

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: 20260829T182715+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 [NIF](#) .

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

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.

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.