

# MacVector 11.1

for Mac OS X

## System Requirements

MacVector 11.1 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 11 uses approximately 95 MB of disk space.

## Changes for MacVector 11.1

Rather than add just a few major new features for MacVector 11.1, we have instead added a large number of minor enhancements throughout the entire application, all designed to either fix longstanding bugs, improve the Mac OS X look and feel of the application or simplify and improve existing workflows.

Many of the analysis functions now use drop down window-modal sheets rather than application modal dialogs, allowing you to continue to work with other windows to prepare, view or copy data required for the analysis. Many of the sheets have a convenient new history combo box that keeps track of the various data files or target folders used in the dialog to allow rapid switching between commonly used files.

Multiple levels of Undo have been added to the Trace, Multiple Sequence Alignment and Contig/Align to Reference editors. All three have also had extensive work to streamline workflows, add keyboard navigation and fix various display glitches and crash bugs.

The specific enhancements and bug fixes in MacVector 11.1 are listed below, broken out by functional area. It's a long list, but if you read it through you should get a lot of hints on how to make the most of this release of MacVector.

## Miscellaneous Enhancements

There is a new Genetic Code reference window accessed from the **Window | Genetic Code Key** menu item that displays the codons of the currently selected genetic code.

There are now keyboard shortcuts to switch between tabs – hold down the apple command key and type “1” to switch to the first tab, “2” for the second tab etc.

Many dialogs that have file selections (e.g. restriction enzymes, matrix files) or directory paths (e.g. Align to Folder and Auto-annotation) now have a history combo box. Not only can you quickly switch to a different file you've used before, but you can even drag and drop files or folders onto the control (OS X 10.5 and later). If you hover the mouse pointer over the control, a tooltip will reveal the full path of the file/folder.

“Dirty” windows now display a dot in the red window close button.

Text windows and tabs now support standard keyboard and mouse selections. You can also drag selected text out of a result window and drop it into other acceptor windows e.g. Microsoft Word or Text Edit (OS X 10.5 and above only).

Dialogs to locate auxiliary data files (Restriction Enzymes, Matrices, Codon Bias tables etc) now all default to the appropriate location in the MacVector distribution folder.

## Miscellaneous Bug Fixes

You can now copy selections of enzymes/subsequences from one enzyme/subsequence editor and paste into a different window without MacVector crashing.

A problem where menu shortcuts were not always immediately active after switching windows has been fixed.

The Proofreader has been fixed to solve an occasional crash, to prevent “double voices” from playing and to reset the progress bar when cancelled.

An occasional problem where the Primers and Phylogenetic Analysis submenus would become permanently disabled has been fixed.

## Analysis Functions

Align to Folder, Restriction Enzyme, Proteolytic Enzyme, Nucleic Acid Subsequence, Protein Subsequence, Translation and Reverse Translation are now all window modal dialog sheets.

Align to Folder – now scans hierarchical sub-folders as well as the selected folder.

Align to Folder – now can handle many different types of non-sequence data without hanging.

Auto-annotation and Align to Folder – now have a new history combo box for the selected folder so you can quickly switch to different folders you commonly use. A tooltip reveals the full path of the folder when you hover over the control.

Auto-annotation – now has a defaults button to revert to factory settings.

Restriction/Proteolytic Enzyme – you can now specify the minimum number of cuts as well as the maximum number of cuts when filtering (or setting up) the results. The selected enzyme data file is now displayed in a history control so you can quickly swap between commonly used files.

Translation – there is now no limit to the text you can add in the “segments to translate” edit box.

Translation – the translation settings now automatically fill out the segments to translate and phase if you have a segmented CDS feature selected when you invoke the analysis.

Protein Analysis Toolbox – the AA Composition, pI and MW protocol now also displays the predicted extinction coefficients and aliphatic index. In addition, the pI and molecular weight calculations have been revised for increased accuracy.

BLAST – the result windows now come to the front if you repeat a search instead of staying hidden in the background.

BLAST – the aligned output now honors the selected “-1” character from the Aligned Display preferences pane to flag mismatches.

BLAST – the alignment result window numbering now honors any origin set in the parental sequence.

BLAST – TBLASTN result numbering is now correct.

Primer3 – the “allow ambiguous residues” setting is now remembered between runs.

Primer3 – you can now copy individual primers from the spreadsheet result window.

Primer3 – the primers from the spreadsheet results can now be exported as a fasta format file.

Primer3 – gap characters are no longer permitted in the edit boxes, preventing occasional calculation problems.

NA/AA Subsequence – the graphical Map result window is now linked back to the parent

sequence so that selections in the result window are propagated to the parent editor.  
Open Reading Frames – the Map result window now opens with the graphics fitted to the size of the window.

## Sequence Editor

Printing now honors the selected page range.

The interpretation of copied sequence data on the clipboard has been improved so that many non-sequence characters (such as forward slashes) are now accepted and skipped.

The Range control now discards non-numeric input.

The Range control selection mechanism has been changed – after typing in the control, press <enter>, <return>, <tab> or <esc> to change the focus to the sequence editor so you can copy sequence data.

