

Resource Summary Report

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[jcv](#)**i**

RRID:SCR_021641

Type: Tool

Proper Citation

jcv*i* (RRID:SCR_021641)

Resource Information

URL: <https://pypi.org/project/jcv/>

Proper Citation: jcv*i* (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: jcv*i*_PyPI, jcv*i* 1.1.17

Resource Type: software library, software toolkit, software resource

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

Availability: Free, Available for download, Freely available

Resource Name: jcv*i*

Resource ID: SCR_021641

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

License: BSD

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260803T040814+0000

Ratings and Alerts

No rating or validation information has been found for jcv*i*.

No alerts have been found for jcv*i*.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#).

Chen M, et al. (2025) The genome of Hippophae salicifolia provides new insights into the sexual differentiation of sea buckthorn. GigaScience, 14.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. GigaScience, 14.

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.

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.

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

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.

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.

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).

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

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.