

2. Annotate and Visualize

Annotate

SnapGene includes a database of common features that can be used as a database to annotate features on your sequences. This database contains a variety of features commonly seen on plasmids, such as promoters, terminators and marker genes. This document will outline a basic task of annotating a sequence using the common features database in SnapGene.

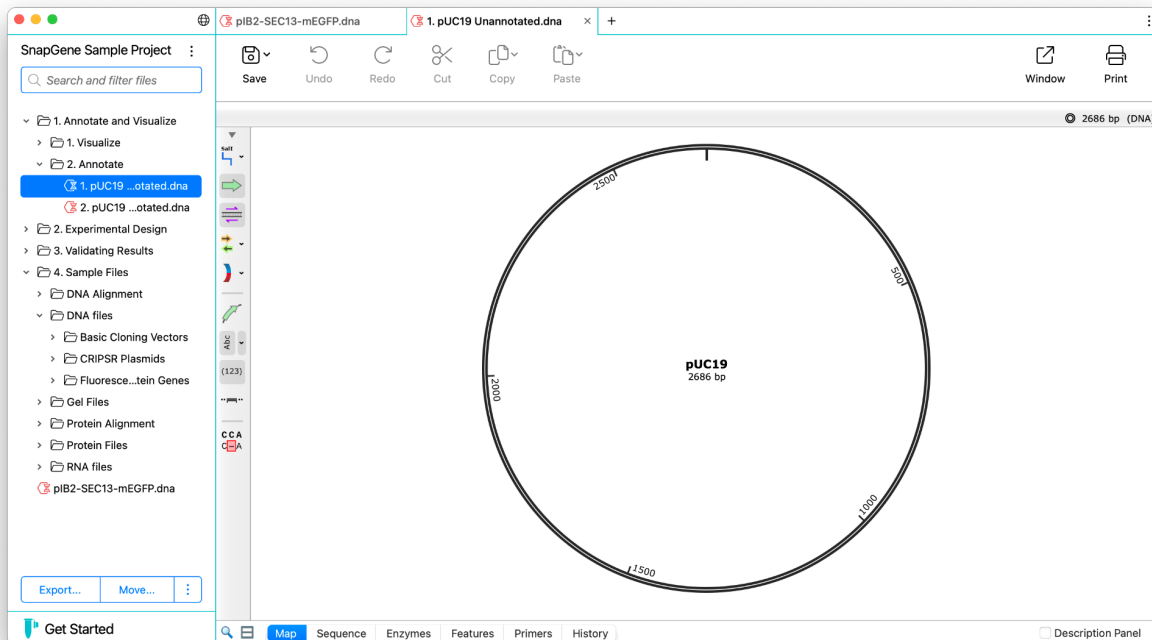
In this folder you will find two files:

1. pUC19 unannotated.dna
2. pUC19 annotated.dna

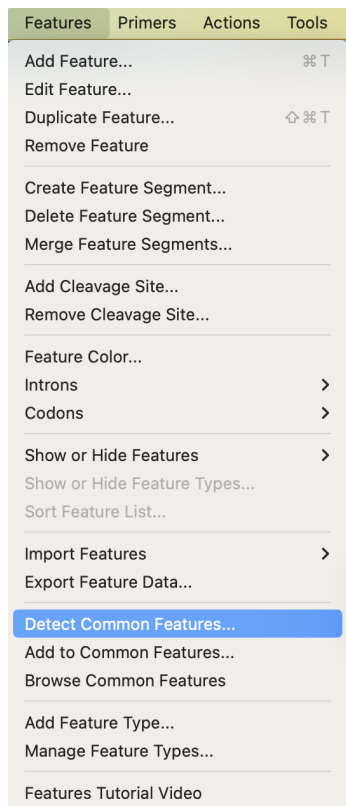
The first file is the unannotated version of the pUC19 DNA sequence that has no annotated features. The second file is the same sequence annotated using the **Detect Common Features** tool in SnapGene. This file has a number of different types of features annotated, including promoters, an origin of replication and an antibiotic resistance marker. The steps taken to create this annotated sequence will now be listed so that you can produce your own annotated version of this sequence.

