

SoftMax® Pro

Data Acquisition and Analysis Software

Version 7.0

User Guide

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Chapter 1: Installation and Setup

SoftMax® Pro Data Acquisition and Analysis Software controls Molecular Devices® spectrophotometers and absorbance, luminescence, and fluorescence microplate readers and detection platforms. For a complete list of the instruments supported by this release of the SoftMax Pro Software, see [Supported Instruments on page 201](#).

The software provides extensive data calculation and analysis capabilities under a Good Manufacturing Practices (GMP), Good Laboratory Practices (GLP) work environment for pharmaceutical, biotechnology, academic, hospital, and government customers.

Over 120 assay protocols are included in the software to speed life science research and drug discovery assay development and screening. Researchers can customize experiment protocols, analyze and display data, and create meaningful reports. The straightforward yet powerful programming capabilities of the SoftMax Pro Software can further enhance specialized data collection and analysis needs through custom assay development.

SoftMax Pro Software is widely integrated with industry-leading robotics systems.

The SoftMax Pro Software can collect data from one or more microplates and store it in a single data file, using the same or different instrument settings for different microplates. Assays requiring a read in two or more read modes or read types can be combined in a single experiment and run with a single command in the software, by defining separate microplate reads and enabling **Auto Read**. See [Enabling Auto Read on page 340](#).

This guide describes features available in SoftMax Pro Software version 6 and later. SoftMax Pro Software 6 is available for a computer using the Windows 7, Windows 8, or Windows 10 operating system.

This section contains the following topics:

- [Computer System Requirements on page 8](#)
- [Installing the SoftMax Pro Software on page 9](#)
- [Uninstalling SoftMax Pro Software on page 14](#)
- [Starting the Software on page 14](#)
- [Registering the Software on page 15](#)
- [Selecting and Connecting to an Instrument on page 16](#)
- [Setting Instrument Calibration Options on page 19](#)
- [Troubleshooting Instrument Connections on page 18](#)
- [Unlocking the SpectraMax Paradigm Instrument on page 20](#)
- [Getting Help on page 22](#)

Computer System Requirements

The SoftMax Pro Software version 7.0 can be installed on a computer with the following system specifications.

Table 1-1: Minimum and Recommended Requirements for SoftMax Pro Software

Item	Minimum	Recommended
Processor	Single-core, 2 GHz or faster	Quad core or faster
Operating system	Windows 7 (SP1 or newer), 32-bit or 64-bit (x86 or x64) and .NET Framework 4.6 (.NET Framework 4.6 is installed automatically by the SoftMax Pro Software installer if required.)	Windows 7 (SP1 or newer), 32-bit or 64-bit (x86 or x64), Windows 8, 32-bit or 64-bit (x86 or x64), or Windows 10, 32-bit or 64-bit (x86 or x64) The SoftMax Pro MiniMax Imaging Edition must be installed on a 64-bit operating system.
Data connection	RS-232 serial port or USB 2.0 port (depending on the instrument)	USB 2.0 ports For instruments that require an RS-232 serial port, you can use a USB 2.0 port with a Keyspan USB-to-serial adapter. Keyspan USB-to-serial adapters have been field tested and given approval by Molecular Devices.
Memory	2 GB RAM	4 GB RAM If running on a virtual machine, Molecular Devices recommends a minimum of 6 GB RAM. For automation, Molecular Devices recommends a minimum of 8 GB RAM.
Hard drive	500 MB of available space	1 GB of available space, or more
Graphics display	Graphics display adapter 1024 x 768 or higher-resolution display	32-bit graphics display with 256 MB video RAM 1280 x 1024 or higher-resolution display
Software installation and activation	CD/DVD drive Internet connection or external USB drive	CD/DVD drive Internet connection or external USB drive



Note: Installing and using the SoftMax Pro Software on the Windows XP operating system is no longer supported. The software is neither tested nor validated on Windows XP.

To prevent data loss, turn off all sleep and hibernation settings for the hard disk, the CPU, and the USB ports. Also, disable automatic Windows Updates. You can update Windows manually when the instrument is not being used by the software. You can set these options in Windows Control Panel. See [Required Computer Settings on page 11](#).

The SpectraMax MiniMax 300 Imaging Cytometer is shipped with a computer that meets greater minimum computer system specifications than those required for the standard installation of the SoftMax Pro Software. See [Optimizing Your Computer for Image Acquisition on page 337](#).

Installing the SoftMax Pro Software



Note: Molecular Devices recommends that you disable your anti-virus program before installing SoftMax Pro Software, as it might interfere with the installation process.

To install the SoftMax Pro Software:

1. Make sure that all connected instruments are powered off.
2. Start the installation program.
 - If you downloaded the software installation, double-click the **SoftMaxPro7.0Setup.exe** file to start the installation program.
 - If you are installing from a USB flash drive, insert the SoftMax Pro Software flash drive into a USB port, and then navigate to the flash drive and double-click **SoftMaxPro7.0Setup.exe**.
 - If you are installing from a CD, insert the SoftMax Pro Software CD into the CD-ROM drive. If the installation program does not automatically start, navigate to your CD-ROM drive and double-click **SoftMaxPro7.0Setup.exe**.
3. Select the edition of the SoftMax Pro Software that you need to install.
 - The **SoftMax Pro Standard Edition** supports most Molecular Devices microplate readers. This edition does not support the SpectraMax MiniMax 300 Imaging Cytometer. For a complete list of the instruments supported by this release of the SoftMax Pro Software, see [Supported Instruments on page 201](#).
 - The **SoftMax Pro MiniMax Imaging Edition** must be installed to support the features of the SpectraMax MiniMax 300 Imaging Cytometer. This edition requires a 64-bit operating system.
 - The **SoftMax Pro GxP Edition** supports using the software in a regulated environment. This edition does not support the SpectraMax MiniMax 300 Imaging Cytometer. For information about using the features of this edition, see [Using SoftMax Pro GxP Software Features on page 467](#).



Note: You must have the correct license for the edition of the software that you need to install.

4. Follow the on-screen instructions to finish installing the software.
5. Before starting the software, power on the connected instruments.



Note: If you have anti-virus programs installed, Molecular Devices recommends that you add the SafeNet HASP License Manager Service (hasplms.exe) to the list of trusted applications.

Installing the Software Remotely or From a Command Line

You can install the SoftMax Pro Software silently from a command line. Make sure that you install the correct edition of the software.

- To silently install the **SoftMax Pro Standard Edition**, type the command:
`SoftMaxPro7.0Setup.exe /s`
- To silently install the **SoftMax Pro MiniMax Imaging Edition**, type the command:
`SoftMaxPro7.0Setup.exe /s EDITIONIMAGING=TRUE`
- To silently install the **SoftMax Pro GxP Edition**, type the command:
`SoftMaxPro7.0Setup.exe /s EDITIONGXP=TRUE`

To view and follow the wizard during the installation, omit `/s` in the command line.

To uninstall the software, without regard to edition, type the command:

```
SoftMaxPro7.0Setup.exe UNINSTALL=YES
```



Note: Some IT environments, such as those using remote installation with deployment tools like SCCM, require an installer in MSI format. To obtain a copy of the MSI installer, contact Molecular Devices technical support. See [Obtaining Support on page 23](#).

Required Computer Settings

Allowing your computer to hibernate or turn off during data acquisition can interrupt the transfer of data from the instrument to the software and result in data loss.

To prevent data loss, turn off all sleep and hibernation settings for the hard disk, the CPU, and the USB ports. Also, disable automatic Windows Updates. You can update Windows manually when the instrument is not being used by the software.

You can set these options in Windows Control Panel.

1. Open **Control Panel**.
2. Click **Hardware and Sound**.
3. Under **Power Options**, click **Change when the computer sleeps**.
4. Click **Change advanced power settings**.
5. In the **Power Options** dialog, set **Hard disk > Turn off hard disk after** to **Never**.
6. Set **Sleep > Sleep after** to **Never**.
7. Set **Sleep > Hibernate after** to **Never**.
8. Set **USB settings > USB selective suspend setting** to **Disabled**.
9. Click **OK**.
10. Return to the home screen of **Control Panel**.
11. Click **System and Security**.
12. Under **Windows Update**, click **Turn automatic updating on or off**.
13. Under **Important Updates**, make sure that **Install updates automatically** is not selected. Select one of the other options.
14. Click **OK**.
15. Close **Control Panel**.

Decimal Symbol Must be a Period

For the SoftMax Pro Software to properly parse or execute calculations, the regional options for the computer must use the period symbol (“.”) for the decimal symbol. This can be an issue if the **Region and Language** setting for the computer is something other than English.

To set custom regional settings, go to **Control Panel > Regional and Language**.

Manually Installing USB Drivers in Windows 7

For some Windows 7, 64-bit operating system installations, automatic installation of the USB instrument driver for some instruments does not occur due to elevated security settings.

If the SoftMax Pro Software cannot connect to your instrument after installing the software, try shutting down the software and then restarting Windows.

If restarting Windows does not permit access to the instrument, then do the following steps to install the driver:

1. Open **Control Panel**.
2. Click **Hardware and Sound**.
3. Under **Devices and Printers**, click **Device Manager**.
4. In **Device Manager**, double-click the unknown device with the yellow warning icon.
5. Click the **Driver** tab and then click **Update Driver**.
6. Click **Browse my computer for driver software**.
7. Click **Browse** and select the SoftMax Pro Software installation folder.

The default installation path is:

C:\Program Files (x86)\Molecular Devices\SoftMax Pro 7.0

8. In the Windows Security warning, click **Install this driver software anyway**.

Granting TCP/IP Access to MDC File Server

When using the SoftMax Pro GxP Software with MDC File Server in a Windows 7, 64-bit operating system, the Windows Firewall sometimes prevents user access to MDC File Server through TCP/IP.

To grant user access through TCP/IP, create a new inbound rule and a new outbound rule in the Windows Firewall Advanced Settings.

Accessing Windows Firewall Advanced Settings

1. Open **Control Panel**.
2. Click **System and Security**.
3. Click **Windows Firewall**.
4. In the left pane, click **Advanced settings** to open the **Windows Firewall with Advanced Security** dialog.

Creating a New Inbound Rule

1. In left pane of the **Windows Firewall with Advanced Security** dialog, click **Inbound Rules**.
2. In the right pane, click **New Rule**.
3. In the **New Inbound Rule Wizard**, click **Port**.
4. Click **Next**.
5. Click **TCP**.
6. Click **Specify local ports**.
7. Type **9001** in the field.
8. Click **Next**.
9. Complete the rest of the wizard based on your network configuration and access rules defined by your system administrator.

Creating a New Outbound Rule

1. In left pane of the **Windows Firewall with Advanced Security** dialog, click **Outbound Rules**.
2. In the right pane, click **New Rule**.
3. In the **New Outbound Rule Wizard**, click **Port**.
4. Click **Next**.
5. Click **TCP**.
6. Click **Specify local ports**.
7. Type **9001** in the field.
8. Click **Next**.
9. Complete the rest of the wizard based on your network configuration and access rules defined by your system administrator.

Uninstalling SoftMax Pro Software

Before uninstalling the program, make sure to back up your data and saved files to a folder outside of the SoftMax Pro Software folder.

1. Click **Start > Control Panel**.
2. Click **Programs and Features**.
3. In the list that is displayed, click **SoftMax Pro 7.0**.
To uninstall the GxP edition, click **SoftMax Pro 7.0 GxP**.
4. Click **Uninstall** or **Remove**.
5. Follow the on-screen instructions to finish uninstalling the program.



Note: This is the recommended method of removing SoftMax Pro Software from a Windows-based computer since it also removes related information from the Windows Registry.

Starting the Software

To start the software under normal conditions, wait for the connected instrument to complete its start-up sequence, and then double-click the **SoftMax Pro 7.0** icon on your desktop to start the program. To start the program from the Windows Start menu, click **Start > All Programs > Molecular Devices > SoftMax Pro 7.0 > SoftMax Pro 7.0**.

For the GxP edition, double-click the **SoftMax Pro 7.0 GxP** icon or click **Start > All Programs > Molecular Devices > SoftMax Pro 7.0 GxP > SoftMax Pro 7.0 GxP**.

If you are using the SoftMax Pro GxP Software, you are prompted to log on before you can continue. Type your administrator-assigned user ID and your password, and then click **Log On**. See [Logging onto SoftMax Pro GxP Software on page 472](#).



Note: When connecting to the SpectraMax i3x and i3 Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, or the FilterMax F3 and F5 Multi-Mode Microplate Readers for the first time, the latest firmware updates automatically install as needed.



Note: You can start the SoftMax Pro Software with or without an attached instrument. When no instrument is attached you cannot acquire data. To do operations that require data you must open an existing data file.

Registering the Software

The software product key is included with the SoftMax Pro Software package. The instrument serial number is located on a label affixed to the rear of the instrument.

Activating Your Software License

If your license is inactive or is ready to expire, then the **Software License Activation** dialog is displayed when you start the SoftMax Pro Software.

If the software is already running, click the **Help** tab in the ribbon and then click **Software**

License  .

The **Software License Activation** dialog lists the current status for each of the available licenses. For information about the features of your license or to obtain a new license key, contact your Molecular Devices representative.

To activate your SoftMax Pro Software license, click **Activate** to open the **Activate Online** dialog.

- If you have access to the internet, type the **Product Key** in the field, click **Activate Online**, and then follow the on-screen instructions to activate your license.
- If you do not have access to the internet, then click **Activate Offline** and follow the on-screen instructions to activate your license.

To activate offline, you need your product key, a computer that has access to the internet, and a USB drive for transferring files between the computers.

On the Internet-enabled computer, go to:

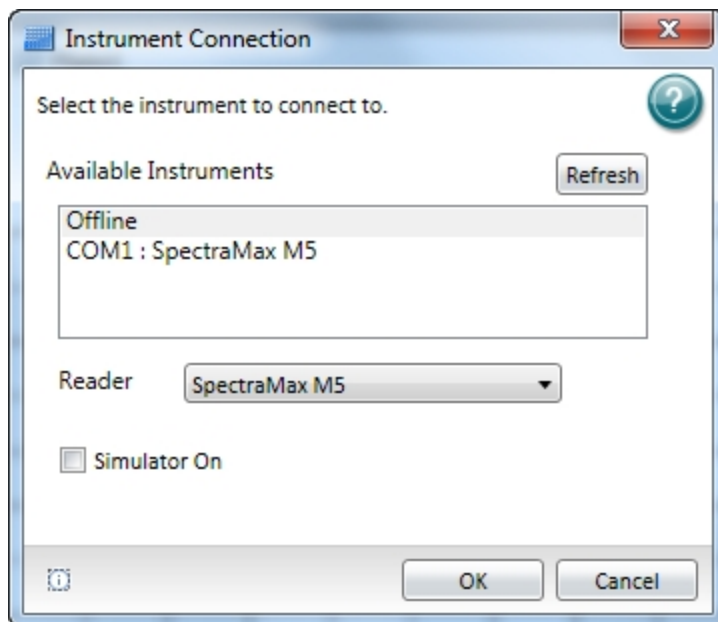
<https://smplicensing.moleculardevices.com>

Follow the on-screen instructions to activate your license.

Selecting and Connecting to an Instrument

To select a reader instrument:

1. Click on the **Instrument** icon on the **Home** tab. The **Instrument Connection** dialog is displayed.



2. In the **Available Instruments** list, select the communication port to which the instrument is connected or select **Offline**.
If the instrument you are connecting to does not show in the list, click **Refresh**.



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument, select **Offline** and then select the instrument from the **Reader** list.

3. If you are working offline, select **Offline** and then select the instrument from the **Reader** list.
4. Optionally, to work in simulation mode, select **Offline**, select the instrument from the **Reader** list, and then select the **Simulator On** check box.
5. Click **OK**. An icon for the selected instrument is displayed on the **Home** tab.



Note: The **Information** button in the lower-left area of the dialog is provided for troubleshooting purposes only.

SoftMax Pro Software supports the following instruments:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms on page 202](#)
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
- [VersaMax Microplate Reader, see page 205](#)
- [SpectraMax Plus 384 Absorbance Microplate Reader, see page 205](#)
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M3 Multi-Mode Microplate Reader, see page 208](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [SpectraMax 340PC 384 Absorbance Microplate Reader, see page 210](#)
- [SpectraMax 190 Absorbance Microplate Reader, see page 210](#)
- [Gemini XPS Microplate Reader, see page 211](#)
- [Gemini EM Microplate Reader, see page 211](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader, see page 214](#)
- [DTX 800 and DTX 880 Multi-Mode Microplate Readers, see page 214](#)
- [Vmax Kinetic Microplate Reader, see page 215](#)
- [EMax Endpoint Microplate Reader, see page 215](#)
- [EMax Plus Microplate Reader on page 215](#)
- [StakMax Microplate Handling System, see page 216](#)

A detection cartridge contains its own independent light source, optics, and electrical components needed to do specific read modes for specific applications.

- The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.




See [Supported Detection Cartridges on page 218](#).

Troubleshooting Instrument Connections

If the instrument is properly connected and turned on, the icon for the instrument is displayed in the **Home** tab of the SoftMax Pro Software main window, and the correct instrument is shown as selected.

The instrument icon shows the connection status of the instrument.

Table 1-2: Instrument Connection Status

Icon	Status
	Instrument Connected
	Instrument Disconnected
	Instrument Simulated

If the instrument status shows as disconnected, make sure that the instrument is powered on and that the connections between the instrument and the computer are secure.

If the instrument you are connecting to does not appear in the **Instrument Connection** dialog, click **Refresh**.

Setting Instrument Calibration Options



Note: Air-calibration applies to absorbance reads only. No microplate or cuvette is required for the instrument calibration. If you are doing a cuvette calibration, the cuvette chamber must be empty.

During calibration, the instrument steps through all available wavelengths one-by-one to measure the signal that reaches the detector when there is no sample in the optical path. The software calculates air-calibration values and stores these values in the firmware. The stored air-calibration values are used when **Speed Read** is enabled or **Calibrate** is disabled in the **Settings** dialog. See [Speed Read on page 262](#) and [Calibrate on page 285](#).

To calibrate the microplate reader:

1. Click **Calibration** on the **Operations** tab in the ribbon.
 2. In the **Calibration** dialog, select either **Plate** or **Cuvette**.
 - To calibrate for microplates, select **Plate**.
 - To calibrate for cuvettes, select **Cuvette**.
 3. Click **Calibrate Now**.
 4. When the calibration indicator shows that the calibration is complete, click **Close**.
-



Note: If the **Calibration** button is not active in the **Operations** tab, then either the instrument is not connected to the computer or the connected instrument does not support the air-calibration process.

Using a Barcode Reader

A barcode reader is an input device similar a keyboard. When you place the cursor in a text field and then use the barcode reader to read a barcode, the barcode reader passes the text embedded in the barcode to the text field.

Before using a barcode reader with the SoftMax Pro Software, make sure that the correct driver is installed and that the barcode reader is functioning correctly. To test a barcode reader, open a text editor, such as Notepad, and then use the barcode reader to read a barcode. If the reader is functioning correctly, the text embedded in the barcode appears in the text editor.

Barcodes can be created in several different formats, such as MSI or Pharmacode. Make sure that the barcode reader you are using supports the type of barcode that you need to read. See the documentation that came with your barcode reader.

Using a barcode reader to input text can be useful for naming a **Plate** section to match the barcode affixed on a microplate. See [Renaming an Experiment or a Section on page 30](#).

Unlocking the SpectraMax Paradigm Instrument

When a SpectraMax Paradigm Instrument is first installed, the hardware transport locks need to be removed as described in the SpectraMax Paradigm Instrument user guide or unpacking guide. As a safety precaution, internal locks controlled by the software prevent the drawers from opening until the instrument is detected and initialized by the SoftMax Pro Software.



Note: Do not install detection cartridges until after you have completed the following instructions to unlock the drawers and initialize the instrument.

To unlock the drawers and initialize the instrument:

1. Make sure that the hardware transport locks have been removed. See the SpectraMax Paradigm Instrument user guide or unpacking guide.



CAUTION! The instrument can be damaged if all the transport locks are not removed before unlocking the drawers and initializing the instrument.

2. Make sure that all drawers have been pushed back into the instrument, the front panels have been replaced, and the microplate door is closed.
3. Make sure that the instrument is connected to the host computer and to a power source, and that the has been installed on the host computer. See the SpectraMax Paradigm Instrument unpacking guide or user guide.



Note: If you are using a 9-pin serial-to-USB adapter cable, install the driver for the adapter on your computer before connecting the cable to the instrument. To make sure the adapter has been correctly installed, open the Windows Device Manager and check for the presence of a COM port, and that there are no conflicts with the COM port.

4. Turn on the power switch on the rear of the instrument.

If the **Standby** button on the front lower-right corner of the instrument is illuminated, press the button to take the instrument out of standby mode.

The LEDs on the status panel flash and turn off, and then the amber LED turns on indicating that the instrument drawers are locked.

5. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).

The amber LED on the status panel turns off and the green LED turns on, indicating a successful connection between the instrument and the SoftMax Pro Software.

6. After successfully connecting to the instrument, the **Instrument Unlocking Procedure** wizard is displayed.

7. If the **Instrument Unlocking Procedure** wizard does not open, then use the **Instrument Connection** dialog to select and connect to the instrument. See [Selecting and Connecting to an Instrument on page 16](#).




Note: If the instrument does not show in the **Available Instruments** list of the **Instrument Connection** dialog, then click **Refresh** above the list.


8. Follow the on-screen instructions in the **Instrument Unlocking Procedure** wizard to unlock the drawers and initialize the instrument.

After completing the **Instrument Unlocking Procedure** wizard, the instrument does an initialization procedure that moves the optics and microplate drawers to home positions. The green LED on the status panel turns on, the amber LED flashes and turns off, and then the green LED remains on. You can install the desired detection cartridges in the instrument. See "Installing Detection Cartridges" in the *SpectraMax Paradigm Instrument User Guide*. To lock the drawers again for shipment, use the **Instrument Information** dialog. See [Using the Instrument Information Dialog on page 457](#).

Getting Help

SoftMax Pro Software has a comprehensive help library. You can open the application help documents from the **Help** tab in the ribbon.





- Click **SoftMax Pro Help**  to view the *SoftMax Pro Software Application Help*. This help contains task-oriented information about how to use SoftMax Pro Software. You can find topics through the table of contents and by using the search function. This document also features a linked index and glossary.

- Click **Formula Reference**  to view the *SoftMax Pro Software Formula Reference Guide*. This document is broken into four main sections:

The first section provides a general introduction to SoftMax Pro Software formulas.

- **Operators** describes the different types of operators that can be used to assemble formulas.
- **Functions** describes the different types of built-in functions that can be used to assemble formulas.
- **Accessors** describes the special functions that provide access to other specific information.

You can find topics through the table of contents and by using the search function. This document also features a linked index.

- Click **Release Notes**  to view the *SoftMax Pro Software Release Notes* for this release of the software. This document is in PDF format and can be viewed using a PDF viewer like Adobe Reader.
- Click **Contact Us**  to display the SoftMax Pro Software What's New page, view the Molecular Devices home page, access the knowledge base, or request technical support. The knowledge base contains documentation supporting Molecular Devices products. You can use the customer login tools and featured links to help you get the information you need.
- Click **Software License**  and follow the instructions in the **Software License Activation** dialog to activate your SoftMax Pro Software license.
- Click **SoftMax Pro**  in the **About** section to see release information about this release of the SoftMax Pro Software application.



Context-sensitive help is available for the dialogs that have a  help button.

More documentation in PDF format can be found in the Windows **Start** menu.

- To view the *SoftMax Pro Software User Guide*, the *Formula Reference Guide*, or the *Software Release Notes*, click **Start > All Programs > Molecular Devices > SoftMax Pro 7.0** and then click the document you want to view.
- To view user guides for the supported instruments, click **Start > All Programs > Molecular Devices > SoftMax Pro 7.0 > Hardware User Guides** and then click the document you want to view.

These documents are in PDF format and can be viewed using a PDF viewer like Adobe Reader.

Obtaining Support

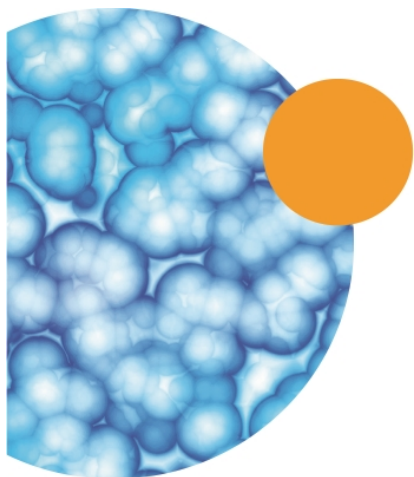
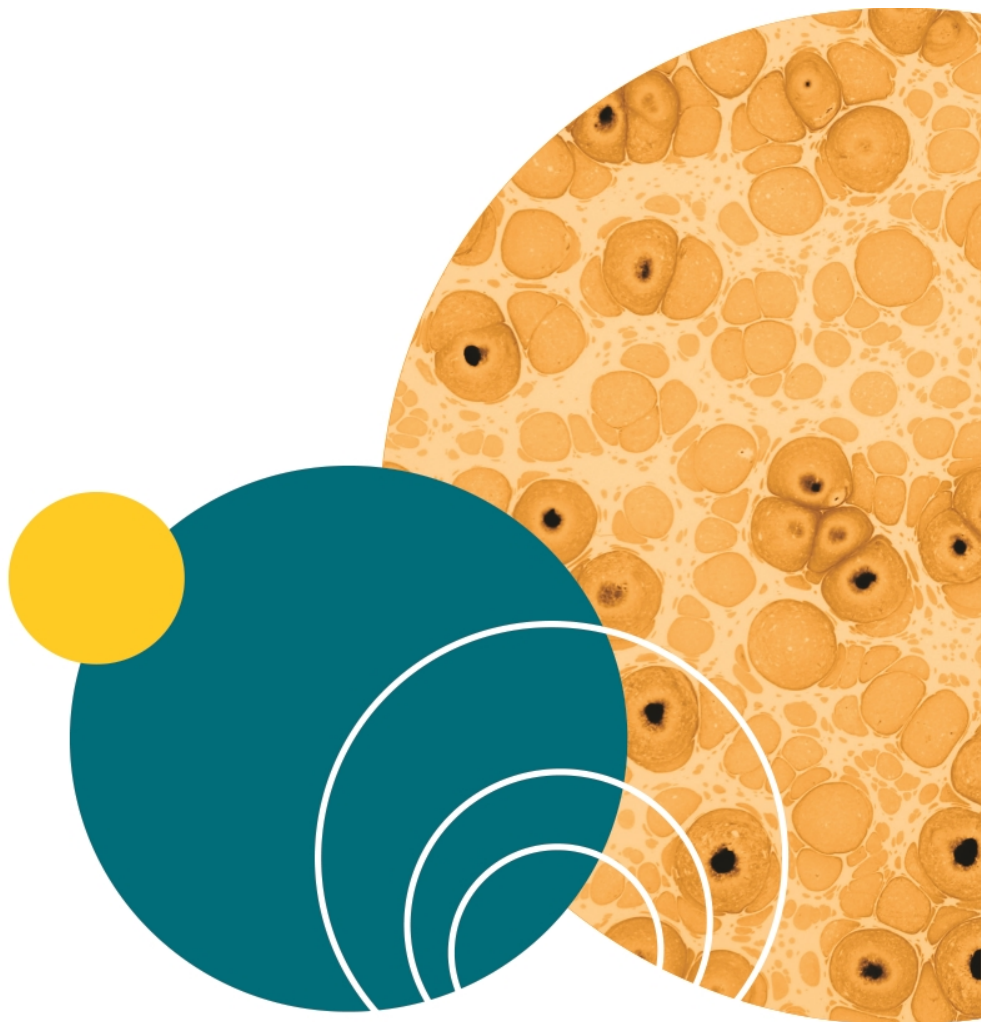
Molecular Devices is a leading worldwide manufacturer and distributor of analytical instrumentation, software, and reagents. We are committed to the quality of our products and to fully supporting our customers with the highest possible level of technical service.

Our support web site, www.moleculardevices.com/support, has a link to the Knowledge Base with technical notes, software upgrades, safety data sheets, and other resources. If you do not find the answers you are seeking, follow the links to the Technical Support Service Request Form to send an email message to a pool of technical support representatives.

You can contact your local representative or contact Molecular Devices Technical Support by telephone at 800-635-5577 (North America only) or +1 408-747-1700. In Europe call +44 (0) 118 944 8000.

To find regional support contact information, visit www.moleculardevices.com/contact.

Please have your instrument serial number or Work Order number, and your software version number available when you call.




Chapter 2: User Interface Overview


If you are familiar with earlier versions of SoftMax Pro Software, adapting to the new SoftMax Pro Software 6 user interface is quick and easy. The SoftMax Pro Software 6 user interface provides advanced features and state-of-the-art navigation, analysis, and data display tools, plus it also supports a version of the classic SoftMax Pro Software interface. SoftMax Pro Software 6 improves the basic functionality of earlier versions of the software, and it adds new features that further contribute to the usability of the powerful computing engine of SoftMax Pro Software.

General Workflow Overview


SoftMax Pro Software lets you set up and run a complete protocol for the supported instruments. Instrument settings can be saved as a protocol (template) file and used repeatedly for reading different microplates or cuvettes. All standalone instrument functions can be controlled using the software.

The following steps give a general overview of the workflow for acquiring and analyzing microplate data using the SoftMax Pro Software. You might need to modify the workflow as it applies to your specific application and the standard operating procedures of your laboratory.


1. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).
You can add as many **Plate** sections or **Cuvette Set** sections as your experiment requires.
2. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
The **Home** tab changes to reflect the tools available for the active **Plate** section or **Cuvette Set** section.
After selecting a **Plate** section, you can use the **Plate Setup Helper** to help you set up a microplate experiment. See [Using the Plate Setup Helper on page 27](#).
3. Create a protocol. Click the **Settings**  button to set the instrument options. See [Selecting Instrument Settings on page 236](#).
4. Click **OK** to save the settings.

As you create the protocol, you might need to click the **Template**  button to add a microplate template that can include defining groups, blank cells, and a sample series, as needed for your application. See [Configuring a Microplate Template on page 301](#).

5. Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

6. Click the **Read**  button to run the protocol and have SoftMax Pro Software collect and store all raw data received from the instrument. See [Collecting Data from a Microplate on page 339](#), [Collecting Data From a Cuvette on page 350](#), or [Collecting Data from a Membrane Holder on page 352](#).

As information is read, the SoftMax Pro Software displays updates showing the new data. Data is displayed in a grid format that corresponds to the wells in a microplate or individual cuvettes.

During the read, the read button changes to . You can click this button to stop the read operation.

SoftMax Pro Software can collect data from one or more microplates or cuvettes and store it in a single data file, using the same or different instrument settings for different microplates or cuvettes. For example, microplates containing different samples can be read using the same or different modes, all within the same experiment.


7. View and analyze the data. See [Setting the Data Display Options on page 358](#), [Doing Data Reduction on page 367](#), [Graphing Data on page 388](#), and [Viewing Western Blot Membrane Data on page 443](#).

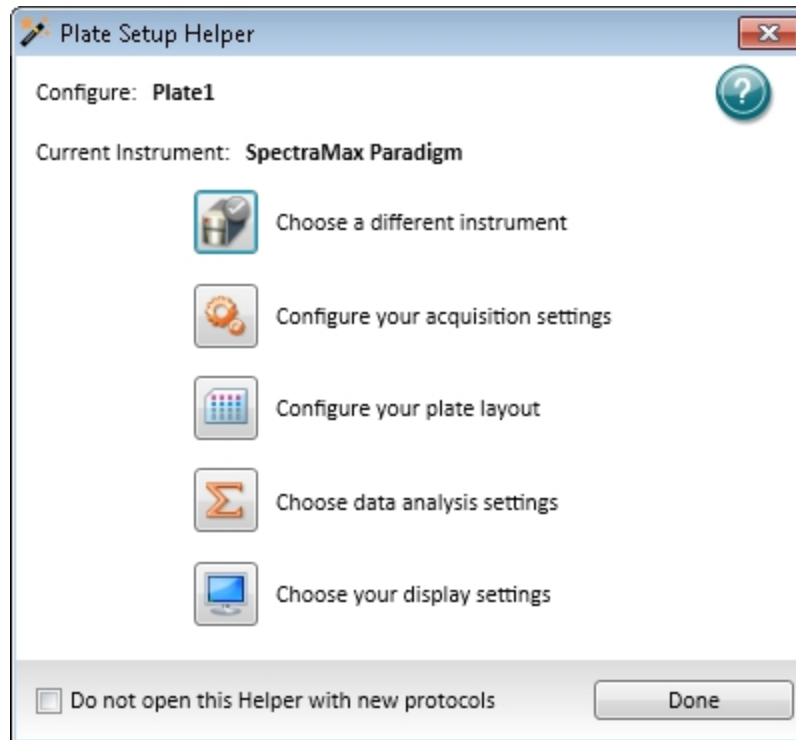
You can manipulate or reduce the raw data using dozens of built-in formulas or define your own analysis structure to quickly and easily summarize the raw data. More than one reduction can be shown, and results from different microplates and cuvettes can be compared within the same experiment.



Note: After you have defined instrument settings, and have optionally customized the SoftMax Pro Software data file with assay information, reduction settings, custom columns in Group sections, and summary objects, you can save the file as a Protocol file type to create an assay template. This template can then be used and distributed throughout a department or company for highly repeatable data collection and analysis.

Using the Plate Setup Helper

When you open a new SoftMax Pro Software file, the **Plate Setup Helper** is displayed to help you set up a microplate experiment. You can also open the **Plate Setup Helper** by clicking **Plate Setup Helper**  in the toolbar at the top of the active **Plate** section.







The wizard-like **Plate Setup Helper** visually guides you through the tasks available in the software to setup a microplate to acquire data. To complete a task, click its button. After you complete a task, the settings for the task are saved, and you return to the helper to select a different task. The tasks do not need to be done in the order they are presented in the helper. However, you must select the instrument before defining your acquisition settings, since the settings are specific to the instrument.

Configure tells you the name of the active **Plate** section. Acquisition settings are applied to the entire **Plate** section. If you have a plate clone selected, then the layout, analysis, and display settings are applied to the selected clone. For information about **Plate** sections, see [Using a Plate Section on page 118](#).

Current Instrument tells you the name of the currently selected instrument. The image in the button below it shows you the instrument and its connection status. You must select the instrument before defining your acquisition settings, since the settings are specific to the instrument. To choose a different instrument or change its status, click the button. See [Selecting an Instrument on page 36](#).

To complete a task, click its button.

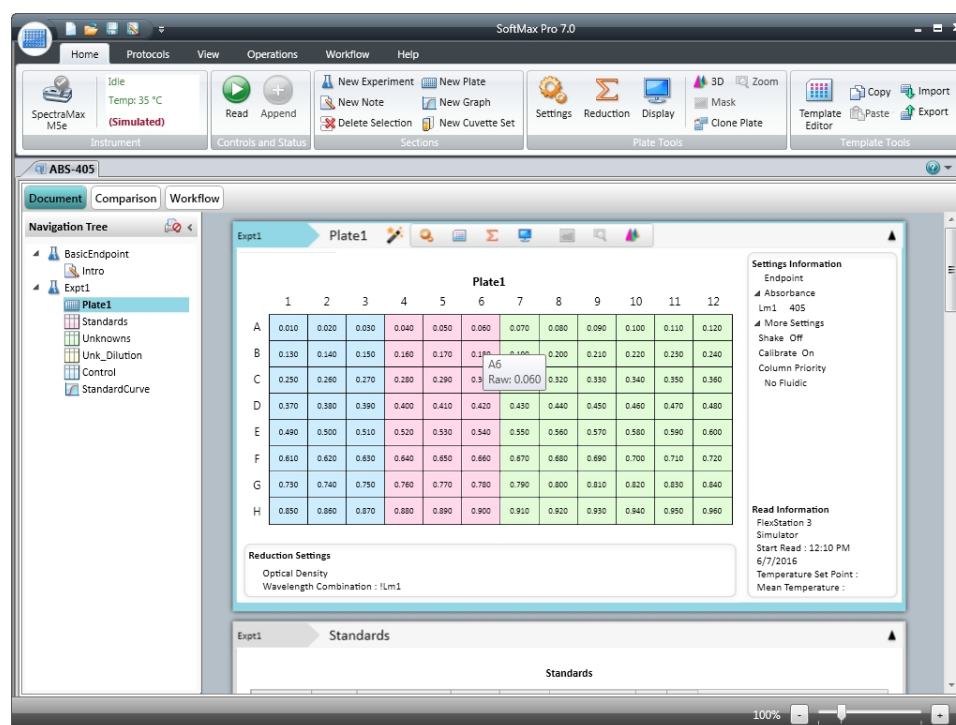
- To configure your acquisition settings, click . See [Instrument Settings](#) on page 246.
- To configure your plate layout, click . See [Configuring a Microplate Template](#) on page 301.
- To choose data analysis settings, click . See [Doing Data Reduction](#) on page 367.
- To choose your display settings, click . See [Setting the Data Display Options](#) on page 358.

To prevent the **Plate Setup Helper** from automatically starting each time you open a new protocol, select the **Do not open this Helper with new protocols** check box. You can enable this option again in the **SoftMax Pro Options** dialog. See [Setting Application Options](#) on page 104.

To close the **Plate Setup Helper**, click **Done**.

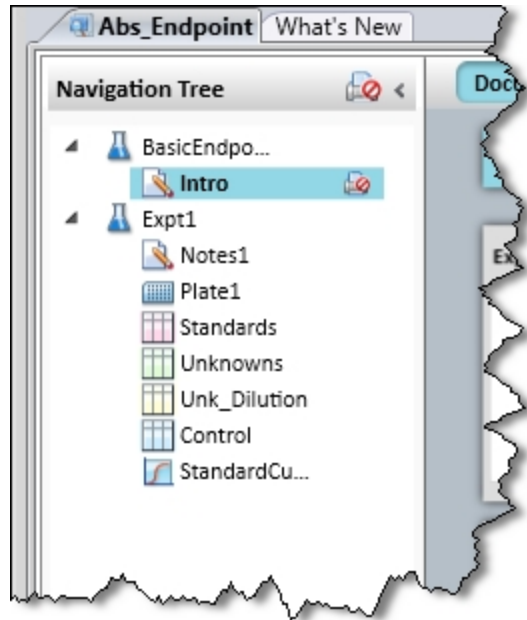
Main Window

The SoftMax Pro Software window has three main areas: the navigation tree on the left, the workspace area on the right, and the ribbon toolbar along the top. Also, the application menu and quick-access toolbar in the upper-left corner give you easy access to file and application management features.



Navigation Tree

The **Navigation Tree** shows the sections in the data file that is currently open and that are available for display in your Workspace.



When you save a data file, the name that you give the file is displayed on the tab above the Navigation Tree. You can have more than one data file open at a time. Each data file can contain an unlimited number of experiments. Each experiment can contain an unlimited number sections. Section types include: Notes, Plate, Cuvette Set, Group, and Graph. See [Workspace Sections on page 107](#).

To change the order of the sections in a experiment, drag the section name to the desired location. The order of the sections can be moved within an experiment only, and cannot be moved between experiments.

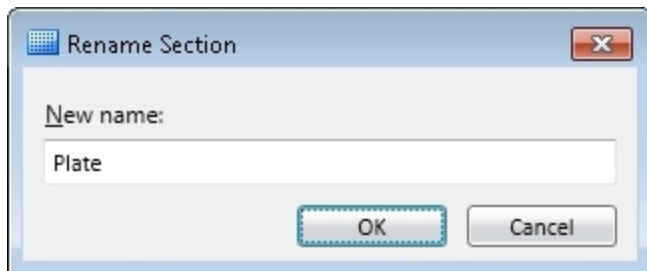
You can right-click an experiment or section in the **Navigation Tree** to rename, duplicate, or delete the section or experiment.

When you duplicate an **Experiment**, all sections in the experiment are duplicated in a new experiment, but without data. When you duplicate a **Notes** or **Graph** section, an exact duplicate is made of the section. When you duplicate a **Group** section, a new group is created with the same properties as the original section. When you duplicate a **Plate** section, the new section contains all the settings from the original section, but without data.

To rename an experiment or a section, see [Renaming an Experiment or a Section on page 30](#).

Renaming an Experiment or a Section

To rename an experiment or section, right-click the experiment or section in the **Navigation Tree** and then click **Rename**.



Edit the text in the **New name** field and then click **OK**.

The new name appears in the **Navigation Tree** and at the top of the section in the Workspace.

To rename an experiment or section using the automation interface, see the description of the **setTitle()** command in the *SoftMax Pro Software Automation API Reference Guide*.

*** Tip:** You can use a barcode reader to input the text embedded in a barcode. See [Using a Barcode Reader on page 19](#).

Workspace Views

The SoftMax Pro Software workspace has two main views that change the way the sections are displayed in the workspace.

- The **Document** view provides you with a scrollable area for viewing the sections. See [Document View on page 31](#).
- The **Comparison** view lets you move the sections around in the workspace to position them where they are most useful. See [Comparison View on page 32](#).

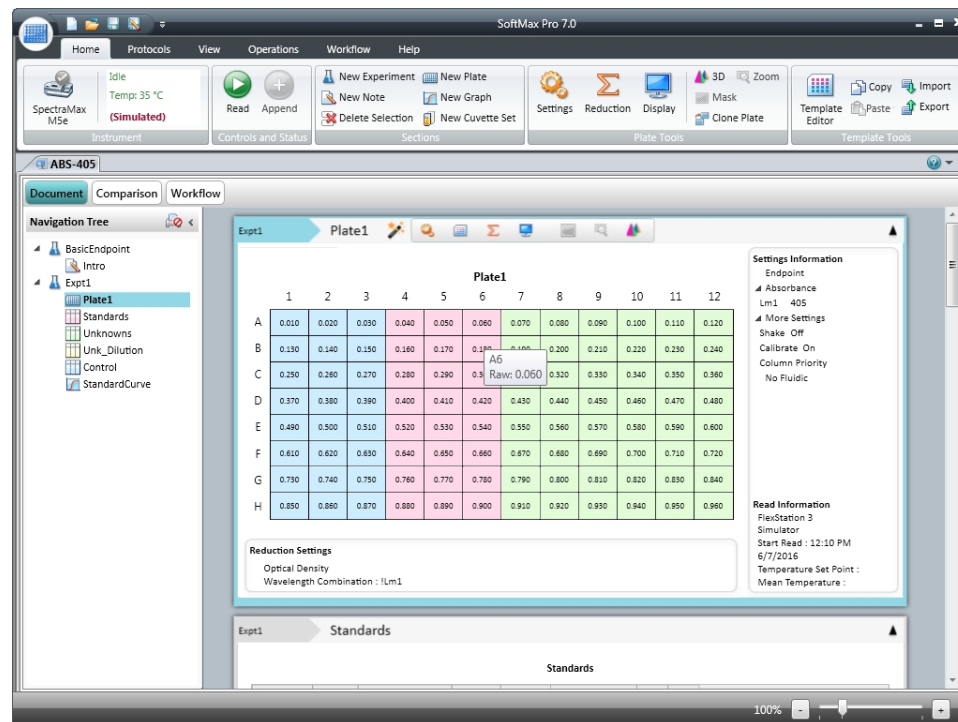
You can also split the workspace to view multiple data files at the same time. See [Using the View Tab on page 44](#).

For information about working with the sections in the workspace, see [Workspace Sections on page 107](#).

The **Workflow** view provides you with a drag-and-drop workflow editor and tools to run and monitor a workflow. See [Workflow View on page 33](#).

Document View

Document view displays information in a manner that is similar to previous SoftMax Pro Software releases. The Document view provides you with a scrollable area for viewing the sections. To view a section either click on it in the navigation tree or use the scroll bar until the desired section comes into view.

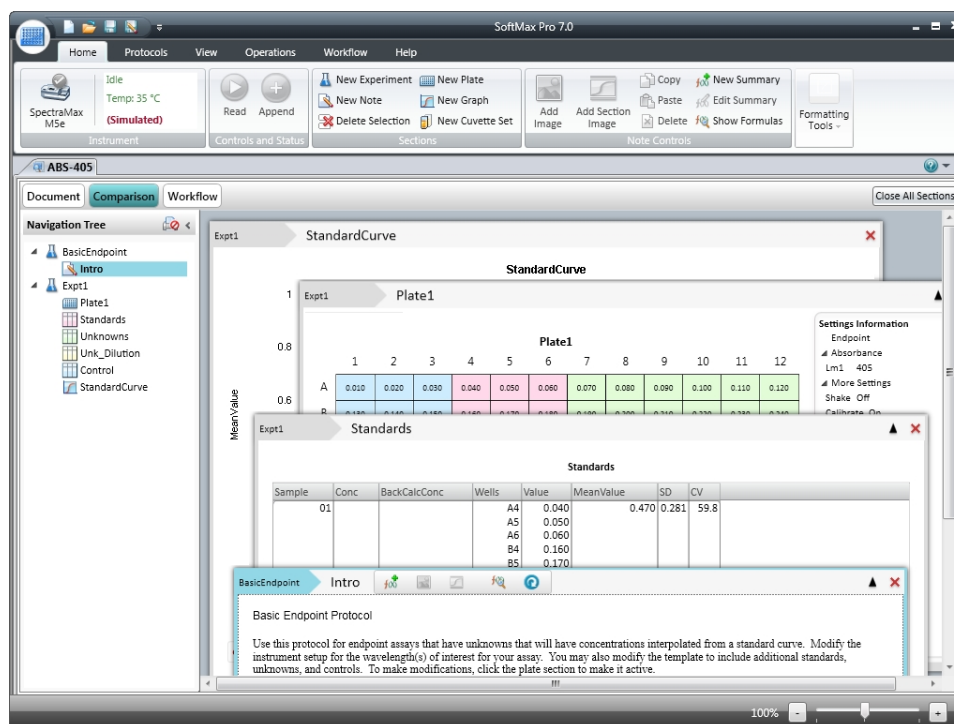


For information about working with the sections in the workspace, see [Workspace Sections on page 107](#).

Comparison View

To change to the Comparison view, click the **Comparison** button.

The **Comparison** view provides you with flexible display options. In Comparison view you can move the sections around in the workspace to position them where they are most useful.



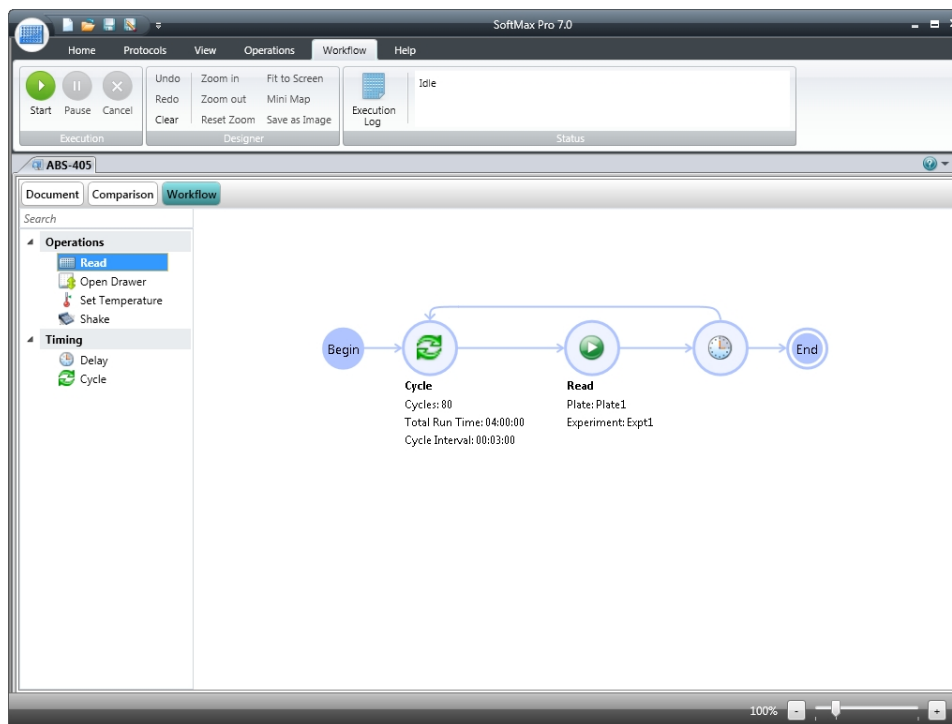
- You can drag sections from the navigation tree and position them in the workspace.
- Sections can overlap.
- Double clicking a section in the navigation tree adds that section to the bottom of the workspace.

For information about working with the sections in the workspace, see [Workspace Sections on page 107](#).

Workflow View

To change to the Workflow view, click the **Workflow** button.

The **Workflow** view provides you with a drag-and-drop workflow editor and tools to run and monitor a workflow. In Workflow view you can define a workflow using the defined **Plate** sections and instrument settings to run multitask kinetic reads that last hours or days.



- Drag tasks from the menu on the left to the timeline on the right.
- Define repeated tasks by placing the tasks in a defined **Cycle** task.
- Click the workflow options in the ribbon to start, pause, resume, and cancel the workflow.

For more information, see [Defining and Running a Workflow on page 297](#).

Ribbon Toolbar

The application ribbon contains tabs with the tools needed to work with SoftMax Pro Software.

Home Tab

The Home tab always contains the following sections:

- Instrument
- Controls and Read Status
- Sections

See [Using Instrument Controls in the Home Tab on page 36](#) and [Using Section Controls in the Home Tab on page 39](#).

The contents of the **Home** tab change depending on the section type that is active in the workspace.

Notes Section Tools

When a **Note** section is active the Home tab contains:

- Notes Controls
- Formatting Tools

See [Using a Note Section on page 108](#).

Plate Section Tools

When a **Plate** section is active, the Home tab contains:

- Plate Tools
- Template Tools

See [Using Plate Tools on page 119](#).

Cuvette Section Tools

When a Cuvette Set section is active, the Home tab contains:

- Cuvette Tools
- Template Tool

See [Using Cuvette Tools on page 130](#).

Group Section Tools

When a **Group** section is active, the Home tab contains:

- Column Tools
- Summary Tools
- Formatting Tools

See [Using Column Tools on page 143](#).

Graph Section Tools

When a **Graph** section is active, the Home tab contains:

- Graph Type
- Graph Tools

See [Working with Graphs on page 389](#).

Protocols Tab

The **Protocols** tab contains the following:

- Protocol Manager
- Community

See [Using the Protocols Tab to Manage Protocols on page 42](#).

View Tab

The **View** tab contains the following:

- Show/Hide Panel
- Window
- Expand/Collapse Sections

See [Using the View Tab on page 44](#).

Operations Tab

The **Operations** tab contains the following:

- Instrument Commands
- Instrument Tools
- Calculations
- Automation

See [Using the Operations Tab on page 44](#).

Workflow Tab

The **Workflow** tab contains the following:

- Execution
- Designer
- Status

See [Defining and Running a Workflow on page 297](#).

GxP Tab

The **GxP** tab is available only when using the SoftMax Pro GxP Software and contains the following:

- User Account
- Data

See [Using the GxP Tab on page 50](#).

Help Tab

The **Help** tab contains the following:

- Help
- About

See [Using the Help Tab on page 51](#).

Using Instrument Controls in the Home Tab

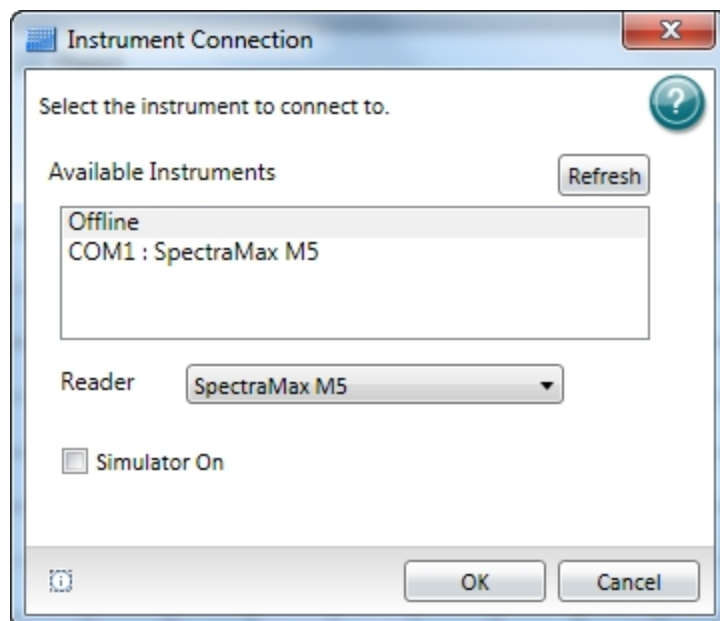
The **Instrument** and **Controls and Status** options on the **Home** tab contain the following controls:

- [Selecting an Instrument, see page 36](#)
- [Reading Data, see page 38](#)

Selecting an Instrument

To select a reader instrument:

1. Click on the **Instrument** icon on the **Home** tab. The **Instrument Connection** dialog is displayed.



2. In the **Available Instruments** list, select the communication port to which the instrument is connected or select **Offline**.

If the instrument you are connecting to does not show in the list, click **Refresh**.



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument, select **Offline** and then select the instrument from the **Reader** list.

3. If you are working offline, select **Offline** and then select the instrument from the **Reader** list.
4. Optionally, to work in simulation mode, select **Offline**, select the instrument from the **Reader** list, and then select the **Simulator On** check box.
5. Click **OK**. An icon for the selected instrument is displayed on the **Home** tab.



Note: The **Information** button in the lower-left area of the dialog is provided for troubleshooting purposes only.

SoftMax Pro Software supports the following instruments:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms on page 202](#)
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
- [VersaMax Microplate Reader, see page 205](#)
- [SpectraMax Plus 384 Absorbance Microplate Reader, see page 205](#)
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M3 Multi-Mode Microplate Reader, see page 208](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [SpectraMax 340PC 384 Absorbance Microplate Reader, see page 210](#)
- [SpectraMax 190 Absorbance Microplate Reader, see page 210](#)
- [Gemini XPS Microplate Reader, see page 211](#)
- [Gemini EM Microplate Reader, see page 211](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader, see page 214](#)
- [DTX 800 and DTX 880 Multi-Mode Microplate Readers, see page 214](#)
- [Vmax Kinetic Microplate Reader, see page 215](#)
- [EMax Endpoint Microplate Reader, see page 215](#)
- [EMax Plus Microplate Reader on page 215](#)
- [StakMax Microplate Handling System, see page 216](#)

Reading Data

After you have your experiment defined and your prepared microplate or cuvette inserted in the microplate reader, you can start a read.




Note: Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

To start a read, click the plate or cuvette section in the workspace, and then click the **Read**




button in the **Home** tab of the ribbon.

As information is read, the SoftMax Pro Software displays updates showing the new data. The data display in a grid format that corresponds to the wells in a microplate or individual cuvettes.


During the read, the read button changes to . You can click this button to stop the read operation. The read stops immediately.

To stop and restart a Kinetic read while the **Plate** section is being read, click the **Interrupt**



button to pause the read, and then click the **Append**  button to continue the Kinetic read from where it left off. When you interrupt a read, the instrument finishes reading all the selected wells in the microplate and then waits for user input before continuing. This type of discontinuous kinetic read can help with acquisition development.

After a Kinetic read ends successfully, you can read the same **Plate** section again and append

the data to the data that already exists in the **Plate** section by clicking the **Append**  button.



Note: If you stop a Kinetic read before it completes, you cannot restart the read or append data to the read. To use these features, you must either let the read finish on its own or click **Interrupt** to pause the read.

SoftMax Pro Software can collect data from one or more microplates or cuvette sets and store the data in a single data file, using the same or different instrument settings for different microplates or cuvette sets. For example, microplates containing different samples can be read using the same or different modes, all within the same experiment.


Using Section Controls in the Home Tab

The Section controls are displayed on the Home tab in the ribbon. For information about the section controls, see the following topics:

- [Creating an Experiment on page 39](#)
- [Creating a Note Section on page 40](#)
- [Deleting a Section on page 40](#)
- [Creating a Plate Section on page 40](#)
- [Creating a New Graph Section on page 41](#)
- [Creating a Cuvette Set Section on page 41](#)

Creating an Experiment

To create a new Experiment:


1. Open a data file in the workspace.
2. If you have more than one Experiment, select the Experiment that you want to duplicate to make the new Experiment.
3. Click **New Experiment**  in **Sections** on the **Home** tab in the ribbon.

A duplicate of the selected Experiment is displayed below the selected Experiment in the **Navigation Tree**. The sections and settings are duplicated, but the data is not.

To change the name of the experiment, right-click the experiment in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

Creating a Note Section

To create a **Note** section:

1. Select the experiment where you want to add a **Note** section in the **Navigation Tree**.
2. If you have more than one section in the Experiment, select the section above where you want the new **Note** section to be displayed in the **Navigation Tree**.
3. Click **New Note**  in **Sections** on the **Home** tab in the ribbon.

A new blank **Note** section is displayed below the selected section in the **Navigation Tree**. See [Using a Note Section on page 108](#).

To change the name of the **Note** section, right-click the **Note** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

Deleting a Section

To delete a section:

1. Select the section or sections that you want to delete in either the **Navigation Tree** or a section in the Workspace. To delete an entire Experiment, select the Experiment in the **Navigation Tree**.




Note: To select multiple sections, press and hold the **Ctrl** or **Shift** key and then click the sections you want to select in the **Navigation Tree**.

2. Click **Delete Selection**  in **Sections** on the **Home** tab in the ribbon.

Deleting a section or experiment cannot be undone. When you delete a **Plate** section, the data from the **Plate** section is also deleted.

Creating a Plate Section

To create a new **Plate** section:


1. Select the experiment where you want to add a **Plate** section in the **Navigation Tree**.
2. If you have more than one section in the Experiment, select the section above where you want the new **Plate** section to be displayed in the **Navigation Tree**.
3. Click **New Plate**  in **Sections** on the **Home** tab in the ribbon.

A blank **Plate** section is displayed in the Workspace. You can add as many **Plate** sections as you need to your data file. See [Using a Plate Section on page 118](#).

To change the name of the **Plate** section, right-click the **Plate** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

Creating a New Graph Section

To create a new graph:


1. Select the **Plate** section to relate to the graph in either the **Navigation Tree** or the **Workspace**.
2. Click **New Graph**  in **Sections** on the **Home** tab in the ribbon.
3. In the **New Graph** dialog, set the options for the graph. See [Creating a New Graph on page 392](#).
4. When the graph options have been set, click **OK**.

A new **Graph** section is displayed below the selected section in the **Navigation Tree**. See [Using a Graph Section on page 149](#).

To change the name of the **Graph** section, right-click the **Graph** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

Creating a Cuvette Set Section

To create a new **Cuvette Set** section:

1. Select the experiment you want to add the **Cuvette Set** section to in the **Navigation Tree**.
2. If you have more than one section in the Experiment, select the section above where you want the new **Cuvette Set** section to be displayed in the **Navigation Tree**.
3. Click **New Cuvette Set**  in **Sections** on the **Home** tab in the ribbon.

A new blank **Cuvette Set** section is displayed below the selected section in the **Navigation Tree**. See [Using a Cuvette Set Section on page 129](#).

To change the name of the **Cuvette Set** section, right-click the **Cuvette Set** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

Using the Protocols Tab to Manage Protocols

The **Protocols** tab in the ribbon provides easy access to protocol files that are stored in the file system. It also gives you access to the SoftMax Pro Software user community for protocol sharing, exchanging tips and tricks, and networking with other experienced users. Protocol files are experiment template files that contain microplate well layout assignments and all other reader configuration information, but no data.

After the SoftMax Pro Software is installed, the Basic Endpoint protocol is set as the default protocol with the filename **default.spr**. Whenever you create a new document, the **default.spr** protocol file is opened as an untitled document that contains the settings from the default protocol file.

You can save the settings of the file currently active in the workspace as the default protocol. After you save the active protocol file as the default, whenever you create a new document, the settings in the **default.spr** file that you have saved are loaded into an untitled document.

Several predefined protocols are installed with SoftMax Pro Software and are placed in the SoftMax Pro Software **Protocols** folder.

You can use the predefined protocols and you can create your own protocols. For more information on protocols, see [Creating a Protocol on page 235](#). When you create protocols, save them into folders on your file system. Name the folders in such a way that you can find the protocols later.

The following buttons are provided on the **Protocol Manager** area of the **Protocols** tab:

- Click **Folder Locations** to add the folders containing the protocols you want to use to the short cut menu you can access by clicking **Protocol Manager**. See [Adding or Removing a Folder in the Protocol Manager on page 70](#).
- Click **Save As Default** to overwrite the default.spr file with the protocol setting of the experiment that is active in your workspace. See [Saving a Protocol as the Default Protocol on page 69](#).



Note: When you save the file as the default protocol, the data you have collected in the current experiment remains unchanged. If you want to keep the data, you need to save the data into a data file.

- Click **Protocol Manager** to open the Protocol Manager shortcut and select a protocol to be assigned to the open experiment. See [Using the Protocol Manager to Open a File on page 68](#).



Note: When you add a new plate or cuvette section to an experiment, you can configure settings using the **Settings** dialog or apply a pre-defined or saved protocol to the new section.

The following buttons are provided in the **Community** area of the **Protocols** tab:

- Click **Protocol Home Page** to access the SoftMax Pro Software community web site for protocol sharing, exchanging tips and tricks, and networking with other experienced users. To access this site, you must have internet access on your computer.
- Click **Export for Sharing** to export the active protocol to an encrypted file format for sharing with the online community. No data is exported with the protocol. Before exporting the protocol, make sure that the first **Note** section has a clear description of the protocol, since the first **Note** section will be used as the description of the protocol on the web site.




After exporting a protocol for sharing, you can upload the exported protocol to the community web site. Protocols exported for sharing have a **.spz** extension. Do not rename the file. The file is encrypted and will not upload properly if it is renamed. To upload your exported protocol, follow the instructions on the SoftMax Pro Software community web site.

Using the View Tab

The **View** tab in the ribbon contains three sections: **Show/Hide Panel**, **Window**, and **Expand/Collapse Sections**.

In the **Show/Hide Panel** section, select or clear the **Navigation Tree** check box to show or hide the **Navigation Tree** in the workspace.

In the **Document View** section, click an option to change the layout of the tabs in the workspace.

- Click **Single Tab Group**  to view one tab group at a time.
- Click **New Horizontal Tab Group**  to split the workspace horizontally. The selected tab moves below inactive tabs in the workspace. You can have as many horizontal areas as you have tabs in the workspace.
- Click **New Vertical Tab Group**  to split the workspace vertically. The selected tab moves to the right of inactive tabs in the workspace. You can have as many vertical areas as you have tabs in the workspace.

In the **Expand/Collapse Sections** section, click an option to **Collapse All Sections** or to **Expand All Sections** in the workspace.

Using the Operations Tab

Instrument Commands

The buttons that are displayed in the **Instrument Commands** group depend on the currently selected instrument.

- **Temperature:** When connected to an instrument with temperature control, you can set the temperature in the microplate or cuvette chamber in degrees Celsius. See [Setting the Temperature on page 47](#).
- **Shake:** If the selected instrument permits manual shaking of the microplate, then the **Shake** button is available. See [Shaking the Microplate on page 48](#).
- **Open / Close:** For most instruments, you can open and close the microplate drawer using the software. For some instrument, other drawers can be opened and closed using the software. See [Opening and Closing a Drawer on page 49](#).

Instrument Tools

The buttons that are displayed in the **Instrument Tools** group depend on the currently selected instrument.

- **Calibration:** The instrument calibration values are stored in the firmware of the instrument. For information about updating the instrument calibration, see [Calibrating the Microplate Reader on page 455](#).
- **Filters:** The positions of the filters in the EMax and Vmax Microplate Readers can be defined using the **Filter Configuration** dialog. For instructions, see [Configuring the Filters for the EMax and Vmax Microplate Readers on page 456](#). EMax Plus Microplate Reader
- **Configure:** In the **Configuration** dialog, you can adjust the intensity of the lamp for each of the installed filters in the EMax Plus Microplate Reader. You can view the positions and wavelengths of the installed filters. This dialog also lists other instrument information like the serial number and firmware version. See [Adjusting the Lamp for the EMax Plus Microplate Reader on page 456](#).
- **Initialize:** To return EMax Plus Microplate Reader microplate carrier to its home position, click the **Initialize** button.
- **Info:** In the **Instrument Information** dialog, you can view a list of the installed detection cartridges in a SpectraMax i3x or i3 Multi-Mode Detection Platform or in a SpectraMax Paradigm Multi-Mode Microplate Reader, or view the installed filters in FilterMax F3 and F5 Multi-Mode Microplate Readers. This dialog also lists other instrument information like the serial number and firmware version. For FilterMax F3 and F5 Multi-Mode Microplate Readers, you can configure the excitation and emission filter slides. See [Using the Instrument Information Dialog on page 457](#).
- **Refresh:** To update the software with the currently installed detection cartridges in a SpectraMax i3x or i3 Multi-Mode Detection Platform or in a SpectraMax Paradigm Multi-Mode Microplate Reader, or with the currently installed filter slides in FilterMax F3 and F5 Multi-Mode Microplate Readers, click the **Refresh** button.

Calculations

By default, SoftMax Pro Software does continuous recalculation of the data when you read plates, create or change formulas, or change settings that have an effect on data. At certain times, it is useful to disable recalculations so that you can edit the Experiment without waiting for recalculations to be completed.

- **Suspend Calculations** disables automatic recalculation. While suspended, no recalculation occurs regardless of what you change, add, or delete from the Experiment. This is useful when creating or changing column formulas within Group sections.
- **Resume Calculations** re-enables automatic recalculation.
- When recalculation has been suspended, you might want to see the results of the changes you have made but might still not want to enable continuous recalculation. Click **Recalculate Now** to recalculate all data once without enabling continuous recalculation.

Under certain circumstances, a calculation status message is displayed in the workspace footer.

- **Calculating** is displayed when SoftMax Pro Software is calculating an entire experiment automatically or when **Recalculate Now** is selected.
- **Calculating Suspended** is displayed when the **Suspend Calculation** is selected.
- Under all other conditions, no message is displayed.

For technical information about SoftMax Pro Software calculations, see [Calculations and Numerical Precision on page 356](#).

Automation

The following automation commands are available.

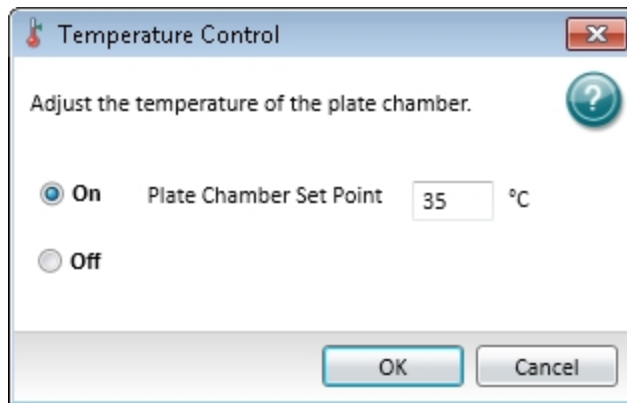
- **Auto Read:** You can automatically read plate sections as they are displayed within an experiment. See [Enabling Auto Read on page 340](#).
- **Plate Stacker:** The StakMax Microplate Handling System runs using the StakMax Software that is integrated with the SoftMax Pro Software. See [StakMax Microplate Handling System on page 216](#).
- **Automation Mode:** You can place the software in automation mode, letting the software accept legacy commands from scripts written for the SoftMax Pro Software version 5.x automation interface. See [Using Automation Mode on page 56](#).

Setting the Temperature

When connected to an instrument with temperature control, you can set the temperature in the microplate or cuvette chamber in degrees Celsius.

To set the temperature:

1. Connect to an instrument that is capable of temperature control.
2. Click **Temperature** on the **Operations** tab in the ribbon.



3. In the **Temperature Control** dialog, click **On**.
4. Type the desired temperature in degrees Celsius.
5. Click **OK**.

The instrument monitors the temperature of the air inside the microplate chamber, and the software displays the air temperature of the chamber on the **Instrument** section of the **Home** tab. The temperature display is continuously updated with the current air temperature.

You can set the temperature 2°C or more above the current air temperature in the chamber. After turning on the temperature control, the chamber can take from 10 to 30 minutes to reach the desired temperature, depending on the difference between the starting temperature and the desired temperature.

With the SpectraMax M2, M2e, M3, M4, M5, M5e, and Plus 384 instruments, the **Instrument** section of the **Home** tab shows the temperature within the microplate chamber. This can be different from the front panel of the instrument that displays the temperature within the cuvette chamber. The readings should be very similar to each other after both chambers have reached equilibrium. During warm-up, you might notice a discrepancy in temperatures, which is normal.



Note: The temperature sensors detect the temperature of the air inside the chamber, not the temperature of the samples in the microplate. If you use the instrument to warm the samples, Molecular Devices recommends that you use a seal or lid on the microplate to prevent evaporation of the sample. Using a seal or lid also helps to maintain uniform temperature. Letting the prepared sample equilibrate inside the microplate chamber can take an hour or more. You can speed up equilibration by pre-warming the sample and the assay reagents to the desired temperature before placing the microplate in the chamber. Validate the data quality to determine whether the seal or lid can stay on the microplate for the read.




CAUTION! The SpectraMax Paradigm, SpectraMax i3x, and FilterMax F5 instruments have an automatic read-height (Z-height) adjustment for fluorescence and luminescence reads. For top reads, the lens or the microplate can be damaged if the microplate height is not set properly. If the microplate has a lid on top, you must indicate that the microplate is lidded and make sure that the microplate height with a lid is set accurately in the **Plate Editor** before starting a read.

After turning off the temperature control, you can help the microplate chamber cool to the ambient temperature by opening the microplate drawer.

Shaking the Microplate

If the selected instrument permits manual shaking of the microplate, then the **Shake** button is available in the **Instrument Commands** section on the **Operations** tab in the ribbon.

To shake the plate:

1. Insert the prepared microplate into the connected instrument.
2. Click and hold **Shake**  on the **Operations** tab in the ribbon.
3. Release the mouse button to stop the shaking operation.





Tip: You can also have the instrument shake the microplate by holding down the **F8** key.

Opening and Closing a Drawer

For most instruments, you can open and close the microplate drawer using the software.

To open and close the microplate drawer on a connected instrument:

1. Click **Open / Close**  on the **Operations** tab in the ribbon to open the microplate drawer.
2. Insert or remove the prepared microplate in the instrument.
3. With the microplate drawer open on the connected instrument, click **Open / Close**  on the **Operations** tab in the ribbon to close the microplate drawer.



Note: The microplate carrier on the EMax Plus Microplate Reader moves in and out of the read chamber during the read, and then returns to the home position after the read ends. If the microplate carrier does not return to the home position, you can initialize the carrier to return it to its home position by clicking **Initialize** in the **Operations** tab of the ribbon. See [Using the Operations Tab on page 44](#).

For some instruments, other drawers can be opened and closed using the software. For example, the three drawers on the FlexStation 3 reader can be opened using the software. Go to the **Operations** tab on the ribbon and then click **Tips** for the tip rack drawer, **Reagent** for the compound plate drawer, or **Open / Close** for the read chamber drawer.

Use the **Instrument Information** dialog to open and close the cartridge drawers on the SpectraMax i3x Instrument or SpectraMax Paradigm Instrument or to open and close the filter drawers on the FilterMax F3 and F5 Instruments. See [Using the Instrument Information Dialog on page 457](#).

Using the GxP Tab

The **GxP** tab is available only when using the SoftMax Pro GxP Software. See [Using SoftMax Pro GxP Software Features on page 467](#).

User Account

The buttons in the **User Account** group provide access to information and management of the current user account.

- **Account Information:** The **User Account Information** dialog provides information about the current user. See [Viewing the User Information on page 472](#).
- **User Log On:** Click the **Log On** button to log on after previously logging off. See [Logging onto SoftMax Pro GxP Software on page 472](#).
- **User Log Off:** Click the **Log Off** button to log the current user off without closing the program.
- **Change Password:** The **Change Password** dialog lets the current user change the password required for logging onto the software. See [Changing the User Password on page 474](#).
- **Select Account Database:** The **User Accounts Connection** dialog lets the GxP Admin Software administrator define the location of the User Accounts file related to this installation of the SoftMax Pro GxP Software. See [Connecting a User Accounts File on page 469](#).


Data


The buttons in the **Data** group provide access to features that are unique to the SoftMax Pro GxP Software.

- **Statements:** The **Statements** dialog lets you view, edit, and add statements. A user with the proper permission can add an electronic signature to statements. See [Working with GxP Statements on page 475](#).
- **Audit Trail:** The **Audit Trail** dialog gives you read-only access to the audit trail for the open data file, and lets you attach a note to the audit trail. See [Viewing the GxP Audit Trail on page 482](#).

Using the Help Tab

SoftMax Pro Software has a comprehensive help library. You can open the application help documents from the **Help** tab in the ribbon.





- Click **SoftMax Pro Help**  to view the *SoftMax Pro Software Application Help*. This help contains task-oriented information about how to use SoftMax Pro Software. You can find topics through the table of contents and by using the search function. This document also features a linked index and glossary.


- Click **Formula Reference**  to view the *SoftMax Pro Software Formula Reference Guide*. This document is broken into four main sections:

The first section provides a general introduction to SoftMax Pro Software formulas.

- **Operators** describes the different types of operators that can be used to assemble formulas.
- **Functions** describes the different types of built-in functions that can be used to assemble formulas.
- **Accessors** describes the special functions that provide access to other specific information.

You can find topics through the table of contents and by using the search function. This document also features a linked index.

- Click **Release Notes**  to view the *SoftMax Pro Software Release Notes* for this release of the software. This document is in PDF format and can be viewed using a PDF viewer like Adobe Reader.
- Click **Contact Us**  to display the SoftMax Pro Software What's New page, view the Molecular Devices home page, access the knowledge base, or request technical support. The knowledge base contains documentation supporting Molecular Devices products. You can use the customer login tools and featured links to help you get the information you need.
- Click **Software License**  and follow the instructions in the **Software License Activation** dialog to activate your SoftMax Pro Software license.
- Click **SoftMax Pro**  in the **About** section to see release information about this release of the SoftMax Pro Software application.

Context-sensitive help is available for the dialogs that have a  help button.

More documentation in PDF format can be found in the Windows **Start** menu.

- To view the *SoftMax Pro Software User Guide*, the *Formula Reference Guide*, or the *Software Release Notes*, click **Start > All Programs > Molecular Devices > SoftMax Pro 7.0** and then click the document you want to view.
- To view user guides for the supported instruments, click **Start > All Programs > Molecular Devices > SoftMax Pro 7.0 > Hardware User Guides** and then click the document you want to view.

These documents are in PDF format and can be viewed using a PDF viewer like Adobe Reader.

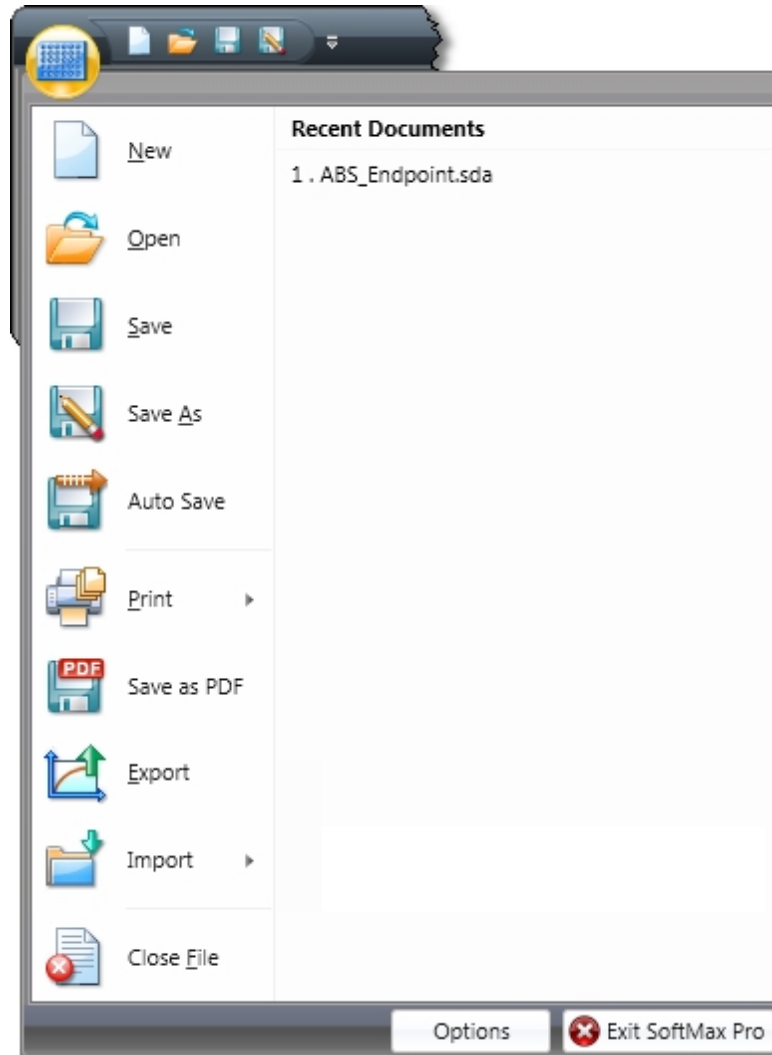
Viewing the On-Screen Help


On-screen help is displayed when the dialog requires specific user interaction. When more information about the topic is available, click the **More Information** link to open a help topic that is specific to the option being set.



Application Menu

The **Application** menu in the upper-left corner of the window contains options for working with files, printing, and managing the application.



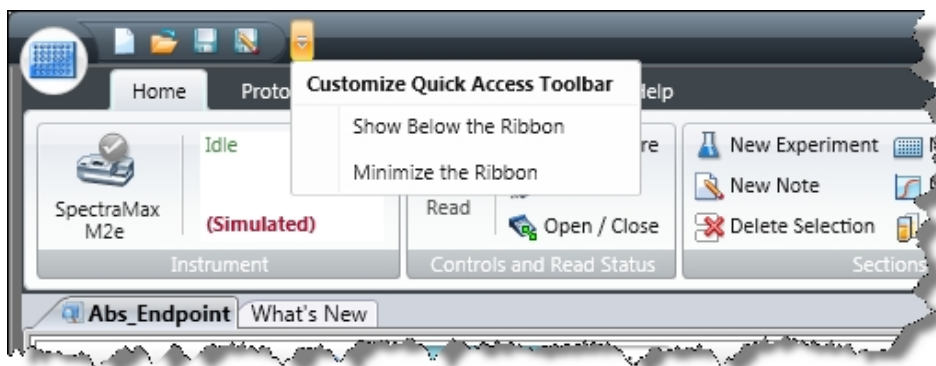
Click the **Application**  button to open the **Application** menu and then click a menu option.

- To create a new blank data file or protocol file, click **New**. See [Creating a New Data File on page 63](#) or [Creating a New Protocol File on page 73](#).
- To open an existing data file or protocol file, click **Open** or select the file from the list of **Recent Documents** on the right. See [Opening a Data File on page 64](#) or [Opening a Protocol File on page 74](#).
- To save an open data file or protocol file, click **Save** or **Save As**. See [Saving Data Files on page 65](#) or [Saving Protocol Files on page 75](#).

- To set up automatic saving options, click **Auto Save**. See [Setting Auto Save Options on page 76](#).
- To print the sections of an experiment, preview a print job, or set printing options, click **Print** and then click the option you want on the right. See [Printing on page 80](#).
- To save the defined printed output of a file in portable document format (PDF), click **Save As PDF**. See [Saving Data in a PDF File on page 451](#).
- To export the data in a data file, click **Export**. See [Exporting Plate Data on page 85](#).
- To import data to a data file, click **Import**. See [Importing Microplate Data on page 99](#).
The data import feature requires a separate license. To obtain a license for this feature, contact your Molecular Devices representative.
- To close the currently open document in the workspace, click **Close File**.
- To set application options, click **Options** at the bottom of the menu. See [Setting Application Options on page 104](#).
- To exit the program, click **Exit SoftMax Pro** at the bottom of the menu.

Quick-Access Toolbar

The Quick-Access toolbar is available for your customization. The Quick-Access toolbar initially is displayed directly to the right of the Application button in the upper-left corner of the SoftMax Pro Software application window.



You can move the location to above or below the ribbon and add function buttons that you want to have quick-access to.

The Quick Access Toolbar initially has buttons to do the following tasks:

- Create a new data file
- Open a data file
- Save a data file
- Save (Save as) a data file or protocol file with a new name
- The actions button

Repositioning the Quick-Access Toolbar

The Quick-Access toolbar can be displayed above or below the application ribbon.

To reposition the Quick-Access toolbar:

1. Click the actions button to the right of the Quick-Access toolbar.
2. From the menu that is displayed, click either **Show Below the Ribbon** or **Show Above the Ribbon**.

Adding a Button

To add a function button to the Quick-Access toolbar:

1. Right-click the button you want to add in the ribbon.
2. From the menu that is displayed, click **Add to Quick-Access Toolbar**.

Removing a Button

To remove a function button from the Quick-Access toolbar:

1. Right-click the button you want to remove in the Quick-Access toolbar.
2. From the menu that is displayed, click **Remove from Quick-Access Toolbar**.

Minimizing the Ribbon

To minimize the ribbon display:

1. Click the actions button to the right of the Quick-Access toolbar.
2. From the menu that is displayed, click **Minimize the Ribbon**.

To return the minimized ribbon to the display:

1. Click the actions button to the right of the Quick-Access toolbar.
2. From the menu that is displayed, click **Minimize the Ribbon** to remove the check mark next to the option.

Integrated Web Browser

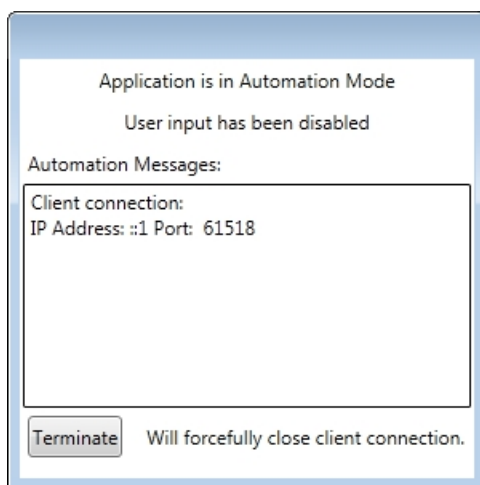
The **What's New** tab in the document area contains a built-in web browser to keep you informed of new or updated products and to give you access to the technical support knowledge base.

This tab automatically starts each time you start the SoftMax Pro Software. To hide this tab on start up, select the **Hide web browser tab when application starts** check box in the **SoftMax Pro Options** dialog. See [Setting Application Options on page 104](#).

Using Automation Mode

The SoftMax Pro Software automation mode prevents user interaction when the software is being controlled by the automation interface through third-party automation software or the StakMax Software. To write scripts to use with the SoftMax Pro Software version 7 automation interface, Molecular Devices recommends that you use the most recent version of the automation commands as described in the *SoftMax Pro Software Automation API Reference Guide*.

To show that the SoftMax Pro Software is in automation mode, a dialog is displayed in front of the main window.




When the automation software acquires data, the related **Plate** section is displayed in the SoftMax Pro Software main window behind the automation mode dialog and displays the acquired data.

If the automation software encounters an error, an error message is displayed in the **Automation Messages** area of the automation mode dialog.

If you need to stop the automation process and regain control of the SoftMax Pro Software, click **Terminate**.

To let the software accept legacy commands from scripts written for the SoftMax Pro Software version 5.x automation interface, go to the **Operations** tab in the ribbon, and then

in the **Automation** section click **Automation Mode** . The legacy script must use the Windows message WM_COPYDATA command. The WM_SETTEXT command is not supported. Legacy scripts might not work correctly with the new automation interface. If your legacy script does not work properly, Molecular Devices recommends that you rewrite the script using the most recent version of the automation commands as described in the *SoftMax Pro Software Automation API Reference Guide*.

For more information on automation, see [Writing and Running Automation Scripts on page 57](#), [StakMax Microplate Handling System on page 216](#), or the *SoftMax Pro Software Automation API Reference Guide*.

Writing and Running Automation Scripts

The automation commands in the SoftMax Pro Software can be scripted and run through the automation API. If you are an experienced automation programmer, consult the *SoftMax Pro Software Automation API Reference Guide* for information about the available commands and their parameters. If you are using the StakMax Microplate Handling System, the StakMax Software has a built in scripting tool. See [StakMax Microplate Handling System on page 216](#). The SoftMax Pro Software also supports a Microsoft Excel Add-In to write and run Excel Workflows.

SoftMax Pro Excel Workflows

The SoftMax Pro Excel workflows are designed to expand the industry-leading handling of Plate Format Data by the SoftMax Pro Software with Excel-based handling of List Format Data. You can use SoftMax Pro Excel workflows to run discontinuous kinetic reads, multiplexed reads, kinetic well scan reads, and temperature-triggered reads.

The SoftMax Pro Automation SDK is the underlying mechanism used by SoftMax Pro Excel workflows to access SoftMax Pro Software functionality. If you want to write your own workflows, you need to be familiar with the available Automation Commands. See the *SoftMax Pro Software Automation API Reference Guide*.

Before you can use Excel to create and run automated workflows, you must install the custom Add-In in Excel. With the Add-In installed you can run or edit the provided workflows or create your own.

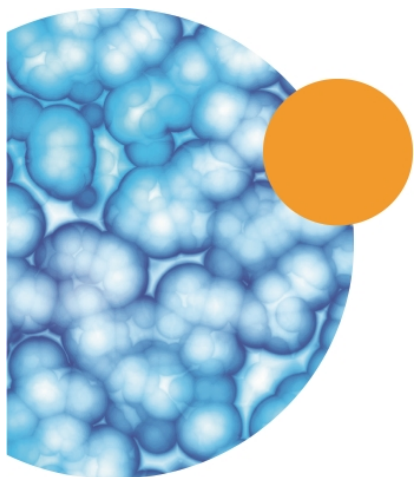
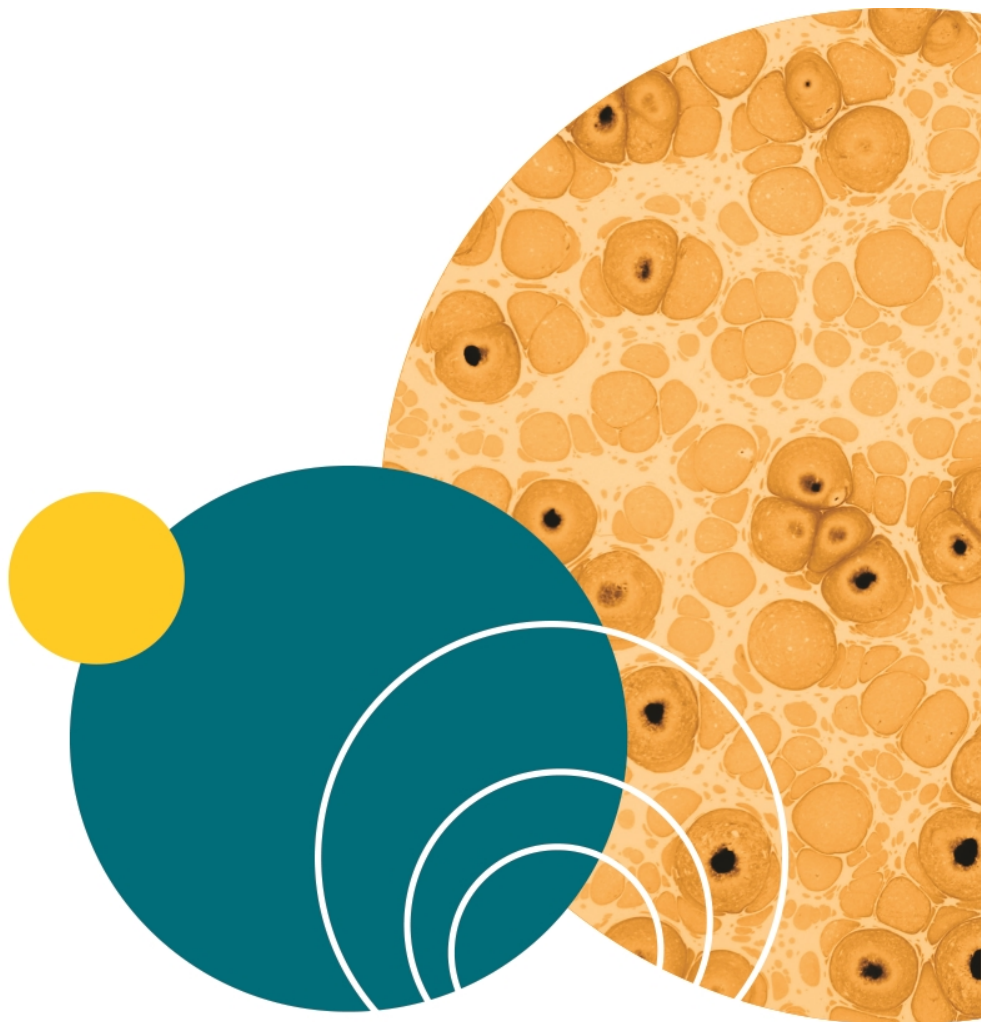
The provided Excel workflows are installed in the same folder as the Excel Add-In files.

- For a 32-bit installation, the workflows are in the following folder:
C:\Program Files\Molecular Devices\SoftMax Pro 7.0 Automation SDK\ExcelAddIn
- For a 64-bit installation, the workflows are in the following folder:
C:\Program Files (x86)\Molecular Devices\SoftMax Pro 7.0 Automation SDK\ExcelAddIn

The Excel workflow files have an extension of **.xlsm**.


Before running or editing a provided Excel workflow, save a copy of the workflow on your computer.

For complete information about setting up and using SoftMax Pro Excel Workflows, see the *SoftMax Pro Software Automation API Reference Guide*.



Chapter 3: File and Application Management

The **Application** menu in the upper-left corner of the SoftMax Pro Software window contains options for working with files, printing, and managing the application.

Click the **Application**  button to open the **Application** menu and then click a menu option. See [Application Menu on page 53](#).

File Types

SoftMax Pro Software uses two basic file types: data files and protocol files.

Data files

Data files contain the experiment settings, the raw data collected by your reader, and the data analysis you might have completed.

SoftMax Pro Software 6 can open files created by version 4.0 or later. Before you open a file you must make sure that your currently selected instrument is the same model as the one used to create the file, or a model with instrument settings that are compatible with the model used to create the file.



Note: Files with data acquired from a FlexStation® 3 Multi-Mode Microplate Reader can be opened for data analysis only.

You can open data files that have the following file extensions:

- .sda (SoftMax Pro Software 6 data files)
- .sdax (SoftMax Pro GxP Software 6 data files)
- .pda (SoftMax Pro Software 4 and 5 data files)
- .eda (SoftMax Pro GxP Software 4 and 5 data files)

See [Opening a Data File on page 64](#).

All SoftMax Pro Software 6 data files are saved with the .sda or .sdax extension. See [Saving Data Files on page 65](#).

When you create a data file for an imaging experiment or a Western Blot experiment, the SoftMax Pro Software creates a folder with the same name as the data file. See [Image Data Files and Folders on page 61](#).

The Auto Save feature can be used to prevent data loss. For more information and a description of the data file types, see [Setting Auto Save Options on page 76](#).

Data Export Formats

You can export the data from a SoftMax Pro Software data file using the following file extensions:

- .xml
- .txt (list)
- .txt (plate)
- .xls (list)
- .xls (plate)

See [Exporting Plate Data on page 85](#).

Protocol Files

Protocol files are experiment template files that contain microplate well layout assignments and all other reader configuration information, but no data.

You can open protocol files that have the following file extensions:

- .spr (SoftMax Pro Software 6 protocol files)
- .sprx (SoftMax Pro GxP Software 6 protocol files)
- .ppr (SoftMax Pro Software 4 and 5 protocol files)
- .epr (SoftMax Pro GxP Software 4 and 5 protocol files)

See [Opening a Protocol File on page 74](#).

All SoftMax Pro Software 6 protocol files are saved with the .spr or .sprx extension. Saving a data file as a protocol file removes the data in the file, leaving only the configuration information. See [Saving Protocol Files on page 75](#).

Predefined Protocols

Several predefined protocols are installed with SoftMax Pro Software and are placed in the default protocols folder. During software installation, the Basic Endpoint protocol is set as the default protocol. Whenever you open a new file, the new file contains the settings from the default protocol file. To change the default protocol file, see [Saving a Protocol as the Default Protocol on page 69](#).

You can use the features available in the **Protocols** tab in the application ribbon to manage and share protocol files. See [Using the Protocols Tab to Manage Protocols on page 42](#).

Image Data Files and Folders

Before starting an image acquisition for Imaging mode or a Western Blot scan, you must save the data file in a location with enough capacity for the image files. You create and save data files for image-based experiments the same as you do for other experiments. See [Creating a New Data File on page 63](#).

For best results, save your imaging data file on a secondary internal hard drive. You can use an external hard drive, but this can slow the data acquisition and is not recommended.



Note: To prevent data loss, do not save your imaging data file on a USB flash drive or to a network location. These methods are not supported by Molecular Devices.


When you create a data file for an imaging experiment or a Western Blot experiment, the SoftMax Pro Software creates a folder with the same name as the data file. For example, if you save the data file with the name **Imaging_Data**, then a new folder named **Imaging_Data** is also created in the same folder where the data file is saved. This folder stores the acquired images and analysis results.



The acquired images are stored separately for each microplate in the **IMAGES** folder in TIFF format. The image analysis data are stored in the **RESULTS** folder. For a Western Blot scan, the **RESULTS** folder is not created or used.



CAUTION! Do not manually rename the data file. Do not manually rename, move, or delete the related folders or files. If you make changes to the structure of these files and folders, then the SoftMax Pro Software possibly cannot open the data file, or it can display inaccurate results.

To make a copy of the data file, image files, and analysis data files, click the **Application**  button in the ribbon to open the **Application** menu, and then click **Save As**. See [Saving Data Files on page 65](#).

To delete the acquired images or the analysis data for an Imaging mode read of a microplate, in the **Navigation Tree** right-click the **Plate** section and then click **Delete Images** or **Delete Cell Data**. See [Navigation Tree on page 29](#).

If you delete the TIFF file for a Western Blot scan, the SoftMax Pro Software recreates the TIFF image from the intensity data stored in the data file.

Molecular Devices recommends that you always use the file-management tools in the SoftMax Pro Software to copy or delete your imaging files.



Note: When you save an imaging experiment as a protocol, only the protocol file is saved. No other folders or files are created. See [Creating a New Protocol File on page 73](#).

Acquiring images in Imaging read mode requires a large portion of computer memory and resources.

Each acquired image file for an Imaging mode read can be larger than 2 megabytes. Acquiring the image of a single site in each well of a 96-well microplate can generate 300 megabytes of image data. A 384-well microplate can generate 1 gigabyte of image data. Acquiring images of multiple sites increases the data-storage requirement. Molecular Devices recommends that you use a data management system.

Before starting an image acquisition, minimize the demands on computer memory and resources by turning off all other programs. When the SoftMax Pro Software has limited access to computer memory and resources, image acquisition can take a long time. In some cases, images of some of the wells can be lost.

To prevent data loss, turn off all sleep and hibernation settings for the hard disk, the CPU, and the USB ports. Also, disable automatic Windows Updates. You can update Windows manually when the instrument is not being used by the software. You can set these options in Windows Control Panel. See [Optimizing Your Computer for Image Acquisition on page 337](#).


Molecular Devices recommends that you use Auto Save with imaging data for saving to text files only. If you use Auto Save to save multiple imaging data files, each new data file is saved without the related folders required for saving images and analysis results. See [Setting Auto Save Options on page 76](#).

Creating a New Data File

You can create a new empty data file and save it into a folder.

The **Application** menu **New** command opens a new data file named **Untitled**, based on the default protocol.

To create a new data file:

1. Click the **Application**  button to open the **Application** menu.
2. Click **New**. A new blank file opens and a new tab is displayed above the navigation tree.



Note: Molecular Devices recommends that you name and save the file before you configure settings and collect data.

3. Click the **Application** button to open the **Application** menu.
4. Click **Save as** to open the **Save As** dialog.
5. Navigate to where you want to save the file.
6. Type the file name in the **File name** field.
7. In the **Save as type** list, select **Data Files (*.sda)**.
If you are working with the SoftMax Pro GxP Software, select **Data Files (*.sdax)**.
8. Click **Save**.

The name of the data file is displayed on the tab above the navigation tree.

When you create a data file for an imaging experiment or a Western Blot experiment, the SoftMax Pro Software creates a folder with the same name as the data file. See [Image Data Files and Folders on page 61](#).

Opening a Data File

To open a supported protocol or data file, use the **Application** menu. SoftMax Pro Software 6 can open files created by version 4.0 or later. However, after you save a file, it is readable only by the current version.

You can open data files that have the following file extensions:

- .sda (SoftMax Pro Software 6 data files)
- .sdax (SoftMax Pro GxP Software 6 data files)
- .pda (SoftMax Pro Software 4 and 5 data files)
- .eda (SoftMax Pro GxP Software 4 and 5 data files)



Note: Before you open a file you must make sure that your currently selected instrument is the same model as the one used to create the file, or a model with instrument settings that are compatible with the model used to create the file.

Files with data acquired from a FlexStation® 3 Multi-Mode Microplate Reader can be opened for data analysis only.

SoftMax Pro Software 6 can open files created by version 4.0 or later. If you want to open a file created in a version earlier than version 4.0, you must first open the file in SoftMax Pro Software 4.0 or later, and then save it as a version 4.0 or later file. Instrument compatibility requirements also must be met.

This version of the SoftMax Pro Software saves the new file with a different file extension from the extension used in previous versions. The file created with the older version can continue to be used with the older version without affecting the contents of the new file.

After opening a file from a previous version, it is good practice to review the file to make sure that the conversion went well. In some cases, the file conversion might change instrument settings, curve fits, or other items that have been updated for version 6.

To open a data file:

1. Click the **Application**  button to open the **Application** menu.

2. Select **Open**. The **Data Files** file type is selected by default.

SoftMax Pro Software 6 can open files created by version 4.0 or later.

When you open a file from a previous version, it is converted to SoftMax Pro Software version 6 format.

3. Navigate to the data file you want to open.

4. Select the file.

5. Click **Open**.

A tab with the name of the file opens above the navigation tree, and the file opens in the workspace.

Saving Data Files

Use the **Application** menu **Save** or **Save As** commands to save data files.

If you want to save data in PDF format, see [Saving Data in a PDF File on page 451](#).

To save a data file:

1. Click the **Application**  button to open the **Application** menu.

2. Click **Save** (for first time file saving) or **Save As**.

3. In the **Save As** dialog, navigate to where you want the file to be saved.

4. In the **File name** field, type a name for the file.

5. From the **Save as type** field, select **Data Files (*.sda)**.

If you are working with the SoftMax Pro GxP Software, select **Data Files (*.sdax)**.

6. Click **Save**.

Molecular Devices recommends that you save your data file frequently. When you want to save the data file, click the **Application**  button to open the **Application** menu and then click **Save** to save the file without opening the **Save As** dialog.

When you create a data file for an imaging experiment or a Western Blot experiment, the SoftMax Pro Software creates a folder with the same name as the data file. See [Image Data Files and Folders on page 61](#).

Copying and Pasting Data

You can copy plate data from one **Plate** section to a different **Plate** section within the same data file or between different data files. The format of the copied plate data must match the format of the target **Plate** section. If you want to copy plate data between **Plate** sections in the same file, it might be easier to use the **Clone Plate** feature. See [Cloning a Plate Section on page 127](#).

In some cases, you can paste endpoint plate data copied from an external program, such as a spreadsheet or text editor. When pasting data from an external program, the format of the copied endpoint data must exactly match the format of the target **Plate** section. Only endpoint data can be pasted from an external program.

For more information about **Plate** sections, see [Using a Plate Section on page 118](#).

To copy data from a **Plate** section:

1. View the **Plate** section that has the data you want to copy.
2. Right-click the plate data area and click **Copy Plate Data** to copy all of the data in the entire plate.

To paste data in a **Plate** section:

1. View the **Plate** section where you want to paste the data.
2. Right-click the plate data area and click **Paste Plate Data**.

If you are pasting data from an external program, click **Paste Data**.

3. When pasting over existing data, click **Yes** in the message box that is displayed.

If the format of the data does not match the format of the target plate, a message is displayed informing you of this. Click **OK** to close the message without pasting the data.

After the data is pasted into the **Plate** section, the **Read Information** on the right indicates that the data was pasted and shows the time and date of when it was pasted.

Managing Protocol Files

Protocol files are experiment template files that contain microplate well layout assignments and all other reader configuration information and reduction parameters, but no data. Protocol files can be useful if you repeat a particular type of experiment frequently.

The **Protocols** tab in the ribbon provides easy access to protocol files that are stored in the file system. It also gives you access to the SoftMax Pro Software user community for protocol sharing, exchanging tips and tricks, and networking with other experienced users. See [Using the Protocols Tab to Manage Protocols on page 42](#).

Over 120 assay protocols are included in the software to speed life science research and drug discovery assay development and screening. Researchers can customize experiment protocols, analyze and display data, and create meaningful reports. The straightforward yet powerful programming capabilities of the SoftMax Pro Software can further enhance specialized data collection and analysis needs through custom assay development.

The predefined protocols installed with SoftMax Pro Software are placed in the SoftMax Pro Software Protocols folder. You can use the Protocol Manager to quickly find and open a protocol. See [Using the Protocol Manager to Open a File on page 68](#).

During software installation, the Basic Endpoint protocol is set as the default protocol. Whenever you open a new file, the new file contains the settings from the default protocol file. You replace the default protocol with the settings from an open file so that future new files will use those settings. See [Saving a Protocol as the Default Protocol on page 69](#).

