

MacVector 26.0.2

for Mac OS X

The online updater for this release is 271 MB in size

THE ONLINE UPDATER WILL NOT WORK!!
DOWNLOAD THE FULL INSTALLER HERE!

System Requirements

MacVector 26 is a Universal Binary supported on any Intel or Apple Silicon Macintosh running **macOS 11.5** (Big Sur) or higher, up to and including macOS Tahoe. There are no other specific hardware requirements for MacVector – if your machine can run macOS 11.5 or above, it can run MacVector. A complete installation of MacVector 26 uses approximately 800MB of disk space. Please note this release will NOT run on OS X 11.0 or earlier versions of OS X.

ASSEMBLER NOTE: If you are performing contig assembly using *MacVector with Assembler*, we recommend you have **at least** 4 GB of **FREE** RAM available on your machine. For any serious NGS work using *phrap*, *velvet*, *SPAdes*, *Flye*, *bowtie* or *minimap2*, you should have at least 16 GB and preferably 32 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 May 1st 2026 or later, MacVector 26 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 26.0.2

Bug Fixes

You can now **File | Export** files (e.g. consensus sequences) without a write error. This was caused by the way we “safe write” files, making a copy of the file and writing before moving the file into its user-selected location. This failed when running in a sandbox.

All remaining Intel-only binaries have been removed from MacVector. Some of these were completely unused but had been left in builds inadvertently, others have been replaced by alternate functionality. MacVector 26.0.2 is now a Universal Binary for all its embedded applications.

The **Auto-Annotation via BLAST** functionality has been reworked to do a better job of handling occasional internet glitches and failed BLAST or Entrez jobs. You should find this is now far more stable, even when annotating large (>100kb) genomes.

Changes for MacVector 26.0.1

Bug Fixes

There have been some changes to better handle licensing changes due to MacVector now running in a sandbox. You should now get appropriately prompted to allow MacVector access to the new file system locations where we keep the license file.

Changes for MacVector 26.0

Why The Version Jump From 18.8?

Over the last 12 months, Apple have committed to numbering their operating system release by year, so the latest release “macOS Tahoe” is “macOS 26”. That makes it easy to remember the year the version was released. Accordingly, we have decided to match that, so, going forwards, all major MacVector releases will be numbered based on the year of release. We will still release complimentary bug fixes as e.g. “26.0.1” etc, so there may be maintenance releases in 2027 that still have “26” as the initial version number.

Running in the macOS Sandbox

Reasoning

At MacVector, we do try to look ahead and future-proof MacVector against Apple’s announced or predicted changes to macOS so that your purchased version will have a long life on future machines and with macOS updates. Apple have been encouraging developers to enable applications to run in a macOS “sandbox” for several years. Currently, any applications downloaded from the App Store **MUST** be sandbox enabled. Apple have made it clear that at some stage **ALL** applications will have to be sandbox-enabled to run on future macOS releases. So that will at some stage include MacVector.

What is a Sandbox?

The basic concept of a “sandbox” is that any running app only has access to a very restricted file system – that way, a rogue or poorly implemented application cannot intentionally or accidentally corrupt your file system or steal your data. However, if you use the standard file system dialogs to open (or save) a file, then macOS “blesses” those files so you can open them from anywhere on your machine and the OS remembers that

those files are “OK”. Typically, for simple applications, you would never realize it was running in a sandbox. You run the app, open a file, save a file and all looks great.

