

hard disk space, a Pentium processor running at least Windows 95, and a monitor with a minimum resolution of 800 x 600 pixels and 8-bit (256) color, although true color mode (24-bit) is recommended.

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TECHSIGHTING SOFTWARE

Pretty Plasmids

Recombinant plasmids are commonly constructed in molecular biology laboratories. The Gene Construction Kit 2 (GCK2) simplifies the design, manipulation, and presentation of plasmid maps. Previously, this program was only available for use on Macintosh systems, but now it is available to Windows 95, 98, and NT users. Files created by Macintosh and Windows GCK2 versions are interchangeable, simplifying collaborations between colleagues with different computers.

Twelve short tutorials provide step-by-step directions to help experienced or new users to rapidly learn program features and increase productivity. More advanced program functions are logically organized and presented in a paperback user's manual, a virtual manual (installed with the program), and at the Textco, Inc. Web site. The tutorials, which require several hours to complete, are highly recommended.

Plasmid map construction in GCK2 begins with entry of the sequence(s) of a parental plasmid or any other DNA molecules. This may be accomplished manually via the keyboard or by importing sequences in a variety of formats (DNA Inspector, GenBank, Intelligenetics, FASTA, NBRF, text, GCG, EMBL, Staden, and Gene Inspector). DNA segments are viewed as either text (sequence) or as a graphic. Once imported, DNA sequences can be cut from one plasmid and pasted into another construct, edited, and annotated with restriction sites and icons. GCK2 can create color illustrations containing multiple constructs, sequences, text, and legends. The program can also manipulate much larger and more complex plasmids, such as the *Agrobacterium tumefaciens* Ti plasmid (~200 kb).

GCK2 will automatically track and document the parent-descendant connection for any given DNA segment within a construct. Students and professionals no

longer need to labor over handwritten notes to describe complex plasmid designs. Users can assign keywords to specific DNA segments and place them in defined subdatabases to make future access more efficient.

GCK2 offers a DNA sequence manipulation package combined with basic graphic illustration features that allow rapid production of professional-quality presentations. Graphics may be exported as illustrations, PICT, or JPEG images for editing in more powerful graphic applications.

Other useful features of the program include identification of silent mutations that create or remove restriction sites in coding sequences, agarose gel simulations for single-, partial-, or multiple-enzyme digests, and an open reading frame finder with translation capability. GCK2 also contains a ligation dialogue feature that disallows DNA segment insertions with incompatible ends.

GCK2 supplies a user-friendly and affordable graphic interface to manipulate complex plasmids and produce professional color illustrations. To add to the program's attractiveness, the company offers a technical support telephone line and a Web site. GCK2 is an especially good choice for labs with students because it is an easy-to-learn program that documents each step of plasmid construction. This program would be an excellent addition to any molecular biology lab.

GCK2 is supplied on a single CD-ROM and requires a system with a Windows 95, 98, or NT platform and at least 8.5-MB hard disk space. Some Windows 95 users will need to download a free driver directly from Microsoft.

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TECHSIGHTING SOFTWARE

Manage Your Microbes

Researchers performing investigations in microbial genetics create many modified strains of microbes in a relatively short time, and many find it difficult to keep the information organized and accessible. Recently, Caesar Software

launched their first software product, StrainMan (version 1.0), to ease this problem. StrainMan is a predefined database application for tracking and logging information about bacterial strains. It not only keeps track of where a vial is stored, it also gives essential data about the genetics of the microbe, its growth needs, and other information. Only basic computer skills are required to run the program. Help is supplied through tutorials and on the company Web site.

StrainMan provides blank database records for the user to fill in information describing their bacterial stocks. The entries include genotype, phenotype, genetic modifications, growth requirements, mutations, and notes. The developers estimate that 1500 strain records occupy about 6 MB of hard disk space. Maneuvering in the program is simple and convenient. StrainMan uses numerous options that reduce typographical errors upon data entry. The attention paid to detail is noteworthy.

Filling in a new strain record is easy. After selecting the Genus window, a pop-up window with over 50 entries beginning with the letter "a" appears. To view a genus beginning with a different letter, one only needs to enter that letter. Clicking on the desired genus in the list selects it for entry into the record. This intuitive, simple design is also available for other records, such as antibiotic resistance, genetic makeup, nutrients, plasmids, transposons, and sources. The last category consists of a catalog of 1309 vendors with their complete contact information.

StrainMan users will spend little time searching for strains after entering relevant information into their records because all the microbes will be cataloged. User-specified parameters combined with Boolean logic search capabilities enable rapid retrieval of desired information. Users may also publish their strain database on a Web site, thus providing wider access to collaborators. Password protection allows control over who may view and search the library.

StrainMan is well-suited for its task. A downloadable trial version is available on the Web for those who wish to browse through the program before purchase. StrainMan version 1.0 is available on both Macintosh and Windows platforms.

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