yesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyes
yesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyes
yesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyes
yesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyesyes

yesyesyesyesyesyesyes yesyesyesyes**Main Contents**

Vised help contents

Select an item from the list below to see the contents for that section.

Vised Basicis
Starting and exiting Vised, accessing menu commands, getting help, and definitions

Workplace
Fonts, keyboard, toolbar, status bar, scrolling, Vised windows, and menu

Editor
Working with documents, entering and editing data, working with sequences

Sequence analysis
Vised sequence analysis functions

Dialog boxes
Vised dialog box help

Information
Registration, distrubution, credits, about Vised (version info etc)

Definitions

Clipboard
Current sequence
Current position
Cursor

Editor window

Insert mode
Insertion point

Landscape

Menu

Overtype mode

Non-scrolling position line

Path

Scroll bar
Sequence block
Sequence name
Sequence number
Sequence type
Status bar

Title bar
Toolbar

Insert mode

An option for inserting typed characters into a sequence by moving existing characters down stream. You can select the insertion mode by pressing the INS key. When you select the Insert option, the letters "INS" appear in the status bar at the bottom of the Vised window.

Sequence name

The Sequence name appears to the left of each line of sequence data.   When you import a sequence from a disk file, the file name is used as a sequence name.

Sequence number

The sequence number appears to the left of the sequence name, and indicates the position of the sequence in the editor.

Sequence type

One letter code to the left ot the sequence name indicating the sequence type.   Sequence types may be 'N' for nucleic acids, 'P' for proteins, 'A' for alignment or 'U' for unassigned.

Caret

The caret is the flashing vertical line that indicates the current insertion point.

Cursor

The cursor is the mouse pointer.   Its shape depends on where on the screen the pointer is located.   For example, in the menu bar, the cursor is an arrow .   In the document window the cursor is an I-beam

Current sequence

The sequence that is currently active is the sequence that contains the caret.   All Vised commands that apply to individual sequences are applied to the current sequence.   The number of the current sequence is indicated on the Status bar after "Seq".

Current position

The current position is the position in the current sequence where the caret is located, and is the position where data is inserted.   Many Vised commands that apply to individual sequences are applied at the current position.   The current position number is indicated on the Status bar after "Pos".

Editor window

The window containing open sequences in an editor document.   Note that you cannot close the editor window.

Insertion point

Vertical blinking bar on the Vised screen that shows your current location and where data are inserted. The insertion point also determines where Vised will begin an action, such as translation or removing spaces.

Landscape

A term used to refer to horizontal page orientation; opposite of "portrait," or vertical, orientation.

Landscape

Portrait

Non-scrolling position line

The Non-scrolling position line is a position line displayed at the bottom of the screen.   It is primarily used to indicate what positions are on screen when there are too many sequences open to fit on the screen.

Overtype mode

An option for replacing existing characters one by one as you type. You can select overtype by pressing the INS key. When you select the Overtype option, the letters "OVR" appear in the status bar at the bottom of the Vised window.

Path

Drive, directory, and filename. For example, the complete path for Vised might be C:\VISED\VISED.EXE.

Scroll bar

A graphical device for moving vertically and horizontally through a document with a mouse. Scroll bars are located at the right and bottom edges of the document window. You can display or hide scroll bars with the Horizontal Scroll Bar and Vertical Scroll Bar check boxes in the Options dialog box (Settings menu).

Sequence block

A veritical group of sequence lines.

Title bar

The horizontal bar at the top of a window that shows the name of the document or application that appears in that window.

Toolbar

A bar containing buttons that perform some of the most common commands in Vised, such as opening, saving, and printing files.   To display the Toolbar, select the Toolbar check box from options dialog box (Settings menu). You may need to enlarge the Vised window to the full width of the screen to see the entire Toolbar.

Statusbar

A line at the bottom of the Vised window that displays information about the current status of the document.

Menu

A list of commands that drops down from the menu bar. The menu bar is displayed across the top of the Vised window and lists the menu names, such as File and Edit.

Clipboard

A temporary storage area for cut or copied text or graphics. You can paste the contents of the Clipboard into any Vised sequence or into a file of another application, such as a word processor. The Clipboard holds the information until you cut or copy another piece of text.

Vised Basicis

[Starting Vised](#)
[Exiting Vised](#)
[Accessing menu commands](#)
[Getting help](#)
[Definitions](#)

Getting help

To view the Vised Help File from the editor, select 'Contents' from the <u>Help Menu</u>.   To search help topics, select 'Index' from the <u>Help Menu</u>.   To learn how to use Help, select 'Help on Help' from the <u>Help Menu</u>.

To get help within dialog boxes, click on the Help button.

Shortcut:
▶ Press the 'Help' icon on the <u>tool bar</u>.
▶ Press F1.

Accessing menu commands

Menu commands can be accessed with the mouse or with the keyboard.

Mouse:

To access the menu with a mouse, position the pointer on the desired menu item and click the left mouse button once.   Items from drop down menus are selected in the same way.

Keyboard:

To access the menu using the keyboard, press ALT and the underlined letter in the menu item name.   For example, to access the File menu, press ALT-F.   To select an item in a drop down menu, press the letter that is underlined in the item name, or use the arrow keys to select the desired item and then press ENTER.

Many menu commands have keyboard shortcuts.   When this is the case, the keystrokes are indicated beside the menu item in the dropdown menu.

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Related topics:

Menu
Keyboard

Exiting Vised

When you exit Vised, you will be prompted to save any changes you have made to Vised documents

To exit:

You can exit Vised through the Vised menu or the system menu, or by using a keyboard shortcut.

To exit Vised through the menu:

1. Select the File menu with the mouse or by typing ALT-F
2. Select exit from the File Menu with the mouse, or by typing X

To exit through the system menu: Double click on the system menu box at the upper left hand corner of the main Vised Window.

To exit using the keyboard shortcut:,   Type ALT-F4

Starting Vised

You can start Vised from either Windows or the command prompt:

From the program manager:
To start Vised from the Windows Program Manager

1. Switch to the Program Manager window.
2. Open the group window that contains the Vised icon.
3. Do one of the following:

    Double-click the Vised icon.
    Use the arrow keys to select the Vised icon, and then press ENTER.

From the windows file menu
To start Vised from the Windows File menu

1. From the Program Manager File menu, choose Run.
2. Do one of the following:

    If Vised is in your path, type Vised
    If Vised is not in your path, type the path for Vised -- for example:
    c:\Vised\Vised.exe

3. Choose the OK button.

From the DOS Command prompt
To start Vised from the command prompt

1. At the command prompt, type win Vised
2. Press ENTER.

Note: If a message appears stating that the command failed, the directory containing Vised is not on your path. Change to the directory containing VISED.EXE and try again.

Workplace

[Menu](#)
[Editor toolbar](#)
[Pretty display   tool bar](#)
[Moving the insertion point](#)
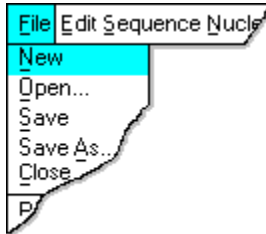[Scrolling through the editor](#)
[Status bar](#)
[Vised windows](#)
[Keyboard](#)
[Selecting fonts](#)

Menu

The menu bar is located below the aplication title bar, along the top of the main window.   All Vised commands can be acessed through the menu bar.

To view all the commands in a menu, do one of the following:

▶ Click the menu name.
▶ Press ALT+n, where n is the underlined letter in the menu name. For example, press ALT+F to open the File menu.

Menu bar items:
File menu
Edit menu
Sequence menu
Options menu
Window menu
Help menu

_____
Related topics:

Accessing menu commands

 File menu

Commands For Manipulating Files: Create, Open, Print And Save Files, And Exit.

New Document
> Creates An New Vised Document.   All All Sequences In The Editor Window Are Discarded.
> You Will Be Prompted To Save Changes, If Any.

Open Document
> Opens An Vised Document That Has Already Been Saved To A Disk File.   Calls The Open
> File Dialog Box.

Save Document
> Saves The Active Vised Document To A Disk.   Calls The Save As Dialog Box.   To Save
> The File Under Its Original Name, Just Press Enter.   If You Want To Save The File Under A
> New Name, Enter The Name In The File Name Edit Box Before You Press Enter.

Print Document
> Prints the Editor Window.   Calls The Print Dialogbox.

Print Pretty Display
> Prints The Contents of the Pretty display Window.

Exit
> Exits Vised.   You Will Be Prompted To Save Documents That Have Been Changed Before
> Exiting.

Recent File List
> A List Of The Last Four Files Saved Is Displayed At The Bottom Of The File Menu.
> Selecting Any One Of These Files Causes That File To Be Opened.

Edit menu

Commands for editing: undo, cut, copy, paste, convert to upper or lower case, insert or remove spaces, and search.

Undo
Undoes the last change made in the editor.

Cut
Deletes selected (highlighted) sequence data from the <u>current sequence</u> and copies it to the clipboard.

Copy
Copies selected (highlighted) sequence data from the <u>current sequence</u> from the edit window, or a selection from the pretty display window, to the clipboard.

Paste
Copies information from the clipboard into the <u>current sequence</u>.   If sequence data is selected, Paste overwrites the selection with the data in the clipboard.   Otherwise, the data is inserted at the <u>current position</u>.

Remove spaces
Removes spaces deletes blanks from a sequence.   If sequence data is selected, spaces are removed from the selection only.   Otherwise, spaces are removed from the <u>current position</u> to the end of the sequence.

Insert spaces
Inserts a specified number of spaces at a given interval.   Calls the Insert Spaces dialog box.   If sequence data is selected, spaces are inserted into the selection only. Otherwise, spaces are inserted from the <u>current position</u> to the end of the sequence.

