

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

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

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: 20260729T044330+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 999 mentions in open access literature.

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

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Marks RA, et al. (2026) The architecture of resilience: a genome assembly of *Myrothamnus flabellifolia* sheds light on desiccation tolerance and sex determination. *The New phytologist*, 249(2), 1063.

Maustad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Cao S, et al. (2025) *Lactuca* super-pangenome provides insights into lettuce genome evolution and domestication. *Nature communications*, 16(1), 7257.

Zhao K, et al. (2025) Pangenome analysis reveals structural variation associated with seed size and weight traits in peanut. *Nature genetics*, 57(5), 1250.

Zeng Y, et al. (2025) Chromosome-level genomes of Arctic and Antarctic mosses: *Aulacomnium turgidum* and *Polytrichastrum alpinum*. *Scientific data*, 12(1), 705.

Zhang RG, et al. (2025) Reticulate allopolyploidy and subsequent dysploidy drive evolution and diversification in the cotton family. *Nature communications*, 16(1), 7480.

Luo S, et al. (2025) Genome assembly at the chromosome level of *Clinopodium barosmum*. *Scientific data*, 12(1), 1406.

Wang Y, et al. (2025) Comparative genomic analyses reveal different genetic basis of two types of fruit in *Maloideae*. *Nature communications*, 16(1), 7463.

Ledoux JB, et al. (2025) Chromosome-Level Genome Assembly and Annotation of *Corallium rubrum*: A Mediterranean Coral Threatened by Overharvesting and Climate Change. *Genome biology and evolution*, 17(2).

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.

Teterina AA, et al. (2025) Pervasive Conservation of Intron Number and Other Genetic Elements Revealed by a Chromosome-level Genome Assembly of the Hyper-polymorphic Nematode *Caenorhabditis brenneri*. *Genome biology and evolution*, 17(3).

Feng Y, et al. (2025) Unveiling the Genomic Features and Biocontrol Potential of *Trichoderma hamatum* Against Root Rot Pathogens. *Journal of fungi (Basel, Switzerland)*, 11(2).

Sheikh SI, et al. (2025) A shared gene but distinct dynamics regulate mimicry polymorphisms in closely related species. *bioRxiv : the preprint server for biology*.

Alves-Ferreira EVC, et al. (2025) Whole Genome Sequence of the gut commensal protist *Tritrichomonas musculus* isolated from laboratory mice. *Scientific data*, 12(1), 590.

Diaz IA, et al. (2025) A haplotype-resolved chromatin landscape connects cis-regulatory variants to trait variation in Citrus. *BMC genomics*, 26(1), 978.

Chang M, et al. (2025) Chromosome-level genome assembly and annotation of the spottedtail morwong (*Cheilodactylus zonatus*). *Scientific data*, 12(1), 1741.

Bu X, et al. (2025) A chromosome-level genome assembly of the Chinese herbal medicine *Chelidonium majus*. *Scientific data*, 12(1), 1642.