### Jellyfish

**RRID:** SCR_005491  
**Type:** Tool

#### Proper Citation

Jellyfish (RRID:SCR_005491)

#### Resource Information

**URL:** [http://www.genome.umd.edu/jellyfish.html](http://www.genome.umd.edu/jellyfish.html)

**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.

**Resource Name:** Jellyfish

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**Resource Type:** Resource, software resource

**Keywords:** c++

**Resource ID:** SCR_005491

**Parent Organization:** University of Maryland; Maryland; USA

**References:** [PMID: 21217122](http://www.ncbi.nlm.nih.gov/pubmed/21217122)

**Availability:** GNU General Public License

**Website Status:** Last checked up

**Alternate IDs:** OMICS_01056
Abbreviations: Jellyfish

Mentions Count: 196

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 196 mentions in open access literature.

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


Choo LQ, et al. (2020) Novel genomic resources for shelled pteropods: a draft genome and target capture probes for Limacina bulimoides, tested for cross-species relevance. BMC

Wu H, et al. (2020) Genome Assembly ofFurther Supports That and Belong to Different Sections. G3 (Bethesda, Md.), 10(2), 455-466.

Renny-Byfield S, et al. (2020) Repetitive DNA content in the maize genome is uncoupled from population stratification at SNP loci. BMC genomics, 21(1), 98.


