

# MacVector 17.0.10

for Mac OS X

***The online updater for this release is 143.5 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 17.0 is supported on any Intel Macintosh running **Mac OS X 10.9** or higher. There are no other specific hardware requirements for MacVector – if your machine can run OS X 10.9 or above, it can run MacVector. A complete installation of MacVector 17.0 uses approximately 253 MB of disk space. Please note this release will NOT run on OS X 10.7 or earlier and is likely to have problems on OS X 10.8.

**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 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 November 1<sup>st</sup> 2018 or later, MacVector 17 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 17.0.10

### Bug Fixes

There have been some tweaks to the Map tab layout code for linear sequences to do a

better job of automatically deciding when to hide labels on crowded maps.

The Multiple Alignment Picture tab now updates correctly when changes are made to the consensus preferences.

A bug where MacVector would crash trying to open very old corrupted MacVector files has been resolved.

A bug where the Align to Reference Problems tab would sometimes crash MacVector has been fixed.

Some missing MUSCLE parameters have been restored.

## Changes for MacVector 17.0.9

### Bug Fix

The ability to copy sequence data from the Map tab when only the sequence line or residues was selected has been restored.

## Changes for MacVector 17.0.8

### macOS 10.15 “Catalina” Compatibility

A glitch in the **Analyze | Primer Design/Test (pairs)** dialog has been resolved where the advanced parameters either could not be viewed or were displayed in a garbled form.

A crash double-clicking on a feature item in the floating *Graphics Palette* window has been fixed.

## Changes for MacVector 17.0.7

### Bug Fixes and Enhancements

Toolbar buttons are now correctly enabled/disabled in the *Restriction Enzyme* window.

The *Primer Design/Test (pairs)* function no longer gets in an invalid state under certain circumstances when a hybridization primer is not specified.

## Changes for MacVector 17.0.6

### Bug Fixes and Enhancements

You can now use **File | Export** to export all contig consensus sequences from an Assembly Project (e.g. after a SPAdes assembly) in a fastq file. Previously this only worked for fasta exports.

You can now “slide” reads in the *Contig* and *Align to Reference* Editors. This is only functional for simple “memory-based” assemblies in the *Contig* Editor, not the NGS assemblies that use a read-only BAM file as the backing store.

You can now dissolve individual contigs in phrap job results. Again, this is only for “memory-based” assemblies such as ABI or plain sequence files, not NGS-based data.

A bug where features would get duplicated when overwriting a sequence by pasting has been fixed.

## Changes for MacVector 17.0.5

### Bug Fixes

A problem connecting to network KeyServers due to the “code-hardening” we had to add

to support notarizing has now been resolved.

A crash when editing certain LOCUS lines has been fixed.

Another “code hardening” issue with importing BAM files into the Assembly Project interface has been fixed.

## Changes for MacVector 17.0.4

### Bug Fixes

A problem where MacVector would crash on exit and not save changes to the global symbol preferences has been resolved.

Occasionally, the *Test Primer Pairs* function would erroneously report an incorrect product with large sequences with many weak binding sites. This has been fixed.

A bug where assembling Gibson Assembly fragments would complement the last few residues when regenerating restriction sites has been fixed.

A hang when undoing deletion of reads in the Align to Reference editor has been fixed.

### Enhancements

The *Restriction Enzyme Picker* can now be resized to a smaller size where the upper panel will become hidden to make better use of smaller screens.

The MacVector application has been “code-hardened” and notarized by Apple. This will help ensure forward-compatibility with future macOS releases that will have increased security requirements.

## Changes for MacVector 17.0.3

### Bug Fixes

Colors have been changed in the Bowtie graphical output to more clearly show the areas with no overlapping reads.

An issue where the Restriction Enzyme File selection dialog could become permanently hidden when invoked from the RE Picker has been resolved.

When you copy Map graphics from circular sequences, the graphical format is now the default when pasted into applications such as MS Word and Keynote.

## Changes for MacVector 17.0.2

### Bug Fixes

Multi-segmented CDS features are now correctly translated in text output windows.