The clipboard code has been reworked to resolve occasional problems copying and pasting into other applications such as Microsoft Word.

There is a new context-sensitive menu item to “Reset Origin to 1” – use this if you have copied a segment of a larger sequence to a new window and don’t want to retain the original numbering.

Setting the origin is now redo/undoable.

You can now drag a selection from one sequence window and drop it into another single sequence window or into an external application (e.g. TextEdit or Microsoft Word) that can accept drag and drop text.

## Map View

A number of crashes have been resolved in the Map view.

The layout of cut sites on crowded maps has been improved.

The layout of crowded restriction enzyme has been dramatically speeded up (~20-fold).

MacVector now automatically suppresses the display of feature labels for large sequences with many features – you can control this from the Map View preferences pane.

When you hover the mouse over a feature, a tooltip displays the label of the feature – useful for crowded maps or when labels are switched off.

Better use is made of the inside region of circular maps to prevent features from overlapping each other or the sequence title.

Restriction enzyme sites are now not displayed if the Map is so crowded that they will not individually resolve. You can view the hidden sites by zooming in to a smaller region or by right-clicking on the display and choosing “Show Results”.

The graphics view is now refreshed more optimally to reduce flickering and avoid multiple redraws of complicated layouts.

A crash when undoing a paste into the Map has been fixed.

The sequence characters no longer disappear when the display is set to unlimited line length and the sequence is longer than ~3,000 residues.

You can now select any graphical object (e.g. a feature) and Edit | Copy will copy a blunt ended copy of the underlying sequence to the clipboard.

Clicking on a feature expands the tree view in the graphics palette to show the feature.

Double-clicking on a restriction enzyme selects all the cut sites for that enzyme.

There is a new Show/Hide Graphics Palette toolbar button (“Palette”) that you can optionally add to the Map Tab toolbar (right-click on the toolbar to bring up the

**Customize Toolbar...** menu item). Add this if you find yourself frequently toggling the visibility of the graphics palette.

There is a new optional Fit to Window/Zoom to Sequence (“Zoom”) toolbar button.

The Range control from the Editor tab is now displayed by default in the Map tab – 11.0 users will need to add the button using the **Customize Toolbar...** option.

If you close the active default restriction enzyme file without saving changes, the Map now refreshes to reflect the status of the unedited file.

The Ligation dialog now treats sequences copied from external sources or the sequence editor as blunt-ended fragments.

There is new **<Size>** meta-tag for graphics labels – use this to display the size of a feature in the label (you can also use **<Length>**).

There are new **<Total>** and **<Index>** meta-tags for graphics labels – these can be used for restriction enzyme cut sites e.g. “<Desc> (<Index>/<Total>)” would generate labels like “BamHI (1/3)”, “BamHI (2/3)” etc.

You can now correctly combine qualifier based metatags so that e.g. “<gene> (<number>)” will display “My Gene (1)” if the qualifiers /gene=”My Gene” and /number=”1” are present in the feature description.

Qualifier based meta-tags are now skipped if the qualifier doesn’t exist in the feature description (previously the actual meta-tag text e.g. “<gene>” would be displayed).

There is a new popup menu in the feature symbol editor that lets you view all of the available meta-tags and insert them into the label. Click on the small triangle to the left of the label edit box.

“Vertical” labels no longer display upside down on circular maps.

## **Trace Editor**

There are now multiple levels of Undo.

The Range edit box now correctly updates when you drag-select in the trace editor.

The editor now scrolls to display any selections input in the range control or in the drop down feature selection menu.

The editor now displays the appropriate selection when you select a feature in a different tab or replica window.

The window now correctly responds to Full Window Title.

Printing now works correctly (broken in 11.0).

## **Multiple Sequence Alignment Editor**

There are now multiple levels of Undo.

The **% Consensus** color group consensus match color is now applied correctly.

Changing the selected color group now correctly updates in replica windows.

The Picture tab in a replica window is now correctly updated when activated if the underlying alignment has changed.

You can now insert a column of gaps in the editor by selecting a column and pressing the period or hyphen (minus) keys.

A PowerPC/Intel endian problem in saved files was resolved.

You can now use “forward delete” as well as “backspace delete” in the editor.

There are now optional toolbar buttons to add and remove sequences from the alignment.

The left hand name panel now automatically resizes to fit the longest name.

You can now fully select in the editor using just the arrow and <shift> keys.  
ClustalW alignments no longer crash if an input sequence has a ">" in the name.  
MacVector no longer hangs when cancelling a long Print Preview from the editor.  
Hiliting is now shown in grey when the window is in the background.  
The display is now immediately updated if you delete a trailing column of gaps.  
The phylogenetic analysis parameters are now remembered between runs.  
There is a new "Show Dots" button that can optionally be added to the editor toolbar.  
Right-click on the toolbar and choose **Customize Toolbar...** to add the button.  
You can now paste sequence data from external applications into the editor.  
The display now automatically scrolls vertically if you drag-select downwards in linear display mode.

