

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 15, 2026

Platanus

RRID:SCR_015531

Type: Tool

Proper Citation

Platanus (RRID:SCR_015531)

Resource Information

URL: <http://platanus.bio.titech.ac.jp/>

Proper Citation: Platanus (RRID:SCR_015531)

Description: De novo sequence assembler that can reconstruct genomic sequences of highly heterozygous diploids from massively parallel shotgun sequencing data., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: PLATform for Assembling NUcleotide Sequences, Platanus - PLATform for Assembling NUcleotide Sequences, Platanus Genome Assembler

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

Defining Citation: [DOI:10.1101/gr.170720.113](https://doi.org/10.1101/gr.170720.113)

Keywords: de novo sequence assembly, genomic sequence reconstruction, shotgun sequence data

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Platanus

Resource ID: SCR_015531

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260815T042716+0000

Ratings and Alerts

No rating or validation information has been found for Platanus.

No alerts have been found for Platanus.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 201 mentions in open access literature.

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

Jung D, et al. (2025) Comparative genomic analysis of Escherichia coli isolated from cases of bovine clinical mastitis and the dairy farm environment. Microbial genomics, 11(6).

Garcia-Erill G, et al. (2025) Genomes of critically endangered saola are shaped by population structure and purging. Cell, 188(12), 3102.

Ibrahim A, et al. (2025) Low Heterozygosity and Historical Bottleneck Effect Depicted From the Genome Assembly of the Indus River Dolphin (Platanista minor). Ecology and evolution, 15(5), e71462.

Kamakura S, et al. (2025) Reminiscent of the pre-diatom? A hitherto undescribed scaly bolidophyte *Lepidoparma frigida* gen. et sp. nov. in a new order Lepidoparmales based on morphology, phylogeny, and ecology. Journal of phycology, 61(4), 757.

Záhonová K, et al. (2025) Comparative genomic analysis of trypanosomatid protists illuminates an extensive change in the nuclear genetic code. mBio, 16(6), e0088525.

Vangestel C, et al. (2024) Chromosomal inversions from an initial ecotypic divergence drive a gradual repeated radiation of Galápagos beetles. Science advances, 10(22), eadk7906.

Vargas AM, et al. (2024) Morphological and dietary changes encoded in the genome of *Beroë ovata*, a ctenophore-eating ctenophore. NAR genomics and bioinformatics, 6(2), lqae072.

Grybchuk D, et al. (2024) Identification of diverse RNA viruses in *Obscuromonas* flagellates (Euglenozoa: Trypanosomatidae: Blastocrithidiinae). Virus evolution, 10(1), veae037.

Bian C, et al. (2024) Chromosome-level genome assembly of the glass catfish (*Kryptopterus vitreolus*) reveals molecular clues to its transparent phenotype. Zoological research, 45(5), 1027.

Katahira K, et al. (2024) Mobile genetic element-driven genomic changes in a community-associated methicillin-resistant *Staphylococcus aureus* clone during its transmission in a regional community outbreak in Japan. Microbial genomics, 10(7).

Du K, et al. (2024) Phylogenomic analyses of all species of swordtail fishes (genus *Xiphophorus*) show that hybridization preceded speciation. Nature communications, 15(1), 6609.

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

Fukao M, et al. (2024) Genome-based assessment of safety characteristics of *Lactocaseibacillus paracasei* NY1301 and genomic differences in closely related strains marketed as probiotics. *Bioscience of microbiota, food and health*, 43(2), 145.

Borstein SR, et al. (2024) The macroevolutionary dynamics of pharyngognathy in fishes fail to support the key innovation hypothesis. *Nature communications*, 15(1), 10325.

Liu Y, et al. (2023) Genomic Analysis of the Rare Slightly Halophilic Myxobacterium "Paraliomyxa miuraensis" SMH-27-4, the Producer of the Antibiotic Miuraenamides A. *Microorganisms*, 11(2).

Samuels ME, et al. (2023) Genomic Sequence of Canadian *Chenopodium berlandieri*: A North American Wild Relative of Quinoa. *Plants (Basel, Switzerland)*, 12(3).

Feng X, et al. (2023) Chromosome-level genomes of multicellular algal sisters to land plants illuminate signaling network evolution. *bioRxiv : the preprint server for biology*.

Sato A, et al. (2023) The chromosomal evolutionary lineage of the genus *Zygosaccharomyces*. *FEMS yeast research*, 23.

Yamaguchi K, et al. (2023) Elasmobranch genome sequencing reveals evolutionary trends of vertebrate karyotype organization. *Genome research*, 33(9), 1527.

Tang T, et al. (2023) A Chromosome-Level Genome Assembly of the Reef Stonefish (*Synanceia verrucosa*) Provides Novel Insights into Stonustoxin (sntx) Genes. *Molecular biology and evolution*, 40(10).