Saving a data file as a protocol file removes the data in the file, leaving only the configuration information. You can add or remove folders in the Protocol Manager to help you find the protocols you use most often. See [Adding or Removing a Folder in the Protocol Manager on page 70](#).


Using the Protocol Manager to Open a File

The predefined protocols installed with SoftMax Pro Software are placed in the SoftMax Pro Software Protocols folder. You can use one of the predefined protocols, or you can create your own protocol. For more information on protocols, see [Creating a Protocol on page 235](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol.

To open a protocol file in the Protocol Manager:

1. Click **Protocol Manager**  on the **Protocols** tab to open the Protocol Manager where you can select a protocol to be assigned to a new file.
2. Select **Protocol Library** > *foldername* to view the available protocols in that folder.
To open the default protocol, click **Default** at the bottom of the Protocol Library.
3. Click the protocol you want to open.
4. When you save the section as a data file the settings from the protocol are saved along with the data.




Note: When you add a new Plate section or Cuvette Set section to an experiment, you can configure the instrument settings using the **Settings** dialog. See [Instrument Settings on page 246](#).

Saving a Protocol as the Default Protocol

After the SoftMax Pro Software is installed, the Basic Endpoint protocol is set as the default protocol with the filename **default.spr**. Whenever you create a new document, the **default.spr** protocol file is opened as an untitled document that contains the settings from the default protocol file.

You can save the settings of the file currently active in the workspace as the default protocol. After you save the active protocol file as the default, whenever you create a new document, the settings in the **default.spr** file that you have saved are loaded into an untitled document.

Saving a Default Protocol

1. Click **Save as Default**  to overwrite the default.spr file with the protocol setting of the experiment that is active in your workspace.
2. Click **OK** to overwrite the default protocol file with this file. With the exception of acquired data, all settings and sections (with their contents) are saved as part of the new default protocol. When you create a new file, it will initially be identical to this current data file (minus existing data).



Note: When you save the file as the default protocol, the data you have collected in the current experiment remains unchanged. If you want to keep the data, you need to save the data into a data file. See [Saving Data Files on page 65](#).

Adding or Removing a Folder in the Protocol Manager

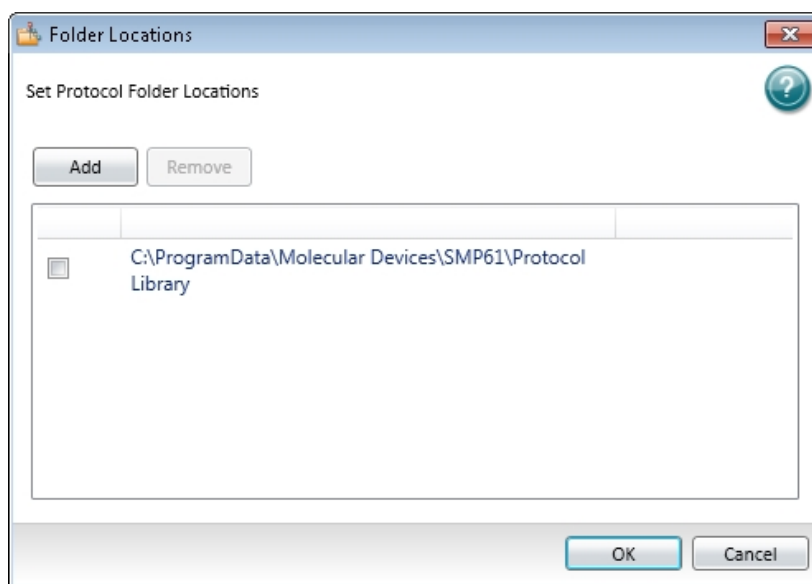
You can add folders in your file system to those folder where protocols can be stored. See [Adding a Protocol Folder Location on page 70](#) and [Deleting a Protocol Folder Location on page 72](#).

Whenever you store protocol files in the added folder, those protocols are available in the **Protocol Manager**. See [Using the Protocol Manager to Open a File on page 68](#).

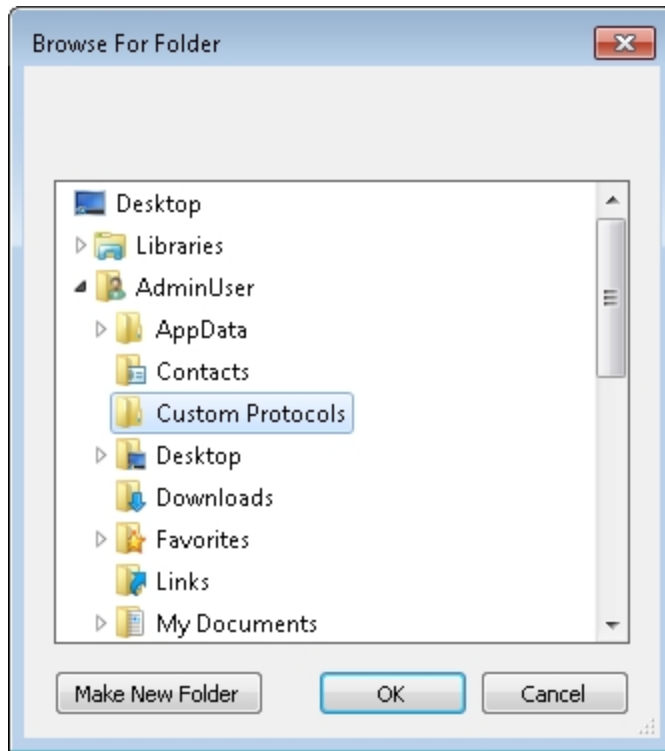
Adding a Protocol Folder Location

To add a protocol folder location to the Protocol Manager:

1. Click **Folder Locations**  to open the **Folder Locations** dialog.




2. Click **Add** to browse the file system to the folder to be added.

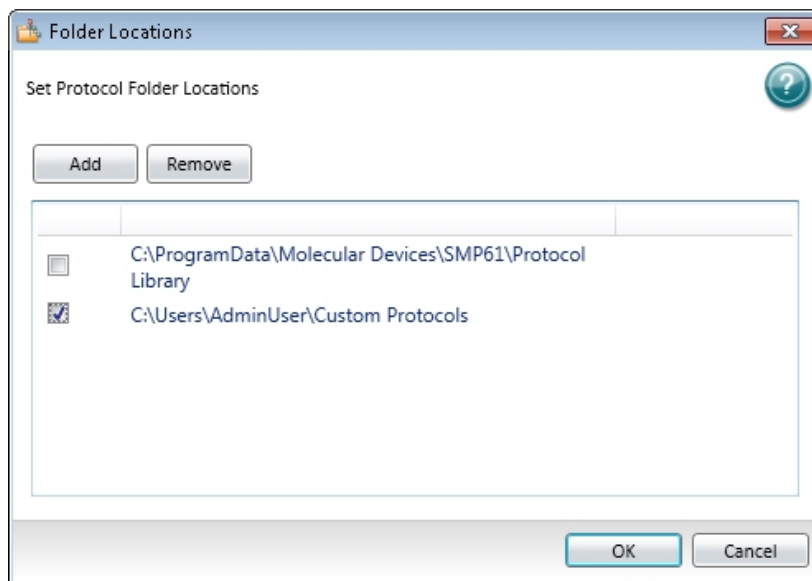


3. Select the folder where you want to store protocols.
4. Optionally, click **Make New Folder** to add a New Folder inside the selected folder and then type a name for the folder.
5. Click **OK**. The selected folder is added to the folder list in the **Folder Locations** dialog.
6. Click **OK** to close the **Folder Locations** dialog.

Deleting a Protocol Folder Location

To remove a protocol folder location from the Protocol Manager:

1. Click **Folder Locations**  to open the **Folder Locations** dialog.
2. Click the check box to select the folder location you want to remove.



3. Click **Remove**. The selected folder is removed from the folder list in the **Folder Locations** dialog.
4. Click **OK** to close the **Folder Locations** dialog.




Note: Removing a protocol folder location from the Protocol Manager does not remove the folder or the files from your computer.

Creating a New Protocol File

You can create a new blank protocol file and save it into a folder.

To create a new protocol file from a predefined protocol in the Protocol Manager, see [Using the Protocol Manager to Open a File on page 68](#).

To create a new protocol file:

1. Click the **Application**  button to open the **Application** menu.
2. Click **New**. A new blank file opens and a new tab is displayed above the navigation tree.
3. Configure the protocol settings, see [Creating a Protocol on page 235](#).



Note: Molecular Devices recommends that you save and name the protocol file before you collect data with the settings.

4. Click the **Application** button to open the **Application** menu.
5. Click **Save as** to open the **Save As** dialog.
6. Navigate to where you want to save the protocol file.
7. Type the file name in the **File name** field.
8. In the **Save as type** list, select **Protocol Files (*.spr)**.
If you are working with the SoftMax Pro GxP Software, select **Protocol Files (*.sprx)**.
9. Click **Save**.

Before using the protocol to collect data, save it as a data file. See [Saving Data Files on page 65](#).

Opening a Protocol File

To open a supported protocol file, use the **Application** menu. SoftMax Pro Software 6 can open files created by version 4.0 or later. However, after you save a file, the new file is readable only by the current version.

You can open protocol files that have the following file extensions:

- .spr (SoftMax Pro Software 6 protocol files)
- .sprx (SoftMax Pro GxP Software 6 protocol files)
- .ppr (SoftMax Pro Software 4 and 5 protocol files)
- .epr (SoftMax Pro GxP Software 4 and 5 protocol files)



Note: Before you open a file you must make sure that your currently selected instrument is the same model as the one used to create the file, or a model with instrument settings that are compatible with the model used to create the file.


SoftMax Pro Software 6 can open files created by version 4.0 or later. If you want to open a file created in a version earlier than version 4.0, you must first open the file in SoftMax Pro Software 4.0 or later, and then save it as a version 4.0 or later file. Instrument compatibility requirements also must be met.

If you need to continue using a protocol file with an older version of SoftMax Pro Software, then save the file with a different name or in a different location after you open the file with the current version.

After opening a file from a previous version, it is good practice to review the file to make sure that the conversion went well. In some cases, the file conversion might change instrument settings, curve fits, or other items that have been updated for version 6.

To open a predefined protocol in the Protocol Manager, see [Using the Protocol Manager to Open a File on page 68](#).

To open a protocol file:

1. Click the **Application**  button to open the **Application** menu.
2. Select **Open**. The **Data Files** file type is selected by default.
3. Select a protocol file type from the list.

SoftMax Pro Software 6 can open files created by version 4.0 or later.


When you open a file from a previous version, it is converted to SoftMax Pro Software version 6 format.

4. Navigate to the protocol file you want to open.
5. Select the file.
6. Click **Open**.

An untitled file opens in the workspace with the settings of the selected protocol applied to it. Before using the protocol to collect data, save it as a data file. See [Saving Data Files on page 65](#).

Saving Protocol Files

Use the **Application** menu **Save As** command to save a file as a protocol file.

1. Click the **Application**  button to open the **Application** menu.
2. Click **Save As**.
3. In the **Save As** dialog, navigate to where you want the protocol file to be saved.
4. In the **File name** field, type a name for the file.
5. From the **Save as type** field, select **Protocol Files (*.spr)**.

If you are working with the SoftMax Pro GxP Software, select **Protocol Files (*.sprx)**.

6. Click **Save**.

Saving a data file as a protocol file removes the data in the file, leaving only the configuration information.

Before using the protocol to collect data, save it as a data file. See [Saving Data Files on page 65](#).

Setting Auto Save Options

When Auto Save is enabled, the collected data is saved automatically to a user-defined location immediately after each plate read is completed. Auto Save reduces the likelihood of lost data, particularly when Auto Save is set to save files to corporate network volumes that are backed up on a regular basis.

You can add as many Auto Save instances as desired, each with its own settings.





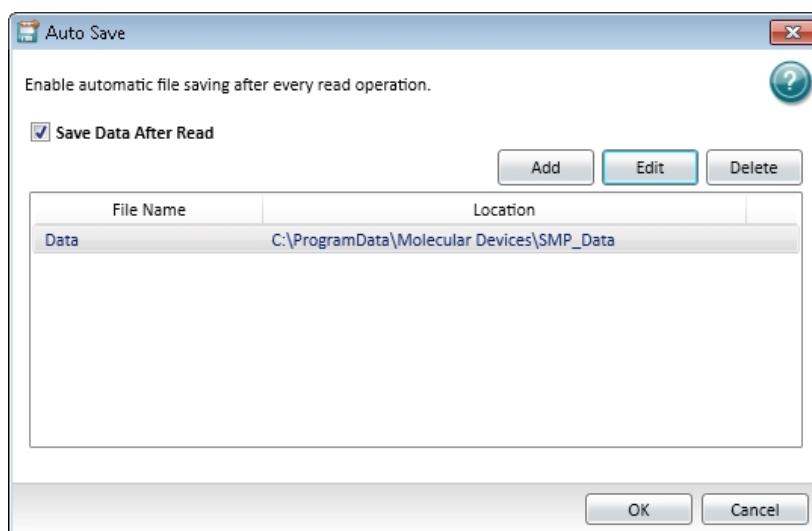
Note: Auto Save settings are saved with each document.

This feature helps prevent data loss when used with automated reads, such as with the StakMax Microplate Handling System. See [StakMax Microplate Handling System on page 216](#).

Molecular Devices recommends that you use Auto Save with imaging data for saving to text files only. If you use Auto Save to save multiple imaging data files, each new data file is saved without the related folders required for saving images and analysis results. See [Image Data Files and Folders on page 61](#).

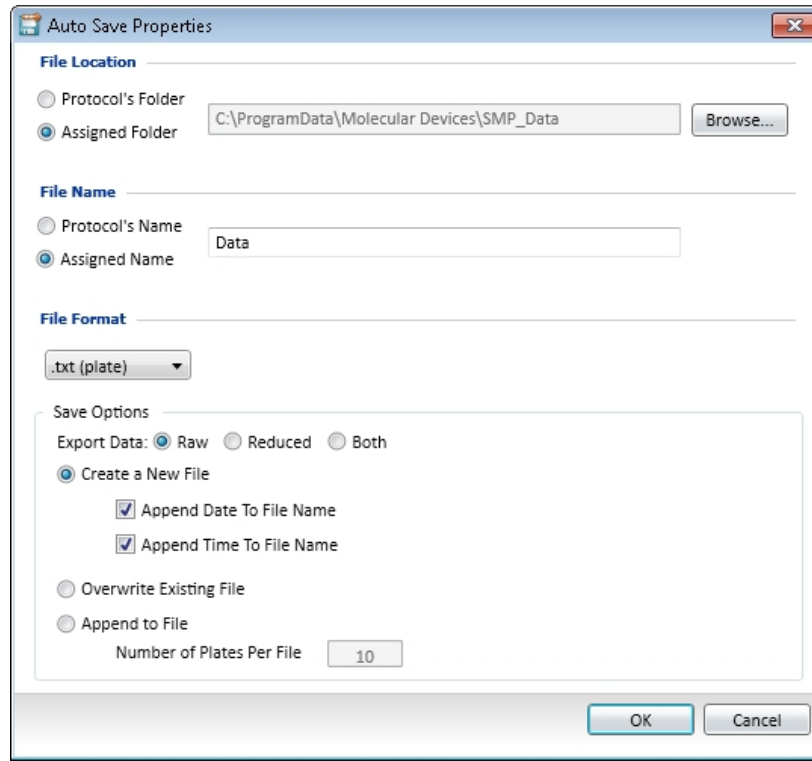
To set Auto Save options:

1. Click the **Application**  button in the ribbon to open the **Application** menu and then click **Auto Save**  to open the **Auto Save** dialog.



2. To enable Auto Save, select **Save Data After Read**.
3. To create a new Auto Save location, click **Add**.
4. To modify an existing Auto Save location, select the location in the list and then click **Edit**.
5. When you are finished setting Auto Save options, click **OK**.

Defining Auto Save Properties



The **Auto Save Properties** dialog contains the following options:

File Location

You can choose to automatically save files to the current protocol's folder or to assign a different folder.

To assign a folder click **Assigned Folder** and then click the **Browse** button to locate the folder where you want to save the data.

File Name

To name the automatically saved file with the current protocol's name, select **Protocol's Name**.

To assign a name to the automatically saved file, select **Assigned Name** and then type a name for the file. The text in this field is automatically inserted at the start of each automatically saved file name.

File Format

Select a data format from the menu. Options include:

- .sda or .sdax
- .xml
- .txt (list)
- .txt (plate)
- .xls (list)
- .xls (plate)

Format options let you specify what type of file is automatically saved. Version 6 supports the following file formats: SoftMax Pro (.sda), XML (.xml), tab-delimited text (.txt) in list or plate layouts, and Excel (.xls) in list or plate layout.

SoftMax Pro File Format

When **.sda** or **.sdax** is selected, your data is automatically saved as a proprietary SoftMax Pro Software file format.

XML File

When **.xml** is selected, your data is automatically saved in XML format. XML is supported for data export and Auto Save. XML is the best file format if you plan to import all read data into other data collection and storage applications—specifically, LIMS (Laboratory Information Management System) or SDMS (Scientific Data Management System) packages.

Tab-Delimited File

When either **.txt (list)** or **.txt (plate)** is selected, your data is automatically saved as a tab-delimited text file, which can be opened by most word processor, spreadsheet, or database programs.

Excel

When either **.xls (list)** or **.xls (plate)** is selected, your data is automatically saved in a format that can be opened by Microsoft Excel. The Excel output has the same format as a tab-delimited file with the .xls file extension which lets the file be opened easily by Excel.

Save Options

The available save options depend on the selected file format for the automatically saved file.

Export Data

For all data formats except .sda, you can specify the type of data to save.

- Select **Raw** to export only the raw data.
- Select **Reduced** to export only the reduced data.
- Select **Both** to export both the raw and the reduced data in the same file.

Create a New File

When you choose to create a new file after each read, you can also choose to append the date and time to the file name.

- Select **Append Date to File Name** to add the date after the specified file name.
- Select **Append Time to File Name** to add the time after the specified file name.

If you select to append both the date and the time to the file name, the time follows the date.

If you do not select to append the date or the time to the file name, files with the same name are numbered sequentially, for example **Data 1**, **Data 2**, and so on.

If you select to append only the date to the file name, SoftMax Pro Software indexes the runs for that day starting with **1** and increments with each successive run. For example, the first file named **Data** that is automatically saved on February 12th, 2014 would be named as **Data-02-12-14 1**, while the second automatically saved file would be named **Data-02-12-14 2**, and so on.

Overwrite Existing File

This option should be used carefully as overwriting a file can cause loss of data. To help ensure against data loss, a file can overwrite only itself. If a different file with the same name exists in the defined autosave directory, the SoftMax Pro Software appends a number to the end of the file name.



Append to File





If either a .txt or .xls format is selected, you can choose to append the plate data to the current file. Enter the maximum number of plates to append per file.

If you are reading 10 microplates using the StakMax Microplate Handling System, you can use **Append to File** to save the data from all 10 microplates in a single data file.

Printing

You can print the contents of the currently selected file. You can print all the sections, or select the sections that you want to print. You can preview the print job before you print it. You can define the header and footer of the pages and the print quality in the **Printing Options** dialog.

To print the file or set the printing options, Click the **Application**  button to open the **Application** menu, and then click **Print** . The following options are displayed on the right:

- Click **Print All**  to print all the included sections in the file. See [Printing All Included Sections on page 81](#).
- Click **Print Preview**  to preview the print job before printing it. See [Previewing a Print Job on page 81](#).
- Click **Print Selected**  to select the sections that you want to print for the print job. See [Printing Selected Sections on page 82](#).
- Click **Printing Options**  to define the header and footer of the pages and the print quality for your print jobs. See [Setting Printing Options on page 83](#).




You can also predefine the sections that you want to exclude from your future print jobs by disabling printing for the sections in the **Navigation Tree**. See [Disabling Sections from Printing on page 84](#).

To print to a PDF file, select the **Molecular Devices (PDF Writer)** in the **Print** dialog or open the **Application** menu and click **Save As PDF**. See [Defining PDF File Settings on page 452](#).

Printing All Included Sections




When you select to print all the sections in the file, all the included sections print in the order they are listed in the **Navigation Tree**. If you have excluded a section from printing by disabling printing for the section in the **Navigation Tree**, the section does not print. See [Disabling Sections from Printing on page 84](#).

To print all the included sections in the file:

1. Click the **Application**  button to open the **Application** menu, and then click **Print**  .
2. From the list on the right, click **Print All**  .
3. In the **Print** dialog, select the printer you want to use and set the print settings available for that printer, including the number of copies that you want to print.
To print to a PDF file, select the **Molecular Devices (PDF Writer)**. See [Defining PDF File Settings on page 452](#).
4. Click **Print**.

Previewing a Print Job

To preview the print job before printing it:

1. Click the **Application**  button to open the **Application** menu, and then click **Print**  .
2. From the list on the right, click **Print Preview**  .
3. In the **Print Preview** dialog, you can scroll through the pages and zoom in and out.
4. Click the **Print** button in the toolbar at the top of the dialog.
5. In the **Print** dialog, select the printer you want to use and set the print settings available for that printer, including the number of copies that you want to print.
To print to a PDF file, select the **Molecular Devices (PDF Writer)**. See [Defining PDF File Settings on page 452](#).
6. Click **Print**.

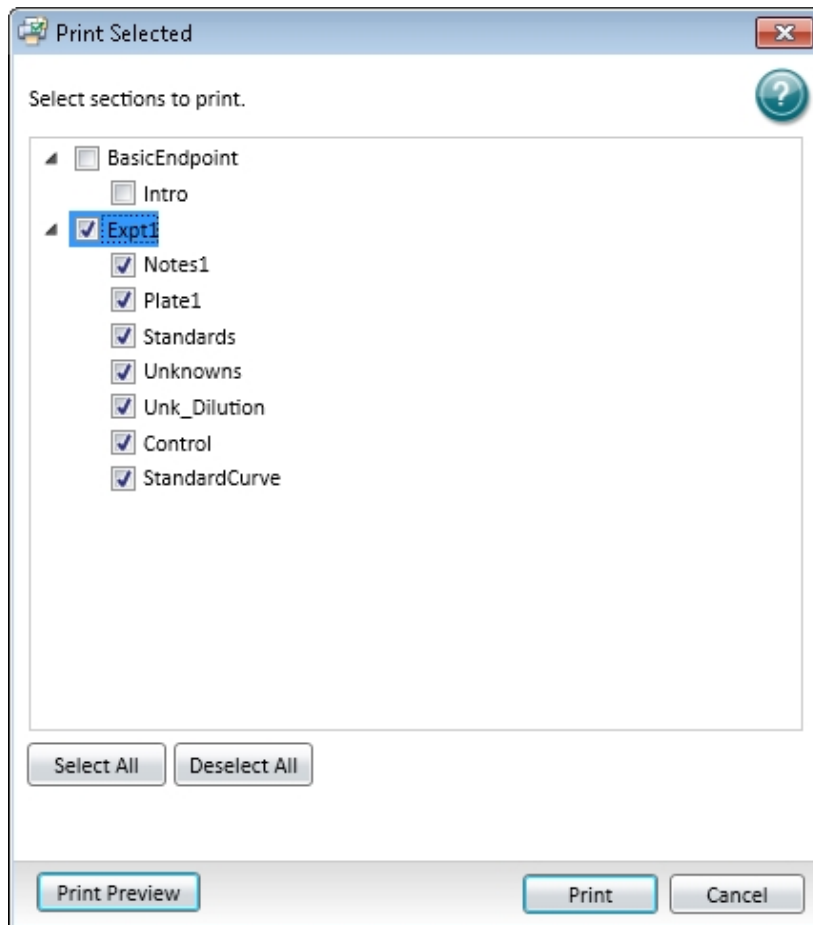
Printing Selected Sections

To select the sections that you want to print:

1. Click the **Application**  button to open the **Application** menu, and then click **Print**



2. Click **Print Selected** .



3. In the **Print Selected** dialog, select the check boxes next to the sections you want to print and clear the check boxes next to the sections that you do not want to print.
 - To select all the check boxes, click **Select All**.
 - To clear all the check boxes, click **Deselect All**.
 - To preview the print job before printing, click **Print Preview**. See [Previewing a Print Job on page 81](#).
4. Click **Print** to print the selected sections.


- In the **Print** dialog, select the printer you want to use and set the print settings available for that printer, including the number of copies that you want to print.

To print to a PDF file, select the **Molecular Devices (PDF Writer)**. See [Defining PDF File Settings on page 452](#).

- Click **Print**.

Setting Printing Options

To define the contents of the header and footer and the quality of the printed output:

- Click the **Application**  button to open the **Application** menu, and then click **Print**



- Click **Printing Options** .

Printing Options

Choose options which affect the appearance of the printed document.

Header and Footer

Left	Center	Right
Header		
<input checked="" type="checkbox"/> Experiment Name		<input type="checkbox"/> Add Image
<input type="text"/>	<input type="text"/>	<input type="text"/>
		<input type="button" value="Browse..."/>
Footer		
<input checked="" type="checkbox"/> File Path and Name		<input type="checkbox"/> SoftMax Pro 6.1
<input checked="" type="checkbox"/> Date and Time		<input checked="" type="checkbox"/> Page Number

Print Quality


Draft Better Best

Improving the print quality may increase the amount of time required to print a document.

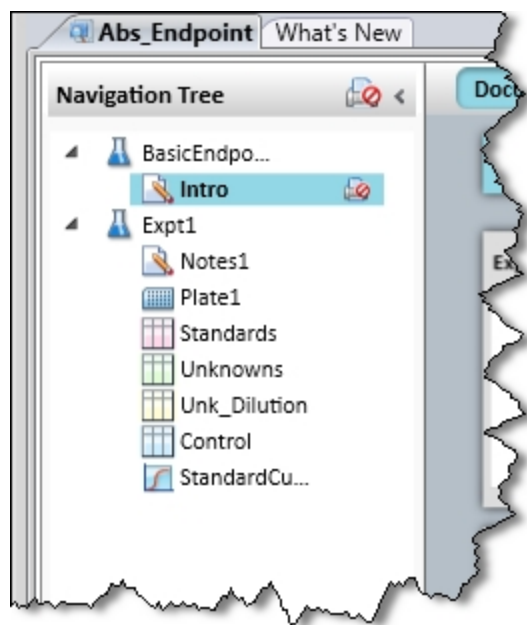
3. In the **Printing Options** dialog, define the header and footer of the pages.
 - To include the predefined text, select the check box next to the text.
 - To include custom text in the header, type the text in the fields.
 - To add a JPEG image, such as a logo, to the right side of the header, select the **Add Image** check box and then click the **Browse** button to locate and select the image file. When printing, the selected image is sized to fit in the image area in the upper-right area of the page.
4. Adjust the print quality by dragging the **Print Quality** slider to the desired quality level.
5. Click **OK** to save the printing options and close the dialog.

Disabling Sections from Printing


To predefine the sections that you want to exclude from your future print jobs:

1. In the **Navigation Tree**, click the section you want to exclude from printing.
2. Click the **Disable printing for the selection**  icon in the upper-right corner of the **Navigation Tree**.

The icon is displayed to the right of the section in the **Navigation Tree**.



To enable printing the selected section, click the **Disable printing for the selection** icon again.

To disable or enable all the sections in an Experiment for printing, click the Experiment to select it and then click the **Disable printing for the selection**  icon in the upper-right corner of the **Navigation Tree**.

Exporting Plate Data

The **Export** feature creates a data file from the selected sections in a SoftMax Pro Software file.

The precision of the data displayed in a **Plate** section varies based on the space available to view the characters.

You can customize the data display to **Numeric notation** or **Scientific notation** format, and specify the number of **Significant Figures** or **Decimal Places**. These options can be set separately for raw data and reduced data.

When the number of digits is increased, the font size of the values in the **Plate** section is decreased. If the value becomes too long, then the numbers are cut off at the edge of the wells.

When SoftMax Pro Software exports plate data, the values are not limited by space and can have more digits for each well.



The values displayed in a **Plate** section are only a representation of the data. In both the **Plate** section and in the exported data, the last digit displayed or exported is rounded based on the actual data value.

For information on exporting membrane data, see [Viewing Western Blot Membrane Data on page 443](#).

For information on exporting Imaging data to Microsoft Excel or PowerPoint, see [Viewing the Imaging Data in a Well on page 365](#).

If you want to export data in PDF format, see [Saving Data in a PDF File on page 451](#).

To export the data from a file:

1. Click the **Application**  button to open the **Application** menu.
2. Click **Export** .
3. In the **Export** dialog, select the sections to export:
 - To include a section in the export, select the check box next to the section.
 - To exclude a section from the export, clear the check box next to the section.
 - To export all plate data, select the **All Plates** check box.
 - To export all group data, select the **All Groups** check box.
 - To export all notes data, select the **All Notes** check box.
4. Click one of the following **Plate Data Options**:
 - **Raw**
 - **Reduced**
 - **Both**



Note: These options apply only if one or more **Plate** sections are selected.

5. Click the **Output Format** you want for the export file:
 - **Columns** exports data in a single column of text for each well.
 - **Plate** exports data in a text matrix corresponding to a microplate grid.
 - **XML** exports data in an XML file format. For a copy of the SoftMax Pro XML schema, contact Molecular Devices Technical Support.



Note: These options apply only if one or more plate sections are selected.

6. Click **OK** to export the data.
7. In the **Save As** dialog, navigate to the folder where you want to save the exported data.
8. In the **File name** field, type a name for the export file.
9. From the **Save as type** list, select the file type for the export file. For XML exports, only **.xml** is available in this list.
10. Click **Save** to save the file with the exported data.

Export File Formats

Whether you save the export as a .txt or .xls, the information is presented as tab-separated values. This topic describes the basic information that is included in these two export formats.

For a copy of the SoftMax Pro XML schema, contact Molecular Devices Technical Support.

The first line of an export file defines the number of sections (or "Blocks") that are included in the export using the following format:

- `##BLOCKS= n`
where *n* is the number of sections that are included in the export file.

The selected sections are exported in the order that they are displayed in the SoftMax Pro Software data file.

Sections are presented in the following format:

- Header line
The header line contains the type of section, such as **Note**, **Plate**, or **Group**, and the title of the section as defined in the SoftMax Pro Software data file. **Plate** sections contain more information in the header line.
- Data lines
The data lines immediately follow the header line and contain the text or data from the exported section. The layout and format of the data lines are dependent on many factors, such as the section type, export type, read mode, and read type.
- End line
The end line of each section is always defined by the text: **~End**

The final line of an export file contains a single field with the original name given to the export file, and the date and time that the file was last saved.

For more detailed information on export formats, see the following topics:

- [Plate Export Formats on page 88](#)
- [Group Section Export Formats on page 98](#)
- [Note Section Export Formats on page 98](#)

Plate Export Formats

This topic describes the format of **Plate** sections that are exported as a .txt or .xls file. For a copy of the SoftMax Pro XML schema, contact Molecular Devices Technical Support.

- The header line contains the type of section, such as **Plate**, and the title of the section as defined in the SoftMax Pro Software data file. **Plate** sections contain more information in the header line. See [Plate Header Fields on page 88](#).
- The data lines immediately follow the header line and contain the data from the exported section. The layout and format of the data lines are dependent on many factors, such as the section type, export type, read mode, and read type. See [Plate Data Lines on page 97](#).

Plate Header Fields

The fields in the header line for a **Plate** section help define the data that is presented in the section. The order and content of the fields are different depending on the read mode used to collect the data.

The tables that follow define the fields in the header line for the different read modes:

- [Table 3-1: Header Fields for Absorbance \(ABS\) Read Mode on page 89](#)
- [Table 3-2: Header Fields for Fluorescence Intensity \(FL\) and AlphaScreen \(ALPHA\) Read Modes on page 90](#)
- [Table 3-3: Header Fields for Luminescence \(LUM\), Time-Resolved Fluorescence \(TRF\), and Fluorescence Polarization \(FP\) Read Modes on page 92](#)
- [Table 3-4: Header Fields for Imaging Read Modes on page 95](#)

Table 3-1: Header Fields for Absorbance (ABS) Read Mode

Position	Name	Description
1.	Section type	Contains the type of section such as Plate
2.	Section name	Contains the title of the section as defined in the SoftMax Pro Software data file
3.	Export version	Contains the version of the export application used for this export
4.	Export format	Contains TimeFormat for Columns output format or PlateFormat for Plate output format as defined in the Export dialog
5.	Read type	Contains the read type used for the acquisition, such as Endpoint, Kinetic, Spectrum, or Well Scan
6.	Read mode	Contains the read mode used for the acquisition, such as Absorbance
7.	Data type	Contains Raw or Reduced to define the type of data in the export file
8.	Pre-read	Always FALSE Pre-read is not a function of SoftMax Pro Software version 6.x
9.	Kinetic points	Contains the number of reads done during the acquisition For Endpoint reads the number is 1
10.	Read time Read pattern	Contains the read time in seconds for a Kinetic read Contains the scan pattern for a Well Scan read Contains no value (blank) for other read types
11.	Kinetic interval Well Scan density	Contains the interval between reads in seconds for a Kinetic read Contains the scan density for a Well Scan read Contains no value (blank) for other read types
12.	Start wavelength	Contains the starting wavelength for a Spectrum read Contains no value (blank) for other read types
13.	End wavelength	Contains the ending wavelength for a Spectrum read Contains no value (blank) for other read types
14.	Wavelength step	Contains the wavelength increment or step for a Spectrum read Contains no value (blank) for other read types
15.	Number of wavelength	Contains the number of wavelengths read for the acquisition Contains no value (blank) for Spectrum reads

Table 3-1: Header Fields for Absorbance (ABS) Read Mode (continued)

Position	Name	Description
16.	Wavelengths	Contains the wavelengths used for the acquisition For multiple-wavelength reads, the values are separated by a space Contains no value (blank) for Spectrum reads
17.	First column	Contains the number of the first column read during the acquisition
18.	Number of columns	Contains the number of columns read during the acquisition
19.	Number of wells	Contains the total number of wells in the microplate, such as 96 or 384
20.	First row	Contains a number corresponding with the first row read during the acquisition
21.	Number of rows	Contains the number of rows read during the acquisition
22.	Time tags	Contains time-tag information if the exported data has read-time tags

Table 3-2: Header Fields for Fluorescence Intensity (FL) and AlphaScreen (ALPHA) Read Modes

Position	Name	Description
1.	Section type	Contains the type of section such as Plate
2.	Section name	Contains the title of the section as defined in the SoftMax Pro Software data file
3.	Export version	Contains the version of the export application used for this export
4.	Export format	Contains TimeFormat for Columns output format or PlateFormat for Plate output format as defined in the Export dialog
5.	Read type	Contains the read type used for the acquisition, such as Endpoint , Kinetic , Spectrum , or Well Scan
6.	Read mode	Contains the read mode used for the acquisition, such as Fluorescence or Luminescence
7.	Bottom read	Contains TRUE if reading from the bottom of the microplate and FALSE if reading from the top
8.	Data type	Contains Raw or Reduced to define the type of data in the export file

Table 3-2: Header Fields for Fluorescence Intensity (FL) and AlphaScreen (ALPHA) Read Modes (continued)

Position	Name	Description
9.	Pre-read	Always FALSE Pre-read is not a function of SoftMax Pro Software version 6.x
10.	Kinetic points	Contains the number of reads done during the acquisition For Endpoint reads the number is 1
11.	Read time Read pattern	Contains the read time in seconds for a Kinetic read Contains the scan pattern for a Well Scan read Contains no value (blank) for other read types
12.	Kinetic interval Well Scan density	Contains the interval between reads in seconds for a Kinetic read Contains the scan density for a Well Scan read Contains no value (blank) for other read types
13.	Start wavelength	Contains the starting wavelength for a Spectrum read Contains no value (blank) for other read types
14.	End wavelength	Contains the ending wavelength for a Spectrum read Contains no value (blank) for other read types
15.	Wavelength step	Contains the wavelength increment or step for a Spectrum read Contains no value (blank) for other read types
16.	Number of wavelengths	Contains the number of wavelengths read for the acquisition Contains no value (blank) for Spectrum reads
17.	Wavelengths	Contains the wavelengths used for the acquisition For multiple-wavelength reads, the values are separated by a space For Fluorescence reads, contains the emission wavelengths Contains no value (blank) for Spectrum reads or Ex/Em sweeps
18.	First column	Contains the number of the first column read during the acquisition
19.	Number of columns	Contains the number of columns read during the acquisition
20.	Number of wells	Contains the total number of wells in the microplate, such as 96 or 384
21.	Excitation wavelengths	Contains the excitation wavelengths used for a Fluorescence read For multiple-wavelength reads, the values are separated by a space Contains no value (blank) for Spectrum reads or Ex/Em sweeps

Table 3-2: Header Fields for Fluorescence Intensity (FL) and AlphaScreen (ALPHA) Read Modes (continued)

Position	Name	Description
22.	Cutoff	Contains Manual or Automatic as defined in the Settings dialog
23.	Cutoff filters	Contains the wavelengths of the cutoff filters with the values separated by a space
24.	Sweep wave	Contains Excitation Sweep or Emission Sweep as defined in the Settings dialog
25.	Sweep fixed wavelength	Contains the fixed wavelength of an Ex/Em sweep
26.	Reads per well	Contains the number of times a well is read during a single reading
27.	PMT gain	Contains Automatic , High , Medium , or Low as defined in the Settings dialog
28.	Start integration time	Contains the time to start integration for a TRF read. Contains no value (blank) for other read modes
29.	End integration time	Contains the time to end integration for a TRF read. Contains no value (blank) for other read modes
30.	First row	Contains a number corresponding with the first row read during the acquisition
31.	Number of rows	Contains the number of rows read during the acquisition
32.	Time tags	Contains time-tag information if the exported data has read-time tags

Table 3-3: Header Fields for Luminescence (LUM), Time-Resolved Fluorescence (TRF), and Fluorescence Polarization (FP) Read Modes

Position	Name	Description
1.	Section type	Contains the type of section such as Plate
2.	Section name	Contains the title of the section as defined in the SoftMax Pro Software data file
3.	Export version	Contains the version of the export application used for this export
4.	Export format	Contains TimeFormat for Columns output format or PlateFormat for Plate output format as defined in the Export dialog
5.	Read type	Contains the read type used for the acquisition, such as Endpoint , Kinetic , Spectrum , or Well Scan
6.	Read mode	Contains the read mode used for the acquisition, such as Luminescence or Time Resolved

Table 3-3: Header Fields for Luminescence (LUM), Time-Resolved Fluorescence (TRF), and Fluorescence Polarization (FP) Read Modes (continued)

Position	Name	Description
7.	Data type	Contains Raw or Reduced to define the type of data in the export file
8.	Pre-read	Always FALSE Pre-read is not a function of SoftMax Pro Software version 6.x
9.	Kinetic points	Contains the number of reads done during the acquisition For Endpoint reads the number is 1
10.	Read time Read pattern	Contains the read time in seconds for a Kinetic read Contains the scan pattern for a Well Scan read Contains no value (blank) for other read types
11.	Kinetic interval Well Scan density	Contains the interval between reads in seconds for a Kinetic read Contains the scan density for a Well Scan read Contains no value (blank) for other read types
12.	Start wavelength	Contains the starting wavelength for a Spectrum read Contains no value (blank) for other read types
13.	End wavelength	Contains the ending wavelength for a Spectrum read Contains no value (blank) for other read types
14.	Wavelength step	Contains the wavelength increment or step for a Spectrum read Contains no value (blank) for other read types
15.	Number of wavelengths	Contains the number of wavelengths read for the acquisition Contains no value (blank) for Spectrum reads
16.	Wavelengths	Contains the wavelengths used for the acquisition For multiple-wavelength reads, the values are separated by a space For Time Resolved reads, contains the emission wavelengths Contains no value (blank) for Spectrum reads or Ex/Em sweeps
17.	First column	Contains the number of the first column read during the acquisition
18.	Number of columns	Contains the number of columns read during the acquisition
19.	Number of wells	Contains the total number of wells in the microplate, such as 96 or 384

Table 3-3: Header Fields for Luminescence (LUM), Time-Resolved Fluorescence (TRF), and Fluorescence Polarization (FP) Read Modes (continued)

Position	Name	Description
20.	Excitation wavelengths	Contains the excitation wavelengths used for a Time Resolved read For multiple-wavelength reads, the values are separated by a space Contains no value (blank) for Spectrum reads or Ex/Em sweeps
21.	Cutoff	Contains Manual or Automatic as defined in the Settings dialog
22.	Cutoff filters	Contains the wavelengths of the cutoff filters with the values separated by a space Contains no value (blank) if no cutoff filter is used
23.	Sweep wave	Contains Excitation Sweep or Emission Sweep as defined in the Settings dialog
24.	Sweep fixed wavelength	Contains the fixed wavelength of an Ex/Em sweep
25.	Reads per well	Contains the number of times a well is read during a single reading
26.	PMT gain	Contains Automatic , High , Medium , or Low as defined in the Settings dialog
27.	Start integration time	Contains the time to start integration for a Time Resolved read. Contains no value (blank) for other read modes
28.	End integration time	Contains the time to end integration for a Time Resolved read. Contains no value (blank) for other read modes
29.	First row	Contains a number corresponding with the first row read during the acquisition
30.	Number of rows	Contains the number of rows read during the acquisition
31.	Time tags	Contains time-tag information if the exported data has read-time tags

Table 3-4: Header Fields for Imaging Read Modes

Position	Name	Description
1.	Section type	Contains the type of section, such as Plate
2.	Section name	Contains the title of the section as defined in the SoftMax Pro Software data file
3.	Export version	Contains the version of the export application used for this export
4.	Export format	Contains TimeFormat for Columns output format or PlateFormat for Plate output format as defined in the Export dialog
5.	Read type	Contains the read type used for the acquisition, such as Endpoint
6.	Read mode	Contains the read mode used for the acquisition, such as Imaging
7.	Data type	Contains Raw or Reduced to define the type of data in the export file
8.	Pre-read	Always FALSE Pre-read is not a function of SoftMax Pro Software version 6.x
9.	Kinetic points	Contains the number of reads done during the acquisition For Endpoint reads the number is 1
10.	Read time	Contains no value (blank) for Imaging reads
11.	Kinetic interval	Contains no value (blank) for Imaging reads
12.	Start wavelength	Contains no value (blank) for Imaging reads
13.	End wavelength	Contains no value (blank) for Imaging reads
14.	Wavelength step	Contains no value (blank) for Imaging reads
15.	Number of wavelengths	Contains the number of wavelengths, or channels, read for the acquisition
16.	Emission wavelengths	Contains the emission wavelengths used for the acquisition For multiple-wavelength reads, the values are separated by a space
17.	First column	Contains the number of the first column read during the acquisition
18.	Number of columns	Contains the number of columns read during the acquisition
19.	Number of wells	Contains the total number of wells in the microplate, such as 96 or 384
20.	First row	Contains a number corresponding with the first row read during the acquisition

Table 3-4: Header Fields for Imaging Read Modes (continued)

Position	Name	Description
21.	Number of rows	Contains the number of rows read during the acquisition
22.	Excitation wavelength	Contains the excitation wavelengths used for the acquisition For multiple-wavelength reads, the values are separated by a space
23.	Analysis type	Contains the analysis type used, such as Discrete Object Analysis
24.	Classification	Contains On if classification is used and Off if it is not used
25.	Find on	Contains the emission wavelength used for finding objects or fields
26.	Measurement	Contains the type of measurement selected in the Display Options dialog, such as Cell Count

Plate Data Lines

The data lines immediately follow the header line.

- The first column shows the time points for a kinetic read, the data points in a well scan read, or the wavelengths in a spectrum read. For endpoint reads, this column is blank.
- The second column shows the temperature for the read, if the incubator is used for the read. If the incubator is off, the value is zero.

The read data starts in the third column. When both raw and reduced data are exported, the reduced data is displayed below the raw data.

The format of the data depends on whether the data were exported in column format or plate format.

For column formats, the data are displayed in a single row. The data for multiple time points for kinetic reads, multiple data points for well scan reads, or multiple wavelengths for spectrum reads are listed in separate rows. For endpoint, kinetic, or well scan reads with multiple wavelengths, the data for each wavelength are displayed in subsequent rows below the previous wavelength. For imaging reads, the data for each measurement are in a separate row.

Time	Temperature	A1	A2	A3	...	B1	B2	B3	...
0:00:00	###	1.596	2.479	2.95	...	3.002	3.103	1.39	...
0:01:58	###	1.564	3.344	2.378	...	2.744	0.113	3.872	...
...	###
Raw Data									
0:00:00	###	3.928	3.645	1.956	...	3.622	2.195	0.519	...
0:01:58	###	2.891	3.824	2.782	...	3.203	1.105	0.281	...
...	###
Reduced Data									
		A1	A2	A3	...	B1	B2	B3	...
		203.45455	-18.91525	-28.13251	...	106.53005	82.585516

Figure 3-1: Kinetic data exported in column format

For plate formats, the data are displayed in a table to indicate the columns and rows of the microplate. The data for multiple time points for kinetic reads, multiple data points for well scan reads, or multiple wavelengths for spectrum reads are listed in separate tables below the previous table. For endpoint, kinetic, or well scan reads with multiple wavelengths, the data for each wavelength are displayed in separate tables to the right of the previous table. For imaging reads, the data for each measurement are in a separate tables to the right of the previous table.

		wavelength 1				wavelength 2			
Temperature		1	2	3	...	1	2	3	...
0:00:00	##	1.596	2.479	2.95	...	3.103	1.39	1.97	...
		1.024	0.308	3.925	...	2.381	1.957	3.722	...
		0.195	0.287	2.638	...	0.967	1.049	1.422	...
	
0:01:58	##	1.564	3.344	2.378	...	0.113	3.872	0.637	...
		0.82	1.797	1.064	...	3.58	2.603	0.996	...
		0.421	3.066	3.906	...	0.915	0.57	2.251	...
	
...	##	1.169	1.092	3.969	...	1.126	0.004	1.934	...
		1.105	3.022	2.845	...	1.933	2.834	0.657	...
		3.602	2.033	3.737	...	0.437	3.242	1.337	...
	
		1	2	3	...	1	2	3	...
		203.45455	-18.91525	-28.13251	...	106.53905	82.585516	121.96918	...
		74.597843	107.62096	-88.65948	...	376	-77.66718	-83.94453	...
		-134.6718	68.810478	-52.5208	...	246.51772	60.674884	48.51772	...
	

Figure 3-2: Kinetic data exported in plate format

Group Section Export Formats

This topic describes the format of **Group** sections that are exported as a .txt or .xls file. For a copy of the SoftMax Pro XML schema, contact Molecular Devices Technical Support.

The header line contains the type of section, such as **Group**, and the title of the section as defined in the SoftMax Pro Software data file.

The data lines immediately follow the header line and contain the text and data from the exported section.

- The data from the group table are displayed in a table that contains the column headings in the first row followed by the data from the table.
- Group summaries, if present, are displayed in the rows at the end of the section.

Note Section Export Formats

This topic describes the format of **Note** sections that are exported as a .txt or .xls file. For a copy of the SoftMax Pro XML schema, contact Molecular Devices Technical Support.

The header line contains the type of section, such as **Note**.

The data lines immediately follow the header line and contain text and summary formulas from the exported section.

Images and section images from the Note section are not included in the export file.

Importing Microplate Data



Note: The data import feature requires a separate license. To obtain a license for this feature, contact your Molecular Devices representative.

You can import microplate data that was acquired by the SoftMax Pro Software or another microplate data acquisition software program.

The data import feature can directly import data from files that were exported in Plate format from version 5.x and 6.x of the SoftMax Pro Software.

Before you can import microplate data that was acquired from a different software program, you must first use that software program to export the data into a compatible format. Templates for importing data in the Plate format and a schema for the XML format are installed with the software.

- To import data from another program in Plate format, the tab-delimited text file must match the format of an import template. See [Using a Plate Format Template for Importing Data on page 101](#).
- To import data from another program in XML format, the XML file must be formatted using the SoftMax Pro Software XML schema. See [Using the XML Schema for Importing Data on page 103](#).

When you import the microplate data, the SoftMax Pro Software creates a new **Plate** section using the section name from the import file. If the named **Plate** section already exists, then the imported data overwrites the existing data in the section.

When you import microplate data into an existing **Plate** section, the SoftMax Pro Software microplate template and reduction settings in the existing **Plate** section are preserved if the imported data are compatible with the settings in the existing section.



If you want to preserve the template and reduction settings, make sure that the name of the **Plate** section in the import file exactly matches the name of the **Plate** section in the SoftMax Pro Software protocol into which you plan to import the data. If the name of the **Plate** section in the text file does not match the name of a **Plate** section in the protocol, then the import process creates a new **Plate** section in the protocol.

Another way to preserve template and reduction settings is to copy the imported data from the new **Plate** section and then paste the data into an existing **Plate** section to use the template and reduction settings in the section where you pasted the data. See [Copying and Pasting Data on page 66](#).



Note: To maximize the number of data points used for reduction, the end time reduction parameter is changed to match the read time from the import file.

To import the microplate data:

1. Open or create a new protocol file.
2. If required, define a **Plate** section for importing the microplate data with the same name as the **Plate** section in the import file.
3. Click the **Application**  button to open the **Application** menu.
4. Click **Import**  and then click the data format of the import file.
 - To import tab-delimited text data, click **Plate Format**.
 - To import XML data, click **XML Format**.
5. In the **Open** dialog, locate and select the file that you want to import.
6. Click **Open**.

The **Plate** section displays the imported data.
7. Save the file as a data file. See [Saving Data Files on page 65](#).

After the data is imported into the **Plate** section, the **Read Information** on the right indicates that the data was imported and shows the time and date of when it was imported. For the GxP edition, the **Read Information** includes the name of the user who imported the data.

Using a Plate Format Template for Importing Data

The data import feature can directly import data from files that were exported in Plate format from version 5.x and 6.x of the SoftMax Pro Software.

Before you can import microplate data that was acquired from a different software program, you must first use that software program to export the data into a compatible format. Templates for importing data in the Plate format and a schema for the XML format are installed with the software. To import data from another program in XML format, the XML file must be formatted using the SoftMax Pro Software XML schema. See [Using the XML Schema for Importing Data on page 103](#).

The data import templates are installed with the SoftMax Pro Software, and can be found in a sub-folder of the Program Files folder where the SoftMax Pro Software program is installed. The default installation path is as follows:

```
C:\Program Files
(x86)\Molecular Devices\SoftMax Pro 7.0\Plugins\Import-PlateFormat\Templates
```

The templates are supplied in .xlsx format, but must be saved in .txt format with tab-separated values before importing the data.

The cells in the template are color-coded. Do not alter the data in cells that have a white background. Cells with colored backgrounds can be edited. A green background color indicates cells that require information, and a light yellow background color indicates cells that optionally can contain information.

You can paste your data directly into the template, or use the template as a model for a script that converts your data to the acceptable format for importing.

Plate Data Layout

The first line of an import template defines the number of **Plate** sections (or "Blocks") that are included in the data file.

- `##BLOCKS= 1`

Each **Plate** section is presented in the following format:

- Header lines

The first header line contains descriptive titles for the data in the second header line. The second header line contains the type of section, **Plate**, and the title to be given to the **Plate** section in the SoftMax Pro Software data file.

The fields in the header lines define the type of read, the number of wells in the microplate, and the wavelengths used for the read, among other relevant information. The layout and format of the header lines are dependent on the read type. For more information, see the template for the read type of your data.

- Data lines

The data lines follow the header lines with a blank row between the header lines and data lines. The layout and format of the data lines are dependent on the read mode and read type.

- The first column shows the time points for a kinetic read, the data points in a well scan read, or the wavelengths in a spectrum read. For endpoint reads, this column is blank.
- The second column shows the temperature for the read, if an incubator is used for the read. If the incubator is off, the value is zero.
- The third column is where the read data starts.

The data are displayed in a table to indicate the columns and rows of the microplate used for the read. The data for multiple time points for kinetic reads, multiple data points for well scan reads, or multiple wavelengths for spectrum reads are listed in separate tables below the previous table. For endpoint, kinetic, or well scan reads with multiple wavelengths, the data for each wavelength are displayed in separate tables to the right of the previous table.

		wavelength 1				wavelength 2			
Temperature		1	2	3	...	1	2	3	...
0:00:00	##	1.596	2.479	2.95	...	3.103	1.39	1.97	...
		1.024	0.308	3.925	...	2.381	1.957	3.722	...
		0.195	0.287	2.638	...	0.967	1.049	1.422	...
	
0:01:58	##	1.564	3.344	2.378	...	0.113	3.872	0.637	...
		0.82	1.797	1.064	...	3.58	2.603	0.996	...
		0.421	3.066	3.906	...	0.915	0.57	2.251	...
	
...	##	1.169	1.092	3.969	...	1.126	0.004	1.934	...
		1.105	3.022	2.845	...	1.933	2.834	0.657	...
		3.602	2.033	3.737	...	0.437	3.242	1.337	...
	

Figure 3-3: Kinetic data in Plate format for importing

- End line

The end line follows the data lines with a blank row between the data lines and end line.

The end line of each **Plate** section is defined by the text: **~End**

To import data from more than one **Plate** section in a single text file, include the header lines, the data lines, and the end line for each **Plate** section immediately after the end line of the previous **Plate** section.

The final line of an import file contains a single field with the original name given to the import file, and the date and time that the file was saved. This information immediately follows the end line for the last **Plate** section in the file.

Using the XML Schema for Importing Data

To import data in XML format, the XML file must be formatted using the SoftMax Pro Software XML schema from software version 6.4.1 or newer.

Before you can import microplate data that was acquired from a different software program, you must first use that software program to export the data into a compatible format. Templates for importing data in the Plate format and a schema for the XML format are installed with the software. To import data from another program in Plate format, the tab-delimited text file must match the format of an import template. See [Using a Plate Format Template for Importing Data on page 101](#).

The XML schema file for data import (XMLImportSchema.xsd) is installed with the SoftMax Pro Software, and can be found in a sub-folder of the Program Files folder where the SoftMax Pro Software program is installed. The default installation path is as follows:

C:\Program Files (x86)\Molecular Devices\SoftMax Pro 7.0\Plugins\Import-XML\Schema


For information about the XML elements and their usages, see the comments in the schema file.

To import data from more than one **Plate** section in a single XML file, make sure that all the **Plate** sections are between the <PlateSections> tags and that each **Plate** section is defined between a set of <PlateSection> tags.

```
<PlateSections>
  <PlateSection>
    [Data from the first Plate section]
  </PlateSection>
  <PlateSection>
    [Data from the second Plate section]
  </PlateSection>
</PlateSections>
```

Figure 3-4: Importing data from more than one Plate section in XML format

Setting Application Options

Click the **Application**  button to open the **Application** menu, and then click the **Options** button at the bottom of the menu.

The **SoftMax Pro Options** dialog contains settings for the following options:

- **Data Recovery**

The **Data Recovery** option contains an informational setting to inform you that opened files will automatically be saved to a temporary file every five minutes to assist with data recovery. This option cannot be turned off. For more information, see [Enabling Data Recovery on page 105](#).

- **Web Browser**

The **Web Browser** option contains a setting to let you hide the integrated web browser tab when the SoftMax Pro Software starts. The web browser automatically starts with the program when this check box is cleared. For more information, see [Integrated Web Browser on page 55](#).

- **Plate Setup Helper**

The **Plate Setup Helper** option contains a setting to prevent the **Plate Setup Helper** from automatically starting each time you open a new protocol. The **Plate Setup Helper** automatically appears each time you open a new SoftMax Pro Software file when this check box is cleared. For more information, see [Using the Plate Setup Helper on page 27](#).

- **Plate Height Warning**

The **Plate Height Warning** option contains a setting to prevent the plate height warning from automatically being displayed when you start a read. To prevent damage to the SpectraMax i3 Multi-Mode Detection Platform, the plate height warning is displayed as a reminder to make sure that the **Plate Height** for the microplate is defined correctly. The plate height warning is automatically displayed when you start a read if this check box is cleared. For more information, see [Using the Plate Editor on page 251](#).

- **Plate Eject After Read**

The **Plate Eject After Read** option contains a setting to prevent the microplate drawer from automatically opening after you finish a read. When this check box is cleared, the microplate drawer opens after a read completes. When this check box is selected, the microplate drawer remains closed after a read completes.

- **Remote Control**

The **Remote Control** option contains settings for connecting an Apple mobile device to control the running software and the connected microplate reader. To allow control by the mobile app, select the **Enable Remote Control** check box, make sure that both the app and the software use the same **Port**, and type the **Host** name or IP address of the computer into the settings in the app. You can download the **SoftMax Pro Remote** app from the Apple App Store.


- **Calculation**

The **Calculation** option allows the software to do data calculations of the kinetic data while a kinetic acquisition is in progress. To enable kinetic data calculations during a read, select the **Calculate during acquisition** check box and then type the number of kinetic reads between successive calculations in the **Calculate every ___ cycle(s)** field.

To close the **SoftMax Pro Options** dialog and save your settings, click **OK**.

Enabling Data Recovery

To verify that data recovery is enabled:

1. Click the **Application**  button to open the **Application** menu.
2. Click the **Options** button at the bottom of the menu.
3. In the **SoftMax Pro Options** dialog, verify that **Save open files for data recovery every five minutes** is selected.
4. Click **OK** to close the dialog.

When Data Recovery is enabled, opened files are automatically saved to a temporary file every five minutes to assist with data recovery.

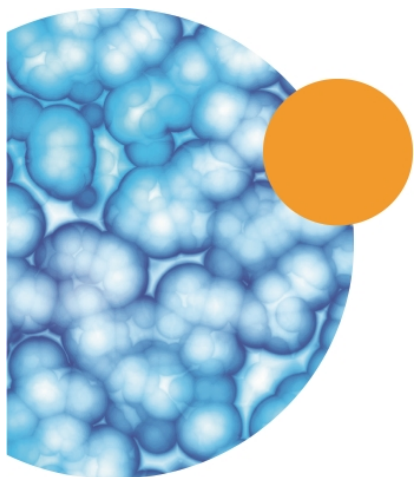
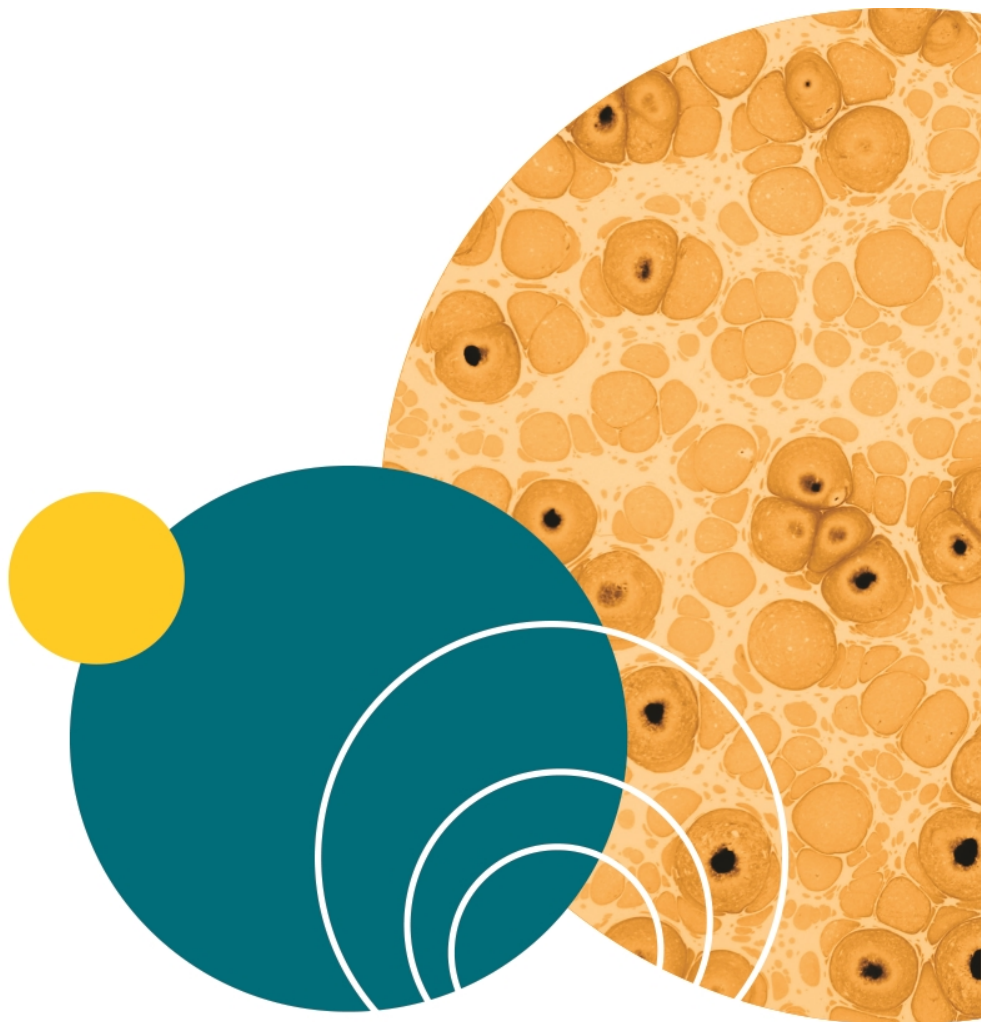
Recovering Files

If the SoftMax Pro Software experiences an unexpected application interruption, then when the SoftMax Pro Software restarts, it lists the files that are available for recovery.

1. Select the file or files you want to recover.
2. Click **Close** to close the dialog.
3. The selected files open in the SoftMax Pro Software.


The files that are not selected from the list are deleted after the dialog closes.

Saving a recovered file overwrites the original file. If an "untitled" file is recovered and opened, the SoftMax Pro Software prompts for a file name and location when the file is saved.



Chapter 4: Workspace Sections

The workspace can contain five different types of sections.

- **Note** sections are used to record text or to report summary data pertaining to the experiment. **Note** sections can contain text and graphics, and can contain images of the other sections in the file. You can have as many **Note** sections as you want in the file. For more information, see [Using a Note Section on page 108](#).
- **Plate** sections are used to collect data from the instrument, and to define data display and data reduction. You can have as many **Plate** sections as you want, and each **Plate** section can have different instrument settings from the other **Plate** sections in the file. For more information, see [Using a Plate Section on page 118](#).
- **Cuvette Set** sections are used to collect data from a cuvette port. You can have as many **Cuvette Set** sections as you want, and each **Cuvette Set** section can have different instrument settings from the other **Cuvette Set** sections in the file. For more information see [Using a Cuvette Set Section on page 129](#).
- Unlike other section types, **Group** sections are created automatically when you create and assign a Group to a **Plate** section within the **Template Editor** dialog (after clicking **Template**  in a **Plate** section). For more information, see [Using a Group Section on page 139](#).
- **Graph** sections are used to plot information from groups as scatter plots or bar graphs. You can have as many **Graph** sections as you want in a file. For more information, see [Using a Graph Section on page 149](#).

The sections are contained in an **Experiment**. Experiments can be used as an organizational tool within the file to maintain separate data sets. You can have as many Experiments as you want in a file.

Experiments and sections are listed in the **Navigation Tree**. See [Navigation Tree on page 29](#).

To rename an experiment or a section, see [Renaming an Experiment or a Section on page 30](#).

When you use the **AutoRead** feature, only the **Plate** sections within the selected **Experiment** are run. See [Enabling Auto Read on page 340](#).

In the SoftMax Pro GxP Software, you can lock the individual sections in an experiment to prevent changes to them. See [Locking and Unlocking Sections on page 484](#).

Using a Note Section

Note sections are used to record text or to report summary data pertaining to the experiment.

You can type text in a **Note** section, add images, and create summaries containing formulas for displaying reduced data.

- A **Summary** is part of a **Note** section or **Group** section that is generated by a user-entered formula applied to data in the file. It can also be text or a user-entered constant, such as certificate value.
- Text in **Note** sections can be formatted (font face, font size, and font style) using the **Notes Controls** formatting tools on the **Home** tab.
- Images can be inserted into the **Note** section including, images from other programs and section images from the current document.



Note: Each image must be placed in its own frame, and the frame cannot contain text.


You can create multiple **Note** sections within the same experiment.

To work in a **Note** section, see the following topics:

- [Adding a Note Section on page 109](#)
- [Inserting an Image on page 109](#)
- [Deleting an Image on page 109](#)
- [Inserting an Image of a Section on page 110](#)
- [Refreshing Section Images on page 110](#)
- [Deleting a Section Image on page 111](#)
- [Adding Text to a Note Section on page 111](#)
- [Aligning Text on page 111](#)
- [Editing Text in a Text Frame on page 112](#)
- [Formatting Text in a Text Frame on page 113](#)
- [Positioning a Text Frame in a Note Section on page 114](#)
- [Resizing a Text Frame on page 114](#)
- [Deleting a Text Frame on page 114](#)
- [Adding a New Summary Formula on page 115](#)
- [Deleting a Summary Formula on page 117](#)
- [Enabling Syntax Helper on page 116](#)

Adding a Note Section

To create a **Note** section:

1. Select the experiment where you want to add a **Note** section in the **Navigation Tree**.
2. If you have more than one section in the Experiment, select the section above where you want the new **Note** section to be displayed in the **Navigation Tree**.
3. Click **New Note**  in **Sections** on the **Home** tab in the ribbon.

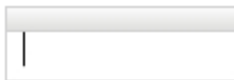
A new blank **Note** section is displayed below the selected section in the **Navigation Tree**.

To change the name of the **Note** section, right-click the **Note** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).


Inserting an Image

To insert an image into a **Note** section:

1. With a **Note** section active in the workspace, click in a blank area of the **Note** section to place the cursor in a new frame where you want to insert the image.



Note: Each image must be placed in its own frame, and the frame cannot contain text.

2. Click **Add Image**  in **Note Controls** on the **Home** tab in the ribbon or in the toolbar at the top of the **Note** section.
3. In the **Open** dialog, browse to locate the image to be inserted.
4. Select the image and click **Open**.
The image is displayed in the **Note** section.

Deleting an Image

To delete an image from a **Note** section:

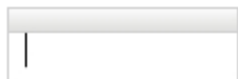
1. Click the image to be deleted.
2. Right-click the image and then click **Delete**.

The image is deleted from the **Note** section.


Inserting an Image of a Section

To insert an image of a section from the current data file into a **Note** section:

1. With a **Note** section active in the workspace, click in a blank area of the **Note** section to place the cursor in a new frame where you want to insert the section image.



Note: Each image must be placed in its own frame, and the frame cannot contain text.


2. Click **Add Section Image**  in **Note Controls** on the **Home** tab in the ribbon or in the toolbar at the top of the **Note** section.
3. In the **Add Section Image** dialog, locate the section to be inserted.
4. Select the section and then click **Add Section Image**.

The section image is displayed in the **Note** section.



Note: You can also right-click in the **Note** section and then click **Add Section Image** to select the section from the cascading menus.

Refreshing Section Images

To refresh all the section images in a **Note** section, click **Refresh Section Images**  in the toolbar at the top of the **Note** section.

All the section images in the **Note** section are updated to their current state. For example, if you inserted an image of a **Graph** section and then made changes to the graph section, you can refresh the **Graph** section image in the **Note** section.



Note: The section images are automatically refreshed periodically, such as when you open the data file, scroll up and down, switch between Document and Comparison views, or start to print or print preview the file.

Deleting a Section Image

To delete a section image from a **Note** section:

1. Click the section image to be deleted.
2. Right-click the section image and then click **Delete**.

The section image is deleted from the **Note** section.

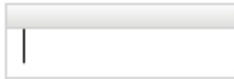


Note: When you delete a section from the data file, images of that section are also deleted from the **Note** sections. When you delete an experiment from the data file, images of the sections in the experiment are also deleted from the remaining **Note** sections.

Adding Text to a Note Section

To add text to a **Note** section:

1. With a **Note** section active in the workspace, click in a blank area of the **Note** section to place the cursor in a new frame where you want the text.



2. Type the text you want to be displayed.
3. To exit from the text frame, click somewhere else in the **Note** section.



Note: You can add more text to a text frame by clicking where you want to add text within the frame.

Aligning Text

Text in a text frame is aligned on a line by line basis. Each line in the text frame can be aligned separately.

To adjust the alignment of text within a text frame, click to select the line of text to be aligned, or click and drag to select multiple lines of text.

The following alignment options are in **Formatting Tools** on the **Home** tab in the ribbon:

- To align the line to the left edge, click **Align Left**
- To center the line, click **Align Center**
- To align the line to the right edge, click **Align Right**
- To left and right justify the line, click **Justify**
- To outdent an indented line, click **Decrease Indent**
- To indent the selected line, click **Increase Indent**

Editing Text in a Text Frame

To edit text in a text frame:

1. Click on the word or click and drag on a group of words to select the text to be edited.
2. Type the revised text.

The selected text is replaced with the text you typed.

Copying Text

To copy text in a text frame:

1. Click on the word or click and drag on a group of words to select the text to be copied.
2. Right-click and then click **Copy**, or press **Ctrl+C**.

The selected text is placed in the clipboard.

Pasting Text

To paste text from the clipboard into a text frame:

1. Copy text into the clipboard.
2. Click to place the cursor in the text frame where you want to insert the text.
3. Right-click and then click **Paste**, or press **Ctrl+V**.

The text in the clipboard is pasted into the text frame.

Cutting Text

To cut text out of a text frame:

1. Click on the word or click and drag on a group of words to select the text to be cut.
2. Right-click and then click **Cut**, or press **Ctrl+X**.

The selected text is cut from the text frame and placed in the clipboard.

Deleting Text

To delete text from a text frame:


1. Click on the word or click and drag on a group of words to select the text to be deleted.
2. Press **Delete**.

The selected text is removed from the text frame and not placed in the clipboard.

Formatting Text in a Text Frame

You can format text in a text frame using the formatting tools found in **Note Controls** on the **Home** tab in the ribbon.

Click and drag or double-click text in a text frame to select the text and then click the formatting tools to do the following functions:

- Select a font face
- Select a font size
- Create **Subscript** x_2 or **Superscript** x^2 characters
- Format **Bold** **B**, **Italic** *.*, or **Underline** . characters
- Add **Bullets** ☰
To add a blank line between lines of bulleted text, click at the end of a line and then press **Shift+Enter** to add a soft line break.
- Add **Numbering** ☰
To add a blank line between lines of numbered text, click at the end of a line and then press **Shift+Enter** to add a soft line break.
- Change the **Font Color** 





You can also click **Undo Previous Action**  or **Redo Previous Action**  for quick formatting changes.

Positioning a Text Frame in a Note Section

You can manually position a text frame within the **Note** section:

1. Click and hold down the mouse button on the border of a text frame.
The four-arrowhead cursor is displayed.
2. Drag the text to the desired location and release the mouse button.

To automatically position text frames within a **Note** section:

1. Click on a text frame border to select the text frame.
You can also select multiple text frames, summaries, and images by pressing **Ctrl** and then clicking on the frame borders.
2. Click an alignment option in **Note Controls** on the **Home** tab in the ribbon.
 - To align a single text frame to the left edge of the **Note** section or align the left edges of multiple frames to the left-most text frame, click **Align Lefts** .
 - To align a single text frame to the right edge of the **Note** section or align the right edges of multiple frames to the right-most text frame, click **Align Rights** .
 - To align a single text frame to the top edge of the **Note** section or align the top edges of multiple frames to the top-most text frame, click **Align Tops** .
 - To align a single text frame to the bottom edge of the **Note** section or align the bottom edges of multiple frames to the bottom-most text frame, click **Align Bottoms** .

Resizing a Text Frame

To resize a text frame:

1. Click the text frame to select it.
2. Click and hold on the right or left side border of the text frame.
A double-ended arrow is displayed.
3. Drag the box to the desired size and release the mouse button.

Deleting a Text Frame


To delete a text frame:

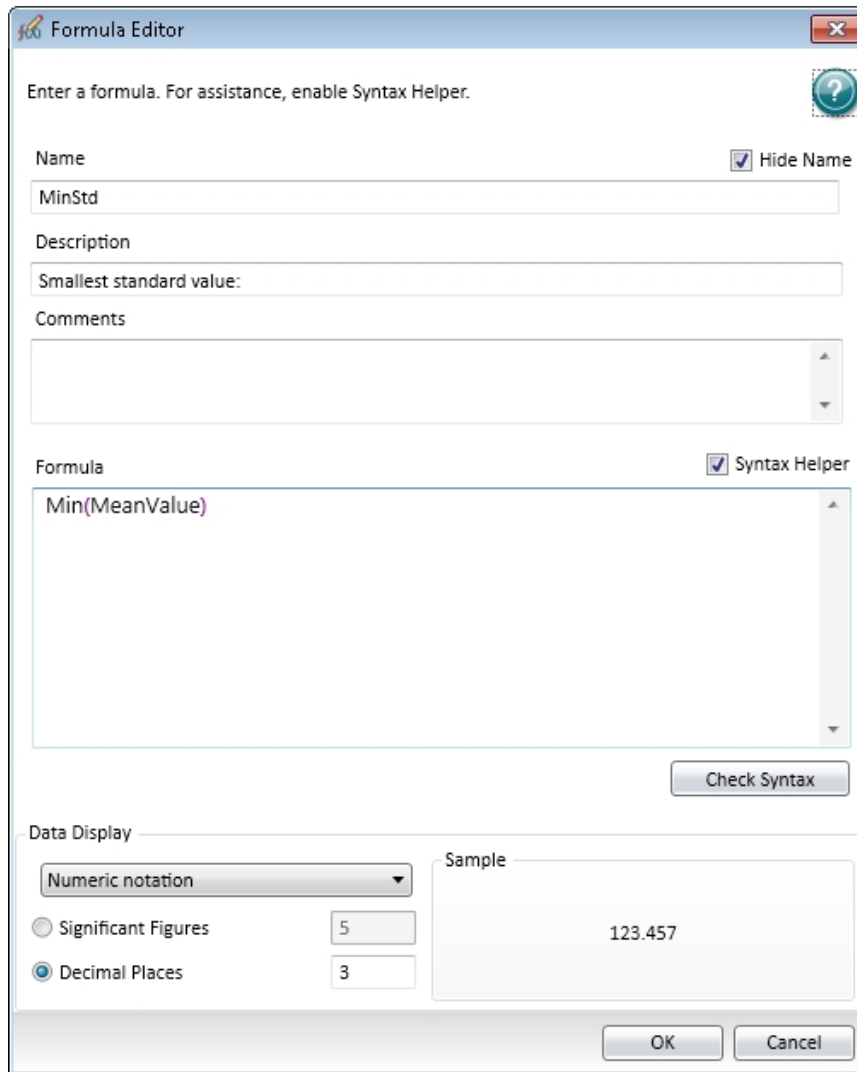
1. Click on the border of the text frame to select the text frame.
2. Right-click and then click **Delete**, or press **Delete** on your keyboard.

The text frame is deleted from the **Note** section.

Adding a New Summary Formula

To add a new Summary Formula to a **Note** section:

1. Click the **Note** section to make it active in the Workspace.
2. Click **New Summary**  in **Note Controls** on the **Home** tab in the ribbon.



3. In the **Formula Editor** dialog, in the **Name** field, type a short descriptive name for the formula.



Note: If you plan to reference this formula in a different formula, for example referencing the formula in a column of a group table, make sure that you do not use reserved characters or names of operators, functions, or accessors in this name. For information about reserved characters and words, see “Rules to Follow When Writing Formulas” in the *SoftMax Pro Software Formula Reference Guide*.

4. Optionally, click **Hide Name** to hide the name of the Summary in the **Note** section or **Group** section.
5. Optionally, type a brief text **Description** of the formula to be displayed in the section.
6. Optionally, type text **Comments** to annotate the formula.
7. Optionally, click **Syntax Helper** to turn on the formula completion tool. See [Enabling Syntax Helper on page 116](#).
8. Type a **Formula** to be used for the Summary or column.
9. Optionally, click **Check Syntax** check the validity of the formula. A message is displayed to the left of the button to help you troubleshoot the syntax of the formula.
10. Specify the **Data Display** characteristics:
 - From the drop-down list select either **Numeric notation** or **Scientific notation**.
 - Click **Decimal Places** and type the number of places to display or click **Significant Figures** and type the number of figures to display.

A preview of the **Data Display** is displayed in the **Sample** on the right.
11. Click **OK**.

For a complete guide to the formulas used in the SoftMax Pro Software, click **Formula**

Reference  on the **Help** tab in the ribbon.

Enabling Syntax Helper

For assistance creating formulas in the **Formula Editor** dialog, click **Syntax Helper**. To disable the Syntax Helper, click **Syntax Helper** to clear the check box.


When you first start typing a formula, a list is displayed below your text as you type. This is **Syntax Helper**, a technology that analyzes text as you type and compares it to formulas that are available for use in the SoftMax Pro Software.

Syntax Helper lets you quickly see what formulas are available and what parameters these formulas expect to receive.

By default, **Syntax Helper** is enabled when you start the SoftMax Pro Software. You can enable and disable this feature whenever you are working in the **Formula Editor** dialog.

Editing a Summary Formula

To edit an existing summary formula:

1. Click the summary formula text frame in the **Note** section to select the text frame.
2. Click **Edit Summary**  in **Note Controls** on the **Home** tab in the ribbon.
You can also double-click the formula to open the **Formula Editor** dialog.
3. In the **Formula Editor** dialog, make the required edits. See [Adding a New Summary Formula on page 115](#).
4. Click **OK**.

Showing or Hiding the Formula in a Summary Formula

Generally, the summary formula in the **Note** section displays the result of the formula. You can show or hide the formula as well as the result.

To show the formula in the summary formula:


1. Click the summary formula text frame.
2. Click **Show Formulas**  in the **Note Controls** section of the **Home** tab in the ribbon.

To hide the formula in the summary formula:

1. Click the summary formula text frame.
2. Click **Hide Formulas**  in the **Note Controls** section of the **Home** tab in the ribbon.

Deleting a Summary Formula

To delete an existing summary formula:

1. Click the summary formula text frame.
2. Click **Delete**  in the **Note Controls** section of the **Home** tab in the ribbon.

Using a Plate Section

A **Plate** section is used to collect data from the instrument, and to define data display and data reduction. If you need to read the same physical plate twice with different instrument settings, then use two **Plate** sections. You can create as many **Plate** sections as you need.


The precision of the data displayed in a **Plate** section varies based on the space available to view the characters.

You can customize the data display to **Numeric notation** or **Scientific notation** format, and specify the number of **Significant Figures** or **Decimal Places**. These options can be set separately for raw data and reduced data.

When the number of digits is increased, the font size of the values in the **Plate** section is decreased. If the value becomes too long, then the numbers are cut off at the edge of the wells.

When SoftMax Pro Software exports plate data, the values are not limited by space and can have more digits for each well.

The values displayed in a **Plate** section are only a representation of the data. In both the **Plate** section and in the exported data, the last digit displayed or exported is rounded based on the actual data value.

To change the properties of the plate, such as the number of wells, click **Settings**  on the **Home** tab in the ribbon to open the **Settings** dialog, and then click the **Plate Type** category to view a list of the available plate definitions. See [Plate Type Settings on page 250](#).

The **Template Editor** in the **Plate** section is used to create a map of the contents of the microplate.

Plate sections have the following areas:

- Tool bar (above the data display)
- Data display (in a microplate grid format)
- Instrument Settings Information and Read Information (to the right of the data display)
- Reduction settings (below the data display)


If the plate grid in the **Plate** section is colored, then a template has been defined for the **Plate** section. Each group defined in the template has a different color and the corresponding group table has the same color.

For information about using a **Plate** section, see the following topics:

- [Adding a Plate Section on page 119](#)
- [Using Plate Tools on page 119](#)
- [Using Template Tools on page 128](#)

Adding a Plate Section

To add a **Plate** section:

1. Select the experiment where you want to add a **Plate** section in the **Navigation Tree**.
2. If you have more than one section in the Experiment, select the section above where you want the new **Plate** section to be displayed in the **Navigation Tree**.
3. Click **New Plate**  in **Sections** on the **Home** tab in the ribbon.

A blank **Plate** section is displayed in the Workspace. You can add as many **Plate** sections as you need to your data file. See [Using a Plate Section on page 118](#).

To change the name of the **Plate** section, right-click the **Plate** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

Using Plate Tools

When a **Plate** section is active in the Workspace, **Plate Tools** are available on the **Home** tab in the ribbon.

Many of the **Plate Tools** available in **Home** tab are also available in the toolbar at the top of the **Plate** section.

For information about using the **Plate Tools**, see the following topics:

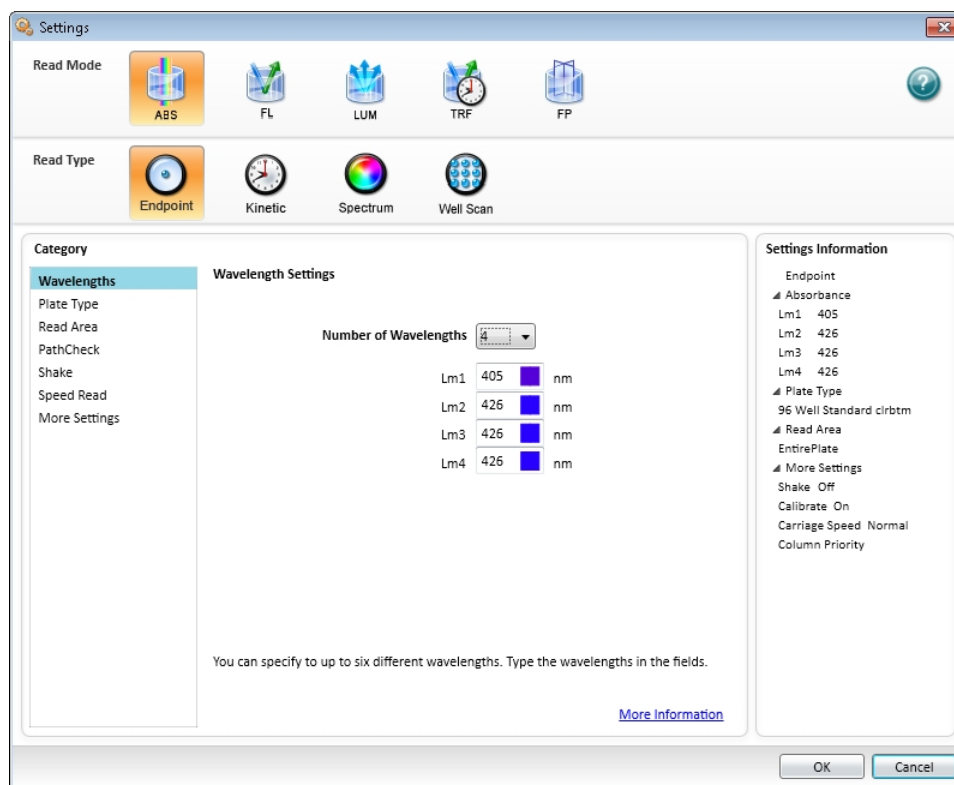
- [Modifying Instrument Settings on page 120](#)
- [Modifying Data Reduction Settings on page 120](#)
- [Modifying the Data Display on page 121](#)
- [Showing Reduced Data in a Three-Dimensional Graph on page 124](#)
- [Zooming the Well Display on page 125](#)
- [Masking Wells on page 126](#)
- [Cloning a Plate Section on page 127](#)
- [Viewing a Membrane Image on page 127](#)

Modifying Instrument Settings

Instrument settings are part of the protocol used to collect data. To modify settings for the selected instrument, select a **Plate** section or **Cuvette Set** section in the Workspace and then


click **Settings**  on the **Home** tab in the ribbon.

The **Settings** dialog is displayed.



Use the options in the **Settings** dialog to define the parameters for acquiring data from a microplate or cuvette. See [Selecting Instrument Settings on page 236](#).


Modifying Data Reduction Settings

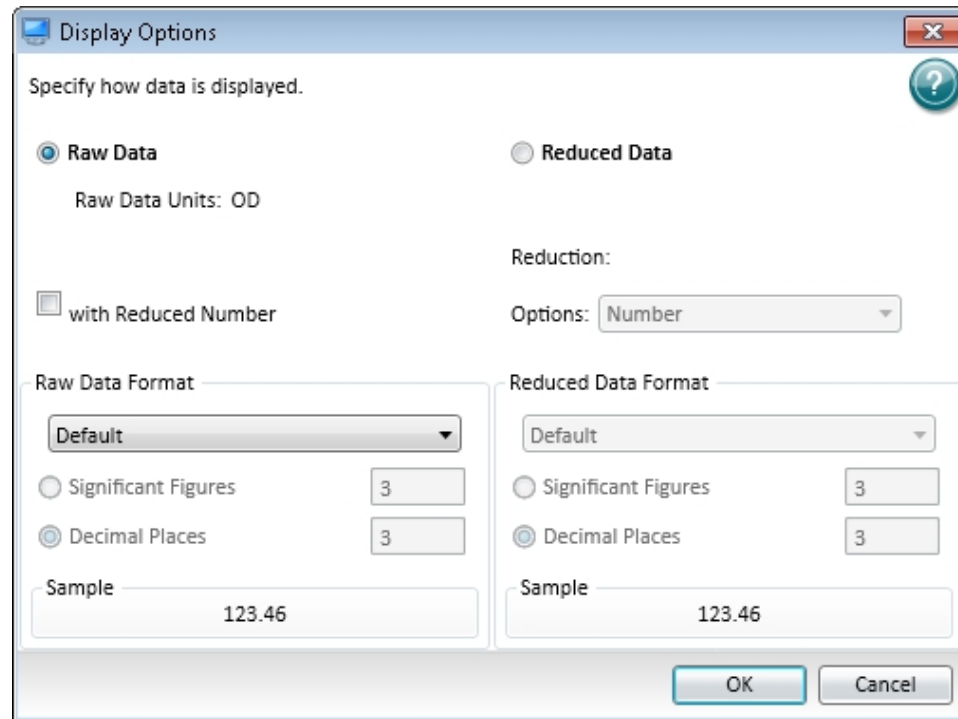
To modify the data reduction settings for a plate or cuvette, click **Reduction**  on the **Home** tab in the ribbon to view the **Data Reduction** dialog.

The **Data Reduction** dialog displays only the reduction options that are available for the instrument you are using, the options that have been selected in the **Settings** dialog, and the options defined in the template.

For more information, see [Doing Data Reduction on page 367](#).

Modifying the Data Display

In an active **Plate** section or **Cuvette Set** section, you can change how the data is presented by clicking **Display**  on the **Home** tab in the ribbon or in the toolbar at the top of the section.



The choices available in the **Display Options** dialog include selecting between **Raw Data** and **Reduced Data**.

For Imaging read mode **Imaging Data** replaces the **Raw Data** option.

You can customize the data display to **Numeric notation** or **Scientific notation** format, and specify the number of **Significant Figures** or **Decimal Places**. These options can be set separately for raw data and reduced data.

The **Default** format determines the number of decimal places to display based on the space available. For example, for a plate with 96 wells or fewer, each well is limited to five digits, plus one character for the decimal point, if applicable. For a 384-well plate, each well is limited to four characters, including the decimal point. If the value requires greater precision than can fit in the available space, the format changes to scientific notation.

Raw Data

Selecting **Raw Data** displays the default data type for the selected read type:

- **Endpoint:** Raw absorbance, fluorescence, or luminescence values.
- **Kinetic:** The change in raw OD/RFU/RLU values over time, displayed as a plot.
- **Spectrum:** Raw OD/RFU/RLU values for the range of wavelengths, displayed as a plot.
- **Well Scan:** Raw OD/RFU/RLU values as shades of blue to red.

To see a reduced number, select **with Reduced Number**.

Reduced Data

The reduced data display is based on the selections made in the **Data Reduction** dialog. See [Doing Data Reduction on page 367](#).

The reduced number is reported in the **Group** section when a template has been defined.

- Select **Number** to view only the reduced number.
- Select **Plot** for Kinetic reads to display a plot of the raw and reduced data. To also view the reduced number, select the **Reduced Number** check box.
- Select **Grayscale** to display the raw data in eight shades of gray, changing from light, for values less than or equal to the low limit, to dark, for values greater than or equal to the high limit. To define the **High Limit** and the **Low Limit** for the grayscale map, type values in the fields. To also view the reduced number, select the **Reduced Number** check box.
- Select **Color Map** to display the raw data in eight colors, changing from blue, for values less than or equal to the low limit, to red, for values greater than or equal to the high limit. To define the **High Limit** and the **Low Limit** for the color map, type values in the fields. To also view the reduced number, select the **Reduced Number** check box.

You can view both raw and reduced data or multiple reductions of the same data by cloning a plate. See [Cloning a Plate Section on page 127](#).

Imaging Data

The **Imaging Data** option is available for Imaging read mode only, and replaces the **Raw Data** option.


To see a reduced number, select **with Reduced Number**.

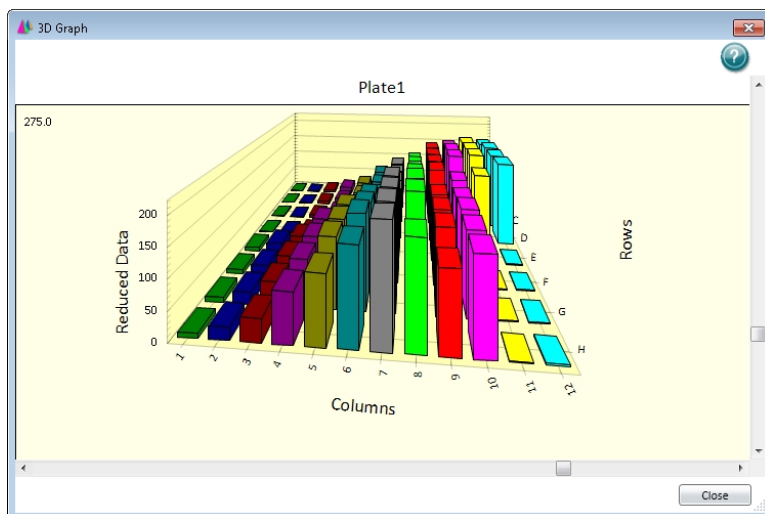
The **Data Type** list contains the measurement selections from the **Image Analysis Settings** in the **Settings** dialog. See [Viewing and Selecting Measurement Statistics on page 273](#).

The available **Data Types** for imaging data are as follows:

- **Object Count** gives the total number of objects detected in the image. This measurement is not used for field analysis of confluent areas.
- **Field Count** gives the total number of confluent areas detected in the image. This measurement is not used for discrete object analysis.
- **Object Percentage** gives the percentage the objects detected in the image by classification. This measurement is not used for field analysis of confluent areas.
- **Covered Area** gives the combined area of all the objects or confluent areas detected in the image as a percentage of the entire image area.
- **Object Area** gives the average area of the objects detected in the image expressed in μm^2 . This measurement is not used for field analysis of confluent areas.
- **Field Area** gives the average area of the confluent areas detected in the image expressed in μm^2 . This measurement is not used for discrete object analysis.
- **Object Roundness** gives the average roundness of each object detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for field analysis of confluent areas.
- **Field Roundness** gives the average roundness of each confluent area detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for discrete object analysis.
- **Object Average Intensity** gives the average fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Average Intensity** gives the average fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Object Intensity** gives the average total fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Intensity** gives the average total fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Total Intensity** gives the combined total fluorescent signal intensity of the objects or confluent areas detected in the image expressed in million intensity counts. This measurement is not used for transmitted light (TL).

Showing Reduced Data in a Three-Dimensional Graph

To view a three-dimensional graphical representation of reduced plate data, view the **Plate** section and then click the  **3D Graph** button in the **Plate Tools** area of the **Home** tab in the ribbon or in the toolbar at the top of the **Plate** section. See [Viewing Data in a Three-Dimensional Graph on page 382](#).





To close the **3D Graph** dialog, click **Close**.

Zooming the Well Display

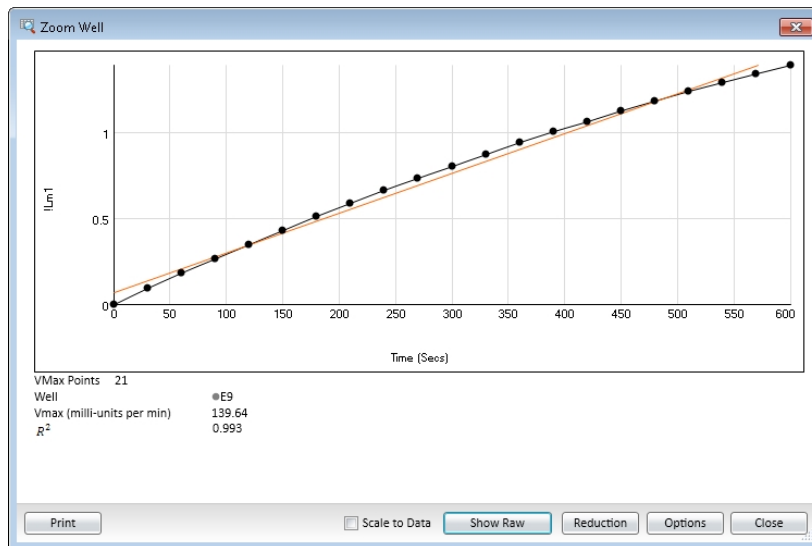
The **Zoom** icon becomes active when the data in a well is available for a zoomed display.

To magnify the display of imaging data in a well, see [Viewing the Imaging Data in a Well on page 365](#).

To display the **Zoom Well** dialog:

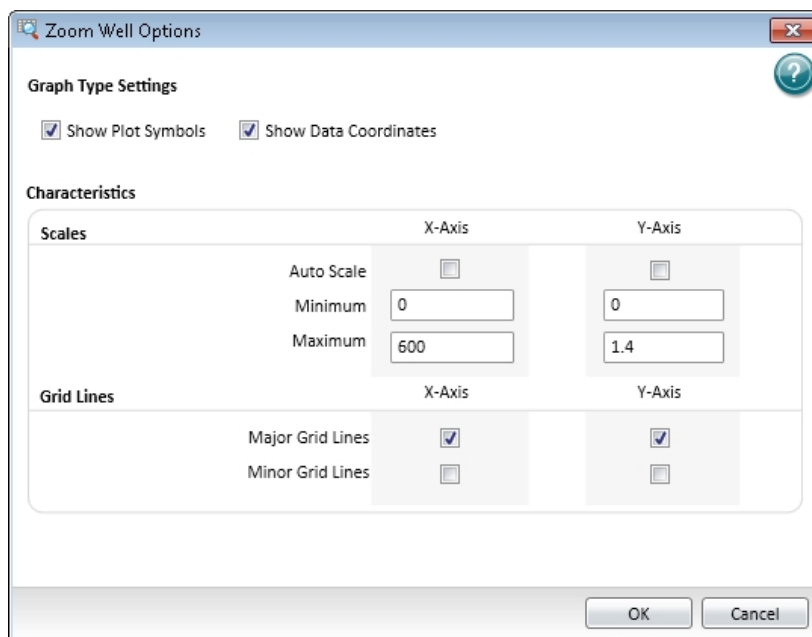
1. Click the well or cuvette that you want to zoom.
2. Click **Zoom**  on the **Home** tab in the ribbon or **Zoom**  in the toolbar at the top of the section. You can also double-click the well to open the **Zoom Well** dialog.

The data from the selected well or cuvette is displayed in a zoomed graph window.



3. To print the graph window, click **Print**.
4. To scale the display to the data, select **Scale to Data**.
5. To toggle between reduced and raw data, click **Show Reduced** or **Show Raw**.
6. To modify the reduction settings, click **Reduction**. The **Data Reduction** dialog is displayed. See [Doing Data Reduction on page 367](#).

7. To modify the zoom well display settings, click **Options**. The **Zoom Well Options** dialog is displayed.



- **Graph Type Settings** lets you enable or disable connected points or plotted symbols on the graph.
- **Characteristics** lets you set Auto Scale parameters and choose the minimum and maximum values for the selected axis. You can also add or remove grid lines from the display.


To save the settings and return to the **Zoom Well** dialog, click **OK**. These changes have an effect on only the well graph being viewed.

8. To close the **Zoom Well** dialog, click **Close**.

Masking Wells

The Mask feature hides selected data so that they are not used for calculations and are not reported. Masking is commonly used to suppress outliers from data reduction calculations. Masking can be used as a “what if?” tool. For example, if you have included a group blank in a template and want to see the data both with and without the blank, masking the group blanks suppresses the blanking function, while unmasking them enables it again.

To mask wells:

1. In an active **Plate** section, click to select a single well or click and drag to select multiple wells.
2. Click **Mask**  in **Plate Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the **Plate** section.


You can also right-click a well and select **Mask** from the shortcut menu.

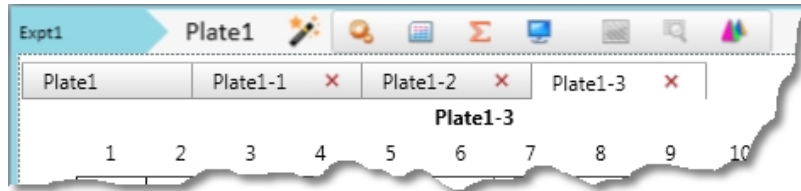
To unmask masked wells, select the wells and then click **Mask**.

Cloning a Plate Section

Cloning a plate adds a duplicate copy of the active plate to the **Plate** section. This can let you apply multiple templates and reductions to the same set of raw data.

To clone a plate:

1. With the **Plate** section you want to clone active in the workspace, click **Clone Plate**  on the **Home** tab in the ribbon.
2. The cloned plate is added to the active plate section.




You can add as many plate clones as needed for your experiment. The cloned plates are shown in tabs at the top of the **Plate** section. The first tab on the left is the original plate. Clones are listed with the original plate name followed by the number of the clone.


- To make a cloned plate active in the section, click the tab for the cloned plate.
- To delete a cloned plate, click the **X** in the tab for the cloned plate.

Viewing a Membrane Image

After scanning a membrane for Western Blot data, the data are displayed in the SoftMax Pro Software as an image. You can use the image tools in the **Plate** section to zoom, crop, colorize, and adjust the intensity of the image. You can also select a region of interest (ROI) and rescan the membrane at a higher resolution. See [Viewing Western Blot Membrane Data on page 443](#).

Western Blot membrane data are saved as a TIFF image that can be analyzed by the image-analysis tool of your choice. The SoftMax Pro Software comes with an installed version of the ImageJ software from U.S. National Institute of Health (NIH). See [Analyzing a Western Blot Image on page 450](#).

To view the membrane image in the ImageJ software, click  in the toolbar at the top of the section and then click **ImageJ Editor**.

To view the membrane image in your selected image-analysis tool, click  in the toolbar at the top of the section and then click **External Image Editor**. This option is available only if you have .tif files associated with a program other than ImageJ software. The icon used for this tool changes depending on the selected image-analysis tool. See [Defining the Membrane Image-Analysis Tool on page 451](#).



Note: The image tools are available only when viewing a **Plate** section that contains membrane data.

Using Template Tools

When a **Plate** section is active in the Workspace, **Template Tools** are available on the **Home** tab in the ribbon.

A Template is a map of the microplate or cuvette that is used to describe the location of samples in the microplate or cuvette, and it provides the link between raw data and analysis groups.

Each template contains samples and groups:

- A set of one or more replicate wells makes up a sample.
- A set of related samples forms a group.

For example, you can have a group named “Standards” that contains seven samples named STD01, STD02, ..., STD07, and a group named “Unknowns” that contains five samples named UNK01, UNK02, ..., UNK05.

Each sample would be generally applied to a column or some other subset of wells on a microplate, or to one or more cuvettes. Each well designated as being part of a group has related to it a group name, a sample name (or replicate ID), a sample descriptor (optional), and a column format for the calculations and data reported in the related **Group** section.

Samples and groups can exist across multiple **Plate** sections and **Cuvette Set** sections as well as within a single **Plate** section or **Cuvette Set** section. Deleting the wells assigned to a group from the template does not delete the group. To delete a group name in the **Template Editor** you must delete the corresponding **Group** section from the data file.

For information about using the **Template Tools**, see [Configuring a Microplate Template on page 301](#).

Using a Cuvette Set Section

Cuvette Set sections are used to collect data from the cuvette port of the SpectraMax M2 and M2e Multi-Mode Microplate Readers, SpectraMax M5 and M5e Multi-Mode Microplate Readers, and the SpectraMax Plus 384 Absorbance Microplate Reader. You can use a **Cuvette Set** section to define an analysis template and to define data display and data reduction. The **Template Editor** in the **Cuvette Set** section is used to describe the contents of each cuvette within the Cuvette Set.

You can add up to 96 cuvettes in a single **Cuvette Set** section or create as many **Cuvette Set** sections as you need. Cuvettes are read one at a time.

Cuvette Set sections have the following areas:

- Tool bar (above the data display)
- Cuvette data display
- Instrument Settings Information and Read Information (to the right of the data display)
- Reduction settings (below the data display)

When colors are displayed in the name labels above individual cuvettes, this means a template has been defined for the **Cuvette Set** section.


Each group defined in the template has a different color. The icon of the corresponding group table has the same color.

For information about using a **Cuvette Set** section, see the following topics:

- [Adding a Cuvette Set Section on page 130](#)
- [Using Cuvette Tools on page 130](#)
- [Using the Template Tool with a Cuvette Set on page 138](#)

Adding a Cuvette Set Section

To add a new **Cuvette Set** section:

1. Select the experiment where you want to add a **Cuvette Set** section in the **Navigation Tree**.
2. If you have more than one section in the Experiment, select the section above where you want the new **Cuvette Set** section to be displayed in the **Navigation Tree**.
3. Click **New Cuvette Set**  in **Sections** on the **Home** tab in the ribbon.

A new **Cuvette Set** section is displayed in the Workspace. You can add as many **Cuvette Set** sections as you need to your data file. Each **Cuvette Set** section can have up to 96 cuvettes defined in the section.

