

# MacVector 12.7.5

## for Mac OS X

### System Requirements

MacVector 12.7 runs on any PowerPC or Intel Macintosh running **Mac OS X 10.5** or higher. It 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 10.5 or above, it can run MacVector. A complete installation of MacVector 12.7 uses approximately 167 MB of disk space.

### Installation and License Activation

Install MacVector 12.7 by double-clicking on the MacVector 12.7.5.pkg installer application. You will be prompted for a system administrator account and password during installation. Once installation is complete, you must enter a valid license owner, serial number and activation code the first time you run MacVector. This information is usually sent by e-mail and is also printed on the inside of the CD sleeve. If you previously installed an earlier version of MacVector and have a serial number with a maintenance end date of Sep 1<sup>st</sup> 2012 or later, MacVector 12.7 will automatically use your existing license and you will not be required to enter the details again.

### Changes for MacVector 12.7.5

#### Bug Fixes

**Edit | Cut** now places the cut fragment on the global pasteboard

Some long term issues pasting copied fragments containing truncated features that cross the origin of circular molecules have been resolved.

Double-headed arrow features are now displayed correctly at the residue level.

Features created from a selection where one end is formed from a restriction site that crosses the circular origin are now correctly created and saved.

A few issues creating and reading .sqn and .tbl files for use with Sequin have been fixed.

### Changes for MacVector 12.7.4

#### Deprecated Functions

This is the last release of MacVector that will retain the now obsolete **Find PCR Primer Pairs** and **Test PCR Primer Pairs** functions. All of the functionality in these interfaces have been replaced by, and improved upon, by the **Primer Design (Primer3)** and **Quickest Primer** functions. For more information on using these new functions, take a look at the [Primer Design Tutorial.pdf](#) tutorial that you can find in the `/Applications/MacVector 12.7/Documentation/` folder.

#### Bug Fixes

Contigs generated by phrap assembly now have quality values.

You can now use the Find function to search for gaps (make sure you have the “Literal” checkbox selected).

A one-out bug displaying the [size] metatag label in Map views has been fixed.

Protein sequences no longer display spurious text in the feature labels.

Restriction enzyme sites are now correctly regenerated on the cloning clipboard when creating constructs in the flipped orientation.

Some display glitches drawing restriction enzyme sites when zoomed in to the origin of a circular plasmid have been fixed.

Restriction sites where the cut location is just before the first residue of the sequence are not correctly reported.

We have coded a workaround to enable saving to Windows 2008R2 servers.

## **Changes for MacVector 12.7.3**

### **Bug Fixes**

Primer3 now works as expected on Mac OS X 10.8.

## **Changes for MacVector 12.7.2**

### **Bug Fixes**

A problem where Align To Reference projects saved on OS X 10.5 could not be reopened has been resolved.

Chromatogram files can now be opened on PowerPC machines.

A bug causing phrap assemblies to occasionally fail with certain filenames has been fixed.

## **Changes for MacVector 12.7.1**

### **Bug Fixes**

A bug where the numbering of the alternative binding sites in the Quicktest Primer dialog was incorrect for sequences with a non-zero origin has been fixed.

A crash problem deleting reads extending beyond the end of the reference sequence in an Align To Reference alignment has been fixed.

Creating a misc\_feature from a subsequence analysis result window no longer adds an additional residue to the end of the feature.

The reaction conditions parameters are now correctly shared with all algorithms that need to calculate melting temperatures.

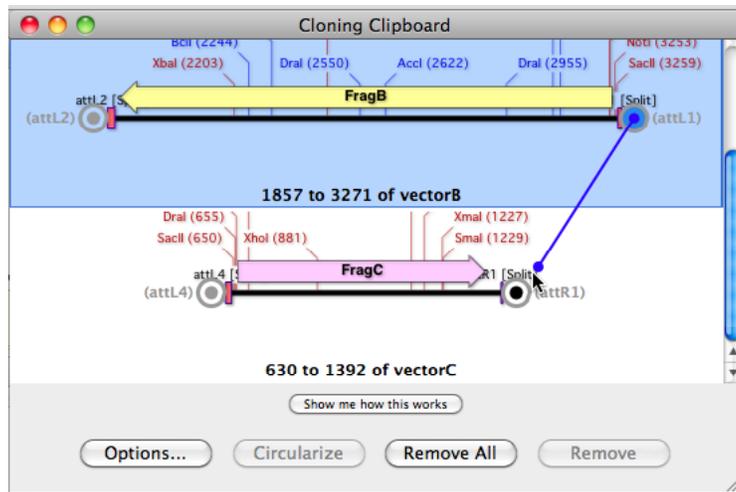
You can now run Primer3 on sequences with a negative origin.

