

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Jellyfish

Synonyms: Jellyfish mer counter

Resource Type: software resource

Defining Citation: [PMID:21217122](#), [DOI:10.1093/bioinformatics/btr011](#)

Keywords: c++, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260903T234806+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 1134 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ningsih F, et al. (2026) *Thermus javaensis* sp. nov., a novel thermophilic bacterium isolated from litter of a geyser in Cisolok, West Java, Indonesia. *International journal of systematic and evolutionary microbiology*, 76(5).

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. *BMC biology*, 24(1).

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

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.

Mouratidis I, et al. (2025) Identification of the shortest species-specific oligonucleotide sequences. *Genome research*, 35(2), 279.

Ji X, et al. (2025) Mapping and identification of QTLs for low light tolerance traits in grapevine. *BMC plant biology*, 25(1), 927.

Yue D, et al. (2025) Chromosome-level genome assembly of *Ampulex clypeocomplana* Chen & Li (Hymenoptera: Ampulicidae). *Scientific data*, 12(1), 1328.

Ren M, et al. (2025) Chromosome-level genome assembly of hawthorn spider mite, *Amphitetranynchus viennensis* (Acari: Tetranychidae). *Scientific data*, 12(1), 1342.

Lv Z, et al. (2025) Near telomere-to-telomere genome assembly of *Camellia pitardii*. *Scientific data*, 12(1), 1422.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Rana A, et al. (2025) Genome assembly and annotation of the parasitoid jewel wasp *Nasonia oneida*. *Scientific data*, 12(1), 1096.

Wang Y, et al. (2025) A chromosome-level genome assembly of *Electrophorus voltai*, a species of electric eel. *Scientific data*, 12(1), 1367.

Chen M, et al. (2025) Chromosome-level genome assembly of the Durum wheat cultivar Langdon. *Scientific data*, 12(1), 1372.

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Liu Y, et al. (2025) Two haplotype-resolved telomere-to-telomere genome assemblies of *Xanthoceras sorbifolium*. *Scientific data*, 12(1), 791.

Serivichyaswat PT, et al. (2025) Metagenomic biodiversity assessment within an offshore wind farm. *Scientific reports*, 15(1), 16786.

Bisht MS, et al. (2025) A high-quality genome assembly of *Annona squamosa* (custard apple) provides functional insights into an emerging fruit crop. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(3).

Ibrahim A, et al. (2025) Low Heterozygosity and Historical Bottleneck Effect Depicted From the Genome Assembly of the Indus River Dolphin (*Platanista minor*). *Ecology and evolution*, 15(5), e71462.

Biar CG, et al. (2025) Protocol to perform multiplexed assays of variant effect using curated loci prime editing. *STAR protocols*, 6(2), 103851.