To change the name of the **Cuvette Set** section, right-click the **Cuvette Set** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).



Note: When you create a new Cuvette Set section with an existing Cuvette Set section active in the workspace, SoftMax Pro Software makes a copy of the active Cuvette Set section and the new Cuvette Set section is a duplicate of the active Cuvette Set section.

Using Cuvette Tools


Cuvette Tools are displayed on the **Home** tab when a **Cuvette Set** section is active in the workspace. **Cuvette Tools** include the following:

- [Modifying Instrument Settings for Cuvettes on page 131](#)
- [Modifying Data Reduction Settings for Cuvettes on page 131](#)
- [Modifying the Cuvette Data Display on page 132](#)
- [Zooming the Cuvette Display on page 134](#)
- [Masking Cuvettes on page 135](#)
- [Adding a Cuvette to a Cuvette Set on page 136](#)
- [Deleting a Cuvette from a Cuvette Set on page 136](#)
- [Copying a Cuvette Set Section on page 136](#)
- [Copying and Pasting Cuvette Data on page 137](#)

Modifying Instrument Settings for Cuvettes


Changing the instrument settings for a cuvette changes the setting for all the cuvettes in the **Cuvette Set** section.

To change the instrument settings:

1. Click the **Cuvette Set** section to make it active in the workspace.
2. Click **Settings**  in the **Cuvette Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the **Cuvette Set** section. The **Settings** dialog is displayed.
3. Set the instrument settings options as needed. See [Selecting Instrument Settings on page 236](#).
4. Click **OK**.

Modifying Data Reduction Settings for Cuvettes

To change the data reduction settings:


1. Click **Reduction**  in the **Cuvette Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the **Cuvette Set** section. The **Data Reduction** dialog is displayed.
The **Data Reduction** dialog displays only the reduction options that are available for the instrument you are using, the options that have been selected in the **Settings** dialog, and the options defined in the template.
2. Change the reduction settings as needed. See [Doing Data Reduction on page 367](#).
3. Click **OK**.

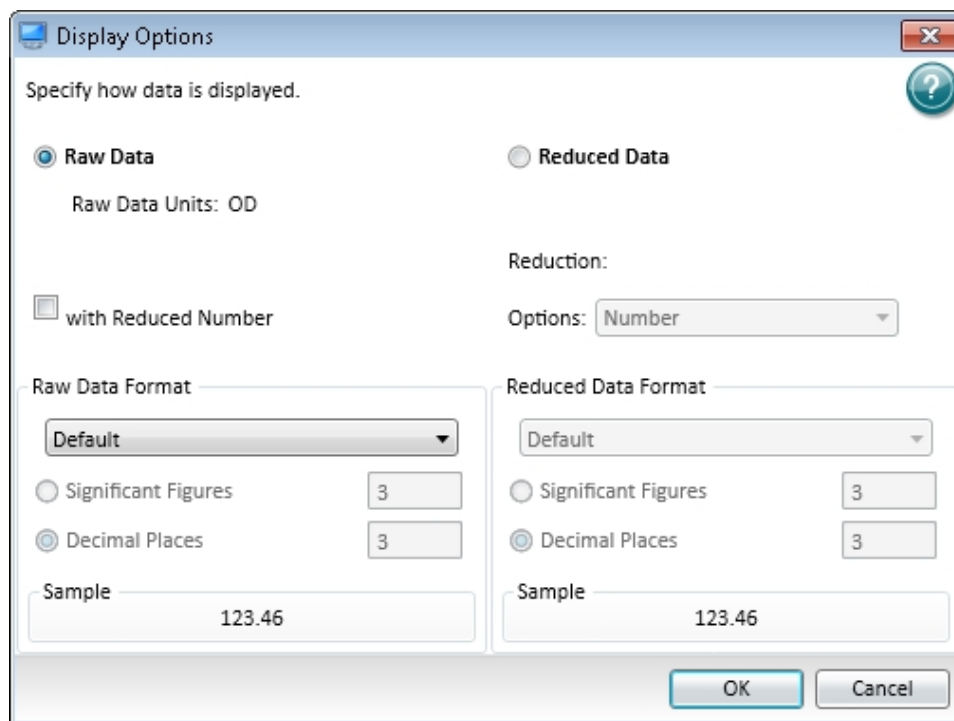


Note: Changing the data reduction setting for one cuvette, changes the settings for all the cuvettes in the active Cuvette Set section.

Modifying the Cuvette Data Display

In an active **Plate** section or **Cuvette Set** section, you can change how the data is presented

by clicking **Display**  on the **Home** tab in the ribbon or in the toolbar at the top of the section.



The choices available in the **Display Options** dialog include selecting between **Raw Data** and **Reduced Data**.

You can customize the data display to **Numeric notation** or **Scientific notation** format, and specify the number of **Significant Figures** or **Decimal Places**. These options can be set separately for raw data and reduced data.

The **Default** format determines the number of decimal places to display based on the space available. For example, for a plate with 96 wells or fewer, each well is limited to five digits, plus one character for the decimal point, if applicable. For a 384-well plate, each well is limited to four characters, including the decimal point. If the value requires greater precision than can fit in the available space, the format changes to scientific notation.

Raw Data

Selecting **Raw Data** displays the default data type for the selected read type:

- **Endpoint:** Raw absorbance, fluorescence, or luminescence values.
- **Kinetic:** The change in raw OD/RFU/RLU values over time, displayed as a plot.
- **Spectrum:** Raw OD/RFU/RLU values for the range of wavelengths, displayed as a plot.
- **Well Scan:** Raw OD/RFU/RLU values as shades of blue to red.

To see a reduced number, select **with Reduced Number**.

Reduced Data

The reduced data display is based on the selections made in the **Data Reduction** dialog. See [Doing Data Reduction on page 367](#).

The reduced number is reported in the **Group** section when a template has been defined.

- Select **Number** to view only the reduced number.
- Select **Plot** for Kinetic reads to display a plot of the raw and reduced data. To also view the reduced number, select the **Reduced Number** check box.
- Select **Grayscale** to display the raw data in eight shades of gray, changing from light, for values less than or equal to the low limit, to dark, for values greater than or equal to the high limit. To define the **High Limit** and the **Low Limit** for the grayscale map, type values in the fields. To also view the reduced number, select the **Reduced Number** check box.
- Select **Color Map** to display the raw data in eight colors, changing from blue, for values less than or equal to the low limit, to red, for values greater than or equal to the high limit. To define the **High Limit** and the **Low Limit** for the color map, type values in the fields. To also view the reduced number, select the **Reduced Number** check box.

You can view both raw and reduced data or multiple reductions of the same data by cloning a plate. See [Cloning a Plate Section on page 127](#).





Note: Changing the display setting for one cuvette changes the display settings for all the cuvettes in the active **Cuvette Set** section.

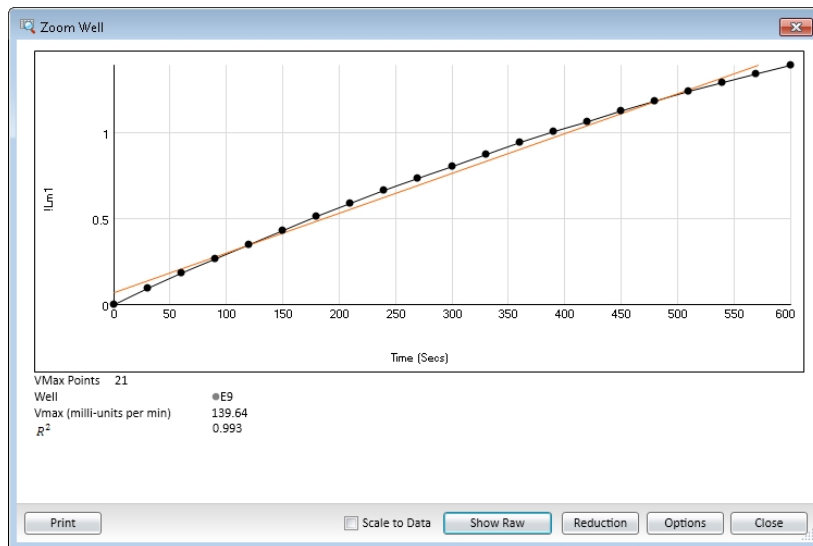
Zooming the Cuvette Display

The **Zoom** icon becomes active when the data in a cuvette is available for a zoomed display.

To display the **Zoom Well** dialog:

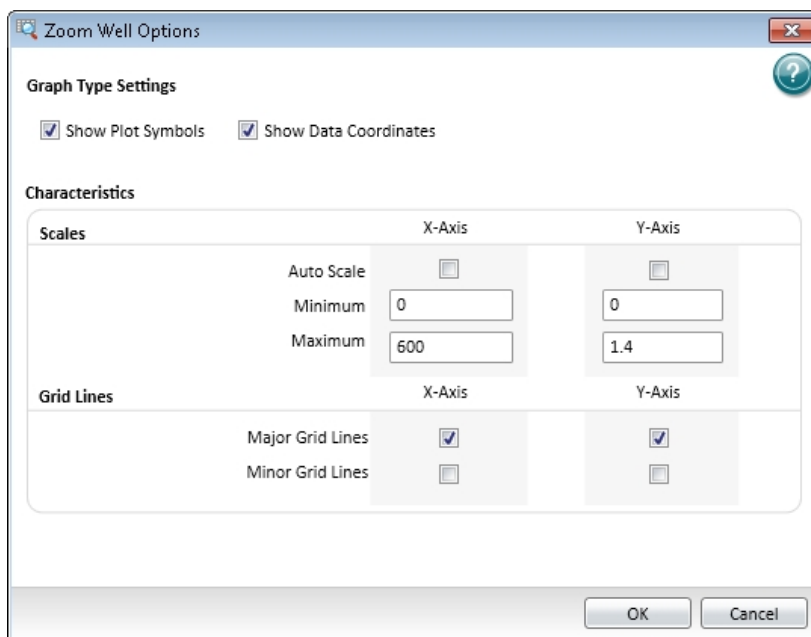
1. Click the well or cuvette that you want to zoom.
2. Click **Zoom**  on the **Home** tab in the ribbon or **Zoom**  in the toolbar at the top of the section. You can also double-click the well to open the **Zoom Well** dialog.

The data from the selected well or cuvette is displayed in a zoomed graph window.



3. To print the graph window, click **Print**.
4. To scale the display to the data, select **Scale to Data**.
5. To toggle between reduced and raw data, click **Show Reduced** or **Show Raw**.
6. To modify the reduction settings, click **Reduction**. The **Data Reduction** dialog is displayed. See [Doing Data Reduction on page 367](#).

7. To modify the zoom well display settings, click **Options**. The **Zoom Well Options** dialog is displayed.



- **Graph Type Settings** lets you enable or disable connected points or plotted symbols on the graph.
- **Characteristics** lets you set Auto Scale parameters and choose the minimum and maximum values for the selected axis. You can also add or remove grid lines from the display.


To save the settings and return to the **Zoom Well** dialog, click **OK**. These changes have an effect on only the well graph being viewed.

8. To close the **Zoom Well** dialog, click **Close**.

Masking Cuvettes

The Mask feature hides selected data so that they are not used for calculations and are not reported. Masking is commonly used to suppress outliers from data reduction calculations. Masking can be used as a “what if?” tool. For example, if you have included a group blank in a template and want to see the data both with and without the blank, masking the group blanks suppresses the blanking function, while unmasking them enables it again.

To mask cuvettes:


1. In an active **Cuvette Set** section, click to select a single cuvette or hold down the **Ctrl** key and click to select multiple cuvettes.
2. Click **Mask**  in **Cuvette Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the **Cuvette Set** section.

You can also right-click a cuvette and select **Mask** from the shortcut menu.

To unmask masked cuvettes, select the cuvettes and then click **Mask**.

Adding a Cuvette to a Cuvette Set

To add a cuvette to a **Cuvette Set** section:

1. Click on a **Cuvette Set** section to make it active in the workspace.
2. Click **New**  in **Cuvette Tools** on the **Home** tab in the ribbon.


Up to 96 cuvettes can be added to one **Cuvette Set** section.

The cuvettes in a **Cuvette Set** are numbered as if they were wells in a microplate. The first 12 cuvettes are numbered A1 through A12, and then the next new cuvette is numbered B1. This representation provides easy access to the data analysis capabilities of the SoftMax Pro Software.

You can also add cuvettes with the Template Editor. See [Using the Template Tool with a Cuvette Set on page 138](#).


Deleting a Cuvette from a Cuvette Set

To delete a cuvette from a **Cuvette Set** section:

1. In an active **Cuvette Set** section, click to select a single cuvette or hold down the **Ctrl** key and click to select multiple cuvettes.
2. Click **Delete**  in **Cuvette Tools** on the **Home** tab in the ribbon.

Copying a Cuvette Set Section

To make a duplicate copy of a **Cuvette Set** section:

1. Click the **Cuvette Set** section you want to duplicate to make it active in the workspace.
2. Click **New Cuvette Set**  in **Sections** on the **Home** tab in the ribbon.
3. A new **Cuvette Set** section that is a duplicate of the active **Cuvette Set** section is added to the Experiment and is displayed on the Navigation Tree.

A new **Cuvette Set** section is displayed in the Workspace that is a duplicate copy of the active **Cuvette Set** section.

You can add as many **Cuvette Set** sections as you need to your data file. Each **Cuvette Set** section can have up to 96 cuvettes defined in the section.

Copying and Pasting Cuvette Data

You can copy cuvette data from one or more cuvettes in a **Cuvette Set** section to a cuvette or cuvettes in the same or a different **Cuvette Set** section. Data can be copied and pasted within the same data file or between different data files.

If you want to copy all the cuvette data from one **Cuvette Set** section to all the cuvettes in a different **Cuvette Set** section in the same file, it might be easier to make a duplicate copy of the **Cuvette Set** section. See [Copying a Cuvette Set Section on page 136](#).

To copy cuvette data:

1. In an active **Cuvette Set** section, click to select a single cuvette or hold down the **Ctrl** key and click to select multiple cuvettes.
2. Right-click and select **Copy Cuvette Data** from the shortcut menu.
3. The data is copied into the clipboard.

To paste cuvette data that is stored in the clipboard:

1. Click the cuvette that the data should be pasted into.
2. If you copied data from multiple cuvettes, click the first cuvette where you want to paste the data. SoftMax Pro Software pastes cuvette data into consecutive cuvettes. For example, if you copied data from three cuvettes and then click cuvette A6 to paste the data, the data will be pasted into cuvettes A6, A7, and A8.
3. Right-click and select **Paste Cuvette Data** from the shortcut menu.

After data is pasted into a cuvette, the **Read Information** on the right indicates that the data was pasted and shows the time and date of when it was pasted.

Using the Template Tool with a Cuvette Set

When a **Cuvette Set** section is active in the Workspace, the **Template Tool** is available on the **Home** tab in the ribbon.

A Template is a map of the microplate or cuvette that is used to describe the location of samples in the microplate or cuvette, and it provides the link between raw data and analysis groups.

Each template contains samples and groups:

- A set of one or more replicate wells makes up a sample.
- A set of related samples forms a group.

For example, you can have a group named “Standards” that contains seven samples named STD01, STD02, ..., STD07, and a group named “Unknowns” that contains five samples named UNK01, UNK02, ..., UNK05.

Each sample would be generally applied to a column or some other subset of wells on a microplate, or to one or more cuvettes. Each well designated as being part of a group has related to it a group name, a sample name (or replicate ID), a sample descriptor (optional), and a column format for the calculations and data reported in the related **Group** section.

Samples and groups can exist across multiple **Plate** sections and **Cuvette Set** sections as well as within a single **Plate** section or **Cuvette Set** section. Deleting the wells assigned to a group from the template does not delete the group. To delete a group name in the **Template Editor** you must delete the corresponding **Group** section from the data file.

When working within a **Cuvette Set** section, adding template information in the form of groups automatically adds cuvettes to the active **Cuvette Set** section.

Up to 96 cuvettes can be added to one **Cuvette Set** section.

When you open the template editor with a **Cuvette Set** section active in the workspace, the template editor window contains 96 wells in the column and row format of a 96-well microplate. The cuvettes in the template are numbered as if they were wells in a microplate. This representation provides easy access to the data analysis capabilities of the SoftMax Pro Software.

For information about using the **Template Tools** with a **Cuvette Set** section, see [Configuring a Microplate Template on page 301](#).

Using a Group Section

Unlike other section types, **Group** sections are created automatically when you create and assign a **Group** to a **Plate** section or **Cuvette Set** section from within the **Template Editor** dialog. See [Configuring a Microplate Template on page 301](#).

Reduced numbers from the **Plate** section or **Cuvette Set** section are displayed in the **Values** column of the **Group** section tables by default.

Custom reduction formulas require the use of accessors and operators that are understood by SoftMax Pro Software. For a list of these accessors and operators see the *SoftMax Pro Formula Reference Guide*.

Reusing Formulas

Formulas are used in **Group** columns and custom reductions. Sometimes it is useful to copy an existing formula or column from one area of the program to a different area, or from one Experiment to a different Experiment, rather than recreating it. After pasting, formulas can be edited.

Formulas in contiguous column formulas can be copied and then pasted as a unit.

When a **Group** section is active in the workspace **Column Tools**, **Summary Tools**, and **Formatting Tools** are displayed on the **Home** tab in the ribbon.

For information about using a **Group** section, see the following topics:

- [Using the Group Settings Dialog on page 139](#)
- [Using Column Tools on page 143](#)
- [Using Summary Tools on page 147](#)
- [Using Formatting Tools in a Group Section on page 149](#)

Using the Group Settings Dialog


The **Group Settings** dialog lets you define the name for a group of related samples, a descriptor related to the samples, and the initial column format for the data calculated and reported in the related **Group** section.

Whenever a new group is created (whether or not wells are selected in the template), a **Group** section is created in your Experiment. To delete a group, you must delete the **Group** section. Clearing a group from the Template Editor removes only the assignment of wells to that group name. It does not delete the group.

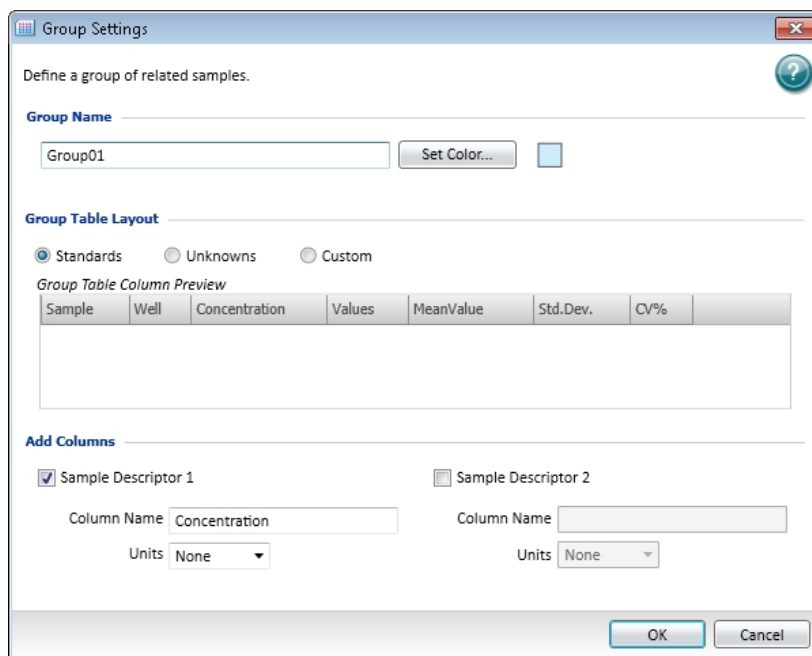
To define a new group, see [Creating a Group on page 140](#).

For information about the column formats, see [Group Table Column Format on page 142](#).

Creating a Group

1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Template Editor**  in **Template Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the active section. This displays the **Template Editor**.
The **Template Editor** contains a representation of the rows and columns of the microplate in the active **Plate** section.
When you open the template editor with a **Cuvette Set** section active in the workspace, the template editor window contains 96 wells in the column and row format of a 96-well microplate. The cuvettes in the template are numbered as if they were wells in a microplate. This representation provides easy access to the data analysis capabilities of the SoftMax Pro Software.
3. Use your mouse to drag the pointer to select one or more wells to be defined as a group.
4. In the **Groups** area, click **Add**.

To modify an existing group, select the group and click **Edit**.



The **Group Settings** dialog box is used to define a group of related samples. It includes the following sections:

- Group Name:** A text field containing "Group01" and a "Set Color..." button with a color selection box.
- Group Table Layout:** Radio buttons for "Standards" (selected), "Unknowns", and "Custom".
- Group Table Column Preview:** A table with columns: Sample, Well, Concentration, Values, MeanValue, Std.Dev., and CV%.
- Add Columns:** Two sections for adding sample descriptors. "Sample Descriptor 1" is checked and has a "Concentration" column name and "None" units. "Sample Descriptor 2" is unchecked and has empty fields.

Buttons for "OK" and "Cancel" are at the bottom right.

5. In the **Group Settings** dialog, in the **Group Name** field, type the name to assign to the group.
6. If you want to set a color for the group, click **Set Color** and select the color to be displayed for the group.

- In the **Group Table Layout** area, click **Standards**, **Unknowns**, or **Custom** to specify the column format.

For information about the column formats, see [Group Table Column Format on page 142](#).

When the **Standards** group type is selected, **Sample Descriptor1** is automatically activated and the assumption is that it will be used for concentration information. However, it could be used for all numerical data, that is, dilution factor or fraction number. The other two group types do not have sample descriptors by default.

- In the **Add Columns** area, if it is not selected, click **Sample Descriptor1** to apply a descriptor and its units to the group.
- Type a short descriptive name for the sample descriptor in the **Column Name** field.



Note: If you plan to reference the name of this column in a formula, make sure that you do not use reserved characters or names of operators, functions, or accessors in this name. For information about reserved characters and words, see “Rules to Follow When Writing Formulas” in the *SoftMax Pro Software Formula Reference Guide*.

- Select a set of units from the list or type them directly in the **Units** field.
- Optionally, click **Sample Descriptor2** to define a second sample descriptor. The **Group Table Column Preview** shows an example of how the columns will be displayed in the group table.
- Click **OK** to close the **Group Settings** dialog. The selected wells are placed in the newly defined group. To define a series for the selected wells, click **Series**. See [Creating a Series on page 304](#).
- Click **OK** to close the **Template Editor** and apply the template.



Note: No sample descriptor is assigned automatically for the Unknowns column format. You can assign a sample descriptor to these column formats manually, but the information is not displayed automatically in the **Group** section. To see it, create a new column containing the formula **!Sampledescriptor**, **!factor**, or **!concentration**. For more information about creating columns, see [Adding a New Column on page 143](#).

Group Table Column Format

The type of **Group Table Layout** defines the default columns for the data calculated and reported in the related **Group** section of the current sample group.

Each of the three column formats (Standard, Unknown, and Custom), creates a different set of columns in a new or existing group. The following table shows the default columns created with each selection type.

Table 4-1: Group Type Column Format

Name	Formula	Standard	Unknown	Custom
Sample	!SampleNames	✓	✓	✓
Wells	!WellIDs	✓	✓	✓
Sample#	Index			
Concentration	!Concentration	✓		
Mean Value	Average(Values)	✓		
Values	!WellValues	✓		
R (Outside Standard Range)	If(Values)>='MinStd @Standards' and Values<='MaxStd@ Standards', "", "R"		✓	✓
Result	InterpX(STD@ StandardCurve, Values)		✓	✓
MeanResult	Average(Result)		✓	✓
Std.Dev.	Stdev(Result)	✓	✓	✓
CV%	Cv(Result)	✓	✓	✓
Dilution	!Factor			✓
Adj.Result	MeanResult*!Factor			✓

Using Column Tools

When a column (or the data in a column) is selected in the group table, the **Column Tools** that can be used on the selected items are active. Actions not applicable for a selected item are disabled.


After selecting a column or data in a group table, functions applicable to the selected item are available by right-clicking to open the Group tools shortcut menu.

For information about using the **Column Tools** on the **Home** tab, see the following topics:

- [Adding a New Column on page 143](#)
- [Modifying a Column on page 144](#)
- [Copying Column Contents on page 145](#)
- [Pasting Column Contents on page 145](#)
- [Cutting Column Content on page 145](#)
- [Deleting a Column on page 146](#)
- [Autosizing a Column on page 146](#)
- [Hiding Columns on page 146](#)
- [Showing Hidden Columns on page 147](#)
- [Hiding Replicates on page 147](#)

Adding a New Column

To add a new column to a group:

1. Click a **Group** section to make it active in the workspace.
2. Click **New**  in **Column Tools** on the **Home** tab in the ribbon.
3. In the **Formula Editor** dialog, in the **Name** field, type a short descriptive name for the formula.



Note: If you plan to reference this formula in a different formula, for example referencing the formula in a column of a group table, make sure that you do not use reserved characters or names of operators, functions, or accessors in this name. For information about reserved characters and words, see “Rules to Follow When Writing Formulas” in the *SoftMax Pro Software Formula Reference Guide*.

4. Optionally, type text **Comments** to annotate the formula.
5. Optionally, click **Syntax Helper** to turn on the formula completion tool. See [Enabling Syntax Helper on page 116](#).
6. Type a **Formula** to be used for the Summary or column.
7. Optionally, click **Check Syntax** check the validity of the formula. A message is displayed to the left of the button to help you troubleshoot the syntax of the formula.

8. Specify the **Data Display** characteristics:

- From the drop-down list select either **Numeric notation** or **Scientific notation**.
- Click **Decimal Places** and type the number of places to display or click **Significant Figures** and type the number of figures to display.

A preview of the **Data Display** is displayed in the **Sample** on the right.

9. Click **OK**.

- If no columns are selected, the column is added at the end of the group on the right.
- If you select a column first, the new column is added to the right of the selected column.

New columns can contain references to other columns, either in the current section or in a different one. For example, if you wanted to subtract the mean values in one group from those in a different group, you could create a new column (in either group) to do this. If the two groups were named “Group 1” and “Group 2,” for example, and both groups contained a column entitled “Mean,” you could create a column within “Group 1” that would subtract the mean values in “Group 2” from those in “Group 1.” The column formula needed to do this would be:

Mean – (Mean@Group2)

Many possibilities exist for creating and editing column formulas. For a complete discussion, see the *SoftMax Pro Formula Reference Guide*.

Modifying a Column


To modify a column formula:

1. Click a **Group** section to make it active in the workspace.
2. To modify a column formula, double click the column heading to open the **Formula Editor** dialog. See [Adding a New Summary Formula on page 115](#).
3. To resize the column width, click and hold the column border and then drag it to the desired column width.

Copying Column Contents

To paste content into a column you must first copy applicable content into the clipboard using the copy operation provided in the **Column Tools**.


To copy content to the clipboard:

1. Click a **Group** section to make it active in the workspace.
2. Select the content to be copied.
3. Click **Copy**  in **Column Tools** on the **Home** tab in the ribbon.

Pasting Column Contents

The content to be pasted into a column must be copied from a different column location and be present in the clipboard.

To paste content into a column:


1. Click a **Group** section to make it active in the workspace.
2. Click to select the target column location.
3. Click **Paste**  in **Column Tools** on the **Home** tab in the ribbon.



Note: If the **Paste** button is disabled when you try this operation, there is no applicable content present in the clipboard. You must first copy content to the clipboard.

Cutting Column Content

To cut content out of a column:


1. Click a **Group** section to make it active in the workspace.
2. Select the content to be removed.
3. Click **Cut**  in **Column Tools** on the **Home** tab in the ribbon.



Note: Content that is cut from a column is not placed in the clipboard. To place content in the clipboard, the content must be copied.


Deleting a Column

To delete a column:

1. Click a **Group** section to make it active in the workspace.
2. Click a column title to select the column.
To select multiple columns, hold down the **SHIFT** key and click to select a range of columns or hold down the **CTRL** key and click to select non-contiguous columns.
3. Click **Delete**  in **Column Tools** on the **Home** tab in the ribbon, or right-click and select **Delete Column** from the shortcut menu.


Autosizing a Column

You can autosize a column to set the width of the selected column to hold the longest text string:

1. Click a **Group** section to make it active in the workspace.
2. Click a column title to select the column.
To select multiple columns, hold down the **SHIFT** key and click to select a range of columns or hold down the **CTRL** key and click to select non-contiguous columns.
3. Click **Auto Size**  in **Column Tools** on the **Home** tab in the ribbon, or right-click and select **Auto Size** from the shortcut menu.


Hiding Columns

To hide one or more columns:

1. Click a **Group** section to make it active in the workspace.
2. Click **Show/Hide**  in **Column Tools** on the **Home** tab in the ribbon or above the right side of the group table.
3. In the **Show Hide group table columns** dialog, clear the check boxes next to the columns that you want to hide.
 - To clear all the check boxes, click **Hide All**.
 - To select all the check boxes, click **Show All**.
4. Click **OK**.


Showing Hidden Columns

To show hidden columns:

1. Click a **Group** section to make it active in the workspace.
2. Click **Show/Hide**  in **Column Tools** on the **Home** tab in the ribbon or above the right side of the group table.
3. In the **Show Hide group table columns** dialog, select the check boxes next to the columns that you want to show.
 - To select all the check boxes, click **Show All**.
 - To clear all the check boxes, click **Hide All**.
4. Click **OK**.

Hiding Replicates

To hide data for all replicates:

1. Click a **Group** section to make it active in the workspace.
2. Click **Hide Replicates**  in the **Column Tools** on the **Home** tab in the ribbon.

Using Summary Tools



When a **Group** section is active in the workspace, the **Home** tab in the ribbon displays the **Summary Tools**.

For information about using the **Summary Tools**, see the following topics:

- [Copying and Pasting a Formula on page 147](#)
- [Deleting a Formula on page 148](#)
- [Adding a New Formula on page 148](#)
- [Editing a Formula on page 148](#)
- [Showing and Hiding the Formulas in a Group Section on page 148](#)


Copying and Pasting a Formula

To copy a formula and paste it into a new summary:

1. Click a **Group** section to make it active in the workspace.
2. Select the Summary formula to be copied.
3. Click **Copy**  in **Summary Tools** on the **Home** tab in the ribbon.
4. Click the location where you want to paste the copy of the Summary formula.
5. Click **Paste**  in **Summary Tools** on the **Home** tab in the ribbon.


Deleting a Formula

To delete a formula:

1. Click a **Group** section to make it active in the workspace.
2. Click a formula to select the formula to be deleted.
3. Click **Delete**  in **Summary Tools** on the **Home** tab in the ribbon.


Adding a New Formula

To add a new formula to a **Group** section:

1. Click on a **Group** section to make it active in the workspace.
2. Click **New Summary**  in **Summary Tools** on the **Home** tab in the ribbon to open the **Formula Editor** dialog. For more information, see [Adding a New Summary Formula on page 115](#).
3. Type the formula to be added and click **OK**.

Editing a Formula


To edit a formula in a **Group** section:

1. Click a **Group** section to make it active in the workspace.
2. Click the formula to be changed to select it.
3. Click **Edit Summary**  in **Summary Tools** on the **Home** tab in the ribbon to open the **Formula Editor** dialog. For more information, see [Adding a New Summary Formula on page 115](#).
4. Type the changes to formula and click **OK**.


Showing and Hiding the Formulas in a Group Section

Generally, the summary formulas in the **Group** section display the results of the formulas. You can show or hide the formulas as well as the results.

To show the formulas in the **Group** section:

1. Click a **Group** section to make it active in the workspace.
2. Click **Show Formulas**  in **Summary Controls** on the **Home** tab in the ribbon.

To hide the formula in the Group section:

1. Click a **Group** section to make it active in the workspace.
2. Click **Hide Formulas**  in **Summary Controls** on the **Home** tab in the ribbon.

Using Formatting Tools in a Group Section

When a **Group** section is active in the workspace, the **Home** tab in the ribbon displays the Formatting Tools.

You can format the text in the summaries and text frames in the **Group** section using the available **Formatting Tools**. Formatting text in a **Group** section is similar to formatting text in a **Note** section. See the following topics:

- [Adding Text to a Note Section on page 111](#)
- [Aligning Text on page 111](#)
- [Editing Text in a Text Frame on page 112](#)
- [Formatting Text in a Text Frame on page 113](#)
- [Positioning a Text Frame in a Note Section on page 114](#)
- [Resizing a Text Frame on page 114](#)
- [Deleting a Text Frame on page 114](#)

Using a Graph Section

Graph sections are used to plot information from groups as scatter plots or bar graphs.

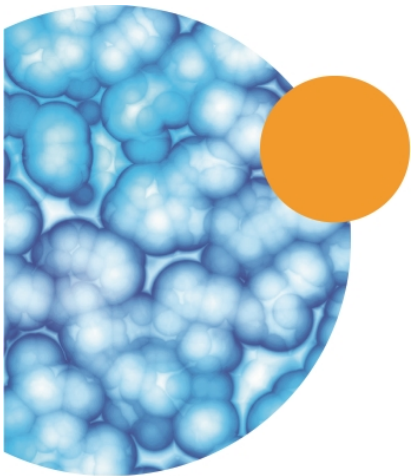
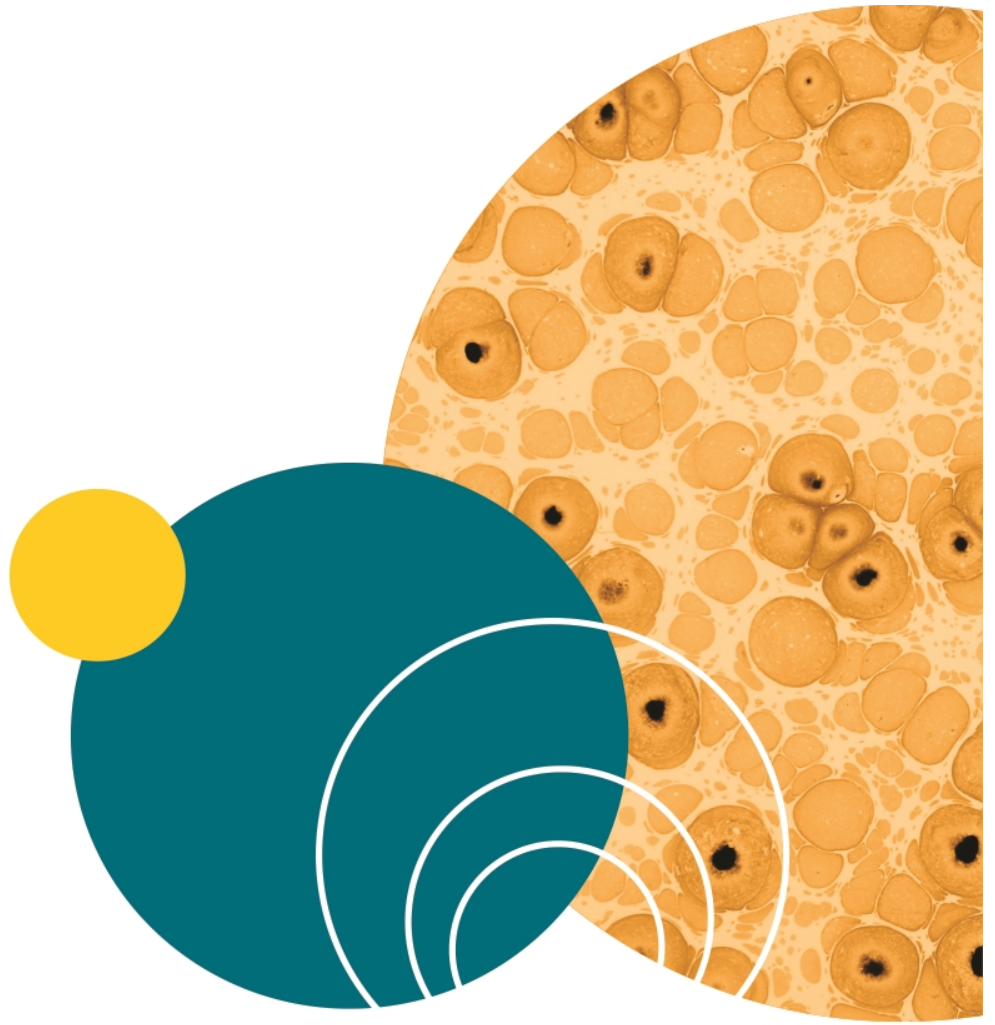
You can create more than one **Graph** section within a data file, and plots in the **Graph** section can be created from any Experiment in the file.

After a graph has been created, new plots can be added and deleted, the axes can be customized, and the size and type of graph can be changed. The grid lines for the graph can be enabled or disabled. The default setting has grid lines enabled.

Graph sections are divided into the following areas:

- The body of the **Graph** section.
- The Legend.

For more information see [Working with Graphs on page 389](#).



Chapter 5: Read Modes and Read Types

Use the SoftMax Pro Software to define the parameters for the read mode and read type of your assay.

For more information on the supported read modes, see the following topics:

- [Absorbance Read Mode on page 154](#)
- [Fluorescence Intensity Read Mode on page 160](#)
- [Luminescence Read Mode on page 166](#)
- [Time-Resolved Fluorescence Read Mode on page 171](#)
- [HTRF Read Mode on page 179](#)
- [FRET Read Mode on page 178](#)
- [Fluorescence Polarization Read Mode on page 185](#)
- [AlphaScreen Read Mode on page 189](#)
- [Western Blot TRF Read Mode on page 193](#)
- [Imaging Read Mode on page 197](#)

Application notes with specific application protocol suggestions can be found in the Information Center and the Knowledge Base on the Molecular Devices web site at www.moleculardevices.com.

Supported Read Types

For most read modes, endpoint, kinetic, multi-point well-scan, and spectrum microplate applications can be set up and run with the SoftMax Pro Software. In addition, the FlexStation 3 reader support the flex read type that can integrate fluid transfer with a kinetic read.

For more information on the supported read types, see the following topics:

- [Endpoint Read Type on page 152](#)
- [Kinetic Read Type on page 152](#)
- [Well Scan Read Type on page 152](#)
- [Spectrum Read Type on page 152](#)
- [Flex Read Type on page 153](#)
- [Membrane Read Type on page 153](#)

Endpoint Read Type

In an endpoint read, a reading of each microplate well is taken in the center of each well, at a single wavelength or at multiple wavelengths. Depending on the read mode, raw data values are reported as optical density (OD), %Transmittance (%T), relative fluorescence units (RFU), or relative luminescence units (RLU).

Kinetic Read Type

In a kinetic read, the instrument collects data over time with multiple readings taken in the center of each well at regular intervals. To get the shortest possible interval for multiple-wavelength Kinetic readings, choose wavelengths in ascending order.

The values calculated based on raw kinetic data include VMax, VMax per Sec, Time to VMax, and Onset Time. Kinetic readings can be single-wavelength or multiple-wavelength readings. Kinetic analysis can collect data points in time intervals of seconds, minutes, hours, or days. The kinetic read interval depends on the instrument setup parameters selected in the SoftMax Pro Software.

Kinetic analysis has many advantages when determining the relative activity of an enzyme in different types of microplate assays, including ELISAs and the purification and characterization of enzymes and enzyme conjugates. Kinetic analysis is capable of providing improved dynamic range, precision, and sensitivity relative to endpoint analysis.

Peak Pro™ Analysis functions provide advanced peak detection and characterization for applicable kinetic reads. See the *SoftMax Pro Software Formula Reference Guide*.

Spectrum Read Type

Depending on the read mode selected, a spectrum read measures optical density (OD), %Transmittance (%T), relative fluorescence units (RFU), or relative luminescence units (RLU) across a spectrum of wavelengths.

Well Scan Read Type

A well scan read can take readings at more than one location within a well. A well scan read takes one or more readings of a single well of a microplate on an evenly spaced grid inside of each well at single or multiple wavelengths.

Some applications involve the detection of whole cells in large-area tissue culture plates. Well scan reads can be used with such microplates to permit maximum surface area detection in whole-cell protocols. Since many cell lines tend to grow as clumps or in the corners of microplate wells, you can choose from several patterns and define the number of points to be scanned to work best with your particular application.

Depending on the read mode selected, the values are reported as optical density (OD), %Transmittance (%T), relative fluorescence units (RFU), or relative luminescence units (RLU).

Flex Read Type

The fluidics module in the FlexStation 3 reader is designed to aspirate fluids from a compound source plate and dispense them into an assay plate. Fluid transfer is made possible with an 8-channel or 16-channel pipettor that is fully automated, including changing the tips from a tip rack.

In the Flex read type, one to eight or one to sixteen wells in one column of the assay plate are read repeatedly for a selected total experimental time. At a preselected point or points during that time sequence, the pipettor can transfer up to three reagents from the compound plate to the assay plate. The instrument continues to read at the preselected time intervals before and after each fluid transfer. After completion of reading the column (or partial column) for a preselected time, the instrument can repeat this cycle with other columns. All the data are collected in one data file represented as a 96-well or 384-well microplate.

For example, an experiment with a two-minute run time accommodates a 96-well microplate in about 24 minutes.

$$\text{Run time} \times \text{Number of columns} = \text{Plate time}$$

$$2 \text{ minutes} \times 12 \text{ columns} = 24 \text{ minutes}$$

Membrane Read Type

The Membrane read type is used for a time-resolved fluorescence reading of a Western Blot membrane. The selected area is read, and a TIFF image is generated with the results of the read.

The Molecular Devices ScanLater™ Western Blot Assay Kit is a novel system for protein analysis that is incorporated into a SpectraMax® Paradigm® or SpectraMax® i3x Multi-Mode Detection Platform. Membranes are incubated with Eu-chelate labeled secondary antibodies or streptavidin that bind specifically to the target protein-specific primary antibody. For more information, contact your Molecular Devices representative or search the knowledge base for **ScanLater** or **Western Blot** at www.moleculardevices.com/support.

If you are using the SoftMax Pro GxP Software, you must enable the following permissions to complete a Western Blot membrane read:

- **Read empty plates/cuvettes** to start a read.
- **Save data files** to save the data file before the read.
- **Overwrite plate/cuvette data** to do a high-resolution ROI read.

See [Using SoftMax Pro GxP Software Features on page 467](#).

Absorbance Read Mode

In the Absorbance (ABS) read mode, the instrument measures the Optical Density (OD) of the sample solutions.

Absorbance is the quantity of light absorbed by a solution. To measure absorbance accurately, it is necessary to eliminate light scatter. If there is no turbidity, then absorbance = optical density.

$$A = \log_{10}(I_0 / I) = -\log_{10}(I / I_0)$$

where I_0 is incident light before it enters the sample, I is the intensity of light after it passes through the sample, and A is the measured absorbance.

For Absorbance reads, you can choose whether to display absorbance data as Optical Density (OD) or %Transmittance (%T) in the Reduction dialog.

Optical Density

Optical density (OD) is the quantity of light passing through a sample to a detector relative to the total quantity of light available. Optical Density includes absorbance of the sample plus light scatter from turbidity and background. You can compensate for background using blanks.

A blank well contains everything used with the sample wells except the chromophore and sample-specific compounds. Do not use an empty well for a blank.

Some applications are designed for turbid samples, such as algae or other micro-organisms in suspension. The reported OD values for turbid samples are likely to be different when read by different instruments.

For optimal results, Molecular Devices recommends that you run replicates for all blanks, controls, and samples. In this case, the blank value that can be subtracted is the average value of all blanks.

% Transmittance

%Transmittance is the ratio of transmitted light to the incident light for absorbance reads.

$$T = I / I_0$$

$$\%T = 100T$$

where I is the intensity of light after it passes through the sample and I_0 is incident light before it enters the sample.

Optical Density and %Transmittance are related by the following formulas:

$$\%T = 10^{2-OD}$$

$$OD = 2 - \log_{10}(\%T)$$

The factor of two comes from the fact that %T is expressed as a percent of the transmitted light and $\log_{10}(100) = 2$.

When in %Transmittance analysis mode, the SoftMax Pro Software converts the raw OD values reported by the instrument to %Transmittance using the above formula. All subsequent calculations are done on the converted numbers.

Applications of Absorbance

Absorbance-based detection has been commonly used to evaluate changes in color or turbidity, permitting widespread use including ELISAs, protein quantitation, endotoxin assays, and cytotoxicity assays. With absorbance readers that are capable of measuring in the ultraviolet (UV) range, the concentration of nucleic acids (DNA and RNA) can be found using their molar extinction coefficients.

For micro-volume measurements, you can use SpectraDrop 24-well Micro-Volume Microplates and SpectraDrop 64-well Micro-Volume Microplates.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up an Absorbance mode protocol, see [Creating an Absorbance Mode Protocol on page 312](#).

Absorbance Instruments

The following instruments have absorbance read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
To do absorbance reads, the SpectraMax Paradigm Multi-Mode Microplate Reader requires the [Absorbance Detection Cartridge, see page 219](#).
- [VersaMax Microplate Reader, see page 205](#)
- [SpectraMax Plus 384 Absorbance Microplate Reader, see page 205](#)
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M3 Multi-Mode Microplate Reader, see page 208](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [SpectraMax 340PC 384 Absorbance Microplate Reader, see page 210](#)
- [SpectraMax 190 Absorbance Microplate Reader, see page 210](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader, see page 214](#)
- [Vmax Kinetic Microplate Reader, see page 215](#)
- [EMax Endpoint Microplate Reader, see page 215](#)
- [EMax Plus Microplate Reader, see page 215](#)

PathCheck Pathlength Measurement Technology

You can enable PathCheck technology in the SoftMax Pro Software **Settings** dialog by selecting the **PathCheck** check box in the **PathCheck Settings** for absorbance endpoint reads.

The temperature-independent PathCheck® Pathlength Measurement Technology normalizes your absorbance values to a 1 cm path length based on the near-infrared absorbance of water.

The Beer–Lambert law states that absorbance is proportional to the distance that light travels through the sample:

$$A = \epsilon bc$$

where A is the absorbance, ϵ is the molar absorptivity of the sample, b is the pathlength, and c is the concentration of the sample. The longer the pathlength, the higher the absorbance.

Microplate readers use a vertical light path so the distance of the light through the sample depends on the volume. This variable pathlength makes it difficult to do extinction-based assays and also makes it confusing to compare results between microplate readers and spectrophotometers.

The standard pathlength of a 1 cm cuvette is the conventional basis for quantifying the unique absorptivity properties of compounds in solution. Quantitative analysis can be done on the basis of extinction coefficients, without standard curves (for example, NADH-based enzyme assays). When using a cuvette, the pathlength is known and is independent of sample volume, so absorbance is directly proportional to concentration when there is no background interference.

In a microplate, pathlength is dependent on the liquid volume, so absorbance is proportional to both the concentration and the pathlength of the sample. Standard curves are often used to determine analyte concentrations in vertical-beam photometry of unknowns, yet errors can still occur from pipetting the samples and standards. The PathCheck technology automatically determines the pathlength of aqueous samples in the microplate and normalizes the absorbance in each well to a pathlength of 1 cm. This way of correcting the microwell absorbance values is accurate to within $\pm 4\%$ of the values obtained directly in a 1 cm cuvette.

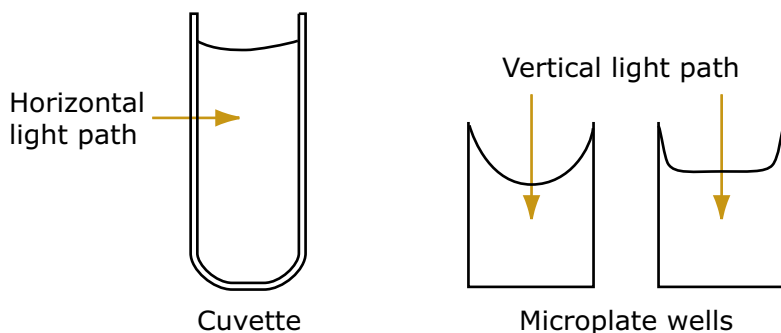


Figure 5-1: Cuvette and Microplate Well Light Paths

The 1 cm values can be obtained by using the factory installed *Water Constant*. PathCheck technology is used to normalize the data acquired from absorbance endpoint microplate readings to a 1 cm pathlength, correcting the OD for each well to the value expected if the sample were read in a 1 cm cuvette.

Water Constant

The Water Constant correction method is supported for absorbance endpoint reads.

The PathCheck technology is based on the absorbance of water in the near infrared spectral region (between 900 nm to 1000 nm). If the sample is completely aqueous, has no turbidity and has a low salt concentration (less than 0.5 M), the Water Constant is sufficient. The Water Constant is determined for each instrument during manufacture and is stored in the instrument.

Cuvette Reference

The Cuvette Reference correction method is supported by the SpectraMax M2, M2e, M3, M4, M5, M5e, and Plus 384 readers.

If the sample contains an organic solvent such as ethanol or methanol, we recommend using the Cuvette Reference. It is important that the solvent does not absorb in the 900 nm to 1000 nm range. To determine whether or not a given solvent would interfere, see the discussion of interfering substances in [Interfering Substances on page 159](#). When a non-interfering solvent is added to the aqueous sample, the water absorbance decreases proportionally to the percentage of organic solvent present. For example, 5% ethanol decreases the water absorbance by 5% and results in a 5% underestimation of the pathlength. You can minimize the error by putting the same water/solvent mixture in a cuvette and using the Cuvette Reference.

To use the Cuvette Reference, place into the cuvette port a standard 1 cm cuvette containing the aqueous/solvent mixture that is used for the samples in the microplate. The cuvette must be in place when you read the microplate. When you click the Read button, the instrument first makes the 900 nm and 1000 nm measurements in the cuvette, and then makes the designated measurements in the microplate. The cuvette values are stored temporarily and used in the PathCheck calculations for the microplate samples.

Use of Cuvette Reference with the PathCheck Pathlength Measurement Technology is different from a reference reading of a cuvette in a CuvetteSet section (by clicking the Ref button in the CuvetteSet section tool bar). The cuvette reference used for PathCheck calculations (measurements at 900 nm and 1000 nm) does not produce data that can be directly viewed in a CuvetteSet section and is used only with data in microplates, not cuvettes. However, you can obtain these values using accessors in the formula editor. See the !PathCheckLm1000 and !PathCheckLm900 accessor described in the *SoftMax Pro Software Formula Reference Guide*.



Note: After you have read a plate with PathCheck technology turned on, PathCheck information is stored permanently in the data file. You have the option of applying, or not applying, PathCheck technology to the absorbance values. If you do not have PathCheck technology turned on during the plate read, you cannot apply the PathCheck Pathlength Measurement Technology feature after the read.

Eliminating the Pathlength-Independent Component

Raw OD measurements of microplate samples include both pathlength-dependent components (sample and solvent) and a pathlength-independent component (OD of microplate material). The pathlength-independent component must be eliminated from the calculation to get valid results that have been normalized by the PathCheck technology. You can do this using a plate blank or using a plate background constant.

Using a Plate Blank

This method can be used if all samples in the microplate are the same volume and you are not depending on the PathCheck technology to correct for variability in volumes.

To use this method:

1. Designate a minimum of one well (preferably several) as Plate Blank.
2. Pipette buffer (for example, your sample matrix) into those wells and read along with your samples. Do not use an empty well for a blank.

The SoftMax Pro Software automatically subtracts the average of the blank wells from each of the samples. The OD of the microplate material is subtracted as part of the blank.

3. Make sure that **Use Plate Blank** is checked under **Other Options** in the **Data Reduction** dialog.

Using a Plate Background Constant

If your sample volumes are not identical or if you choose not to use a Plate Blank, then you must use a Plate Background Constant. Omitting a Plate Background Constant results in artificially high values after being normalized by the PathCheck technology.

To determine the Plate Background Constant:

1. Fill a clean microplate with water.
2. Read at the wavelengths that you will be reading your samples.

The average OD value is the Plate Background Constant. If you intend to read your samples at more than one wavelength, there should be a corresponding number of Plate Background Constant values for each wavelength.



Note: It is important that you put water in the wells and not read a dry microplate for the Plate Background Constant. A dry microplate has a slightly higher OD value than a water-filled microplate because of differences in refractive indices. Using a dry microplate results in PathCheck technology normalized values that are lower than 1 cm cuvette values.

Interfering Substances

Material that absorbs in the 900 nm to 1000 nm spectral region could interfere with PathCheck technology measurements. Fortunately, there are few materials that do interfere at the concentrations generally used.

Turbidity is the most common interference. If you can detect turbidity in your sample, you should not use the PathCheck technology. Turbidity elevates the 900 nm measurement more than the 1000 nm measurement and causes an erroneously low estimate of pathlength. Using Cuvette Reference does not reliably correct for turbidity.

Samples that are highly colored in the upper-visible spectrum might have absorbance extending into the near-infrared (NIR) spectrum and can interfere with the PathCheck technology. Examples include Lowry assays, molybdate-based assays, and samples containing hemoglobins or porphyrins. In general, if the sample is distinctly red or purple, you should check for interference before using the PathCheck technology.

To determine possible color interference, do the following:

- Measure the OD at 900 nm and 1000 nm (both measured with air reference).
- Subtract the 900 nm value from the 1000 nm value.

Do the same for pure water.

If the delta OD for the sample differs significantly from the delta OD for water, then it is recommended to not use the PathCheck technology.

Organic solvents could interfere with the PathCheck technology if they have absorbance in the region of the NIR water peak. Solvents such as ethanol and methanol do not absorb in the NIR region, so they do not interfere, except for causing a decrease in the water absorbance to the extent of their presence in the solution. If, however, the solvent absorbs between 900 nm and 1000 nm, the interference would be similar to the interference of highly colored samples as previously described. If you are considering adding an organic solvent other than ethanol or methanol, you should run a Spectrum scan between 900 nm and 1000 nm to determine if the solvent would interfere with the PathCheck technology.

Fluorescence Intensity Read Mode

Fluorescence occurs when absorbed light is re-radiated at a longer wavelength. In the Fluorescence Intensity (FL) read mode, the instrument measures the intensity of the re-radiated light and expresses the result in Relative Fluorescence Units (RFU).

The governing equation for fluorescence is:

$$\text{Fluorescence} = \text{extinction coefficient} \times \text{concentration} \times \text{quantum yield} \times \text{excitation intensity} \times \text{pathlength} \times \text{emission collection efficiency}$$

Fluorescent materials absorb light energy of a characteristic wavelength (excitation), undergo an electronic state change, and instantaneously emit light of a longer wavelength (emission). Most common fluorescent materials have well-characterized excitation and emission spectra. The following figure shows an example of excitation and emission spectra for a fluorophore. The excitation and emission bands are each fairly broad, with half-bandwidths of approximately 40 nm, and the difference between the wavelengths of the excitation and emission maxima (the Stokes shift) is generally fairly small, about 30 nm. There is considerable overlap between the excitation and emission spectra (gray area) when a small Stokes shift is present.

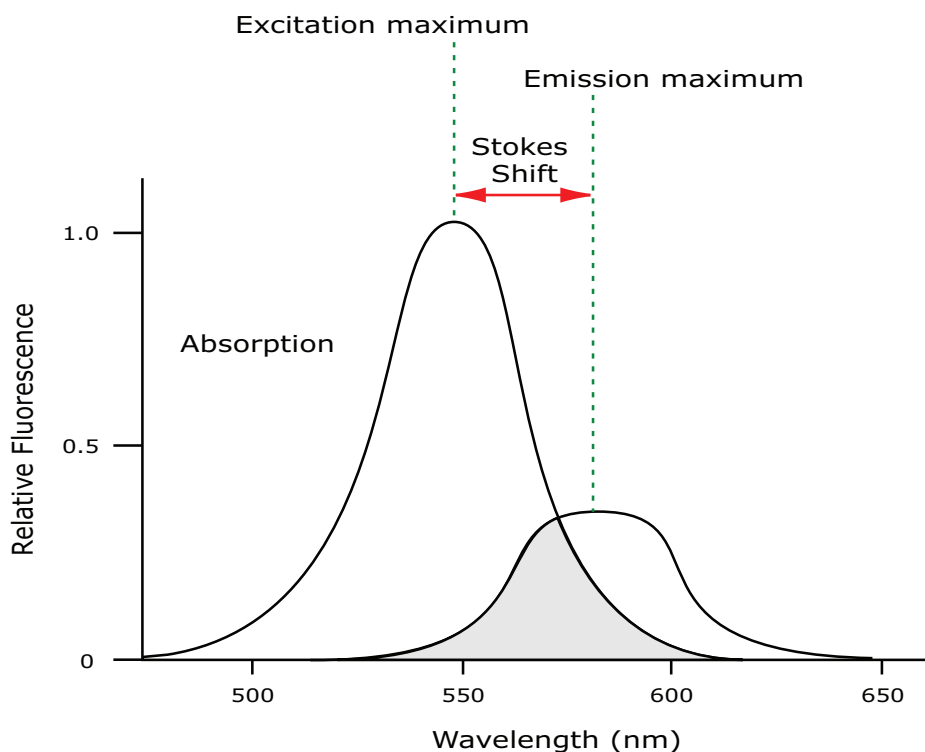


Figure 5-2: Excitation and Emission Spectra

Because the intensity of the excitation light is usually many tens of thousands of times greater than that of the emitted light, you must have sufficient spectral separation to reduce the interference of the excitation light with detection of the emitted light.

* **Tip:** If the Stokes shift is small, you should choose an excitation wavelength that is as far away from the emission maximum as possible while still being capable of stimulating the fluorophore so that less of the excited light overlaps the emission spectrum, permitting better selection and quantitation of the emitted light.

The **Spectral Optimization Wizard** in the SoftMax Pro Software provides the best settings for maximizing the signal to background window, $(S-B)/B$, while minimizing the optimization time. You can use this wizard with the SpectraMax i3x Multi-Mode Detection Platform or with a Tunable Wavelength (TUNE) Detection Cartridge installed in the SpectraMax Paradigm Multi-Mode Microplate Reader. See [Spectral Optimization on page 348](#).

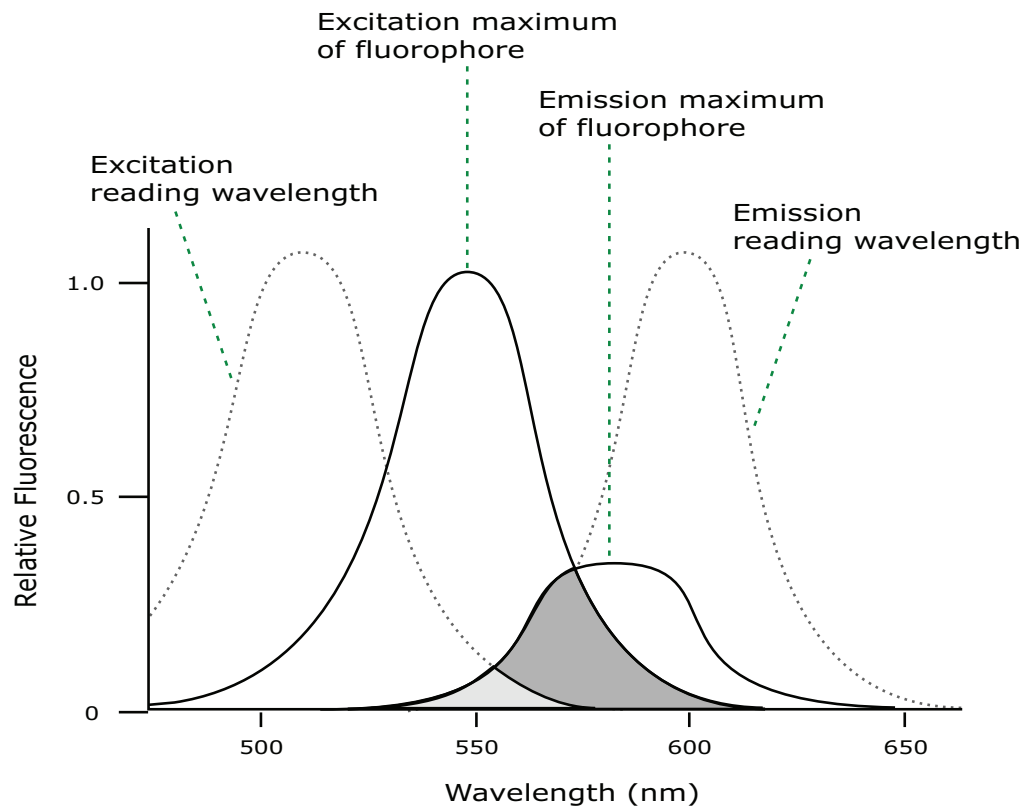


Figure 5-3: Optimized Excitation and Emission Reading Wavelengths

The previous figure shows that the best results are often obtained when the excitation and emission wavelengths used for reading are not the same as the peak wavelengths of the excitation and emission spectra of the fluorophore. When the reading wavelengths for excitation and emission are separated, a smaller quantity of excitation light passes through to the emission monochromator (gray area) and on to the PMT, resulting in a purer emission signal and more accurate data.

The instrument permits scanning of both excitation and emission wavelengths, using separate tunable dual monochromators. One benefit of scanning emission spectra is that you can determine more accurately whether the emission is, in fact, the expected fluorophore, or multiple fluorophores, and not one generated by a variety of background sources or by contaminants. One more benefit is that you can find excitation and emission wavelengths that prevent interference when interfering fluorescent species are present.

For this reason, it is desirable to scan emission for both an intermediate concentration of labeled sample, as well as the background of unlabeled sample. The optimal setting is where the ratio of the sample emission to background emission is at the maximum.

Fluorescence intensity data is dependent on a number of variables. See [Analyzing Fluorescence Intensity Data on page 164](#).

Applications of Fluorescence Intensity

Fluorescence intensity is used widely in applications such as fluorescent ELISAs, protein assays, nucleic acid quantitation, reporter gene assays, cell viability, cell proliferation, and cytotoxicity. One more major application of this mode is to study the kinetics of ion release.

Some assays use a fluorescent label to selectively attach to certain compounds. The quantity or concentration of the compound can then be quantified by measuring the fluorescence intensity of the label, which is attached to the compound. Such methods are often used to quantify low concentrations of DNA or RNA, for example.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a fluorescence intensity mode protocol, see [Creating a Fluorescence Intensity Mode Protocol on page 314](#).

Fluorescence Intensity Instruments and Detection Cartridges

The following instruments have fluorescence intensity read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M3 Multi-Mode Microplate Reader, see page 208](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [Gemini XPS Microplate Reader, see page 211](#)
- [Gemini EM Microplate Reader, see page 211](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader, see page 214](#)

The following detection cartridges have fluorescence intensity read mode capability:

- [Tunable Wavelength \(TUNE\) Detection Cartridge, see page 220](#)
- [Multi-Mode \(MULTI\) Detection Cartridge, see page 221](#)
- [Fluorescence Intensity \(FI\) Detection Cartridges, see page 225](#)
- [Fluorescence Intensity \(FI\) GeneBLAzer Detection Cartridge, see page 226](#)
- [Fluorescence Intensity Dual Label \(FI-DL\) \(MultiTox-Fluor\) Detection Cartridge, see page 228](#)



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

Fluorescence Intensity Reads with Injectors

Injectors in a microplate reader are used to automatically deliver a specified volume of a reagent to the wells of a microplate. They are generally used when delivery of the reagent initiates a reaction that occurs rapidly and results in a luminescent or fluorescent signal that must be detected quickly.

The SpectraMax i3x Instrument with the Injector Cartridge installed can be set up to inject and read well by well to reduce signal loss.

Common inject-and-read assays include calcium flux assays.

Analyzing Fluorescence Intensity Data

Fluorescence intensity data is dependent on a number of variables. Raw data is compared to a standard curve with known concentrations of a reference label.

A standard curve consists of, at a minimum, a blank sample and a reference standard sample of known concentration. The raw data can then be expressed in equivalent concentration of a reference label.

Analyzing and validating fluorescence intensity data generally consists of the following:

- [Background Correction and Quantification on page 164](#)
- [Detection Limit on page 165](#)
- [Linearity and the Linear Dynamic Range on page 165](#)

Background Correction and Quantification

A blank well contains everything used with the sample wells except the label and sample-specific compounds. Do not use an empty well for a blank.

The blank sample reveals the offset underlying each data sample. This offset does not carry information on the label, and is generally subtracted before data reduction is done.

The blank-subtracted raw data are proportional to the quantity of label in a sample such that the label concentration is quantified by the following equation.

$$\text{conc}_{\text{label}} = \frac{(\text{sample} - \text{blank})}{\frac{\text{std} - \text{blank}}{\text{conc}_{\text{std}}}}$$

where conc_{std} is the concentration of the *standard*, and *sample*, *blank*, and *standard* are average values of replicates for the sample, blank, and standard wells. In the general case where the standard curve covers a concentration range of more than a few linear logs, $(\text{standard} - \text{blank}) / \text{conc}_{\text{std}}$ is equivalent to the slope of the standard curve, and so the concentration of the label is determined by $(\text{sample} - \text{blank}) / (\text{slope of standard curve})$.

For optimal results, Molecular Devices recommends that you run replicates for all blanks, controls, and samples. In this case, the blank value that can be subtracted is the average value of all blanks.

Detection Limit

The detection limit is the smallest sample concentration that can be measured reliably above the blank. Determining the detection limit requires taking a number of blank measurements and calculating an average value and standard deviation for the blanks. The detection threshold is defined as the average blank plus three standard deviations. If the average sample value measures above the threshold, the sample can be detected at a statistically significant level.

The detection limit can be described by the following equation:

$$\text{Det Limit} = \frac{3 \text{ Stdev}_{\text{blank}}}{\frac{\text{std} - \text{blank}}{\text{conc}_{\text{std}}}}$$

where conc_{std} is the concentration of the standard, $\text{StDev}_{\text{Blank}}$ is the standard deviation of the blank replicates, and blank and Std are average values of the replicates for the blank and standard wells.

Determining the detection limit for an assay requires multiple blanks to calculate their standard deviation.

Linearity and the Linear Dynamic Range

Within a wide range at moderately high concentrations, blanked raw data is proportional to the quantity of label in a sample.

The linear dynamic range (LDR) is defined by:

$$\text{LDR} = \log_{10} \left(\frac{\text{max conc lin}}{\text{detection limit}} \right)$$

where LDR is expressed as a log, and max conc lin is the highest concentration in the linear range that can be quantified.

When the standard curve after blank reduction is not linear in concentration at the lower end, there might be an incorrect or contaminated blank.

Luminescence Read Mode

In luminescence read mode, no excitation is necessary as the species being measured emit light naturally. For this reason, the lamp does not flash, so no background excitation interference occurs.

In the Luminescence (LUM) read mode, the instrument provides measurements in Relative Luminescence Units (RLUs).

Luminescence is the emission of light by processes that derive energy from essentially non-thermal changes, the motion of subatomic particles, or the excitation of an atomic system by radiation. Luminescence detection relies on the production of light from a chemical reaction in a sample.

To help eliminate background luminescence from a microplate that has been exposed to light, Molecular Devices recommends dark adaptation of the microplate by placing the sample-loaded microplate in the instrument for several minutes before starting the read.

For some monochromator-based instruments, the default setting for luminescence is the “zero order” position where the grating monochromator acts as a mirror that reflects all light to the PMT detector.

The SpectraMax i3x Instrument bypasses the emission monochromator for luminescence reads that detect all wavelengths.

If wavelength selection is desired, you can choose the wavelength where peak emission is expected to occur. Also, multiple wavelength choices let species with multiple components be differentiated and measured easily.

Luminescence can be read from the top or the bottom of a microplate. Solid white microplates or white microplates with clear bottoms are recommended for luminescence reads.

Concentrations or qualitative results are derived from raw data with a standard curve or by comparison with reference controls. See [Analyzing Luminescence Data on page 168](#).

Applications of Luminescence

Chemiluminescent or bioluminescent reactions can be induced to measure the quantity of a particular compound in a sample. Examples of luminescent assays include the following:

- Reporter gene assays (the measurement of luciferase gene expression)
- Quantitation of adenosine triphosphate (ATP) as an indication of cell counts with cell-proliferation, cytotoxicity, and biomass assays
- Enzyme measurements with luminescent substrates, such as immunoassays

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a luminescence mode protocol, see [Creating a Luminescence Mode Protocol on page 322](#).

Luminescence Instruments and Detection Cartridges

The following instruments have luminescence read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M3 Multi-Mode Microplate Reader, see page 208](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [Gemini XPS Microplate Reader, see page 211](#)
- [Gemini EM Microplate Reader, see page 211](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader, see page 214](#)

The following detection cartridges have luminescence read mode capability:

- [Tunable Wavelength \(TUNE\) Detection Cartridge, see page 220](#)
- [Multi-Mode \(MULTI\) Detection Cartridge, see page 221](#)
- [Glow Luminescence \(LUM\) Detection Cartridges, see page 227](#)
- [Dual Color Luminescence \(LUM\) \(BRET2\) Detection Cartridge, see page 230](#)
- [Dual Color Luminescence \(LUM\) \(Chroma-Glo\) Detection Cartridge, see page 231](#)



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

Luminescence Reads with Injectors

Injectors in a microplate reader are used to automatically deliver a specified volume of a reagent to the wells of a microplate. They are generally used when delivery of the reagent initiates a reaction that occurs rapidly and results in a luminescent or fluorescent signal that must be detected quickly.

The SpectraMax i3x Instrument with the Injector Cartridge installed can be set up to inject and read well by well to reduce signal loss.

Common inject-and-read assays include luciferase reporter assays.

The Injector Cartridge is DLReady™ certified by Promega for the Dual-Luciferase Reporter (DLR™) assay system.



DLReady, DLR, and the DLReady logo are trademarks of Promega Corporation.

Analyzing Luminescence Data

The conversion rate of photons to counts is individual for each reader. Therefore, raw data from the same plate can seem significantly different from one instrument to the next. Also, the data format used by other manufacturers might not be counts per second and can be different by several orders of magnitude. It is important to know that the number of counts and the size of figures is in no way an indication of sensitivity. See [Detection Limit on page 169](#).

Concentrations or qualitative results are derived from raw data with a standard curve or by comparison with reference controls. A standard curve consists of, at a minimum, a blank sample and a reference standard sample of known concentration. The raw data can then be expressed in equivalent concentration of a reference label. The raw data is normalized to counts per second by dividing the number of counts by the read time per well.

Analyzing and validating luminescence data generally consists of the following:

- [Background Correction on page 168](#)
- [Detection Limit on page 169](#)
- [Sample Volumes and Concentration of Reactants on page 169](#)
- [Data Optimization on page 170](#)

Background Correction

The light detected in a luminescent measurement generally has two components: specific light from the luminescent reaction and an approximately constant level of background light caused by various factors, including the plate material and impurities in the reagents. The background can be effectively measured using blank replicates. Blanks should include the luminescent substrate (chemical energy source) but not the luminescence agent (generally an enzymatic group which makes the substrate glow).

A blank well contains everything used with the sample wells except the label and sample-specific compounds. Do not use an empty well for a blank.

The blank sample reveals the offset underlying each data sample. This offset does not carry information on the label, and is generally subtracted before data reduction is done.

For optimal results, Molecular Devices recommends that you run replicates for all blanks, controls, and samples. In this case, the blank value that can be subtracted is the average value of all blanks.

To help eliminate background luminescence from a microplate that has been exposed to light, Molecular Devices recommends dark adaptation of the microplate by placing the sample-loaded microplate in the instrument for several minutes before starting the read.

Detection Limit

The detection limit is the smallest sample concentration that can be measured reliably above the blank. Determining the detection limit requires taking a number of blank measurements and calculating an average value and standard deviation for the blanks. The detection threshold is defined as the average blank plus three standard deviations. If the average sample value measures above the threshold, the sample can be detected at a statistically significant level.

The detection limit can be described by the following equation:

$$\text{Det Limit} = \frac{3 \text{ Stdev}_{\text{blank}}}{\frac{\text{std} - \text{blank}}{\text{conc}_{\text{std}}}}$$

where conc_{std} is the concentration of the standard, $\text{StDev}_{\text{Blank}}$ is the standard deviation of the blank replicates, and blank and Std are average values of the replicates for the blank and standard wells.

Determining the detection limit for an assay requires multiple blanks to calculate their standard deviation.

Sample Volumes and Concentration of Reactants

The concentration of the luminescent agent impacts the quantity of light output in a luminescent reaction. Light is emitted as a result of a reaction between two or more compounds. Therefore, the quantity of light output is proportional to the quantity of the limiting reagent in the sample.

For example, in an ATP/luciferin-luciferase system, when total volume is held constant and ATP is the limiting reagent, the blanked light output is proportional to the concentration of ATP in the sample, at very high concentrations of ATP. Substrate can be used up and become rate-limiting, providing it is the rate-limiting component. In this case, the non-linearity is an effect of the assay and not caused by the microplate reader.



Note: Very bright samples can exceed the linear dynamic range of the instrument. If so, reading can be done using an attenuation filter.

Data Optimization

The measurement noise is dependent on the read time per sample (time per plate or time per well). In particular, the detection limit improves when the read time is increased. Therefore, it is important to specify the read time when comparing measurements.

All low-light-level detection devices have some measurement noise in common. To average out the measurement noise, optimization of the time per well involves accumulating as many counts as possible. Within some range, you can reduce noise (CVs, detection limit) by increasing the read time per well, as far as is acceptable from throughput and sample stability considerations.

Z' is the standard statistical parameter in the high-throughput screening community for measuring the quality of a screening assay independent of test compounds. It is used as a measure of the signal separation between the positive controls and the negative controls in an assay.

The value of Z' can be determined using the following formula:

$$Z' = 1 - \frac{3(SD_{c+}) + 3(SD_{c-})}{|Mean_{c+} - Mean_{c-}|}$$

where **SD** is the standard deviation, **c+** is the positive control, and **c-** is the negative control.

A Z' value greater than or equal to 0.4 is the generally acceptable minimum for an assay. Higher values might be desired when results are more critical.

Z' is not linear and can be made unrealistically small by outliers that skew the standard deviations in either population. To improve the Z' value, you can increase the quantity of label in the sample, if acceptable for the assay, or increase the read time per well.

Time-Resolved Fluorescence Read Mode

Time-resolved fluorescence (TRF) is a measurement technique that depends on three characteristics that lead to better discrimination between the specific signal, proportional to the quantity of label, and the unspecific fluorescence resulting from background and compound interference:

- Pulsed excitation light sources
- Time-gated electronics faster than the fluorescence lifetime
- Labels with prolonged fluorescence lifetime

The time-gating electronics introduce a delay between the cut off of each light pulse and the start of signal collection. During the delay, the unspecific fluorescence (caused by test compounds, assay reagents, and the microplate) vanishes while only a small portion of the specific fluorescence from the label is sacrificed. Enough of the specific signal remains during the decay period with the added benefit of reduced background.

In Time-Resolved Fluorescence read mode, the instrument detects the extremely long emission half-lives of rare earth elements called lanthanides such as europium (lifetime of about 700 μ s), samarium (lifetime of about 70 μ s), or terbium (lifetime of about 1000 μ s).

Applications of Time-Resolved Fluorescence

Time-resolved fluorescence (TRF) is widely used in high throughput screening applications such as kinase assays, and is useful in some fluorescence immunoassays, such as DELFIA (dissociation-enhanced enzyme linked fluorescence immunoassay). TRF is also useful in some assay variants of TR-FRET (time-resolved fluorescence resonance energy transfer) in which the FRET acceptor label acts as a quencher only and does not emit fluorescence. The proximity between donor label and acceptor (quencher) is then quantified by the intensity decrease of the donor label.

DELFIA requires washing steps as in an ELISA, but the TR-FRET assay involving quenching is a homogeneous microplate assay technique and requires only mixing and measuring—no wash steps are required. It can also be miniaturized, which makes it useful for high-throughput screening applications.

The Cisbio Bioassays HTRF (Homogeneous Time-Resolved Fluorescence) technology is a proprietary time-resolved fluorescence technology that overcomes many of the drawbacks of standard Fluorescence Resonance Energy Transfer (FRET) techniques, such as the requirements to correct for autofluorescence and the fluorescent contributions of unbound fluorophores. See [HTRF Read Mode on page 179](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a time-resolved fluorescence mode protocol, see [Creating a Time-Resolved Fluorescence Mode Protocol on page 324](#).

Time-Resolved Fluorescence Instruments and Detection Cartridges

The following instruments have time-resolved fluorescence read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
The SpectraMax i3x Instrument requires detection cartridges to do time-resolved fluorescence reads.
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [Gemini XPS Microplate Reader, see page 211](#)
- [Gemini EM Microplate Reader, see page 211](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)

The following detection cartridges have time-resolved fluorescence read mode capability:

- [Tunable Wavelength \(TUNE\) Detection Cartridge, see page 220](#)
- [Multi-Mode \(MULTI\) Detection Cartridge, see page 221](#)
- [Cisbio HTRF Detection Cartridge on page 223](#)
- [Time Resolved Fluorescence \(TRF-EUSA\) Detection Cartridge, see page 224](#)



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

Analyzing Time-Resolved Fluorescence Data

A time-resolved fluorescence (TRF) measurement includes a number of pulses. Each pulse consists of turning the light source on and off (Excitation Time), pausing for a specified length of time (Measurement Delay), and measuring the fluorescence intensity of the sample for a specified length of time (Integration Time). These pulses are repeated several times, as specified in the protocol parameters.

Analyzing and interpreting TRF data generally consists of the following:

- [Blank Correction on page 173](#)
- [Data Normalization on page 173](#)
- [Data Optimization on page 174](#)

Blank Correction

Although background is significantly lower than with fluorescence intensity measurements, Molecular Devices recommends that you use blanks or assay controls.

A blank well contains everything used with the sample wells except the label and sample-specific compounds. Do not use an empty well for a blank.

The blank sample reveals the offset underlying each data sample. This offset does not carry information on the label, and is generally subtracted before data reduction is done.

For optimal results, Molecular Devices recommends that you run replicates for all blanks, controls, and samples. In this case, the blank value that can be subtracted is the average value of all blanks.

Data Normalization

TRF raw data changes in magnitude when the timing parameters are changed. However, TRF data are normalized for a number of 1000 pulses. This means that the sample raw data does not change when only the number of pulses is changed.

When selecting a fast read mode, the raw data becomes slightly lower because during the continuous plate movement, some signal is collected under non-optimal focusing conditions.

Data Optimization

There are two timing parameters which can be optimized to adjust the performance of the measurement as desired: time per well and integration time per cycle.

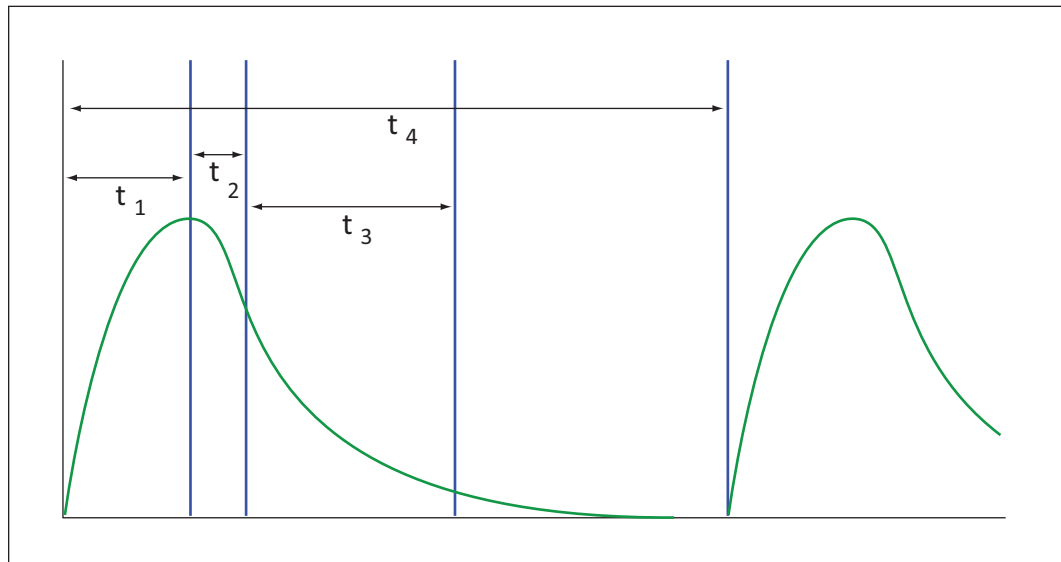
The measurement noise is dependent on the read time per sample (time per plate or time per well). In particular, the detection limit improves when the read time is increased. Therefore, it is important to specify the read time when comparing measurements. For TRF, the read time per well increases with the selected number of pulses. The time between pulses and the intensity of each pulse, however, can be different on various systems.

All low-light-level detection devices have some measurement noise in common. To average out the measurement noise, optimization of the time per well involves accumulating as many counts as possible. Within some range, you can reduce noise (CVs, detection limit) by increasing the read time per well, as far as is acceptable from throughput and sample stability considerations.

To further optimize measurement results, optimize the timing parameters. The following table and figure can be used as guidelines for the selection of timing parameters.

Table 5-1: Time-resolved fluorescence timing parameters example

Parameter	Value	Comment
Pulse length	0.100 ms	The period for excitation of the sample, shown as t_1 in the following figure. This is the suggested value for the TUNE, MULTI, and TRF detection cartridges.
Measurement delay	0.010 ms	The delay to ensure the excitation pulse is no longer detectable, shown as t_2 in the following figure. This is the suggested value for the TUNE, MULTI and TRF detection cartridges.
Integration time per cycle (pulse)	0.890 ms	The period for accumulating the signal, shown as t_3 in the following figure. This is the suggested value for the TUNE and MULTI detection cartridges.
Integration time per cycle (pulse)	1.890 ms	The period for accumulating the signal, shown as t_3 in the following figure. This is the suggested value for the TRF detection cartridge.

**Figure 5-4: Timing parameters for time-resolved fluorescence**

When neglecting the time delay t_2 compared to the integration time window t_3 , the accumulated signal A can be approximated with the following equation:

$$A / A_{\max} = (1 - \exp(-M)) \times 100\%$$

In the previous equation, M is the size of the time window (or integration time) divided by the exponential decay time constant (or the fluorescence lifetime of the label).

$$M = (\text{integration time}) / (\text{fluorescence lifetime})$$

For example, using Europium, which has a fluorescence lifetime of 700 μs , and the suggested integration time per cycle of 1.890 ms (or 1890 μs), $M = 1890 / 700 = 2.7$. Inserting this value of M into the first equation yields $A / A_{\max} = 93\%$.

To optimize the integration time per cycle (pulse), the integration time should be set such that the value of M produces the desired signal. For example, to get more than 86% signal, select an integration time such that M is greater than 2.0. Using the previous Europium example and solving for the integration time, the integration time can be set to M (2.0) times the fluorescence lifetime (700 μs), or 1400 μs (1.4 ms).

Table 5-2: Achievable accumulated signal percentage compared to M

M	0.25	0.50	0.75	1.00	1.25	1.50	2.00	3.00
A / A_{max}[%]	22	39	53	63	71	78	86	95

M can be technically limited by the time between pulses. Further gain in signal above some value of M can be negligible to improve results.

When performing a dual-label Europium-Samarium measurement, there are more timing parameters. There is some residual cross-talk of the Samarium signal captured in the Europium emission channel. Samarium has a much shorter fluorescence lifetime, so to reduce the cross-talk of Samarium in the Europium channel, Europium is measured in a time window shifted away from the time window for Samarium. This lets the Europium be quantified without cross contamination from the Samarium. The known Europium concentration can then be used to remove the Europium cross-contamination in the Samarium channel.

Suggested timing parameters for a dual-label Europium-Samarium measurement are listed in the following table.

Table 5-3: Time-resolved fluorescence timing parameters for dual-label Europium-Samarium

Parameter	Value	Comment
Pulse length	0.100 ms	The time interval for flash monitoring This is the suggested value for the TRF detection cartridge.
Measurement delay (first window)	0.010 ms	The delay to ensure the excitation pulse is no longer detectable This is the suggested value for the TRF detection cartridge.
Integration time (first window)	0.100 ms	The period for accumulating the Samarium signal This is the suggested value for the TRF detection cartridge.
Measurement delay (second window)	0.140 ms	The read out of the Samarium signal This is the suggested value for the TRF detection cartridge.
Integration time (second window)	0.750 ms	The period for accumulating the Europium signal This is the suggested value for the TRF detection cartridge.

FRET Read Mode

Fluorescence resonance energy transfer (FRET) is a distance-dependent interaction between the electronic excited states of two dye molecules in which excitation is transferred from a donor molecule to an acceptor molecule *without emission of a photon*.

FRET relies on the distance-dependent transfer of energy from a donor molecule to an acceptor molecule. Due to its sensitivity to distance, FRET has been used to investigate molecular interactions. FRET is the radiationless transmission of energy from a donor molecule to an acceptor molecule. The donor molecule is the dye or chromophore that initially absorbs the energy and the acceptor is the chromophore to which the energy is subsequently transferred. This resonance interaction occurs over greater than interatomic distances, without conversion to thermal energy, and without a molecular collision. The transfer of energy leads to a reduction in the fluorescence intensity and excited state lifetime of the donor, and an increase in the emission intensity of the acceptor. A pair of molecules that interact in such a manner that FRET occurs is often referred to as a donor/acceptor pair.

While there are many factors that influence FRET, the primary conditions that need to be met for FRET to occur are relatively few:

- The donor and acceptor molecules must be in close proximity to each other.
- The absorption or excitation spectrum of the acceptor must overlap the fluorescence emission spectrum of the donor.

The degree to which they overlap is referred to as the spectral overlap integral (J).

- The donor and acceptor transition must be approximately parallel.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a FRET mode protocol, see [Creating a FRET Mode Protocol on page 327](#).

FRET Instruments and Detection Cartridges

The following instruments have FRET read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
To do HTRF reads, the SpectraMax i3x Instrument requires the [Cisbio HTRF Detection Cartridge, see page 223](#).
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
To do HTRF reads, the SpectraMax Paradigm Multi-Mode Microplate Reader requires the [Cisbio HTRF Detection Cartridge, see page 223](#).
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader on page 214](#)



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

HTRF Read Mode

Homogeneous time-resolved fluorescence (HTRF) is a measurement technique based on fluorescence resonance energy transfer (FRET) using the advantages of time-resolved fluorescence (TRF) reading.

Fluorescence resonance energy transfer (FRET) is a distance-dependent interaction between the electronic excited states of two dye molecules in which excitation is transferred from a donor molecule to an acceptor molecule *without emission of a photon*.

FRET relies on the distance-dependent transfer of energy from a donor molecule to an acceptor molecule. Due to its sensitivity to distance, FRET has been used to investigate molecular interactions. FRET is the radiationless transmission of energy from a donor molecule to an acceptor molecule. The donor molecule is the dye or chromophore that initially absorbs the energy and the acceptor is the chromophore to which the energy is subsequently transferred. This resonance interaction occurs over greater than interatomic distances, without conversion to thermal energy, and without a molecular collision. The transfer of energy leads to a reduction in the fluorescence intensity and excited state lifetime of the donor, and an increase in the emission intensity of the acceptor. A pair of molecules that interact in such a manner that FRET occurs is often referred to as a donor/acceptor pair.

While there are many factors that influence FRET, the primary conditions that need to be met for FRET to occur are relatively few:

- The donor and acceptor molecules must be in close proximity to each other.
- The absorption or excitation spectrum of the acceptor must overlap the fluorescence emission spectrum of the donor.
The degree to which they overlap is referred to as the spectral overlap integral (J).
- The donor and acceptor transition must be approximately parallel.

HTRF uses a donor fluorophore with a long fluorescence lifetime, such as Europium. The acceptor fluorophore acts as if it also has a long fluorescence lifetime. This lets the time-gating principle of time-resolved fluorescence be applied to the acceptor emission to separate specific signal from background and signal caused by compound interference.

Time-gating electronics introduce a delay between the flashes and the start of signal collection. During the delay, the unspecific fluorescence caused by test compounds, assay reagents, and the microplate vanishes while only a small portion of the specific fluorescence from the acceptor fluorophore is sacrificed. Enough of the specific signal remains, with the benefit of reduced background.

Applications of Homogeneous Time-Resolved Fluorescence

Homogeneous time-resolved fluorescence (HTRF) is used in competitive assays to quantify the binding between two labeled molecules, or the disintegration of a bound complex. Binding partners can have similar molecular weights as opposed to fluorescence polarization read modes. HTRF is a homogeneous assay that requires only mixing and measuring—no wash steps are required. It can also be miniaturized, which makes it useful for high-throughput screening applications.

The fluorescence ratio related to the HTRF readout is a correction method developed by Cisbio, for which Cisbio has granted a license to Molecular Devices. Its application is strictly limited to the use of HTRF reagents and technology, excluding other TR-FRET technologies such as IMAP TR-FRET calculations of acceptor to donor ratios.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

HTRF Instruments and Detection Cartridges

The following instruments have HTRF read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
To do HTRF reads, the SpectraMax i3x Instrument requires the [Cisbio HTRF Detection Cartridge, see page 223](#).
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
To do HTRF reads, the SpectraMax Paradigm Multi-Mode Microplate Reader requires the [Cisbio HTRF Detection Cartridge, see page 223](#).



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

HTRF is a registered trademark of Cisbio Bioassays.

Analyzing HTRF Data

A Homogeneous Time-Resolved Fluorescence (HTRF) measurement includes a number of flash intervals. Each flash interval consists of flashing the lamp, pausing for a specified length of time, and measuring the fluorescence intensity of the sample. These flash intervals are repeated several times, as specified in the protocol parameters. See [Data Optimization on page 182](#).

Analyzing and interpreting HTRF data generally consists of the following:

- [Data Reduction on page 182](#)
- [Data Optimization on page 182](#)

Data Reduction

Data reduction for HTRF reads consists of two steps.

First, a ratio of the signal measured by the emission from the acceptor label at 665 nm to the signal measured by the emission of the donor label at 616 nm is calculated and multiplied by a factor of 10,000. This generates what is called the HTRF ratio.

In the second step, ratios are calculated that represent the relative change in the HTRF signal compared to that of the assay background, represented by assay controls potentially named negative or Standard 0. This relative response ratio is called the Delta F and is formatted as a percentage, although values greater than 100 can be generated.

Data Optimization

The measurement noise is dependent on the read time per sample (time per plate or time per well). In particular, the detection limit improves when the read time is increased. Therefore, it is important to specify the read time when comparing measurements. For TRF, the read time per well increases with the selected number of pulses. The time between pulses, however, can be different on various systems.

Table 5-4: HTRF timing parameters example

Parameter	Value	Comment
Number of pulses	30	The number of flashes per read.
Measurement delay	30 μ s	The delay to ensure the excitation pulse is no longer detectable.
Integration time per cycle (pulse)	400 μ s	The period for accumulating the signal.

Defining the number of flashes (pulses) cannot be used for comparative purposes because the flash and intensity rate varies from system to system.

There are two timing parameters which can be optimized to adjust the performance of the measurement as desired: time per plate or time per well, and integration time per cycle.

All low-light-level detection devices have some measurement noise in common. To average out the measurement noise, optimization of the time per well involves accumulating as many counts as possible. Within some range, you can reduce noise (CVs, detection limit) by increasing the read time per well, as far as is acceptable from throughput and sample stability considerations.

As the number of flashes (read time per well) is increased, several aspects of the data improve:

- Delta F values show less variability (better CVs).
- Small Delta F values are better distinguished from noise.
- Noise of background is reduced.

The second timing parameter which can be optimized is the Integration time per cycle. Care must be taken in optimizing the integration time to consider noise. Delta F is higher at low integration times, but noise is also high at low integration times. The optimal integration time is where noise is minimized while maximizing Delta F.

In the following example, the optimal integration time (read time per cycle) is displayed to be in the 500 μs to 1000 μs range, as noise is minimized and Delta F is still relatively high. Going greater than 1000 μs shows a sharp decline in Delta F without apparent improvement in noise.

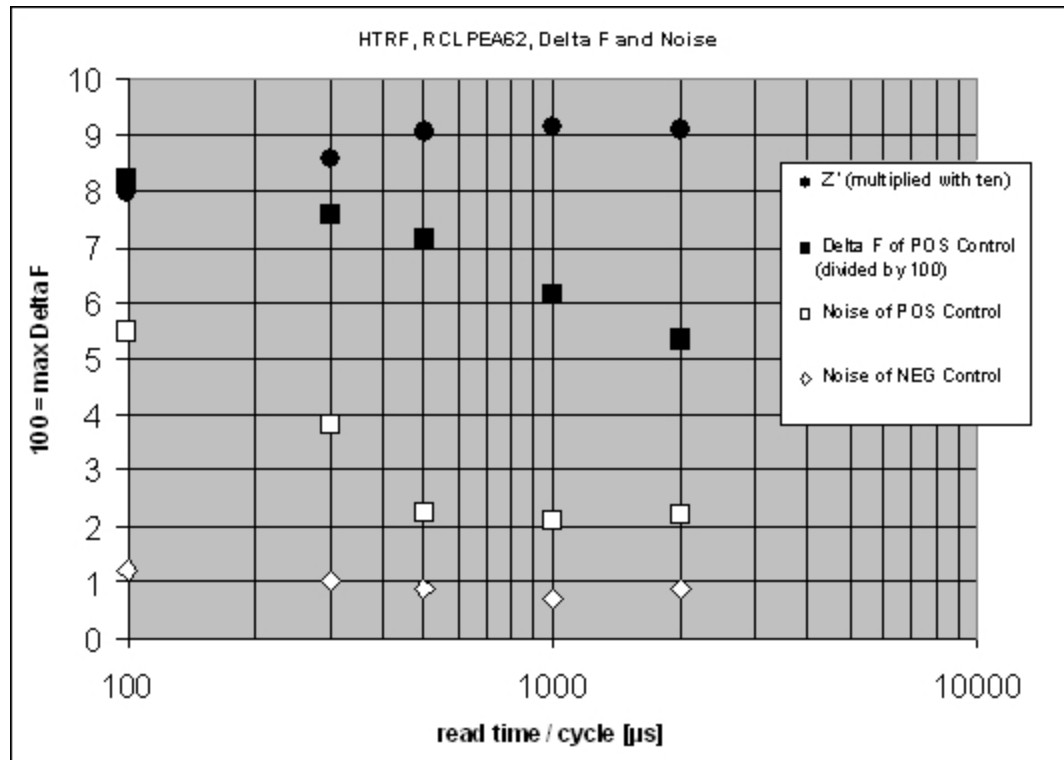


Figure 5-5: Relationship Between Integration Time, Noise, and Delta F

Z' is the standard statistical parameter in the high-throughput screening community for measuring the quality of a screening assay independent of test compounds. It is used as a measure of the signal separation between the positive controls and the negative controls in an assay.

The value of Z' can be determined using the following formula:

$$Z' = 1 - \frac{3(SD_{c+}) + 3(SD_{c-})}{|Mean_{c+} - Mean_{c-}|}$$

where **SD** is the standard deviation, **c+** is the positive control, and **c-** is the negative control.

A Z' value greater than or equal to 0.4 is the generally acceptable minimum for an assay.

Higher values might be desired when results are more critical.

Z' is not linear and can be made unrealistically small by outliers that skew the standard deviations in either population. To improve the Z' value, you can increase the quantity of label in the sample, if acceptable for the assay, or increase the read time per well.

Fluorescence Polarization Read Mode

Fluorescence polarization (FP) mode measures the relative change of polarization of emitted fluorescent compared to excitation light.

Fluorescence polarization detection is similar to fluorescence intensity, with the important difference that it uses plane-polarized light, rather than non-polarized light. Plate readers measure FP of the sample by detecting light emitted both parallel and perpendicular to the plane of excitation.

By using a fluorescent dye to label a small molecule, its binding to a different molecule of equal or greater size can be monitored through its speed of rotation.

When molecules are excited with polarized light, the polarization of the emitted light depends on the size of the molecule to which the fluorophore is bound. Larger molecules emit a higher percentage of polarized light, while smaller molecules emit a lower percentage of polarized light because of their rapid molecular movement. For this reason FP is generally used for molecular binding assays in high-throughput screening (HTS).

Fluorescence polarization mode returns two sets of data: one for fluorescence intensity parallel (P) to the excitation plane, and the other for fluorescence intensity perpendicular (S) to the excitation plane. These S and P values are used to calculate the Polarization (mP) and Anisotropy (r) values in the SoftMax Pro Software.

The Fluorescence Polarization data for a sample is evaluated based on its relative position between the low and high control values. See [Analyzing Fluorescence Polarization Data on page 186](#).

Applications of Fluorescence Polarization

Fluorescence polarization measurements provide information on molecular orientation and mobility, and are generally used to quantify the success of a binding reaction between a smaller labeled ligand and a binding site at a much larger or immobilized molecule. FP can also be used to quantify the dissociation or cleavage of the labeled ligand from a binding site.

FP is a homogeneous microplate assay technique and requires only mixing and measuring—no wash steps are required as in an ELISA. It can also be miniaturized, which makes it useful for high-throughput screening applications.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a fluorescence polarization mode protocol, see [Creating a Fluorescence Polarization Mode Protocol on page 329](#).

Fluorescence Polarization Instruments and Detection Cartridges

The following instruments have fluorescence polarization read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
To do fluorescence polarization reads, the SpectraMax i3x Instrument requires a [Fluorescence Polarization \(FP\) Detection Cartridges, see page 229](#).
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
To do fluorescence polarization reads, the SpectraMax Paradigm Multi-Mode Microplate Reader requires a [Fluorescence Polarization \(FP\) Detection Cartridges, see page 229](#).
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

Analyzing Fluorescence Polarization Data

Fluorescence polarization mode returns two sets of data: one for fluorescence intensity parallel (P) to the excitation plane, and the other for fluorescence intensity perpendicular (S) to the excitation plane. These S and P values are used to calculate the Polarization (mP) and Anisotropy (r) values in the SoftMax Pro Software.

FP assays in microplates are generally designed with two control samples:

- LOW control sample: minimal polarization value resulting from unbound labeled ligand only
- HIGH control sample: maximum polarization value resulting from bound labeled ligand only

The FP data for a sample is evaluated based on its relative position between the low and high control values. Total intensity can also be determined from the raw data and is proportional to the quantity of label in a sample.

Analyzing and interpreting fluorescence polarization data generally consists of the following:

- [Blank Correction on page 187](#)
- [Data Reduction on page 187](#)
- [Data Qualification and Validation on page 188](#)

Blank Correction

Many fluorescence polarization assays use small fluorescent label concentrations in the lower nm range. In this range, blank controls become significant when compared to samples.

A blank well contains everything used with the sample wells except the label and sample-specific compounds. Do not use an empty well for a blank.

Background wells, containing all assay components minus the fluorophore, should be tested. If the signal in the background wells is more than 1/10 the signal in the wells containing fluorophore, then background wells should be run on each assay plate. The average raw signal from the background's parallel and perpendicular readings must be subtracted from the raw parallel and perpendicular readings of each sample well before the mP calculation is done.

For optimal results, Molecular Devices recommends that you run replicates for all blanks, controls, and samples. In this case, the blank value that can be subtracted is the average value of all blanks.

Data Reduction

Fluorescence polarization mode returns two sets of data: one for fluorescence intensity parallel (P) to the excitation plane, and the other for fluorescence intensity perpendicular (S) to the excitation plane. These S and P values are used to calculate the Polarization (mP) and Anisotropy (r) values in the SoftMax Pro Software.

Although the raw S and P values are the true actual values returned from the instrument, the calculated Polarization (mP) and Anisotropy (r) values are treated as the raw data and become the basis for further reduction calculations.

Polarization (mP) is calculated as follows:

$$mP = 1000 * \frac{(\text{parallel} - (G * \text{perpendicular}))}{(\text{parallel} + (G * \text{perpendicular}))}$$

Anisotropy (r) is calculated as follows:

$$r = \frac{(\text{parallel} - (G * \text{perpendicular}))}{(\text{parallel} + (2G * \text{perpendicular}))}$$

The G factor, or grating factor, is used in fluorescence polarization to correct polarization data for optical artifacts, converting relative mP data to theoretical mP data. Optical systems, particularly with reflective components, pass light of different polarization with different efficiency. G factor corrects this instrumental bias.

Data Qualification and Validation

When validating the data of a fluorescence polarization measurement and the assay, the two factors to look at are the precision value and the Z' parameter.

The FP precision value is a measure of replicate uniformity determined by the standard deviation of replicates at a label concentration of 1 nM. Since the precision of a measured signal also depends on the read time, the read time must also be specified. A longer read time leads to a lower (better) precision value.

Z' is the standard statistical parameter in the high-throughput screening community for measuring the quality of a screening assay independent of test compounds. It is used as a measure of the signal separation between the positive controls and the negative controls in an assay.

The value of Z' can be determined using the following formula:

$$Z' = 1 - \frac{3(SD_{c+}) + 3(SD_{c-})}{|Mean_{c+} - Mean_{c-}|}$$

where **SD** is the standard deviation, **c+** is the positive control, and **c-** is the negative control.

A Z' value greater than or equal to 0.4 is the generally acceptable minimum for an assay. Higher values might be desired when results are more critical.

Z' is not linear and can be made unrealistically small by outliers that skew the standard deviations in either population. To improve the Z' value, you can increase the quantity of label in the sample, if acceptable for the assay, or increase the read time per well.

The assay window is dependent on the fluorophore lifetime and relative size of the receptor to the ligand. Precision values are better (lower) at higher signals, which normally come from higher label concentrations.

For a given assay window, Z' is a downward sloping linear function. That is, as precision values get higher (worse), the Z' value gets lower (worse).

Precision is dependent upon assay characteristics (sample volume, label concentration) and read time. In many assays, the characteristics are defined and cannot be changed. In this case, the only way to improve precision is to increase the read time per well.

AlphaScreen Read Mode

ALPHA stands for Amplified Luminescent Proximity Homogeneous Assay. AlphaScreen® is a bead-based chemistry used to study molecular interactions between moieties A and B, for example. When a biological interaction between A and B moves beads (coated with A and B, respectively) together, a cascade of chemical reactions produce a greatly amplified signal.

