

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: 20260801T190442+0000

Ratings and Alerts

No rating or validation information has been found for RepeatMasker.

No alerts have been found for RepeatMasker.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9750 mentions in open access literature.

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

Jarrell AF, et al. (2026) Building genomic resources to facilitate the study and use of *Solanum microdontum*, a wild relative of cultivated potato. *G3* (Bethesda, Md.), 16(1).

Garc??a JF, et al. (2026) Intraspecies sequence-graph analysis of the *Phytophthora theobromicola* genome reveals a dynamic structure and variable effector repertoires. *G3* (Bethesda, Md.), 16(1).

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.

Bonamici L, et al. (2026) Characterization of Copy Number Variants in Hereditary Cancer Patients Through NGS Shows a Distinctive PALB2 Contribution to the Diagnostic Yield. *Human mutation*, 2026, 6601291.

Kulikov N, et al. (2026) The Chromosome-Scale Genome Assembly of the Redlip Blenny, *Ophioblennius macclurei* (Blenniidae). *Genome biology and evolution*, 18(1).

Hirase S, et al. (2026) Ancestral Origin and Structural Characteristics of Non-Syntenic Homologous Chromosomes in Abalones (*Haliotis*). *Molecular ecology resources*, 26(1), e70057.

Miglierina E, et al. (2026) DIS3 licenses B cells for plasma cell differentiation in humans. *Cellular & molecular immunology*, 23(1), 31.

Banno A, et al. (2026) A simple, efficient, and scalable method to generate oocyte-like cells in vitro. *Life science alliance*, 9(2).

Telonis AG, et al. (2026) Synergistic intragenic epigenetic deregulation by IDH2 and SRSF2 mutations causes mis-splicing of key transcriptional regulators. *Science advances*, 12(1), eadu8292.

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Dockman RL, et al. (2026) Improved chromosome-level genome assembly of the American cockroach, *Periplaneta americana*. *G3 (Bethesda, Md.)*, 16(1).

Sperschneider J, et al. (2026) The fungal pathogen *Rhizoctonia solani* AG-8 has 2 nuclear haplotypes that differ in abundance. *G3 (Bethesda, Md.)*, 16(1).

Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3 (Bethesda, Md.)*, 16(1).

Li R, et al. (2026) Whole-genome sequence-based association analysis of African American individuals with bipolar disorder and schizophrenia. *HGG advances*, 7(1), 100499.

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Nachtigall PG, et al. (2026) The Golden Lancehead Genome Reveals Distinct Selective Processes Acting on Venom Genes of an Island Endemic Snake. *Genome biology and evolution*, 18(1).

Chen J, et al. (2026) Genomic and transcriptomic analysis of yield enhancement mechanism of lipopeptide iturin W by tryptone supplementation. *Microbiology spectrum*, 14(1), e0324725.

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