

Resource Summary Report

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Rebase

RRID:SCR_021169

Type: Tool

Proper Citation

Rebase (RRID:SCR_021169)

Resource Information

URL: <https://www.girinst.org/rebase/>

Proper Citation: Rebase (RRID:SCR_021169)

Description: Database of repetitive DNA elements.Database of prototypic sequences representing repetitive DNA from different eukaryotic species. Used in genome sequencing projects worldwide as reference collection for masking and annotation of repetitive DNA.

Resource Type: database, data or information resource

Keywords: repetitive DNA elements, prototypic sequences, eukaryotic species, repetitive DNA masking, repetitive DNA annotation, reference collection, FASEB list

Resource Name: Rebase

Resource ID: SCR_021169

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260808T190435+0000

Ratings and Alerts

No rating or validation information has been found for Rebase.

No alerts have been found for Rebase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 942 mentions in open access literature.

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

LaVigne CA, et al. (2026) Plagl1 and Lrrc58 control mammalian body size by triggering target-directed microRNA degradation of miR-322 and miR-503. *Genes & development*, 40(3-4), 215.

Li Z, et al. (2026) A near-telomere-to-telomere genome assembly of the Chinese soft-shelled turtle (*Pelodiscus sinensis*). *Scientific data*, 13(1), 202.

Kuang Z, et al. (2026) Genomic insights into chromosomal fusion and its evolutionary implications for zokors. *Molecular biology and evolution*, 43(2).

Olver J, et al. (2026) ATRX safeguards cellular identity during *C. elegans* development. *bioRxiv : the preprint server for biology*.

Lu X, et al. (2026) Functional analysis and identification of miRNAs associated with lipid metabolism from milk-derived exosomes. *Journal of animal science and biotechnology*, 17(1), 20.

Zhang Z, et al. (2026) Haplotype-resolved chromosome-level genome assembly of an autohexaploid oil camellia tree *Camellia osmantha*. *Scientific data*, 13(1).

Li H, et al. (2026) Comparative genome analysis provides a foundation for defining salvinatorin A biosynthesis in *Salvia divinorum*. *Nature communications*, 17(1).

Zhang W, et al. (2026) Chromosome level genome assembly of *Camellia sinensis* 'Yuwan Xiaoye'. *Scientific data*, 13(1).

Wu J, et al. (2026) Extracellular vesicle microRNA signature as a highly accurate diagnostic biomarker for human brucellosis. *Frontiers in cellular and infection microbiology*, 16, 1806232.

Qin Q, et al. (2026) Development of a serum-based microRNA panel for Alzheimer's disease diagnosis. *Journal of translational internal medicine*, 14(3), 456.

Senti KA, et al. (2026) Co-evolving infectivity and expression patterns drive the diversification of endogenous retroviruses. *The EMBO journal*, 45(6), 1889.

Liu J, et al. (2026) Telomere-to-Telomere Genome Assembly of Two Hemiculter Species Provide Insights into the Genomic and Morphometric Bases of Adaptation to Flow Velocity. *Biomolecules*, 16(1).

Ahmad A, et al. (2026) Transposable element dynamics in Arthropoda genomes and their impacts on the evolution of functional genes. *BMC biology*, 24(1), 31.

Wang J, et al. (2026) A chromosomal-level genome assembly of *Phoxinus grumi* (Cypriniformes: Leuciscidae). *Scientific data*, 13(1).

Shi X, et al. (2026) Chromosome-level genome assembly of narrow-leaf bur-reed (*Sparganium angustifolium* Michx., Typhaceae). *Scientific data*, 13(1).

Droc G, et al. (2026) A Super-Pangenome for Cultivated Citrus Reveals Evolutive Features During the Allopatric Phase of Their Reticulate Evolution. *Plant biotechnology journal*, 24(5), 3345.

Chen X, et al. (2026) A de novo assembled chromosome-level genome of *Ainsliaea gracilis* Franch. (Pertyeae, Asteraceae) and its comparative phylogenomics within Asteraceae. *BMC plant biology*, 26(1).

Wu B, et al. (2026) Chromosome-level genome assembly of masu salmon (*Oncorhynchus masou masou*). *Scientific data*, 13(1).

Chen Q, et al. (2026) Chromosome-level genome assembly and annotation of the critically endangered Siberian crane (*Leucogeranus leucogeranus*). *Scientific data*, 13(1).

Jiang XL, et al. (2026) Population genomics of *Quercus gilva* provides insights into the conservation of fengshui forests. *Communications biology*, 9(1).