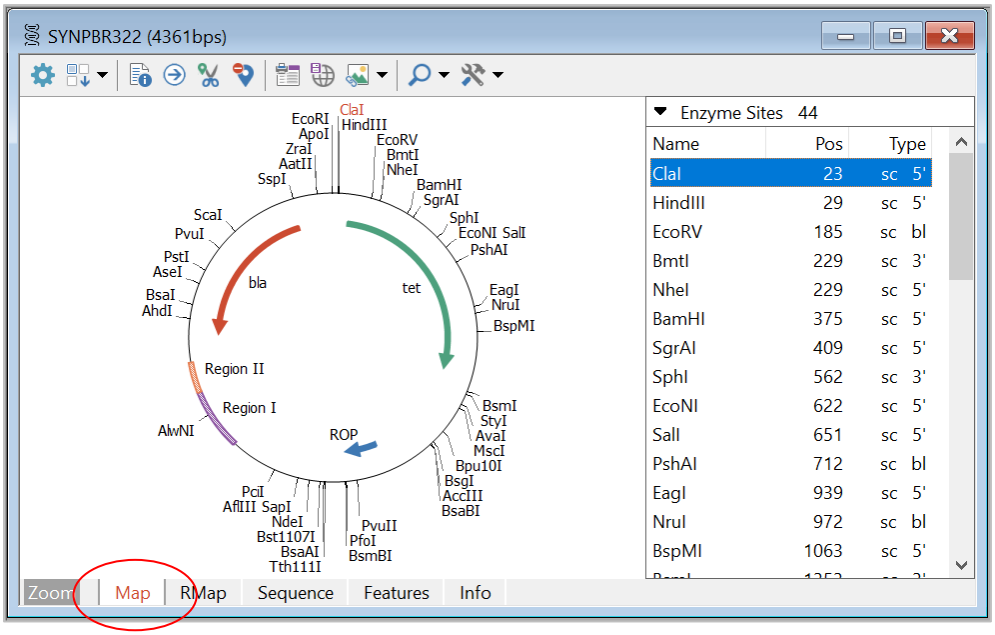
Molecule Viewer Window – Map View



Custom styles and colors applied to some genes in this map. Enzyme sites list shown at right.

Helpful toolbar buttons:

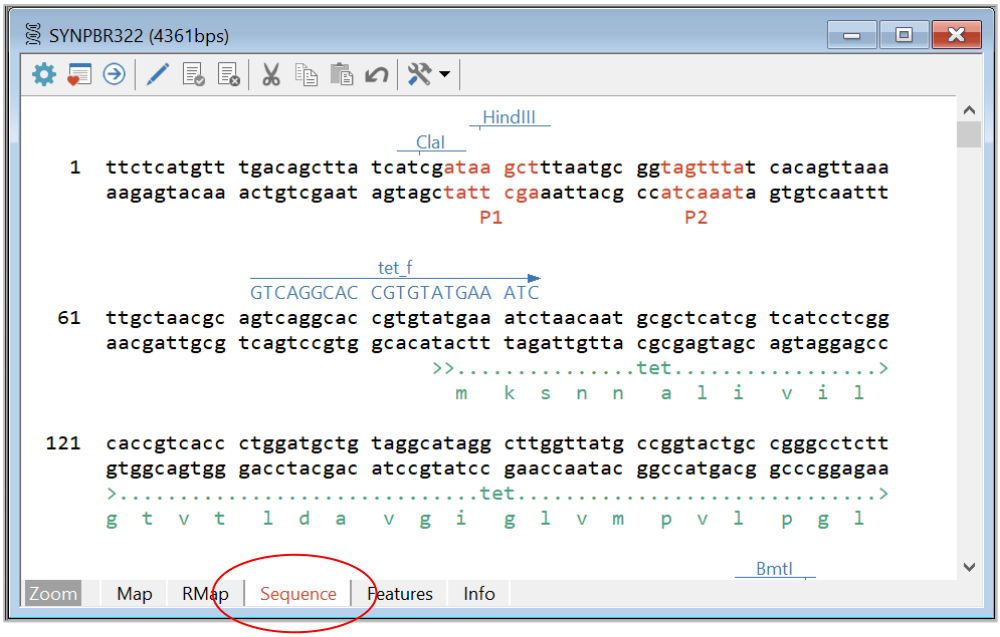
- Change Sites
- Site Properties
- Go To Sequence
- Save for Web
- Enhanced View