Segmented alignments are now correctly displayed in the *Align to Reference* **Map** tab.

The *Base Composition* text output now correctly calculates the “T” composition.

We have found a workaround for problems printing many graphical image views under macOS Mojave.

## Changes for MacVector 17.0.1

### Bug Fixes

The *cDNA Alignment* algorithm in the **Align to Reference** function now generates results similar to MacVector 16.

A crash when hovering the mouse pointer over a tab bar with the <option> key held down has been fixed.

A problem opening saved Gibson Assembly projects on macOS versions prior to 10.14 has been resolved.

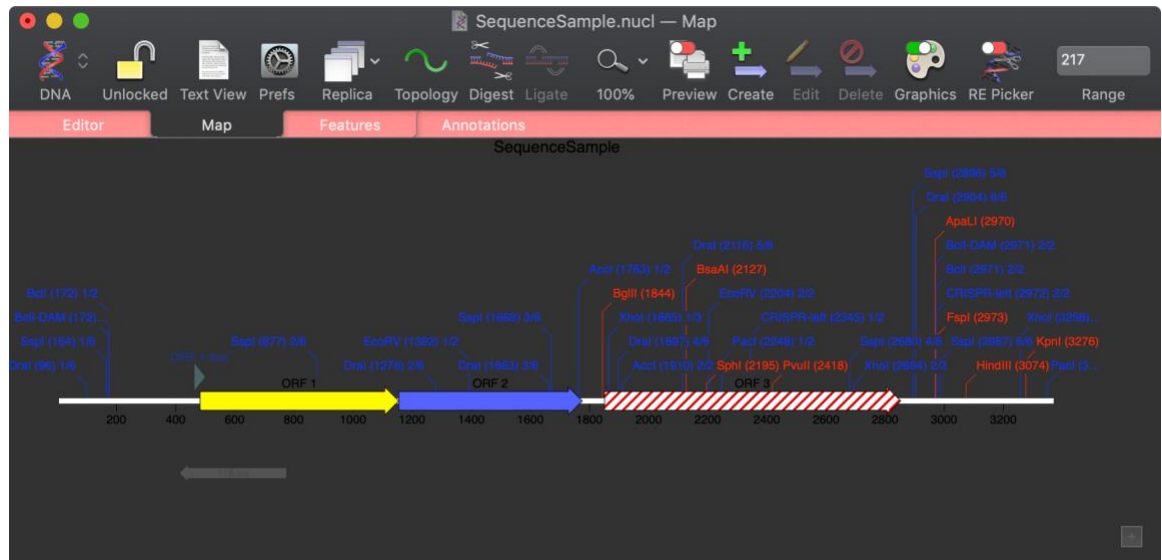
A variety of issues editing and selecting sequences in the *Multiple Sequence Alignment Editor* have been fixed.

When you select an ORF in the *Open Reading Frame* analysis results window, the corresponding region in the parental sequence is now selected.

