

Resource Summary Report

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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 analysis software, software application, software resource, sequence analysis software, data processing software

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: 20260801T190738+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 [RRID](#) .

Eichert A, et al. (2025) An unusually large genome from an unusually large stonefly: A chromosome-length genome assembly for the giant salmonfly, *Pteronarcys californica* (Plecoptera: Pteronarcyidae). *The Journal of heredity*, 116(3), 315.

Schöneberg Y, et al. (2025) Three Novel Spider Genomes Unveil Spidroin Diversification and Hox Cluster Architecture: *Ryuthela nishihirai* (Liphistiidae), *Uloborus plumipes* (Uloboridae) and *Cheiracanthium punctorium* (Cheiracanthiidae). *Molecular ecology resources*, 25(1), e14038.

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

Polinski JM, et al. (2025) Chromosome-level reference genome for the Jonah crab, *Cancer borealis*. *G3 (Bethesda, Md.)*, 15(1).

González-Ramírez IS, et al. (2025) A genome assembly for the California endemic liverwort *Calasterella californica*. *The Journal of heredity*, 116(3), 389.

Choi SS, et al. (2025) Multiple hybridization events and repeated evolution of homoeologue expression bias in parthenogenetic, polyploid New Zealand stick insects. *Molecular ecology*, 34(15), e17422.

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

Ragasa LRP, et al. (2025) Comparative genomics reveals putative copper tolerance genes in a *Fusarium oxysporum* strain. *G3 (Bethesda, Md.)*, 15(1).

Santos PKF, et al. (2025) The genome of the solitary bee *Tetrapedia diversipes* (Hymenoptera, Apidae). *G3 (Bethesda, Md.)*, 15(2).

Zhou Z, et al. (2025) Chromosome-level assembly and gene annotation of *Kappaphycus striatus* genome. *Scientific data*, 12(1), 249.

Dong Z, et al. (2025) Chromosome-level genome sequencing and assembly of the parasitoid wasp *Leptopilina myrica*. *Scientific data*, 12(1), 235.

Vea IM, et al. (2025) The B Chromosome of *Pseudococcus viburni*: A Selfish Chromosome that Exploits Whole-Genome Meiotic Drive. *Genome biology and evolution*, 17(1).

Ren L, et al. (2025) Genomes reveal pervasive distant hybridization in nature among cyprinid fishes. *GigaScience*, 14.

Zhang Y, et al. (2025) Metabolic enhancement contributed by horizontal gene transfer is essential for dietary specialization in leaf beetles. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2415717122.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of *Cerasus* species and the selection of genetic characteristics in edible cherries. *Molecular horticulture*, 5(1), 6.

Liu R, et al. (2025) Chromosome-level reference genome and annotation of the Arctic fish *Anisarchus medius*. *Scientific data*, 12(1), 68.

Chudhary A, et al. (2025) Characterization of chemosensory genes in the subterranean pest *Gryllotalpa Orientalis* based on genome assembly and transcriptome comparison. *BMC genomics*, 26(1), 33.

Li R, et al. (2025) Photosymbiosis shaped animal genome architecture and gene evolution as revealed in giant clams. *Communications biology*, 8(1), 7.

Zhang D, et al. (2025) Chromosome level genome assembly of 'Wanfeng' almond (*Prunus dulcis*). *Scientific data*, 12(1), 179.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (*Rosa laevigata*). *Scientific data*, 12(1), 132.