Delete to end of seq
Deletes the sequence from the <u>current position</u> to the end of the sequence.

Upper case
Convert data to upper case characters

Lower case
Convert data to lower case characters

Find
Searches the <u>current sequence</u> for the next occurance of a text string.   Calls the Find dialog box.

Seacrh again
Repeats the last find operation.

Sequence menu

The Sequence menu contains commands that apply to both nucleotide (type N) and protein (Type P) sequences.

Create
Generates an empty sequence.   If too many sequences are already open, or if there is insufficient memory to create the sequence, an error message is displayed.

Import
Opens formated sequence file that has already been saved to a disk.   Calls the Import dialog box.   See Importing a sequence for supported formats.

Export
Saves the current sequence to a disk file.   Calls the Export dialog box.

Delete
Deletes the current sequence.   You will be prompted to save the sequence and given an opportunity to cancel the command.

Reverse
Causes a sequence to be written out the reverse orientation.   This command does not create a new sequence.

Complement
Creates a new sequence that is the complement of the current sequence.

Translate in frame
Creates a new sequence that is the translation product of the current sequence.

Translate all
Translate the sequence in all six frames.

Match
Identifies identical posistions in a sequence with the sequence above.   If sequence data is selected, the match is applied to the selected portion of the sequence only.
Otherwise, the match is applied from the current position to the end of the sequence.
Note that the sequences must have be the same type.

Pretty display
Displays all open sequences for formatted output.

Pattern search
Search the current sequence for a pattern using the prosite data base pattern syntax.

Options menu

Commands to set options for analysis functions, editor, individual sequences, and fonts.

Editor options
Set editor options.

Pretty display opitons
Set options used for Pretty display.

Sequence options
Sets the sequence name, type and position, and Display mode numbering options for the <u>current sequence</u>.   Calls the Sequence Info dialog box.

Title font
Set the font used in pretty display title.

Font
Set the font used in the editor and pretty display windows.

Window menu

Commands for manipulating Vised windows: tile, cascade, set active window.

Cascade
Arranges document windows in a cascaded format.

Tile
Arranges document windows in a tiled format.

Edit window
Brings the editor window to the foreground and makes it active.

Pretty display window
Brings the prettyt display window to the foreground and makes it active.

Help menu

Commands for displaying the help index, the help search dialog box, and the Vised About dialog box.

Contents
   Displays the Vised Help File contents.

Search
   Displays the Vised Help File Search dialog box.

Help on help
   How to use help.

About Vised
   Displays a copyright notice and information about Vised.

Editor toolbar

The tool bar is a collection of buttons displayed under the menu bar that you can use to accomplish common tasks quickly.   To use the tool bar, position the mouse cursor over the desired button and click the left mouse button.

Vised displays two tool bars, an editor tool bar that is displayed when the editor window is active, and a graph/data tool bar that is displayed when the graph or data window is active:

Editor tool bar
This tool bar is displayed when the editor window is active
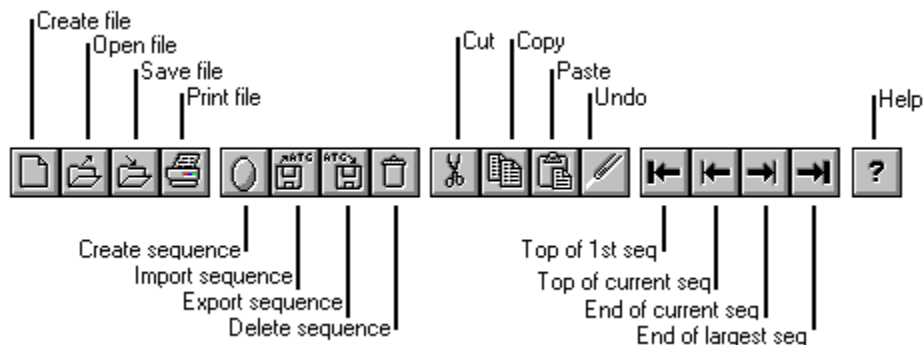
Create file
  Creates a new Vised file by clearing all currently open sequences.

Open file
  Open an Vised file from a disk.

Save file
  Save an Vised file to a disk.

Print file
  Print the contents of the Editor window

Create sequence
  Create a new blank sequence.

Import sequence
  Import a sequence from a disk file.

Export sequence
  Export a sequence to a disk file.

Delete sequence
  Delete the current sequence.

Cut
  Delete highlighted data from the current sequence and copy the data to the clipboard.

Copy
  Copy highlighted data to the clipboard.

Paste
  Insert data from the clipboard into the current position.

Undo
  Undo the most recent edit.

Top of 1st sequence
    Move the insertion point to position one of the first sequence.

Top of the current sequence
    Move the insertion point to postion one of the current sequence.

End of the current sequence
    Move the insertion point to the last position of the current sequence.

End of the largest sequence
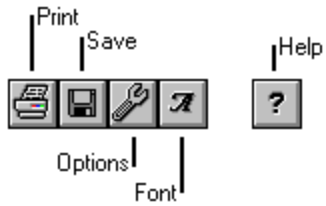   Move the insertion point to the last position of the largest sequence.

Help
    Veiw the help file contents.

Pretty display tool bar

This tool bar is displayed when the pretty display window is active.

Print
Print the contents of the active window.

Save
Save table or graph/map as picture

Options
Set analysis function options.

Font
Set the font for the current window.

Help
View the help file contents.

Moving the insertion point

To change the current position or current sequence, you must move the insertion point, which is shown by the caret.   You can move the caret using the keyboard or the mouse. You can also scroll through the editor window without moving the current position.

To set the current position:

With the mouse:

1. Scroll to the desired location

2. Position the cursor over the desired sequence position

3. Click the left mouse button once.   The caret will move to the new position.

With the keyboard:

To move:	Press:
One position down stream	→
One position up stream	←
Up one sequence	↑
Down one sequence	↓
Start of the current line	HOME
End of the current line	END
Start of the current sequence	CONTROL + HOME
End of the current sequence	CONTROL + END
Start of the 1st sequence	CONTROL + PAGEDOWN
End of the largest sequence	CONTROL + PAGEUP

_____
Related topics:

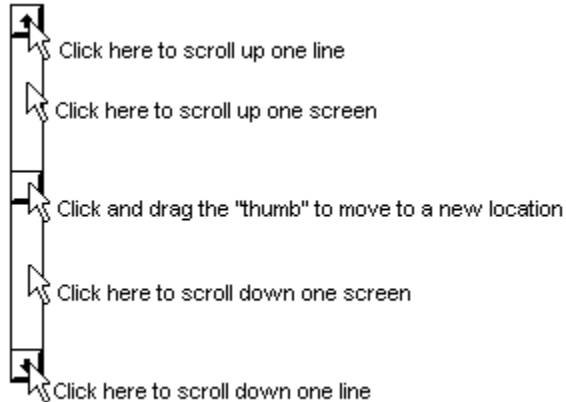Scrolling through the editor

Scrolling through the editor

You can scroll through the editor window without changing the current positon using either the mouse or the keyboard.

To scroll through the editor

With the mouse:
Use the horizontal and vertical scroll bars, as illustrated below:

Click here to scroll up one line

Click here to scroll up one screen

Click and drag the "thumb" to move to a new location

Click here to scroll down one screen

Click here to scroll down one line

With the keyboard:

To scroll:	Press:
up by one screen	PAGE UP
down by one screen	PAGE DOWN

Related topics:

Moving the insertion point
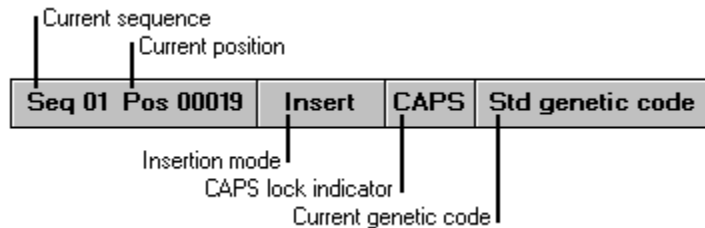
![Workplace icon] **Status bar**

The Status bar is located at the bottom of the Vised window.   When the menu is active, the status bar displays a message descibing what the selected menu command does.   Otherwise, the contents of the status bar depend on what window is active.

Editor status bar
When the editor window is active, the status bar displays:

Current sequence
Current position

Seq 01 Pos 00019 | Insert | CAPS | Std genetic code

Insertion mode
CAPS lock indicator
Current genetic code

    Current sequence
        Indicates which of the sequences in the editor currently has the carret (the <u>caret</u> is the flashing vertical bar that indicates the inserion point).

    Current position
        Indicates the position of the <u>caret</u> in the <u>current sequence</u>.

    Insertion mode
        Indicates whether keystrokes will be inserted at the current position or will be typed over the existing data.

    CAPS
        Indicates the status of the caps lock key.   If the caps lock key is on, CAPS will be displayed.   Otherwise, this section will be blank.

    Current genetic code
        Indicates what genetic code is in use.   This may be either the standard genetic code or a user defined genetic code.

Vised windows

Vised displays either one or two windows at any given time: the Editor window, and the pretty display window.   The Editor window is always open.   The pretty display window is shown when you select the pretty display function from the <u>sequence menu</u>..

Editor window

The editor window displays your sequence data   You will use the editor window to enter and edit data.   You will also use the editor as a launch pad for sequence analysis functions.   The editor window displays up to twenty sequences simultaneously, and also displays the sequence number, type and name.

Pretty display window

The pretty display window displays all of your sequences in user defined formats.   You cannot edit the data in the pretty display window.

