

Resource Summary Report

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[jcv](#)[i](#)

RRID:SCR_021641

Type: Tool

Proper Citation

jcv (RRID:SCR_021641)

Resource Information

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

Proper Citation: jcv (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_PyPI, jcv 1.1.17

Resource Type: software library, software resource, software toolkit

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

Availability: Free, Available for download, Freely available

Resource Name: jcv

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: 20260905T132943+0000

Ratings and Alerts

No rating or validation information has been found for jcv.

No alerts have been found for jcv.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

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.

Tang H, et al. (2024) JCVI: A versatile toolkit for comparative genomics analysis. *iMeta*, 3(4), e211.

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

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

Cheng Z, et al. (2023) Comparatively Evolution and Expression Analysis of GRF Transcription Factor Genes in Seven Plant Species. *Plants (Basel, Switzerland)*, 12(15).

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

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.

Liu DK, et al. (2022) Genome-wide analysis of the TCP gene family and their expression pattern in *Cymbidium goeringii*. *Frontiers in plant science*, 13, 1068969.

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

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

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).

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.

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.