Resource Summary Report

Generated by NIF on Apr 19, 2025

jcvi

RRID:SCR_021641
Type: Tool

Proper Citation

jcvi (RRID:SCR_021641)

Resource Information

URL: https://pypi.org/project/jcvi/

Proper Citation: jcvi (RRID:SCR_021641)

Description: Software tool as collection of Python libraries to parse bioinformatics files, or perform computation related to assembly, annotation, and comparative genomics.

Synonyms: jcvi_PyPI, jcvi 1.1.17

Resource Type: software toolkit, software library, software resource

Keywords: Python libraries, parse bioinformatics files, assembly, annotation, comparative genomics

Funding:

Availability: Free, Available for download, Freely available

Resource Name: jcvi

Resource ID: SCR_021641

Alternate URLs: https://github.com/tanghaibao/jcvi/tree/v0.5.7, https://zenodo.org/record/31631#.YRaieYhKhPa

License: BSD

Record Creation Time: 20220129T080356+0000

Record Last Update: 20250419T055726+0000

Ratings and Alerts

No rating or validation information has been found for jcvi.

No alerts have been found for jcvi.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Xia W, et al. (2024) Chromosome-level genome provides new insight into the overwintering process of Korla pear (Pyrus sinkiangensis Yu). BMC plant biology, 24(1), 773.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. GigaScience, 13.

Pu Y, et al. (2024) A high-quality chromosomal genome assembly of the sea cucumber Chiridota heheva and its hydrothermal adaptation. GigaScience, 13.

Yuan L, et al. (2024) The genomes of 5 underutilized Papilionoideae crops provide insights into root nodulation and disease resistance. GigaScience, 13.

Dong Z, et al. (2023) A chromosome-level genome assembly of Ostrea denselamellosa provides initial insights into its evolution. Genomics, 115(2), 110582.

Zheng J, et al. (2022) Molecular mechanisms underlying hematophagia revealed by comparative analyses of leech genomes. GigaScience, 12.

Lötter A, et al. (2022) Haplogenome assembly reveals structural variation in Eucalyptus interspecific hybrids. GigaScience, 12.

Wang L, et al. (2022) The Capparis spinosa var. herbacea genome provides the first genomic instrument for a diversity and evolution study of the Capparaceae family. GigaScience, 11.

Wu W, et al. (2021) Characterization of the Liriodendron Chinense MYB Gene Family and Its Role in Abiotic Stress Response. Frontiers in plant science, 12, 641280.

Sun WH, et al. (2021) The Euscaphis japonica genome and the evolution of malvids. The Plant journal : for cell and molecular biology, 108(5), 1382.

Ai Y, et al. (2021) The Cymbidium genome reveals the evolution of unique morphological traits. Horticulture research, 8(1), 255.

Huang R, et al. (2021) De novo screening of disease-resistant genes from the chromosome-level genome of rare minnow using CRISPR-cas9 random mutation. GigaScience, 10(11).

Llorens-Marès T, et al. (2015) Connecting biodiversity and potential functional role in modern euxinic environments by microbial metagenomics. The ISME journal, 9(7), 1648.