Sequence View

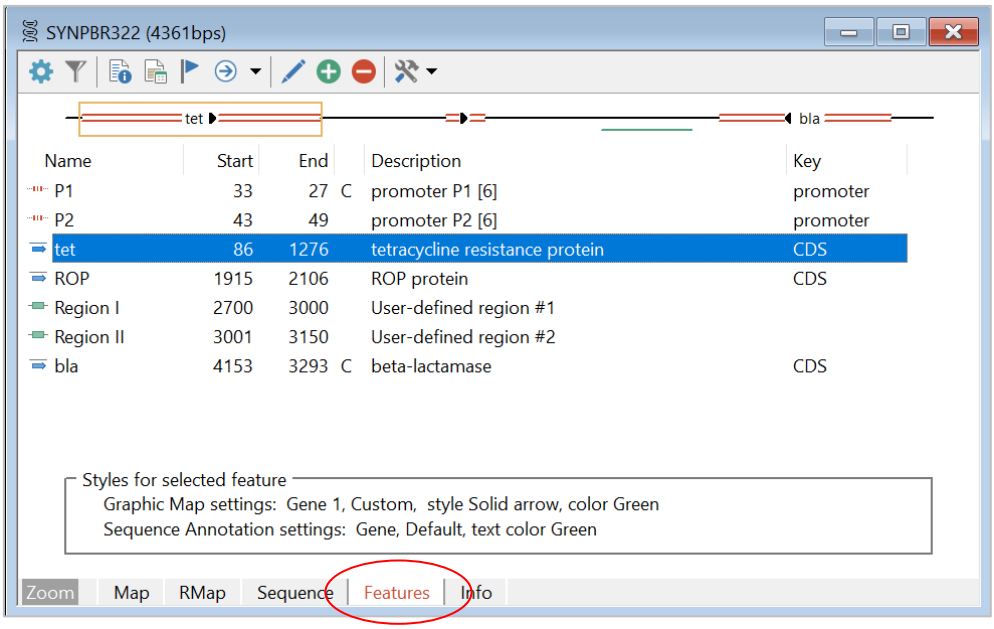
Formatted sequence shows enzyme sites, sequence labels, primers, translated genes.

Helpful toolbar buttons:

- My Style
- Go To BP Number
- Edit Sequence
- Tools > Find
- Tools > Enter as Feature



Features View



Set to show simple features map above list and selected feature style in boxed area below list.

Helpful toolbar buttons:

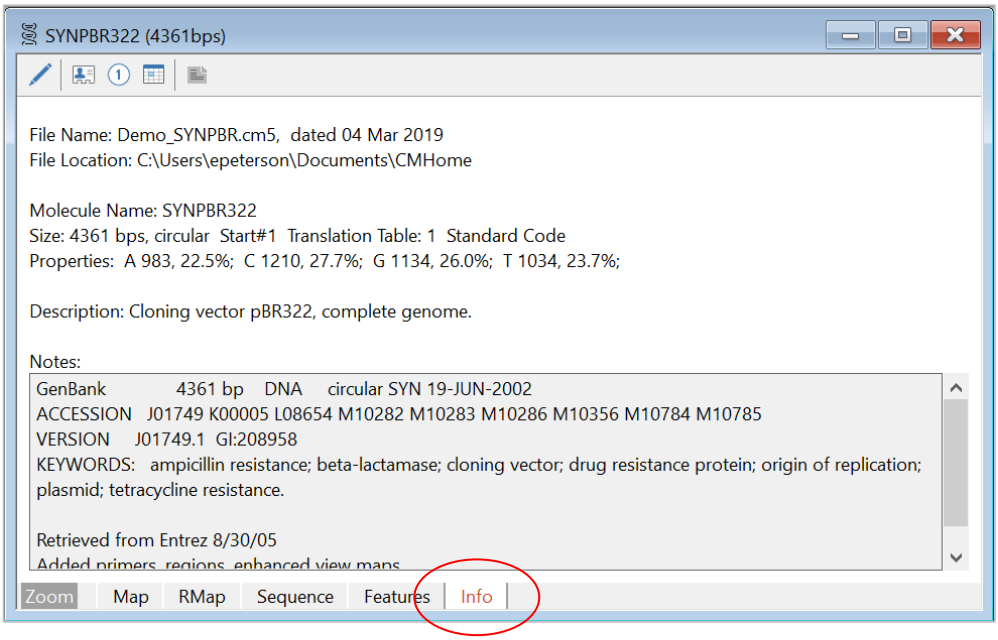
- Filter
- Feature Properties
- Customize Feature
- Go To Sequence
- Tools > Make Fragment

