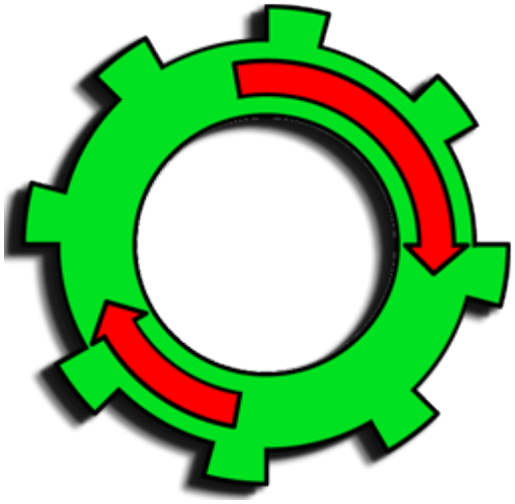


XPlasMap

Users' Guide

version 0.99

Questions, bug reports, feature requests:
Please write to xplasmap@iayork.com

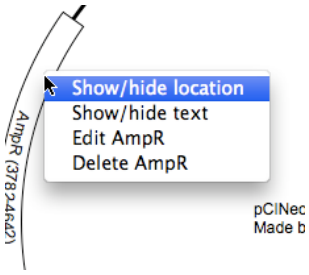
Table of Contents

Notes and tips

What XPlasMap can and can't do. XPlasMap draws DNA maps: Circular DNA (e.g. plasmids) or linear DNA (e.g. genomic views). The maps can be annotated, fragments can be added or deleted to plan or match your cloning, and so on. XPlasMap can perform restriction mapping and open reading frame analysis, but **only when importing a new sequence**. The sequence is not saved after import, so you can't make modifications to the map and then search for restriction sites. (There are several excellent free programs for Mac OSX that will do sequence analysis.)

More than one answer. There are generally several ways to do common actions. For example, a ***new gene*** can be added by (1) clicking on a menu item ("Features → New Gene"); (2) typing ⌘-G; (3) clicking on the toolbar icon. ***Pre-existing genes*** can be edited by (1) selecting (highlighting) the gene and clicking a menu item ("Edit → Edit selected"); (2) selecting the gene and typing ⌘-E; (3) double-clicking the gene; (4) using the contextual menu item for the gene; (5) double-clicking on the description of the gene in the "List View".

The "Add new gene" toolbar icon

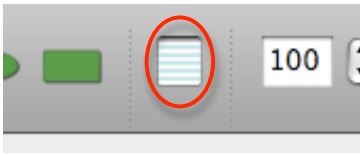


The contextual menu for a gene

Check out contextual menus. Most features have a contextual menu (control-click, or right-click) that offers quick access to modifications, edits, or deletions.

Check out Preferences. Set various default values in the Preferences, including whether to look for open reading frames in imported sequences; how to identify open reading frames; favourite sets of restriction enzymes for mapping during import; and default fonts and exported image resolutions.

Check out List View. The List View ("Maps → List View", ⌘-L, or toolbar icon) is particularly useful for complicated maps with many features or restriction sites. List View shows all the features in a table view that can be sorted by start, end, type, etc. Features can be edited individually (select and double-click), or as a group (select several and double-click).



The "List view" toolbar icon

If in doubt, try ⌘-click. Dragging on a gene moves the text, not the gene itself. To move the gene itself, hold down the command (⌘) key and drag. To edit the shape of an arrow, oval, or rectangle, command-click (⌘-click) on it; a red cross-hair will appear at the "end" of the annotation. Drag the cross-hair to change the shape.

