

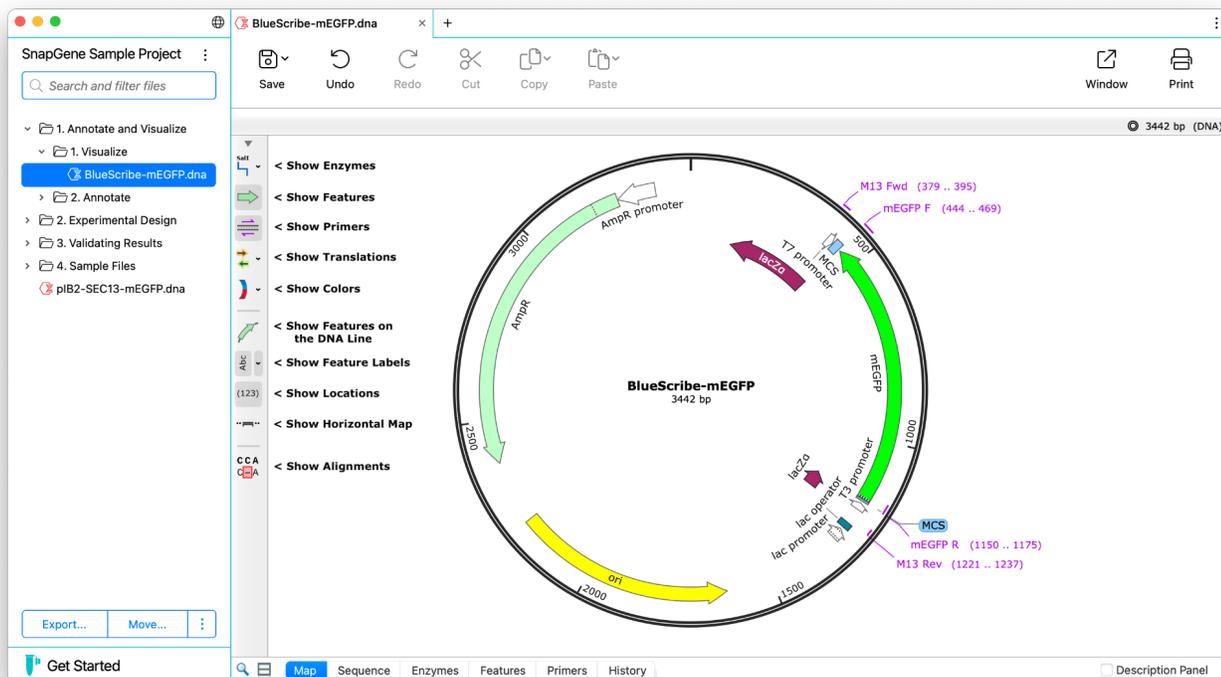
1. Annotate and Visualize

Visualize

SnapGene offers a large number of tools and settings to visualize your sequences. These vary depending on the sequence type that you are working with. For the purposes of this document we will only look at a DNA sequence, but note that when you are working with other file types such as protein, or RNA, these settings might be different. For more information about how to use these view settings, the [SnapGene User Guide](#) is a useful resource that covers these settings in far more detail.