Info View

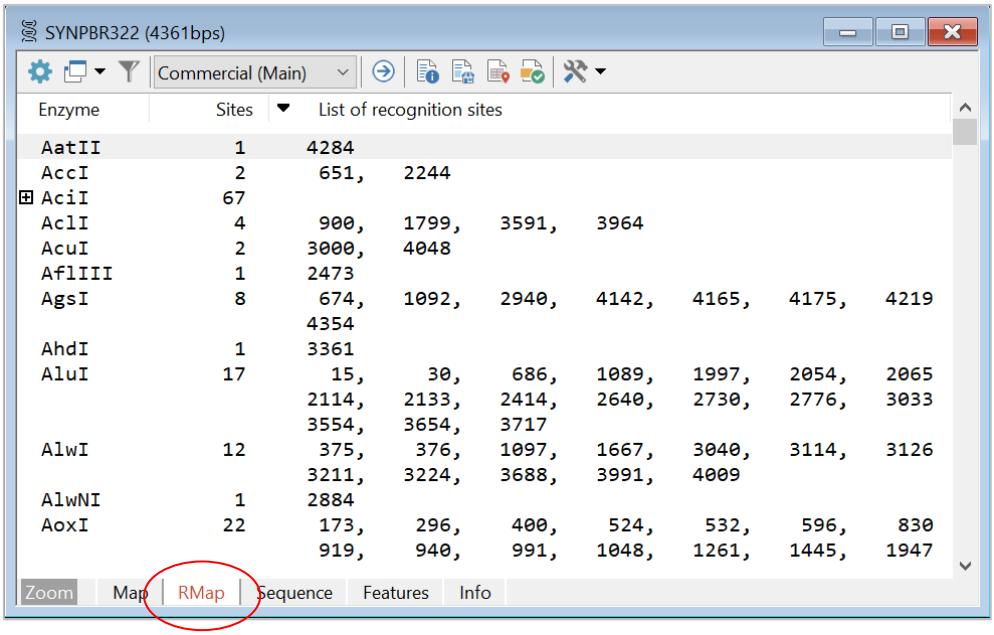
Modify molecule name and description. Add Notes to document molecule source or changes made.

Helpful toolbar buttons:

- Edit
- Author Stamp
- Base Number Start
- Translation Table
- GenBank Annotations



RMap View



Select to display List of Recognition Sites, Map of Recognition Sites, Fragment Sizes, or Gel View.

Helpful toolbar buttons:

