

# Resource Summary Report

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## RepeatMasker

RRID:SCR\_012954

Type: Tool

### Proper Citation

RepeatMasker (RRID:SCR\_012954)

### Resource Information

**URL:** <http://repeatmasker.org/>

**Proper Citation:** RepeatMasker (RRID:SCR\_012954)

**Description:** Software tool that screens DNA sequences for interspersed repeats and low complexity DNA sequences. The output of the program is a detailed annotation of the repeats that are present in the query sequence as well as a modified version of the query sequence in which all the annotated repeats have been masked (default: replaced by Ns). Currently over 56% of human genomic sequence is identified and masked by the program. Sequence comparisons in RepeatMasker are performed by one of several popular search engines including nhmmer, cross\_match, ABblast/WUblast, RMBlast and Decypher. RepeatMasker makes use of curated libraries of repeats and currently supports Dfam ( profile HMM library ) and RepBase ( consensus sequence library ).

**Synonyms:** repeatmasker.org

**Resource Type:** software resource

**Defining Citation:** [DOI:10.1007/978-1-61779-603-6\\_2](https://doi.org/10.1007/978-1-61779-603-6_2)

**Resource Name:** RepeatMasker

**Resource ID:** SCR\_012954

**Alternate IDs:** nlx\_156840, OMICS\_09436

**Old URLs:** <https://sources.debian.org/src/repeatmasker/>

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20260808T190018+0000

### Ratings and Alerts

No rating or validation information has been found for RepeatMasker.

No alerts have been found for RepeatMasker.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 10730 mentions in open access literature.

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

Adami A, et al. (2026) Protocol for efficient CRISPRi-mediated silencing of retrotransposons in human pluripotent stem cells. STAR protocols, 7(1), 104398.

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.

Vuong TT, et al. (2026) DNA Methyltransferase Inhibition Prevents Platinum-Induced Ovarian Cancer Stem Cell Enrichment. Cancer research communications, 6(7), 1721.

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

Li C, et al. (2026) ARID1A deficiency unleashes centromeric RNA transcription to drive chromosomal instability and boosts PKMYT1 inhibitor efficacy via RNA sensing. bioRxiv : the preprint server for biology.

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.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. GigaScience, 15.

Li SY, et al. (2026) TGF $\beta$ 1 Activates Lnc-APUE to Promote Tumor Metastasis via the Alu Element-Driven STAU1-Mediated Decay of CDH1 mRNA. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(20), e18731.

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

Shi M, et al. (2026) Transcriptomic landscape of transposable elements reveals LTR7-PLAAT4 as a potential oncogene and therapeutic target in pancreatic adenocarcinoma. Genome research, 36(2), 275.

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

Zanella E, et al. (2026) Damage-induced i-loops generate eccDNA from repetitive elements. *Molecular cell*, 86(10), 1856.

Yunusbaev U, et al. (2026) The Evolution and Origin of Allotetraploid *Aegilops geniculata* Revealed by the Homoeolog-Resolved Genome Assembly. *Plant biotechnology journal*, 24(3), 1866.

Chen Z, et al. (2026) Evaluating Probe Design for Phylogenomics Across Taxonomic Scales: First Steps for Applying Ultraconserved Elements in an Understudied Class (Mollusca: Polyplacophora). *Molecular ecology resources*, 26(1), e70076.

Wood JC, et al. (2026) Chromosome-scale genome assembly for yellow wood sorrel, *Oxalis stricta*. *G3 (Bethesda, Md.)*, 16(3).

Helmy M, et al. (2026) High-quality mouse reference genomes reveal the structural complexity of the murine protein-coding landscape. *Cell genomics*, 6(2), 101074.

Robinson BR, et al. (2026) Acute testicular hyperthermia leads to rapid loss of global piRNA and a concurrent increase in LINE1 activity within heat sensitive male germ cells. *Mobile DNA*, 17(1), 7.

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(17), e18238.

Konno H, et al. (2026) PacBio long-read amplicon sequencing of dog leukocyte antigen genes at full-length level in beagle dogs. *Experimental animals*, 75(2), 250.

Dhakad P, et al. (2026) Comparative gene annotation and orthology assignments across 301 species of *Drosophilidae*. *bioRxiv : the preprint server for biology*.