

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>

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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: 20260912T195835+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 [SPARC SAWG](#) .

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.