

MacVector 13.0.7

for Mac OS X

The online updater for this release is 43.5 MB in size

System Requirements

MacVector 13 runs on any Intel Macintosh running **Mac OS X 10.6** or higher. There are no other specific hardware requirements for MacVector – if your machine can run OS X 10.6 or above, it can run MacVector. A complete installation of MacVector 13 uses approximately 172 MB of disk space.

Installation and License Activation

Install MacVector 13 by dragging the MacVector folder onto the Applications folder. You may be prompted for a system administrator account and password during this copy. You can then optionally drag the “Shortcut” icon for the MacVector application itself onto your desktop or onto the Dock for easy access. Don’t worry if the shortcut icon appears blank, it will reset to a MacVector icon the when you first run it. 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 but is also printed on the inside of the CD sleeve if you opted to receive MacVector on physical media. If you previously installed an earlier version of MacVector and have a serial number with a maintenance end date of November 1st 2013 or later, MacVector 13 will automatically use your existing license and you will not be required to enter the details again.

Changes for MacVector 13.0.7

Bug Fixes

We FINALLY tracked down the bug that some of our European customers have been seeing with the multiple alignment color groups! Thanks for your patience on that one, it was related to using French/German/Spanish localization.

The residues that appear on the Y axis of a “dot plot” matrix when zoomed in to the residue level are now displayed correctly on all versions of Mac OS X.

Changes for MacVector 13.0.6

Bug Fixes

Velvet now correctly honors the Long Read Threshold setting to distinguish between short and long reads..

The codon usage table information is now reset between runs.

A bug that caused the DNA color group values to get cleared has been fixed. There may still be another intermittent bug that some users have reported that we have not been able

to reproduce.

An intermittent crash when repeating certain analysis functions has been fixed.

Changes for MacVector 13.0.5

Bug Fixes

The **Multiple Sequence Alignment (MSA) Editor** no longer has missing regions in the display when in linear mode with blocking switched on.

Printing from the **MSA Editor** and **MSA Picture** tabs has been improved for multiple-page printing.

Changes for MacVector 13.0.4

Bug Fixes

The **Multiple Sequence Alignment Editor** “name” pane can now be resized much narrower to reduce white space when printing.

A crash when deleting the entire contents of the Annotations “Comments” section has been resolved.

The **Align To Reference** and **Contig Editor Map** tabs now calculate and display the selected range (bp) in the **Range** toolbar item.

Clicking to deselect in the **Map** tab when in “sequence select” mode no longer scrolls back to the top.

The **Test Sequencing Primer** function no longer crashes if multiple alternate binding sites are present in the target sequence.

Changes for MacVector 13.0.3

Bug Fixes

BLAST now works on OS X 10.6

A crash when opening multiple sequence alignment files containing terminator characters (*) has been fixed.

A problem where features with no description could crash MacVector has been fixed.

Changes for MacVector 13.0.2

Bug Fixes

A critical crash bug encountered during delete/paste/reverse+complement operations in feature-rich sequences has been fixed.

Repeat invocations of the **Analyze | Translate** function now work as expected.

Zooming in the **Map** tab of sequences when the line length is set to “unlimited” now works correctly.

Base Composition plots have been re-enabled.

Changes for MacVector 13.0.1

Bug Fixes

A bug where inserting a single residue using the trace editor would insert 99 residues has

been fixed.

The various *Fit To Printer Page* actions in MacVector (**Preview** in the single sequence **Map** tab, the **Fit To Print** options in the Chromatogram editor and the **Fit To** options in the Phylogenetic Tree Window) now all respond correctly after **Page Setup** has been used to change paper or print orientation.

The correct primer is now copied after sorting then copying primers in the **Primer Design Spreadsheet** window.

The feature numbering in the **Features** tab now correctly responds to changes in the numbering origin of linear sequences. This also fixed a bug where features that became out of range disappeared after insertions and deletions and other numbering became corrupted.

Changing the topology now correctly changes the **Map** from linear to circular (or vice-versa) on all versions of the OS.

The cloning clipboard **Digest** function now works on OS X 10.6.

Changing preferences in the multiple sequence alignment window now correctly flags the underlying document as dirty.

The Phylogenetic window **Export Tab Contents As** menu item is now enabled and lets you export the tree in a number of different graphical formats.

The **Align To Reference Editor** tab now displays the numbering for traces aligned to the minus strand.

The **Reverse Translation** function now lets you create probes longer than 15 nt.

Changes for MacVector 13

Interface Enhancements

All of the toolbar icons have been reworked to have a more consistent look and feel and to display at high resolution on Retina screens.

The tab bars have been redesigned on all of the primary windows.

All result windows now get collated into a single result window per sequence, with tabs for each result. If you want to view more than one result at a time, you can “tear off” any tab into its own window.

There is a new **File | Export Tab Contents** menu item that can be used to save tab-specific data (e.g. graphics or text).

Primer Design Enhancements

The **Quickest Primer** interface now shows restriction enzyme cut sites in the parental sequence around the primer binding site.

The **Quickest Primer** interface also shows “one out” restriction enzyme sites. These are colored according to the effect that changing the mismatched base would have on any overlapping annotated ORFs. Potential silent mutations, which would not change the amino acid sequence of any coding sequences, are shown in red, those that would change the code are shown in green.

Hovering over a restriction site with the mouse displays the actual recognition sequence of the site.

Clicking and holding on a site, temporarily changes the sequence of the primer to match the mutated site and changes to the amino acid sequence of any ORFs are displayed

above the sequence.

Double-clicking on a one-out site changes the primer sequence to match the selected site.

The **Primer3** interface has been enhanced for testing pairs of primers. There is now a fourth “testing” mode that is automatically invoked when a pair of primers are entered. This mode removes most of the constraints to ensure pairs of binding primers are correctly identified.

The optimal annealing temperature for pairs of primers is now displayed in the spreadsheet result.

Primer3 will now include primers that overlap the ends of the region to be amplified. Previously, primers had to be entirely outside of the region.

Assembling *de novo* NGS Sequences With Velvet

The popular **Velvet** algorithm has been added to the Assembly module. You can use this to assemble large numbers of NGS sequences supplied in fastq files. In our hands, around 20 million 90nt Illumina reads can be assembled into a 6 Mb bacterial genome in around an hour on a retina MacBook Pro with 16 GB RAM.

Apple Scripting

Some basic Applescripting capabilities have been added to MacVector 13. In particular, there are now commands to open and save files in specified formats, so you can create Applescripts that can iterate through a folder of sequences and save each of them into a different folder in any format supported by MacVector. There is a new Applescripts folder with some example scripts to get you started.

Chromatogram Files

There is a new **Raw Data** tab that lists the peak positions, basecalls, quality values and areas under the curve for the chromatogram trace data. There are also columns that indicate the potential presence of “mixed” residues at a variety of confidence levels. It is in a tab-delimited format that can be copied and pasted directly into Excel for additional analysis.

Miscellaneous Changes

The **Starting Point** dialog now has links to the **Entrez** browser and to help pages to help new users understand the many different ways you can get sequences into MacVector.

The **Align To Folder** function now reads fastq formatted files in the target folder. The Description result window now displays the full name of each sequence, even with the typically long names from NGS experiments.

The **phrap** default parameters have been tweaked to generate better assemblies of both NGS and chromatogram data.

All of the “plain text” views now automatically adjust their formatting when printed to ensure that they are no more than a single page in width.

The **Page Preview** and **Magnify** controls have been moved from the bottom left corner of map windows onto the toolbar.

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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