Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 1, 2025

GapCloser

RRID:SCR_015026 Type: Tool

Proper Citation

GapCloser (RRID:SCR_015026)

Resource Information

URL: https://sourceforge.net/projects/soapdenovo2/files/GapCloser/

Proper Citation: GapCloser (RRID:SCR_015026)

Description: Module of SOAPdenovo2 commonly used independently to close gaps in genome assemblies.

Resource Type: software resource, data processing software, source code, software application, sequence analysis software, data analysis software

Defining Citation: PMID:23587118

Keywords: gap closure, genome assembly, sequence

Funding:

Availability: Free, Available for download

Resource Name: GapCloser

Resource ID: SCR_015026

License: GNU General Public License version 3.0 (GPLv3)

Record Creation Time: 20220129T080323+0000

Record Last Update: 20250501T081225+0000

Ratings and Alerts

No rating or validation information has been found for GapCloser.

No alerts have been found for GapCloser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 661 mentions in open access literature.

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

Wu Y, et al. (2025) Characterization of the Phosphotransferase from Bacillus subtilis 1101 That Is Responsible for the Biotransformation of Zearalenone. Toxins, 17(1).

Vignale FA, et al. (2025) Yerba mate (Ilex paraguariensis) genome provides new insights into convergent evolution of caffeine biosynthesis. eLife, 14.

Patel J, et al. (2025) Whole genome sequencing, assembly and annotation of the Southern Ground Hornbill - Bucorvus leadbeateri. Scientific data, 12(1), 58.

Shin HD, et al. (2025) Chromosome-level Genome Assembly of Korean Long-tailed Chicken and Pangenome of 40 Gallus gallus Assemblies. Scientific data, 12(1), 51.

Xiao R, et al. (2025) Phylogeographic and genetic insights into Sinonychia martensi: an endemic cave-dwelling harvestman in Beijing. BMC ecology and evolution, 25(1), 5.

Tian R, et al. (2024) Sirenian genomes illuminate the evolution of fully aquatic species within the mammalian superorder afrotheria. Nature communications, 15(1), 5568.

Mira-Jover A, et al. (2024) Taking advantage of reference-guided assembly in a slowlyevolving lineage: Application to Testudo graeca. PloS one, 19(8), e0303408.

Hu J, et al. (2024) A new chromosome-scale duck genome shows a major histocompatibility complex with several expanded multigene families. BMC biology, 22(1), 31.

Wang L, et al. (2024) Fecal PCR survey and genome analysis of Lawsonia intracellularis in China. Frontiers in veterinary science, 11, 1324768.

Liu J, et al. (2024) Chromosome-level genome assembly of humpback grouper using PacBio HiFi reads and Hi-C technologies. Scientific data, 11(1), 51.

Zhang M, et al. (2024) Genomic Characterization of Phage ZP3 and Its Endolysin LysZP with Antimicrobial Potential against Xanthomonas oryzae pv. oryzae. Viruses, 16(9).

Li H, et al. (2024) The Genome of Vitis zhejiang-adstricta Strengthens the Protection and Utilization of the Endangered Ancient Grape Endemic to China. Plant & cell physiology, 65(2), 216.

Póti Á, et al. (2024) Mutational profile of the regenerative process and de novo genome assembly of the planarian Schmidtea polychroa. Nucleic acids research, 52(4), 1779.

Han Y, et al. (2024) Longitudinal multi-omics analysis uncovers the altered landscape of gut microbiota and plasma metabolome in response to high altitude. Microbiome, 12(1), 70.

Shang B, et al. (2024) A Novel Transposon Tn7709 Harbors Multidrug Resistance Genes in a Pathogenic Aeromonas media Strain QST31. Microorganisms, 12(3).

Shen X, et al. (2024) Exploring the cobia (Rachycentron canadum) genome: unveiling putative male heterogametic regions and identification of sex-specific markers. GigaScience, 13.

Wörheide G, et al. (2024) The genomes of the aquarium sponges Tethya wilhelma and Tethya minuta (Porifera: Demospongiae). F1000Research, 13, 679.

Huang B, et al. (2024) Isolation, characterization, and genomic analysis of a lytic bacteriophage, PQ43W, with the potential of controlling bacterial wilt. Frontiers in microbiology, 15, 1396213.

Peng JF, et al. (2024) Draft genome sequence data of Pythium cedri Chen 4, the causal pathogen of deodar cedar root rot. Data in brief, 57, 110930.

Liu S, et al. (2024) Biosynthetic potential of the gut microbiome in longevous populations. Gut microbes, 16(1), 2426623.