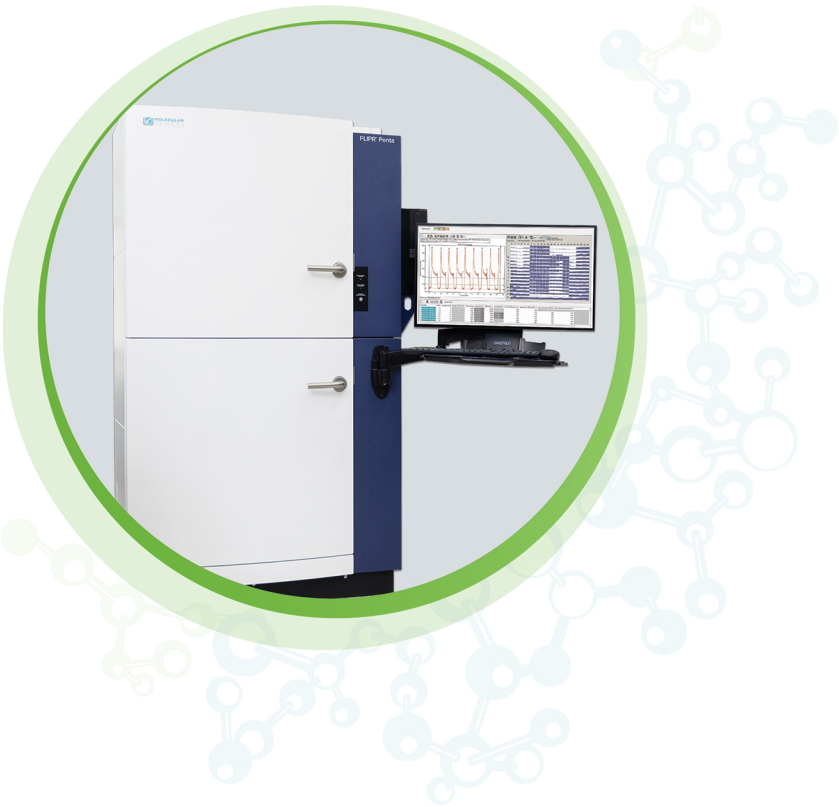

FLIPR Penta

High-Throughput Cellular Screening System

Hardware and ScreenWorks Software Version 5.1

Quick Start Guide

MOLECULAR DEVICES

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Patents: http://www.moleculardevices.com/patents

Product manufactured by Molecular Devices, LLC.
3860 N. First Street, San Jose, California, 95134, United States of America.
Molecular Devices, LLC is ISO 9001 registered.

FLIPR Penta High-Throughput Cellular Screening System Quick Start

The FLIPR® Penta High-Throughput Cellular Screening System provides an automated solution for identifying early leads in the drug discovery process and for evaluating drug efficacy and toxicity. With simultaneous pipette and read function, the system supports fast kinetic cellular assays. It can be quickly configured based on library size, detection mode, screening format, assay and target. A fully integrated solution from assay development to lead optimization.

The FLIPR Penta System includes:

- Simultaneous 96-well, 384-well or 1536-well liquid or cell transfer
- Expanded wavelength support
- User-configurable pipettors and optics
- FLIPR® Cycler, internal robotic plate handler option that works in conjunction with external robotic software
- Choice of camera:
  - EMCCD camera for fluorescence applications
  - HS EMCCD high-speed, high-sensitivity camera for fluorescence and luminescence
- Cell suspension option
- Compact platform with minimal facilities requirements
- ScreenWorks® Software and optional ScreenWorks® Peak Pro™ Software modules for analysis

This guide includes the following quick start topics:

Note: Refer to the *FLIPR Penta High-Throughput Cellular Screening System User Guide* for additional details and procedures that are not covered in this quick start guide.

Workflow

The FLIPR Penta High-Throughput Cellular Screening System uses the following sequence of processes:

1. Prepare the cells.
2. Power on the system.
3. Run a system check.
4. Load cell dye.
5. Prepare source plates.
6. Set up an assay protocol.
7. Run the experiment.
8. Analyze the data.

Before You Start

CAUTION! Before using the instrument, it is very important that you read and understand all the safety instructions. See the *FLIPR Penta High-Throughput Cellular Screening System User Guide* for safety details and more. Then follow the procedures in Powering On the System.

Powering On and Powering Off the System

Note: Molecular Devices installs and configures your FLIPR Penta High-Throughput Cellular Screening System in your laboratory.

The following procedures are for powering on and powering off the FLIPR Penta System, which includes connecting the ScreenWorks Software to the instrument.

Powering On the System

Before continuing, do as instructed in Before You Start.

To power on the FLIPR Penta System:

1. Power on the computer and monitor.
2. Simultaneously press the **CTRL+ALT+DELETE** keys to launch the Windows operating system.
3. At the prompt type your password.

   Note: The first time you log in after your system installation, the default password is *fliprtetra*.
   Wait for the operating system to finish starting-up before continuing.

4. Power on the external chiller with the switch located on the left side of the chiller.
5. Power on the FLIPR Penta System power switch located on the right side of the instrument.

   CAUTION! The system goes through an initialization cycle to register all of the instrument components. This cycle is not complete until the green **Assay Finished (Unlock)** light on the upper door is the only light illuminated on the instrument status panel.

6. Double-click on the desktop icon to start the ScreenWorks Software.

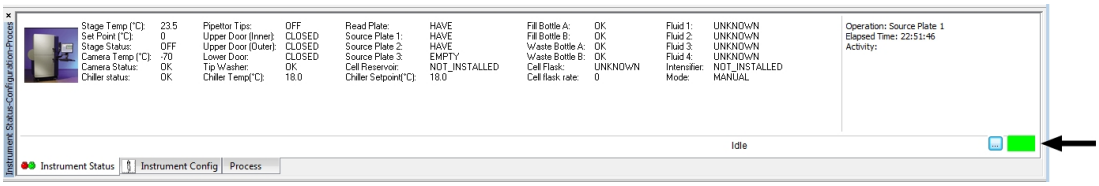
   Tip: Do not repeatedly double-click the software icon. Starting the software can take several seconds.

Note: The system is ready for use when the camera temperature is at operating temperature. The camera temperature and status display in the ScreenWorks Software Instrument Status panel. The camera operating temperature depends on the camera in your instrument.

Connecting the Software to the Instrument

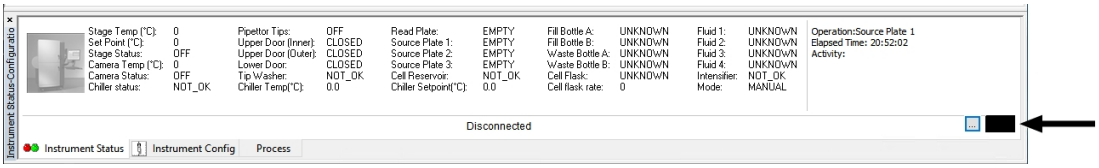
After powering on the instrument, when you start the ScreenWorks Software, it should automatically connect to the instrument. In the software, in the Instrument Status panel, in the lower right corner of the screen, a green connection status icon indicates the connection and in the toolbar, the 

button displays.



If you see a black connection status icon, the software is disconnected from the instrument, and in the toolbar, the 

button displays.



To connect to the instrument, click 

.

