

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

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: 20260905T133006+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 1123 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

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.

Nie Y, et al. (2026) Identification of sex chromosome, sex-biased gene expression and dosage compensation in the pygmy mole cricket *Xya riparia* (Orthoptera: Tridactyloidea). *BMC genomics*, 27(1).

Xin G, et al. (2026) The chromosome-scale genome assembly, annotation of *Bischofia polycarpa* (H. L?v.) Airy Shaw, Phyllanthaceae. *Scientific data*, 13(1).

Han D, et al. (2026) Pan-genome assembly of vine tea (*Nekemias grossedentata*) reveals structural variation in its dihydromyricetin biosynthesis diversity. *Horticulture research*, 13(2), uhaf307.

Wu Y, et al. (2026) Telomere-to-telomere gapless genome assembly of *Siniperca scherzeri*. *Scientific data*, 13(1).

Wang J, et al. (2026) A high-quality chromosome-level genome assembly of a feather star *Glyptometra* sp. from a deep seamount. *Scientific data*, 13(1).

Kale SM, et al. (2026) Extensive variation between chromosomes of North American and European hop. *Nature communications*, 17(1).

Niu Y, et al. (2026) Chromosome-level genome assembly of the blackchin tilapia (*Sarotherodon melanotheron*). *Scientific data*, 13(1).

Sun Y, et al. (2026) Chromosome level genome assembly of taro (*Colocasia esculenta*). *Scientific data*, 13(1).

Ding S, et al. (2026) Chromosome-level genome assembly of a Chinese evergreen sweetgum (*Liquidambar gracilipes*, Altingiaceae). *Scientific data*, 13(1), 66.

Liu T, et al. (2026) Chromosome-level genome assembly and annotation of the endangered plant *Primula kwangtungensis* (Primulaceae). *Scientific data*, 13(1), 212.

Luo Y, et al. (2026) A chromosome-level genome assembly and multi-omics analyses provide insights into the biosynthesis of piperlongumine in *Piper sarmentosum*. *Communications biology*, 9(1), 170.

Wu H, et al. (2026) A telomere-to-telomere genome assembly of Chinese water deer (*Hydropotes inermis*). *Scientific data*, 13(1).

Wang ZL, et al. (2026) Centromeric tandem repeats expansions in plateau zokor enhance chromosome stability for high-altitude adaptation. *Genome biology*, 27(1).

Yu ZX, et al. (2026) Chromosome-level genome of *Mosla chinensis* from alpine ecotype provides insights into terpenoid biosynthesis and germplasm exploration. *Frontiers in plant science*, 17, 1819008.

Hu H, et al. (2026) Structural variation drives rhizome innovation and adaptive divergence in sister *Medicago* species. *Journal of integrative plant biology*, 68(2), 406.

Tan S, et al. (2026) A chromosome-scale genome assembly of Wu's rock agama (*Laudakia wui*) from low-altitude habitats. *Scientific data*, 13(1).

Dong Z, et al. (2026) Fungal photobiont and microbiome genome composition in the *Cladonia uncialis* tripartite symbiosis. *Scientific data*, 13(1).

Zhou C, et al. (2026) Chromosome-level genome assembly of the deep-sea solemyid bivalve *Acharax haimaensis*. *Scientific data*, 13(1).