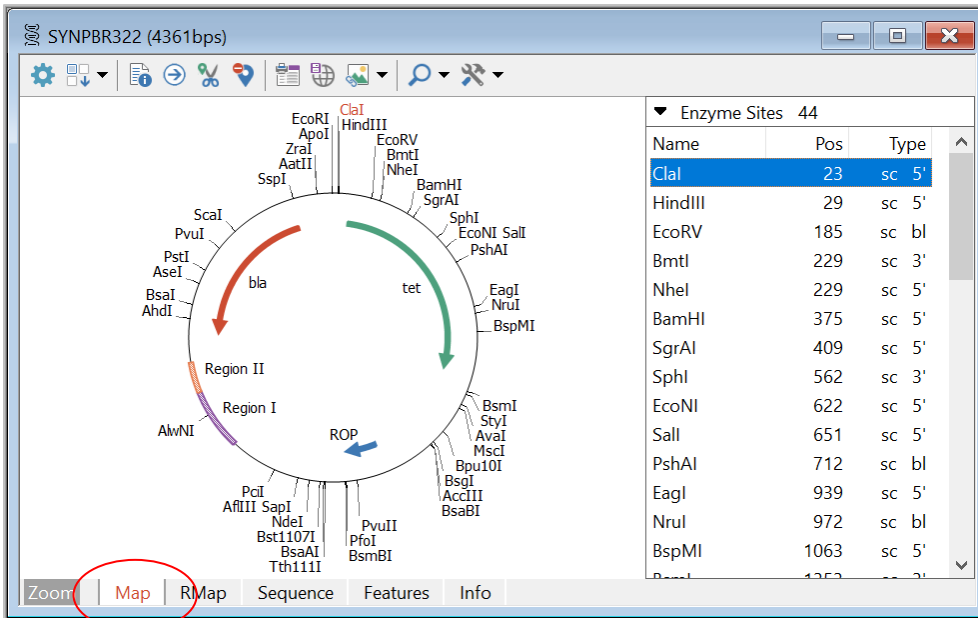


Molecule Viewer Window – Map View



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

Helpful toolbar buttons:

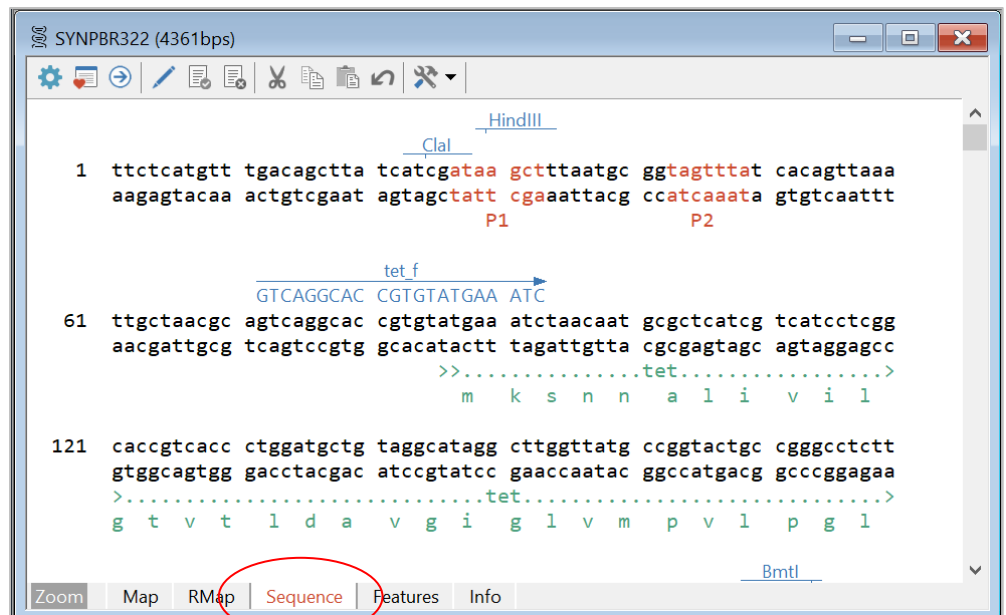
- Change Sites
- Site Properties
- Go To Sequence
- Save for Web
- Enhanced View

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

Name	Start	End	Description	Key
P1	33	27	C promoter P1 [6]	promoter
P2	43	49	C promoter P2 [6]	promoter
tet	86	1276	tetracycline resistance protein	CDS
ROP	1915	2106	ROP protein	CDS
Region I	2700	3000	User-defined region #1	
Region II	3001	3150	User-defined region #2	
bla	4153	3293	C beta-lactamase	CDS

Styles for selected feature

Graphic Map settings: Gene 1, Custom, style Solid arrow, color Green

Sequence Annotation settings: Gene, Default, text color Green

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

File Name: Demo_SYNPBR.cm5, dated 04 Mar 2019
File Location: C:\Users\epeterson\Documents\CMHome

Molecule Name: SYNPBR322
Size: 4361 bps, circular Start#1 Translation Table: 1 Standard Code
Properties: A 983, 22.5%; C 1210, 27.7%; G 1134, 26.0%; T 1034, 23.7%;

Description: Cloning vector pBR322, complete genome.

