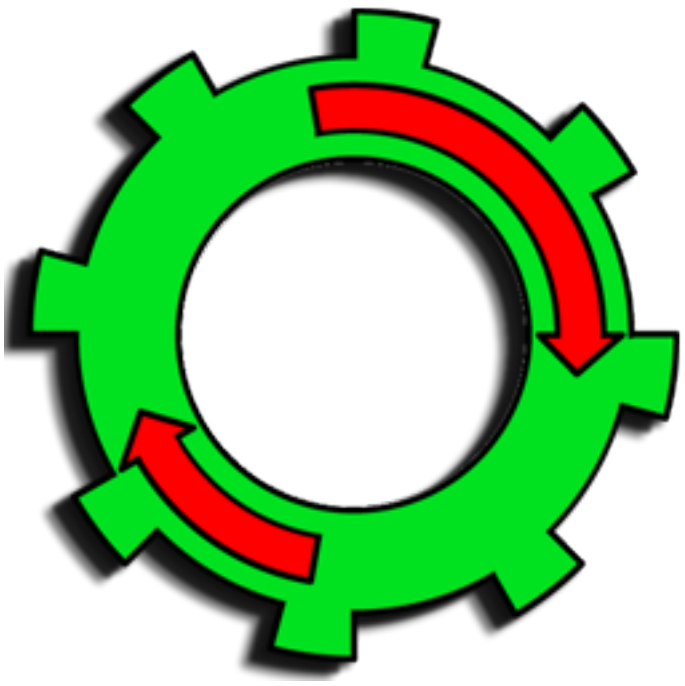


XPlasMap Users' Guide

version 0.9

Quick start

- Start a new map from the **Maps** menu (⌘-N for circular, ⌘-Shift-N for linear map)
  - **Maps** menu **/ Linear <> Circular** to convert between circular and linear maps
- Draw linear DNA maps directly from GenBank files:
  - Save a file to your computer, from GenBank in "GenBank (Full)" format
  - Import (**File** menu **/ Import / from GenBank (.gb files)**)
  - Choose which features listed in the GenBank (genes, mRNA, CDS, etc) you want to include on the map
- Draw maps directly from FastA or plain-text sequence files (**File** menu **/ Import / from FastA or Text**)
- Add new genes, new multiple cloning sites, or new restriction sites from the **Edit** menu (or ⌘-G, ⌘-Shift-M, or ⌘-R)
  - Genes on linear (but not circular) maps can be shown as exon/intron diagrams, or as a single block
  - Multiple cloning sites can be displayed in several styles
- Edit by double-clicking on the feature
  - To edit a plasmid, click on the text in the center, or on the comment at the bottom (or "Edit plasmid info" from the **Edit** menu)
  - Quick edits via contextual menu (control-click or right-click on the feature)
- Click and drag to move a feature
  - Hold down ⌘ and drag to move a gene (click-and-drag moves the text of the gene only)
- Copy a fragment (⌘-C or **Edit / Copy** menu) for later pasting, or draw it as a linear fragment (**Maps / New linear DNA** or ⌘- Shift-N).
- Inserting a fragment (**Edit** menu): insert either a new, featureless section of DNA, a copied fragment from memory, or a linear DNA fragment from a saved file
- Cut a fragment (⌘-X or **Edit** menu) is the equivalent of collapsing out a region
- View as list (⌘-L or "View as list" in the **Maps** menu) for a sortable text summary of all DNA features
  - Edit multiple features simultaneously using "View as list"
- Print maps (**File / Print**) or export as images (**File / Export / to PNG** or **File / Export / to JPG**)

XPlasMap FAQ

Most of XPlasMap's functions should be fairly obvious. This section is aimed at clarifying some less obvious points.

1. How can I use my DNA map in a slide show or as a figure? Export to PNG or JPG (File menu), then insert that image into whatever program you're using. (For practical purposes, the main difference between Save as JPG and Save as PNG is that the JPGs have a solid background, the PNGs have a transparent background.) Or, go to the Print menu and Save As PDF.

2. How do I draw a map from a plain text file? From a FastA file? Select "Import / from FastA or text" in the File menu, and select a file of the appropriate format.

3. What's the advantage of drawing a map from a plain text or FastA file? At this point (XPlasMap v.0.9), not much. You'll get a plain, featureless linear map of the proper length. With FastA format, you can include multiple sequence in FastA in the same file, and each will be made into a separate map. Also, FastA imports will give a name to the sequence (copied from the identifier header).

4. How do I draw a map from a GenBank file? First, go to GenBank, find your sequence of interest, and select "GenBank (Full)", and "Send to File" to save the sequence to your drive. Then select "Import / from GenBank (.gb format)" in the File menu, and select the file. You'll be asked which of the features you want to display on your map. (The features can be sorted in various way, and you can limit the features that are shown to only include the kind you're interested in.) Check them off, and you're done, though you may need to edit some points.

5. My gene of interest doesn't have its genomic information in GenBank. If the organisms has had its genome sequenced, even if you don't easily find an individual file for your gene, you can usually readily find a longer stretch of DNA containing your gene of interest, even if it may have many other features as well as the one you want. Download the long stretch (make sure you select GeneBank (full)Make a map from that, copy the region that contains your gene, and make a new linear map from the copied region (just select "New linear DNA", and tick the checkbox for "Make linear map from copied fragment". (If the stretch of DNA you originally downloaded has many features and it's hard to identify your gene, use "List view" to quickly limit and sort the features and find the start and end positions of the gene.)

If the genome hasn't been sequenced, you're on your own.

6. What's the advantage of drawing a map from a GenBank file? The map will include any of the features listed in the GenBank files that you want to import. You can map entire chromosomes this way (though it takes a minute or so, and the results often look pretty cluttered).

7. What's the "List view" for? List view (in the Maps menu) shows all the maps' features in text form. If you've turned off display of a feature on the map view, the List view is the only way you can edit it to turn it back on. As well, because you can limit the List view display to one kind of feature and sort by position, name, kind, etc, you can sort restriction sites etc. in various ways. Having sorted, you can also edit groups of features as a batch.

8. What are the different gene styles for? With circular maps, there's only one basic gene style ("Simple"), an arc with or without an arrow, although you can vary many aspects of the arc (presence, absence, direction of arrow; location of arc relative to plasmid backbone; color; text color; text position). Linear DNA maps are more likely to show genomic views, and so there are two other gene styles available in Linear view: "Exons" and "Hybrid". These styles are very similar to each other: Both show a gene as a series of exons (if the information is available). "Exons" style indicates the orientation of the gene by making the last exon an arrow; "Hybrid" style draws an arrow underneath or above the gene, to indicate the orientation. "Exons" view is a little less cluttered, but when the exons are small (e.g. when a long stretch of DNA is being mapped) the arrows are hard to see. "Simple" view makes gene location clearer. "Hybrid" view shows exons, and makes gene orientation easier to see, but also makes the view a little more cluttered.

9. How do I enter and edit exons in a gene? The simple way is to import the genomic view from GenBank. XPlasMap will pick the exon info from the .gb file.

The other way to enter exon info is by hand. Enter a new gene, if necessary. It will be shown as a "Simple" style, no matter what style you choose in the New Gene dialog, because there's no exon information. Now select "Exons" from the gene's contextual menu. This opens a form where you can enter exon information. Enter the start and end of each exon relative to the gene start, not to the overall map, and ignore gene orientation: If gene starts at 1000 bp on the map, and the third exon starts at 6000 on the map, then enter 5000 (the distance from the gene start) as the exon's start.. After your exon info is entered, make sure the gene style is either "Exons" or "Hybrid" to see the exons. (Remember that only linear maps accept these styles.)

10. What are the different multiple cloning site styles for? The three different MCS styles are purely for show, they don't indicate anything functional about the MCS. "Arc" style (especially for circular maps) look good (at least to me) unless there are a lot of enzymes listed, when "Boxed" or "Text" style is less cluttered.

11. I turned off display of an enzyme (or gene, or MCS). How can I edit it to show it again? Normally, to edit a feature you double-click it on the Map view. Obviously, if you've turned off display of the feature, you can't do that. Use the List view (Maps menu) to reveal all features in a sortable text view, and double-click the feature to get the edit dialog again.

12. How do I change the font? Preferences menu.

13. How do I ... ? If there's a feature you want added, something you can't figure out, or (especially) if you find a bug, please send email to

iayork@iayork.com
or
iayork@gmail.com

(Please include "XPlasMap" in the subject, to make sure the email isn't caught by spam filters)

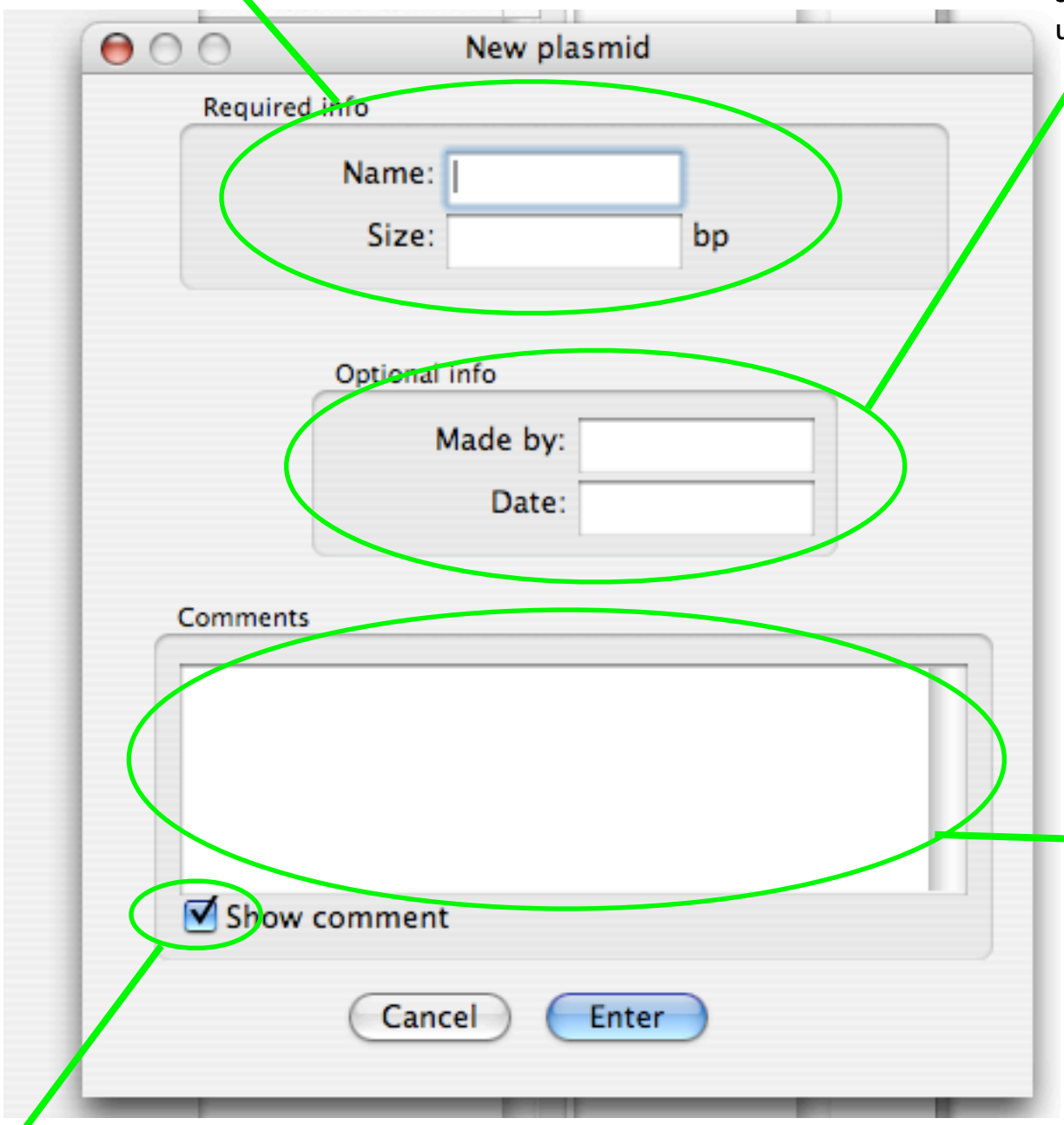
XPlasMap Users' Guide
Table of Contents

Detailed instructions/screenshots

Starting a new plasmid map

The ***New circular plasmid*** menu option in the ***Maps*** menu (or ⌘-N)

Plasmid name and size (in base pairs) are required information. They are shown in the center of the plasmid, like this:
pNewPlasmid (5555bp)



"Made by" and "Date" are optional fields. If they're filled in, they'll be shown in the center of the plasmid, under the name, thus:

pNewPlasmid (5555bp)
Made by Ian York (Aug. 2006)

"Comment" is another optional field. Text entered in here will be shown at the lower left of the map.

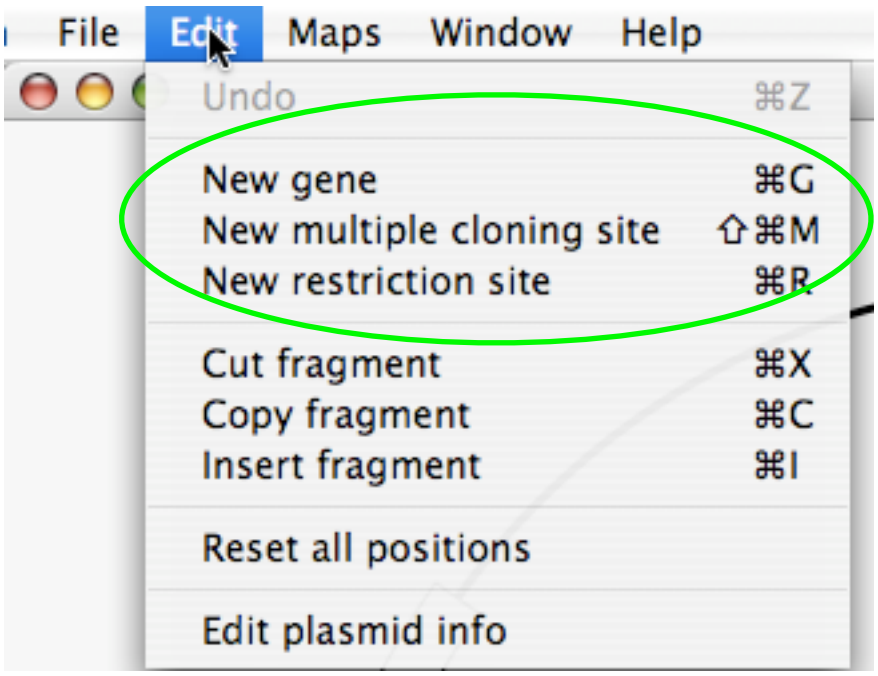
You may wish to have a comment hidden under some circumstances (e.g. make notes for your records, but print off a map with less clutter). Uncheck the "Show Comment" checkbox to hide the comment. (Edit the plasmid information to show the comment again.)

Tips

- To make a new linear DNA map, select "New linear DNA" from the "Maps" menu instead of "New circular plasmid". The linear DNA dialog is almost exactly the same
- This is the same dialog as when you edit a plasmid (although for editing the the information is already filled in)
- To edit any of the information entered here:
  1. Go to "Edit plasmid info" in the "Edit" menu; or
  2. Double-click on the plasmid text (Name/size/made by; or
  3. Right-click on the plasmid text for contextual menu.
- If you wish to make a map from a DNA sequence or from a GenBank record, you can skip this and go directly to "Import" (See below)

Entering a new feature

The ***New gene, New multiple cloning site,*** and ***New restriction site*** menu options in the ***Edit*** menu



Tips

- New gene" and "New enzyme" allow you to enter multiple new genes or enzymes without having to go through this menu again
- "New multiple cloning site" only enters one at a time

Entering a new gene

The ***New gene*** menu option in the ***Edit*** menu (or ⌘-G)

The default option is to enter the start and end position of the new gene (e.g. from 150 to 1050bp). You can also enter the start position and the length of the gene (e.g. a 900bp gene starting at 150bp).