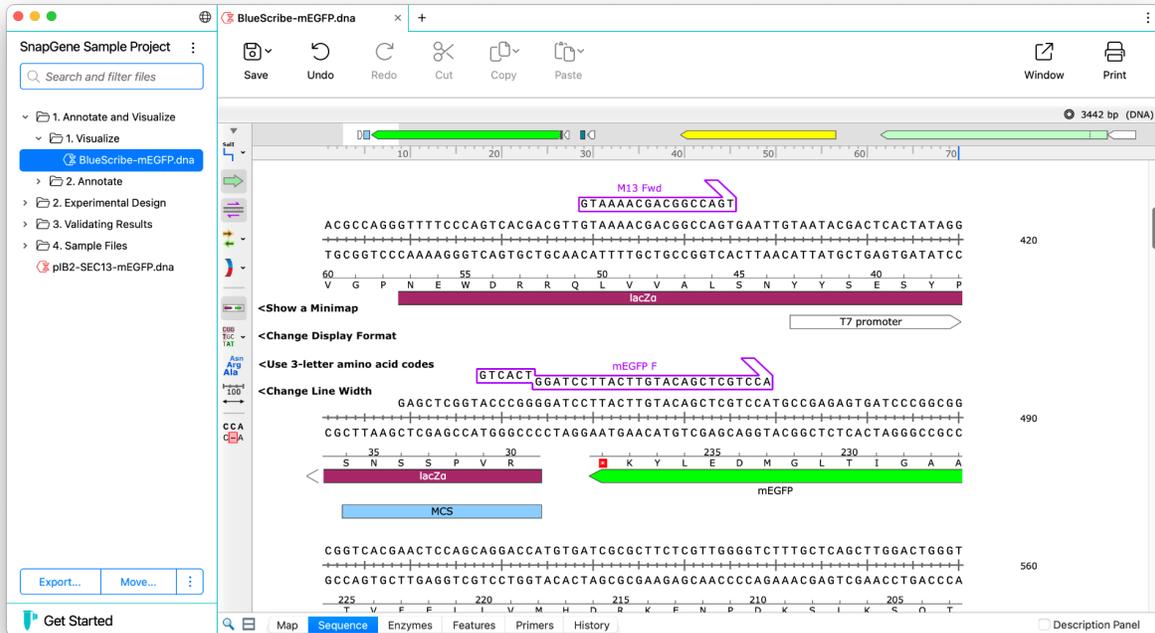
The Map View

When you open the pUC57-kan.dna file in this folder, you will see the following document. By default SnapGene will open this to the Map view. You can change this to the Sequence view by selecting the Sequence tab at the bottom of the document. A document in the Map view will have a number of settings that you can alter to change the visualization of the document - these are outlined on the screenshot below.



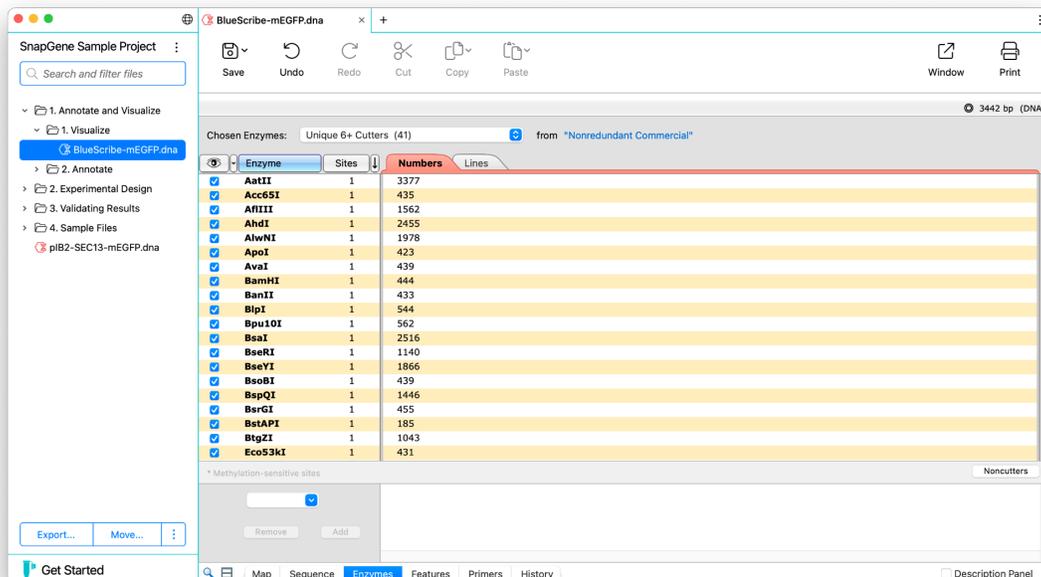
The Sequence View

Switch to the Sequence view by selecting the Sequence tab at the bottom of the screen. This will show you the sequence of pUC57-kan.dna. Like the Map view, this has a number of settings that you can use to alter the display of your sequence. A number of these are shared with the map view, but the new settings introduced by this view are outlined in the screenshot below.



The Enzymes View

This view displays a detailed view of the restriction enzyme sites in your sequence, and the cut site locations. The **Chosen Enzymes** dropdown box allows you to change the enzyme set that is displayed to those held by a certain supplier, or key sets that might be relevant for certain types of cloning such as the type IIS enzymes used by cloning methods such as Golden Gate. The **Noncutters** button at the bottom-right of this table will provide a list of enzymes that do not cut your sequence.



The Features View

Selecting the **Features** tab at the bottom of the window will take you to a table with detailed information about each of the features present in your sequence. The information for individual features can be seen by hovering over the feature in the map or sequence view, but this view instead provides the information for all of your features in a single place. From here you can select a feature in the list and switch back to the **Sequence** or **Map** tab to be taken to that feature.

Feature	Location	Size	Type
<input checked="" type="checkbox"/> lacZa	146 .. 444	299 bp	CDS
/codon_start = 1 /gene = lacZ fragment /product = LacZa fragment of β -galactosidase /translation = RVPSSNSPYSESYNSLAVLQRRDWNENPGVTQLNRLAAHPFASWRNSEEARTDRPSQQRLSLNGEWRMLRMYFLLLHLCGISHRIWCTLSTICSDAA 98 amino acids = 11.3 kDa			
<input checked="" type="checkbox"/> T7 promoter	402 .. 420	19 bp	promoter
/note = promoter for bacteriophage T7 RNA polymerase			
<input checked="" type="checkbox"/> MCS	423 .. 444	22 bp	misc_feature
/note = pUC18/19 multiple cloning site			
<input checked="" type="checkbox"/> mEGFP	450 .. 1169	720 bp	CDS
3 segments /product = enhanced GFP /note = mammalian codon-optimized /translation = MYSKGEELFTGVVPILVLELDGVDVNGHKFSVSGEGEDATYGKLT LKFICTTGKLPVWP TLVTTLYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERT IFFKDDGNYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKLENYNSHNVYIMADKQNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGGGPVLL PDNHYLSTQSKLSKDPNEKRDMHVLVLFVTAAGITLGMDELK*			

