MacVector 18.8.0

for Mac OS X

The online updater for this release is 269 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 18.8 is a Universal Binary supported on any Intel or Apple Silicon Macintosh running **Mac OS X 11.5** (macOS Big Sur) or higher, up to and including macOS Tahoe. There are no other specific hardware requirements for MacVector – if your machine can run OS X 11.5 or above, it can run MacVector. A complete installation of MacVector 18.8 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** 2 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 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 May 1st 2025 or later, MacVector 18.8 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 18.8

Auto-annotation via BLAST

You can now automatically annotate a bare sequence with a couple of clicks using the NCBI BLAST and *Entrez* functionality. Open your sequence of interest and choose **Database | Auto-annotate Sequence (via BLAST)…** and accept the default values. Behind the scenes, MacVector splits up the sequence into shorter overlapping segments (by default, 1kb with 500nt overlaps) and BLASTs each one against the selected NCBI BLAST database. It then downloads the best hits from each BLAST result using Entrez and saves them into a common folder, optimizing as it runs to avoid duplications. It then runs an **Auto-annotation** against that folder to annotate the starting sequence. Small (<20 kb) plasmid sequences typically complete in less than 10 minutes, whereas modest genomes (~2 Mbp) might take a few hours. The rate of submission of BLAST and Entrez searches is throttled by default to avoid running afoul of the NCBI submission limits.

Note that you can also do this for multiple sequences in a “batch” mode using the same approach described below for **Batch BLAST**.

Batch BLAST

You can now run BLAST with a single click on a large collection of sequences, such as a set of NGS reads, or the contigs resulting from an NGS assembly, and view the results in a spreadsheet-style window. To invoke this, use **File | New | Assembly Project** to create a new **Project** window and add your sequences of interest to that by clicking on the **Add Seqs** toolbar button. You can choose any nucleic acid file format that MacVector can recognize, including fasta and fastq data files, though if they contain more than 10,000 sequences they will be brought in as a reference to a disk file, rather than as individual sequences. You can always use the `SplitFastQFile.app` applet in `/MacVector/AppleScripts/` to break up fastq files into smaller chunks.

Select the sequences or contigs that you want to BLAST (or leave unselected to BLAST all of them) and choose **Database | Online Search for Similar Sequences (BLAST)…** to start the job. As well as running a blast search on each sequence, MacVector downloads some of the best hits for each sequence using *Entrez* to help identify the actual genes or CDS features that match each test sequence.

The results are presented in as a sortable spread sheet with one line for each input sequence and as a text format with hyperlinks to retrieve the corresponding matches. There is also a **Details** tab that updates dynamically to show the specific alignment information for any selected line in the spread sheet. You can “tear off” the details tab to open it in a separate window, allowing you to have side-by-side windows where you can click on a spreadsheet line and watch the **Details** window update.

Miscellaneous Enhancements and Bug Fixes

The **Auto-annotate Sequence…** function has been improved to now report and annotate partial feature matches. So, for example, you can analyze a short sequence that matches within a known CDS feature and it will be correctly identified and annotated using the standard GenBank format for “starts before” and “ends after” notation.

There have been a lot of behind-the-scenes changes to the floating **Graphics Palette** so that it retains its display position and does not scroll when you turn features and **Restriction Enzymes** on and off.

The SPAdes executables have been updated to be a Universal Binary (version 4.2.0).

The Bowtie executables have been updated to version 2.5.3.

A few display bugs in the output of the genome comparison tool have been fixed. These particularly affected the alignment of individual matches to the opposite strand or alignments that were not the full length of a feature. These were display glitches only – the underlying data was correct regarding the quality of the match.

You can now assemble pre-designed **Gibson Assembly** fragments where the end identities are greater than 40 nucleotides.

The **Align to Reference Map** view now displays the clipped section at each end for segmented matches. Previously this was only shown for single segment matches.

The protein pI calculation has been optimized to account for embedded `Cys` and `Tyr` residues that rarely practically contribute to the observed pI for a non-denatured protein.

The **Multiple Sequence Alignment Editor** display scrolling and editing has been dramatically speeded up for large alignments.

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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