

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 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: data processing software, software resource, image analysis software, alignment software, software application

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: 20260731T043000+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 66 mentions in open access literature.

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

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.

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.

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.

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

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.

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 Korea*. *Scientific reports*, 15(1), 26912.

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

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.

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.

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

Wang Y, et al. (2024) Evolution of Sex-linked Genes and the Role of Pericentromeric Regions in Sex Chromosomes: Insights from Diploid Willows. *Molecular biology and evolution*, 41(11).

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).

Ohdera AH, et al. (2024) The microbiome of a Pacific moon jellyfish *Aurelia coerulea*. *PloS one*, 19(4), e0298002.

Yang Z, et al. (2024) A near-complete assembly of the *Houttuynia cordata* genome provides insights into the regulatory mechanism of flavonoid biosynthesis in Yuxingcao. *Plant communications*, 5(10), 101075.

Kuhl H, et al. (2024) Multi-genome comparisons reveal gain-and-loss evolution of anti-Mullerian hormone receptor type 2 as a candidate master sex-determining gene in Percidae. *BMC biology*, 22(1), 141.

Hsiang TF, et al. (2024) The haplotype-phased genome assembly facilitated the deciphering of the bud dormancy-related QTLs in *Prunus mume*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(1).