Powering Off the System and the Software

To power off the FLIPR Penta System:

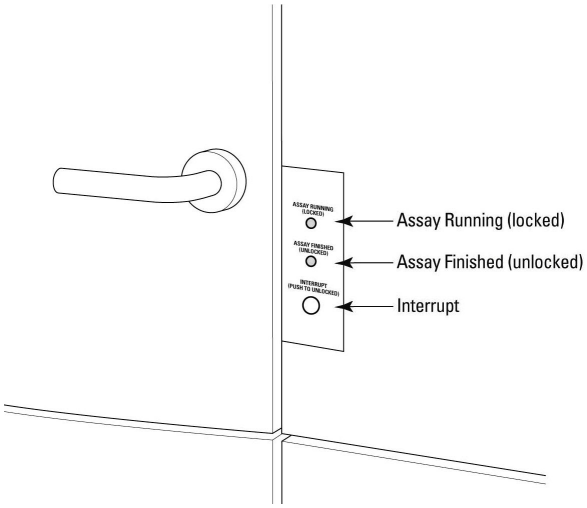
1. At the end of an experiment run, wait for the **Assay Finished (Unlocked)** light on the upper door, Instrument Status Panel turns green, indicating the experiment is finished.
2. If the last protocol run did not remove the tips from the pipettor head, we recommend making sure that you remove them using the manual command. Failure to remove tips can result in an error on next start.
3. Exit ScreenWorks Software by selecting **File** > **Exit**.
4. Power off the computer and monitor.
5. Power off the FLIPR Penta instrument.
6. Power off the chiller.

Checking Instrument Status and Configuration

You can check instrument status on the front of the instrument and from within the ScreenWorks Software. You can only check the instrument configuration status from within the ScreenWorks Software. For more details see System Status Panel and Software Status Tabs on page 7.

System Status Panel

The system status panel, located next to the upper door handle, indicates if the door is locked or unlocked, depending on the instrument activity. It also includes an emergency Interrupt button to stop any running processes.



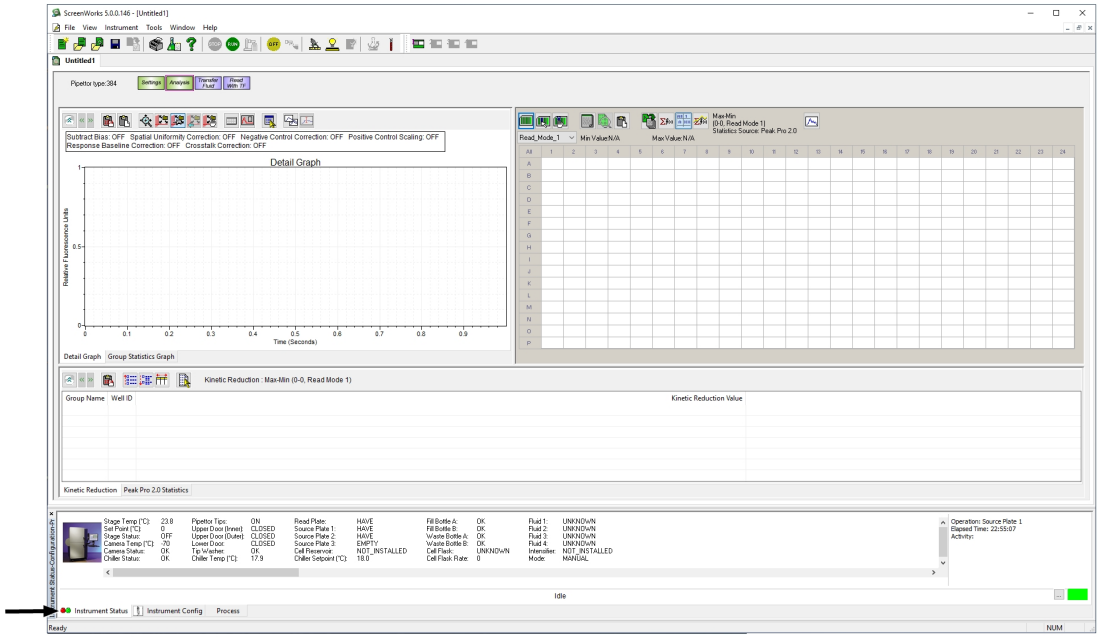
The panel has two lights and the Interrupt button. From the top of the panel these are:

- **Assay Running (Locked)**—Yellow light
  The FLIPR Penta System is performing a task. The upper and lower doors are locked until the task finishes or is stopped using the Interrupt button.
- **Assay Finished (Unlocked)**—Green light
  No tasks are being run and it is safe to open the upper and lower instrument doors.
- **Interrupt**—Flashing green light
  A system override to stop all tasks, so you can access the instrument. When pressed, the light flashes until the system has reached a safe state to open the doors.

CAUTION! The Interrupt button immediately ends the experiment and should only be used in emergencies. Before you can use the instrument normally again, the system might need to be reinitialized from within the software by selecting **Instrument > Reset** from the menu.

Software Status Tabs

Within the ScreenWorks Software, the **Instrument Status-Configuration-Process** tab panel, located on the bottom of the main screen, is open automatically and reports the status of and settings for the FLIPR Penta System hardware; and it includes the processes used to create protocols. For more details, refer to the *FLIPR Penta High-Throughput Cellular Screening System User Guide*.



Instrument Status Tab

The current status of the system hardware components report in the **Instrument Status** tab panel.

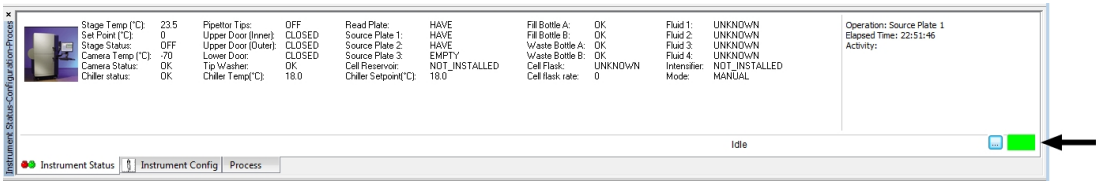


Figure 1-1: Example Instrument Status Tab Panel With Online Status Indicator

Table 1-1: Instrument Status Options

Options	Description
Stage Temp (°C)	Displays what the stage temperature is currently.
Set Point	Displays the stage temperature setting.
Stage Status	Displays whether the heated stage is turned on or off.

Table 1-1: Instrument Status Options (continued)

Options	Description
Camera Temp (°C)	Displays the camera temperature. Operating temperature for the camera depends on the installed camera. EMCCD camera: -70°C (-94°F) ± 2°C HS EMCCD camera: -70°C (-94°F) ± 2°C ICCD camera: -20°C (-4°F) ± 5°C
Camera Status	Indicates whether the camera is turned on or off.
Chiller status	Indicates whether the chiller is available or not.
Pipettor Tips	Reports when tips are loaded on the pipettor head.
Upper Door (Inner)	Reports whether the inner-upper door (observation panel) is open or closed. **Note**: The system runs as long as the inner door is closed, however data might not be valid if the outer door is open.
Upper Door (Outer)	Reports whether the outer-upper door is open or closed.
Lower Door	Reports whether the lower door is open or closed.
Tip Washer	Indicates the status of the tip washer.
Chiller Temp (°C)	Reports the current temperature in the chiller.
Read Plate	Reports when a plate is present in Position 3 (Read Plate position).
Source Plate 1	Reports when a plate is present in Position 1 (Source Plate 1 or Tip Loading position).
Source Plate 2	Reports when a plate is present in Position 2 (Source Plate 2).
Source Plate 3	Reports when a plate is present in Position 4 (Source Plate 3 or Cell Reservoir).
Cell Reservoir	Reports if **Installed** or **Not_Installed**.
Chiller Setpoint (°C)	Reports the set point from the chiller.
Fill Bottle A	Reports when bottle A is empty of wash solution.
Fill Bottle B	Reports when bottle B is empty of wash solution.
Waste Bottle A	Reports when waste bottle A is full.
Waste Bottle B	Reports when waste bottle B is full.
Cell Flask	Reports the last known state of the stir Cell Flask. At start the state is *Unknown* until the Cell Flask is used.
Cell flask rate	Reports the set stir rate of the cell flask. If the **Cell Suspension** option is installed and the stir rate is 0, an exclamation sign displays.
Fluid 1	Reports the last known state of the Fluid 1 bottle. At the start the status is *Unknown* until that Fluid is used.