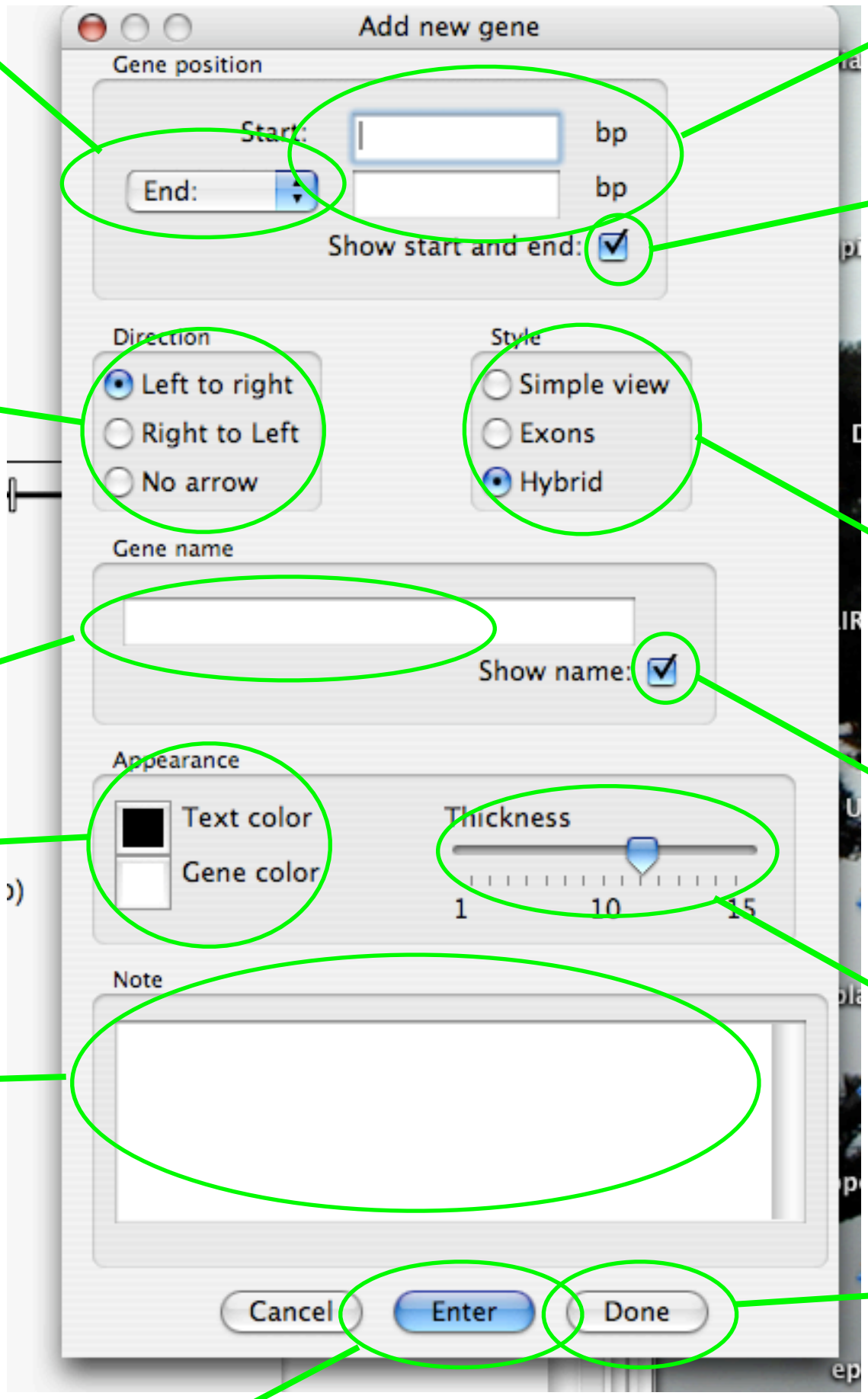
Gene orientation can be right to left or left to right for linear DNA (Clockwise and counterclockwise for circular plasmids). This selection overrides the start and end selection entered in the "Gene position" box above.

Gene name. Not required information

Change the color of the text (i.e. name and location) or of the gene itself

You can make a short note about the gene, This will **not** be shown on the map. You can read it by clicking on the gene (the note is shown in the statusbar at the bottom of the window), by selecting List View, or by editing the gene (which takes you back to this dialog)

If you have several new genes to enter all at once, click "Enter" as each one is done; the gene info will be entered, the dialog will be cleared, but the dialog won't be dismissed -- you can enter the next gene immediately



Position of the gene (in base pairs) is required information

By default, genes are labeled with their name and positions (e.g. NewGene (150-1050). Use this checkbox to not show the locations (e.g. for very short genes, where the text becomes too long with locations included)

In linear maps, genes can be shown with several styles. See below for examples of each. This is not an option with circular plasmids

By default, genes are labeled with their name and positions. Use this checkbox if you don't want the name to be shown

The thickness of the gene can be adjusted. See below for examples

If you only have one new gene to enter, or if you've entered the info for the final gene of a series of new genes, click "Done" to commit the info and dismiss the dialog

Tips

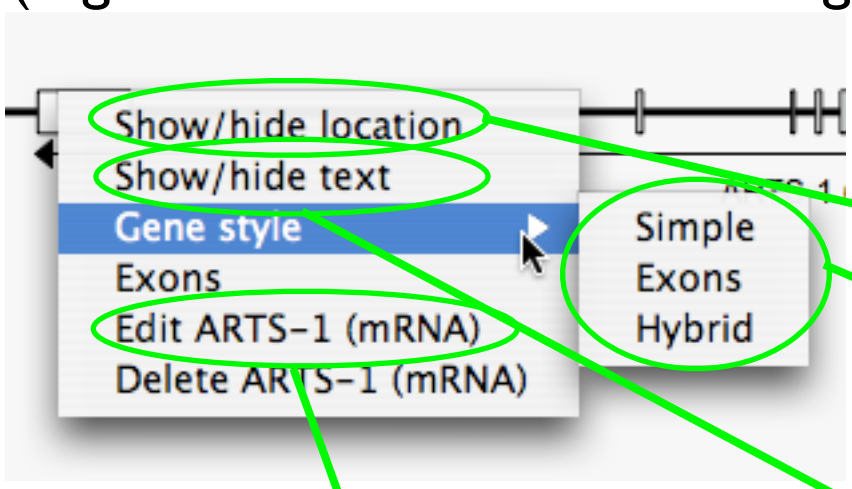
- There are a lot of options here, but the defaults are (hopefully!) sensible enough that you shouldn't have to touch most of them
- As with other features, genes can be edited by double-clicking on them, or through their contextual menus (right-click or control-click on the gene)
- Genes and their text can be dragged to new vertical positions once made. To drag a gene, hold down the Command (⌘) key while dragging

Editing a gene's appearance

The ***New gene*** menu option in the ***Edit*** menu, *or*
the ***Edit gene*** dialog after double-clicking a gene, *or*
The gene contextual menu

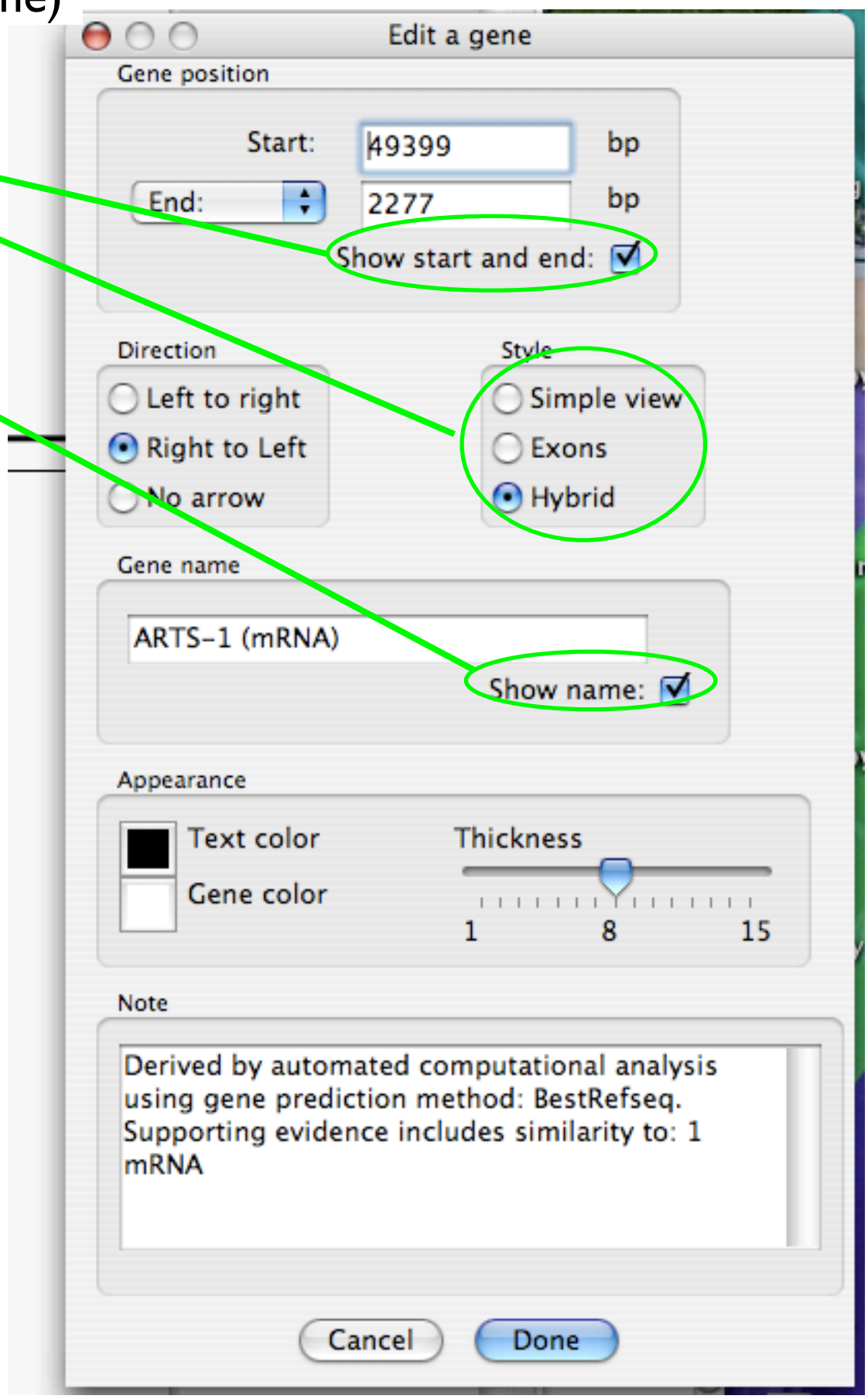
The gene contextual menu offers quick access to several appearance options in the full edit menu

Contextual menu
(Right-click or control-click on gene)



Open the edit gene dialog

Edit gene: Double-click on gene, or select Edit (gene name) from contextual menu



Editing a gene's appearance

The ***Exons*** dialog (Gene contextual menu)

Control-click or right-click on a gene, select "Exons"
(Linear DNA maps only)

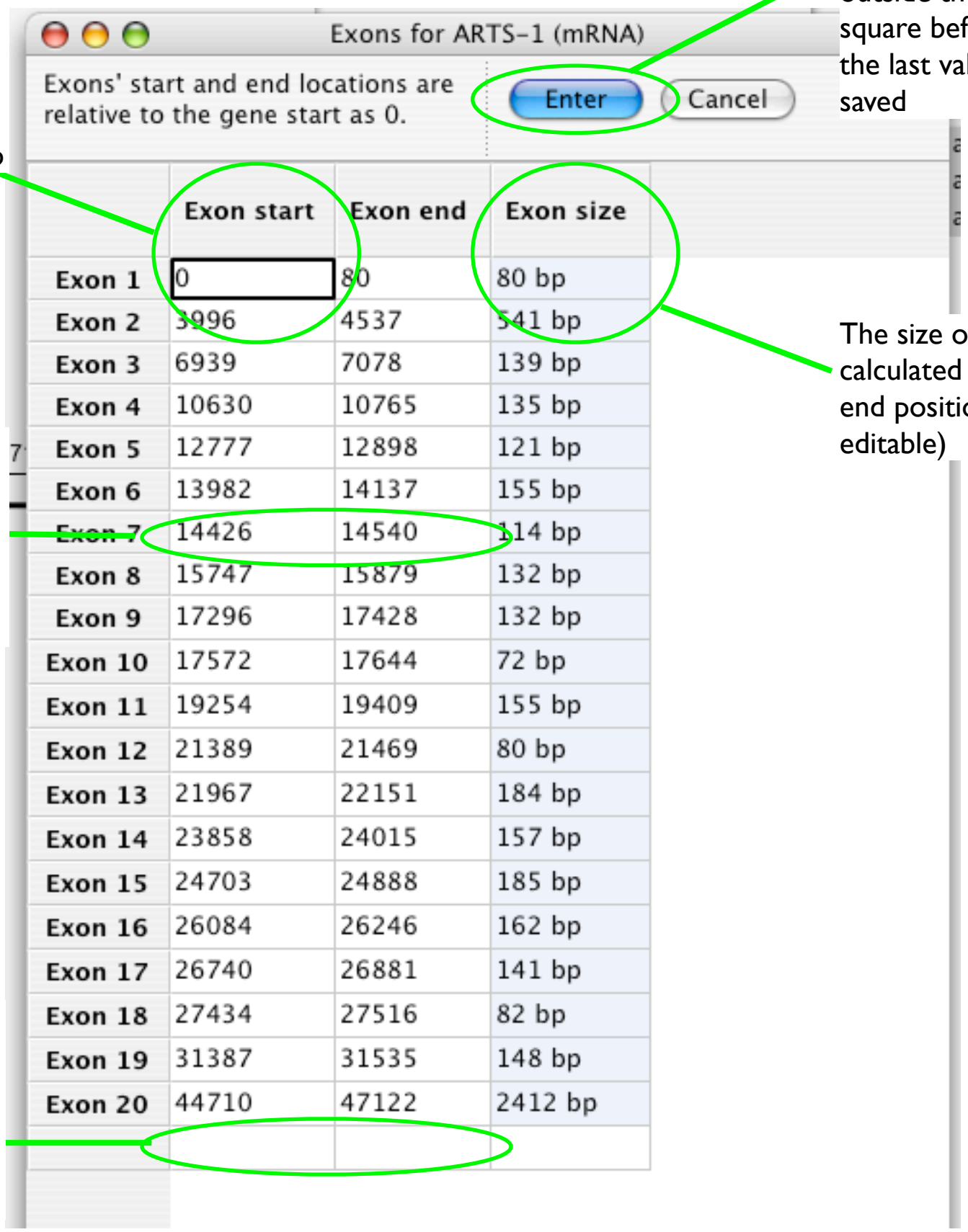
Exon start and end are relative to the gene start, regardless of gene orientation or gene position on the map

Select "Enter" when finished. Be sure to click outside the edited grid square before entering, or the last value won't be saved

Double-click on a grid square to edit an exon's position. Click outside the square when finished

The size of each exon is calculated from start and end positions (not user-editable)

Enter start and end in the last (empty) row to enter a new exon. Double-click on the grid square to enter



	Exon start	Exon end	Exon size
Exon 1	0	80	80 bp
Exon 2	3996	4537	541 bp
Exon 3	6939	7078	139 bp
Exon 4	10630	10765	135 bp
Exon 5	12777	12898	121 bp
Exon 6	13982	14137	155 bp
Exon 7	14426	14540	114 bp
Exon 8	15747	15879	132 bp
Exon 9	17296	17428	132 bp
Exon 10	17572	17644	72 bp
Exon 11	19254	19409	155 bp
Exon 12	21389	21469	80 bp
Exon 13	21967	22151	184 bp
Exon 14	23858	24015	157 bp
Exon 15	24703	24888	185 bp
Exon 16	26084	26246	162 bp
Exon 17	26740	26881	141 bp
Exon 18	27434	27516	82 bp
Exon 19	31387	31535	148 bp
Exon 20	44710	47122	2412 bp

