

Resource Summary Report

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

Defining Citation: [PMID:23587118](#)

Keywords: gap closure, genome assembly, sequence

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: 20260805T044334+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

Usage and Citation Metrics

We found 696 mentions in open access literature.

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

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.

Zhang M, et al. (2025) Widespread distribution of BpfA-mediated bisphenol F degradation among members of the Pseudomonadota and Actinomycetota. *The ISME journal*, 19(1).

Santhosh A, et al. (2025) Genomic characterization of an environmental *Burkholderia thailandensis* strain from Kerala, India reveals virulence and antimicrobial resistance signatures. *BMC genomics*, 26(1), 1146.

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

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

Hu J, et al. (2025) Characteristics and Mechanisms of Simultaneous Quinoline and Ammonium Nitrogen Removal by a Robust Bacterium *Pseudomonas stutzeri* H3. *Microorganisms*, 13(3).

Sun T, et al. (2025) Interactions with native microbial keystone taxa enhance the biocontrol efficiency of *Streptomyces*. *Microbiome*, 13(1), 126.

Roberts WR, et al. (2025) Three reference genomes for freshwater diatom ecology and evolution. *Journal of phycology*, 61(2), 267.

Lin Z, et al. (2025) Identification and analysis of VOCs released by *Rhodococcus ruber* GXMZU2400 to promote plant growth and inhibit pathogen growth. *BMC plant biology*, 25(1), 559.

Mulati M, et al. (2025) Diversity of glyphosate-degrading bacteria and degradation genes from Xinjiang cotton field's unique soil environment. *Environmental microbiome*, 20(1), 138.

Sun S, et al. (2025) Screening microbial inhibitors of *Pseudogymnoascus destructans* in Northern China. *Microbiology spectrum*, 13(12), e0124125.

Chakraborty A, et al. (2025) Life inside a bag: multiomics insights into the bagworm species *Eumeta cramer*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).

Chu C, et al. (2025) Characterization of Homeodomain Proteins at the A? Sublocus in *Schizophyllum commune* and Their Role in Sexual Compatibility and Development. *Journal of fungi* (Basel, Switzerland), 11(6).

Ma T, et al. (2025) Familial Reclassification Within Order Lysobacterales and Proposal of Four Novel Species. *Microorganisms*, 13(6).

Li Y, et al. (2025) TELLBASE: a novel tool of TELL-seq barcode-assisted scaffold assembler for bacterial genomes. *Briefings in bioinformatics*, 26(5).

Zhao J-X, et al. (2025) Investigation of the genetic diversity of gut mycobiota of the wild and laboratory mice. *Microbiology spectrum*, 13(5), e0284024.

Luo J, et al. (2025) *Glycyrrhiza* plastid paternal inheritance and a new DNA barcode provide new strategies for molecular identification of three medicinal licorice hybrid complexes. *BMC plant biology*, 25(1), 885.

Wen X, et al. (2025) The genome of giant waterlily provides insights into the origin of angiosperms, leaf gigantism, and stamen function innovation. *Plant communications*, 6(6), 101342.

Záhonová K, et al. (2025) Comparative genomic analysis of trypanosomatid protists illuminates an extensive change in the nuclear genetic code. *mBio*, 16(6), e0088525.