

MacVector 18.1.3

for Mac OS X

The online updater for this release is 224 MB in size

You must be running MacVector **15.5.4** or later for this updater to work!

If the updater fails, [DOWNLOAD THE FULL INSTALLER HERE!](#)

System Requirements

MacVector 18.1 is a Universal Binary supported on any Intel or Apple Silicon Macintosh running **Mac OS X 10.12** (macOS Sierra) or higher, up to and including macOS Big Sur. There are no other specific hardware requirements for MacVector – if your machine can run OS X 10.12 or above, it can run MacVector. A complete installation of MacVector 18.1 uses approximately 496 MB of disk space. Please note this release will NOT run on OS X 10.10 or earlier versions of OS X.

ASSEMBLER NOTE: If you are performing contig assembly using *MacVector with Assembler*, we recommend you have **at least** 2 GB of **FREE** RAM available on your machine. For any serious NGS work using phrap, velvet, SPAdes, Flye 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.

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 February 1st 2021 or later, MacVector 18.1 will automatically use your existing license and you will not be required to enter the details again. NOTE: you can optionally activate a license for your own use without requiring Administrative privileges.

Changes for MacVector 18.1.3

InterProScan Update

The European Bioinformatics Institute (EBI) have changed the programming interface to their popular protein “*InterProScan*” online functionality, requiring a major update to the MacVector *InterProScan* code. They no longer return html code that we could integrate into MacVector, so the graphical appearance of the results has changed substantially.

When you invoke *InterProScan*, there is a new **Map** results tab that is very similar to **Map** results returned by many other MacVector functions. Currently, to reduce clutter, we display a subset of the full *InterProScan* results, but you can always turn on all remaining results using the floating *Graphics Palette*. If you “mouse-over” the graphic representing a “hit” you will see a tool tip summarizing the hit information. If you select a graphic item and right-click (or <ctrl>-click) a popup menu will appear. This has options to add the feature to the parental protein sequence and also has options to view more information about the hit in your default web browser.

Bug Fixes

An issue where gap residues were not getting placed correctly in the chromatogram pane of the *Align to Reference* Editor has been fixed.

Sequence selections in the chromatogram pane of the *Align to Reference* Editor are no longer offset by 16 pixels.

Changes for MacVector 18.1.2

Bug Fixes

Multiple Alignments of RNA sequences now generate U/T residues in the consensus.

A bug where Assembly Projects created by earlier versions of MacVector could not be re-saved and re-opened has been fixed.

Changes for MacVector 18.1.1

Universal Binary

MacVector 18.1.1 is a Universal Binary, meaning that it can run natively on both Intel and Apple Silicon Macintosh computers. Other than the ability to run natively on M1 processors, MacVector 18.1.1 is essentially identical to MacVector 18.0.1 with the exception that the embedded Python framework has been updated to version 3.9. Currently, all of the embedded 3rd party algorithms are included as Universal Binaries with the exception of SPAdes and Bowtie – these run under Rosetta2 emulation on Apple Silicon machines. However, in our hands, they still out-perform equivalent older Intel-based computers.

Changes for MacVector 18.0.1

Cosmetic Changes for Big Sur

The main application icon and window toolbar appearance have been updated to match the macOS Big Sur “look and feel”. MacVector 18.0.1 is still just an x86_64 “Intel” native binary, meaning that it runs under Rosetta2 emulation on Apple Silicon machines. There is a parallel MacVector 18.1.1 release that [you should download](#) if you are using an M1 machine and want to take advantage of a version of MacVector compiled to run

natively on arm64 processors.

Improved Align to Reference SNP Reporting

The align to reference algorithm has been slightly tweaked to do a better job of aligning reads that have insertions relative to the reference. The SNPa tab has been revised to use standard reporting for both nucleic acid SNPs and for corresponding changes to amino acid sequences in CDS features. In addition, small deletions are now reported, again using standard nomenclature.

Bug Fixes

The use of a comma as the decimal point separator is now supported throughout MacVector for international localization.

Flye now assembles long read NGS data as expected.

A crash bug when “flipping” primer sequences in the *Quicktest Primer* interface has been resolved.

Using the *Position Mask* in multiple sequence alignments now works as documented.

Drag and drop is now disabled *within* an individual window as it could sometimes cause inadvertent corruption of the sequence.

Import of GFF files has been improved.

A crashing bug when extensively using the magnification function in the **Map** tab has been resolved.

Changes for MacVector 18.0.0

Searching for CRISPR PAM Sites

There is a new feature accessed by the **Analyze | CRISPR PAM sites...** menu item that will scan Nucleic Acid sequences for Protospacer Adjacent Motifs associated with the CRISPR Cas9 and related enzymes cleavage and modification functions. By default, MacVector uses a file called *Protospacer Adjacent Motifs.pam* that is located in the */Applications/MacVector/Subsequences/* folder. It contains most of the current (July 2020) characterized Cas9-like enzymes, but you can always open the file and add your own.

While MacVector does not search genomes for potential off-target sites, this is still a very useful function to alert you to potential CRISPR target sites. The output is a mix between the current *Restriction Enzyme* and *Nucleic Acid Subsequence* searches, so you can easily see and copy the guide sequences.

You can also have MacVector automatically scan for CRISPR PAM sites whenever you open a DNA sequence file. You can control this using the **MacVector | Preferences | Scan DNA** pane.

Enhancements to Outlining Shared Domains in Aligned Sequences

First added in MacVector 17.5, this functionality has been significantly enhanced to expose additional Feature-related functionality in Multiple Sequence Alignment documents. There is a new **Features** tab in the protein multiple sequence alignment window where you can view, edit, create and/or delete features in each of the aligned sequences.

When the **Editor** or **Picture** tabs are active, a new floating *Graphics Palette* is displayed (similar in concept to the Graphics Palette for the single sequence **Map** tab), allowing you to turn features on and off permitting greater control over how shared domains are displayed and outlined.

Additional File Formats

MacVector now reads the following sequence formats;

SnapGene *.dna* files

SerialCloner *.xdna* files

Sequencher *.spf* assembly project files

Trim by Quality

Both the **Align to Reference** and **Assembly Project** windows now let you trim reads based on quality. The reads (typically Sanger sequencing reads in ABI or SCF format) should not be aligned prior to running the algorithm. A typical workflow might thus be to add *.ab1* or *.scf* files to a project, optionally base call with *phred*, if needed, then *Trim by Quality* prior to aligning or assembling.

Miscellaneous Enhancements

There have been a large number of minor enhancements. Some, such as reworking code behind the scenes to replace deprecated Apple functions and refactoring code for better stability and performance to help ensure that MacVector will continue to work on upcoming releases of macOS and take advantage of improved hardware. There have also been improvements to Dark Mode support in many areas and much better handling of the labels in crowded **Map** views.

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.

USA

Toll Free: (866) 338 0222

Telephone: (919) 303 7450

Fax: (919) 303 7449

E-mail: support@macvector.com

Europe

Telephone: + 44 (0)1223 410552

Fax: +44 (0)1223 709429

E-mail: support@macvector.com

Worldwide

Telephone: + 1 919 303 7450

E-mail: support@macvector.com

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>

MacVector, Inc.
Software for Scientists