

Resource Summary Report

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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 U24 HG010136;
NHGRI R01 HG002939

Availability: Free, Freely available

Resource Name: Dfam

Resource ID: SCR_021168

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260801T191041+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 82 mentions in open access literature.

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

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.

MacDonald ZG, et al. (2025) Whole-Genome Evaluation of Genetic Rescue: The Case of a Curiously Isolated and Endangered Butterfly. *Molecular ecology*, 34(4), e17657.

Souza LHB, et al. (2025) New Insights into the Sex Chromosome Evolution of the Common Barker Frog Species Complex (Anura, Leptodactylidae) Inferred from Its Satellite DNA Content. *Biomolecules*, 15(6).

Zhu M, et al. (2025) A chromosomal-level genome assembly of *Odontolabis cuvera* Hope, 1842 (Coleoptera: Lucanidae). *Scientific data*, 12(1), 1258.

Peng G, et al. (2025) The high-quality telomere-to-telomere genome assembly of the earthworm (*Amyntas aspergillum*). *Scientific data*, 12(1), 931.

McGrath N, et al. (2025) A high-quality Oxford Nanopore assembly of the hourglass dolphin (*Lagenorhynchus cruciger*) genome. *G3 (Bethesda, Md.)*, 15(5).

Jiang Z, et al. (2025) Chromosomal-level genome assembly of *Trichogramma japonicum* (Hymenoptera: Trichogrammatidae). *Scientific data*, 12(1), 1537.

Li Y, et al. (2025) Chromosome-level genome assembly and annotation of the *Triplophysa pappenheimi*. *Scientific data*, 12(1), 1859.

Zhang Y, et al. (2025) Chromosome-level genome assembly of black carp *Mylopharyngodon piceus* using Nanopore and Hi-C technologies. *Scientific data*, 12(1), 145.

Shin HD, et al. (2025) Chromosome-level Genome Assembly of Korean Long-tailed Chicken and Pangenome of 40 *Gallus gallus* Assemblies. *Scientific data*, 12(1), 51.

Lee JH, et al. (2025) Chromosome level de Novo hybrid assembly of Asian honeybee, *Apis cerana* Koreana. *Scientific reports*, 15(1), 26912.

Qi J, et al. (2025) Genomic Sequencing and Characterization of Two *Auricularia* Species from the Qinling Region: Insights into Evolutionary Dynamics and Secondary Metabolite Potential. *Journal of fungi (Basel, Switzerland)*, 11(5).

Cheung TY, et al. (2025) Exceptionally low genomic diversity in the underutilised legume Kersting's groundnut. *Nature communications*, 16(1), 5183.

Vignale FA, et al. (2025) Yerba mate (*Ilex paraguariensis*) genome provides new insights into convergent evolution of caffeine biosynthesis. *eLife*, 14.

Peterson JK, et al. (2025) First whole-genome sequence of *Triatoma sanguisuga* (Le Conte, 1855), vector of Chagas disease. *G3* (Bethesda, Md.), 15(3).

Yan Y, et al. (2025) Degenerated vision, altered lipid metabolism, and expanded chemoreceptor repertoires enable *Lindaspio polybranchiata* to thrive in deep-sea cold seeps. *BMC biology*, 23(1), 13.

Li R, et al. (2025) Chromosome-Level Genome Assembly of the Heptageniid Mayfly *Parafronurus youi* (Ephemeroptera), and Its Annotation. *Genome biology and evolution*, 17(3).

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: *Phoxinus phoxinus*) provide evidence of haplotype diversity. *GigaScience*, 14.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Bulzu PA, et al. (2025) Lineage-specific expansions of polinton-like viruses in photosynthetic cryptophytes. *Microbiome*, 13(1), 154.