Notes:

GenBank 4361 bp DNA circular SYN 19-JUN-2002
ACCESSION J01749 K00005 L08654 M10282 M10283 M10286 M10356 M10784 M10785
VERSION J01749.1 GI:208958
KEYWORDS: ampicillin resistance; beta-lactamase; cloning vector; drug resistance protein; origin of replication; plasmid; tetracycline resistance.

Retrieved from Entrez 8/30/05
Added primers regions enhanced view maps

RMap View

Enzyme	Sites	List of recognition sites							
AatII	1	4284							
AccI	2	651, 2244							
AciI	67								
AcI	4	900, 1799, 3591, 3964							
AcuI	2	3000, 4048							
AflIII	1	2473							
AgsI	8	674, 1092, 2940, 4142, 4165, 4175, 4219							
AhdI	1	4354							
AluI	17	3361							
AlwI	12	15, 30, 686, 1089, 1997, 2054, 2065							
		2114, 2133, 2414, 2640, 2730, 2776, 3033							
		3554, 3654, 3717							
AlwNI	12	375, 376, 1097, 1667, 3040, 3114, 3126							
		3211, 3224, 3688, 3991, 4009							
AlwNI	1	2884							
AoxI	22	173, 296, 400, 524, 532, 596, 830							
		919, 940, 991, 1048, 1261, 1445, 1947							

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.

Filter Restriction Map Data ✕

Molecule: SYNBPBR322 4361 bps circular

Filter by Cut Information

Cut N times. Where N < or = 1

Cut outside region. No cuts here: 86 - 1276 ?

Cut inside region. Must cut here: - ?

Filter by Enzyme Characteristics

Ends produced by cut: (leave blank to accept all ends)

Show: 5' overhang 3' overhang Blunt ends

Recognition element size: (leave blank to accept all sizes)

Show: >6 base 6 base 5 base 4 base

Clear
OK
Cancel

Simulate Cloning – Use Cloning Wizards

PCR Cloning 1 Results

Solution 1

Recombinant Molecule: Solution 1, 6999 bps DNA Circular

Insert (amplified product) final size: 2636 bps

Insert Source Molecule: HIV2ROD, 9671 bps DNA

Forward Primer: Pos 2306, 18 bp len, Tm 58°C ATAATGACAGGCGACACC

Reverse Primer: Pos 4941C, 20 bp len, Tm 60°C GGCTATGCCATTCTCCATC

Vector Molecule: SYNPNR322, 4361 bps DNA Circular

Cut with EcoRV after base 187; Thymine bases added to 3' termini

Insert orientation: Clockwise

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

Ligation 2

SYNPUC19V*

EcoRI Sacl

5' -AATCACTGG 2684 bps GTACCGAGCT-3'

3' - GTGACC CATGGC -5'

Fragments in order of ligation

1	2	3
HIV2ROD* 171 bps	AF169635* 2321 bps	SYNPUC19V* 2684 bps
Sacl Sacl	Sacl	EcoRI Sacl
HIV2ROD cut fragment Sacl..5705 to Sacl..5875	'NPC1 AF169635 cut fragment Sacl..2080 to rightend	SYNPUC19V cut fragment EcoRI..285 to Sacl..282

Cut Molecule

Cut Molecule

Molecule: HIV2ROD 9671 bps Change...

Enzyme(s)

Cut with:

Enter 1, 2 or 3 enzyme names, separated by commas, or paste (right)

Map site

Cut at site:

Base Position(s)

Cut after bp:

Enter 1 or 2 bp numbers, separated by commas Features...

Enzyme list:

Enzyme	Recognition
AarI	CACCTGC
AatII	GACGTC
AbsI	CCTCGAGG
Acc65I	GGTACC
AccI	GTMKAC
AcI	CCGC
AdI	AACGTT
AgeI	CTCAAC

Double-click to paste enzyme

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.

Join Sequences

Sequences A and B can be joined to create a larger molecule. You can invert (reverse complement) a starting sequence, if needed. Molecule features will be retained during this operation and enzyme sites can be retained or scanned anew.

Sequence A

Molecule: Change...

Invert molecule

Sequence B

Molecule: Change...

Invert molecule

Operation

Append -- simply add Sequence B to the end of Sequence A

Circularize resulting molecule

Splice -- merge Sequence B with A, removing overlaps (min 10 bases)

Insert -- insert Sequence B after bp in Sequence A

Auto-scan for enzyme sites Features...

OK Cancel

Open Reading Frame Search

Open Reading Frames Found

Molecule: SYNPR322 4361 bps circular

Search: Start codon = ATG; Stop codons = TAA,TAG,TGA

Report: Min size = 100 aas; Max number = 20 ORFs

ORFs: 7

Start	Frame	AAs
86	2	396
4153	2 C	286
1081	2 C	152
259	1	127
1883	1 C	122
780	3 C	116

Enter the selected Open Reading Frame as a Gene or Enter All.

Show Overview

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.

Open Reading Frames

Frame

Molecule: SYNPR322 4361 bps

Terminators = full height bars (black); ATG Start codons = half height (color)