

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

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: 20260905T133006+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 3249 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte* (Hong Kong, China), 2026, gigabyte174.

Jian J, et al. (2026) The genome of *Pleurosigma* provides insights into the evolutionary adaptations of pelagic diatoms. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

Tahir MS, et al. (2026) Chromosome-level genome and transcriptome analysis of *Trichophyton verrucosum* reveals pathogenicity mechanisms and antifungal response. *Virulence*, 17(1), 2677294.

Wang L, et al. (2026) Chromosome-level genome assembly, annotation, evolutionary analysis, and establishment of transformation systems in *Carex rigescens*. *Plant cell reports*, 45(5).

Yu C, et al. (2026) Graph pan-genome advances genetic discoveries and the improvement of eggplant. *Horticulture research*, 13(1), uhaf248.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Xin G, et al. (2026) The chromosome-scale genome assembly, annotation of *Bischofia polycarpa* (H. Lév.) Airy Shaw, *Phyllanthaceae*. *Scientific data*, 13(1).

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Huang CH, et al. (2026) Genome-Wide Characterization of Sex-Linked Regions in the Sangzhi Horned Toad (*Boulenophrys sangzhiensis*) Reveals Complex Sex Determination Mechanisms. *Molecular ecology resources*, 26(3), e70136.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Hulsey CD, et al. (2026) Divergence at the IRX gene cluster underlies extreme trophic polymorphism in a cichlid fish (*Herichthys minckleyi*). *Communications biology*, 9(1).

Plasil M, et al. (2026) A chromosome-level genome assembly of the snow leopard, *Panthera uncia*. *The Journal of heredity*, 117(2), 272.

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.

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.

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

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

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