## Changes for MacVector 17.0.0

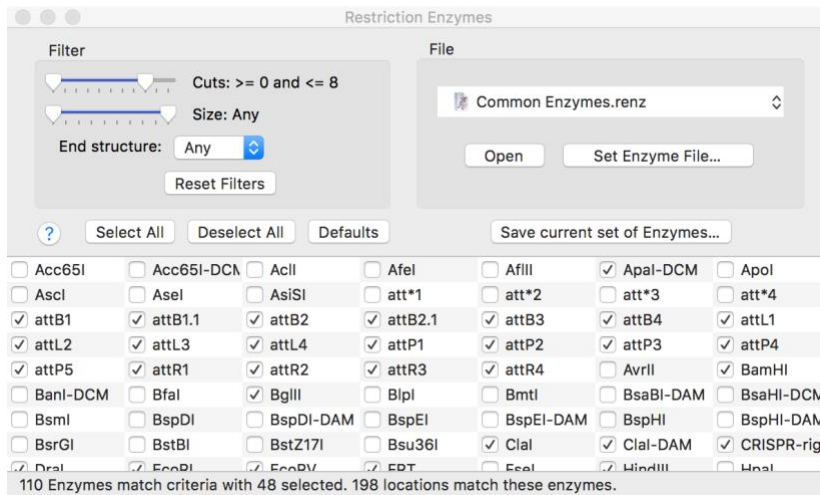
### Dark Mode Support

MacVector 17 has basic support for the macOS Mojave “Dark Mode”. Many of the icons have been reworked and the background and foreground colors and the tab bars of most windows are now dynamic so that text and graphics are clear and legible under both Dark and Light modes.

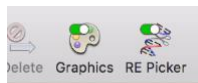


### Restriction Enzyme Picker

There is a new floating window that displays a list of Restriction Enzymes that cut the currently active sequence, even if those enzymes are not currently visible in the **Map** tab.



The entire interface is interactive, so you can move the sliders to filter by number of cuts or site size, or choose the end structure (5' overhang, 3' overhang, blunt) or toggle individual enzymes on and off. You can save any set of enzymes in a separate file for use in **Analyze | Restriction Enzymes...** analysis. You can show/hide the window when you are not interested in restriction enzymes using the **RE Picker** toolbar button (note there is also now a companion button to show/hide the **Graphics Palette**);



## Gibson/Ligase Independent Cloning

There is a completely new interface and document type to handle a variety of ligase-independent cloning strategies. The interface supports both the 5' exonuclease driven “Gibson” assembly technique as well as the T4 DNA Polymerase 3' exonuclease “Ligase Independent Cloning” approach. You can have MacVector automatically design primers for you, or you can provide custom primers you have designed yourself manually, or with popular internet tools such as the NEBuilder website. You can also just provide existing fragments with overlapping ends for MacVector to assemble. The interface also shows the exact structure of the junctions between fragments, including relevant CDS translations so that you can check you have protein fusions in the correct frame.

The interface is highly interactive – you can drag features into it from other sequence documents and even drag a restriction enzyme(s) into it from a vector to use the cut vector as a base for you cloning experiment. The recommended primers are listed in a separate tab that can be printed or copied to other applications, so you can document them before sending them off for synthesis. A simple click creates the new circular molecule once all ends have been accounted for. The entire project can be saved as a new document type, and any fragment can be separately opened in a normal sequence window either before or after applying PCR primers.

The screenshot shows the MacVector software interface for editing a pUC19 plasmid. The main window displays the plasmid map with features like `lacZalpha`, `AmpR`, and `pMB1 ori`. Below the map, there are sections for 'Primers' and 'ORF1' analysis. The 'Primers' section shows two 'Automatic Primer' options with their respective sequences and melting temperatures (Tm = 52.3°C and Tm = 52.6°C). The 'ORF1' section shows the ORF1 sequence and its translation: ProSerLeuHisAlaCysArgSerThrLeuGluMetProAspLeuThrSerPheTrpIleSerPhe. The interface also includes a circular map of the plasmid on the right side.