Table 1-1: Instrument Status Options (continued)

Options	Description
Fluid 2	Reports the last known state of the Fluid 2 bottle. At the start the status is *Unknown* until that Fluid is used.
Fluid 3	Reports the last known state of the Fluid 3 bottle. At the start the status is *Unknown* until that Fluid is used.
Fluid 4	Reports the last known state of the Fluid 4 bottle. At the start the status is *Unknown* until that Fluid is used.
Intensifier	Reports if **Installed** or **Not_Installed**.
Mode	Reports if ScreenWorks Software is in **Manual** or **Remote** mode.

Identify Connection Status

To view the connection status:

- In the bottom-right corner of the panel, identify the color-coded connection status icon, which reports the connection status between ScreenWorks Software and the instrument. Green means connected, and black means disconnected.

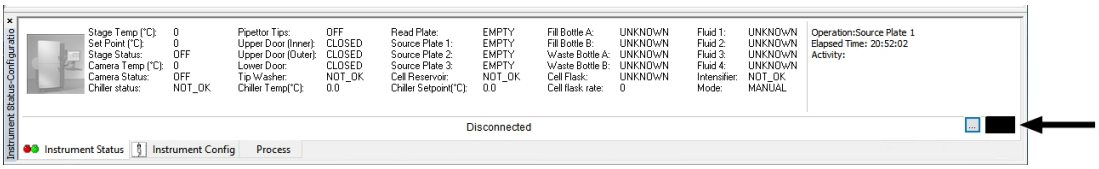


Figure 1-2: Example Instrument Status Tab Panel With Offline Status Indicator

View Messages and Faults

To view status messages and faults:

- Next to the color-coded connection status icon, click … **Instrument Status** to see a list of the last thousand messages in the Instrument Status History dialog.

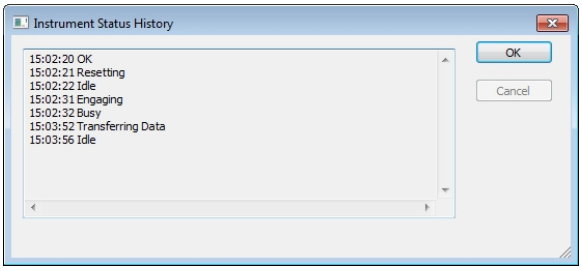
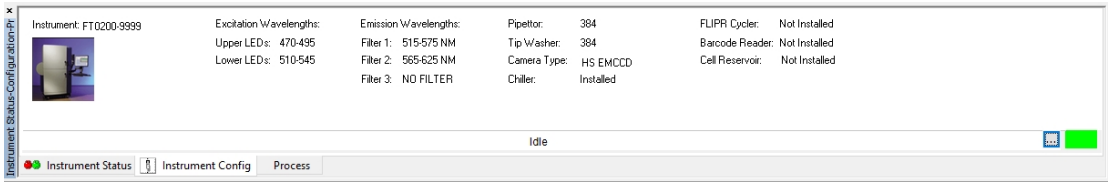


Figure 1-3: Example Instrument Status History Dialog

Tip: If needed, the dialog text can be copied to the clipboard to paste elsewhere.

Instrument Configuration Tab

The **Instrument Configuration** tab indicates the current instrument configuration of the LED banks, emission filters, pipettor head, and optional FLIPR Cycler.



If the system is Offline, you can configure these settings to define protocols. For camera types details, see the *CCD Camera Options* section of the *FLIPR Penta High-Throughput Cellular Screening System User Guide*. See Online Mode vs. Offline Mode on page 11.

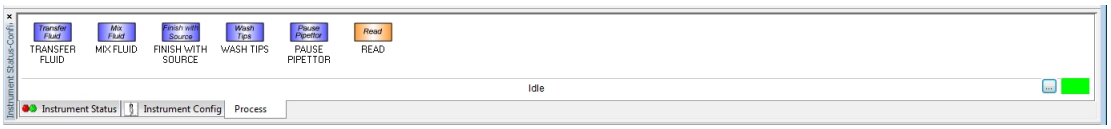
CAUTION! If a protocol created offline does not match the Instrument Configuration when opened online, the protocol does not run until the configuration of the protocol and instrument match.

Table 1-2: Instrument Configuration Options

Options	Description
Excitation Wavelengths	Displays the excitation wavelengths installed on the system. **Upper LEDs**—Displays the wavelength range of the top set of LED banks in the LED modules. **Lower LEDs**—Displays the wavelength range of the lower set of LED banks in the LED modules.
Emission Wavelengths	Displays the emission filter wavelengths installed on the system. Up to three filters can be installed at the same time.
Pipettor	Displays the type of pipettor head (96, 384, 1536, 384 pin tool, or 1536 pin tool) installed on the system. **Note**: The pipettor head format must agree with the tip wash reservoir format. A warning is issued if these are different.
Tip Washer	Displays the type of tip washer (96, 384 or 1536) installed on the system.
Camera Type	Select from EMCCD, HS EMCCD, or ICCD camera.
Chiller	Reports when a chiller is installed.
FLIPR Cycler	Reports when the FLIPR Cycler is installed.
Barcode Reader	Reports when a barcode reader is installed.
Cell Reservoir	Use the check box to indicate whether or not the Cell Reservoir is installed.

Process Tab

The Process tab is used to create new protocols and edit existing protocols.

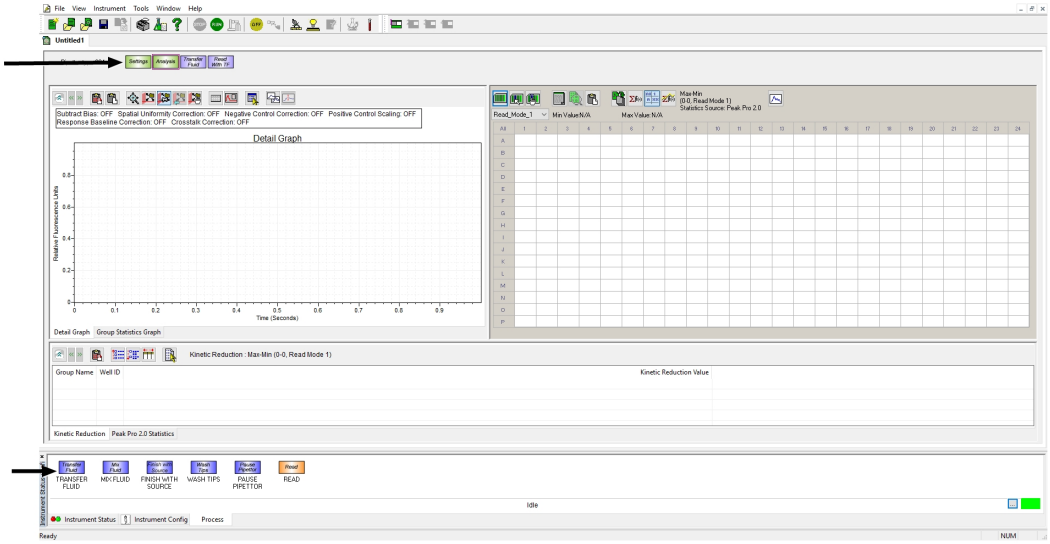


The Process tab panel displays processes that can be incorporated into your experiment protocols. See Using Protocols on page 14. The color of the process icon depends on the function in the protocol. See Protocol Process Icon Colors.

Note: The available processes vary according to the instrument configuration. For example, different process opts appear when the instrument is configured to use a pin tool instead of a pipettor.

For details about each process, see the *FLIPR Penta High-Throughput Cellular Screening System User Guide*.

Protocol Process Icon Colors



- Green—indicates that the process is required to run an experiment and cannot be deleted.
- Blue—indicates that the process involves liquid handling. These steps are always run series with each other, and never run simultaneously.
- Orange—indicates that the process runs simultaneously with any liquid handling process, if possible.
- Purple—indicates linked processes, such as **Mix with TF** and **Read with TF**, which are connected to the **Transfer Fluid** process.

