

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

PBJelly

RRID:SCR_012091

Type: Tool

Proper Citation

PBJelly (RRID:SCR_012091)

Resource Information

URL: <http://sourceforge.net/projects/pb-jelly/>

Proper Citation: PBJelly (RRID:SCR_012091)

Description: Software that automates the finishing process using long sequence reads in a reference-guided assembly process.

Resource Type: software resource

Defining Citation: [PMID:23185243](#)

Keywords: standalone software, roche, pacific biosciences

Resource Name: PBJelly

Resource ID: SCR_012091

Alternate IDs: OMICS_05098

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260725T190728+0000

Ratings and Alerts

No rating or validation information has been found for PBJelly.

No alerts have been found for PBJelly.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 170 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Cassin-Sackett L, et al. (2025) Rapid adaptation to a globally introduced virulent pathogen in a keystone species. PNAS nexus, 4(7), pgaf199.

Piovani L, et al. (2025) The genomic origin of the unique chaetognath body plan. Nature, 645(8082), 964.

Zhou J, et al. (2025) Whole-genome analysis and antimicrobial resistance phenotype of *Vagococcus fluvialis* isolated from wild Niviventer. Frontiers in microbiology, 16, 1546744.

Hall N, et al. (2025) FHY3/FAR1 transposable elements generate adaptive genetic variation in the *Bassia scoparia* genome. Pest management science, 81(8), 4393.

Shaw PL, et al. (2025) Chromosome-level genome assemblies for the latent pine pathogen, *Diplodia sapinea*, reveal two accessory chromosomes with distinct genomic features and evolutionary dynamics. G3 (Bethesda, Md.), 15(12).

Du H, et al. (2025) A near-complete genome assembly of *Fragaria iinumae*. BMC genomics, 26(1), 253.

Passari AK, et al. (2025) Comparative genomics of the *Streptomyces* genus: insights into multi-stress-resistant genes for bioremediation. World journal of microbiology & biotechnology, 41(12), 492.

Marlétaz F, et al. (2024) The hagfish genome and the evolution of vertebrates. Nature, 627(8005), 811.

Konuma J, et al. (2024) Odd-Paired is Involved in Morphological Divergence of Snail-Feeding Beetles. Molecular biology and evolution, 41(6).

Lai Y, et al. (2024) High-quality chromosome-level genome assembly and multi-omics analysis of rosemary (*Salvia rosmarinus*) reveals new insights into the environmental and genome adaptation. Plant biotechnology journal, 22(7), 1833.

Hoshino M, et al. (2024) Parallel loss of sexual reproduction in field populations of a brown alga sheds light on the mechanisms underlying the emergence of asexuality. Nature ecology & evolution, 8(10), 1916.

Talenti A, et al. (2024) Continent-wide genomic analysis of the African buffalo (*Syncerus caffer*). Communications biology, 7(1), 792.

Hu Z, et al. (2024) Genomics insights into flowering and floral pattern formation: regional duplication and seasonal pattern of gene expression in *Camellia*. BMC biology, 22(1), 50.

Rüber L, et al. (2024) The genome sequence of the Dracula fish, *Danionella dracula* (Britz, Conway & Rüber, 2009). Wellcome open research, 9, 194.

Hogg CJ, et al. (2024) Extant and extinct bilby genomes combined with Indigenous knowledge improve conservation of a unique Australian marsupial. *Nature ecology & evolution*, 8(7), 1311.

Jung H, et al. (2024) The identification of small molecule inhibitors with anthelmintic activities that target conserved proteins among ruminant gastrointestinal nematodes. *mBio*, 15(3), e0009524.

Carpinteyro-Ponce J, et al. (2024) The Complex Landscape of Structural Divergence Between the *Drosophila pseudoobscura* and *D. persimilis* Genomes. *Genome biology and evolution*, 16(3).

Yuan N, et al. (2024) Comprehensive assessment of long-read sequencing platforms and calling algorithms for detection of copy number variation. *Briefings in bioinformatics*, 25(5).

Silliman K, et al. (2023) Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate. *Genome biology and evolution*, 15(2).

Wang YW, et al. (2023) Invasive Californian death caps develop mushrooms unisexually and bisexually. *Nature communications*, 14(1), 6560.