

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

RepeatScout

RRID:SCR_014653

Type: Tool

Proper Citation

RepeatScout (RRID:SCR_014653)

Resource Information

URL: <http://bix.ucsd.edu/repeatscout/>

Proper Citation: RepeatScout (RRID:SCR_014653)

Description: Algorithm used to identify de novo repeat families in newly sequenced genomes. Repeat libraries for *C. briggsae*, *M. musculus* (X chromosome), *R. norvegicus* (X chromosome), armadillo, *H. sapiens* (X chromosome), and various other mammals created using RepeatScout are available on the main site., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16, 2025.

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

Defining Citation: [PMID:15961478](#)

Keywords: algorithm, sequence analysis, repeat, genome sequence, de novo, repeat family, repeat library, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RepeatScout

Resource ID: SCR_014653

Alternate IDs: BioTools:RepeatScout, biotools:RepeatScout

Alternate URLs: <https://bio.tools/RepeatScout>, <https://bio.tools/RepeatScout>, <https://bio.tools/RepeatScout>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260905T132749+0000

Ratings and Alerts

No rating or validation information has been found for RepeatScout.

No alerts have been found for RepeatScout.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 818 mentions in open access literature.

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

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

Pan T, et al. (2025) Genomic insights and the conservation potential of captive breeding: The case of Chinese alligator. Science advances, 11(14), eadm7980.

Tittarelli E, et al. (2025) Transposable element dynamics in *Xenopus laevis* embryogenesis: a tale of two coexisting subgenomes. Mobile DNA, 16(1), 17.

Hospodářská M, et al. (2025) Multiple Origins of Sex Chromosomes in Nothobranchius Killifishes. Molecular ecology, 34(16), e70029.

Rana A, et al. (2025) Genome assembly and annotation of the parasitoid jewel wasp *Nasonia oneida*. Scientific data, 12(1), 1096.

Wang R, et al. (2025) Chromosome-level genome assembly of *Malus niedzwetzkyana*, the mother of Rosybloom crabapple. Scientific data, 12(1), 211.

Zhao X, et al. (2025) Chromosome-level genome assembly of an endoparasitoid *Cotesia ruficrus*. Scientific data, 12(1), 508.

Mondo SJ, et al. (2025) Consecutive low-frequency shifts in A/T content denote nucleosome positions across microeukaryotes. iScience, 28(5), 112472.

Wang J, et al. (2025) Resolving floral development dynamics using genome and single-cell temporal transcriptome of *Dendrobium devonianum*. Plant biotechnology journal, 23(8), 2997.

Navasca A, et al. (2025) Dispensable genome and segmental duplications drive the genome plasticity in *Fusarium solani*. Frontiers in fungal biology, 6, 1432339.

Deng K, et al. (2025) Decoding Pecan's Fungal Foe: A Genomic Insight into *Colletotrichum plurivorum* Isolate W-6. Journal of fungi (Basel, Switzerland), 11(3).

Lv Z, et al. (2025) Near telomere-to-telomere genome assembly of *Camellia pitardii*. Scientific data, 12(1), 1422.

Sun D, et al. (2025) Chromosome-level genome assembly of scalloped spiny lobster *Panulirus homarus homarus*. *Scientific data*, 12(1), 900.

DeWeese K, et al. (2025) Scaffolded and annotated nuclear and organelle genomes of the North American brown alga *Saccharina latissima*. *Frontiers in genetics*, 16, 1494480.

Li X, et al. (2025) Genomic Insights into Post-Domestication Expansion and Selection of Body Size in Ponies. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(16), e2413023.

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

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Bhadauria V, et al. (2025) Near-complete genome and infection transcriptomes of the maize leaf and sheath spot pathogen *Epicoccum sorghinum*. *Scientific data*, 12(1), 261.

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.

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