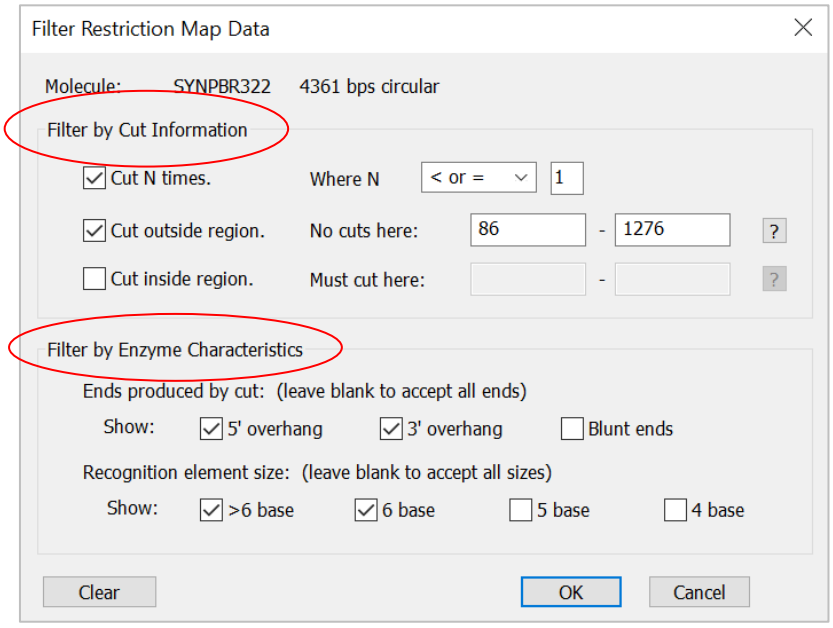
- Go To Enzyme
- Enzyme Properties
- Enzyme Suppliers
- Isoschizomers
- Compatible Ends

Filter RMap Display

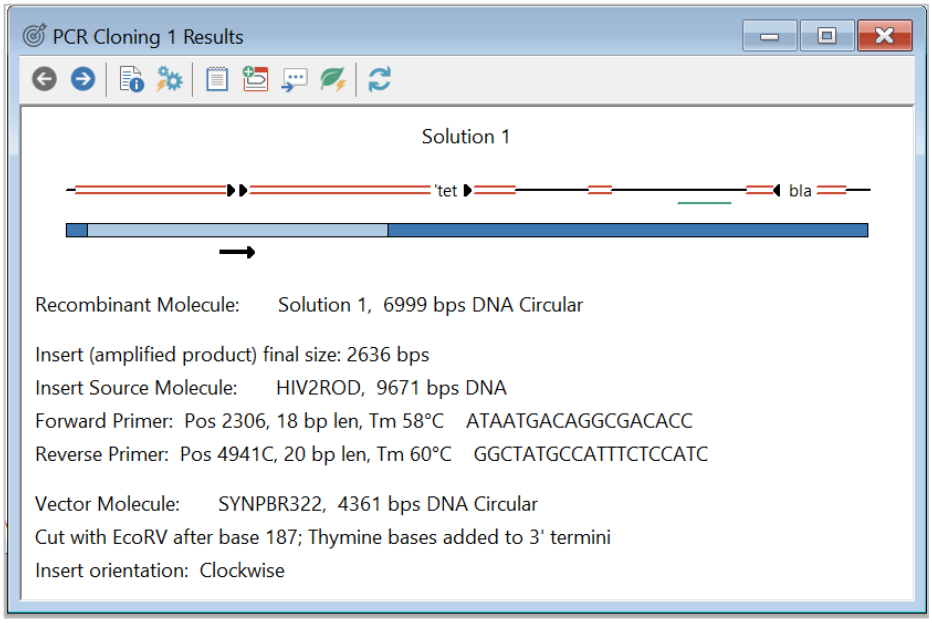
Filter restriction map data by Cut Information and/or filter by Enzyme Characteristics.

Filtered restriction map data can be used to build a user enzyme list or enter all sites to your molecule map in one easy step.

Click the Tools button in the RMap display window to use these options on filtered data.



Simulate Cloning – Use Cloning Wizards



Cloning wizards will help you to select the appropriate components, show you the proposed result, and create the resulting recombinant molecule.

