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, sequence analysis software, data processing software, software resource

Defining Citation: PMID:9862982

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

Funding:

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: 20250509T060400+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 436 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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.

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

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

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.

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.

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

Li J, et al. (2023) The nearly complete assembly of the Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. Plant communications, 4(1), 100422.

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

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.

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

Guo Y, et al. (2023) Hologenome analysis reveals independent evolution to chemosymbiosis by deep-sea bivalves. BMC biology, 21(1), 51.

Payne ZL, et al. (2023) A gap-free genome assembly of Chlamydomonas reinhardtii and detection of translocations induced by CRISPR-mediated mutagenesis. Plant communications, 4(2), 100493.

Johnson AR, et al. (2023) Chromosome-level Genome Assembly of Euphorbia peplus, a Model System for Plant Latex, Reveals that Relative Lack of Ty3 Transposons Contributed to Its Small Genome Size. Genome biology and evolution, 15(3).

Macas J, et al. (2023) Assembly of the 81.6 Mb centromere of pea chromosome 6 elucidates the structure and evolution of metapolycentric chromosomes. PLoS genetics, 19(2), e1010633.

Alekseeva M, et al. (2023) A Set of Highly Polymorphic Microsatellite Markers for Genetic Diversity Studies in the Genus Origanum. Plants (Basel, Switzerland), 12(4).

Ikemoto K, et al. (2023) Localized assembly for long reads enables genome-wide analysis of repetitive regions at single-base resolution in human genomes. Human genomics, 17(1), 21.