Why is it a Problem for MacVector

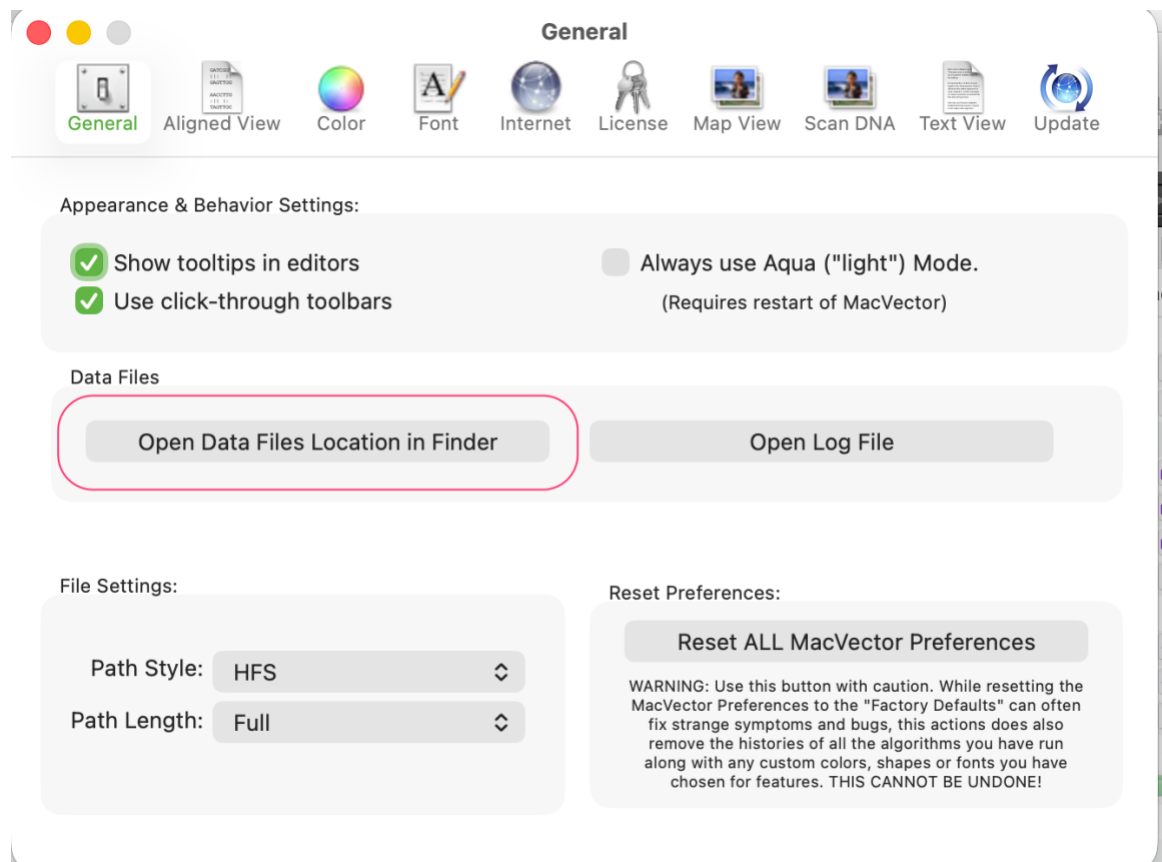
The problem comes when an application tries to access a file that you have not specifically “blessed” by choosing it through a file dialog. MacVector has many of these – there are default files for Restriction Enzyme Analysis, Primer Database searches, Gel Markers, Codon Usage analysis etc. Unless you have specifically changed the selection, MacVector will be denied access to the file when it tries to run an analysis with the default data files.

How Do We Solve the Problem?

MacVector now contains an internal copy of all its default auxiliary files and copies those into a specific location accessible to the sandbox, recommended by Apple. MacVector can then freely access the files in that location. You can add your own files to that location, edit the files, copy them or do anything you want with them. They are located at:

`<Your Home Folder>/Library/ Application Support/MacVector/`

But, MacVector 26 simplifies this whole URL issue by having a handy shortcut button in the **MacVector | Settings | General** pane that will drop you in the parental folder.



Note that if you have already changed any of the auxiliary file settings to point to a non-default location, these will be honored and should be read and used successfully by MacVector 26

Any Issues I Should be Aware Of?

Other than the possibility of auxiliary files not being available to read because they are in private locations, the other main problem comes from existing saved **Assembly Project** files. They often contain pointers to e.g. read fastq files. When you re-open those projects and try to run an analysis again, you will be prompted to allow access to those fastq files. Going forwards, all data in saved projects has additional information stored with references to external files that lets macOS know these have been “blessed”.

Golden Gate Cloning

One of the major new functions in MacVector is support for the popular Golden Gate Cloning strategy. The basic idea behind this is that you can design primers to create PCR products where you can cut with Type IIS enzymes that asymmetrically cleave to one side leaving 4 nt overhangs and then design multiple inserts, each with a different but complementary 4 nt overhang such that you can (potentially) assemble 20 or more fragments to a viable clone in a one-pot reaction. The detailed explanation of this technique is beyond this simple set of release notes but can be found here:

<https://en.wikipedia.org/wiki/Golden_Gate_Cloning>.

MacVector goes way beyond simple Golden Gate Cloning interfaces such as the popular NCBI tool (<https://goldengate.neb.com>). With MacVector you can;

