



CHLOROBOX

GeSeq

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GeSeq - Annotation of Organellar Genomes

GeSeq has been developed for a rapid and accurate annotation of organelle genomes, in particular chloroplast genomes.

Please take a look at our [documentation](#) which includes a quickstart section.

Citations keep this server running. If you use GeSeq please cite:

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R and Greiner S (2017) GeSeq – versatile and accurate annotation of organelle genomes. *Nucleic Acids Research* 45: W6-W11

Hover over buttons for tips. To load an example job, press "Example" in the "Actions" field.

FASTA file(s) to annotate

1 file in list [+ Upload File\(s\)](#)

OX359233.1.fna [×](#)

☒ Circular ☐ Linear

Sequence source
☐ Plastid (land plants) ☐ Plastid (algae)
☒ Mitochondrial

Annotation Options
☐ Annotate plastid Inverted Repeat (IR)
☐ Annotate plastid trans-spliced *rps12*

Annotation Support
☐ Support annotation by Chloë
☐ Support annotation by MFannot

Annotation revision
☒ Keep best annotation only
☐ Keep all annotations

Annotation

BLAT search

Protein search identity
 25 [▼](#)

rRNA, tRNA, DNA search identity
 85 [▼](#)

Annotate
☒ CDS ☒ tRNA ☒ rRNA

Options
☒ Ignore genes annotated as locus tag
☐ Ignore genes annotated as ORFs

☐ HMMER profile search

3rd Party tRNA annotators

☒ ARAGORN v1.2.38

Genetic code
 Standard [▼](#)

Max intron length
 3000 bp

Options
☐ Allow overlaps
☐ Fix intron
☐ Report low scoring tRNAs

☐ ARWEN v1.2.3

☒ tRNAscan-SE v2.0.7

BLAT Reference Sequences

3rd Party References

[Add NCBI RefSeq\(s\)](#)

Mesua ferrea [×](#)

Manihot esculenta [×](#)

Ricinus communis [×](#)

MPI-MP Reference Set

☐ chloroplast land plants (CDS + rRNA)

User References

GenBank/EMBL

0 files in list [+ Upload File\(s\)](#)

FASTA Nucleotide (CDS)

0 files in list [+ Upload File\(s\)](#)

FASTA Nucleotide (tRNA, rRNA, primer, other DNA or RNA)

0 files in list [+ Upload File\(s\)](#)

3rd Party Stand-Alone Annotators

☐ Chloë v0.1.0

☐ MFannot v1.34

Output Options

☒ Generate multi-GenBank
☒ Generate multi-GFF3
☒ Generate multi-GBSON

Actions

[Submit](#) [Reset](#) [Example](#)

☒ I have read and accept the [Disclaimer](#)

Results

GeSeqJob-20240601-125101

ID gs_job_6666a962d8f5a

Status: finished

OX359233.1-Mercurialis-annua-genome-assembly%2C-organelle-mitochondrion

Primary Output Annotation Tools

[blatX](#) [ARAGORN v1.2.38](#) [blatN](#)

[tRNAscan-SE v2.0.7](#)

Annotation

[GenBank](#) [GFF3](#) [GFF3 + FASTA](#)

[GBSON](#)

Visualization

[OGDRAW](#)

CHLOROBX

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Search mode
Default

Genetic Code
Universal

Cut-off score for reporting tRNAs
15

Score and report output options

- ☒ Disable pseudogene checking
- ☐ Display detailed prediction output
- ☐ Show origin of first-pass hits
- ☐ Show primary and secondary structure components to scores

- LOLA
- GBSON
- ISE-G 2015
- Contact
- Disclaimer