

Resource Summary Report

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Tandem Repeats Finder

RRID:SCR_022065

Type: Tool

Proper Citation

Tandem Repeats Finder (RRID:SCR_022065)

Resource Information

URL: <https://github.com/Benson-Genomics-Lab/TRF>

Proper Citation: Tandem Repeats Finder (RRID:SCR_022065)

Description: Software tool to locate and display tandem repeats in DNA sequences. Used to analyze DNA sequences.

Resource Type: data analysis software, software application, software resource, data processing software, sequence analysis software

Defining Citation: [PMID:9862982](#)

Keywords: locate and display tandem repeats, analyze DNA sequences, tandem repeat, DNA sequence

Availability: Free, Available for download, Freely available

Resource Name: Tandem Repeats Finder

Resource ID: SCR_022065

License: GNU AFFERO GENERAL PUBLIC LICENSE

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260812T044416+0000

Ratings and Alerts

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

No alerts have been found for Tandem Repeats Finder.

Data and Source Information

Usage and Citation Metrics

We found 443 mentions in open access literature.

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

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Doré G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte (Hong Kong, China)*, 2026, gigabyte176.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 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.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

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

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

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.

Xu Y, et al. (2024) Chromosome-level genome of the poultry shaft louse *Menopon gallinae* provides insight into the host-switching and adaptive evolution of parasitic lice. *GigaScience*, 13(1).

Cui G, et al. (2023) *Meliaceae* genomes provide insights into wood development and limonoids biosynthesis. *Plant biotechnology journal*, 21(3), 574.

López-Cortegano E, et al. (2023) Rates and spectra of de novo structural mutations in *Chlamydomonas reinhardtii*. *Genome research*, 33(1), 45.

Jin M, et al. (2023) Chromosome-level genome of black cutworm provides novel insights into polyphagy and seasonal migration in insects. *BMC biology*, 21(1), 2.

Sun B, et al. (2023) The chromosome-level genome and key genes associated with mud-dwelling behavior and adaptations of hypoxia and noxious environments in loach (*Misgurnus anguillicaudatus*). *BMC biology*, 21(1), 18.

Craig RJ, et al. (2023) The *Chlamydomonas* Genome Project, version 6: Reference assemblies for mating-type plus and minus strains reveal extensive structural mutation in the laboratory. *The Plant cell*, 35(2), 644.

Hu W, et al. (2023) A molecular atlas reveals the tri-sectional spinning mechanism of spider dragline silk. *Nature communications*, 14(1), 837.

Fajkus P, et al. (2023) Telomerase RNA in Hymenoptera (Insecta) switched to plant/ciliate-like biogenesis. *Nucleic acids research*, 51(1), 420.

Tang CY, et al. (2023) Genetic mapping and molecular mechanism behind color variation in the Asian vine snake. *Genome biology*, 24(1), 46.

Rojrung R, et al. (2023) Analysis of sequence diversity in *Plasmodium falciparum* glutamic acid-rich protein (PfGARP), an asexual blood stage vaccine candidate. *Scientific reports*, 13(1), 3951.

Yang Y, et al. (2023) Chromosome-Level Genome Assembly of *Herpetospermum pedunculatum* (Cucurbitaceae). *Genome biology and evolution*, 15(2).