To run the **Detect Common Features** tool on the unannotated sequence, do the following:

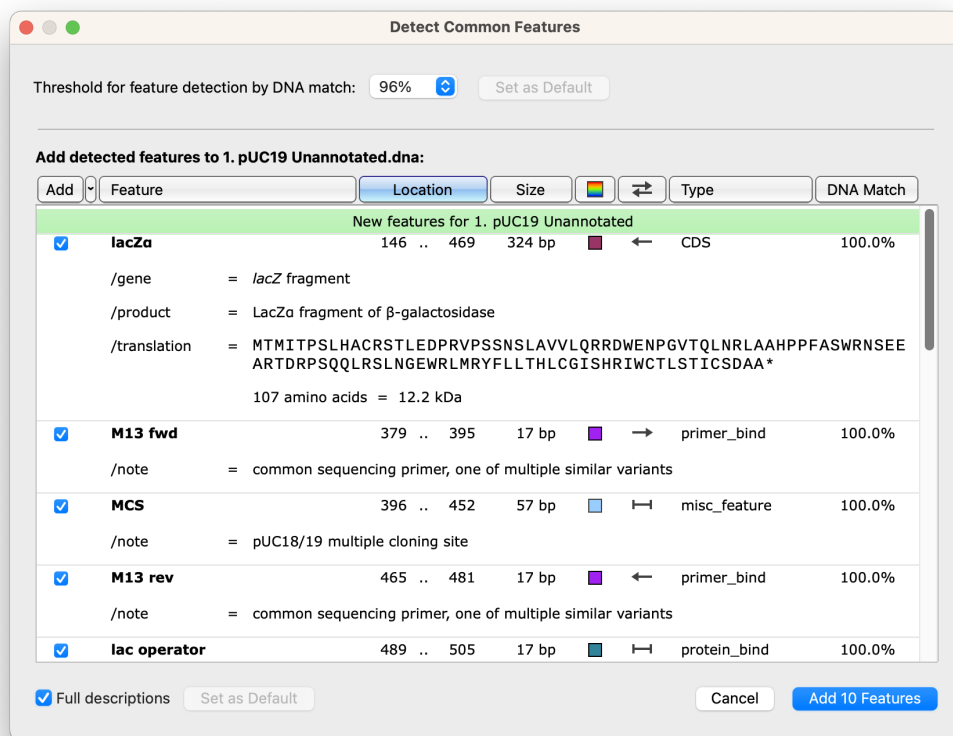
1. Select pUC19 unannotated in the file explore inside the project browser



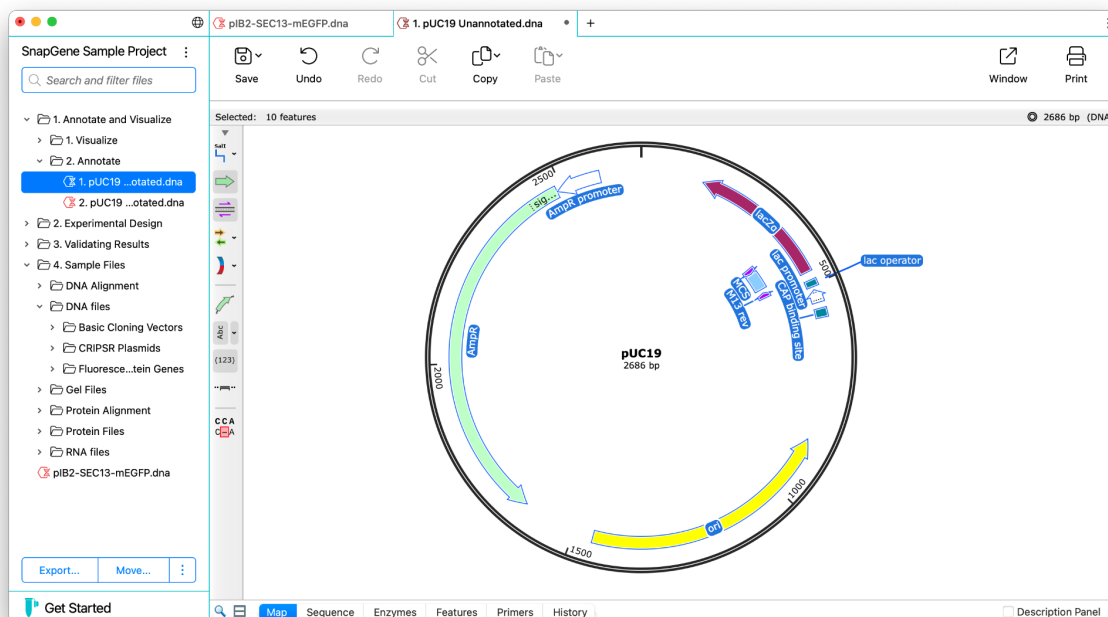
2. Press the **Features** button in the actions menu, then select **Detect Common Features...**