Keyboard

Many commands can be executed more quickly using keyboard short cuts.   These are the key combinations you can press to execute menu commands.

Control Key combinations:

Press:	To:
Ctrl+N	Create a new document
Ctrl+O	Open an existing document from a disk file
Ctrl+S	Save the active document
Ctlr+P	Print the active document
Ctrl+X	Cut the selected data
Ctrl+C	Copy the selected data to the clipbord
Ctrl+V	Paste data from the clipboard to the current position
Ctrl+A	Create a new sequence
Ctrl+M	Import a sequence from a disk file
Ctrl+E	Export the current sequence to a disk file
Ctrl+D	Delete the current sequence
Ctrl + Home	Move to start of current sequence
Ctrl + End	Move to end of current sequence
Ctrl + Pageup	Move to start of first sequence
Ctrl + Pagedown	Move to end of largest sequence
Alt+BackSpace	Undo

Function Keys:

Key:	Command:
F1	Help contents
Shift+F1	Help search
F2	Remove spaces
Shift+F2	Insert spaces
Ctrl+F3	Delete to end of sequence
F3	Find
Shift+F3	Find again
Alt+F4	Exit Vised
F5	Match
Ctrl+F5	Pattern search
Alt+F5	Pretty display
F7	Translate in frame
Shift+F7	Translate all

Alt+F7	Reverse
Ctrl+F7	Complement
F10	Pretty display options
Shift+F10	Sequence options
Alt+F10	Editor options
F11	Editor font
Ctrl+F11	Title font

Selecting fonts

To set the font used in the editor and pretty display windows, select 'Font' from the options menu. To set the font used in the pretty display title, select 'Title font' from the options menu. Both of these commands call the <u>font dialog box</u>.

Note: The editor and pretty display windows use fixed pitch fonts only.

Editor

Documents
Creating a document
Opening an existing document
Saving a document
Printing documents
Editor options

Editing
Undo
Entering data
Editing data
Selecting data
Cutting sequence data
Copying sequence data
Pasting sequence data
Deleting to the end of a sequence
Removing spaces from a sequence
Inserting spaces into a sequence
Finding text

Sequences
Creating a sequence
Importing a sequence
Exporting a sequence
Moving a sequence
Sequence options: name,   type, and number

Creating a document

To Create a new document:
Select "New document" from the <u>file menu</u>.

Shortcut:
Press the 'New document' icon on the <u>tool bar</u>.

Notes:
If you have made changes to the current document, you will be prompted to save your work.

_____
Related topics:

<u>Opening an existing document</u>
<u>Saving a document</u>

 Opening an existing document

To open an existing document, do the following:

 select 'Open' from the <u>file menu</u>.   This will open the **File open dialog box**
.

 In the **File Name** box, type or select the document you want to open.

 If the document you want to open is not listed in the **File Name** box, do one or more of the following:

      --In the **Drives** box, select a new drive.
      --In the **Directories** box, select a new directory.
      --In the **List Files Of Type** box, select the type of document you want to open with
       its 3-character extension.

 Choose the OK button.

Shortcuts:

 Press the 'Open' icon on the <u>tool bar</u>.

 If the document was recently saved, you can open it by selecting the file name from the recent file list in the <u>file menu</u>.

Notes:

Vised will automatically recognize and import Macaw files.

You can see a list of all the files with a specific extension in a drive or directory with a specific extension. In the File Name box, type an asterisk (*), before a period (.) and the extension. For example, to see all the files with a .DAT extension in a directory, type *.DAT in the File Name box. To see all the files in a directory, type *.*

—————————

Related topics:

[Creating a document](#)
[Saving a document](#)
[File open dialog box](#)

 Saving a document

To Save a document, do the following:

 select 'Save' from the file menu.   This will open the File save dialog box.

 In the **File Name** box, type or select the document you want to Save.

 If the document you want to Save is not listed in the **File Name** box, do one or more of the following:

> --In the **Drives** box, select a new drive.
> --In the **Directories** box, select a new directory.
> --In the **List Files Of Type** box, select the type of document you want to Save with its 3-character extension.

 Choose the OK button.

Shortcut:

 Press the 'Save' icon on the tool bar.

Notes:

You can see a list of all the files with a specific extension in a drive or directory with a specific extension. In the File Name box, type an asterisk (*), before a period (.) and the extension. For example, to see all the files with a .DAT extension in a directory, type *.DAT in the File Name box. To see all the files in a directory, type *.*

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Related topics:

Creating a document
Opening an existing document
File save dialog box

Printing documents

You can print the contents of the Editor and Pretty display windows.   The commands used to print are:

Window	Menu	Command
Editor window	File menu	Print document
Pretty display window	File menu	Print pretty display

To print a file:

1. Select the appropriate print command from the File menu as listed in the above table. This will call the Print dialog box.

2. Select the desired numer of copies and print quality.

3. Press the Setup button if you wish to change the printer in use, or to set the paper size, source and orientation.   This will call the Print setup dialog box, shown below:

4. Press the OK button.

Cancelling a print job:

Printing takes place in two stages.   First the out put is sent to a print spooler, such as the Print manager that comes with MS Windows.   Then the print spooler sends the output to the printer.

While Vised is sending its output to the spooler, the "printing file" message box is displayed .   You can cancel the job by pressing Cancel in the message box,.

Once the file acutally starts to print, you must use the print manager to cancel the job.

 Editor options

You can set editor options to change the appearance of the editor, or to determine what genetic code is used in the translation of nucleic acid sequences.

The editor options are:

Line length: Sets the number of characters displayed on each line.   The line length must be an even mutlple of 10, and may not be greater than 250.

Name field width: Sets the number of characters displayed of the name of each sequence.   The name field width may be any number bewteen 0 and 16.   If the name field width is less than the number of characters in the name of a sequence, the name is truncated.

Genetic code: You may choose to use the standard genetic code, or a user defined genetic code to translate your Nucleic acid sequences.   You can edit the user defined genetic code by pressing the button labeled "Edit user defined code".

To set the editor options:

      1. Select Editor options from the <u>options menu</u>.

      2. Enter the desired options.

      3. Press the OK button.

_____
Related topics:

<u>Selecting fonts</u>
<u>Editor options dialog box</u>

 Creating a sequence

To Create a new sequence:

 select "Create" from the <u>sequence menu</u>.

Shortcut:

 Press the 'Create sequence' icon on the <u>tool bar</u>.

Notes:

 The newly created sequence is type "U" (Unassigned).

 If there are too many sequences open, an error message is displayed (the maximum number of sequences is 30).

_____
Related topics:

<u>Sequence options: name,   type, and number</u>
<u>Importing a sequence</u>

Importing a sequence

Vised automatically detects and reads sequences in a variety of formats.   If the format is not recoginzed, Vised reads in the whole file, including information that may not be part of the sequence.   If this happens, you can remove the extraneous information using the editor.

Currently, Vised recognizes sequence data in the following formats:

DNAStrider	NBRF
EMBL	Olsen
Fitch	Pearson/Fasta
GCG	PIR/CODATA
GenBank/GB	Plain/Raw
IG/Stanford	Zuker

To import an existing sequence:

 select 'Import' from the sequence menu.   This will open the Import Ascii File dialog box.

 In the File Name box, type or select the sequence you want to import.

 If the sequence you want to import is not listed in the **File Name** box, do one or more of the following:

>   --In the **Drives** box, select a new drive.
>   --In the **Directories** box, select a new directory.
>   --In the **List Files Of Type** box, select the type of file you want to open with its 3-
>   character extension.

 Choose the OK button.

Shortcut:

 Press the 'Import' icon on the tool bar.

Notes:

You can see a list of all the files with a specific extension in a drive or directory

with a specific extension. In the File Name box, type an asterisk (*), before a period (.) and the extension. For example, to see all the files with a .DAT extension in a directory, type *.DAT in the File Name box. To see all the files in a directory, type *.*

If the file name specifies a library (a file that contains more than one sequence), the Select sequence dialog box will be called.   This dialog box alows you to select which sequence you wish to import from the library.   Note that this alows you to import individual sequences from Vised files, as well as sequences from libraries in any of the formats listed above.

_____
Related topics:

Creating a sequence
File open dialog box
Select sequence dialog box.

Exporting a sequence

To Export a sequence:

 select 'Export' from the <u>sequence menu</u>.   This will open the Export Ascii File dialog box.

 In the **File Name** box, type or select the sequence you want to Export.

 If the sequence you want to Export is not listed in the **File Name** box, do one or more of the following:

> --In the **Drives** box, select a new drive.
> --In the **Directories** box, select a new directory.
> --In the **File format** box, select the sequence format you want.
>   Supported formats are:

DNAStrider	NBRF
EMBL	IG/Stanford
Fitch	Pearson/Fasta
GCG	PIR/CODATA
GenBank/GB	Plain/Raw

 Choose the OK button.

Shortcut:

 Press the 'Export' icon on the <u>tool bar</u>.

Notes:

You can see a list of all the files with a specific extension in a drive or directory with a specific extension. In the File Name box, type an asterisk (*), before a period (.) and the extension. For example, to see all the files with a .DAT extension in a directory, type *.DAT in the File Name box. To see all the files in a directory, type *.*

_____
Related topics:

<u>File save dialog box</u>

 Moving a sequence

The sequence postion is indicated by a number to the right of the sequence name in Edit Mode.

To change the sequence order:

 Open the Sequence Info dialog box by selecting 'Sequence Options' from the sequence menu or by double clicking on the name field of the sequence you wish to move.

 Enter a new position for the sequence in the Number edit box to the left of the sequence name.

