

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

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: data or information resource, database

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: 20260801T191023+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 822 mentions in open access literature.

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

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.

Michel M, et al. (2025) Noninvasive Multicancer Detection Using DNA Hypomethylation of LINE-1 Retrotransposons. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(7), 1275.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.

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.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (*Rosa laevigata*). *Scientific data*, 12(1), 132.

Wu B, et al. (2025) Identification and analysis of miRNA - mRNA regulatory modules associated with resistance to bacterial leaf streak in rice. *BMC genomics*, 26(1), 207.

Song Y, et al. (2025) Haplotype-Phased Chromosome-Level Genome Assembly of *Cryptoporus qinlingensis*, a Typical Traditional Chinese Medicine Fungus. *Journal of fungi (Basel, Switzerland)*, 11(2).

Cho H, et al. (2025) Chromosome-level genome assembly and improved annotation of onion genome (*Allium cepa* L.). *Scientific data*, 12(1), 336.

He H, et al. (2025) Chromosome-level genome assembly of *Monolepta hieroglyphica*, two-spotted leaf beetle (Coleoptera: Chrysomelidae). *Scientific data*, 12(1), 1.

Chen P, et al. (2025) Chromosome-scale assembly of *Artemia tibetiana* genome, first aquatic invertebrate genome from Tibet Plateau. *Scientific data*, 12(1), 777.

Ning Y, et al. (2025) Chromosome-level genome assembly for clubrush (*Scirpus × mariqueter*) endemic to China. *Scientific data*, 12(1), 839.

Zhao Y, et al. (2025) A chromosome-level genome assembly of the *Bullacta exarata* (Cephalaspidea: Haminoeidae). *Scientific data*, 12(1), 1008.

Huang T, et al. (2025) Chromosome-level genome assembly of the aphid *Megoura crassicauda*. *Scientific data*, 12(1), 994.

Yang Y, et al. (2025) The Nearly Complete Genome of *Grifola frondosa* and Light-Induced Genes Screened Based on Transcriptomics Promote the Production of Triterpenoid Compounds. *Journal of fungi (Basel, Switzerland)*, 11(4).

Kang Z, et al. (2025) Genomic and Multi-Omics Analysis of *Phlebopus portentosus*: Effects of Cultivation on Secondary Metabolites. *Journal of fungi (Basel, Switzerland)*,

11(4).

Newman AG, et al. (2025) Glial reactivity and cognitive decline follow chronic heterochromatin loss in neurons. *Nature communications*, 16(1), 7325.

Xiang N, et al. (2025) Chromosomal level genome assembly of medicinal plant *Chrysosplenium macrophyllum*. *Scientific data*, 12(1), 1224.

Chen Y, et al. (2025) Non-disruptive 3D profiling of combinations of epigenetic marks in single cells. *bioRxiv : the preprint server for biology*.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Lv Y, et al. (2025) Chromosome-level genome assembly reveals adaptive evolution of the invasive Amazon sailfin catfish (*Pterygoplichthys pardalis*). *Communications biology*, 8(1), 616.