## **Changes for MacVector 12.7**

### **Cloning Clipboard**

There is a new window called the **Cloning Clipboard** that can be opened and closed

from the **Window** menu. Whenever a restriction fragment is generated using the **Digest** button (or **Edit | Digest** menu item), the fragment is placed on the cloning clipboard. You can then join fragments on the clipboard by selecting the end of one fragment and dragging it onto the end of another fragment;



When you release the mouse over an end, you are presented with a dialog that lets you fill or cut back ends if you wish. Finally, after building up a molecule from multiple pieces, you can click on the circularize button to create a new circular molecule, or just double-click on a fragment to open it in a new MacVector sequence window. For more information, check out the file `Cloning Clipboard Tutorial.pdf` in the `/Applications/MacVector 12.7/Documentation/` folder.

### Optimized Reverse Translations

There are new options in the **Analyze | Reverse Translation** dialog, allowing you to optimize codon usage when reverse translating a protein. You can now request that the generated DNA sequence uses only the most popular codons from a given codon bias file, or that the generated sequence should have an overall codon usage that most closely matches that file.

### Align To Reference Performance Enhancements

A number of operations in the **Align To Reference** functionality have been optimized to be of more use for aligning large numbers of Next Generation Sequencing reads against large genomes. Importing reads is now very much faster (in many cases 100x faster) and aligning reads is from 5x to 50x faster. With the appropriate parameters, you can now align several hundred thousand reads against a typical bacterial chromosome in just a few hours. Individual edits in the **Editor** tab with several hundred thousand reads are now effectively instantaneous (previously they could take many minutes while the consensus was recalculated). In addition the text in the **SNP** tab is generated anywhere from 10x to 1,000x faster than previously. Finally, although generation of the text in the **Text** tab has also been significantly speeded up (again up to 1,000x) it also now runs as a separate thread so you can cancel the operation if it takes too long.

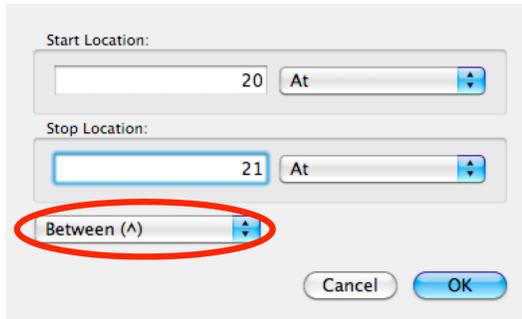
### MacVector Free

One major change that will primarily affect users of the trial version is that, starting with MacVector 12.7, once a trial license expires, MacVector will no longer simply refuse to run. Instead, MacVector will continue to run, but all of the functions in the **Analyze**

menu become disabled. This means users can still open, edit, save and print MacVector documents, or save MacVector files in other formats. They can still perform simple click cloning operations (but not the new **Cloning Clipboard**), generate new constructs and have full control over the appearance of features. **Entrez** and **BLAST** are still available along with the **Find** functionality. This will let licensed users share MacVector files and data with more casual users without having to convert sequences into a common format, often losing information (such as graphical appearance and layout) in the process.

### Miscellaneous Changes/Bug Fixes

You can now create a feature “between residues” which can be displayed as a line graphic in the **Map** tab.



The image shows a dialog box with the following fields and controls:

- Start Location:** A text input field containing the number "20" and a dropdown menu set to "At".
- Stop Location:** A text input field containing the number "21" and a dropdown menu set to "At".
- Feature Type:** A dropdown menu with the option "Between (^)" selected and highlighted by a red oval.
- Buttons:** "Cancel" and "OK" buttons at the bottom right.

If you subsequently select that feature the caret becomes positioned between the residues in the **Editor** tab.

Updated Short Protein Motifs.psub file. Thanks to Dr Peter Friedman, this subsequence file has been updated with many more useful entries.

Updated Gateway att sites. The att sites in the Gateway.renz and Common Enzymes.renz file have been updated to be more discriminating and to support newer att3, att4 and att5 vectors.

The installer is now signed with a MacVector, Inc certificate to prevent OS X 10.7 and later from warning that the installer is not from a trusted source.

## 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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