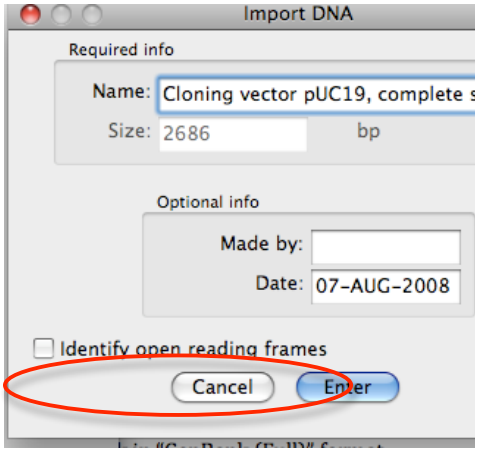
Quick start

New maps

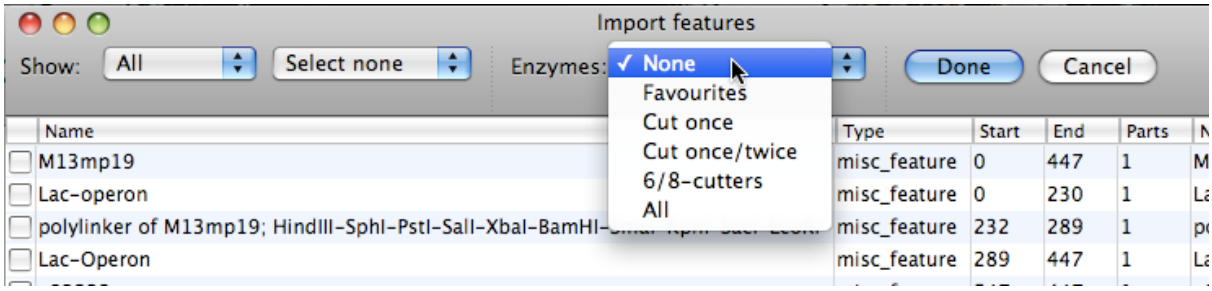
- Start a new map from the **Maps** menu (**⌘-N** for circular, **⌘-Shift-N** for linear map)
    - **Maps → Linear <> Circular** to convert between circular and linear maps

Importing from GenBank, FastA, text, or EMBOSS format

- Draw maps directly from GenBank, EMBOSS, FastA, or plain-text files
    - Save a file to your computer, from GenBank in "GenBank (Full)" format
    - Import (**File → Import → from GenBank (.gb files)**)
    - Choose which features listed in the GenBank (genes, mRNA, CDS, etc) you want to include on the map
- Imported sequences (GenBank, FastA, text files): Optional open reading frame identification and restriction mapping during import.



While importing a sequence: The "Identify open reading frames" checkbox



After importing a sequence: the restriction mapping pull-down menu

Adding new features (Genes, enzymes, multiple cloning sites)

- Add new genes, new multiple cloning sites, new restriction sites, or new text from the **Features** menu (or **⌘-G**, **⌘-Shift-M**, **⌘-R**; or toolbar icons)
    - Genes on linear (but not circular) maps can be shown as exons (with direction indicated on the last exon, or with the whole gene , as a single block
    - Multiple cloning sites can also be displayed in several styles

Editing and modifying features

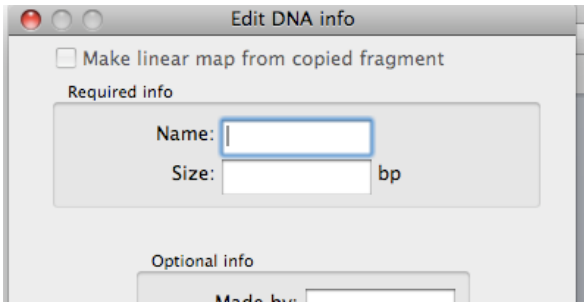
- Edit a feature by double-clicking on it, by selecting "**Edit** … " in the Contextual menu, by selecting (highlighting) the feature and clicking "**Edit → Edit selected"**, or by selecting it and typing **⌘-E**
- contextual menu (control-click or right-click on the feature)
- Click and drag to move a feature
    - Click-and-drag moves only the text of gene
    - Hold down ⌘ and drag to move a gene itself

