

Resource Summary Report

Generated by [dkNET](#) on Aug 27, 2026

Dfam

RRID:SCR_021168

Type: Tool

Proper Citation

Dfam (RRID:SCR_021168)

Resource Information

URL: <https://dfam.org/home>

Proper Citation: Dfam (RRID:SCR_021168)

Description: Open collection of Transposable Element DNA sequence alignments, hidden Markov Models, consensus sequences, and genome annotations. Dfam 3.2 provides early access to uncurated, de novo generated families.

Synonyms: Dfam 3.2

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1186/s13100-020-00230-y](https://doi.org/10.1186/s13100-020-00230-y)

Keywords: Transposable Element, DNA sequence alignments, hidden Markov Models, consensus sequences, genome annotations

Funding: NHGRI R01 HG002939;
NHGRI U24 HG010136

Availability: Free, Freely available

Resource Name: Dfam

Resource ID: SCR_021168

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260821T194151+0000

Ratings and Alerts

No rating or validation information has been found for Dfam.

No alerts have been found for Dfam.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 110 mentions in open access literature.

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

Sobreiro MB, et al. (2026) De Novo Chromosome-Level Assembly of the Endangered *Pilocarpus Microphyllus* Highlights Genomic Resources for Conservation and Sustainable *Pilocarpine* Extraction. *Genome biology and evolution*, 18(3).

Shi X, et al. (2026) Chromosome-level genome assembly of *Sinodiscula camellicola* strain Scam5. *Scientific data*, 13(1).

Cajigas Gandia A, et al. (2026) Transcriptomic genotyping elucidates the population structure and demographic history of the endangered poison frog *Oophaga vicentei* (Anura: Dendrobatidae). *BMC genomics*, 27(1).

Griem-Krey H, et al. (2026) Transposable elements hitchhike on Starships across fungal genomes. *Nature communications*, 17(1).

Zhang J, et al. (2026) A Set of Novel Venom Proteins Enables Parasitoid Wasps to Exploit Older Hosts and Coexist with Competitors. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e12654.

Adami A, et al. (2026) Protocol for efficient CRISPRi-mediated silencing of retrotransposons in human pluripotent stem cells. *STAR protocols*, 7(1), 104398.

Stratakis M, et al. (2026) Unravelling the thread of *Podarcis* omics; insights into the genome and transcriptome of the Cretan wall lizard. *Genes & genomics*, 48(1), 27.

Miao B, et al. (2026) Expression spectrum of TE-driven transcripts in human adult tissues. *Genome biology*, 27(1).

Bibi AC, et al. (2026) High-Quality Genome Assembly and Annotation of *Ceratonia siliqua* Provide Insights Into the Secondary Loss of Symbiotic Nitrogen Fixation. *Physiologia plantarum*, 178(1), e70803.

Wang J, et al. (2026) The chromosomal-level genome assembly and annotation of *Phyllospadix iwatensis* (Surfgrass). *Scientific data*, 13(1).

Bodelón A, et al. (2026) Male sterility in *Drosophila* hybrids revealed by a multi-generational transcriptomic analysis of genes and transposable elements in testes. *BMC biology*, 24(1).

Méndez M, et al. (2026) First draft genome and genomic analysis of *Neofusicoccum parvum* isolated from mango (*Mangifera indica* L.) in Paraguay. *Frontiers in fungal biology*, 7, 1813584.

Quintanilla-Mena M, et al. (2026) De novo Genome Assembly, Annotation, and Comparative Analysis of the Lined Sole *Achirus lineatus* as a Resource for Evolutionary and Environmental Genomics. *Marine biotechnology* (New York, N.Y.), 28(4).

Aoyagi YB, et al. (2026) Chromosome-level genome assembly of the *Gerbera* (*Gerbera hybrida*) using HiFi long-read and Hi-C technologies. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 33(1).

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

Veseljak D, et al. (2026) *Tribolium madens* satellitome reveals a network of highly abundant satellite DNAs in megabase-sized regions hallmarked by macro-dyad symmetries. *Genome biology*, 27(1).

Lin F, et al. (2026) A chromosome-level genome assembly of the panda loach (*Yaoshania pachychilus*). *Scientific data*, 13(1).

Huang R, et al. (2026) IAPez retrotransposons regulate the first lineage segregation in mouse pre-implantation development. *Nucleic acids research*, 54(11).

Zanella E, et al. (2026) Damage-induced i-loops generate eccDNA from repetitive elements. *Molecular cell*, 86(10), 1856.

Lind AL, et al. (2025) Contiguous and complete assemblies of *Blastocystis* gut microbiome-associated protists reveal evolutionary diversification to host ecology. *Genome research*, 35(6), 1377.