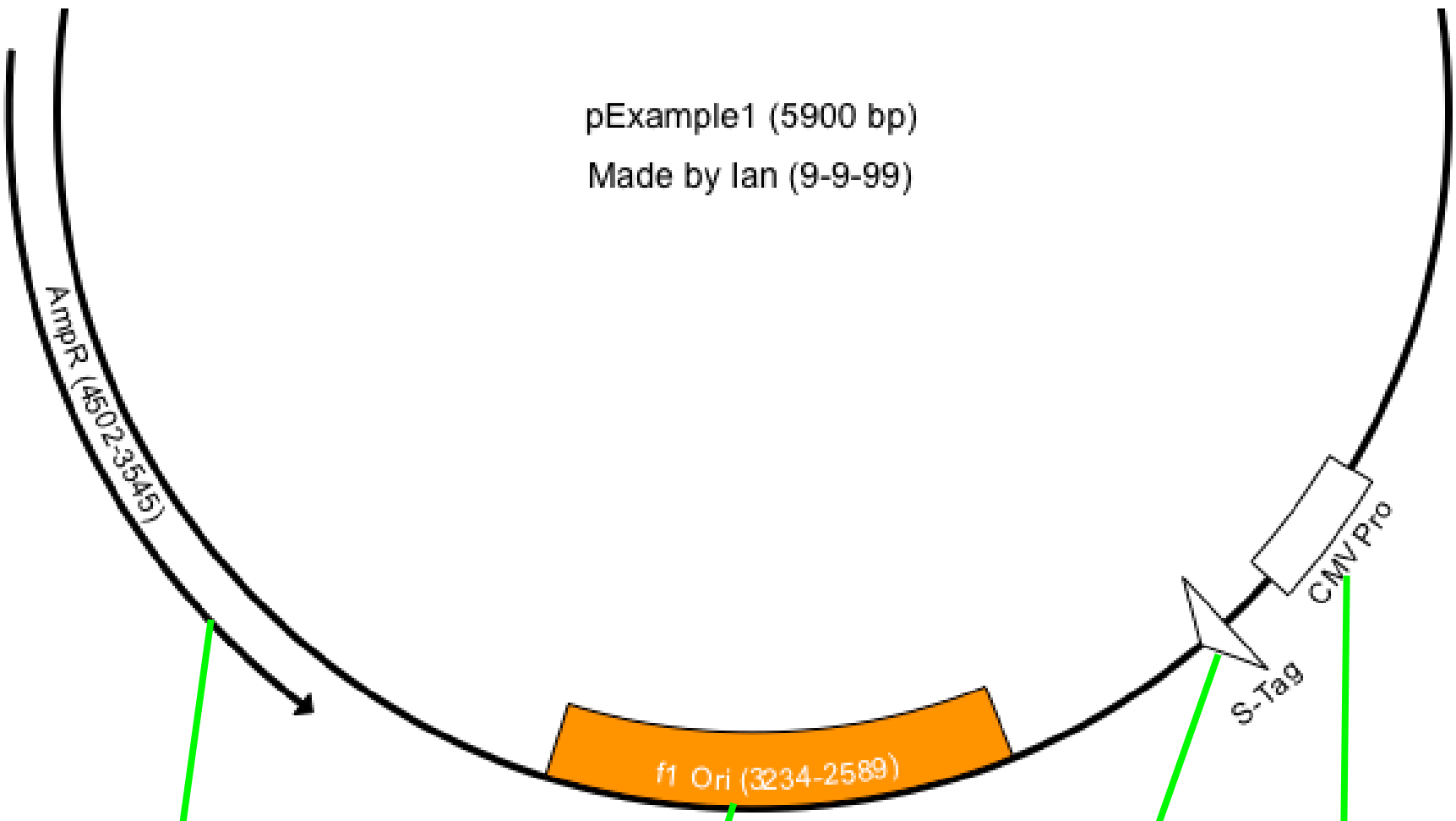
Tips

- Click outside the selected square when finished editing, or the changes won't be saved

Editing a gene's appearance

Examples - gene styles for circular maps

Circular maps allow editing of the color, text color, thickness, and vertical position of genes



Counterclockwise
Thickness = 1
Dragged gene
Dragged text
Gene color = black

No arrow
Thickness = 15
Dragged gene
Dragged text
Gene color = Orange
Text color = white

Clockwise
Don't show location
Thickness = 10
Dragged text

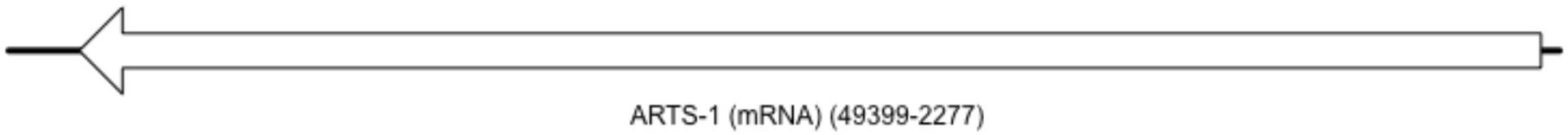
No arrow
Don't show location
Thickness = 10
Dragged text

Editing a gene's appearance

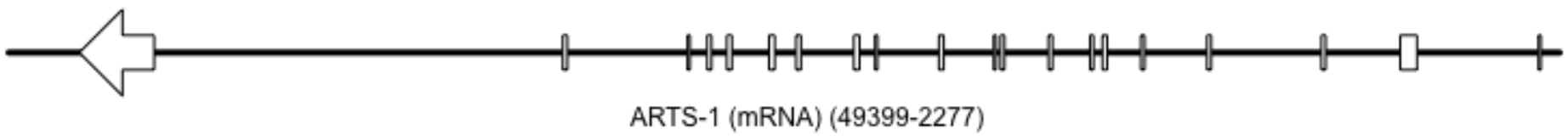
Examples - gene styles for linear maps

Linear maps offer three different gene styles,
as well as the color, thickness, and position edits available in circular maps

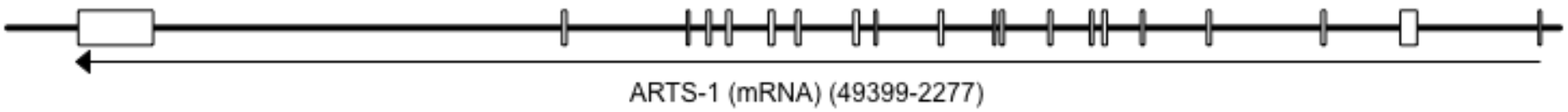
Simple style



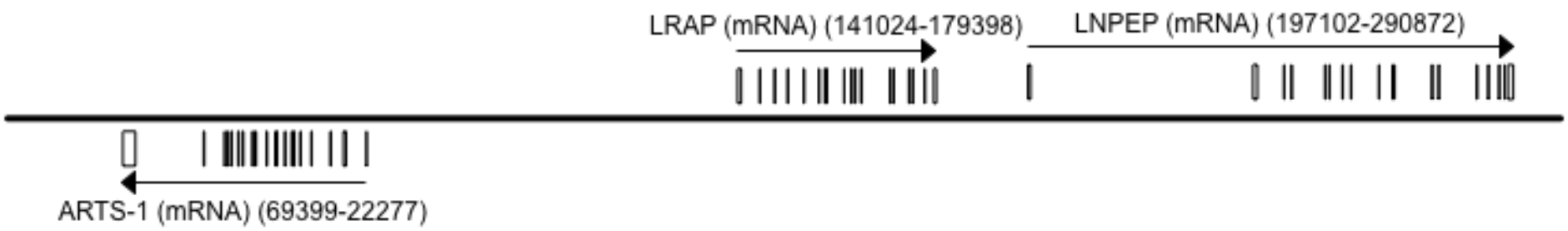
Exon style



Hybrid style



Hybrid style (Repositioned genes)



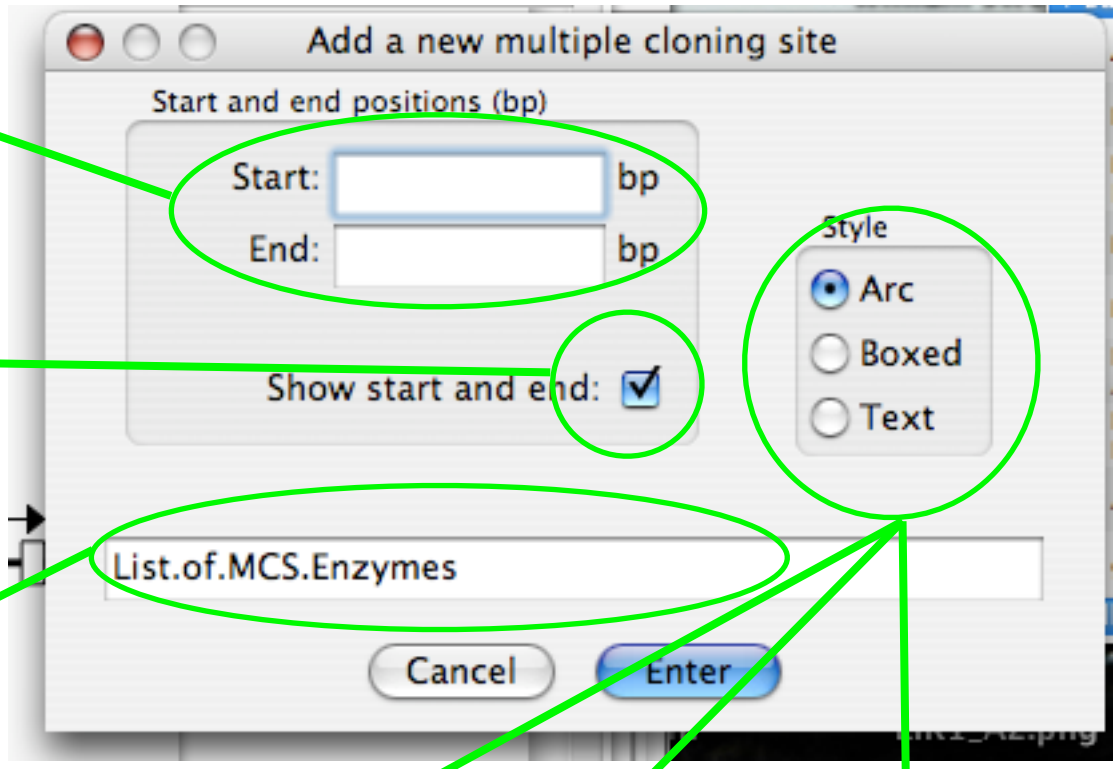
Entering a new multiple cloning site

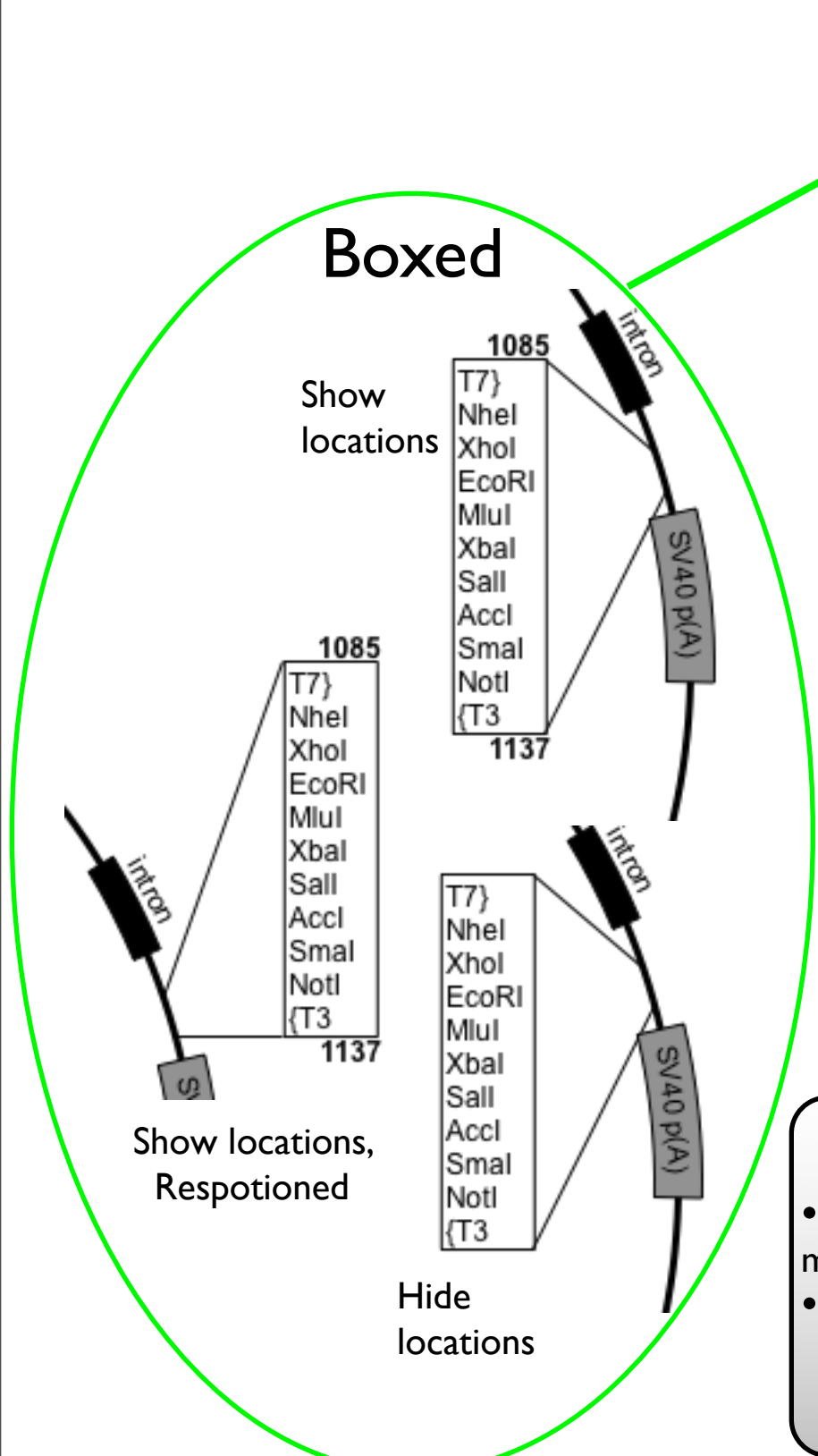
The ***New multiple cloning site*** menu option in the ***Edit*** menu (or ⌘-Shift-M))

