

MacVector[®] 10.6

for Mac OS X

System Requirements

MacVector 10.6 runs on any PowerPC or Intel Macintosh running Mac OS X 10.4 or higher. It is a Universal Binary, meaning that it runs natively on both PowerPC and Intel based Macintosh computers. There are no specific hardware requirements for MacVector – if your machine can run OS X 10.4 or above, it can run MacVector. A complete installation of MacVector 10.6 uses approximately 85 MB of disk space.

Changes for MacVector 10.6

Vector NTI Database Reading

There is a new function that allows you to directly import sequence data from databases created by Vector NTI Advance v10 or earlier. Select the new **Database->Vector NTI Import...** menu item and then click on the **Choose** button to locate the Vector NTI database folder on your file system. The database can reside on a remote Windows machine if required – make sure you share the parental directory containing the Vector NTI Database folder on the remote machine, then connect to that machine using the Finder **Go->Connect to Server...** menu item.

Once a database has been selected, MacVector will display a list of all of the sequences available in the database. There is a popup menu to toggle between Nucleic Acid and Protein sequences. The list can be sorted to more easily identify sequence(s) of interest. Select one or more sequences and then click either the **To Desktop** button to open those sequences in MacVector, or **To Disk** to save the sequences in MacVector format to a folder on your hard drive.

MacVector will read all of the standard features and annotations associated with each sequence. For this release, feature appearance information is discarded and the default MacVector feature representation are used instead. In addition, MacVector ignores any restriction enzyme sites annotated in the database sequence and replaces them with the default dynamic set of sites used by the **Map** tab.

Changes for MacVector 10.5.3

Bug Fixes

A number of bugs were inadvertently introduced while adding the exon/frame translation enhancements in 10.5.2. All have now been fixed. The specific bugs were; (a) if you created a protein through a translation, the last two amino acids were always missing; (b) proteins created from minus strand translations were reversed and (c) there were occasional crashes when a result window containing a translation was refreshed (e.g. after changing the Text Display preferences).

You can now create “point” features – i.e. features where the start and stop locations are the same residue.

The trace file editor has been modified to solve the occasional appearance of extra gaps and to prevent lower case characters from being entered. Also, if the editor has been opened from an Assembly Project, you no longer get unnecessarily prompted to save changes.

The name of the second aligned sequence is now correctly displayed in the Pustell Matrix alignment text window.

When you “Save As...” a multiple sequence alignment file, the current window now gets its title changed to reflect the new name.

Changes for MacVector 10.5.2

New Functionality

MacVector now honors the standard GenBank `/codon_start` qualifier to define the start frame of a coding region. This is useful when annotating exons in eukaryotic sequences where the triplet codons may not be in phase due to the presence of introns. Valid values are 1, 2 or 3. The annotated sequence output now correctly displays the translated amino acids for all segmented features in addition to honoring the `/codon_start` qualifier.

Bug Fixes

Several crashes that occurred when saving modified sequences have been fixed.

Occasional hangs during startup with the trial version have been resolved.

Sequences containing quotes in the annotation comments can now be saved correctly in BSMML and Assembly file formats.

Junk characters are no longer appended to certain textual result windows.

Copying sequence data from a Read feature in the Contig Editor now works correctly.

When exiting MacVector with jobs still running, the job manager now waits for your input rather than exiting after 5 seconds.

A range selection discrepancy in the Primer3 dialog has been fixed.

Selections in the multiple sequence alignment editor now display correctly even when blocking is set to be non-zero.

The Results section of the Default Symbols editor dialog now displays the correct labels in the list of results.

A “one-out” calculation bug in the pairwise alignment and pairwise matrix result tabs of multiple sequence alignments has been fixed.

Changes for MacVector 10.5.1

Bug Fixes

A problem where sequence document icons would sometimes be replaced by generic icons was fixed.

A crash bug when zooming in the Restriction Enzyme results Map window of large sequences was fixed.

Align to Folder now correctly displays the sequence alignments.

A crash when importing slightly malformed GenBank files (such as those exported from Vector NTI) has been resolved.

A problem where the last line of reports in text windows would be missing has been fixed. This would lead to e.g. the last Restriction Enzyme not getting reported in the Enzyme Cutters list.

Changes for MacVector 10.5

cDNA Alignments and Splice Site Identification

The Sequence Confirmation algorithm from MacVector 10.0 has been rewritten to allow you to align cDNA clones against corresponding genomic sequences and accurately identify the splice site junctions between intron and exon sequences. Actual splice sites at ambiguous junctions are determined using the standard GT..AG intron rule. Once identified you can quickly save each intron or exon as a feature on the parental sequence. The analysis function has been renamed from “Sequence Confirmation” to “Align to Reference” to more accurately reflect the new functionality. The algorithm is sensitive enough to let you align random cDNA sequencing chromatogram reads directly against a genome and identify the splice junctions even with typical sequencing errors.

