

Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

LR Gapcloser

RRID:SCR_016194

Type: Tool

Proper Citation

LR Gapcloser (RRID:SCR_016194)

Resource Information

URL: http://www.fishbrowser.org/software/LR_Gapcloser/

Proper Citation: LR Gapcloser (RRID:SCR_016194)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 18th, 2023. Software that uses long reads to close gaps in the assemblies.

Synonyms: LR_Gapcloser

Resource Type: alignment software, data processing software, image analysis software, software application, software resource

Defining Citation: [PMID:30576505](#)

Keywords: long, short, read, alignment, assembly, gap, closer, sequence, gene

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: LR Gapcloser

Resource ID: SCR_016194

Alternate IDs: SCR_017021

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260829T182508+0000

Ratings and Alerts

No rating or validation information has been found for LR Gapcloser.

No alerts have been found for LR Gapcloser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 71 mentions in open access literature.

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

Chen W, et al. (2026) A near telomere-to-telomere genome assembly of *Pterocryptis cochinchinensis*. *Scientific data*, 13(1).

Chen D, et al. (2026) The Neijiang pig T2T genome reveals domestication history and germplasm traits of Southwest Chinese local breeds. *Communications biology*, 9(1), 278.

Wang Y, et al. (2026) Recurrent sex chromosome turnover mediated by distinct *ARR17* and *PISTILLATA* duplications in willows. *Genome biology*, 27(1).

Zhou Y, et al. (2026) A telomere-to-telomere reference genome assembly of the *Hypomesus nipponensis*. *Scientific data*, 13(1).

Zhang X, et al. (2026) A telomere-to-telomere gap-free genome assembly of the protandrous maroon clownfish (*Premnas biaculeatus*). *Scientific data*, 13(1), 220.

Bian C, et al. (2025) A complete telomere-to-telomere chromosome-level genome assembly of X-ray tetra (*Pristella maxillaris*). *Scientific data*, 12(1), 496.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Wen H, et al. (2025) TRFill: synergistic use of HiFi and Hi-C sequencing enables accurate assembly of tandem repeats for population-level analysis. *Genome biology*, 26(1), 227.

Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the striped catfish (*Pangasianodon hypophthalmus*). *Scientific data*, 12(1), 1890.

Alvarez-Costes S, et al. (2025) Leveraging Synteny to Generate Reference Genomes for Conservation: Assembling the Genomes of Hector's and Maui Dolphins. *Molecular ecology resources*, 25(7), e14109.

Liang YY, et al. (2025) Pan-Genome Analysis Reveals Local Adaptation to Climate Driven by Introgression in Oak Species. *Molecular biology and evolution*, 42(5).

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the protandrous hermaphrodite Asian seabass (*Lates calcarifer*). *Scientific data*, 12(1), 1457.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

Teterina AA, et al. (2025) Pervasive Conservation of Intron Number and Other Genetic Elements Revealed by a Chromosome-level Genome Assembly of the Hyper-polymorphic Nematode *Caenorhabditis brenneri*. *Genome biology and evolution*, 17(3).

Lee JH, et al. (2025) Chromosome level de Novo hybrid assembly of Asian honeybee, *Apis cerana Koreana*. *Scientific reports*, 15(1), 26912.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Hashiguchi Y, et al. (2024) Draft Genome of Akame (*Lates Japonicus*) Reveals Possible Genetic Mechanisms for Long-Term Persistence and Adaptive Evolution with Low Genetic Diversity. *Genome biology and evolution*, 16(8).