

Resource Summary Report

Generated by T1D on Aug 5, 2026

RepeatModeler

RRID:SCR_015027

Type: Tool

Proper Citation

RepeatModeler (RRID:SCR_015027)

Resource Information

URL: <http://www.repeatmasker.org/RepeatModeler/>

Proper Citation: RepeatModeler (RRID:SCR_015027)

Description: Sequence analysis software that performs repeat family identification and creates models for sequence data. RepeatModeler utilizes RepeatScout and RECON to identify repeat element boundaries and family relationships., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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

Keywords: sequence analysis, sequence repeats, repeat identification, bio.tools

Funding: Institute for Systems Biology ;
NHGRI R44 HG02244;
NHGRI R01 HG002939

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RepeatModeler

Resource ID: SCR_015027

Alternate IDs: biotools:repeatmodeler

Alternate URLs: <https://bio.tools/repeatmodeler>

License: Open Source License v2.1

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260805T044333+0000

Ratings and Alerts

No rating or validation information has been found for RepeatModeler.

No alerts have been found for RepeatModeler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3193 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Peng G, et al. (2025) The high-quality telomere-to-telomere genome assembly of the earthworm (*Amyntas aspergillum*). *Scientific data*, 12(1), 931.

Chen SH, et al. (2025) Pathways to Recovery: Genomics and Resistance Assays for Tree Species Devastated by the Myrtle Rust Pathogen. *Molecular ecology*, 34(16), e70030.

Zhang R, et al. (2025) Chromosome-level genome assembly of an Arctic fish species pale eelpout (*Lycodes pallidus*). *Scientific data*, 12(1), 1187.

Xiang N, et al. (2025) Chromosomal level genome assembly of medicinal plant *Chrysosplenium macrophyllum*. *Scientific data*, 12(1), 1224.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Zhu M, et al. (2025) A chromosomal-level genome assembly of *Odontolabis cuvera* Hope, 1842 (Coleoptera: Lucanidae). *Scientific data*, 12(1), 1258.

Liu Y, et al. (2025) Identification of a gene conferring broad-spectrum orthospovirus resistance in Solanaceae. *Science advances*, 11(25), eadw4333.

Dong Z, et al. (2025) A rare, evolutionarily conserved venom protein benefits endoparasitism across parasitoids. *Cell genomics*, 5(8), 100920.

Luo Z, et al. (2025) The first high-quality chromosome-level genome of *Parupeneus biaculeatus* using HiFi and Hi-C data. *Scientific data*, 12(1), 1042.

Chen CC, et al. (2025) High-quality chromosome-level genome of three *Meretrix* species using Nanopore and Hi-C technologies. *Scientific data*, 12(1), 1141.

Huang K, et al. (2025) Super-large record-breaking mitochondrial genome of *Cathaya argyrophylla* in Pinaceae. *Frontiers in plant science*, 16, 1556332.

Zeng Z, et al. (2025) Chromosome-level genome assembly of *Hippophae salicifolia*. *Scientific data*, 12(1), 1503.

Roa-Var??n A, et al. (2025) Chromosome-level genome assembly of the Vermilion Snapper (*Rhomboplites aurorubens*). *Scientific data*, 12(1), 1281.

Lyu H, et al. (2025) A chromosome-level genome assembly of *Coffea arabica* L. var. 'Kona Typica'. *Scientific data*, 12(1), 1314.

Tian X, et al. (2025) Insights into the genetic basis of bilateral head asymmetry in a scale-eating cichlid fish. *Science advances*, 11(31), eadw4406.

Zhao Z, et al. (2025) Evolutionary Consequences of Unusually Large Pericentric TE-rich Regions in the Genome of a Neotropical Fig Wasp. *Genome biology and evolution*, 17(9).

Zhang Y, et al. (2025) Chromosome-level genome assembly and annotation of Amur Pike (*Esox reichertii*). *Scientific data*, 12(1), 1454.

Achakkagari S, et al. (2025) Better together: Subgenomes for allotetraploid potato wild relative *Solanum acaule* Bitt. reveal origins in Petota Clade 3 and 4. *The plant genome*, 18(3), e70095.

Omufwoko KS, et al. (2025) Developmental transcriptomes predict adult social behaviours in the socially flexible sweat bee, *Lasioglossum baleicum*. *Molecular ecology*, 34(15), e17244.

Huang R, et al. (2025) High-quality genome assembly and annotation of the crested gecko (*Correlophus ciliatus*). *G3 (Bethesda, Md.)*, 15(2).