Helpful toolbar buttons:

- Solution Details
- Primer Pair Report
- Export Primer Sequences
- Create Molecule

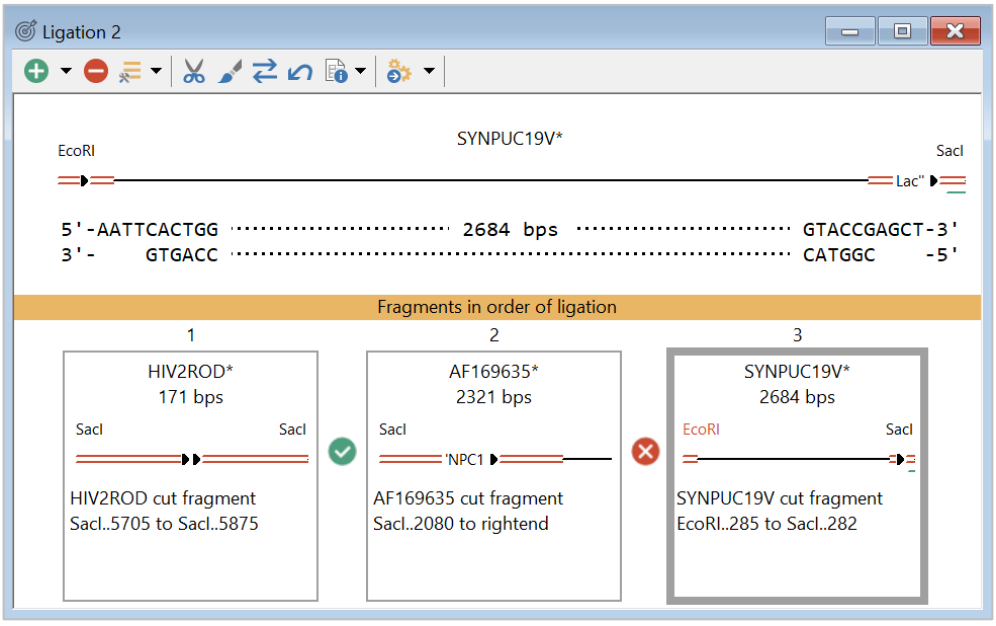
Ligate

Or use the Ligate module to do the cloning simulation.

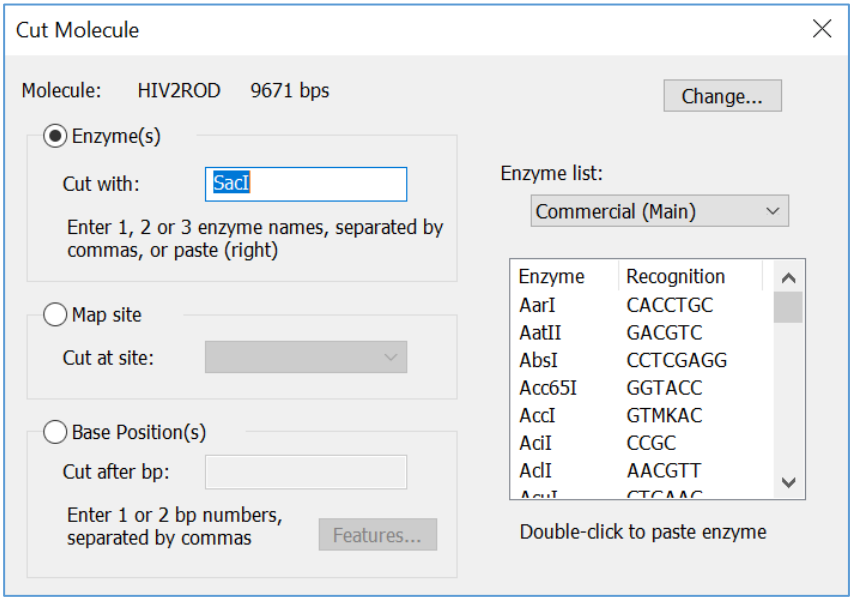
Upper area: active molecule you can modify (cut, etc.)
Lower area: fragments in correct order as they are being prepared for ligation.

Helpful toolbar buttons:

- Cut
- Modify Ends
- Invert Fragment
- Fragment Information



Cut Molecule



You can cut circular DNA to make it linear, cut out a region to be cloned, or cut with an enzyme to make a compatible end.

Cut at all enzyme cut sites for 1, 2 or 3 enzymes, or cut at one enzyme site on your map, or cut at user-specified basepair positions.

