for Consed.

No alerts have been found for Consed.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 595 mentions in open access literature.

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

Washington JM, et al. (2025) Expanding the Diversity of Actinobacterial Tectiviridae: A Novel Genus from Microbacterium. *Viruses*, 17(1).

Culot A, et al. (2025) High-Performance Genome Annotation for a Safer and Faster-Developing Phage Therapy. *Viruses*, 17(3).

Danbaki AS, et al. (2025) Pathogenic FANCC Variants Are Associated with Accessory Breasts in a Sub-Saharan African Multiplex Family. *Current issues in molecular biology*, 47(11).

Mu W, et al. (2025) Characterization of the complete mitochondrial genomes of two sea cucumbers, *Deima validum* and *Oneirophanta mutabilis* (Holothuroidea, Synallactida, Deimatidae): Insight into deep-sea adaptive evolution of Deimatidae. *PloS one*, 20(5), e0323612.

Shu W, et al. (2025) Description of *Streptomyces explomaris* sp. nov., isolated from the coastal soil rhizosphere of *Juniperus excelsa* and reclassification of *Streptomyces libani* as a later heterotypic synonym of *Streptomyces nigrescens*. *International journal of systematic and evolutionary microbiology*, 75(5).

Cao Yao JC, et al. (2024) Complete Genome Sequences of Four Mycobacteriophages Involved in Directed Evolution against Undisputed *Mycobacterium abscessus* Clinical Strains. *Microorganisms*, 12(2).

Baumgartner BM, et al. (2024) Genome sequences of actinobacteriophages JorRay, Blocker23, Nibbles, and OlgasClover. *Microbiology resource announcements*, 13(4), e0125623.

Grabner F M, et al. (2024) *Lacticaseibacillus parahuelsenbergensis* sp. nov., *Lacticaseibacillus styriensis* sp. nov. and *Lacticaseibacillus zeae* subsp. *silagei* subsp. nov., isolated from different grass and corn silage. *International journal of systematic and evolutionary microbiology*, 74(7).

Willner DL, et al. (2024) Transcriptional dynamics during *Rhodococcus erythropolis* infection with phage WC1. *BMC microbiology*, 24(1), 107.

deCarvalho T, et al. (2023) Simultaneous entry as an adaptation to virulence in a novel satellite-helper system infecting *Streptomyces* species. *The ISME journal*, 17(12), 2381.

Loney RE, et al. (2023) A Novel Subcluster of Closely Related Bacillus Phages with Distinct Tail Fiber/Lysin Gene Combinations. *Viruses*, 15(11).

Dulberger CL, et al. (2023) Mycobacterial nucleoid-associated protein Lsr2 is required for productive mycobacteriophage infection. *Nature microbiology*, 8(4), 695.

Amarh ED, et al. (2023) Unusual prophages in Mycobacterium abscessus genomes and strain variations in phage susceptibilities. *PloS one*, 18(2), e0281769.

Baptista LC, et al. (2023) Multiomics profiling of the impact of an angiotensin (1-7)-expressing probiotic combined with exercise training in aged male rats. *Journal of applied physiology* (Bethesda, Md. : 1985), 134(5), 1135.

Aoki K, et al. (2023) Association between Genetic Variation in the TAS2R38 Bitter Taste Receptor and Propylthiouracil Bitter Taste Thresholds among Adults Living in Japan Using the Modified 2AFC Procedure with the Quest Method. *Nutrients*, 15(10).

Angst P, et al. (2023) Near chromosome-level genome assembly of the microsporidium *Hamiltosporidium tvaerminnensis*. *G3* (Bethesda, Md.), 13(10).

Mathes HN, et al. (2023) Complete Genome Sequences of Chop, DelRio, and GrandSlam, Three *Gordonia* Phages Isolated from Soil in Central Arkansas. *Microbiology resource announcements*, 12(5), e0002323.

Gan X, et al. (2022) Emerging of Multidrug-Resistant *Cronobacter sakazakii* Isolated from Infant Supplementary Food in China. *Microbiology spectrum*, 10(5), e0119722.

Curran E, et al. (2022) Genome Sequences of *Gordonia rubripertincta* Bacteriophages AnarQue and Figliar. *Microbiology resource announcements*, 11(1), e0108521.

Pheiffer F, et al. (2022) Bioassay-Guided Fractionation Leads to the Detection of Cholic Acid Generated by the Rare *Thalassomonas* sp. *Marine drugs*, 21(1).