

Resource Summary Report

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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, data analysis software, data processing software, data visualization software, image analysis software, sequence analysis software, software application, software resource

Defining Citation: [PMID:26801397](#)

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

Funding: NHGRI U54 HG00455;
Wellcome Trust Grant 098051

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: 20260821T194050+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 84 mentions in open access literature.

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

Lim ZH, et al. (2025) Diatom heterotrophy on brown algal polysaccharides emerged through horizontal gene transfer, gene duplication, and neofunctionalization. PLoS biology, 23(4), e3003038.

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) Deconvolf 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.

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.

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.

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).

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

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

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

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

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.