

## A Five Minutes Crash Course for using CPGAVAS2

Last updated on March 15th, 2019

CPGAVAS2 is a significant update of our previous CPGAVAS web server. It allows automated annotation and analysis of newly and previously sequenced plastid genome. The web server can be accessed at <http://www.herbalgenomics.org/cpgavas2>. In case of DNS server problem, it can be accessed from <http://47.96.249.172:16019/analyzer/view>.

### Step I. Upload a sequence for annotation and analysis.

1. Go to “**AnnoGenome**” page, download the sample fasta files.
2. Fill in the information for Project Name and Species Name.
3. Upload the sample fasta sequences for your genome.
4. Click the “Submit” button and you will see a message like the following:  
*“You job xxx has been submitted and it is under processing. It usually takes up to xx minutes to finish the annotation of a 150 kb long plastom sequence. Please keep a note of your project id, as this is the only information by which you can access your data through <http://www.herbalgenomics.org/cpgavas2> under “ViewAnno”.*
5. You should keep a note of the job ID and comes back to the page in 20 (depending on the job load of sever) minutes to check the results.

### Step II. Visualize and editing the annotations.

1. Once you come back, go to the “**ViewAnno**” page, enter the ID for your job. A report page will show up. Browse through this page to see the results for gene models in GFF3 format, circular map image in png format, sequences for predicted DNA and proteins in FASTA format and analysis reports organized in Tables.
2. Through our own research work, we become big fans of Apollo genome editor and believe that there is no need or it is not possible to reinvent a genome annotation editor just as powerful. As a result, we make CPGAVAS2 output compatible with Apollo for editing. Download the gene models in GFF format. Open it up in Apollo, please select GFF3 format for “**Choose Data Source**”. And Check the “**Embed FASTA in GFF**”.
3. Edit the annotations using Apollo. Apollo is a very powerful editor that supports all sorts of editing of the predicted gene models. Of course, other editors can be used as well.
4. Export the annotation to a file in GFF3 format for updating of the analysis (see below).

### Step III. Retrieve sequences from other plastid genomes for comparative study.

1. Go to “**ExtractSeq**” page,
2. Select the species and the gene ids for which you would like to retrieve the sequences.
3. Select the type of sequence you would like to retrieve.

4. Select if you want the output sequences to be concatenated or not.
5. Click “submit”. The corresponding sequences will be retrieved and can be used for comparative studies.

Now you can run the CPGAVAS2 for your analyses. For detailed information, please refer to CPGAVAS2’s full documentation. If you have any questions or comments, please contact us at the following email address: [cliu@implad.ac.cn](mailto:cliu@implad.ac.cn) or [cpgavas@aliyun.com](mailto:cpgavas@aliyun.com).