## Genome Comparison

In recent years that has been an explosion of whole-genome sequencing projects. One common question coming out of this has been to ask “Exactly what are the genetic differences between my sequenced organism and another related strain?” MacVector to the rescue! A new **Analyze | Compare Genomes By Feature...** feature lets you see the differences between two annotated genomes in fine detail. The function takes every annotated feature from the source genome and looks for the presence of that feature in the comparison genome based on sequence similarity. CDS features are even translated so that the predicted amino acid sequences are compared. The results are then tabulated to show identical, closely related, and weakly related features in separate tabs, with additional tabs for features that are completely missing and a “details” tab that shows the low-level alignment details for any matching pair of features. Hot-links in the result tabs let you quickly scroll the parent sequences to any individual feature of interest.

```

Campylobacter jejuni 35925.nucl — Results
Details
Campylobacter jejuni 35925.nucl
CDS
  complement(179918..180028)
  /codon_start=1
  /db_xref=GI:761233174
  /inference=ab initio prediction:Prodigal:2.60
  /locus_tag=UC78_0176
  /product=hypothetical protein
  /protein_id=AJP34688.1
  /transl_table=11
  /translation=MKKIILFLLCVGFACSEHSHTDFKDLNKTEYNSQ

Campylobacter jejuni subsp. jejuni IA3902.nucl
CDS
  complement(172572..172697)
  /codon_start=1
  /db_xref=GI:284925468
  /locus_tag=CJ5A_0166
  /product=putative lipoprotein
  /protein_id=ADC27820.1
  /transl_table=11
  /translation=MKKIILFLLCVGFACSEHSHTDFKDLNKTEYNSQLKDKI

Aligned Length = 41      Gaps = 5
Identities = 36 (87.8%)  Similarities = 0 (0.0%)

Campylobacter jejuni      1 MKKIILFLLCVGFACSEHSHTDFKDLNKTEYNSQ----      36
Campylobacter jejuni      1 MKKIILFLLCVGFACSEHSHTDFKDLNKTEYNSQLKDKI      41
*****

Aligned length = 112  Unaligned residues = 14
Raw alignment score = 213 (maximum raw score = 222) = 95.9%
Overall score (accounting for unaligned residues) = 90.6%

Campylobacter jejuni 179918 ATGAAAAAATAATTTTATTTTACTATGCGTTGGCTTTGCTTTGCTGCTGAACAT 179977
|||||
Campylobacter jejuni 172586 ATGAAAAAATAATTTTATTTTACTATGCGTTGGCTTTGCTTTGCTGCTGAACAT 172645
|||||
Campylobacter jejuni 179978 TCTCATACTGATTTTAAAGATCTTAATAAACCGAGTATAATTCCTCAAT-AA 180037
|||||
Campylobacter jejuni 172646 TCTCATACTGATTTTAAAGATCTTAATAAACCGAGTATAATTCCTCAATAAaggataaa 172705
|||||
Campylobacter jejuni 180038
Campylobacter jejuni 172706 atatga

```

## Assembly Jobs

You can now run multiple jobs in an assembly project and each job is encapsulated in its own job object in the Assembly Project window. This gives you much greater flexibility in organizing your assembly tasks and each job is given an intuitive name.

The screenshot shows the 'Properties' tab of the Assembly Project window. It displays a table of jobs with columns for Name, Status, Length, #, ClipR, and Stop. The jobs listed include 'AnnotatedGenome', 'Cj-RM35925\_S23-1643\_L001\_R1\_001.fastq', 'Cj-RM35925\_S23-1643\_L001\_R2\_001.fastq', 'Cj-RM35925\_S23\_L001\_R1\_001.fastq.gz', 'Cj-RM35925\_S23\_L001\_R2\_001.fastq.gz', 'Cj-RM35925\_S23\_L001\_R2\_001.fastq.gz', 'Bowtie 2 - 16:00 - Dec 14, 2018', 'Unaligned\_Reads\_71.fq.gz', 'AnnotatedGenome Contig 71', 'Velvet 1 - 15:38 - Dec 14, 2018', 'Velvet Cj-RM35925\_S23-1643\_L001\_Rx\_001 - 15:32 - Dec 14, 2018', 'Unaligned\_Reads\_1', and 'Contig 2' through 'Contig 9'.

