

Resource Summary Report

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GeSeq

RRID:SCR_017336

Type: Tool

Proper Citation

GeSeq (RRID:SCR_017336)

Resource Information

URL: <https://chlorobox.mpimp-golm.mpg.de/geseq.html>

Proper Citation: GeSeq (RRID:SCR_017336)

Description: Software tool for rapid and accurate annotation of organelle genomes, in particular chloroplast genomes.

Resource Type: software resource, software application, data processing software, service resource

Defining Citation: [PMID:28486635](#)

Keywords: rapid, accurate, annotation, organelle, genome, chloroplast, bio.tools

Funding: Human Frontier Science Program ;
Max Planck Society ;
German Science Foundation

Availability: Free, Freely available

Resource Name: GeSeq

Resource ID: SCR_017336

Alternate IDs: biotools:geseq

Alternate URLs: <https://bio.tools/geseq>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260801T042808+0000

Ratings and Alerts

No rating or validation information has been found for GeSeq .

No alerts have been found for GeSeq .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 375 mentions in open access literature.

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

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

Zhou G, et al. (2025) De novo assembly of the mitochondrial genome of *Glycyrrhiza glabra* and identification of two types of homologous recombination configurations caused by repeat sequences. *BMC genomics*, 26(1), 13.

Yuan J, et al. (2025) Comparative and phylogenetic analyses of the chloroplast genomes of mangrove plants. *Scientific reports*, 15(1), 3915.

Chen D, et al. (2025) Largest genome assembly in Brassicaceae: retrotransposon-driven genome expansion and karyotype evolution in *Matthiola incana*. *Plant biotechnology journal*, 23(9), 4109.

Zhang S, et al. (2025) Comparative genomics uncovers organellar genome structural divergence in Caryophyllales and reveals widespread non-coding transcription in *Bougainvillea glabra* organellar. *BMC genomics*, 26(1), 722.

Sulaiman S, et al. (2025) The complete plastome of the Antarctic moss *Andreaea regularis* (Andreaeaceae) and its comparative analyses within Bryophyta. *BMC genomics*, 26(1), 667.

Jiang Y, et al. (2025) Comparative chloroplast genomes of *Incarvillea* species (Bignoniaceae) unveiled genomic diversity and shed light on phylogenetic relationships. *BMC plant biology*, 25(1), 399.

Jiao B, et al. (2025) Global phylogeny and taxonomy of *Artemisia*. *Nature communications*, 16(1), 8648.

Dharmayanthi AB, et al. (2025) The mitochondrial genome sequence of the Bornean orang-utan (*Pongo pygmaeus*) malaria parasite, *Plasmodium pitheci*. *Malaria journal*, 24(1), 321.

Robbins MD, et al. (2025) Haplotype-resolved genome assembly of 'Manhattan' perennial ryegrass (*Lolium perenne* L.) and characterization of drought responsive late

embryogenesis abundant genes. BMC genomics, 26(1), 1125.

Al-Andal A, et al. (2025) Plastome diversity and phylogenetic insights among modern Egyptian wheat cultivars: Genome-Wide and Gene-Level perspectives. BMC plant biology, 25(1), 1781.

Wu T, et al. (2025) Ancient Hybridisation Fuelled Diversification in Acropora Corals. Molecular ecology, 34(22), e17615.

Ren Z, et al. (2025) A combined treatment regimen for *Trichuris rhinopittheroxella* infection in *Rhinopithecus roxellana* in southern China. International journal for parasitology. Parasites and wildlife, 26, 101036.

Witharana EP, et al. (2025) Subfamily evolution analysis using nuclear and chloroplast data from the same reads. Scientific reports, 15(1), 687.

Nie L, et al. (2025) Plastome data provides new insights into population differentiation and evolution of Ginkgo in the Sichuan Basin of China. BMC plant biology, 25(1), 48.

Liu B, et al. (2025) Complete chloroplast genome data of *Trollius ledebourii* Rehb, an important medicinal plant species. Data in brief, 59, 111408.

Univaso L, et al. (2025) The rps15-rpl32 intergenic locus is a phylogeographic marker for Latin American *Zea mays* landrace varieties and subspecies. BMC genomics, 26(1), 672.

Liu X, et al. (2025) Assembly and comparative analysis of the complete mitochondrial genome of *Abies beshanzuensis*: insights into conservation genomics of a critically endangered fir. BMC plant biology, 25(1), 1049.

Fujiwara K, et al. (2025) A Near Complete Genome Assembly of the Oshima Cherry *Cerasus speciosa*. Scientific data, 12(1), 162.

Yong Q, et al. (2025) Complete chloroplast genomes of 13 species of the *Impatiens* genus for genomic features and phylogenetic relationships studies. Scientific reports, 15(1), 4258.