

MacVector 16.0.8

for Mac OS X

The online updater for this release is 80.1 MB in size

System Requirements

MacVector 16.0 runs on any Intel Macintosh running **Mac OS X 10.7** or higher. There are no other specific hardware requirements for MacVector – if your machine can run OS X 10.7 or above, it can run MacVector. A complete installation of MacVector 16.0 uses approximately 210 MB of disk space. Please note this release will NOT run on OS X 10.6 or earlier.

ASSEMBLER NOTE: If you are performing contig assembly using MacVector with Assembler, we recommend you have **at least 1 GB** of FREE RAM available on your machine. For any serious NGS work using phrap, velvet, SPAdes or bowtie, you should have at least 8 GB and preferably 16 GB or more for satisfactory performance.

Installation and License Activation

You can choose to install MacVector in one of two ways; if you want to install MacVector for all users of the computer, simply drag the MacVector folder onto the Applications folder. You will be prompted for a system administrator account and password during this copy. If you don't have administrative privileges, or if you want to install it for just your own use, you can install MacVector in the /Applications/ folder in your own personal home directory. To do that, double-click on the **OpenUserApplicationsFolder** icon to open the folder in a separate window, then drag the MacVector folder into that window.

Once installation is complete, when you first run MacVector you must enter a valid license owner, serial number and activation code, if one does not already exist on your computer. 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 September 1st 2017 or later, MacVector 16 will automatically use your existing license and you will not be required to enter the details again. NOTE: one important change for MacVector 14.0 and later is that you can now activate a license for your own use without requiring Administrative privileges.

Changes for MacVector 16.0.8

Bug Fixes

The NCBI changed the behavior of the Entrez server for retrieving sequences in the BLAST hit list. This release has some changes to restore that functionality.

Changes for MacVector 16.0.7

Bug Fixes

The ability to copy Feature information from the Features tab has been restored.
MacVector no longer hangs when analyzing Protein sequences with over 32,000 residues.
MacVector now does a better job of opening multiple sequence alignment files with internally corrupted Newick guide trees.
There have been additional changes to improve the stability of large Align To Reference alignment jobs.

Changes for MacVector 16.0.6

Bug Fixes

Some minor issues with Align To Reference when reads aligned starting at the last residue of circular sequences has been fixed.
MacVector now does a better job of parsing malformed Genbank LOCUS lines.

Changes for MacVector 16.0.5

Bug Fixes

A crash when editing names in the MSA Editor with fewer than 4 sequences in the alignment has been fixed.
There have been some changes to the threading of Align To Reference jobs to help prevent occasional crashes on certain machine/OS combinations.
New features once again honor the settings in the default Symbol Editor. This was inadvertently broken in MacVector 16.0.3.

Changes for MacVector 16.0.4

Bug Fixes

You can now change RNA sequences to DNA using the toolbar button.
Some occasional issues calculating the consensus sequence for Align To Reference assemblies have been resolved.

Changes for MacVector 16.0.3

Bug Fixes

An occasional crash when rapidly moving the mouse pointer around the Quicktest Primer dialog has been fixed.
A problem recalculating phylogenetic trees has been fixed.
You can now select multiple features in the Map view, double-click on one and the multiple-Symbol Editor will be displayed.
Using the Free-form Feature Editor tab no longer deletes qualifiers.
All of the controls in the MSA Editor Preferences are now wired up correctly.
Some extraneous asterisks in the MSA text output have been removed.

Changes for MacVector 16.0.2

Bug Fixes

A crash when invoking the Align to Reference **Add Seqs** function on OS X 10.7 and OS X 10.8 has been fixed.

When you Export a sequence in GenBank format, MacVector now writes out all GenBank features, even if they are currently obsolete.

