

Resource Summary Report

Generated by [dkNET](#) on Aug 12, 2026

RepeatScout

RRID:SCR_014653

Type: Tool

Proper Citation

RepeatScout (RRID:SCR_014653)

Resource Information

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

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

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: 20260812T044249+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 [dkNET](#).

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

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

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.

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

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.

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

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

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

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).

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

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

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.