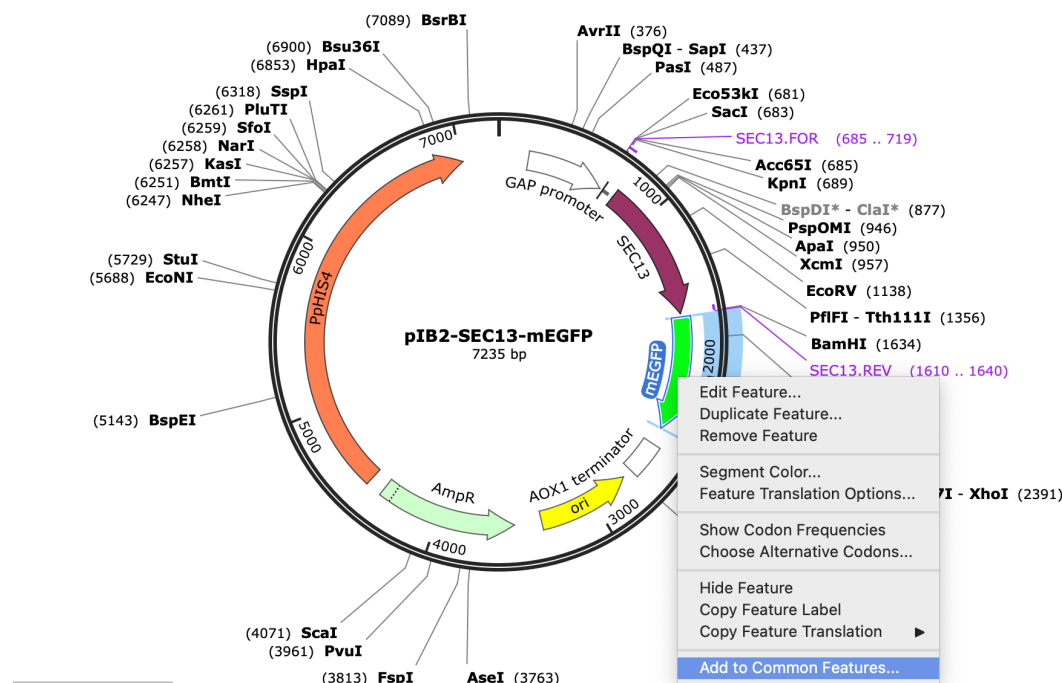
3. This will bring up the dialog shown below. SnapGene has detected features present in the pUC19 sequence you have selected from the common features database. From here you can change the detection threshold if you know that the sequence you are using diverges from the sequence present in the common features database.



4. All 10 features that SnapGene has detected will be selected by default. You can select or unselect particular features using the checkboxes in the Add column, then select **Add 10 Features** to add all the features listed to the pUC19 sequence.



It is also possible to add your own features to this database so that these can be used to annotate other sequences. In order to do this you will need an annotated version of your desired feature already present on a sequence. You can then right-click this feature and select **Add to Common features**, as shown in the screenshot below. This will add this feature to your database so that it can be used by the **Detect Common Features** tool.



More information about this tool can be found at our [User Guide](#). If you believe we have missed a feature that should be present in our common features database, let us know by [contacting support](#). We frequently add new features to this database, or update existing features based on user feedback.