Shortcut:

 Use the mouse to click on the name field of the sequence you wish to move and drag it to the new position.   A black box will appear around the sequence that is being moved, as shown below:

Related topics:

Sequence options: name,   type, and number
Sequence options dialog box

Sequence options: name, type, and number

Options for each sequence are:

Name: The sequence name can be any combination of characters, up to 16 characters total.   When you import a sequence from a disk file, the file name is automatically used as the seqence name.

Type: Sequences may be type 'N' for nucleic acids, 'P' for protein, 'A' for alignment, or 'U' for unclassified.   The sequence analysis fuctions available for a given sequence depend on the sequence type.

Number: This option specifies the position of the sequence in the editor.   For example, entering a 3 in this edit field will cause the sequence to be moved to the third position.   Note that the number you enter must not be greater than the total number of sequences open.

To set the options for a given sequence:

1. Position the caret in the sequence whose option you wish to change

2. Select Sequence options from the options menu

3. Enter the desired options in the sequence options dialog box.

4. Press the OK button.

Short cut: Position the cursor over the sequence name or number and Double click the mouse left button to call the sequence options dialog box.

Undo

You can undo an error in the editor using the Undo command in the <u>edit menu</u>.   This command reverses the most recent edit.

To undo the most recent edit:

Select undo from the <u>edit menu</u>

shortcuts:

   Press Alt+Backspace.

Press the undo button on the <u>toolbar</u>

Entering data

When you start Vised, a single type 'N' sequence is created, and the insertion point, or <u>caret</u>, is positioned at position 1, ready to receive your typed data.

To enter sequence data from the key board, position the <u>caret</u> within the desired sequence. Data can be entered from the keyboard in either insert mode or typeover mode:

Insert mode: Keystrokes are inserted into the sequence at the <u>current position</u>, and the characters downstream from the <u>current position</u> are moved to the right to make room for the insertion.

Typeover mode: Typed characters displace the characters already present.

Notes:

If any data is highligted, typing replaces the highlighted data regardless of insertion mode.

You cannot enter data after the end of sequence marker.   If you attempt to do so, an error message will be displayed.

_____

Related topics:

<u>Editing data</u>
<u>Selecting data</u>

 Selecting data

Selected (highlighted) data appears as white characters on a black background.   You can select data using the mouse or the keyboard.

 With the mouse:
To select part of the sequence:

1. Place the cursor over the desired selection start point.

2. Click the left mouse button and hold it down.

3. Drag the cursor to the desired end point.

Note: If you drag the mouse outside of the editor window, the window will be scrolled.

To select all of a sequence:

1. Place the cursor over the desired sequence.

2. Double click the left button.

 With the keyboard:

1. Position the caret at the point where you wish the selection to begin.

2. Hold down the shift key, and press the arrow keys to extend the selection in the desired direction.

Editing data

Data may be cut, copied, pasted or deleted, just as text is in a word processor.   You can also use the commands in the <u>edit menu</u> to remove or insert spaces in the sequence, convert the sequence to upper or lower case, or delete to the end of the sequence.   If you make an error when editing your data, immediately select undo from the edit menu, or press the undo icon on the <u>toolbar</u>.

Note: You cannot edit beyond the end of sequence marker.   If you try to do so, an error message will be displayed.

For step by step instructions on specific editing tasks, view the help topics listed below:

<u>Undo</u>
<u>Entering data</u>
<u>Selecting data</u>
<u>Cutting sequence data</u>
<u>Copying sequence data</u>
<u>Pasting sequence data</u>
<u>Deleting to the end of a sequence</u>
<u>Removing spaces from a sequence</u>
<u>Inserting spaces into a sequence</u>

Cutting sequence data

To cut data from the <u>current sequence</u> use the mouse to select the data that you wish to cut. Then select 'Cut' from the <u>edit menu.</u>

Shortcut:

 Press the 'Cut' icon on the <u>tool bar</u>.

Note:

 If no data is selected, the 'Cut' command in the <u>edit menu</u> is disabled (grayed)

Related topics:

<u>Selecting data</u>
<u>Copying sequence data</u>
<u>Pasting sequence data</u>

Copying sequence data

To copy data to the clipboard:

1. Use the mouse to select the data that you wish to copy.

2. Then select 'Copy' from the <u>edit menu</u>.

Shortcut:

 Press the 'Copy' icon on the <u>tool bar</u>.

Note:

 If no data is selected, the 'Copy' command in the <u>edit menu</u> is disabled (grayed)

Related topics:

<u>Selecting data</u>
<u>Cutting sequence data</u>
<u>Pasting sequence data</u>

 Pasting sequence data

To paste data from the clipboard into a sequence:

    1. Position the <u>caret</u> at the point in the sequence where you would like to insert the data.

    2. Select 'Paste' from the <u>edit menu</u>

Shortcut:

 Press the 'Paste' icon on the <u>toolbar</u>.

Notes:

 If no data in the target sequence is selected (highlighted), pasting will cause the data in the clipboard to be inserted into the sequence at the <u>current position</u>.

 If data in the target sequence is selected, pasting will cause the data in the clipboard to replace the highlighted data.

 If the clipboard is empty, the 'Paste' comand in the <u>edit menu</u> is disabled (grayed).

_____
Related topics:

<u>Selecting data</u>
<u>Cutting sequence data</u>
<u>Copying sequence data</u>

Deleting to the end of a sequence

To delete to the end of a sequence:

    1. Position the <u>caret</u> at the point you wish to delete from.

    2. Select 'Delete to end of seq' from the <u>edit menu</u>.

Note:

If the <u>caret</u> is positioned beyond the end of the sequence, an error message is displayed.

Removing spaces from a sequence

To remove spaces from a sequence:

1. Position the <u>caret</u> at the point in the sequence where you want the removal of spaces to start.

2. Select 'Remove spaces' from the <u>edit menu</u>.

Notes:

 If no data is selected (highlighted), spaces will be removed from the <u>current position</u> to the end of the sequence.   Spaces located at positions upstream from the <u>current position</u> will not be removed.

 If data is selected, spaces will be removed from the highlighted portion of the sequence.   Spaces will not be removed from the unhighlighted portions of the sequence.

_____
Related topics:

<u>Selecting data</u>

Inserting spaces into a sequence

To insert spaces into a sequence:

1. Position the <u>caret</u> at the point in the sequence where you want the insertion of spaces to start.

2. Select 'Insert spaces' from the <u>edit menu</u>.

3. Enter the frequency of insertion and the number of spaces to insert in the <u>Insert spaces dialog box</u>.

4. Press the OK button.

Notes:

 If no data is selected (highlighted), spaces will be inserted from the <u>current position</u> to the end of the sequence.   Spaces will not be inserted at positions upstream from the <u>current position</u>.

 If data is selected, spaces will be inserted into the highlighted portion of the sequence only.   Spaces will not be inserted into the unhighlighted portions of the sequence.

_____
Related topics:

<u>Selecting data</u>
<u>Insert spaces dialog box</u>.

 Finding text

You can search your sequence data for short substrings as follows:

1. Position the caret at the point where you wish to search from.

2. Select Find from the edit menu.   This will call the <u>Find dialog box</u>.

3. Enter the desired string in the 'Find what' field.

4. Select the 'Match case' and 'Search up' or 'Search down' options as desired.

4. Press the OK button.

Notes

If the string is found in the data, the editor will scroll to the position of the string, and the string will be selected.

To repeat a search without using the Find dialog box, select Search again from the edit menu, or press Shift+F3

Sequence analysis

Reverse
Complement
Translate in frame
Translate all
Match
Pretty display
Pattern Search

 Reverse

Reversing causes a sequence to be written out backwards.

To reverse a sequence:

1. Position the <u>caret</u> in the sequence you wish to reverse.

2. Select 'Reverse' from the <u>sequence menu</u>.

Note:

 Only nucleotide sequences (type 'N') can be reversed.   Reversing other sequence types causes an error message to be displayed.

_____
Related topics:

<u>Sequence options: name, type, and number</u>

Complement

Creates a new sequence that is the complement of the <u>current sequence</u>.

To complement a sequence:

1. Position the <u>caret</u> in the sequence you wish to complement.

2. Select 'Complement' from the <u>sequence menu</u>.

Notes:

 Only nucleotide sequences (type 'N') can be reversed.   Complementing other <u>sequence</u> types causes an error message to be displayed.

 Only the nucleotides A, G, T, C, U, R and Y are complemented.   All other <u>characters</u> are copied into the new sequence without change.

 If no data in the <u>current sequence</u> is selected, complementation begins at the <u>current position</u> and continues to the end of the sequence.

 If data in the <u>current sequence</u> is selected, complementation extends along the length of the selection only.

 If there are too many sequences open to create the new sequence, an error message is displayed.

 Translate in frame

Translate in frame predicts an amino acid sequence in the reading frame starting at the <u>current position</u>, or at the begining of the current selection.   The function creates a new protein sequence, containing the translation product shown below the translated sequence.

To translate in frame:

1. Position the <u>caret</u> in the sequence you wish to translate.

2. Select 'Translate in frame' from the <u>sequence menu</u>.

Setting the genetic code:

You may choose to use the universal genetic code or a user defined genetic code that you can edit.   To set genetic code options, select <u>Editor options</u> from the Options menu, then choose from the following:

Universal: Use the standard genetic code

User defined: Use the user defined genetic code.

Edit user defined code: Calls the <u>edit genetic code dialog box</u>.

Notes:

This function applies to type 'N' (nucleic acid) sequences   only.   If you attempt to apply this fuction to other sequence types, an error message will be displayed.

 If no data in the <u>current sequence</u> is selected, translation begins at the <u>current position</u> and continues to the end of the sequence.

 If data in the <u>current sequence</u> is selected, translation extends along the length of the selection only.