Editing map parameters (Size, notes, date, etc)

- **Edit → Plasmid Info** (or **⌘-I**, or toolbar "info" icon)

Copying and cutting fragments

- To copy or cut out a fragment, "**Edit → Copy fragment" (or ⌘-C) or** "**Edit → Cut fragment" (⌘-X)** brings up a dialog that lets you select start and end points
- Or, select the restriction site that starts the fragment, hold down "Shift" key, click the enzyme that ends the fragment, and type **⌘-C** to copy **(⌘-X** to cut**)**



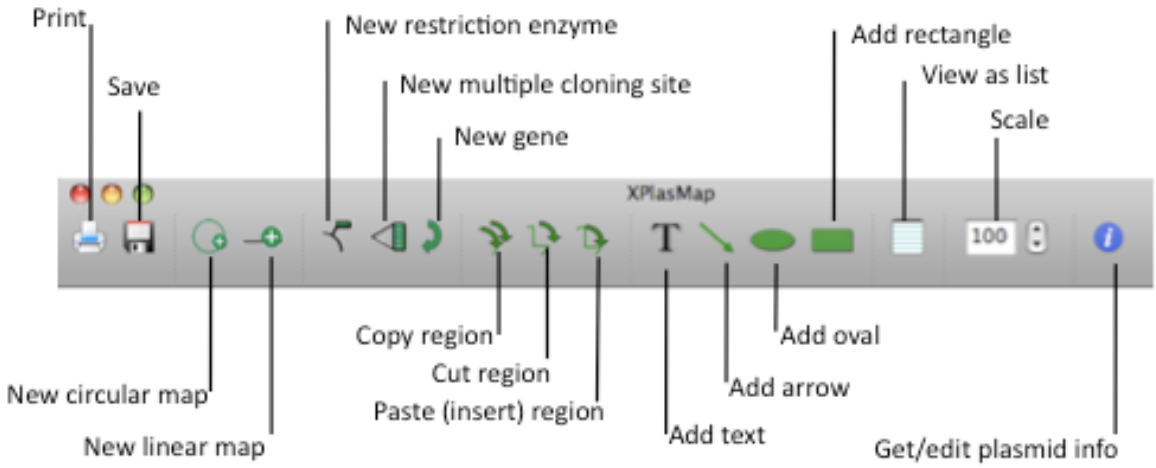
The "Make linear map from copied fragment" checkbox in the New Linear DNA dialog

- Cut and copied fragments can be drawn as a linear map. "**Maps → New linear DNA"** or type **⌘- Shift-N**, then check the "Make linear map … " checkbox
- Cut and copied fragments can be inserted into the same, or different, plasmids.
- "Cut" fragments are saved for later use. Deleted fragments are not saved

Inserting fragments

- Inserting a fragment (**Edit→Insert fragment**" or **⌘-V**): 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