Changes for MacVector 16.0.1

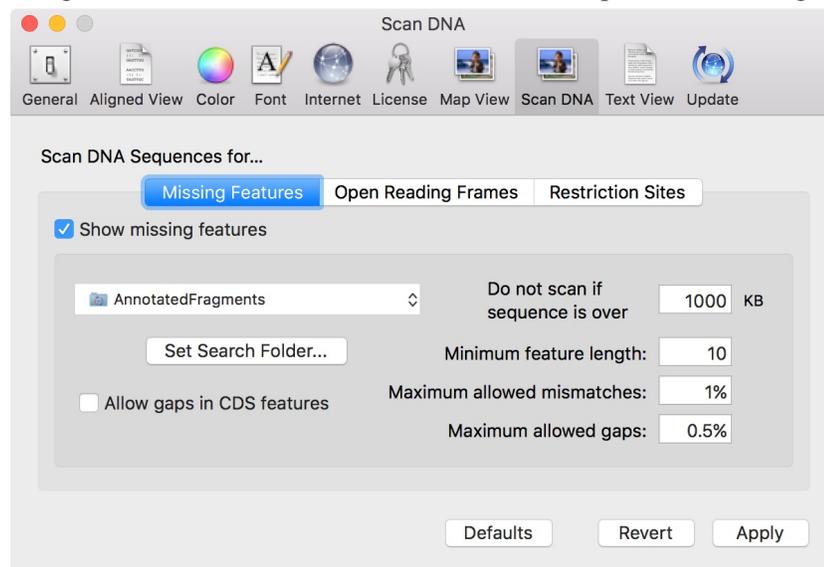
Bug Fixes

A critical bug where MacVector crashed when unlocking a document after invoking **Options | Symbols For Xxx...** has been fixed.

Changes for MacVector 16.0.0

Scan For Missing Features

Whenever you open a DNA sequence, MacVector now scans it to identify common features that are not already annotated on the sequence. It shows these in faded colors in the **Map** tab so that you can see what features are missing from your sequence. By default, MacVector uses the collection of features in the /MacVector/Common Vectors/Annotated Fragments/ folder, but you can use any folder you like, configured using the new **MacVector | Preferences | Scan DNA** preference settings.



You can right-click on any faded feature to add it to your sequence, or select all of them and add with a single mouse-click.

Combined Feature/Symbol Editor

If you double-click on an individual feature in the **Map** tab, it now brings up a dialog with two tabs – one for the **Feature Editor** and one for the **Symbol Editor**. This lets you edit both the basic Genbank-style feature information and the graphical symbol appearance in a single dialog. Note: this is only displayed when you are editing a single individual feature. If you want to change the appearance of multiple features at the same time, you

will get the normal **Symbol Editor**.

Assembler Improvements

We have added the popular SPAdes algorithm to Assembler for MacVector 16.0. This is a high-performance assembler that uses very little RAM, allowing it to run on relatively modest machines, though we do recommend 16GB+ of RAM for optimal performance. It is a little slower than our existing velvet algorithm, but does a better job of resolving repeats at the ends of contigs, so you generally find it produces longer contigs with the same input data. One drawback of SPAdes is that it does not generate alignments, only contig consensus sequences, so we have added an option to generate alignments within MacVector using bowtie. This does increase processing time.

You can now use interleaved paired read files for all NGS assembly algorithms (velvet, bowtie and SPAdes). MacVector will automatically identify them where possible.

MacVector now directly supports compressed fasta and fastq formatted files (.zip or .gzip) and will submit those directly to assembly algorithms. This dramatically reduces the amount of temporary disk space required when assembling large datasets.

There are now more options to control the type of read that you are using (unpaired, paired-end, mate pair, HQ mate pair, NxSeq long mate pair), or the source of the reads (Illumina, IonTorrent, PacBio, Nanopore etc). Double-click on a read after importing into a project to set these parameters. SPAdes in particular will optimize assembly based on these settings.

There is now a right-click option to circularize contigs in the **Contig Editor**. If there are direct repeats at the ends of a contig, you can right-click and the item will show you the length of the repeat. If you select the item, a new circular sequence will be created from the consensus.

Miscellaneous Enhancements

In the single nucleic acid sequence editor view, when you hover the pointer over a residue, the tooltip now displays the nucleic acid residue number under the pointer, and also the amino acid residue number of any annotated CDS feature at that position.

The **Align To Reference** assembly algorithm has been improved to better handle reads crossing the circular origin of a reference sequence. It is also now significantly faster when aligning longer reads with multiple regions of mismatches.

Multiple Sequence Alignments now have an option to “**unalign**” selected sequences, or the entire alignment – it’s an option on the **Align** toolbar button.

By default, MacVector now uses a smaller arrow for ORF results, with a pale red color for matches on the plus strand and pale grey for matches on the minus strand to distinguish them from annotated features.

MacVector 16 has had yet more functions added to the AppleScript directory. To see what functions are available, open the apple-supplied Script Editor, choose **File | Open Dictionary** and select the MacVector.app application. For examples of using AppleScript to drive MacVector, see sample files in the /Applications/MacVector/AppleScripts/ folder.

Bug Fixes

Find Sequencing Primers/Probes now honors the % GC and Tm limits.

Some parameters in the **Analyze | Primer Design/Test (pairs)** “Test Primer Pair” function which were previously hidden have now been revealed.

The **Analyze | Base Composition** algorithm now generates the correct Tm data for very

short window sizes.

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 or licensing 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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