Name	Status	Length	#	ClipR	Stop
AnnotatedGenome	REF	1618194		1	1618194
Cj-RM35925_S23-1643_L001_R1_001.fastq	Illumina Paired-e...	301	854542		
Cj-RM35925_S23-1643_L001_R2_001.fastq	Illumina Paired-e...	301	854542		
Cj-RM35925_S23_L001_R1_001.fastq.gz	Illumina Paired-e...	301	859505		
Cj-RM35925_S23_L001_R1_001.fastq.gz	Illumina Paired-e...	301	749965		
Cj-RM35925_S23_L001_R2_001.fastq.gz	Illumina Paired-e...	301	870000		
Cj-RM35925_S23_L001_R2_001.fastq.gz	Illumina Paired-e...	301	770000		
▼ Bowtie 2 - 16:00 - Dec 14, 2018					
Unaligned_Reads_71.fq.gz	Illumina Unpaired	301	28175		
AnnotatedGenome Contig 71		1618194	1581295		
▶ Velvet 1 - 15:38 - Dec 14, 2018					
▼ Velvet Cj-RM35925_S23-1643_L001_Rx_001 - 15:32 - Dec 14, 2018					
Unaligned_Reads_1	454	301	734000		
Contig 2		166101	95368	1	166101
Contig 3		36487	24718	1	36487
Contig 4		87616	44983	1	87616
Contig 5		241784	137195	1	241784
Contig 6		191924	103696	1	191924
Contig 7		38682	20543	1	38682
Contig 8		159227	99478	1	159227
Contig 9		47436	25686	1	47436

There is a properties tab that lists all of the relevant details for the currently selected job, including input parameters, total assembled reads, average contig length, total contig length and even N50 to give you an idea of the quality of genome assemblies. A popup menu lets you quickly switch between different jobs.

## Coverage Tab

Assembly projects now have a **Coverage** report that allows you to select a reference sequence and directly compare multiple reference assemblies. You can compare different



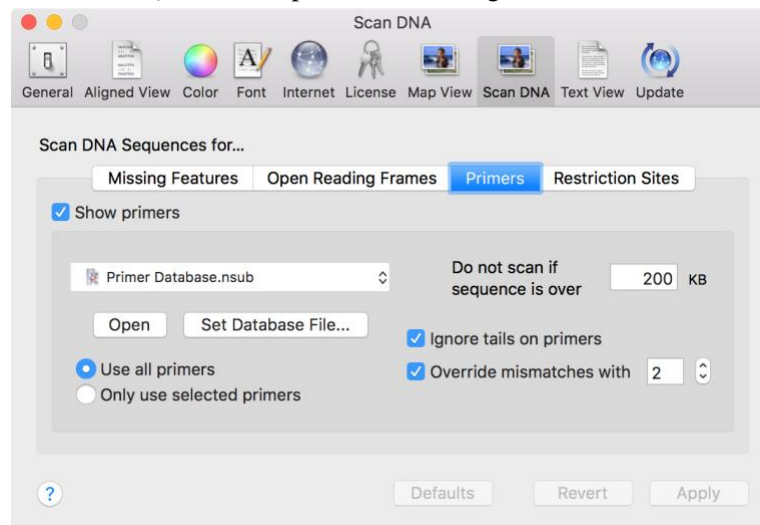
sequencing datasets assembled against the same reference sequence with expression level comparison. Now that you can store multiple assembly jobs in a single Assembly Project, then you can also directly compare multiple runs of the same dataset against a single reference sequence to compare which is the best assembly.

## Assembly Problems

*Align to Reference* now has a **Problems** tab that helps you identify mis-assembled genomic sequences based on excessive mismatches, discontinuous reads and other common problems. The primary aim of this tab is to help you identify potential assembly issues with genomic sequencing projects. You can use *Align to Reference* to assemble several million reads against a typical small genome (practically, up to ~10 Mbp or so) and the tab will report those regions that are most likely to be misassembled.

## Scan for Primers

MacVector now automatically scans DNA sequences for primer binding sites whenever you open a DNA sequence, in addition to the Restriction Enzymes, Open Reading Frames and Missing Features introduced in previous versions. By default, the collection of primers in the `/MacVector/Subsequences/PrimerDatabase.nsub` file are used, but you can use any `.nsub` file you like, configured using the updated **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.