The cascade finally resulting in signal is triggered by laser excitation (680 nm), making a photosensitizer on the A-beads convert oxygen to an excited (singlet) state. That energized oxygen diffuses away from the A-bead. When reaching the B-bead in close proximity, it reacts with a thioxene derivative on the B-bead generating chemiluminescence at 370 nm. Energy transfer to a fluorescent dye on the same bead shifts the emission wavelength into the 520 nm to 620 nm range. The limited lifetime of singlet oxygen in solvent (~4 microseconds) lets diffusion reach up to only around 200 nm distance. Thus, only B-beads in the proximity of A-beads yield signal, which indicates binding between moieties A and B.

An AlphaScreen measurement includes a light pulse, by turning on the laser diode for a specified time, turning off the laser diode, followed by the measurement of the AlphaScreen signal, as specified in the measurement protocol timing parameters.



Note: AlphaScreen beads are light sensitive. Beads are best handled under subdued (<100 lux) or green filtered (Roscolux filters #389 from Rosco, or equivalent) light conditions. Do incubation steps in the dark.

The raw data can be normalized to counts per second. See [Analyzing AlphaScreen Data on page 191](#).

Applications of AlphaScreen

AlphaScreen reagent and assays are used for drug discovery purposes. Examples of AlphaScreen assays include:

- G-protein coupled receptor (GPCR) assay kits, for cAMP quantification or IP3 quantification.
- Tyrosine Kinase assays.
- Cytokine detection kits, such as TNF-alpha detection (immunoassay).

AlphaScreen read mode can also capture the Europium emission line of AlphaLISA®.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a fluorescence polarization mode protocol, see [Creating a Fluorescence Polarization Mode Protocol on page 329](#).

AlphaScreen Instruments and Detection Cartridges

The following instruments have AlphaScreen read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
To do AlphaScreen reads, the SpectraMax i3x Instrument requires [AlphaScreen Detection Cartridges](#), see [page 222](#).
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
To do AlphaScreen reads, the SpectraMax Paradigm Multi-Mode Microplate Reader requires [AlphaScreen Detection Cartridges](#), see [page 222](#).



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

For more information, go to www.perkinelmer.com.

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Analyzing AlphaScreen Data

The conversion rate of photons to counts and relative fluorescence units (RFU) is individual for each reader. Therefore, raw data from the same microplate can seem to be different from one instrument to the next. Also, the data format used by instrument manufacturers might be counts normalized per second or not normalized counts, and therefore the raw data can be different by several orders of magnitude. It is important to know that the number of counts and the size of figures is in no way an indication of sensitivity. See [Detection Limit on page 192](#).

The raw data can be normalized to counts per second by selecting the **Normalization** option in the **Settings** dialog. See [Creating a Protocol on page 235](#).

Analyzing and validating AlphaScreen data can consist of the following:

- [Background Correction on page 191](#)
- [Detection Limit on page 192](#)
- [Data Qualification and Validation on page 192](#)

Background Correction

Although background is significantly lower than with fluorescence intensity measurements, Molecular Devices recommends that you use blanks or assay controls for background correction. The background can be effectively measured using blank replicates. When reading a sample with small signal, an interference can occur from the afterglow of a very strong emitting adjacent sample that was measured just before. Such cross talk can occur through the wall of a white 384-well plate. To prevent such interference, you can select the **Interlaced Reading** option in the SoftMax Pro Software Settings dialog. This option reads only every other well in a checkerboard pattern, and then reads the microplate again to read the previously omitted wells.

A blank well contains everything used with the sample wells except the label and sample-specific compounds. Do not use an empty well for a blank.

For optimal results, Molecular Devices recommends that you run replicates for all blanks, controls, and samples. In this case, the blank value that can be subtracted is the average value of all blanks.

Detection Limit

The detection limit is the smallest sample concentration that can be measured reliably above the blank. Determining the detection limit requires taking a number of blank measurements and calculating an average value and standard deviation for the blanks. The detection threshold is defined as the average blank plus three standard deviations. If the average sample value measures above the threshold, the sample can be detected at a statistically significant level.

The detection limit can be described by the following equation:

$$\text{Det Limit} = \frac{3 \text{ Stdev}_{\text{blank}}}{\frac{\text{std} - \text{blank}}{\text{conc}_{\text{std}}}}$$

where conc_{std} is the concentration of the standard, $\text{StDev}_{\text{Blank}}$ is the standard deviation of the blank replicates, and blank and Std are average values of the replicates for the blank and standard wells.

Data Qualification and Validation

Z' is the standard statistical parameter in the high-throughput screening community for measuring the quality of a screening assay independent of test compounds. It is used as a measure of the signal separation between the positive controls and the negative controls in an assay.

The value of Z' can be determined using the following formula:

$$Z' = 1 - \frac{3(\text{SD}_{\text{c}^+}) + 3(\text{SD}_{\text{c}^-})}{|\text{Mean}_{\text{c}^+} - \text{Mean}_{\text{c}^-}|}$$

where **SD** is the standard deviation, **c+** is the positive control, and **c-** is the negative control. A Z' value greater than or equal to 0.4 is the generally acceptable minimum for an assay. Higher values might be desired when results are more critical.

Z' is not linear and can be made unrealistically small by outliers that skew the standard deviations in either population. To improve the Z' value, you can increase the quantity of label in the sample, if acceptable for the assay, or increase the read time per well.



CAUTION! The assay plate and the instrument should be kept at room temperature, since temperature variations cause fluctuations in signal.

Western Blot TRF Read Mode

Protein detection is an important task for pharmaceutical and clinical research, and Western Blots (WB), or protein immunoblots, are one of the most common methods employed for this purpose. Various techniques are used to detect proteins on Western Blot membranes including fluorescence, silver staining, and chemiluminescence. However, each technique has its limitations, and there is a continuous need to improve quantitation, accuracy, and dynamic range of Western Blots.

The Molecular Devices ScanLater™ Western Blot Assay Kit is a novel system for protein analysis that is incorporated into a SpectraMax® Paradigm® or SpectraMax® i3x Multi-Mode Detection Platform. Membranes are incubated with Eu-chelate labeled secondary antibodies or streptavidin that bind specifically to the target protein-specific primary antibody. Europium has a long fluorescence lifetime, on the order of 1 msec, and detection is done in Time Resolved Fluorescence (TRF) mode which significantly reduces background from auto-fluorescence or other sources of short lifetime emissions. The membranes are placed into a microplate reader where they are scanned with the ScanLater Western Blot (WB) Detection Cartridge.

The method does not involve enzyme detection, and the Eu-chelates are resistant to photo-bleaching, so the signal remains stable for long periods of time (weeks to months). This permits repeat reading of membranes and the potential for comparison of band intensities to known standards for more accurate quantitation.

The TRF detection employs photon counting, so the theoretical dynamic range is $>10^5$. In practice, however, dynamic range is limited by saturation of binding sites on high-abundant bands and non-specific binding to background membrane. There is also no camera blooming, as can occur with chemiluminescence or fluorescence detection, so the system gives sharp bands and excellent image quality.

The SpectraMax Western Blot system is a simple, sensitive, and stable platform that provides excellent Western Blot capability in a SpectraMax Paradigm or SpectraMax i3x Multi-Mode Detection Platform extending the uses of these essential laboratory instruments.

Applications

- Identify the nature of the protein or epitope effectively. Also, it can be used as a tool for quantitative analysis of protein.
- Use for chromatography components analysis, sucrose gradient analysis.
- Test the endogenous or exogenous expression of phosphoprotein so as to detect the phosphorylation signal.
- Protein resilience in the function experiment.
- Structure domain analysis.
- Analysis of the protein expression level.
- Analysis of protein content in the serum.
- Analysis of regulatory proteins expressed in the cell cycle.

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about setting up a Western Blot TRF mode protocol, see [Creating a Western Blot TRF Mode Protocol on page 333](#).

If you are using the SoftMax Pro GxP Software, you must enable the following permissions to complete a Western Blot membrane read:

- **Read empty plates/cuvettes** to start a read.
- **Save data files** to save the data file before the read.
- **Overwrite plate/cuvette data** to do a high-resolution ROI read.

See [Using SoftMax Pro GxP Software Features on page 467](#).

Western Blot TRF Instruments and Detection Cartridges

The following instruments have Western Blot TRF read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)
To do Western Blot TRF reads, the SpectraMax i3x Instrument requires the ScanLater Western Blot (WB) Detection Cartridge.
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
To do Western Blot TRF reads, the SpectraMax Paradigm Multi-Mode Microplate Reader requires the ScanLater Western Blot (WB) Detection Cartridge.

The ScanLater Western Blot (WB) Detection Cartridge can be used for top reads only.

Analyzing Western Blot TRF Data

After scanning a membrane for Western Blot data, the data are displayed in the SoftMax Pro Software as an image. You can use the image tools in the **Plate** section to zoom, crop, colorize, and adjust the intensity of the image. You can also select a region of interest (ROI) and rescan the membrane at a higher resolution. See [Viewing Western Blot Membrane Data on page 443](#).

Western Blot membrane data are saved as a TIFF image that can be analyzed by the image-analysis tool of your choice. The SoftMax Pro Software comes with an installed version of the ImageJ software from U.S. National Institute of Health (NIH). See [Analyzing a Western Blot Image on page 450](#).

For best results, use the Molecular Devices ScanLater™ Western Blot Assay Kit that matches your application.

To ensure successful acquisition of Western Blot data, see the following topics:

- [Blocking Nonspecific Binding on page 195](#)
- [Handling the Membrane on page 196](#)

Blocking Nonspecific Binding

To reduce noise, use blocking buffer to reduce non-specific protein from binding with the membrane.

No single-blocking reagent is optimal for every antigen-antibody pair. Some primary antibodies can exhibit greatly reduced signal or different nonspecific binding in different blocking solutions. If you have difficulty detecting your target protein, changing the blocking solution can dramatically improve the performance. If the primary antibody has worked well in the past using chemiluminescent detection, try that same blocking solution for detection. Other commonly used blocking buffers other than BSA are 3% casein and 5% non-fat milk.

Milk-based blockers can contain IgG that can crossreact with anti-goat antibodies. This can significantly increase background and reduce antibody titer. Milk-based blockers can also contain endogenous biotin or phosphoepitopes that can cause higher background.

To prevent background speckles on blots, use high-quality, ultra-pure water for buffers.

Do not over-block. Extended blocking times can cause loss of target protein from the membrane.

Handling the Membrane

To scan the membrane in a SpectraMax Paradigm or SpectraMax i3x Instrument, the membrane must be placed in a Molecular Devices ScanLater™ Membrane Holder. See [Loading the Membrane into the Membrane Holder on page 335](#).



Note: Handle membranes by their edges only, using clean forceps. Do not touch the membrane with gloved or bare hands.

The maximum size for a membrane is 109 mm x 77 mm to let it fit in the membrane holder.

The Western Blot should be prepared using standard blotting procedures for the membrane being used. For optimal results, use Millipore Immobilon FL (IPFL00010). If using PVDF, pre-wet the membrane in 100% methanol.

Use enough antibody volume so that the entire membrane surface is sufficiently covered with liquid at all times. Use heat-seal bags if the volume is limiting. Do not let an area of the membrane dry out. Use agitation for all antibody incubations.

Small proteins can pass through the membrane during transfer (“blow-through”). To prevent this, use a membrane with a smaller pore size or reduce the transfer time.

Allow the blot to dry for a minimum of 1 hour before detection.

Do not wrap the membrane in plastic when scanning.

Imaging Read Mode

To use this read mode, you must have the SpectraMax MiniMax 300 Imaging Cytometer installed with the SpectraMax i3x Instrument.

Imaging read mode does whole-cell imaging assays.

Whole-cell imaging assays are cell-based, or object-based, rather than the single-point measurements found in other types of microplate reads. These types of assays can yield more biologically meaningful results that can discriminate the fluorescence related to objects, such as cells or beads, from the bulk solution within a microplate well.

The measurement is primarily fluorescent with quantification of cell size, shape, area, and intensity. Label-free quantification is also supported through brightfield, transmitted light imaging. The camera resolution in the SpectraMax MiniMax 300 Imaging Cytometer is sufficient to determine the approximate shape of small 8 micron objects, such as blood cells.

Other advantages of these assays include, the direct interrogation of individual cells instead of whole well or cell lysates that permit controlling for cell numbers and heterogeneity in cell-based assays. Also, increased sensitivity by both detecting a few fluorescent cells per well, as well as detecting cells that are, on average, less fluorescent.

The SpectraMax® MiniMax™ 300 Imaging Cytometer 300 is capable of acquiring image data using transmitted light and two fluorescent channels during the same microplate read. In the SoftMax Pro Software **Settings** dialog, you can select the channels that you want to use for the acquisition. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

You can obtain imaging data through visual inspection of the image or by using the analysis tools available in the SoftMax Pro Software. See [Analyzing Imaging Data on page 198](#).

Applications of Whole-Cell Imaging

Whole-cell imaging assays measure a diverse set of cellular responses, such as fluorescent protein expression (phosphorylated and total), cell viability (cell toxicity), cell apoptosis, and cell cycle analysis.

Supported dyes include the following:

- EarlyTox™ Cell Integrity Kit
- Fluorescein isothiocyanate (FITC)
- Calcein AM
- Alexa Fluor 488 or Alexa Fluor 647
- Cy5
- DRAQ5

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

For information about creating Imaging read mode protocols, see [Creating an Imaging Mode Protocol on page 336](#).

Imaging Instruments and Detection Cartridges

The following instrument has Imaging read mode capability:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms, see page 202](#)

The SpectraMax® MiniMax™ 300 Imaging Cytometer adds imaging capability to the SpectraMax i3x Instrument to visually inspect your sample and to run cell-based assays at cellular or whole-cell resolution.

To do brightfield, transmitted-light imaging, you must install the SpectraMax Transmitted Light (TL) Detection Cartridge in the detection cartridge drawer. See [Transmitted Light \(TL\) Detection Cartridge on page 233](#).

Analyzing Imaging Data

You can obtain imaging data through visual inspection of the image or by using the analysis tools available in the SoftMax Pro Software.

In fluorescent imaging, the fluorescence in the sample is excited with light of a specified wavelength. The fluorophore emits at a longer wavelength that is captured in the image.

The software measures the intensity of the emitted fluorescence and estimates the intensity of the background in the image.

You can select one of the following image analysis types.

Discrete Object Analysis

Discrete Object Analysis uses proprietary algorithms to analyze separate objects, or cells, based on multiple parameters including the signal intensity over the background and the size of the objects.

When you click **Discrete Object Analysis**, The **Wavelength for Finding Objects** list appears below the list of analysis types. Select the wavelength from this list to use to identify the objects in the well images. You can use transmitted light or a fluorescent wavelength to find nuclei or easily separable objects in the image. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

The **Image Analysis Settings** category on the left expands to show the subcategories that follow:

- Click **Find Objects** to enter size and intensity values or use proprietary algorithms with the provided drawing tools to graphically define the objects and the background areas for the analysis. See [Finding Discrete Objects or Confluent Areas on page 267](#).
- Click **Classify Objects** to define separate measurements for different types of found objects, or cells. See [Classifying Discrete Objects on page 271](#).
- Click **Select Measurements** to view the results of the analysis for the selected wells. See [Viewing and Selecting Measurement Statistics on page 273](#).

Field Analysis

Field Analysis uses proprietary algorithms to analyze confluent areas based on multiple parameters including the signal intensity over the background and the size of the areas.

When you click **Field Analysis**, The **Wavelength for Finding Confluent Areas** list appears below the list of analysis types. Select the wavelength from this list to use to identify the confluent areas in the well images. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

The **Image Analysis Settings** category on the left expands to show the subcategories that follow:

- Click **Find Confluent Areas** to use proprietary algorithms with the provided drawing tools to graphically define the confluent areas and the background areas for the analysis. See [Finding Discrete Objects or Confluent Areas on page 267](#).
- Click **Select Measurements** to view the results of the analysis for the selected wells. See [Viewing and Selecting Measurement Statistics on page 273](#).

The SoftMax Pro Software proprietary algorithms with the provided drawing tools help the software learn the patterns of the objects that you want to find. Depending on the complexity of the object patterns, this teaching process can take several iterations before you get your desired results. See [Resolving Common Issues with Drawing and Finding Objects on page 275](#).

Analysis Measurement Parameters

Depending on the needs of your application, you can use one or more of the following analysis measurement parameters for the region of interest (ROI) in your experiment:

- **Object Count** gives the total number of objects detected in the image. This measurement is not used for field analysis of confluent areas.
- **Field Count** gives the total number of confluent areas detected in the image. This measurement is not used for discrete object analysis.
- **Object Percentage** gives the percentage the objects detected in the image by classification. This measurement is not used for field analysis of confluent areas.
- **Covered Area** gives the combined area of all the objects or confluent areas detected in the image as a percentage of the entire image area.
- **Object Area** gives the average area of the objects detected in the image expressed in μm^2 . This measurement is not used for field analysis of confluent areas.
- **Field Area** gives the average area of the confluent areas detected in the image expressed in μm^2 . This measurement is not used for discrete object analysis.
- **Object Roundness** gives the average roundness of each object detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for field analysis of confluent areas.
- **Field Roundness** gives the average roundness of each confluent area detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for discrete object analysis.
- **Object Average Intensity** gives the average fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Average Intensity** gives the average fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Object Intensity** gives the average total fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Intensity** gives the average total fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Total Intensity** gives the combined total fluorescent signal intensity of the objects or confluent areas detected in the image expressed in million intensity counts. This measurement is not used for transmitted light (TL).

Chapter 6: Supported Instruments and Detection Cartridges

SoftMax® Pro Data Acquisition and Analysis Software controls Molecular Devices® spectrophotometers and absorbance, luminescence, and fluorescence microplate readers and detection platforms.

A detection cartridge contains its own independent light source, optics, and electrical components needed to do specific read modes for specific applications.

- The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.

Supported Instruments

User guides for each of the supported instruments are installed during the SoftMax Pro Software installation. You can view these user guides from the Windows Start menu at **Start > All Programs > Molecular Devices > SoftMax Pro 7.0 > Hardware User Guides**.

SoftMax Pro Software supports the following instruments:

- [SpectraMax i3x and i3 Multi-Mode Detection Platforms on page 202](#)
- [SpectraMax Paradigm Multi-Mode Microplate Reader, see page 204](#)
- [VersaMax Microplate Reader, see page 205](#)
- [SpectraMax Plus 384 Absorbance Microplate Reader, see page 205](#)
- [SpectraMax M5 and M5e Multi-Mode Microplate Readers, see page 206](#)
- [SpectraMax M4 Multi-Mode Microplate Reader, see page 207](#)
- [SpectraMax M3 Multi-Mode Microplate Reader, see page 208](#)
- [SpectraMax M2 and M2e Multi-Mode Microplate Readers, see page 209](#)
- [SpectraMax 340PC 384 Absorbance Microplate Reader, see page 210](#)
- [SpectraMax 190 Absorbance Microplate Reader, see page 210](#)
- [Gemini XPS Microplate Reader, see page 211](#)
- [Gemini EM Microplate Reader, see page 211](#)
- [FlexStation 3 Multi-Mode Microplate Reader, see page 212](#)
- [FilterMax F5 Multi-Mode Microplate Reader, see page 213](#)
- [FilterMax F3 Multi-Mode Microplate Reader, see page 214](#)
- [DTX 800 and DTX 880 Multi-Mode Microplate Readers, see page 214](#)
- [Vmax Kinetic Microplate Reader, see page 215](#)
- [EMax Endpoint Microplate Reader, see page 215](#)
- [EMax Plus Microplate Reader on page 215](#)
- [StakMax Microplate Handling System, see page 216](#)

A detection cartridge contains its own independent light source, optics, and electrical components needed to do specific read modes for specific applications.

- The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.

See [Supported Detection Cartridges on page 218](#).

SpectraMax i3x and i3 Multi-Mode Detection Platforms

The SpectraMax i3x Multi-Mode Detection Platform is a monochromator-based, multi-mode detection platform. An external computer running the SoftMax® Pro provides integrated instrument control, data display, and statistical data analysis.

The built-in read modes include:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).

The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges. A detection cartridge contains its own independent light source, optics, and electrical components needed to do specific read modes for specific applications. Up to four detection cartridges can be installed in the detection cartridge drawer. For information about the different detection cartridges, see [Supported Detection Cartridges on page 218](#).

For most read modes, endpoint, kinetic, multi-point well-scan, and spectrum microplate applications can be set up and run with the SoftMax Pro Software.

For more information on the supported read types, see the following topics:

- [Endpoint Read Type on page 152](#)
- [Kinetic Read Type on page 152](#)
- [Well Scan Read Type on page 152](#)
- [Spectrum Read Type on page 152](#)
- [Flex Read Type on page 153](#)
- [Membrane Read Type on page 153](#)

The SpectraMax® MiniMax™ 300 Imaging Cytometer adds imaging capability to the SpectraMax i3x Instrument to visually inspect your sample and to run cell-based assays at cellular or whole-cell resolution. See [SpectraMax MiniMax 300 Imaging Cytometer on page 203](#).

Depending on the application, the instrument can read 6, 12, 24, 48, 96, and 384-well microplates. For micro-volume measurements, the instrument supports the SpectraDrop 24-well Micro-Volume Microplates and the SpectraDrop 64-well Micro-Volume Microplates. With some detection cartridges, the instrument is capable of reading 1536-well microplates.

Features of the SpectraMax i3x Multi-Mode Detection Platform include:

- Built-in, 2x2 monochromators for absorbance, fluorescence, and luminescence reads
- Top and bottom read capability
- More capabilities with detection cartridges, including AlphaScreen
- Adjustable read height (Z-height) for top reads
- Up to 1536-well format with some detection cartridges
- Temperature control
- PathCheck Pathlength Measurement Technology

SpectraMax MiniMax 300 Imaging Cytometer

The SpectraMax® MiniMax™ 300 Imaging Cytometer adds imaging capability to the SpectraMax i3x Instrument to visually inspect your sample and to run cell-based assays at cellular or whole-cell resolution. The cytometer uses solid-state illumination, a digital camera, a 4x objective lens, laser auto-focus, and auto-exposure to capture fluorescent or label-free images of a sample at the bottom of the microplate wells. The cytometer supports 96-well and 384-well, flat-bottom, clear-bottom microplates.

The measurement is primarily fluorescent with quantification of cell size, shape, area, and intensity. Label-free quantification is also supported through brightfield, transmitted light imaging. The camera resolution in the SpectraMax MiniMax 300 Imaging Cytometer is sufficient to determine the approximate shape of small 8 micron objects, such as blood cells.

The SpectraMax® MiniMax™ 300 Imaging Cytometer 300 is capable of acquiring image data using transmitted light and two fluorescent channels during the same microplate read. In the SoftMax Pro Software **Settings** dialog, you can select the channels that you want to use for the acquisition. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

To do brightfield, transmitted-light imaging, you must install the SpectraMax Transmitted Light (TL) Detection Cartridge in the detection cartridge drawer. See [Transmitted Light \(TL\) Detection Cartridge on page 233](#).

SpectraMax Paradigm Multi-Mode Microplate Reader

The SpectraMax Paradigm Multi-Mode Microplate Reader is a modular multi-mode microplate reader. User-installable detection cartridges let the microplate reader be configured for specific applications, and they expand the capabilities of the microplate reader. The measurement capabilities of the microplate reader are defined by the installed detection cartridges.

Up to six detection cartridges can be installed in each of the two detection cartridge drawers of the SpectraMax Paradigm Multi-Mode Microplate Reader.

Most detection cartridges start with an excitation energy source either in the form of long-life, high-powered LED, a xenon flash lamp, or a laser diode. By concentrating the excitation energy on the sample through label-specific optics, high levels of sensitivity and performance are reached.

For information about the different detection cartridges, see [Supported Detection Cartridges on page 218](#).

Features of the SpectraMax Paradigm Multi-Mode Microplate Reader include:

- Array of detection cartridge capabilities
- Automatic read height (Z-height) optimization for both top and bottom read
- LED intensity adjustment
- Up to 1536-well format
- Temperature control
- Monochromator and filter based options available
- PathCheck Pathlength Measurement Technology
- AlphaScreen

VersaMax Microplate Reader

The VersaMax™ Microplate Reader provides rapid and sensitive measurements of a variety of analytes across a wide range of concentrations. You can run both standard spectrophotometer and microplate reader applications on the same instrument. Read one sample or up to 96 at a time. Use standard 96-well microplates.

Detection mode includes:

- Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).

VersaMax Microplate Reader features include:

- Full spectral range: 340 nm to 850 nm, tunable in 1 nm increments.
- Superior performance: 2 nm bandwidth provides exceptional accuracy and linearity for the widest range of assays.
- Endpoint and Kinetic reads.

SpectraMax Plus 384 Absorbance Microplate Reader

The SpectraMax® Plus 384 Absorbance Microplate Reader has a built-in cuvette port and microplate drawer. You can run both standard spectrophotometer and microplate reader applications on the same instrument. Read one sample or up to 384 at a time. Use a standard cuvette, 12 x 75 mm test tube, or 96-well or 384-well microplate. For more sample throughput, the SpectraMax Plus 384 Absorbance Microplate Reader can be integrated into a full robotic system.

Detection mode includes:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).

SpectraMax Plus 384 Absorbance Microplate Reader features include:

- Full spectral range: 190 nm to 1000 nm, tunable in 1 nm increments.
- Superior performance: 2 nm bandwidth provides exceptional accuracy and linearity for the widest range of assays.
- Speed read mode: Reads 96-well microplates in just 5 seconds and 384-well microplates in 16 seconds for ultra-fast sample throughput.
- PathCheck Pathlength Measurement Technology reports the microplate data as standard 1 cm cuvette values.

SpectraMax M5 and M5e Multi-Mode Microplate Readers

The SpectraMax M5 and M5e Multi-Mode Microplate Readers are modular, upgradable, dual-monochromator microplate reader platforms offering a wide range of high performance multi-mode capabilities ideal for life science research and drug discovery screening.

The SpectraMax M5 and M5e Multi-Mode Microplate Readers offer triple-mode cuvette port, accurate temperature control, and microplate shaking capability.

Detection modes include:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).
- Fluorescence Polarization (FP), see [Fluorescence Polarization Read Mode on page 185](#).

Features of the SpectraMax M5 and M5e Multi-Mode Microplate Readers include:

- Three-mode cuvette port for assay development
- Dual monochromator tunability
- PathCheck Pathlength Measurement Technology
- Endpoint, kinetic, spectral, and well-scanning read types
- Comprehensive Data Analysis with SoftMax Pro Software
- Validation and compliance
- Automation compatibility

SpectraMax M4 Multi-Mode Microplate Reader

The SpectraMax M4 Multi-Mode Microplate Reader is a modular, dual-monochromator microplate reader platform offering a wide range of high performance multi-mode capabilities ideal for life science research and drug discovery screening.

The SpectraMax M4 Multi-Mode Microplate Reader offers a triple-mode cuvette port, accurate temperature control, and microplate shaking capability.

Detection modes include:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).

Features of the SpectraMax M4 Multi-Mode Microplate Reader include:

- Three-mode cuvette port for assay development
- Dual monochromator tunability
- PathCheck Pathlength Measurement Technology
- Endpoint, kinetic, spectrum, and well scan read types
- Comprehensive Data Analysis with SoftMax Pro Software
- Validation and compliance
- Automation compatibility

SpectraMax M3 Multi-Mode Microplate Reader

The SpectraMax M3 Multi-Mode Microplate Reader is a modular, dual-monochromator microplate reader platform offering a wide range of high performance multi-mode capabilities ideal for life science research and drug discovery screening.

The SpectraMax M3 Multi-Mode Microplate Reader offers a triple-mode cuvette port, accurate temperature control, and microplate shaking capability.

Detection modes include:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).

Features of the SpectraMax M3 Multi-Mode Microplate Reader include:

- Three-mode cuvette port for assay development
- Dual monochromator tunability
- Automated Absorbance Pathlength Correction with PathCheck Pathlength Measurement Technology
- Endpoint, kinetic, spectral and well-scanning read types
- Comprehensive Data Analysis with SoftMax Pro Software
- Validation and compliance
- Robotics compatibility

SpectraMax M2 and M2e Multi-Mode Microplate Readers

The SpectraMax M2 and M2e Multi-Mode Microplate Readers are instruments with two monochromators, dual-mode cuvette ports, and top-plate and bottom-plate reading capability (top-reading only on the SpectraMax M2 Multi-Mode Microplate Reader). Area-well scanning read types and the PathCheck® Pathlength Measurement Technology let homogeneous and heterogeneous microplate assays be done in one flexible system.

Detection modes include:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).

Features of the SpectraMax M2 and M2e Multi-Mode Microplate Readers include:

- Multi-detection capability
- Top-read and bottom-read (SpectraMax M2e Instrument only)
- Dual-mode cuvette port
- Two monochromators
- PathCheck Pathlength Measurement Technology and well volume sensors
- Instrument and software validation
- Automation compatible

SpectraMax 340PC 384 Absorbance Microplate Reader

The SpectraMax® 340PC 384 Absorbance Microplate Reader provides rapid and sensitive measurements of a variety of analytes across a wide range of concentrations. You can run both standard spectrophotometer and microplate reader applications on the same instrument. Read one sample or up to 384 at a time. Use standard 96-well or 384-well microplates.

Detection mode includes:

- Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).

SpectraMax 340PC 384 Absorbance Microplate Reader features include:

- Full spectral range: 340 nm to 850 nm, tunable in 1 nm increments.
- Superior performance: 2 nm bandwidth provides exceptional accuracy and linearity for the widest range of assays.
- PathCheck Pathlength Measurement Technology reports the microplate data as standard 1 cm cuvette values.

SpectraMax 190 Absorbance Microplate Reader

The SpectraMax® 190 Absorbance Microplate Reader provides rapid and sensitive measurements of a variety of analytes across a wide range of concentrations. Read one sample or up to 96 at a time. Use standard 96-well microplates.

Detection mode includes:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).

SpectraMax 190 Absorbance Microplate Reader features include:

- Full spectral range: 190 nm to 850 nm, tunable in 1 nm increments.
- Superior performance: 2 nm bandwidth provides exceptional accuracy and linearity for the widest range of assays.
- PathCheck Pathlength Measurement Technology reports the microplate data as standard 1 cm cuvette values.

Gemini XPS Microplate Reader

The Gemini XPS Microplate Reader can do a variety of fluorescent applications. The extreme flexibility and high sensitivity makes the Gemini XPS Microplate Reader useful for applications within the fields of biochemistry, cell biology, immunology, molecular biology, and microbiology.

Detection modes include:

- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).

Gemini XPS Microplate Reader features include:

- Dual monochromators let you select wavelengths in 1 nm increments.
- Cutoff filters reduce stray light and minimize background interference.
- Wavelength scanning ensures that the most sensitive assay conditions are used.

Gemini EM Microplate Reader

The Gemini EM Microplate Reader can do a variety of fluorescent applications. The extreme flexibility and high sensitivity makes the Gemini EM Microplate Reader useful for applications within the fields of biochemistry, cell biology, immunology, molecular biology, and microbiology. The top-read and bottom-read optical design permits measurements for solution and cell-based assays.

Detection modes include:

- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).

Gemini EM Microplate Reader features include:

- Dual monochromators let you select wavelengths in 1 nm increments.
- Cutoff filters reduce stray light and minimize background interference.
- Wavelength scanning ensures that the most sensitive assay conditions are used.

FlexStation 3 Multi-Mode Microplate Reader

The FlexStation® 3 Multi-Mode Microplate Reader combines the performance of a dual-monochromator, multi-mode microplate reader and an integrated 8-channel or 16-channel pipettor into one compact bench-top reader. This integrated system provides a multi-detection platform capable of increasing liquid-handling throughput and flexibility for biochemical-based and cell-based assays. The system is equally amenable to agonist and antagonist assay formats. Combining fluid transfer with multi-detection optics provides a microplate reader capable of doing a broad span of applications for the drug discovery and research environments.

Detection modes include:

- UV and Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).
- Fluorescence Polarization (FP), see [Fluorescence Polarization Read Mode on page 185](#).

The dual monochromators in the FlexStation 3 reader let you target the optimal assay excitation and emission wavelengths, while eliminating the need to change expensive band pass filters between experiments.

For most read modes, endpoint, kinetic, multi-point well-scan, and spectrum microplate applications plus the dedicated flex read type can be set up and run with the SoftMax Pro Software.

FilterMax F5 Multi-Mode Microplate Reader

The FilterMax F5 Multi-Mode Microplate Reader is ideal for a broad range of applications, including drug discovery, genomics, proteomics, and cell-based research. The unique patented design ensures precise performance and sensitivity across all detection modes.

Detection modes include:

- UV and Visible Absorbance (ABS) at wavelengths between 230 nm and 650 nm, see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL) at wavelengths between 230 nm and 700 nm for top reading, or between 300 nm and 650 nm for bottom reading, see [Fluorescence Intensity Read Mode on page 160](#).
- Glow-type Luminescence (LUM) at wavelengths between 400 nm and 700 nm, see [Luminescence Read Mode on page 166](#).
- Time-Resolved Fluorescence (TRF) at wavelengths between 340 nm and 700 nm, see [Time-Resolved Fluorescence Read Mode on page 171](#).
- Fluorescence Polarization (FP) at wavelengths between 300 nm and 700 nm, see [Fluorescence Polarization Read Mode on page 185](#).
- Fluorescence Resonance Energy Transfer (FRET), see [FRET Read Mode on page 178](#).

Other features of the FilterMax F5 Multi-Mode Microplate Reader include:

- A deuterium light source that extends sensitivity into the deep UV band.
- Endpoint, kinetic, multiple wavelength, linear scan, and area scan read types
- Measurements on samples in 6, 12, 24, 48, 96, 384, 1536-well microplates.
- PathCheck Pathlength Measurement Technology
- Automatic read height (Z-height) optimization for top read
- Temperature control in the microplate chamber during measurements.
- Comprehensive Data Analysis with SoftMax Pro Software

The filters used to do measurements are mounted on two types of interchangeable slides. One slide is reserved for excitation filters used in absorbance and fluorescence measurements, the other is used for emission filters used in fluorescence and some luminescence measurements. Each slide can hold up to six filters. For more information, see [Configuring Filter Slides on page 458](#).

FilterMax F3 Multi-Mode Microplate Reader

The FilterMax F3 Multi-Mode Microplate Reader is ideal for a broad range of applications, including drug discovery, genomics, proteomics, and cell-based research. The unique patented design ensures precise performance and sensitivity across all detection modes.

Detection modes include:

- Visible Absorbance (ABS) at wavelengths between 340 nm and 650 nm, see [Absorbance Read Mode on page 154](#).
- Fluorescence Intensity (FL) for top reading at wavelengths between 340 nm and 650 nm, see [Fluorescence Intensity Read Mode on page 160](#).
- Glow-type Luminescence (LUM) at wavelengths between 400 nm and 650 nm, see [Luminescence Read Mode on page 166](#).
- Fluorescence Resonance Energy Transfer (FRET), see [FRET Read Mode on page 178](#).

Other features of the FilterMax F3 Multi-Mode Microplate Reader include:

- Endpoint, kinetic, multiple wavelength, linear scan, and area scan read types.
- Measurements on samples in 96-well and 384-well microplates.
- Linear and orbital microplate shaking.
- Comprehensive Data Analysis with the SoftMax Pro Software.

The filters used to do measurements are mounted on two types of interchangeable slides. One slide is reserved for excitation filters used in absorbance and fluorescence measurements, the other is used for emission filters used in fluorescence and some luminescence measurements. Each slide can hold up to six filters. For more information, see [Configuring Filter Slides on page 458](#).

DTX 800 and DTX 880 Multi-Mode Microplate Readers

The DTX 800 and DTX 880 Multi-Mode Microplate Readers are earlier models of the FilterMax F3 and F5 Multi-Mode Microplate Readers. For information about the DTX 800 and DTX 880 Multi-Mode Microplate Readers, refer to information in this documentation regarding the FilterMax F3 and F5 Multi-Mode Microplate Readers.

- For information about the DTX 800 Multi-Mode Microplate Reader, see [FilterMax F3 Multi-Mode Microplate Reader on page 214](#).
- For information about the DTX 880 Multi-Mode Microplate Reader, see [FilterMax F5 Multi-Mode Microplate Reader on page 213](#).

Vmax Kinetic Microplate Reader

The Vmax Kinetic Microplate Reader measures optical density (OD) and can do a kinetic analysis, the rate of optical density change per minute (milliOD/min). The optical array is designed to analyze the absorbance of multiple sample sites with 9 mm centers. Read one sample or up to 96 at a time. Use standard 96-well microplates.

Detection mode includes:

- Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).

Vmax Kinetic Microplate Reader features include:

- Filter range: 400 nm to 750 nm
- Filter capacity: 6
- Optical density: single wavelength and dual wavelength

EMax Endpoint Microplate Reader

The EMax Endpoint Microplate Reader measures optical density (OD). The optical array is designed to analyze the absorbance of multiple sample sites with 9 mm centers. Read one sample or up to 96 at a time. Use standard 96-well microplates.

Detection mode includes:

- Visible Absorbance (ABS), see [Absorbance Read Mode on page 154](#).

EMax Endpoint Microplate Reader features include:

- Filter range: 400 nm to 750 nm
- Filter capacity: 6
- Optical density: single wavelength and dual wavelength

EMax Plus Microplate Reader

The EMax[®] Plus Microplate Reader is a filter-based absorbance microplate reader, with eight standard filters for a wide range of applications. The instrument can read standard 96-well microplates.

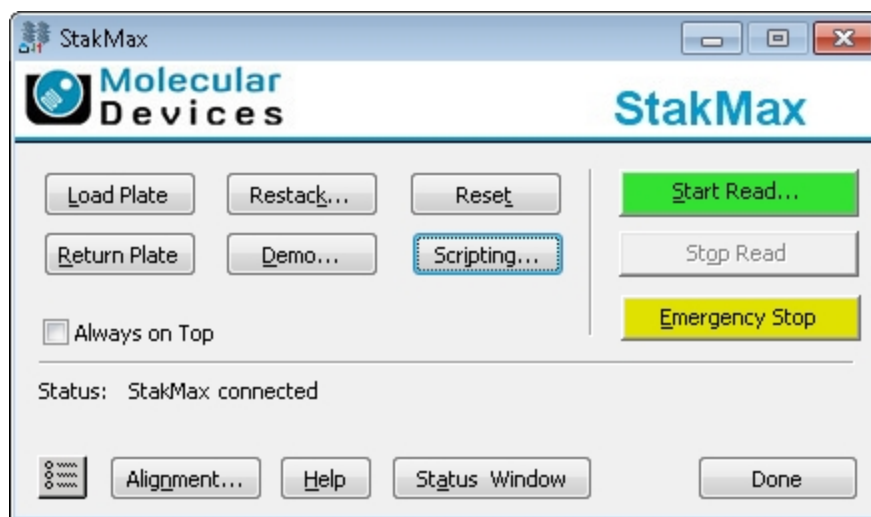
The instrument has a built-in read mode for visible absorbance (ABS) measurements, see [Absorbance Read Mode on page 154](#).

Endpoint and kinetic read types are supported. See [Endpoint Read Type on page 152](#) and [Kinetic Read Type on page 152](#).

StakMax Microplate Handling System

The StakMax® Microplate Handling System is an integrated microplate stacker for use with Molecular Devices® microplate readers, providing simple, powerful, walk-away benchtop automation.

The StakMax Software is accessed from the **Operations** tab in the ribbon. When you click **Plate Stacker**, the SoftMax Pro Software is placed in automation mode, and then the StakMax Software starts and automatically connects to the StakMax Microplate Handling System. The current status of the instrument is displayed in the status line of the StakMax Software window.



CAUTION! To prevent data loss, make sure that **Auto Save** is enabled for each protocol you want to run before you start the StakMax Software to run automated reads. See [Setting Auto Save Options on page 76](#).

To exit the StakMax Software, click **Done** and then click **Terminate** in the SoftMax Pro Software Automation dialog.

Compatible Instruments

The StakMax Microplate Handling System is compatible with the following microplate readers:

- SpectraMax® Paradigm® Multi-Mode Microplate Reader
- SpectraMax® M2 and M2e Multi-Mode Microplate Readers
- SpectraMax® M3 Multi-Mode Microplate Reader
- SpectraMax® M4 Multi-Mode Microplate Reader
- SpectraMax® M5 and M5e Multi-Mode Microplate Readers
- SpectraMax® L Microplate Reader
- Gemini™ EM and XPS Microplate Readers

Newer models of the following readers are compatible with the StakMax Microplate Handling System:

- SpectraMax® Plus 384 Absorbance Microplate Reader
- SpectraMax® 340PC 384 Absorbance Microplate Reader
- SpectraMax® 190 Absorbance Microplate Reader
- VersaMax™ Microplate Reader

For more information about using the StakMax Microplate Handling System, see the *StakMax Microplate Handling System User Guide* or the help available in the StakMax Software.

For information about the SoftMax Pro Software automation mode, see [Using Automation Mode on page 56](#).

Supported Detection Cartridges

A detection cartridge contains its own independent light source, optics, and electrical components needed to do specific read modes for specific applications.

- The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.



Note: For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

The SoftMax Pro Software supports the following detection cartridges:

- [Absorbance Detection Cartridge on page 219](#)
- [Tunable Wavelength \(TUNE\) Detection Cartridge, see page 220](#)
- [Multi-Mode \(MULTI\) Detection Cartridge, see page 221](#)
- [AlphaScreen Detection Cartridges , see page 222](#)
- [Cisbio HTRF Detection Cartridge on page 223](#)
- [Time Resolved Fluorescence \(TRF-EUSA\) Detection Cartridge, see page 224](#)
- [Fluorescence Intensity \(FI\) Detection Cartridges, see page 225](#)
- [Fluorescence Intensity \(FI\) GeneBLAzer Detection Cartridge, see page 226](#)
- [Fluorescence Intensity Dual Label \(FI-DL\) \(MultiTox-Fluor\) Detection Cartridge, see page 228](#)
- [Fluorescence Polarization \(FP\) Detection Cartridges, see page 229](#)
- [Glow Luminescence \(LUM\) Detection Cartridges, see page 227](#)
- [Dual Color Luminescence \(LUM\) \(BRET2\) Detection Cartridge, see page 230](#)
- [Dual Color Luminescence \(LUM\) \(Chroma-Glo\) Detection Cartridge, see page 231](#)
- [ScanLater Western Blot \(WB\) Detection Cartridge on page 232](#)
- [Injector Cartridge on page 233](#)
- [Transmitted Light \(TL\) Detection Cartridge on page 233](#)

For complete descriptions and specifications for each of the supported detection cartridges, see the *SpectraMax i3x Multi-Mode Detection Platform User Guide* or the *SpectraMax Paradigm Multi-Mode Microplate Reader User Guide*.

Custom detection cartridges can be designed to meet the specific needs of your application. For more information, see your Molecular Devices representative.

Absorbance Detection Cartridge

The Absorbance Detection Cartridge combines wavelength scanning and a broad spectrum wavelength range necessary to address a variety of nucleic acids, proteins, ELISAs, and immunoassays found in the laboratory. The Absorbance Detection Cartridge uses a monochromator to do absorbance endpoint, kinetic, well scan, and spectrum read types (wavelength scanning) measurements.

The Absorbance Detection Cartridge consists of two components: a detection component (ABS-DET) which measures the absorbance, and an excitation component (ABS-MONO) which sets the absorbance wavelengths. The detection component is installed in the top read detection cartridge drawer and occupies one (1) detection cartridge slot. The excitation component is installed in the bottom read detection cartridge drawer and occupies two (2) detection cartridge slots. The two components must be installed to do absorbance measurements with the SpectraMax Paradigm Multi-Mode Microplate Reader.

The SpectraMax i3x Multi-Mode Detection Platform does not support the Absorbance Detection Cartridge.

Typical Applications

- Nucleic Acid Quantitation
- Protein Quantitation
- ELISA
- Immunoassay
- Proliferation/Viability

You can create protocols that use the Absorbance Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Tunable Wavelength (TUNE) Detection Cartridge

The Tunable Wavelength (TUNE) Detection Cartridge enables several detection modes, including:

- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).

The spectral optimization feature of the Tunable Wavelength (TUNE) Detection Cartridge can help to get the maximum signal-to-background ratio for most fluorophores or luminescence labels that are compatible with the wavelength ranges.

Using a Spectrum read, you can define a fixed excitation wavelength and scan the emission wavelengths, or define a fixed emission wavelength and scan the excitation wavelengths. The spectral optimization helps to get the maximum signal-to-background ratio from a fluorescent or fluorescently labeled analyte. For more information on using the spectral optimization feature, see the SoftMax Pro Software application help or user guide.

The Tunable Wavelength (TUNE) Detection Cartridge occupies three (3) slots in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).
- Spectrum, see [Spectrum Read Type on page 152](#).

You can create protocols that use the Tunable Wavelength (TUNE) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Multi-Mode (MULTI) Detection Cartridge

Optimized for 96-well and 384-well plates, the Multi-Mode (MULTI) Detection Cartridge enables several detection modes, including:

- Fluorescence Intensity (FL), see [Fluorescence Intensity Read Mode on page 160](#).
- Time-Resolved Fluorescence (TRF), see [Time-Resolved Fluorescence Read Mode on page 171](#).
- Luminescence (LUM), see [Luminescence Read Mode on page 166](#).

The Multi-Mode (MULTI) Detection Cartridge occupies three (3) slots in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Multi-Mode (MULTI) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

AlphaScreen Detection Cartridges

The AlphaScreen® Detection Cartridges use a 680 nm laser diode to provide a sensitive reading system for AlphaScreen assays. The design isolates each well and enables the optimal performance for AlphaScreen assays. The detection cartridges also capture the Europium emission line of AlphaLISA®.

The following AlphaScreen Detection Cartridges are available:

- AlphaScreen 384 Std Detection Cartridge
- AlphaScreen 384 HTS Detection Cartridge
- AlphaScreen 1536 HTS Detection Cartridge

Each AlphaScreen Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The AlphaScreen Detection Cartridges can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the AlphaScreen Detection Cartridges in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

ALPHASCREEN and ALPHALISA are registered trademarks of PerkinElmer, Inc.

Cisbio HTRF Detection Cartridge

The Cisbio HTRF Detection Cartridge uses a high-energy Xenon flash lamp for sensitive reading of HTRF reagents. Also, the standard dual-emission design gives the most accurate results in short overall read time. This detection cartridge enables time-resolved fluorescence read modes for europium cryptate and europium acceptors.

The fluorescence ratio related to the HTRF readout is a correction method developed by Cisbio, for which Cisbio has granted a license to Molecular Devices. Its application is strictly limited to the use of HTRF reagents and technology, excluding other TR-FRET technologies such as IMAP TR-FRET calculations of acceptor to donor ratios.

The Cisbio HTRF Detection Cartridge is a dual-emission detection cartridge and occupies two (2) slots in the detection cartridge drawer.

The Cisbio HTRF Detection Cartridges can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Cisbio HTRF Detection Cartridges in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

HTRF is a registered trademark of Cisbio Bioassays.

Time Resolved Fluorescence (TRF-EUSA) Detection Cartridge

The Time Resolved Fluorescence (TRF-EUSA) Detection Cartridge enables time-resolved fluorescence read modes for Europium and Samarium. It is ideal for protein interaction, GPCR, and enzyme activity applications.

The Time Resolved Fluorescence (TRF-EUSA) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

Well scan is not available for dual-label assays.

You can create protocols that use the Time Resolved Fluorescence (TRF-EUSA) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Fluorescence Intensity (FI) Detection Cartridges

The Fluorescence Intensity (FI) Detection Cartridges use an ultra high power LED for the excitation of various fluorescent labels, enabling fluorescence intensity read modes. Also, the standard dual-emission design enables simple, straightforward fluorescence resonance energy transfer (FRET) measurement.

The following Fluorescence Intensity (FI) Detection Cartridges are available:

- Fluorescence Intensity (FI) (coum-fluor) Detection Cartridge
- Fluorescence Intensity (FI) (fluor-rhod) Detection Cartridge
- Fluorescence Intensity (FI) (Cy3-Cy5) Detection Cartridge
- Fluorescence Intensity (FI) (CFP-YFP) Detection Cartridge

Other Fluorescence Intensity (FI) Detection Cartridges include the [Fluorescence Intensity \(FI\) GeneBLAzer Detection Cartridge on page 226](#) and the [Fluorescence Intensity Dual Label \(FI-DL\) \(MultiTox-Fluor\) Detection Cartridge on page 228](#).

Each Fluorescence Intensity (FI) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The Fluorescence Intensity (FI) Detection Cartridges can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Fluorescence Intensity (FI) Detection Cartridges in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Fluorescence Intensity (FI) GeneBLAzer Detection Cartridge

The Fluorescence Intensity (FI) GeneBLAzer Detection Cartridge is designed for use with GeneBLAzer assays from Invitrogen. Also, the standard dual-emission design enables fluorescence resonance energy transfer (FRET) measurement.

The Fluorescence Intensity (FI) GeneBLAzer Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Fluorescence Intensity (FI) GeneBLAzer Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Glow Luminescence (LUM) Detection Cartridges

The Glow Luminescence (LUM) Detection Cartridges enable luminescence read modes.

The three Glow Luminescence (LUM) Detection Cartridges are individually optimized for 1536-well, 384-well, or 96-well microplate formats:

- Glow Luminescence (LUM) Detection Cartridge
- Glow Luminescence (LUM) Detection Cartridge (384)
- Glow Luminescence (LUM) Detection Cartridge (96)

For dual-color luminescence, see the [Dual Color Luminescence \(LUM\) \(BRET2\) Detection Cartridge on page 230](#) and the [Dual Color Luminescence \(LUM\) \(Chroma-Glo\) Detection Cartridge on page 231](#).

Each Glow Luminescence (LUM) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The Glow Luminescence (LUM) Detection Cartridges can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Glow Luminescence (LUM) Detection Cartridges in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Fluorescence Intensity Dual Label (FI-DL) (MultiTox-Fluor) Detection Cartridge

The Fluorescence Intensity Dual Label (FI-DL) (MultiTox-Fluor) Detection Cartridge uses ultra high-powered LEDs for the excitation of a dual set of fluorescent labels. This detection cartridge has been optimized for detection of the label set used in the MultiTox-Fluor Multiplex Cytotoxicity Assay from Promega:

- AFC (amino-fluorocoumarin)
- R110 (rhodamine 110)

The Fluorescence Intensity Dual Label (FI-DL) (MultiTox-Fluor) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Fluorescence Intensity Dual Label (FI-DL) (MultiTox-Fluor) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Fluorescence Polarization (FP) Detection Cartridges

The Fluorescence Polarization (FP) Detection Cartridges enable fluorescence polarization read modes for specific labels, depending on the cartridge.

Fluorescence Polarization (FP) Detection Cartridges are available for the following labels:

- Fluorescence Polarization (FP) (Fluorescein) Detection Cartridge
- Fluorescence Polarization (FP) (Rhodamine) Detection Cartridge

Each Fluorescence Polarization (FP) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).

You can create protocols that use the Fluorescence Polarization (FP) Detection Cartridges in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Dual Color Luminescence (LUM) (BRET2) Detection Cartridge

The Dual Color Luminescence (LUM) (BRET2) Detection Cartridge enables read modes for luminescence and is designed to provide the optimal performance when used with Perkin Elmer BRET² reagents.

For luminescence measurements that do not require emission filters, see [Glow Luminescence \(LUM\) Detection Cartridges on page 227](#).

The Dual Color Luminescence (LUM) (BRET2) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Dual Color Luminescence (LUM) (BRET2) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

BRET² is a trademark of PerkinElmer, Inc.

Dual Color Luminescence (LUM) (Chroma-Glo) Detection Cartridge

The Dual Color Luminescence (LUM) (Chroma-Glo) Detection Cartridge enables read modes for luminescence and is designed to provide the optimal performance when used with Promega Chroma-Glo™ reagents.

For luminescence measurements that do not require emission filters, see [Glow Luminescence \(LUM\) Detection Cartridges on page 227](#).

The Dual Color Luminescence (LUM) (Chroma-Glo) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

The can do the following read types:

- End Point, see [Endpoint Read Type on page 152](#).
- Kinetic, see [Kinetic Read Type on page 152](#).
- Well Scan, see [Well Scan Read Type on page 152](#).

You can create protocols that use the Dual Color Luminescence (LUM) (Chroma-Glo) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

Chroma-Glo is a trademark of Promega Corporation.

ScanLater Western Blot (WB) Detection Cartridge

The ScanLater™ Western Blot (WB) Detection Cartridge enables time-resolved fluorescence read mode for Western Blot membranes.

The Molecular Devices ScanLater™ Western Blot Assay Kit is a novel system for protein analysis that is incorporated into a SpectraMax® Paradigm® or SpectraMax® i3x Multi-Mode Detection Platform. Membranes are incubated with Eu-chelate labeled secondary antibodies or streptavidin that bind specifically to the target protein-specific primary antibody. For more information, contact your representative or search the knowledge base for **ScanLater** or **Western Blot** at www.moleculardevices.com/support.

The ScanLater Western Blot (WB) Detection Cartridge occupies two (2) slots in the detection cartridge drawer.

Western Blot reads use time-resolved fluorescence read mode with a membrane read type. See [Membrane Read Type on page 153](#).

You can create protocols that use the ScanLater Western Blot (WB) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

If you are using the SoftMax Pro GxP Software, you must enable the following permissions to complete a Western Blot membrane read:

- **Read empty plates/cuvettes** to start a read.
- **Save data files** to save the data file before the read.
- **Overwrite plate/cuvette data** to do a high-resolution ROI read.

See [Using SoftMax Pro GxP Software Features on page 467](#).

Injector Cartridge

The SpectraMax® Injector Cartridge adds injector capability to the SpectraMax i3x Instrument. You can use the injectors and optics in the Injector Cartridge for luminescence reads from the top of the sample, or use the injectors in the cartridge along with the built-in Monochromator in the SpectraMax i3x Instrument for fluorescence intensity reads from the bottom of the sample. To do a read with injection, you must first install the Injector Cartridge in the detection cartridge drawer.

The Injector Cartridge is installed in the two rear-most slots (3 and 4) in the detection cartridge drawer.

You can create protocols that use the Injector Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).

You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).

To define the settings for a read with injection, you must use the **Acquisition View** of the **Settings** dialog. See [Using the Acquisition View on page 240](#).

Transmitted Light (TL) Detection Cartridge

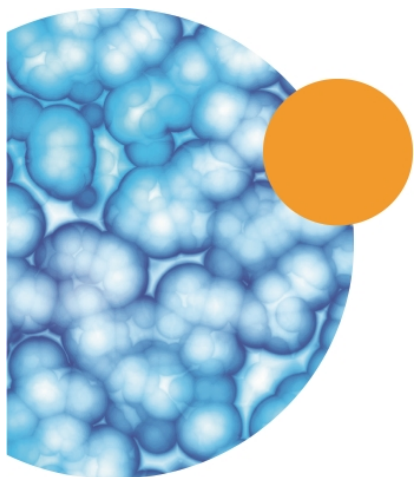
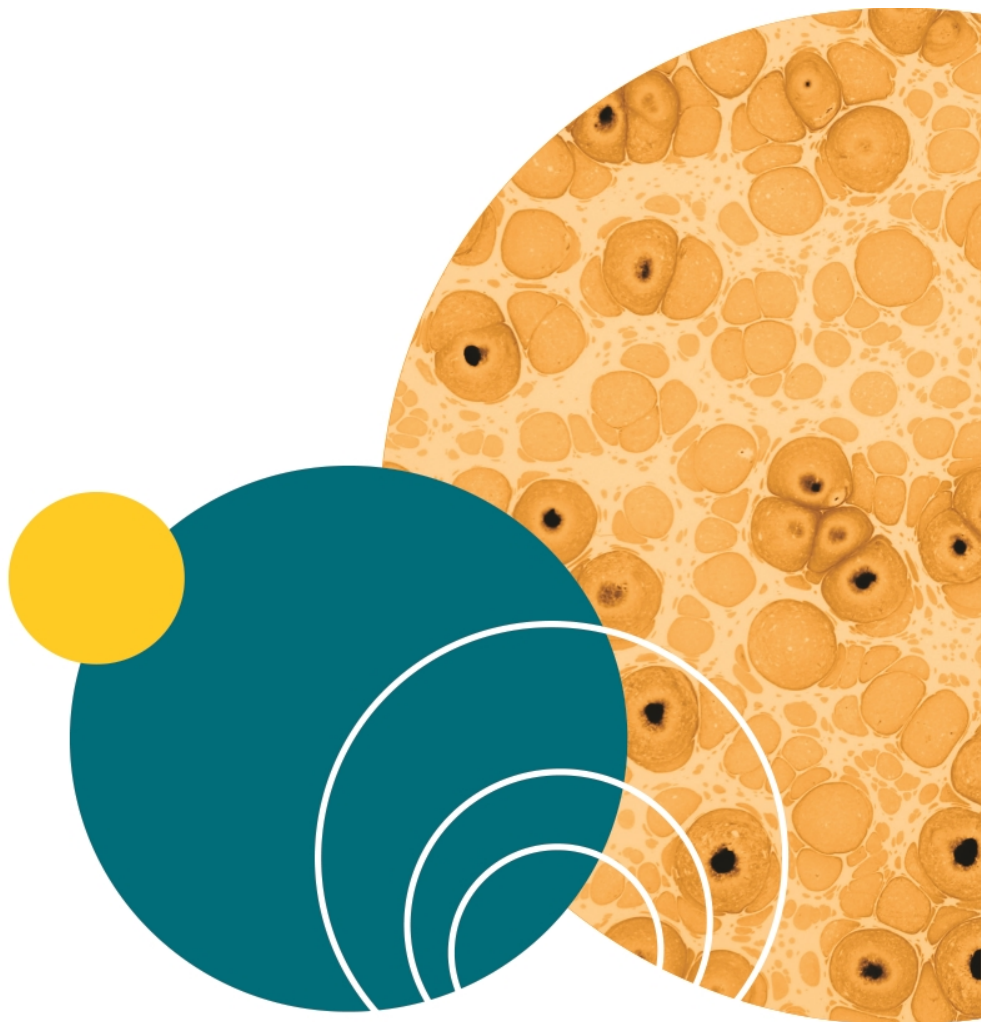
To do brightfield, transmitted-light imaging, you must install the SpectraMax Transmitted Light (TL) Detection Cartridge in the detection cartridge drawer. The Transmitted Light (TL) Detection Cartridge provides white LED illumination for transmitted-light imaging when used with the SpectraMax MiniMax 300 Imaging Cytometer. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

The Transmitted Light (TL) Detection Cartridge occupies one (1) slot in the detection cartridge drawer.

You can create protocols that use the Transmitted Light (TL) Detection Cartridge in the SoftMax Pro Software. See [Creating a Protocol on page 235](#).


You can use the Protocol Manager in the SoftMax Pro Software to quickly find and open a predefined protocol. See [Using the Protocol Manager to Open a File on page 68](#).

More protocols and updated protocols can be downloaded from the protocol sharing web site (www.softmaxpro.org). See [Using the Protocols Tab to Manage Protocols on page 42](#).



Chapter 7: Collecting Data

A general process for preparing, collecting, and analyzing data is as follows:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).
3. Choose a data acquisition protocol. You can use an existing protocol or create a new one.
 - To use an existing protocol, see [Opening a Protocol File on page 74](#).
 - To set up a new protocol, see [Creating a Protocol on page 235](#).
4. Prepare the microplate or the cuvette and insert it into the instrument.
5. Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).
6. Click the **Read**  button to read the microplate or the cuvette. See [Collecting Data from a Microplate on page 339](#), [Collecting Data From a Cuvette on page 350](#), or [Collecting Data from a Membrane Holder on page 352](#).
7. Analyze the data. See [Analyzing Data on page 355](#).
8. Save the acquired data, see [Saving Data Files on page 65](#).

Creating a Protocol

Protocols contain instrument settings, template maps, data reduction, and display options. Templates are maps to the contents of a microplate or the cuvettes in a cuvette set, and how the data will be collected and displayed.

Application notes with specific application protocol suggestions can be found in the Information Center and the Knowledge Base on the Molecular Devices web site at www.moleculardevices.com.

You can manage protocols using the **Protocol Manager** on the **Protocols** tab in the ribbon. See [Using the Protocols Tab to Manage Protocols on page 42](#).

You can create as many different protocols as you need. You can create a new protocol from a blank file or by modifying an existing protocol and saving it under a new name.

To create a protocol, follow these steps:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select the instrument to be used with the protocol. See [Selecting and Connecting to an Instrument on page 16](#).
3. Define the instrument settings to use with the protocol. See [Selecting Instrument Settings on page 236](#).
4. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
5. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).

6. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).
7. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).


Selecting Instrument Settings

The **Plate** sections or **Cuvette Set** sections in a file or experiment generally use the same instrument, but they can have different parameters for the instrument settings.

Use the **Settings** dialog to configure all parameters for a microplate or cuvette read, such as the read type (Endpoint, Kinetic, Spectrum, Well Scan, Membrane), the read mode (Absorbance, Fluorescence, Luminescence, Time Resolved Fluorescence, Fluorescence Polarization, ALPHAScreen, FRET, Imaging), wavelength settings, microplate type, wells to read, PathCheck technology, optics settings, shake parameters, timing for Kinetic runs, speed read, and more.

To select and connect to an instrument see, [Selecting and Connecting to an Instrument on page 16](#).

To open the **Settings** dialog:

1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Settings**  on the **Home** tab in the ribbon or in the toolbar at the top of the active section.

The available options in the **Settings** dialog depend on the instrument, read mode, and read type that is selected.

For the SpectraMax i3 and i3x Instruments, the **Settings** dialog has two methods available for configuring a microplate read.

- The **Standard View** uses a table-like design, with selectable categories where you can configure your settings. See [Using the Standard View on page 237](#).
- The **Acquisition View** uses a workflow design, with drag-and-drop tools to configure your settings. See [Using the Acquisition View on page 240](#).

To switch between the views, click **Standard View** or **Acquisition View** in the lower-left corner of the **Settings** dialog.

Standard View **Acquisition View**

After defining the settings for the protocol, click **OK** to close the **Settings** dialog.

To continue creating the protocol see the following:

- Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
- Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
- Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

Using the Standard View

The **Standard View** uses a table-like design, with selectable categories where you can configure your settings. This view is available for all supported instruments. It does not support reads with injection. To define the settings for a read with injection, use the **Acquisition View**. See [Using the Acquisition View on page 240](#).



Note: If you have defined an Imaging read or a ScanLater Western Blot read, switching to **Acquisition View** removes the related settings.



For the SpectraMax Paradigm, SpectraMax i3, and i3x Instruments, select the optical configuration or detection cartridge to use. See [Selecting the Optical Configuration or Detection Cartridge on page 239](#).

For all instruments, select the read mode and read type for the protocol. See [Selecting the Read Mode on page 240](#) and [Selecting the Read Type on page 240](#).

Select a **Category** from the list on the left to view and edit the available settings in the center pane. The **Settings Information** pane displays the defined settings.

The available options in the **Settings** dialog depend on the instrument, read mode, and read type that is selected. For information about the available settings, see the following topics:

- [Wavelength Settings on page 247](#)
- [Plate Type Settings on page 250](#)
- [Read Area Settings on page 255](#)

- [PathCheck Technology Settings on page 257](#)
- [TRF Settings on page 258](#)
- [PMT and Optics Settings on page 258](#)
- [Timing Settings on page 260](#)
- [Well Scan Settings on page 261](#)
- [Shake Settings on page 262](#)
- [Speed Read on page 262](#)
- [Well Area Settings on page 263](#)
- [Image Acquisition Settings on page 264](#)
- [Image Analysis Settings on page 266](#)
- [Region of Interest Settings on page 281](#)
- [Settings for Reads with Injection on page 282](#)
- [More Settings on page 285](#)
- [Compound Transfer Settings on page 289](#)
- [Compound Source Settings on page 292](#)
- [Pipette Tips Layout Settings on page 293](#)
- [Compound and Tips Columns Settings on page 293](#)
- [Triturate Settings on page 296](#)

After defining the settings for the protocol, click **OK** to close the **Settings** dialog.

Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

Selecting the Optical Configuration or Detection Cartridge

Select an **Optical Configuration** or a **Cartridge** from those shown at the top of the **Settings** dialog.

A detection cartridge contains its own independent light source, optics, and electrical components needed to do specific read modes for specific applications.

- The read capabilities of the SpectraMax i3x Instrument can be upgraded with user-installable detection cartridges.
- The SpectraMax Paradigm Multi-Mode Microplate Reader requires detection cartridges to do reads.

For the SpectraMax i3x Instrument, you can select **Monochromator** to use the built-in read modes. To use an installed SpectraMax MiniMax 300 Imaging Cytometer for imaging reads, select **MiniMax**. For transmitted light imaging, you need to install the Transmitted Light (TL) Detection Cartridge, but do not need to select it in the **Settings** dialog.



Note: When you select to work **Offline** in the **Instrument Connection** dialog, you can see all the detection cartridges that the SpectraMax i3x Multi-Mode Detection Platform or SpectraMax Paradigm Multi-Mode Microplate Reader can support.

When you are actually connected to the instrument, you see only the detection cartridges that are installed in the instrument.

For the SpectraMax i3x Multi-Mode Detection Platform, the detection cartridges can be used for top reads only.

For information on the available detection cartridges, see [Supported Detection Cartridges on page 218](#).

After selecting the optical configuration or detection cartridge to use, select the read mode and read type for the protocol. See [Selecting the Read Mode on page 240](#) and [Selecting the Read Type on page 240](#).

Selecting the Read Mode

In the **Settings** dialog, select the **Read Mode** for the protocol.

For more information on the supported read modes, see the following topics:

- [Absorbance Read Mode on page 154](#)
- [Fluorescence Intensity Read Mode on page 160](#)
- [Luminescence Read Mode on page 166](#)
- [Time-Resolved Fluorescence Read Mode on page 171](#)
- [HTRF Read Mode on page 179](#)
- [FRET Read Mode on page 178](#)
- [Fluorescence Polarization Read Mode on page 185](#)
- [AlphaScreen Read Mode on page 189](#)
- [Western Blot TRF Read Mode on page 193](#)
- [Imaging Read Mode on page 197](#)

After selecting the **Read Mode**, select a **Read Type**. See [Selecting the Read Type on page 240](#).

Selecting the Read Type

After selecting the **Read Mode**, select a **Read Type** for the protocol.

For more information on the supported read types, see the following topics:

- [Endpoint Read Type on page 152](#)
- [Kinetic Read Type on page 152](#)
- [Well Scan Read Type on page 152](#)
- [Spectrum Read Type on page 152](#)
- [Flex Read Type on page 153](#)
- [Membrane Read Type on page 153](#)

After selecting the **Read Mode** and **Read Type**, select a **Category** from the list and edit the available settings.

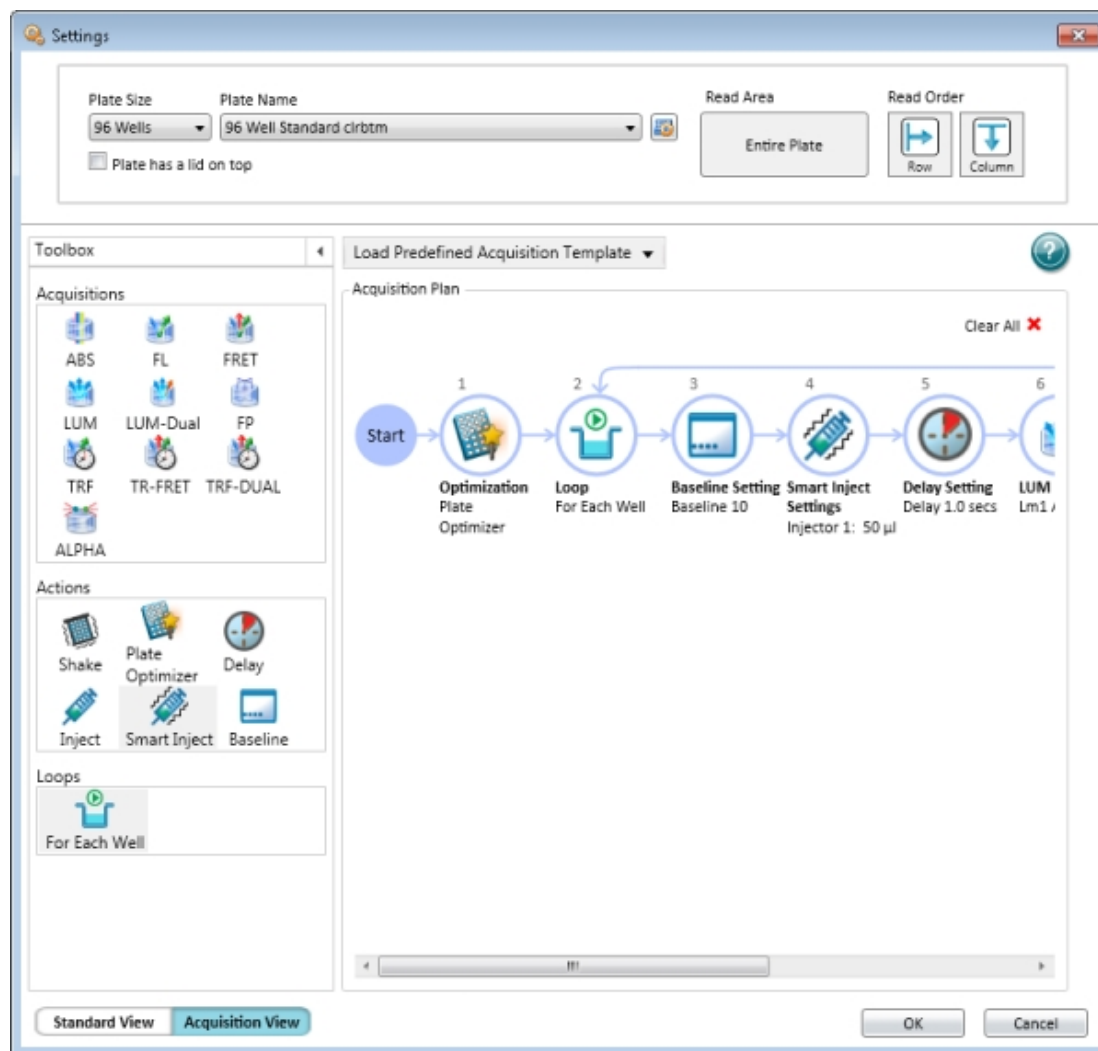
After defining the settings for the protocol, click **OK** to close the **Settings** dialog.

Using the Acquisition View

The **Acquisition View** uses a workflow design, with drag-and-drop tools to configure your settings. This view is available for the SpectraMax i3 and i3x Instruments. It does not support Imaging reads and ScanLater Western Blot reads. To define the settings for a Imaging reads and Western Blot reads, use the **Standard View**. See [Using the Standard View on page 237](#).



Note: If you have defined a read with injection, switching to **Standard View** removes the related settings.



From the top section, select the microplate type and configuration, including the **Read Area** and the **Read Order**. See the following topics:

- [Plate Type Settings on page 250](#)
- [Read Area Settings on page 255](#)
- [Read Order on page 286](#)

The **Acquisition Plan** section displays the time line of steps that have been defined for the protocol. The defined steps occur in order from left to right between the **Start** and **End** nodes. When an step has multiple settings, these setting are displayed below the step in the time line.

- To quickly start an acquisition plan, select a template from the **Load Predefined Acquisition Template** list.
- To delete the existing plan and start from scratch, click **Clear All**.

You can drag **Acquisitions**, **Actions**, and **Loops** from the **Toolbox** to the time line. The time line lets you drop nodes only in appropriate places for the specific step. For example, the **Optimization** node can be placed only at the beginning of the time line.

You can double-click **Acquisitions**, **Actions**, and **Loops** in the **Toolbox** to place the node in the first appropriate position for that node on the time line.

When you drop an **Acquisition** node onto the time line, you must select from the available options.

- Some **Acquisition** nodes require you to **Select Hardware**, or the optical configuration for the read. This can be the Monochromator or a related detection cartridge. See [Supported Detection Cartridges on page 218](#).
- All **Acquisition** nodes require you to select the read type, such as endpoint or kinetic. For more information on the supported read types, see the following topics:
 - [Endpoint Read Type on page 152](#)
 - [Kinetic Read Type on page 152](#)
 - [Spectrum Read Type on page 152](#)
 - [Well Scan Read Type on page 152](#)

For information about adding **Actions** and **Loops**, see [Adding Actions and Loops to the Time Line on page 243](#).

For information about creating a read with injectors, see [Defining Reads with Injection on page 244](#).

When you click an editable node, a pencil icon appears. Click the pencil icon to open a settings window related to that node.



To delete the node, click the red X, if available.

After you finish editing the settings, click the workspace outside of the settings window to close the window.

For information about the available settings, see the following topics:

- [Wavelength Settings on page 247](#)
- [Timing Settings on page 260](#)
- [Shake Settings on page 262](#)
- [Speed Read on page 262](#)
- [PathCheck Technology Settings on page 257](#)
- [Well Scan Settings on page 261](#)
- [PMT and Optics Settings on page 258](#)
- [Normalization of AlphaScreen Data on page 288](#)
- [Background Correction with Interlaced Readings on page 288](#)

After defining the settings for the protocol, click **OK** to close the **Settings** dialog.

Before starting a read, it is a good practice to save your data file. See [Saving Data Files on page 65](#).








Adding Actions and Loops to the Time Line

You can drag **Actions** and **Loops** from the **Toolbox** to the time line. The time line lets you drop nodes only in appropriate places for the specific action or loop. For example, the **Plate Optimizer** node can be placed only at the beginning of the time line.

When you double-click **Actions** and **Loops** in the **Toolbox**, the node is placed in the first appropriate position for that node on the time line.

The following **Actions** and **Loops** are available in the **Toolbox**.

Table 7-1: Available Actions and Loops

Node	Description
	Shake lets you define options for automated shaking of the microplate in the chamber. See Shake Settings on page 262 . To shake the microplate at the same time as an injection step, use the SmartInject technology.
	Plate Optimizer causes the Pre-Read Optimization Options dialog to open before the microplate is read. This step can be placed only at the beginning of the time line. See Show Pre-Read Optimization Options on page 287 .
	Delay lets you define the number of seconds to wait between steps in the time line. You can set the delay from 0.001 seconds to 100 seconds. For information on setting a delay after an injection, see Defining Reads with Injection on page 244 .
	Inject adds a step for injection. See Defining Reads with Injection on page 244 .
	SmartInject™ technology adds a step for injection while shaking the microplate. The microplate continues to shake through the following delay step, if included, and stops shaking before the well is read. See Defining Reads with Injection on page 244 .
	Baseline takes the defined number of baseline reads before the Inject or SmartInject step of a kinetic read with injection. The baseline data can be subtracted from the reads that follow the injection. See Defining Reads with Injection on page 244 .
	For Each Well runs the steps in the time line for each well individually with all the defined injections, delays, and reads before running the steps again for the next well. The Next Well node is also added to the end of the time line.

Defining Reads with Injection

To define the settings for a read with injection, you must use the **Acquisition View** of the **Settings** dialog.

To do a read with injection, you must first install the Injector Cartridge in the SpectraMax i3x Instrument. You can use the Injector Cartridge for luminescence reads, or use the built-in Monochromator in the SpectraMax i3x Instrument for fluorescence intensity reads with injection.

- When you add a luminescence (LUM) step to the time line, select **INJECTOR** from the **Select Hardware** list to use the Injector Cartridge for the read. A luminescence read with injection is taken from the top of the microplate.
- When you add a fluorescence intensity (FL) step to the time line select **MONO** from the **Select Hardware** list to use the built-in Monochromator for the read. A fluorescence intensity read with injection is taken from the bottom of the microplate.

Reads with injection are generally done well-by-well. Double-click **For Each Well** in the **Toolbox** to have the steps in the time line run for each well individually with all the defined injections, delays, and reads before running the steps again for the next well. The **Next Well** node is also added to the end of the time line. Add the steps for your assay between these nodes.

To add a simple injection step, drag the **Inject** node to the time line and drop the node before the **LUM Read** or **FL Read** step.

- To shake the microplate after the injection, add a **Shake** step between the injection step and the read step.
- To shake the microplate during the injection, use the **SmartInject** node instead of the **Inject** node, and do not add a **Shake** step. The SmartInject™ technology shakes the microplate during the injection and continues to shake through the following delay step, if a **Delay** node follows the **SmartInject** node. The microplate stops shaking before the well is read.

To define the settings for the injection step, click the **Inject** node or the **SmartInject** node and then click the pencil icon to open a settings window. Select the injector to use and type the number of microliters (µL) to dispense. You can dispense from 1 µL to the maximum allowable volume of the well, based on the selected microplate type. Define the dispense volume based on the requirements of your assay and the net volume available in the well.

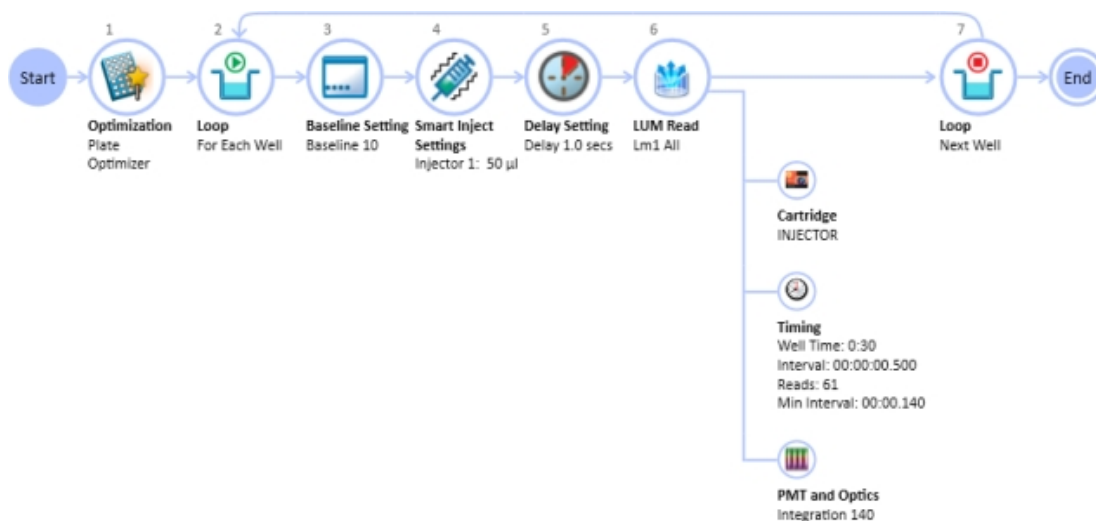
You can add a **Delay** step after the injection ends and before the read begins, if required. You can set the delay from 0.001 seconds to 100 seconds.

- For luminescence reads, there is always a delay of 0.3 seconds after the injection ends and before the read begins to allow time for the detector to move into position for the read.
- For fluorescence intensity reads, there is no delay for injector number 1. The read starts at the same time as the injection unless a **Delay** step is added. For injector number 2, there is always a delay of 0.3 seconds after the injection ends and before the read begins.

The **Delay** step compensates for the hardware delay. If the defined delay is longer than the hardware delay, then the actual delay time is the defined delay time. However, if the defined delay is shorter than the hardware delay, then the actual delay time is the hardware delay time. For example, if a luminescence read has a defined delay of 1 second, then the actual delay time between the end of the injection and the beginning of the read is 1 second. However, if a luminescence read has a defined delay of 0.05 seconds, then the actual delay time between the end of the injection and the beginning of the read is 0.3 seconds due to the hardware delay.

You can take baseline reads before the injection step of a kinetic read by double-clicking **Baseline** in the **Toolbox**. The **Baseline** step is added to the time line before the injection step. Click the pencil icon and type the number of baseline reads. You can define from 1 to 999 baseline reads. Baseline reads use the settings defined in the **LUM Read** or **FL Read** step. The baseline data can be subtracted from the reads that follow the injection. You can use the Formula Editor to automate baseline subtraction. See [Adding a New Summary Formula on page 115](#). More information about baseline subtraction can be found in the Formula Reference Guide.

The following illustration shows a time line for a luminescence kinetic read with SmartInject technology. It starts with microplate optimization and does 10 baseline reads before the injection step. It then delays 1 second after the injection ends before starting the read.




Note: With SmartInject™ technology, the microplate shakes during the injection and continues to shake through the following delay step. The microplate stops shaking before the well is read.

Instrument Settings

Each **Plate** section or **Cuvette Set** section in a file or experiment must use the same instrument, but can have different parameters for the instrument settings.

Use the **Settings** dialog to configure all parameters for a microplate or cuvette read, such as the read type (Endpoint, Kinetic, Spectrum, Well Scan, Membrane), the read mode (Absorbance, Fluorescence, Luminescence, Time Resolved Fluorescence, Fluorescence Polarization, ALPHAScreen, FRET, Imaging), wavelength settings, microplate type, wells to read, PathCheck technology, optics settings, shake parameters, timing for Kinetic runs, speed read, and more.

To open the **Settings** dialog:

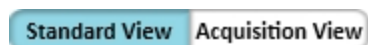
1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Settings**  on the **Home** tab in the ribbon or in the toolbar at the top of the active section.

The available options in the **Settings** dialog depend on the instrument, read mode, and read type that is selected.

For the SpectraMax i3 and i3x Instruments, the **Settings** dialog has two methods available for configuring a microplate read.

- The **Standard View** uses a table-like design, with selectable categories where you can configure your settings. See [Using the Standard View on page 237](#).
- The **Acquisition View** uses a workflow design, with drag-and-drop tools to configure your settings. See [Using the Acquisition View on page 240](#).

To switch between the views, click **Standard View** or **Acquisition View** in the lower-left corner of the **Settings** dialog.



For information about the available settings, see the following topics:

- [Wavelength Settings on page 247](#)
- [Plate Type Settings on page 250](#)
- [Read Area Settings on page 255](#)
- [PathCheck Technology Settings on page 257](#)
- [TRF Settings on page 258](#)
- [PMT and Optics Settings on page 258](#)
- [Timing Settings on page 260](#)
- [Well Scan Settings on page 261](#)
- [Shake Settings on page 262](#)
- [Speed Read on page 262](#)
- [Well Area Settings on page 263](#)
- [Image Acquisition Settings on page 264](#)

- [Image Analysis Settings on page 266](#)
- [Region of Interest Settings on page 281](#)
- [Settings for Reads with Injection on page 282](#)
- [More Settings on page 285](#)
- [Compound Transfer Settings on page 289](#)
- [Compound Source Settings on page 292](#)
- [Pipette Tips Layout Settings on page 293](#)
- [Compound and Tips Columns Settings on page 293](#)
- [Triturate Settings on page 296](#)

Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

Wavelength Settings

The available wavelength settings vary depending on the selected instrument, read mode, and read type.

Procedures to optimize excitation and emission wavelengths for a given protocol are described in the instrument user guides for the microplate readers that support this function. For more information, see those user guides.

Endpoint, Kinetic, Well Scan, or Flex Reads

Specify the number of wavelengths to read, and then type or select a wavelength value within the available range for the instrument for each wavelength.

For filter-based instruments, select from the available filters.

Bandwidth

Bandwidth selection is available only for fluorescence intensity (FL) and luminescence (LUM) reads the SpectraMax i3 or SpectraMax i3x Multi-Mode Detection Platforms using the built-in Monochromator.

Select the spectral bandwidth of the wavelength for the read. The selected bandwidth is used for all the wavelengths in a multiple wavelength read.

For fluorescence intensity reads, select separate bandwidths for the excitation and emission wavelengths.

Spectrum Reads

Choose a **Start** and a **Stop** wavelength value within the available range for the instrument, and choose a wavelength **Step** for each increment between reads.

The minimum selectable **Step** increment is 1 nm.

Cutoffs

The choices in this portion of the Wavelengths setting depend on the selections for read type (Endpoint, Kinetic, Spectrum, or Well Scan) and read mode (Fluorescence, Fluorescence Polarization, or Time Resolved Fluorescence).

The term cutoff refers to filters used to block unwanted residual excitation light and minimize background interference.

No emission cutoff filter is used when a Luminescence read mode is selected. With other read modes, choices are to enable or disable Auto Cutoff with specific filter settings available if it is disabled (manual cutoff selection). When Auto Cutoff is enabled, the instrument sets the cutoffs based on the wavelengths chosen for reading. When a Spectrum read type is selected, a manual setting for the emission monochromator is required, with the default being no cutoff filter.

Determining a manual setting for a cutoff filter is based on the known value of the Stokes shift, which is the difference between the wavelengths of the excitation and emission maxima. If the Stokes shift is small, choose an excitation wavelength that is as far as possible from the emission maximum while still being capable of exciting the fluorophore. Doing this causes less of the excited light to overlap the emission spectrum, permitting better selection and quantitation of the emitted light. See the individual instrument user guides for more information about cutoff filter settings.

Imaging Reads

Select one or more wavelengths, or channels, to use for the acquisition. Images are acquired separately for each wavelength or channel, and can be analyzed separately.

The SpectraMax MiniMax 300 Imaging Cytometer captures images from the bottom of each microplate well. You can choose to illuminate the sample with white transmitted light from the top of the microplate using the Transmitted Light (TL) Detection Cartridge, or use fluorescent excitation from the bottom of the microplate.

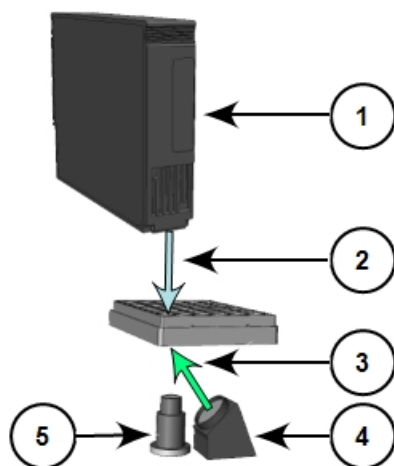


Figure 7-1: Path of Selected Light Sources

Item	Description
1	Transmitted Light (TL) Detection Cartridge
2	Path of white light from the Transmitted Light (TL) Detection Cartridge
3	Path of fluorescent excitation
4	Light source for fluorescent excitation
5	Camera lens

To illuminate the sample from the top, you need to have the Transmitted Light (TL) Detection Cartridge installed in the detection cartridge drawer. See [Transmitted Light \(TL\) Detection Cartridge on page 233](#).

For best results with transmitted-light reads, use a microplate with no cover. A clear cover can be used, if required. For fluorescent reads, you can use a solid cover on the microplate.

Plate Type Settings


The Plate Type settings determine the display of the wells in the **Plate** section. Set the plate type to match the microplate type, the number of wells, the clarity or opaqueness of the wells, and the round or square shape of the wells in the microplate to be read.

Changing the Plate Type for a **Plate** section causes the well assignments stored in the previous template to be discarded. The groups created previously remain, however, so you can select new wells and apply existing groups to these wells.

The Plate Library includes entries for microplates of various sizes with standard dimensions. If you are uncertain which microplate to select, then select the Standard plate definition. You can choose to edit the dimensions of a microplate or add a custom microplate to the microplate library.

- To edit the dimensions of a microplate in the library, select the microplate from the list and click **Edit Plate** to open the **Plate Editor** dialog.

In the **Acquisition View**, click  to open the **Plate Editor** dialog.

- To add a new microplate to the library, select a microplate from the list and click **Edit Plate** or click . Type a name for the new microplate in the **Plate Name** field of the **Plate Editor** dialog.
- To include a microplate from a predefined microplate description, click **Import Plate** and use the file system browser to locate the microplate description file.



Note: The **Import Plate** option is available only in the **Standard View** for the SpectraMax Paradigm Multi-Mode Microplate Reader, the SpectraMax i3x Multi-Mode Detection Platform, and the FilterMax F3 and F5 Multi-Mode Microplate Readers.

- To delete a microplate from the microplate library, select the microplate to be removed and click **Remove**.

In the **Acquisition View**, click . In the **Plate Editor** dialog, make sure that the name of the microplate to be removed is in the **Plate Name** field, and then click **Delete**.

For information about defining custom microplate dimensions, see [Using the Plate Editor on page 251](#).



Note: Only the custom microplate definitions created or edited in Imaging mode can be used for Imaging reads. Microplate definitions created, edited, or optimized for other read modes are not included in the list of available microplates for Imaging reads.

When using a SpectraMax Paradigm Multi-Mode Microplate Reader, you can define the microplate orientation.

Choose the microplate orientation to match the orientation of the microplate in the microplate drawer.

- **Landscape** puts the A1 location in the upper-left corner closest to the instrument.
- **Portrait** puts the A1 location in the upper-right corner closest to the instrument.
- **Opposite Landscape** puts the A1 location in the lower-right corner farthest from the instrument.
- **Opposite Portrait** puts the A1 location in the lower-left corner farthest from the instrument.

If the microplate has a lid, select **Is Lidded** in the **Standard View**, or **Plate has a lid on top** in the **Acquisition View**.




CAUTION! If the microplate has a lid on top, you must indicate that the microplate is lidded and make sure that the microplate height with a lid is set accurately in the **Plate Editor** before starting a read.

Using the Plate Editor

Use the Plate Editor to modify the definition of an existing microplate, or to add a new microplate definition to the Plate Library.

If you opened the Plate Editor from the **Acquisition View**, you can remove the custom microplate that is named in the **Plate Name** field by clicking **Delete**. The **Delete** button is available only for saved custom microplate definitions.

To view the Plate Editor:

1. Click a **Plate** section to make it active in the workspace.
2. Click **Settings**  on the **Home** tab in the ribbon or in the toolbar at the top of the active section.
3. In the **Settings** dialog, click the **Plate Type** category.
4. In the **Plate Type Settings**, click **Edit Plate**.

In the **Acquisition View**, click  to open the **Plate Editor** dialog.

The Plate Editor has fields and check boxes that you can use to define the microplate dimensions, in millimeters.



Note: SoftMax Pro Software comes with plate definitions for the SpectraDrop 24-well Micro-Volume Microplates and SpectraDrop 64-well Micro-Volume Microplates.

Modifying the Dimension of an Existing Plate

To modify the dimension of an existing plate when you do not want to change the name of the plate:

1. In the **Plate Type Settings**, click the plate in the list and then click **Edit Plate**.

In the **Acquisition View**, click  to open the **Plate Editor** dialog.

2. Type the custom dimensions as needed.
3. Click **Save**.

The changed plate has an asterisk at the end of the plate name.

Importing a Plate Definition

Importing a previously saved microplate definition is available only with the SpectraMax i3 and i3x Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers. For the SpectraMax i3x Multi-Mode Detection Platform, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers.

1. In the **Plate Type Settings**, click **Import Plate**.
2. In the **Open** dialog, navigate to the location where the microplate definition is saved.
3. Select the **Microplate File (*.plt)** or **Multimode File (*.xml)** file type.
4. Select the plate definition file.
5. Click **Open** to add the plate definition to the list.

Creating a New Plate

1. In the **Plate Type Settings**, click a plate in the plate list then and click **Edit Plate**.

Defining a new plate can be easier if you select a similar plate from the list before opening the Plate editor.

In the **Acquisition View**, click  to open the **Plate Editor** dialog.

2. In the **Plate Editor**, in the **Plate Name** field, type a name for the new plate definition.
3. Type the dimensions of the new plate as needed.
4. Click **Save**.

The new plate name is displayed in the plate list.

Table 7-2: Plate Editor Tools








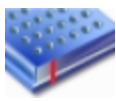


Field Name	Image	Description
Left Edge to Left Well Center		Type the distance from the left edge of the plate to the center of well A1 in millimeters.
Horizontal Center to Center		Type the horizontal distance between well centers in millimeters.
Top Edge to Top Left Well Center		Type the distance from the top edge of the plate to the center of well A1 in millimeters.
Vertical Center to Center		Type the vertical distance between well centers in millimeters.
Well Diameter and Well Shape		Type the diameter of a round well or the width of a square well in millimeters. Select the Well Shape Square check box if the wells have a square shape, rather than round. The setting is available only with the SpectraMax i3 and i3x Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers.
Well Bottom Type / Thickness		Select the Clear well bottom check box if the wells have a clear bottom, rather than opaque. For the SpectraMax i3x Multi-Mode Detection Platform used with a SpectraMax MiniMax 300 Imaging Cytometer, type the thickness of the bottom of the well of the microplate. This setting is used to determine the initial focus distance for Imaging reads.
Well Volume / Depth		Type the depth of the well in millimeters. This setting is available only with the SpectraMax i3 and i3x Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers. For the SpectraMax i3x Multi-Mode Detection Platform used with a SpectraMax Injector Cartridge, type the working volume of the well for the microplate in microliters. This setting is used to determine the maximum allowed dispense volume for reads with injection.

Table 7-2: Plate Editor Tools (continued)

Field Name	Image	Description
Plate Height		Type the height of the microplate in millimeters and also the height of the microplate with a lid in millimeters. This setting is used to determine the read height for top reads, and is available only with the SpectraMax i3 and i3x Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers.
Plate Length		Type the length of the microplate in millimeters. This setting is available only with the SpectraMax i3 and i3x Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers.
Plate Width		Type the width of the microplate in millimeters. This setting is available only with the SpectraMax i3 and i3x Multi-Mode Detection Platforms, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers.

The distance from the left edge of the microplate to the center of well A1 must also include an offset for the angle of the optics.

To determine the correct settings for these fields, measure the applicable areas of the microplate in the lab.



CAUTION! To prevent damage to the instrument, the microplate height and read height must be set accurately before starting a read with a SpectraMax i3 Multi-Mode Detection Platform.

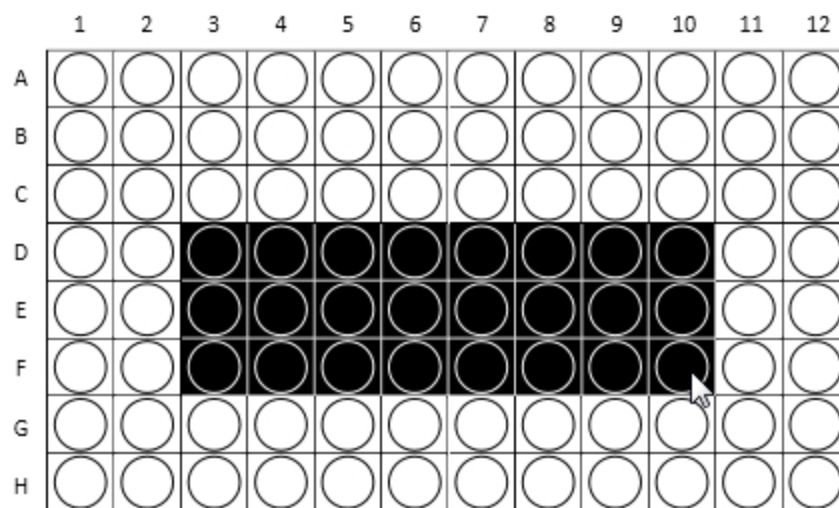
Microplate definitions are saved in a *.plt file in a sub-folder of the **ProgramData** folder. A custom microplate definition is specific to the computer on which it is saved, when a protocol that has a custom microplate selected is opened on a different computer, the SoftMax Pro Software gives an option to save the custom microplate definition on the new computer.

Read Area Settings

Partial-microplate reading is available for all read types, although it is most useful for fast kinetic analysis or image acquisition. The time required for kinetic readings or acquiring images can be significantly reduced using this setting since the instrument does not have to read the entire microplate.

You can choose to read an entire microplate or a subset of wells.

To select a contiguous, rectangular region on the microplate, use your mouse to drag the pointer and select the wells to be read.



Columns do not need to start with “1” but must be contiguous.

To read all the wells in the microplate, select the **Select All** check box.

For the SpectraMax i3 and SpectraMax i3x Instruments, you can select non-contiguous wells if you are using a **Well** read order in the **Standard View**, or have added a **For Each Well** loop in the **Acquisition View**. To select non-contiguous wells, hold down the **CTRL** key as you click each well.

If you select a partial microplate reading, only the wells to be read are visible in the data display, indicating that no data will be collected for the other wells. However, all wells are displayed in the Template Editor. See [Configuring a Microplate Template on page 301](#).

Western Blot Membrane Read Area Settings

To scan the membrane in a SpectraMax Paradigm or SpectraMax i3x Instrument, the membrane must be placed in a Molecular Devices ScanLater™ Membrane Holder. See [Loading the Membrane into the Membrane Holder on page 335](#).

A high-resolution scan of the entire surface can take approximately 15 minutes. To reduce the scanning time, you can define a smaller area for the scan.

Select the area to scan from the **Target Read Area** list.

- **Mini Membrane** scans an area 85 mm x 65 mm.
- **Whole Membrane Holder** scans an area 109 mm x 77 mm.
- **ROI Selection** scans an area based on the region of interest (ROI) defined and acquired in the **Plate** section.

If no region of interest has been defined and acquired in the **Plate** section, then **ROI Selection** is not available in the list.

The example in the Read Area settings shows the approximate area to be scanned.

PathCheck Technology Settings

You can enable PathCheck Technology in the SoftMax Pro Software **Settings** dialog by selecting the **PathCheck** check box in the **PathCheck Settings** for absorbance endpoint reads.

The temperature-independent PathCheck® Pathlength Measurement Technology normalizes your absorbance values to a 1 cm path length based on the near-infrared absorbance of water.

The Beer–Lambert law states that absorbance is proportional to the distance that light travels through the sample:

$$A = \epsilon bc$$

where A is the absorbance, ϵ is the molar absorptivity of the sample, b is the pathlength, and c is the concentration of the sample. The longer the pathlength, the higher the absorbance.

Microplate readers use a vertical light path so the distance of the light through the sample depends on the volume. This variable pathlength makes it difficult to do extinction-based assays and also makes it confusing to compare results between microplate readers and spectrophotometers.

The standard pathlength of a 1 cm cuvette is the conventional basis for quantifying the unique absorptivity properties of compounds in solution. Quantitative analysis can be done on the basis of extinction coefficients, without standard curves (for example, NADH-based enzyme assays). When using a cuvette, the pathlength is known and is independent of sample volume, so absorbance is directly proportional to concentration when there is no background interference.

See [PathCheck Pathlength Measurement Technology on page 156](#).

TRF Settings

TRF measures fluorescence as a function of time after excitation. You can set the integration delay before collecting data and the integration time of the fluorescence signal.

- The integration delay is the amount of time that elapses between the flash of the lamp (excitation) and the beginning of data acquisition from the well (emission).
- The integration time is the amount of time that the well is read.

See [Time-Resolved Fluorescence Read Mode on page 171](#).

PMT and Optics Settings

The sensitivity settings can be set in **PMT and Optics Settings** in the **Settings** dialog.

PMT sensitivity can be set to **Low**, **Medium**, or **High**. To get optimal PMT response without saturation, set the PMT gain to **High** for samples having lower concentration (dim samples), or use a lower PMT gain for samples having a higher concentration (bright samples).

To define the exact voltage to use for the **PMT Gain**, select **Manual** and then type a value in the field.

The **Automatic** setting, when available, lets the instrument adjust the PMT voltage automatically for varying concentrations of sample in the microplate.

The SpectraMax i3x Instrument uses two light sources. The Spectral Fusion™ Illumination uses the spectral range of a high power Xenon flash lamp intensified by LEDs in the visible range. Automatic LED power adjustment is used with high PMT Gain when the excitation wavelength is between 430 nm and 680 nm for high sensitivity across multiple fluorophores. In multiple-wavelength reads, the **PMT Gain** is set to **High** and cannot be changed.

For some instruments, the PMT sensitivity is always set to **Automatic** for Luminescence (LUM) and Time Resolved Fluorescence (TRF) read modes. For these instruments, the **PMT Gain** setting is not available for these read modes.

For Western Blot membrane scans, you can choose the resolution for the full scan and for a secondary scan of a region of interest.

- The **Default Scan Resolution** applies to the entire read area of the membrane defined in the **Read Area** settings.
- The **ROI Scan Resolution** applies to the region of interest (ROI) defined in the **Plate** section.

A **High** resolution scan provides the best results, while a **Low** resolution scan provides the fastest read.

The general workflow for acquiring Western Blot data, is to scan the defined read area of the membrane with a low resolution, and then define a region of interest (ROI) to be scanned at a high resolution.

For some instruments in certain read modes, you can type the desired number of **Flashes per read**. For the SpectraMax i3x Instrument when the excitation wavelength is between 430 nm and 680 nm, 60 flashes is equal to 1 second of integration time.

For the SpectraMax Paradigm Multi-Mode Microplate Reader, and for some detection cartridges with the SpectraMax i3x Multi-Mode Detection Platform, you can select **On the Fly Detection** options.

On-the-Fly Detection, when enabled, yields considerably faster read times while the microplate moves continuously as each well is measured, as opposed to when it is disabled (**Off-stop and go**) and the microplate stops moving for each read.

To use On-the-Fly Detection, select an option to specify whether the detection method should be optimized for **Performance** or **Speed**.

- Selecting **Performance** results in a faster read time than not using On-the-Fly Detection, but not as fast as the Speed mode. Performance provides considerably better results than Speed for demanding assays.
- Selecting **Speed** results in the fastest possible read time per microplate. However, there is a trade-off between the data quality and read speed because each well is sampled for shorter integration times.

For the SpectraMax Paradigm Multi-Mode Microplate Reader and the FilterMax F5 Multi-Mode Microplate Reader, and some detection cartridges with the SpectraMax i3x Instrument, you can set the **Integration Time**. Type a value in the **Integration Time** field in milliseconds, to specify the measurement time per well to be validated.

Select the **Read From Bottom** check box to have an instrument with bottom-read capability read up through the bottom of the microplate rather than down from the top.

For the SpectraMax i3x Instrument, the SpectraMax Paradigm Multi-Mode Microplate Reader, and the FilterMax F5 Multi-Mode Microplate Reader, you can specify the **Read Height**.

