

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

Defining Citation: [PMID:28204566](#)

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

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

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

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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 202 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wu L, et al. (2026) High-quality genome assembly and annotation of the white-cheeked goby, *Rhinogobius duospilus* (Herre, 1935) (Gobiiformes: Oxudercidae). *G3* (Bethesda, Md.), 16(2).

Premachandra T, et al. (2026) Persistence of an unusual triple sex chromosome system through allopolyploidization in African clawed frogs (*Xenopus*, subgenus *Silurana*). *Evolution; international journal of organic evolution*, 80(3), 584.

Wei X, et al. (2026) Mitochondrial genomes of Terebelliformia: gene rearrangements, phylogenetic relationships, and evolutionary insights. *BMC genomics*, 27(1).

Yang NY, et al. (2026) Integrative Taxonomy of *Nuchequula longicornis* (Teleostei: Leiognathidae) from Chinese Waters: Morphological Analysis, Mitogenomic Characterization, and Phylogenetic Implications. *Biology*, 15(3).

Kmentová N, et al. (2026) Geographic differentiation of ectoparasitic flatworms in the pelagic zone of Lake Tanganyika, Africa. *Frontiers in zoology*, 23(1).

Alikhanova A, et al. (2026) Complete chloroplast genome sequence data of *Iris kuschakewiczii* B.Fedtsch., an endemic species of the Northern Tien Shan mountains. *Data in brief*, 65, 112563.

Lin YT, et al. (2026) Glass scallop genome reveals key adaptations to deep-sea environments and ectosymbiosis. *Nature communications*, 17(1).

Park JM, et al. (2026) Complete chloroplast genome sequence of *Rhamnella franguloides* (Maxim.) Weberb. (Rhamnaceae). *Mitochondrial DNA. Part B, Resources*, 11(4), 504.

Alharbi SA, et al. (2026) Conservation Status, Plastome Diversity, and Evolutionary Diversification of Three Arabian *Desmidorchis* Endemics (Apocynaceae). *Biology*, 15(10).

Liu X, et al. (2026) Complete chloroplast genome sequence and phylogenetic analysis of *Gloiopeltis furcata* (Gigartinales, Florideophyceae). *Mitochondrial DNA. Part B, Resources*, 11(3), 404.

Chen K, et al. (2026) The complete chloroplast genome sequence of *Camellia obtusifolia* (Theaceae). Mitochondrial DNA. Part B, Resources, 11(3), 414.

Huynh TTT, et al. (2026) Complete mitochondrial genome sequence data of *Pterygoplichthys gibbiceps* (Actinopterygii, Loricariidae). Data in brief, 67, 112963.

Kim IH, et al. (2026) Morphology and mitochondrial genome-based analysis of the systematics and evolution of *Acanthochitona* species (Polyplacophora: Acanthochitonidae). Marine life science & technology, 8(1), 49.

Ma D, et al. (2026) The complete mitochondrial genome of *Prinsepia uniflora* (Rosaceae): De novo assembly, characterization, and phylogenetic analysis. BMC genomics, 27(1).

Alharbi SA, et al. (2026) First Plastome Sequences of Two Endemic Taxa of *Orbea* Haw. from the Arabian Peninsula: Comparative Genomics and Phylogenetic Relationships Within the Tribe Ceropegieae (Asclepiadoideae, Apocynaceae). Biology, 15(3).

Ye F, et al. (2026) Revisiting a Chinese Endemic Termite Genus of Building Timber Pests: Mitochondrial Genomic and Morphological Dissection and Phylogenetic Positioning of *Xiaitermes* Gao & He, 1994 (Termitidae: Nasutitermitinae). Insects, 17(6).

Fauskee BD, et al. (2026) Losing genes, gaining edits: how relaxed selection and inverted repeat expansion shape RNA editing in Schizaeaceae plastomes. The Plant journal : for cell and molecular biology, 126(5), e70919.

Cha Y, et al. (2026) The complete mitochondrial genome of *Fusicolla acetilerea* (Nectriaceae, Hypocreales). Mitochondrial DNA. Part B, Resources, 11(3), 419.

Cheng Y, et al. (2026) Phylogenetic Reconstructions Based on Mitogenomes Reveal the Paraphyly of the Subfamily Isotominae of Isotomidae (Collembola: Entomobryomorpha). Genes, 17(2).

Ali RLMN, et al. (2026) Evidence of a putative new species *Haemagogus* 'Trinidad sp. A' from the Caribbean sharing mitogenome lineages with species endemic to the Amazon. Scientific reports, 16(1).