Online Mode vs. Offline Mode

The software has two startup modes:

- 

Online—the software is connected to the instrument.
- 

Offline—the software is disconnected from the instrument.

The default start-up mode is determined during software installation in the **Online/Offline** dialog. Regardless of the startup mode, pipettor head and tip washer type must always match.

Note: To be able to select either mode while generating protocols, you must install the software in Offline mode.

When the software is open, you can switch modes by selecting from the **Instrument** menu, **Go Online** or **Go Offline**.

Note: Switching modes after the software is opened does not change the software startup mode chosen at the time of installation. To change the default startup mode, the ScreenWorks Software must be reinstalled.

Online Mode

When started in Online mode, ScreenWorks Software checks for instrument connections. If no connections are sensed, you are notified. You can then either check the connections and attempt to connect again, or choose to run the software in Offline mode.

Create new protocols in Online mode.

When ScreenWorks Software starts in Online mode and connects to the instrument, the default installation configuration file is overwritten using the current instrument settings and plate library information.

If you are working in Online mode and then switch to Offline mode, the instrument setup configuration is remembered as the last setting.

Offline Mode

When ScreenWorks Software starts and no instrument connection registers, you are notified and can then either check the connections and attempt to connect again in Online mode, or choose to run the software in Offline mode.

When ScreenWorks Software starts in Offline mode, you can configure the following hardware options:

- Camera Type
- Pipettor Format

Protocols created in Offline mode with hardware settings that do not match current hardware settings are flagged. You must change the hardware settings to match those in the protocol in order to run it.

Checking the System

Once a day, before running your first assay plate, do the following system checks:

1. Make sure that the system is turned on and the camera is cooled to proper operating temperature.
   - EMCCD camera: -70°C (-94°F) ± 2°C
   - HS EMCCD camera: -70°C (-94°F) ± 2°C
   - ICCD camera: - 20°C (-4°F) ± 5°C

2. Run a Yellow Plate Signal Test to ensure the system is operating according to specifications. See Running the Yellow Plate Signal Test on page 13.

   A yellow signal test plate is provided with each corresponding pipettor head supplied with the system.

   A signal test plate only needs to be run once a day unless system components such as pipettor heads or LEDs are changed.

CAUTION! To avoid damaging the yellow signal test plates:
Avoid scratching the plate bottom because scratches can affect the standard deviation.
Store the plates in a safe place away from bright light on an even surface.

Running the Yellow Plate Signal Test

Use the Yellow Plate Signal Test once a day to verify that the system optics are calibrated. Additionally use the Yellow Plate Signal Test after you recalibrate or change the optics.

To run a Yellow Plate Signal Test:

1. Place the yellow signal test plate on the stage in the read position.
2. In the ScreenWorks Software, select **Instrument** > **Manual Operation** > **Yellow Plate Signal Test** or click  **Yellow Plate Signal Test**.

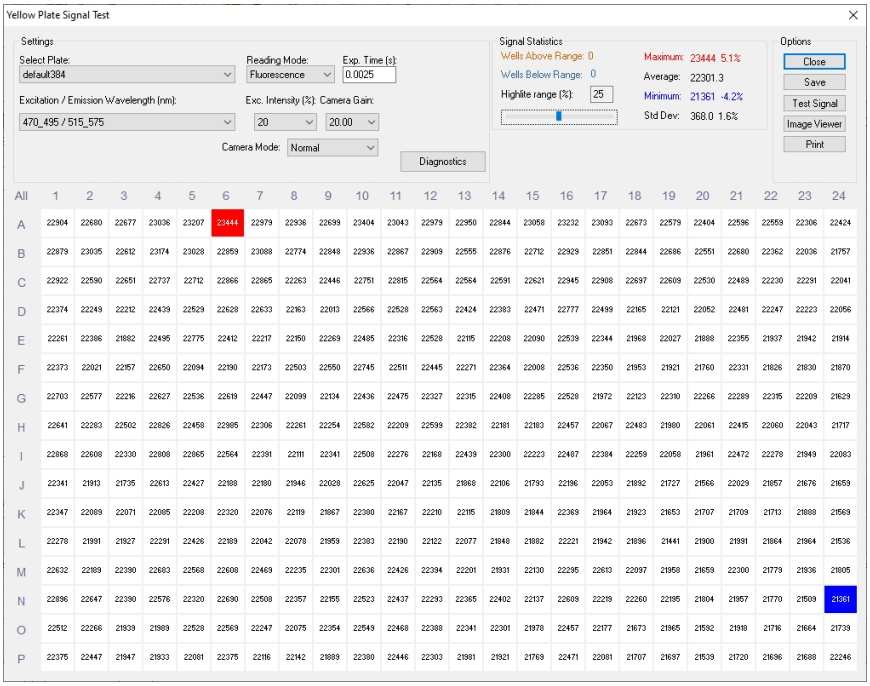


Figure 1-4: Yellow Plate Signal Test Dialog

3. Set the following parameters:
   a. Select the correct plate from the **Select Plate** list.
   b. Select **Reading Mode** > **Fluorescence** only.

      CAUTION! Although both Fluorescence and Luminescence are available options in the test dialog, currently there is no easy way of testing signal strength in Reading Mode > Luminescence.
      Do not run any Reading Mode > Luminescence signal tests.

   c. Select the appropriate **Excitation/Emission Wavelengths**.
   d. Set the **Excitation Intensity** to 50.
   e. Set the **Exposure Time** to 0.1 seconds.
   f. Adjust the following variable camera settings:
      - For the EMCCD camera, set the **Camera Gain** to 80.
      - For the ICCD camera, set the **Gate Factor** to 6%.
      - For the HS EMCCD camera:
        - In **Camera Mode** > **Normal**, set the **Camera Gain** to 1.5 and the **Exposure Time** to 0.005 seconds.
        - In **Camera Mode** > **HighSpeed**, set the **Camera Gain** to 20 and the **Exposure Time** to 0.001 seconds.
4. Take a picture by clicking **Test Signal**.

   When the instrument is calibrated with the yellow test plate for the appropriate plate format and optics, normal test plate results are a relative standard deviation less than 5%.

   If the test results are abnormal values, look at the **Image Display** for any anomalies on the plate.
5. Print the results and keep them in a “Maintenance” folder by the instrument to track the standard deviation of the yellow signal test plate over time.

   Note: The **Yellow Plate Signal Test** and **Image Display** results are not saved within a data file.

   Alternatively, you can save the files on the hard drive in the signal test directory (**C:\Documents and Settings\[your_user_name]\My Documents\Molecular Devices\ScreenWorks\MySignalTests**) as a ***.sig** file, which can be opened in third-party spreadsheet software.

Note: The relative standard deviation should be less than 5% if the flat-field calibration was performed using the Flat Field Calibration Plate of the respective plate format (96-wells, 384-wells, or 1536-wells). See Flat-Field Calibration.

Using Protocols

The protocols you create determine how the system functions while running an experiment. Protocols consist of a series of process configurations. As you create your experiment protocol, you configure each process. See Creating New Protocols. Process options are located in the Process tab in the Instrument Status-Configuration-Process panel. See Process Tab on page 11.

