Resource Summary Report

Generated by RRID on Apr 19, 2025

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: database, data or information resource

Defining Citation: DOI: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: 20250412T060318+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 67 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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.

Lai Y, et al. (2025) Genome assembly of the grassland caterpillar Gynaephora qinghaiensis. Scientific data, 12(1), 158.

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.

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

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.

Sylvester T, et al. (2024) A reference quality genome assembly for the jewel scarab Chrysina gloriosa. G3 (Bethesda, Md.), 14(6).

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

Wang C, et al. (2024) Comprehensive characterization of ERV-K (HML-8) in the chimpanzee genome revealed less genomic activity than humans. Frontiers in cellular and infection microbiology, 14, 1349046.

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex

communication. GigaScience, 13.

Xia W, et al. (2024) Chromosome-level genome provides new insight into the overwintering process of Korla pear (Pyrus sinkiangensis Yu). BMC plant biology, 24(1), 773.

Chen HM, et al. (2024) A chromosome-scale reference genome of the Banna miniature inbred pig. Scientific data, 11(1), 1345.

Wang Y, et al. (2024) Chromosome-scale genome, together with transcriptome and metabolome, provides insights into the evolution and anthocyanin biosynthesis of Rubus rosaefolius Sm. (Rosaceae). Horticulture research, 11(4), uhae064.

Kim B, et al. (2024) Chromosome-level genome assembly of Korean holoparasitic plants, Orobanche coerulescens. Scientific data, 11(1), 714.

Zhu X, et al. (2024) An expanded odorant-binding protein mediates host cue detection in the parasitic wasp Baryscapus dioryctriae basis of the chromosome-level genome assembly analysis. BMC biology, 22(1), 196.

Peterson JK, et al. (2024) Genome report: First whole genome sequence of Triatoma sanguisuga (Le Conte, 1855), vector of Chagas disease. bioRxiv : the preprint server for biology.

Wei T, et al. (2024) Chromosome-level genome assembly of two cultivated Jujubes. Scientific data, 11(1), 1144.

Ivancevic A, et al. (2024) Endogenous retroviruses mediate transcriptional rewiring in response to oncogenic signaling in colorectal cancer. Science advances, 10(29), eado1218.

Li Z, et al. (2024) Intraspecific diploidization of a halophyte root fungus drives heterosis. Nature communications, 15(1), 5872.

Chen M, et al. (2024) Comprehensive Identification and Characterization of HML-9 Group in Chimpanzee Genome. Viruses, 16(6).