## Use of APIKeys with Entrez and BLAST

The NCBI have introduced a new system for accessing the Entrez database over the internet. They now throttle general accesses to the Entrez server to no more than 3 calls per second per IP address. This might seem a lot, but if you want to download a list of 100 sequences, this can really slow things down, especially if you are sharing a public IP address behind a company or university firewall and others are using MacVector. They have introduced a new “APIKey” concept – you can request one of these from the NCBI for your own personal use and that increases the permitted rate to 10 calls per second and is independent of the IP address. Thus, you can share a public IP address with colleagues

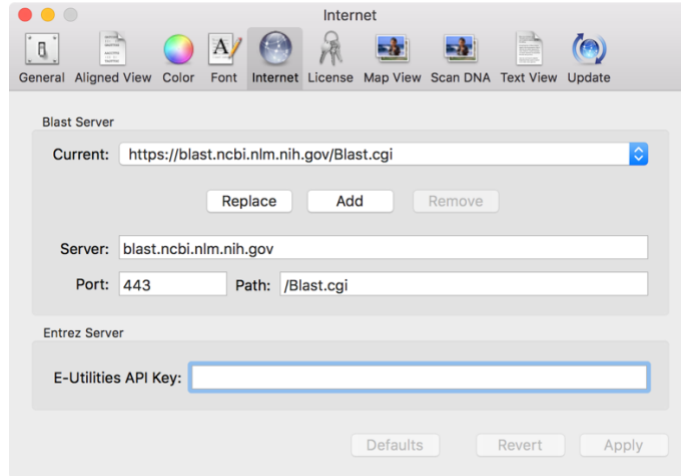


and still each have the full 10 calls per second access.

Here's what the NCBI have to say about APIKeys;

<https://ncbiinsights.ncbi.nlm.nih.gov/2017/11/02/new-api-keys-for-the-e-utilities/>

Once you get one, you can tell MacVector to use it using the **MacVector | Preferences | Internet** tab;



## How Do I?

There's a brand new **How Do I** menu that shows common workflows with simple step by step guides and short videos.

Every tool dialog now has direct access to a simple video/tutorial on how to use it.

## Miscellaneous Enhancements

You can now copy and paste features between sequence documents. Simply select the feature in the Features tab of one sequence, **Edit | Copy**, then switch to another sequence Features tab and choose **Edit | Paste**.

You can now select a short sequence in a Read in the Align To Reference **Editor** tab, right-click to bring up a context sensitive menu, and then select all of the other aligned reads that contain that a sequence. It's a great way of selecting all the reads with a specific SNP(s). Combine it with selecting the pairs for each read with NGS data and saving the selected reads and you have a very powerful way of analyzing SNPs or resolving repeat sequences in genomic assemblies.

Some of the nomenclature and interactions in the Primer3 dialog box have been cleaned up to simplify its use.

You can now add sequences to the *Align To Reference* window from multi-sequence GenBank files.

GenBank multi-sequence files now open by default as individual sequences.

When results are generated for the Bowtie **Coverage** tab, the name of each feature is now displayed exactly as per the label used in the **Map** tab allowing you more control over exactly how the text appears.

There is now an option in the **Database | Auto-annotate Sequence...** interface to automatically "fix" CDS features. This will change the stop location if the match creates a longer or shorter open reading frame and will also change the contents of any /translation= qualifier to reflect the new translated coding sequence.

The *Align to Reference* algorithm is now multi-threaded. You will see a significant speed up, particularly if you are using larger *Sensitivity* values, though we still recommend keeping *Sensitivity* to a low (<4) value and the *Hash Value* to the maximum possible value for optimal performance when searching through large amounts of NGS data.

## Bug Fixes

The plain text output from the **Analyze | Restriction Enzymes** function has been re-worked to correct some problems introduced in MacVector 15 where the reported restriction enzyme cut sites were not correctly aligned.

Some inconsistencies in outlining similarities in the Multiple Sequence Alignment **Picture** tab have been resolved.

Some problems in the *Align to Reference* consensus calculation when aligning reads that wrap around circular sequences has been resolved.

Some strand-specific quirks with the *Auto Annotation* function have been resolved.

Network Licensing: Some issues with MacVector not cleanly releasing Sassafras KeyServer licenses have been cleaned up. In addition, the error messages reported with KeyServer are now more informative.

The scale bar has been restored to the *Phylogram* view in the *Phylogeny* window.

## 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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