Release Notes for
Molecular Analyst Macintosh
Densitometry
Version 2.1.2

FOR MOLECULAR IMAGERS
If you are using a PCI based Power Macintosh (7200, 7500, 8500, or 9500) make sure that you are running either System 7.5.3 or have the System 7.5 Update 2.0 installed.

**********ACQUISITION MODULES**********

MOLECULAR IMAGERS
- Full Support for GS-250, GS-363, GS-505, and GS-525 Molecular Imagers.
- Fixed problem with scanning with ATTO board with virtual memory on.
- There was a problem where you could not communicate with Imager using ATTO card.
  This occured when user had more than ID 5 checked in the Bio-Rad INIT/SExpress control panel. This has been fixed.
- Now Power Macintosh native.

DENSITOMETERS
- Full Support for GS-670, GS-690 and GS-700.

GEL DOC
- Full Support for Gel Doc 1000.
- Full Support for Gel Doc 1000 on PCI Power Macintoshes.

ALL
- Made KanjiTalk compatible.

**********APPLICATION**********

MOLECULAR ANALYST 2.1.1

- Added support for video printing on PCI Power Macintoshes via Gel Doc 1000 system.
- Made KanjiTalk compatible.

MOLECULAR ANALYST 2.1

- TIFF import
- New preferences dialog box

- Pallete control affects print output
- Color printing
- Video printing (Need a video printer connected to Gel Doc frame grabber board)
- Increased number of displayed significant figures in volume results table, profile display window and exported volume analysis data.
- Improved tick mark display on profile graph axis.

Bugs Fixed 2.1

General:

- The file compatibility warning dialog is not displayed in Revert of image or profile files now because the dialog has been displayed once when the files are opened.
- Hitting the forward delete key in the transform window no longer locks up the appication.

Image:

- For data just below saturation, attenuation could cause dark lines of data. This is fixed.
- Preview of a 1600 magnified image is not messy any more.
- The preview image at the left bottom corner on the Transform window displays correctly for a 1600 magnified image.
- The Preview window correctly shows the outline of the image when the image is resized smaller.
- Weighted Noise Reduction filtering of a large image (more than 10M) does not mess up the image any more.
- The %Total and %Max radio buttons in the Spot Parameters dialog box work properly now.
- Changing a saved, previously unmodified image with the Transformation command does enable the Save command now.
- Renaming an opened image file in the Finder and then trying to save the image second time in the application do not crash the application any more.
- Every time switching between the triangle and scrollbar controls or moving the bottom triangle in the Transformation window does not alter the maximum value any more.
- Images can be printed on LaserWriter IIIp and HP DeskWriter 560 printers now.

Overlay:

- Any long text overlay, with most part of it hanging off the left edge of an image, is not off the image any more when the text length is shortened.
- Dragging a long text overlay to the left edge of an image sometimes shortened and truncated the text. This is fixed.

- The Font menu marks the currently selected font for any fonts below the 31st menu item now.
- Strictly vertical or horizontal multi-segment profile extraction lines can be moved now.
- Hitting the delete key while creating a multi-segment profile extraction line does not crash the application any more.
- Labels of overlays are duplicated in overlay duplication on an image.
- Font size of text overlays other than the standard ones are saved and can be recalled now.
- Corrected menu bar access when the Overlay Info windows are up.
- Removed left over outlines in the rotation of a rectangular volume overlay.
- Some of the horizontal and vertical line profile overlays were sometimes not included in image cropping. This is fixed.

Regression:

- In Auto Integrate mode of an image, all concentration, molecular weight (MW), and isoelectric point (PI) columns on the Report window are correctly changed and updated when the regression type is changed with the Regression window is up.
- % Volume column in the Report window is always updated for grid overlay changes.
- The Report window displays valid values now for concentration, molecular weight (MW), and isoelectric point (pI) after Revert to Saved of an image with newly created overlays on it.
- Zero values are allowed in concentration, molecular weight, and isoelectric point (pI) analysis.
- A scroll bar was sometimes shown in the Regression window. This is corrected.

Profile:

- Boost Factor item in the Smooth Options dialog could sometimes be highlighted even if it was hidden. This is fixed.
- Improved the DWMTM filtering algorithm.
- One decimal point is added in displaying the profile values in counts.

KNOWN PROBLEMS

GEL DOC 1000 ACQUISITION

Issues with long image acquisition/integration times:
Gel Doc can acquire an image of an Ethidium Bromide stained DNA gel in about 0.5/5.0 seconds. When integration times are increased beyond about 5 seconds, you may begin to notice delays in performing requested commands.

You should investigate these issues before a long integration time is attempted with an important sample exposed to UV illumination.

Let us examine what happens with an example. Set the Gel Doc acquisition option "Live/Integrate" to "Integrate" and use a time of 10 seconds. The camera's CCD is exposed to incoming light for 10 seconds, the image is transferred to the computer and then the CCD is exposed to light for another 10 seconds. This cycle is repeated until the capture button is pressed or the acquisition window is closed or the capture options are changed.

The Molecular Analyst software does not respond to any user input during the 10 seconds that the CCD is exposed to light. Keystrokes and mouse clicks are stored in the computer, but they are not acted upon until an image has been fully acquired and transferred to the computer. The stored key clicks and key strokes are executed during the short time interval between transfer of the image to the computer and the next round of CCD light exposure.

Thus the first delay is caused by the integration time itself. For example, If you should decide to capture an image you see on the screen and press the capture button while the CCD has been exposed to light for 3 seconds in its current cycle, the program will not react to the Capture command for another 7 seconds. The software will then expose the CCD to light for another 10 seconds and then display the image in a new untitled window.

For short integration times, this does not cause any problem. With long integration times, however, there will be correspondingly long delays in performing requested commands.

A second source of delay comes from the fact that generally only one to three mouse clicks or key strokes are acted upon during the interval between successive image transfers. Thus, if during an image integration cycle you have clicked the mouse many times on the image or on various controls, there could be a large backlog of commands to execute.