_____
Related topics:

<u>Translate all</u>
<u>Selecting data</u>

 Translate all

This function creates six new protein sequences, one for each reading frame.   The forward translation products are shown above the translated sequence, and are give names starting with a plus sign.   The reverse translation products are shown below the translated sequence, and are give names starting with a minus sign.

To translate all six frames:

1. Posistion the <u>caret</u> in the sequence you wish to translate.

2. Select 'Translate all' from the <u>sequence menu</u>..

Setting the genetic code:

You may choose to use the universal genetic code or a user defined genetic code that you can edit.   To set genetic code options, select <u>Editor options</u> from the Options menu, then choose from the following:

Universal: Use the standard genetic code

User defined: Use the user defined genetic code.

Edit user defined code: Calls the <u>edit genetic code dialog box</u>.

Notes:

This function applies to type 'N' (nucleic acid) sequences   only.   If you attempt to apply this fuction to other sequence types, an error message will be displayed.

This function is applied to the whole sequence regardless of data selection.

_____

Related topics:

<u>Translate in frame</u>

Pretty display

Pretty display is intended to provide you with a flexible way of displaying the sequences in the editor.   When you select Pretty display, all of the sequences in the editor are included. So if you want to display just one sequence, you will have to delete all the other open sequences before you select pretty display.

How to: To display your sequences with pretty display:

1. Make sure that only the sequences you want to display are open in the editor.

2. Select Pretty display from the sequence menu

To set display options:

1. Select Pretty display options from the options menu.   This calls the Pretty display options dialog box.

2. Choose from the following options:

Line length: The number of characters to display on each line.

Name field: The number of characters from the sequence names to display. For example, if the Name field is set to 8, only the first 8 characters of each sequences name is displayed.

Vert. spaces: The number of veritical spaces to place between groups of lines.

Space every: Displays the sequence in groups of n characters.   For example, if Space every is set to 10, a space in inserted after every 10th charater.

Box identities: Draws boxes around each sequence character that is identical to the character in the same position in the first sequence.   Note that this option only applies to the display of more than one sequence.   The Space every option is ignored when Box identities is selected

Numbers: Determines the placement of sequence numbering.   The options are:
   None: No numbers are displayed.

   Left: Numbers are displayed to the left of the sequence.   Note: The sequence names are not displayed when this option is choosen.

   Right: Numbers are displayed to the right of the sequence.

   Top: Numbers are displayed above the sequence.

   Bottom: Numbers are displayed below the sequence.

4. Press the OK button

Notes:

This function is applied to all sequences currently open in the editor.

 The start and end point values are not used for this function.

You can copy from the pretty display window.   Position the mouse at the point you want to start at.   Click the left mouse button and hold it down while you move the mouse.   This will draw a box.   Release the left button and select copy from the edit menu.   You can then paste the selection into your drawing program or word processor.

 Pattern Search

Pattern Search alows you to search both nucleotide and amino acid sequences for patterns using the prosite data base syntax.   The results of the search are displayed as a map in the graph window and as a table in the data window.   In addition, the sites are highlighted on the sequence in the editor.

To search for a pattern:

1. Position the caret in the sequence you wish to search.

2. Select Pattern search from the Edit menu.

3. Enter a pattern in the Pattern search dialog box.

4. Press the OK button.

Pattern syntax:

Pattern search uses the prosite data base pattern syntax as specified in the prosite database (Bairoch A., Bucher P., PROSITE: recent developments. Nucleic Acids Res. 22:3583-3589(1994)).

The patterns are described using the following conventions:

The standard IUPAC one-letter codes for the amino acids are used.

The symbol `x' is used for a position where any amino acid is accepted.

Ambiguities are   indicated by   listing the acceptable amino acids for a given position,   between square   parentheses `[   ]'. For example: [ALT] stands for Ala or Leu or Thr.

Ambiguities are   also indicated   by listing between a pair of curly brackets `{   }' the   amino acids that are not accepted at a given position. For example: {AM} stands for any amino acid except Ala and Met.

Each element in a pattern is separated from its neighbor by a `-'.

Repetition of   an element   of the pattern can be indicated by following that element   with a   numerical value   or   a   numerical   range   between parenthesis. Examples: x(3) corresponds to x-x-x, x(2,4) corresponds to x-x or x-x-x or x-x-x-x.

When a pattern is restricted to either the N- or C-terminal of a sequence, that pattern either starts with a `<' symbol or respectively ends with a `>' symbol.

Examples:

[AC]-x-V-x(4)-{ED}.

This pattern is translated as: [Ala or Cys]-any-Val-any-any-any-any-{any but Glu or Asp}

<A-x-[ST](2)-x(0,1)-V.

This pattern, which must be in the N-terminal of the sequence (`<'), is translated as: Ala-any-[Ser or Thr]-[Ser or Thr]-(any or none)-Val

Matching two sequences

Matching is used to identify data points in a sequence that are identical to the same data points at the same position in the sequence imediately above it.   Identical elements are connected by a vertical line.

For example, matching the sequence ATGACGA with the sequence ATGGATA results in a match that looks like this:

```
ATGACGA
|||||||
ATGTAGA
```

To match data from the current sequence with the sequence above, select 'Match' from the sequence menu.

Shortcuts:

Press the 'Match' icon on the tool bar.

Type the keys <CTRL>-M

Notes:

If no data in the current sequence is selected, the match extends from the current position to the end of the current sequence or the end of the sequence above, whichever is smaller.

If data in the current sequence is selected, the match extends along the length of the selection only.

If there is no sequence above the current sequence, or if there are too many sequences open, an error message is displayed.

_____
Related topics:

Selecting data

Dialog boxes

[Edit genetic code](#)
[Editor options](#)
[File open](#)
[File save](#)
[Find](#)
[Fonts](#)
[Insert spaces](#)
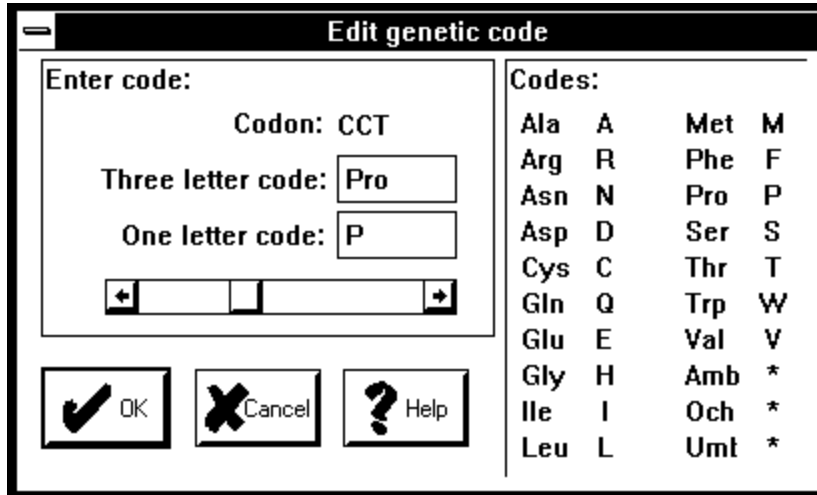[Pretty display options dialog box](#)
[Pattern search](#)
[Print setup](#)
[Print](#)
[Sequence options](#)
[Select sequence](#)

Edit genetic code dialog box

This dialog box is used to edit the user defined genetic code:

```
┌─────────────────────────────────────────────────────┐
│ ▬              Edit genetic code                     │
├─────────────────────────────────────────────────────┤
│ ┌─Enter code:──────────────┐  ┌─Codes:──────────────┐│
│ │                          │  │ Ala   A    Met   M  ││
│ │      Codon: CCT          │  │ Arg   R    Phe   F  ││
│ │                          │  │ Asn   N    Pro   P  ││
│ │ Three letter code: │Pro │ │  │ Asp   D    Ser   S  ││
│ │                          │  │ Cys   C    Thr   T  ││
│ │ One letter code:   │P   │ │  │ Gln   Q    Trp   W  ││
│ │                          │  │ Glu   E    Val   V  ││
│ │  ◄────────█──────────►   │  │ Gly   H    Amb   *  ││
│ └──────────────────────────┘  │ Ile   I    Och   *  ││
│                                │ Leu   L    Umt   *  ││
│ ┌──────┐ ┌──────┐ ┌──────┐    │                     ││
│ │✔ OK  │ │✖Cancel│ │? Help│   └─────────────────────┘│
│ └──────┘ └──────┘ └──────┘                           │
└─────────────────────────────────────────────────────┘
```

Enter code:

    Codon: Displays the current codon.

    Three letter code: Enter the three letter code for the residue you wish to associate with the current codon.

    One letter code: Enter the one letter code for the residue you wish to associate with the current codon.

    Scroll bar: Sets the current codon. Use the scroll bar to scroll through the availble codons.

Codes:

    Lists the standard three and one letter codes for reference purposes.

_____
Related topics:

Editor options
Translate in frame
Translate all

 Editor options dialog box

Use this dialog box to set editor options to change the appearance of the editor, or to determine what genetic code is used in the translation of nucleic acid sequences.   The editor options are:

Lines:

> **Line length:**   Sets the number of characters displayed on each line.   The line length must be an even mutlple of 10, and may not be greater than 250.

> **Name field width:**   Sets the number of characters displayed of the name of each sequence.   The name field width may be any number bewteen 0 and 16.   If the name field width is less than the number of characters in the name of a sequence, the name is truncated.

Non-scrolling position line:

> **Always on:**   Non-scrolling position line   displayed at all times.

> **Always off:**   Non-scrolling position line of at all times.

> **On when screen full:**   Non-scrolling position line   line displayed only when there are too many sequences to fit on the screen.

