## **Resource Summary Report**

Generated by FDI Lab - SciCrunch.org on May 14, 2024

# **Jellyfish**

RRID:SCR\_005491

Type: Tool

## **Proper Citation**

Jellyfish (RRID:SCR\_005491)

#### **Resource Information**

URL: <a href="http://www.genome.umd.edu/jellyfish.html">http://www.genome.umd.edu/jellyfish.html</a>

**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.

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

Resource ID: SCR 005491

Alternate IDs: biotools:jellyfish, OMICS\_01056

Alternate URLs: https://bio.tools/jellyfish, https://sources.debian.org/src/jellyfish1/

## 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.

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.

Sun N, et al. (2024) Chromosome-level genome provides insight into the evolution and conservation of the threatened goral (Naemorhedus goral). BMC genomics, 25(1), 92.

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).

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

Song Y, et al. (2024) Chromosome level genome assembly of endangered medicinal plant Anisodus tanguticus. Scientific data, 11(1), 161.

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).

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).

Wang X, et al. (2024) De novo chromosome-level genome assembly of Chinese motherwort (Leonurus japonicus). Scientific data, 11(1), 55.

Li H, et al. (2024) A chromosome-level genome assembly of Sesamia inferens. Scientific data, 11(1), 134.

Zhou H, et al. (2024) De novo Phased Genome Assembly, Annotation and Population Genotyping of Alectoris Chukar. Scientific data, 11(1), 162.

Sudalaimuthuasari N, et al. (2024) Near-chromosomal-level genome of the red palm weevil (Rhynchophorus ferrugineus), a potential resource for genome-based pest control. Scientific data, 11(1), 45.

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

Chen M, et al. (2024) Chromosome-level genome assembly of Hippophae gyantsensis. Scientific data, 11(1), 126.

Stevens L, et al. (2024) The genome of Litomosoides sigmodontis illuminates the origins of Y chromosomes in filarial nematodes. PLoS genetics, 20(1), e1011116.

Wu S, et al. (2024) High-quality genome assembly of a C. crossoptilon and related functional and genetics data resources. Scientific data, 11(1), 247.

Gao YF, et al. (2024) Chromosome-level genome assembly of the Japanese sawyer beetle Monochamus alternatus. Scientific data, 11(1), 199.

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

Zheng J, et al. (2024) Chromosome-level genome assembly of Acrossocheilus fasciatus using PacBio sequencing and Hi-C technology. Scientific data, 11(1), 166.