Resource Summary Report

Generated by RRID on Apr 8, 2025

Dotter

RRID:SCR_016080
Type: Tool

Proper Citation

Dotter (RRID:SCR_016080)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/seqtools

Proper Citation: Dotter (RRID:SCR_016080)

Description: Software for sequence alignment that is a graphical dot-matrix program for detailed comparison of two sequences.

Synonyms: Seqtools Dotter

Resource Type: alignment software, software application, data visualization software, sequence analysis software, data analysis software, data processing software, image analysis software, software resource

Defining Citation: PMID:26801397

Keywords: sequence, alignment, graphical, dot-matrix, program, comparison, two, detail

Funding: Wellcome Trust Grant 098051;
NHGRI U54 HG00455

Availability: Free, Available for download

Resource Name: Dotter

Resource ID: SCR_016080

License: GNU GPL version 3, Apache Version 2.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250407T220307+0000

Ratings and Alerts

No rating or validation information has been found for Dotter.

No alerts have been found for Dotter.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Kobrlová L, et al. (2024) First insight into the genomes of the Pulmonaria officinalis group (Boraginaceae) provided by repeatome analysis and comparative karyotyping. BMC plant biology, 24(1), 859.

Wernersson E, et al. (2024) Deconwolf enables high-performance deconvolution of widefield fluorescence microscopy images. Nature methods, 21(7), 1245.

Schwartz JC, et al. (2024) A genome assembly and transcriptome atlas of the inbred Babraham pig to illuminate porcine immunogenetic variation. Immunogenetics, 76(5-6), 361.

Trunova D, et al. (2024) Does time matter? Intraspecific diversity of ribosomal RNA genes in lineages of the allopolyploid model grass Brachypodium hybridum with different evolutionary ages. BMC plant biology, 24(1), 981.

Zhao H, et al. (2023) A 1.5-Mb continuous endogenous viral region in the arbuscular mycorrhizal fungus Rhizophagus irregularis. Virus evolution, 9(2), vead064.

Mota A, et al. (2022) FRET-FISH probes chromatin compaction at individual genomic loci in single cells. Nature communications, 13(1), 6680.

Mota A, et al. (2022) Simultaneous visualization of DNA loci in single cells by combinatorial multi-color iFISH. Scientific data, 9(1), 47.

Zhang M, et al. (2021) Definition of a High-Resolution Molecular Marker for Tracking the Genetic Diversity of the Harmful Algal Species Eucampia zodiacus Through Comparative Analysis of Mitochondrial Genomes. Frontiers in microbiology, 12, 631144.

Kolodziej MC, et al. (2021) A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. Nature communications, 12(1), 956.

Moolhuijzen P, et al. (2020) PacBio genome sequencing reveals new insights into the genomic organisation of the multi-copy ToxB gene of the wheat fungal pathogen Pyrenophora tritici-repentis. BMC genomics, 21(1), 645.

Bornancini VA, et al. (2020) Reconstruction and Characterization of Full-Length Begomovirus and Alphasatellite Genomes Infecting Pepper through Metagenomics. Viruses, 12(2).

Zwyrtková J, et al. (2020) Comparative analyses of DNA repeats and identification of a novel Fesreba centromeric element in fescues and ryegrasses. BMC plant biology, 20(1), 280.

Ventimiglia M, et al. (2020) On the Trail of Tetu1: Genome-Wide Discovery of CACTA Transposable Elements in Sunflower Genome. International journal of molecular sciences, 21(6).

Merski M, et al. (2020) Self-analysis of repeat proteins reveals evolutionarily conserved patterns. BMC bioinformatics, 21(1), 179.

Usai G, et al. (2020) Interspecific hybridisation and LTR-retrotransposon mobilisation-related structural variation in plants: A case study. Genomics, 112(2), 1611.

Báez M, et al. (2019) Together But Different: The Subgenomes of the Bimodal Eleutherine Karyotypes Are Differentially Organized. Frontiers in plant science, 10, 1170.

Gelali E, et al. (2019) iFISH is a publically available resource enabling versatile DNA FISH to study genome architecture. Nature communications, 10(1), 1636.

Thind AK, et al. (2018) Chromosome-scale comparative sequence analysis unravels molecular mechanisms of genome dynamics between two wheat cultivars. Genome biology, 19(1), 104.

El Baidouri M, et al. (2018) Genic C-Methylation in Soybean Is Associated with Gene Paralogs Relocated to Transposable Element-Rich Pericentromeres. Molecular plant, 11(3), 485.

Buti M, et al. (2018) The genome sequence and transcriptome of Potentilla micrantha and their comparison to Fragaria vesca (the woodland strawberry). GigaScience, 7(4), 1.