

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

Tandem Repeats Database

RRID:SCR_005659

Type: Tool

Proper Citation

Tandem Repeats Database (RRID:SCR_005659)

Resource Information

URL: <http://tandem.bu.edu/cgi-bin/trdb/trdb.exe>

Proper Citation: Tandem Repeats Database (RRID:SCR_005659)

Description: A public repository of information on tandem repeats in genomic DNA and contains a variety of tools for their analysis. These currently include the Tandem Repeats Finder algorithm, query and filtering capabilities for finding particular repeats of interest, repeat clustering algorithms based on sequence similarity, polymorphism prediction based on common patterns of mutation, PCR primer selection, and data download in a variety of formats. In addition, TRDB serves as a centralized research workbench, provides storage space for results of analysis, and permits collaborators to privately share their data and analysis.

Abbreviations: TRDB

Synonyms: Tandem Repeats Database

Resource Type: data or information resource, database

Resource Name: Tandem Repeats Database

Resource ID: SCR_005659

Alternate IDs: nif-0000-03584

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260815T182844+0000

Ratings and Alerts

No rating or validation information has been found for Tandem Repeats Database.

No alerts have been found for Tandem Repeats Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Alves SIA, et al. (2024) What are microsatellites and how to choose the best tool: a user-friendly review of SSR and 74 SSR mining tools. *Frontiers in genetics*, 15, 1474611.

Hemedan AA, et al. (2024) Cohort-specific boolean models highlight different regulatory modules during Parkinson's disease progression. *iScience*, 27(10), 110956.

Kumar S, et al. (2023) Evolution of Resistance to Irinotecan in Cancer Cells Involves Generation of Topoisomerase-Guided Mutations in Non-Coding Genome That Reduce the Chances of DNA Breaks. *International journal of molecular sciences*, 24(10).

Çilingir FG, et al. (2022) Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. *GigaScience*, 11.

Ikegami M, et al. (2021) MicroSEC filters sequence errors for formalin-fixed and paraffin-embedded samples. *Communications biology*, 4(1), 1396.

Gonçalves MFM, et al. (2021) Genomic and Metabolomic Analyses of the Marine Fungus *Emericellopsis cladophorae*: Insights into Saltwater Adaptability Mechanisms and Its Biosynthetic Potential. *Journal of fungi (Basel, Switzerland)*, 8(1).

Gonçalves MFM, et al. (2021) Genome and Metabolome MS-Based Mining of a Marine Strain of *Aspergillus affinis*. *Journal of fungi (Basel, Switzerland)*, 7(12).

Li Y, et al. (2020) Pacific Biosciences assembly with Hi-C mapping generates an improved, chromosome-level goose genome. *GigaScience*, 9(10).

Fumasoni M, et al. (2020) The evolutionary plasticity of chromosome metabolism allows adaptation to constitutive DNA replication stress. *eLife*, 9.

Cserhati M, et al. (2019) K-mer-Based Motif Analysis in Insect Species across *Anopheles*, *Drosophila*, and *Glossina* Genera and Its Application to Species Classification. *Computational and mathematical methods in medicine*, 2019, 4259479.

Lu S, et al. (2019) Chromosomal-level reference genome of Chinese peacock butterfly (*Papilio bianor*) based on third-generation DNA sequencing and Hi-C analysis. *GigaScience*, 8(11).

Cameron DL, et al. (2019) Comprehensive evaluation and characterisation of short read general-purpose structural variant calling software. *Nature communications*, 10(1), 3240.

Ahmed M, et al. (2012) Transposable elements are a significant contributor to tandem repeats in the human genome. *Comparative and functional genomics*, 2012, 947089.

Polato NR, et al. (2011) Gene discovery in the threatened elkhorn coral: 454 sequencing of the *Acropora palmata* transcriptome. *PloS one*, 6(12), e28634.