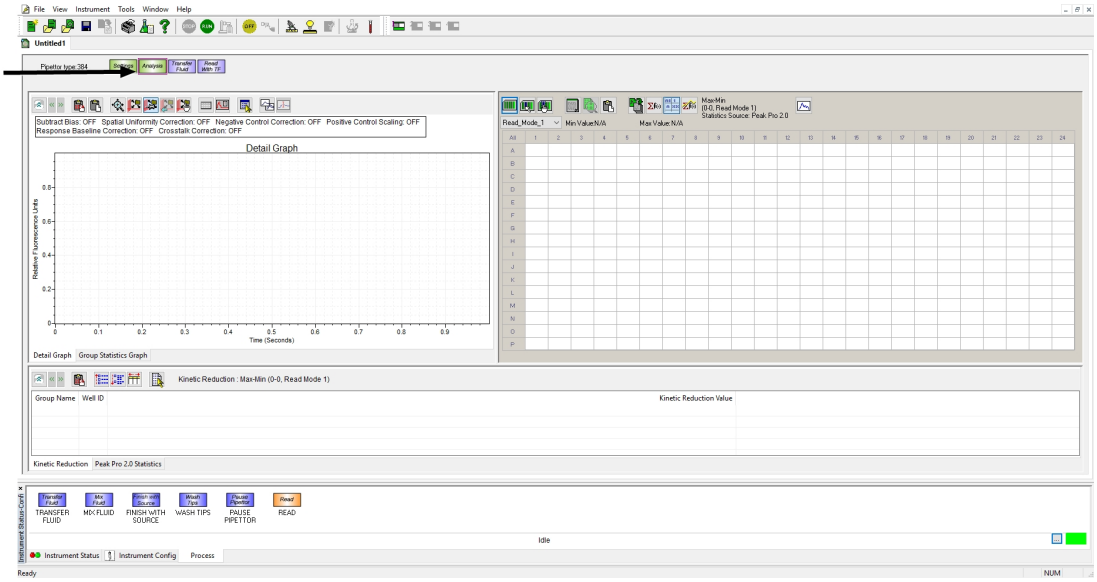
Tip: Refer to the *FLIPR Penta High-Throughput Cellular Screening System Protocol Guide* for specific assay protocols.

To save a data file as a protocol file, see Saving Data Files as Protocol Files on page 18.

Creating New Protocols

In the ScreenWorks Software, creating a protocol involves combining processes represented in the protocol builder as colored block icons at the top of the Experiment window. The available processes depend on your instrument configuration. See Instrument Configuration Tab on page 9. The color of the process icon depend on the function in the protocol. See Protocol Process Icon Colors on page 11.

A red box around the process in the protocol list indicates the process selection and indicates which configuration settings dialog is open.



Protocols contain combinations of the following processes. Available options depend on the components installed in your instrument.

- **Settings**—required for every protocol, automatically included at the beginning of every new protocol file, and cannot be removed.
- **Analysis**—required for every protocol, automatically included at the beginning of every new protocol file, and cannot be removed.
- **Transfer Fluid**—automatically included in new protocols and have the following selectable linked processes:
  - **Read with TF**—automatically included in new protocols after Transfer Fluid, and timed precisely to coincide with compound addition to the read plate. This setting can be deselected from within the Transfer Fluid configuration settings dialog.
  - **Mix with TF**—optional selection within the Transfer Fluid configuration settings dialog.
- **Mix Fluid**
- **Wash Reservoir**—only available when the **Cell Suspension** option is installed.
- **Wash Tips**—available only with pipettor configuration.
- **Wash Pins**—available only with pintool configuration.
- **Blot Pins**—available only with pintool configuration.
- **Pause Pipettor**
- **Finish with Source**
- **Read**

To create a new protocol:

1. Open the **Process** tab panel. See Process Tab on page 11.
2. In the **Process** tab panel, add the assays steps. Do one of the following:
   - To place the new process at the end of your developing protocol list, drag and drop the process anywhere in the Experiment window.
   - To place the new process somewhere specific in your developing protocol list, drag and drop the process where you want it. You are notified when the position is invalid.

3. When the configuration screen opens for the added process, adjust settings as needed.
4. Repeat steps 2 and 3 until you are finished building your protocol.
5. Define the **Analysis** parameters.

   Click the **Analysis** process, and then click **Grouping**, **Correction**, and **Export** to specify the analysis parameters for the experiment data.
6. Click on any other process icon to open its configuration screen and make changes as needed.

> **Note:** When using the HS EMCCD camera, depending on your **Protocol** > **Settings** > **Edit read mode** > **Camera Mode** setting, when using a fast Read time interval value, the plate matrix panel updating might be delayed until the end of the data acquisition rather than updating during the data acquisition.
>
> Specifically, the following settings result in the plate matrix panel updating at the end of the data acquisition:
> For **Camera Mode** > **HighSpeed**—a **Read time interval(s)** setting of 0.018 seconds or shorter
> For **Camera Mode** > **Normal or Sensitivity**—a **Read time interval(s)** setting of 0.029 or shorter

7. Select **File** > **Save**.
8. In the **Save As** dialog, in the **File name** field, type a name for your protocol, and then click **Save**.

> Tip: Protocol files are saved as an ***.fmp** file. Unless you change the **Save in** location for your protocols, the default save location is **C:\Documents\Molecular Devices\ScreenWorks\MyProtocols**.

9. Run your experiment.

Refer to the *FLIPR Penta High-Throughput Cellular Screening System Protocol Guide* for specific protocol settings.

Deleting Processes from the Protocol

Protocol processes are either linked to the Transfer Fluid process or not linked.

To delete processes that are not linked:

- In the protocol list, select a non-purple process icon, and then on your keyboard, press **DELETE**.

To delete a Transfer Fluid linked process:

1. In the protocol list, select the purple **Transfer Fluid** icon.
2. In the configuration settings dialog, deselect the linked process you want deleted, either **Read** or **Mix Fluid**.

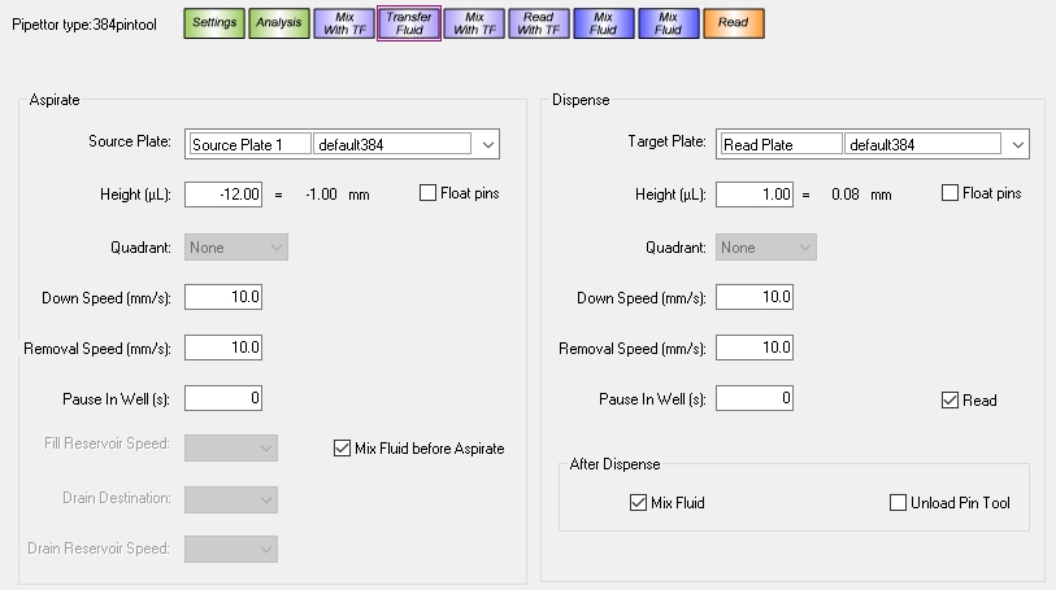


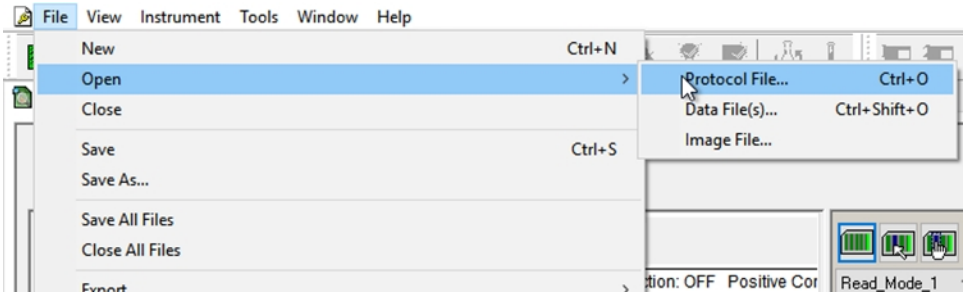
Figure 1-5: Transfer Fluid Configuration Settings Dialog With Linked Processes

