

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

Jellyfish

RRID:SCR_005491

Type: Tool

Proper Citation

Jellyfish (RRID:SCR_005491)

Resource Information

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

Proper Citation: Jellyfish (RRID:SCR_005491)

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 [SPARC SAWG](#) .

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.

Dishuck PC, et al. (2025) Structural variation, selection, and diversification of the NPIP gene family from the human pangenome. bioRxiv : the preprint server for biology.

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

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.

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.

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

Barak N, et al. (2025) Jellyfish blooms through the microbial lens: temporal changes, cross-species and Jellyfish-water comparisons. Environmental microbiome, 20(1), 49.

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.

- Fu Z, et al. (2025) A chromosome-level genome assembly of Gray's grenadier anchovy, *Coilia grayii*. *Scientific data*, 12(1), 656.
- Lu J, et al. (2025) Haplotype-resolved chromosome-level genome assembly of *Fragaria × ananassa* Duch. cv. 'Yuexin'. *Scientific data*, 12(1), 974.
- Lu K, et al. (2025) Chromosome-Level Genome and Variation Map of Eri Silkworm *Samia cynthia ricini*. *Biology*, 14(6).
- Ryan K, et al. (2025) New Genome Assemblies for Poeciliidae: A Foundation for Adaptation Studies. *Genome biology and evolution*, 17(6).
- 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.
- 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.
- 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.
- 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.