Long Filenames

The 31 and 63 character limits on filenames in previous versions has

been removed for this release for all sequence related files.

Universal File Reading

The file reading code in MacVector 10.5 has been consolidated so that any sequence format that MacVector can read can be used as input to any MacVector function. Specifically, this means that you can now use any supported single or multiple sequence file format for;

- Importing into multiple sequence alignments.
- Importing into Align to Reference (formerly Sequence Confirmation) windows.
- Importing into Contig Assembly Projects (Assembler only).
- Target files for the Align to Folder function.

In particular, you can now create FastA format database files and use them in the Align to Folder function. Because of performance and memory related issues, we recommend you keep any FastA databases under 100 MB in size for use in Align to Folder.

Combined Preferences

The various global settings in MacVector have now been combined into a single multiple pane Preferences dialog, accessible from the standard OS X Preferences menu item. This simplifies the configuration of many of the default settings allowing you to customize MacVector to your own personal tastes.

Align to Reference Text Printing

There is a new tab in the Align to Reference (previously called Sequence Confirmation) window called "Text". This is a summary of the alignment that uses the Editor tab settings to generate a printable text display of the entire alignment. You can use this to print the alignment or copy interesting sections of the alignment for pasting into other documents.

Toolbar Customization

The OS X style toolbars introduced in MacVector 10.0 are now fully customizable using the standard OS X editor. You can add, remove and rearrange the toolbar buttons so that you have just the icons you regularly use close at hand.

Profile Scans

There is now a simple profile scanning capability built in to the Coding Preference Plot feature, which has been renamed "Nucleic Acid Analysis Toolkit". MacVector reads profile files using the transfac profile format.

Online Help

The online help has been significantly revised, new content added and

the layout has been improved.

Licensing Enhancements

If you have purchased more than one MacVector license, you can now have multiple licenses installed on one machine. If the currently selected license is already in use elsewhere on the network, you can quickly toggle to a different license without needing to re-enter the license details.

Miscellaneous Enhancements

The graphical outputs of the Pustell Matrix analyses, the Protein Analysis Toolkit and the Nucleic Acid Analysis Toolkit (formerly Coding Preference Plot) have been recoded so that they are resized along with the window. This allows the display of large matrices or wide profiles in far greater detail than was possible in MacVector 10.0.

There are new keyboard equivalents for File->New->Nucleic Acid (command-N), File->New->Protein (command-option-N), File->New->Assembly Project (command-control-N), and last File->New-><type> (command-shift-option-N).

Replica toolbar item now has a drop down menu to quickly open to any available view.

There are a number of additional toolbar items e.g. Add Feature in Sequence Editor view, Add Seqs and Remove Seqs in MSA Editor view, and Add, Edit and Delete feature in the Map view.

All MacVector files now use File extensions for maximal file system compatibility and the File Save dialogs use optional extension hiding

File proxy items in window title bars to show the path and to drag either the file or the path (e.g. the file can be moved or copied by dragging the proxy item or one can drag the icon to the terminal window to use the complete path in a command line tool).

There is a new Starting Point dialog. Although experienced users will not typically need this (it can be switched off with a checkbox in the dialog itself), new users can quickly find and open sample files or other sequences to get them started more easily.

A new Software Update preference pane gives you greater control over notifications of new releases and bug fixes. This also now includes custom news items and hyperlinks in the dialog.

MacVector 10.5 now handles downloading extremely large sequences more gracefully. In addition to performance enhancements, you also now have the option of skipping particularly large sequences.

The window title bar and Window menu have been enhanced to include the name of the currently selected tab.

When MacVector has completed jobs that you haven't yet looked at, the

dock icon now indicates how many results are ready for you to view.

Editing and navigation in the Contig Editor and Align to Reference editor has been enhanced. For example, you can now insert residues by holding down the <option> key and typing a residue.

You can now select a single segment of a multi-segmented feature by holding down the <option> key while clicking on it. The Feature list now has a group disclosure triangle to let you toggle between selecting the entire feature, or selecting individual segments.

Updated Third Party Tools and Libraries

Support for NCBI-GenBank Flat File Release 168.0 (October 2008)

DDBJ/Embl/GenBank features version 8 October 2008

clustalw 2.0.9

primer3 1.1.4

NCBI toolkit version ncbi3_2_2008 (March 2008)

REBase version 811 (Nov 2008)

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 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:

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