Genetic code:

> **Universal:**   Use the universal genetic code for translation of DNA sequences.

> **User defined:**   Use the user defined genetic code for translation of DNA sequences.

> **Edit user defined code:**   Calls the edit genetic code dialog box.   Alows you to edit the

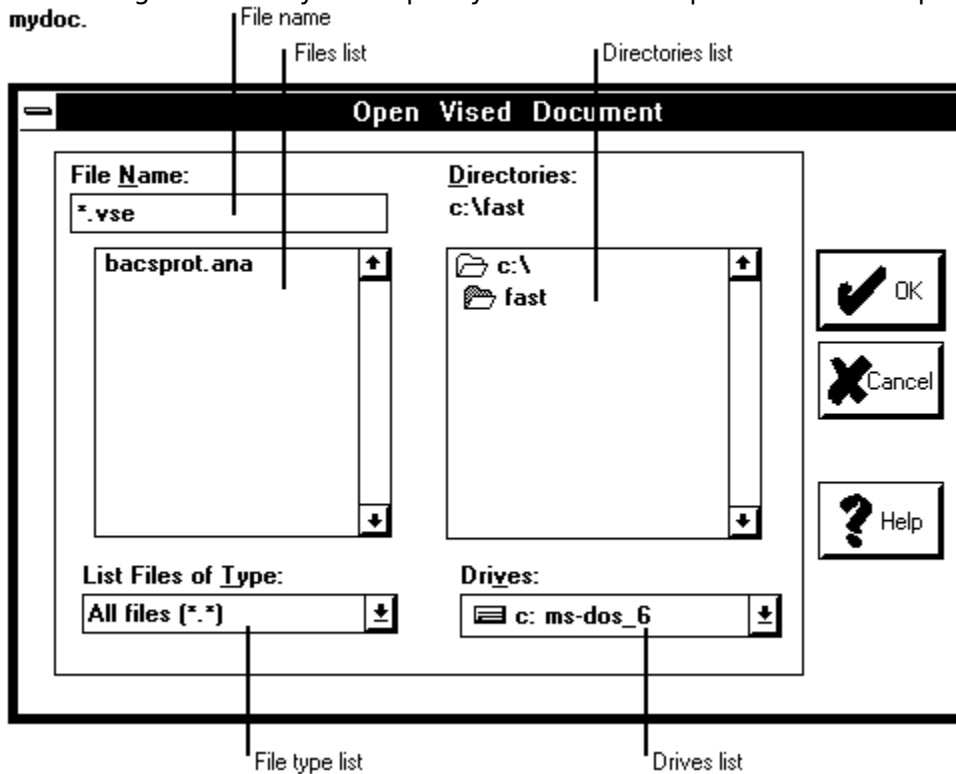genetic code used when the user defined option is selected.

_____

Related topics:

<u>Editor options</u>

File open dialog box

This dialog box alows you to specify the name and path of a file to open.

File Name

Type or select the filename you want to open.

Files list

This box lists files with the extension you select in the List Files Of Type box.   Click once on a file name in this box to place the file in the file name box.   Click twice to open the file.

Note: To see a list of files with a particular extension, type an asterisk (*), a period, and the three-character extension in the File name box. For example, if you want to see all files with a .TXT extension in a directory, type *.txt.

List Files Of Type

Select the type of file you want to open.

Drives

Select the drive that has the file that you want to open.

Directories

Select the directory that has the file that you want to open.

OK button: Opens the file in the file name box.   If the file name in the name box is not complete, the OK button is ignored.

Cancel button: Closes the dialog box without opening the file.

_____
Related topics:

Opening an existing document
Importing a sequence

Pretty display options dialog box

Title:

Sets the title displayed at the top of the pretty display window.

Line length:

The number of characters to display on each line.

Name field:

The number of characters from the sequence names to display. For example, if the Name field is set to 8, only the first 8 characters of each sequences name is displayed.

Vert. spaces:

The number of veritical spaces to place between groups of lines.

Space every:

Displays the sequence in groups of n characters.   For example, if Space every is set to 10, a space in inserted after every 10th charater.

Box identities:

Draws boxes around each sequence character that is identical to the character in the same position in the first sequence.   Note that this option only applies to the display of more than one sequence.   The Space every option is ignored when Box identities is selected

Numbers:

Determines the placement of sequence numbering.   The options are:

None: No numbers are displayed.

Left: Numbers are displayed to the left of the sequence.   Note: The sequence names are not displayed when this option is choosen.

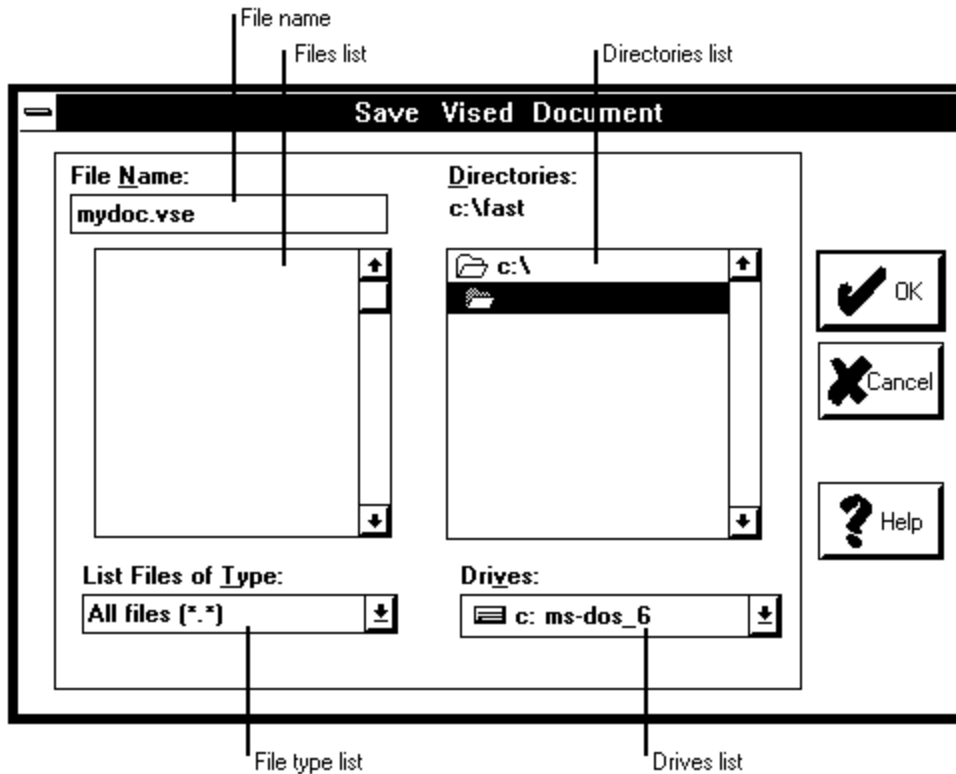**Right**:   Numbers are displayed to the right of the sequence.

Top: Numbers are displayed above the sequence.

Bottom: Numbers are displayed below the sequence.

File save dialog box

This dialog box alows you to specify the name and path of a file to save.

File Name

Type or select the filename you want to save.

Files list

This box lists files with the extension you select in the List Files Of Type box.   Click once on a file name in this box to place the file in the file name box.   Click twice to save the file.

Note: To see a list of files with a particular extension, type an asterisk (*), a period, and the three-character extension in the File name box. For example, if you want to see all files with a .TXT extension in a directory, type *.txt.

List Files Of Type

Select the format that you want the file to be saved under.

Drives

Select the drive that you want the file to be saved to.

Directories

Select the directory that you want the file to be saved to.

OK button

Saves the file in the file name box.   If the file name in the name box is not complete, the OK button is ignored.

Cancel button

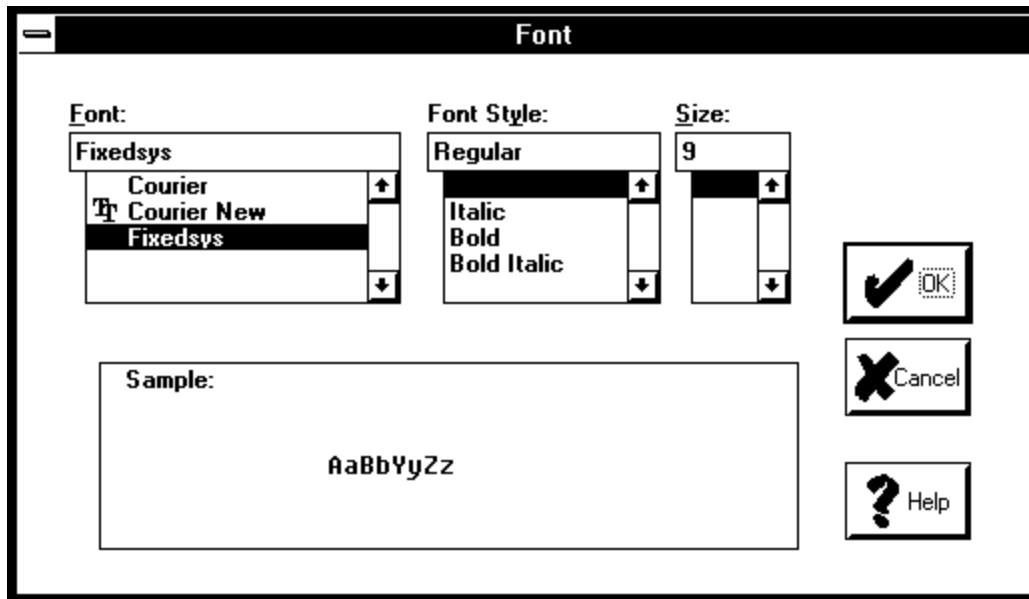Closes the dialog box without opening the file.