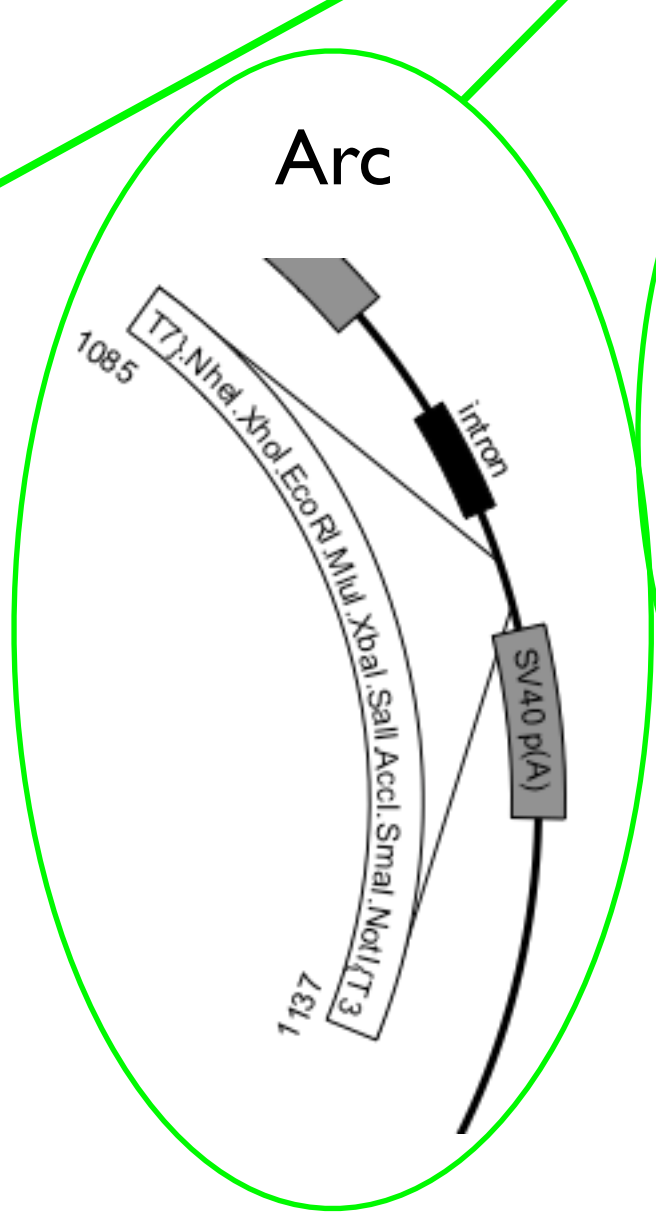
Start and end positions of the MCS (in base pairs) are required

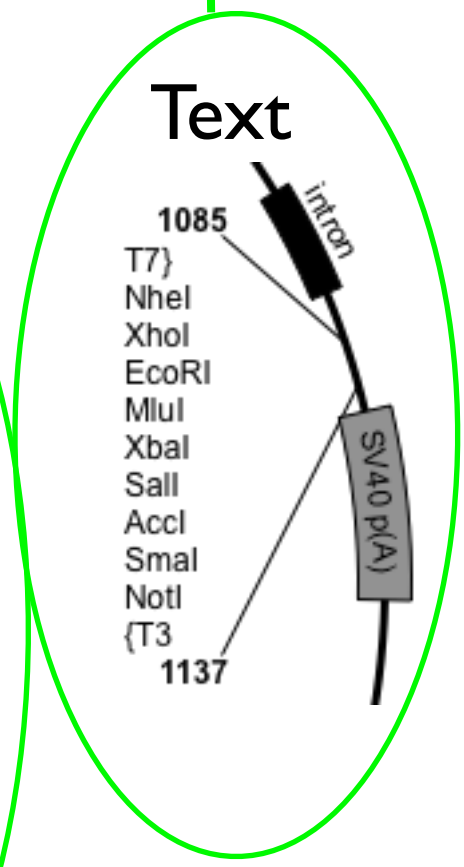
By default, the start and end positions of a multiple cloning site are shown along with the enzyme list. This can be turned off

The enzyme list can be written in any format *However*, in "Boxed" and "Text" styles, the text will be split at periods ("."). In Arc style the text will be displayed jsut as you wrote it









Tips

- Multiple cloning sites can be dragged to new positions once made.
- Contextual menus give quick access to edit options

Entering a new restriction site

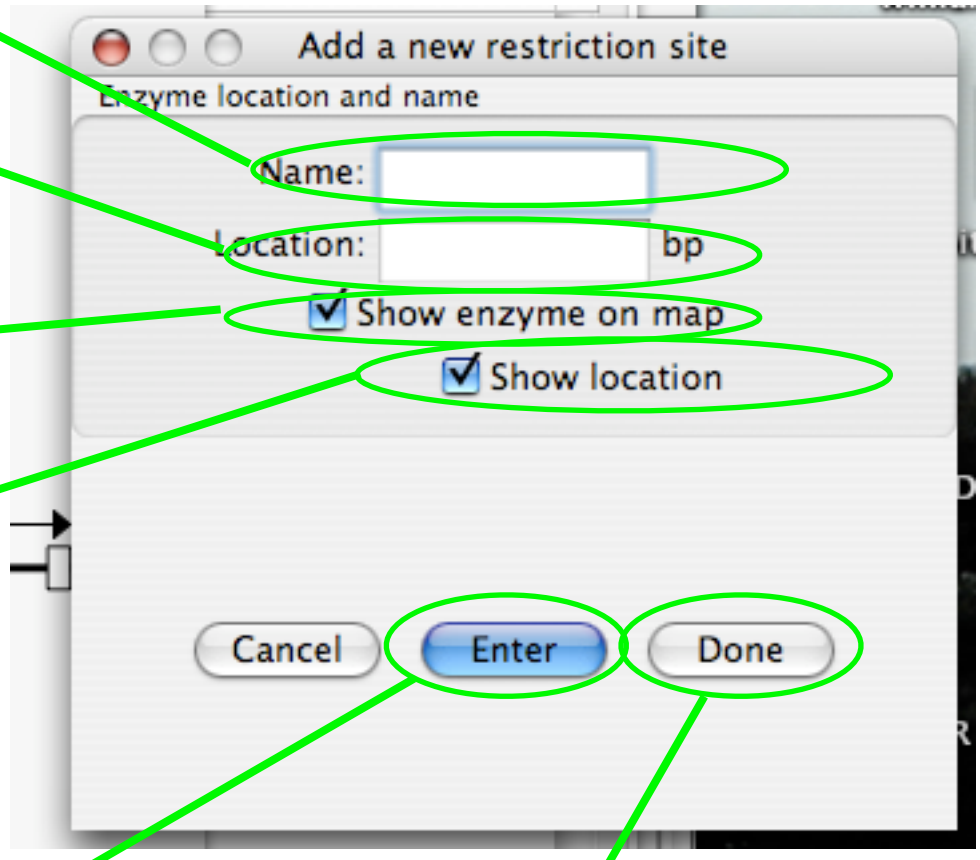
The ***New restriction site*** menu option in the ***Edit*** menu (or ⌘-R)

Name of the enzyme

Location (in base pairs) of the enzyme is required

You can enter an enzyme, and then not show it on the map (e.g. if you want to include a long list of enzymes for planning cloning, but keep an uncluttered map for overviews). If you Hide the enzyme, you need to go to List View to edit it and show it again

Show the enzyme location (e.g. BamHI (1234)) or hide it in the map (e.g. BamHI)



When entering new enzymes, if you click "Enter" after putting in the enzyme info, the info will be committed, the dialog will be cleared, and you can enter another enzyme immediately.

When entering new enzymes, if you click "Done" after putting in the enzyme info, the info will be committed, the dialog will be closed, and you will be returned to the map

An enzyme (with location shown)

Tips

- You can drag the enzyme to a different position (the text will move but will remain connected to its location on the map
- If you have many enzymes, List view can help make batch edits (e.g. turn on or off display of many enzymes at once)
- List view is also useful for sorting enzymes by name (e.g. group together all HindIII sites), or by location

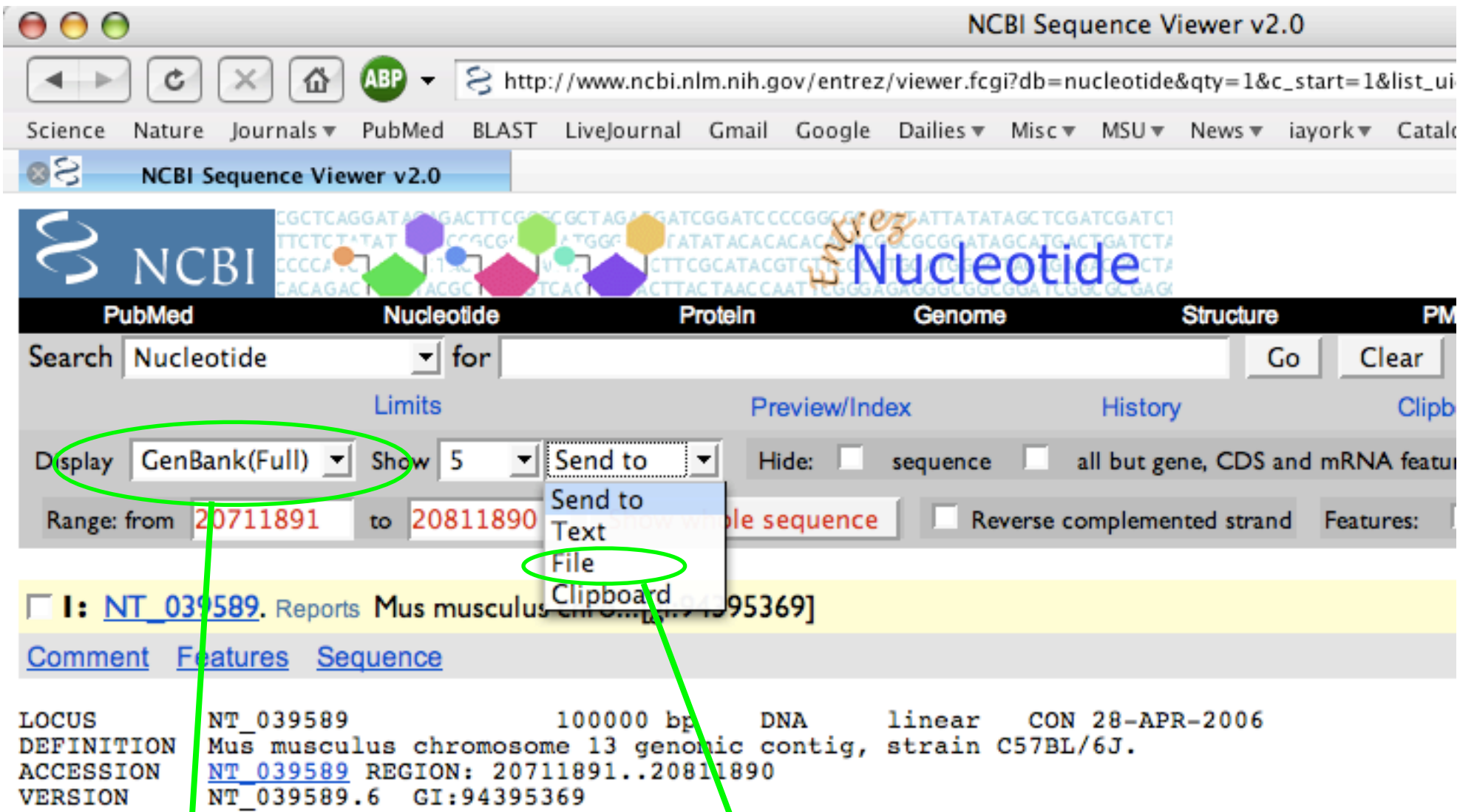
Making maps from imported sequence files

Import / from GenBank (.gb files) in the ***File*** menu

1. Download a nucleotide file in GenBank (Full) format

   http://www.ncbi.nlm.gov

   Save the file as GenBank (Full)
2. Import the file into XPlasMap
3. Select features to include in the map



GenBank (Full) format
(For shorter sequences, "GenBnk" format works as well, but "Full" format is safer.)

"Send to file" to download the full set of info to your hard drive.

Tips

- See http://www.ncbi.nlm.nih.gov/Genbank/index.html for an introduction to GenBank
- http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=handbook.chapter.ch1 for a more detailed discussion of GenBank

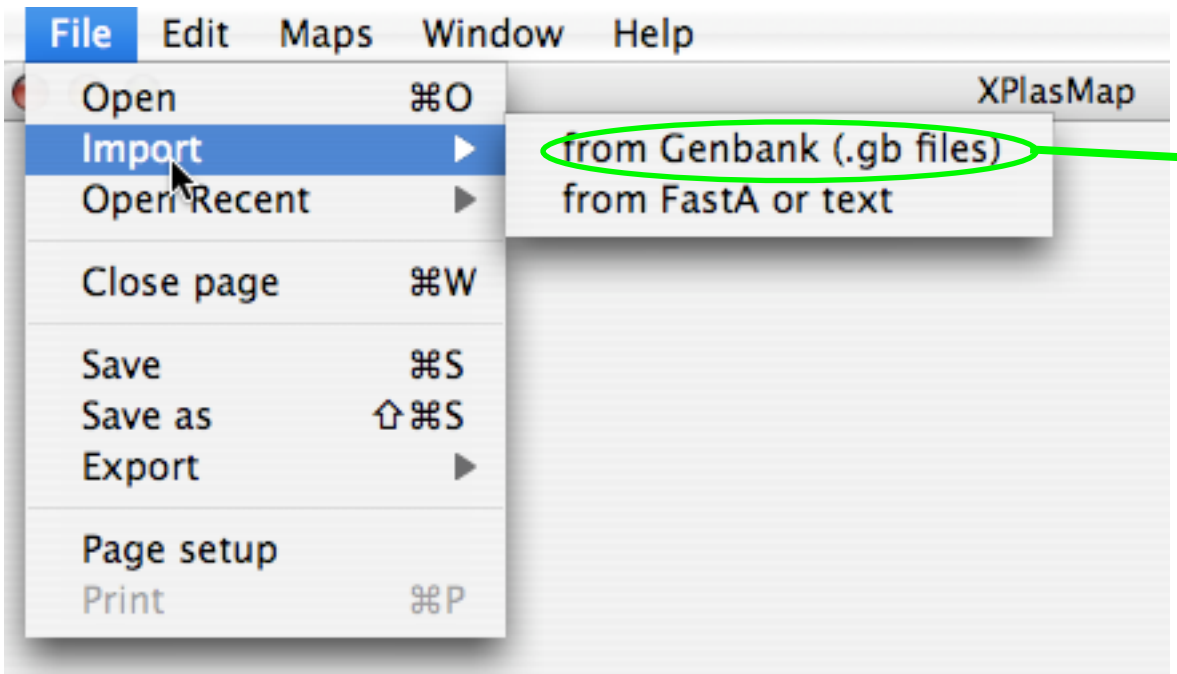
Making maps from imported sequence files

