

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: sequence analysis software, data analysis software, software resource, software application, 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: 20260728T043445+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.

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

Liu HJ, et al. (2025) Morphological differences between residual childhood hip dysplasia with previous osteotomy and adolescent-onset hip dysplasia. *Journal of orthopaedic surgery and research*, 20(1), 271.

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).

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).

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).

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

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.

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

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

Conn T, et al. (2025) Genome assembly and annotation of *Acropora pulchra* from Mo'orea French Polynesia. *GigaByte (Hong Kong, China)*, 2025, gigabyte153.

Chen L, et al. (2025) A telomere-to-telomere gap-free assembly integrating multi-omics uncovers the genetic mechanism of fruit quality and important agronomic trait associations in pomegranate. *Plant biotechnology journal*, 23(7), 2852.

Liu S, et al. (2025) CgABR1-CgFAD negatively regulates the fruit neck length in citrus. *Plant biotechnology journal*, 23(8), 3083.

Han X, et al. (2025) The telomere-to-telomere genome assembly and annotation of the rock carp (*Procypris rabaudi*). *Scientific data*, 12(1), 781.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

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.

Qi J, et al. (2025) Genomic Sequencing and Characterization of Two *Auricularia* Species from the Qinling Region: Insights into Evolutionary Dynamics and Secondary Metabolite Potential. *Journal of fungi (Basel, Switzerland)*, 11(5).