Read Height specifies the distance in millimeters between the objective lens and the microplate. You can type a value for the read height in this field.

To have SoftMax Pro Software find the optimized read height before the read, use the **Read Height Optimization** feature in the **Pre-Read Optimization** dialog by selecting the **Show Pre-Read Optimization Options** check box in the **More Settings** tab.

Read Height is available for the SpectraMax i3x Multi-Mode Detection Platform and the FilterMax F5 Multi-Mode Microplate Reader for top-read only.



CAUTION! To prevent damage to the instrument, the microplate height and read height must be set accurately before starting a read with a SpectraMax i3 Multi-Mode Detection Platform.

Timing Settings

For Kinetic and Flex reads you can define the total run time and the time interval between reads.

Type values for the **Total Run Time** and the **Interval** between readings in **hh:mm:ss** format.


For the SpectraMax i3x or i3 Multi-Mode Detection Platform and the SpectraMax Paradigm Multi-Mode Microplate Reader, selecting a **Well** read order in the **Standard View**, or adding a **For Each Well** loop in the **Acquisition View**, for a kinetic read lets you define timing parameters in milliseconds.

The minimum permitted interval values are shown below the **Interval** field.

The **Number of Reads** is calculated based on the values in the **Total Run Time** and **Interval** fields.

To read only one time point, click **Single Point Read** to set the **Total Run Time** and the **Interval** to the same value. This can be useful for running a multitask kinetic read with alternating read modes within a cycle. See [Defining and Running a Workflow on page 297](#).

The minimum permitted read interval is determined by the instrument, and depends on many factors including the number of wavelengths, the number of wells being read, and the distance the instrument's filter wheel must move. Maximum read intervals also vary by instrument, for example the SpectraMax M2 Multi-Mode Microplate Reader has a maximum read interval of 2 hours and 45 minutes, and the SpectraMax Paradigm Multi-Mode Microplate Reader has a maximum read interval of 18 hours and 12 minutes. If you type a non-allowed read interval, a message is displayed defining the minimum or maximum permitted value for the read interval.

 **Tip:** In some cases, choosing wavelengths in ascending order can get the shortest possible interval.

Well Scan Settings

A well scan read can take readings at more than one location within a well. A well scan read takes one or more readings of a single well of a microplate on an evenly spaced grid inside of each well at single or multiple wavelengths.

Some applications involve the detection of whole cells in large-area tissue culture plates. Well scan reads can be used with such microplates to permit maximum surface area detection in whole-cell protocols. Since many cell lines tend to grow as clumps or in the corners of microplate wells, you can choose from several patterns and define the number of points to be scanned to work best with your particular application.

Well Scan reads let readings be taken at more than one location within a well. Well Scan settings let you specify how a Well Scan is done.

You can specify the scanning pattern and the scanning density.

The number of points that are available depend on the well size of the selected microplate.

Up to four scanning patterns are available, depending on the selected instrument:

- A horizontal line
- A vertical line
- A cross (which is a combination of a horizontal and vertical line)
- A fill pattern

The fill pattern can be either round or square to match the shape of the well. The image in the Well Scan settings shows the shape of the well as defined for the selected microplate. See [Plate Type Settings on page 250](#).

The following are determined by **Density**:

- The number of points that are read in the line patterns.
- The maximum number of horizontal and vertical points that are included in the cross or fill pattern.

Shake Settings

Shake lets you set options for automated shaking of the microplate in the chamber. The options available for Shake depend on the read type and the instrument.

Before First Read

This setting can be used with all read types. Whether you read at a single wavelength or at multiple wavelengths, selecting the **Before First Read** shakes the plate for the set quantity of time before the first wavelength reading only.

Between Reads

This option is available only when a Kinetic read type is selected.

For readings at a single wavelength, enabling **Between Reads** shakes the plate for the specified quantity of time before each reading at that wavelength.

For readings at multiple wavelengths, enabling **Between Reads** shakes the plate for the specified quantity of time before each reading at the first wavelength only.



Note: The **Before First Read** and **Between Reads** options are available only in the **Standard View**. To enable shaking in the **Acquisition View**, place the **Shake** node in the time line where you want the shake to occur.

For the SpectraMax i3x Multi-Mode Detection Platform and the SpectraMax Paradigm Multi-Mode Microplate Reader, you can specify the method for the microplate shaking operation. The microplate shaking options include to following:

- **Intensity:** Low, Medium, or High. The actual shake speed is based on the microplate format.
- **Direction:** Linear or Orbital patterns.
- **Duration:** Length of time in seconds.

Speed Read

Enable **Speed Read** for an Absorbance read to read the plate faster by decreasing the number of lamp flashes.

The **Speed Read** option is particularly useful in Spectrum scans and can greatly reduce the time needed to run the protocol.

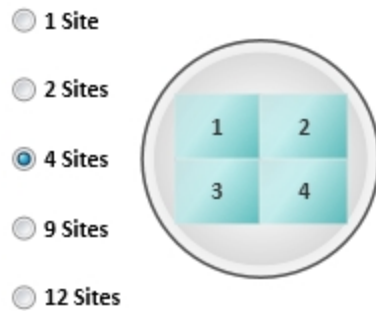
For instruments that support software calibration, **Speed Read** turns off **Calibration** and uses the air calibration values stored in the firmware of the instrument. As a result, **Speed Read** might not provide as accurate an absorbance measurement at each wavelength of a scan as with the normal read.

Well Area Settings

The Well Area Settings for Imaging reads let images be acquired at more than one location, or site, within a well to form a single seamless tiled image.

Select the number of sites that you want to acquire.

Well Area Settings



If you select to acquire images of more than one site in the well, the images are "tiled" together into a single image for analysis.

Image acquisition time increases with each site selected. For faster image acquisition, select fewer sites.


Image Acquisition Settings

In the Image Acquisition Settings, you can define the exposure time and focus adjustment for two sample wells. These settings are used for every well in the entire microplate during acquisition. The exposure and focus adjustment can be set separately for each wavelength, or channel.


Acquiring Images for Maximum Intensity and Minimum Intensity

Only one site is acquired in each well. If you selected to acquire more than one site, the first site is acquired.

To acquire the image for maximum intensity:

1. Click  to the right of the **Well** field above the maximum intensity image area.
2. Click the microplate well that you expect to have the brightest image.
The well filled with red is used to determine maximum intensity, and the well filled with blue is used to determine minimum intensity.
3. Click **Acquire Max Image** and wait for the image to be acquired.

To acquire the image for minimum intensity:

1. Click  to the right of the **Well** field above the minimum intensity image area.
2. Click the microplate well that you expect to have the darkest image.
The well filled with red is used to determine maximum intensity, and the well filled with blue is used to determine minimum intensity.
3. Click **Acquire Min Image** and wait for the image to be acquired.

For some multi-channel experiments, the brightest and darkest images for one channel can be different than the brightest and darkest images for another channel. In this case, try to locate the wells that give you the best results between the different channels.

To view the image for a specific wavelength, click the tab above the image for that wavelength. To view an image with all the wavelengths, click **Composite**.

To zoom the acquired image in and out, right-click the image and click **Zoom In** or **Zoom Out**. You can also hold the **CTRL** key down and press **+** or **-**, or use the mouse wheel to zoom in or out. Drag the scroll bars to move the zoomed image in the image area, or click the image and drag it into position. To view a larger version of the image area, double-click the image to open the **Zoom Well** dialog. See [Zooming the Image in a Well on page 338](#).

Setting the Exposure Time and Focus Adjustment

The exposure and focus adjustment can be set separately for each wavelength, or channel. To view the image for a specific wavelength, click the tab above the image for that wavelength. To view an image with all the wavelengths, click **Composite**. Set the exposure and focus adjustment in the row designated for the specific channel.

To have the SoftMax Pro Software determine the best exposure, click **Auto Expose**. The new value in the **Exposure** field is based on the perceived best intensity for the **Max Intensity** or **Min Intensity** image, whichever is brightest. To view what effect the new exposure value has on the images, acquire the maximum intensity and minimum intensity images again.

To continue to adjust the intensity of the images, type a value in the **Exposure** field for the number of milliseconds to hold the camera shutter open. Increasing the exposure time increases the intensity of the image, while decreasing the exposure time decreases the intensity of the image. After each adjustment, acquire the images again to view what effect the change has on their intensity.

The system optics use a laser automatic focus system and software algorithms to find the initial focus distance for the cells in the microplate wells. You can adjust the focus by typing a value in the **Focus Adjustment** field for the number of microns to move the objective lens closer to or farther away from the sample.

- Increasing the **Focus Adjustment** value moves the objective lens closer to the sample.
- Decreasing the **Focus Adjustment** value moves the objective lens farther away from the sample.

After each adjustment, acquire the images again to view what effect the change has on their focus.

For transmitted light images, make sure that enough contrast exists between the objects and the background. The sharper the focus is, the less contrast exists. For best results when you use a preset drawing analysis, make sure that the objects are brighter than the background.

These settings are used for every well in the entire microplate during acquisition.

Image Analysis Settings

In the **Image Analysis Settings** category, select an analysis type to use.

To acquire images without analysis, click **No Analysis**.

Discrete Object Analysis

Discrete Object Analysis uses proprietary algorithms to analyze separate objects, or cells, based on multiple parameters including the signal intensity over the background and the size of the objects.

When you click **Discrete Object Analysis**, The **Wavelength for Finding Objects** list appears below the list of analysis types. Select the wavelength from this list to use to identify the objects in the well images. You can use transmitted light or a fluorescent wavelength to find nuclei or easily separable objects in the image. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

The **Image Analysis Settings** category on the left expands to show the subcategories that follow:

- Click **Find Objects** to enter size and intensity values or use proprietary algorithms with the provided drawing tools to graphically define the objects and the background areas for the analysis. See [Finding Discrete Objects or Confluent Areas on page 267](#).
- Click **Classify Objects** to define separate measurements for different types of found objects, or cells. See [Classifying Discrete Objects on page 271](#).
- Click **Select Measurements** to view the results of the analysis for the selected wells. See [Viewing and Selecting Measurement Statistics on page 273](#).

Field Analysis

Field Analysis uses proprietary algorithms to analyze confluent areas based on multiple parameters including the signal intensity over the background and the size of the areas.

When you click **Field Analysis**, The **Wavelength for Finding Confluent Areas** list appears below the list of analysis types. Select the wavelength from this list to use to identify the confluent areas in the well images. The StainFree™ Cell Detection Algorithm eliminates cell staining for cell counting and confluency measurements using proprietary transmitted light analysis technology.

The **Image Analysis Settings** category on the left expands to show the subcategories that follow:



- Click **Find Confluent Areas** to use proprietary algorithms with the provided drawing tools to graphically define the confluent areas and the background areas for the analysis. See [Finding Discrete Objects or Confluent Areas on page 267](#).
- Click **Select Measurements** to view the results of the analysis for the selected wells. See [Viewing and Selecting Measurement Statistics on page 273](#).

The SoftMax Pro Software proprietary algorithms with the provided drawing tools in the **Find Objects** or **Find Confluent Areas** settings help the software learn the patterns of the objects that you want to find. Depending on the complexity of the object patterns, this teaching process can take several iterations before you get your desired results. See [Resolving Common Issues with Drawing and Finding Objects on page 275](#).

Finding Discrete Objects or Confluent Areas

In the **Find Objects** or **Find Confluent Areas** settings, the minimum and maximum images from the **Image Acquisition Settings** are displayed.

To make it easier to select the objects or areas in the images, view this page in full screen.

- Click  to view the page in full screen.
- Click  to restore the page to its original size.

In full-screen view, click the tabs at the top of the page to switch between the different pages of the analysis settings.

To zoom the acquired image in and out, right-click the image and click **Zoom In** or **Zoom Out**. You can also hold the **CTRL** key down and press **+** or **-**, or use the mouse wheel to zoom in or out. Drag the scroll bars to move the zoomed image in the image area, or click the image and drag it into position.

Click the buttons above the image to switch the view of the image between wavelengths, and to show or hide found objects (or confluent areas) and drawings.



- When a button is filled in, the related wavelength, objects (or confluent areas), and drawings are displayed in the image.
- When a button is outlined, the related wavelength, objects (or confluent areas), and drawings are not displayed in the image.

When you click a button above one of the images, it effects the display of both images. Use the controls below the image to separately adjust the intensity of each wavelength. From the list on the left, select the wavelength that you want to adjust.



Drag the sliders to adjust the intensity range of the image.



- The bar on the left controls the low level of intensity.
- The bar on the right controls the high level of intensity.

When you drag a bar, the intensity level is displayed above the bar.

To move the sliders to the outside edges, click the double-arrow button on the left.

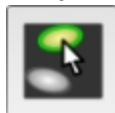
From the list on the right, select the color for the view.

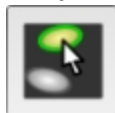


For fluorescent acquisition and discrete object analysis, you can select a **Finding Method**:

- Click **Set Size and Intensity** to define the intensity threshold above the background intensity to be applied separately to each object in the image that meets the defined size range. This type of analysis helps to detect objects in areas of the image where the intensity is uneven.
- Click **Draw on Images** to use the drawing tools to help the software learn the patterns of the objects that you want to find.

The **Set Size and Intensity** settings are available for fluorescent acquisition and discrete



object analysis. Click  and then click four or more representative objects on the images that you want to detect as cells. In the **Min Width** and **Max Width** fields, type values to define the size range in microns of the objects to be found. In the **Intensity Above Background** field, type a value to indicate the intensity threshold above the background intensity at which the dimmest object is to be detected. For example, if the background intensity is 1000 and the intensity of the dimmest object is 1200, type 200. After you enter new settings, click **Apply**.

The **Grow** setting allows you to define the number of pixels to increase the diameter of the found objects in one wavelength, so that they can be measured at the new size in another wavelength of the acquisition. For example, if you are using a stain for nuclei, you can find the object in the first wavelength and then increase the diameter to find the protein of interest in another fluorescence wavelength. The innovative "grow without touching" algorithm increases the size of the measured areas without letting the areas touch or overlap their edges.


Draw on Images is available for every type of image acquisition and analysis. You can use the drawing tools to help the software learn the patterns of the objects or confluent areas that you want to find. Depending on the complexity of the object or area patterns, this teaching process can take some time before you get your desired results.

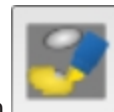
To use a preset drawing analysis, select the preset from the **Settings** list. Each preset drawing analysis is designed to work with specific cell types. Select the preset analysis that works best with your images. Click **Apply** to find objects or confluent areas using the preset.

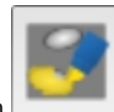
After you have acquired data, you can select **Stored Setting** from the **Settings** list to use the previously defined analysis settings.

To start from scratch, select **Create New Setting** from the **Settings** list.

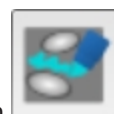
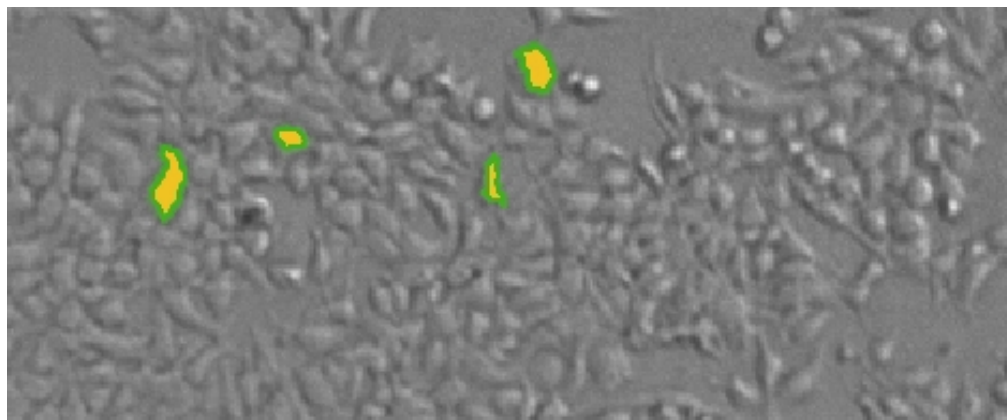


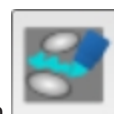
To select the objects for fluorescent acquisition and discrete object analysis, click  and then click a line width. Click four or more representative objects on the images. This method is not available for transmitted light acquisition or for confluent area analysis.

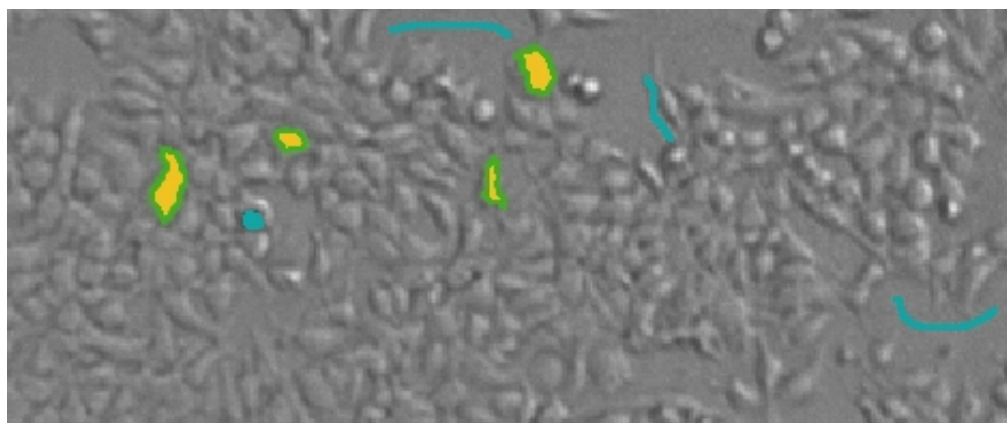


To define the objects or confluent areas, click the object or area pen  and then click a line width.

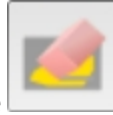
- For discrete object analysis, draw inside the object up to the edge, but do not include the edge. When the object is filled in with yellow, the drawing is outlined in green. For best results, fill in four or more representative objects.
- For field analysis, draw across confluent areas, avoiding background. For best results, draw across four or more representative areas.



To define the background, click the background pen  and then click a line width. Draw on the image to define artifacts and background areas in blue. For best results, define four or more representative background areas.

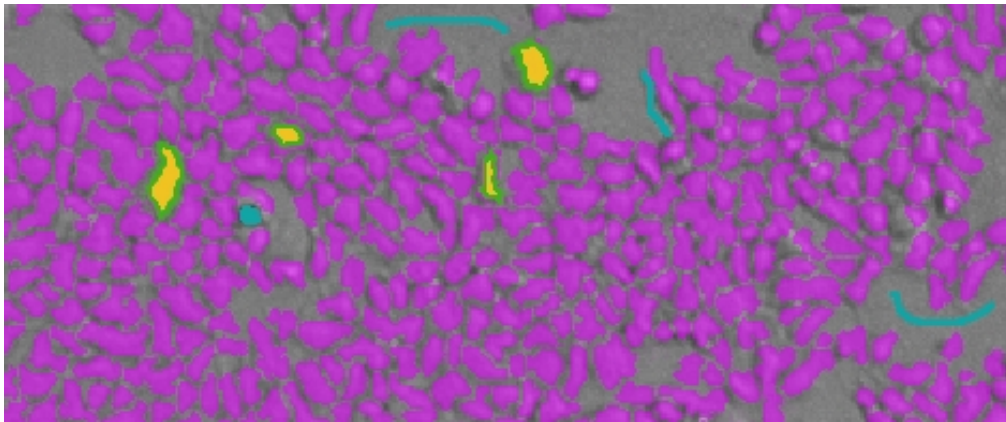


If you draw an object or area incorrectly, click **Undo** to remove it. If you undo something that you want to keep, click **Redo** to restore it. To clear the drawings from the image, click **Start Over**.



To erase parts of drawings, click the eraser and then click a line width. Drag the eraser across drawings to remove them.

After you have the objects and areas defined, click **Apply** to have the software find the objects or confluent areas in the image. Continue to draw and to apply until you get satisfactory results. See [Resolving Common Issues with Drawing and Finding Objects on page 275](#).



After you are satisfied with the found objects or confluent areas, you can classify objects or view the measurement statistics. See [Classifying Discrete Objects on page 271](#) or [Viewing and Selecting Measurement Statistics on page 273](#).

Classifying Discrete Objects

In the **Classify Objects** settings, the minimum and maximum images from the **Image Acquisition Settings** are displayed along with the found objects from the **Find Objects** settings. The **Classify Objects** settings are not available for field analysis of confluent areas.



Note: Before you can classify objects, you must first find objects in the **Find Objects** settings. See [Finding Discrete Objects or Confluent Areas on page 267](#).

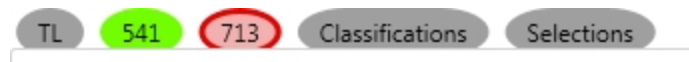
To make it easier to select the objects in the images, view this page in full screen.

- Click to view the page in full screen.
- Click to restore the page to its original size.

In full-screen view, click the tabs at the top of the page to switch between the different pages of the analysis settings.

To zoom the acquired image in and out, right-click the image and click **Zoom In** or **Zoom Out**. You can also hold the **CTRL** key down and press + or -, or use the mouse wheel to zoom in or out. Drag the scroll bars to move the zoomed image in the image area, or click the image and drag it into position.

Click the buttons above the image to switch the view of the image between wavelengths, and to show or hide classified objects or selections.



- When buttons are filled in, the related wavelengths, classifications, or selections are displayed in the image.
- When a button is outlined, the related wavelengths, classifications, or selections are not displayed in the image.

When you click a button above one of the images, it effects the display of both images.

Use the controls below the image to separately adjust the intensity of each wavelength.

From the list on the left, select the wavelength that you want to adjust.



Drag the sliders to adjust the intensity range of the image.



- The bar on the left controls the low level of intensity.
- The bar on the right controls the high level of intensity.

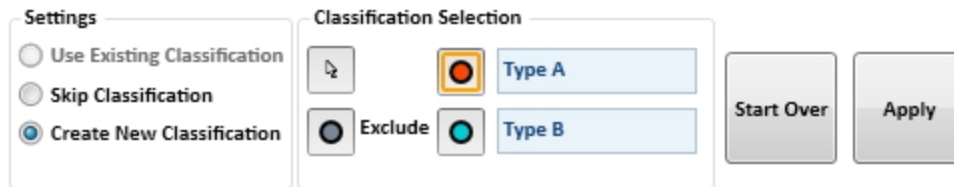
When you drag a bar, the intensity level is displayed above the bar.

To move the sliders to the outside edges, click the double-arrow button on the left.

From the list on the right, select the color for the view.



Use the selection tools at the bottom of the page to classify the found objects in the images into two separate classifications.



In **Re-Analysis** mode, you can select and apply **Use Existing Classification** to use the previously defined classification settings.

If you do not want to use classification in your analysis, click **Skip Classification**.

You can replace the **Type A** and **Type B** titles with your own titles for the classifications. Titles must use only letters, numbers, and spaces, and can be up to 16 characters long, including spaces. They must start and end with a letter. The titles cannot be the same as each other. Also, you cannot use "Exclude" as a title, since this is a reserved word.

To start classifying objects from scratch, click **Create New Classification**.

- To select objects for the first classification, click the red button and then click the objects in the images.
- To select objects for the second classification, click the blue button and then click the objects in the images.
- To exclude objects from being classified, click the gray button and then click the objects in the images. If you exclude objects, you must also use at least one of the classifications types to include objects.

To deselect a selected object click it again. To remove all the selections from the images, click **Start Over**.



After you have several classified objects selected, click **Apply** to have the software find and classify the objects in the image. Continue to select and to apply until you get satisfactory results.

After you are satisfied with the classified objects, you can view the measurement statistics. [Viewing and Selecting Measurement Statistics on page 273.](#)

Viewing and Selecting Measurement Statistics

In the **Measurement Selections** settings, a table is displayed with the analysis results for the minimum intensity and maximum intensity images.

To make it easier to view the measurements table, view this page in full screen.

- Click  to view the page in full screen.
- Click  to restore the page to its original size.

In full-screen view, click the tabs at the top of the page to switch between the different pages of the analysis settings.

The results are displayed separately for each measured wavelength and classification, if applicable. Each measurement row displays two bars and numerical data representing the **Max Intensity** or **Min Intensity** images.

The possible included measurements are as follows:

- **Object Count** gives the total number of objects detected in the image. This measurement is not used for field analysis of confluent areas.
- **Field Count** gives the total number of confluent areas detected in the image. This measurement is not used for discrete object analysis.
- **Object Percentage** gives the percentage the objects detected in the image by classification. This measurement is not used for field analysis of confluent areas.
- **Covered Area** gives the combined area of all the objects or confluent areas detected in the image as a percentage of the entire image area.
- **Object Area** gives the average area of the objects detected in the image expressed in μm^2 . This measurement is not used for field analysis of confluent areas.
- **Field Area** gives the average area of the confluent areas detected in the image expressed in μm^2 . This measurement is not used for discrete object analysis.
- **Object Roundness** gives the average roundness of each object detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for field analysis of confluent areas.
- **Field Roundness** gives the average roundness of each confluent area detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for discrete object analysis.
- **Object Average Intensity** gives the average fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Average Intensity** gives the average fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Object Intensity** gives the average total fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).

- **Field Intensity** gives the average total fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Total Intensity** gives the combined total fluorescent signal intensity of the objects or confluent areas detected in the image expressed in million intensity counts. This measurement is not used for transmitted light (TL).

To select the measurements that you want to include in the analysis, click **Select Measurements** in the lower-right area of the page. This places a **Remove** button next to each measurement in the table.

- To exclude a measurement, click **Remove**.
- To include a measurement, click **Add**.
- To exclude all measurements, click **Remove All**.
- To include all measurements, click **Add All**.

After you have selected the measurements that you want to include and exclude, click **Done**.

The selected measurements are dynamically added to the data reduction list that you can use to view data in the **Plate** section or to add to a **Group** section for further analysis. See [Using a Plate Section on page 118](#) or [Using a Group Section on page 139](#).

To view the measurements in an interactive image, data table, and chart, click **Show Details**. See [Viewing the Imaging Data in a Well on page 365](#).

If no measurements are displayed, and you did not make changes to the analysis settings since the last measurement, click **Measure** to analyze the selected wells. This can be useful if you change acquisition wells and want to analyze the new wells.

Resolving Common Issues with Drawing and Finding Objects

The SoftMax Pro Software proprietary algorithms with the provided drawing tools in the **Find Objects** or **Find Confluent Areas** settings help the software learn the patterns of the objects that you want to find. Depending on the complexity of the object patterns, this teaching process can take several iterations before you get your desired results.

The SoftMax Pro Software uses a complex algorithm to learn the properties of the cells or confluent areas in the image. The algorithm examines each pixel and how it relates to its surrounding area. Cells change shapes and sizes under different conditions such as confluency. Artifacts can look like cells or confuse the algorithm. Cells that are touching are more difficult to find than sparse cells in an image. Complex images can require more drawing examples to create a good training set.

Some common issues with finding cells and confluent areas are as follows:

- Under splitting finds multiple cells or confluent areas that can also include background. See [Resolving Under-Splitting Issues on page 277](#).
- Over splitting finds portions of cells or confluent areas and can include several found objects within a single cell or confluent area. See [Resolving Over-Splitting Issues on page 278](#).
- Artifacts can be found and counted as cells or confluent areas. See [Resolving Artifact Issues on page 279](#).
- Ghosting finds background areas next to cells or confluent areas. See [Resolving Ghosting Issues on page 280](#).

Molecular Devices recommends that you start with a preset drawing analysis. Select the preset from the **Settings** list and then click **Apply** to find objects or confluent areas using the preset. Each preset drawing analysis is designed to work with specific cell types. Select the preset analysis that works best with your images.

For transmitted light images, make sure that enough contrast exists between the objects and the background. The sharper the focus is, the less contrast exists. To increase the contrast between the objects and the background, move the lens closer to or farther away from the microplate.

Adjust the focus in the **Image Acquisition Settings**. Increasing the **Focus Adjustment** value moves the objective lens closer to the sample, while decreasing the **Focus Adjustment** value moves the objective lens farther away from the sample. In general, moving the lens closer makes the objects darker than the background, while moving the lens farther away makes the objects brighter than the background.



Note: For best results when you use a preset drawing analysis, make sure that the objects are brighter than the background.

To create an iterative training set for complex images can require the following steps:

1. Carefully draw four or more cells or confluent areas that best represent your target population. Draw inside the cell or confluent area up to the edge, but do not include the edge.
2. Define the artifacts and background areas in the image.
3. Apply the drawing and then try to fix the problems.
4. Continue to adjust the drawings. After fixing some problems the results can actually look worse as the algorithm emphasizes the fixes. Keep making adjustments to create a complete training set.
5. After the result looks reasonable, scroll and look around the image for other issues.
6. Stop when you are satisfied or you get diminishing returns. As the training data set grows, more drawings will have less impact. At some point changes will be of little benefit.

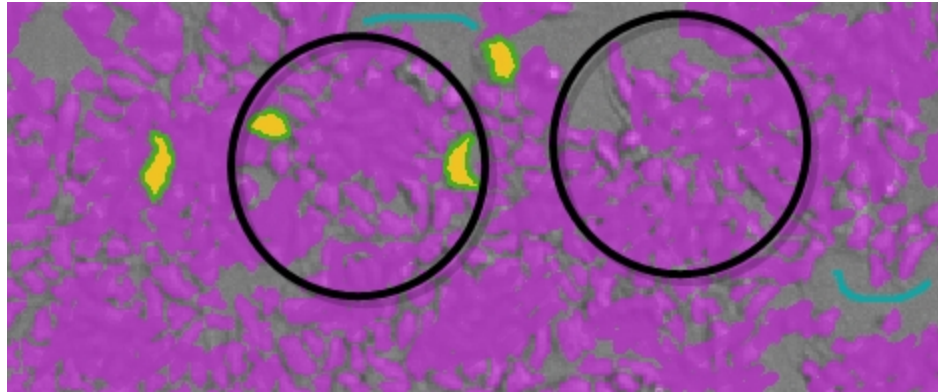
If, at the end of the process, it is still not right, start again and repeat all the steps.

Sometimes there is something that had an unexpected influence on the algorithm, and starting over can produce a better result.

If, after trying multiple iterations, ask someone else with experience to try. This person can possibly notice specific issues, or will draw larger or smaller.

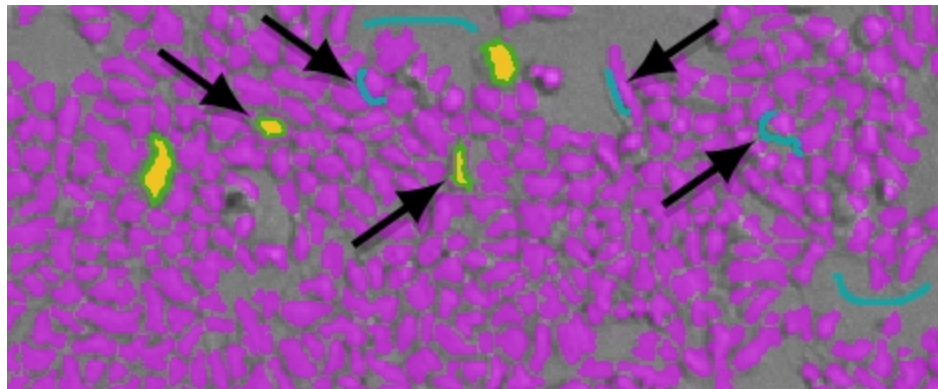
Resolving Under-Splitting Issues

Under splitting finds multiple cells or confluent areas that can also include background.



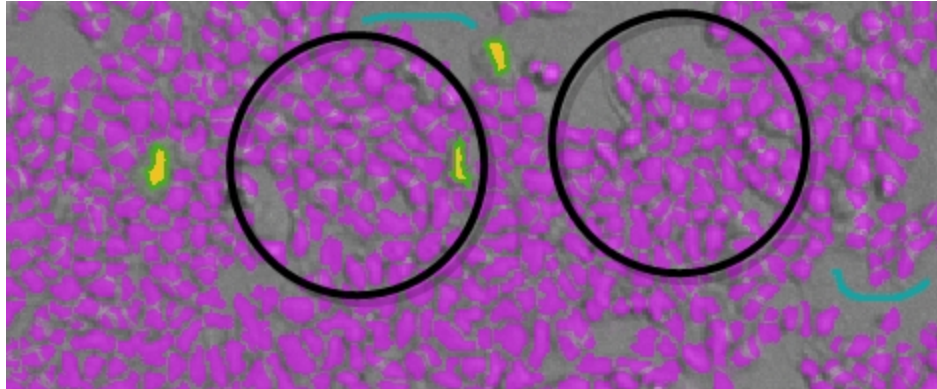
Under splitting can be caused by drawing outside of the edge of the cells or confluent areas. The lines between the cells or confluent areas are interpreted as being part of the cell or confluent-area structure.

To resolve under-splitting issues, draw inside the cell or confluent area up to the edge, but do not include the edge. You can also use the background pen to draw on the lines between the cells or confluent areas.

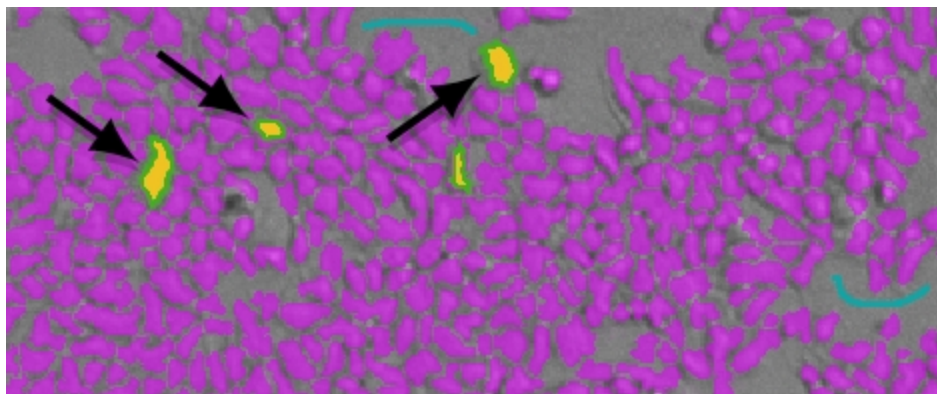


Resolving Over-Splitting Issues

Over splitting finds portions of cells or confluent areas and can include several found objects within a single cell or confluent area.



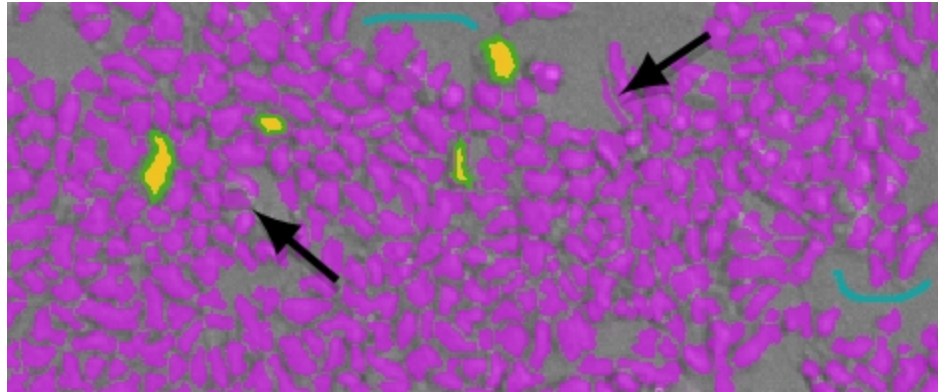
Over splitting can be caused by drawing too small within the cells or confluent areas. Sometimes over splitting can happen after using the background pen to remove an artifact. To resolve over-splitting issues, draw inside the cell or confluent area up to the edge, but do not include the edge.



If over splitting is the result of artifact removal, try erasing the blue from the artifact defined by the background pen.

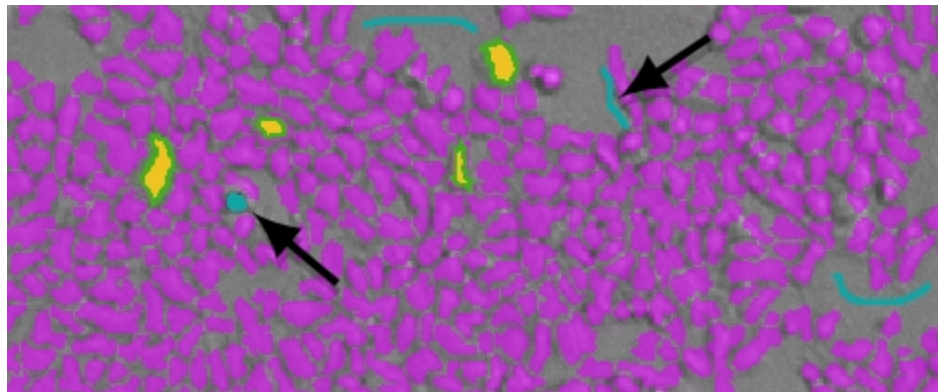
Resolving Artifact Issues

Artifacts can be found and counted as cells or confluent areas.



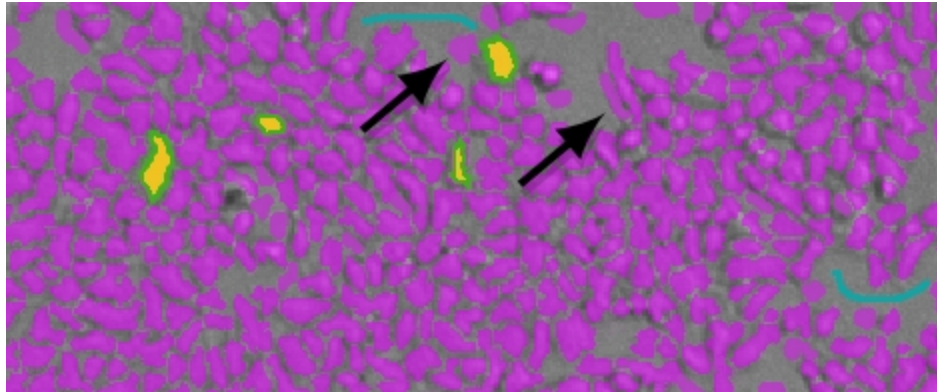
Artifact issues can be caused by debris or other artifacts in the image where the edges and surrounding pixels confuse the software.

To resolve artifact issues, use the background pen to define artifacts as background and not cells or confluent areas.



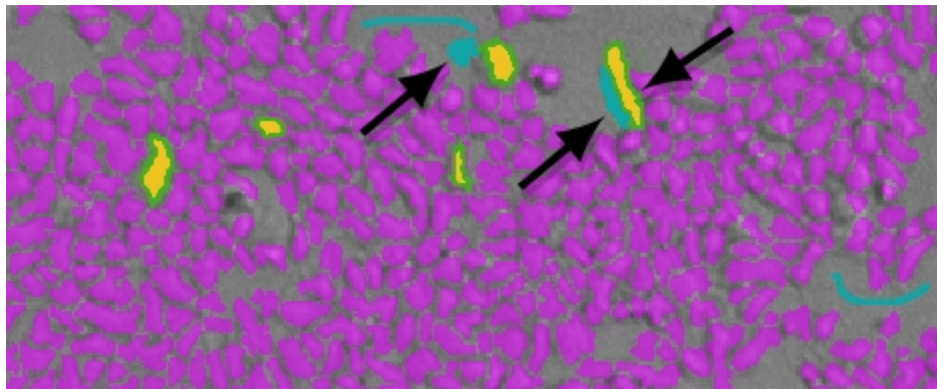
Resolving Ghosting Issues

Ghosting finds background areas next to cells or confluent areas .




Ghosting can be caused by the edges of cells or confluent areas and the surrounding pixels that confuse the software.

To resolve ghosting issues, use the background pen to draw over the area of the ghost. Draw this area right to the edge of the cell or confluent area. If necessary, use the object pen to draw on the cell or confluent area so that the drawing goes out to the edge of the cell or confluent area.



Region of Interest Settings

You can define a region of the images in all the wells to be analyzed, if needed for your application. Only the selected region of interest (ROI) is used for the analysis. This can be useful if cells tend to congregate in the same region of the wells.

To select the well to use for defining the region of interest, click  to the right of the **Well** field above the image area. The well filled with red is used to determine the region of interest. Click the well that you want to use, and then click **Acquire All Sites**.

To view the image for a specific wavelength, click the tab above the image for that wavelength. To view an image with all the wavelengths, click **Composite**.

To zoom the acquired image in and out, right-click the image and click **Zoom In** or **Zoom Out**. You can also hold the **CTRL** key down and press **+** or **-**, or use the mouse wheel to zoom in or out. Drag the scroll bars to move the zoomed image in the image area, or click the image and drag it into position.

To define a region of interest:

1. Select the **Enable Region Selection** check box.
A rectangle is displayed on the image.
2. Click **Resize** and then drag the corners of the rectangle to redefine the size of the region.
3. To start over, click **Draw** and then drag a new rectangle on the image to define the region.

To use the entire image for the analysis, clear the **Enable Region Selection** check box.

Settings for Reads with Injection

To define the settings for a read with injection, you must use the **Acquisition View** of the **Settings** dialog.

To do a read with injection, you must first install the Injector Cartridge in the SpectraMax i3x Instrument. You can use the Injector Cartridge for luminescence reads, or use the built-in Monochromator in the SpectraMax i3x Instrument for fluorescence intensity reads with injection.

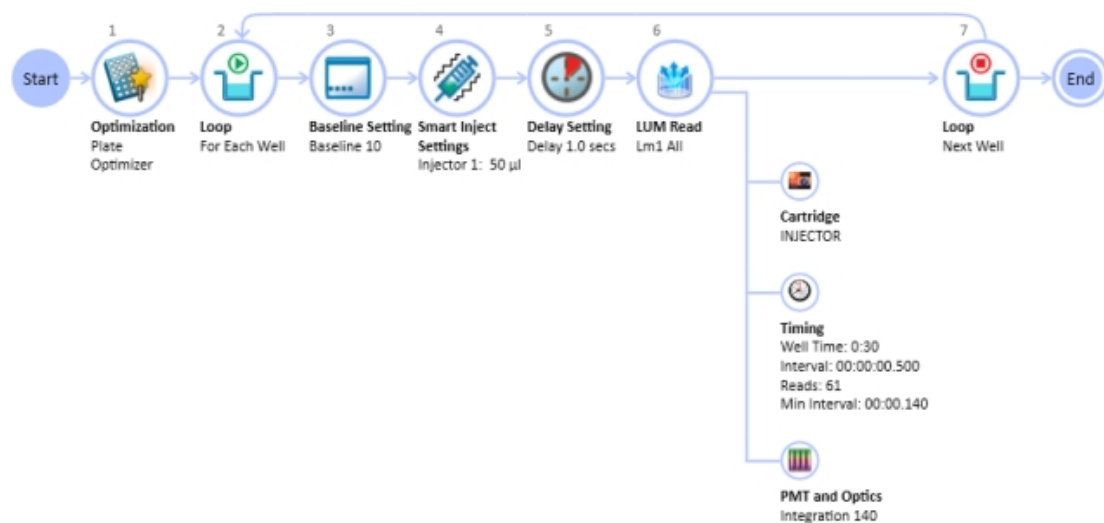
- When you add a luminescence (LUM) step to the time line, select **INJECTOR** from the **Select Hardware** list to use the Injector Cartridge for the read. A luminescence read with injection is taken from the top of the microplate.
- When you add a fluorescence intensity (FL) step to the time line select **MONO** from the **Select Hardware** list to use the built-in Monochromator for the read. A fluorescence intensity read with injection is taken from the bottom of the microplate.

The following options are specific to reads with injections.

For Each Well and Next Well

Reads with injection are generally done well-by-well. Double-click **For Each Well** in the **Toolbox** to have the steps in the time line run for each well individually with all the defined injections, delays, and reads before running the steps again for the next well. The **Next Well** node is also added to the end of the time line. Add the steps for your assay between these nodes.

The following illustration shows a time line for a luminescence kinetic read with SmartInject technology. It starts with microplate optimization. All the acquisition steps are between the **For Each Well** and **Next Well** nodes.



Inject

To add a simple injection step, drag the **Inject** node to the time line and drop the node before the **LUM Read** or **FL Read** step.

- To shake the microplate after the injection, add a **Shake** step between the injection step and the read step. See [Shake Settings on page 262](#).
- To shake the microplate during the injection, use the **SmartInject™** node instead of the **Inject** node, and do not add a **Shake** step. The microplate shakes during the injection, continues to shake through the following delay step, if a **Delay** node follows the **SmartInject** node, and then stops shaking before the well is read. See [SmartInject Technology on page 283](#).

To define the settings for the injection step, click the **Inject** node and then click the pencil icon to open a settings window. Select the injector to use and type the number of microliters (μL) to dispense. You can dispense from 1 μL to the maximum allowable volume of the well, based on the selected microplate type. Define the dispense volume based on the requirements of your assay and the net volume available in the well.

You can add a **Delay** step after the injection ends and before the read begins, if required. You can set the delay from 0.001 seconds to 100 seconds. See [Delay on page 284](#).

SmartInject Technology

To shake the microplate during the injection, drag the **SmartInject** node to the time line and drop the node before the **LUM Read** or **FL Read** step.

The SmartInject™ technology shakes the microplate during the injection and continues to shake through the following delay step, if a **Delay** node follows the **SmartInject** node. The microplate stops shaking before the well is read.

To define the settings for the injection step, click the **SmartInject** node and then click the pencil icon to open a settings window. Select the injector to use and type the number of microliters (μL) to dispense. You can dispense from 1 μL to the maximum allowable volume of the well, based on the selected microplate type. Define the dispense volume based on the requirements of your assay and the net volume available in the well.

You can add a **Delay** step after the injection ends and before the read begins, if required. You can set the delay from 0.001 seconds to 100 seconds. See [Delay on page 284](#).

Delay

You can add a **Delay** step after the injection ends and before the read begins, if required. You can set the delay from 0.001 seconds to 100 seconds.

- For luminescence reads, there is always a delay of 0.3 seconds after the injection ends and before the read begins to allow time for the detector to move into position for the read.
- For fluorescence intensity reads, there is no delay for injector number 1. The read starts at the same time as the injection unless a **Delay** step is added. For injector number 2, there is always a delay of 0.3 seconds after the injection ends and before the read begins.

The **Delay** step compensates for the hardware delay. If the defined delay is longer than the hardware delay, then the actual delay time is the defined delay time. However, if the defined delay is shorter than the hardware delay, then the actual delay time is the hardware delay time. For example, if a luminescence read has a defined delay of 1 second, then the actual delay time between the end of the injection and the beginning of the read is 1 second. However, if a luminescence read has a defined delay of 0.05 seconds, then the actual delay time between the end of the injection and the beginning of the read is 0.3 seconds due to the hardware delay.

Baseline

You can take baseline reads before the injection step of a kinetic read by double-clicking **Baseline** in the **Toolbox**. The **Baseline** step is added to the time line before the injection step. Click the pencil icon and type the number of baseline reads. You can define from 1 to 999 baseline reads. Baseline reads use the settings defined in the **LUM Read** or **FL Read** step. The baseline data can be subtracted from the reads that follow the injection. You can use the Formula Editor to automate baseline subtraction. See [Adding a New Summary Formula on page 115](#). More information about baseline subtraction can be found in the Formula Reference Guide.

More Settings

The **More Settings** category in the **Settings** dialog provides more settings options. The options vary depending on the selected instrument, read mode, and read type.

Calibrate

For Absorbance reads, the **Calibrate** setting tells the instrument to make an air-calibration measurement at each wavelength before reading the microplate, as determined by the type of instrument and the read settings. If you turn calibration off, SoftMax Pro Software uses the air-calibration values stored in the firmware of the instrument, or the values from the previous calibration.

For Fluorescence and Luminescence reads, the instrument makes a reference read on the internal reference chip at each wavelength before reading the microplate. If you turn calibration off, SoftMax Pro Software uses the default values stored in the firmware of the instrument, or the values from the previous calibration.

For kinetic readings the calibration measurement is made between readings during a run, unless the read interval is too short to allow calibration.

If **Calibrate** is set to **On** in the **More Settings** tab, the instrument runs calibration for the wavelengths specified in the protocol before each read.

These new calibrations overwrite the calibration setting stored in firmware for the current data acquisition read, and for any subsequent read with calibration turned off. When the instrument is powered off and on, the calibrations revert to those stored in firmware.

The air-calibration values stored in the firmware for Absorbance reads can be updated using the **Calibration** button on the **Operations** tab in the ribbon. See [Calibrating the Microplate Reader on page 455](#).

Turning off calibration allows the instrument to begin or complete readings more quickly. Molecular Devices recommends that you calibrate at your assay wavelengths for at least one microplate before turning off calibration.

Carriage Speed

Carriage Speed can be slowed down for samples (such as, fragile clots) that can be disrupted by rapid carriage movement. Select a **Carriage Speed** of Normal or Slow.

Read Order

The Read Order options in the **More Settings** category in the **Settings** dialog vary depending on the selected instrument, read mode, and read type.

Read Order Column/Wavelength

Choosing column or wavelength priority determines the order in which a plate is read in multi-wavelength readings:

- In column priority, the instrument reads the entire microplate (or chosen number of strips) at the first wavelength, and then goes back and reads the microplate at the second and other selected wavelengths.
- In wavelength priority, the instrument reads all wavelengths for the first column of wells in the microplate first, and then reads all wavelengths for the second column, third column, and so on.

Microplate Read Order

- **Row** reads the entire microplate row-by-row.
- **Column** reads the entire microplate column-by-column.
- **Well** reads each well individually with all wavelengths and intervals defined for the read before reading the next well. This can be useful for spectral scans, area scans, and specialized, fast-kinetic applications.

For the SpectraMax i3x or i3 Multi-Mode Detection Platform and the SpectraMax Paradigm Multi-Mode Microplate Reader, selecting a **Well** read order in the **Standard View**, or adding a **For Each Well** loop in the **Acquisition View**, for a kinetic read lets you define timing parameters in milliseconds.

Settling Time

For some instruments, the **Settling Time** option is available in the **More Settings** category in the **Settings** dialog.

Settling Time is the delay between the motion of the reader and the start of the read. This delay allows time for the meniscus motion to cease, potentially improving precision, especially in the low-density, high-volume microplates with fewer than 96 wells.

To specify a settling time, select the **Settling Time** check box, and then type a time between 100 and 1000 milliseconds.

The specified delay is added between the reading of each column. There is no delay between each well in a column.

Show Pre-Read Optimization Options

For some instruments, **Show Pre-Read Optimization Options** can be selected in the **More Settings** category in the **Settings** dialog.

In the **Acquisition View**, **Plate Optimization** can be added to the beginning of the time line.

Selecting **Show Pre-Read Optimization Options** causes the **Pre-Read Optimization Options** dialog to open before the microplate is read. The available optimization options are dependent on the read mode.

Microplate Optimization

Microplate dimensions can vary slightly between production lots, which can have a potential effect on measurement accuracy. SoftMax Pro Software lets labware dimensions be optimized by determining the centers of the four corner wells on the plate. Each time a labware type is optimized before a read, a new plate definition is added to the Plate Library with dimensions from the labware optimization.

If a microplate type is to be used in different plate orientations for measurements, labware optimization must be done for each plate orientation separately.

Read Height Optimization

The SpectraMax i3x Multi-Mode Detection Platform and the SpectraMax Paradigm Multi-Mode Microplate Reader feature an objective lens that can be moved up and down to optimize the read height used in luminescence, fluorescence intensity, fluorescence polarization, and time-resolved fluorescence protocols. Read height is the distance between the top (using top reading) or bottom (using bottom reading) surface of the microplate being read and the surface of the objective lens. Optimizing read height matches the focus of the optics with the sample volume. This maximizes the raw signal, which yields the highest precision and maximum sensitivity.

Read Height Optimization is available for the SpectraMax i3x Multi-Mode Detection Platform for top-read only.

Read Height Optimization is available for the FilterMax F5 Multi-Mode Microplate Reader for top-read only.

Read Height Optimization is not available for the FilterMax F3 Multi-Mode Microplate Reader.

Attenuation

Very bright samples can exceed the linear dynamic range of the detection system. To reduce the intensity, use an attenuation filter for the read.

Normalization of AlphaScreen Data

For AlphaScreen reads, the **Normalization** option is available. In the **Standard View**, this option is available in the **More Settings** category of the **Settings** dialog.

The conversion rate of photons to counts is individual for each detector. Therefore, raw data from the same plate can seem to be different from one instrument to the next. Also, the data format used by instrument manufacturers can be counts normalized-per-second or not-normalized counts, therefore raw data can be different by several orders of magnitude. It is important to know that the number of counts and the size of figures is in no way an indication of sensitivity.

The raw data can be normalized to counts per second by selecting the **Normalization** option.

Background Correction with Interlaced Readings

For AlphaScreen Endpoint reads, the **Interlaced Reading** option is available. In the **Standard View**, this option is available in the **More Settings** category of the **Settings** dialog.

Although background is significantly lower with AlphaScreen than with fluorescence intensity measurements, Molecular Devices recommends that you use blank or assay controls for background correction. The background can be effectively measured using blank replicates. When reading a sample with small signal, an interference can occur from the afterglow of a very strong emitting adjacent sample that was measured just before. Such cross talk can occur through the wall of a white 384-well microplate. To prevent such interference, you can select the **Interlaced Reading** option, which reads only every other well in a checkerboard pattern, and adds a different plate run to read the previously omitted wells.

For improved results, Molecular Devices recommends that you use replicates for all blanks, controls, and samples.

This setting is available for the SpectraMax i3x Multi-Mode Detection Platform and the SpectraMax Paradigm Multi-Mode Microplate Reader with an AlphaScreen Detection Cartridge installed.

Compound Transfer Settings

Compound transfer settings are supported by the FlexStation 3 Multi-Mode Microplate Reader.

The **Compound Transfer** settings must be configured correctly. In addition to configuring precise fluid transfers for your experiments, these settings also help prevent flooding of the assay plate.

The settings let you define volumes for up to three transfers. However, you must keep in mind the actual maximum volume allowed in the wells you are using as you define the settings. The maximum cumulative volume depends on the assay plate type you select. See [Plate Type Settings on page 250](#).

For the Endpoint and Kinetic read types, the transfers are done to all the selected wells before the first read.

For the Flex read type, the transfers are done for a column while that column is being read. All transfers and reads are done for that column before moving to the next column.

No. of Compound Transfers

You can enable up to three compound transfers in each column during a read.

From the **No. of Compound Transfers** drop-down list, select the number of transfers required for the assay.

- With **0** selected, no other options are displayed.
- With **1**, **2**, or **3** selected, color-coded images representing each of the transfers and the transfer settings are displayed.

Initial Volume

In the **Initial Volume** field, type a value that equals the largest initial volume in the wells of the assay plate before the compound transfers.

- For a 96-well microplate, this value can be set from 0 μL to 269 μL , although typical values are about 10 μL to 200 μL .
- For a 384-well microplate, this value can be set from 0 μL to 120 μL , although typical values are about 5 μL to 80 μL .

If there is no fluid volume in the assay plate before the compound transfers, type **0** in this field.

The software defines all wells as having the same initial volume. The software uses this value to compute the total volume in each well after all fluids have been dispensed. The software makes this calculation to warn you in the **Compound & Tips Columns** settings of the potential for overflow of fluid from the wells. See [Compound and Tips Columns Settings on page 293](#).

The entered value is saved with the file but the value is displayed only in the **Compound Transfer** settings and in the **Compound & Tips Columns** settings.

Transfer Settings

After you click one of the color-coded transfer images, that image is displayed with a light blue background.



After you click a transfer image, you can then define the parameters for that transfer.



Note: There are no other indications in the transfer settings for which transfer you are defining, so pay close attention to which transfer settings you are modifying.

- In the **Pipette Height** field, type a value of 1 μL to 300 μL for a 96-well microplate or 1 μL to 130 μL for a 384-well microplate. This setting determines the volume of fluid in microliters, measured from the bottom of the assay plate well, above which the tip of the pipette will remain during the dispensing portion of the transfer event. This setting helps make sure that the tip of the pipette is below the surface of the liquid at the end of the transfer, minimizing the possibility that undispensed drops remain on the tips.



Note: As you configure subsequent transfers, calculate the amount of fluid added and set the pipette height accordingly. For example, if the initial volume is 15 μL and the first transfer dispenses 20 μL , then you can set the pipette height for the first transfer to 25 μL . If the second transfer dispenses 15 μL , then you can set the pipette height for the second transfer to 45 μL .

- In the **Volume** field, type a value to define the volume of liquid to be dispensed from the source to each individual well chosen to receive that transfer.
 - For a 96-well microplate, the range is 1 μL to 200 μL .
 - For a 384-well microplate, the range is 1 μL to 30 μL .



Note: Keep in mind the maximum total volume each well can hold as you accumulate volumes with multiple transfers.

- In the **Rate** field, type a value of 1 to 8. This setting determines the rate at which the fluid is dispensed into the well of the assay microplate.
 - In a 96-well microplate, a setting of 1 is equal to 26 μL per second and each subsequent number increases in increments of 26 μL per second, so that a setting of 2 is equal to 52 μL per second.
 - In a 384-well microplates, a setting of 1 is equal to 6 μL per second and each subsequent number increases in increments of 6 μL per second, so that a setting of 2 is equal to 12 μL per second.

A setting of 3 or 4 can help minimize cell damage or dislodgment. For non-contact dispensing, use a rate of 8 to make sure that all liquid is dispensed from the pipette tip.

- In the **Time Point** field, type a value that is equal to or greater than the value in the **Minimum Time** up to 9999 seconds. This setting determines the time after the start of the read when the fluid is scheduled to begin being dispensed. Your time point becomes your baseline time. This is not the time interval between transfers. In Endpoint and Kinetic reads, **Time Point** defines the time at which the first dispense occurs. The Endpoint or Kinetic read begins after all transfers are made.



Note: The **Time Point** value cannot be smaller than the **Minimum Time** identified by the software for each transfer.

- The **Minimum Time** field automatically displays the minimum time required before a pipetting event can occur. This minimum time value is cumulative, not an interval between pipetting events. The value is the minimum number of seconds of elapsed time from the beginning of the read. It takes into account the mechanical speed of the pipette head and the time needed to load and unload tips, aspirate and dispense fluids, triturate fluids, and shake the microplate.

The minimum time for the second pipetting event depends on when the first pipetting event occurred. The calculation for the second event starts at the end of the first event and adds the total time necessary to load pipette tips, aspirate new fluids from the compound plate, and dispense them into the assay plate.

Leave Tips On Between Columns

For a Flex read type, the pipettor returns the tips to the tip rack after all the transfers for a column are complete, and then installs tips from the tip rack before the first transfer for the next column. If you are using tips from the same position in the tip rack for the first and last transfers in each column, then you can reduce the cycle time between columns by selecting the **Leave tips on between columns** check box. The tip assignments are defined in the **Compound & Tips Columns** settings.

Avoiding Problems

Time point calculations are based on the number of wells read, and the tip column and the compound column used during the transfer. If you select time points that are not long enough to be compatible with the selected volumes and transfer speed, the software notifies you that the time point needs to be increased.

If you select transfer volumes that add up to more than the maximum that can fit in the assay plate, an overflow warning is displayed indicating that you have exceeded the volume limits of the assay plate.

Pay attention to the minimum time value displayed under the time point field for each transfer, as the minimum time values are different depending on which transfer you are configuring.

The **Compound Transfer** settings work together with the **Compound & Tips Columns** settings. Until well assignments are made in the **Compound & Tips Columns** settings, the **Compound Transfer** settings display **No targets assigned**. See [Compound and Tips Columns Settings on page 293](#).

Compound Source Settings

The **Compound Source** settings let you select a compound source plate. Compound plates store fluids that are aspirated (or withdrawn) from the compound plate and then dispensed (or injected) into the assay plate during the run.

Make sure that you select a plate type that matches the type and well configuration of the actual compound plate you are using. It must also be compatible with the number of wells selected in the plate type settings for the assay plate.

The well bottom height is different for different types of microplates. Select the plate type correctly to prevent jamming the pipette tips into the bottom of the well.

- For 96-well microplates, the instrument aspirates using a pipette height of 20 μL above the bottom of the well.
- For 384-well microplates, the instrument aspirates using a pipette height of 10 μL above the bottom of the well.

The pipette height for the compound source plate is set automatically. The pipette height for the assay plate is defined in the Compound Transfer settings.

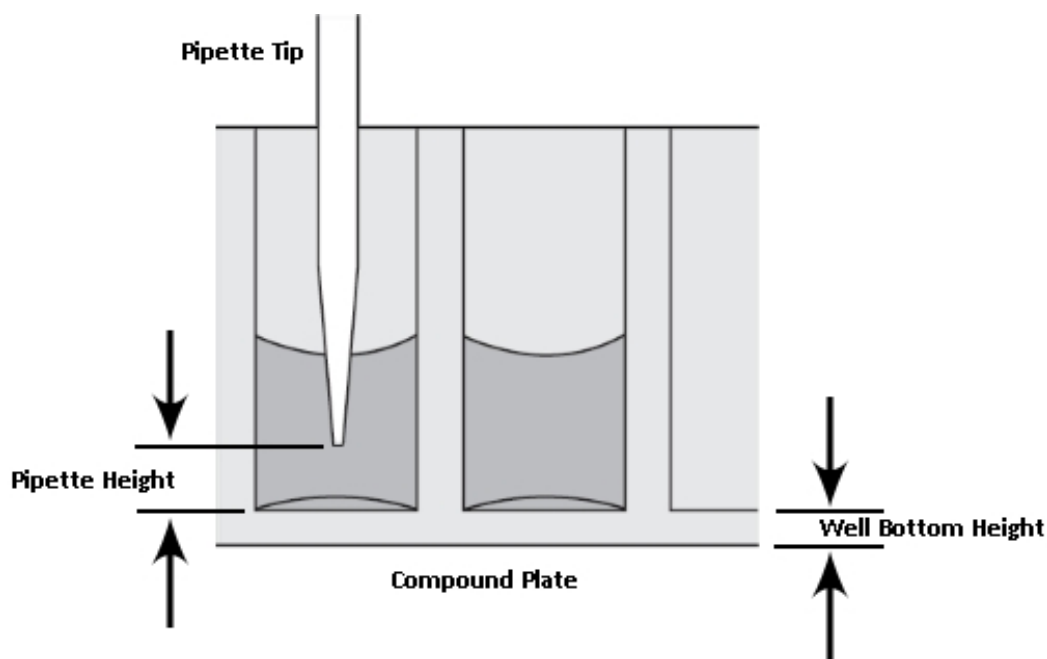


Figure 7-2: Well Bottom Height



CAUTION! Selecting an incorrect compound plate type can result in the pipette tips jamming into the wells and damaging the microplate, the tips, and the instrument.

Pipette Tips Layout Settings

The **Pipette Tips Layout** settings display a column of tips in a 96-well (12 tips) or 384-well (24 tips) layout that matches the selection made in the **Plate Type** settings for the assay plate.

If you use a partial rack of tips, make sure that the **Pipette Tips Layout** settings match the configuration of the partial rack inserted in the tip drawer. The selected tips must be contiguous.

To select a contiguous set of tips, use your mouse to drag the pointer and select the tips to use.



To use all the tips in the rack, select the **Select All** check box.

If you change the selection in the **Plate Type** settings for the assay plate to a microplate with a different number of wells (for example, from 96-wells to 384-wells), the selection in the **Pipette Tips Layout** settings defaults to selecting the full rack of tips.

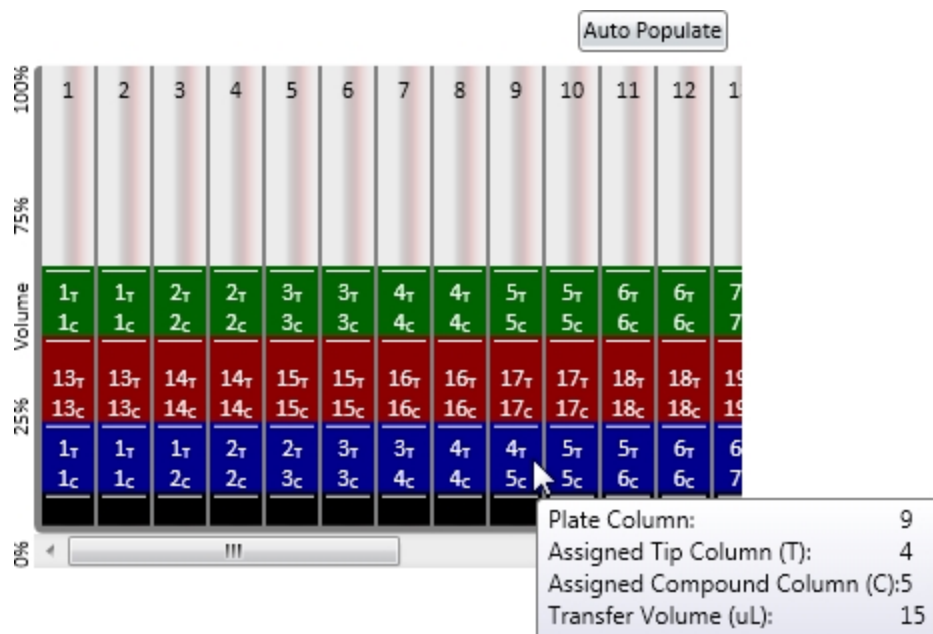


CAUTION! Molecular Devices recommends using a full rack of tips each time you do a fluid transfer. If you mistakenly enable a pipetting function from a tip that is not present, your samples will not receive the intended compound. There is also a potential of damaging the microplate, the tips, and the instrument.

Compound and Tips Columns Settings

The **Compound & Tips Columns** settings that are available depend on the selection made in the **Plate Type** settings for the assay plate and the number of transfers defined in the **Compound Transfer** settings.

If one or more transfers are enabled, then these settings let you choose the tips and compounds to be used for each of the transfers.



Each color-coded transfer is stacked on top of the previous transfer, with the black area at the bottom representing the initial volume in the wells.

- For a 96-well assay plate, all 12 columns are displayed.
- For 384-well columns, the first 12 columns are displayed. To view the other columns, drag the scroll bar to the right.

You can restrict the number of columns that are available in the **Read Area** or **Wells to Read** settings, and restrict the number of tips that are available in the **Pipette Tips Layout** settings.

Each transfer is assigned a set of tips from the tip rack and a column from the source plate:


- To select a set of tips from the tip rack for a transfer, click the tip assignment indicated by the letter **t** and then select the number of the tip set from the list.
- To select a column from the source plate for a transfer, click the column assignment indicated by the letter **c** and then select the number of the source column from the list.

If the assay requires that no fluid is to be transferred to the assay microplate for a column during one or more transfer operations, click the red **X** at the top of the drop-down list. A color-coded drop icon is displayed for that column indicating that it will be skipped.



To enable a transfer for a skipped column, click the drop icon and then assign the tip and source columns for the transfer.

You can manually assign tips and source columns for each and every transfer.

 **Tip:** To leave the tips on between columns for a Flex read type, select the same set of tips in the tip rack for the first transfer of a column as was selected for the last transfer of the previous column.

Assigning Compound and Tip Columns Automatically

To have the software automatically assign the tips and columns, click **Auto Populate**.

The SoftMax Pro Software automatically enters information in the **Compound and Tip Columns** settings taking into consideration the number of transfers and the **Read Area** or **Wells to Read** settings. The software assigns fluid to be aspirated from the compound plate starting with the first available column. Aspirated fluid is then be dispensed to the first available column in the assay plate as indicated in the **Read Area** or **Wells to Read** settings.

The software makes the assignments based on the following conditions:

- All columns selected in the **Read Area** or **Wells to Read** settings are to receive fluid.
- The fluids are transferred from left to right. The read-transfer-read sequence in each column is initiated only after the read-transfer-read event from the previous column is completed (the total read time for that column).
- The fluid transfer targets are cumulative from transfer to transfer. That is, the targets for the second transfer start with the next available clean tip and untargeted compound column rather than reusing tips and compound columns targeted by the preceding fluid transfer.
- Each fluid transfer uses a new tip.

For example, suppose the instrument is configuring for three fluid transfers as follows:

- A selection in the **Read Area** or **Wells to Read** settings of columns 1 through 4.
- A Compound Source selection of a 12-column compound source plate, such as a 96-well microplate.
- A selection in the **Pipette Tips Layout** settings of a full rack of tips.

From this configuration, the SoftMax Pro Software selects tip and compound columns 1 through 4 for the first transfer. The second transfer uses the next four columns (5 through 8), and the third transfer uses the remaining four unused columns (9 through 12).



Note: The SoftMax Pro Software does not assign targets beyond the limitations of the available tips and compound source columns. After all available tips and compound source columns have been assigned, the software stops assigning targets.

Triturate Settings

Trituration is mixing of the contents of the wells in a microplate by using the pipettor to alternately aspirate the fluid from a well and then dispense it back into the well. You can choose to triturate in either the compound source plate or the assay plate, or both.

Applications for which trituration is recommended include when the compound in the source plate needs to be resuspended before the addition, when transferring low volumes of fluid to the assay plate, or when transferring fluid before or during an absorbance read to make sure that the well contents are properly mixed.

The **Triturate** settings are based on the number of compound transfers you specified in the **Compound Transfer** settings. If no transfers are enabled, no triturate settings are available.

Select the transfer during which trituration is to be done, and then select either the **Compound Source** or the **Assay Plate** check box, or both.

Type values for the **Volume** of fluid in microliters to be withdrawn from the well, and for the number of **Cycles**, or times, to aspirate and dispense the fluid in the well.

For the **Assay Plate** settings, you must also type a value for the **Height** at which the trituration occurs. The height setting must take into account the defined trituration volume and the total volume in the well, so that the tips remain below the liquid surface and do not aspirate air.

If you have selected dispense times that are incompatible with the **Triturate** settings, an error message appears. To modify the dispense time, return to the **Compound Transfer** settings.

Defining and Running a Workflow

The **Workflow** view provides you with a drag-and-drop workflow editor and tools to run and monitor a workflow. In Workflow view you can define a workflow using the defined **Plate** sections and instrument settings to run multitask kinetic reads that last hours or days.



To change to the Workflow view, click the **Workflow** button.

Drag tasks from the menu on the left to the timeline on the right.



Define repeated tasks by placing the tasks in a defined **Cycle** task.

*** Tip:** You can gather data over long periods of time by using a Kinetic read type and then defining the Timing settings to acquire a single point with each read. See [Timing Settings on page 260](#).

Note: Place only Kinetic reads within a cycle. Using other read types causes the software to overwrite the previously acquired data in the Plate section. You can place an Endpoint, Well Scan, Spectrum, or Flex read before or after a cycle to preserve the acquired data.

When you click a task in the timeline, a pencil icon appears. Click the pencil icon to edit the settings for that task. See [Editing Workflow Tasks on page 298](#).



To remove the task from the timeline, click the red X.

In the **Workflow** tab of the ribbon, click the options in the **Designer** group to undo or redo actions, clear all tasks from the editor, and zoom in and out of the editor. Click **Mini Map** to open the **Overview** window that can help you navigate a long timeline. To export an image of the timeline in JPG, PNG, GIF or XPS format, click **Save as Image**.

Click the options in the **Execution** group to start, pause, resume, and cancel the workflow. See [Running a Workflow on page 300](#).

The **Status** group displays the current status of the workflow. Click **Execution Log** to view the status of the tasks of a running workflow in real time.

Editing Workflow Tasks

In the **Workflow** editor, drag tasks from the menu on the left to the timeline on the right and then click the pencil icon to edit the settings for that task.




Select options from the drop-down lists or type text in the fields. When you have finished editing the task, press **ENTER** or click on a blank area of the workflow editor.

Each task has its own set of options:

Read

From the **Experiment** drop-down list, select the name of the experiment that contains the **Plate** section for the read.

From the **Plate Section** drop-down list, select the name of the **Plate** section for the read.

The read is done using the instrument settings defined for the selected **Plate** section. To edit the instrument settings, click . See [Instrument Settings on page 246](#).

*** Tip:** If you have placed a Kinetic read in a Cycle for a SpectraMax i3x, SpectraMax Paradigm, or FilterMax reader, turn off **Show Pre-Read Optimization Options** for the read to prevent having the software wait for user interaction before each read. See [Show Pre-Read Optimization Options on page 287](#).

Open Drawer

Mark the **Wait while drawer is open** check box to pause the workflow until the drawer is manually closed. If you require the workflow to continue to the next task with the drawer open, clear this check box.

In the **Message to Show**, type a message that software displays when the drawer opens. You might want to type instructions for the operator.

Set Temperature

To set the temperature in the read chamber, click **On** and then type the desired temperature in degrees Celsius in the **Plate Chamber Set Point** field.

Mark the **Wait while the temperature changes** check box to pause the workflow until the read chamber reaches the required set point. If you require the workflow to continue to the next task before the chamber reaches its set point, clear this check box.

To turn off temperature control, click **Off**.

For more information, see [Setting the Temperature on page 47](#).

Shake

In the **Shake time** field, type the number of seconds to shake the microplate.

Delay

Type values for the delay in Days:Hours:Minutes:Seconds, or click one of the values and then click the arrow button on the right to increment or decrement that value.



Note: The **Delay** task continues even if the workflow has been paused.

Cycle

Total Run Time defines the total time for all the cycles to complete. Type values in Days:Hours:Minutes:Seconds, or click one of the values and then click the arrow button on the right to increment or decrement that value.

Cycle Interval defines the time from the start of one cycle to the start of the next cycle. Type values in Days:Hours:Minutes:Seconds, or click one of the values and then click the arrow button on the right to increment or decrement that value.

The number of cycles is calculated based on how many Cycle Intervals can be completed within the Total Run Time.

To include a task in the cycle, drag the task between the start and end points of the **Cycle** task.



When you define the timing for a Cycle, make sure that the tasks in the Cycle can be completed within the allotted time. The workflow editor cannot calculate the time it takes to do a read. If the read takes longer than the time allotted for the Cycle, then the next Cycle begins immediately after the Cycle tasks have completed.






Note: The **Cycle Interval** continues even if the workflow has been paused.

Running a Workflow

After you have your workflow defined and your prepared microplate inserted in the microplate reader, you can run the workflow.




Note: Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

- To run a workflow, click the **Start**  button in the **Workflow** tab of the ribbon.
- To stop a running workflow, click the **Cancel**  button.
- To temporarily stop a running workflow, click the **Pause**  button. Pausing a workflow lets you work with other features in the software, such as defining protocols or running short reads, while the software is waiting to do the next non-timing task in the workflow.

When a workflow is paused, all delays and cycle timings continue to run. When the workflow reaches a non-timing task, such as a read, the task is started after the workflow is resumed. If the workflow is resumed after the scheduled time for a task to start, then the task starts when the workflow is resumed and all subsequent tasks are rescheduled to a later time.


For example, if a delay before a read is set for 30 minutes and the workflow is resumed after 40 minutes, then the read starts when the workflow is resumed and all subsequent tasks are rescheduled to start 10 minutes later than their original times.

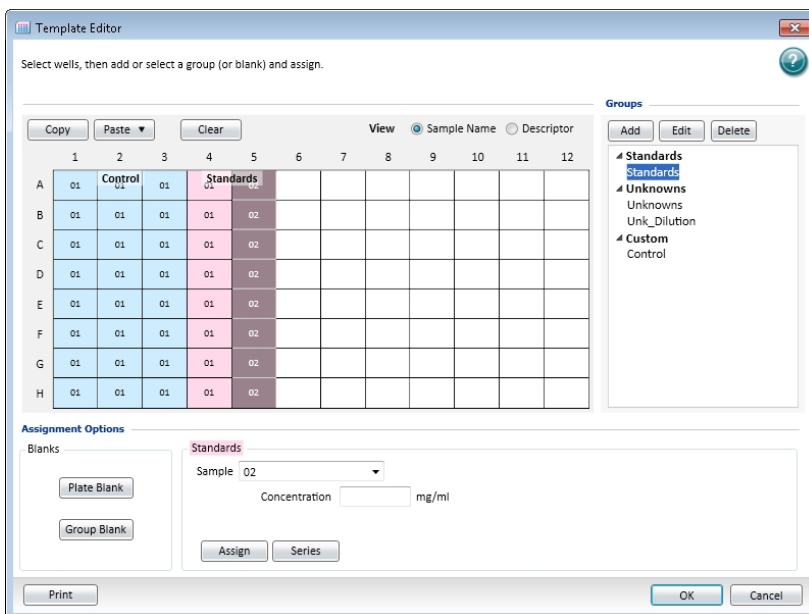
- To restart a paused workflow, click the **Resume**  button

Configuring a Microplate Template

The **Template Editor** is a representation of the microplate or set of cuvettes shown as a grid of wells that can be used to designate the location of blanks, standards, controls, unknowns, empty wells, or to assign wells to other groups you create.

When you select multiple wells in the **Template Editor**, the selection must be a rectangular group of contiguous wells.

1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Template**  in the **Template Tools** section of the **Home** tab in the ribbon or in the toolbar at the top of the section. This opens the **Template Editor**.



The screenshot shows the **Template Editor** window. At the top, it says "Select wells, then add or select a group (or blank) and assign." Below this are buttons for **Copy**, **Paste**, and **Clear**. There are also **View** options for **Sample Name** (selected) and **Descriptor**. To the right are **Groups** buttons: **Add**, **Edit**, and **Delete**.

The main area is a grid of wells. The columns are numbered 1 to 12, and the rows are lettered A to H. The grid shows the following assignments:

Row	1	2	3	4	5	6	7	8	9	10	11	12
A	01	Control	01	Standards								
B	01	01	01	01	02							
C	01	01	01	01	02							
D	01	01	01	01	02							
E	01	01	01	01	02							
F	01	01	01	01	02							
G	01	01	01	01	02							
H	01	01	01	01	02							

On the right side, the **Groups** list includes: **Standards**, **Standards**, **Unknowns**, **Unk_Dilution**, and **Custom Control**.

Below the grid are **Assignment Options**. Under **Blanks**, there are buttons for **Plate Blank** and **Group Blank**. Under **Standards**, there is a **Sample** dropdown menu set to **02** and a **Concentration** input field with the unit **mg/ml**. There are also **Assign** and **Series** buttons.

At the bottom of the window are **Print**, **OK**, and **Cancel** buttons.

The **Template Editor** contains a representation of the rows and columns of the microplate in the active **Plate** section.

When you open the template editor with a **Cuvette Set** section active in the workspace, the template editor window contains 96 wells in the column and row format of a 96-well microplate. The cuvettes in the template are numbered as if they were wells in a microplate. This representation provides easy access to the data analysis capabilities of the SoftMax Pro Software.

3. Define a group of wells, see [Defining a Group on page 303](#).
 - To assign wells to an existing group, select the wells to add to the group, click the group name, and then click **Assign**.
 - To specify wells as Plate Blank, select the wells and then click **Plate Blank**.
 - To specify wells as Group Blank, select the wells, click **Group Blank**, and then click **Assign**.




Note: For more information about using blanks, see [Defining Blanks on page 308](#).

- To remove wells from a group, select the wells to be removed and then click **Clear**.
 - To print the **Template Editor** dialog, click the **Print** button.
4. To assign wells to a series, select the wells and then click the **Series** button. See [Creating a Series on page 304](#).
 5. Click **OK** to close the **Template Editor** and apply the template.

To save the template in a protocol file for use on future experiments, see [Saving Protocol Files on page 75](#).

Modifying a Template


To modify a template:

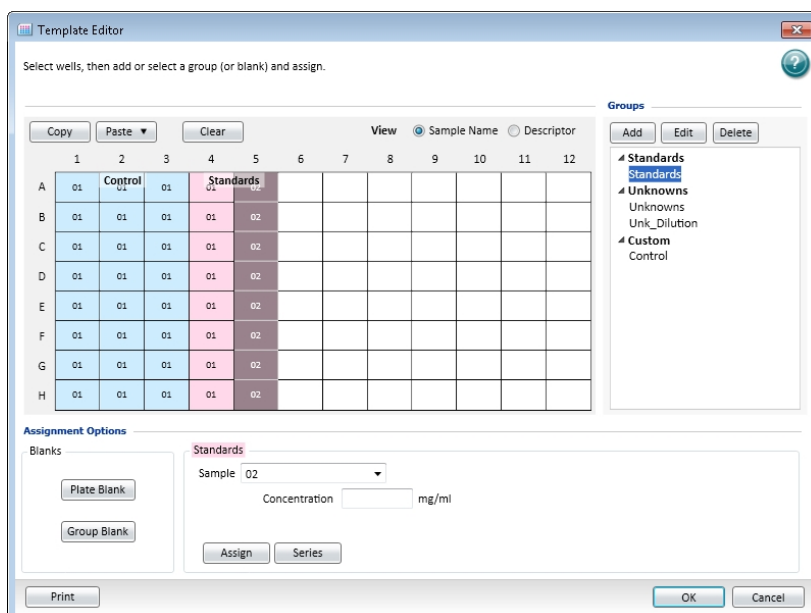
1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Template Editor**  in **Template Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the active section.
3. In the **Template Editor**, modify the template as needed. See [Configuring a Microplate Template on page 301](#).
4. Click **OK** to close the **Template Editor**.

Defining a Group

Wells can be assigned to group types using the Template Editor. Depending on the protocol, certain group types, such as Standard or Unknown, can be created automatically. You can create other groups as required.

To define the group for selected wells:

1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Template Editor**  in **Template Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the active section. This displays the **Template Editor**.



The **Template Editor** contains a representation of the rows and columns of the microplate in the active **Plate** section.

When you open the template editor with a **Cuvette Set** section active in the workspace, the template editor window contains 96 wells in the column and row format of a 96-well microplate. The cuvettes in the template are numbered as if they were wells in a microplate. This representation provides easy access to the data analysis capabilities of the SoftMax Pro Software.

3. Use your mouse to drag the pointer to select one or more wells to be defined as a group.
4. In the **Groups** area, select an existing group and click **Edit**.
To create a new group, click **Add**. See [Creating a Group on page 140](#).
5. In the **Group Settings** dialog, if a sample descriptor has been defined for the selected group, type an applicable value in the field for the descriptor.
6. Click **OK** to close the **Group Settings** dialog.
7. Click **Assign** to assign the group to the selected wells.
To define a series for the selected wells, click **Series**. See [Creating a Series on page 304](#).
8. Click **OK** to close the **Template Editor** and apply the template.


Creating a Series

You can define several samples as a series, letting you easily enter incremental sample descriptors (for example, dilutions or concentrations) and sample names to the template as long as the increment can be expressed as a mathematical operation. This lets you work with groups of wells in the Template so that the standard value or dilution factor increases or decreases in specified steps. The series name can be incremented as well.

You can assign the same group or sample definition (same sample name and description within a group) to multiple wells to create replicates. For example, you might want to read standards in replicate to ensure that anomalies can be excluded before generating a standard curve. To create replicates, click the **Assign** button or use the **Series** dialog.

A series is defined in one direction (starting from left, right, top, or bottom) and therefore samples must be configured sequentially in either ascending or descending order.

To create a series:

1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Template Editor**  in **Template Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the active section.
3. In the **Template Editor** dialog, click and drag the mouse to select one or more wells to be part of the series.

4. In the **Groups** area, select an existing group name.



Note: A series is related to a group. If no groups have been defined, you will need to define a group and then define the series. To create a new group, click **Add** to open the **Group Settings** dialog. See [Using the Group Settings Dialog on page 139](#).

5. Click the **Series** button.
6. Select options in **Series Layout**.
 - Choose a fill direction to describe how the series fills the wells from the **Start From** options. Select one of **Top to Bottom**, **Bottom to Top**, **Left to Right**, or **Right to Left**.
 - In **Patterns of Replicates**, type the number of replicates in the Y-Direction and type the number of replicates in the X-Direction.
 The maximum number of replicates depends on the selection of wells. For example, if you are filling down from the top and you have chosen a block of wells that is 4 wells wide by 8 wells high, the maximum number of replicates will be four. With the same block of wells selected, filling from the left would permit eight replicates. If the number of replicates you choose does not divide evenly into the number of rows or columns you select, depending on the filling direction, the remaining wells that cannot contain replicates will be labeled as more individual wells in the series. To create a series that includes all the wells in the microplate, select all the wells, select the fill direction, and then set the replicates to 1.
 - Optionally, click **Reverse Series Order** to reverse the order of the series.
7. In **Sample Information** type the name of the first sample in the series in the **Starting Sample Name** field. Subsequent replicates use this name as a base and either increment the number within the name or append a number to it.
8. If a sample descriptor has been defined for the selected group, type an applicable value in the **Starting Value** field for the descriptor.
9. From the **Step by** list, select the operator for the series (+, -, *, or /) and then enter a value for the increment. For example, with a starting value of 0.5, the division operator (/) and the increment 2, the series will start with 0.5 and divide each subsequent sample by 2 to produce the series 0.5, 0.25, 0.125, and so on.
10. Click **OK** to save the series and close the dialog.

Incrementing the Names Only

To increment the names of a series of samples without applying a concentration or dilution:

1. Create a series in the **Series** dialog.
2. If a sample descriptor has been defined for the selected group, clear the check box next to the descriptor.

Incrementing with a Constant

To increment the names of a series of samples with a constant concentration or dilution:

1. Create a series in the **Series** dialog.
2. In the **Starting Value** field for the sample descriptor, type a value for the concentration or dilution.
3. From the **Step by** list, select the multiplication operator (*) and then enter a value of 1 for the increment.

If sample names are set to increment automatically using the Series function, then the SoftMax Pro Software automatically truncates the sample name to three or four characters, including the incrementing number if the sample name starts with letters. If the sample name is entirely numeric, it is not truncated. If sample names are very long, and they must be kept long for reference, you need to set up your replicates manually.

Copying and Pasting Template Contents

The content of a template can be copied and pasted to a different section within the same experiment or between different experiments. Only contiguous subsets can be copied in the template.

Within the Same Experiment Section

The destination template is an extension of the original template and all wells on the destination plate are considered replicates of the wells on the source plate, with the same group and sample names.

- Changes made to the template on the destination plate are also made on the source plate.
- Data from the two **Plate** sections are analyzed together.

Between Different Experiment Sections


When copying and pasting between different Experiment sections, make sure that the group names and sample names of the pasted template are identical to those from the source template. Since they are in different Experiments, however, the full name is different, for example: group@experiment#2 instead of group@experiment#1.

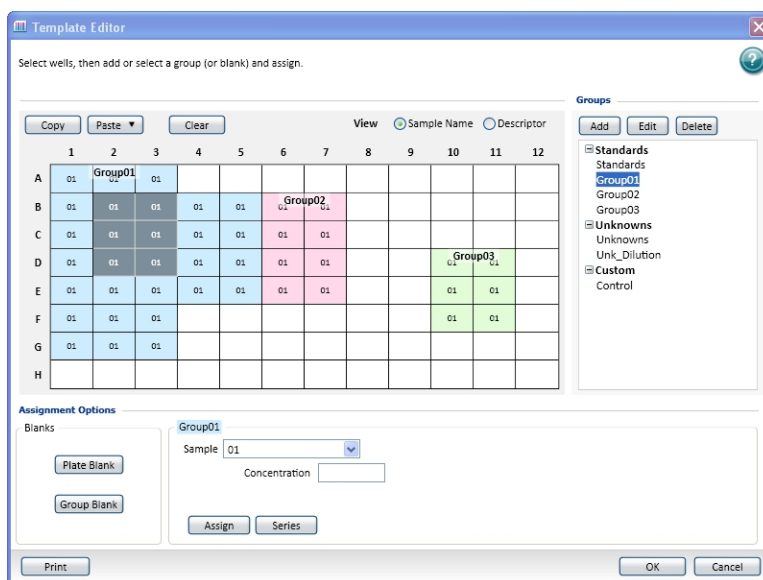
- Changes made to the template of the destination **Plate** section have no effect on the source section.
- Data from the two **Plate** sections are not analyzed together.

Regions within a Template

Only contiguous subsets can be copied and pasted in a template.

To copy and paste a region of a template:

1. Click the source **Plate** section to make it active in the workspace.
2. Click **Template Editor**  in **Template Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the active section.
3. Click and drag to select the wells to copy.
4. Click the **Copy** button on the left above the template.



5. Click a different location in the same template and then click **Paste**.



Note: You can select the same footprint, or click the top-left well of the desired target.

6. From the menu click **Paste** or **Paste With New Group**.

- **Paste** adds the copied wells to the current group.
- **Paste With New Group** pastes a the copied cells into a new group.

If more wells are selected for pasting than were selected for copying, the extra wells are left empty.

The real value in this method is the means to copy a complicated template and then to analyze the data separately from the original plate.

Defining Blanks

In the **Template Editor** you can configure **Plate Blanks** and **Group Blanks**.

The different blank types have the following features:

- **Plate Blanks** are used to correct readings when all samples on a plate have been prepared in the same buffer or matrix, and therefore can use the same correction value. Plate blanks are subtracted from the raw data, or after pathlength correction if PathCheck is selected.
- **Group Blanks** are used to correct readings when samples on a plate have been prepared in a different buffer or matrix, and therefore have to be individually corrected. Group blanks can be subtracted from raw data, like plate blank, or after post-reduction calculations, for example, wavelength, kinetic reduction, and so on.


Blanks can be used in combination and have cumulative effects.

Plate Blanks

Plate Blanks can be assigned in **Plate** sections and in **Cuvette Set** sections.

Plate Sections

Wells can be assigned to a **Plate Blank**:


1. Click a **Plate** section to make it active in the workspace.
2. Click **Template Editor**  on the **Home** tab in the ribbon or in the toolbar above the active section.
3. In the **Template Editor**, select the wells to be used for the **Plate Blank**.
4. Click **Plate Blank**.

Use **Plate Blanks** when all samples on the plate have been prepared in the same way, and therefore can be corrected from a single blank reading. **Plate Blank** subtraction can be turned off in the **Data Reduction** dialog so that the data can be reviewed with or without **Plate Blank** subtraction. See [Doing Data Reduction on page 367](#).

For Kinetic and Spectrum data, the blank value is averaged and subtracted from each point in the read.

Cuvette Set Sections

To do a similar function to Plate Blanking for Cuvette Set sections, you can assign cuvettes to a Blank group in the Template Editor of the Cuvette Set section and create a Template Blank:

1. Click a **Cuvette Set** section to make it active in the workspace.
2. Click **Template Editor**  on the **Home** tab in the ribbon or in the toolbar above the active section.
3. In the **Template Editor**, select the cuvettes to be used for the Template Blank.
4. Click **Blank**.


The average value of all the cuvettes in a Template Blank group is subtracted from individual cuvette readings in the same Cuvette Set section.

For Kinetic and Spectrum data, the blank value is averaged and subtracted from each point in the read.

Template blanks are subtracted after the cuvette reference reading is subtracted.

Group Blanks (Plates and Cuvettes)

Blank wells can be assigned within a group (other than the “Blank” group) in the Template Editor:

1. Click a **Plate** section or **Cuvette Set** section to make it active in the workspace.
2. Click **Template Editor**  on the **Home** tab in the ribbon or in the toolbar above the active section.
3. In the **Template Editor**, select the wells or cuvettes to be used for the group blank. These should be wells or cuvettes that are assigned to a Group, but not the “Blank” group.
4. Select a group from the **Group Types** list.
5. Click **Group Blank** and then click **Assign**.

In a plate blank group the average value of all the wells in the Blank group is subtracted from each individual well value on the microplate. If you have an instrument that supports PathCheck Pathlength Measurement Technology, the Plate Blank is subtracted after pathlength correction. The average reduced value of the blank wells or cuvettes within that group is subtracted from individual reduced values within that group only.


Use Group Blanks when samples on the plate have been prepared differently, and therefore require individual blank correction.

The Group Blank function offers the options of subtraction before or after data reduction. When a group blank has been assigned, it is automatically subtracted and you do not have the option of reviewing the uncorrected data. To see the reduced number without the group blank subtracted, you must mask the group blank wells or cuvettes. See [Masking Wells or Cuvettes on page 367](#).

Group blanks apply to all wells or cuvettes in a group and can be subtracted from wells or cuvettes in more than one **Plate** section or **Cuvette Set** section.

Exporting a Template

To export template information from a **Plate** section:

1. Click the **Plate** section with the template to be exported to make it active in the workspace.
2. Click **Export**  in **Template Tools** on the **Home** tab in the ribbon.
3. In the **Save As** dialog, navigate to the location in the file system where you want to save the template file.
4. Type a name for the file in the **File name** field
5. From the **Save as type** list, select **Text files (*.txt)** or **Excel files (*.xls)**.
Text files are save in tab-delimited format.
6. Click **Save**.

For information about the format of an imported or exported template file, see [Template File Formats on page 311](#).


Importing a Template

Template information can be imported into a **Plate** section from a tab-delimited ASCII text file in Unicode (UTF-8) format. Template files can be prepared outside SoftMax Pro Software and then imported as needed when ready to run samples.

For information about the format of an imported or exported template file, see [Template File Formats on page 311](#).



Tip: A good way to determine the correct format for importing a template is to export a template from SoftMax Pro Software and examine the contents of the resulting file.

1. Click the **Plate** section where you want to import template information to make it active in the workspace.
2. Click **Import**  in **Template Tools** on the **Home** tab in the ribbon.
3. In the **Open** dialog, navigate to and select the text file to be imported.
4. Click **Open**.

Template File Formats

Template information saved as a tab-delimited ASCII text file in Unicode (UTF-8) format can be imported to or exported from **Plate** sections. A template file consists of ten columns of data separated by tabs. Each line of the file provides information for a single well in the microplate.

When template information is exported, the first line of data contains template information for well A1, the second line of data contains template information for well A2, and so on, until a line has been created in the export file for each well in the microplate. If no template information exists for a well in a plate, that line is left blank.

The order for importing template information must match the export order. Similarly, blank lines in the file are assigned to a well, providing a well with no template setting.

A tab-delimited ASCII file can be opened with a spreadsheet program, such as Microsoft Excel. If the file is edited in Microsoft Excel, it cannot be imported back into SoftMax Pro Software unless the layout of the cells match the correct format for importing, and the file is saved as an ASCII text file in Unicode (UTF-8) format.

Table 7-3: ASCII Template File Columns and Descriptions

Column	Column Entry	Description
A	Well Location	In this column, the wells do not need to be in order.
B	Group Name	Assigned in the Group Settings dialog. If this field is missing, the rest of the line is ignored. A text string can be entered in this field.
C	Group Type	Assigned in the Template Editor dialog. Three text strings are supported in SoftMax Pro Software: Standards, Unknowns, Custom. Blank groups have an Empty column format. If this field is left blank, no sample name will be assigned to the well, although the sample name will be included in the group.
D	Sample Name	The sample name is set in the Sample field of the Template Editor dialog. If this field is left blank, no sample name will be assigned to the well, although the sample name will be included in the group.
E	Descriptor1 Name	Assigned in the Group column name assigned to the descriptor 1 is shown here.
F	Descriptor1 Value	Assigned in the Group Settings dialog. A numeric value can be entered in this field or it can be left blank.
G	Descriptor1 Units	Assigned in the Group Settings dialog. Supported strings are unit/ml, mg/ml, µg/ml*, ng/ml, mg, ng, and ml. If this column is left blank, unit/ml is assigned.

Table 7-3: ASCII Template File Columns and Descriptions (continued)

Column	Column Entry	Description
H	Descriptor2 Name	Assigned in the Group column name assigned to the descriptor 2 is shown here.
I	Descriptor2 Value	Assigned in the Group Settings dialog. A numeric value can be entered in this field or it can be left blank.
J	Descriptor2 Units	Assigned in the Group Settings dialog. Supported strings are unit/ml, mg/ml, µg/ml*, ng/ml, mg, ng, and ml. If this column is left blank, unit/ml is assigned.

* The µ symbol can be imported only if the ASCII text file is saved in Unicode (UTF-8) format.


Creating an Absorbance Mode Protocol

To create an Absorbance Mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.
4. When working with a SpectraMax Paradigm Multi-Mode Microplate Reader, click the Absorbance Detection Cartridge from the **Cartridges** list. When working with the SpectraMax i3x Multi-Mode Detection Platform, use the built-in monochromator.
5. Click **ABS** to select the Absorbance read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Absorbance Mode Protocol Overview

Absorbance is the quantity of light absorbed by a solution. To measure absorbance accurately, it is necessary to eliminate light scatter. If there is no turbidity, then absorbance = optical density.

$$A = \log_{10}(I_0 / I) = -\log_{10}(I / I_0)$$

where I_0 is incident light before it enters the sample, I is the intensity of light after it passes through the sample, and A is the measured absorbance.

Applications of Absorbance

Absorbance measurements are used to quantify the concentration of an absorbing species. It must be known at what wavelength a species absorbs light. For example, the concentration of nucleic acids can be quantified by measuring the absorbance at 260 nm.

Optimizing Absorbance Assays

The wavelength of the incident light can be adjusted in 1 nm increments. SoftMax Pro Software also permits reading up to six wavelengths per plate or cuvette for **Endpoint** and **Kinetic** read types, and four wavelengths for **Well Scan** reads.

It is always good scientific practice to designate wells in the microplate to serve as plate blanks or group blanks. This can be done in the **Template Editor** dialog of the **Plate** section in the SoftMax Pro Software. See [Configuring a Microplate Template on page 301](#).

If desired, the PathCheck Pathlength Measurement Technology feature can be used to normalize the data to a 1 cm pathlength. See [PathCheck Pathlength Measurement Technology on page 156](#).



Note: Assay optimization requires the use of a computer and SoftMax Pro Software.


Creating a Fluorescence Intensity Mode Protocol

To create a Fluorescence Intensity protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.
4. When working with the SpectraMax Paradigm Multi-Mode Microplate Reader, click one of the Fluorescence Intensity (FI) cartridges from the **Cartridges** list. When working with the SpectraMax i3x Multi-Mode Detection Platform, use the built-in monochromator or click one of the Fluorescence Intensity (FI) cartridges from the **Cartridges** list.
5. Click **FL** to select the Fluorescence Intensity read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Fluorescence Intensity Mode Overview

Fluorescence occurs when absorbed light is re-radiated at a longer wavelength. In the Fluorescence Intensity (FL) read mode, the instrument measures the intensity of the re-radiated light and expresses the result in Relative Fluorescence Units (RFU).

The governing equation for fluorescence is:

$$\text{Fluorescence} = \text{extinction coefficient} \times \text{concentration} \times \text{quantum yield} \times \text{excitation intensity} \times \text{pathlength} \times \text{emission collection efficiency}$$

Fluorescent materials absorb light energy of a characteristic wavelength (excitation), undergo an electronic state change, and instantaneously emit light of a longer wavelength (emission). Most common fluorescent materials have well-characterized excitation and emission spectra. The following figure shows an example of excitation and emission spectra for a fluorophore. The excitation and emission bands are each fairly broad, with half-bandwidths of approximately 40 nm, and the difference between the wavelengths of the excitation and emission maxima (the Stokes shift) is generally fairly small, about 30 nm. There is considerable overlap between the excitation and emission spectra (gray area) when a small Stokes shift is present.

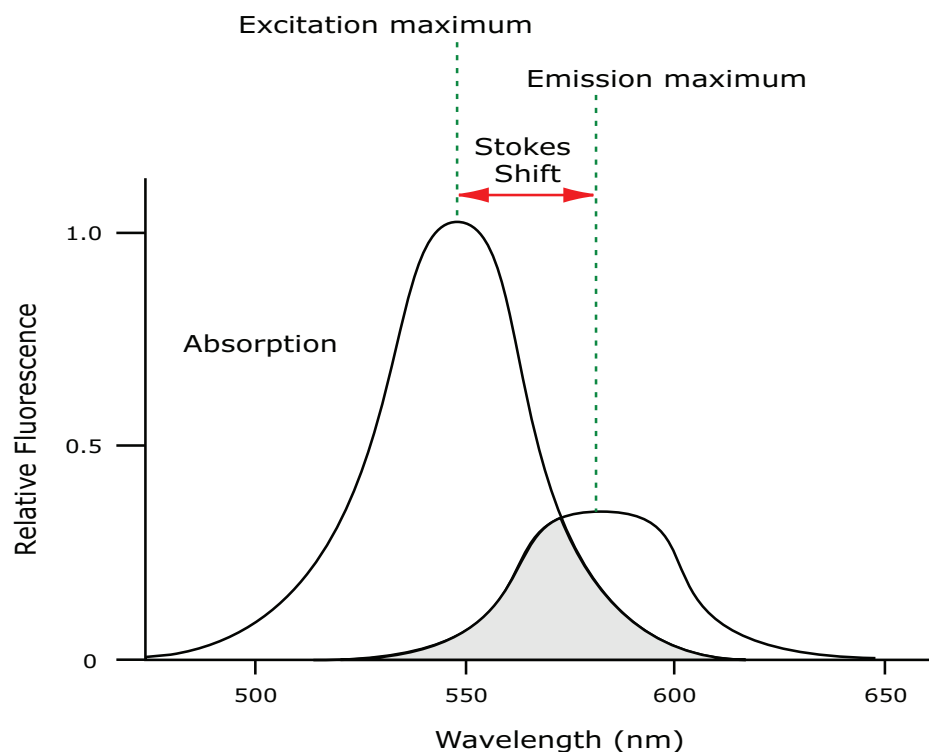


Figure 7-3: Excitation and Emission Spectra

*** Tip:** If the Stokes shift is small, choose an excitation wavelength that is as far away from the emission maximum as possible while still being capable of stimulating the fluorophore so that less of the excited light overlaps the emission spectrum, permitting better selection and quantitation of the emitted light.

Because the intensity of the excitation light is usually many tens of thousands of times greater than that of the emitted light, some type of spectral separation is necessary to reduce the interference of the excitation light with detection of the emitted light.

