Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 1, 2025

Jellyfish

RRID:SCR_005491
Type: Tool

Proper Citation

Jellyfish (RRID:SCR_005491)

Resource Information

URL: http://www.genome.umd.edu/jellyfish.html

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Description: A software tool for fast, memory-efficient counting of k-mers in DNA. A k-mer is a substring of length k, and counting the occurrences of all such substrings is a central step in many analyses of DNA sequence. JELLYFISH can count k-mers quickly by using an efficient encoding of a hash table and by exploiting the compare-and-swap CPU instruction to increase parallelism. Jellyfish is a command-line program that reads FASTA and multi-FASTA files containing DNA sequences. It outputs its k-mer counts in an binary format, which can be translated into a human-readable text format using the jellyfish dump command.

Abbreviations: Jellyfish

Synonyms: Jellyfish mer counter

Resource Type: software resource

Defining Citation: PMID:21217122, DOI:10.1093/bioinformatics/btr011

Keywords: c++, bio.tools

Funding:

Availability: GNU General Public License

Resource Name: Jellyfish

Resource ID: SCR_005491

Alternate IDs: biotools:jellyfish, OMICS_01056

Alternate URLs: https://bio.tools/jellyfish, https://sources.debian.org/src/jellyfish1/

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250214T183124+0000

Ratings and Alerts

No rating or validation information has been found for Jellyfish.

No alerts have been found for Jellyfish.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 935 mentions in open access literature.

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

Choi S, et al. (2025) Chromosome-level genome assembly of Salvia sclarea. Scientific data, 12(1), 14.

Yang Y, et al. (2025) Systematic identification of secondary bile acid production genes in global microbiome. mSystems, 10(1), e0081724.

Liang Y, et al. (2025) The giant genome of lily provides insights into the hybridization of cultivated lilies. Nature communications, 16(1), 45.

Zhang W, et al. (2025) Chromosome-level genome assembly of tetraploid Chinese cherry (Prunus pseudocerasus). Scientific data, 12(1), 136.

Patankar HV, et al. (2025) A Chromosome level assembly of pomegranate (Punica granatum L.) variety grown in arid environment. Scientific data, 12(1), 73.

Lan L, et al. (2025) Chromosome-level and haplotype-resolved genome assembly of Bougainvillea glabra. Scientific data, 12(1), 107.

Yang Y, et al. (2025) A Chromosome-Scale Genome of Trametes versicolor and Transcriptome-Based Screening for Light-Induced Genes That Promote Triterpene

Biosynthesis. Journal of fungi (Basel, Switzerland), 11(1).

Yang G, et al. (2025) Chromosome-level genome assembly of Megachile sculpturalis Smith (Hymenoptera, Apoidea, Megachilidae). Scientific data, 12(1), 46.

Yan Y, et al. (2025) Degenerated vision, altered lipid metabolism, and expanded chemoreceptor repertoires enable Lindaspio polybranchiata to thrive in deep-sea cold seeps. BMC biology, 23(1), 13.

Wang GF, et al. (2025) Chromosome-level genome assembly of a destructive leaf-mining moth Eriocrania semipurpurella alpina. Scientific data, 12(1), 2.

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.

Guan DL, et al. (2025) A high-quality chromosome-level genome assembly of the mulberry looper, Phthonandria atrilineata. Scientific data, 12(1), 186.

Liu JN, et al. (2025) Pan-genome analyses of 11 Fraxinus species provide insights into salt adaptation in ash trees. Plant communications, 6(1), 101137.

Zhang Y, et al. (2025) Chromosome-level genome assembly of black carp Mylopharyngodon piceus using Nanopore and Hi-C technologies. Scientific data, 12(1), 145.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (Eleusine indica). Scientific data, 12(1), 156.

Schöneberg Y, et al. (2025) Three Novel Spider Genomes Unveil Spidroin Diversification and Hox Cluster Architecture: Ryuthela nishihirai (Liphistiidae), Uloborus plumipes (Uloboridae) and Cheiracanthium punctorium (Cheiracanthiidae). Molecular ecology resources, 25(1), e14038.

He H, et al. (2025) Chromosome-level genome assembly of Monolepta hieroglyphica, two-spotted leaf beetle (Coleoptera: Chrysomelidae). Scientific data, 12(1), 1.

Zhang X, et al. (2025) Intestinal TM6SF2 protects against metabolic dysfunction-associated steatohepatitis through the gut-liver axis. Nature metabolism, 7(1), 102.

Biar CG, et al. (2025) Curated loci prime editing (cliPE) for accessible multiplexed assays of variant effect (MAVEs). ArXiv.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries. Molecular horticulture, 5(1), 6.