Opening Protocols

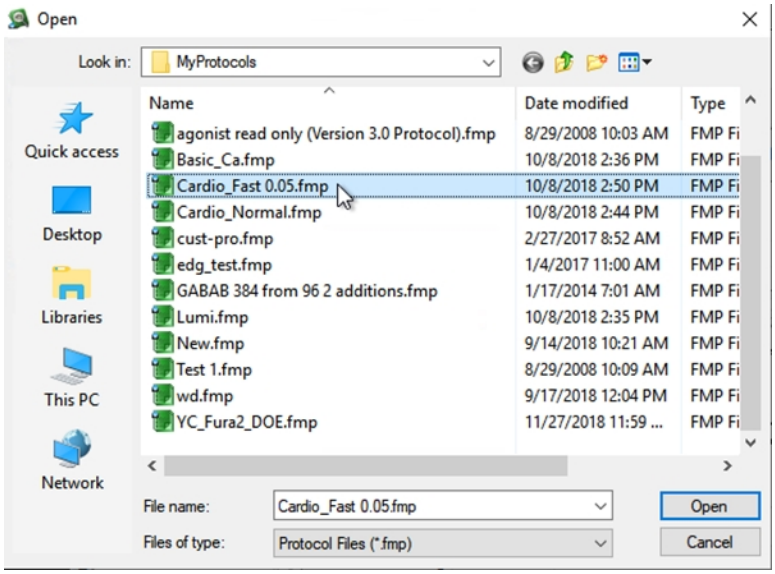
If you have saved protocol files to use, you can open an existing protocol file, rather than create a new one in the ScreenWorks Software.

To open a protocol file:

1. Select **File** > **Open** > **Protocol File**.



2. In the **Open** dialog, select your protocol file name, then click **Open**.



Deleting Protocols

You cannot delete a protocol from within ScreenWorks Software.

To delete a protocol:

1. In your Windows File Explorer navigate to where the protocols are saved.

> Tip: During the creation process, unless you changed the **Save in** location for your protocols, the default location for all of your protocol files is **C:\Documents\Molecular Devices\ScreenWorks\MyProtocols**.

2. Select the ***.fmp** file you want removed, and then on your keyboard, press **DELETE**.

Saving Data Files as Protocol Files

Protocol information stored in data files (*.fmd) cannot be edited, nor used to run a new experiment; however, you can extract this information to a new protocol file. Experiments run using this new protocol file have exactly the same protocol steps as used to create the data file.

> Tip: When using a protocol file (*.fmp), you can add, remove, or change processes in the file, then save the amended protocol and run it.

To store a data file as a protocol file:

1. Select **File** > **Save As**.
2. In the **File name** field, type a protocol name.
3. In the **Save as type** field, select **Protocol Files (*.fmp)** option and click **Save**.

   The stored file is stripped of all data and only associated protocol information is stored in the protocol file.

> **Note:** Saved changes only affect the protocol. The data file from which the protocol was derived remains intact.

Exporting Data

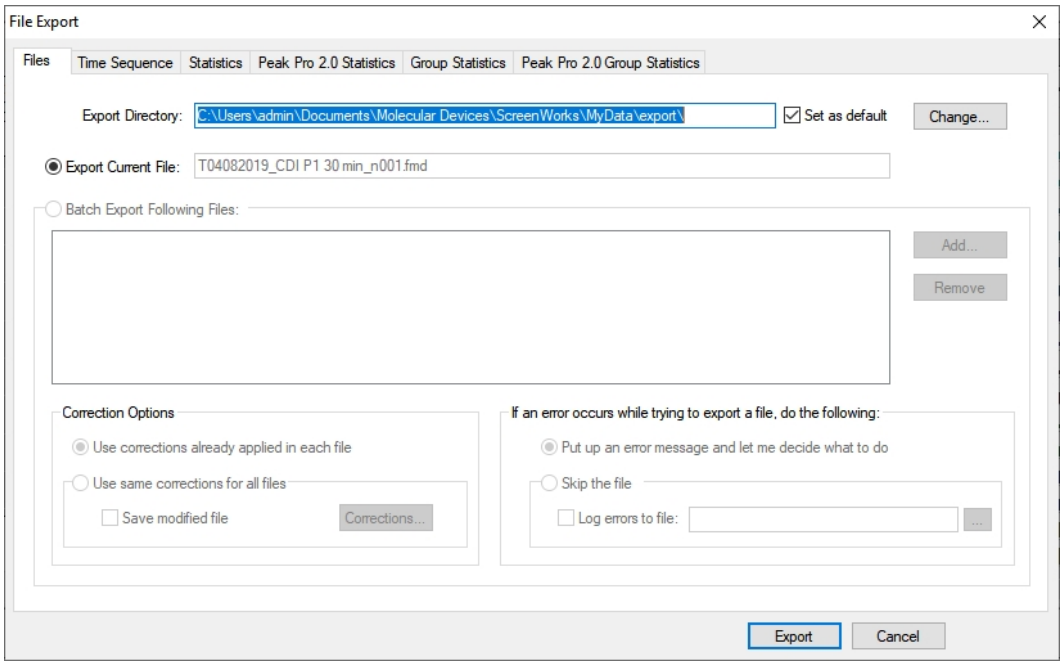
You can export data the following two ways:

- Automatic export when a protocol is run.
- Export from already acquired data.

To configure the data export:

- In protocol files, in the **Analysis** screen, click  **Configure Auto Export**.
- For data files, use **File** > **Export**, **File** or **Batch Export**.

> **Note: Auto-Export** and **Batch Export** do not support the ScreenWorks® Peak Pro™ Software Version 2.0.



Data is exported as ASCII text format files with a separate file exported for each measurement configuration specified. When you export data , you specify a folder in which to write the output files.The default export folder is:

C:\Documents and Settings\[your_user_name]\My Documents\Molecular Devices\ScreenWorks\MyData

The **File Export** dialog has the following tabs:

- **Files**—Export directory setting or batch files selections.
- **Time Sequence**—Exports time-point measurements for selected read modes. The measurement values that are exported have any corrections configured in the **Correction** dialog applied. If there are two read modes and **Ratiometric Options** is selected in the **Correction** dialog, you can also export the ratio for each time point.
  Files have a *.seq*n* extension, where n increments for each file generated in the export.
- **Statistics**—Exports averages, maximums, and other kinetic reduction values for selected numbers of reads for each well.
  Files have a *.stat*n* extension, where n increments for each file generated in the export.

- **Peak Pro 2.0 Statistics**—You must run the analysis in the Peak Pro 2.0 software module before you can do the export. After running the analysis, this export works the same way as Statistics.

  Note: The ScreenWorks Peak Pro Software Version 2.0 requires the purchase of a separate module license.

- **Group Statistics**—Exports the group statistical values for selected numbers of reads for each group and are based on user-defined kinetic reduction settings.
  Files have a *.gstat*n* extension, where n increments for each file generated in the export.
- **Peak Pro 2.0 Group Statistics**—You must run the analysis in the Peak Pro 2.0 software module before you can do the export. After running the analysis, this export works the same way as Group Statistics.

  Note: The ScreenWorks Peak Pro Software Version 2.0 requires the purchase of a separate module license.

CAUTION! Data created in ScreenWorks Software Version 2.0 cannot be viewed or exported by ScreenWorks Software Version 5.x.

