

# Resource Summary Report

Generated by [RRID](#) on Aug 9, 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/](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:** image analysis software, software resource, software application, alignment software, data processing software

**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:** 20260808T190050+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 [RRID](#) .

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).

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.

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

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.

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

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).

Zhang X, et al. (2025) A telomere-to-telomere gap-free genome assembly of the protandrous hermaphrodite Asian seabass (*Lateolabrax japonicus*). *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).