Import / from GenBank (.gb files) in the ***File*** menu

1. Download a nucleotide file in GenBank (Full) format
2. Import the file into XPlasMap

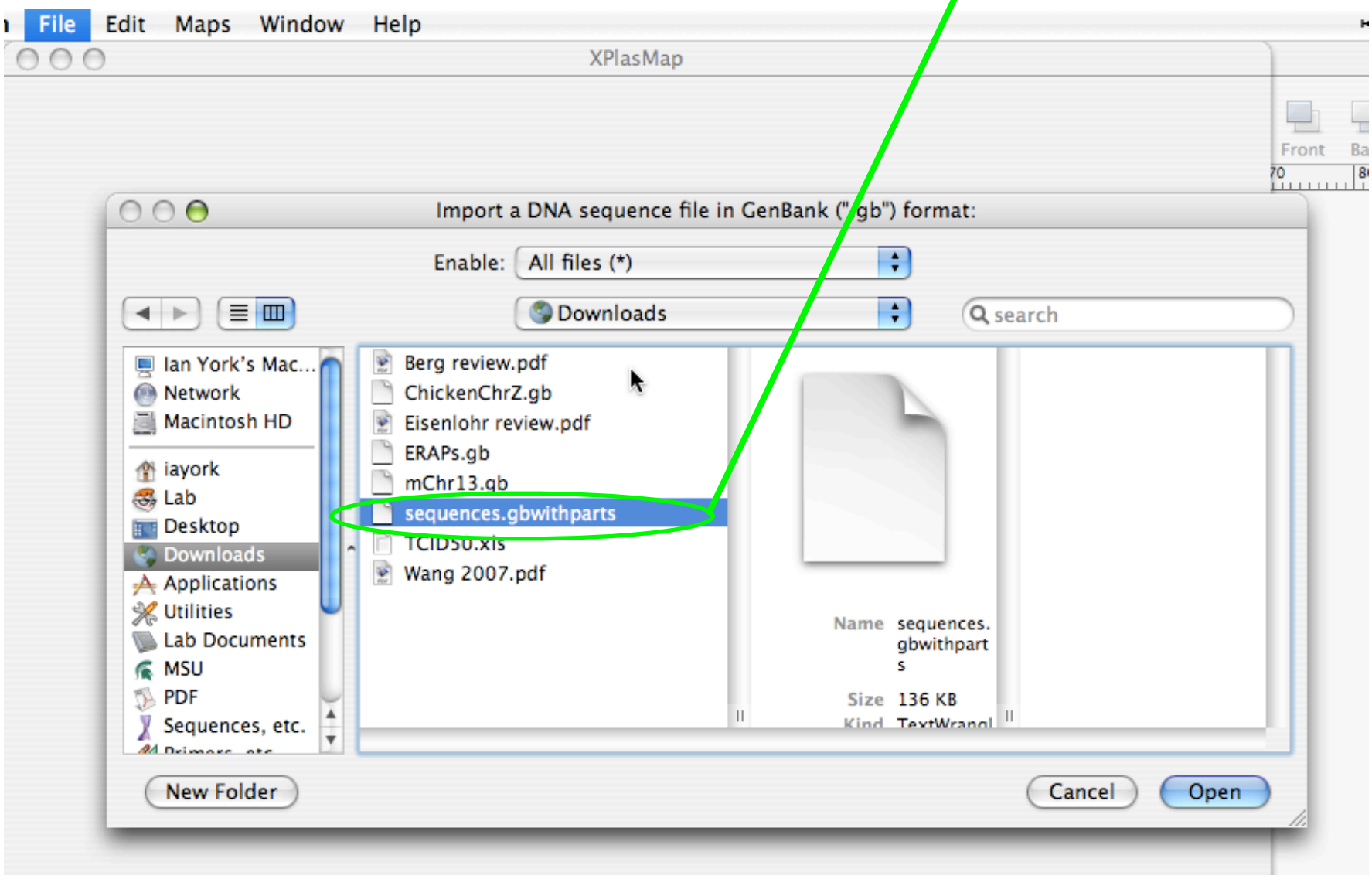
   File -> Import -> from GenBank (.gb files)

   Select the file you downloaded
3. Select features to include in the map



Import from GenBank menu selection

Open the GeneBank file you downloaded (.gb or .gbwithparts file extension)



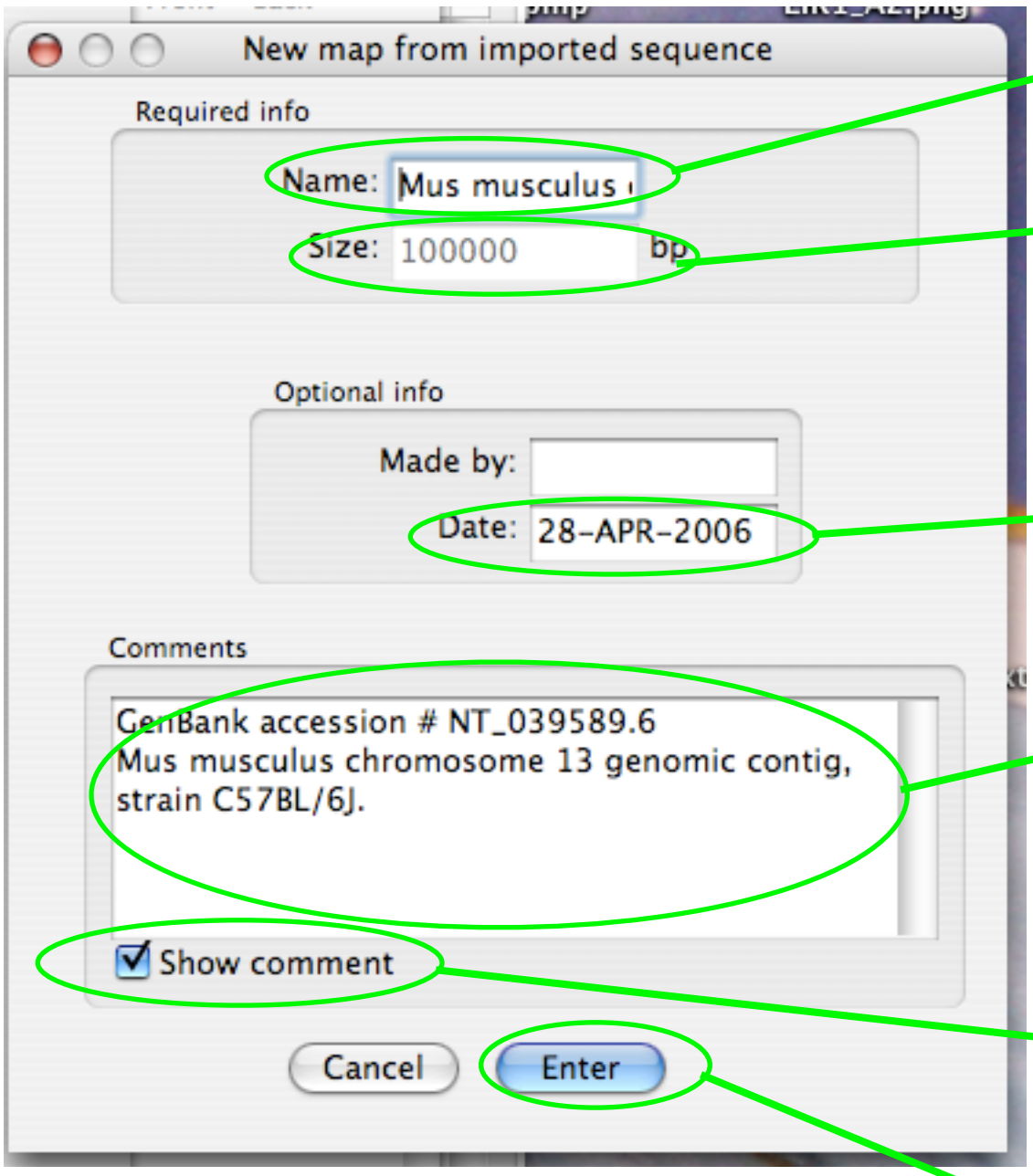
Making maps from imported sequence files

Import / from GenBank (.gb files) in the ***File*** menu

1. Download a nucleotide file in GenBank (Full) format
2. Import the file into XPlasMap

   You're shown a "New map from imported sequence" dialog

   Default information is filled in; most of it can beedited
3. Select features to include in the map



The default name is the "Definition" line in the GenBank record. Edit if you want a different name

The size if taken from the sequence. This can't be edited

Default date is the last modification date of the GenBank record

Default comments include the GenBank accession number and the Definition line

As with any map, you can hide or show the comment

Once you've made any changes to the default values, click "Enter" and you can select features to display

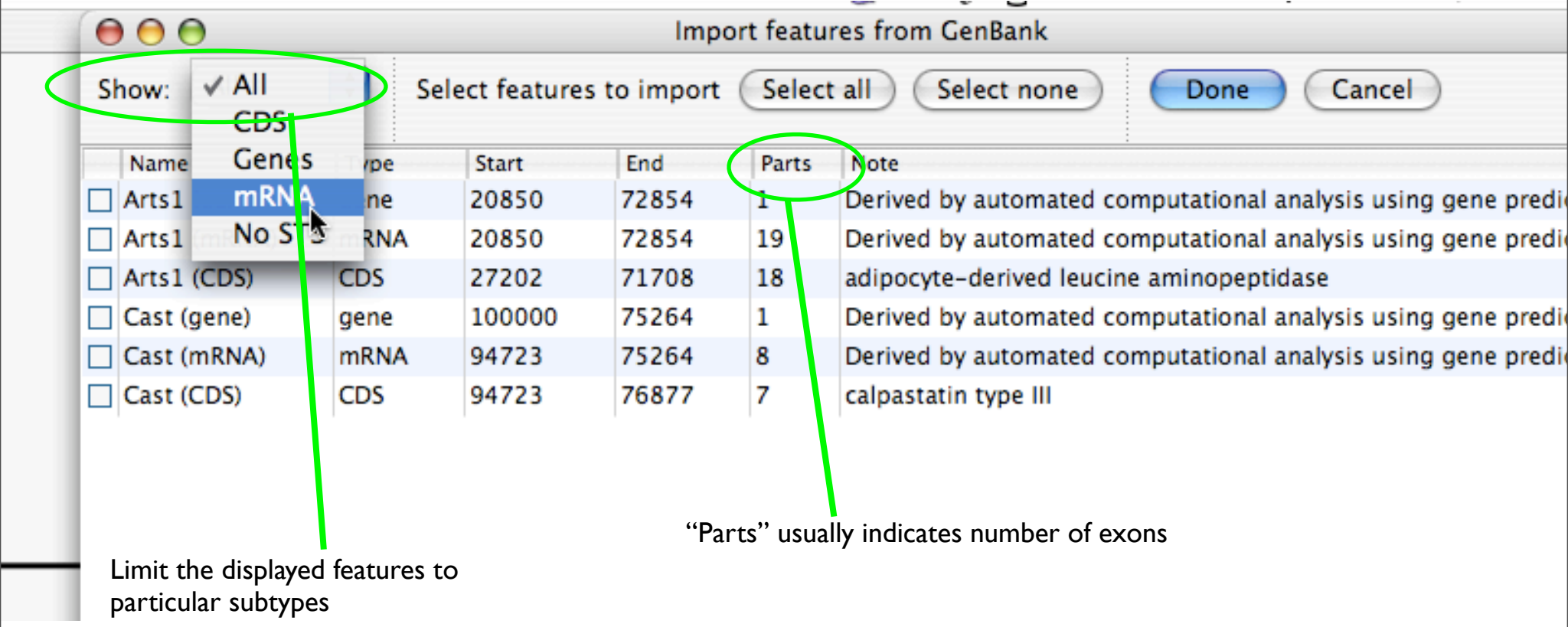
Making maps from imported sequence files

Import / from GenBank (.gb files) in the ***File*** menu

1. Download a nucleotide file in GenBank (Full) format
2. Import the file into XPlasMap
3. Select features to include in the map

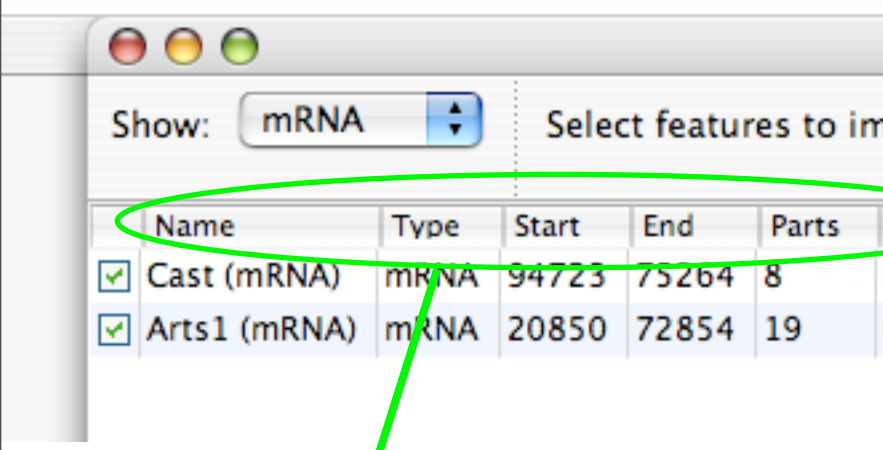
   Select the relevant rows

   Sort and/or limit the displayed feature to make choosing the right ones easier



Limit the displayed features to particular subtypes

"Parts" usually indicates number of exons



Click on a column name ("Name", "Type", "Start", End", Parts", or "Note") to sort by that parameter. Click again to reverse sort order

Tips

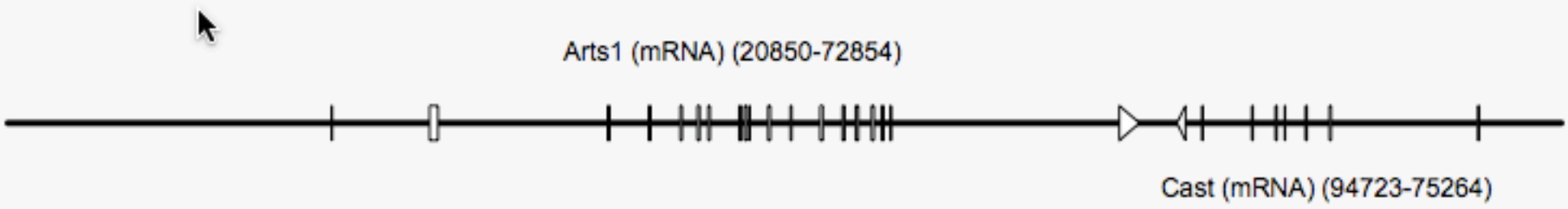
•Use the "Show:" pull-down menu to limit features to the kind you want, e.g. only mRNA (which shows exons), only Genes (which usually don't indicate exons), "No STS" to exclude sequence-tagged sites

Making maps from imported sequence files

Import / from GenBank (.gb files) in the ***File*** menu

1. Download a nucleotide file in GenBank (Full) format
2. Import the file into XPlasMap
3. Select features to include in the map

Once you've selected the features you want to import, click "Done"
XPlasMap will draw a linear map with the features you selected



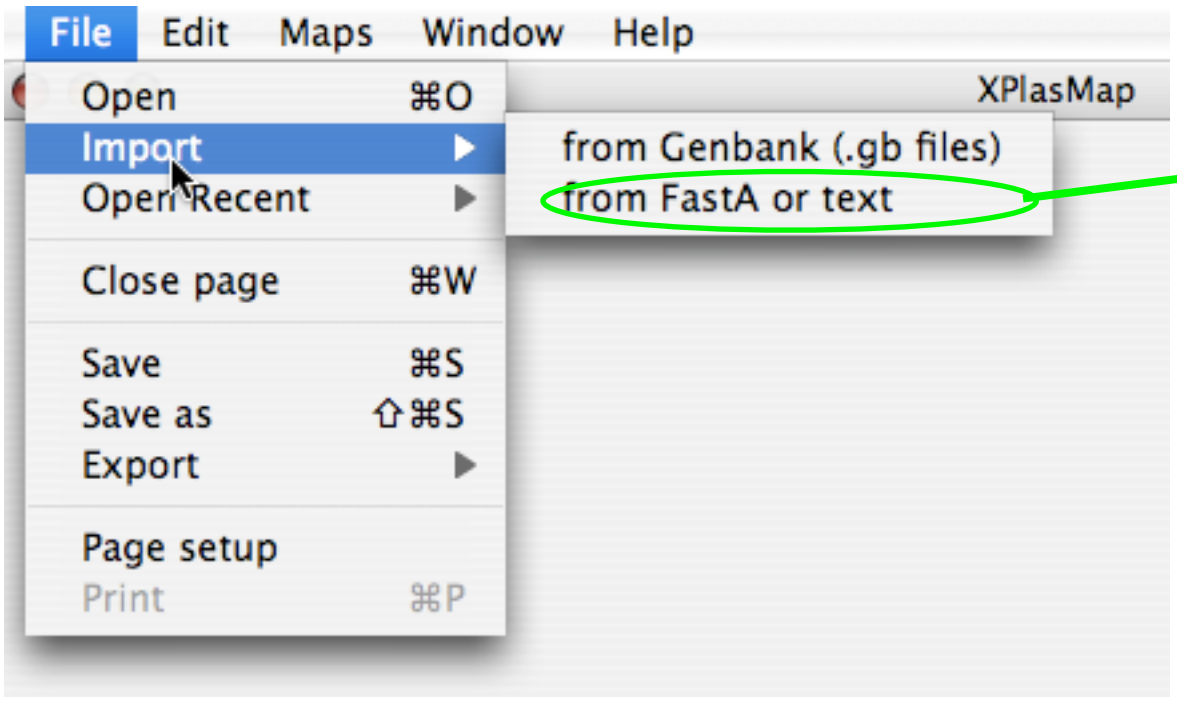
Mus musculus chromosome 13 genomic contig, strain C57BL/6J. (100000 bp)
(28-APR-2006)

