

Resource Summary Report

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[NOVOPlasty](#)

RRID:SCR_017335

Type: Tool

Proper Citation

NOVOPlasty (RRID:SCR_017335)

Resource Information

URL: <https://github.com/ndierckx/NOVOPlasty>

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Description: Software package as de novo assembler and heteroplasmy variance caller for short circular genomes. Used for de novo assembly of organelle genomes from whole genome data.

Resource Type: image analysis software, alignment software, software application, software resource, data processing software

Defining Citation: [PMID:28204566](#)

Keywords: de novo, assembler, heteroplasmy, variance, caller, short, circular, genome, organelle, whole, data

Funding: Interuniversity Institute of Bioinformatics in Brussels ;
Belgian Kids Fund ;
Hôpital Universitaire des Enfants Reine Fabiola

Availability: Free, Available for download, Freely available

Resource Name: NOVOPlasty

Resource ID: SCR_017335

License URLs: <https://github.com/ndierckx/NOVOPlasty/blob/master/LICENSE>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260801T190601+0000

Ratings and Alerts

No rating or validation information has been found for NOVOPlasty.

No alerts have been found for NOVOPlasty.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 161 mentions in open access literature.

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

Nguyen PAT, et al. (2025) The Complete Chloroplast Genome of *Baccaurea ramiflora* Lour. Cultivar Ha Chau (Phyllanthaceae, Malpighiales). *Ecology and evolution*, 15(3), e71145.

Ali RLMN, et al. (2025) Mitogenomes of mosquito species of Harris County in Texas. *Scientific reports*, 15(1), 22013.

Zhang L, et al. (2025) Hybridization of *Lycium qingshuiheense* and *L. ningxiaense* revealed using morphological, SSR markers, and chloroplast genomic data. *BMC genomics*, 26(1), 965.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Huang Y, et al. (2025) Characterization of the complete mitochondrial genome of *Hynobius bambusicolus* Wang, Othman, Qiu and Borzée, 2023 (Amphibia, Caudata, Hynobiidae) and its phylogenetic implications. *Mitochondrial DNA. Part B, Resources*, 10(4), 278.

Patil MP, et al. (2025) Characterization of the Complete Mitochondrial Genome of the Red Alga *Ahnfeltiopsis flabelliformis* (Rhodophyta, Gigartinales, Phyllophoraceae) and Its Phylogenetic Analysis. *Biology*, 14(6).

Usmani S, et al. (2025) Phylogenetic taxonomy of the *Zambian Anopheles coustani* group using a mitogenomics approach. *Research square*.

Povill C, et al. (2025) Unveiling the Evolutionary History of *cis*-Andean *Alouatta* (Atelidae, Alouattinae) Through Mitochondrial Genomes. *American journal of primatology*, 87(5), e70043.

Kuppusamy S, et al. (2025) Mitochondrial genomics and phylogeny of noctuid moths: Implications for *Macroheterocera*. *PloS one*, 20(10), e0333540.

Lin D, et al. (2025) Phylogenomics of angiosperms based on mitochondrial genes: insights into deep node relationships. *BMC biology*, 23(1), 45.

Yang Y, et al. (2025) The Integrative Taxonomy and Mitochondrial Genome Evolution of Freshwater Planarians (Platyhelminthes: Tricladida): The Discovery of a New Clade in Southern China. *Genes*, 16(6).

Liu L, et al. (2025) Complete chloroplast genome sequencing of *Pseudocodon convolvulaceus*, a medicinal herb from Qinghai-Tibet Plateau in China. *PloS one*, 20(8), e0328307.

Zhao Q, et al. (2025) The first two complete mitochondrial genomes of *Butyriboletus roseoflavus* (Hai B. Li & Hai L. Wei) D. Arora & J.L. Frank 2014 (Boletales: Boletaceae) and phylogenetic analysis. *Mitochondrial DNA. Part B, Resources*, 10(7), 646.

Barcyt? D, et al. (2025) Expanded diversity of pedinophytes provides a window into the evolution of the genetic code in organelles. *PLoS genetics*, 21(10), e1011901.

De Thier O, et al. (2025) First chromosome-level genome assembly of the colonial chordate model *Botryllus schlosseri* (Tunicata). *GigaScience*, 14.

Ye F, et al. (2025) Evolutionary insights from the mitochondrial genomes of invasive scale insects (Hemiptera: Coccothraupidae): large-scale transfer RNA gene truncations and tandem repeat-driven intraspecific gene rearrangements. *BMC genomics*, 26(1), 1003.

De Luca D, et al. (2025) The plastid genome of the critically endangered *Valeriana trinervis* (= *Centranthus trinervis*) and insights from comparison with other *Valeriana* plastomes (Caprifoliaceae). *Planta*, 262(4), 100.

Chen Y, et al. (2025) The complete chloroplast genome of *Stachyurus himalaicus*. *Mitochondrial DNA. Part B, Resources*, 10(6), 513.

Xing G, et al. (2025) Characterization and Phylogenetic Analysis of the Complete Mitogenomes of *Valsa mali* and *Valsa pyri*. *Journal of fungi (Basel, Switzerland)*, 11(5).

He ZS, et al. (2025) Specimen Identification Through Multilocus Species Tree Constructed From Single-Copy Orthologs (SCOs): A Case Study in *Cymbidium* Subgenus *Jensoa*. *Ecology and evolution*, 15(4), e71323.