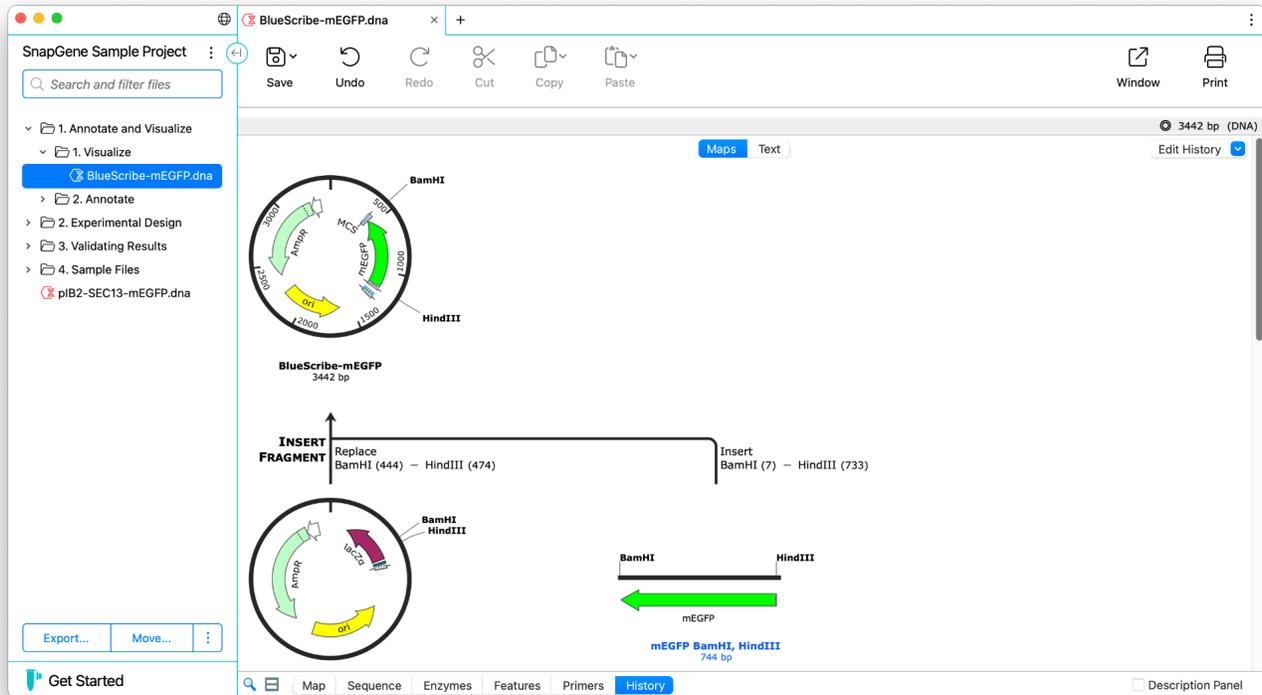
The Primers View

This view is similar to the Features view, but instead gives you the information for all of the primers that are present on your sequence. This includes information that is relevant for primers, such as the binding sites, binding temperature and the length of the primer.

Primer	Length	Binding Sites	Tm	Date Added
<input checked="" type="checkbox"/> M13 Fwd	17-mer	379 .. 395	56°C	2 Jun 2023
/sequence = GTAAACGACGGCCAGT 53% GC / 5228.5 Da				
<input checked="" type="checkbox"/> mEGFP F	32-mer	444 .. 469	61°C	2 Jun 2023
/sequence = GTCACGGATCCTTACTTGTACAGCTCGTCCA 50% GC / 9726.4 Da				
<input type="checkbox"/> A206K.REV	39-mer	531 .. 569	71°C	
/sequence = GTTGGGGTCTTTGCTCAGCTTGACTGGGTGCTCAGGTA 56% GC / 12,107.9 Da /note = For introducing the monomerizing A206K mutation				
<input type="checkbox"/> A206K.FOR	39-mer	531 .. 569	72°C	
/sequence = TACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAAC 56% GC / 11,868.7 Da /note = For introducing the monomerizing A206K mutation				
<input checked="" type="checkbox"/> mEGFP R	32-mer	1150 .. 1175	65°C	2 Jun 2023
/sequence = TCAGTGAAGCTTATGGTGAGCAAGGGCCAGGA 53% GC / 10,018.6 Da				
<input checked="" type="checkbox"/> M13 Rev	17-mer	1221 .. 1237	49°C	2 Jun 2023

The History View

The **History** tab will allow you to see the history of a sequence, giving information of any actions that were performed in SnapGene to generate that document. Selecting on the name of an ancestor sequence in this view will open that ancestral document, and selecting on the names of any primers used listed for any of the steps will bring up the information about those primers. The history view can be switched from the map view to text view by selecting the **Text** tab at the top of the window.



This provides a basic summary of the view of a DNA file in SnapGene. The tabs and view settings for other sequence types will be slightly different. For example, for single-stranded RNA files you will also have the Secondary Structure tab available to you that will allow you to run RNA structure analyses