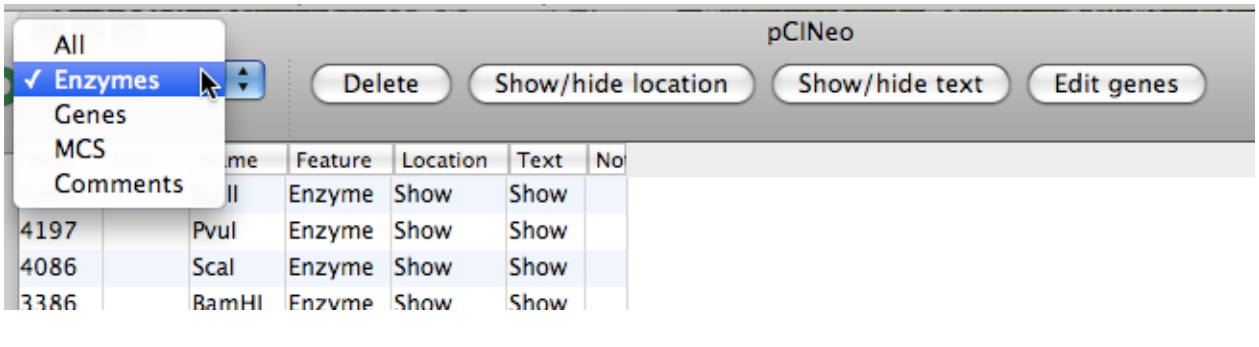
Toolbar icons



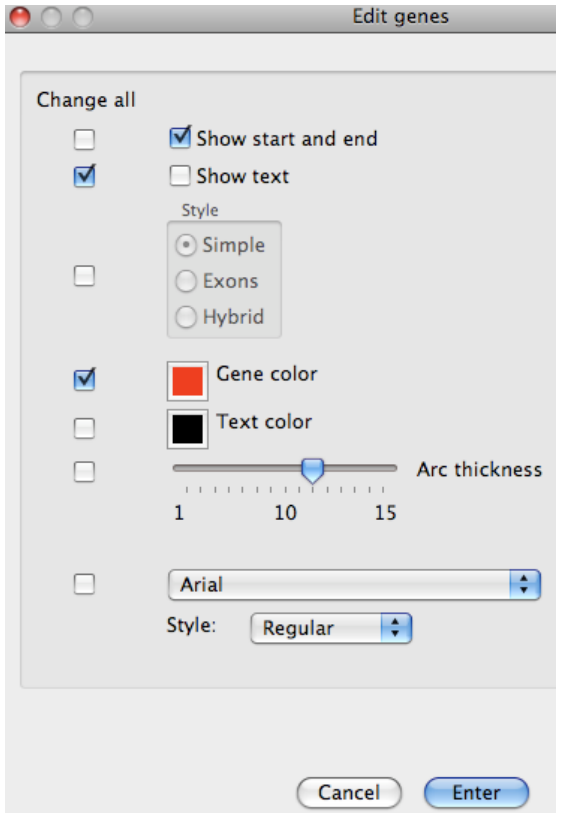
Functions of the toolbar icons

View as list

- View as list ("**Maps→View as list**" or ⌘-**L**) for a sortable text summary of all DNA features
- Select and double-click to edit individual features
- To edit the appearance of multiple genes at once, select the genes and click the "Edit genes" button



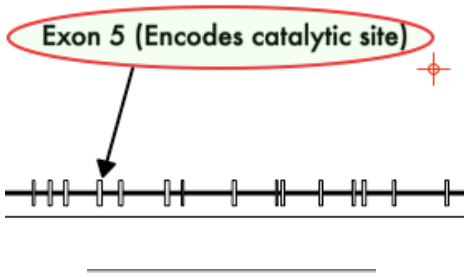
The List View



The "Edit multiple genes" dialog (from List View)

Annotations

- Add ovals, rectangles, arrows, or text using the Features menu or the toolbar icons
- Annotation features can be dragged
- To change the shape of an oval or rectangle, or change the arrow direction, command-click (**⌘-click**) on the feature. A red cross-hair will appear; drag this cross-hair to change the annotation feature's shape



Annotation with an oval, an arrow, and text. Note the crosshair (lower left of the oval) used to change the shape of the oval

Edit fonts

- Set default font in Preferences.
- To change fonts for an individual feature, select (highlight) the feature and click "Edit → Set font"
- To set fonts for a group of features (e.g. all genes, or all enzymes) make sure no feature is highlighted, then select "Edit → Set font".

