

MacVector 12.5.1

for Mac OS X

System Requirements

MacVector 12.5 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 12.5 uses approximately 160 MB of disk space.

Installation and License Activation

Install MacVector 12.5 by double-clicking on the MacVector 12.5.mpkg installer application. You will be prompted for a system administrator account and password during installation. As with MacVector 12.0, once installation is complete, you must enter a valid 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 MacVector 12.0 and have a serial number with a maintenance end date of Oct 1st 2011 or later, MacVector 12.5 will automatically use your existing license and you will not be required to enter the details again.

Changes for MacVector 12.5.1

Bug Fixes

Several occasional crashes have been fixed.

Printing from the multiple sequence alignment editor now no longer prints additional blank pages.

A bug leading to corrupted data when copying and pasting items between Restriction Enzyme documents has been fixed.

The CDS translations display in the single sequence editor now updates correctly when residues are inserted before CDS features in the editor.

Changes for MacVector 12.5

Reference Alignments of Next Generation Sequencing Data

The add-on Assembler product is now able to align millions of reads from next generation sequencing projects against one or more genomic reference sequences. Please see the *Assembler 12.5 Release Notes* for more details

New Multiple Sequence Alignment Algorithms

DNA and Protein sequence alignments can now be automatically aligned with the popular T-Coffee and Muscle alignment algorithms as well as the existing ClustalW algorithm.

Alignments are now scored using the matrix selected in the ClustalW parameters dialog. Scoring is calculated by adding the scores of each pairwise alignment in the multiple alignment.

You can also now use the **Edit | Find** function to search for subsequences in the Multiple Sequence Alignment Editor.

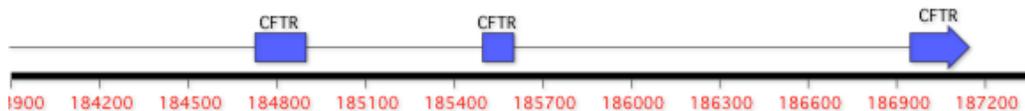
Rewritten Windows

The restriction enzyme, proteolytic enzyme, DNA and protein subsequence editors and the Matrix editor have all been rewritten using Cocoa table views. Apart from an improved appearance, this change makes it easier to navigate and select entries in the editors, simplifying the creation of subsets (you can copy and paste between windows). In addition, you can sort the columns by clicking on the titles.

The **Entrez** browser has been rewritten and now permits an unlimited number of search terms to be combined for a search.

Sequence Window Enhancements

There are new “Segmented Hollow Arrow”, “Segmented Hollow Box” and “Segmented Full Height Hollow Box” symbol. You can use these for segmented features (e.g. CDS features containing introns) in the **Map** tab and the exon segments will be shown joined by a line e.g.



The **Editor** tab can now display the translations of CDS features above or below the sequence – turn this on using the **Strands** button.

Miscellaneous Enhancements

Segmented subsequence matches now have all segments displayed in the text and graphical outputs. This lets you e.g. search for canonical *E. coli* promoter sequences and see both the -35 and -10 regions displayed in the Map.

The **Align to Reference** algorithm now runs as a standard job so that you can switch to other windows and carry on using MacVector while waiting for lengthy alignments to complete.

When using a Roaming license off the network, there is no longer a temporary hang when MacVector attempts to reconnect to the license server.

Many dialogs have had error handling code added so that red information text will be displayed explaining why the OK button is not enabled if invalid parameters have been entered.

The maximum number of results that can be returned by the **Align to Folder** function has been increased to 32,767.

Protein sequences now support the same relative numbering options as DNA sequences so you can have them start at a number other than 1.

The SNP tab of the **Align to Reference** Window now lists all of the changes between the consensus and the reference sequence and includes the codon change and amino acid change of any CDS feature crossing each SNP.

Primer3 has been updated to version 2.2.3.

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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