Tips

•At this point the map is just like any other XPlasMap map. Edit existing data, or add new features, as you would for any other map

Making maps from imported sequence files

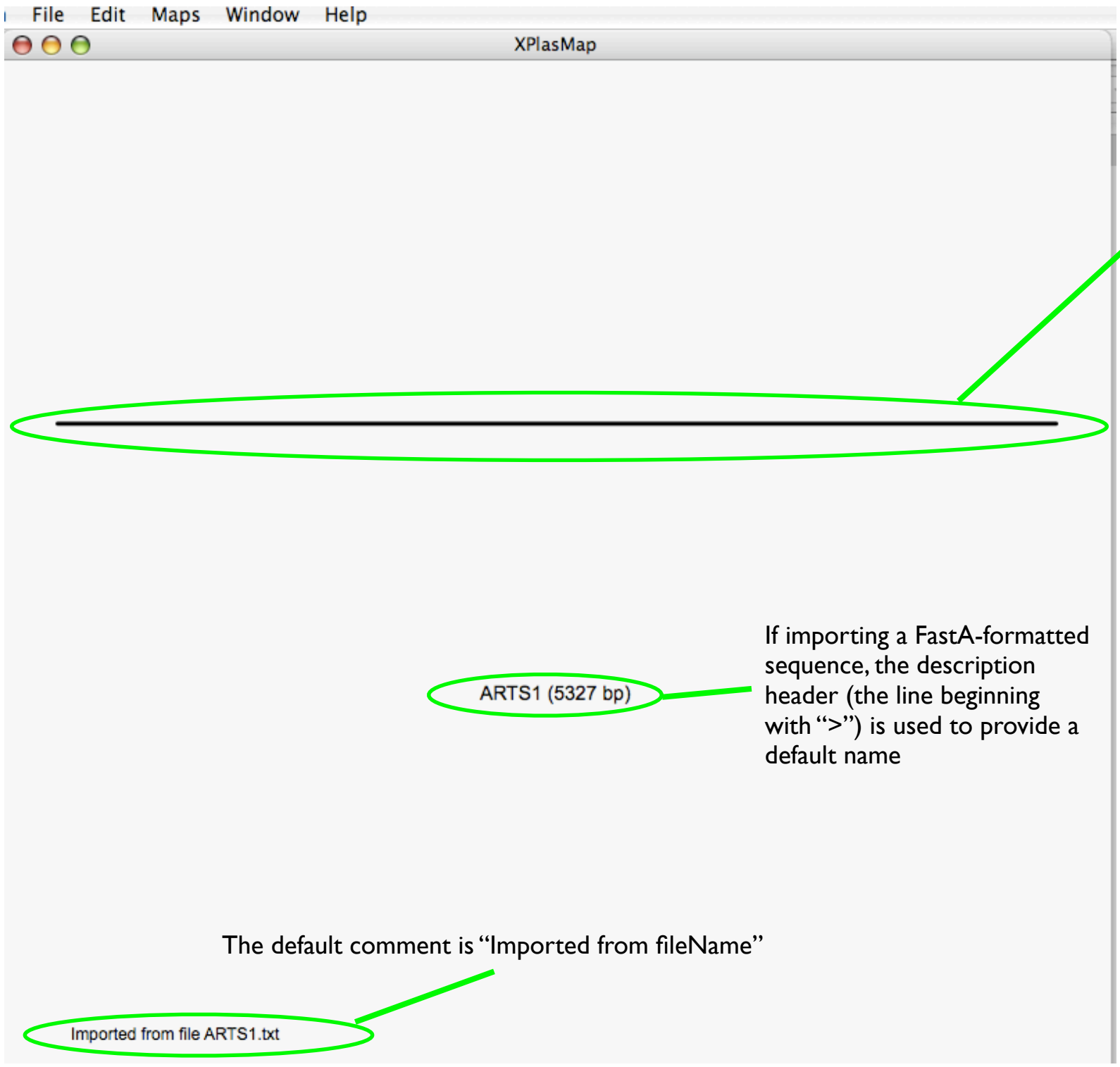
Import / from FastA or text) in the ***File*** menu



FastA files are a plain-text sequence preceded by a descriptive line starting with ">". Several sequences can be in the same file, so long as they're separated by the line starting with ">"

Plain text files have nothing but a nucleotide sequence.

In either case, any characters other than nucleotide characters (A, C, G, T, or U) or N are converted to N.



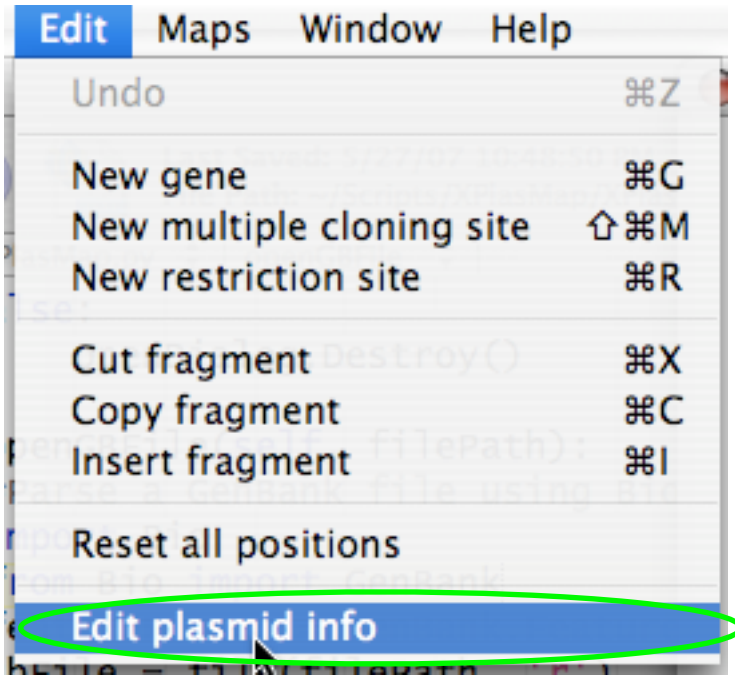
The result of the import is not very exciting: A featureless linear DNA map of the appropriate length

If importing a FastA-formatted sequence, the description header (the line beginning with ">") is used to provide a default name

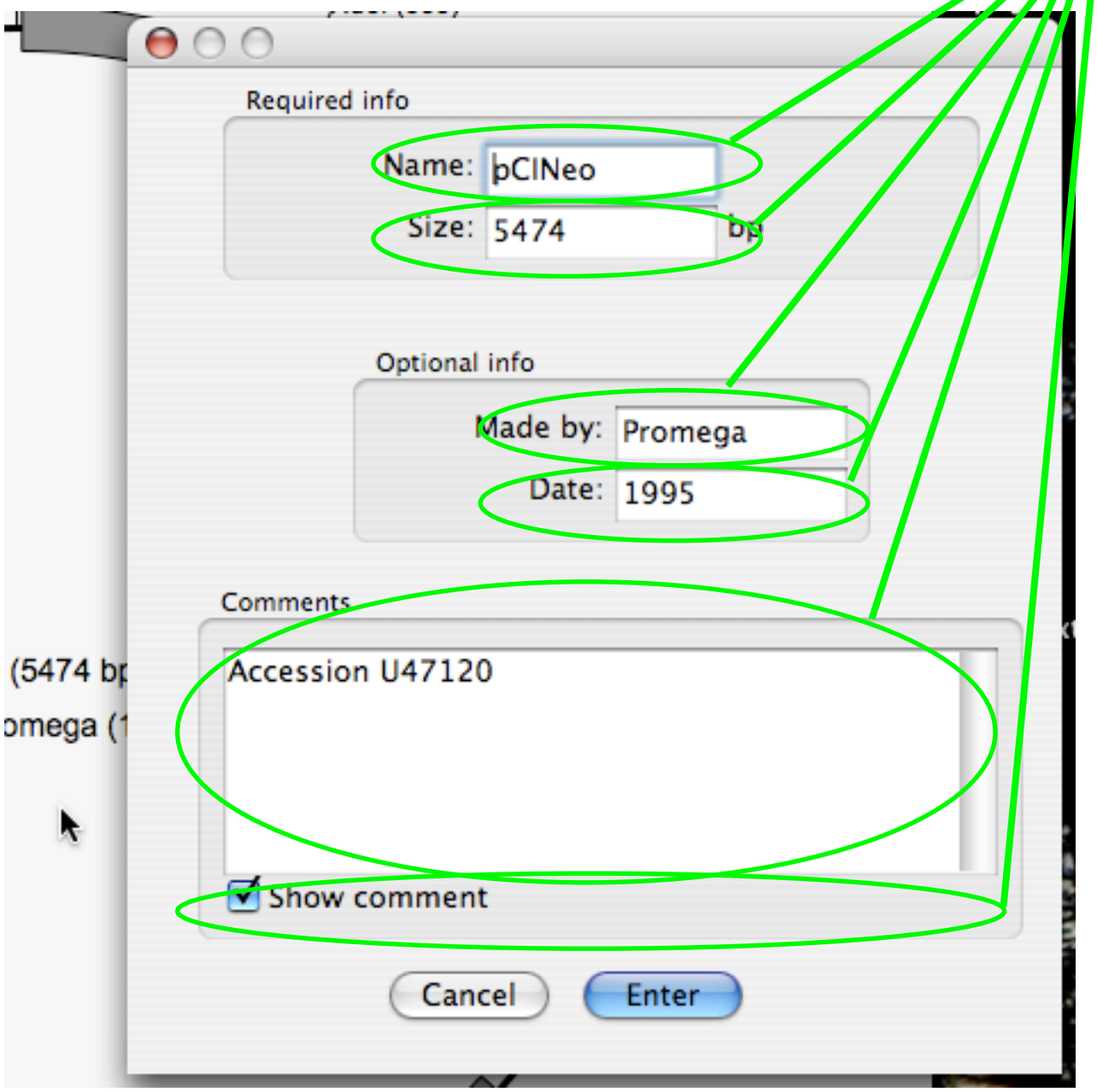
The default comment is "Imported from fileName"

Modifying existing maps

The ***Edit plasmid info*** menu item in the ***Edit*** menu

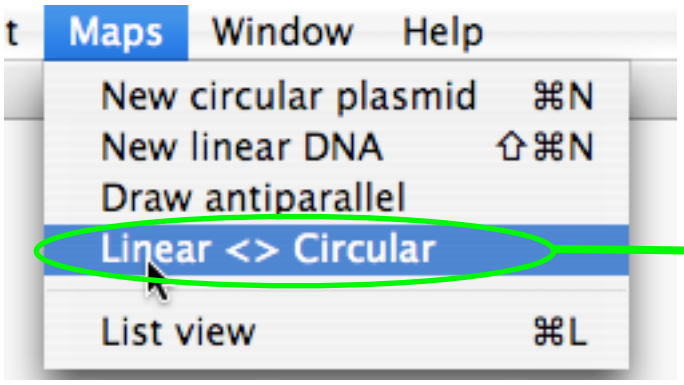


Any of the original information about the plasmid can be changed

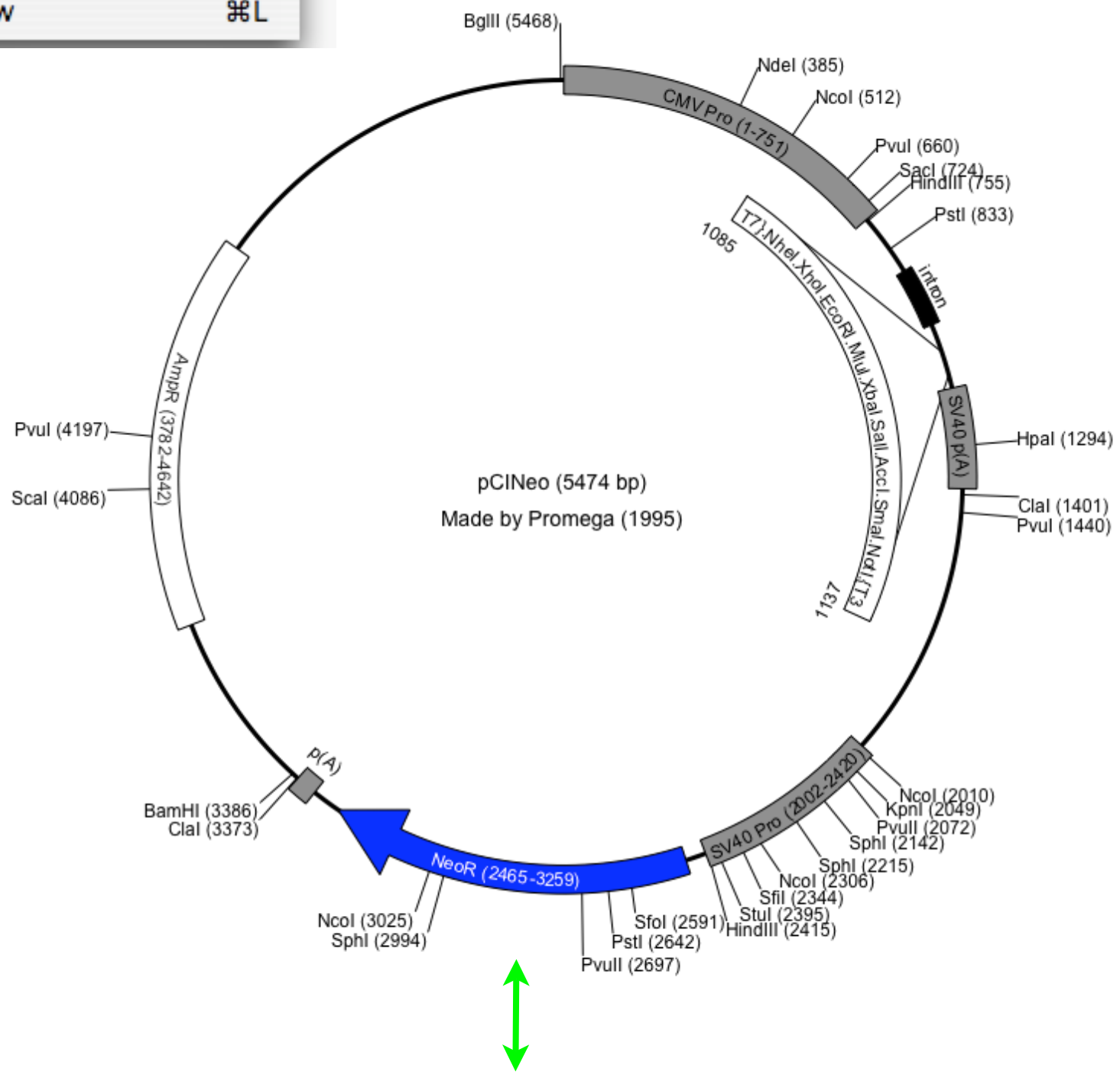


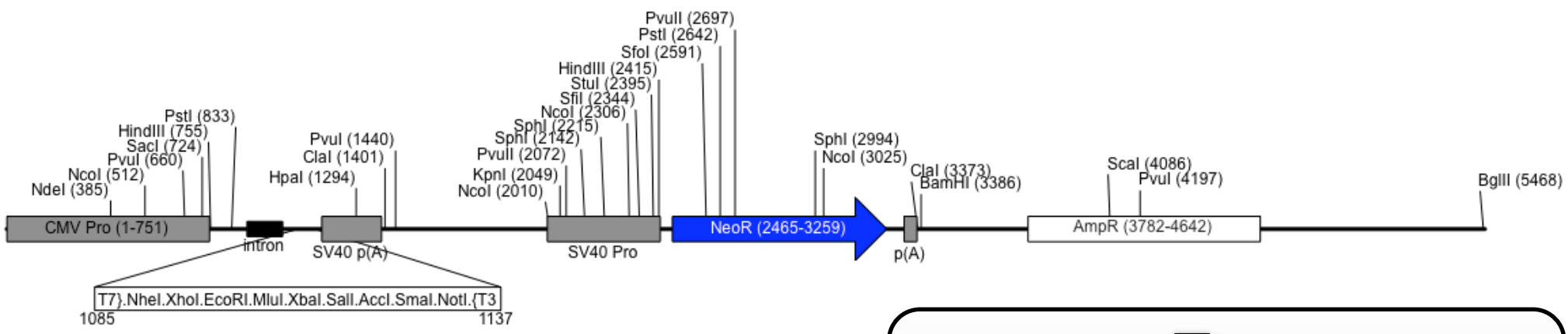
Modifying existing maps

Linear <> Circular in the ***Maps*** menu



Convert circular maps to linear maps and vice-versa





pCINeo (5474 bp)