Open reading frame identification

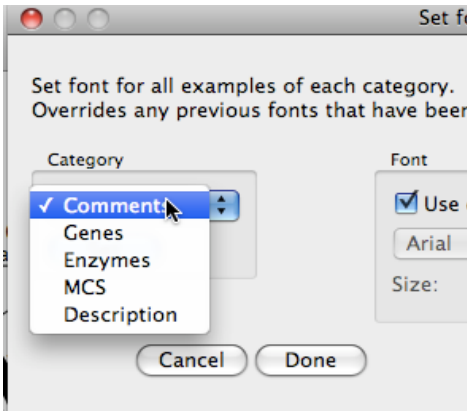
- Open reading frames can be identified while importing a new sequence from text, FastA, or GenBank format
- Minimum length to be called an ORF, and requirement for an initiating ATG, can be set in Preferences

Enzyme sets

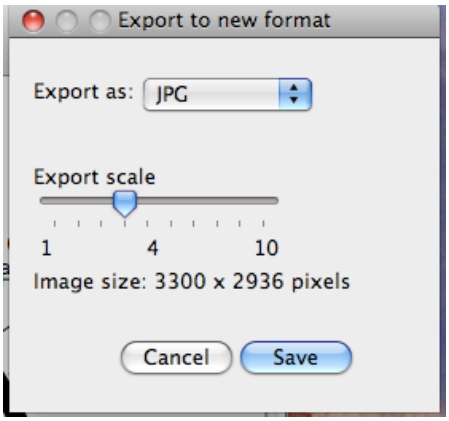
- Define your own enzyme set in Preferences
- On importing a sequence, select an appropriate set of restriction enzymes for mapping the sequence

Printing; exporting as an image

- Print maps (**File → Print;** you can also save as PDF using the standard OSX print dialog) or export as JPG or PNG (**File → Export**)
- JPG has a white background, PNG has a transparent background
- The "Export scale" default size can be set in Preferences
- Can adjust the "Export scale" to save as a higher resolution, larger file, or as a lower resolution, smaller file



Set the font for all of one kind of feature



The "Export to new format" dialog box

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? The main advantage is that you can map open reading frames and restriction enzymes on import. (Note that ***the sequence is not saved***, so after the map is imported you can't go back and find more restriction sites or open reading frames.)

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 organism 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 additional 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 List View (**Maps → List View**) 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? Change the default font in the **Preferences** menu. To change the font for individual items, highlight the item and **Edit → Set Font**. To change the font for, e.g. all genes or all enzymes, make sure no feature is highlighted, and click **Edit → Set font**.

13. How do I restriction-map my DNA? When you import from a DNA file (FastA, text, or GenBank) select an enzyme set from the “Enzymes” pull-down menu. Be aware that mapping a large piece of DNA will take a minute or two.

14. How can I map with just the enzymes I’m interested in? In Preferences, “Select Enzyme Set”. You can choose enzymes and give the set a name. Next time you import DNA, that set will be an option. (The default enzyme sets offer enzymes that cut once or twice, as well as 6 and 8-cutters.)

15. How I can identify restriction sites after I’ve already imported a DNA sequence? At least for now, you can’t. Sequence information isn’t kept after the map is drawn. You would have to import again.

16. How do I map open reading frames? Make sure the “Identify ORFs” option is checked in the import dialog. Set the definition of an ORF (length, etc) in Preferences.

17. 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 **xplasmap@iayork.com**.

What's new; what's different in v. 0.99

- **Ovals, rectangles, and arrows for annotations**
- **Auto-positioning for enzymes and gene text**
- **Checkbox to identify ORFs in Genbank during import**
- **Import from EMBOSS**
- **Highlight features when selected**
- **Convert restriction sites to MCS/MCS to restriction sites**
- **Change feature fonts on an individual basis**
- **Insert, copy, and cut fragments by restriction site**
- **Export to plain text**
- **Determine PNG and JPG resolution at export**
- **Import circular DNA from GenBank correctly**
- **Plasmid name and description are moveable**
- **Change "Insert fragment" shortcut from "⌘I" to "⌘V"**
- **Change "Edit plasmid info" shortcut to "⌘I"**
- **"Info" icon in toolbar to edit plasmid info**