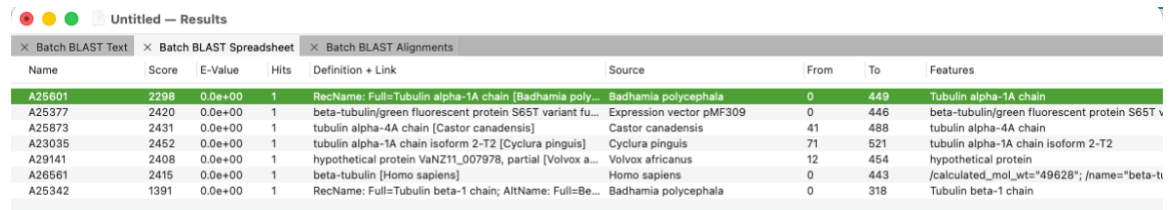
- Select the primary enzyme you would like to use for a cloning (e.g. BsaI, but all Type II enzymes are available).
- Add a circular vector to a project and have MacVector automatically identify that it has suitable Type IIS sites to be a vector
- Add “pre-cut” vectors to a project which will then honor the existing overhangs.
- Add one or more fragments that can be blunt ended or cut and MacVector will sort them out and automatically generate primers if needed to make them assemble.
- Directly edit any primer to modify how the fragment will butt up to the adjacent fragment to adjust open reading frames etc.
- View the junctions between fragments to confirm the fusion looks correct.
- Export the predicted result of the assembly as a new sequence.
- Print/Export a list of all the required primers
- And (perhaps most impressive of all), if you give MacVector a collection of existing constructs (e.g. by drag and drop or **File | Open** selection), it will automatically work out if a new construct can be created by combining those vectors, the selected enzyme and T4 DNA ligase into the same one-pot tube. Fans of the MoClo system (and many similar) should love this.

Batch BLAST of Protein Sequences

One important change for MacVector 26 is that you can now add protein sequences to assembly projects. Accordingly, we have changed the name from “**Assembly Project**” to “**Sequence Project**” as it can now contain both DNA and protein sequences. Future releases of MacVector will take advantage of this to use **Sequence Projects** as a general organizational project for sequences where many different analysis functions will be able to directly operate on items in the projects.

For MacVector 26, you can select one or more protein sequences and select **Database | Online Search for Similar Sequences (BLAST)...** and this will run BLAST on the selected sequences. The results contain a summary window that lists the best hits for each input sequence. This is interactive, so you can “drill down” and view the individual

results for any sequence if you wish.



The screenshot shows the 'Batch BLAST Alignments' tab in MacVector. The table lists search results with columns for Name, Score, E-Value, Hits, Definition + Link, Source, From, To, and Features. The results show several matches for tubulin sequences from various sources like Badhamia polycephala, Castor canadensis, and Cyclura pinguis.

Name	Score	E-Value	Hits	Definition + Link	Source	From	To	Features
A25601	2298	0.0e+00	1	RecName: Full=Tubulin alpha-1A chain [Badhamia poly...	Badhamia polycephala	0	449	Tubulin alpha-1A chain
A25377	2420	0.0e+00	1	beta-tubulin/green fluorescent protein S65T variant fu...	Expression vector pMF309	0	446	beta-tubulin/green fluorescent protein S65T v...
A25873	2431	0.0e+00	1	tubulin alpha-4A chain [Castor canadensis]	Castor canadensis	41	488	tubulin alpha-4A chain
A23035	2452	0.0e+00	1	tubulin alpha-1A chain isoform 2-T2 [Cyclura pinguis]	Cyclura pinguis	71	521	tubulin alpha-1A chain isoform 2-T2
A29141	2408	0.0e+00	1	hypothetical protein VaNZ11_007978, partial [Volvox a...	Volvox africanus	12	454	hypothetical protein
A26561	2415	0.0e+00	1	beta-tubulin [Homo sapiens]	Homo sapiens	0	443	/calculated_mol_wt="49628"; /name="beta-t
A25342	1391	0.0e+00	1	RecName: Full=Tubulin beta-1 chain; AltName: Full=Be...	Badhamia polycephala	0	318	Tubulin beta-1 chain

All Internal 3rd Party Executables Are Now Universal Binaries

MacVector itself, and most of the embedded 3rd party executables like ClustalW, phred/phrap/cross_match, primer3 etc, have been Universal Binaries since MacVector 18.2 was released. However, some of the executables needed significant rewrites to generate Apple Silicon binaries. The last two hold outs were `bowtie2` and the embedded `perl` that we ship within MacVector. With MacVector 26 these are now both Universal Binaries. This will prevent any messages from macOS warning about components within MacVector needing to be updated and will ensure forward compatibility with future macOS releases when support for Intel binaries is withdrawn. As a bonus, **Bowtie** assemblies are now a little faster on Apple Silicon machines.

Minor Enhancements and Bug Fixes

When you download a fragment from the **BLAST Map** tab, the downloaded fragment now contains an additional ~1kb of sequence from either side of the hit region. For many matches to genomes or large sequences, this allows you to easily retrieve a more informative segment of DNA containing the features of interest around your hit.

There is a new **Analyze | Optimize CDS...** menu item. This is active whenever a CDS feature is selected in a sequence. This functionality was available previously only as a context-sensitive right-click option.

The **File | New** menu now has separate entries for the various cloning project implementations within MacVector: **Gibson Assembly**, **Ligation Independent Cloning**, **Golden Gate Cloning** and **Pre-existing Fragment Assembly**.

You can now export features in GFF format.

The setting in the **Translation** analysis dialogs are now correctly remembered between invocations.

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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