Exporting Time Sequence

Configure parameters for export of time-sequence data in the **Export Time Sequence** tab. The exported files contain a value for every read interval for each well, for the read mode or ratio selected. This contrasts with the Statistics file, which contains one kinetic reduction per well.

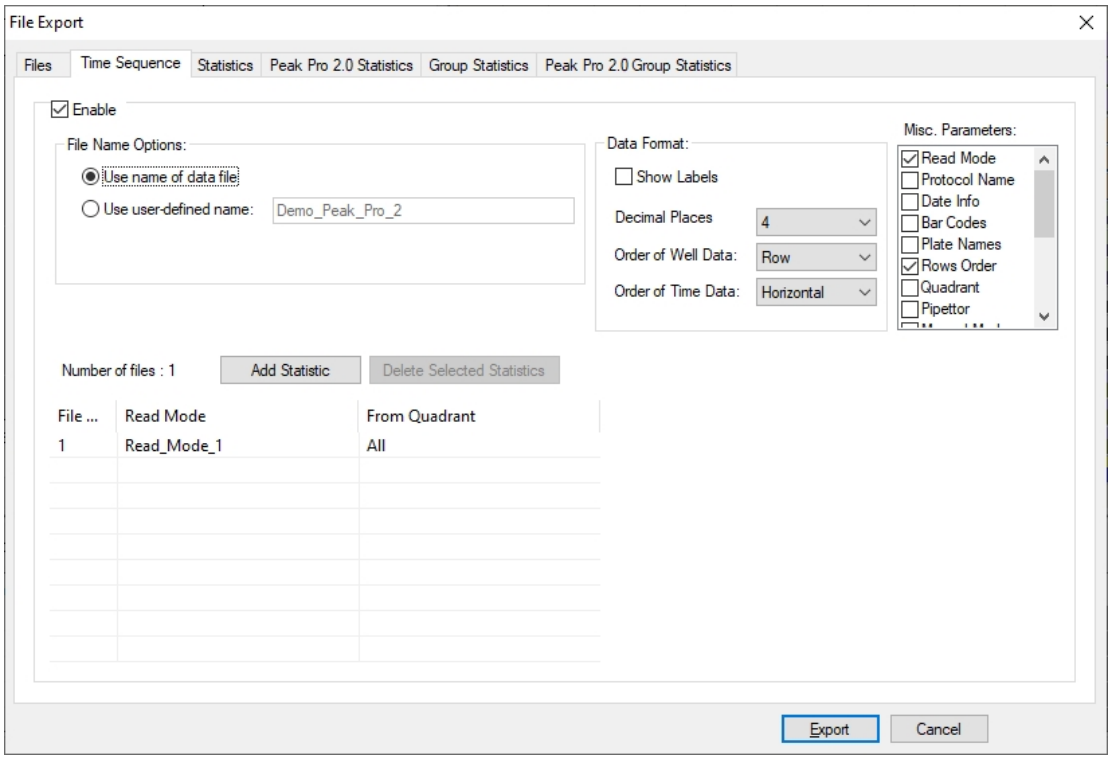


Table 1-3: Export Time Sequence Options

Options	Description
Enable	Check this option to have a time sequence export file created.
File Name Options	Choose a name for the exported time sequence file. **Use name of data file**—Export files with the data or protocol file name, with *.seq*n* extension, where *n* is an integer ≥ 1. **Use user-defined name**—Enter your own name for the export files (maximum of 25 characters). Files are given *.seq*n* extension, where *n* is an integer ≥ 1.

Table 1-3: Export Time Sequence Options (continued)

Options	Description
Data Format	Format the output from this group of options: **Show Labels**—Check to include information about the processing options selected (for example, name of *.fmd file and well labels). Any corrections prior to export (e.g., negative control correction) are reported at the top of the exported ASCII file. **Decimal Places**—Select 2, 3, or 4 decimal places for your data export. Your setting applies only if the selected number of decimal places exist in the data. **Order of Well Data**—Order the data by column (for example, A1, B1, C1) or by row (for example, A1, A2, A3). Set this option in accordance to the way your spreadsheet or database handles well data. **Order Time Data**—Select vertical or horizontal ordering of the data.
Misc. Parameters	Select experimental parameters and group statistics to export with the data.
Individual File Parameters	Use the bottom section of the dialog to choose the number and type of time sequence files to be created from the same data set. **Number of Files**—Click the **Add Statistic** button to add to the number of statistic files to be created from the same data set. **Read Mode**—Enter the read mode (or ratiometric data) from which you want to export data. **From Quadrant**—You can choose a specific quadrant from which to export, or export data from all quadrants. This enables you to export data from one plate into four different spreadsheet files, if desired. **Note**: This option is only available for data created in 384-well or 1536-well formats.

Exporting Statistics

Use the **Export Statistics** tab to configure kinetic reductions, for example, averages and maximum and minimum values, for selected numbers of reads within each well. Multiple kinetic reductions can be configured, each resulting in another export file. Within each file only one value is reported per well.

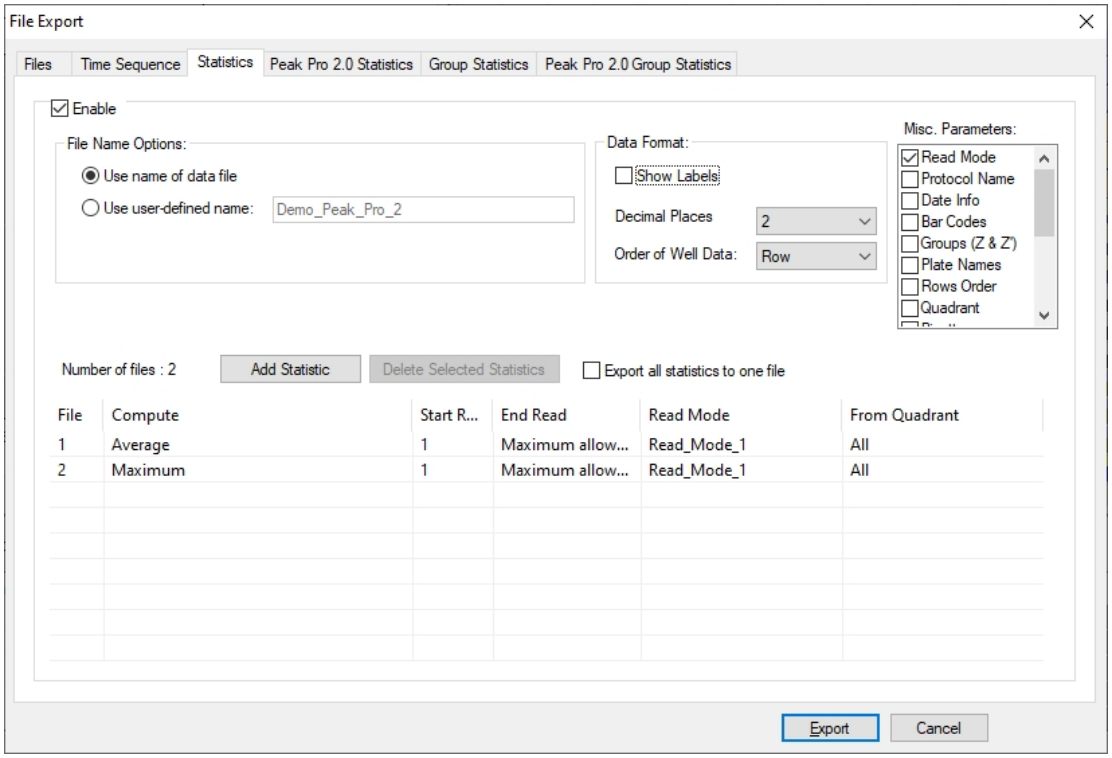


Table 1-4: Export Statistics Options

Options	Description
Enable	Check this box to have a statistic file created.
File Name Options	Choose a name for the exported statistic file. **Use name of data file**—Export files with the data or protocol file name, with *.stat*n* extension, where *n* is an integer ≥ 1. **Use user-defined name**—Enter your own name for the export files (maximum of 25 characters). Files are given *.stat*n* extension, where *n* is an integer ≥ 1.