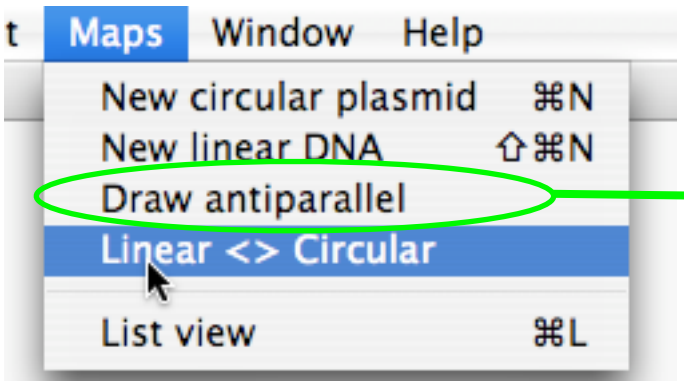
Made by Promega (1995)

Tips

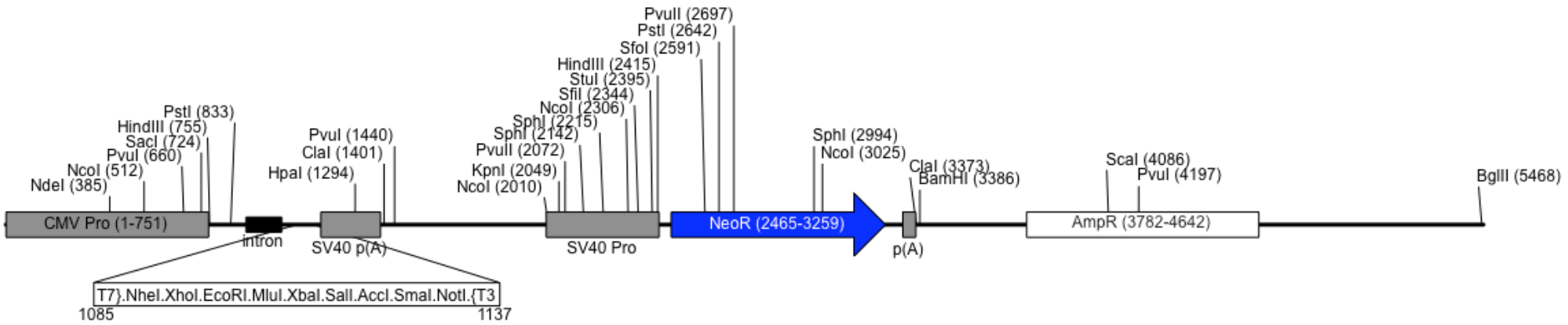
- Positions are all set to default after a linear/ circular conversion, so for any but the most simple maps you'll need to adjust

Modifying existing maps

Draw antiparallel in the ***Maps*** menu

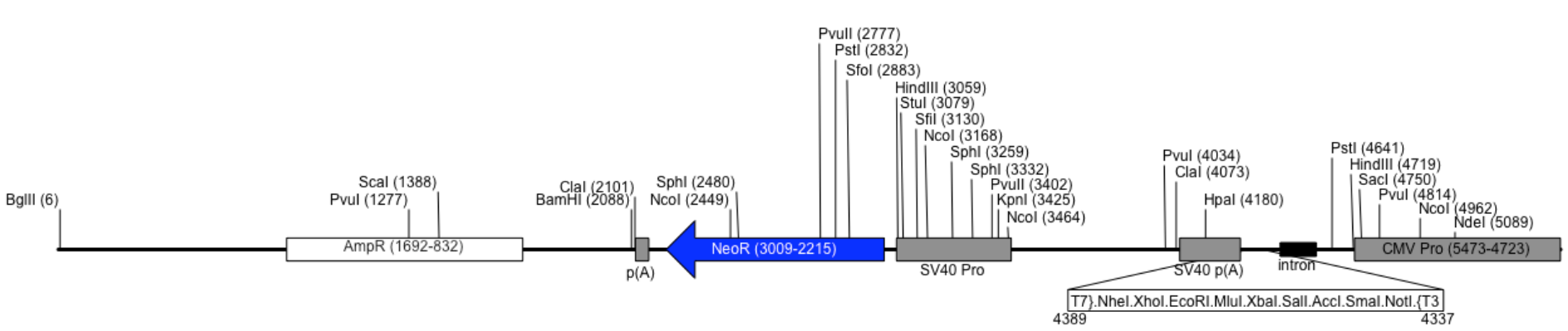


Draw the reverse complement of the map
(Linear maps only)



pCINeo (5474 bp)

Made by Promega (1995)



pCINeo (Reversed) (5474 bp)

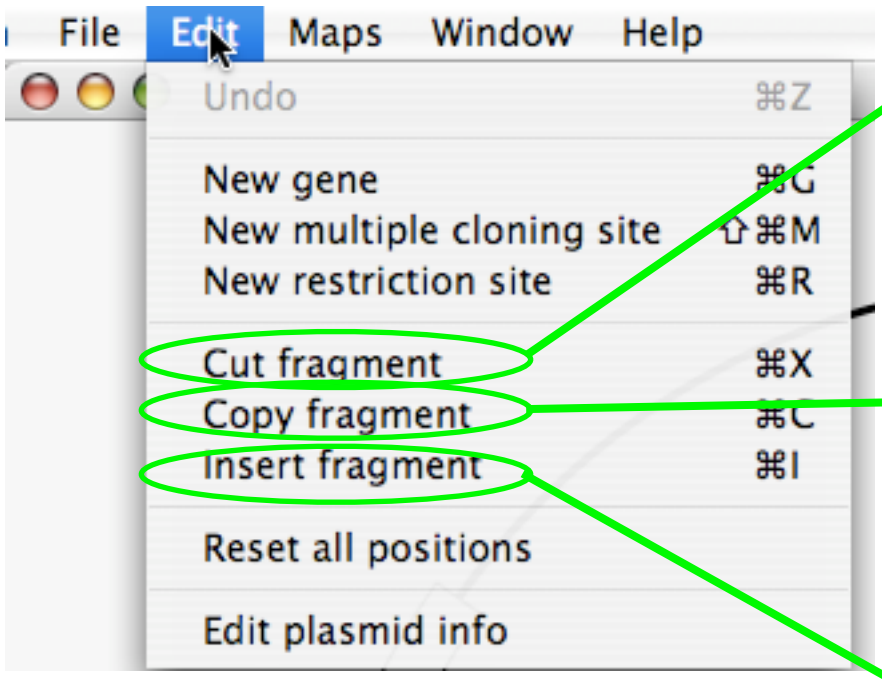
Made by Promega (1995)

Tips

- Draw antiparallel is only available for linear maps.
- Positions are all set to default after drawing the antiparallel strand, so for any but the most simple maps you'll need to adjust the text. (In the example maps here, the text positions have been manually fixed after the antiparallel strand was drawn)

Modifying existing maps

Cut, Copy, and ***Insert fragment*** in the ***Edit*** menu



Remove a section of DNA, and all its associated features, from the map, reducing the total size of the DNA. You can save the deleted fragment in memory, or just throw it away

Select a region of DNA (and all its associated features) to copy for later insertion into a new map, or to make a new map of the region alone

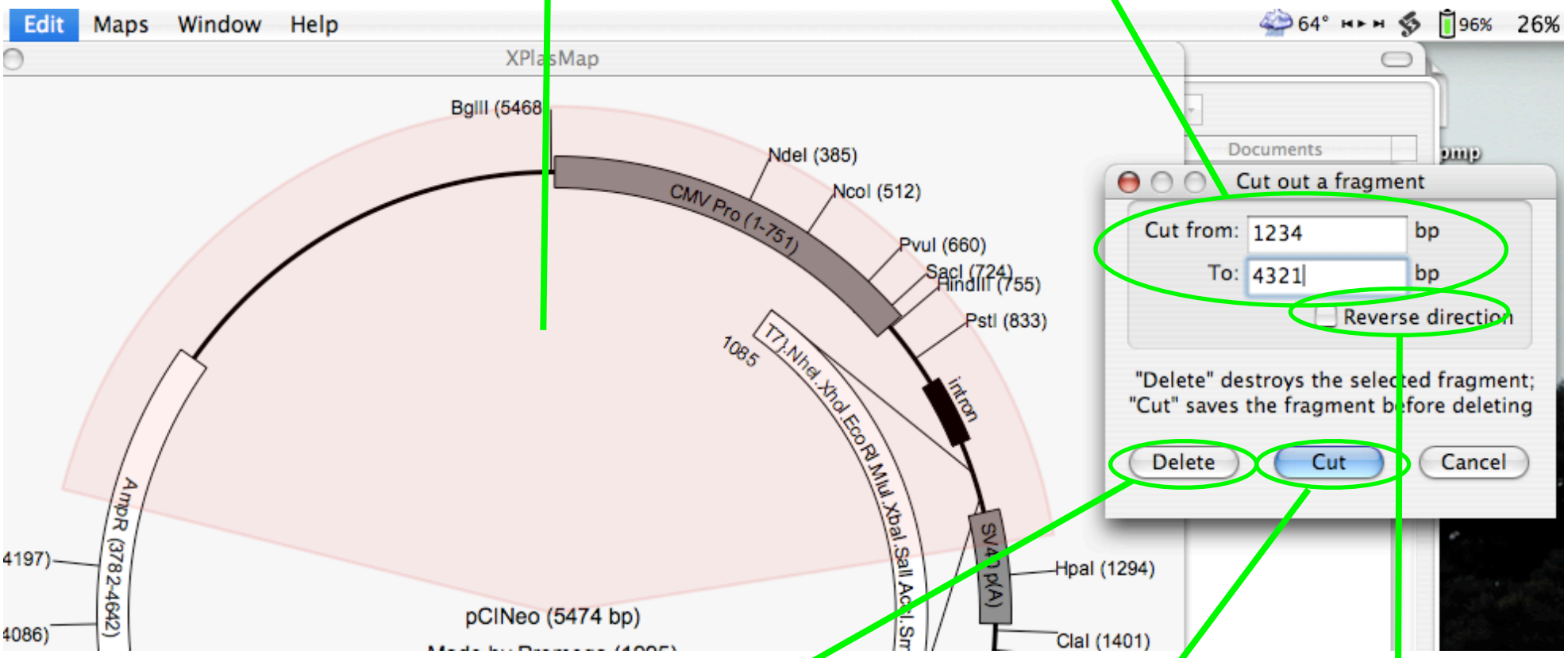
Inserted a previously copied section of DNA, or a previously saved linear DNA map, into an existing map

Modifying existing maps

The ***Cut fragment*** menu option in the ***Edit*** menu (or ⌘-X)

The highlighted region indicates the part of the map that will be cut out

Cut from: .. To: .. The start and end of the fragment to be deleted



"Delete" just deletes the selected fragment and associated features, without saving the fragment in memory

"Cut" deletes the selected region and associated fragments from the plasmid, and also saves a copy of the fragment in memory. See "Copy fragment" (p. 27) for more information

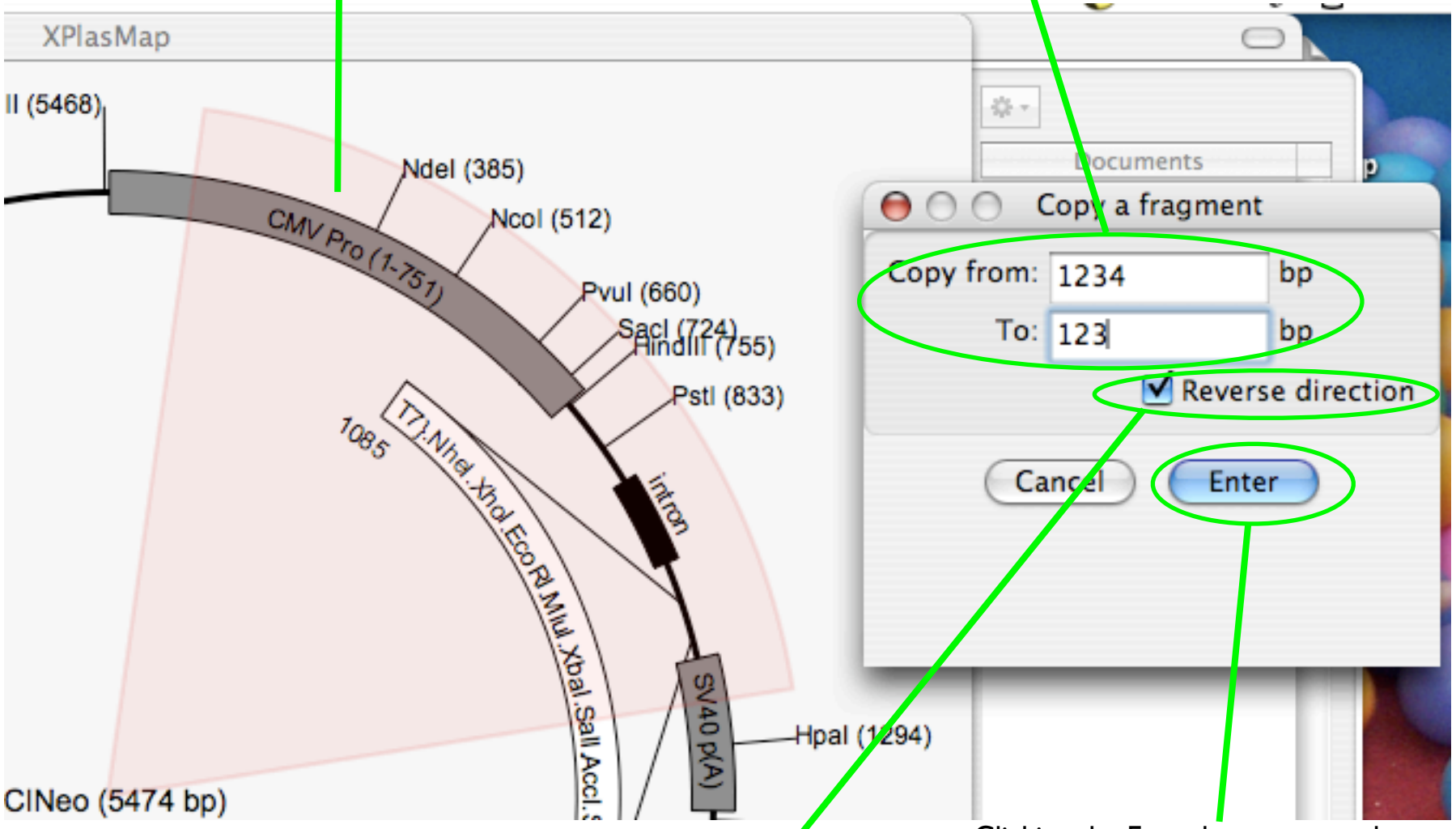
Reverse direction: Check here to cut from the same ends, but in the other direction (Circular plasmids only)

Modifying existing maps

The ***Copy fragment*** menu option in the ***Edit*** menu (or ⌘-C)

