SoftMax® Pro Software Version 5.4.2 Software Release Notes

Introduction

The SoftMax® Pro Software version 5.4.2 update is a minor release. The following is a summary of the changes incorporated in this update as compared to version 5.4.1, the last general release of the SoftMax Pro Software.

New in SoftMax Pro v5.4.2

Updated Support for Operating Systems

SoftMax Pro Software v5.4.2 is now supported for MAC OS v10.6, as well as Windows 7, 32-bit and 64-bit operating systems supported in the SoftMax Pro Software v5.4.1 release.

Additional Windows 7 installation considerations for the SpectraMax® L Microplate Reader, StakMax® Microplate Handling System, and the MDC FileServer are addressed in an insert to the SoftMax Pro Software User Guide included with the software.

Modifications Made to SoftMax Pro Software v5.4.2

Protocol Modifications

The following protocol files were added, removed, or updated:

- **Assay Development**
  - Fluorescence Optimization
    Updated the introduction and instruction sections to enhance clarity and usability.
  - Z Factor Assay Development
    Changed from FlexStation® 3 Reader type to FI mode, and updated reader suitability to enhance the protocol's usability.
- **Cell Signaling and Transport**
  - QBT Fatty Acid Uptake-Endpoint
    Removed and replaced with QBT Fatty Acid Uptake protocol
  - QBT Fatty Acid Uptake-Kinetic
    Removed and replaced with QBT Fatty Acid Uptake protocol
  - QBT Fatty Acid Uptake (added)
    Added to combine QBT Fatty Acid Uptake-Endpoint and QBT Fatty Acid Uptake-Kinetic protocols into a single protocol.
- **Early ADME-Permeability & Solubility**
  - MScreen PAMPA
    Updated the introduction section to enhance clarity and usability.

- **ELISA-Kinetic**
  - HRP and ABTS-Kinetic
    Corrected group table reference in standard curve to ensure users get accurate results.
- **Molecular Devices**
  - Calcium
    Changed PMT to medium to accommodate firmware change and prevent PMT saturation with typical assays to improve user experience and avoid bad or lost data.
  - QBT Fatty Acid Uptake-Endpoint
    Removed and replaced with QBT Fatty Acid Uptake protocol
  - QBT Fatty Acid Uptake-Kinetic
    Removed and replaced with QBT Fatty Acid Uptake protocol
  - QBT Fatty Acid Uptake (added)
    Added to combine QBT Fatty Acid Uptake-Endpoint and QBT Fatty Acid Uptake-Kinetic protocols into a single protocol.
- **Nucleic Acids**
  - PicoGreen Fluorescence
    Updated the introduction section to enhance clarity and usability.
- **Reporter Assays**
  - GeneBLAzer
    Improved readers suitability.
  - Ready-To-Glow Secreted Luciferase
    Improved readers suitability.
- **Statistics**
  - Z-Factor Determination
    Changed from FlexStation® 3 Reader type to FI mode, and updated reader suitability to enhance the protocol's usability.
- **TR-FRET**
  - HTRF_Competitive
    Added a note to indicate that this protocol is for use with Europium reagents only.
  - HTRF_Immunoassay
    Added a note to indicate that this protocol is for use with Europium reagents only.
  - HTRF_Protease
    Added a note to indicate that this protocol is for use with Europium reagents only.
  - HTRF_Terbium Cryptate
    Added a new protocol for Terbium reagents from Cisbio.

Note: In version 5.4.1, the protocol folder titled **MDS Analytical Technologies** was renamed to **Molecular Devices**.

General Software Issues Addressed in SoftMax Pro Software v5.4.2

The "M3 M4 M5 M5e ABS1" and "M3 M4 M5 M5e FL1" validation protocols are not included in v5.4.1

Defect ID: FB 2570

These two validation protocols are not included in the v5.4.1 release preventing the protocols from being used for validation.

Resolution:

The validation protocols are included in the v5.4.2 release.

Impact of fix:

This fix has no impact on current workflow or data.

The LM1 protocol on a SpectraMax L reader produces out-of-range results

Defect ID: FB 2355

Running the LM1 protocol on a SpectraMax L reader produces out-of-range results due to incorrect calculations in the protocol.

Resolution:

The corrected calculations in the LM1 protocol now display values within the acceptable range.

Impact of fix:

If validation was performed using the uncorrected protocol, validation should be performed again using the corrected protocol. This fix has no other impact on current workflow or data.

Performing a multi-well read on the SpectraMax L reader returns all the same values for each well

Defect ID: FB 2356

When performing a multi-well read on the SpectraMax L reader, the software returns all the same values for each well if the system calibration is incorrect.

Resolution:

When system calibration is incorrect, the software has been enhanced to prompt the user that the calibration values are not acceptable.

Impact of fix:

This fix impacts workflow to require system calibration if the system has incorrect calibration values. If reads were performed using a system with incorrect calibration, some of the data might be invalid.

Incorrect column formula for Vmax850 in Kinetic Baseline Noise group

The Kinetic Baseline Noise evaluation done in the Helma validation protocols Plus Helma and M Series Helma have incorrect Vmax reduction formulas that can lead to failures of the result to meet the specified limits for the instruments.

Defect ID: FB 2442

Resolution:

The Vmax reduction formulas in these protocols have been corrected for the 850 nm and 405 nm wavelengths.

Impact of fix:

If validation was performed using the uncorrected protocols, validation should be performed again using the corrected protocols. This fix has no other impact on current workflow or data.

After multiple plate reads using a SpectraMax L reader, some of the data is not being displayed

Defect ID: FB 2289

After multiple plate reads using a SpectraMax L reader, some of the data is not being displayed when the software retains data from previous reads.

Resolution:

The software is now forcing a recalculation in the background which enhances the capability to display all the calculated data.

Impact of fix:

This fix has no impact on current workflow. If multiple plate reads were performed using v5.4.1, some of the data might be invalid.

Exported data in .xml format when Plate kinetic data contains fewer than 96 wells does not contain all the data

Defect ID: FB 2304

When exporting data in .xml format from Plate kinetic data that contains fewer than 96 wells, some of the data is not included in the exported .xml file.

Resolution:

The exported .xml file contains plate kinetic data for all the selected wells.

Impact of fix:

If incomplete data was exported using v5.4.1, the data can be exported correctly from the saved data file using v5.4.2. The fix has no other impact on current workflow or data.

After a reading in GxP, the saved data file does not retain the "read by" information

Defect ID: FB 2082

After performing a read using SoftMax Pro GxP Software, the saved data file does not retain the "read by" information.

Resolution:

The saved data includes the "read by" information.

Impact of fix:

This fix has no impact on current workflow or data.

Fluorescence Polarization mode becomes disabled after a well scan read on a FlexStation 3 reader

Defect ID: FB 1801

After performing a well scan read on a FlexStation 3 reader, the Fluorescence Polarization (FP) mode becomes disabled.

Resolution:

After a well scan read, the Fluorescence Polarization mode is enabled.

Impact of fix:

This fix has no impact on current workflow or data.

How to Update to SoftMax Pro Software v5.4.2

Within-version updates (such as from v5.4) are provided online at no charge to customers who have registered their previous software version with Molecular Devices. Please visit the SoftMax Pro Software home page for more information about registering your products. You will need your software serial number to complete the process.

http://www.moleculardevices.com/softmax

Note: To upgrade from version 4.x or older, please contact your local Molecular Devices representative.

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