_____

Related topics:

<u>Exporting a sequence</u>
<u>Saving a document</u>

Fonts dialog box

This dialog box alows you to set a font for a given window or for the title displayed in the graph window.

Font

> The name of the font.   You can type the name in the font edit box, or you can select a font from the font list box by clicking on it with the left mouse button.

Font Style

> The style of the font.   You can type the style in the font style edit box, or you can select a style from the style list box by clicking on it with the left mouse button.

Size

> The size of the font.   You can type the size in the font size edit box, or you can select a size from the font size list box by clicking on it with the left mouse button.

Sample

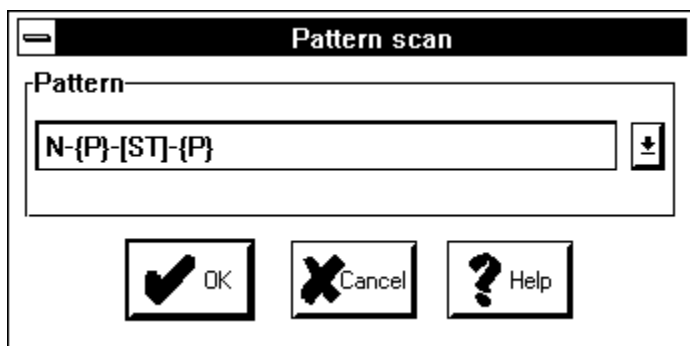> Displays a sample of what your selected font will look like.

_____
Related topics:

Selecting fonts

Pattern search dialog box

This dialog box alows you to enter the pattern you wish to search the current sequence with.

Pattern: Enter the search pattern using the prosite data base syntax (see <u>Pattern search</u>). To choose a   recently used pattern, press the down arrow, select the desired pattern with the mouse and press OK.
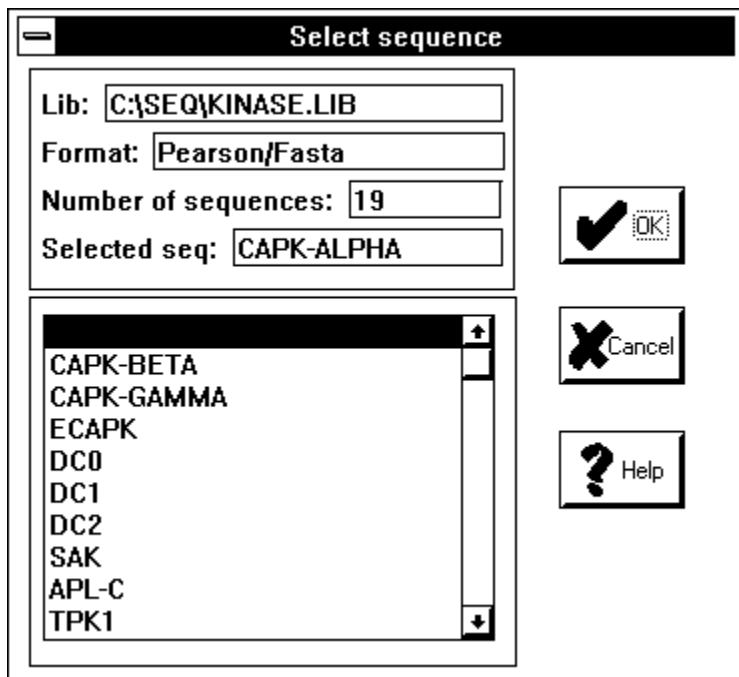
_____

Related topics:

<u>Pattern search</u>.

Select sequence dialog box

This dialog box alows you to select a sequence to be imported from a library.

Sequence information:

    Lib: Name of the library file.

    Format: Format of the library file.

    Number of sequences: Number of sequences in the file.

    Selected seq: The currently selected sequence.

Sequence list:

    Lists the sequences in the library.   To select a sequence to import, scroll the list until the desired sequence name is visible, click on the sequence name with the mouse and press OK.
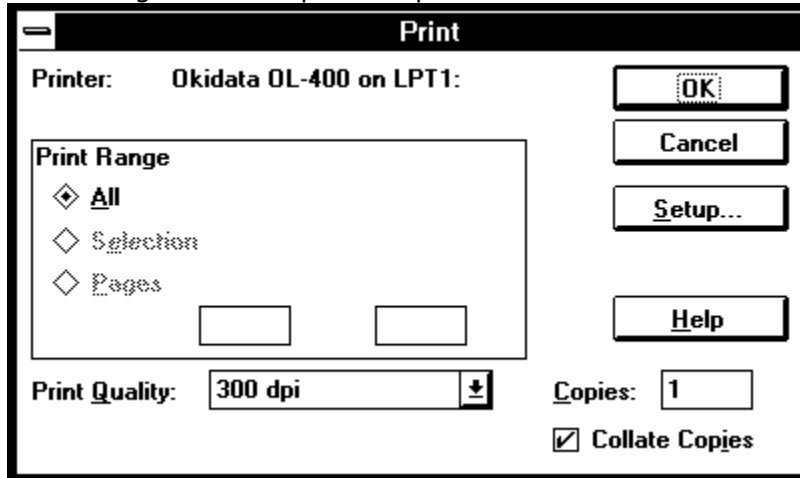
_____

Related topics:

Importing sequences.

Print dialog box

This dialog sets basic printer options.

Printer

   Displays the currently selected printer.

Print Range

   All: Print the whole document, table or graph.

   Selection: Print the selected parts of the document only.

   Pages: Print the specified pages only.

Print Quality

   Sets the printer resolution.

Copies

   Sets the number of copies to print.

Collate copies

   Sort copies.

Setup

   Calls the Print setup dialog box.   Selects the printer and sets printer options.
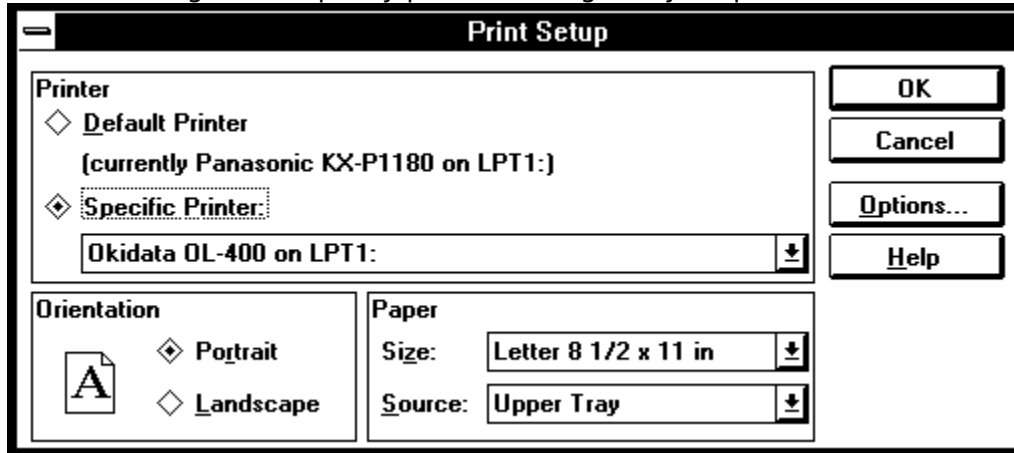
_____

Related topics:

Printing

Print setup dialog box.

Workplace **Print setup**

Use this dialog box to specify printer settings for your printer.

```
┌─────────────────────────────────────────────────────────────────┐
│ ▬                        Print Setup                             │
├─────────────────────────────────────────────────────────────────┤
│ ┌─Printer──────────────────────────────────────┐   ┌──────────┐ │
│ │ ◇ Default Printer                            │   │    OK    │ │
│ │   (currently Panasonic KX-P1180 on LPT1:)    │   └──────────┘ │
│ │ ◆ Specific Printer:                          │   ┌──────────┐ │
│ │   ┌────────────────────────────────────────┐ │   │  Cancel  │ │
│ │   │ Okidata OL-400 on LPT1:              ▼ │ │   └──────────┘ │
│ │   └────────────────────────────────────────┘ │   ┌──────────┐ │
│ ├──Orientation──────────┬──Paper───────────────┤   │ Options… │ │
│ │          ◆ Portrait   │ Size:  ┌───────────┐▼│   └──────────┘ │
│ │   ┌───┐               │        │Letter 8 1/2 x 11 in│ ┌──────┐│
│ │   │ A │  ◇ Landscape  │ Source:┌───────────┐▼│   │  Help  ││
│ │   └───┘               │        │Upper Tray │ │   └────────┘│
│ └───────────────────────┴──────────────────────┘               │
└─────────────────────────────────────────────────────────────────┘
```

Printer

   Default Printer: Use the printer that you defined as the default printer from the windows control panel.

   Specific Printer: Select a printer other than the default.   Note: you must install printers from the windows control panel before you can select them with this dialog box.

Orientation

   Portrait: Print using the portrait orientation (height is greater than width).

   Landscape: Print using the landscape orientation (height is greater than width).

Paper

   Size: Select the size of the paper used.

   Source: Select the source of the paper for printers that use more than one source.

