

MacVector[®] 10.0.2

for Mac OS X

System Requirements

MacVector 10.0.2 runs on any PowerPC or Intel Macintosh running Mac OS X 10.3 or higher. This release is a Universal Binary, meaning that it runs natively on both PowerPC and Intel based Macintosh computers. There are no specific hardware requirements for MacVector – if your machine can run OS X 10.3, it can run MacVector. A complete installation of MacVector 10.0 uses approximately 110 MB of disk space.

Changes for MacVector 10.0.2

Crashes when editing annotations and features under OS X 10.3.9 have been fixed.

MacVector now writes EMBL format files in the "new" format and can automatically read EMBL files in either the "new" or "old" format.

<Shift> button editing functions have been added to the Multiple Sequence Alignment editor.

New Nucleic Acid and Protein windows now default to the Editor tab.

Changes for MacVector 10.0.1

MacVector 10.0.1 is primarily a bug fix release. It is a complimentary upgrade for all users of MacVector 10.0. When you install MacVector 10.0.1 it will replace your existing copy of MacVector 10.0. The following changes have been made to MacVector 10.0.1;

Crashes while editing certain chromatogram (trace) files have been fixed.

The graphics palette "Filter" button now works as documented

The ability to jump to specific restriction enzymes in the restriction enzyme editor by typing a few characters has been restored.

The Restriction Enzyme Map Results window is now fully interactive - you can copy/paste into selected restriction enzyme sites just as you could with MacVector 9.5.

EMBL file import has been reworked to handle the latest changes in the format.

When you select a feature in the Map tab, MacVector now scrolls all replica windows to reflect that same selection. A number of other selection bugs have been fixed so that all replica windows and tabs now correctly reflect the current selection.

A long standing bug where subsequence searches would show the wrong location of the match in the graphic result window has been fixed.

Handling of the /note qualifier has been dramatically improved. There is a new "Free-form" tab in the Feature Editor that allows you to enter any text which will then be assigned to the /note qualifier. The problem seen previously where the /note qualifier would get duplicated has been fixed. Finally, the display of labels in the Map tabs has been modified so that features with only a /note qualifier are labeled with the contents of the qualifier, not the entire description.

Find and Jump To now work in the Contig, Sequence Confirmation and Trace Editor windows.

The Range edit box is now updated in real time and includes the length of the selected region.

The first click on an inactive MacVector window no longer modifies any selection in that window.

A number of issues with the new Primer3 parameters have been fixed.

Sassafras Network licensing errors are now handled correctly. Also, Assembler licenses are no longer checked out if the machine does not have an Assembler-enabling activation code installed.

Crashes when editing Restriction Enzymes under OS X 10.3 have been fixed.

Problems selecting databases in Entrez searches under OS X 10.3 have been fixed.

A number of issues related to copy/pasting sequences to/from the Multiple Sequence Alignment Editor have been resolved.

Several issues with the graphical display have been cleaned up - the "Single Arrow" graphic no longer gets compressed at low resolution and the zoom function no longer changes the currently selected line length of the graphics display. The "Fit in Window" scaling popup menu now works the same as it did in MacVector 9.5.

Several selection/highlighting glitches have been fixed in the Phylogenetic Tree viewer.

Changes for MacVector 10.0

Licensing Changes

This release of MacVector no longer supports the use of USB Eve3 hardware keys for copy protection. There is a new replacement licensing implementation that ensures that only one copy of MacVector with a given serial number can be running on a network at any one time. All installers now create a temporary license so that you have 30 days to activate the full license. This can be done at any time by choosing "Activate License..." from the "Options" menu. If you believe you are entitled to a license and you have not already been contacted by MacVector, Inc, please send an e-mail to support@macvector.com with the license owners name and original serial number.