The SpectraMax readers incorporate many features designed to restrict interference from reflected excitation light. These features include a set of long-pass emission cutoff filters that can be set automatically by the instrument or manually by the user.

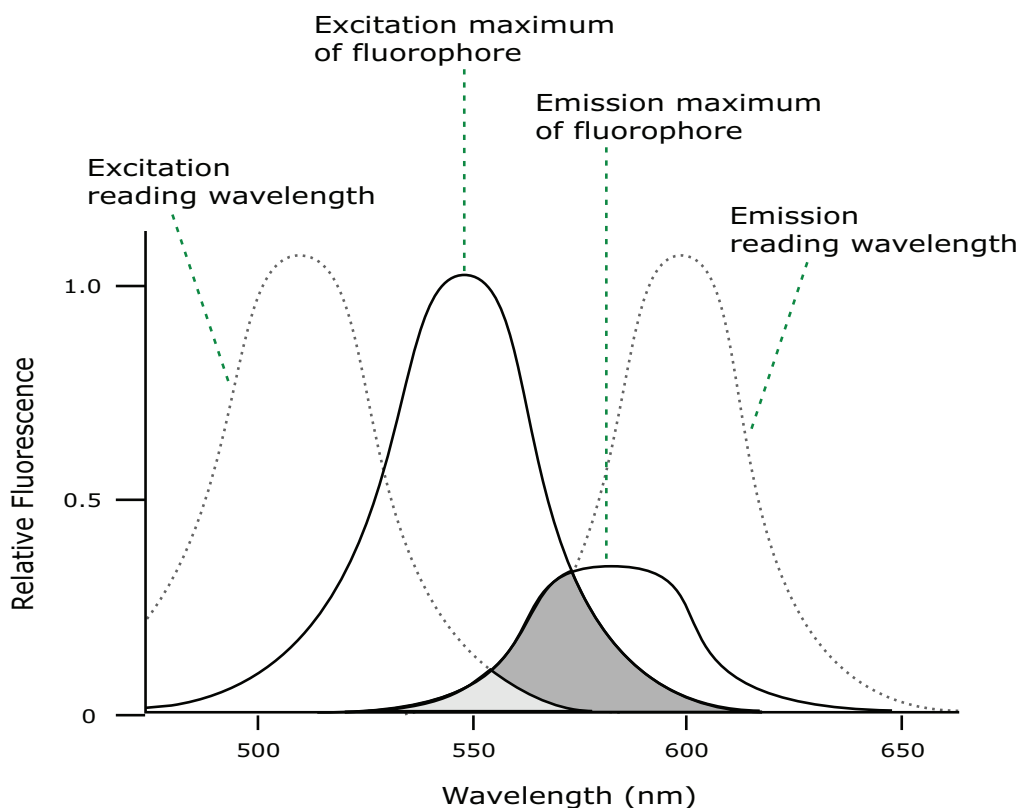


Figure 7-4: Optimized Excitation and Emission Reading Wavelengths

The previous figure shows that the best results are often obtained when the excitation and emission wavelengths used for reading are not the same as the peak wavelengths or maxima of the excitation and emission spectra of the fluorophore. When the reading wavelengths for excitation and emission are separated, a smaller quantity of excitation light passes through to the emission monochromator (gray area) and on to the PMT, resulting in a purer emission signal and more accurate data.

The SpectraMax readers permits scanning of both excitation and emission wavelengths, using separate tunable monochromators. One benefit of scanning emission spectra is that you can determine more accurately whether the emission is, in fact, the expected fluorophore, or multiple fluorophores, and not one generated by a variety of background sources or by contaminants. One more benefit is that you can find excitation and emission wavelengths that prevent interference when interfering fluorescent species are present.

For this reason, it is desirable to scan emission for both an intermediate concentration of labeled sample, as well as the background of unlabeled sample. The optimal setting is where the ratio of the sample emission to background emission is at the maximum.

Optimizing Fluorescence Intensity Assays

The optimal instrument settings for detection of a particular fluorophore depend on a number of different factors. Settings that can be adjusted for assay optimization include the excitation and emission wavelengths, emission cutoff filter, readings per well, the PMT voltage, and the temperature of the reading chamber.

Another important factor that is independent of the instrument but can affect assay optimization is the Stokes shift, which is the difference between the wavelengths of the excitation and emission maxima. When the Stokes shift is very small, optimizing the excitation and emission wavelengths and correct cutoff filter choices are very important.

- **Excitation and Emission Wavelengths**

The excitation and emission wavelengths can be set in 1 nm increments between 250 nm and 850 nm. The available wavelengths are dependent on the instrument. For more information about the available wavelengths, see the documentation for the instrument you are using.

A procedure to optimize excitation and emission wavelengths for a given assay is outlined in [Spectral Scanning on page 318](#).

- **Emission Cutoff Filter**

The emission cutoff filters assist in reducing background. Sources of background include stray excitation light and native fluorescence of plate materials, sample constituents, and solvents (including water). The default setting lets the instrument and SoftMax Pro Software determine which cutoff filter should be used in endpoint and kinetic modes. The spectral scan mode default uses no cutoff filter.

- **Readings Per Well**

The number of readings per well can vary between 1 (used for a quick estimate) and 100 (for very precise measurements). The default number of readings per well varies with the read mode: for fluorescence, the default is 6, and for luminescence the display shows 1 read per well.

- **PMT Voltage**

The voltage of the photomultiplier tube can be set to low (for higher concentration samples), medium, or high (for lower concentration samples) in all read modes. In endpoint and spectrum mode, there is a different setting, automatic, in which the instrument automatically adjusts the PMT voltage for varying concentrations of sample in the plate.

- **Temperature Control**

The chamber of the instrument is isothermal at ambient as well as at elevated temperatures.

The temperature in the reading chamber can be adjusted from 2°C (3.6°F) above ambient to the maximum temperature for the instrument. See the user guide for your instrument.

Spectral Scanning

This procedure optimizes excitation and emission wavelengths for fluorescence assays using spectral scanning.

If you are using the SpectraMax i3x Multi-Mode Detection Platform or using the SpectraMax Paradigm Multi-Mode Microplate Reader with a Tunable Wavelength (TUNE) Detection Cartridge, see [Spectral Optimization on page 348](#).

Pipette 200 μ L of sample that includes the fluorophore and 200 μ L of a buffer control into separate wells of a microplate.

Do the Excitation Scan

1. Using SoftMax Pro Software, set up a Plate section for a fluorescence read, spectrum mode, Em Fixed/Ex Scan, with no cutoff filter (default), and medium PMT.
2. Set the emission wavelength based on the tentative value from the literature (or from a customary filter set used to measure your fluorophore). If the emission wavelength is not known, select a tentative emission wavelength about 50 nanometers greater than the absorbance maximum of the fluorophore. If necessary, the absorbance maximum can be determined by performing an optical density spectral scan first.
3. Set the excitation scan to start/stop approximately 50 nm below/above the tentative excitation value obtained from the literature (or the customary excitation filter).
4. Set the step increment to 2 nm or 3 nm. You can choose to do a preliminary scan with a 10 nm increment to determine the approximate peak location, and then repeat the scan over a narrower wavelength range with a 2 nm or 3 nm increment.
5. Do the scan and view the results as a plot of emission fluorescence vs. excitation wavelength. Note the excitation wavelength at the emission peak and the maximum RFU value.

If an error message reporting missing data points occurs, it can be due to possible saturation reported by the SoftMax Pro Software program at the end of the spectral scan. Reset the PMT to “low” and rescan the sample (scan the buffer blank with the PMT set to “medium” or “high”). If the error occurs after scanning with the PMT set to “low,” it can be necessary to dilute the sample.

If the excitation scan shows no apparent peak, change the PMT setting to “high” and rescan the sample. If the spectral scan still shows no apparent peak, adjust the Y-scale of the zoom plot so that the plot fills the graph.

6. Select the optimal excitation wavelength.
 - If the excitation peak wavelength and emission wavelength are separated by more than 80 nm, use the excitation peak wavelength value.
 - If the excitation and emission wavelengths are less than 80 nm apart, use the shortest excitation wavelength that gives 90% maximal emission. Follow the plot to the left of the peak until the RFU value falls to approximately 90% of the maximum, and then drop a line from the 90% point on the plot to the x-axis as shown in the following figure.

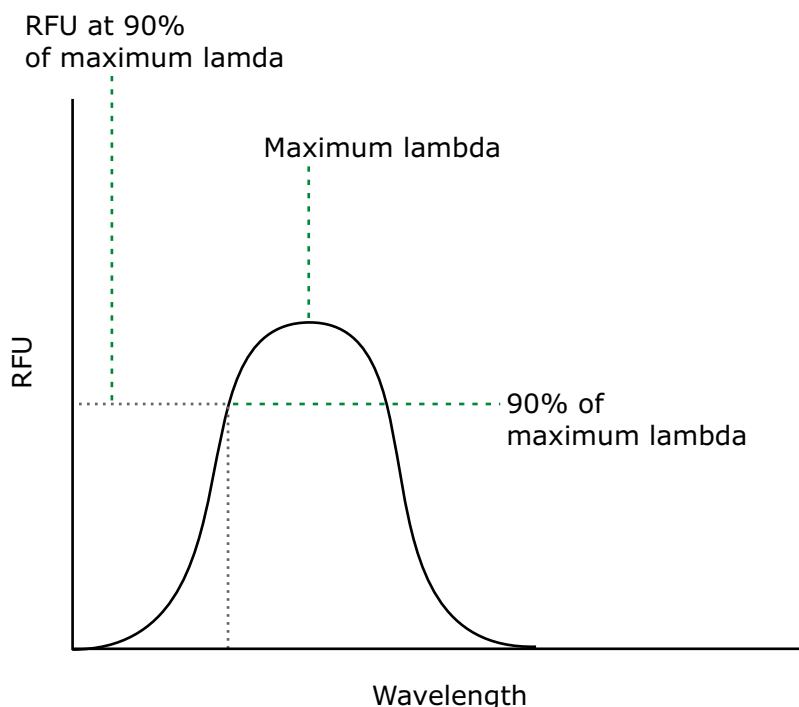


Figure 7-5: Plot of RFU and Wavelength

Do Emission Scan #1

1. In the SoftMax Pro program, set up a second plate section for a fluorescence read, spectrum mode, Ex Fixed/Em Scan, with no cutoff filter (default), and medium PMT.
2. Set the excitation wavelength to the value determined in [Do the Excitation Scan on page 318](#).
3. Set the emission scan to start/stop approximately 50 nm below or above the tentative emission value obtained from the literature (or existing filter pair).



Note: If the Stokes shift is less than 50 nm, then start the emission scan above the excitation wavelength.

4. Set the step increment to 2 nm to 3 nm (or do a preliminary scan with a 10 nm increment to determine the approximate peak location and then repeat the scan over a narrower wavelength range using a 2 nm to 3 nm increment.)
5. Do the scan and view the results as a plot of fluorescence vs. emission wavelength.

Choose the Emission Filter

Select an emission cutoff filter that blocks as much of the residual excitation light as possible without unduly reducing the fluorescence signal. The cutoff wavelength choices are 325, 420, 435, 475, 495, 515, 530, 550, 570, 590, 610, 630, 665, or 695 nm. The cutoff value should be near the maximum emission wavelength (preferably between the excitation wavelength and the maximal emission wavelength) but a minimum of 10 nm less than the emission wavelength. If you have questions about this procedure, contact Molecular Devices Technical Support and speak to an application scientist.

Do Emission Scan #2

1. In the SoftMax Pro Software, set up a third plate section for an emission scan as specified in [Do Emission Scan #1 on page 319](#), except selecting Manual Cutoff Filter and setting the wavelength to that determined in [Choose the Emission Filter on page 320](#).
2. Do the scan and view the results as a plot of fluorescence vs. emission wavelength. Note the wavelength giving the maximum emission (the optimal emission wavelength).
3. Compare the spectra of the sample containing the fluorophore to the spectra of the buffer blank to get an estimate of the signal-to-noise ratio. If there is significant background interference, repeat [Choose the Emission Filter on page 320](#) and [Do Emission Scan #2 on page 320](#) with a different choice of cutoff filter.

Results

The optimal excitation and emission wavelengths are those determined in [Do the Excitation Scan on page 318](#) and [Do Emission Scan #2 on page 320](#).

Comments

- In endpoint or kinetic fluorescence modes, the **AutoCutoff** feature generally selects the same cutoff filter wavelength as the previously described optimization method. If desired, however, you can specify the cutoff filters manually.
- For emission wavelengths less than 325 nanometers, experimental iteration is usually the best method of determining the optimal emission and excitation wavelengths. Start the previously described optimization procedure. Try emission and excitation wavelength combinations with the 325 cutoff or with no cutoff filter. Similarly, for excitation wavelengths greater than 660 nanometers, try emission and excitation wavelength combinations with the 695 cutoff or with no cutoff filter.

The following table lists default settings for the emission cutoff filters.

Table 7-4: Emission cutoff filter default settings for SpectraMax M2, M2e, M3, M4, M5, M5e, and FlexStation readers

#	Automatic Cutoff Selection Wavelength (nm)	Endpoint and Kinetic Modes Emission Wavelength (nm)
1	None	< 415
2	420	415–434
3	435	435–454
4	455	455–474
5	475	475–494
6	495	495–514
7	515	515–529
8	530	530–549
9	550	550–569
10	570	570–589
11	590	590–609
12	610	610–629
13	630	630–664
14	665	665–694
15	695	695–850


Creating a Luminescence Mode Protocol

To create a Luminescence Mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.
4. When working with the SpectraMax Paradigm Multi-Mode Microplate Reader, click one of the Luminescence (LUM) detection cartridge from the **Cartridges** list. When working with the SpectraMax i3x Multi-Mode Detection Platform, use the built-in monochromator or click one of the Luminescence (LUM) cartridges from the **Cartridges** list.
5. Click **LUM** to select the Luminescence read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Luminescence Mode Protocol Overview

Luminescence is the emission of light by processes that derive energy from essentially non-thermal changes, the motion of subatomic particles, or the excitation of an atomic system by radiation. Luminescence detection relies on the production of light from a chemical reaction in a sample.

In luminescence read mode, no excitation is necessary as the species being measured emit light naturally. For this reason, the lamp does not flash, so no background interference occurs. A dark estimate is done over a dark reference, and multiple readings are averaged together into one reading per well.

The default setting for luminescence is the “zero order” position where the grating monochromator acts as a mirror that reflects all light to the PMT detector. If wavelength selection is desired, you can choose the wavelength where peak emission is expected to occur. Also, multiple wavelength choices let species with multiple components be differentiated and measured easily. In luminescence read mode, no emission cutoff filter is used.

Optimizing Luminescence Assays

Luminescence can be read from the top or the bottom of a microplate. Solid white microplates or white microplates with clear bottoms are recommended for luminescence reads.

For standard luminescence a separate light path without monochromators carries the emitted light to a dedicated PMT. The optimal emission wavelength is between 360 nm and 630 nm. In the **Settings** dialog the emission says **All**.

For wavelength-selectable luminescence, the emission monochromator is used to differentiate the wavelengths being emitted from the well. Multiple emission wavelengths within the specified reader range can be defined.

If reading only one luminescent event in the well, you can get the best sensitivity using the standard luminescence measurement, without a wavelength selected.

Luminescence read times are not designated by multiple reads per well, but rather by choosing the total integration time desired between 1 ms and 1500 ms. Typical luminescence assays require between 500 ms and 1000 ms integration.

If wells have been incubating for a long period of time, it is a good idea to mix the plate before reading. This can be done using the Shake setting.

If it seems that the signal is always higher in the first wells read (for example, column A), the plate might need to be “dark adapted” to reduce the auto-luminescence of the white plastic. To help eliminate background luminescence from a microplate that has been exposed to light, Molecular Devices recommends dark adaptation of the microplate by placing the sample-loaded microplate in the instrument for several minutes before starting the read.


Creating a Time-Resolved Fluorescence Mode Protocol

To create a Time-Resolved Fluorescence Mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.
4. When working with the SpectraMax Paradigm Multi-Mode Microplate Reader or the SpectraMax i3x Multi-Mode Detection Platform, click a TRF-capable detection cartridge from the **Cartridges** list.
5. Click **TRF** to select the **Time-Resolved Fluorescence** read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Time-Resolved Fluorescence Mode Overview

In Time-Resolved Fluorescence (TRF) read mode, the instrument detects the extremely long emission half-lives of rare earth elements called lanthanides.

Time-resolved fluorescence (TRF) is a measurement technique that depends on three characteristics that lead to better discrimination between the specific signal, proportional to the quantity of label, and the unspecific fluorescence resulting from background and compound interference:

- Pulsed excitation light sources
- Time-gated electronics faster than the fluorescence lifetime
- Labels with prolonged fluorescence lifetime

The time-gating electronics introduce a delay between the cut off of each light pulse and the start of signal collection. During the delay, the unspecific fluorescence (caused by test compounds, assay reagents, and the microplate) vanishes while only a small portion of the specific fluorescence from the label is sacrificed. Enough of the specific signal remains during the decay period with the added benefit of reduced background.

The use of long-lived fluorophores combined with time-resolved detection (a delay between excitation and emission detection) minimizes interference from fluorescence excitation light. Assays with these long-lifetime fluorophores have the advantage of very low background fluorescence. TRF detection is widely used in high throughput screening applications such as kinase assays.

In normal Fluorescence Intensity mode, the readings are taken while the lamp is on. The most common limitation to sensitivity in normal fluorescence is excitation energy or background fluorescence that cannot be eliminated from the emission signal. Since the lamp is the source of excitation energy, turning it off provides the best means of eliminating background excitation. The elimination of background excitation is the critical difference between fluorescence intensity measurements and TRF measurements.

Optimizing Time-Resolved Fluorescence Assays

Time-resolved fluorescence is done by flashing the excitation lamp and, after it is off, collecting the delayed emission for a period of time before the lamp is flashed again. Long-lifetime rare-earth lanthanide dyes are generally used to provide a long-lived fluorescent signal that persists after the lamp is turned off. Background fluorescence usually fades, while lanthanide chelates and cryptates have fluorescent lifetimes between 100 μs and 2 ms.

Time-resolved fluorescence (TRF) assays can be read from the top or bottom of a microplate. Solid white plates are recommended for top time-resolved fluorescence reads, and white plates with clear bottoms are recommended for bottom reads.

To optimize data collection for a particular assay, you can select when to start and end data acquisition—the minimum is 50 μs after the lamp has been turned off, and the maximum is 1450 μs , in 50 μs or 200 μs steps.

If the time-resolved fluorescence assay you are using has low signal or gives results with high %CV, use 100 readings per well. If a faster read speed is required, turn the settling time off and experiment with fewer flashes per well until acceptable precision and speed are achieved.

The important settings for getting the best results in TRF assays are integration delay and integration time:

- The integration delay is the amount of time that elapses between the flash of the lamp (excitation) and the beginning of data acquisition from the well (emission).
- The integration time is the amount of time that the well is read.

The integration delay and integration time are usually specified in the package insert of commercially available TRF reagent kits. If a kit is not used, start with a delay of 50 μs and try different delays up to 400 μs with a fixed integration time of 400 μs . After the optimal delay is chosen, based on the highest ratio of a well containing a fluorophore divided by wells containing only buffer, optimize the integration time, which is generally between 400 μs and 1000 μs .

Some examples of TRF assays are:

- IMAP® TR-FRET
- Cisbio HTRF
- LanthaScreen TR-FRET
- LANCE TR-FRET
- DELFIA TRF


Creating a FRET Mode Protocol

To create a Fluorescence Resonance Energy Transfer (FRET) protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.
4. When working with the SpectraMax Paradigm Multi-Mode Microplate Reader or the SpectraMax i3x Multi-Mode Detection Platform, click a FRET-capable detection cartridge from the **Cartridges** list.
5. Click **FRET** to select the FRET read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Fluorescence Resonance Energy Transfer Overview

Fluorescence resonance energy transfer (FRET) is a distance-dependent interaction between the electronic excited states of two dye molecules in which excitation is transferred from a donor molecule to an acceptor molecule *without emission of a photon*.

FRET relies on the distance-dependent transfer of energy from a donor molecule to an acceptor molecule. Due to its sensitivity to distance, FRET has been used to investigate molecular interactions. FRET is the radiationless transmission of energy from a donor molecule to an acceptor molecule. The donor molecule is the dye or chromophore that initially absorbs the energy and the acceptor is the chromophore to which the energy is subsequently transferred. This resonance interaction occurs over greater than interatomic distances, without conversion to thermal energy, and without a molecular collision. The transfer of energy leads to a reduction in the fluorescence intensity and excited state lifetime of the donor, and an increase in the emission intensity of the acceptor. A pair of molecules that interact in such a manner that FRET occurs is often referred to as a donor/acceptor pair.

While there are many factors that influence FRET, the primary conditions that need to be met for FRET to occur are relatively few:

- The donor and acceptor molecules must be in close proximity to each other.
- The absorption or excitation spectrum of the acceptor must overlap the fluorescence emission spectrum of the donor.

The degree to which they overlap is referred to as the spectral overlap integral (J).

- The donor and acceptor transition must be approximately parallel.


Creating a Fluorescence Polarization Mode Protocol

To create a Fluorescence Polarization Mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select an instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.
4. When working with the SpectraMax Paradigm Multi-Mode Microplate Reader or the SpectraMax i3x Multi-Mode Detection Platform, click a Fluorescence Polarization (FP) Detection Cartridge from the **Cartridges** list.
5. Click **FP** to select the Fluorescence Polarization read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Fluorescence Polarization Mode Protocol Overview

Fluorescence polarization detection is similar to fluorescence intensity, with the important difference that it uses plane-polarized light, rather than non-polarized light. Plate readers measure FP of the sample by detecting light emitted both parallel and perpendicular to the plane of excitation.

By using a fluorescent dye to label a small molecule, its binding to a different molecule of equal or greater size can be monitored through its speed of rotation.

Fluorescence polarization mode returns two sets of data: one for fluorescence intensity parallel (P) to the excitation plane, and the other for fluorescence intensity perpendicular (S) to the excitation plane. These S and P values are used to calculate the Polarization (mP) and Anisotropy (r) values in the SoftMax Pro Software.

Although the raw S and P values are the true actual values returned from the instrument, the calculated Polarization (mP) and Anisotropy (r) values are treated as the raw data. These become the basis for further reduction calculations.

You can choose to display these data types in the Plate section. When raw (S&P) is displayed, the mP value is by default used for all reduction calculations. When exporting, the displayed raw values are exported, whether mP, r, or Raw (S&P).

Polarization (mP) is calculated as follows:

$$mP = 1000 * \frac{(\text{parallel} - (G * \text{perpendicular}))}{(\text{parallel} + (G * \text{perpendicular}))}$$

Anisotropy (r) is calculated as follows:

$$r = \frac{(\text{parallel} - (G * \text{perpendicular}))}{(\text{parallel} + (2G * \text{perpendicular}))}$$

Optimizing Fluorescence Polarization Assays

Fluorescence polarization for the SpectraMax i3x Multi-Mode Detection Platform, the SpectraMax Paradigm Multi-Mode Microplate Reader, the SpectraMax M5 and M5e Multi-Mode Microplate Readers, the FlexStation 3 Multi-Mode Microplate Reader, and the FilterMax F3 and F5 Multi-Mode Microplate Readers can be read only from the top of a microplate. The plastic from which a microplate is formed has an effect on the light polarization, precluding reading from the bottom and also reading a covered plate from the top.

Solid black plates are recommended for fluorescence polarization reads. If the assay components seem to bind to the microplate, as evidenced by poor mP dynamic range (small difference between bound and unbound tracer), we suggest using plates treated to minimize binding, or polypropylene plates and adding a very small quantity of detergent, to the assay buffer.

Background wells, containing all assay components minus the fluorophore, should be tested. If the signal in the background wells is more than 1/10 the signal in the wells containing fluorophore, then background wells should be run on each assay plate. The average raw signal from the background's parallel and perpendicular readings should be subtracted from the raw parallel and perpendicular readings of each sample well before the mP calculation is done.

For best precision in assays using a low quantity of fluorophore (for example, <5 nm fluorescein), set the PMT sensitivity to High and the number of readings to 100. If a faster read speed is required, turn the settling time off and experiment with fewer flashes per well until acceptable precision and speed are achieved.



Note: Fewer flashes result in a higher speed, but with less precision.


Creating an AlphaScreen Mode Protocol

To create an AlphaScreen Mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select the SpectraMax i3x Multi-Mode Detection Platform or the SpectraMax Paradigm Multi-Mode Microplate Reader. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate section active, click **Settings**  on the **Home** tab in the ribbon.
4. Click one of the AlphaScreen Detection Cartridges from the **Cartridges** list.
5. Click **Screen** to select the AlphaScreen read mode.
6. Click a Read Type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
10. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
11. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
12. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

AlphaScreen Mode Protocol Overview

ALPHA stands for Amplified Luminescent Proximity Homogeneous Assay. AlphaScreen® is a bead-based chemistry used to study molecular interactions between moieties A and B, for example. When a biological interaction between A and B moves beads (coated with A and B, respectively) together, a cascade of chemical reactions produce a greatly amplified signal.

The cascade finally resulting in signal is triggered by laser excitation (680 nm), making a photosensitizer on the A-beads convert oxygen to an excited (singlet) state. That energized oxygen diffuses away from the A-bead. When reaching the B-bead in close proximity, it reacts with a thioxene derivative on the B-bead generating chemiluminescence at 370 nm. Energy transfer to a fluorescent dye on the same bead shifts the emission wavelength into the 520 nm to 620 nm range. The limited lifetime of singlet oxygen in solvent (~4 microseconds) lets diffusion reach up to only around 200 nm distance. Thus, only B-beads in the proximity of A-beads yield signal, which indicates binding between moieties A and B.

An AlphaScreen measurement includes a light pulse, by turning on the laser diode for a specified time, turning off the laser diode, followed by the measurement of the AlphaScreen signal, as specified in the measurement protocol timing parameters.



Note: AlphaScreen beads are light sensitive. Beads are best handled under subdued (<100 lux) or green filtered (Roscolux filters #389 from Rosco, or equivalent) light conditions. Do incubation steps in the dark.

For more information, see [AlphaScreen Read Mode on page 189](#).


Creating a Western Blot TRF Mode Protocol

To create a Western Blot TRF Mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select a SpectraMax Paradigm or SpectraMax i3x Instrument. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the **Plate** section active, click **Settings**  on the **Home** tab in the ribbon.
4. In the **Cartridges** list, click **SCANLATER WB** for the ScanLater Western Blot (WB) Detection Cartridge.
5. Click **TRF** to select the **Time-Resolved Fluorescence** read mode.
6. Click the **Membrane** read type.
7. Define the settings.
For more information about the settings, see the **SoftMax Pro Application Help**.
8. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
9. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Western Blot TRF Mode Overview

Protein detection is an important task for pharmaceutical and clinical research, and Western Blots (WB), or protein immunoblots, are one of the most common methods employed for this purpose. Various techniques are used to detect proteins on Western Blot membranes including fluorescence, silver staining, and chemiluminescence. However, each technique has its limitations, and there is a continuous need to improve quantitation, accuracy, and dynamic range of Western Blots.

The Molecular Devices ScanLater™ Western Blot Assay Kit is a novel system for protein analysis that is incorporated into a SpectraMax® Paradigm® or SpectraMax® i3x Multi-Mode Detection Platform. Membranes are incubated with Eu-chelate labeled secondary antibodies or streptavidin that bind specifically to the target protein-specific primary antibody. Europium has a long fluorescence lifetime, on the order of 1 msec, and detection is done in Time Resolved Fluorescence (TRF) mode which significantly reduces background from auto-fluorescence or other sources of short lifetime emissions. The membranes are placed into a microplate reader where they are scanned with the ScanLater Western Blot (WB) Detection Cartridge.

The method does not involve enzyme detection, and the Eu-chelates are resistant to photo-bleaching, so the signal remains stable for long periods of time (weeks to months). This permits repeat reading of membranes and the potential for comparison of band intensities to known standards for more accurate quantitation.

The TRF detection employs photon counting, so the theoretical dynamic range is $>10^5$. In practice, however, dynamic range is limited by saturation of binding sites on high-abundant bands and non-specific binding to background membrane. There is also no camera blooming, as can occur with chemiluminescence or fluorescence detection, so the system gives sharp bands and excellent image quality.

The SpectraMax Western Blot system is a simple, sensitive, and stable platform that provides excellent Western Blot capability in a SpectraMax Paradigm or SpectraMax i3x Multi-Mode Detection Platform extending the uses of these essential laboratory instruments.

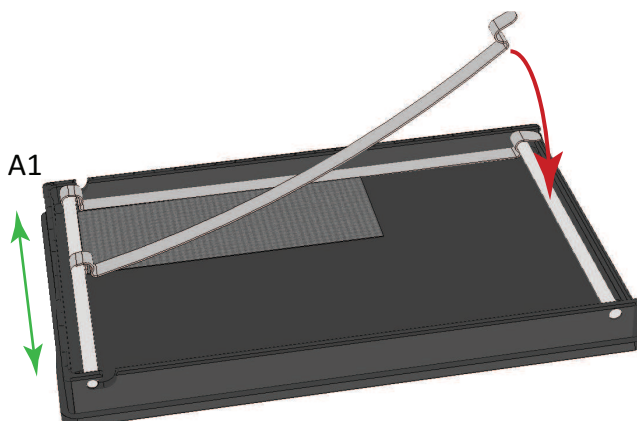
Loading the Membrane into the Membrane Holder



Note: Handle membranes only by the edges using clean forceps. Take care to not touch the membrane with gloved or bare hands.

To scan the membrane in a SpectraMax Paradigm or SpectraMax i3x Instrument, the membrane must be placed in a Molecular Devices ScanLater™ Membrane Holder. The maximum size for a membrane is 109 mm x 77 mm to let it fit in the membrane holder.

1. Place the membrane on the membrane holder with one corner of the membrane aligned with the A1 corner of the membrane holder.



2. Slide the holder clips to place them over the membrane as close to the edges of the membrane as possible to expose the maximum scanning area of the blot.
3. Lower the holder clips into place and then gently press the end of each holder clip to snap it into place and secure the membrane to the holder.



CAUTION! To prevent damage to the instrument or the membrane holder, make sure that all the holder clips are securely snapped into place before inserting the membrane holder into the microplate reader.

4. Load the membrane holder into the microplate drawer with the A1 corner in the A1 position of the drawer. See the user guide for your instrument.


Creating an Imaging Mode Protocol

To create an Imaging mode protocol:

1. Start the SoftMax Pro Software. See [Starting the Software on page 14](#).
2. Select the SpectraMax i3x Multi-Mode Detection Platform using the **Instrument Connection** dialog. See [Selecting and Connecting to an Instrument on page 16](#).



Note: It is not necessary to be physically connected to an instrument to create a protocol. If you are not connected to an instrument you can select the target instrument and work offline.

3. With the plate or cuvette section active, click **Settings**  on the **Home** tab in the ribbon.



4. Click **MiniMax** in the **Optical Configuration** list.
5. Click **Imaging** in the **Read Modes** list.

If you have previously acquired images and want to make changes to the analysis settings for those images, click **Re-analysis** in the **Read Modes** list.

4. Define the **Imaging** read settings or the **Re-analysis** settings.

For more information about the **Imaging** read settings or **Re-analysis** settings, see the **SoftMax Pro Application Help**.

6. After defining the settings for the protocol, click **OK** to close the **Settings** dialog.
7. Create a template, if applicable. See [Configuring a Microplate Template on page 301](#).
8. Set Data Reduction parameters, if applicable. See [Doing Data Reduction on page 367](#).
9. Set Display options, if applicable. See [Setting the Data Display Options on page 358](#).
10. Save the settings to a protocol file. See [Saving the Settings to a Protocol File on page 338](#).

Imaging Mode Protocol Overview

Imaging read mode does whole-cell imaging assays.

Whole-cell imaging assays are cell-based, or object-based, rather than the single-point measurements found in other types of microplate reads. These types of assays can yield more biologically meaningful results that can discriminate the fluorescence related to objects, such as cells or beads, from the bulk solution within a microplate well.

The measurement is primarily fluorescent with quantification of cell size, shape, area, and intensity. Label-free quantification is also supported through brightfield, transmitted light imaging. The camera resolution in the SpectraMax MiniMax 300 Imaging Cytometer is sufficient to determine the approximate shape of small 8 micron objects, such as blood cells.

For more information, see [Imaging Read Mode on page 197](#).

Optimizing Your Computer for Image Acquisition

Acquiring images requires a large portion of computer memory and resources.

Before starting an image acquisition, you must save the data file in a location with enough capacity for the image files. When you create a data file for an imaging experiment or a Western Blot experiment, the SoftMax Pro Software creates a folder with the same name as the data file. See [Image Data Files and Folders on page 61](#).

Each acquired image file for an Imaging mode read can be larger than 2 megabytes. Acquiring the image of a single site in each well of a 96-well microplate can generate 300 megabytes of image data. A 384-well microplate can generate 1 gigabyte of image data. Acquiring images of multiple sites increases the data-storage requirement. Molecular Devices recommends that you employ a data management system.

For best results, save your imaging data file on a secondary internal hard drive. You can use an external hard drive, but this can slow the data acquisition and is not recommended.



Note: To prevent data loss, do not save your imaging data file on a USB flash drive or to a network location. These methods are not supported by Molecular Devices.

Before starting an image acquisition, minimize the demands on computer memory and resources by turning off all other programs. When the SoftMax Pro Software has limited access to computer memory and resources, image acquisition can take a long time. In some cases, images of some of the wells can be lost.

To prevent data loss, turn off all sleep and hibernation settings for the hard disk, the CPU, and the USB ports. Also, disable automatic Windows Updates. You can update Windows manually when the instrument is not being used by the software. You can set these options in Windows Control Panel. See [Required Computer Settings on page 11](#).

Molecular Devices recommends that you use Auto Save with imaging data for saving to text files only. If you use Auto Save to save multiple imaging data files, each new data file is saved without the related folders required for saving images and analysis results. See [Setting Auto Save Options on page 76](#).

Zooming the Image in a Well


An image of the selected well is displayed in the **Image Acquisition**, **Image Selection**, and **Region of Interest** categories of the **Settings** dialog. To view a larger version of the image area, double-click the image to open the **Zoom Well** dialog.

In the **Zoom Well** dialog, the image area displays the acquired image from the selected well. To zoom the acquired image in and out, right-click the image and click **Zoom In** or **Zoom Out**. You can also hold the **CTRL** key down and press **+** or **-**, or use the mouse wheel to zoom in or out. Drag the scroll bars to move the zoomed image in the image area, or click the image and drag it into position.

To close the dialog, click **Close**.

Saving the Settings to a Protocol File

To save the settings for the experiment into a protocol file:

1. Click the **Application**  button to open the **Application** menu.
2. Click **Save As**.
3. In the **Save As** dialog, navigate to where you want the protocol file to be saved.
4. In the **File name** field, type a name for the file.
5. From the **Save as type** field, select **Protocol Files (*.spr)**.

If you are working with the SoftMax Pro GxP Software, select **Protocol Files (*.sprx)**.

6. Click **Save**.

Saving a data file as a protocol file removes the data in the file, leaving only the configuration information.

Collecting Data from a Microplate




You can start a read after defining the instrument settings. It is not necessary to define groups and assign wells in the Template Editor first. The values received from the instrument are raw values. The settings in the Template Editor have no effect on these raw values.



Note: Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

To automatically read multiple **Plate** sections in the same experiment, see [Enabling Auto Read on page 340](#).

To read a microplate:

1. Open the microplate drawer of the instrument by clicking **Open/Close**  on the **Operations** tab in the ribbon.
The microplate carrier on the EMax Plus Microplate Reader moves in and out of the read chamber during the read, and then returns to the home position after the read ends. If the microplate carrier does not return to the home position, you can initialize the carrier to return it to its home position by clicking **Initialize** in the **Operations** tab of the ribbon. See [Using the Operations Tab on page 44](#).
2. Insert the prepared microplate matching well A1 with position A1 in the microplate drawer. Make sure the microplate is flat against the drawer bottom or against the adapter.
3. Click **Open/Close**  to close the microplate drawer.
4. For information about opening and closing other drawers on your instrument, see .
5. Open a SoftMax Pro Software data file or protocol file that contains the applicable experiment settings for the plate read. As an alternative, create new settings by selecting the **Plate** section in the SoftMax Pro Software program and configuring the instrument settings using the **Settings** dialog. See [Selecting Instrument Settings on page 236](#).
6. Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).
7. Click **Read**  on the **Home** tab in the ribbon.


The Read button changes to **Stop** , letting you terminate a read if required.

You can also use the controls in the **Home** tab to interrupt and restart a read in progress. See [Reading Data on page 38](#).

8. The active **Plate** section is read.
 - If you are using the SpectraMax i3x Multi-Mode Detection Platform, the SpectraMax Paradigm Multi-Mode Microplate Reader, or the FilterMax F3 and F5 Multi-Mode Microplate Readers and selected to do pre-read optimizations, the **Pre-Read Optimization Options** dialog is displayed. See [Doing Pre-Read Optimization on page 342](#).
 - If you are using the SpectraMax i3x Multi-Mode Detection Platform or using the SpectraMax Paradigm Multi-Mode Microplate Reader with a Tunable Wavelength (TUNE) Detection Cartridge and selected to run spectral optimization, the **Spectral Optimization Wizard** runs before the microplate is read. See [Spectral Optimization on page 348](#).
9. After the read is complete, the microplate drawer of the instrument opens letting you remove the microplate. If temperature control is on, the drawer closes again after approximately 10 seconds.

If you prefer to have the microplate remain inside the instrument after the read is complete, you can set this option in the **SoftMax Pro Options** dialog. See [Setting Application Options on page 104](#).



Note: If you return to the instrument and find the microplate drawer closed after a reading has finished, click **Open/Close**  on the **Operations** tab in the ribbon or press the **Drawer** button on the instrument. After the drawer opens, you can remove the microplate.

After the read is complete, save the data. See [Saving Data Files on page 65](#).

For information on the data-analysis tools in the SoftMax Pro Software, see [Analyzing Data on page 355](#).


Enabling Auto Read

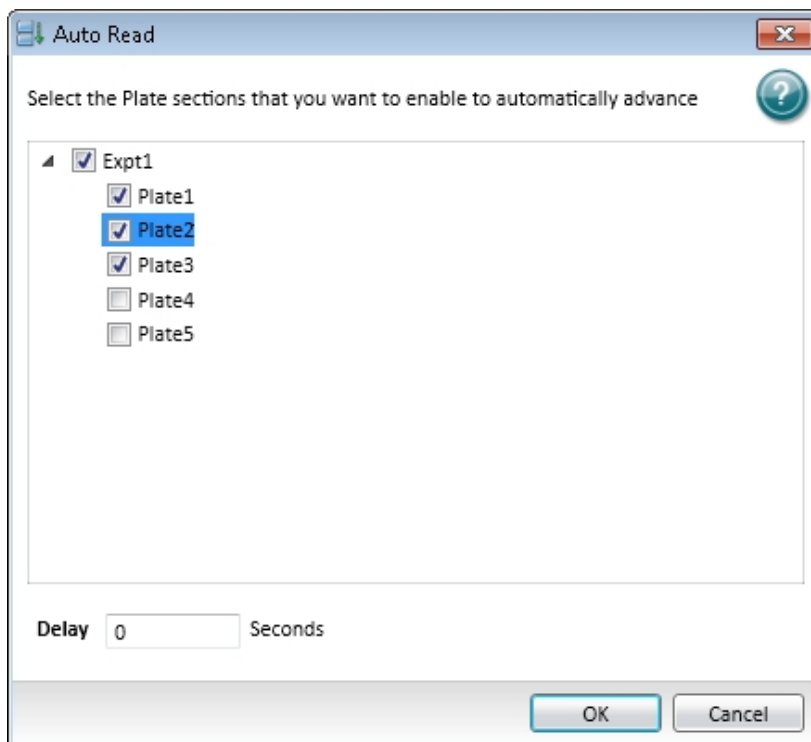
Auto Read automatically advances to the next **Plate** section after a read in the order that the **Plate** sections are displayed within a single Experiment. When you start a read for a **Plate** section that is enabled to automatically advance with AutoRead, the Auto Read feature advances to the next **Plate** section in the Experiment and then reads that plate. If multiple **Plate** sections are enabled to automatically advance with AutoRead, the Auto Read feature reads all enabled **Plate** sections until it reads a non-enabled **Plate** section or the last **Plate** section in the Experiment. **Plate** sections that come before the selected **Plate** section are not read.

For example, if you have five **Plate** sections (Plate 1, Plate 2, Plate 3, Plate 4, and Plate 5) in an Experiment, you can enable Plate 1, Plate 2, and Plate 3 to automatically advance with Auto Read. If you start a Read operation for Plate 2, then Plate 2, Plate 3, and Plate 4 are read in sequence. Plate 1 is not read, since it comes before Plate 2. Plate 5 is not read since Plate 4 is not enabled to automatically advance with AutoRead.

You can set an interval, or delay time, between the plate readings, if desired.

The SoftMax Pro Software can collect data from one or more microplates and store it in a single data file, using the same or different instrument settings for different microplates. Assays requiring a read in two or more read modes or read types can be combined in a single experiment and run with a single command in the software, by defining separate microplate reads and enabling **Auto Read**.

1. In the **Navigation Tree** or the workspace, select the Experiment that has the **Plate** sections that you want to enable to automatically advance with Auto Read.
2. Click **Auto Read**  in the **Operations** tab of the ribbon.



3. In the **Auto Read** dialog, select the **Plate** sections that you want to enable to automatically advance with Auto Read.
4. Optionally, type the number of seconds to delay (the interval) between reading each **Plate** section.
5. Click **OK** to close the dialog.



Note: If you have a **Cuvette Set** section following an enabled **Plate** section, Auto Read will not advance to or beyond the **Cuvette Set** section.

Doing Pre-Read Optimization

When using the SpectraMax i3x Multi-Mode Detection Platform, the SpectraMax Paradigm Multi-Mode Microplate Reader, or the FilterMax F3 and F5 Multi-Mode Microplate Readers in certain read modes, you can use pre-read optimization options. Using this function lets you do microplate optimization and read height adjustment, when available.

The **Pre-Read Optimization Options** dialog is displayed when the **Show Pre-Read Optimization Options** check box is selected on the **More Settings** tab of the Settings dialog. In the **Acquisition View**, **Plate Optimization** can be added to the beginning of the time line. The available optimization options are dependent on the selected instrument and the read mode.



Note: If you are using the SpectraMax i3x Multi-Mode Detection Platform or using the SpectraMax Paradigm Multi-Mode Microplate Reader with a Tunable Wavelength (TUNE) Detection Cartridge and selected to run spectral optimization, the Spectral Optimization Wizard runs before the Pre-Read Optimization Options dialog is displayed. See [Spectral Optimization on page 348](#).

To select pre-read optimization options:

1. Select the **Run Microplate Optimization** check box to run the Microplate Optimization Wizard before reading the microplate. See [Microplate Optimization on page 343](#).
2. Select the **Run Read Height Adjustment** check box to run the Read Height Optimization Wizard before reading the plate. See [Read Height Optimization on page 346](#).
3. Click **Run Optimization** to run the selected optimization options.
4. If the microplate has a lid on it, you must select the **Plate is Lidded** check box.
5. Optionally, for some instruments you can select the orientation for the microplate:
 - Landscape
 - Portrait
 - Opposite Landscape
 - Opposite Portrait
6. Click **Read Plate** to start the read.

Microplate Optimization

Microplate dimensions can vary slightly between production lots, which can have a potential effect on measurement accuracy. SoftMax Pro Software lets microplate dimensions be optimized by determining the centers of the four corner wells on the plate. Each time a microplate is optimized, a new microplate definition is created with dimensions specific to that lot.



Note: If a microplate type is to be used in different plate orientations for measurements, microplate optimization must be done for each plate orientation separately.

The microplate is optimized using the Microplate Optimization Wizard.

You can select to run the Microplate Optimization Wizard in the Pre-Read Optimization Options dialog that is displayed if the **Show Pre-Read Optimization Options** check box is selected on the **More Settings** tab of the **Settings** dialog. In the **Acquisition View, Plate Optimization** can be added to the beginning of the time line. See [Selecting Instrument Settings on page 236](#).

When selected, the **Pre-Read Optimization Options** dialog runs after the **Read** button is clicked.

To do microplate optimization:

1. In the **Pre-Read Optimization Options** dialog, select the **Run Microplate Optimization before reading the plate** check box.
2. Click **Run Optimization**.

The Microplate Optimization Wizard takes you through the optimization process:

- [Insert the Microplate on page 344](#)
- [Running Optimization on page 344](#)
- [Selecting the Centers of the Four Corner Wells on page 345](#)
- [Verifying Microplate Dimensions on page 345](#)

Insert the Microplate

Microplate dimensions are optimized by reading the four corner wells of the plate. The **Insert the Microplate** step provides controls to load and eject the microplate from the instrument and to select the orientation of the plate in the microplate drawer.

To insert the prepared microplate for optimization:

1. Click **Open the Microplate Drawer** to move the microplate drawer carrier outside the instrument.
2. Fill the corner wells of the plate with identical samples. To ensure accuracy, samples must be correct for the selected read mode detection method. Sample concentration and volume must be identical in each well.
3. Place the prepared microplate on the microplate drawer.
4. Click **Close the Microplate Drawer** to load the microplate into the instrument.
5. In **Select the Microplate Orientation**, select the orientation of the plate on the microplate drawer. The selected orientation is displayed graphically on the right, with well A1 marked in red. Make sure this orientation is the same as the orientation of the microplate in the drawer selected in the **Pre-Read Optimization Options** dialog.
6. Click **Next** to start the optimization. See [Running Optimization on page 344](#). The optimization read starts automatically.

Running Optimization

Optimization in Progress displays the status of the optimization read and provides the means to cancel the optimization in progress. The optimization read requires several minutes to complete.

To cancel the optimization process and close the **Microplate Optimization** wizard without saving the optimization data, click the **Cancel** button.

When the optimization read is complete, you can select the centers of each of the four corner wells. See [Selecting the Centers of the Four Corner Wells on page 345](#).

Selecting the Centers of the Four Corner Wells

Use the **Select the Center** steps to precisely define the centers of the corner wells read in the optimization. Each **Select the Center** step displays an image of the well generated by the optimization read. Define the well centers by dragging the cross hairs to the position visually identified as the center. Do a **Select the Center** step for each corner well individually.

To define the centers of the wells:

1. Place the pointer in the well image.
2. Click-and-drag the cross hairs to the desired center of the well.



Note: The cross hairs are displayed after the cursor is placed in the well image.

3. Click **Next** to define the centers of the remaining well reads.

After all four well centers are defined, the **Verify Microplate Dimensions** step is displayed. See [Verifying Microplate Dimensions on page 345](#).

Verifying Microplate Dimensions

Use the **Verify Microplate Dimensions** step to verify that the x and y offsets and distances between rows and columns are correct. The offsets, distances, and lot name can be edited in the **Verify Microplate Dimensions** step.

1. If necessary, click the + next to **Microplate Dimensions** to display the fields in the category.
2. Verify that the x and y offset and distances between rows and columns are correct. If necessary, you can edit the dimension. All offsets and well-spacing dimensions are defined in millimeters.
3. If necessary, click the + next to **Microplate Name** to display the default name assigned to the new microplate definition.
4. Type a new Microplate Name, if desired.
5. Click **Save** to save the optimization data and create the new Microplate definition.

This new microplate definition can be selected from the plate types listed in the Plate Type Library. For more information, see [Plate Type Settings on page 250](#).

If you have selected the **Run Read Height Adjustment** check box in the **Pre-Read Optimization Options** dialog, the **Read Height Optimization Wizard** runs before reading the plate. See [Read Height Optimization on page 346](#).

Read Height Optimization

The SpectraMax i3x Multi-Mode Detection Platform and the SpectraMax Paradigm Multi-Mode Microplate Reader feature an objective lens that can be moved up and down to optimize the read height used in luminescence, fluorescence intensity, fluorescence polarization, and time-resolved fluorescence protocols. Read height is the distance between the top (using top reading) or bottom (using bottom reading) surface of the microplate being read and the surface of the objective lens. Optimizing read height matches the focus of the optics with the sample volume. This maximizes the raw signal, which yields the highest precision and maximum sensitivity.

A single sample with a known maximum signal and volume is placed on the same type of microplate used in the protocol. The sample is measured using the same, or very similar, read mode used in the protocol.

The optimized read height is saved in the protocol and is used for all subsequent runs of the protocol until reset by performing a new optimization or manually selecting a read height option.

You can select to run the **Read Height Optimization Wizard** in the **Pre-Read Optimization Options** dialog that is displayed if the **Show Pre-Read Optimization Options** check box is selected on the **More Settings** tab of the **Settings** dialog. In the **Acquisition View, Plate Optimization** can be added to the beginning of the time line. See [Selecting Instrument Settings on page 236](#).

When selected, the **Pre-Read Optimization Options** dialog is displayed after the **Read** button is clicked.

To do Read Height optimization:

1. Select the **Run Read Height Adjustments before reading the plate** check box.
2. Select **Microplate options**.
3. Click **Run Optimization**.

Running Read Height Optimization

Select the well to be measured to do the optimization.

Use a standard or sample position with a good signal or pipette liquid with a known maximum signal to a well on the microplate used in the optimization. The concentration of the optimization sample should be a minimum of ten times greater than the detection limit. The sample volume should be the same as that of samples measured in the protocol. If using a layout with standards, the standard well closest to the center of the plate is pre-selected. If not using a layout with standards, the first sample is pre-selected.



Note: When optimizing read height for a fluorescence protocol, make sure the optimization sample is the same fluorescent substance that the detection method is configured to detect.

1. Load the plate into the instrument.
2. In the **Select Well** step, select the well containing the optimization sample.
3. Click **Next** to start the optimization.

The **Optimization in Progress** step is displayed. The optimization can take from several seconds to several minutes depending on the detection methods used.

4. When the read is finished, the **Optimization Complete** step is displayed, displaying the Optimized Read Height. To specify a different read height, type a value in the **Custom Read Height** field. The read height is measured in millimeters.
5. Click **Save** to save the specified read height in the protocol. The specified read height is used for all subsequent runs of the protocol until reset by performing a new optimization or manually selecting a read height option.

When **Read Height Optimization** is complete and you return to the **Pre-Read Optimization** dialog, you can choose to change the microplate options and rerun Microplate Optimization or Read Height Optimization. When all you have completed all the desired optimization, click **Read Plate** to start reading the plate.

After the wizard closes, the **Pre-Read Optimization Options** dialog is displayed.

Spectral Optimization

Spectral optimization in spectral assays improves accuracy while reducing data acquisition and computational burden. Spectral optimization can help to get the maximum signal-to-background ratio for most fluorophores or luminescence labels that are compatible with the wavelength ranges of the instrument or detection cartridge.

Spectral optimization for fluorescence intensity reads is available for the SpectraMax i3x Multi-Mode Detection Platform using its built-in monochromator.

Spectral Optimization for both fluorescence intensity and luminescence reads is available for the SpectraMax Paradigm Multi-Mode Microplate Reader with the Tunable Wavelength (TUNE) Detection Cartridge.

To run the **Spectral Optimization Wizard**, select **Unknown** for the **Wavelengths** in the **Settings** dialog.

When **Unknown** is selected, the **Spectral Optimization Wizard** dialog is displayed after the **Read** button is clicked.

Running Spectral Optimization

1. In the **Read Settings** step, specify the wavelength ranges and other parameters for the optimization.

The **Start Emission Wavelength** value must be a minimum of 20 nm greater than the **Start Excitation Wavelength** value. Molecular Devices recommends using an emission value that is a minimum of 40 nm greater than the excitation value.

To do Spectral Optimization, there must be a minimum of 10 data points in the range for both the excitation and emission wavelengths. Make sure that the **Wavelength Increment** permits a minimum of 10 data points in each range.

For a luminescence read, only emission values can be specified.

2. To specify the **Reading Height** or **Integration Time**, click **Advanced parameters** and then type the desired values in the fields.

For Time-Resolved Fluorescence (TRF) reads, you can also specify **Pulse Length**, **Number of Pulses**, and **Measurement Delay**.

3. Click **Next** to continue.
4. In the **Blank Well** step, select the well in the plate layout that corresponds with a well in the microplate that contains buffer or other liquid for background correction.
5. Click **Next** to continue.
6. In the **Sample Well** step, select the well in the plate layout that corresponds with the well in the microplate that contains your sample.
7. Click **Next** to continue.
8. Wait while the indicator in the **Optimization in Progress** step displays the operation's progress.

9. In the **Optimization Complete** step, a 3-dimensional heat map image is displayed. The heat map is generated using the formula $(S - B) / B$, where S = signal and B = background.



Note: For a luminescence read, the Spectral Optimization Wizard generates a 2-dimensional graph.

The cross hair in the image indicates the optimized peak wavelengths. To change the wavelengths for the read, drag the cross hair to a new location or type values in the fields.

The Emission value must be a minimum of 20 nm greater than the Excitation value. Molecular Devices recommends using an emission value that is a minimum of 40 nm greater than the excitation value.

For a luminescence read, only emission values can be specified.

To change the way the a 3-dimensional heat map image is displayed, select or clear the **Use LogScale** check box.

- If you have edited the Wavelength (Custom) values and want to reset the values to the wizard-defined optimized peak, click **Reset to Optimized Peak**.
- If you want to redefine the settings and run the wizard again, click **Restart Wizard**.
- If you want to save the wavelength values without immediately reading the microplate, click **Cancel**, and then click **Yes** in the message that is displayed.


Right-click on the image to display the shortcut menu, and then you can select from the following options:

- **Copy Raw Data** copies the data in tab-delimited format that can be pasted into a spreadsheet or text editor. This option is available only when using the Monochromator of the SpectraMax i3x Instrument.
- **Copy Image** copies the image into a bitmap file that can be pasted into an image editing program.
- **Save Raw Data to Disk** saves the data into a text file in tab-delimited format. This option is available only when using the Monochromator of the SpectraMax i3x Instrument.
- **Save Image to Disk** saves the image into a .bmp file.

10. Click **Read** to save the protocol with the specified excitation and emission wavelengths and use these values to read the microplate.

If you selected to do pre-read optimizations, the **Pre-Read Optimization Options** dialog is displayed before the microplate is read. See [Doing Pre-Read Optimization on page 342](#).

Collecting Data From a Cuvette

Two types of data collection are possible using a cuvette: a reference and a sample reading. You can start a reading after defining the instrument settings. It is not necessary to define groups and assign cuvettes in the Template Editor first, but you can use the Template Editor to create the required number of cuvettes in the section. As an alternative, you can create a small number of cuvettes one at a time with **New Cuvette Set**  on the **Home** tab in the ribbon.

Instrument settings must be the same for all cuvettes in a **Cuvette Set** section.

Sample Reading

You can select a cuvette in the **Cuvette Set** section and choose to read it by clicking **Read**



on the **Home** tab in the ribbon.

The Read button changes to **Stop** , letting you terminate a reading if desired.

If you select more than one cuvette, the software starts with the left-most selected cuvette that does not contain sample read data.

Cuvette Set sections have a limit of 96 cuvettes. If this limit is reached, create a new **Cuvette Set** section.

Reference Reading

A reference reading can be taken either on air or using a cuvette containing the buffer of your sample.

The reference can be read before or after reading samples.

If no reference has been taken in a **Cuvette Set** section before samples were read and you then read a reference, the following occurs:

- The reference reading is applied to all cuvettes in the **Cuvette Set** section if it is the first reference reading.
- In subsequent reference readings, if you select one or more cuvettes, it will selectively replace the reference reading for those selected cuvettes.
- The time and date of the reading are displayed under each cuvette in the section.
- The reference is applied to new cuvettes subsequently created in that section.

You can have more than one reference per **Cuvette Set** section.

To apply a different reference to cuvettes:

1. Select the cuvettes in the **Cuvette Set** section.
2. Place the correct reference in the cuvette port.
3. Click the **Ref** button.


The time and date stamp of the reference for the selected cuvettes changes.

Any new cuvettes created in the **Cuvette Set** section after reading a second reference use the new reference reading.

The reference reading is applied to all cuvettes in the **Cuvette Set** section, unless you have selected specific cuvettes. The reference value is not displayed in SoftMax Pro Software. If you want to see the reference value, you can use one of the following procedures.

Procedure 1:

1. Create a cuvette in the **Cuvette Set** section and Ref on air (empty cuvette port).
2. Read a cuvette containing the blanking solution.
If you want to have both reference and read values available, do the following:
3. Create a cuvette set with up to the maximum of 96 cuvettes.
4. Define a template blank in the **Cuvette Set** section.
5. Place buffer in the cuvette and click **Read**.

6. Click **Read**  again to read the remaining samples.

The optical density of the cuvette designated as the template blank is subtracted from the optical density of all the other cuvettes in the **Cuvette Set** section.

Procedure 2:

1. Create a **Cuvette Set** with up to the maximum of 96 cuvettes.
2. Reference and read the cuvette.
3. Create a template with the applicable groups.
4. Create a column in each Group table with the formula !wellprereadLm1.

If you have a multiple-wavelength reading and want to see the reference at each wavelength, create more columns with the formula !wellprereadLmx where **x** is 2, 3, or 4, corresponding to the wavelength for which you want to see a reference.

The OD/RFU/RLU with the reference subtracted is displayed in the Values column. The reference value for each sample is displayed in the custom column you have created.

Collecting Data from a Membrane Holder

You can start a read after defining the instrument settings.



Note: Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).


To automatically read multiple **Plate** sections in the same experiment, see [Enabling Auto Read on page 340](#).

If you are using the SoftMax Pro GxP Software, you must enable the following permissions to complete a Western Blot membrane read:

- **Read empty plates/cuvettes** to start a read.
- **Save data files** to save the data file before the read.
- **Overwrite plate/cuvette data** to do a high-resolution ROI read.


See [Using SoftMax Pro GxP Software Features on page 467](#).


To read a membrane:

1. Open the drawer of the instrument by clicking **Open/Close**  on the **Home** tab in the ribbon.
2. Insert the prepared membrane holder matching the A1 position on the membrane holder with the A1 position in the drawer in landscape orientation. Make sure the membrane holder is flat against the drawer bottom.





CAUTION! To prevent damage to the instrument or the membrane holder, make sure that all the holder clips are securely snapped into place before inserting the membrane holder into the microplate reader.

3. Click **Open/Close**  to close the drawer.
4. Open a SoftMax Pro Software data file or protocol file that contains the applicable experiment settings for the membrane read. As an alternative, create new settings by selecting the **Plate** section in the SoftMax Pro Software program and configuring the instrument settings using the **Settings** dialog. See [Selecting Instrument Settings on page 236](#).
5. Before starting a read, it is good practice to save your data file. For Imaging reads and Western Blot reads, you must save your data file before starting the read. See [Saving Data Files on page 65](#).

6. Click **Read**  on the **Home** tab in the ribbon.

The Read button changes to **Stop** , letting you terminate a read if desired.

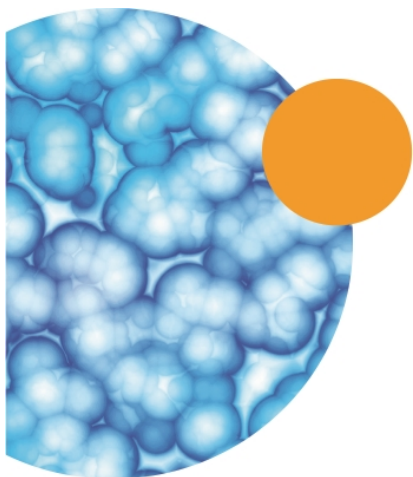
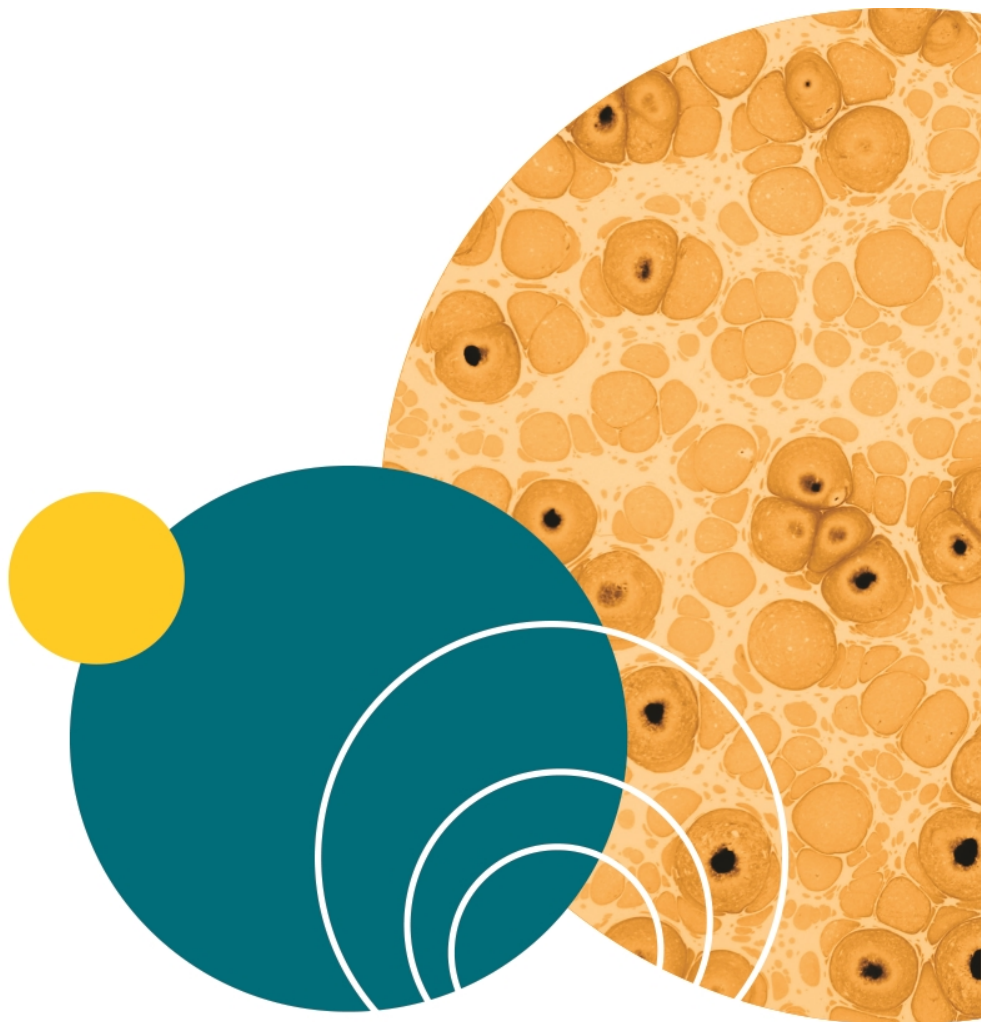
7. The active **Plate** section is read.
8. To select and scan a region of interest (ROI), click  on the left side of the **Plate** section

and then drag across the image to define the region. Click **Read**  on the **Home** tab in the ribbon to scan the region using the **ROI Scan Resolution** defined in the **Settings** dialog. The data from the ROI scan replaces the data from the original scan. See [Viewing Western Blot Membrane Data on page 443](#).

9. When the read is complete, click **Open/Close**  to open the drawer letting you remove the membrane holder.

After the read is complete, save the data. See [Saving Data Files on page 65](#).

For information on the data-analysis tools for Western Blot images, see [Viewing Western Blot Membrane Data on page 443](#).



Each SoftMax Pro Software data file has a minimum of one **Plate** section or one **Cuvette Set** section. Most files also have an assigned plate template and related **Group** sections, **Graph** sections, and **Note** sections. However, depending upon the protocol and how you want to report the data, only some of these sections might be present in every file.

Some simple protocols, such as reading the absorbance of proteins at 280 nm in a cuvette or in a microplate with PathCheck Pathlength Measurement Technology, let you calculate concentration in the **Plate** section or **Cuvette Set** section. In such an example, **Group** sections and **Graph** sections are necessary only if you want to display the data in tables or graphically.

Many common protocols consist of data acquired in a **Plate** section or **Cuvette Set** section. Standards and unknowns are defined in a template. Unknowns are then interpolated from a standard curve.

For more information see:

- [Calculations and Numerical Precision on page 356](#)
- [Setting the Data Display Options on page 358](#)
- [Doing Data Reduction on page 367](#)
- [Viewing Data in a Three-Dimensional Graph on page 382](#)
- [Graphing Data on page 388](#)
- [Analyzing a Western Blot Image on page 450](#)

Calculations and Numerical Precision

The calculations done by the SoftMax Pro Software on real numbers use 64-bit double-precision (15+ digits of precision) as defined by the *Institute of Electrical and Electronics Engineers standard for floating point arithmetic (IEEE 754)*. Computations always use the maximum available precision. Rounding occurs only as required for display formatting purposes, or in the evaluation of a formula in which the **Round** operator is used.

See “Technical Details of Numerical Calculations in the SoftMax Pro Software” in the application help.

Numbers from **Plate** sections, **Cuvette Set** sections, **Group** sections, and Summaries are displayed, printed, and exported with as many digits after the decimal point as specified by the user. All numbers saved in the SoftMax Pro Software data files are stored with full 64-bit double-precision.

The precision of the data displayed in a **Plate** section varies based on the space available to view the characters.

You can customize the data display to **Numeric notation** or **Scientific notation** format, and specify the number of **Significant Figures** or **Decimal Places**. These options can be set separately for raw data and reduced data.

When the number of digits is increased, the font size of the values in the **Plate** section is decreased. If the value becomes too long, then the numbers are cut off at the edge of the wells.

When SoftMax Pro Software exports plate data, the values are not limited by space and can have more digits for each well.

The values displayed in a **Plate** section are only a representation of the data. In both the **Plate** section and in the exported data, the last digit displayed or exported is rounded based on the actual data value.

Although the SoftMax Pro Software can display readings and numbers derived from those readings with more than four decimal places, the resolution of the microplate reader ultimately determines the precision of the calculations. For more information about the numerical resolution of a reader, see the documentation for that reader.



Note: In versions of the SoftMax Pro Software older than version 6.0, the software used a text-conversion algorithm with a slight upward bias. This can result in a mismatch between the rounded values in the newer version and the older version. For example, when rounding the raw value 14.849999... to one decimal place, versions 6.0 and newer display 14.8, while older versions display 14.9. This does not affect the accuracy of the calculations, since rounding occurs only as required for display formatting purposes, or in the evaluation of a formula in which the **Round** operator is used. Computations always use the maximum available precision.

For information on suspending and resuming calculations, see [Using the Operations Tab on page 44](#).

More information on SoftMax Pro Software calculations can be found in the following topics or references:

- For information on Optical Density and %Transmittance calculations, see [Absorbance Read Mode on page 154](#).
- For information on pathlength calculations, see [PathCheck Pathlength Measurement Technology on page 156](#).
- For information on Fluorescence Polarization calculations, see [Fluorescence Polarization Read Mode on page 185](#).
- For information on kinetic and spectrum reductions, see [Kinetic Data Reduction Options on page 378](#) and [Spectrum Data Reduction Options on page 380](#).
- For information on curve fit calculations, see [Curve Fit Functions on page 404](#).
- For a technical discussion of calculations and numerical precision, see “Technical Details of Numerical Calculations in the SoftMax Pro Software” in the application help.
- For information on statistical functions, see the *SoftMax Pro Software Formula Reference Guide*.


Calculation Hierarchy

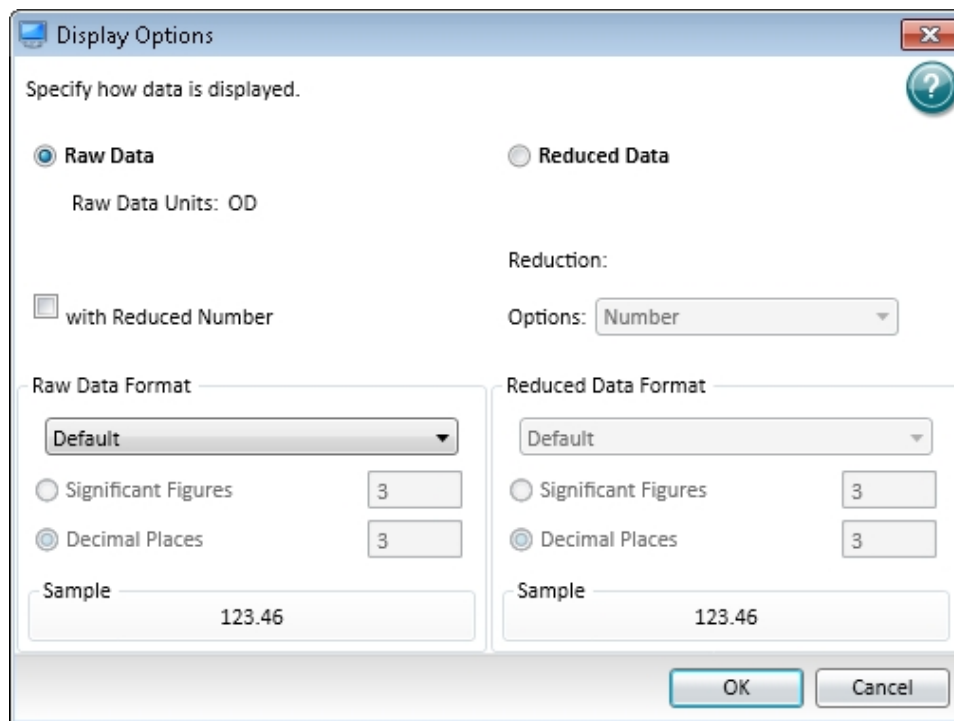
When reducing the data collected from the instrument, the SoftMax Pro Software does calculations hierarchically. If an option in the hierarchy has not been selected in the **Settings** dialog, is not available for the instrument being used, is not applicable to the type of read being done, or has not been defined in the **Template** dialog or the **Reduction** dialog, then the SoftMax Pro Software continues with the next listed calculation in the hierarchy.

The following is the general hierarchy of reduction calculations:

1. Apply Well Masking
2. Subtract Plate Background constant
3. Apply PathCheck Technology normalization
4. Subtract Plate Blank
5. Apply Smoothing
6. Time Alignment (Interpolate Raw Data)
7. Subtract Group Blank (pre-reduction option)
8. Calculate mP or Anisotropy
9. Set first data point to zero
10. Convert OD to %T
11. Apply Reduction Limits
12. Apply Wavelength Combination
13. Apply Baseline Options
14. Apply Kinetic or Spectrum Reduction
15. Subtract Group Blank (post-reduction option)

Setting the Data Display Options

In an active **Plate** section or **Cuvette Set** section, you can change how the data is presented by clicking **Display**  on the **Home** tab in the ribbon or in the toolbar at the top of the section.



The choices available in the **Display Options** dialog include selecting between **Raw Data** and **Reduced Data**.

For Imaging read mode **Imaging Data** replaces the **Raw Data** option.

You can customize the data display to **Numeric notation** or **Scientific notation** format, and specify the number of **Significant Figures** or **Decimal Places**. These options can be set separately for raw data and reduced data.


The **Default** format determines the number of decimal places to display based on the space available. For example, for a plate with 96 wells or fewer, each well is limited to five digits, plus one character for the decimal point, if applicable. For a 384-well plate, each well is limited to four characters, including the decimal point. If the value requires greater precision than can fit in the available space, the format changes to scientific notation.

When SoftMax Pro Software exports plate data, the values are not limited by space and can have more digits for each well.

The values displayed in a **Plate** section are only a representation of the data. In both the **Plate** section and in the exported data, the last digit displayed or exported is rounded based on the actual data value.

You can view both raw and reduced data or multiple reductions of the same data by cloning a plate. See [Cloning a Plate Section on page 127](#).

Viewing Raw Data

1. Click **Display**  on the **Home** tab in the ribbon or in the toolbar at the top of the section.
2. In the **Display Options** dialog, click **Raw Data**.
3. Optionally, click **with Reduced Number** to include the reduced data number on the display.
4. Click **OK**.


Raw Data Options

Selecting **Raw Data** displays the default data type for the selected read type:

- **Endpoint:** Raw absorbance, fluorescence, or luminescence values.
- **Kinetic:** The change in raw OD/RFU/RLU values over time, displayed as a plot.
- **Spectrum:** Raw OD/RFU/RLU values for the range of wavelengths, displayed as a plot.
- **Well Scan:** Raw OD/RFU/RLU values as shades of blue to red.

To see a reduced number, select **with Reduced Number**.

Viewing Reduced Data

1. Click **Display**  on the **Home** tab in the ribbon or in the toolbar at the top of the section.
2. In the **Display Options** dialog, click **Reduced Data**.
3. Select an option from the **Options** list.
4. Click **OK**.


Reduced Data Options

The reduced data display is based on the selections made in the **Data Reduction** dialog. See [Doing Data Reduction on page 367](#).

The reduced number is reported in the **Group** section when a template has been defined.

- Select **Number** to view only the reduced number.
- Select **Plot** for Kinetic reads to display a plot of the raw and reduced data. To also view the reduced number, select the **Reduced Number** check box.
- Select **Grayscale** to display the raw data in eight shades of gray, changing from light, for values less than or equal to the low limit, to dark, for values greater than or equal to the high limit. To define the **High Limit** and the **Low Limit** for the grayscale map, type values in the fields. To also view the reduced number, select the **Reduced Number** check box.
- Select **Color Map** to display the raw data in eight colors, changing from blue, for values less than or equal to the low limit, to red, for values greater than or equal to the high limit. To define the **High Limit** and the **Low Limit** for the color map, type values in the fields. To also view the reduced number, select the **Reduced Number** check box.

Viewing Imaging Data

1. Click **Display**  on the **Home** tab in the ribbon or in the toolbar at the top of the section.
2. In the **Display Options** dialog, click **Imaging Data**.
To display reduced imaging data, see [Viewing Reduced Data on page 360](#).
3. Select a **Data Type**. The options available in the measurement selections from the **Image Analysis Settings** in the **Settings** dialog. See [Viewing and Selecting Measurement Statistics on page 273](#).
4. Optionally, click **with Reduced Number** to include the reduced data number on the display.
5. Click **OK**.

Imaging Data Options

The **Data Type** list contains the measurement selections from the **Image Analysis Settings** in the **Settings** dialog. See [Viewing and Selecting Measurement Statistics on page 273](#).

Select from one of the **Data Types** that follow. Separate data types are available for each measured wavelength and classification, if applicable.

- **Object Count** gives the total number of objects detected in the image. This measurement is not used for field analysis of confluent areas.
- **Field Count** gives the total number of confluent areas detected in the image. This measurement is not used for discrete object analysis.
- **Object Percentage** gives the percentage the objects detected in the image by classification. This measurement is not used for field analysis of confluent areas.
- **Covered Area** gives the combined area of all the objects or confluent areas detected in the image as a percentage of the entire image area.
- **Object Area** gives the average area of the objects detected in the image expressed in μm^2 . This measurement is not used for field analysis of confluent areas.
- **Field Area** gives the average area of the confluent areas detected in the image expressed in μm^2 . This measurement is not used for discrete object analysis.
- **Object Roundness** gives the average roundness of each object detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for field analysis of confluent areas.
- **Field Roundness** gives the average roundness of each confluent area detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for discrete object analysis.
- **Object Average Intensity** gives the average fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).



- **Field Average Intensity** gives the average fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Object Intensity** gives the average total fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Intensity** gives the average total fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Total Intensity** gives the combined total fluorescent signal intensity of the objects or confluent areas detected in the image expressed in million intensity counts. This measurement is not used for transmitted light (TL).

Zooming the Display of a Well or Cuvette

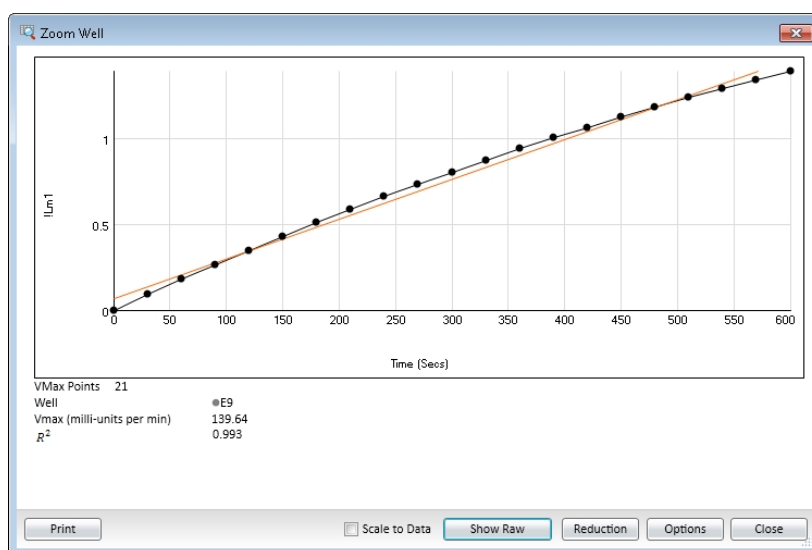
The **Zoom** icon becomes active when the data in a well or cuvette is available for a zoomed display.

To magnify the display of imaging data in a well, see [Viewing the Imaging Data in a Well on page 365](#).

To display the **Zoom Well** dialog:

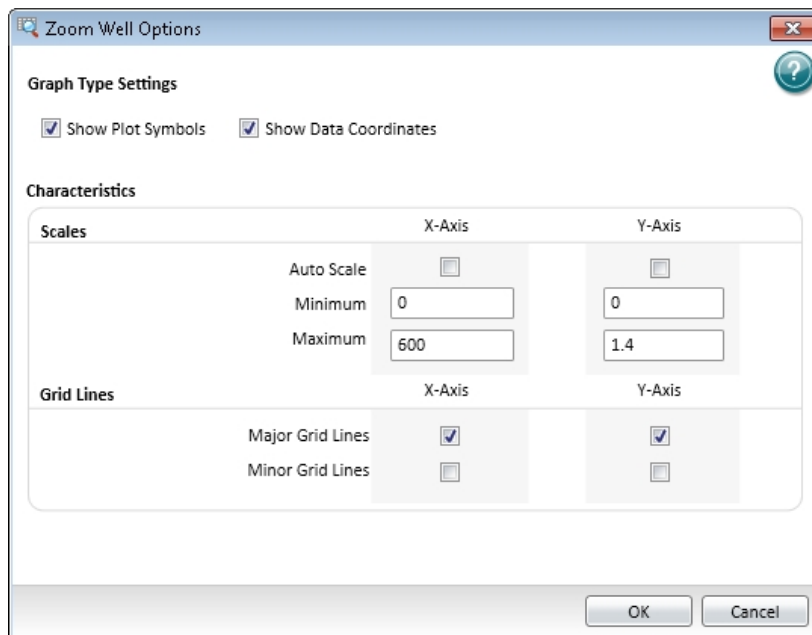
1. Click the well or cuvette that you want to zoom.
2. Click **Zoom**  on the **Home** tab in the ribbon or **Zoom**  in the toolbar at the top of the section. You can also double-click the well to open the **Zoom Well** dialog.

The data from the selected well or cuvette is displayed in a zoomed graph window.



3. To print the graph window, click **Print**.
4. To scale the display to the data, select **Scale to Data**.
5. To toggle between reduced and raw data, click **Show Reduced** or **Show Raw**.
6. To modify the reduction settings, click **Reduction**. The **Data Reduction** dialog is displayed. See [Doing Data Reduction on page 367](#).

- To modify the zoom well display settings, click **Options**. The **Zoom Well Options** dialog is displayed.



- **Graph Type Settings** lets you enable or disable connected points or plotted symbols on the graph.
- **Characteristics** lets you set Auto Scale parameters and choose the minimum and maximum values for the selected axis. You can also add or remove grid lines from the display.



To save the settings and return to the **Zoom Well** dialog, click **OK**. These changes have an effect on only the well graph being viewed.

- To close the **Zoom Well** dialog, click **Close**.

Viewing the Imaging Data in a Well

You can view a combination of the raw image and the analysis data in up to four wells from a **Plate** section or the two wells from the Image Analysis Settings. See [Using a Plate Section on page 118](#) or [Image Analysis Settings on page 266](#).

The **Zoom** icon becomes active for a **Plate** section when the imaging data in a well is available for a zoomed display.

To display the **SoftMax Pro MiniMax Well Viewer** dialog from a **Plate** section, double-click the well that you want to zoom. You can also click **Zoom**  on the **Home** tab in the ribbon or **Zoom**  in the toolbar at the top of the section. In the Image Analysis Settings Measurement Selection, click **Show Details**.

To view more than one well in a **Plate** section, drag your pointer to select up to four wells before opening the **Zoom Well** dialog.

It can take some time before the **SoftMax Pro MiniMax Well Viewer** dialog is displayed. It can also be displayed behind the SoftMax Pro Software window. To bring the well viewer to the front, click the **SoftMax Pro MiniMax Well Viewer** icon in the Windows task bar.



The **SoftMax Pro MiniMax Well Viewer** dialog displays a zoomed image of the well, a table of data, and chart of the data. To choose to display one or more of these areas, select or clear the **Show Images**, **Show Tables**, or **Show Charts** check boxes in the lower-left area of the dialog.

The three areas in the dialog are interactive.

- Click the cells in the image to highlight the data in the table and the data in the chart.
- Click the data in the table to highlight the cells in the image and the data in the chart.
- Click the data in the chart to highlight the cells in the image and the data in the table.

To use an image of the **SoftMax Pro MiniMax Well Viewer** dialog in a Microsoft PowerPoint presentation, click **Send to PowerPoint**. A new document opens in PowerPoint with an image of the **Zoom Well** dialog in a slide.

Image Area Options

The image area displays the acquired image from the selected well. To zoom the acquired image in and out, right-click the image and click **Zoom In** or **Zoom Out**. You can also hold the **CTRL** key down and press **+** or **-**, or use the mouse wheel to zoom in or out. Drag the scroll bars to move the zoomed image in the image area, or click the image and drag it into position.

Click the buttons above the image to switch the view of the image between wavelengths, and to display or hide the found objects or confluent areas.



- When a button is filled in, the related wavelength, objects, or areas are displayed in the image.
- When a button is outlined, the related wavelength, objects, or areas are not displayed in the image.

When you click a button above the images, it effects the display of all the images.

Use the controls below the image to separately adjust the intensity of each wavelength.

From the list on the left, select the wavelength that you want to adjust.



Drag the sliders to adjust the intensity range of the image.



- The bar on the left controls the low level of intensity.
- The bar on the right controls the high level of intensity.

When you drag a bar, the intensity level is displayed above the bar.

To move the sliders to the outside edges, click the double-arrow button on the left.

From the list on the right, select the color for the view.



To automatically scale the intensity of all the wavelengths in the image, click **Auto Scale All Wavelengths**.

Table Area Options

In the table area, you can change the size the columns by dragging the separator lines. Drag the scroll bars to view the data in the table.

To use the table data in Microsoft Excel, click **Send to Excel**. A new spreadsheet opens in Excel with the data from the table in the cells.

Chart Area Options

To change the type of chart displayed in the chart area, click **Histogram** or **Scatter Plot**.


- For a histogram, you can select a data type for the **X Axis Data**.
- For a scatter plot, you can select data types for the **X Axis Data** and the **Y Axis Data**.

Masking Wells or Cuvettes

The Mask feature hides selected data so that they are not used for calculations and are not reported. Masking is commonly used to suppress outliers from data reduction calculations.

Masking can be used as a “what if?” tool. For example, if you have included a group blank in a template and want to see the data both with and without the blank, masking the group blanks suppresses the blanking function, while unmasking them enables it again.

To mask wells or cuvettes:

1. In an active **Plate** section or **Cuvette Set** section, select a well or cuvette or select multiple wells or cuvettes.
 - To select multiple wells in a **Plate** section, click and drag across the desired wells.
 - To select multiple cuvettes in a **Cuvette Set** section, hold down the **Ctrl** key and click the desired wells.
2. Click **Mask**  in **Plate Tools** or **Cuvette Tools** on the **Home** tab in the ribbon or in the toolbar at the top of the section.

You can also right-click a well or cuvette and select **Mask** from the shortcut menu.

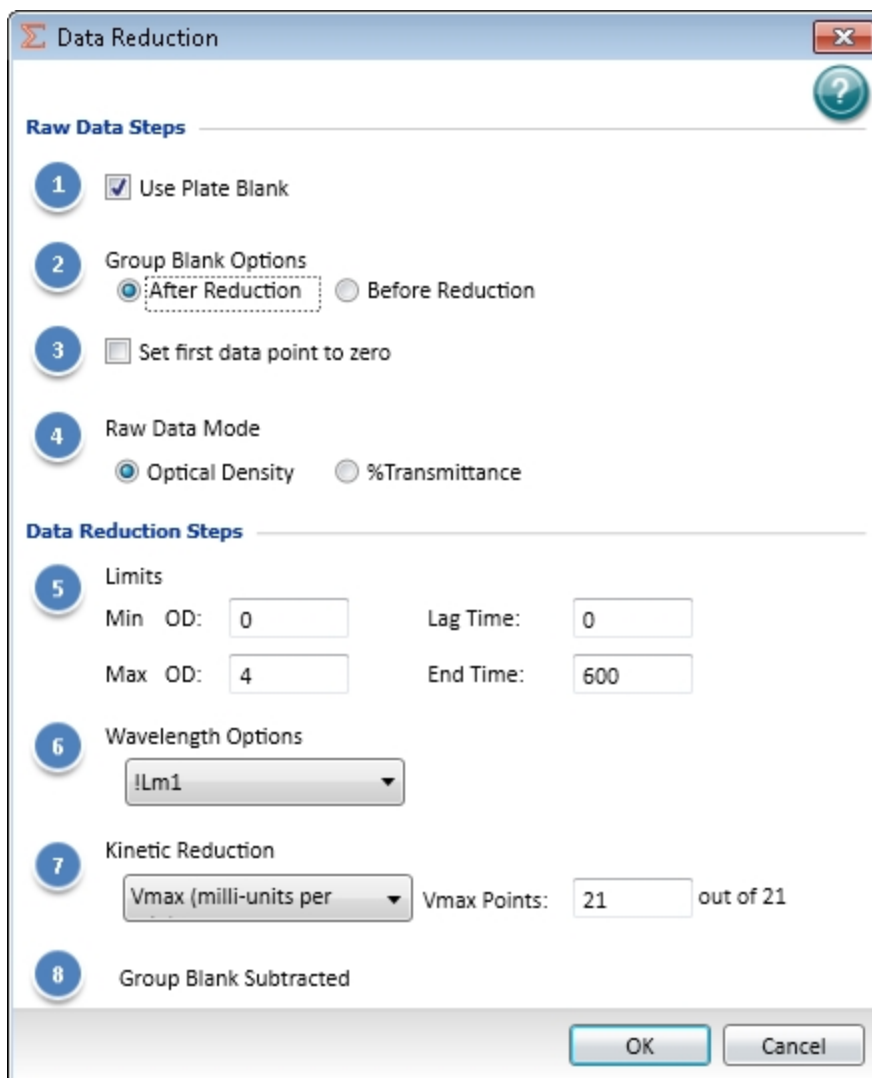
To unmask masked wells or cuvettes select them and then click **Mask**.

Doing Data Reduction

The reduction process in SoftMax Pro Software is based on formulas that reduce the raw data to show a single number for each well or cuvette. Further analysis of this reduced number is done in **Group** and **Graph** sections.

When reducing raw information collected from the instrument, SoftMax Pro Software does calculations hierarchically. Only the data reduction calculations that apply to the data based on the instrument read mode, read type, and settings are done. See [Calculation Hierarchy on page 357](#).

Click **Reduction** on the **Home** tab in the ribbon or in the toolbar at the top of the section to open the **Data Reduction** dialog.



The **Data Reduction** dialog displays only the reduction options that are available for the instrument you are using, the options that have been selected in the **Settings** dialog, and the options defined in the template.

SoftMax Pro Software does the applicable calculations in the **Plate** section or **Cuvette Set** section in the order displayed in the **Data Reduction** dialog. If an option has either not been selected in the **Instrument Settings** dialog, is not available for the instrument you are using, or has not been defined in the template, SoftMax Pro Software continues with the next applicable calculation.

Raw Data Steps

Raw data displays are calculated using the following steps that apply to the selected mode, type, and settings:

Apply PathCheck (Absorbance Endpoint only)

PathCheck Pathlength Measurement Technology normalization calculations apply to the data only when PathCheck has been enabled in the PathCheck settings for an Absorbance Endpoint read. When PathCheck is enabled, this calculation can be disabled in the **Data Reduction** dialog by clearing the **Apply Pathcheck** check box. For more information, see [PathCheck Pathlength Measurement Technology on page 156](#).

The screenshot shows the 'Data Reduction' dialog box with the following settings:

- Raw Data Steps:**
 - 1. Pathcheck Options:
 - Apply Pathcheck
 - Apply Plate Background OD
 - Lm1: 0
 - 2. Use Plate Blank
 - 3. Group Blank Options:
 - After Reduction
 - Before Reduction
 - 4. Raw Data Mode:
 - Optical Density
 - %Transmittance
- Data Reduction Steps:**
 - 5. Wavelength Options: !Lm1

Apply Plate Background OD (Absorbance Endpoint only)

Subtraction of the Plate Background constant applies to the data only when PathCheck has been enabled in the PathCheck settings for an Absorbance Endpoint read. To define the constant, type a value in the field. When PathCheck is enabled, this calculation can be disabled in the **Data Reduction** dialog by clearing the **Apply Plate Background OD** check box.

Use Plate Blank

The **Use Plate Blank** calculation is available when a plate blank is specified in the template settings for the plate. To enable subtraction of the plate blank value, select the **Use Plate Blank** check box. For more information about plate blanks, see [Defining Blanks on page 308](#).

Smoothing

Smoothing is used to reduce noise in kinetic reads for FlexStation Instrument data. This setting takes the moving average of the raw data and displays the plot using the averaged values.

The default is no smoothing, or a setting of 1 “averaged” point.

- A setting of 3 provides the least amount of smoothing, where the value of the center point is added to the values of the points on either side. The sum of these points is then divided by three and the resulting value is substituted for the center point.
- A setting of 9 averages the center point with the four points on each side.

When multiple wavelengths are read, smoothing is done before doing wavelength combination calculations such as ratios or multiplication. For example, if you read at two wavelengths and choose to take a ratio of those wavelengths, smoothing is performed on each individual wavelength and the wavelength ratio is calculated using smoothed data.

Time Alignment

For FlexStation Instrument data, each data value is logged with its own read time. The SoftMax Pro Software can align the time points by **Wavelength** or by **Well** and interpolate the data against a single time point.

- Select the **Time Alignment** check box and then click **Wavelength** so that you can do wavelength combination calculations correctly. For example, you can take a ratio of two different wavelengths ($Lm1/Lm2$) in a single well that have been read at two different time points. The **Wavelength** option is available only when two or more wavelengths are present in the data.

With **Wavelength** selected, the SoftMax Pro Software uses quadratic interpolation to calculate the interpolated values. This results in the loss of one point at each end of the plot. Before starting the calculation, the software determines the starting point by averaging the initial data points of the separate wavelengths. For example, if the first data points of the two wavelengths have time values of 0.3 and 0.5 seconds, the software averages these data points and uses 0.4 seconds as its initial point for interpolation.

- Select the **Time Alignment** check box and then click **Well** to normalize the kinetic read times of the wells in the column against the read time of the first well in the column. Injection occurs at the same time in all the wells of a column, but each of the wells is read sequentially. So, each well is read at a different time point during the reaction from the injection. With **Well** selected, the data in the wells are interpolated against the time point of the read of the first well.

Group Blank Options

The **Group Blank Options** calculation is available when a group blank is specified in the template settings for the plate. The subtraction of the group blank value can be selected as a pre-reduction process or a post-reduction process.

- To enable the group blank value subtraction calculation as a pre-reduction process, click **Before Reduction**.
- To enable the group blank value subtraction calculation as a post-reduction process, click **After Reduction**. When **After Reduction** is selected under **Group Blank Options**, the last step in the **Data Reduction** dialog shows **Group Blank Subtracted**.

For more information about group blanks, see [Defining Blanks on page 308](#).

Polarization or Anisotropy (Fluorescence Polarization only)

Fluorescence polarization mode returns two sets of data: one for fluorescence intensity parallel (P) to the excitation plane, and the other for fluorescence intensity perpendicular (S) to the excitation plane. These S and P values are used to calculate the Polarization (mP) and Anisotropy (r) values in the SoftMax Pro Software. Click the data type to use as the raw data for the reduction.

G Factor

The G factor, or grating factor, is used in fluorescence polarization to correct polarization data for optical artifacts, converting relative mP data to theoretical mP data. Optical systems, particularly with reflective components, pass light of different polarization with different efficiency. G factor corrects this instrumental bias. To define the **G Factor**, type a value in the field.

Set first data point to zero (Kinetic only)

Select this check box to offset the first data point to (0,) and shift all other data accordingly. Clearing this check box can cause some data points that do not fall within the reduction limits to disappear.

To see more data and still display absolute values, increase the reduction limits for **Min OD**, **Min RLU**, or **Min RFU** and the **Max OD**, **Max RLU**, or **Max RFU**.

Raw Data Display Mode (Absorbance only)

For Absorbance reads, you can choose whether to display absorbance data as Optical Density or %Transmittance.

- **Optical Density:** The quantity of light passing through a sample to a detector relative to the total quantity of light available. Optical Density includes absorbance of the sample plus light scatter from turbidity.
- **% Transmittance** is the ratio of transmitted light to the incident light (for absorbance readings).

Click the data type to use as the raw data for the reduction.



Note: Separate mathematical calculations are used for handling Optical Density (OD) and %Transmittance (%T) calculations for Pre-read plate blanking, PathCheck Pathlength Measurement Technology, and Reference, because OD calculations are done on a linear scale, while %T calculations are done on a logarithmic scale. However, SoftMax Pro Software does not do other calculations differently for OD and %T modes. Because of this, Molecular Devices recommends that %T be used only for raw OD, raw OD with Pre-read plate blank subtraction, or raw OD readings which are normalized by the PathCheck Pathlength Measurement Technology. Use caution when using %T on reduced numbers or the readings that apply to other calculations since the data might not be calculated correctly.

Data Reduction Steps

Data Reduction display includes one or more of the following calculations:

Baseline Options

Baseline options affect the way that the data is graphed for FlexStation Instrument data.

- **Absolute** displays the raw data without any change in the way it is graphed. Raw data is used in subsequent reduction calculations.
- **Zero Baseline** offsets the graph slightly. For example, if you type **5** for the number of points, then the average of the first 5 points is used as the baseline value, and all raw data are subtracted from this value.

Baseline subtraction is applied only to the reduced data. The raw data plots do not change. To view the plot with baseline subtraction, select **Reduced Plot** in the **Display** dialog or select **Show Reduced** in a **Zoom Well** dialog.

If two or more wavelengths are present in a reading, and you combine these wavelengths while **Zero Baseline** is selected, the zero baseline applies only after the wavelength combination.

- **% Baseline** makes data from a FlexStation Instrument look similar to data from a FLIPR System. Data from a FLIPR System can be imported into the SoftMax Pro Software, and this option modifies the plot and reduction calculations to make data from a FlexStation Instrument comparable to data from a FLIPR System.

This method averages the first number of points you specify (the upper box), divides the raw data by this average value, and then multiplies by 100 (%). Type a value from 0.001 to 99999 to be used to multiply the % Baseline value.

This calculation is done only on the reduced data and only after any wavelength combinations are calculated.

To view the modified plot, select **Reduced Plot** in the **Display** dialog or select **Show Reduced** in a **Zoom Well** dialog.

Limits

Apply the specified reduction limits to the reduced data after this step. To specify the limits, type values in the fields.

Limits define the data that are viewed and included in data reduction. If you change a limit to show less data, you can always display the excluded data again by changing the limit.

The display of OD, RFU, or RLU values is relative to the first point measured for each well.


Negative Kinetic values decrease with time, and limits should be set accordingly (below 0) to view negative Kinetic data.

- **Min OD, Min RFU, or Min RLU** defines the limit for the minimum value to report. Values from the reading that are under this limit are not shown and are excluded from data reduction. The default is 0 OD or RFU/RLU. To display negative Kinetics, the value should be set below 0 (zero).


- **Max OD, Max RFU, or Max RLU** defines the limit for the minimum value to report. Values from the reading that are under this limit are not shown and are excluded from data reduction. The default is 0 OD or RFU/RLU. To display negative Kinetics, the value should be set below 0 (zero).
- **Lag Time** in a kinetic read defines the period of very slow growth of microorganisms or the rate of reaction that can precede the rapid or linear phase of reaction. The lag time specifies how many initial data points are excluded from the calculation of **Vmax Rate**. Lag time truncates the data used in the calculation, but does not prevent data from being collected. Kinetic plots do not display the data collected before the lag time.
- **End Time** in a kinetic read specifies the time at which to stop showing data in the display and exclude it from data reduction. Values occurring after this limit are not reported in the display and are excluded from data reduction. The default setting is the total assay time for the kinetic read.
- **Start** in a spectrum read specifies the limit in nm for the minimum wavelength setting to report. Values from the reading that are under this limit are not shown and are excluded from data reduction.
- **End** in a spectrum read specifies the limit for the maximum wavelength setting to report. Values from the reading that are above this limit are not shown and are excluded from data reduction.

Wavelength Options

Select an available wavelength formula from the list. To use a custom reduction, select

Custom from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).


Kinetic Reduction

Select a Kinetic reduction mode from the list. To use a custom reduction, select **Custom** from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).

For more information about kinetic reductions, see [Kinetic Data Reduction Options on page 378](#).


The number of Vmax Points is determined by the Timing settings.

Spectrum Reduction

Select a Spectrum reduction mode from the list. To use a custom reduction, select **Custom** from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).

For more information about spectrum reductions, see [Spectrum Data Reduction Options on page 380](#).

Well Scan Reduction

Select **Maximum**, **Minimum**, **Average**, or **Custom** from the list. **Average** provides the average value for all points in the Well Scan. To use a custom reduction, select **Custom** from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).

Group Blank Subtracted

When **After Reduction** is selected under **Group Blank Options**, the last step in the **Data Reduction** dialog shows **Group Blank Subtracted**.

After all applicable data reduction options have been set, click **OK**.

Data Reduction Formulas

The reduction process in SoftMax Pro Software is based on formulas that reduce the raw data to show a single number for each well or cuvette. Further analysis of this reduced number is done in **Group** sections and **Graph** sections. See [Using a Group Section on page 139](#) and [Graphing Data on page 388](#).

Custom Reduction Formulas

If the predefined reduction formulas do not meet your needs, you can create custom reduction formulas. Selecting **Custom** from the menus or dialogs displays a **Formula** button that you can click to open a **Formula** dialog.

Examples of some formulas that can be used when combining multiple wavelengths in a **Formula** dialog are given in the following tables.

Table 8-1: Wavelength Reduction Formula Examples for Specific Wavelength Combinations

2 Wavelengths	3 Wavelengths	4 to 6 Wavelengths
$!Lm1 + !Lm2$	$Lm1 + !Lm2 + !Lm3$	$!Lm1 + !Lm2 + \dots + !Lmn$
$!Lm1 - !Lm2$	$(!Lm1 - !Lm3) / (!Lm2 - !Lm3)$	$(!Lm1 - !Lm6) / (!Lm2 - !Lm5) / (!Lm3 - !Lm4)$
$!Lm1 / !Lm2$	$!Lm1 / !Lm3$	$!Lm1 / !Lmn$
$!Lm1 * !Lm2$	$!Lm1 * !Lm3$	$!Lm1 * !Lmn$
$\text{Log}10(!Lm1/!Lm2)$	$\text{Log}10(!Lm1/!Lm3)$	$\text{Log}10(!Lm1/!Lmn)$
$!Pathlength$	$!Pathlength$	$!Pathlength$

Table 8-2: Wavelength Reduction Formula Examples for all Wavelength Combinations

Formula	Description
$!Lmx / \text{constant}$	For example, $Lm1 / 1.44$ for quantitating a polyclonal antibody by measuring the absorbance at A280 with PathCheck Pathlength Measurement Technology on.
$\text{Average}(!Lm1\&!Lm2\&!Lm3)$	Averages together the optical densities for multiple readings at the same wavelength (for example, if you read the well six times at 280 nm).
$\text{Min}(!Lm1\&!Lm2\&!Lm3)$	Reports the minimum OD/RFU/RLU recorded for multiple wavelength readings in each well.
$\text{Max}(!Lm1\&!Lm2\&!Lm3)$	Reports the maximum OD/RFU/RLU recorded for multiple wavelength readings in each well.
$\text{If}(!Lmz < A, \text{makeerr}(118), (\text{if}(!Lmx > B, \text{makeerr}(117), !Lm1)))$	Reports “low” for a well with an OD/RFU/RLU less than A, “high” for an OD/RFU/RLU greater than B, and the OD/RFU/RLU of a well lies between A and B.

Custom reduction formulas using mathematical operators or terms can be used to obtain specific types of data. The following table provides some examples of such formulas for Kinetic and Spectrum readings.

Table 8-3: Kinetic Reduction Formula Examples

Formula	Description
Vmaxcorr(!combinedplot, !Vmaxpoints,!readinterval)	Reports Vmax correlation coefficient for plots in all 96 wells.
Vmax(Delta(!combinedplot), !Vmaxpoints,!readinterval)	Reports the Vmax Rate of the delta between each time point.

Table 8-4: Spectrum or Kinetic Reduction Formula Example

Formula	Description
Nthitem(!Lm1,X)	Reports the optical density at item X in the list of readings. For example, if you have a Kinetic run with 20 time points and X is 10, it reports the OD/RFU/RLU of the 10th time point. Similarly, if you have a Spectrum scan with 20 measurements and X is 10, it reports the OD/RFU/RLU of the 10th wavelength measured.

