

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 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: 20260905T132536+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 [PRECISE-TBI](#) .

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.

Cho W, et al. (2025) An annotated haplotype-resolved genome sequence assembly of diploid German chamomile, *Matricaria chamomilla*. *Scientific data*, 12(1), 358.

Shi Y, et al. (2025) Chromosome-level genome assembly of the traditional medicinal plant *Lindera aggregata*. *Scientific data*, 12(1), 565.

Zolkiewicz K, et al. (2025) Mutations of the brassinosteroid biosynthesis gene HvDWARF5 enable balance between semi-dwarfism and maintenance of grain size in barley. *Physiologia plantarum*, 177(2), e70179.

Liu HL, et al. (2025) Chromosome-level genome assembly of the Adonis ladybird *Hippodamia variegata*. *Scientific data*, 12(1), 558.

Zhang L, et al. (2025) A high-quality chromosome-level genome assembly for the agricultural pest *Mythimna separata*. *Scientific data*, 12(1), 540.

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

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

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

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

Yin M, et al. (2025) The haplotype-resolved genome assembly of an ancient citrus variety provides insights into the domestication history and fruit trait formation of loose-skin mandarins. *Genome biology*, 26(1), 61.

Lu K, et al. (2025) Chromosome-Level Genome and Variation Map of Eri Silkworm *Samia cynthia ricini*. *Biology*, 14(6).

Godec T, et al. (2025) Haplotype-resolved genome assembly of the tetraploid potato cultivar Désirée. *Scientific data*, 12(1), 1044.

Ryan K, et al. (2025) New Genome Assemblies for Poeciliidae: A Foundation for Adaptation Studies. *Genome biology and evolution*, 17(6).

Fu Z, et al. (2025) A chromosome-level genome assembly of Gray's grenadier anchovy, *Coilia grayii*. *Scientific data*, 12(1), 656.

Derilus D, et al. (2025) Chromosome-scale genome assembly and annotation of two geographically distinct strains of malaria vector *Anopheles albimanus*. *Scientific reports*, 15(1), 19448.

Lu J, et al. (2025) Haplotype-resolved chromosome-level genome assembly of *Fragaria × ananassa* Duch. cv. 'Yuexin'. *Scientific data*, 12(1), 974.

Wu H, et al. (2025) Construction of the super pan-genome for the genus *Actinidia* reveals structural variations linked to phenotypic diversity. *Horticulture research*, 12(6), uhaf067.