**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

**Availability:** GNU General Public License

**Resource Name:** Jellyfish

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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 714 mentions in open access literature.

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

Khalaf A, et al. (2024) Polyploidy is widespread in Microsporidia. Microbiology spectrum, 12(2), e0366923.

Flynn JM, et al. (2024) High-Quality Genome Assemblies Reveal Evolutionary Dynamics of Repetitive DNA and Structural Rearrangements in the Drosophila virilis Subgroup. Genome biology and evolution, 16(1).


Garg KM, et al. (2024) Hybrid de novo genome assembly of the sexually dimorphic Lady Amherst's pheasant. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(1).

Wolf M, et al. (2024) Near chromosome-level and highly repetitive genome assembly of the snake pipefish Entelurus aequoreus (Syngnathiformes: Syngnathidae). GigaByte (Hong Kong, China), 2024, gigabyte105.


Zhang H, et al. (2024) The haplotype-resolved genome assembly of autotetraploid rhubarb
Rheum officinale provides insights into its genome evolution and massive accumulation of anthraquinones. Plant communications, 5(1), 100677.

Wang ZF, et al. (2024) Chromosome-level genome assembly and demographic history of Euryodendron excelsum in monotypic genus endemic to China. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(1).

Qian ZH, et al. (2024) The chromosome-level genome of the submerged plant Cryptocoryne crispatula provides insights into the terrestrial-freshwater transition in Araceae. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(1).


Howell AA, et al. (2024) Computational host range prediction-The good, the bad, and the ugly. Virus evolution, 10(1), vead083.


Park HY, et al. (2024) Genome of Raphanus sativus L. Bakdal, an elite line of large cultivated Korean radish. Frontiers in genetics, 15, 1328050.