Table 1-4: Export Statistics Options (continued)

Options	Description
Data Format	Format the output from this group of options: **Show Labels**—When checked, the output file contains information about the processing options selected (for example, name of *.fmd file and well labels). Any corrections done prior to exporting the data (e.g., negative control correction) are indicated in text format at the top of the exported ASCII file. **Decimal Places**—Select 2, 3, or 4 decimal places for your data export. Your setting applies only if the selected number of decimal places exist in the data. **Order of Well Data**—Order the data by column (for example, A1, B1, C1) or by row (for example, A1, A2, A3). Set this option in accordance to the way your spreadsheet or database handles well data.
Misc. Parameters	Select experiment parameters and group statistics to export with the data.
Individual File Parameters	Use the bottom section of the dialog to designate the number and type of statistic files to be created from the same data set. **Number of Files**—Click the **Add Statistic** button to add to the number of statistic files to be created from the same data set. **Compute**—Select a kinetic reduction type. **Start Read**—Enter the first read number to be included in the kinetic reduction. **End Read**—Enter the last read number to be included in kinetic reduction. This can equal the Start Read, if you want to extract values from a single read. **Read Mode**—Enter the read mode (or ratiometric data) from which the data processes. **From Quadrant**—You can choose a specific quadrant from which to export, or export data from all quadrants. This enables you to export data from one plate into four different spreadsheet files, if desired. **Note**: This option is only available for data created in 384-well or 1536-well formats.

Exporting Group Statistics

Use the **Export Group Statistics** tab to configure a group statistics export report, for example, average, standard deviation and z-scores, based on the kinetic reduction types defined for a select number of reads as set up on the Analysis screen.

Note: If there are no groups defined on the Analysis screen, an empty report exports.

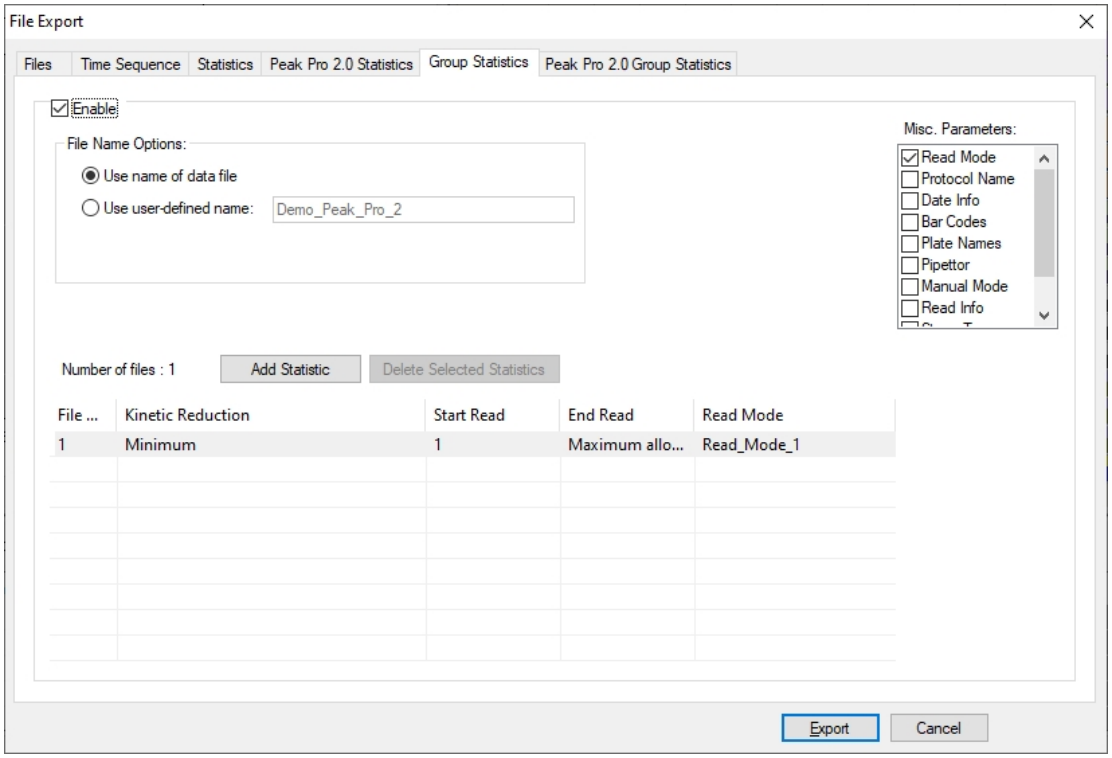


Table 1-5: Export Group Statistics Options

Options	Description
Enable	Check this box to have a group statistic file created.
File Name Options	Choose a name for the exported group statistic file. **Use name of data file**—Export files with the data or protocol file name, with *.gstat*n* extension, where *n* is an integer ≥ 1. **Use user-defined name**—Enter your own name for the export files (maximum of 25 characters). Files are given *.gstat*n* extension, where *n* is an integer ≥ 1.

Table 1-5: Export Group Statistics Options (continued)

Options	Description
Kinetic Reduction	Configures the parameters used to define the kinetic reduction. **Reduction Type**—Defines the reduction to be applied to the kinetic data traces exported. See Kinetic Reduction Types for details. **Start Read**—Define the first read to be used to determine the kinetic reduction. **End Read**—Define the last read used to determine the kinetic reduction. **Read Mode**—Select the read mode to apply the kinetic reduction.
Misc. Parameters	Select experiment parameters to export with the data.

Batch Exporting

Note: Batch Export does not support the separately licensed analysis module ScreenWorks Peak Pro Software Version 2.0.

Manual export of files is accessed through **File** > **Export**, **File** or **Batch Export**. **Manual Export** allows the same files as defined above to be exported.

Table 1-6: Batch Export Options

Options	Description
Export Directory	User defines where export files are to be sent. The default export folder is: **C:\Documents and Settings\[your_user_name]\My Documents\Molecular Devices\ScreenWorks\MyData**
Batch Export Following Files	Selecting **Add** opens the **Open File** dialog to choose data files to be exported. **Note**: Hold down the **SHIFT** or **CTRL** key to select data files.
Correction Options	During export, either the existing or new corrections can be applied. **Use corrections already applied in each data file**—Applies the existing corrections saved with each data file during export. **Use same corrections for all files**—Applies and saves new corrections to all data files. Useful when exporting all data files with same parameters or saving the same correction to multiple data files. Details regarding available corrections can be found under Correction.

Table 1-6: Batch Export Options (continued)

Options	Description
If an error occurs while trying to export a file, do the following	**Put up an error message and let me decide what to do**—Enables the user to decide how to proceed when an error is encountered. **Skip the file**—Does not include the data in the export, but continues to export data. The option to write the error to a log file is available.

When batch exporting data, the export files produced vary depending on the options you select in the individual export statistic, time sequence and group statistic sections. If a single export file is needed for each data file exported, select **Use name of data file** in the respective section you want to export. Export files created using this method are labeled with the name of the data file from which it was created. However, if a single export file is needed that contains information for multiple data files, select **Use user-defined name** in the respective section. In this instance, all exported information combines into one file labeled with the desired user-defined name. When the file is open, the individual data file names which the information was exported from are used as the header for each data set within the export file.

Obtaining Support

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

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

WARNING! BIOHAZARD. It is your responsibility to decontaminate components of the instrument before you return parts to Molecular Devices for repair. Molecular Devices does not accept items that have not been decontaminated where it is applicable to do so. If parts are returned, they must be enclosed in a sealed plastic bag stating that the contents are safe to handle and are not contaminated.

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