OS X Toolbars

All of the primary windows in MacVector have been rewritten to use OS X-style toolbars. This includes the following windows;

Sequence editor, multiple sequence alignment editor, enzyme editor, subsequence editor, map/graphics window, phylogenetic tree window, matrix editor, trace/chromatogram editor, sequence confirmation editor, contig editor and assembly project window. The text and PICT result windows do not use toolbars.

Tabbed Windows

To reduce screen clutter and simplify the interface, many of the common windows in MacVector 10.0 have been combined into a single window with tabbed views. For most windows, a "Replica" toolbar button lets you open a second window for those times when you need to see more than one tab at a time.

Sequence Window. This now has Editor, Map, Features and Annotations tabs. The corresponding toolbar buttons from the editor window have been removed as they are no longer needed.

Trace/Chromatogram Window. This now has Editor, Map, Features and Annotations tabs.

Sequence Confirmation Window. This now has Editor, Map, Features and Annotations tabs.

Multiple Sequence Alignment Window. The multiple alignment result windows (Text, Pairwise, Matrix, Picture, Guide Tree) have now been added as separate tabs to the main editor window.

Contig Window. This now has Editor, Map, Features and Annotations tabs.

Feature Editing

The feature list has been rewritten to use OS X style lists. This removes the old 8,000 feature limit in earlier versions of MacVector.

The feature editor has been completely rewritten to directly support Genbank qualifiers as well as keywords.

You can now use the “Find” function to search sequence features based on type and/or text appearing in features or qualifiers.

Primer3

There is a new primer design function in MacVector 10.0. This is based on the popular Primer3 algorithm and is accessed through the Analyze->Primers sub menu.

The default Primer3 implementation lets you choose a region to amplify and will automatically find the best 5 pairs of primers. You can also find primers based on product size or by defining flanking regions.

There is an option to have Primer3 find a third “Hybridizing Primer” for use in real-time PCR.

You can also specify your own primer(s) and have Primer3 evaluate them for suitability.

The results are displayed in tabular and graphical format. The views are interactive and linked to the parent sequence so that you can select primers and/or products and copy/paste to other windows or use to create new features on the sequence.

Automatic Restriction Enzyme Searching

You can now have sequences be automatically scanned for restriction enzymes and have these displayed in the default map view. This is configured from the revised Graphic Options dialog, now accessible from a new Preferences button on the Map tab toolbar. By default, this is set to use selected enzymes in the “Common Enzymes” file.

This dramatically simplifies the use of MacVector for “click cloning”. You can open a source destination sequence, click on the appropriate restriction sites, choose Edit->Copy to copy the fragment, and paste directly into a matching site in a suitable target sequence.

Miscellaneous Changes

Menu options are no longer disabled when a target sequence is locked. Instead, you are prompted to allow automatic unlocking when you try to invoke a function that would modify the document.

You can now save sequence features in a format suitable for use in the NCBI Sequin program for submitting sequences to Genbank. Choose File->Save As... and select the Sequin Feature Table format.

There is a new toolbar option in the Sequence Confirmation and Contig Editor windows to display 3 or 6 frame translations underneath the consensus sequence.

The Entrez Browser window now supports searching of all available databases at the NCBI, although you can still only directly retrieve sequence entries or PubMed documents. A new preview pane contains a

direct web interface to the NCBI web site to view and open non-sequence related links. All downloads now occur as a job in the background, particularly useful as MacVector can now download the large “contig” entries that may contain many MegaBases of sequence.

Support information

For assistance with MacVector, please contact your local MacVector, Inc office. You will need a current MacVector maintenance contract to be eligible for technical support other than for basic installation problems. New sales of MacVector include 12 months of support that also entitles you to any upgrades to MacVector released during the maintenance period.

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When contacting Customer Support with a technical problem, please be prepared to give your product serial number as well as a detailed description of your problem and any error messages you encounter. Visit the MacVector Web site for details of any available updates, and any relevant information that could not be added to these release notes in time for publication:

<http://www.macvector.com>

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