

Resource Summary Report

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PASA

RRID:SCR_014656

Type: Tool

Proper Citation

PASA (RRID:SCR_014656)

Resource Information

URL: <http://pasapipeline.github.io/>

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Description: Gene structure annotation and analysis tool that uses spliced alignments of expressed transcript sequences to automatically model gene structures. It also incorporates gene structures based on transcript alignments into existing gene structure annotations. It is one component of a larger eukaryotic annotation pipeline implemented at the Broad Institute.

Synonyms: Program to Assemble Spliced Alignments (PASA), Program to Assemble Spliced Alignments

Resource Type: data processing software, data analysis software, sequence analysis software, software resource, software application

Defining Citation: [DOI:10.1093/nar/gkg770](https://doi.org/10.1093/nar/gkg770)

Keywords: gene structure, annotation, gene structure analysis tool, spliced alignment, transcript sequence, bio.tools

Funding:

Availability: Available for download

Resource Name: PASA

Resource ID: SCR_014656

Alternate IDs: biotools:PASA

Alternate URLs: <https://bio.tools/PASA>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250426T060417+0000

Ratings and Alerts

No rating or validation information has been found for PASA.

No alerts have been found for PASA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 772 mentions in open access literature.

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

Zhang Y, et al. (2025) Chromosome-level genome assembly of black carp *Mylopharyngodon piceus* using Nanopore and Hi-C technologies. *Scientific data*, 12(1), 145.

Yang Y, et al. (2025) Chromosome-level genome assembly of the sweet potato rot nematode *Ditylenchus destructor*. *Scientific data*, 12(1), 174.

Ma C, et al. (2025) Chromosome-level Genome Assembly and Annotation of the Arctic Moss *Ptychostomum knowltonii*. *Genome biology and evolution*, 17(1).

Tenger-Trolander A, et al. (2025) Genomic Resources for the Scuttle Fly *Megaselia abdita*: A Model Organism for Comparative Developmental Studies in Flies. *bioRxiv : the preprint server for biology*.

Clancy SM, et al. (2025) The *Calicophoron daubneyi* genome provides new insight into mechanisms of feeding, eggshell synthesis and parasite-microbe interactions. *BMC biology*, 23(1), 11.

Chudhary A, et al. (2025) Characterization of chemosensory genes in the subterranean pest *Gryllotalpa Orientalis* based on genome assembly and transcriptome comparison. *BMC genomics*, 26(1), 33.

Krawczyk K, et al. (2025) Chromosome-scale telomere to telomere genome assembly of common crystalwort (*Riccia sorocarpa* Bisch.). *Scientific data*, 12(1), 77.

Kariba R, et al. (2025) Draft genome sequence of Kei apple, an underutilized African tree crop. *Scientific data*, 12(1), 70.

Wang Y, et al. (2025) A high-quality chromosome-scale genome assembly of the Cherokee rose (*Rosa laevigata*). *Scientific data*, 12(1), 132.

Ye F, et al. (2025) Comprehensive genome annotation of the model ciliate *Tetrahymena thermophila* by in-depth epigenetic and transcriptomic profiling. *Nucleic acids research*, 53(2).

Lan L, et al. (2025) Chromosome-level and haplotype-resolved genome assembly of *Bougainvillea glabra*. *Scientific data*, 12(1), 107.

Öztoprak H, et al. (2025) Chromosome-scale genome dynamics reveal signatures of independent haplotype evolution in the ancient asexual mite *Platynothrus peltifer*. *Science advances*, 11(4), eadn0817.

Wang GF, et al. (2025) Chromosome-level genome assembly of a destructive leaf-mining moth *Eriocrania semipurpurella alpina*. *Scientific data*, 12(1), 2.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Amiri EE, et al. (2025) Conservation of symmetry breaking at the level of chromatin accessibility between fly species with unrelated anterior determinants. *bioRxiv : the preprint server for biology*.

Liu C, et al. (2025) A chromosome-scale genome assembly of the pioneer plant *Stylosanthes angustifolia*: insights into genome evolution and drought adaptation. *GigaScience*, 14.

Zhao Q, et al. (2025) Near telomere-to-telomere genome assemblies of Silkie *Gallus gallus* and Mallard *Anas platyrhynchos* restored the structure of chromosomes and "missing" genes in birds. *Journal of animal science and biotechnology*, 16(1), 9.

Medrano JF, et al. (2025) De novo whole-genome assembly and annotation of *Coffea arabica* var. Geisha, a high-quality coffee variety from the primary origin of coffee. *G3 (Bethesda, Md.)*, 15(1).

Zhang L, et al. (2025) Chromosome-level genome assembly and annotation of the gynogenetic large-scale loach (*Paramisgurnus dabryanus*). *Scientific data*, 12(1), 155.

Ding R, et al. (2025) Chromosome-Level Genome Assembly and Whole-Genome Resequencing Revealed Contrasting Population Genetic Differentiation of Black Bream (*Megalobrama skolkovii*) (Teleostei: Cyprinidae) Allopatric and Sympatric to Its Kin Species. *Ecology and evolution*, 15(1), e70874.