

MacPlasmap 2.1

Reviewed by A. Malcolm Campbell, Ph.D.

Overview

MacPlasmap version 2.1 is a user-friendly program that facilitates the drawing of linear and circular maps of plasmids. As in its predecessor, MacPlasmap 2.0, the maps can be modified with insertions and deletions, genes can be drawn and labeled, restriction sites can be indicated, and the files can be exported as PICT or TEXT formats. This latest version has some added features: DNA sequences in certain formats can be used directly to generate maps; text can be converted into features on the map and conversely, map features can be converted into text; the maps can be drawn with rulers; and under certain circumstances, GenBank and EMBL features can be converted into map features. As the name indicates, it is a Macintosh program, and it makes good use of menus, but it is not accelerated for Power Macs and is somewhat slow opening files and modifying figures.

System Requirements

MacPlasmap 2.1 requires System 7 or above, and a minimum of 1MB of RAM (though this is not stated in the documentation). Installation is simple and the program supports all standard printers. It is useful to have a color monitor to enhance different features on the map. Evaluation of this program was conducted on a PowerMac 7100/66 with 24 MB RAM.

Key Features

MacPlasmap 2.1 allows DNA sequences in a limited number of formats (GenBank, EMBL, native DNA Strider, Plain Text, BioNet, NBRF, GCG, and IntelliGenetics) to be converted into maps. Figure 1 was generated from a linear DNA sequence in DNA Strider format. The three "genes" (ori, amp, and arg7) were drawn manually, but the restriction sites were inserted by selecting a subset of enzymes from a menu containing a long list of sites recognized by the program. This particular plasmid was converted into a circle (Figure 2) by adjusting the map parameters. When the **Circularize** command was used, the program quit.

Converting Features to Text

Figure 3 shows how the map features can be converted into text. Similarly, text can be used to generate features. For example, if the position and length of the arg7 gene is provided, the program will generate the appropriate feature on the map. This ability is very nice, since genes can be drawn easily at exactly the right location, instead of having to manually draw a box at the approximate location.

The documentation is awkward, since two manuals are provided: one covers the basics that were available in version 2.0, while a smaller supplemental manual

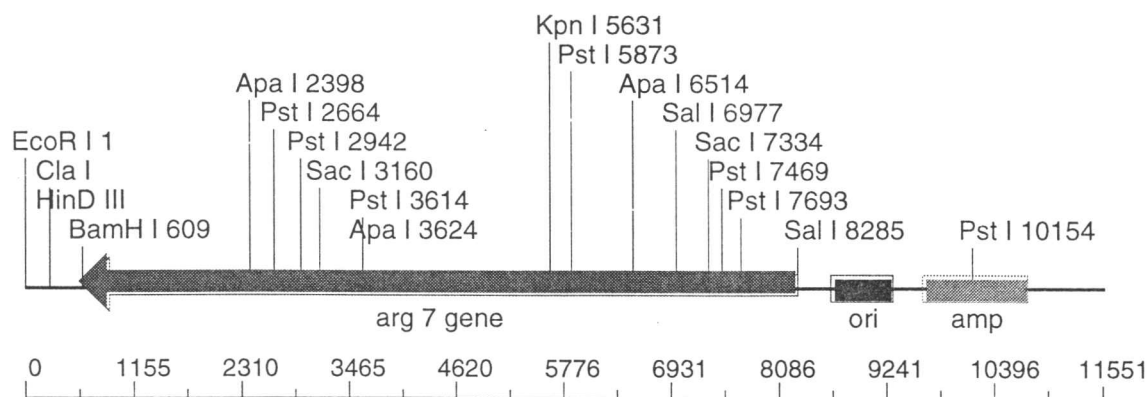


Figure 1. Linear map of a plasmid that was generated from a DNA sequence file. The three genes were drawn manually and the ruler is in base pairs.

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