

Resource Summary Report

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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: 20260725T190605+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 1130 mentions in open access literature.

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

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

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.

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

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

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

Guo Y, et al. (2025) Chromosome-level genome assembly of the intertidal lucinid clam *Indoaustriella scarlatoi*. *Scientific data*, 12(1), 275.

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

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

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

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.

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).

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

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.

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

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

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

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