The highlighted region indicates the part of the map that will be copied

Copy from: .. To: .. The start and end of the fragment to be copied



Reverse direction: Check here to copy from the same ends, but in the other direction (Circular plasmids only)

Clicking the Enter button saves the fragment and its associated features to memory. You can now Insert the fragment into an existing map, or draw a new map from the fragment

Tips

- After you've Copied a fragment, you can either Insert it directly into an existing DNA map (see p. 28), or you can make a standalone map from it (New linear map menu item in the Maps menu, check off the "Make new map from copied fragment" option; see p. 29)
- Copied fragments in memory will not be saved when you close XPlasMap. If you want to use the fragment in a new XPlasMap session, you must save it as a linear map

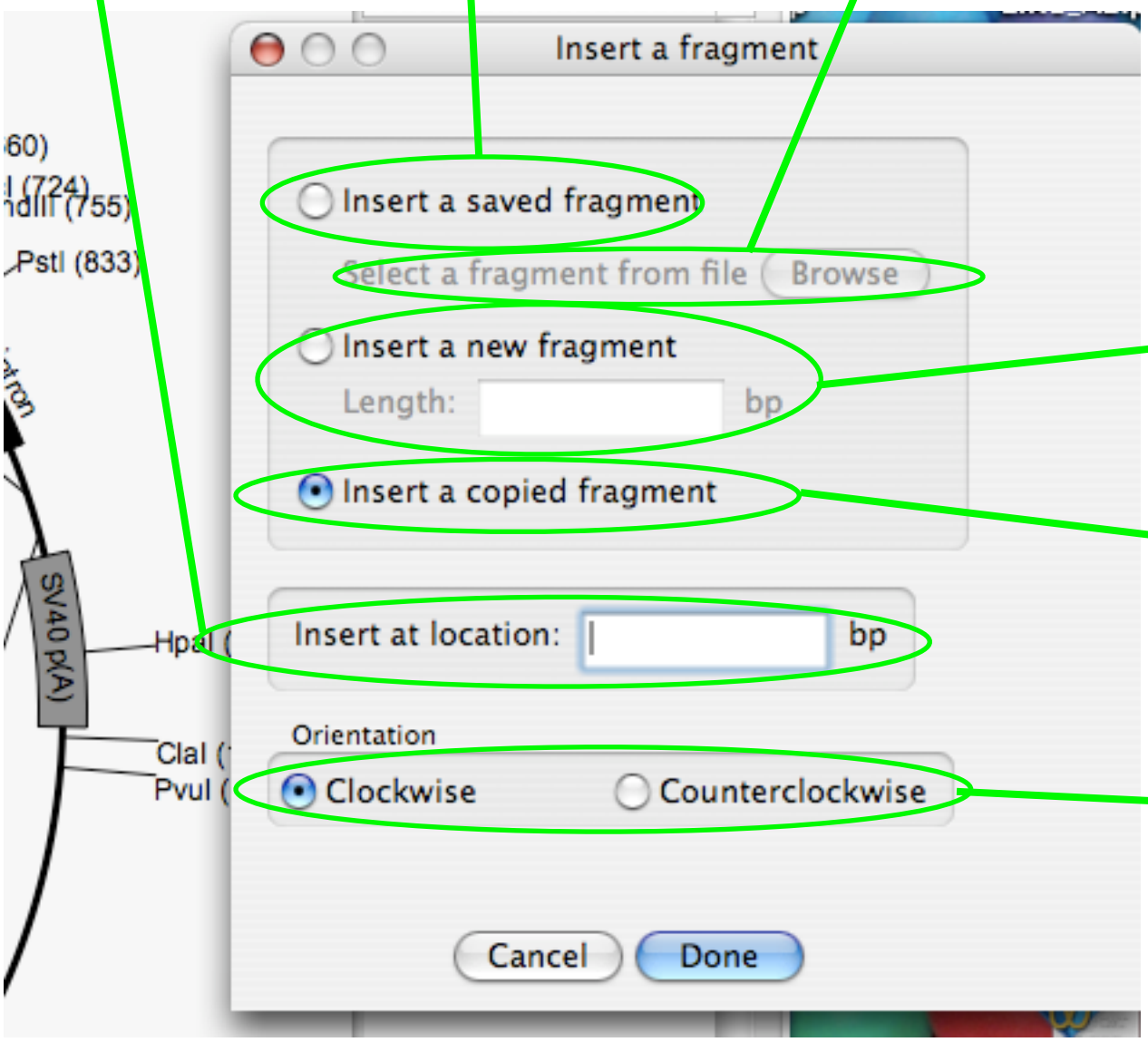
Modifying existing maps

The ***Insert fragment*** menu option in the ***Edit*** menu (or ⌘-I)

The location (in base pairs) At which to insert a new fragment of DNA. Required info

Insert a fragment from a file. The file must contain a <u>linear</u> DNA map in .xpmp format

Click the "Browse" button to select the file containing the linear DNA map to insert



Enter a new stretch of blank (featureless) DNA at the location you define

Insert a previously-copied fragment that's saved in memory

Orientation of the inserted fragment (not relevant for "new" (featureless) fragments). "Counterclockwise" reverses the orientation of the fragment

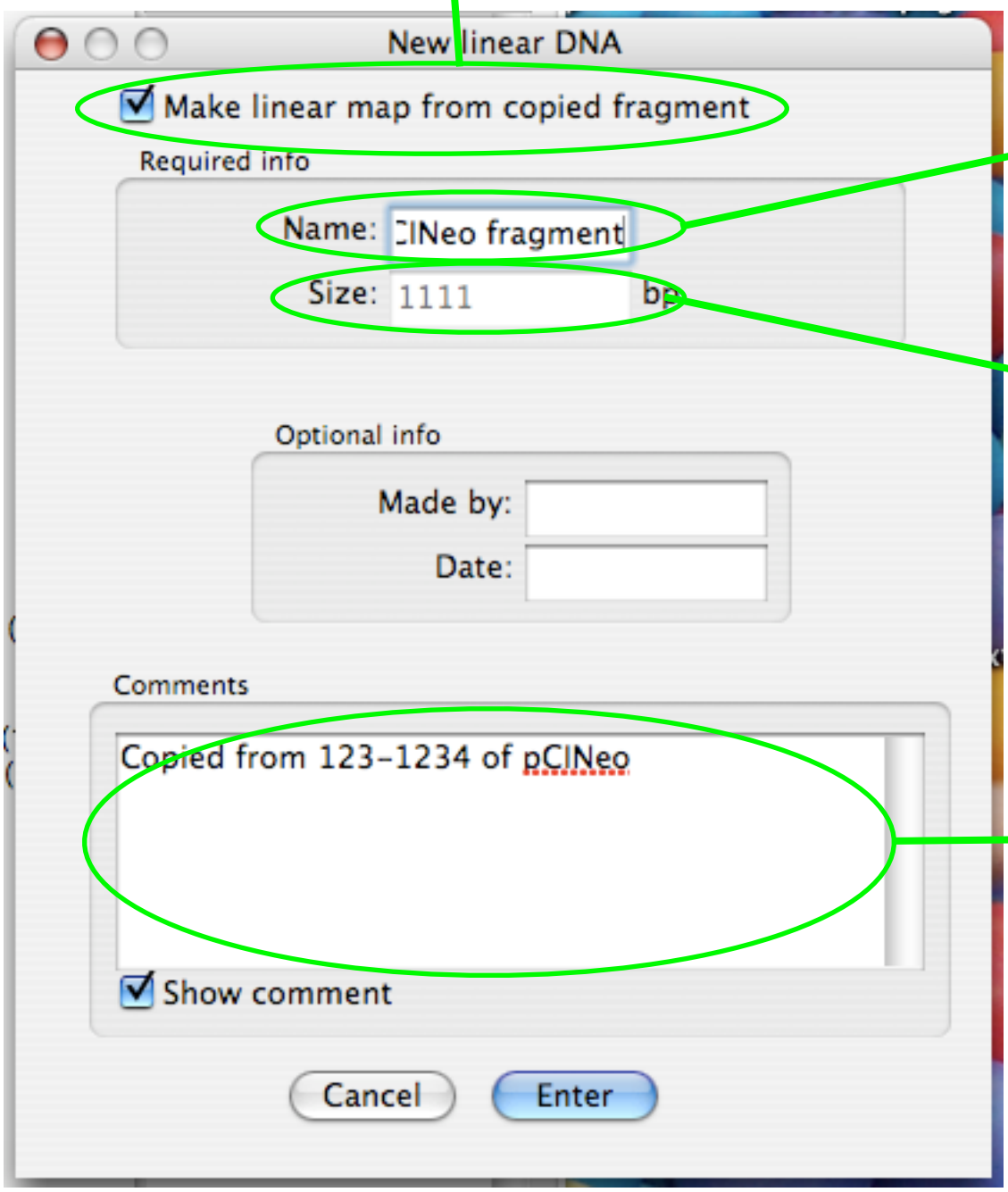
Tips

- Inserting a fragment increases the size of the DNA; to add a new feature without changing the DNA size, use New Gene (or MCS, etc)

Modifying existing maps

The ***Make new map from copied fragment*** checkbox in the ***New linear map*** menu option in the ***Maps*** menu (or ⌘-Shift-N)

The checkbox is enabled when a copied fragment has been stored in memory



Name and comment default information is offered, but can be edited

Default size of the insert can't be changed, because it's the size of the copied fragment

Name and comment default information is offered, but can be edited

Tips

- The new map is linear, right-to-left. After it's made, it's just the same as any other map you've created
- You can reverse the map orientation with "Draw antiparallel" in the Maps menu
- Convert to a circular map with "Linear <> Circular" in the Maps menu

The List view for text overviews

The ***List view*** menu option in the ***Maps*** menu (or ⌘-L)

Limit the display to show only one type of feature

Batch operations: Select multiple features, edit them as a group.
See p. 31 for Edit Genes batch operation

pCINeo

All
Enzymes
Genes
MCS

Delete | Show/hide location | Show/hide text | Edit genes

S	me	Feature	Location	Text	Note
1		MCS	Show		T7}.NheI.XhoI.EcoRI.MluI.XbaI.SalI.AccI.SmaI.NotI.{T3
3782	4642	AmpR	Gene	Show	Show
3323	3371	p(A)	Gene	Hide	Show
2002	2420	SV40 Pro	Gene	Show	Show
1167	1388	SV40 p(A)	Gene	Hide	Show
890	1022	intron	Gene	Hide	Show
1	751	CMV Pro	Gene	Show	Show
5468		BglII	Enzyme	Show	Show
4197		PvuI	Enzyme	Show	Show
4086		ScaI	Enzyme	Show	Show
3386		BamHI	Enzyme	Show	Show
3373		ClaI	Enzyme	Show	Show
3025		NcoI	Enzyme	Show	Show
2994		SphI	Enzyme	Show	Show
2697		PvuII	Enzyme	Show	Show
2642		PstI	Enzyme	Show	Show
2591		SfoI	Enzyme	Show	Show
2415		HindIII	Enzyme	Show	Show
2395		StuI	Enzyme	Show	Show
2344		SfiI	Enzyme	Show	Show
2306		NcoI	Enzyme	Show	Show
2215		SphI	Enzyme	Show	Show

List view, Status bar, and Edit Gene dialog box are the three places that allow you to see Notes for genes

Sortable columns - click to sort, click again to sort by reverse order

Select by highlighting (Can select multiple rows)

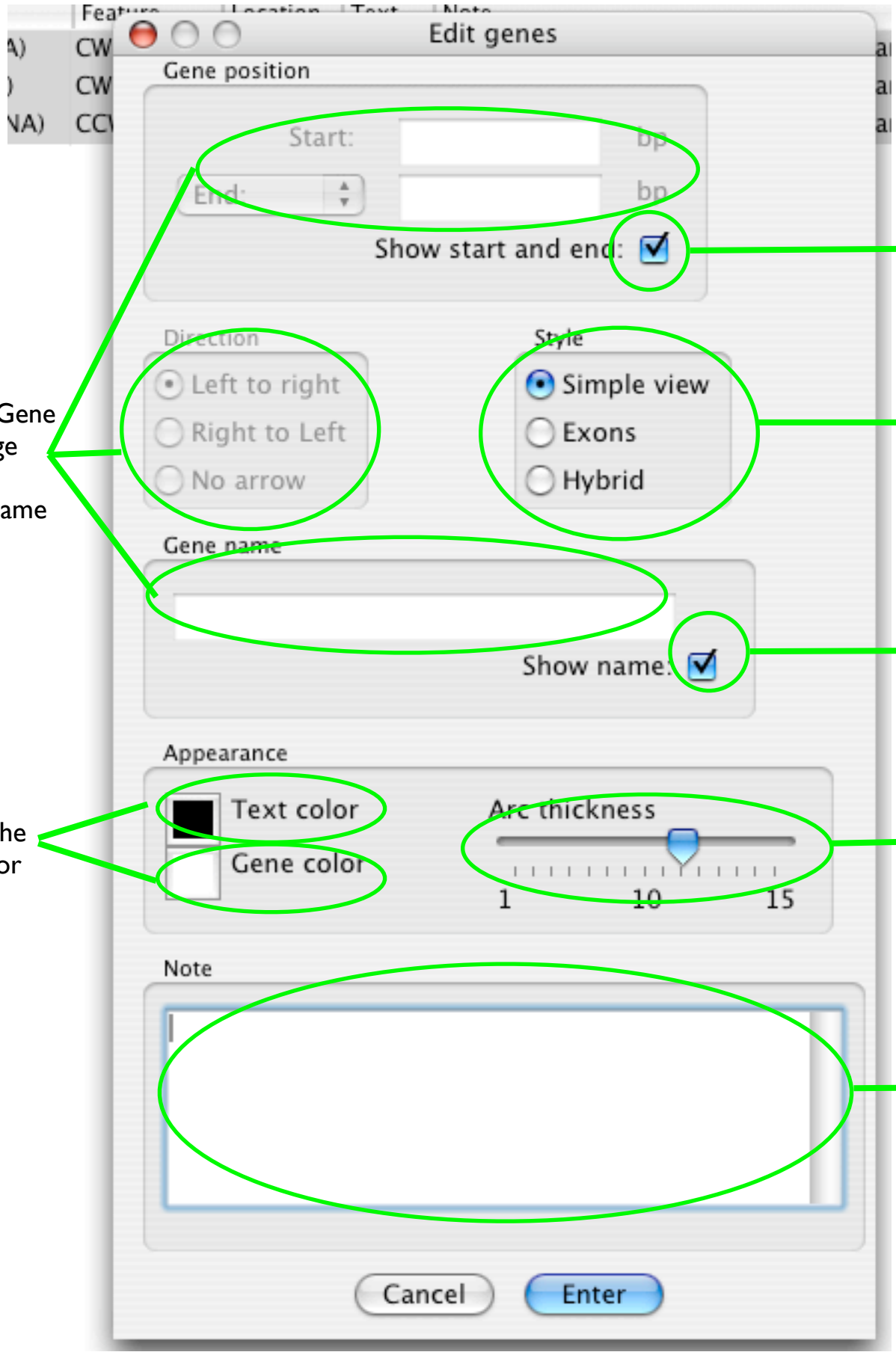
Tips

- Double-click on a row (feature) to get the edit dialog for that feature
- Select multiple rows using ⌘-click (for discontinous rows) or shift-click (selects all rows between the clicks)

The List view for text overviews

Edit genes in the ***List view*** menu option in the ***Maps*** menu

Edit multiple genes at once



Unlike the usual Edit Gene dialog, you can't change start or end position, orientation, or gene name

Show or hide the start and end positions

Change the genes' style

Show or hide the name

Change the color of the genes, or the text color

Change the arc thickness

Make a note for all selected genes

Tips

•Be careful! Even if you don't specifically select an aspect to change, it will still be edited for all the genes you've selected. E.g. if you've change the color of one gene to red, and make no changes in gene color in this dialog, your gene will be white when you're finished.