The accessor names for custom reduction formulas for imaging data are enclosed in square brackets to prevent conflicts with other formula elements.

Table 8-5: Imaging Reduction Formula Example

Formula	Description
![TypeAObjectCount] - ![TypeBObjectCount]	Reports the difference between the number of Type A and Type B cells detected in the image.

For a full discussion of custom formulas, see the *SoftMax Pro Software Formula Reference Guide*.

When you finish your entry in the **Calculation** dialog and click **OK**, the formula is displayed and becomes the default selection for the **Custom** option.

Kinetic Data Reduction Options

Kinetic reductions are applied to the value at each time point after the wavelength combination formula is applied.

Vmax

Vmax is the maximum slope of the Kinetic display of mOD/min or RFU/RLU per second. Vmax is calculated by measuring the slopes of a number of straight lines, where Vmax Points determines the number of contiguous points over which each straight line is defined.

This is an alternative method for analyzing non-linear Kinetic reactions that reports the elapsed time until the maximum reaction rate is reached, rather than reporting the maximum rate itself. Used in conjunction with Vmax Points, Time to Vmax is the time to the midpoint of the line defined by Vmax Points and used to calculate Vmax.

Vmax Rate is reported as signal/min (milli-OD, RFU, or RLU units per minute) for a Kinetic read. It is calculated using a linear curve fit, $y = Ax + B$. A creeping iteration is done using Vmax Points and the slope of the steepest line segment is reported as Vmax Rate. It can also be reported as units per second (the default for Fluorescence and Luminescence modes).

Vmax (milli-units per min) and **Vmax (units per sec)** reductions are available for all instruments that are capable of Kinetics. The default Kinetic reduction is **Vmax (milli-units per min)**.

Time to Vmax elapsed time data is useful for applications including coagulation chemistry where the changing concentration of the reagents does not change Vmax, but rather changes the time at which the reaction reaches the maximum rate.

The number of available Vmax Points is determined by the Timing settings. Typing a value in the **Vmax Points** field defines the maximum size of the line segment used to determine the slope of the line used in calculating the rate of the reaction. The default is the total number of points taken in the reading.

The first slope is calculated for a line drawn that starts at the first reading as defined by **Lag Time** and ends at a total number of readings equal to the **Vmax Points** setting. The second and subsequent slopes are calculated to start at the second time point and end at a total number of readings equal to the **Vmax Points** setting. The steepest positive or negative slope is reported as Vmax.

If the data plot displays fewer time points (data points) than Vmax Points, all of the time points are used to determine the slope of the data.

Onset Time

Onset time is a method for analyzing non-linear Kinetic reactions. Onset Time reports the time required for a Kinetic reaction to reach a specified OD or RFU/RLU (onset OD/RFU/RLU).

This elapsed time data is useful for cascade reactions including clot formation (such as, endotoxin testing) and clot lysis applications where the change in reagent concentration does not have an effect on the maximum optical density change but changes the time required for the reaction to reach completion.

Time at Minimum

This setting reports the time at the minimum OD, RFU/RLU, or %T that falls within the reduction limits.

Time at Maximum

This setting reports the time at the maximum OD, RFU/RLU, or %T that falls within the reduction limits.

Time at 1/2 Maximum

This setting reports the time at the half of the maximum OD, RFU/RLU, or %T that falls within the reduction limits.

To calculate this reduction, SoftMax Pro Software determines the Kinetic point (within the reduction limits) that has the maximum signal level (OD or %T) and divides it by 2 to get the 1/2 Maximum value. Then it finds the time value at the 1/2 Maximum.


Area Under Curve

This reduction estimates the area under the curve as defined by the data plots within the reduction limits. The data plots are treated as a series of trapezoids with vertices at successive data points and at the X-axis coordinates of the data points. The areas defined by each of the trapezoids are then computed and summed.

Slope

The slope reduction option determines the slope of the combined plot (for example, the slope of the line using linear regression after the wavelength combination reduction). This reduction uses all visible time points in the reduction window.

Slope is the same as Vmax Rate when Vmax Rate is set to the same number of points as the run, but is different if you have modified Vmax Points.

To use a custom reduction, select **Custom** from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).

Spectrum Data Reduction Options

The **Spectrum Reduction** formula is applied to the list of numbers in each well (values at each wavelength) after the wavelength combination formula is applied. The default reduction for a Spectrum read is **Lambda at Maximum**.

Maximum

This reduction reports the maximum absorbance (optical density) or percent transmittance (%T), RFU, or RLU within the reduction limits.

Minimum

This reduction reports the minimum absorbance (optical density) or percent transmittance (%T), RFU, or RLU within the reduction limits.

Lambda at Maximum


This reduction reports the wavelength at which maximum absorbance (optical density) or percent transmittance (%T), RFU, or RLU within the reduction limits.

Lambda at Minimum

This reduction reports the wavelength of minimum absorbance (optical density) or percent transmittance (%T), RFU, or RLU within the reduction limits.

Area Under Curve

This reduction estimates the area under the curve as defined by the data plots, within the reduction limits. The data plots are treated as a series of trapezoids with vertices at successive data points and at the X-axis coordinates of the data points. The areas defined by each of the trapezoids are then computed and summed.


To use a custom reduction, select **Custom** from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).

Imaging Data Reduction Options


The **Imaging Data** list contains the measurement selections from the **Image Analysis Settings** in the **Settings** dialog. See [Viewing and Selecting Measurement Statistics on page 273](#).

Select from one of the reduction data types that follow. Separate data types are available for each measured wavelength and classification, if applicable.

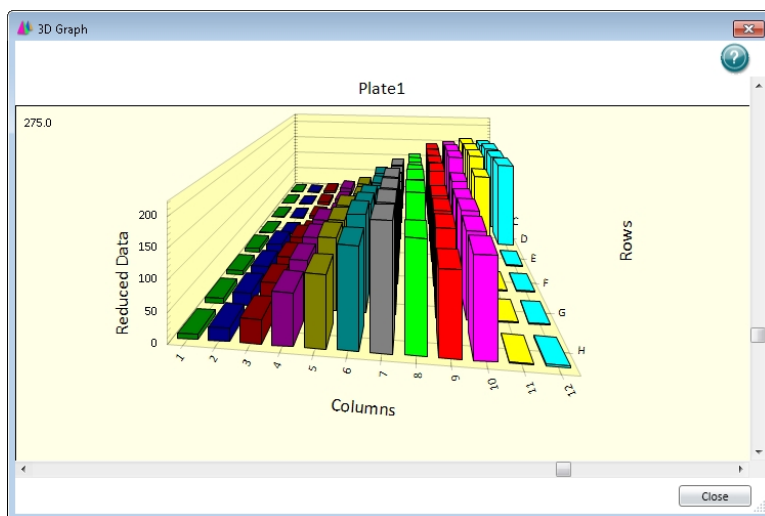
- **Object Count** gives the total number of objects detected in the image. This measurement is not used for field analysis of confluent areas.
- **Field Count** gives the total number of confluent areas detected in the image. This measurement is not used for discrete object analysis.
- **Object Percentage** gives the percentage the objects detected in the image by classification. This measurement is not used for field analysis of confluent areas.
- **Covered Area** gives the combined area of all the objects or confluent areas detected in the image as a percentage of the entire image area.
- **Object Area** gives the average area of the objects detected in the image expressed in μm^2 . This measurement is not used for field analysis of confluent areas.
- **Field Area** gives the average area of the confluent areas detected in the image expressed in μm^2 . This measurement is not used for discrete object analysis.
- **Object Roundness** gives the average roundness of each object detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for field analysis of confluent areas.
- **Field Roundness** gives the average roundness of each confluent area detected in the image. A shape factor of 1.00 is perfectly round, while a shape factor of 0.00 is not round at all. This measurement is not used for discrete object analysis.
- **Object Average Intensity** gives the average fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Average Intensity** gives the average fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Object Intensity** gives the average total fluorescent signal intensity of the objects detected in the image. This measurement is not used for field analysis of confluent areas. This measurement is not used for transmitted light (TL).
- **Field Intensity** gives the average total fluorescent signal intensity of the confluent areas detected in the image. This measurement is not used for discrete object analysis. This measurement is not used for transmitted light (TL).
- **Total Intensity** gives the combined total fluorescent signal intensity of the objects or confluent areas detected in the image expressed in million intensity counts. This measurement is not used for transmitted light (TL).

To use a custom reduction, select **Custom** from the list and then, click  to open the **Formula Editor**. See [Data Reduction Formulas on page 376](#).

Viewing Data in a Three-Dimensional Graph

To view a three-dimensional graphical representation of reduced plate data, view the **Plate** section and then click the  **3D Graph** button in the **Plate Tools** area of the **Home** tab in the ribbon or in the toolbar at the top of the **Plate** section.

You can rotate a 3D graph vertically and horizontally.



To rotate the 3D graph:

- To rotate the 3D graph vertically, drag the vertical scroll bar located to the right of the 3D graph.
- To rotate the 3D graph horizontally, drag the horizontal scroll bar located below the 3D graph.
- To start or stop a continuous animated horizontal rotation of the 3D graph, double-click the 3D graph.

You can resize the **3D Graph** dialog by dragging a side or a corner of the dialog.

For customization and export options, right-click on the 3D graph.

You can quickly choose a customization option from the menu, or click **Customization Dialog** to change several options at the same time. See [Customizing a Three-Dimensional Graph on page 383](#).

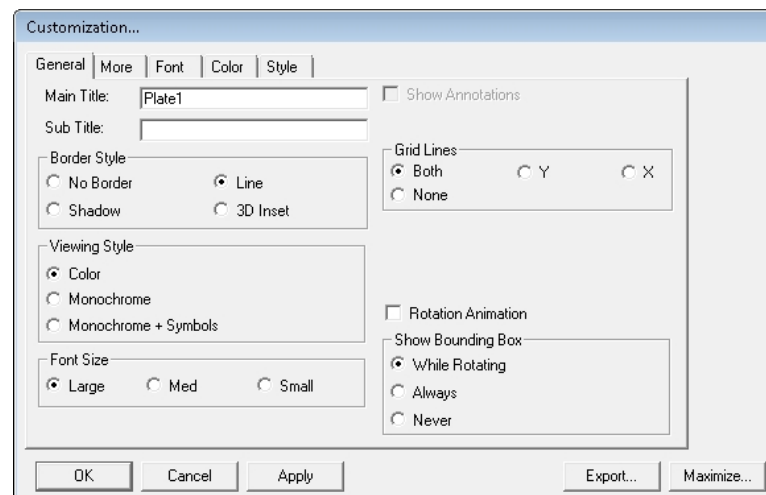
Other options in the 3D graph dialog include:

- **Plotting Method** lets you view the graphed data in **Wire Frame**, **Surface**, **Surface with Shading** views.
- **Maximize** expands the 3D graph to a full screen view. To return to the normal view, click the title bar or press **Esc**.
- **Export dialog is displayed** the **Export Control** dialog letting you export the graphical image to your choice of formats, or export the data to a text format. See [Exporting a Three-Dimensional Graph on page 386](#).

To close the **3D Graph** dialog, click **Close**.

Customizing a Three-Dimensional Graph

The customization dialog has five tabs that contain customization options for the current 3D graph.



Click a tab to work with the options under that tab.

- For the **General** tab, see [General Customization Options for a 3D Graph on page 384](#).
- For the **More** tab, see [More Customization Options for a 3D Graph on page 384](#).
- For the **Font** tab, see [Font Customization Options for a 3D Graph on page 385](#).
- For the **Color** tab, see [Color Customization Options for a 3D Graph on page 385](#).
- For the **Style** tab, see [Style Customization Options for a 3D Graph on page 386](#).

After making changes to the options in this dialog, you can click **Apply** to view how the changes are applied to the 3D graph.

To close the **Customization** dialog and save unapplied changes, click **OK**.

Click **Export** to close the **Customization** dialog and open the **Export Control** dialog that lets you export the graphical image to your choice of formats, or to export the data to a text format. See [Exporting a Three-Dimensional Graph on page 386](#).

Click **Maximize** to close the **Customization** dialog and expand the 3D graph to a full screen view. To return to the normal view, click the title bar or press **Esc**.

General Customization Options for a 3D Graph

Click the **General** tab to customize the 3D graph with the following options:

- **Main Title:** Type the text you want for the title of the 3D graph.
- **Sub Title:** Type the text you want below the title of the 3D graph.
- **Show Annotations:** To show notes, select this check box. This option is not available if there are no notes available.
- **Border Style:** To change the border around the outside of the graphical image, click **No Border**, **Line**, **Shadow**, or **3D Inset**.
- **Viewing Style:** To change the display of the image background, click **Color**, **Monochrome**, or **Monochrome + Symbols**.
- **Font Size:** To change the font size for all the text, click **Large**, **Med**, or **Small**.
- **Grid Lines:** To view both the Y and X grid lines, click **Both**. To view only the grid lines for the Y-axis, click **Y**. To view only the grid lines for the X-axis, click **X**. To remove the grid lines, click **None**.
- **Rotation Animation:** To start a continuous animated horizontal rotation of the 3D graph, select this check box.
- **Show Bounding Box:** To display a wire-frame box around the 3D graph under specific conditions, click **While Rotating**, **Always**, or **Never**.

More Customization Options for a 3D Graph

Click the **More** tab to customize the 3D graph with the following options:

- **Rotation Detail:** To change the display style when the 3D graph rotates, click **Wireframe** to display only the outlines of the 3D graph, **Plotting Method** to display the data plot in full 3D while displaying only outlines for the grid, or **Full** to display the entire 3D graph in full 3D during rotation.
- **Rotation Increment:** To control the speed and direction of the animated rotation, select an increment from the list. Values closer to zero rotate slower, while values farther from zero rotate faster. To rotate counter-clockwise, select a negative value.
- **Shading Style:** To change the display of the shading, click **White** or **Color**. This option has no effect on the display if there is no shading in the 3D graph.
- **Plotting Method:** To change the display of the data plot, click **Wire Frame**, **Surface**, or **Surface with Shading**.

Font Customization Options for a 3D Graph

Click the **Font** tab to customize the text in the 3D graph:

- **Main Title** includes only the title of the 3D graph.
- **Sub-Title** includes only the text directly below the title of the 3D graph, if applicable.
- **Subset/Point/Axis Labels** includes all of the other text in the 3D graph.

For each text area, you can select the font and select a check box to add **bold**, **italic**, and **underline** styles to the text.

A **sample** is displayed at the bottom to help you with your selections.

Color Customization Options for a 3D Graph

Click the **Color** tab to customize the colors used in the 3D graph.

Changes in the **Color** tab are automatically applied to the 3D graph as they are selected.

Click an option from the **Graph Attributes** group and then click a color to apply to the selected attribute:

- **Desk Foreground** includes the text of the title and subtitle of the 3D graph.
- **Desk Background** includes the area behind the title and subtitle of the 3D graph.
- **Shadow Color** includes the border shadowing when Shadow is select for the Border Style in the General tab.
- **Graph Foreground** includes all the text other than the title and subtitle, and the border around the 3D graph.
- **Graph Background** includes the area within the border and behind the 3D graph.
- **X and Z Axis Plane** includes the floor of the 3D graph.
- **Y Axis Plane** includes the walls of the 3D graph.

Quick Styles group lets you select from pre-defined styles for the 3D graph:

- Select the **Bitmap/Gradient Styles** check box to add texture to the 3D graph.
- Click the **Inset**, **Shadow**, **Line**, and **No Border** options in the **Light**, **Medium**, and **Dark** columns to view what effect the selected styles have on the 3D graph.

Style Customization Options for a 3D Graph

Click the **Style** tab to customize colors used in the 3D graph.

Changes in the **Style** tab are automatically applied to the 3D graph as they are selected.

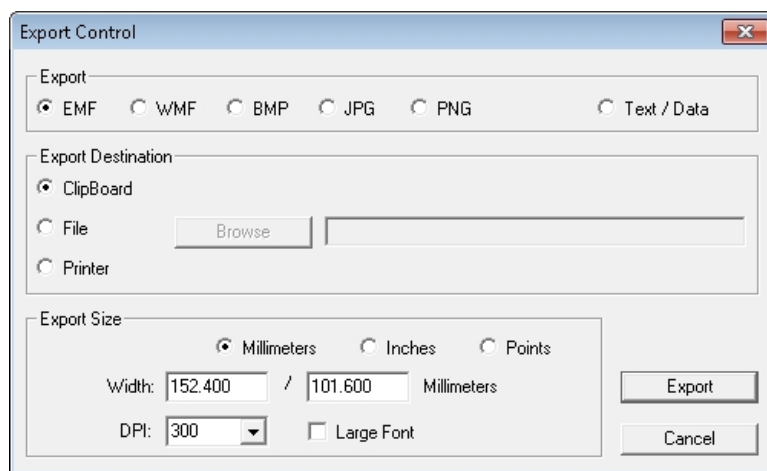
The customizable items in the list on the left are dependent on the some of the selections in the other tabs, and on the type of data.

Click an item in the list, and then click a color to apply to it.

Exporting a Three-Dimensional Graph

Before exporting an image of a 3D graph, make sure that you have rotated the 3D graph to the view that you want and that you have set your customization options. See [Customizing a Three-Dimensional Graph on page 383](#).

For export options, right-click on the 3D graph and then click **Export Dialog** to open the **Export Control** dialog.



Click the graphic format from the **Export** area. If you select **Text/Data**, only the data is exported. For more information about exporting the data, see [Exporting Data from a Three-Dimensional Graph on page 387](#).

In the **Export Destination** area, select how you want to export the image or data:

- Click **Clipboard** to export the image or data to the Windows clipboard so that you can paste it into a different program like a word processor or a spreadsheet.
- Click **File** to save the image or data in a file on your computer or network. Click **Browse** to choose the destination and give the file a name.
- Click **Printer** to export the image or data directly to a printer. After you click **Print**, you can select the printer and printer options.

The options in the **Export Size** area are dependent on the selected **Export** format and the **Export Destination**:

- **Full Page** is available for exporting to a Printer.
- **No Specific Size** is available for the WMF format exported to the clipboard or a file. Click this option to let the export operation select the size for the image.
- **Pixels** is available for BMP, JPG, and PNG formats exported to the clipboard or a file.
- **Millimeters, Inches, and Points** are available for EMF and WMF formats exported to the clipboard or a file, and for all graphic formats exported to a printer.
- If you have selected measurement units, type the width and height for the exported image.
- For all graphic formats exported to the clipboard or a file, select the **DPI** (dots per inch) for the exported image.
- For all graphic formats exported to the clipboard or a file, You can select the **Large Font** check box to increase the size of the text in the exported image.

When you have finished selecting your export options, click **Export** or **Print**.

If you are exporting the data as text, then the Export dialog is displayed with more options for formatting the exported data. See [Exporting Data from a Three-Dimensional Graph on page 387](#).

Exporting Data from a Three-Dimensional Graph

To export just the data from a 3D graph:

1. Right-click on the 3D graph and then click **Export Dialog**.
2. In the **Export Control** dialog, click **Text/Data**.
3. In the **Export Destination** area, select how you want to export the data:
 - Click **Clipboard** to export the data to the Windows clipboard so that you can paste it into a different program like a word processor or a spreadsheet.
 - Click **File** to save the data in a file on your computer or network. Click **Browse** to choose the destination and give the file a name.
4. Click **Export**.
5. In the **Export** dialog, in the **Select Subsets and Points** area, choose to export **All Data** or **Selected Data**.

If you choose **Selected Data**, you can export columns of data by clicking the numbers that correspond to the column numbers on the microplate, or you can export rows of data by clicking the letters that correspond to the row letters on the microplate. If you want to export a single well or a group of wells, click the column numbers and row letters that correspond to the well or group of wells on the microplate. To select more than one column or row in each list, hold down the **Shift** or **Ctrl** key as you click.


6. In the **Export What** area choose to export just the **Data** or the **Data and Labels**.
7. If you have multiple values available in your data, choose an option from the **Data to Export** area.

8. In the **Export Style** area, click **List** or **Table**.
 - When you choose to export a **List**, define the delimiter for the data in each line by clicking **Tab** or **Comma**. The type of delimiter you choose must match the requirements of the program where you want to use the exported data.
 - When you choose to export a **Table**, you can click **Subsets/Points** to place the data from the microplate column numbers into the rows of the table and the data from the microplate row letter into the columns of the table, or click **Point/Subsets** to place the data from the microplate row letters into the rows of the table and the data from the microplate column numbers into the columns of the table.
9. In the **Numeric Precision** area, click **Current Precision** to export the data using the rounding defined in the 3D graph, or click **Maximum Precision** to export the rounding available in the data file.
10. Click **Export** to export the data to the format defined in Step 3.



Note: If you exported the data to the Windows clipboard, you need to immediately open the program where you want to use the data and paste the data into that program.

Graphing Data

Click **New Graph**  in **Sections** on the **Home** tab in the ribbon to open the **Plot Editor** dialog where you can create a graph from the collected data.

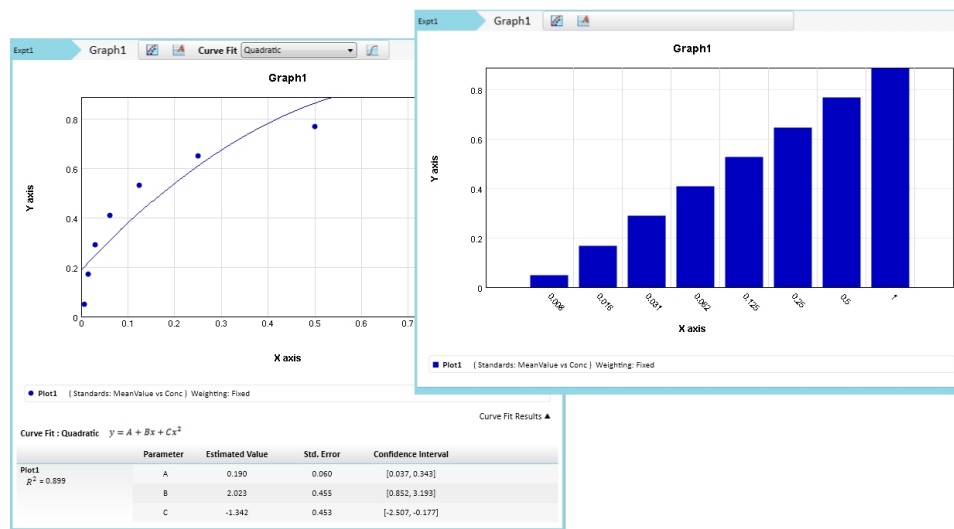
After a graph has been created, new plots can be added and deleted, the axes can be customized, and the size and type of graph can be changed. The grid lines for the graph can be enabled or disabled. The default setting has grid lines enabled.

Other methods of visualizing data include viewing a zoomed well plot of the data in a well in a **Plate** section or a cuvette in a **Cuvette Set** section, and viewing a three-dimensional graphical display of the data. See [Zooming the Display of a Well or Cuvette on page 363](#) and [Viewing Data in a Three-Dimensional Graph on page 382](#).

Working with Graphs

Graph sections are used to plot information from groups as scatter plots or bar graphs.

You can create more than one **Graph** section within a data file, and plots in the **Graph** section can be created from any Experiment in the file.



Graph sections are divided into the following areas:

- The body of the **Graph** section.
- The Legend. See [Graph Legend on page 389](#).

To change the name of the **Graph** section, right-click the **Graph** section in the **Navigation Tree** and then click **Rename**. See [Renaming an Experiment or a Section on page 30](#).

For more information about graphs, see the following topics:

- [Creating a New Graph on page 392](#)
- [Editing an Existing Graph on page 394](#)
- [Selecting Curve Fit Settings on page 394](#)
- [Changing the Name of the Graph Section on page 439](#)
- [Changing the Appearance of a Graph on page 440](#)
- [Zooming the Graph Display on page 442](#)
- [Exporting an Image of a Graph Section on page 442](#)

Graph Legend

The graph legend for a scatter plot contains information about the contents of the graph. To view or hide the graph legend, click **Curve Fit Results** on the right below the graph. A bar graph does not have a legend.

Independent Fits

For each curve fit function:


- The formulas for the selected curve fits
- For each plot:
 - R^2 value
 - EC_{50} value (where applicable)
 - For each parameter:
 - Estimated Value
 - Standard Error (Std. Error) of the estimate
 - Confidence Interval of the estimate: The confidence interval for a given confidence level is a range such that the true value lies within the range with the desired probability. The confidence level is usually specified as a percentage. The greater the confidence level, the wider the resulting confidence interval. Calculation of the confidence interval is based on sampling statistics. For example, suppose that many data sets are obtained, and the confidence interval is calculated for each data set based on a chosen statistic. The percentage of those confidence intervals containing the true value is the specified confidence level. Select the Confidence Interval Method in the Statistics tab of the Curve Fit Settings dialog. See [Curve Fit Statistics Tab on page 402](#).
 - Independence: Parameter *Independence* is one way to examine the suitability of a given curve fit for the data set. It is a measure of the extent to which the best value of one parameter depends on the best values of the other parameters, and is a number between 0 and 1, with 1 being the ideal. In the graph fit legend, parameter independence has been translated into bars, where 10 bars indicate a high degree of independence. Because only very small values indicate a problem, a nonlinear transformation is used for this translation. If one or more parameters have few bars or no bars, the curve fit might not be a good fit for the data set.

For example, if the data set is sigmoidal with clear lower and upper asymptotes, 4-parameter fits should be applicable with many bars for all parameters. However, if one or both of the asymptotes is missing, the A or the D parameter will have few bars, indicating that reliable values cannot be deduced from the data set.

Global Fits

- The formula for the selected curve fit
- For each plot:
 - Estimated Relative Potency (Estimated Rel. Pot.)
 - Standard Error (Std. Error) of the estimate
 - Confidence Interval of the estimate (see explanation under [Independent Fits on page 390](#))
 - Independence (see explanation under [Independent Fits on page 390](#))
 - EC₅₀ value (where applicable)
- The list of weighting formulas
- R² value
- For each parameter:
 - Estimated Value
 - Standard Error (Std. Error) of the estimate
 - Confidence Interval of the estimate
 - Independence

Creating a New Graph

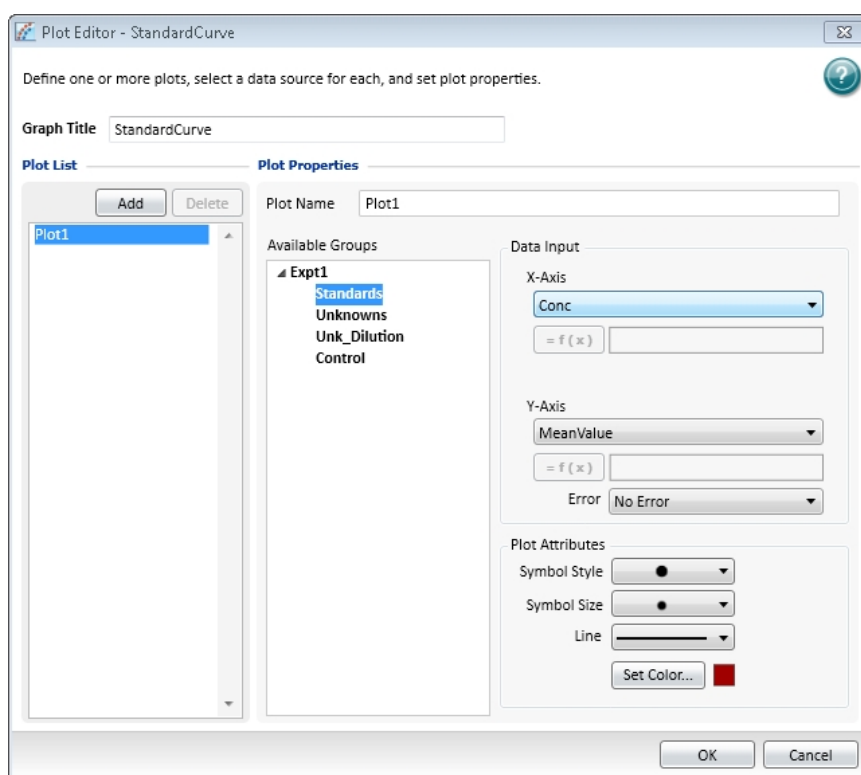
Click **New Graph**  in **Sections** on the **Home** tab in the ribbon to open the **Plot Editor** dialog where you can create a graph from the collected data. Graphing is enabled both during data collection and after data has been acquired for a Kinetic, Spectrum, and Well Scan read.

In the **Plot Editor** dialog, you can name the graph, assign specific information to be plotted on the X and Y axes, and choose which icon and color to use.

All groups that have been created or assigned within the file are shown in the **Available Groups** list.

To create a new graph:

1. Click **New Graph** on the **Plate** section **Home** tab to open the **Plot Editor** dialog.



2. In the **Graph Title** field, type a name for the graph.
3. Select a plot.

The **Plot List** shows the existing plots. One plot is shown by default.

- To add a new plot to the graph, click **Add**.
- To remove a plot from the list, select a plot and then click **Delete**.

When you select a plot from the list, the parameters for the selected plot are displayed in the **Plot Properties** area of the dialog.

4. Optionally, type a name for the plot in the **Plot Name** field. The plot name changes in the plots list.

5. Select a group from the **Available Groups** list. Data from the selected group is plotted in the graph.



Note: Groups are defined using the template editor. If no groups are displayed in the list, you must go to the **Template Editor** dialog and define one or more groups. See [Defining a Group on page 303](#).

6. In the **Data Input** area, select column types from those listed to assign to the plot in the X-Axis and Y-Axis. The list contains only the group column names available for the group that is selected in **Available Groups**. When you select the **Custom** type, the Formula Editor opens for you to define the custom formula.
7. Select a column or **No Error** in the **Error** field to define the display of error bars.



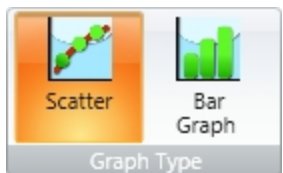
Note: When data is displayed as a scatter plot, you can choose to display error bars for the plot of the data for the X-axis and Y-axis. Error bars are lines that extend outside of a plotted value in either or both directions and graphically represent some error in plotted data.

8. Use the **Plot Attributes** area to change the appearance of the graph:
 - Select the **Symbol Style** to define the symbol to be used to mark each data point in a scatter plot.
 - Select the **Symbol Size** to define the size of the selected symbol in a scatter plot.
 - Select the **Line Style** to define the line to be used between data points in a scatter plot.
 - Click **Set Color** and select the color from the color picker to define the color of the symbol and line in a scatter plot or the color of the bar in a bar graph.
9. Click **OK** to apply the settings and close the **New Graph** dialog.


A new **Graph** section is added to the experiment with the resulting data plots displayed as specified.

Editing an Existing Graph

You can change a graph by changing the type of graph, by editing the appearance of the graph, or by using the **Plot Editor** dialog to change the plots and the data or plot attributes. You can display the data in a scatter plot or a bar graph. To change the graph type, click **Scatter** or **Bar Graph** in the **Graph Type** section on the **Home** tab in the ribbon.



To edit the appearance of the graph, see [Changing the Appearance of a Graph on page 440](#). To use the **Plot Editor** dialog to change the plots and the data or plot attributes:

1. With a **Graph** section active in the workspace, click **Plot Editor**  in the **Graph Tools** section on the **Home** tab in the ribbon or in the toolbar at the top of the **Graph** section.
2. Make the required changes to the graph definitions. See [Creating a New Graph on page 392](#).
3. Click **OK** to apply the settings and close the **Plot Editor** dialog.



Note: You can add as many plots as you need during one editing session. To add more plots click **Add**. To delete a plot from the graph select the plot and click **Delete**.

Selecting Curve Fit Settings



Note: Curve fits are used only in scatter plots.

When you first create a graph of the data, it does not have a fit related to it. You can fit a plot to one of the curve fit selections. These selections are shown in the **Fit** list in the toolbar at the top of the **Graph** section. You can filter the list of curve fits by selecting a category from the **Category** list. All plots on a graph must have the same type of fit.

Generally, a standard curve refers to the curve fitted to the plot of concentration compared to the mean value for the Standard group.

After you have selected a fit type, SoftMax Pro Software determines the parameter values that best fit the data. The function with these parameters is drawn on the graph.



Note: Ideally, the type of fit used is determined by the underlying chemistry of the assay and can be set before data is read.


When a fit is done, the parameter values are tabulated in the legend at the bottom of the graph. The parameter table also contains information regarding the uncertainty of the parameters, specifically standard errors and (optionally) confidence intervals.

A good discussion of curve fitting appears in “Data Analysis and Quality Control of Assays: A Practical Primer” by R. P. Channing Rogers in *Practical Immuno Assay*, edited by Wilfrid R. Butt (published by Marcel Dekker, Inc., New York, 1984).

Judging a Good Curve Fit

Visual inspection is always useful for evaluating a curve fit. The legend at the bottom of the graph contains information summarizing the numerical output of the fit. This includes the coefficient of determination R^2 , a traditional measure of goodness of fit. R^2 is the fraction of the variance of the y-values explained by the fit, and is 1 for a perfect fit. However, this should not be used to determine the statistical significance of the fit, or to compare the suitability of different curve fit functions. For such purposes, statistics such as chi-squared or Fisher-F can be used. These statistics can be obtained from the formula system.

Even for a good fit, as judged by eye or R^2 , some parameters might have high uncertainty.

To define a curve fit for the plots in a graph, click **Curve Fit Settings**  in the **Graph Tools** section on the **Home** tab in the ribbon or in the toolbar at the top of the **Graph** section.

The **Curve Fit Settings** dialog has three tabs available for defining the curve fit:

- **Curve Fit**, see [Curve Fit Tab on page 396](#).
- **Weighting**, see [Curve Fit Weighting Tab on page 401](#).
- **Statistics**, see [Curve Fit Statistics Tab on page 402](#).

After you finish defining the curve fit, click **OK**.

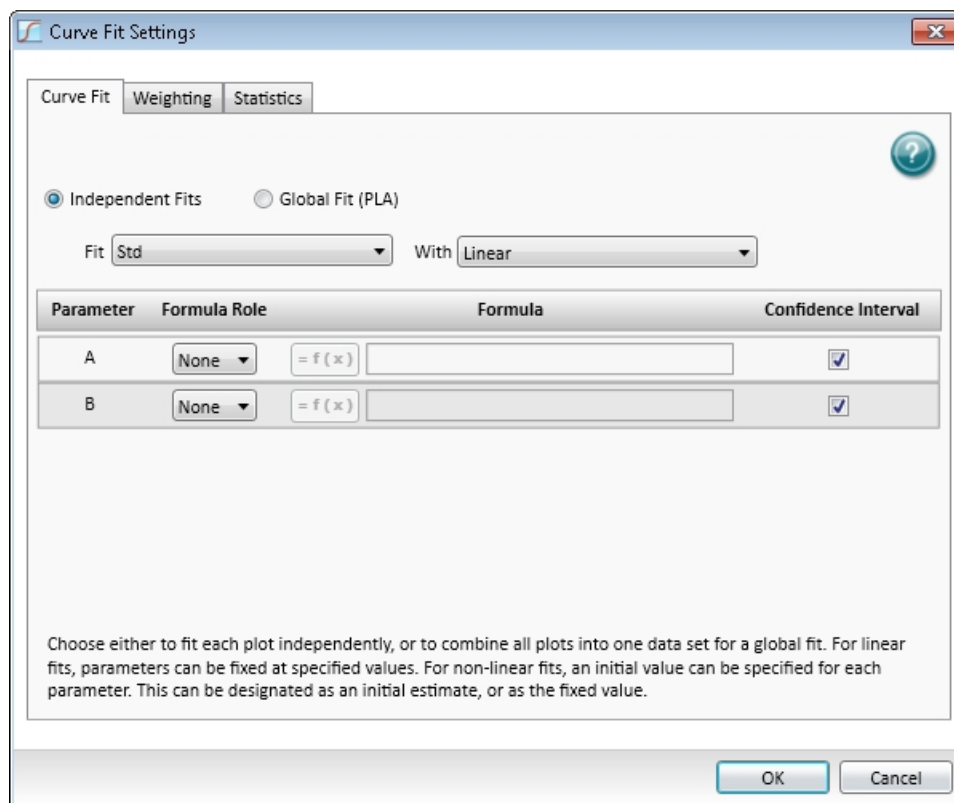
Curve Fit Tab

When you first create a graph of the data, it does not have a fit related to it. You can fit a plot to one of the predefined curve-fit functions.


These selections are shown in the **Fit** list in the **Graph** section toolbar. You can filter the list of curve fits by selecting a category from the **Category** list.

For information about the available curve fit functions, see [Curve Fit Functions on page 404](#).

You can also select a plot from the graph and a curve fit to apply to that plot from the list on the **Curve Fit** tab in the **Curve Fit Settings** dialog.



All plots on a graph can have the same type of fit or each plot can have a different fit applied individually. The **Curve Fit** tab of the **Curve Fit Settings** dialog provides the means to set a different fit to individual plots.

To define a curve fit for the plots in a graph, click **Curve Fit**  in the **Graph Tools** section on the **Home** tab in the ribbon or in the toolbar at the top of the **Graph** section. You can choose to fit each plot independently or to combine all plots into one data set for a global fit.

- To fit each plot independently, see [Independent Fits on page 398](#).
- To combine all plots into one data set, see [Global Fit \(PLA\) on page 399](#).

Generally, a standard curve refers to the curve fitted to the plot of concentration versus mean value for the Standard group.

After you have selected a fit type, SoftMax Pro Software determines the parameter values that best fit the data. The function with these parameters is drawn on the graph.



Note: Ideally, the type of fit used is determined by the underlying chemistry of the assay and can be set before data is read.



Note: A good discussion of curve fitting appears in “Data Analysis and Quality Control of Assays: A Practical Primer” by R. P. Channing Rogers in *Practical Immuno Assay*, edited by Wilfrid R. Butt (published by Marcel Dekker, Inc., New York, 1984).


- For linear fits, parameters can be fixed at specified values.
- For nonlinear fits, an initial value can be specified for each parameter. This can be designated as an initial estimate (the seed value), or as the fixed value.

You can specify whether a Confidence Interval should be calculated for each parameter.

The confidence interval for a given confidence level is a range such that the true value lies within the range with the desired probability. The confidence level is usually specified as a percentage. The greater the confidence level, the wider the resulting confidence interval. Calculation of the confidence interval is based on sampling statistics. For example, suppose that many data sets are obtained, and the confidence interval is calculated for each data set based on a chosen statistic. The percentage of those confidence intervals containing the true value is the specified confidence level.

Independent Fits

When plots in a graph are to be fit with curve fit functions independently:


1. Open a **Graph** section with multiple plots in the workspace.
2. Click **Curve Fit Settings**  in the **Graph Tools** section on the **Home** tab in the ribbon or in the toolbar at the top of the **Graph** section.
3. In the **Curve Fit Settings** dialog, in the **Curve Fit** tab, select **Independent Fits**.
4. Select a plot from the **Fit** list.
You can filter the list of curve fits by selecting a category from the **Category** list.
5. Select which curve fit function to apply to the plot from the **With** list.
6. Continue selecting plots and applying curve fit functions as needed.
7. If applicable, click the **Weighting** tab. See [Curve Fit Weighting Tab on page 401](#).
8. If applicable, click the **Statistics** tab. See [Curve Fit Statistics Tab on page 402](#).
9. When all curve fit options have been set, click **OK**.

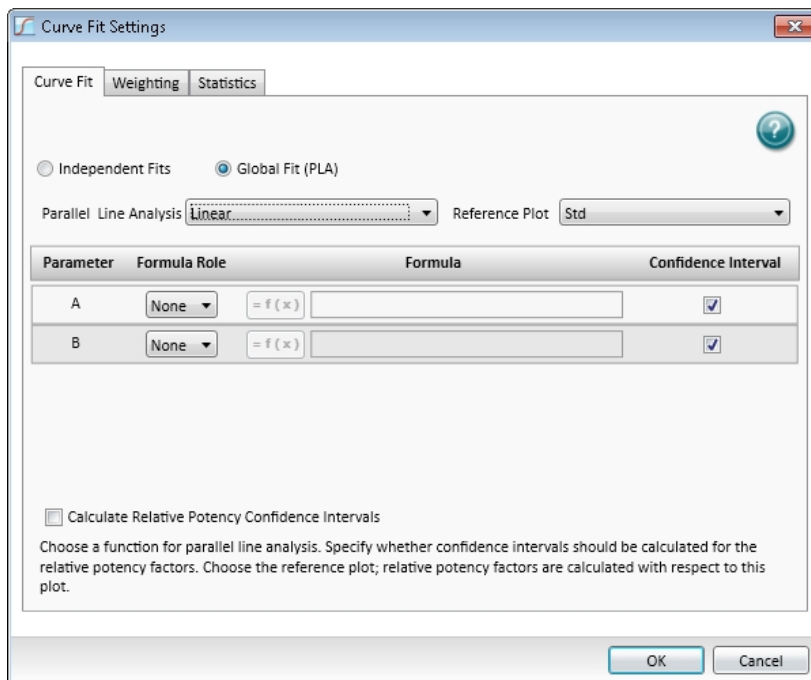


Note: For independent fits (and global to a limited extent), you can fix values. Curve fit parameter values can either be fixed, or "manually seeded" to start the curve fit algorithm search.

Global Fit (PLA)

When all the plots in a graph are to have the same curve fit functions applied:

1. Open a **Graph** section with multiple plots in the workspace.
2. Click **Curve Fit Settings**  in the **Graph Tools** section on the **Home** tab in the ribbon or in the toolbar at the top of the **Graph** section.
3. In the **Curve Fit Settings** dialog, select **Global Fit (PLA)**.



The available global fit is parallel line analysis. See [Parallel Line Analysis on page 400](#).

4. Select the plot from the **Fit** list.
You can filter the list of curve fits by selecting a category from the **Category** list.
5. Select an option, except point-to-point or cubic spline, from the **With** list.
6. If applicable, select **Relative Potency Confidence Interval**.
7. Select a plot for the **Reference Plot** list.
8. If applicable, click the **Weighting** tab. See [Curve Fit Weighting Tab on page 401](#).
9. If applicable, click the **Statistics** tab. See [Curve Fit Statistics Tab on page 402](#).
10. When all curve fit options have been set, click **OK**.

Parallel Line Analysis

Parallel line analysis (PLA) is available for all Global fits except point-to-point and cubic spline fits.

Determining parallelism between a standard and test compound, and subsequent estimation of relative potency, are fundamentals of bioassay use in biopharmaceutical development and testing. For linear data, parallelism can be evaluated by examining the similarity between the slopes of straight lines.

Bioassay data and immunoassays in particular, have been demonstrated to fit well with a sigmoidal shape defined by a 4-parameter or 5-parameter curve fit. The basic question of whether a curve with a specified shape can fit both standard and test data sets when shifted along the X-axis can be addressed following a method detailed by Gottschalk and Dunn (Journal of Biopharmaceutical Statistics, 15:437- 463, 2005).

The parameters are those for the fit function, plus a relative potency factor for each data set relative to one designated as a reference. Below the graph are displayed their values, standard errors, and (optionally) confidence intervals.

Function operators are included with SoftMax Pro Software that can be used to summarize this information in a Notes section. For more details, see the *SoftMax Pro Formula Reference Guide*.

Curve Fit Weighting Tab

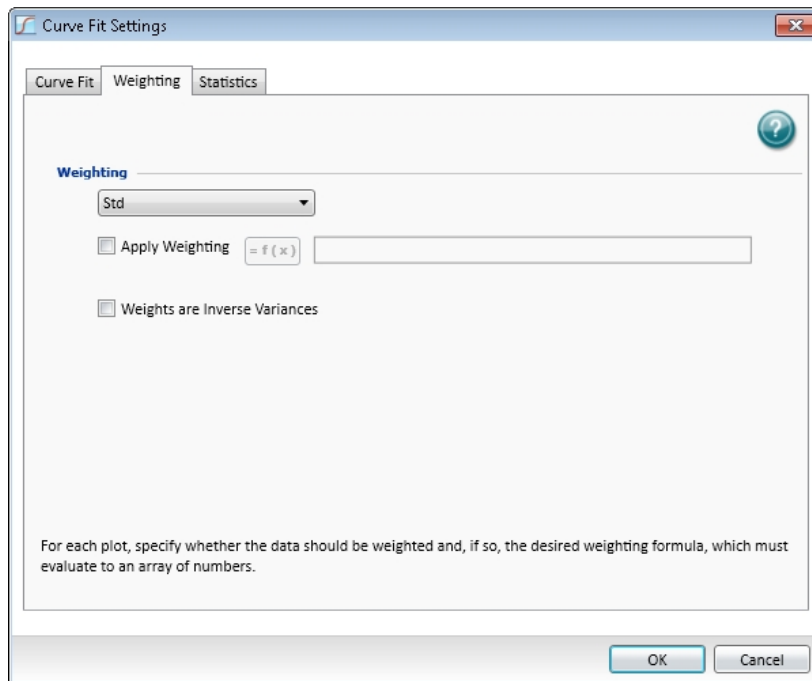
For each plot, specify whether the data should be weighted and, if so, the desired weighting formula, which must evaluate to an array of numbers.

Least-squares fitting is based on the assumption that errors are normally distributed. If the variance of each point in the fit is known, or can be estimated by some means, its inverse should be specified as the weight for the point. If the variances are not known, but are believed to be non-uniform across the data, that is, a known function of y , then a weighting function should be used to reflect this information. If a formula for the weighting is not provided, then all points have equal weight.

The weighting feature permits independent weighting of individual plots within a **Graph** section.

To apply weighting to a plot:

1. On the graph, select **Curve Fit Settings**.
2. In the **Curve Fit Settings** dialog, click the **Weighting** tab.



3. Select a plot from the **Weighting** list.
4. Select **Apply Weighting**.
5. Click the **Formula** button.
6. In the **Formula** field, type the formula to be applied as the weighting.
If a formula for the weighting is not provided, then all points have equal weight.

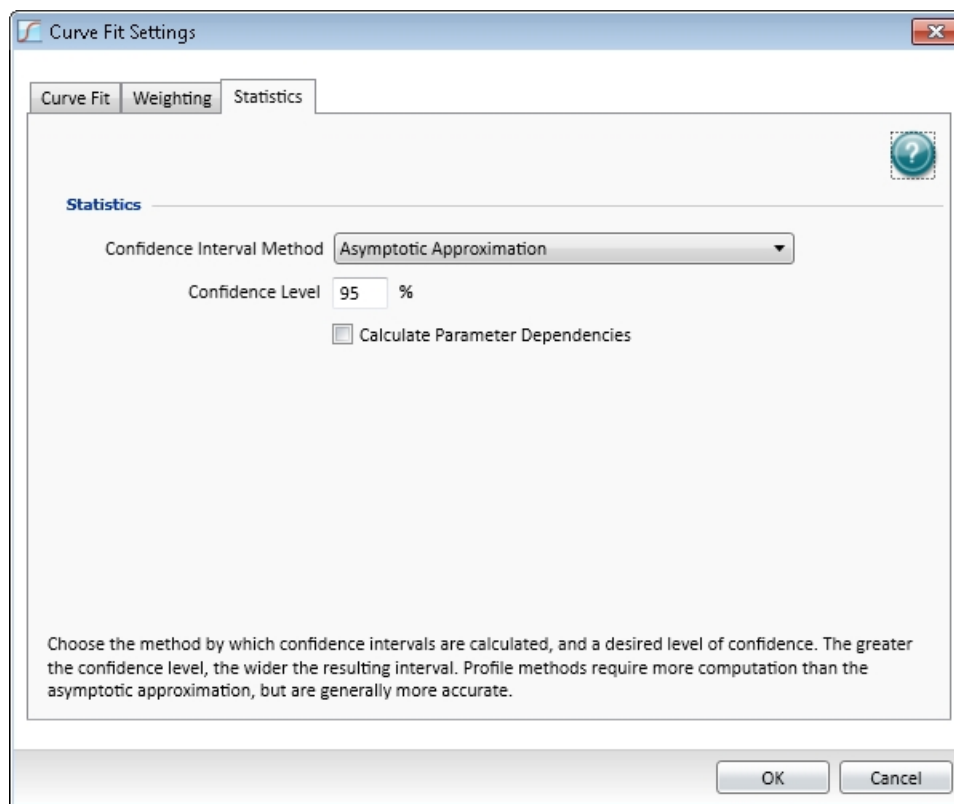
7. If the data are weighted with the inverse of their variances, then select the **Weights are Inverse Variances** check box.

If the **Apply Weighting** and the **Weights are Inverse Variances** check boxes are both selected in the **Weighting** tab for each plot, then the **Profile Method (Chi-Squared distribution)** option is available in the **Confidence Interval Method** list in the **Statistics** tab. See [Curve Fit Statistics Tab on page 402](#).

8. Click **OK**.

Curve Fit Statistics Tab

In the **Statistics** tab, you can specify the statistics display.



Choose the method by which confidence intervals are calculated, and a desired level of confidence. See [Table 8-6: Confidence Interval Method on page 403](#).

Confidence Interval Method

The confidence interval for a given confidence level is a range such that the true value lies within the range with the desired probability. The confidence level is usually specified as a percentage. The greater the confidence level, the wider the resulting confidence interval. Calculation of the confidence interval is based on sampling statistics. For example, suppose that many data sets are obtained, and the confidence interval is calculated for each data set based on a chosen statistic. The percentage of those confidence intervals containing the true value is the specified confidence level.

To specify the method used to establish the confidence interval, select a confidence interval method from the list.

Table 8-6: Confidence Interval Method

Confidence Interval Method	Description
Asymptotic Approximation	Calculates Wald confidence interval, which is simply related to the standard error.
Profile Method (F distribution)	Based on model comparison with F-statistic.
Profile Method (Chi-Squared distribution)	Based on model comparison with chi-squared-statistic. If the Apply Weighting and the Weights are Inverse Variances check boxes are both selected in the Weighting tab for each plot, then the Profile Method (Chi-Squared distribution) option is available in the Confidence Interval Method list in the Statistics tab. See Curve Fit Weighting Tab on page 401 .
Profile Method (t distribution)	Based on T-profile function.



Note: Profile methods require more computation than the asymptotic approximation, but are generally more accurate.

Confidence Level

How likely the interval is to contain the parameter is determined by the **Confidence Level**. Increasing the desired confidence level usually widens the confidence interval.

Calculate Parameter Dependencies

To calculate dependencies between parameters, select **Calculate Parameter Dependencies**. With this option selected, the graphical representation in the graph legend represents the parameter independence of the curve fit. See [Graph Legend on page 389](#).

Parameter *Independence* is one way to examine the suitability of a given curve fit for the data set. It is a measure of the extent to which the best value of one parameter depends on the best values of the other parameters, and is a number between 0 and 1, with 1 being the ideal. In the graph fit legend, parameter independence has been translated into bars, where 10 bars indicate a high degree of independence. Because only very small values indicate a problem, a nonlinear transformation is used for this translation. If one or more parameters have few bars or no bars, the curve fit might not be a good fit for the data set.

For example, if the data set is sigmoidal with clear lower and upper asymptotes, 4-parameter fits should be applicable with many bars for all parameters. However, if one or both of the asymptotes is missing, the A or the D parameter will have few bars, indicating that reliable values cannot be deduced from the data set.

Curve Fit Functions

Generally, a standard curve refers to the curve fitted to the plot of concentration versus mean value for the Standard group.

After you have selected a fit type, SoftMax Pro Software determines the parameter values that best fit the data. The function with these parameters is drawn on the graph. Ideally, the type of fit used is determined by the underlying chemistry of the assay and can be set before data is read.

When a fit is done, the parameter values are displayed in the legend at the bottom of the graph. The correlation coefficient describes how well a change in x values correlates with a change in the y values. The R^2 value should be used only for linear curve fits.

A good discussion of curve fitting appears in "Data Analysis and Quality Control of Assays: A Practical Primer" by R. P. Channing Rogers in *Practical Immuno Assay*, edited by Wilfrid R. Butt (published by Marcel Dekker, Inc., New York, 1984).

When you first create a graph of the data, it does not have a fit related to it. You can fit a plot to one of the following curve-fit functions.

These selections are shown in the **Fit** list in the toolbar at the top of the **Graph** section. You can filter the list of curve fits by selecting a category from the **Category** list.

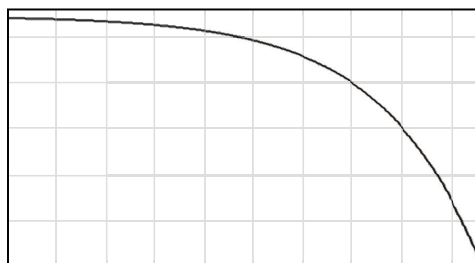
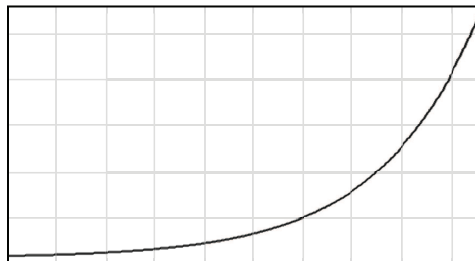
No Fit

Select **No Fit** to apply no curve fit, and to plot the scatter of the data points.

2-Parameter Exponential

The **2-Parameter Exponential** curve fit is also known as:

- 2P Exponential
- [Exponential Growth on page 406](#)
- [Exponential Decay on page 407](#)



$$y = A \times e^{Bx}$$

y = Concentration

x = Time

A = Y_0

B = k

For exponential growth, $B > 0$

For exponential decay, $B < 0$

A 2-parameter exponential curve fit is commonly used for radioactive decay, first order kinetics, and unimolecular decay. It is also used for exponential growth:

$$\text{Doubling time} = B \times \ln(2) = B \times 0.693$$

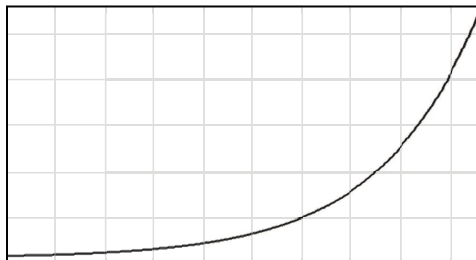
Mathematically, a 2-parameter exponential curve fit is a special case of a 3-parameter exponential curve fit. See [3-Parameter Exponential on page 408](#).

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a 2-parameter exponential curve fit algorithm is 2.

Exponential Growth

The **Exponential Growth** curve fit is also known as:

- [2-Parameter Exponential on page 405](#)



$$y = A \times e^{Bx}$$

y = Concentration

x = Time

A = Y_0

B = k

For exponential growth, $B > 0$

An exponential growth curve fit is commonly used for radioactive decay, first order kinetics, and unimolecular decay.

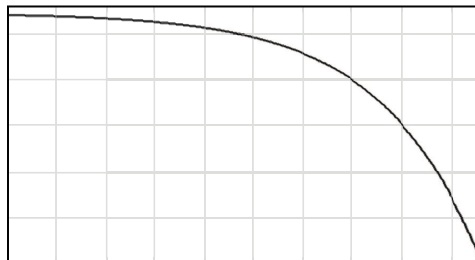
Mathematically, this is a special case of a 3-parameter exponential curve fit. See [3-Parameter Exponential on page 408](#).

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for an exponential growth curve fit algorithm is 2.

Exponential Decay

The **Exponential Decay** curve fit is also known as:

- [2-Parameter Exponential on page 405](#)



$$y = A \times e^{Bx}$$

y = Concentration

x = Time

A = Y_0

B = k

For exponential growth, $B > 0$

For exponential decay, $B < 0$

A 2-parameter exponential curve fit is commonly used for exponential growth:

$$\text{Doubling time} = B \times \ln(2) = B \times 0.693$$

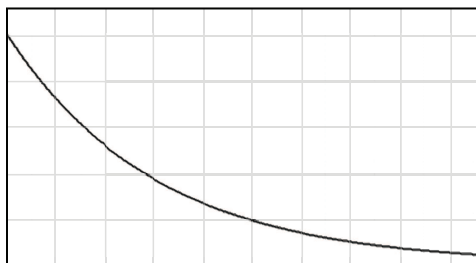
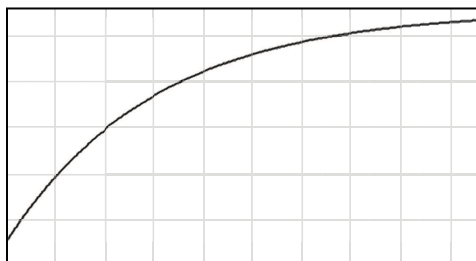
Mathematically, this is a special case of a 3-parameter exponential curve fit. See [3-Parameter Exponential on page 408](#).

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a 2-parameter exponential curve fit algorithm is 2.

3-Parameter Exponential

The **3-Parameter Exponential** curve fit is also known as:

- Exponential (in previous versions of the SoftMax Pro Software)
- 3P Exponential
- [One-Phase Exponential Decay, see page 409](#)
- [One-Phase Exponential Association, see page 410](#)



$$y = A + B \times (1 - e^{-x/C})$$

x = Time (usually)

y = Specific + Nonspecific Binding or Response

One-Phase Exponential Decay (B negative)

$$A = Y_0 = Y_{\max} = \text{Plateau} + \text{Span}$$

$$B = -\text{Span}$$

$$C = 1/k = 1/\text{decay constant}$$

One-Phase Exponential Association (B positive)

$$A = Y_0 = Y_{\min}$$

$$B = \text{Span} = Y_{\max} - Y_0$$

$$C = 1/k = 1/\text{association constant}$$

An exponential curve fit is commonly used for drug elimination, dissociation of ligand from a receptor, and radioisotope decay. It is also used for pseudo-first order kinetics of ligand/receptor interaction or substrate/enzyme interaction.

The SoftMax Pro Software expresses C as the reciprocal of k, so it has same units as X.

$$t_{1/2} = C \times \ln 2 = C \times 0.693$$

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for an exponential curve fit algorithm is 3.

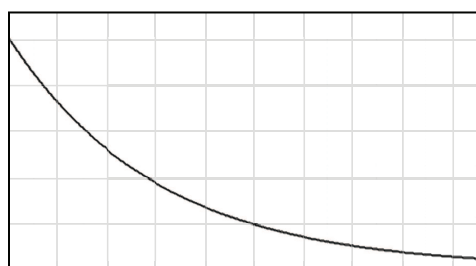


Note: In previous versions of SoftMax Pro Software, it was possible to select a linearized version of this fit. This option is not available in SoftMax Pro Software 6.

One-Phase Exponential Decay

The **One-Phase Exponential Decay** curve fit is also known as:

- [3-Parameter Exponential](#), see page 408
- 3P Exponential



$$y = A + B \times (1 - e^{-x/C})$$

x = Time (usually)

y = Specific + Nonspecific Binding or Response

A = $Y_0 = Y_{\max}$ = Plateau + Span

B = -Span

C = $1/k = 1/\text{decay constant}$

The SoftMax Pro Software expresses C as the reciprocal of k, so it has same units as X.

$$t_{1/2} = C \times \ln 2 = C \times 0.693$$

A one-phase exponential decay curve fit is commonly used for drug elimination, dissociation of ligand from a receptor, and radioisotope decay.

The curve is the same as one-phase exponential association, except B is negative instead of positive. See [One-Phase Exponential Association on page 410](#).

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a one-phase exponential decay curve fit algorithm is 3.

One-Phase Exponential Association

The **One-Phase Exponential Association** curve fit is also known as:

- [3-Parameter Exponential](#), see page 408
- 3P Exponential



$$y = A + B \times (1 - e^{-x/C})$$

x = Time (usually)

y = Specific + Nonspecific Binding or Response

$A = Y_0 = Y_{\min}$

$B = \text{Span} = Y_{\max} - Y_0$

$C = 1/k = 1/\text{association constant}$

A one-phase exponential association curve fit is commonly used for pseudo-first order kinetics of ligand/receptor interaction or substrate/enzyme interaction.

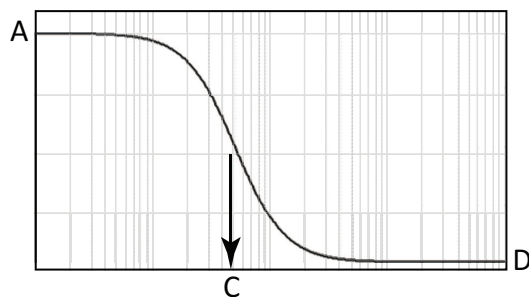
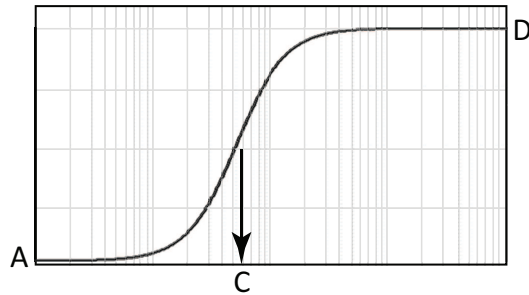
The curve is the same as one-phase exponential decay, except B is positive instead of negative. See [One-Phase Exponential Decay](#) on page 409.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a one-phase exponential association curve fit algorithm is 3.

4-Parameter Logistic

A **4-Parameter Logistic** equation is also known as:

- Sigmoidal Dose-Response (variable slope)
- Four-Parameter Logistic Equation
- Four-Parameter Dose-Response Curve
- Hill Equation



$$y = D + \frac{A - D}{1 + \left(\frac{X}{C}\right)^B}$$

A = First Asymptote

B = Slope Factor/Hill Coefficient

C = EC₅₀/IC₅₀

D = Second Asymptote



Note: In the SoftMax Pro Software, B is always positive, assuming neither A nor D is fixed. A is always the first asymptote, and D is always the last asymptote. So A and D can swap between top and bottom according to the shape of the curve, whether rising or falling with increasing concentration. However, if either A or D has been fixed in the software, the B parameter is no longer required to be positive. In such cases, A and D might or might not be the first and last asymptotes respectively.

A 4-parameter curve fit is commonly used in dose-response studies and estimation of EC₅₀/IC₅₀ values. It can also be used as standard curves.

A 4-parameter curve fit assumes a sigmoidal data set with clear lower and upper asymptotes. If either asymptote is not clearly defined or is missing (as in a marginal data set), it is nearly impossible to estimate where the asymptote lies, or if exists at all. Likewise the EC_{50} cannot be estimated.

The 4-parameter curve possesses rotational symmetry about the point:

$$\{C, (A+D)/2\}$$

This point is sometimes referred to erroneously as an inflection point. In reality, for $B > 1$, the inflection point is:

$$\left\{ C \left(\frac{(B-1)}{(B+1)} \right)^{\left(\frac{1}{B} \right)}, \frac{((A+D)+(A-D)/B)}{2} \right\}$$

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a 4-parameter curve fit algorithm is 4.



Note: For 3-parameter sigmoidal dose-response curves, use the 4-parameter curve fit and fix B or one of the asymptotes to a constant. See [3-Parameter Dose-Response Curves on page 413](#).

The minimization method for the 4-parameter equation is based on the Levenberg-Marquardt Method. Discussion of these methods can be found in *The Art of Scientific Computing* by William H. Press, Brian P. Flannery, Saul A Teukolski, and William T. Vetterling, published by Cambridge University Press, New York, 1988.

3-Parameter Dose-Response Curves

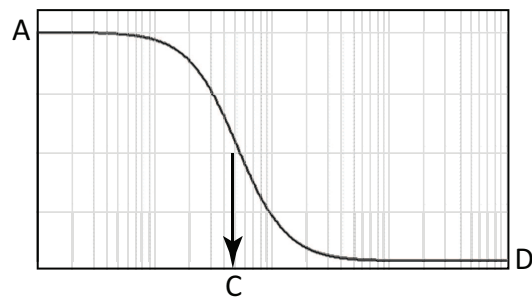
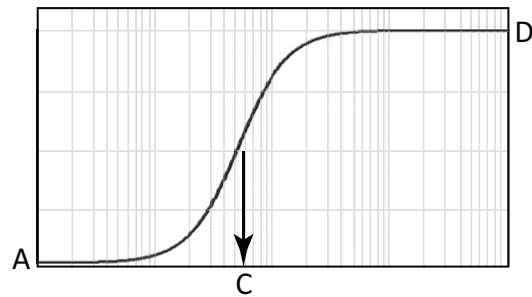
3-Parameter Dose-Response Curves are special cases of a 4-Parameter Logistic equation with one parameter fixed. See [4-Parameter Logistic](#) on page 411.

3-Parameter Dose-Response Curves with a fixed slope are also known as:

- Sigmoidal Dose-Response (Fixed Slope)
- One-Site Competition
- Three-Parameter Logistic Equation
- Hill Equation (Hill Slope = -1)

3-Parameter Dose-Response Curves with a fixed asymptote are also known as:

- Sigmoidal Dose-Response (Fixed Asymptote)
- Three-Parameter Logistic Equation
- Hill Equation (Bottom Asymptote is Fixed to 0)



$$y = D + \frac{A - D}{1 + \left(\frac{x}{C}\right)^B}$$

Fixed Slope

If B is positive:

A = First Asymptote

B = Fixed (generally to 1)

C = EC_{50}/IC_{50}

D = Second Asymptote

If B is negative:

A = Second Asymptote

B = Fixed (generally to -1)

C = EC_{50}/IC_{50}

D = First Asymptote

Fixed Asymptote

A = First Asymptote (A or D fixed)

B = Slope Factor/Hill Coefficient

C = EC_{50}/IC_{50}

D = Second Asymptote (A or D fixed)

3-parameter dose-response curves are commonly used in dose-response studies and estimation of EC_{50}/IC_{50} values. They can also be used as standard curves.

3-parameter dose-response curves assume a sigmoidal data set with clear lower and upper asymptotes. If either asymptote is not clearly defined or is missing (as in a marginal data set), it is nearly impossible to estimate where the asymptote lies, or if exists at all. Likewise the EC_{50} cannot be estimated.

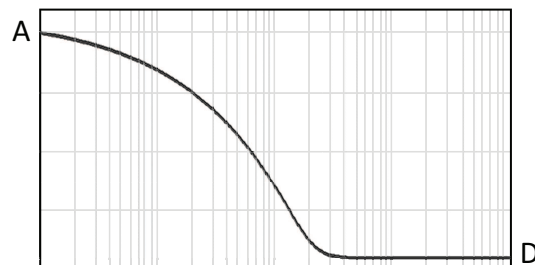
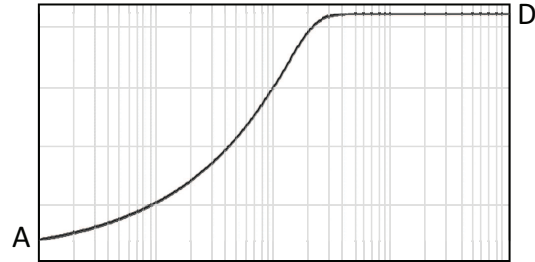
For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a 4-parameter curve fit algorithm is 4.

The minimization method for the 3-parameter dose-response curves equation is based on the Levenberg-Marquardt Method. Discussion of these methods can be found in *The Art of Scientific Computing* by William H. Press, Brian P. Flannery, Saul A Teukolski, and William T. Vetterling, published by Cambridge University Press, New York, 1988.

5-Parameter Logistic

A **5-Parameter Logistic** equation is also known as:

- Five-Parameter Logistic Equation



$$y = D + \frac{A - D}{\left\{ 1 + \left(\frac{X}{C} \right)^B \right\}^G}$$

A = First Asymptote

B = Slope Factor

C = [no physical meaning]

D = Second Asymptote

G = Asymmetry Factor



Note: In the SoftMax Pro Software, B is always positive, assuming neither A nor D is fixed. A is always the first asymptote, and D is always the last asymptote. So A and D can swap between top and bottom according to the shape of the curve, whether rising or falling with increasing concentration. However, if either A or D has been fixed in the software, the B parameter is no longer required to be positive. In such cases, A and D might or might not be the first and last asymptotes respectively.

A 5-parameter curve fit is commonly used in dose-response studies and estimation of EC_{50}/IC_{50} values. It can also be used as standard curves.

A 5-parameter curve fit assumes an asymmetric sigmoidal data set with clear lower and upper asymptotes. If either asymptote is not clearly defined or is missing (as in a marginal data set), it is nearly impossible to estimate where the asymptote lies, or if exists at all. Likewise the EC_{50} cannot be estimated.

Unlike the 4-parameter logistic equation, C is not the IC_{50} value. The IC_{50} value needs to be calculated separately. This is described in the *SoftMax Pro Software Formula Reference Guide*.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a 5-parameter curve fit algorithm is 5.

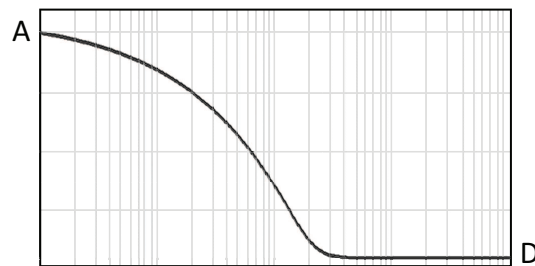
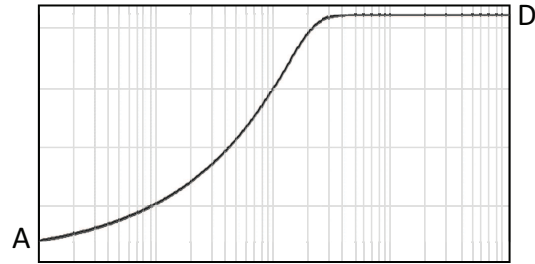
The minimization method for the 5-parameter equation is based on the Levenberg-Marquardt Method. Discussion of these methods can be found in *The Art of Scientific Computing* by William H. Press, Brian P. Flannery, Saul A Teukolski, and William T. Vetterling, published by Cambridge University Press, New York, 1988.

5-Parameter Logistic Alternate

This is a re-parameterization of the standard five-parameter logistic, such that parameters B and C have the same interpretation as in the case of the four-parameter logistic. In particular, the EC_{50} value is given by C.

A **5-Parameter Logistic Alternate** equation is also known as:

- Five-Parameter Alternate Logistic Equation
- 5P Alternate



$$y = D + (A - D) \left\{ 1 + \left(2^{\frac{1}{G}} - 1 \right) \left(\frac{X}{C} \right)^{B/2G} \left(1 - 2^{-\frac{1}{C}} \right) \right\}^{-G}$$

A = First Asymptote

B = Slope Factor

C = EC_{50}/IC_{50}

D = Second Asymptote

G = Asymmetry Factor



Note: In the SoftMax Pro Software, B is always positive, assuming neither A nor D is fixed. A is always the first asymptote, and D is always the last asymptote. So A and D can swap between top and bottom according to the shape of the curve, whether rising or falling with increasing concentration. However, if either A or D has been fixed in the software, the B parameter is no longer required to be positive. In such cases, A and D might or might not be the first and last asymptotes respectively.

A 5-parameter logistic alternate equation is commonly used in dose-response studies and estimation of EC_{50}/IC_{50} values. It can also be used as standard curves.

The 5-parameter logistic alternate equation is identical to the 5-parameter logistic equation, except that it has been re-parameterized such that the C parameter is the estimated EC_{50}/IC_{50} value.

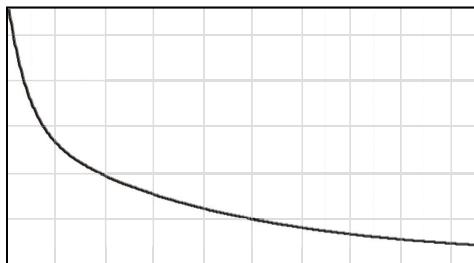
A 5-parameter logistic alternate equation assumes a asymmetric sigmoidal data set with clear lower and upper asymptotes. If either asymptote is not clearly defined or is missing (as in a marginal data set), it is nearly impossible to estimate where the asymptote lies, or if exists at all. Likewise the EC_{50} cannot be estimated.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a 5-parameter logistic alternate equation algorithm is 6.

Bi-Exponential

The **Bi-Exponential** curve fit is also known as:

- [Two-Phase Exponential Decay, see page 419](#)
- Double Exponential Decay



$$y = Ae^{Bx} + Ce^{Dx} + G$$

A = Span1

B = k1

C = Span2

D = k2

G = Plateau

When the curve is decaying, B and D are both negative.

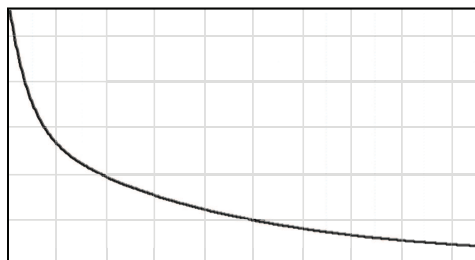
The bi-exponential curve fit is commonly used when the decay is the result is the sum of a fast and a slow exponential decay.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a bi-exponential curve fit algorithm is 5.

Two-Phase Exponential Decay

The **Two-Phase Exponential Decay** curve fit is also known as:

- [Bi-Exponential, see page 418](#)
- Double Exponential Decay



$$y = Ae^{Bx} + Ce^{Dx} + G$$

A = Span1

B = k1

C = Span2

D = k2

G = Plateau

When the curve is decaying, B and D are both negative.

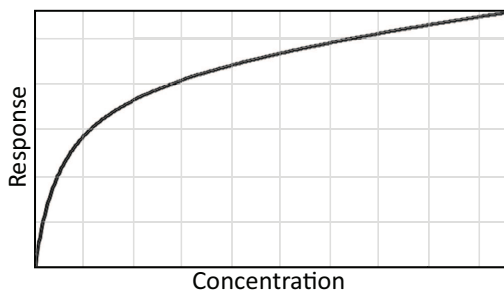
The two-phase exponential decay curve fit is commonly used when the decay is the result is the sum of a fast and a slow exponential decay.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a two-phase exponential decay curve fit algorithm is 5.

Bi-Rectangular Hyperbola

The **Bi-Rectangular Hyperbola** curve fit is also known as:

- [Two-Site Equilibrium Binding \(specific binding\)](#), see page 421
- [Michaelis-Menten with Two Isozymes](#), see page 422



$$Y = \frac{Ax}{x + B} + \frac{Cx}{x + D}$$

Two-Site Equilibrium Binding (specific binding)

y = Specific binding

A = Maximum binding (high affinity)

B = Kd(high)

C = Maximum binding (low affinity)

B = Kd(low)

Michaelis-Menten with Two Isozymes

Y = V_i

A = V_imax (1)

B = Km (1)

C = V_imax (2)

B = Km (2)

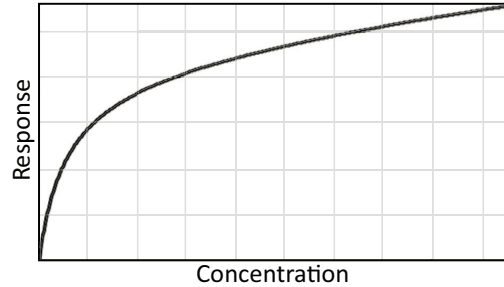
A bi-rectangular curve fit is commonly used for estimation of maximum (specific) binding and Kd values in the presence of two binding sites: high-affinity and low-affinity. It is also used for evaluation of enzyme activity, as function of [S] when two isozymes are present.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a bi-rectangular hyperbola curve fit algorithm is 4.

Two-Site Equilibrium Binding (specific binding)

The **Two-Site Equilibrium Binding (specific binding)** curve fit is also known as:

- [Bi-Rectangular Hyperbola on page 420](#)



$$Y = \frac{Ax}{x + B} + \frac{Cx}{x + D}$$

y = Specific binding

A = Maximum binding (high affinity)

B = Kd(high)

C = Maximum binding (low affinity)

D = Kd(low)

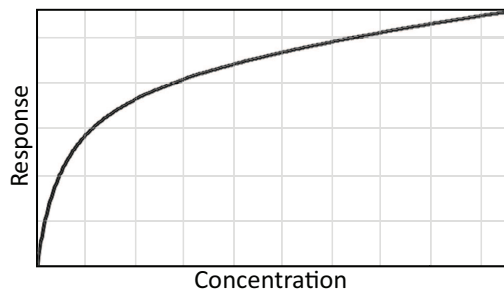
A two-site equilibrium binding (specific binding) curve fit is commonly used for estimation of maximum (specific) binding and Kd values in the presence of two binding sites: high-affinity and low-affinity.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a two-site equilibrium binding (specific binding) curve fit algorithm is 4.

Michaelis-Menten with Two Isozymes

The **Michaelis-Menten with Two Isozymes** curve fit is also known as:

- [Bi-Rectangular Hyperbola](#), see page 420



$$Y = \frac{Ax}{x + B} + \frac{Cx}{x + D}$$

$$Y = V_i$$

$$A = V_{i\max} (1)$$

$$B = K_m (1)$$

$$C = V_{i\max} (2)$$

$$D = K_m (2)$$

A Michaelis-Menten with two isozymes curve fit is commonly used for evaluation of enzyme activity, as function of [S] when two isozymes are present.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a Michaelis-Menten with two isozymes curve fit algorithm is 4.

Brain Cousens

The Brain Cousens curve fit is also known as:

- Sigmoidal Dose-Response with Hormesis



$$y = D + \frac{A - D + Gx}{1 + \left(1 + \frac{2CG}{A - D}\right) \left(\frac{x}{C}\right)^B}$$

A = First Asymptote

B = Slope Factor

C = EC_{50}/IC_{50}

D = Second Asymptote

G = Hormesis Factor

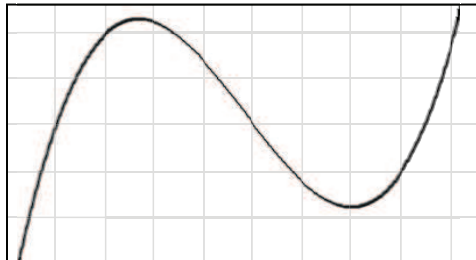
A brain cousens curve fit is commonly used for studies of test systems that show hormesis (opposite responses at low and high doses). An example is when an inhibitor shows an enhanced response at low doses and an inhibitory response at high doses.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a brain cousens curve fit algorithm is 4.

Cubic

A **Cubic** curve fit is also known as:

- Polynomial Third Order



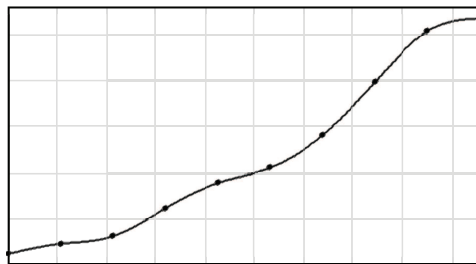
$$y = A + Bx + Cx^2 + Dx^3$$

A cubic curve fit can be used for standard curves, but there is risk of multiple inflection points, and so ambiguity in InterpX results.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a cubic curve fit algorithm is 4.

Cubic Spline

A **Cubic Spline** curve fit is a series of cubic segments joining adjacent pairs in a set of points such that the first and second derivatives match at the joints. There is no simple formula for the entire function.



A cubic spline curve fit is commonly used for cosmetic curve smoothing.

Gaussian

The **Gaussian** function consists of a single peak.



$$y = A * e^{-\left(\frac{x-B}{C}\right)^2} + D$$

A = Height – D

B = Peak Center

C is related to the peak width

D = Baseline

Peak width at half-height = $\text{ParmC}(\text{Plot@Graph}) * 2 * \text{Sqrt}(\text{Ln}(2))$

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a gaussian curve fit algorithm is 4.

Linear

A **Linear** curve fit is also known as:

- Polynomial First Order



$$y = A + Bx$$

A = Intercept

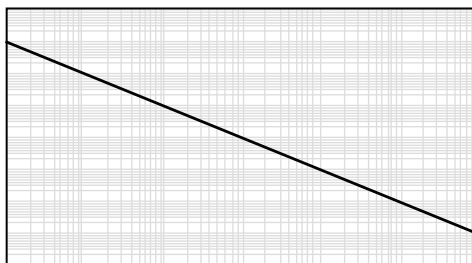
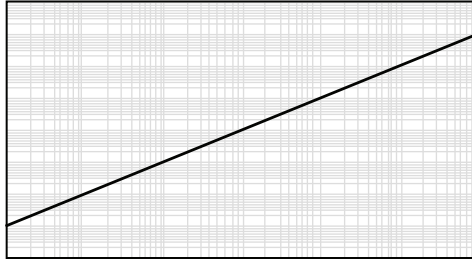
B = Slope

Use a linear fit when the values seem to lie on or are scattered around a straight line.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a linear curve fit algorithm is 2.

Log-Log

The **Log-Log** curve fit fits the best straight line to the set of data that consists of the logarithm of the readings on the Y-axis (the response) and the logarithm of the dose on the X-axis.



$$\text{Log}(y) = A + B \times \text{Log}(x)$$

A = Intercept

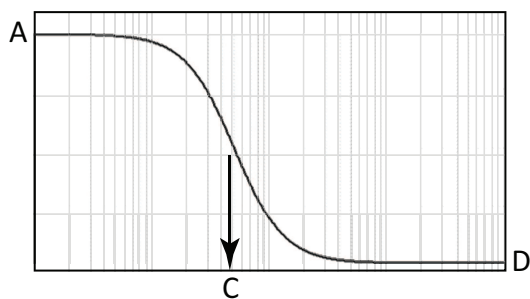
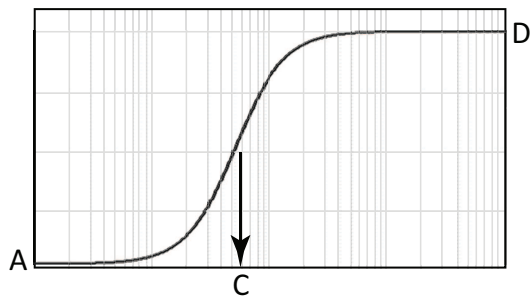
B = Slope

Log in this equation is the common or base-10 logarithm.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a log-log curve fit algorithm is 2.

Log-Logit

The **Log-Logit** curve fit routine uses the same equation as the **4-Parameter** curve fit, but uses a different curve fitting algorithm. It is an older method and might be considered outdated. See [4-Parameter Logisitic on page 411](#).



$$y = D + \frac{A - D}{1 + \left(\frac{x}{C}\right)^B}$$

A = First Asymptote

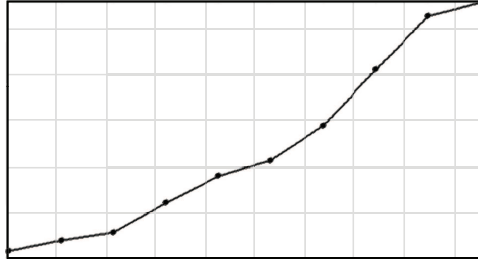
B = Slope Factor/Hill Coefficient

C = EC₅₀/IC₅₀

D = Second Asymptote

Point-to-Point

The **Point-to-Point** curve fit uses a linear equation to fit each pair of data points.



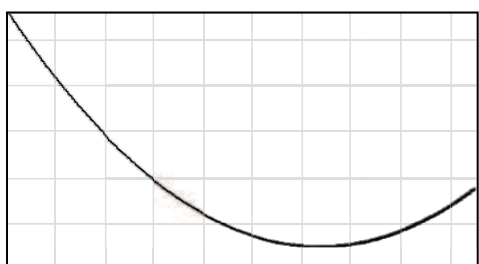
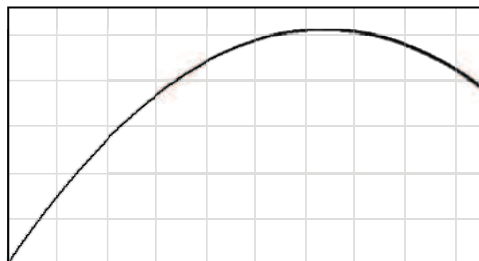
This curve fit is composed of multiple linear pieces joining the points. The line segment defined by each pair is used to interpolate data between those points.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a point-to-point curve fit algorithm is 2.

Quadratic

A **Quadratic** curve fit is also known as:

- Polynomial Second Order



$$y = A + Bx + Cx^2$$

A = Intercept

B = Slope of the Curve at the Intercept

C = a measure of the curvature of the parabola

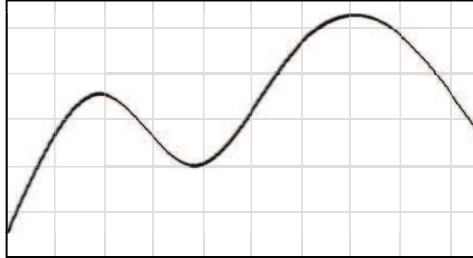
The quadratic fit is useful for standard curves.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a quadratic curve fit algorithm is 3.

Quartic

A **Quartic** curve fit is also known as:

- Polynomial Fourth Order



$$y = A + Bx + Cx^2 + Dx^3 + Gx^4$$

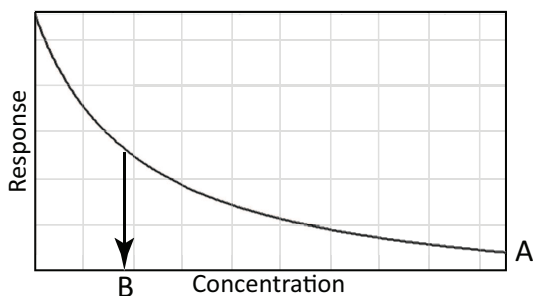
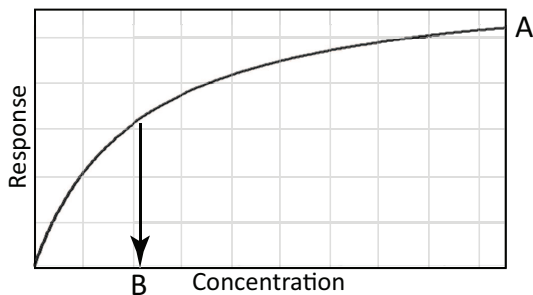
A quartic curve fit can be used for standard curves, but there is risk of multiple inflection points, and so ambiguity in InterpX results.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a quartic curve fit algorithm is 5.

Rectangular Hyperbola

A **Rectangular Hyperbola** curve fit is also known as:

- [Michaelis-Menten](#), see page 433
- [One-Site Equilibrium Binding \(specific binding\)](#), see page 434



$$Y = \frac{Ax}{x + B}$$

For Michaelis-Menten:

$$y = V_i$$

$$A = V_i \text{max}$$

$$B = K_m$$

For One-Site Equilibrium Binding (specific binding):

$$y = \text{Specific Binding}$$

$$A = \text{Maximum Binding}$$

$$B = K_d$$

A rectangular hyperbola curve fit is commonly used estimation of $V_i \text{max}$, K_m , maximum binding, and K_d .

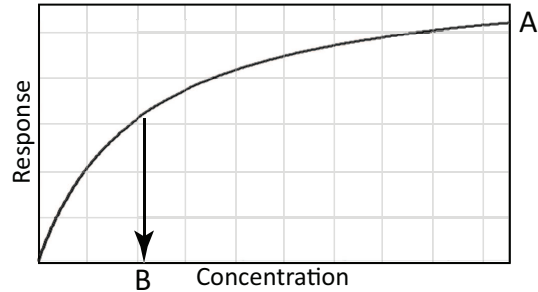
A rectangular hyperbola curve fit is a special case of the 4-parameter curve fit where $B = 1$, $D = 0$, and x is $1/\text{concentration}$.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a rectangular hyperbola curve fit algorithm is 2.

Michaelis-Menten

A **Michaelis-Menten** curve fit is also known as:

- [Rectangular Hyperbola, see page 432](#)



$$Y = \frac{Ax}{x + B}$$

$$y = V_i$$

$$A = V_{i\max}$$

$$B = K_m$$

A Michaelis-Menten curve fit is commonly used estimation of $V_{i\max}$ and K_m .

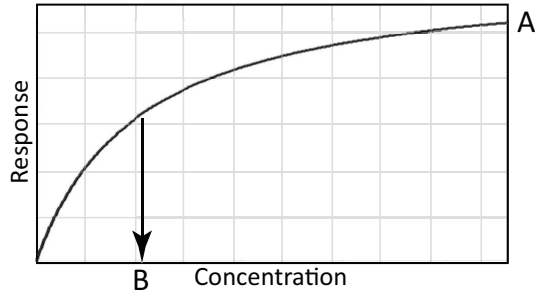
A Michaelis-Menten curve fit is a special case of the 4-parameter curve fit where $B = 1$, $D = 0$, and x is $1/\text{concentration}$.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a Michaelis-Menten curve fit algorithm is 2.

One-Site Equilibrium Binding (specific binding)

A **One-Site Equilibrium Binding (specific binding)** curve fit is also known as:

- [Rectangular Hyperbola, see page 432](#)



$$Y = \frac{Ax}{x + B}$$

y = Specific Binding

A = Maximum Binding

B = Kd

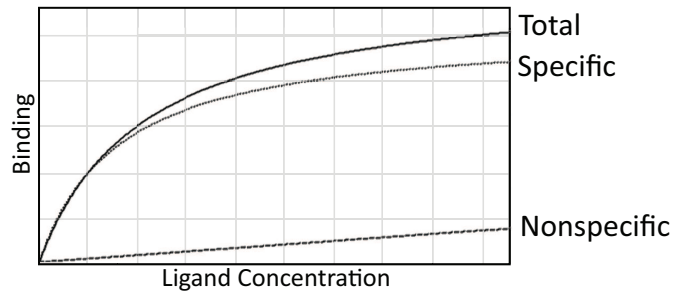
A one-site equilibrium binding (specific binding) curve fit is commonly used estimation of maximum binding and Kd.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a one-site equilibrium binding (specific binding) curve fit algorithm is 2.

Rect. Hyper. Plus Linear

A **Rect. Hyper. Plus Linear** (rectangular hyperbola plus linear) curve fit is also known as:

- RHPlusLinear (in previous versions of the SoftMax Pro Software)
- **One-Site Equilibrium Binding (total and nonspecific)**, see page 436



$$y = \frac{Ax}{x + B} + Cx$$

y = Total binding

A = Specific Binding B_{\max}

B = Kd (specific binding)

C = nonspecific binding coefficient

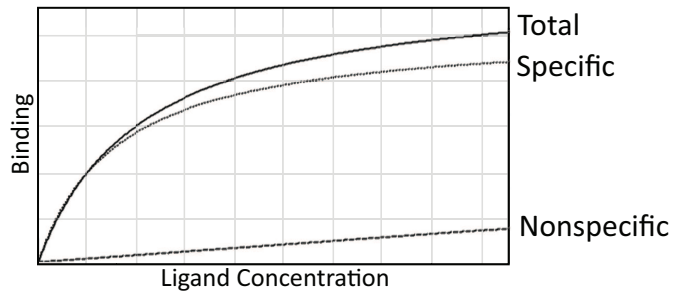
A rectangular hyperbola plus linear curve fit is commonly used for estimation of maximum binding and Kd (of specific binding) in the presence of nonspecific binding.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a rectangular hyperbola plus linear curve fit algorithm is 3.

One-Site Equilibrium Binding (total and nonspecific)

A **One-Site Equilibrium Binding (total and nonspecific)** curve fit is also known as:

- Rectangular Hyperbola Plus Linear
- [Rect. Hyper. Plus Linear, see page 435](#)



$$y = \frac{Ax}{x + B} + Cx$$

y = Total binding

A = Specific Binding B_{\max}

B = Kd (specific binding)

C = nonspecific binding coefficient

A one-site equilibrium binding (total and nonspecific) curve fit is commonly used for estimation of maximum binding and Kd (of specific binding) in the presence of nonspecific binding.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a one-site equilibrium binding (total and nonspecific) curve fit algorithm is 3.

Semi-Log

The **Semi-Log** curve fit fits the best straight line to a set of data for $\log(x)$ plotted against y .



$$y = A + B \times \text{Log}(x)$$

A = y-intercept at $x=1$

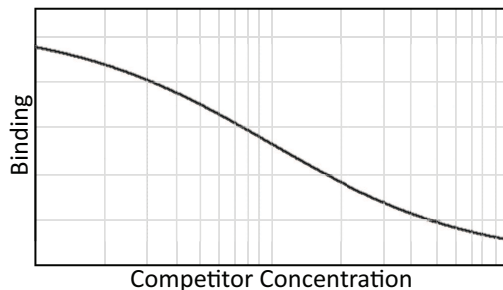
B = Slope

Log in this equation is the common or base-10 logarithm.

For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a semi-log curve fit algorithm is 2.

Two-Site Competition

The **Two-Site Competition** curve fit is applicable to competition studies involving two receptor binding sites.



$$y = D + (A - D) \left(\frac{B}{1 + \left(\frac{X}{C}\right)} + \frac{1 - B}{1 + \left(\frac{X}{G}\right)} \right)$$

A = Y_0 = First Asymptote

B = Fraction of Sites with Affinity Associated with C

C = EC_{50} for One Site

G = EC_{50} for the Other Site

D = Second Asymptote

1 - B = Fraction of Sites with Affinity Associated with G

Assumptions include:

- Ligand has identical affinity for both receptors
- Competitor had different affinities
- Fraction1 = Fraction of Receptors with (1)
- Span = Top - Bottom



Note: To obtain a one-site competition fit, use the 4-parameter logistic and fix B to -1. See [3-Parameter Dose-Response Curves on page 413](#).

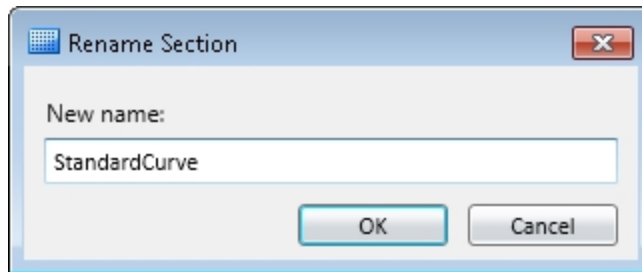
For the best results, you should always exceed the minimum number of standards required for a curve fit. The minimum number of standards required mathematically for a two-site competition curve fit algorithm is 4.

Changing the Name of the Graph Section

To change the name of a graph.

1. Click the **Graph** section to make it active in the workspace.
2. Double click the name of **Graph** section at the top of the section to open the **Rename Section** dialog.


You can also right-click the graph in the **Navigation Tree** and then click **Rename**.



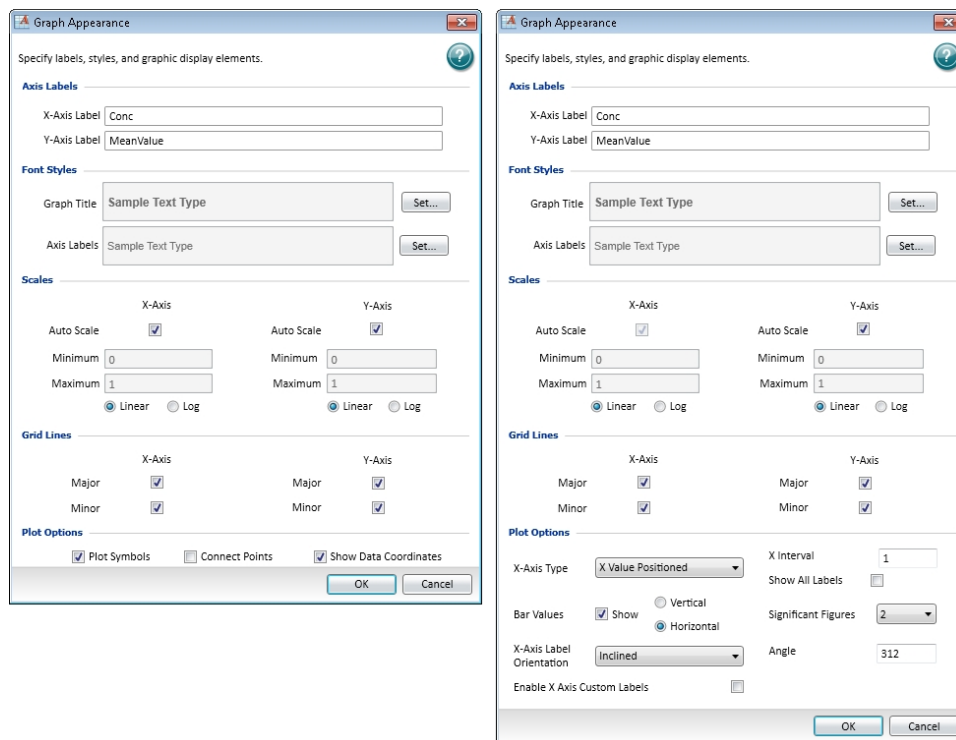
2. In the **New name** field, type the name.
3. Click **OK**.

This changes the name of the **Graph** section, but does not change the title of the graph. To change the title of the graph, see [Editing an Existing Graph on page 394](#).

Changing the Appearance of a Graph

With a **Graph** section active in the workspace, click **Graph Appearance**  in the **Graph Tools** section on the **Home** tab in the ribbon or in the toolbar at the top of the section.

In the **Graph Appearance** dialog, you can specify labels, styles, and graphic-display options.

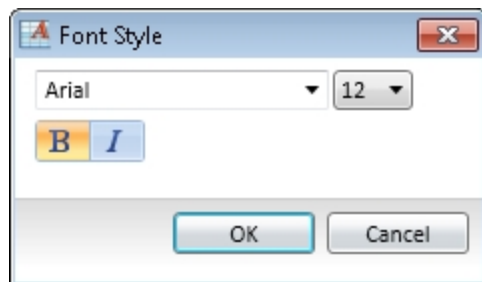


Axis Labels

Define labels for the X-Axis and Y-Axis by typing the text of the labels in the fields. These labels are displayed in the font specified in the **Font Styles** area.

Font Styles

Font Styles provides separate control of the fonts used for the **Graph Title** and **Axis Labels**. Click **Set** to open the **Font Style** dialog.



After you have finished defining the font style, click **OK**. The defined font style is displayed in the **Sample Text Type** example text.

Scales

To automatically scale one or both axes, select the **Auto Scale** check box for the axis.

As an alternative, you can define **Minimum** and **Maximum** scaling values.

You can also select either a **Linear** or a **Log** display of each axis. **Log** is the default selection.

Grid Lines

You can choose to display the major and minor grid lines for the X-Axis and the Y-Axis individually. To display a grid line, select the related check box.

Plot Options

For a scatter plot, you can select the following options:

- Select **Plot Symbols** to display the defined symbol for each data point.
You can define the size and style of the symbol, and the color of the symbol and the line, in the **Plot Editor** dialog. See [Creating a New Graph on page 392](#).
- Select **Connect Points** to display a line connecting each of the data points.
- Show **Data Coordinates** to display the coordinates for each data point when you use your mouse to hover the pointer over the data point.

For a bar graph, you can select the following display options:

- From the **X-Axis Type** drop-down list, select **Evenly Spaced Axis**, **Separated Axis**, or **X Value Positioned**.
For the **X Value Positioned** option, type a value in the **X Interval** field. To display all the labels for the defined interval, select the **Show All Labels** check box. When this check box is cleared, labels are displayed only for the bars that have data.
- To display the data values above each bar, select the **Show Values** check box and then click **Vertical** or **Horizontal**. Select a number from the **Significant Figures** drop-down list.
- From the **X-Axis Label Orientation** drop-down list, select **Horizontal**, **Vertical**, or **Inclined**.

For the **Inclined** option, type a value in the **Angle** field.

- If you want to edit the labels directly in the **Graph** section, then select the **Enable X-Axis Custom Labels** check box.

When this option is selected, you can double-click the label in the **Graph** section to edit the label. Clearing this check box returns the labels to their default values.



Note: When the **Enable X-Axis Custom Labels** check box is selected, the **X-Axis Label Orientation** is set to **Horizontal**. After you edit the labels, you can change the **X-Axis Label Orientation** to **Vertical** or **Inclined**.

Zooming the Graph Display

To zoom in on a section of a graph, use your mouse to draw a rectangle over the section. After you release the mouse button, the display zooms into the selected region.

To return to the default view, double-click the graph body.

Zooming is supported for scatter plots only.

Exporting an Image of a Graph Section


You can export a 300 DPI image of a **Graph** section so that you can import the image into another program. You can also copy the **Graph** section and then paste the 300 DPI image directly into a word processor or spreadsheet program.

To copy a **Graph** section, right-click anywhere on the section and then click **Copy**.



Note: The 300 DPI image might appear very large in the program where it is imported or pasted. You might need to scale or resize the image in that program after importing or pasting the **Graph** section image.





To export an image of a graph to a .png file:


1. Click the **Graph** section to make it active in the workspace.
2. Make sure that the graph is displayed the way you want, including whether or not the graph legend is displayed. See [Graph Legend on page 389](#).
3. Click **Export Graph**  in the **Graph Tools** section on the **Home** tab in the ribbon.
4. In the **Save As** dialog, browse to the file location where you want to save the .png file.
5. In the **File name** field, type a name for the file.
6. Click **Save**.





An image of the active **Graph** section is saved as a .png file at 300 DPI resolution.

Viewing Western Blot Membrane Data




After scanning a membrane for Western Blot data, the data are displayed in the SoftMax Pro Software as an image. You can use the image tools in the **Plate** section to zoom, crop, colorize, and adjust the intensity of the image. You can also select a region of interest (ROI) and rescan the membrane at a higher resolution.

- To zoom the image in or out, drag the slider on the side of the **Plate** section.
- To view the image at its actual size, click **1:1** on the side of the **Plate** section.
- To fit the image to the **Plate** section, click **Fit** on the side of the **Plate** section.
- To zoom in on a specific area of the image, click  on the side of the **Plate** section and then drag across the image to define the area to zoom.
- To move the image within the **Plate** section, click  on the side of the **Plate** section and then drag the image to move it.
- To crop the image, click  on the side of the **Plate** section and then drag across the image to define the cropped area.
- To colorize the image from a look-up table (LUT), from the **LUT** list at the top of the **Plate** section, select a color option.
- To adjust the intensity of the image, in the **Subtract** field at the top of the **Plate** section, type a value to subtract from the image intensity.
- To scale the image intensity, select the **Log** check box.
- To invert the colors of the image, similar to a photographic negative, select the **Invert** check box.
- To select and scan a region of interest (ROI), click  on the left side of the **Plate** section



and then drag across the image to define the region. Click **Read**  on the **Home** tab in the ribbon to scan the region using the **ROI Scan Resolution** defined in the **Settings** dialog. The data from the ROI scan replaces the data from the original scan.