### **Contig/Align to Reference Assembly Editor**

There are now multiple levels of Undo.  
Zooming in the Map tab now repositions the editor to the corresponding location.  
In the Align to Reference editor, you can now overwrite a gap in the Reference sequence with another gap to delete the corresponding residue in each overlapping read. Use this to quickly delete extra mis-called bases in the reads so they match the reference.  
Replica windows now also close if a contig was dissolved due to an edit.  
A number of crashes have been fixed – particularly after deleting residues from the end of a Read or the reference sequence, or after deleting Reads or features from an Assembly.  
Align to Reference calculations now honor any selected sequences in the alignment – if none are selected, then all are aligned.  
Reads that overlap the 3' end of the alignment can now be selected as expected and the titles highlight.  
The Align to Reference algorithm has been tweaked to solve occasional problems where it would not choose the best alignment.  
The Map tab now correctly updates if you delete an existing feature in the view.  
If a contig is saved as a different format file, the file is added to the recent items menu.  
Gap handling has been improved to ensure common gaps are closed up during edits.  
The editor no longer gets confused when you scroll through a large number of gaps in the reference sequence over a short region of the alignment.  
The consensus is updated after sequences are removed.  
Pasting now prompts you to unlock locked documents.  
The Text tab now refreshes in response to changes in replica windows.

### **Feature Editing**

Entering non-standard keywords no longer crashes MacVector.  
The Feature tab has a new context sensitive (right-click) menu item that lets you Join two or more selected features of the same type.  
The Feature tab context menu now lists all /db\_xref and /protein\_id qualifiers – selecting one will open the appropriate database source in the default web browser.  
The drop-down qualifier menu now ignores "/" characters so you can type a character to alphabetically jump to those entries.

Protein features can now have multiple locations.

Read features can now be deleted from sequences exported from the contig editor.

The labels “Create” and “Remove” are now used consistently throughout MacVector for all buttons that add/create or delete/remove features. This avoids conflicts with labels for buttons that add and remove sequences from an alignment.

### **Subsequence Editor**

The editor has been reworked as a dropdown dialog sheet and you can now copy/paste into the Sequence edit box. These changes let you easily paste primers from external applications or from other MacVector windows into a subsequence file to maintain a database of useful primers.

### **File Import/Export**

Vector NTI .ma4 and .pa4 files can now be imported into MacVector.

**File | New From Clipboard** now handles copied multiple sequence alignment data as well as single sequence data.

Imported text files (ASCII, GenBank etc) now appear on the recent file menu and do not prompt you to save when you close a window without editing.

Saving PubMed abstracts now uses a more intuitive Author-based default name, rather than the number of the document.

Sequences downloaded from Entrez are now named with a combination of GID and LOCUS e.g. “432991 (SCU03771)” so you can more easily relate the GID in BLAST and Entrez result lists to the saved file on disk.

Sequences imported from FastA format files are now named by taking the characters from after the “>” to the first white space in the description line (previously, the entire line was taken).

The extra Options button for controlling how Phylip formatted multiple alignment files are saved now appears under OS X 10.5 and OS X 10.6.

### **Preferences**

There are new Default buttons to let you quickly revert to factory settings for the Aligned Display, Colors, Internet, Map View and Text Display panes.

The Map View pane has a new option to enable/disable label hiding for sequences with many features.

The Preferences window is no longer left in a disabled state when all other windows are closed.

### **Job Manager**

MacVector now does a better job of cleaning up after itself if there is a crash while ClustalW is running so that it can be restarted without any problems.

Failed jobs no longer block the parent sequence from initiating new jobs.

It now prompts you to terminate all active jobs when exiting MacVector.

If you have Growl installed on your machine, the Job Manager will use Growl notifications when a job has completed rather than bounce the icon in the dock.

### **Assembler**

You can now open and edit plain sequences from the Assembly Project Window.

When you close a project, all associated open contig/trace/sequence windows are automatically closed.

You can now only open one copy of a contig/trace/sequence from a project – if you attempt to re-open a sequence, the existing window will be brought to the front.

If you attempt to open an assembler file without an active assembler license you now get a warning message.

The phred button is disabled if no trace files are available for base-calling.

Imported sequences can now have spaces in the name (they are converted to underscores as phrap does not permit spaces in the names).

There is a new import dialog for next generation sequencing data. In addition, each type of data gets a different graphical symbol so you can easily distinguish between them.

File type extensions are now stripped off when importing data into assembly projects.

### **Find Functionality**

The Find dialog no longer gets confused by upper and lower case when trying to auto-complete entries.

The Find Feature interface remembers the last feature type searched for.

Find Feature now clears any existing restriction enzyme selections before searching.

Hits are now shown in replica windows as well as the original.

### **Starting Point Dialog**

The recent files are now sorted by last access date

A bug was fixed where MacVector would crash if a file was deleted externally after being displayed in the Starting Point Dialog.

### **Licensing**

The 21-day trial license now overrides any installed license – this lets existing users try out new features before deciding whether or not to upgrade or purchase Assembler.

The License Owner is no longer automatically filled out for new licenses to help prevent users overlooking the need to enter the License Owner exactly as written in the license e-mail.

The startup dialog for the demo version has been reworked to make it clear that there is no need for trial users to enter a valid license to be able to run the demo. version.

## 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:

<http://www.macvector.com>

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