Options

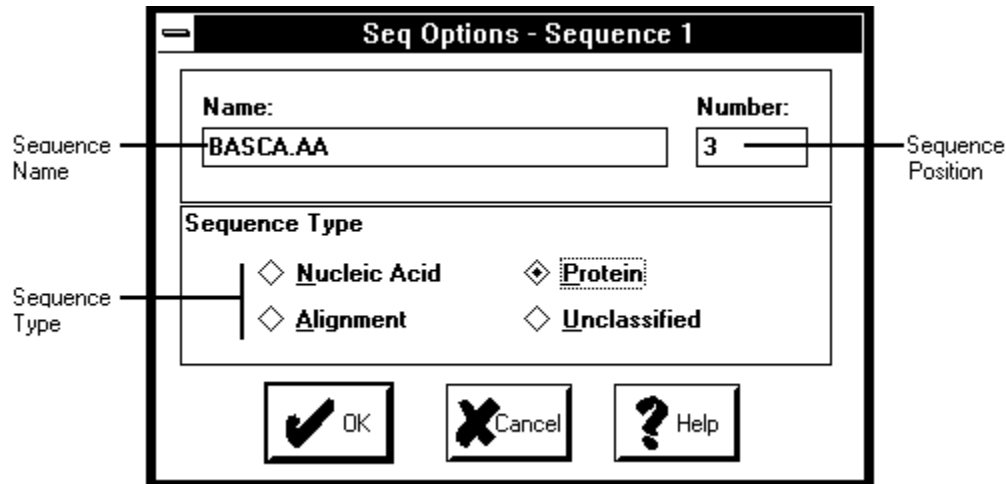   Specify other, printer specific options.

───────────────
Related topics:

Print dialog box
Printing

Sequence options

This dialog box alows you to change options that apply to the current sequence only.

Name

Displays the sequence name.   You can enter a name of up to 15 characters.   Note that the name may be truncated on the screen if the name field width is set to less than 15.

Number

Displays the sequence postion on the screen.   Entering a new postion will cause the sequence postion to change.

Sequence type

To set the sequence type, click on the option you want.

_____
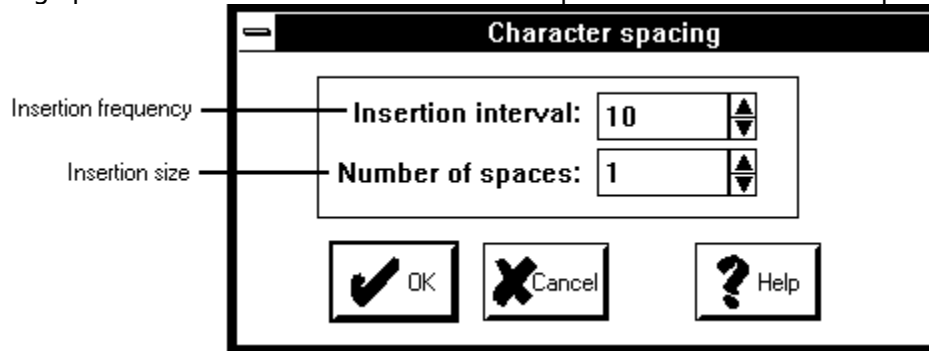
Related topics:

Sequence options: name,   type, and number

Insert spaces

This dialog box alows you to insert spaces into a sequence in a regular pattern.   Any existing spaces are first removed from the sequence before the new spacing is applied.

Insertion interval
    Displays how often spaces are to be inserted.

Number of spaces:
    Displays how many spaces are to be inserted.

Example: If you enter an insertion interval of three, and Number of spaces of two, two spaces will be inserted between every third character.
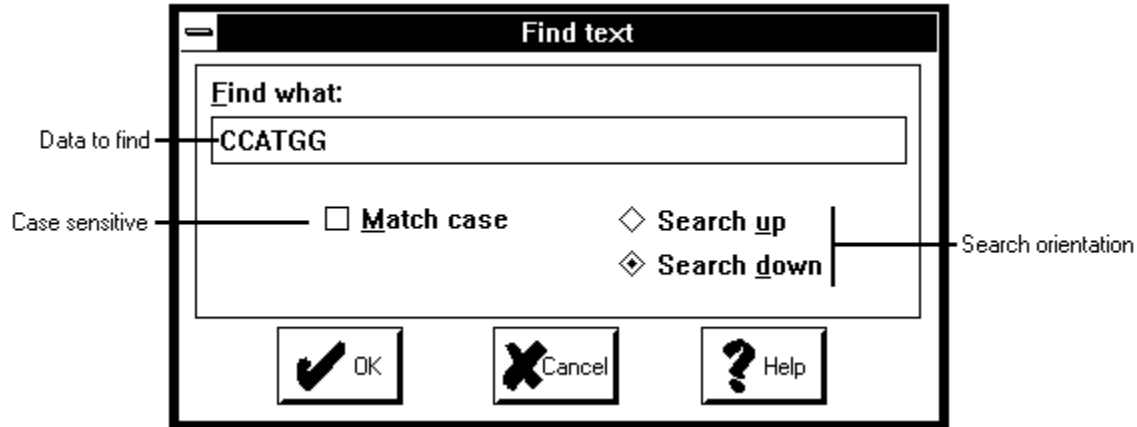
_____
Related topics:

Inserting spaces into a sequence
Removing spaces from a sequence

Find

Use this command to search for specified text in the current sequence.

Find What

Type the text you want to find, or paste it from the Clipboard (CTRL+V).

Match Case

Select this option to find only those occurrences with the combination of uppercase and lowercase letters specified in the Find What box.

Direction

Up: Searches from the insertion point or the end of the selection to the beginning of sequence.

Down: Searches from the insertion point or the beginning of the selection to the end of the sequence.

Information

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Registration

Vised is ShareWare

Vised is "ShareWare".   This entitles you, the customer, to try out the software for up to 30 days without obligation to pay for it.

Shareware (non-registered) Vised is a "full" version.   This means that the same capabilities available in the registered software are present in the non-registered software.   In fact, the non-registered software includes a bonus feature - the shareware nag box

If you use Vised beyond the 30 days, you should register it.   Registration entitles you to free upgrades to the software, which is nice.

How Much Does It Cost To Register?

Registering Vised costs you only $30.00 US.   If you are part of an organization and wish to use several copies, greatly reduced site licensing rates are also available.

How To Register

To register, please print out a registration form and send it to:

Ken Peters
487, Aquila Place
Parksville, BC
Canada.
V9P 1C1

Before you register, please take a look at the Licensing section of this help file.

Unlocking the Software

You will receive a notification of registration   which contains your personal registration name and number.

First, bring up the Reigistration Dialog by first invoking About dialog box, then clicking on the Register button.

Enter your name in the registration dialog.   Be sure to type your name exactly as it appears in your notification, as capitalization, spaces and punctuation are all taken into account when computing your registration number.

Now enter your personal registration number, and select Register   If all is well, Vised will respond with a message thanking you for your registration.   Otherwise Vised will complain that your name and number don't match, and you will have to correct the information.

Software Distribution and Licensing Information

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This shareware software may be freely distributed, provided that:

(1) Such distribution includes only the original archive.   You may not alter, delete or add any files in the distribution archive.

(2) The distrubution does not include a registration number.   In particular, you may not distrubute a registered version of Vised.

(3) No money is charged to the person receiving the software, beyond reasonable cost of packaging and other overhead.

License

By receiving and/or using Vised, you accept the following Evaluation and Registered User Agreement.   This agreement is a binding legal agreement.   If you do not intend to honor this agreement, remove Vised from your computer now.

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Credits

Vised uses sequence import and export functions from Readseq (c) 1990 by Don Gilbert. Thank you, Don for making those functions public!

The multi-sequence editor format used by Vised was inspired by the DOS program, esee, by Eric Cabot.

About Vised

About the author:

> I have a Ph.D. in genetics from the University of British Columbia.   About Three years ago, I decided to stay home with my kids.   In order to keep myself from going crazy, I taught myself how to program and wrote this and several other pieces of software.   I am open to job offers...

How to contact the author:

> **e-mail:**   kpeters@qb.island.net

Version history:

> **Version 1.0** - May 1996.
>   -Initial release.

> **Version 1.0a** - July 1996.
>   -Fixed file open bug that caused vised to crash when the file contained too many
>   sequences.
>
>   -Increased number of sequences from 20 to 30.

> **Version 1.1** - September, 1996
>   -Fixed resource leak in pretty display.
>
>   -Fixed bug that caused loss of pretty display title on setting window focus.
>
>   -Increased number of sequences to 200.
>
>   -Changed scrolling from block-by-block to line-by-line so that more sequences
>   than would fit on the screen at one time could be displayed.
>
>   -Added a non-scrolling position line to aid in navigation when more than a screen
>   full of sequences are open.
>
>   -Added navigation buttons and keyboard shortcuts.

Upcoming:

> Version 2.0 will add the following features:
>
>   - User-definable color display of bases.
>
>   - Support for standard codon tables.
>
>   - Option to turn off line-wrap so that sequences can be displayed on one long line.
>
>   - Support for third party applications.

Registration form

Please print this form, fill it out and send it to:

        Vised
        487 Aquila Place
        Parksville, BC
        Canada
        V9P 1C1

Name_____ Date_____

Company_____ Phone_____

Street_____ FAX_____

City_____ Country_____ ZIP/Postal code_____

Email_____ ___

            ALL AMOUNTS ARE UNITED STATES DOLLARS

SINGLE USER LICENSE: @ $30.00   = _____

SITE LICENSE: Must supply a proper business name.
   3 to 9 computers   @ $21.00 each X ____units   = _____
  10 to 29 computers ...@ $19.00 each X ____units   = _____
  30 to 99 computers   @ $15.00 each X ____units   = _____
 100 & up computers   @ $11.00 each X ____units   = _____

        Total (US funds only)   _____

Method of payment: Cheque__   Money order__
                    Purchase order__   Credit card__

Purchase order number: (universities only)_____

Credit card:

Mastercard__ VISA__

Name exactly as on credit card _____

Card Number_____ Exp.Date_____

Signature_____