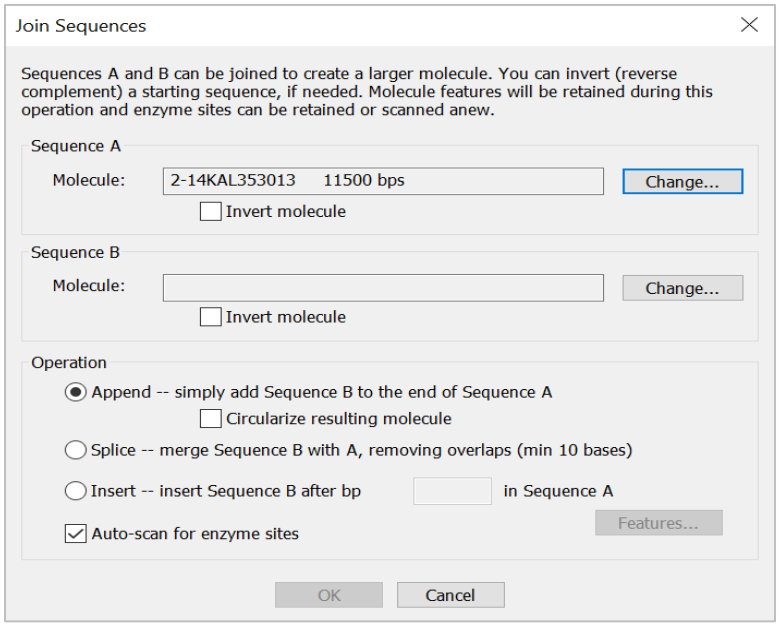
Use Modify Ends function, if needed.

Join Sequences

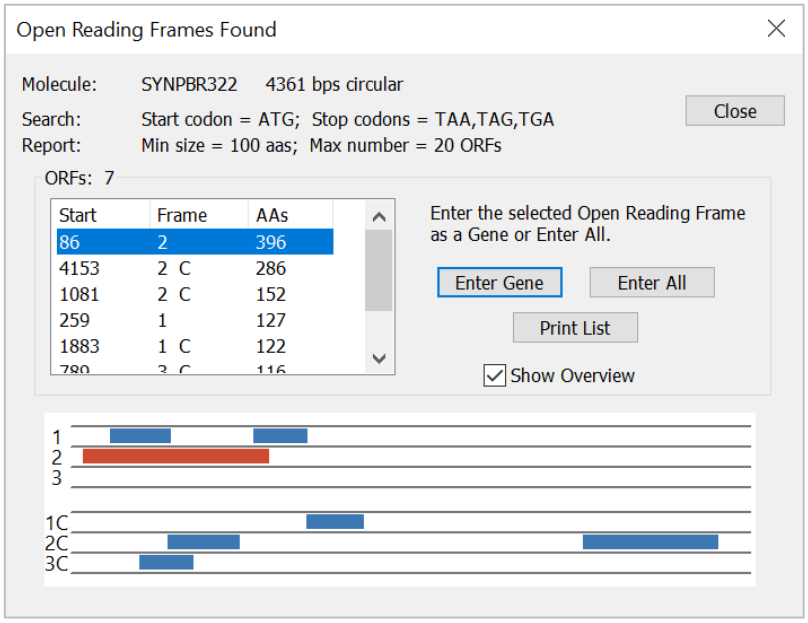
Simply join two sequences to create a larger molecule, selecting the join method.

Add one sequence to the end of the other (Append), or merge, removing overlaps (Splice), or insert within the other sequence (Insert).

Molecule features will be retained and basepair positions recalculated.



Open Reading Frame Search



Use this option to find ORFs for the active molecule. Specify start and stop codons you require and minimum size cutoff.

View overview of results (shown here) or a list of each ORF found, with an arrow marking its location on a simple molecule map.

Click to enter an ORF as a gene in your molecule.

Analyze Open Reading Frames

Use the Analyze option to do an ORF analysis.

View a graphic results display showing an ORF map of all 6 reading frames. Full height bars mark terminators, half height bars mark selected start codons.

Or view a text display showing start and end bp positions, length in amino acids, frame, and Fickett's TESTCODE score values.