

Resource Summary Report

Generated by [T1D](#) on Sep 18, 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: 20260912T195745+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 172 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Martin FM, et al. (2026) Draft Genomes of Geographically Distinct Strains and Progeny of the Ectomycorrhizal Basidiomycete *Laccaria bicolor*. *Journal of genomics*, 14, 10.

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

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

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

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

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.

Hanrahan BJ, et al. (2025) Sex chromosome dosage compensation in a sex reversing skink is not influenced by sexual phenotype. *BMC genomics*, 27(1), 72.

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

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).

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

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

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.

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.

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).

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).

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.

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