- To adjust the resolution of the scanned image, click  to view the image at the scanned resolution, click  to view the image at a fine resolution suitable for external analysis, or click  to view the image at a very fine resolution suitable for publishing.
- To restore the image using the data from the last scan, click  on the top of the **Plate** section.

The **Plate** section also contains options for exporting the image for further analysis or publishing. These tools are on the right side of the top of the **Plate** section

- To open the raw image data in a Microsoft Excel template for analysis, click  and then click **Excel Analysis**. See [Using Excel to Analyze Western Blot Data on page 445](#).
- To open the raw image in the ImageJ software, click  and then click **ImageJ Editor**. See [Analyzing a Western Blot Image on page 450](#).
- To open the raw image in a pre-defined image-analysis tool, click  and then click **External Image Editor**. This option is available only if you have .tif files associated with a program other than ImageJ software. See [Analyzing a Western Blot Image on page 450](#).



Note: If you use the ImageJ software or an external image-analysis tool to make and save changes to the original image file, the edited image is displayed in the **Plate** section and the image cannot be edited from within the SoftMax Pro Software indicated by  at the top of the section. To restore the image using the data from the last scan, click .

-
- To export the raw image data to a text file, click , click **Export as Text**, and then select a name for the exported text file.
 - To export the edited image as it is displayed in the **Plate** section, click , click **Export as Image**, and then select a name and format for the exported image file.

For information on how to locate the generated image, see [Image Data Files and Folders on page 61](#).

Using Excel to Analyze Western Blot Data

You can export the Western Blot image data to a Microsoft Excel template to analyze the image data.

To export the raw image data to an Excel template, click  and then click **Excel Analysis**.

An Excel file opens displaying the exported data. There are three worksheets in the Excel file.

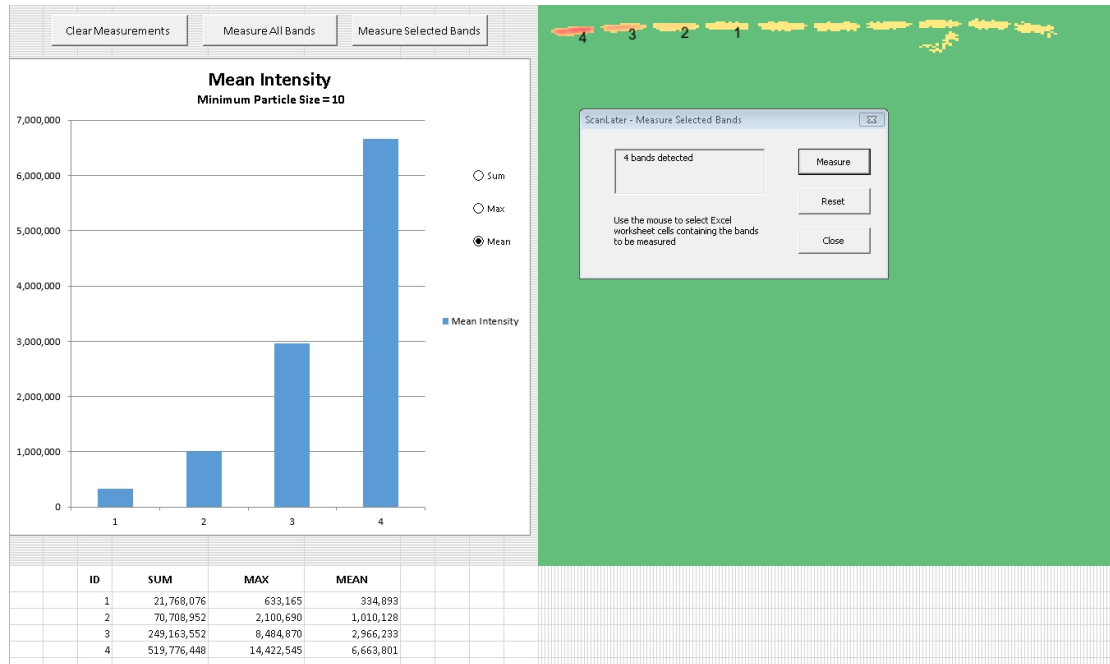


- The **Analysis** worksheet displays the data using automatic background subtraction. You can select the bands to measure and display a bar graph showing an analysis of the selected bands in the **Analysis** worksheet. See [Measuring Selected Bands on page 446](#).
- The **Segmentation** worksheet displays the segmented bands with background subtraction. The segmented bands are displayed on a white background. You can adjust the background noise level and the minimum and maximum band size in the **Segmentation** worksheet. See [Defining Segmentation Criteria on page 447](#).
- The **Data** worksheet displays the TIFF image and a color rendering of the raw data. No further analysis is shown in the **Data** worksheet. If the automatic background subtraction in the **Analysis** worksheet is not sufficient for your data, you can manually define the background for subtraction in the **Data** worksheet. See [Manually Selecting Background for Subtraction on page 449](#).

To save the data and analysis for future reference, save the Excel file.

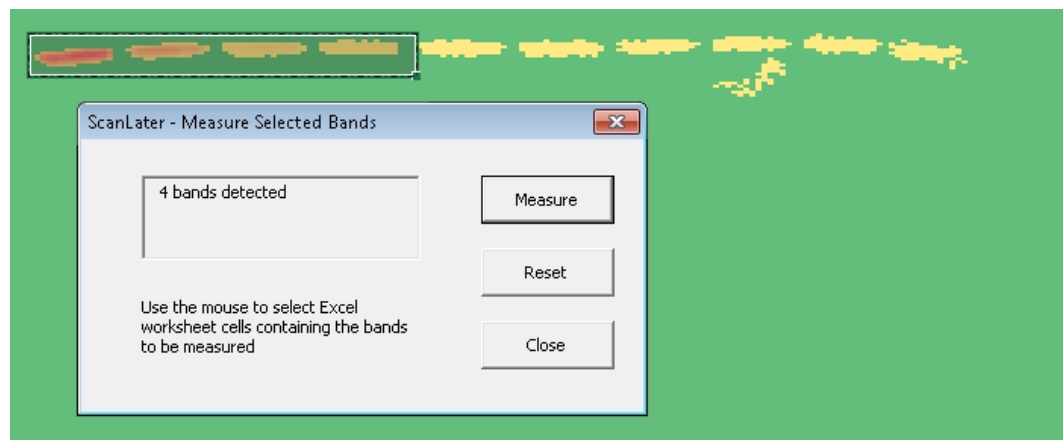
Measuring Selected Bands

You can select the bands to measure and display a bar graph showing an analysis of the selected bands in the **Analysis** worksheet. To view the **Analysis** worksheet, click the **Analysis** tab at the bottom of the Excel window.



The **Analysis** worksheet displays the data using automatic background subtraction.

- To measure all the displayed bands, click **Measure All Bands**.
- To select a group of bands to measure, click **Measure Selected Bands**, and then use your mouse to draw a rectangle around the bands that you want to measure. In the **ScanLater - Measure Selected Bands** dialog, click **Measure**.



- To remove the measurement analysis from the worksheet, click **Clear Measurements**.

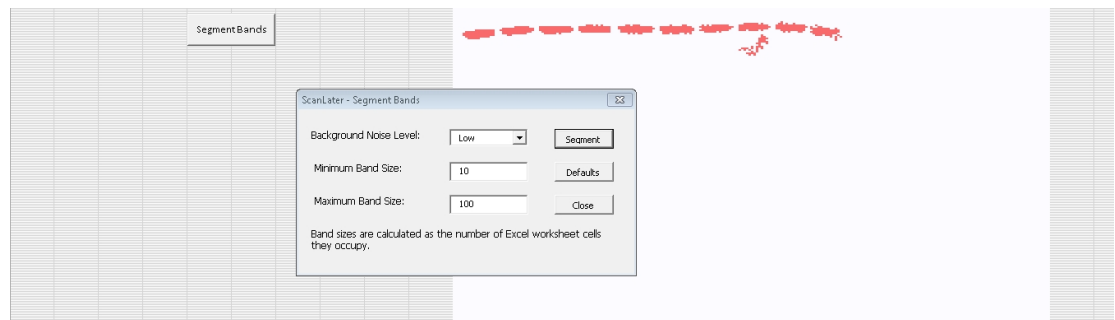
After you select the bands to measure, a bar graph is displayed with a table below it to show an analysis of the bands based on the analysis criteria. Labels on the blot show the locations of the bands that are referenced in the graph and the table.

You can adjust the background noise level and the minimum and maximum band size in the **Segmentation** worksheet. See [Defining Segmentation Criteria on page 447](#).

If the automatic background subtraction is not sufficient for your data, you can manually define the background for subtraction in the **Data** worksheet. See [Manually Selecting Background for Subtraction on page 449](#).

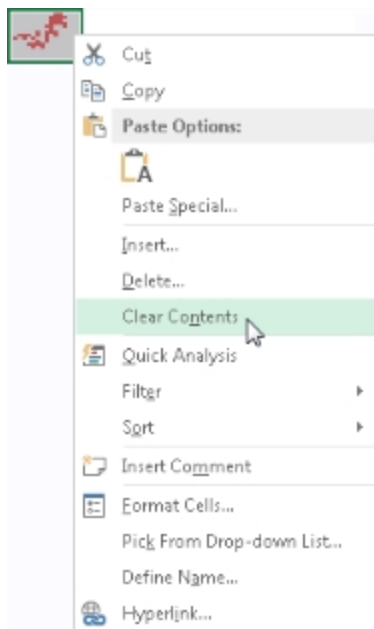
Defining Segmentation Criteria

The **Segmentation** worksheet displays the segmented bands with background subtraction. The segmented bands are displayed on a white background. You can adjust the background noise level and the minimum and maximum band size in the **Segmentation** worksheet. You can also remove artifacts that you do not want to include in your measurements.



To adjust the segmentation of the bands, click **Segment Bands**. In the **ScanLater - Segment Bands** dialog, select either a **Low** or **High** background noise level to subtract, and define the minimum and a maximum band size for the segmentation. The band size is the total number of cells in the Excel worksheet that the band occupies. To view the result of your settings, click **Segment**.

To remove artifacts from the displayed data, use your mouse to drag a rectangle around the artifact, and then right-click the rectangle and select **Clear Contents**.



You can select the bands to measure and display a bar graph showing an analysis of the selected bands in the **Analysis** worksheet. See [Measuring Selected Bands on page 446](#).

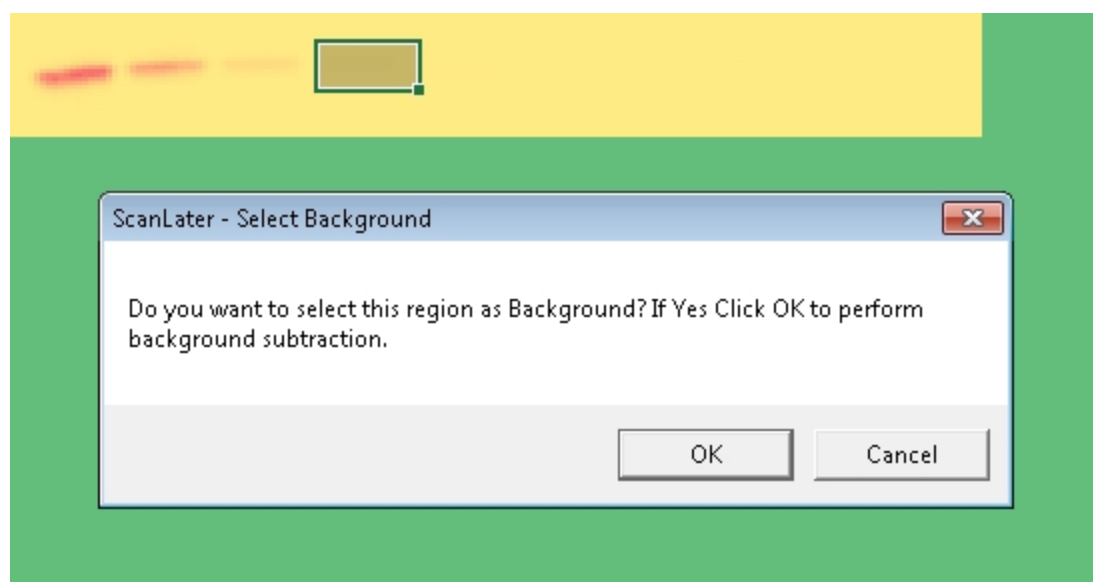
If the automatic background subtraction is not sufficient for your data, you can manually define the background for subtraction in the **Data** worksheet. See [Manually Selecting Background for Subtraction on page 449](#).

Manually Selecting Background for Subtraction

The **Data** worksheet displays the TIFF image and a color rendering of the raw data. No further analysis is shown in the **Data** worksheet. If the automatic background subtraction is not sufficient for your data, you can manually define the background for subtraction in the **Data** worksheet.



To define the background for subtraction, use your mouse to drag a rectangle around the area to use as the background. In the **ScanLater - Select Background** dialog, click **OK**.





You can select the bands to measure and display a bar graph showing an analysis of the selected bands in the **Analysis** worksheet. See [Measuring Selected Bands on page 446](#).

You can adjust the background noise level and the minimum and maximum band size in the **Segmentation** worksheet. See [Defining Segmentation Criteria on page 447](#).



Analyzing a Western Blot Image

Western Blot membrane data are saved as a TIFF image that can be analyzed by the image-analysis tool of your choice. The SoftMax Pro Software comes with an installed version of the ImageJ software from U.S. National Institute of Health (NIH).

To view the membrane image in the ImageJ software, click  in the toolbar at the top of the section and then click **ImageJ Editor**.

To view the membrane image in your selected image-analysis tool, click  in the toolbar at the top of the section and then click **External Image Editor**. This option is available only if you have .tif files associated with a program other than ImageJ software. The icon used for this tool changes depending on the selected image-analysis tool. See [Defining the Membrane Image-Analysis Tool on page 451](#).



Note: If you use the ImageJ software or an external image-analysis tool to make and save changes to the original image file, the edited image is displayed in the **Plate** section and the image cannot be edited from within the SoftMax Pro Software indicated by  at the top of the section. To restore the image using the data from the last scan, click .

To retain the editing capabilities within the SoftMax Pro Software and also edit the image with an external editor, export the image or make a copy of the generated TIFF image to open in the editor. For information on how to locate the generated TIFF image, see [Image Data Files and Folders on page 61](#).

Defining the Membrane Image-Analysis Tool

1. In Windows Explorer, right-click a file that has a **.tif** extension.
2. Click **Open with > Choose default program**.
3. In the **Open with** dialog, select the program you want to use for membrane image-analysis.
 - If the program you want is listed in the **Recommended Programs** list, then select it.
 - If the program you want is not listed in the **Recommended Programs** list, then click **Browse**. Locate and select the **.exe** file for the program that you want to use, and then click **Open**.
4. Make sure that the **Always use the selected program to open this kind of file** check box is selected.
5. Click **OK**.


The ImageJ software **.exe** file installed with the SoftMax Pro Software can be found in the **ImageJ** folder within the SoftMax Pro Software installation folder.

The next time you open a Western Blot data file, the **Image** icon changes to match the selected program.

Saving Data in a PDF File

You can save the contents of the currently selected file in PDF format. Before saving the PDF file, you can define the header and footer of the pages and the print quality in the **Printing Options** dialog, and predefine the sections that you want to exclude from the PDF file by disabling printing for the sections in the **Navigation Tree**. See [Setting Printing Options on page 83](#) and [Disabling Sections from Printing on page 84](#).

To save the data in a PDF file:

1. Click the **Application**  button to open the **Application** menu.
2. Click **Save As PDF**.

You can also select the **Molecular Devices (PDF Writer)** in the **Print** dialog.
3. In the **Molecular Devices (PDF Writer) - Create File** dialog, name the file and define the PDF options. See [Defining PDF File Settings on page 452](#).
4. Click **Save** to save the PDF file.

Defining PDF File Settings

The following tables define the settings for each of the tabs in the **Molecular Devices (PDF Writer) - Create File** dialog:

Table 8-7: PDF File Settings in the General Tab

Option	Description
Option Set	Select a pre-defined set of PDF settings from this list. To define a new set, select <Edit>.
Format	To create a PDF file, select PDF from this list. You can also select from this list to create output in image file formats.
File Name	Type the file name in the path or click <input type="button" value="..."/> to browse for a folder and name the file.
Append if output exists	Select this check box to append this file to an existing file instead of overwriting an existing file.
Open destination folder after creation	Select this check box to open the folder where the file is saved after saving the file.
Open the document after creation	Select this check box to open the file after saving the file.

Table 8-8: PDF File Settings in the Document Tab

Option	Description
Author	Type the name of the author in this field for displaying in the document properties.
Title	Type the title of the document in this field for displaying in the document properties.
Subject	Type the subject of the document in this field for displaying in the document properties.
Keywords	Type keywords for the document in this field for displaying in the document properties.
Quality	Select a quality option from this list to define the size of the PDF file.
Initial zoom level	Select a zoom level from this list to define how the document is displayed each time it is opened.
Compatibility Level	Select a format from this list to make the PDF file compatible with older versions of PDF readers. Some options might not be supported in older version.
PDF/A-1b	Select this check box to use the PDF/A-1b archiving standard.

Table 8-9: PDF File Settings in the Image Tab

Option	Description
DPI	When creating an image file, select the resolution for the image in dots per inch.
Text Alpha Bits	When creating an image file, select the number of bits to use for the alpha channel for text.

Table 8-10: PDF File Settings in the Watermark Tab

Option	Description
Text	Type the text that you want to be displayed in the watermark.
Font	Select the typeface for the watermark.
Color	Click <input type="button" value="..."/> to select the color for the text.
Size	Type the size of the text in points.
Outline width	Type the width of the text outline in pixels to have the text be displayed in outlines. To have the text be displayed as a solid color, leave this field blank.
Layer	To have the watermark text be displayed on top of the document text, select Stamp . To have the watermark text be displayed behind the document text, select Watermark .
Rotation	Select to display the text upward from the lower left-corner or downward from the upper-left corner.
Vertical position	Select to display the text on the top, center, or bottom of the document.
Vertical adjustment	Type a percentage offset for the vertical watermark position.
Horizontal position	Select to display the text on the left, center, or right of the document.
Horizontal adjustment	Type a percentage offset for the horizontal watermark position.

Table 8-11: PDF File Settings in the Merge Tab

Option	Description
Append PDF	Type the name of the file to which you want to append this file. To browse for the file, click <input type="button" value="..."/> .
Position	To append the new file to the end of the old file, select Bottom . To append the new file to the start of the old file, select Top .
Background PDF	If you want to print the data on an existing file, type the file name in this field. This can be used to print on company letterhead. To browse for the file, click <input type="button" value="..."/> .
Layer	To have the new file be displayed on top of the old file, select Stamp . To have the new file be displayed behind the old file, select Watermark .

Table 8-12: PDF File Settings in the Security Tab

Option	Description
Owner password	Type the password that gives owner permissions for the file.
User password	Type the password that gives user permissions for the file.
Key Length	Select the length of the key to be used for document encryption.
Set Permissions	Select this check box to limit access to the document for the user level.
Print	Select whether or not to permit printing and what print quality is permitted.
Copy to clipboard	Select this check box to permit users to copy text from the file to the clipboard.

Chapter 9: Maintaining and Calibrating an Instrument

Instrument maintenance is described in the user guide for the instrument. For instrument maintenance instructions, see the user guide for your instrument.

Information on configuration, maintenance, and calibration tasks that can be done using the SoftMax Pro Software can be found in the following topics:

- [Calibrating the Microplate Reader on page 455](#)
- [Configuring the Filters for the EMax and Vmax Microplate Readers on page 456](#)
- [Adjusting the Lamp for the EMax Plus Microplate Reader on page 456](#)
- [Using the Instrument Information Dialog on page 457](#)
- [Viewing Instrument Software Support on page 465](#)

Calibrating the Microplate Reader

If the connected instrument supports the SoftMax Pro Software air-calibration process, then the **Calibration** button is available in the **Operation** tab in the ribbon.



Note: Air-calibration applies to absorbance reads only. No microplate or cuvette is required for the instrument calibration. If you are doing a cuvette calibration, the cuvette chamber must be empty.

During calibration, the instrument steps through all available wavelengths one-by-one to measure the signal that reaches the detector when there is no sample in the optical path. The software calculates air-calibration values and stores these values in the firmware. The stored air-calibration values are used when **Speed Read** is enabled or **Calibrate** is disabled in the **Settings** dialog. See [Speed Read on page 262](#) and [Calibrate on page 285](#).

To calibrate the microplate reader:

1. Click **Calibration** on the **Operations** tab in the ribbon.
2. In the **Calibration** dialog, select either **Plate** or **Cuvette**.
 - To calibrate for microplates, select **Plate**.
 - To calibrate for cuvettes, select **Cuvette**.
3. Click **Calibrate Now**.
4. When the calibration indicator shows that the calibration is complete, click **Close**.



Note: If the **Calibration** button is not active in the **Operations** tab, then either the instrument is not connected to the computer or the connected instrument does not support the air-calibration process.

Configuring the Filters for the EMax and Vmax Microplate Readers

The EMax and Vmax Microplate Readers have configurable filters. If you change the order of the filters, or add or remove filters, you need to use the **Filter Configuration** dialog to define the positions of the filters. If the filter settings in the **Filter Configuration** dialog are incorrect, the microplate reader will generate incorrect data. For information about changing the filters, see the user guide for the EMax and Vmax Microplate Readers.

To define the filter positions:

1. Click **Filters** on the **Operations** tab in the ribbon.
2. In the **Filter Configuration** dialog, type the wavelength values in the correct positions for each installed filter.

You can define up to six filters. The permitted wavelength range is 400 nm to 750 nm.

3. After all the installed filters have been defined, click **OK**.

The defined filters are available for selection in the **Settings** dialog. See [Creating an Absorbance Mode Protocol on page 312](#).

Adjusting the Lamp for the EMax Plus Microplate Reader

To adjust the halogen lamp, click **Configure** on the **Operations** tab in the ribbon.

In the **Configuration** dialog, you can adjust the intensity of the lamp for each of the installed filters in the EMax Plus Microplate Reader. You can view the positions and wavelengths of the installed filters. This dialog also lists other instrument information like the serial number and firmware version.

The installed filters are available for selection in the **Settings** dialog. See [Creating an Absorbance Mode Protocol on page 312](#).

To adjust the intensity of the lamp for each of the filters, click **Adjust Lamp**. The software and instrument step through each filter one at a time to adjust the lamp intensity for the best implementation of the filter wavelength.



Note: The **Configuration** dialog must remain open until the lamp adjustment has completed.

Using the Instrument Information Dialog


To view the **Instrument Information** dialog, go to the **Operations** tab in the ribbon and click **Info**.

The Instrument Information dialog lists the PIC firmware version, the instrument firmware version, the instrument serial number, and the automation device number for the selected SpectraMax i3x or i3 Multi-Mode Detection Platform, SpectraMax Paradigm Multi-Mode Microplate Reader, FilterMax F3 Multi-Mode Microplate Reader, or FilterMax F5 Multi-Mode Microplate Reader. To update the PIC or instrument firmware, click the **Update** button. For more information about updating firmware, contact Molecular Devices support.

The lower portion of the dialog shows instrument-specific information for either the SpectraMax Paradigm Multi-Mode Microplate Reader or FilterMax F3 and F5 Multi-Mode Microplate Readers.


SpectraMax i3x or i3 Multi-Mode Detection Platform Instrument Information

The software detects the installed detection cartridges and displays them in the **Instrument Information** dialog. The name and serial number for the detection cartridge is displayed under its position in the drawer.

To open or close the detection cartridge drawer, click  to the left of the detection cartridge definitions for the drawer.

SpectraMax Paradigm Multi-Mode Microplate Reader Instrument Information

The software detects the installed detection cartridges and displays them in the **Instrument Information** dialog. The name and serial number for the detection cartridge is displayed under its position in the drawer.

To open or close a detection cartridge drawer, click  to the left of the detection cartridge definitions for that drawer.

You can lock or unlock the detection cartridge drawers when you are using the StakMax Microplate Handling System:

- When the microplate handler is installed, the detection cartridge drawers must be locked. To lock the cartridge drawers, click **Lock Drawers for StakMax**.
- When you need to open a detection cartridge drawer, remove the microplate handler from the detection platform and then unlock the drawers. To unlock the cartridge drawers, click **Unlock Drawers for StakMax**.

For more information, see the user guide for the StakMax Microplate Handling System.

To lock all the drawers closed, click **Lock Instrument for Shipment** and follow the on-screen instructions. For information about preparing an instrument for shipment, contact Molecular Devices support.

For information about unlocking the drawers, see [Unlocking the SpectraMax Paradigm Instrument on page 20](#).

To align the transfer position of the StakMax Microplate Handling System with the plate drawer of the SpectraMax Paradigm Multi-Mode Microplate Reader, click **StakMax Alignment Wizard**. For information about using the StakMax Alignment Wizard, see the user guide for the StakMax Microplate Handling System.

FilterMax F3 and F5 Multi-Mode Microplate Readers Instrument Information

The software detects the installed excitation and emission filter slides and displays their saved configurations in the **Instrument Information** dialog. The identification number for the slide is displayed on the right. Each filter has its defined wavelength, bandwidth, and read mode displayed under its position in the slide.

To eject or retract a filter slide, click  to the left of the slide definition.

To edit the filters in a slide, or to define more slides, click **Edit Slide Configuration**. See [Configuring Filter Slides on page 458](#).

Configuring Filter Slides

The FilterMax F3 and F5 Multi-Mode Microplate Readers have configurable filter slides. If you add or remove filter slides, or change the order of the filters in a slide, you need to use the **Filter Settings** dialog to define the filters in the slide. If the defined filter settings in the **Instrument Information** dialog are incorrect, the microplate reader will generate incorrect data. For information about changing the filter slides, see the user guide for the FilterMax F3 and F5 Multi-Mode Microplate Readers.

To view the **Filter Settings** dialog, go to the **Operations** tab in the ribbon and click **Info**. Then, in the **Instrument Information** dialog, click **Edit Slide Configuration**.

The filters used to do measurements are mounted on two types of interchangeable slides. One slide is reserved for excitation filters used in absorbance and fluorescence measurements, the other is used for emission filters used in fluorescence and some luminescence measurements. Each slide can hold up to six filters.



Note: Excitation and emission filter slides are different sizes to prevent them from being installed in the incorrect position.

When exchanging slides, an identification code built into the slide lets the SoftMax Pro Software recognize the new slide and filter configuration. When a slide with a new configuration is inserted, or the filters on a slide change, the slide must be configured in the **Filter Settings** dialog. Up to 31 excitation filter slides and 31 emission filter slides can be stored in the software at one time.

- For quantitation protocols, a genomic filter slide, which contains narrow bandwidth 260 nm and 280 nm filters must be installed and configured.
- For protocols that use PathCheck Pathlength Measurement Technology, a filter slide designed for PathCheck technology must be used.

To work with a filter slide, click **Excitation** or **Emission** to display a list of the selected type of filter slides. To add, remove, export, or import filter slides, click a button on the left side of the dialog.

- Click **Add Slide** to add a new filter slide to the list. See [Adding a Filter Slide on page 460](#).
- Click **Remove Slide** to delete the selected filter slide. See [Removing a Filter Slide on page 461](#).
- Click **Export selected Slide** to export the filter definitions for the selected filter slide. See [Exporting a Filter Slide on page 461](#).
- Click **Import Slides** to import a filter slide definition file that defines one or more filter slides. See [Importing Filter Slides on page 462](#).
- Click **Load Slides** to replace all the current filter slide definitions with the imported definitions. See [Replacing the Filter Slide Definitions on page 463](#).
- Click **Export Slides** to export all the defined filter slides. See [Exporting the Filter Slide Definitions on page 464](#).



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

Adding a Filter Slide

The filters used to do measurements are mounted on two types of interchangeable slides. One slide is reserved for excitation filters used in absorbance and fluorescence measurements, the other is used for emission filters used in fluorescence and some luminescence measurements. Each slide can hold up to six filters.

To add a filter slide and configure the filters:

1. Go to the **Operations** tab in the ribbon and click **Info**.
2. In the **Instrument Information** dialog, click **Edit Slide Configuration**.
3. In the **Filter Settings** dialog, click **Excitation** or **Emission** to display a list of the selected type of filter slides.
4. Click **Add Slide** to add a new slide to the list.
5. The **Filter Slide Properties** pane displays information about the selected slide.
6. In the **Slide ID** field, type the identification number printed on the slide.
7. In the list of filter slides, click the **+** to the left of the filter slide name to display the list of filters installed on the slide.
8. Click a filter in the list to display the **Filter Properties** for the selected filter.
9. In the **Wavelength** field, type the wavelength of the filter.
10. In the **Technique(s)** field, select the read mode for which the filter applies. The filter can be used only for measurements of the selected read mode. For the FilterMax F5 Multi-Mode Microplate Reader only, you can select **Polarization** for filter positions that have a polarization filter installed.
 - After a read mode is selected, the **Installed** field displays **Yes**.
 - If no read mode is selected, the **Installed** field displays **No**, and the filter position cannot be used for measurements.



Note: The **Installed** and **Position** fields cannot be edited.

11. In the **Bandwidth** field, type the bandwidth of the filter.
12. In the **Order#** field, type the manufacturer's part number for the filter for your reference.
13. Continue configuring the rest of filters on the slide.
14. After the filters on the slide have been properly configured, click **OK**.



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

Removing a Filter Slide

If a filter slide is no longer used with an instrument, it can be removed from the list.



CAUTION! After you remove a filter slide from the list, it cannot be recovered. If you think you might want to use this filter slide definition again, export the slide definition before removing it from the list. See [Exporting a Filter Slide on page 461](#).

To remove a filter slide from the list:

1. Go to the **Operations** tab in the ribbon and click **Info**.
2. In the **Instrument Information** dialog, click **Edit Slide Configuration**.
3. In the **Filter Settings** dialog, click **Excitation** or **Emission** to display a list of the selected type of filter slides.
4. In the slide list, click the slide that you want to remove.
5. Click **Remove Slide** to remove slide from the list.
6. Click **OK**.



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

Exporting a Filter Slide

Exported slide definitions are saved in XML files that can be imported again later or imported into the software on a different computer.

Using the **Export selected Slide** feature exports the definition for a single filter slide. To export all the current filter slide definitions, see [Exporting the Filter Slide Definitions on page 464](#).

To export a filter slide in the list:

1. Go to the **Operations** tab in the ribbon and click **Info**.
2. In the **Instrument Information** dialog, click **Edit Slide Configuration**.
3. In the **Filter Settings** dialog, click **Excitation** or **Emission** to display a list of the selected type of filter slides.
4. In the slide list, click the slide that you want to export.
5. Click **Export selected Slide**.
6. In the **Save As** dialog, navigate to the folder where you want to save the exported XML file and type a name for the file in the **File name** field.

The default location for filter slide definitions is:

C:\ProgramData\Molecular Devices\SMP651\MultiMode\Detection Software\Filters

7. Click **Save**.
8. In the **Filter Settings** dialog, click **OK**.



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

Importing Filter Slides

Filter slide definitions can be imported from XML files that were previously exported or provided by Molecular Devices. Slide definition files can contain definitions of one or more filter slides.

Each filter slide definition must have a unique **Slide ID**. If the **Slide ID** of a filter slide that you want to import exists in the list, rename the **Slide ID** or remove the slide from the list before importing.

To import filter slide definitions into the list:

1. Go to the **Operations** tab in the ribbon and click **Info**.
2. In the **Instrument Information** dialog, click **Edit Slide Configuration**.
3. In the **Filter Settings** dialog, click **Excitation** or **Emission** to display a list of the selected type of filter slides.
4. Click **Import Slides**.
5. In the **Open** dialog, navigate to the folder where XML file is saved and select the file.
The default location for filter slide definitions is:
C:\ProgramData\Molecular Devices\SMP651\MultiMode\Detection Software\Filters
6. Click **Open**.
7. In the **Filter Settings** dialog, click **OK**.



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

Replacing the Filter Slide Definitions

Filter slide definitions can be imported from XML files that were previously exported or provided by Molecular Devices. Slide definition files can contain definitions of one or more filter slides for excitation and emission filters.



CAUTION! When you use the **Load Slides** feature, all the current definitions are deleted, and are replaced by the imported definitions for excitation and emission filters. If you think you might want to use one or more of the current filter slide definitions again, export the slide definitions before replacing them in the list. See [Exporting a Filter Slide on page 461](#) or [Exporting the Filter Slide Definitions on page 464](#).

To replace the current filter slide definitions:

1. Go to the **Operations** tab in the ribbon and click **Info**.
2. In the **Instrument Information** dialog, click **Edit Slide Configuration**.
3. In the **Filter Settings** dialog, click **Load Slides**.
4. In the message that is displayed, click **Yes**.
5. In the **Open** dialog, navigate to the folder where the XML file is saved and select the file.
The default location for filter slide definitions is:
C:\ProgramData\Molecular Devices\SMP651\MultiMode\Detection Software\Filters
6. Click **Open**.
7. In the **Filter Settings** dialog, click **OK**.



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

Exporting the Filter Slide Definitions

Exported filter slide definitions are saved in XML files that can be imported again later or imported into the software on a different computer.

Using the **Export Slides** feature exports all the filter slide definitions in the excitation and emission lists. If you want to export a single filter slide definition, see [Exporting a Filter Slide on page 461](#).

To export all the filter slide definitions in the lists:

1. Go to the **Operations** tab in the ribbon and click **Info**.
2. In the **Instrument Information** dialog, click **Edit Slide Configuration**.
3. In the **Filter Settings** dialog, click **Export Slides**.
4. In the **Save As** dialog, navigate to the folder where you want to save the exported XML file and type a name for the file in the **File name** field.

The default location for filter slide definitions is:

C:\ProgramData\Molecular Devices\SMP651\MultiMode\Detection Software\Filters

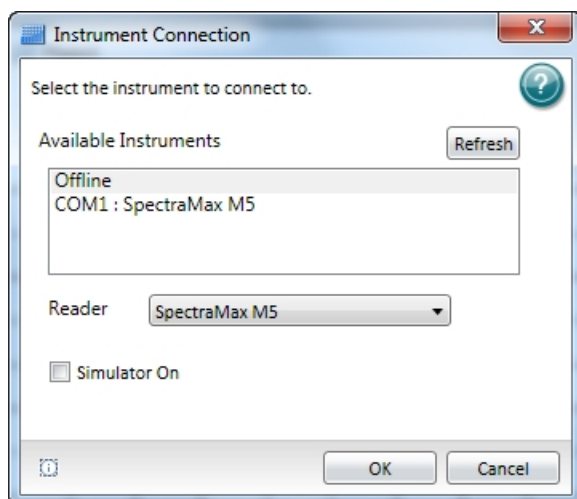
5. Click **Save**.
6. In the **Filter Settings** dialog, click **OK**.



Note: Molecular Devices recommends that you do not reconfigure standard filter slides.

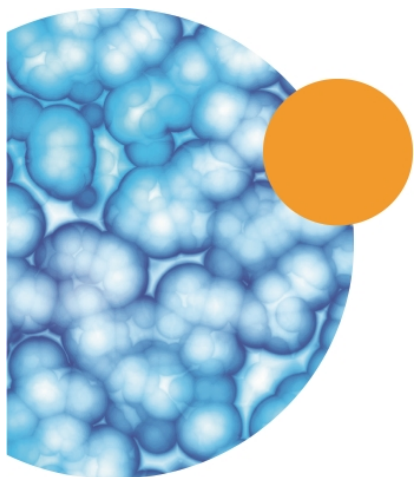
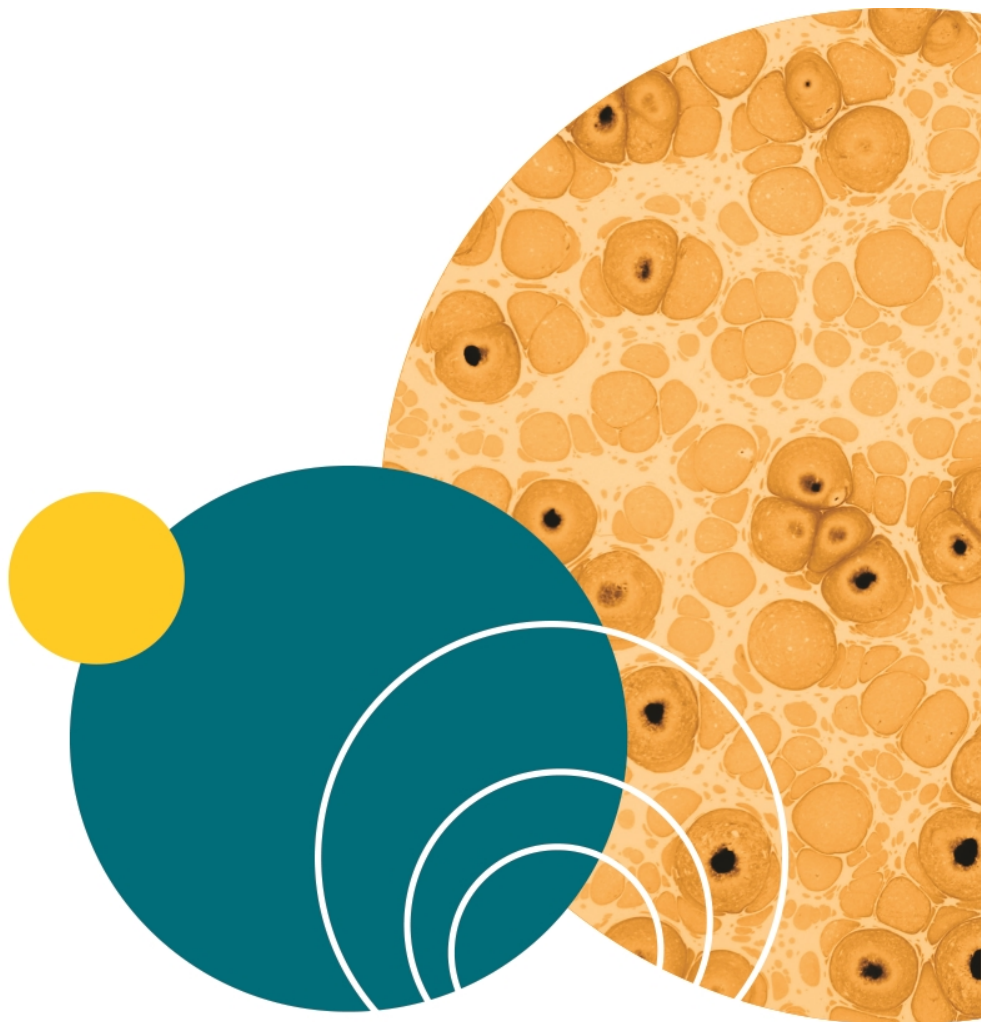
Viewing Instrument Software Support

Each of the supported instruments has related "plug-in" support that defines the interaction between the instrument and the SoftMax Pro Software interface. You can view a list of the of these plug-ins for troubleshooting purposes. Generally, you would view this list after contacting Molecular Devices technical support.



Click the **Information** button on the lower-left of the **Instrument Connection** dialog to open a list of the plug-ins currently installed with the SoftMax Pro Software.

For a list of the instruments that are supported by this version of the SoftMax Pro Software, see [Supported Instruments on page 201](#).



Molecular Devices provides a fully integrated hardware and software solution for adherence to Good Manufacturing Practices (GMP), Good Laboratory Practices (GLP), and many other regulatory compliance requirements including 21 CFR Part 11. The SoftMax® Pro GxP Microplate Data Compliance Software extends the SoftMax Pro Software into regulated laboratories working under GMP, GLP, and 21 CFR Part 11 guidelines for secure electronic records. SoftMax Pro GxP Software provides a method for electronically signing data files, and also automatically maintains a document-based audit trail for electronic records. This audit trail preserves user actions and modifications for review even after microplate data is collected and analyzed.

This integrated solution consists of the following components:

- A Molecular Devices microplate reader.
- SoftMax Pro GxP Software for data collection and analysis.
- GxP Admin Software for user management in SoftMax Pro GxP Software.
- MDC File Server (optional) for TCP/IP-based file serving of the User Accounts files.

The SoftMax Pro GxP Software connects to and controls the Molecular Devices microplate reader, and analyzes all collected data.

Use the GxP Admin Software to set up User Accounts that can be linked to the SoftMax Pro GxP Software through a Network File Server or the optional MDC File Server. See [Setting Up User Accounts for SoftMax Pro GxP Software on page 468](#).

The SoftMax Pro GxP Software is installed on individual computers that are used for data collection or data analysis. Each user account must be linked to a User Accounts file before users can log onto the SoftMax Pro GxP Software and use the software to collect and analyze microplate data.

Setting Up User Accounts for SoftMax Pro GxP Software

Use GxP Admin Software to create and maintain User Accounts (.edb) files. SoftMax Pro GxP Software uses these User Accounts files to regulate user access to the features of SoftMax Pro GxP Software and to provide traceability and accountability in electronic records. The User Accounts file records all approved users and their related information, including the following:

- User names, user logon IDs, and passwords.
- Assigned user permissions to SoftMax Pro GxP Software features.
- Global settings pertaining to all listed users, such as password aging, non-network use, guest access, and so on.
- Audit histories of all administrator actions in GxP Admin, such as user creation, modification, and so on.

If set by the administrator, SoftMax Pro GxP Software users do not require continual access to a User Accounts (.edb) file in order to use the SoftMax Pro GxP Software for data collection and analysis when no network connection is available, such as during a corporate network failure or using SoftMax Pro GxP Software while traveling.

SoftMax Pro GxP Software users can be connected to a User Account file in one of two ways:

- Network File Server (File Path connection) where the User Account file is placed on a secure, shared network file server, and the system browser is used to link each SoftMax Pro GxP Software installation directly to the defined User Account file.
- MDC File Server (TCP/IP Server connection) where the User Account file is placed on a secure network location and each SoftMax Pro GxP Software installation is linked indirectly to the defined User Account file using a TCP/IP address provided by the MDC File Server.

For information about setting up User Accounts files, see the *GxP Admin Software User Guide*.



Connecting a User Accounts File

Before users can log onto the SoftMax Pro GxP Software, the installed program needs to be connected to a User Accounts file. You can also change the related User Accounts file.

To define the User Accounts file connection:

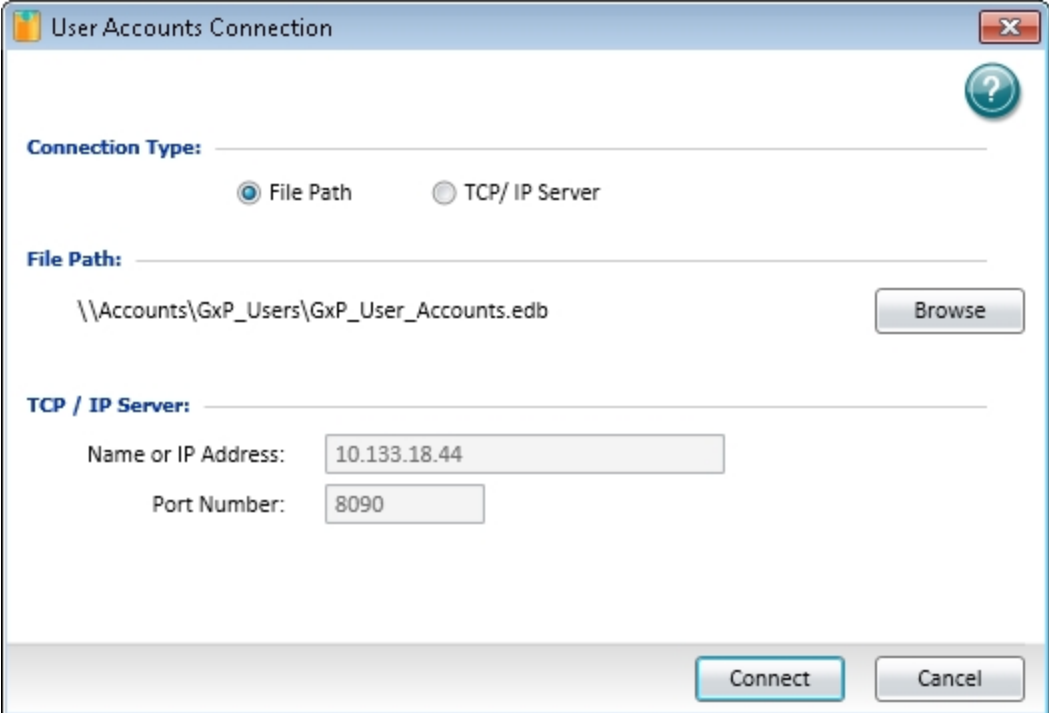
1. Start the SoftMax Pro GxP Software.
2. In the **Log On** dialog, click the **Change** button.

If the software is running with a user logged on, then go to the **GxP** tab in the ribbon. In

the **User Account** area, click **User Log Off**  and then click **Select Account Database** .

3. In the **User Accounts Connection** dialog, click the **Connection Type** for either a **File Path** or **TCP/IP Server** connection.
 - If you are setting up a **File Path** connection, then click the **Browse** button and use the **Open** dialog to locate the User Accounts (.edb) file on your network. Click **Open** to return to the **User Accounts Connection** dialog where the selected file path is shown.
 - If you are setting up a **TCP/IP Server** connection, then type the server computer **Name or IP Address** and the **Port Number** in the fields.

For information about setting up User Accounts files, see the *GxP Admin Software User Guide*.



The screenshot shows the 'User Accounts Connection' dialog box. It features a title bar with a close button and a help icon. The 'Connection Type' section has two radio buttons: 'File Path' (selected) and 'TCP/IP Server'. Below this, the 'File Path' section contains a text field with the path '\\Accounts\GxP_Users\GxP_User_Accounts.edb' and a 'Browse' button. The 'TCP / IP Server' section has two text input fields: 'Name or IP Address' with the value '10.133.18.44' and 'Port Number' with the value '8090'. At the bottom of the dialog are 'Connect' and 'Cancel' buttons.

4. Click **Connect**.

5. In the **Log On** dialog, type your user name and password.
6. Click **Log On**.

After establishing the User Accounts file connection, the defined users can log on and start acquiring and analyzing data with the SoftMax Pro GxP Software.

Granting TCP/IP Access to MDC File Server

When using the SoftMax Pro GxP Software with MDC File Server in a Windows 7, 64-bit operating system, the Windows Firewall sometimes blocks user access to MDC File Server through TCP/IP.

To grant user access through TCP/IP, create a new inbound rule and a new outbound rule in the Windows Firewall Advanced Settings.

Accessing Windows Firewall Advanced Settings

1. Open **Control Panel**.
2. Click **System and Security**.
3. Click **Windows Firewall**.
4. In the left pane, click **Advanced settings** to open the **Windows Firewall with Advanced Security** dialog.

Creating a New Inbound Rule

1. In left pane of the **Windows Firewall with Advanced Security** dialog, click **Inbound Rules**.
2. In the right pane, click **New Rule**.
3. In the **New Inbound Rule Wizard**, click **Port**.
4. Click **Next**.
5. Click **TCP**.
6. Click **Specify local ports**.
7. Type **9001** in the field.
8. Click **Next**.
9. Complete the rest of the wizard based on your network configuration and access rules defined by your system administrator.

Creating a New Outbound Rule

1. In left pane of the **Windows Firewall with Advanced Security** dialog, click **Outbound Rules**.
2. In the right pane, click **New Rule**.
3. In the **New Outbound Rule Wizard**, click **Port**.
4. Click **Next**.
5. Click **TCP**.
6. Click **Specify local ports**.
7. Type **9001** in the field.
8. Click **Next**.
9. Complete the rest of the wizard based on your network configuration and access rules defined by your system administrator.

Logging onto SoftMax Pro GxP Software

Each time you start the SoftMax Pro GxP Software, you are prompted to log on before you can continue. If the software is running and the user has logged off, go to the **GxP** tab in the

ribbon, and then in the **User Accounts** section, click **User Log On** .



The image shows a screenshot of the 'SoftMax Pro 6 - Log On' dialog box. On the left side, there is a graphic with an orange background featuring a grid of small circles and a stylized green leaf. Below this graphic, the letters 'GXP' are displayed in white on a teal background. On the right side, there are two input fields: the top one contains the text 'newton' and the bottom one contains seven black dots representing a password. Below the password field, the text 'Guest Logon is not allowed.' is displayed. A horizontal line separates this section from the user information section below. The user information section includes the following text: 'Last Logged On: Unknown', 'Contact: Addy', and 'User Account File: GxP_User_Accounts.edb'. To the right of the file name is a 'Change' button. At the bottom right of the dialog box, there are two buttons: 'Log On' and 'Cancel'.

In the **Log On** dialog, type your user ID and your password and then click **Log On**.



Note: Although the user ID is not case sensitive, the password is.

If you want to associate the installed program with a User Accounts file, or change the related User Accounts file, click the **Change** button. See [Connecting a User Accounts File on page 469](#).

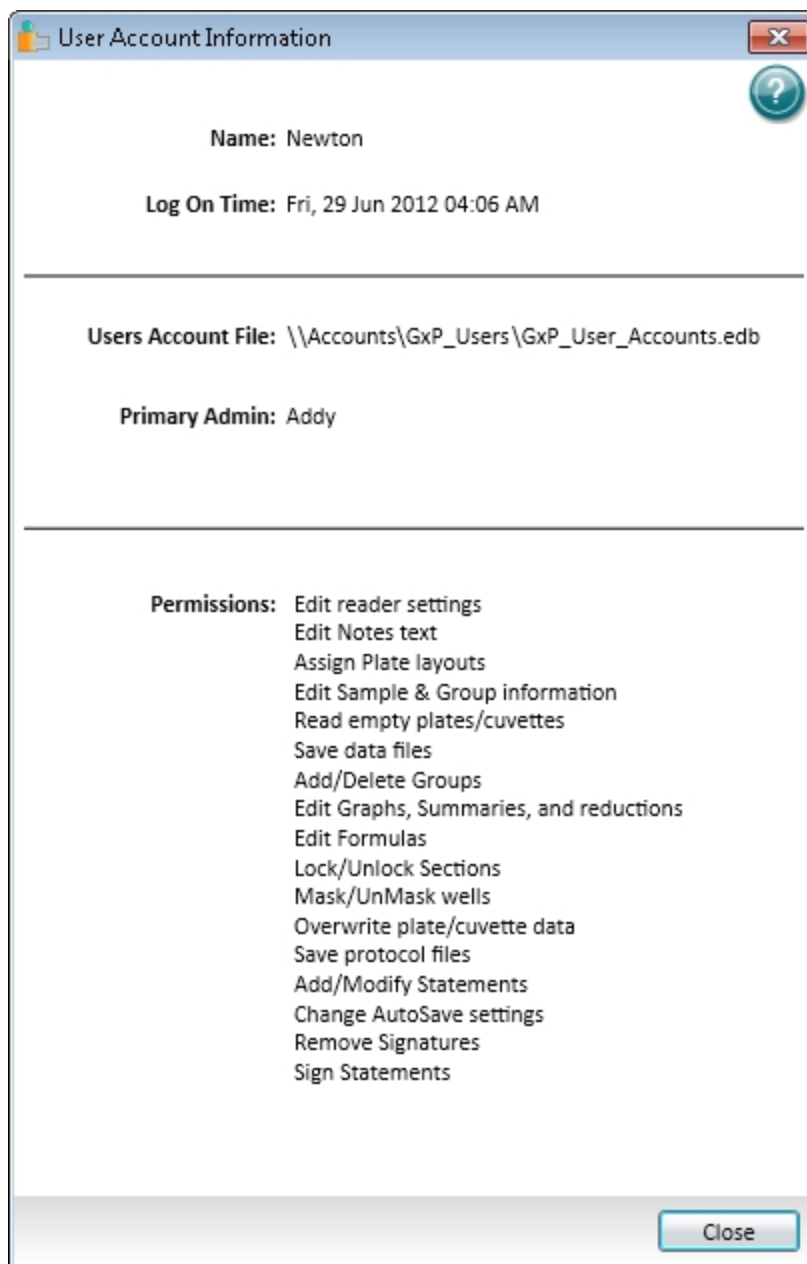
If the GxP Admin Software administrator has permitted it, those without an account can log on as a guest. Guests can open, view, and print existing data files or protocols. They cannot modify or save changes to existing data files or protocols. If guest log on is permitted, the **Log On** dialog explicitly states this, and a **Guest** button is available for logging on as a guest. For more information, see the *GxP Admin Software User Guide*.

Viewing the User Information

To view information about the current user, go to the **GxP** tab in the ribbon, and then in the

User Accounts section, click **Account Information** .

The **User Account Information** dialog provides information about the current user.



- The top section shows the user name and the time that the user logged on.
- The middle section shows the path to the related User Accounts file and the name of the GxP Admin Software administrator.
- The lower section shows the permissions assigned to the user by the GxP Admin Software administrator.

For more information about user accounts, see the *GxP Admin Software User Guide*.

To close the **User Account Information** dialog, click **Close**.

Changing the User Password

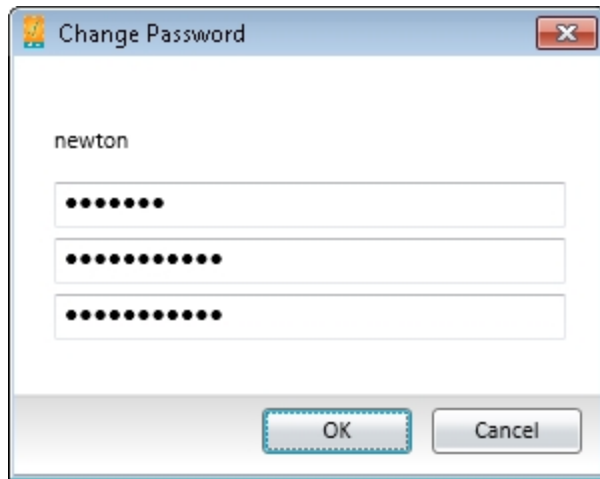
Users cannot change their user names, but they can change their passwords. The GxP Admin Software administrator can also define rules for requiring password changes.

To change your password:

1. Go to the **GxP** tab in the ribbon, and then in the **User Accounts** section, click **Change**

Password .

2. In the **Change Password** dialog, type your old password in the first field.



The image shows a 'Change Password' dialog box with a title bar containing a yellow warning icon and the text 'Change Password' and a close button. The dialog contains a text field with the username 'newton' above it. Below the text field are three password input fields, each filled with black dots. The first field is for the old password, the second for the new password, and the third for the confirmation of the new password. At the bottom of the dialog are two buttons: 'OK' and 'Cancel'.

3. Type your new password in the second field, and then type it again in the third field to confirm it.

The software compares the second and third field to make sure that they match exactly before the new password is saved.



Note: The password must be between 6 and 32 characters with a minimum of one alpha character and a minimum of one numeric character. The password is case sensitive.

4. Click **OK**.

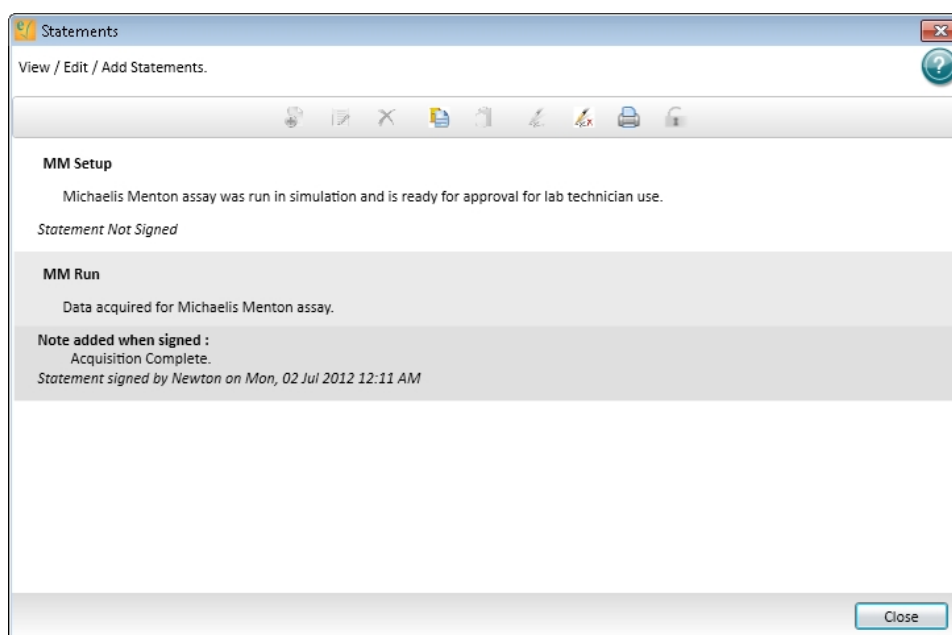
The next time you log onto the software, you will need to use the new password.

Working with GxP Statements

A user with the correct permission can view, add, and edit GxP statements to a SoftMax Pro GxP Software data file. You can use GxP statements to designate that an Experiment has been reviewed, verified, or given approval.

A user with the correct permission can apply an electronic signature to a statement. See [Signing a GxP Statement on page 479](#). After a GxP statement is signed, the SoftMax Pro GxP Software locks the data file to prevent further changes to the file. To unlock the file, remove all the statement signatures.

To work with GxP statements, go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .



In the **Statements** dialog, you can work with GxP statements by clicking the tools in the toolbar at the top of the dialog.

Table 10-1: The Statements Toolbar











Tool	Description
	Add Statement (see Adding a GxP Statement on page 477)
	Edit Statement (see Editing a GxP Statement on page 477)
	Delete Statements (see Deleting All GxP Statements on page 478)
	Copy Statement (see Duplicating a GxP Statement on page 478)
	Paste Statement (see Duplicating a GxP Statement on page 478)
	Sign Statement (see Signing a GxP Statement on page 479)

Table 10-1: The Statements Toolbar (continued)

Tool	Description
	Remove All Signatures (see Removing Signatures from All GxP Statements on page 480)
	Disable printing of Statements (see Printing GxP Statements on page 481)
	Enable printing of Statements (see Printing GxP Statements on page 481)
	Lock Statements (see Locking and Unlocking GxP Statements on page 481)
	Unlock Statements (see Locking and Unlocking GxP Statements on page 481)



To close the **Statements** dialog, click **Close**.

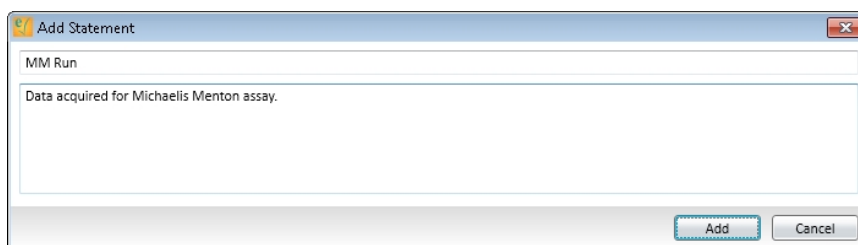
The statements status button in the upper-right corner of the work area displays the number of statements in the file, and how many statements are signed.



To quickly open the **Statements** dialog, click the statements status button.



Adding a GxP Statement

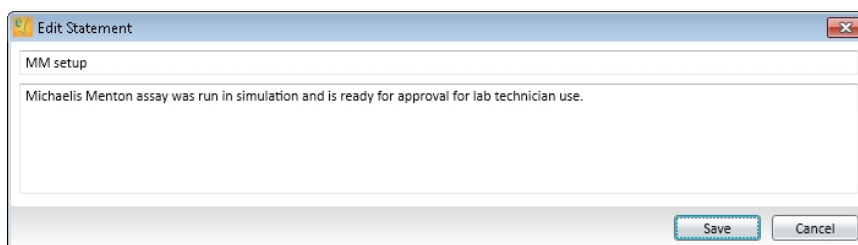
1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .
2. If there is more than one statement displayed in the **Statement** dialog, click the statement directly above where you want to add the new statement.
3. Click **Add Statement**  in the toolbar at the top of the dialog.



4. In the **Add Statement** dialog, click in the upper field and type a title for the statement. A title is required for each statement.
5. Click in the lower field and type the content of the statement.
6. Click **Add**.



Editing a GxP Statement

1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .
2. In the **Statement** dialog, click the statement that you want to edit.
3. Click **Edit Statement**  in the toolbar at the top of the dialog.



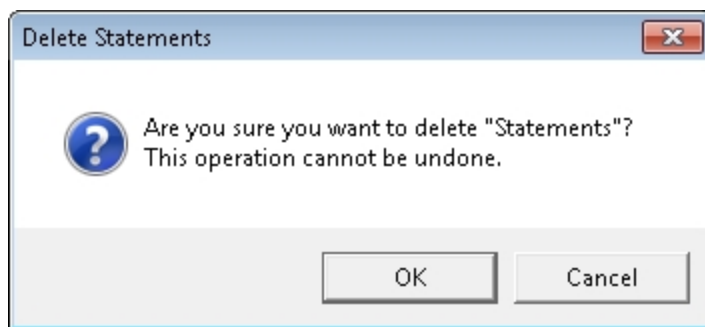
4. In the **Edit Statement** dialog, click in the upper field and edit the title for the statement.
5. Click in the lower field and edit the content of the statement.
6. Click **Save**.

Deleting All GxP Statements

1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .
2. Click **Delete Statements**  in the toolbar at the top of the dialog.







CAUTION! Deleting statements deletes all the GxP statements in the SoftMax Pro GxP Software data file. There is no undo for this. After deleting the statements, they cannot be retrieved.




3. In the **Delete Statements** message, click **OK** to delete all the GxP statements in the SoftMax Pro GxP Software data file.

Duplicating a GxP Statement


1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .
2. In the **Statement** dialog, click the statement that you want to duplicate.
3. Click **Copy Statement**  in the toolbar at the top of the dialog.
4. Click the statement directly above where you want to paste the copied statement.
5. Click **Paste Statement**  in the toolbar at the top of the dialog.


To edit the pasted statement, click the statement to select it and then click **Edit Statement**  in the toolbar at the top of the dialog. See [Editing a GxP Statement on page 477](#).

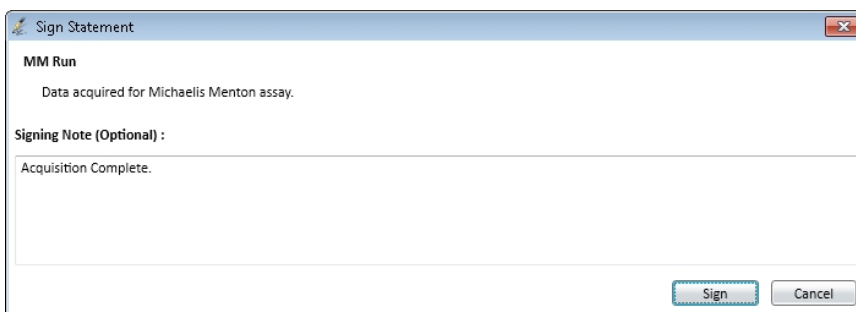
Signing a GxP Statement

1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .
2. In the **Statement** dialog, click the statement that you want to sign.
When a statement is selected, it has a light gray background.

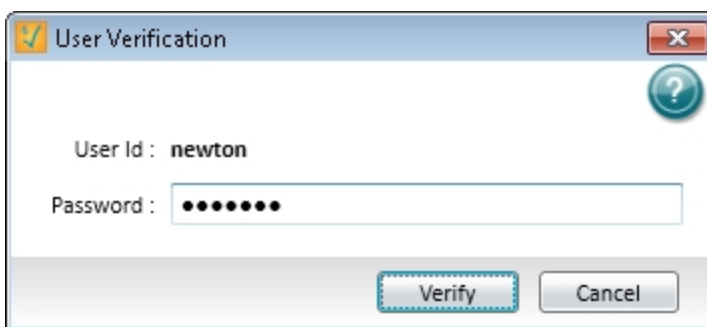


Note: If the statements are locked, they cannot be signed. To unlock the statements, click **Unlock Statements**  in the toolbar at the top of the **Statements** dialog.

3. Click **Sign Statement**  in the toolbar at the top of the dialog.
Sign Statement is not available in the toolbar until after you click the statement that you want to sign.



4. In the **Sign Statement** dialog, verify that the text at the top is the statement that you want to sign.
5. Click in the lower field and type a signing statement, if applicable.
6. Click **Sign**.






7. In the **User Verification** dialog, type your password.
8. Click **Verify**.

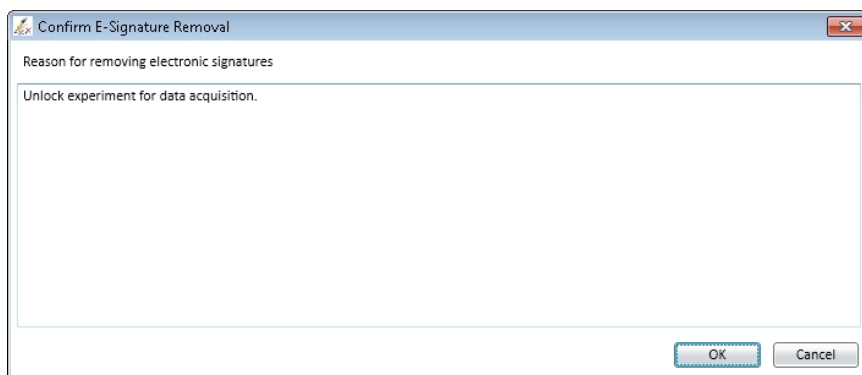


Note: After a GxP statement is signed, the SoftMax Pro GxP Software locks the data file to prevent further changes to the file. To unlock the file, remove all the statement signatures.

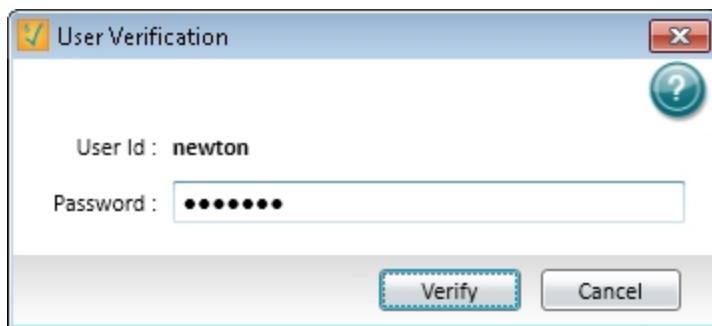
Removing Signatures from All GxP Statements

1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements** .
2. Click **Remove all signatures**  in the toolbar at the top of the dialog.

 **CAUTION!** Removing signatures removes the signatures from all the GxP statements in the SoftMax Pro GxP Software data file. There is no undo for this. After the signatures are removed, the data file is unlocked and changes can be made to the file.




3. In the **Confirm E-Signature Removal** dialog, type a reason for removing the signatures.
4. Click **OK**.







5. In the **User Verification** dialog, type your password.
6. Click **Verify**.

Printing GxP Statements

You can let the statements print or block the statements from printing in the **Statements** dialog .

To change the GxP printing options, go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements**  to open the **Statements** dialog.

- To let the statements be printed with the data file, click **Enable printing of Statements**  in the toolbar at the top of the dialog.
- To prevent the statements from printing with the data file, click **Disable printing of Statements**  in the toolbar at the top of the dialog.


The button switches between  and  to indicate whether or not statements will be printed.



You can also select to print or not to print statements with the data file in the **Print Selected** dialog. For information about printing the contents of a data file, see [Printing on page 80](#).


Locking and Unlocking GxP Statements

You can lock the statements to prevent changes to the **Statements** dialog.

You cannot lock signed statements. After a GxP statement is signed, the SoftMax Pro GxP Software locks the data file to prevent further changes to the file. To unlock the file, remove all the statement signatures.

To change the GxP statements lock options, go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Statements**  to open the **Statements** dialog.

- To prevent changes to the statements, click **Lock Statements**  in the toolbar at the top of the dialog.
- To permit changes to the statements, click **Unlock Statements**  in the toolbar at the top of the dialog.

The button switches between  and  to indicate whether or not statements are locked.

All the statements are locked or unlocked at the same time.

With the statements locked, you can still change the printing options. See [Printing GxP Statements on page 481](#).

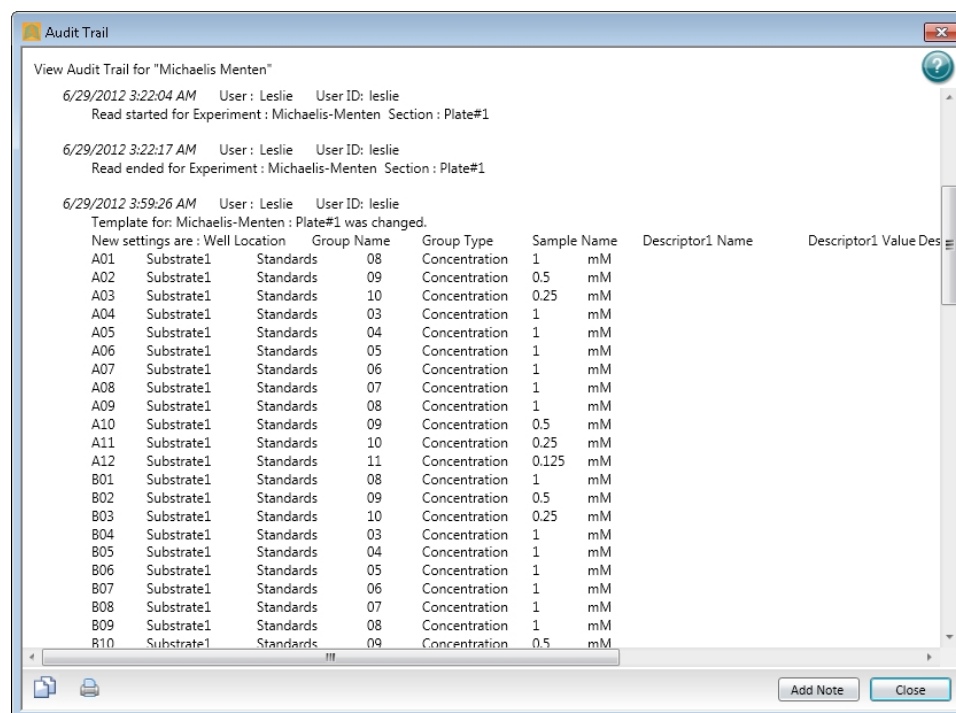
Viewing the GxP Audit Trail

The **Audit Trail** dialog gives you read-only access to the audit trail for the open data file, and lets you attach a note to the audit trail.

To view the audit trail, go to the **GxP** tab in the ribbon, and then in the **Data** section, click




Audit Trail



Each entry in the audit trail has a time-and-date stamp, and identifies the user performing the task.


To add a note to the audit trail, see [Adding a Note to the GxP Audit Trail on page 483](#).

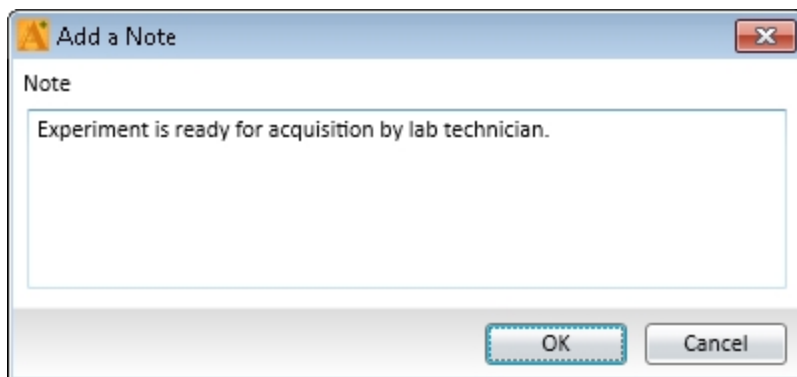
To copy the entire audit trail to the Windows clipboard, click **Copy to clipboard**  in the lower-left corner of the dialog. You can then paste the audit trail into a text editor or word processor for saving or printing.

To let the audit trail print or block the audit trail from printing, see [Printing the GxP Audit Trail on page 483](#).

To close the **Audit Trail** dialog, click **Close**.

Adding a Note to the GxP Audit Trail


1. Go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Audit Trail** .
2. In the **Audit Trail** dialog, click **Add Note**.







3. In the **Add a Note** dialog, type the content of the note.
4. Click **OK**.

The note is added to the end of the audit trail and becomes part of the permanent record for the open data file.

Printing the GxP Audit Trail

You can let the audit trail print or block the audit trail from printing in the **Audit Trail** dialog. To change the GxP printing options, go to the **GxP** tab in the ribbon, and then in the **Data** section, click **Audit Trail**  to open the **Audit Trail** dialog.


- To let the audit trail be printed with the data file, click **Enable printing of the audit trail**  in the toolbar at the bottom of the dialog.
- To prevent the audit trail from printing with the data file, click **Disable printing of the audit trail**  in the toolbar at the bottom of the dialog.

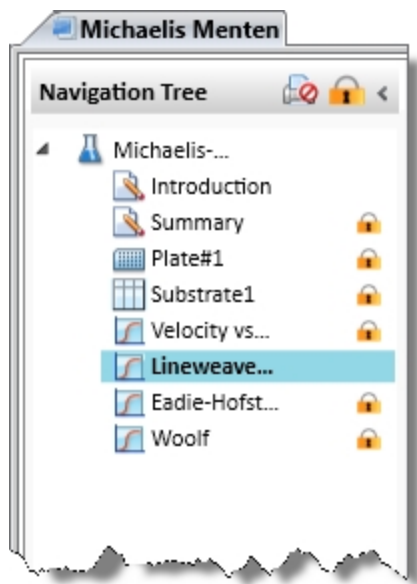
The button switches between  and  to indicate whether or not the audit trail will be printed.


You can also select to print or not to print the audit trail with the data file in the **Print Selected** dialog. For information about printing the contents of a data file, see [Printing on page 80](#).

Locking and Unlocking Sections

In the SoftMax Pro GxP Software, you can lock the individual sections in an experiment to prevent changes to them. A locked section cannot be deleted nor have its data changed. When a locked section is duplicated, the duplicate section is unlocked by default. Locked sections can be printed with the data file.

To lock or unlock a section, click the section to select it and then click **Lock Selection**  at the top of the Navigation Tree.



To lock or unlock all the sections in an Experiment, click the Experiment to select it and then click **Lock Selection**  at the top of the Navigation Tree.

When a section is locked, no direct changes can be made to it, with the following exceptions:

- In a **Plate** section, the data cannot be overwritten. However, a **Plate** section that has no data can have data acquired and added to the section.
- The name of a **Group** section can be changed indirectly in the **Group Settings** dialog.

Glossary

Numerics

21 CFR Part 11

The FDA guidelines for trustworthy electronic records, known as 21 CFR Part 11, requires companies to employ procedures and controls designed to ensure the authenticity, integrity, and when applicable the confidentiality of electronic records, and to ensure that the signer cannot readily repudiate the signed record as not genuine. To satisfy this requirement persons must, along with other things, employ procedures and controls that include the use of computer-generated time stamps.



Note: No software by itself can be 21 CFR Part 11 compliant. The provides features that let users demonstrate compliance with these regulations.

See [Using SoftMax Pro GxP Software Features on page 467](#).

A

Absorbance

Absorbance is the quantity of light absorbed by a solution. To measure absorbance accurately, it is necessary to eliminate light scatter. If there is no turbidity, then absorbance = optical density.

$$A = \log_{10}(I_0 / I) = -\log_{10}(I / I_0)$$

where I_0 is incident light before it enters the sample, I is the intensity of light after it passes through the sample, and A is the measured absorbance.

See [Absorbance Read Mode on page 154](#).

AlphaScreen

ALPHA stands for Amplified Luminescent Proximity Homogeneous Assay. AlphaScreen® is a bead-based chemistry used to study molecular interactions between moieties A and B, for example. When a biological interaction between A and B moves beads (coated with A and B, respectively) together, a cascade of chemical reactions produce a greatly amplified signal.

The cascade finally resulting in signal is triggered by laser excitation (680 nm), making a photosensitizer on the A-beads convert oxygen to an excited (singlet) state. That energized oxygen diffuses away from the A-bead. When reaching the B-bead in close proximity, it reacts with a thioxene derivative on the B-bead generating chemiluminescence at 370 nm. Energy transfer to a fluorescent dye on the same bead shifts the emission wavelength into the 520 nm to 620 nm range. The limited lifetime of singlet oxygen in solvent (~4 microseconds) lets diffusion reach up to only around 200 nm distance. Thus, only B-beads in the proximity of A-beads yield signal, which indicates binding between moieties A and B.

An AlphaScreen measurement includes a light pulse, by turning on the laser diode for a specified time, turning off the laser diode, followed by the measurement of the AlphaScreen signal, as specified in the measurement protocol timing parameters.



Note: AlphaScreen beads are light sensitive. Beads are best handled under subdued (<100 lux) or green filtered (Roscolux filters #389 from Rosco, or equivalent) light conditions. Do incubation steps in the dark.

See [AlphaScreen Read Mode on page 189](#).

AutoRead

Auto Read automatically advances to the next **Plate** section after a read in the order that the **Plate** sections are displayed within a single Experiment. When you start a read for a **Plate** section that is enabled to automatically advance with AutoRead, the Auto Read feature advances to the next **Plate** section in the Experiment and then reads that plate. If multiple **Plate** sections are enabled to automatically advance with AutoRead, the Auto Read feature reads all enabled **Plate** sections until it reads a non-enabled **Plate** section or the last **Plate** section in the Experiment. **Plate** sections that come before the selected **Plate** section are not read.

For example, if you have five **Plate** sections (Plate 1, Plate 2, Plate 3, Plate 4, and Plate 5) in an Experiment, you can enable Plate 1, Plate 2, and Plate 3 to automatically advance with Auto Read. If you start a Read operation for Plate 2, then Plate 2, Plate 3, and Plate 4 are read in sequence. Plate 1 is not read, since it comes before Plate 2. Plate 5 is not read since Plate 4 is not enabled to automatically advance with AutoRead.

You can set an interval, or delay time, between the plate readings, if desired.

See [Enabling Auto Read on page 340](#).

Auto Save

When Auto Save is enabled, the collected data is saved automatically to a user-defined location immediately after each plate read is completed. Auto Save reduces the likelihood of lost data, particularly when Auto Save is set to save files to corporate network volumes that are backed up on a regular basis.

You can add as many Auto Save instances as desired, each with its own settings.



Note: Auto Save settings are saved with each document.

See [Setting Auto Save Options on page 76](#).

B

Baseline

Baseline reads are available for kinetic reads with injection.

The instrument collects baseline data before the injection, so that the baseline data can be subtracted from the reads that follow the injection.

Bottom Read

You can set up a bottom read in the **PMT and Optics** category of the **Settings** dialog. Select the **Read From Bottom** check box to have an instrument with bottom-read capability read up through the bottom of the microplate rather than down from the top.

See [PMT and Optics Settings on page 258](#).

C

Calibrate

For Absorbance reads, the **Calibrate** setting tells the instrument to make an air-calibration measurement at each wavelength before reading the microplate, as determined by the type of instrument and the read settings. If you turn calibration off, SoftMax Pro Software uses the air-calibration values stored in the firmware of the instrument, or the values from the previous calibration.

For Fluorescence and Luminescence reads, the instrument makes a reference read on the internal reference chip at each wavelength before reading the microplate. If you turn calibration off, SoftMax Pro Software uses the default values stored in the firmware of the instrument, or the values from the previous calibration.

For kinetic readings the calibration measurement is made between readings during a run, unless the read interval is too short to allow calibration.

See [More Settings on page 285](#).

Cutoff

The term cutoff refers to filters used to block unwanted residual excitation light and minimize background interference.

No emission cutoff filter is used when a Luminescence read mode is selected. With other read modes, choices are to enable or disable Auto Cutoff with specific filter settings available if it is disabled (manual cutoff selection). When Auto Cutoff is enabled, the instrument sets the cutoffs based on the wavelengths chosen for reading. When a Spectrum read type is selected, a manual setting for the emission monochromator is required, with the default being no cutoff filter.

See [Wavelength Settings on page 247](#).

Cuvette Set Section

Cuvette Set sections are used to collect data from the cuvette port of the SpectraMax M2 and M2e Multi-Mode Microplate Readers, SpectraMax M5 and M5e Multi-Mode Microplate Readers, and the SpectraMax Plus 384 Absorbance Microplate Reader. You can use a **Cuvette Set** section to define an analysis template and to define data display and data reduction. The **Template Editor** in the **Cuvette Set** section is used to describe the contents of each cuvette within the Cuvette Set.

See [Using a Cuvette Set Section on page 129](#).

D

Default Protocol

After the SoftMax Pro Software is installed, the Basic Endpoint protocol is set as the default protocol with the filename **default.spr**. Whenever you create a new document, the **default.spr** protocol file is opened as an untitled document that contains the settings from the default protocol file.

You can save the settings of the file currently active in the workspace as the default protocol. After you save the active protocol file as the default, whenever you create a new document, the settings in the **default.spr** file that you have saved are loaded into an untitled document.

See [Saving a Protocol as the Default Protocol on page 69](#).

E

Emission Spectrum Scan

An emission spectrum scan measures fluorescence or luminescence across a spectrum of wavelengths. Fluorescent reads use the emitted light from a fixed excitation wavelength. The default value reported for each well is the wavelength of maximum emission in either RFU for fluorescence mode or RLU for luminescence mode.

See [Excitation Spectrum Scan on page 489](#).

End Time

End Time in a kinetic read specifies the time at which to stop showing data in the display and exclude it from data reduction. Values occurring after this limit are not reported in the display and are excluded from data reduction. The default setting is the total assay time for the kinetic read.

See [Doing Data Reduction on page 367](#).

Endpoint

In an endpoint read, a reading of each microplate well is taken in the center of each well, at a single wavelength or at multiple wavelengths. Depending on the read mode, raw data values are reported as optical density (OD), %Transmittance (%T), relative fluorescence units (RFU), or relative luminescence units (RLU).

See [Endpoint Read Type on page 152](#).

Excitation Spectrum Scan

An excitation spectrum scan measures fluorescence at a single emission wavelength for the emitted light across a spectrum of excitation wavelengths. The default value reported for each well is the wavelength of maximum fluorescence excitation in RFU.

See [Emission Spectrum Scan on page 489](#).

F

Fluorescence

Fluorescence occurs when absorbed light is re-radiated at a longer wavelength. In the Fluorescence Intensity (FL) read mode, the instrument measures the intensity of the re-radiated light and expresses the result in Relative Fluorescence Units (RFU).

The governing equation for fluorescence is:

$$\text{Fluorescence} = \text{extinction coefficient} \times \text{concentration} \times \text{quantum yield} \times \text{excitation intensity} \times \text{pathlength} \times \text{emission collection efficiency}$$

See [Fluorescence Intensity Read Mode on page 160](#).

Fluorescence Polarization

Fluorescence polarization detection is similar to fluorescence intensity, with the important difference that it uses plane-polarized light, rather than non-polarized light. Plate readers measure FP of the sample by detecting light emitted both parallel and perpendicular to the plane of excitation.

By using a fluorescent dye to label a small molecule, its binding to a different molecule of equal or greater size can be monitored through its speed of rotation.

See [Fluorescence Polarization Read Mode on page 185](#).

Fluorescence Resonance Energy Transfer (FRET)

Fluorescence resonance energy transfer (FRET) is a distance-dependent interaction between the electronic excited states of two dye molecules in which excitation is transferred from a donor molecule to an acceptor molecule *without emission of a photon*.

FRET relies on the distance-dependent transfer of energy from a donor molecule to an acceptor molecule. Due to its sensitivity to distance, FRET has been used to investigate molecular interactions. FRET is the radiationless transmission of energy from a donor molecule to an acceptor molecule. The donor molecule is the dye or chromophore that initially absorbs the energy and the acceptor is the chromophore to which the energy is subsequently transferred. This resonance interaction occurs over greater than interatomic distances, without conversion to thermal energy, and without a molecular collision. The transfer of energy leads to a reduction in the fluorescence intensity and excited state lifetime of the donor, and an increase in the emission intensity of the acceptor. A pair of molecules that interact in such a manner that FRET occurs is often referred to as a donor/acceptor pair.

While there are many factors that influence FRET, the primary conditions that need to be met for FRET to occur are relatively few:

- The donor and acceptor molecules must be in close proximity to each other.
- The absorption or excitation spectrum of the acceptor must overlap the fluorescence emission spectrum of the donor.
The degree to which they overlap is referred to as the spectral overlap integral (J).
- The donor and acceptor transition must be approximately parallel.

See [FRET Read Mode on page 178](#).

Fluorophore

A fluorophore is a material that absorbs light energy of a characteristic wavelength, undergoes an electronic state change, and instantaneously emits light of a longer wavelength.

See [Fluorescence Intensity Read Mode on page 160](#), [Time-Resolved Fluorescence Read Mode on page 171](#), and [Fluorescence Polarization Read Mode on page 185](#).

G

G Factor

The G factor, or grating factor, is used in fluorescence polarization to correct polarization data for optical artifacts, converting relative mP data to theoretical mP data. Optical systems, particularly with reflective components, pass light of different polarization with different efficiency. G factor corrects this instrumental bias.

See [Data Reduction on page 187](#).

Gain

Gain is the quantity of increase in signal power expressed as the ratio of output to input for a photomultiplier tube (PMT).

See [PMT and Optics Settings on page 258](#).

Group

Wells can be assigned to group types using the Template Editor. Depending on the protocol, certain group types, such as Standard or Unknown, can be created automatically. You can create other groups as required.

See [Defining a Group on page 303](#).

I

Imaging

Imaging read mode does whole-cell imaging assays.

Whole-cell imaging assays are cell-based, or object-based, rather than the single-point measurements found in other types of microplate reads. These types of assays can yield more biologically meaningful results that can discriminate the fluorescence related to objects, such as cells or beads, from the bulk solution within a microplate well.

See [Imaging Read Mode on page 197](#).

K

Kinetic

In a kinetic read, the instrument collects data over time with multiple readings taken in the center of each well at regular intervals. To get the shortest possible interval for multiple-wavelength Kinetic readings, choose wavelengths in ascending order.

The values calculated based on raw kinetic data include VMax, VMax per Sec, Time to VMax, and Onset Time. Kinetic readings can be single-wavelength or multiple-wavelength readings.

See [Kinetic Read Type on page 152](#).

L

Lag Time

Lag Time in a kinetic read defines the period of very slow growth of microorganisms or the rate of reaction that can precede the rapid or linear phase of reaction. The lag time specifies how many initial data points are excluded from the calculation of **Vmax Rate**. Lag time truncates the data used in the calculation, but does not prevent data from being collected. Kinetic plots do not display the data collected before the lag time.

See [Doing Data Reduction on page 367](#).

Luminescence

Luminescence is the emission of light by processes that derive energy from essentially non-thermal changes, the motion of subatomic particles, or the excitation of an atomic system by radiation. Luminescence detection relies on the production of light from a chemical reaction in a sample.

See [Luminescence Read Mode on page 166](#).

LUT

A look-up table (LUT) determines the colors to use for the intensity values when displaying an image.

See [Viewing Western Blot Membrane Data on page 443](#).

M

Mask

The Mask feature hides selected data so that they are not used for calculations and are not reported. Masking is commonly used to suppress outliers from data reduction calculations. Masking can be used as a “what if?” tool. For example, if you have included a group blank in a template and want to see the data both with and without the blank, masking the group blanks suppresses the blanking function, while unmasking them enables it again.

See [Masking Wells or Cuvettes on page 367](#).

Membrane

The Membrane read type is used for a time-resolved fluorescence reading of a Western Blot membrane.

See [Membrane Read Type on page 153](#) and [Western Blot TRF Read Mode on page 193](#).

O

Onset Time

Onset time is a method for analyzing non-linear Kinetic reactions. Onset Time reports the time required for a Kinetic reaction to reach a specified OD or RFU/RLU (onset OD/RFU/RLU).

See [Kinetic Data Reduction Options on page 378](#).

Optical Density (OD)

Optical density (OD) is the quantity of light passing through a sample to a detector relative to the total quantity of light available. Optical Density includes absorbance of the sample plus light scatter from turbidity and background. You can compensate for background using blanks.

A blank well contains everything used with the sample wells except the chromophore and sample-specific compounds. Do not use an empty well for a blank.

Some applications are designed for turbid samples, such as algae or other micro-organisms in suspension. The reported OD values for turbid samples are likely to be different when read by different instruments.

See [Absorbance Read Mode on page 154](#).

P

PathCheck Technology

The temperature-independent PathCheck® Pathlength Measurement Technology normalizes your absorbance values to a 1 cm path length based on the near-infrared absorbance of water.

The Beer–Lambert law states that absorbance is proportional to the distance that light travels through the sample:

$$A = \epsilon bc$$

where A is the absorbance, ϵ is the molar absorptivity of the sample, b is the pathlength, and c is the concentration of the sample. The longer the pathlength, the higher the absorbance.

Microplate readers use a vertical light path so the distance of the light through the sample depends on the volume. This variable pathlength makes it difficult to do extinction-based assays and also makes it confusing to compare results between microplate readers and spectrophotometers.

The standard pathlength of a 1 cm cuvette is the conventional basis for quantifying the unique absorptivity properties of compounds in solution. Quantitative analysis can be done on the basis of extinction coefficients, without standard curves (for example, NADH-based enzyme assays). When using a cuvette, the pathlength is known and is independent of sample volume, so absorbance is directly proportional to concentration when there is no background interference.

See [PathCheck Pathlength Measurement Technology on page 156](#).

Photomultiplier Tube (PMT)

A Photomultiplier Tube (PMT) is a vacuum tube that can detect light from dim sources through the use of photo emission and successive instances of secondary emission to produce enough electrons to generate a useful current.

Plate Section

A **Plate** section is used to collect data from the instrument, and to define data display and data reduction. If you need to read the same physical plate twice with different instrument settings, then use two **Plate** sections. You can create as many **Plate** sections as you need.

See [Using a Plate Section on page 118](#).

Protocol File

Protocol files are experiment template files that contain microplate well layout assignments and all other reader configuration information and reduction parameters, but no data.

Protocol files can be useful if you repeat a particular type of experiment frequently.

See [Managing Protocol Files on page 67](#).

R

Raw Data

Raw data is the signal reported from the instrument with no changes made. This is reported as optical density (OD), relative fluorescence units (RFU), or relative luminescence units (RLU), depending on the read mode.

Raw Data Mode

In Absorbance (ABS) read mode or Fluorescence Polarization (FP) read mode, you can select the type of raw data to display and use for reduction calculations.

For Absorbance reads, you can choose whether to display absorbance data as Optical Density or %Transmittance.

Fluorescence polarization mode returns two sets of data: one for fluorescence intensity parallel (P) to the excitation plane, and the other for fluorescence intensity perpendicular (S) to the excitation plane. These S and P values are used to calculate the Polarization (mP) and Anisotropy (r) values in the SoftMax Pro Software.

See [Doing Data Reduction on page 367](#).

Read Mode

For more information on the supported read modes, see the following topics:

- [Absorbance Read Mode on page 154](#)
- [Fluorescence Intensity Read Mode on page 160](#)
- [Luminescence Read Mode on page 166](#)
- [Time-Resolved Fluorescence Read Mode on page 171](#)
- [HTRF Read Mode on page 179](#)
- [FRET Read Mode on page 178](#)
- [Fluorescence Polarization Read Mode on page 185](#)
- [AlphaScreen Read Mode on page 189](#)
- [Western Blot TRF Read Mode on page 193](#)
- [Imaging Read Mode on page 197](#)

Read Type

For more information on the supported read types, see the following topics:

- [Endpoint Read Type on page 152](#)
- [Kinetic Read Type on page 152](#)
- [Well Scan Read Type on page 152](#)
- [Spectrum Read Type on page 152](#)
- [Flex Read Type on page 153](#)
- [Membrane Read Type on page 153](#)

Reduced Data

Data reduction causes the raw signal values reported by the instrument to be calculated and displayed based on user-defined formula settings.

Reference

A reference reading can be taken either on air or using a cuvette containing the buffer of your sample.

See [Collecting Data From a Cuvette on page 350](#).

ROI

A region of interest (ROI) is a small area or region of an image where items of interest can be found.

- For Western Blot Membrane reads, the region of interest is defined in the **Plate** section. See [Viewing Western Blot Membrane Data on page 443](#).
- For Imaging reads, the region of interest is defined in the **Settings** dialog. See [Region of Interest Settings on page 281](#).

S

Series

You can define several samples as a series, letting you easily enter incremental sample descriptors (for example, dilutions or concentrations) and sample names to the template as long as the increment can be expressed as a mathematical operation. This lets you work with groups of wells in the Template so that the standard value or dilution factor increases or decreases in specified steps. The series name can be incremented as well.

See [Creating a Series on page 304](#).

Slope

The slope reduction option determines the slope of the combined plot (for example, the slope of the line using linear regression after the wavelength combination reduction). This reduction uses all visible time points in the reduction window.

Slope is the same as Vmax Rate when Vmax Rate is set to the same number of points as the run, but is different if you have modified Vmax Points.

See [Kinetic Data Reduction Options on page 378](#).

SmartInject

SmartInject™ technology is available for reads with injection.

The SmartInject™ technology shakes the microplate during the injection and continues to shake through the following delay step, if a **Delay** node follows the **SmartInject** node. The microplate stops shaking before the well is read.

Spectrum

Depending on the read mode selected, a spectrum read measures optical density (OD), %Transmittance (%T), relative fluorescence units (RFU), or relative luminescence units (RLU) across a spectrum of wavelengths.

See [Spectrum Read Type on page 152](#), [Emission Spectrum Scan on page 489](#), and [Excitation Spectrum Scan on page 489](#).

Stokes Shift

The Stokes shift is the difference between the wavelengths of the excitation and emission maxima, or peaks.

See [Emission Spectrum Scan on page 489](#) and [Excitation Spectrum Scan on page 489](#).

T

Template Editor

A Template is a map of the microplate or cuvette that is used to describe the location of samples in the microplate or cuvette, and it provides the link between raw data and analysis groups.

The **Template Editor** is a representation of the microplate or set of cuvettes shown as a grid of wells that can be used to designate the location of blanks, standards, controls, unknowns, empty wells, or to assign wells to other groups you create.

See [Configuring a Microplate Template on page 301](#).

Time-Resolved Fluorescence (TRF)

Time-resolved fluorescence (TRF) is a measurement technique that depends on three characteristics that lead to better discrimination between the specific signal, proportional to the quantity of label, and the unspecific fluorescence resulting from background and compound interference:

- Pulsed excitation light sources
- Time-gated electronics faster than the fluorescence lifetime
- Labels with prolonged fluorescence lifetime

The time-gating electronics introduce a delay between the cut off of each light pulse and the start of signal collection. During the delay, the unspecific fluorescence (caused by test compounds, assay reagents, and the microplate) vanishes while only a small portion of the specific fluorescence from the label is sacrificed. Enough of the specific signal remains during the decay period with the added benefit of reduced background.

See [Time-Resolved Fluorescence Read Mode on page 171](#).

%Transmittance

%Transmittance is the ratio of transmitted light to the incident light for absorbance reads.

$$T = I/I_0$$

$$\%T = 100T$$

where I is the intensity of light after it passes through the sample and I_0 is incident light before it enters the sample.

V

Vmax Points

Vmax is the maximum slope of the Kinetic display of mOD/min or RFU/RLU per second. Vmax is calculated by measuring the slopes of a number of straight lines, where Vmax Points determines the number of contiguous points over which each straight line is defined.

This is an alternative method for analyzing non-linear Kinetic reactions that reports the elapsed time until the maximum reaction rate is reached, rather than reporting the maximum rate itself. Used in conjunction with Vmax Points, Time to Vmax is the time to the midpoint of the line defined by Vmax Points and used to calculate Vmax.

See [Kinetic Data Reduction Options on page 378](#).

Vmax Rate

Vmax Rate is reported as signal/min (milli-OD, RFU, or RLU units per minute) for a Kinetic read. It is calculated using a linear curve fit, $y = Ax + B$. A creeping iteration is done using Vmax Points and the slope of the steepest line segment is reported as Vmax Rate. It can also be reported as units per second (the default for Fluorescence and Luminescence modes).

See [Kinetic Data Reduction Options on page 378](#).

W

Well Scan

A well scan read can take readings at more than one location within a well. A well scan read takes one or more readings of a single well of a microplate on an evenly spaced grid inside of each well at single or multiple wavelengths.

Some applications involve the detection of whole cells in large-area tissue culture plates. Well scan reads can be used with such microplates to permit maximum surface area detection in whole-cell protocols. Since many cell lines tend to grow as clumps or in the corners of microplate wells, you can choose from several patterns and define the number of points to be scanned to work best with your particular application.

See [Well Scan Read Type on page 152](#).

Z

Z'

Z' is the standard statistical parameter in the high-throughput screening community for measuring the quality of a screening assay independent of test compounds. It is used as a measure of the signal separation between the positive controls and the negative controls in an assay.

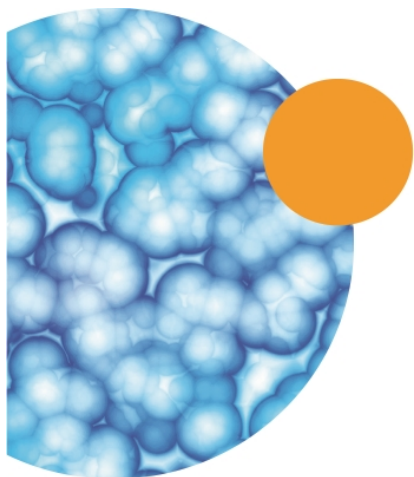
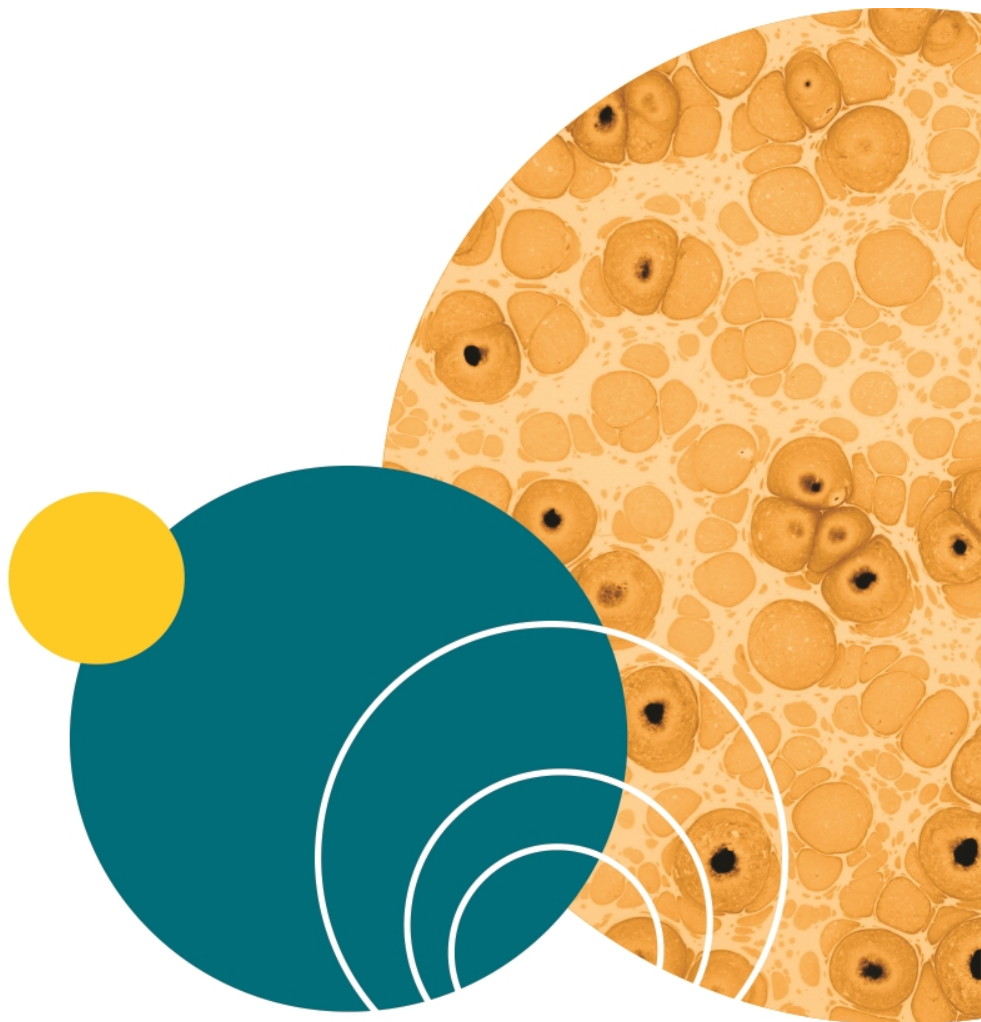
The value of Z' can be determined using the following formula:

$$Z' = 1 - \frac{3(SD_{c+}) + 3(SD_{c-})}{|Mean_{c+} - Mean_{c-}|}$$

where **SD** is the standard deviation, **c+** is the positive control, and **c-** is the negative control.

A Z' value greater than or equal to 0.4 is the generally acceptable minimum for an assay. Higher values might be desired when results are more critical.

Z' is not linear and can be made unrealistically small by outliers that skew the standard deviations in either population. To improve the Z' value, you can increase the quantity of label in the sample, if acceptable for the assay, or increase the read time per well.



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